

Figure S1.

1. 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
MDLYRFVVTREMPSEYHTTFMDKFNHFIFEMVSSSDMNERKGGILAIIVSLTGVDVGN
STRISRFSNYLRNLLPSNDVSVMEMAARAVGWLAYSSGSYAAEYVEHEVKRALEWLTS
DRQESKRLAAVLVVKELAVNTPFFFFQQVQQFFDCIFNAVRDPKPNIREGAVAALRAALAV
TSQRESKATQKAQWYRQCYDEAVKLYDELQGREKKLSRDDWAHGSLLIMNELLRCSNIEGE
RLRMEMEDITNQYQHHERTLKEMSKTHKSPSSSLALQQFQHKAFPINNFMSSGNRHNMQKI
SFESRTCKQLVESHFQKVCALLLRHKNSKSVHIQLILQVIFPRLAFAFKPHEFSRLYLDD
DTINFLLGSLKTTTRDKTSTFQAIGLLAISVQDNIVRYLPGILEVIRASLPPKDLPAKKQ
KNMVVDPSVFTCSMLARAVGPAMIKDVRDLLDSMFATGLSPALTAALRDLAIQIPQLKKEIQ
EGLLNLSLILMGRQLRHPGAPKSPLOFPMSASLTNLADIQDATSITLALKTLGSFDFE
GHSLTQFVQKCAEQYLSDDHKEIRMEAVRTRCARLLTPLLQLLANSQGOISIAAMNTVAE
VLRHKLTVVGITDTEGEEGVIINIRTELEYSVGVGRNKEQAAKMLGHLVANAARLVRPYME
PILNALIPKLKEPDPNPNVTISVLVAIGEQAQVSGTEMKRWMDLLEPLILEMLQDSSSLQK
REVALWTLGQLVESTGYVIEPKRYPSLLEVLNLFKTEQATGIRREVIRVLGLLGALDP
HKHKMNQGMIOQNESNSVSASDTKLSSDSTQPEPENTSEMLANMTASTTLEEIYPAIAIATL
MRIIRDPSLSQHHTMVVQAITFIFKSLGKICVPYIQQVIPAYLAVIRSADQTFREFLFQQ
LGVIIAIVKQHIRNYLNDIFTIIEKEYWSPNSTMQNTIINLVEQIVTALGTEFKIYLPQII
PQILKVFMDSSDNRAVTGKLLNALQLFGANLDDYLHLLLPPVVKLFDSPDVPLSVKRIA
LETVDKLTLLDLTEFASRIIHPLVRTLDSVPELQTAAMD TLCAMVMQMGPKFTIFIPMV
QRVIQKHKIAHQRYFILMARILKASTIAEEEDDPILLKHKRKNRGKATESSESMAADTAVIK
KLHVSFINLQKALEAGRKESKEDWMEWLRRLSIELLKESSPALRSCWALAQTYNLSAKD
LFNAAFVSCWTELTEAQQDELILSLEQALTSQEIPEITQTLNLAEFMEHC DKGPLPLDT
SLLGSRAMRCRAYAKALHYKEEEFHRGPTTATLESLSINNKLQQPESASGVLQYAQNHR
TDVKVQESWYEKLEHEWNKALEAYEKKQEEKPEDFNLTGMRMRCLEALAEWGHHLHQIACEK
WGTSSDENRTDMARMAASAAGWLGQWDSMEEYMCLIPRNSYNGAFYRAVFALHTENYQLA
QQCIDKARDILDTELTAMAGESYNRAYGAMVNVQMLSELEEVMOFKLVPERQEAIKHMWW
DRLQGCQRVVEDWQKI IQVRSLVVSPLEDMKTWLKYASLCRKSGRRLALSQKTLVMLLGM
DPAKNCDKPIPTTNPQVTFAYLKHMMWKSQKKEAYGKLGQHFVQHSLOTRALQLITPEDTQQ
RTQNLNKLARCYLKLGDWMLYGVNEESSVTQILEYSLATEYDKYWKAWHGWALINYE
AVLFYKQSEKSGNQPSPGDIGPPGRGDAPLSPKTDTSVSTASKMHKYCVLAVQGFFRSI
SLSQNKSLQDTRLRLTLTLMFDYDQWLEVYEAALNDGLKTIQVENWLQVIPQLIARIDIPRPL
VSRLISQLLIDIGKAHPQALIYPLTVASKSNVPARQTAANKILKNMCEHSNTLVQQAMLV
SEELIRVAILWHELWHEGLEEASRLYFGERDIKGMFSTLEPLHNMVERGPQTLKETSFNQ
AYGRDLMEAEQEWCRKYQRSENVKDLTQAWDLYYHVFRRI SKQLPQLTSLELQYVSPKLLR
CQDLELAVPGKYEPNQPIVKIKRCQSSLOVITSKQRPRKLSIFGSNGKEFQFLKGHEDL
RQDERVMQLFGLVNSLLVENPETFRRLNTIQRFSVIPLSTNSGLIGWVPHDTLHSLIRD
YREKKKILLNIEHRLMLRMAPDYDHLTLMQKVEVFEHALEHTQGDDLAKILWYKSPSSEV
WFDRTNYTRSLAVMSMVGYVLGGLGDRHPSNLMLDRTSGKVIHIDFGDCFEVAMVREKFP
EKIPFRLTRMLINAMEVTGIDGNYKMTCEVMEVLRHKDSLMAVLEAFVYDPLLNWRLM
DTTAKGKTKTKDSYSGGSQEADMLENVNDINQTAHKRSAPAAASSVSGDNFQAEVINKKA
LSIINRVRDKLTGRDFSQGDPIDVPTQVDLLIKQATSHENLCQCYIGWCPFW
```

```
>XM_020068652.1 PREDICTED: Crassostrea gigas serine/threonine-protein
kinase mTOR (LOC105331599), transcript variant X3, mRNA
ATGACACAACATCTGCAAGAAATTATAACCCAGTTTGTGACAGGGTTAAAAAATAAAAAATGAAGATGTTA
GAAATAAGTCTGCCATGGATTTATACCGCTTTGTGGTCACTGAGTTACGGGAAATGCCCTCCGAGTACCA
CACAACTTCATGGATAAATTCAACCATTTTCAATTTTGAATGGTATCCAGTTCAGATATGAATGAGCGC
AAAGCGGAATATTGGCCATAGTTAGTCTCACTGGAGTTGATGTAGGGAACACCTCCACCAGAATAAGTA
GGTCTCTAATTACCTTCGGAATCTTCTGCCGTCCAATGATGTATCAGTCATGGAGATGGCTGCTCGGGC
AGTGGGCTGGCTGGCCTACTCCTCAGGCTCCTATGCTGCAGAGTACGTGGAGCATGAAGTGAAGCGTGCC
TTAGAGTGGTTAACTAGTGATCGACAGGAGAGCAAGCGACTAGCTGCTGTTCTGGTGTGAAAGAACTTG
CTGTAATAACACCAACATTCTTCTTTCAACAAGTGCAGCAGTTTTTTGATTGTATTTTCAATGCTGTCAG
AGATCCGAAGCCCAACATCAGAGAAGGAGCTGTTGCAGCCCTGAGGGCCGCTCTGGCGGTAACCTCACAG
CGAGAGAGCAAGGCCACTCAGAAGGCTCAGTGGTACAGGCAATGTTATGACGAGGCTGTGAAACTGTATG
ATGAGTTGCAGGGAAGAGAGAAAAAATTATCTCGAGATGACTGGGCTCATGGATCCCTTCTCATAATGAA
TGAAGTGTGAGATGTAGTAATATTGAGGGAGAGAGGCTAAGAATGGAAATGGAAAGATATAACTAACCAG
CAGTATCAACATGAAAGGACTCTTAAGGAGATGTCAAAGACCCACAAATCACCTCCAGTTCTCTAGCCC
TGCAGCAGTTCCAACACAAAGCATTCCCCATCAACAACCTTTATGTCTGGCAATCGGCATAACATGCAGAA
```

AATCAGTTTTGAAAGCCGAACCTTGTAACAGCTTGTGCGAAAGTCATTTTGATAAGGTGTGTGCCCTACTT
TTGAGACACAAGAACAGCAAGAGTGTTTACATCCAGCTGATTCTACAAGTTATCTTTCCACGTCTTGCCG
CCTTTAAACCACATGAATTCTCCCGACTGTACCTGGATGATAACAATCAACTTCTGTGGGGTCACTGAA
AACAAACACGTGACAAGACCTCCACATTCCAGGCCATTGGACTACTGGCCATTTCTGTCCAGGACAACATT
GTCCGATACCTTCCCGGGATCCTGGAGGTCATCAGGGCTTCCCTCCCTCCCAAAGACCTACCAGCCAAGA
AACAGAAGAATATGGTGGTGGATCCATCAGTTTTTACCTGTATCAGCATGCTGGCCAGAGCTGTAGGCC
AGCCATGATTAAGGATGTGAGAGATCTGTTAGACTCCATGTTTGGCGACTGGTCTGAGTCTGCTTTGACT
GCAGCCCTTCGTGATCTGGCCATACAGATCCCACAACATAAAGAAAGAAATTCAGGAAGGGCTGCTGAAGA
ACCTCTCACTCATCTTAATGGGGAGACAACCTCCGCCACCCTGGGGCCCCCAAAAGTCCCTTACAGCCTTT
CCCTATGTGAGCCTCTTTAAACAAATTTGGCAGACATCCAAGATGCCACAAGCATAAACAAGTGGCATTAAAA
ACTCTGGGAAGCTTTGATTTTGAAGGCCACTCTTTGACCCAGTTTGTCCAGCATTGTGCTGAGCAGTACC
TGTCAAGTGACCACAAGGAGATACGCATGGAAGCCGTCCGTACCTGTGCTAGGCTGCTGACACCTCTCCT
ACAGTTGCTTGCCAATAGTCAAGGACAGATCAGCATAGCGGCCATGAATACAGTGGCTGAGGTGTTACAT
AAGCTGCTGGTAGTGGGCATCACAGACACAGATTCTGACATCAGATACTGTGTTCTGGTCTCTATGGATG
ACCGTTTTGATCCTCATCTAGCCCAAGCAGAGAATCTGTCCGCTTTGTTTGTGGCCCTGAATGATGAGGT
GTTTCAGATTCGTGAGCTGGCAATTTGTATCATTGGTTCGACTTAGCAGTAAAAACCCAGCATATGTCATG
CCTTCTTTGAGGAAAACACTTATTCAGATCAGAACAGAGTTGGAGTACAGTGGGGTGGGAAGAAAACAAAG
AACAAAGCCGCTAAAATGCTTGGCCACCTGGTGGCTAATGCTGCCCGCTGGTGGCCCGTACATGGAACC
CATATTGAACGCCCTGATCCCCAAACTGAAGGAGCCCGACCCTAACCCCAACGTCAACCATCAGTGTACTG
GTCGCCATAGGAGAACAGGCACAGGTCAGTGGTACAGAGATGAGAAAAGTGGATGGATGAGTTACTTCCCT
TGATCTTGAAATGTTACAAGACTCGTCTCTACAGAAAAGAGAGGTTGCACTGTGGACCCTGGGACA
GCTGGTTGAGAGTACAGGATACGTGATCGAGCCCTACAAACGCTACCCCTCATTGCTGGAAGTACTCCTT
AACTTCTTGAAAACAGAGCAAGCTACAGGAATTAGAAGAGAGGTGATCCGTGTGCTTGGTTTGTGCTGGAG
CTCTTGATCCACACAACATAAGATGAACCAGGGAATGATTCAGAGGAATGAATCCAACCTCTGTGAGTGC
ATCGGACACAAAGCTATCCTCTGACAGCACCCAGCCTGAGAACACAAGTGAATGTTAGCCAACATGACC
GCTTCTACCCTCTGGAGGAAATCTATCCAGCCATTGCCATAGCAACACTGATGCGGATAATCCGTGATC
CATCTCTCTCACAGCACACAAATGGTGGTCCAGGCGATCACCTTCATCTTCAAGAGTCTGGGAATTA
GTGTGTCCCGTACATCCAGCAGGTGATCCCAGCTTACCTGGCGGTTATCCGGTCCGCGGATCAGACGTTT
AGAGAGTTCTTGTTCACAACAAGTGGGAGTCATCATTGCGATCGTGAAGCAACACATCAGGAACCTACCTCA
ATGATATTTTACCATTATAAAGGAGTACTGGAGTCCCAACAGCACTATGCAGAACACAATCATTAACT
GGTGGAGCAGATGTGACGGCCCTGGGGACAGAGTTCAGATCTACCTCCCCAGATCATCCCCAGATC
CTCAAAGTCTTACAGGACTCCAGCGACAACCCGGGCACTACCCGGCAAGTTACTGAATGCCCTACAGT
TGTTTGGAGCTAACCTTGATGACTACCTCCATCTCCTCCTCCTGTGGTGAAGCTGTTGACAGCCC
AGATGTCCCTCTCTCAGTCAAAGGATTGCCTTGGAAACTGTAGATAAATTGACCTTGACCTTGACCTG
ACAGAGTTTGCTTCCCGGATCATTATCCCTTGTGAGAACCTTGGACTCTGTGCTGAGTTACAGACAG
CCGCCATGGATACACTGTGTGCCATGGTGTGATGAGATGGGTCCAAAGTTCACTATCTTCAATCCGATGGT
CCAGCGTGTGATACAGAAACACAAGATAGCTCACCAGCGATACTTCACTTCTTATGGCAAGGATTCTCAAG
GCATCAACCATTGCTGAGGAAGAAGATGATCCTATTTTATTGAAGCACAGAAAGAATCGTGGGAAGGCAA
CAGAATCTAGTGAATCGATGGCAGACACAGCTGTGATTAAGAAGCTTCATGTGAGCTTTATAAATCTCCA
AAAGGCTTTGGAAGCTGGGAGAAAGGAATCCAAGGAAGACTGGATGGAGTGGCTGAGGAGACTGAGTATA
GAGCTCCTGAAAGAGTCCCCATCCCCCGCCCTCAGGTCTGCTGGGCTCTGGCACAGACCTACAACCTCGC
TGGCCAAAGATCTGTTCAATGCTGCCTTTGTGTCTGCTGGACTGAACTTACAGAAGCTCAGCAAGATGA
ACTCATTCTTAGTCTCGAACAAGCCCTCACATCTCAGGAAATACCCGAGATCACTCAGACTCTTCTTAAT
CTGGCAGAATTCATGGAACACTGTGATAAAGGGCCCCCTGCCTTTAGATACCTCACTATTGGGATCTCGGG
CGATGAGGTGCCGAGCGTATGCCAAGGCTCTACACTACAAGGAAGAGGAGTTCACCCGGGGACCCACCAC
AGCCACTCTCGAATCTCTGATCAGTATTAACAACAAGCTTCAGCAGCCGAGTCAGCCTCTGGTGTGCTA
CAGTACGCACAGAATCACAGGACTGATGTGAAAGTACAAGAAAGCTGGTATGAGAAGCTTCATGAGTGGAA
ATAAAGCTCTAGAGGCCTACGAGAAAAACAGGAGGAGAAACCTGAGGATTTCAACCTGACTCTGGGCAG
AATGAGATGTCTAGAGGCATTAGCAGAGTGGGGTACCTTCATCAGATTGCCTGTGAGAAGTGGGGGACC
AGTAGTGTGAGAACTGCAGTACATGGCAGGAGAAATGCTTGCCTCAGCTGCCTGGGACTGGGTCAGTGGG
ACAGTATGGAGGAGTACATGTGTCTGATCCCAGGAACAGTTACAATGGGGCATTCTACCAGCTGTGTT
CGCTCTCCATACAGAGAACTACCAGTTAGCACAACAGTGCATTGACAAAGCCAGAGATATTCTGGACACA
GAGCTGACAGCTATGGCAGGGGAGAGCTACAACAGAGCCTATGGGGCCATGGTCAATGTCCAGATGTTGT
CGGAGCTTGAGGAGGTCATGCAGTTTAAACTGGTTCCCGAAAGACAGGAGGCCATCAAGCACATGTGGTG
GGACCGCCTCCAAGGCTGTGAGCGCTGGTGGAAAGACTGGCAGAAGATCATCCAGTCCGCTCCCTGGTT
GTGTGCCCCCTGGAAGACATGAAAACATGGCTGAAGTACGCCAGTCTGTGAGGAAGAGTGGAAAGACTGG
CCCTTTCCAGAAGACTCTGGTGTGTTGTTGGGAATGGACCCTGCTAAGAACTGTGATAAGCCTATTTCC
TACCACCAACCCTCAGGTCACCTTTGCTTACCTCAAACACATGTGGAAGAGCAGTCAGAAGAAAGAAGCT
TATGGTAAATGCAACATTTTGTCCAACATTCACCTCAAACCTCGGGCTCTCCAACCTGATAACGCTGAGG
ATACTCAACAAAGAAGTCAACTGAACAAGTTGCTTGTAGGTGTTACCTGAAGCTTGGAGACTGGGCGGA
CATGTTGTATGGAGTGAACGAGGAATCAGTGACCCAGATTCTAGAGTACTACAGCCTGGCCACAGAGTAC
GACAAATACTGGTACAAGGCGTGGCATGGATGGGCTCTAATCAACTATGAAGCGGTCTTATTTTACAAAC
AATCAGAGAAGTCGGGCAATCAGCCCCAGTCCCTGGAGATATTGGCCCTCCGGGGAGAGGAGACGCGCC

CCTCTACCAAAGACGGACACCAGTGTCTCGACTGCCTCCAAGATGCATAAAATACTGTGTTCTAGCTGTA
CAGGGATTCTTTAGGTCCATCTCTCTGTCCCAGAATAAAAGTTTACAGGACACACTCAGGTTGTTGACGC
TGATGTTTTGACTATGGTCAGTGGTTAGAGGTATACGAGGCATTGAATGATGGACTGAAAACCATACAGGT
GGAGAACTGGCTGCAGGTGATTCTCACTGATTGCCAGGATTGACATTCCACGCCCTTGGTCAGTCGT
CTCATCAGTCAGCTCTTGATCGACATCGGCAAGGCTCACCTCAGGCCTTGATTTACCCCCTTACTGTGG
CCTCCAAGTCTAACGTTTCTGCCCGCCAAACAGCAGCCAACAAAATCCTGAAGAACATGTGTGAACACAG
CAACACTTTGGTACAACAGGCCATGCTGGTGGAGTGAGGAGCTGATCCGGGTGGCCATTCTATGGCATGAG
TTGTGGCATGAGGGACTAGAGGAGGCCTCCAGGCTATACTTTGGGGAGAGGGACATCAAGGGCATGTTCT
CTACCCTGGAGCCGCTACATAACATGGTGGAGCGCGGCCCCAGACCCTCAAGGAACTTCATTTAATCA
GGCGTACGGCCGTGACCTGATGGAGGCCAGGAGTGGTGTAGGAAAGTACCAGAGGTGAGAGAACGTCAAG
GACCTGACCCAGGCCTGGGATCTCTACTACCATGTGTTTCCAGGAGGATCTCTAAAACAGCTGCCACAGCTGA
CATCCCTGGAGCTTCAGTATGTTTTCTCCTAAACTTCTTCGCTGTCAAGATCTGGAGTTAGCTGTGCCTGG
GAAGTATGAACCAAACCAACCAATCGTCAAAATCAAACGCTGCCAGAGTTCAGTCAAGTCATTACCTCA
AAGCAGAGGCCAGAAAACACTCAGCATATTTGGTTCCAATGGGAAGGAGTTCAGTTCCTGTGTAAGGGAC
ACGAGGACCTGCGACAAGACGAGCGAGTTCATGCAGCTCTTTGGACTAGTCAACTCTCTCCTGGTGGAAAA
TCCAGAGACCTTCCGAAGGAACCTTACGATTCAGCGGTTCTCCGTTATCCCCCTGTGCGACAAAACCGGC
CTGATTGGCTGGGTACCACACACCCGACACCCTACACTCCCTCATCCGTGACTACCGAGAGAAAAAGAAAA
TTCTGCTCAACATAGAGCACAGGCTGATGCTCAGAATGGCACCAGGACTATGACCATTTGACCCTGATGCA
GAAGGTGGAGGTATTTGAGCATGCTCTGGAGCACACCCAGGGAGATGACCTGGCCAAGATCTTGTGGTAC
AAGAGTCTTAGCTCAGAGGTGTGGTTCGATAGACGTACAACTACACTCGCTCCCTGGCTGTTATGTCTA
TGGTGGGCTATGTGTTGGGTCTTGGAGACAGACATCCTTCCAATCTAATGTTGGATCGTACTAGTGGCAA
AGTCATCCATATCGACTTTGGTACTGCTTTGAGGTTGCCATGGTGAGAGAAAAGTTTCCCGAGAAGATT
CCATTCCGCTTGACTCGCATGTTAATCAATGCTATGGAGGTGACAGGTATCGACGGTAACTACAAGATGA
CCTGTGAGAGTGTGATGGAGGTACTGAGGGAACACAAGGACAGTCTGATGGCCGTGCTCGAGGCCTTTGT
GTACGACCCTCTCCTCAACTGGAGGCTCATGGACACAACAGCCAAAGGGAAAAACAAGACCAAAGATTCA
TACTCTGGTGGAAAGTCAGGAACAGGCGGACATGTTGGAGAACGTGATATCAATCAGACCGCCACAAAC
GCTCCGCCCTGAGGCCGCAAGTTCAGTCAGCGGGGACAATTTCCAGGCAGAGGTTCATCAACAAGAAAGGC
ACTGTCCATCATTAAATCGGGTCAGGGACAAAATAACTGGTTCGTGACTTCTCTCAGGGGGATCCGATTGAT
GTCCCCACCCAGGTGGACCTCCTGATAAAAACAGGCCACCTCCCACGAGAATCTATGTCAGTGTACATTG
GGTGGTGTCCATTCTGGTGAAGGTTCTCGGCTCTGATGTGTGTGCTGTGGTTTTTCCACCTTAAACAC
TGTGTTATGCATGCAACCTGTGATTTATTAAGTTGGTATGTCTTATATACATATGTACATTAACATGTTG
TTTTTTTTTATTGCAATTTATGTATAGATTAATTTGGCAGTTAAATGTGCCTGTGTACAGAAGATAGTTG
CAAAATGCCATTTGAATCTTATTTACTGATTGTATTTGTTTATGGATTATTTATGTAGTAGTACATG
TTTTAGCAATTTGCTAAGCAAATGAACAAGTACTGAAAATGACAGAGAATTATGATACATGTACATGTAT
CCTGGGAATCGTTTTACCCTAAATTAGAGACATGAAAGTATCATAAAAATTTGGGATCTTAAAGTTTTGCTT
CTAAACAAGTTATAAGCTCCACTTTACTTAATGATTACTGGTAATTTATGACAATGTTACTGCAATTCAG
GTTTTTTTTTTACAATCAAACATTGCTAGTAGCTTTACATGTGCAACCACATGCTTCACAACATTTATAT
ATGAACATTCATGCTATGAATGTGTGCGAGGTTCCATATTTTTATGTGTACAGTATGCTTCTATGAATGTA
CTTACTTGTACATGCAGTCATTACCGGTAAGTCTGTTTTGTATTGTCTGATGTACATACTAGTGTGG
CTCTGTTATTTTGTGCTGACAACAGTTTTTATAAGTGTCTATGCGGATAAATCTAAATGTCTTTTTGTAC
ATGTTAATACACATGTAGTTATTACACATGAACATGTTATCAAGGTATCCGATCCATAATAGGATCTAAT
TTTTCCAACCTTGAATATCCATCATGTATTTAATCTTTGATACCTAAAGCATTTTAAACAAGAAAAAGA
TTTACTGAGAGAAATTTTCAAAAATATTATTAATAAGCAGTGATTAATTGATCATAAAGATTGCATTAT
GGTCTATGGGGACAAGCACATTTTTTAAATAAAAAAGTAAATTTCTAAGAATATCAATAAATGCTTTGGT
GGAAAGATGTATTTTATCATTAGGAATACAAAACACTATTGAAAATCAATTTTACACTATATAGATTTTTT
AAAATGAATTTTATAGAATAAAAGCAAAGGGGCGCAATTTTAAAAAAGGAAAAGGTCAATTAATTAGG
ACTCATTCCACTCTTACATATTGATACTTAAACATGAAAATTTATGTCCAAGTATACTGAGTATTAAGCCC
ATACATATCTGTTATGCACCAAATTCATTGAACCTGGGGCTATTATAGATCGGATACCTTAACGAACATT
CATGTTGATGATTTACTCTTTAAACCATGCTTATTAGATTTGACAAAAATATTCTTGTGATATTCGCTG
TGTTATGGAATGGAGCTATATGTACAATTTGTCATGAAAACCTTACATCTACAAATATGCATATTTGAGTA
TGTTAATTATGAGGCAGAAATCTTTTTTTTTTTTATTTGACTCGCAAATTCAGAGAAAAAATCGCAAAAT
ATGAATACTTGAATAAAAACACAAAATTTGTAGATTTTTTAAGTTATCAACCTATTCTTTTTATGAGGG
AAGTATTGGGGTAATTCAAAGAGTTTTTGTAAATATACAGTGCATGTACCAACATTTGTACCGTACATGTA
TGAAGCATTATAATTGTGTCATAAATGAATACTGTTATGTATTACAAATATACTGTTAAAAATGTCCCTT
TAAAGTAATATTGTTTTGTGACAATAAATTAAGATAAAAATGTTAATTCACA

>XM_005263438.2 PREDICTED: Homo sapiens mechanistic target of rapamycin
kinase (MTOR), transcript variant X2, mRNA
CGGGGAAGCGGGCGGTGGGGCAGGGGGCTGAAGCGGCGGTACCGGTGCTGGCGGCGGCAGCTGAGGCC
TTGGCCGAAGCCGCGCAATATTAAGGAACTTCTCTCTAAAGAACCTCAGGGCAAGATGCTTGGAAACC
GGACCTGCCGCCGCCACCACCGCTGCCACCACATCTAGCAATGTGAGCGTCTTCGAGCAGTTTGCCAGTG
GCCTAAAGAGCCGGAATGAGGAAACCAGGGCCAAAGCCGCAAGGAGCTCCAGCACTATGTCACCATGGA
ACTCCGAGAGATGAGTCAAGAGGAGTCTACTCGCTTCTATGACCAACTGAACCATCACATTTTTGAATTTG

GTTCAGCTCAGATGCCAATGAGAGGAAAGGTGGCATCTTGGCCATAGCTAGCCTCATAGGAGTGGAAAG
GTGGGAATGCCACCCGAATTGGCAGATTTGCCAACTATCTTCGGAACCTCCTCCCTCCAATGACCCAGT
TGTCATGGAAATGGCATCCAAGGCCATTGGCCGTCTTGCCATGGCAGGGGACACTTTTACCGCTGAGTAC
GTGGAATTTGAGGTGAAGCGAGCCCTGGAATGGCTGGGTGCTGACCGCAATGAGGGCCGGAGACATGCAG
CTGTCTGGTTCTCCGTGAGCTGGCCATCAGCGTCCCTACCTTCTTCTTCCAGCAAGTGAACCCCTTCTT
TGACAACATTTTTGTGGCCGTGTGGGACCCCAACAGGCCATCCGTGAGGGAGCTGTAGCCGCCCTTCGT
GCCTGTCTGATTCTCACAACCCAGCGTGAGCCGAAGGAGATGCAGAAGCCTCAGTGGTACAGGCACACAT
TTGAAGAAGCAGAGAAGGGATTTGATGAGACCTTGGCCAAAGAGAAGGGCATGAATCGGGATGATCGGAT
CCATGGAGCCTTGTGATCCTTAACGAGCTGGTCCGAATCAGCAGCATGGAGGGAGAGCGTCTGAGAGAA
GAAATGGAAGAAATCACACAGCAGCAGCTGGTACACGACAAGTACTGCAAAGATCTCATGGGCTTCGGAA
CAAAACCTCGTCACATTACCCCTTACCAGTTTCCAGGCTGTACAGCCCCAGCAGTCAAATGCCTTGGT
GGGGCTGCTGGGGTACAGCTCTCACCAGGCCCTCATGGGATTTGGGACCTCCCCAGTCCAGCTAAGTCC
ACCCTGGTGGAGAGCCGGTGTTCAGAGACTTGATGGAGGAGAAATTTGATCAGGTGTCCAGTGGGTGC
TGAATGCAGGAATAGCAAGAACTCGCTGATCCAAATGACAATCCTTAATTTGTTGCCCGCTTGGCTGC
ATTCGACCTTCTGCCTTACAGATACCCAGTATCTCCAAGATACCATGAACCATGTCTAAGCTGTGTC
AAGAAGGAGAAGGAACGTACAGCGGCCCTCCAAGCCTGGGGCTACTTTCTGTGGCTGTGAGGTCTGAGT
TTAAGGTCTATTTGCCTCGCGTGTGGACATCATCCGAGCGGCCCTGCCCCCAAAGGACTTCGCCCATAA
GAGGCAGAAGGCAATGCAGGTGGATGCCACAGTCTTCACTTGCATCAGCATGCTGGCTCGAGCAATGGGG
CCAGGCATCCAGCAGGATATCAAGGAGCTGCTGGAGCCCATGCTGGCAGTGGGACTAAGCCCTGCCCTCA
CTGCAGTGTCTACGACCTGAGCCGTGAGATTCCACAGCTAAAGAAGGACATTAAGATGGGCTACTGAA
AATGCTGTCCCTGGTCTTATGCACAAACCCCTTCGCCACCCAGGCATGCCAAAGGGCCTGGCCATCAG
CTGGCCTCTCCTGGCCTCACGACCTCCCTGAGGCCAGCGATGTGGCAGCATCACTCTTGCCTCCGAA
CGCTTGGCAGCTTTGAATTTGAAGGCCACTCTCTGACCCAATTTGTTCCGCACTGTGCGGATCATTTCT
GAACAGTGAGCACAAGGAGATCCGCATGGAGGCTGCCCCGACCTGCTCCCGCCTGCTCACACCTCCATC
CACCTCATCAGTGGCCATGCTCATGTGGTTAGCCAGACCGCAGTGAAGTGGTGGCAGATGTGCTTAGCA
AACTGCTCGTAGTTGGGATAACAGATCCTGACCCTGACATTCGCTACTGTGTCTTGGCGTCCCTGGACGA
GCGCTTTGATGCACACCTGGCCCAGGCGGAGAAGTTCAGGCCTTGTGTTGGCTCTGAATGACCAGGTG
TTTGAGATCCGGGAGCTGGCCATCTGCACTGTGGGCCGACTCAGTAGCATGAACCTGCCTTTGTTCATGC
CTTTCCTGCGCAAGATGCTCATCCAGATTTTACAGAGTTGGAGCACAGTGGGATTTGGAAGAATCAAAGA
GCAGAGTCCCCGCATGCTGGGGCACCTGGTCTCCAATGCCCCCGACTCATCCGCCCTACATGGAGCCT
ATCTGAAGGCATTAATTTTGAAGTCAAAGATCCAGACCTGATCCAAACCCAGGTGTGATCAATAATG
TCCTGGAACAACATAGGAGAATTGGCACAGGTTAGTGGCCTGGAAATGAGGAAATGGGTGTGAACTTTT
TATTATCATCATGGACATGCTCCAGGATTCCTCTTGTGTTGGCCAAAAGGCAGGTGGCTCTGTGACCTTG
GGACAGTTGGTGGCCAGCACTGGCTATGTAGTAGAGCCCTACAGGAAGTACCCTACTTTGCTTGAGGTGC
TACTGAATTTTCTGAAGACTGAGCAGAACCAGGGTACACGCAGAGAGGCCATCCGTGTGTTAGGGCTTTT
AGGGGCTTTGGATCCTTACAAGCACAAAGTGAACATTGGCATGATAGACCAGTCCCGGGATGCCTCTGCT
GTCAGCCTGTGAGAATCCAAGTCAAGTCAAGTCAAGTATTCTCTGACTATAGCACTAGTGAATGCTGGTCAACA
TGGGAAACTTGCCTCTGGATGAGTTCTACCCAGCTGTGTCCATGGTGGCCCTGATGCGGATCTTCCGAGA
CCAGTCACTCTCTCATCATCACACCATGGTTGTCCAGGCCATCACCTTCATCTTCAAGTCCCTGGGACTC
AAATGTGTGCAGTTCTGCCCCAGGTGCACCCAGTTCCTTAACGTCATTTCAGTCTGTGATGGGGCCA
TCCGGGAATTTTTGTTCCAGCAGCTGGGAATGTTGGTGTCTTTGTGAAGAGCCACATCAGACCTTATAT
GGATGAATAGTACCCTCATGAGAGAATTCTGGGTGCATGAACACCTCAATTCAGAGCAGCATCATTTCT
CTCATTGAGCAAATTTGGTGTAGCTCTTGGGGGTGAATTTAAGCTCTACCTGCCCCAGCTGATCCACACA
TGCTGCGTGTCTTTCATGCATGACAACAGCCAGGCCGATTGTCTCTATCAAGTTACTGGCTGCAATCCA
GCTGTTTGGCGCCAACCTGGATGACTACCTGCATTTACTGCTGCCTCCTATTGTTAAGTTGTTTGTATGCC
CCTGAAGCTCCACTGCCATCTCGAAAGGCAGCGCTAGAGACTGTGGACCGCCTGACGGAGTCCCTGGATT
TCACTGACTATGCCTCCCGGATCATTACCCCTATTGTTGCAACACTGGACCAGAGCCCAGAATGCGCTC
CACAGCCATGGACACGCTGTCTTCACTTGTTTTTTCAGCTGGGGAAGAAGTACCAAATTTTCATTTCAATG
GTGAATAAAGTTCTGGTGCACACCCGAATCAATCATCAGCGCTATGATGTGCTCATCTGCAGAATTGTCA
AGGATACACACTTGTGCTGATGAAGAGGAGGATCCTTTGATTTACCAGCATCGGATGCTTAGGAGTGGCCA
AGGGGATGCATTGGCTAGTGGACCAGTGGAAACAGGACCCATGAAGAAACTGCACGTCAGCACCATCAAC
CTCCAAAAGGCCTGGGGCGCTGCCAGGAGGGTCTCCAAAGATGACTGGCTGGAATGGCTGAGACGGCTGA
GCCTGGAGCTGCTGAAGGACTCATCATCGCCCTCCCTGCGCTCCTGCTGGGCCCTGGCACAGGCCTACAA
CCCGATGGCCAGGGATCTCTTCAATGCTGCATTTGTGTCTGCTGGTCTGAACTGAATGAAGATCAACAG
GATGAGCTCATCAGAAGCATCGAGTTGGCCCTCACCTCACAAGACATCGCTGAAGTCACACAGACCCTCT
TAACTTGGCTGAATTCATGGAACACAGTGACAAGGGCCCCCTGCCACTGAGAGATGACAATGGCATTTGT
TCTGCTGGGTGAGAGAGCTGCCAAGTCCGAGCATATGCCAAAGCACTACACTACAAAGAACTGGAGTTC
CAGAAAGGCCCCACCCCTGCCATTTCTAGAATCTCTCATCAGCATTAATAATAAGCTACAGCAGCCGGAGG
CAGCGGCCGGAGTGTTAGAATATGCCATGAAACACTTTGGAGAGCTGGAGATCCAGGCTACCTGGTATGA
GAACTGCACGAGTGGGAGGATGCCCTTGTGGCCTATGACAAGAAAATGGACACCAACAAGGACGACCCA
GAGCTGATGCTGGGCCGATGCGCTGCCTCGAGGCCCTTGGGGGAATGGGGTCAACTCCACCAGCAGTGT
GTGAAAAGTGGACCCTGGTTAATGATGAGACCCAAGCCAAGATGGCCCCGGATGGCTGCTGCAGCTGCATG
GGGTTTAGGTGAGTGGGACAGCATGGAAGAATACACCTGTATGATCCCTCGGGACACCCATGATGGGGCA

TTTTATAGAGCTGTGCTGGCACTGCATCAGGACCTCTTCTCCTTGGCACAAACAGTGCATTGACAAGGCCA
GGGACCTGCTGGATGCTGAATTAAGTGCATGGCAGGAGAGAGTTACAGTCGGGCATATGGGGCCATGGT
TTCTTGGCCACATGCTGTCCGAGCTGGAGGAGGTTATCCAGTACAAACTTGTCCCCGAGCGACGAGAGATC
ATCCGCCAGATCTGGTGGGAGAGACTGCAGGGCTGCCAGCGTATCGTAGAGGACTGGCAGAAAATCCTTA
TGGTGGCGTCCCTTGTGGTCAGCCCTCATGAAGACATGAGAACCTGGCTCAAGTATGCAAGCCTGTGCGG
CAAGAGTGGCAGGCTGGCTCTTGTCTATAAAACTTTAGTGTGCTCCTGGGAGTTGATCCGTCTCGGCAA
CTTGACCATCCTCTGCCAACAGTTCACCCTCAGGTGACCTATGCCTACATGAAAAACATGTGGAAGAGTG
CCCGCAAGATCGATGCCTTCCAGCACATGCAGCATTTTGTCCAGACCATGCAGCAACAGGCCCCAGCATGC
CATCGCTACTGAGGACCAGCAGCATAAGCAGGAACCTGCACAAGCTCATGGCCCGATGCTTCTTGAAACTT
GGAGAGTGGCAGCTGAATCTACAGGGCATCAATGAGAGCACAATCCCCAAAGTGTGTCAGTACTACAGCG
CCGCCACAGAGCAGCACCAGCAGCTGGTACAAGGCCTGGCATGCGTGGGCAGTGATGAACTTCGAAGCTGT
GCTACACTACAAACATCAGAACCAAGCCCGCGATGAGAAGAAGAAACTGCGTCATGCCAGCGGGGCCAAC
ATCACCACGCCACCCTGCCGCCACCACGGCCGCCACTGCCACCACCCTGCCAGCACCAGGGGCAGCA
ACAGTGAGAGCGAGGCCGAGAGCACCAGAACAGCCCCACCCCATCGCCGCTGCAGAAGAAGGTCACTGA
GGATCTGTCCAAAACCTTCTGATGTACACGGTGCCTGCCGTCCAGGGCTTCTTCCGTTCATCTCCTTG
TCACGAGGCAACAACCTCCAGGATACACTCAGAGTTCTCACCTTATGGTTTGATTATGGTCACTGCCCAG
ATGTCAATGAGGCCTTAGTGGAGGGGGTGAAGCCATCCAGATTGATACCTGGCTACAGGTTATACCTCA
GCTCATTGCAAGAATTGATACGCCCAGACCCTTGGTGGGACGTCTCATTACCCAGCTTCTCACAGACATT
GGTCCGTACCACCCCGAGCCCTCATCTACCCACTGACAGTGGCTTCTAAGTCTACCACGACAGCCCGGC
ACAATGCAGCCAACAAGATTCTGAAGAACATGTGTGAGCACAGCAACACCCTGGTCCAGCAGGCCATGAT
GGTGAGCGAGGAGCTGATCCGAGTGGCCATCCTCTGGCATGAGATGTGGCATGAAGGCCTGGAAGAGGCA
TCTCGTTTTGTACTTTGGGGAAAGGAACGTGAAAGGCATGTTTGGAGTGTGGAGCCCTGCATGCTATGA
TGAACGGGGCCCCAGACTCTGAAGGAAACATCCTTTAATCAGGCCTATGGTCGAGATTTAATGGAGGC
CCAAGAGTGGTGCAGGAAGTACATGAAATCAGGGAATGTCAAGGACCTCACCCAAGCCTGGGACCTCTAT
TATCATGTGTTCCGACGAATCTCAAAGCAGCTGCCTCAGCTCACATCCTTAGAGCTGCAATATGTTTCCC
CAAACCTTCTGATGTGCCGGGACCTTGAATTGGCTGTGCCAGGAACATATGACCCCAACCAGCCAATCAT
TCGCATTACAGTCCATAGCACCGTCTTTGCAAGTCATCACATCCAAGCAGAGGCCCCCGAAAATTGACACTT
ATGGGCAGCAACGGACATGAGTTTTGTTTTCTTCTAAAAGGCCATGAAGATCTGCGCCAGGATGAGCGTG
TGATGCAGCTCTTCGGCCTGGTTAACACCCTTCTGGCCAATGACCCAACATCTCTTCGGAAAAACCTCAG
CATCCAGAGATACGCTGTCTATCCCTTTATCGACCAACTCGGGCCTCATTGGCTGGGTTCCTTCTGTGAC
ACACTGCACGCCCTCATCCGGGACTACAGGGAGAAGAAGAAGATCCTTCTCAACATCGAGCATCGCATCA
TGTTGCGGATGGCTCCGGACTATGACCCTGACTCTGATGCAGAAGGTGGAGGTGTTGAGCATGCCGT
CAATAATACAGCTGGGACACTGGCCAAGCTGTGTGGCTGAAAAGCCCCAGCTCCGAGGTGTGTTTT
GACCGAAGAACCAATTATACCCGTTCTTTAGCGGTTCATGTCAATGGTTGGGTATATTTTAGCCCTGGGAG
ATAGACACCCATCCAACCTGATGCTGGACCGTCTGAGTGGGAAGATCCTGCACATTGACTTTGGGGACTG
CTTTGAGGTTGCTATGACCCGAGAGAAGTTTCCAGAGAAGATTCCATTTAGACTAACAAGAATGTTGACC
AATGCTATGGAGGTTACAGGCCTGGATGGCAACTACAGAATCACATGCCACACAGTGATGGAGGTGCTGC
GAGAGCACAAGGACAGTGTCTATGGCCGTGCTGGAAGCCTTTGTCTATGACCCCTTGCTGAACTGGAGGCT
GATGGACACAATAACCAAAGGCAACAAGCGATCCCGAACGAGGACGGATTCTACTCTGCTGGCCAGTCA
GTCGAAATTTTGGACGGTGTGGAACCTGGAGAGCCAGCCCATAAGAAAACGGGGACCACAGTGCCAGAAT
CTATTCATTCTTTTATTGGAGACGGTTTTGGTGAACCAGAGGCCCTAAATAAGAAAGCTATCCAGATTAT
TAACAGGGTTCGAGATAAGCTCACTGGTCCGGGACTTCTCTCATGATGACACTTTGGATGTTCCAACGCAA
GTTGAGCTGCTCATCAAACAAGCGACATCCCATGAAAACCTCTGCCAGTGCTATATTGGCTGGTGCCTT
TCTGGTAACTGGAGGCCCAGATGTGCCCATCACGTTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTC
CACTAAACTGAAACCATGGTGAGAAAGTTTTGACTTTGTTAAATATTTTGAATGTAAATGAAAAAGACTA
CTGTATATTTAAAGTTGGTTTTGAACCAACTTTCTAGCTGCTGTTGAAGAATATATTGTGCAAAAACAAG
GCTTGATTTGGTTCCCAGGACAGTGAAACATAGTAATACCACGTAATCAAGCCATTCATTTTGGGGAAC
AGAAGATCCATAACTTTAGAAATACGGGTTTTGACTTAACTCACAAAGAGAACTCATCATAAGTACTTGCT
GATGGAAGAATGACCTAGTTGCTCCTCTCAACATGGGTACAGCAAACCTCAGCACAGCCAAGAAGCCTCAG
GTCGTGGAGAACATGGATTAGGATCCTAGACTGTAAAGACACAGAAGATGCTGACCTCACCCCTGCCACC
TATCCCAAGACCTCACTGGTCTGTGGACAGCAGCAGAAATGTTTGAAGATAGGCCAAAATGAGTACAAA
AGGTCTGTCTTCCATCAGACCCAGTGATGCTGCGACTCACACGCTTCAATTCAAGACCTGACCGCTAGTA
GGGAGGTTTTATTAGATCGCTGGCAGCCTCGGCTGAGCAGATGCACAGAGGGGATCACTGTGCAGTGGGA
CCACCCTCACTGGCCTTCTGCAGCAGGGTCTGGGATGTTTTTCAAGTGGTCAAAAATACTCTGTTTAGAGCA
AGGGCTCAGAAAACAGAAATACTGTCTATGGAGGTGCTGAACACAGGGAAGGTCTGGTACATATTGGAAAT
TATGAGCAGAAACAATACTCAACTAAATGCACAAAGTATAAAGTGTAGCCATGTCTAGACACCATGTTGT
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
MEPHEEQIWKSKLLKAANNMMDMDRNVPLAPNLNVNMMNMKNASRNGDEFGLTSSRFDGV
VIGSNGDVNFKPILEKIFRELTSDYKEERKLASISLFDLLVSLEHELSEIEFQAVSNDIN
NKILELVHTKKTSTRVGAVLSIDTLISFYAYTERLPNETSRLAGYLRGLIPSNDEVMRL

AAKTLGKLAVPGGTYTSDFVEFEIKSCLEWLTASTEKNFSSSKPDHAKHAALLIITALA
ENCPLYLLYQYLNLSILDNIWRALRDPHLVIRIDASITLAKCLSTLRNRDPQLTSQWVQRLA
TSCEYGFQVNTLECIHASLLVYKEILFLKDPFLNQVFDQMCLNCIAYENHKAKMIREKIY
QIVPLLASFNPQLFAGKYLHQIMDNYLEILTANAPANKIPLHKDDKQILISIGDIAYEVG
PDIAPYVKQILDYIEHDLQTKFKFRKKFENEIFYCIGRLAVPLGKLLNRNILDLMF
KCPLSDYMQETFOILTERIPSLGPKINDELLNLVLCSTLSGTFPIQPGSPMEIPSFSSRERA
REWRNKNILQKTGESNDDNDNDIKIIIQAFRMLKNIKSRFSLVEFVRIVALSYIEHTDPRV
RKLAAALTSCEIYVKDNICKQTSLSLHSLNTVSEVLSKLLAITIADPLQDIRLEVLKLNLPFCF
DPQLAQPDNLRLLFTALHDESFNIQSVAMELVGRLSSVNPAYVIPSIRKILLELLTKLKF
STSSREKEETASLLCTLRSSKDVAKPYIEPLLNVLKPKFQDTSSTVASTALRTIGELSV
VGGEDMKIYKDLFPLIKTFQDQSNFKAALALGQLAASSGYVIDPLLDYPELLGI
LVNILKTENSQNIRRTVTTLIGILGAIDPYRQKEREVTSTTDISTEQNAPPIDIALLMQG
MSPSNDEYYTTVVIHCLLKILKDPSSLSSYHTAVIQAIMHIFQTLGLKCVSFLDQIIPPTIL
DVMRTCSQSLLLEFYFQQLCSLIIIVRQHIRPHVDSIFQAIKDFSSVAKLQITLVSVIEAI
SKALEGEFVKRLVPLTLTLFLVILENDKSSDKVLSRRVLRLLLESFGPNLEGYSHLITPKIV
QMAEFTSGNLQRSIIITIGKLAQDVDFEMSSSRIVHSLLRVLSSTTSDELKSKVIMNTLSL
LLIQMGTSFAIFIPIVINEVLMKKHIQHTIYDDLNRILNNDVLPKILEANTTDYKPAEQ
MEAADAGVAKLPINQSVLKSAWNSSQORTKEDWQEWKRLSIQLLKESPSHALRACSNLA
SMYYPLAKELFNATAFACVWTELYSQYQEDLIGSLCIALSSPLNPPEIHQTLNLLVEFMEH
DDKALPIPTQSLGEYAERCHAYAKALHYKEIKFIKEPENSTIESLISINNQLNQTDAAG
ILKHAQQHSLQKETFWEKLERWEDALHAYNEREKAGDTSVSVTLGKMRSLHALGEWEQ
LSQLAARKKWKVSKLQTKKLIAPLAAGAAWGLGEWDMLEQYISVMKPKSPDKEFFDAILYL
HKNDYDNASKHILNARDLLVTEISALINESYNRAYSVIVRTQIITEFEEIKYKQLPPNS
EKKLHYQNLWTKRLLGCQKNVDLWQVRVLRVSLVIKPKQDLQIWIKFANLCRKSGRMRLA
NKALNMLLEGGNDPSLPNTFKAPPPVVAQQLKIYIATGAYKEALNHLIGFTSRLAHDGL
DPNNMIAQSVKLSASTAPYVEEYTKLLARCFKQGEWRIATQPNWRNTNPDAILGSYLL
ATHFDKNWYKAWHNWALANFEVISMVQEETKLNNGKNDDDDDTAVNNDNVRIDGSIILGSG
SLTINGNRYPLELIQRHVPAIKGFFHSISLLETSCLODTRLRLTLFNFNGGIKEVSOAM
YEGFNLMKIENWLEVLPLQISRIHQPDPTVSNLSLLSDLGKAHPQALVYPLTVAIKSE
SVSRQKAALSIIEKIRIHSPLVNQAELVSHELIRVAVLWHELWYEGLEDASRQFFVEHN
IEKMFSTLEPLHKHLGNEPQTLSEVSFQKSFGRDLNDAYEWLNKYKSKDINNQLQAWDI
YYNVFRKITRQIQQLTDLQHVSPQLLATHDLELAVPGTYFPGKPTIRIAKFEPLFSVI
SSKQRPKRFYSIKSGDKDYKYVLKGHEDIRQDLSVMQFLGLVNTLLKNDSECFKRHLDIQ
QYPAIPLSPKSGLLGWVNSDTHFVLIREHRDAKKIPLNIEHWVMLQMAPDYENLTLQK
IEVFTYALDNTKGQDLYKILWLKSRSSSETWLERRTTYTRSLAVMSMTGYILGLGDRHPSN
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
MNKYINKYTPPNLLSLRQRAEGKHRTRKKLTHKSHSHDEMSTTSNTDSNHNGPNDSGR
VITGSAGHIGKISFVDSLEDTTFSTLNLIFDKLKSQVQERASGANELSTTLTSLAREVS
AEQFQRFNSNLNKKIFELIHGFTSSEKIGGILAVDTLISFYLSTEELPNQTSRLANYLRV
LIPSSDIEVMRLAANTLGRRLTVPGGTLTSDFVEFEVRTCIDWLTLTADNNSSSSKLEYRR
HAALLIIKALADNSPYLLYPVNSILDNIWVPLRDAKLIIRLDAVALGKCLTIIQDRDP
ALGKQWFQRLFQGCTHGLSLNTNDSVHATLLVFRELLSLKAPYLKDYDDIYKSTMKYKE
YKFDVIRREVYAILPLLAAFDPAIFTKKYLDRIMVHYLRYLKNIIDMNAANNSDKPFILVS
IGDIAFEVGSISPYMTLILDNIREGLRTRKFKVRKQFEKDLFYCIGKLACALGPAFAKHL
NKDLLNMLNCPMSDQMQLMILNEKIPSESTVNSRIILNLLSISLSGEKFIQSNQYDF
NNQFSIEKARKSRNQSFMKKTGESNDDITDAQILIQCFKMLQLIHHQYSLTEFVRLITIS
YIEHEDSSVRKLAALTSCLDFIKDDICKQTSVHALHSVSEVLSKLLMIAITDPVAEIRLE
ILQHLGNSFDPQLAQPDNLRLLFMALNDEIFGIQLEAIKIGRLSSVNPAYVVPVSLRKT
LELLTQLKFSNMPKKEESATLLCTLINSSDEVAKPYIDPILDVILPKCQDASSAVASTA
LKVLGELSVVGGKEMTRYLKEMLPLIINTFQDQSNFKAALALGQLAASSGYVVGPL
LDYPELLGILINILKTENNPHIRRGTVRLIGILGALDPYKHREIEVTSNSKSSVEQNAPS
IDIALLMQGVSPSNDEYYPTVVIHNLKILNDPSLSIHHTAAIQAIMHIFQNLGLRCVSF
LDQIIPGIIILVMRSCPPSQLDFYFQQLGSLISIVKQHIRPHVEKIYGVIREFFPIIKLQI
TIIISVIESISKALEGEFVKRFVPELTFFLDILENDQSNKRIVPIRILKSLVTFGPNLEDY
SHLIMPVVRMTEYSAGSLKKSISITLGRALAKNINLSEMSSRIVQALVRILNNGDRELTK
ATMNTLSLLLLQLGTDVVFVVPVINKALLRNRIQHSVYDQLVNKLLNNECLPTNIFDKE
NEVPERKNEYEDEMQVTKLPVNQNILKNAWYCSQOKTKEDWQEWIRRLSIQLLKESPSACL

RSCSSLVSVYYPLARELFNASFSSCWVELQTSYQEDLIQALCKALSSSENPPPIYQMLLN
LVEFMEHDDKPLPIPIHTLGKYAQKCHAFKALHYKEVEFLEPKNSTIEALISINNQLH
QTDSAIGILKHAQQHNELQKQWYKQKQWEDALAAAYNEKEAAGEDSVEVMMGKLRSY
ALGEWEELSKLASEKWTAKPEVKKAMAPLAAGAAWGLEQWDEIAQYTSVMKSQSPDKEF
YDAILCLHRNNFKKAIEVHIFNARDLLVTELSALVNESYNRAYNVVVRAQIIAELEEIIKY
KKLPQNSDKRLTMRWTRLLGCQKNIDVWQRILRVRSLVIKPKEDAQVRIKIFANLCKR
SGRMALAKKVLNTLLEETDDPDHPNTAKASPPVVAQLKYLWATGLQDEALKQLINFTSR
MAHDLGLDPNNMIAQSVPPQSKRVPRHVEDYTKLLARCFLKQGEWRVCLQPKWRLSNPDS
ILGSYLLATHFDNTWYKAWHNWALANFEVISMILTSVSKKKQEGSDASSVTDINEFDNGMI
GVNTFDAKEVHYSSNLIHRHVIPIAIKGFHHSISLSESSSLQDALRLLTLWFTFGGPIPEAT
QAMHEGFNLIQIGTWLEVLPLQISRIHQPNQIVSRSLLSLSDLGKAHPQALVYPLMVAI
KSELSRQKAALSIIKEMRIHSPVLVDQAEVLSHELIRMAVLWHEQWYEGLDASRQFFG
EHNTEKMFAALEPLYEMLKRGPETLREISFQNSFGRDLNDAYEWMNYKKSVDVSNLQA
WDIYYNVFRKIGKQLPQLQTLLELQHVSPKLLSAHDLELAVPGTRASGGKPIVKISKFEPV
FSVISSKQRPKFCIKGSDGKDYKYVLLKGHEDIRQDSLVMQLFGLVNTLLQNDACEFRRH
LDIQQYPAIPLSPKSGLLGWVNSDTFHVLIHREHREAKKIPLNIEHWVMLQMAPDYDNL
LLQKVEVFTYALNNTQDLYKVLWKLKRSSETWLERRTTYTRSLAVMSMTGYILGLGDR
HPSNMLDRITGKVIHIDFGDCFEAAILREKFPKVPFRLTRMLTYAMEVSGIEGFRIT
CENVMKVLRDNKGLMAILEAFADPLINWGFDLPTKKIEEETGIQLPVMNANELLSNGA
ITEEEVQRVENEHKNAIRNARAMLVLRITDKLTGNDIRRFNDLDVPEQVDKLIQQATSV
ENLCQHYIGWCPFW

2. 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
MEPGRGGTETVGKFEFSRKDLIGHGAFVAVFKGRHREKHDLEAVKCNKKNLAKSQTLGKEIKILKELKHENI
VALYDFQEMANSVYLVMEYCNGGDLADYLHAMRTLSEDTIRLFLQOQIAGAMRLLHSHKGIHHRDLKQPNIILLSNPA
GRRANPNSIRVKIADFGFARYLQSNMMAATLCGSPMYMAPEVIMSQHYDGKADLWSIGTIVYQCLTGKAPFQASS
PQDLRLFYEKNTLVPTIPRETSAPLRQLLLALLQRNHKDRMDFFEFFHHPFLDASPSVRKSPVPVPSYSSGS
GSSSSSSSTSHLASPPSLGEMQQLQKTLASPADTAGFLHSSRDSGGSKDSSCDTDDFVMVPAQFPDGLVAEAPSA
KPPPDSLMCSGSSLVASAGLESHGRTPSPSPCCSSSPSPSGRAGPFSSSRGASVPIPVPTQVQNYQRIERNLQS
PTQFQTPRSSAIRRSGSTSPGLFARASPSPPAAHAHGGVLRKMSLGGGRPYTPSPQVGTIPERPGWSGTPSPQG
AEMRGGRSRPRGSSAPEHSPRTSGLGCRLLHSAPNLSDLHVVRPKLPKPPTDPLGAVFSPPPQASPPQPSHGLQSCR
NLRGSPKLPDFLQRNPLPPIILGSPTKAVPSFDFPKTPSSQNLALLARQGVVMTPPRNRTLPLDLSEVGFHQPPL
GPGLRPGEDPKGPFGRSFTSRLTDLKAAFGTQAPDPGSTESLQEKPMIAPSAGFGGSLHPGARAGGTSSPS
PVVFTVGSPPSGSTPPQGPRTMFSAGPTGSASSARHLVPGPCSEAPAPELPAPGHGCSFADPITANLEGAVTF
EAPDLPEETLMEQEHEILRGLRFTLLFVQHVLEIAALKGSASEAAGGPEYQLQESVVADQISLLSREWGFAEQL
VLYLKVAEELLSSGLQSAIDQIRAGKLCSSSTVKQVVRRLNELYKASVVSCQGLSLRLQRFFLDKQRLLDRIHSIT
AERLIFSHAVQMVQSAALDEMFOHREGCVPRYHKALLLLEGLQHMLSDQADIENVTKCKLCIERRLSALLTGICA

>sp|P53104|ATG1_YEAST Serine/threonine-protein kinase ATG1 OS=Saccharomyces
cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATG1 PE=1 SV=1
MGDIKKNKDHTTSVNHNLASAGNYTAEKEIGKGSFATVYRGLTSDKSQHVAIKEVSRK
LKNKKLLENLEIEIAILKKIKHPHIVGLIDCERTSTDFYLIMEYCALGDLTFLLKRRKEL
MENHPLLRVTVFEEKYPPSPENHNLHRAFLVLSYLQQLASALKFLRSKNLVHRDIKPNLLL
STPLIGYHDSKSFHELGFVGIYNLPILKIADFGFARFLPNTSLAETLCGSPLYMAPEILN
YQKYNKADLWSVGTVFEMCCGTPPFRASNHLELFFKIKRANDVITFPSPYCNIEPELKE
LICSLTTFDPAQRIGFEEFFANKVVNEDLSSYELEDDLPELESKSKGIVESNMVSEYLS
KQPKSPNSNLAGHQSMADNPAELSDALKNSNILTAPAVKTDHTQAVDKKASNKYHNSLV
SDRSFEREYVVVEKKSVEVNSLADEVAQAGFNPNPIKHPTSTQNQNVLLNEQFSPNNQOY
FQNQGENPRLLRATSSSSGGSDGSRPRLVDRRLSISLNPNSNALSALGIASRLFGGA
NQOQQQQOQITSSPPYSQTLNLSQLFHELTENIILRIDHLQHPETLKLNTNIVSILESLA
AKAFVVYSYAEVKFSQIVPLSTTLKGMANFENRRSMDSNIAIAEEQSDDAEEDETLKKY
KEDCLSTKTFGKGRTLSATSQLSATFNKLPRESEMILLCNEAIVLYMKALSILSKSMQVTS
NWWYESQEKSCSLRVNVLVQWLREKFNECLEKADFLRLKINDLRFKHASEVAENQTLLEEK
GSSEEPVYLEKLLYDRALEISKMAAHMELKGENLYNCELAYATSLWMLLETSLDDDDFTNA
YGDYPFKTNHILKSNVEDKEKYHSVLDENDRIIRKYIDSIANRLKILRQKMNHQ

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

ATGGGAGACATTAATAAATAAAGATCACACAACCTCTGTGAACCATAATCTAATGGCAAGTGCAGGAAATTT
ACACCGCTGAGAAAGAAATCGGAAAGGGTTCGTTTGCCACTGTATATAGAGGGCATCTGACATCCGACAA
ATCTCAGCATGTAGCCATAAAGGAAGTATCAAGGGCGAAATTAATAAATAAAGAAATTAAGAAATTTG
GAAATAGAAATCGCTATCTTGAAGAAAATCAAGCATCCTCATATCGTCGGACTTATTGACTGTGAACGAA
CATCAACAGATTTTTTATTTGATCATGGAGTACTGTGCTCTTGGGGACCTAACATTTCTGTGAAAAGGCG
TAAAGAATTGATGGAGAATCATCCTCTACTAAGGACCGTATTTGAAAAATACCCCTCCACCGAGTGAGAAC
CATAACGGCCTGCATAGAGCGTTTTGTCTTGAGTTATTTACAGCAGTTAGCGTCCGCTTTGAAATTTTTGA
GGTCTAAAAACTTGGTTCATAGAGACATCAAGCCTCAAAACTTACTATTATCTACACCCCTAATTGGATA
TCATGATTCAAAAAGCTTCCATGAACCTTGGATTTGTTGGGATCTACAACCTTACCCATTTTTAAAGATAGCA
GATTTCCGGTTTTGCAAGATTTTTGCCAAACACGTCATTAGCAGAAAATCTTTGTGGCTCACCATTTATATA
TGGCACCAGAAATTTTGAATTATCAAAAAATATAACGCTAAAGCAGATCTGTGGTCTGTCCGGTACAGTGGT
ATTCGAAATGTGCTGTGGCACCCACCGTTTAGAGCTTCCAATCATTGGAGTTATCAAGAAAAATTTAAA
AGAGCAAACGATGTCATAACGTTTCCCTTCATATTGCAATATTGAACCAGAGTTAAAAGAGTTGATATGTA
GTTTTATTGACATTTGATCCAGCCCAAAGAATAGGATTTGAGGAGTTTTTGTCAACAAGGTAGTCAACGA
AGACTTGTCTTCTTATGAATTGGAAGATGATTTACCTGAGTTAGAATCCAAATCAAAAGGTATTGTAGAA
AGTAATATGTTTCGTTTCTGAGTATTTTCTTAAACAGCCAAAGAGTCCGAACAGTAATCTGCAGGTCAAT
AATCAATGGCAGATAATCCCGCGGAGCTCAGTGATGCCCTCAAGAACAGCAATATATTAAGTCCCGCAGC
CGTTAAAACAGACCATAACACAAGCCGTAGATAAAAAAGGCTTCAAATAATAAATACCATAATAGCCTAGTT
TCAGATAGAAGCTTTGAAAGAGAATATGTGGTGGTAGAGAAGAAATCGGTTGAAAGTTAATTCATTGGCAG
ACGAGGTTGCTCAAGCAGGATTCAATCCAAATCCTATTAAGCACCCAACTTCAACTCAAAATCAGAACGT
CTTATTGAATGAGCAATTTCTCTCCAAACAATCAACAGTATTTTCAAAATCAAGGAGAAAAATCCGAGGTTA
CTGAGGGCCACATCATCTTCCAGTGGAGGTAGTGATGGGTCTAGGCGACCATCTTTGGTGGATAGACGCT
TGTCTATATCCTCGCTGAATCCATCTAATGCATTATCAAGAGCCCTCGGTATTGCATCAACGAGATTGTT
TGGTGGTGCAATCAACAGCAGCAACAGCAACAAATCACATCTTCCCCACCGTACAGTCAAACCTTTGTTG
AATCCCAACTTTTTTTCATGAACCTTACTGAGAATATAATATTAAGAATAGATCACCTACAGCATCCAGAGA
CACTGAAATTAGATAATACTAATATCGTTAGTATTTTGAATCTCTGGCCGCAAAGGCATTTGTTGTTTA
CTCTTATGCAGAAGTGAAATTTTTCTCAAATTTGTTCCATTATCAACAACATTTAAAAGGCATGGCTAACTTT
GAGAACAGGCGCAGTATGGATAGTAATGCTATTGCAGAAGAACAAGACTCAGACGATGCAGAAGAAGAGG
ATGAAACGTTGAAAAAGTACAAGGAAGATTGCTTATCCACGAAAATTTTTGGAAAGGGTAGAACTTTATC
TGCCACATCTCAGTTGAGTGCAACTTTCAATAAACTACCACGTTTCGAAATGATCCTTCTATGTAATGAG
GCCATTGTCTTATATATGAAGGCATTATCCATTTTATCAAAATCTATGCAGGTAACGTCCAACCTGGTGGT
ATGAATCTCAAGAAAAATCATGTTCTCTAAGAGTTAAACGTGTTGGTACAGTGGCTAAGGGAAAAATTTAA
TGAATGTTTGAAAAAAGCTGATTTCTGAGATTTAAAATTAACGACTTGAGATTCAAGCATGCTTCTGAG
GTAGCTGAAAATCAAACCTTTGGAAGAAAAAGGTAGTTTCGGAAGAGCCAGTATATTTAGAAAAAGCTATTAT
ATGATCGTGCATTAGAAATATCTAAGATGGCCGCACATATGGAATTTAAAAGGAGAAAAATTTGTACAACCTG
TGAATTAGCTTATGCAACTTCACTTTGGATGTTAGAAAATTTCTCTGGACGATGATGATTTTACGAATGCC
TATGGTACTACCCTTTTTAAAATAACATACATCTAAAAAGTAACGACGTTGAAAGATAAAGAGAAATATC
ATAGTGTGTTGGATGAAAATGACAGAATAATCATAAGAAAGTATATTGATAGTATTGCAAAACAGGTTGAA
AATATTGAGGCAGAAGATGAACCACCAAAATTA

3. 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
MEVVGDYEYSKKDLIGHGAFVVFVKGRHRKRPNHVVAIKSITKKNLAKSQNLLSKEIKIL
KELSDLHHENVVALLDCKETTNNHVYLVMEYCNGGDLADYLQAKGTLSEDTIASFLRQIAA
AMQVMNGKGVHRDLKPNILLCHDGKPNTPSTEMRLKIADFGFARFLNDGVMAATLCS
PMYMAPEVIMSLQYCAKADLWSIGTIVFQCLTGKAPFQAQTPQQLKHFYEKHAELKPNIP
KDTSPELRDLKMLKRNADRIEFASPVVPPGRASQGCSSSPTPPRCVSASPLSGKAD
YSTPPSKVVQMVKQQEVAEAMQGSTHDEEFLKVDKGPTPRSNSPTEHDFVLVDPGMSDQS
DGS DKGRAPSTEDLQSLGERAQPQVVRVEPQVGSVAYKKDSGDVSSPSRPSLPMQSNQ
SEPIPVPTQVKAYERIRSSSSPLSSPRKCGTEPSPLDSAKLSSQNIKISPQPESKFSAPD
IGSFSPTVKFVSGTTPNVSTPWRRGSIGSSQGGAIYHPPSNASNSPSRRASMGSSPSGF
NRNFSPPGSLPTILDASPHFELNQEPQFTDNMPTVPVRAFPQGSKPKAIPESKGTKRYHP
SEVDRVKNLNMERCNTDPAAGGMSMLSQQMKVAYMNQQGLNLLLEGQVVRYTSENENLVSP
NDNTVQMDTQRSGLRRTMSATPPSNLMFAQSPPNMEGPVAFVAPGLAEETLMGDHNH
EIMAKLSFVNDLADCVMEELAMAKGAPLNTLSESVNWKQEGEPLHGDQMPKFIEAQRLLLEQ
LVLYVRSLLQLSSSLQLARREIKDERLQISNALKTLKQMNERYHRCVSVCKHIQORLGI
TMQNALTPQVVIATADKLIYNYAIEMCQTAALDELFGNPPQECFKRYNTAHILLHLSLQQA
RNSNDKQLLDKYKDAVERRLSHIQATQNYYPQFEIS

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

```
AGTCGCGCGGGAGCGGGTAGCGCGCGGAGGGCGTTGGGCGCCGCCGCGAGGCGGGGAAGCGGGGGCCG
CGGCGGTGCGGGTCTAGGGCGGGCCGTCGCCGTCGAGCAGCGCCCCGAGCGGGGAGGGCCGAGGAG
GCCCCGACGAGCTGGGGATGGAGAGTACCGGGCCCCCTCACTGCCTCAGAGCGCGTGTGCGGCTCTGGGCGC
GCACAGTGACGGTGACGGCACCCCTGGCCCCGGCAGCGCCGAGGCCGCTTCGCCAGACAGCCAGCGGCCG
CGGCAGGCCGGGCCATGAGCGGCAGGGGCCGGGCCGGCCCTCGCTGACCCTGGCTCCGCGCGGCAGCTTC
CCCAGTTTCCGCTCCGGTCTCTCGGCATGAGAGTCCGCCCGGGCCCCGGGGCTGCGGCTGCCCCAGACCCG
CCGCACGCTGGGCGCGCTCCGGGCCCGCGGAGCCGCGGTGCTGATACCTGCGCCGCACTGCGCCGCCCGCC
CGTCCGCTGTGTGCCCCGGGGGCGCGGCCATGGAGGTGGTGGGTGACTTCGAGTACAGCAAGAGGGATCT
CGTGGGACACGGGGCCTTCGCCGTTGGTCTTCCGGGGGCGGCACCCGCCAGAAAATGATTGGGAGGTAGCT
ATTAAAAGTATTAATAAAAAGAAGTGTCAAATACAAATACTGCTTGAAAAGGAAATTAATAATCTTAA
AGGAACTTCAGCATGAAAATATTGTAGCACTCTATGATGTTTTCAGGAATTACCCAATCTGTCTTTTGGT
GATGGAGTATTGCAATGGTGGAGACCTCGCAGATTATTTGCAAGCGAAAGGGACTCTCAGTGAAGACACG
ATCAGAGTGTCTTCATCAGATTGCTGCTGCCATGCGAATCCTGCACAGCAAAGGAATCATCCACAGAG
ATCTCAAACCACAGAACATCTTGCTGCTTATGCCAATCGCAGAAAATCAAGTGTGAGTGTGATTCGCAT
CAAAATAGCGGATTTTGGTTTTGCTCGTTACCTACATAGTAACATGATGGCTGCAACACTGTGTGGATCC
CCGATGTACATGGCTCCTGAGGTTATTATGTCTCAACATTATGATGCTAAGGCTGACTTGTGGAGCATAG
GAACAGTGATATAACCAATGCCTAGTTGGAAAACACCTTTTTCAGGCCAATAGTCTCAAGACTTAAGGAT
GTTTTATGAAAAAACAGGAGCTTAATGCCTAGTATTTCCAGAGAAACATCACCTTATTTGGCTAATCTC
CTTTTGGGTTTTGCTTCAGAGAAACCAAAAAGATAGAATGGACTTTGAAGCATTTTTTAGCCATCCTTTTC
TTGAGCAAGGTCCAGTAAAAAATCTTGCCAGTTCAGTGCCTATGTATTCTGGTCTGTCTCTGGAAG
CTCCTGTGGCAGCTCTCCATCTTGTGCTTTTTGCTTCTCCACCATCCCTTCCAGATATGCAGCATATTCAG
GAAGAAAATTTATCTTCCCCACCATTGGGTCTCCCAACTATCTACAAGTTTCCAAAGATTCTGCCAGTA
CTAGTAGCAAGAATCTTCTTGTGACACGGATGACTTTGTTTTGGTGCACACAACATCTCGTCAGACCA
CTCATGTGATATGCCAGTGGGGACTGCTGGCAGACGTGCTTCAAATGAATTCTTGGTGTGTGGAGGGCAG
TGTCAGCCTACTGTGTACCTCACAGCGAAACAGCACCAATTCAGTTCCTACTCAAATAAGGAATTTATC
AGCGCATAGAGCAGAATCTTACATCTACTGCCAGCTCAGGCACAAAATGTACATGGTTCTCCAAGATCTGC
AGTGGTACGAAGGTCCAACACCAGCCCCATGGGCTTCTCCGGCCGGGATCATGCTCCCCAGTACCAGCA
GACACAGCACAGACAGTTGGACGAAGGCTCTCCACTGGGTCTTCTAGGCCTTACTCACCTTCCCCTTTGG
TTGGTACCATTCTGAGCAATTCAGTCAGTGTCTGTGTTGGCATTCTCAGGGCCATGACTCCAGGAGTAG
AAACTCTCAGGTTCTCCAGTGCCACAAGCTCAGTCCCCACAGTCTCTTATCGGGTGTAGACTGCAG
AGCGCCCCACCCTCACTGACATCTATCAGAACAAGCAGAAGCTCAGAAAACAGCACTTGACCCCGTGT
GCCATCCCATACTGGGGCTGGGTACAGCTACTCGCCTCAGCCCAGTCCGGCTGGCAGCCTTGGAACTTC
TCCCACCAAGCACTTGGGGTCTCTCCACGGAGTTCTGACTGGTTCTTTAAAACCTCTTTGCCAACAAATC
ATTGGCTCTCCTACTAAGACCACAGCTCCTTTCAAATCCCTAAAACCTCAAGCATCTTCCAACCTGTTAG
CCTTGGTTACTCGTCATGGGCCTGCTGAAGAACAGTCGAAAGATGGGAATGAGCCACGGGAATGTGCCCA
TTGCCTCTTAGTGCAAGGAAGTGAGAGGCAGCGGGCCGAGCAGCAGAGCAAGGCAGTGTGTTGGCAGATCT
GTCAGTACCGGAAGTTATCAGATCAACAAGGAAAGACTCCTATATGTCGACATCAGGGCAGCACAGACA
GTTTAAATACAGAACGACCAATGGATATAGCTCCGGCAGGAGCCTGTGGTGGTGTCTGGCACCTCCTGC
AGGTACAGCAGCAAGTTCCAAGGCTGTCTCTTCACTGTAGGGTCTCCTCCACACAGTGCAGCAGCCCC
ACTTGTACCCACATGTTCTTTCGAACAAGAACAACCTCAGTGGGGCCCAGCAACTCCGGGGGCTCTCTTT
GTGCCATGAGTGGCCGCGTGTGCGTGGGGTCCCCGCCTGGCCCAGGCTTCGGCTCTTCCCCTCCAGGAGC
AGAGGCAGCTCCCAGCCTGAGATACGTGCCTTACGGTGCTTACCCCCCAGCCTAGAGGGGCTCATCACC
TTTGAAGCCCCTGAACTGCCGGAGGAGACGCTGATGGAGCGGGAACACACAGACACCTTACGCCATCTGA
ATGTGATGCTGATGTTCACTGAGTGTGTGCTGGACCTGACAGCCATGAGGGGAGGAAACCTGAGCTGTG
CACATCTGCTGTGTCTTGTACCAGATCCAGGAGAGTGTGGTGGTGGACCAGATCAGTCAGCTGAGCAAA
GACTGGGGGCGGGTGGAGCAGCTGGTGTGTACATGAAAGCAGCACAGCTGCTTGGGGCTTCTCTGCATC
TTGCCAAAGCCCAGATCAAGTCCGGGAAACTGAGCCCATCCACAGCTGTGAAACAAGTTGTCAAGAATCT
GAACGAACGATATAAATCTGCATCACCATGTGCAAGAAACTTACAGAAAAGCTGAATCGATCTTCTCT
GACAAACAGAGGTTTATTGATGAAATCAACAGTGTGACTGCAGAGAAACTCATCTATAATTGTGCTGTAG
AAATGGTTCAGTCTGCAGCCCTGGATGAGATGTTTTCAGCAGACCGAAGATATTGTTTATCGCTATCATAA
GGCAGCCCTTCTTTTGAAGGCCTAAGTAGGATTCTACAGGACCCTGCAGATATTGAAAATGTGCATAAAA
TATAAATGTAGTATTGAGAGAAGACTGTGCGCGCTCTGCCATAGCACCCGAACCGTGTGAGCAGCAGGCT
CATCCCGTGGACCGGTGGTGGGAACGTGAGGAAGAGGGGAAGGAAGGAAGAGCTTTTCCATTTGGTGTCTC
CAATGTCTCCTGCTGGACCCATCTGCCTAGTGGAAAGGCAGCAAAATTTCAAGAAACAGGTGAGGTTGAGC
AGCTTGGTGAACCCCATGGGGCCTGGAGTTGGAGCTCAACAGCAATGGATTTTCAGAGACCACCTGAAA
CTCCAGTAAAAAGACTTGGGAGACATGTTAATAAACTCAAGCATTTGATCGACCCA
```

4. 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
MSRPTSGRPSTAKSVAVIVPKLSGFVFTEKLGSGTYAVVYKAYRKSGSRQVVAIKCVLKS
SLNKASTENLLTEIELLKLKNHENIVRLEDFQWDDQYIYLIMEYCSGGDLNFIKSKRTL
PENILKRFLQQIAKAMRYLREFNIAHMDLKPQNILLTSEYNPTLKIADFGFSKHLFKGDE
LHAMRGSPLYMAPEIICKGTYSRVDLWSIGVIIYECLFGRAPFASRTFKELENKIWDSK
PVEAMILNLQIPYGVNVSENCRDILRLRRDPDERITFDEFFNHPFVDLEHCASNESLS
KAVNIVANAVKKDQNGEYKEAIKLYCDSLGHFMPAIHYEKDERKKEAIRAKVKDYMNRAE
ELKMLKPKRPPPPVNGVKRTISEDPMEEELTELCKDNEELTAAVTLIRAADTENSQEDYE
QALKHYELALSTFIKFLKEEKPGHRKDLIGKLSRSWMDEAEKIKMFLDVQNLQTEDTSAK
EEENEKKYLYTVREAVGDKTISER

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

GGAACCGCCCGCCCGCAGCGAGGAAGCGCCCGCGCGGGCGCAGGCGGCCGGAATGGCGGGGCCCCGGCTGGG
GTCCCCCGCGCCTGGACGGCTTCATCCTCACCGAGCGCCTGGGCAGCGGCACGTACGCCACGGTGTACAA
GGCCTACGCCAAGAAGGACACTCGTGAAGTGGTAGCCATAAAGTGTGTAGCCAAGAAAAGTCTGAACAAG
GCATCGGTGGAGAACCTCCTCACGGAGATTGAGATCCTCAAGGGCATTTCGACATCCCCACATTGTGCAGC
TGAAAGACTTTTCAGTGGGACAGTGACAATATCTACCTCATCATGGAGTTTTGCGCAGGGGGCGACCTGTC
TCGCTTCATCCATACCCGAGGATTCTGCCTGAGAAGGTGGCGCGTGTCTTCATGCAGCAATTAGCTAGC
GCCCTGCAATTCCTGCATGAACGGAATATCTCTCACCTGGATCTGAAGCCACAGAACATTTACTGAGCT
CCTTGGAGAAGCCCCACCTAAAACCTGGCAGACTTTGGTTTTCGCACACACATGTCCCCGTGGGATGAGAA
GCACGTGCTCCGTGGCTCCCCCTCTACATGGCCCCGAGATGGTGTGCCAGCGGCAGTATGACGCCCCG
GTGGACCTCTGGTCCATGGGGGTTCATCCTGTATGAAGCCCTCTTCGGGCAGCCCCCTTTGCCTCCAGGT
CGTTCTCGGAGCTGGAAGAGAAGATCCGTAGCAACCGGGTTCATCGAGCTCCCCCTTGCGGCCCCCTGCTCTC
CCGAGACTGCCGGGACCTACTGCAGCGGCTCCTGGAGCGGGACCCAGCCGTCGCATCTCCTTCCAGGAC
TTTTTTGCGCACCCCTGGGTGGACCTGGAGCACATGCCAGTGGGGAGAGTCTGGGGCGAGCAACCGCCC
TGGTGGTGCAGGCTGTGAAGAAAGACCAGGAGGGGGATTACAGCAGCTGCCTTATCACTTACTGCAAGGC
TCTGGACTTCTTTGTACCTGCCCTGCACTATGAAGTGGATGCCAGCGGAAGGAGGCAATTAAGGCAAAG
GTGGGGCAGTACGTGTCCCGGGCTGAGGAGCTCAAGGCCATCGTCTCCTCTTCCAATCAGGCCCTGCTGA
GGCAGGGGACCTCTGCCCGAGACCTGCTCAGAGAGATGGCCCCGGACAAGCCACGCCTCTAGCTGCCCT
GGAAGTGGCTTACGTGCCATGGCCAAGGAGGAGCCCGCGGGGAGCAGGATGCCCTGGACCTGTATC
CAGCACAGCCTGGGGGAGCTACTGCTGTTGCTGGCAGCGGAGCCCCCGGGCCGGAGCGGGAGCTGCTTC
ACACTGAGGTTTCAAGACCTCATGGCCCCGAGCTGAATACTTGAAGGAGCAGGTCAAGATGAGGGAATCTCG
CTGGGAAGCTGACACCCTGGACAAAGAGGGACTGTGCGGAATCTGTTTCGTAGCTCTTGCACCCTTCAGTGA
CCCTAGAAGAATGATTGGACAGATGTGAGCCATCTGGAGCAGAGGGGCACTAACCCAGGCTGACGCCAAG
AATGAAGTGGCCACTGCAGCCCTGGCGAGCAGGCTTCTTGGATGGACAGTGTGAGACCCCATATCCC
AGAGTCCCCAGCCTCCCTCAGGTTACTCTGCACCCACAGATGGTTTGGATGGCTGTGCTGTATACTGGAG
GGGAGGGCAGGACTCTGGGAGAACAGCACTTCTTTCATGAGACCTTTGTTACTCGGTGGTACTGGGTCC
TGTGCCTGTCCGTTTTGGGGCATGCAGCCCTCTATCATTTTTGGCTCCGAGAAGAGGGCAAGGGGCCCC
GCAGGGTACTTCTGTGCTTGCCTCGCCCTGCCAGCAGGCAGCTGTGCCCTGGCCTGCCCTTCCCGGA
CCCCTTATTCCAACCTCAGCTCCTCTTTGCACTGGAATGGGGCACTCCAACACCCCTCAGGGACCACCTC
CCCACAGTATGCACTCAGCCCCACAGAACCACAGTCTTTCTGGGAACCTCACACCTGCCCGCCATCTTG
GTACTTTAGGTTAATCCCTCAAGCATGAAAGCTGGATCTTTTGGGGTTAAGAAGCCCAAGCCTTGTTC
TGCCCTGGCCTAGGGAGCACTCAGGAGGGTTTCTTGGTCTCATCTCTCCACCTCCGTTCCCTCTGGGC
CCCACACTAGCCACAGCGCGGGCCTTGTGCTGGAGTTTGGACCTGGGACAGGGGAGAGGGAGGCTTGGAGA
CAGTCTGACCCAGTGCCTCTAGGCCACCCACTTCTAGGCCTGCCCTGCCCGCTGGAGCCCTGGGCAAG
CTCTTTCCCTTTCTGGGCCTGGGTCTCCCCATCTCTTCAATGGGGCTGATACCTTACAGCCCACAGCA
TGGGCACTTATGAGGACAAAGTGAATTTAACCTGGAAAAGAATGTATTTGAGAGTTCTTTTAAATAATC
AGCGGGTGTGGTGAATTTGTAGCCCTTCTGCCCTTAAATGCTTCTTGGGCAAGAGCTGTCTGTCTCC
TGCAGGAGGCTGAGTGAAAGAGTATCATTCATTGTTTTCTCTATTAAATTATTTCTCTA

5. 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
MENFVLYEELGRGDNIIYKGRRKGTINFVAIHCIKCRPEVTNTVRMTHDISHPNVVK
FYEWYETS NHLWLVLVVELCTGGSLATLITQDRNLPESSIRSFIDLVGTGIHYIHSGLILFC
DLRPTKILLDGSGLTKYADFGLSRVEGEILEELFEKADAGEMWSNEADLDDNPLSKKYK
TTGAPTYMSPPEGFQSQEITILSDLWSLGCVLYEMFTGHPPFLAESFQQLKEKILHKELPP
PKVKGSRFSSKPSDFHNLLEGLLQKDPDKRMGWPGLVNHSFWQGRLSHLAKDLVTSQEV
RSSIVNTRSSVLVEGTASALGRIKTVDLKKSMDRVPVSTLETETGTRPGSTMGDYMRPKTA

PGNEGGSTLFTLSTRPPTAVPPDEKLAPTQKPTQSPLSTREVRETI GTTGGESQADETKN
EAELELIYHHSDFHITPIVDNTKIQKPGA AKFD AKILPVPPFTA EKMANMSEKELSKHIKA
IIDGLSINEKGPSPQKRIHLLHLYLTGLSTNPQVATALTRNNVLSVLAKVVKETQHLDVKT
KAARVVGLIAGNAEDLDESVTI SE SIATL TEVI IRENVKNGKLGQVLPVAVGELLYFVAQQ
EVKHGKTC DNWSVT SMTYTVITRCCREGEDAVVNHIAAKTVENNVATQSTHAQKFVSNEM
GQSLWYIFKHSTVDSL RITALNALCRITHHNPTVFQSVIDTVGMTTILSALSFGITRIQQ
SIVTMFGALIASGQSLNRVVQDKDFLQKLIRLLDSPSVVIRAKAFVVIHEVVKNNDLLL
NSCQSRLVMIERDSRRQTPREGKAPENNGSESVEYLMQCLDLLINHMVDVVPRLFKIIV
TSLDAVMGRKHPNAVQAKQLRSSLPLIHVFLHLVTSQVFRPKIVNEEFIKNLSSVLSHIK
SIELGETNIEGASGISPSDFVTTTMSVLEGISQHPMIVAEYHQVILESVLP I IADLVVS
QNGETRALSLRFLSEIASVYLNQEYQAAGEKKNVAVGLHKI I TERLLPQFEQ ILLDQEPL
PSYGLKLLLTLLDQNGGFVKQFEQGLVSVIFQVMMDHQSNPLNSSMQSIAGILNCLVAH
KDTNMKDLYEQGLIDYFTTLFFDVTTACL DTEDHADNKIAHSMQLONLLD TLHSMFKYVSE
VVRKALQNKKAGGEGNREAEAEQ LLLTNKSLTDLTTILTQLL CFEDTDIQDFSTKCLS
LLVQLFGGENKDSMTPENMEYYSKALKKSDAKKQKVLRLRI IKRLLSTERVHVESMKQHGE
TLANTIRNLVQTASSHADVAISSLAADILKMTVPQEYYSKALKKADAKKQKVLRLRI IKRL
LSTERVHVESMKQHGETLANTIRNLVQTASSHADVAISSLAADILKMTDIVLPGMEAF TM
ADQNDIRVKNQDFVGCYMDQEPRTLNEKMTVSTTMTVDSCRKTCTDLKFKYYGVEYSAQC
FCGNQPLNVRKMRREGDCLKPCAGDRTQACGGSWRIAVYENPQNI PKFVGCYMDQQARTLN
EKMTVSTTMTVDSCRKTCTDLKFKYYGVEYSSQCFGNQLMNVKMRREGDCLKPCDGDRT
QACGGNWR IAVYENPLYI PKFVGCYVDQTYRTLGEKMTVSTTMTVDSCRKTCTDLKFKYY
GVEYSSQCFGCYDLIHAIKVSEEDCLRPCSGDRTQACGGSWRIAVYENPRYI SREYEEEN
NVEFVGC FVDQARTLNGKMTTSTTMTVYNCRKTCTDLKFMFYGVEVKKAGRKGGNQKAE
HMFPTKSLTDMTTILT SWELLFEECFCGNKLTITTKMRDGDCLKPCGTGDKTQACGGDWRI
AVYENPYITPPKFVGCYMDQQARTLNEKKTVSTTMTVDSCRKTCTDLKFKYYGVEVNICR
ICWLLHGSTS QNLERKDDCLYNNDSGQLPKNVYGVSEV

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

GTGGACCTGTCCTGAGGCAGAGGCCGAGATGCGCGCAACCGCGGGAGCAGCCAAGTGGACTGGACTCTTT
TCTTGACTTAGCTACCAGGAGCTAGAGATGCTGTTATTCTATTGTATGTGAGAAGTCGGCCCCAGAGATGG
AAAAC TTTATTCTGTATGAGGAGATCGGAAGAGGAAGCAAGACTGTTGTCTATAAAGGGCGACGGAAGGG
AACAAATCAATTTTGTAGCCATTCTTTGTACTGATAAGTGCAAAAGGCCTGAAATAACCAACTGGGTCCGT
CTCACCCGTGAAATAAAACACAAGAATATTGTAAC TTTTCATGAATGGTATGAAACAAGCAACCACCTCT
GGCTAGTGGTGGAACTCTGCACAGGTGGTTCCTTAAAAACAGTTATTGCTCAAGATGAAAACCTCCCAGA
AGATGTTGTGAGAGAATTTGGAATTGACCTGATTAGTGGATTACATCATCTTCATAAACTGGCATTCTC
TTTTGTGACATTTCTCCTAGGAAGATACTCTTGGAAAGGGCCTGGCACACTGAAGTTTAGCAACTTTTGCT
TGGCAAAAGTGGAAAGGTGAAAATTTGGAAGAGTTCTTTGCTTTGGTGGCAGCAGAGGAAGGAGGAGTGA
TAATGGGGAAAATGTCCTGAAGAAAAGCATGAAAAGTAGAGTCAAAGGATCTCCTGTATATACAGCACCA
GAAGTTGTGAGGGGTGCTGACTTTTCCATCTCCAGTGACCTCTGGTCTTTGGGCTGTCTGCTTTATGAAA
TGTTTTTCAGGAAAACCTCCATTCTTCTCAGAAAAGTATTT CAGAATTA ACTGAAAAGATCTTATGTGAAGA
TCCTTTGCCACCTATTCCGAAAGATTCTTCTCGTCTAAAGCTTCTT CAGATTTTATTAATTTGCTTGAT
GGGTTACTTCAAAGAGATCTCAGAAAAGATTGACTTGGACAAGGCTACTGCAGCATTCATTTTGGAAGA
AAGCTTTTGTGAGCAGATCAGGAATCAAGCGTCAAGATCTCAGTCTCAGCAGAAAACACTATGGAGTG
TTCTGGGCCACAAGATTCCAAGGAGCTTTTGCAGA ACTCTCAGAGTAGACAAGCAAAAGGGCACAAGAGT
GGTCAACCACTAGGTCACTCTTTCAGACTAGAAAATCCA ACTGAGTTTCGGCCTAAGAGTACTCTTGAGG
GTCAATTGAATGAATCCATGTTTCTTCTCAGTTCTCGTCTACTCCCAGAACTAGCACTGCAGTGGAAAGT
AAGTCTGGTGAGGATATGACTCACTGTTTACCACAGAAGACTTCTCCTCTGACCAAGATTACAAGTGGA
CACCTGAGTCAGCAGGACCTGGAATCCCAGATGAGAGAGCTTATCTACACGGACTCAGATCTTGTGTGCA
CCCCATTATCGACAATCCAAAGATAATGAAAACAGCCACCAGTTAAATTTGATGCAAAAATATTGCATCT
ACCAACATATT CAGTGGATAAGTTATTTCTGAAAGATCAAGATTGGAATGACTTTTTCACAACAAGTG
TGCTCGCAGATCGACTCCACTGAGAAGAGCATGGGGGCTCCCGAGCCAAGCTGAATCTCCTTTGCTATT
TGTGCGTGGTGGCTGGTCAACAGGAGGTGGCCACCAGGCTCCTCCATTCCCCCTGTTCCAATTGCTAAT
CCAGCATTTGCGGATAGCTCCA AACTGGGATATACGGGGCCAAGGTTGCTCACGTAATGGTTACTGGCT
TCGCACACAGCTGAGCTCCAGGAAAATACACCTGTTGTTGAGGCAATTGTTCTCTTA ACTGAATTAATTA
GGGAAA ACTT CAGGAACAGCAAATTA AAAACAGTGCCTTTTACCAACCTTGGGGAGCTGATCTATCTTGT
AGCCACCAGGAAGAAAAAAGAAACCTTAGAGAGTGCTGGGCTGTTCCCTTGGCTGCATACACAGTG
CTAATGAGGTGCCTTCGGGAAGGGGAAGAGCGTGTGTGAATCACATGGCAGCAAAAATATTGAAAATG
TCTGTACCACCTTTTCTGCTCAGTCCCAGGGCTTTATTACAGGAGAAAATAGGACCCATTTTGTGGTACCT
ATTCAGACACTCCACTGCTGATTCTCTTAGGATAACAGCAGTATCGGCCTTGTGTAGAATCACTCGCCAT
TCTCCTACTGCCTTCCAGAATGTTATTGAAAAGGTGGGACTGAACTCAGTAATAAACTCCCTGGCCTCTG
CCATCTGCAAAGTTCAGCAGTACATGTTGACCTTATTTCGCTGCCATGTTGTCTGTGGGATTCATCTTCA

AAGACTAATCCAAGAAAAGGGTTTTGTCTCCACAATTATCCGTTTACTTGACAGCCCTCAACATGCATT
AGAGCAAAAGCCTTCCTGGTTCTTCTATATATTTTTGATTTATAACCGTGAGATGTTGCTGCTCAGTTGCC
AAGCAAGACTGGTGATGTACATCGAGAGAGACAGCAGAAAGACCACTCCAGGCAAGGAGCAGCAAAAGTGG
CAATGAATACCTGTCCAAATGCCTGGATCTTCTCATCTGTACATTGTGCAGGAGCTGCCACGAATCCTG
GGTGACATTCTTAACTCCTTGGCTAATGTTTCTGGACGTAAACACCCATCAACAGTTCAAGTGAACACAGC
TGAAGTTGTGTCTCCCCCTGATGCCTGTAGTGCTTACCTCGTAACTTACAGGTATTTGACCTCAAGT
TGTGACAGAAGAGTTTTCTTTTTCAGCTATGGAAGTATTCTTAGTCATATTAATCTGTAGACTCAGGAGAA
ACGAACATAGATGGAGCCATAGGACTGACAGCATCAGAAGAATTTATCAAGATCACATTGTCAGCTTTTG
AAGCAATAATACAGTATCCTATTTTTATTGAAAGACTATCGCTCCACGGTTGTTGACTATATACTGCCACC
CTTGGTGTCTTGGTTCAAAGCCAAAATGTGGAGTGGAGACTCTTTAGCTTGGCGTTGCTCTCAGAAAACC
ACATCTCTACTCGTGAACCAGGAGTTTGGGGATGGCAAGGAGAAGGCCAGTGTGATTCTGACAGCAATC
TTCTGGCTCTCATTGAGATGTCTTACTTCCCCAGTATGAGCACATTCTTTTAGAACCTGACCCAGTACC
AGCATATGCTCTGAAACTGCTAGTCGCGATGACTGAACACAACCCAACTTTCACAAGACTTGTGGAAGAA
AGCAAAGTATCCCACTCATTCTTGAAGTAACTCTGGAACATCAGGAGAGCATTCTGGGTAATACCATGC
AAAGTGTGATTGCATTACTCAGCAATCTAGTTGCCTGCAAAGATTGCAATATGGAAGTACTTTATGAACA
AGGACTTGTGAGTACATCTGTAACCTGCTCAGTAACTGCCACACTGTGCTTGGATGGACAATAAA
AACAACAATGAGATGGCAGCTCCACTGCTCTTTTCCCTGCTTGTATTTTTGCACAGCATGCTGACCTATA
CCTCCGGTATTGTACGGCTGGCTTTGCAGGCCAGAAAGTCTGGCTCAGGAGAGGACCTCAGGCTGCAGA
AGACCTGCTGCTGCTCAACAGACCTCTGACAGACCTGATTAGCCTGCTCATTCCACTGCTTCCCTAATGAA
GATCCTGAGATTTTTGATGTTTTCATCCAAGTGCCTGTCTATACTGGTTCAGCTGTATGGAGGGGAAAACC
CGGACAGCCTCTCTCTGAAAATGTGGAAATTTTTGCTCATTTACTGACATCCAAGGAGGACCCAAAAGGA
GCAGAAGCTTCTGTTAAGGATTCTCAGAAGAATGATCACCTCCAATGAGAAGCACTTGAGAGCCTCAAG
AATGCAGGCAGCCTCCTGCGGGCTCTGGAGCGGCTGGCCCCCTGGGAGTGGTTCATTTGCCGACAGTGGG
TGGCTCCCTTGGCCCTGGAAATCCTCCAAGCCGTTGGGCACTAGGCAAGAAGGTGCTTAGCACAAAGCCCG
CCCTGTGGCCCCAGCCCTCGGATGCATAAGCAAGGTGAGCTCCAGACACCTTTGCCACATCCCCTCACA
GCTGTCTTTGGACCTAATAAAGTCAGCTTAACCCAGAACCTGGTGGCCCAAGTGTCTACTAACCCAGGG
CCTAGAAAAGTACTCAGAATGGACTTCCCTTGGTTTCTGTGGAATGCATCTGGGAAGCCCAGGTTTTGTTA
GCTGTTCTCAGAAATGTTCTTTCCCTCTCTGTGTGGGCCAGGTGGGCTAAGGTTAGCACTGCCTGTGGTA
ATAAAGCAGTGGATGCAAAGCACA

6. ATG13 (autophagy related 13)

>tr|K1QIF8|K1QIF8_CRAGI Autophagy-related protein 13 OS=Crassostrea gigas
OX=29159 GN=CGI_10016010 PE=3 SV=1
MSKLSQQDRKDLKFTKFLIYKSLQIIVQSRLGEKIQAQSKPFFSSGADWFNLAIKDIVEV
HNETKKALVSQTALLSQNVCEISLKTSEGDSMVLETWYIGLNKETCDVNARISYTVYNR
MGIALKTLFSISRVTTPAYKLSRQGANADEYVICYRFYQGDPPFFMLGDNYQTIKVGSV
TPVGTIYINLAYRKLITPQKSKAIPIEVKDDHFKKDNSPRRPTTPKPCSLGFRNST
SEDLFGDGVGDQDLCTTFDNPGEAFLGTMQHGLVPPNIQQKTALKTDNRENNEAPKK
QENVEKQLSFTSYQKVGAFQNRNSKEINNTDLEDVPPFLNLLQAEGKSEVKMTVQRELQN
DIESNEQVSSNKSEEEKSLEQALSPSESISNTSAPDDFVMVELKTPFAGADPNQDLGKF
YRECQGAPQLTMCSETNVTEALAEISSQIQMFESNIEGFDDFVTSITESVTVE

>NM_001346354.1 Homo sapiens autophagy related 13 (ATG13), transcript
variant 45, mRNA
ACTGCCGCTGCGCGGCTACCTGCGGTTTCTCTCCGCACATTCCACACGCGGCCCAAACGGTCTCTCTCT
CTCTCTCTCAAACACCGCCTTTCCGTCTTTGTTTTATCTTGTAGTAGCTTAGAAAAGATTGGAGAAGAAAAGC
TTACGTGGAATGAAAATCAACTTTTATGGATATTTTTGAGGACTAAAAGAATAAATAGGGCGTCCGTACTG
TAGCGAAAGTGCAGCTAAGGTTAGGCATCTGGATTTCCCCCGTAGCCCTCTTTCACCCCCCCCCCGGC
CATTACCGAAGCGGATGAAAACAAACTAACGATGGCGGCGCCGGAAGCGACCGGCTGCTGGGCTTAA
GGCGGGAGTGACCGCTTAACCAGTGAGGGAAGCACTGAAGAGCGCCAGTCGACGTGGGTGCGACAACCTCG
CGGAGTCTTAGGAGCAAACGTCTGGGGCTGCGAGCCAGGACCCTTCTGAAGCCTTAGGTGTCTATCGG
CGACGTGTACGGTCACTGCAGCTCCGGAGCGCGGAACCCCTCAGCCAGGAGGCGCGGCTGGTCCGTCCAG
GTCCCGGCTCCGTAATGAGAGCCCGGAACCACTCTTGTGCGCGAGCTTCGCAGATTCTATAGGCAAT
GGAAACTGATCTCAATCCCAGGACAGAAAGGACCTGGACAAGTTTATTAAATTTTTTGCCTCAAGACT
GTCCAAGTGATTGTCCAGGCTCGGCTTGGTGAAGATTTGCACTCGTTTCATCATCTTCTCCAACGGGTT
CAGATTGGTTCAACTTAGCAATCAAAGACATCCCAGAGGTTACACATGAAGCAAAGAAGGCACTGGCAGG
ACAGCTGCCTGCAGTCGGGAGGTCCATGTGTGTGGAGATTTCACTTAAGACTTCTGAGGGAGATTCCATG
GAGCTGGAAATATGGTGTCTTGAATGAATGAAAAGTGTGATAAAGAAATCAAAGTTTCTACACGGTGT
ACAACAGACTGTCATTGCTGCTGAAGTCCCTTCTGTCTATAACTAGGGTGACACCAGCCTATAGGCTCTC
CAGGAAACAAGGGCATGAATATGTCATATTATACAGGATATATTTTTGGAGAAGTTCAGCTGAGTGGCTTA
GGAGAAGGCTTCCAGACAGTTCTGTGTTGGGACAGTGGGCACCCCTGTGGGCACCATCACTCTTCTTGTG

CTTACAGAATTAACCTTGGCATTTCATGTCTACCAGGCAATTTGAGAGGACCCACCTATCATGGGGATTAT
TATTGATCACTTTGTGGACCGTCCCTATCCCAGCTCCTCTCCCATGCACCCCTGCAATTACAGAAGTGT
GGTGAGGACACTGGAGTAATATACCCGTCTGTAGAAGACTCTCAAGAAGTGTGTACCACCTCTTTTTCCA
CCTCCCCACCATCCCAGCTGATGGTTCTGGGAAGGAAGGTGGGGTACCCCTTGCTCCCAACCAGCCTGT
CCATGGTACCCAGGCTGACCAGGAGAGACTGGCAACCTGCACCCCTTCTGACAGAACCCTGTGTGCC
ACACCCTCCAGTAGTGAGGATACTGAAACCGTATCAAACAGCAGTGAGGGACGGGCCTCCCTCACGATG
TCTTGGAGACCATCTTTGTCCGAAAAGTGGGGGCTTTTGTCAACAAACCCATTAACCAGGTGACCCCTGAC
GAGTTTGGATATACCCCTTTGCCATGTTTGTCTCCCAAGAATTTGGAGCTGGAGGATACCGATCCAATGGTG
AATCCTCCAGATTCCCCAGAGACTGAATCTCCTCTCCAGGGCAGCCTGCACCTCAGATGGCTCCAGCGGGG
GCAGCAGTGGCAATACCCATGATGACTTTGTTATGATAGACTTTAAACCAGCTTTTTCTAAAAGATGACAT
TCTTCCGATGGACCTGGGGACCTTCTATCGGGAGTTTTCAGAACCACCTCAGCTGAGCAGCCTCTCCATA
GATATTGGAGCACAGTCCATGGCTGAAGACTTGGACTCATTACCAGAGAAGCTGGCTGTGCATGAGAAGA
ATGTCGCGAGTTTGTATGCCTTTGTGGAAACCCTGCAGTAAAAGTATCCTTGAGTCCAGCAGCACCCCT
TTTTTGTGGCCCCAGGGCATAAGCAGCCTCCCATGCATCAGCTGCTCCACCCCTCATCTGTCTGTGAGC
CAGGTGGAAGGAGGCTGGCTTCTCCCATGGGGACCCAGAAGTCCCTACTCTTGGACCTCTGGAGACTC
CGTGGCGGAGTCAAGCCAGTGGCCAGTTGGAGAAGACTCACGTGCTGGCCTTGGAGATGGGAAGAACC
TTCGTACGAAAAGCCCTCAGCAGGGCCATCTGTGTGCCCTGCCCATCACCACCTGCTTCCCAAGGGTGT
CATCCTGTTTCTCTGTGCTGCCGGCCTCCTGCCTGGGCCTGCCTTGCAGCTGGCCCCCTTCCCTGCCTGTG
TCACCATCCACTGTTTGCATTTCCAGCTGGTGGCCAAGAGATTGGTGTGGAGGCAGAAAAGAGGAAGGAGA
CAGTGCCAGGAGGAAGAAGGAAGGAGTCCCTTAGCTCTCTTATTGTTCCCTTTACTTCTGTCTATCTTC
TTCTCCTCTTCTCTCTCTTGCCTCTATGCCTGTATTTCTGGCAATATGACAGGCCTGCCTACCCAAG
ATCAGAACTCCAAAACCCTCCACCCCTGAAGGTCGGGAGGGTCTGAGCAGCCCTGGTGGCTGCCTGTG
CTCAGGTCTCAGCTCCATGGGAAATAAAAATGGCACCCCTGAATCTCTAGGATTTTGTCACTTGGAGTCA
CAGCAAAGTTCTTCTTCTTCTTGTCCCCCGTTGCTGCTCCTTGGTTATAGAACATGGTAAATATTTATTA
CTTTCAGAGAAACCAGATATTTTATAGAGGAAATATGTTTGGAGTGTGTTTTCCTTGGAGAAAGGC
GGAGGGCTCTTCTGGGACGGAGACCTCCTCCTCCGGAGGTTATTGAGAATCCGGGGCTGCTGCTTTGAGG
ATCTTCCCACCATAACAGACAGCGAGATCCAAGAAGAGGGCTGGCCGGGGGCAAAGTCACCTCCCAGTGTG
GCTGCACCTGGAAGTACTAAAGGCTTTACCTTGGATAGTTGCGTATTCCTGGTGAGAGCCTTACATCTCC
CACAGTTTCTGCAGAGTACTGACTCCATTCTGGCAGCCCAGGAAGTCTGGGTGCTAAATGTGATGGCC
ACATGTAGTGGTTAGGGGATGTTGTGTGTGTCCCCAACTGCCTGGGTACTTGTTCCTGATCCCTGGGGC
TGTCTGTGGAGCTTTTCTCCTGCTTGGGCCTAGCTACCATCTCCCTCTAATCCCAGGTTCTCTACACT
GCCCTGGGGTTTACCAGCTGGATTGGCTTCTGGTTGAGAAATCAAAGCTGGGCATGATGACTTAACC
CTTTCAGGTATTGTTACTTGAATAAGTCAAGTCCAGTCCAGCTACCCACCTATGATCTGCTTCCCAGCC
TCGCTGGTAGTCTGGTCAAGGAGATCTAGGTCTACTCCATTCTCCTGGCCACCTGGGGCATTCACTG
GCAGCAGCTGTGCTTCAAGTGGAGCAGGTGGTTCTCAGCTGCTTGTAGTATACTGCATGTGACACTGTTT
CCACATAAAGGCTGACTTCTGAGGATTGGAGCAGGCTCTGGCGGGGACCAGAGCTCTGCGTGTGCTGC
TGCCACCAAGAAGTGTAGCAGAAGCAGTAGCAGCCAACTGGCCCTCCTGACTTTGGCCAGAGCACATG
CGTGGCTTGTGAACCCAGGCTCAGGTTTATCCCCAAGGCCCCAGCTTTGAGAAGGGGGAAGGCCCTGG
TAAGTTATTGATGCCCCATATTTTCCAGCTACTGCTCTCTTTCCAAGGCCTTGCATGGAAAGGCCTAGCCA
TTGTCTGAGGCAGCAATCTTTGGCATCTACAGGTGGCAGCAGCCTTTCACCAGGGCTCCATCTGTGAAGA
GTCTCAGCCATGACTTTGAGCTGAGCTTGGGAGAAGTAAAGCAACTGTTAAGGCCAGCCCTTGGCCCTCA
GACCTGCCATGAAAGGAATGAGCCCTAGACTGACTCCTGCAGCACCCCGGGACAGGCTGGGACCAGCTG
TTTGTCTCCAGGTGTGAGAGTCCCTCCTCCTCCTCCAACCTCTCCAACCTACTTTGTTTGGAAATACCGA
GCTACACTTCAAATGTATTTCAAGGGATTTCCAATAAATTTTTTTTCTGTACTTTACAGCCTCCTGTCTG
TAGGTTGTCTGAAGACCTCGTAACCCCTTCCCCACCCCTGCCCCAGTGCAGGTCTGGGAAAGGGGAGAGT
GGTGCCTTGTGAAGCGCAGAAAGACCTCAAGTGTCTGGGCAAGCCTGTTTTGAGTCCGGTGTGGCCTCTT
AGGGGCTGTATACCCTGGGGTTTCTGGGTGAGGAACTTCTTAGTATTTCTCTTCCCTGGTCCCCTAT
CAGGGGCTTGAATTTGAATATTCAGTTGGAGAATGCATTTAAAATACACCCATAGTAAAATCTCCATAAA
ATGCAGGCCACCGTTATCAGCTCTTTATTGCTCTTACATAACAACCTCACCCCTGGAGGGAAAAACAACAGT
GCAAGGCAGGGAGTGCAGGCTCCCCAAGCCATCTGGGGGATTTGTGGCTGAGCAAGCAGAAGAGAGTA
GCAGGAAGTTAAAGGTCCATGCAAGTTTGTAGCTGCCTTGATCTGACTGGCGGTGCTTGAGCAGCCAGG
AAGAGTAGAAGAGCCCCGGGGTATGCGTCTGTCTGGCTCCTGGGGCCTGGGGCTGCAGGCCTCTCAACC
CGGCCAGGGCCAGCCCCGCTCCTAATTCTCCTAGTTTGTGACCATAGTTAGGGGAGGGAGCTGATTGGT
GGAGACAACATCCCGGAGGTAGGGATGGTTCTAGAGGCAAAAGAGAAGTACAGAACTGGACAGCTGCTG
TCTGGGTTGCTTCCCCACCCGCTTCCAGGCTGAAGCTAGGCCAGGATTTAAAAGGGCTGGTTAGAAAAGT
CCAAATCCAGCCTATTCTGGAGCCAGGAGCTCCTGATTATTAGTAAACCAGGTGACACTGATCATGTGG
CCAGCCAGGACAGTTGCCCAATACCTGAGTCAGAAGTACGAAAAGGCTGTTCTGGTGTTCCTTCAA
TCAGGAACCCCAATAACAAAGTTTTTTCAGTTGCCCATGCCAGCAATGGTGTCTACCTCTTTAAAGCA
TCTCCCTACACTCTACCCCTGGAGGCCATCGTTGTTAAGGCCTTGGTAAATTGGCATTGTGAGTCACTCAG
CAGAGGCCCTGCCAGGAGCCCAACCCAAGTAAACAGTTTCTCGCTCCTGTTTCCCTGGGTCACTGCCCTC
TCTATTCCAGCCACTCAGCTCTAGCTGAGCAGATCCAGAGAGAGAGGAGGCCCCAGTGCCTGGAGGAAG
GCCACCATTTGTGGAATGGGACTTGTCTTGGGGCTGAGGCCCAATGTTTGTAAATCACCATCTGTAAACA
CAGCCTGATCCTGCAGCTCTGGCCCTGCTCCCCAGCCCGACAAGCAAGGAGGAGAAAAACCAGGCCCA

ACTGGGGCCGCTATAGCCTCCTGATTGCCATTAGCAAGCAAGCAGACACCTGGAACCTGACCACTAT
GGGAGGTGAAATTCTGGCCTACCTTCTCACCAACAAACCTGTCAAAAAAAAAATGCGGTAAATAATCATCT
TAACTTTTAAAGCAA

>sp|Q06628|ATG13_YEAST Autophagy-related protein 13 OS=Saccharomyces
cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATG13 PE=1 SV=1
MVAEEDIEKQVLQLIDSFLLKTTLLICSTESSRYQSSTENIFLFDLDFEDHSELVSELP
EIISKWSHYDGRKELPPLVVETYLDRQLNSSLVRLKDHEGHLWNVCKGKQEIWMER
WLIELDSSPTFKSYSEDETVDNELSKQLVLLFRYLLTLIQLLPTTELYQLLIKSYNGPQ
NEGSSNPITSTGPLVSIKTCVLDGSKPILSKGRIGLSKPIINTYSNALNESNLPAHLDQK
KITPVWTKFGLLRVSVSYRRDWKFEINNTNDELFSARHASVSHNSQGPQNQPEQEGQSDQ
DIGKRQPQFQQQQPQQQQQQQQQQRQHQVQTQQQRQIPDRRSLSLSPCTRANSFEPQS
WQKKVYPISRPVQPFKVGSIQSASRNPSNSSFFNQPPVHRPSMSSNYGPMNIEGTSV
GSTSKYSSSFNIRRHSSVKTTENAELKSKAVKSPLOPQESQEDLMDLVKLLLEKPDLT
KKTSGNNPPNINISDSLIRYQNLKPSNDLLEDLSVLSMDPNHTYHRGRSDSHSPLPSI
SPSMHYGSLNSRMSQGANASHLIARGGNSSTSALNSRRNSLDKSSNKQGMGLPPIFGG
ESTSYHHDNKIQKYNQLGVEEDDDENDRLNMQMNSATKFKSSISPRSIDSISSSFIKS
RIPIRQPYHYSQPTTAPFQAQAKFHKPANKLIDNGNRSNSNNNNHNGNDAVGMHNDEDD
QDDDLVFFMSDMNLSKEG

7. RB1CC1 (RB1 inducible coiled-coil 1)

>tr|K1QSI9|K1QSI9_CRAGI RB1-inducible coiled-coil protein 1 OS=Crassostrea
gigas OX=29159 GN=CGI_10019938 PE=4 SV=1
MELKLMsklTVSQALIELKRKHEKEISEMISKLEKEKSDSLTAIHNSLQAEKQVAFNEA
VTKLSQDKDKVIEDLRakeKDLLEQLSTDQETILKLNEEKSKLEDIKTRAMSHLSDKERE
YNAARRQLLEDDLALTRQQLSQYQSQLQAMSTISVPSVMEISQIEDSSRIASLEDELKSKS
EKIAELQQKMMIEISMTTSTRHIAEDKVSITSCNVGDALFLCLDDRHDQYVVFTIGSTLHF
LHTDCQDRTLGLKPNPGETKKSUWVLAIEITEKEYCQAKKPQNRFKVPVGTQFYRVKAKPWRP
ESGARGTSSTAST

>XM_017014112.2 PREDICTED: Homo sapiens RB1 inducible coiled-coil 1
(RB1CC1), transcript variant X17, mRNA
ATGCGCCGCGGAGGAAGAGACGGAGTCGACAATAACAAACCAAGCCGCGGGTGTCCGCGGCCCTGCCG
AGCCCTCGGCCTTGCCCTCAGAATCCCCAGTCGCCTGGGCCCTCGGCTCTGACAGGCCGCGGCCTTCTG
TCCCCCGGCCCCAGACCCAGAGCCGAGGGGCTGCTCGCGTCTTGTCCGCCCCGACCCCTCCCTGCCCTC
CTAGAGTTCGGGGCCGCGCGGGCGGGCGCCCGGGACGCCGCGGTTGTGTCCGCTTAGCGGTGCCGAAT
GGGCGGTTGGTAACCGCTGCCGAGGACTAGGCGGGCGGGCGGAAGATGGTGCCTGGGGGTCGCTGGCTCTGCT
GCTGCCGCGGGCAAGGAGGAGGCGTTGCCGGTTTTCTGAGTTTAAACCAGTAATGCCATTCAGTTGCCAA
TCTCAAGCAAAGCAAACATAAGCCAGTTTTAATCTACTTTTTAAGAAAAGTGGTAGTCCTTTTACAGTG
CCTGACGTAACGTATCAGAGGGTGAGGTATAAGCTCACAGAATTCAGATAAATCATCATGAAGTTATAT
GTATTTCTGGTTAACTGGAACACTCTAACATTTGACACTGAACTTACAGTGCAAATGTGGCAGACC
TTAAGCATGCCATTCAAAGCAAATACAAGATTGCTATTCAACACCAGGTGCTGGTGGTCAATGGAGGAGA
ATGCATGGCTGCAGATCGAAGAGTGTGTACCTACAGTGTGGACGGATACAAATCCAATTTTCTTTTT
AACAAAGAAATGACTCTTATGTGATCGTCCACCTGCTATTCTCTAAAACACTACCTTTTCGACAGAAAATGACA
TGGAATAAAAAGTTGAAGAATCTCTTATGATGCCTGCAGTTTTTTCATACTGTTGCTTCAAGGACACAGCT
TGCATTGGAATGTATGAAGTTGCCAAGAACTTTGTTCTTTTTTGTGAAGGTCTTGTACATGATGAACAT
CTTCAACACCAAGGCTGGGCTGCAATCATGGCCAACCTGGAGGACTGTTCAAATTCATAACAAAAGCTAC
TTTTCAAGTTTGAAAGTATTTATTCAAATTATCTGCAGTCCATAGAAGACATCAAGTTAAAACCTTACTCA
TTTAGGAACTGCAGTTTCAGTAATGGCCAAGATTCCACTGTTGGAGTGCCTAACCCAGACATAGTTACAGA
GAATGTTTGGGAAGACTGGATTCTTTACCTGAACATGAAGACTCAGAAAAAGCTGAGATGAAAAGATCCA
CTGAACTGGTCTCTCTCCTGATATGCCTAGAACAATAACGAATCTTTGTTAACCTCATTTCCTCAAGTC
AGTGGAAACATGTGTCCCAGATACCGCAGATGCTGAAAGTGGCAAAGAAATTAGGGAATCTTGTCAAAGT
ACTGTTTCATCAGCAAGATGAAACTACGATTGACACTAAAGATGGTGTCTGCCCTTTTTTAATGTCTCTT
TGTTAGACTGGATAAATGTTCAAGATAGACCTAATGATGTGGAATCTTTGGTCAGGAAGTCTTTGATTC
TATGAGCAGGCTTGATCCAAGGATTATTCGACCATTTATAGCAGAATGCCGTCAAACCTATTGCCAACTT
GATAATCAGAATATGAAAGCCATTAAAGGACTTGAAGATCGGCTCTACGCCCTGGACCAGATGATTGCTA
GCTGTGGCCGACTGGTGAATGAACAGAAAGAGCTTGCTCAGGGATTTTTAGCTAATCAGAAGAGAGCTGA
AACTTAAAGGATGCATCTGTATTACCTGATTTATGCCTGAGTCACGCAAATCAGTTGATGATTATGTTG
CAAATCATAGAAAACCTGTTAGATATTAAGCAGAAGTGTACCACTGCCAAACAAGAACTAGCAAATAACC
TACATGTCAGACTGAAGTGGTGTGCTTTGTAATGCTTCATGCTGATCAAGATGGAGAGAAGTTACAAGC
TTTGCTCCGCCTCGTAATAGAGCTGTTAGAAAGAGTCAAATTTGTTGAAGCTCTTAGTACAGTTCTCAG

ATGTACTGCTTAGCTGTTGTTGAGGTTGTAAGAAGAAAAATGTTTCATAAAAACTACAGGGAGTGGGCTG
GTGCTTTAGTCAAAGATGGAAAGAGATTATATGAAGCAGAAAAATCAAAAAGGGAATCCTTTGGGAAAT
ATTTAACTCAAAGCCTCGAAAGTTTACTGTGAACCTCCAGATATTTTATTAAAAAGATTTACAGTTTCT
GCAATCATTTTGTCTTTCGGAAGTTTCCAGCATTCCCTCAGGGTTCCCTTACTTTGTGACTTTGAACCTCTA
CACCAGCATGTACTTGCTCTACATAATTTGGTAAAAGCAGCACAAAAGTTTGGATGAAATGTCACAGACCA
TTACAGATCTACTGAGTGAACAAAAGGCATCTGTGAGTCAGACATCCCCACAGTCTGCTTCTCACCAG
GATGGAAAGTACAGCAGGAATTACAACACTACTACCTCACCGAGAACTCCTCCACCCTGACTGTTTCCAGGAT
CCCTTATGTCCTGCAGTTTGTCCCTTAGAAGAATTATCTCCAGATAGTATTGATGCACATACGTTTGATT
TTGAAACTATTCCCCATCCAAACATAGAACAGACTATTCCACCAAGTTTCTTTAGACTTTGGATTTCATTAGC
AGAAAGTCTGAATCAGATTTTTATGTCTGCTGTGAATGAGTTTGTAAATAGAAGAAAAATTTGTGCTCTCCT
AATCCTATAAGTGATCCACAAAGCCCAGAAATGATGGTGAATCACTTTTATTTCATCAGTTATCAATGCGA
TAGACAGTAGACGAATGCAGGATACAAATGTATGTGGTAAGGAGGATTTTGGAGATCATACTTCTCTGAA
TGTCCAGTTGGAAAGATGTAGAGTTGTTGCCCAAGACTCTCACTTCCAGTATACAAACCATTAAAGGAAGAC
CTTTGCCACTTTAGAACATTTGTACAAAAAGAACAGTGTGACTTCTCAAATTCATTAATAATGTACAGCAG
TAGAAATAAGAAACATTTATGAAAAAGTAAAAATGTTCTCTGGAAATAACACTAAAAGAAAAACATCAAAA
AGAACTACTGTCTTTAAAAAATGAATATGAAGGTAAACTTACCGGACTAATAAAGGAACTGAAGAGAAT
GAAAACAAAATTAAAAAATTTGAAGGGAGAGTTAGTATGCCTTGAGGAGGTTTTACAAAATAAAGATAATG
AATTTGCTTTGGTTAAACATGAAAAAGAAGCTGTAATCTGCCTGCAGAATGAAAAGGATCAGAAGTTGTT
AGAGATGGAAAATATAATGCACTCTCAAAAATTTGTGAAATTAAGAAGTGAAGCAGTCACGAGAAAATAGTG
TTAGAAGACTTAAAAAGCTCCATGTTGAAAATGATGAGAAGTTACAGTTATTGAGGGCAGAACTTCAGT
CCTTGGAGCAAAGTCATCTAAAGGAATTAGAGGACACACTTCAGGTTAGGCACATACAAGAGTTTGGAGAA
GGTTATGACAGACCACAGAGTTTCTTTGGAGGAATTAAAAAAGGAAAACCAACAAAATAATTAATCAATA
CAAGAATCTCATGCTGAAATTATCCAGGAAAAAGAAAAACAGTTACAGGAATTAAACTCAAGGTTTCTG
ATTTTGTGACACGAGATGCAAGTTAGAGGTTGAACCTTGCCTTGAAGGAAGCAGAACTGATGAAATAAA
AATTTTGTGGAAGAAAGCAGAGCCCAGCAGAAGGAGACCTTGAAATCTCTTCTTGAACAAGAGACAGAA
AATTTGAGAACAGAAATTAGTAAACTCAACCAAAAGATTGAGGATAATAATGAAAATTTATCAGGTGGGCT
TAGCAGAGCTAAGAACTTTAATGACAATTGAAAAAGATCAGTGTATTTCCGAGTTAATTAGTAGACATGA
AGAAGAATCTAATATACTTAAAGCTGAATTAACAACAAAGTAAACATCTTTGCATAACCAAGCATTGAAA
GAAAAAACCTAAAAGAACAATAATTGAACTGCAGAGTAAATTTGGATTGAGAATTTGAGTGTCTTTGAAA
GACAAAAAGATGAAAAAATTACCAACAAGAAGAGAAATACGAAGCTATTATCCAGAACCTTGAAGAAAG
CAGACAAAAATTTGGTCAGCAGCCAGGAGCAAGACAGAGAACAGTTAATTCAGAAGCTTAATTTGTAAAA
GATGAAGCTATTGAGTGTCCCTAAAAGAATTTAAATTTGGAGAGAGAAGTTGTTGAGAAAGAGTTATTAG
AAAAAGTTAAACATCTTGAGAATCAATAGCAAAAGTCCCTGCCATTGACTCTACAGAGGAGATTTCTTC
AAGCTTAGTTGCTGAACTTCAAGAAAAAGCTTCAAGAAAGAAAAAGCTAAGTTTCTAGAACAACATGAAAG
CAAGAAAAAGAAAGAATGAAGAAATGCAAAATGTTGCAACATCTTTGATTGCGGAACAACAGACCAATT
TTAACACTGTTTTAACAAGAGAGAAAAATGAGAAAAAGAAAAATAATAAATGATCTTAGTGATAAGTTGAA
AAGTACAATGCAGCAACAAGAACGGGATAAAGATTTGATAGAGTCACTTTCTGAAGATCGAGCTCGTTTG
CTTGAGGAAAAGAAAAAGCTTGAAGAAGAAGTCAAGTTGCGTAGTAGCAGTTTTGTTCTTCCACCAT
ATGTAGCTACAGCCCCAGAACTTTATGGAGCTTGTGCACCTGAACTCCAGGTGAATCAGATAGATCCGC
TGTGAAACAGCAGATGAAGGAAGAGTGGATTGAGCAATGGAGACAAGCATGATGTCTGTACAAGAAAAAT
ATTCATATGTTGTCTGAAGAAAAACAGCGGATAATGCTGTTAGAACGAACATTGCAATTGAAAGAAGAAG
AAAATAAACGGTTAAATCAAAGACTGATGTCTCAGAGCATGTCTTCCAGTATCTTCAAGGCATTCTGAAAA
GATAGCTATTAGAGATTTTCCAGGTGGGAGATTTGGTACTCATCATCCTAGACGAACGCCATGACAATTAT
GTGTTATTTACTGTTAGTCTACTTTATATTTTCTACATTCAGAGTCTCTACCTGCCCTGGATCTCAAAC
CAGCTTCAGGTGCATCTAGAAGACCCTGGGTACTTGGAAAAGTAAATGGAAAAAGAACTGTCAAGCCAA
AAAGGCACAAAACAGATTTAAAGTTTCTTTGGGGACAAAGTTTTACAGAGTGAAGCCGTATCATGGAAAT
AAGAAAGTATAACTTATGGACAAAATTAATACATTCTATGACATTTTTTTCTGATTTGTCTTGCAGTGTCT
CATTTCATCACTCCAAAAACAGCAGGCCATCTTTTTATGCAAAAGTCAAGGATGACAATATACTTCACTGGT
GTACATCGTTTACTTTTTAACTGGCTTCATTTTAGGAATAATAAATTCATCAGAATCCTTGGCTGAATTA
AAATGGTTTTGTTTTTTTTTTTTTTTTTTTTTACCAGCAACTCTAGAAATGCGGACCAACTACTTCAT
TTTTCTCAAAGGCATACCTTGTGCATTGTGGCTTATGATGAGCCATATTAATTGCCTGTTAAATATACAC
TAGCTTGAACCTTAGATGTTAAATGTTATTATTACCAGCATTGTCTTTTTGTGAAATCAGTATCAGAATA
CTTGCACTCTTTAACACATTCTTTATAAAAATGTATAAAATTTATTCAGAACTATTTAAAAATAAAGAGGAGTG
TTATTGCATGCTGATAATCATTTTTGAGTTTGCCTCAGTAGATACTAAAGCAAATTTGTTTCCAGTTTTTTA
AATGCCCTTTGATGTTTCAAAAAAAGGAAGTGAATTTGATTGACTGATTTTAAAGTCAAGCCATAA
GTAATCAGCAATCTTCAAAGCACTTTTCCAGTGGATTGGTCATCTGGGTTCTAAAGGGAAGAGTCTGTGCT
ACTAACCATTTCAAATGCAGACTCAAACCTTCCCAACATCTTTATGACTCTAGAATAATCATATTGATGA
AATCGTAATTCATGGTTGAGTTTCCAGAACAAAAGATATTTCATTGCACATTAACCATTTAGAGGTCATTTA
AATAACAAAATATTGTATTGTAAAAGAACTGTACAATTTTAAAACAATAAAGATTTGAACCTGTAAATGT
GTGTGCCTTTTTAAAGAAGGATACATTTTTAATATATTTGAGTGAATGCTGGGAAGTGTGAAAATATTGTT
ATGTATCATATCAAAGAGAAACATGTTTTATTACAAAAATGTTCTTTAACTATATACTATGTAACAGGGTA
AACAGTGTATTGTAGAATAGAATTTGTGTAAACTAGATCTTTAGAGAAGTTGCCATTGAGCAAAAGTTATTT
AAATGAGTTAGTTGAGTTGGATGAGAATTTGTTGAGGTTTGTGCTAGAGAACAATAATAAAAAATTTCT

TTTTTCAGAAAATATTTAATTTCTTCATAAAAAATAAGTTAAATATTTTTTTTAAATATGTATATCTAATAGT
ACAAAATGGAATAAACATCATAGTGTATAGAAAACGAATTTGACAAGTTAATGAATAAATGAACAAATG
ATTTCA

8. ATG101 (autophagy related 101)

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

ATAAATAAATACGACCCGTTTACGGGTAATAAAGGAAAAACAAAGCAGTGAGTCAGATGATAAGATAGAC
GCTGATTTTCAGTGTGGTCTCGGGTGTATGTGTGTAATTTTAAAGGCGAAAATGAAAAATGAACGCTCGAT
CACAAGTGTTCGAATTGTCTAGTAGAAGGAAGACAGATTGAGGAGACTGTTAGCAGTATATTTTCATACCTT
GTTGCTCCAAAGAACAGTCGGAAAGTTTCACTACAAACAAGAAGGAACATACTCTATTGGCACTGTTGGA
GTGGAGGATGTGGATTGTGACTTTGTAGACTTTACTTATGTCTAGAGTGGCTTCTGACACTCTGGATCATA
TGATCAAGAAAGACATAGCTTTTATTTCAGGGACACCCCTTCGGAGTATGGATAATCCAGGATCAGGACAGAT
TTCCTTGGAGTTTTACCAAAGAAGCGAGGCCGATGGCCTTTCCACCCGGAATGTATTCCCTGGGAGGTG
TGGACAGTGAAACTAGACATCTTAACACTCAATAACGAAAGTGAAAGACAAATTTGCAGGGAAAAACTTG
GAGAAATGTTAGGAGAACGAGTCATCACTATAGCAGACCTGATGAATCGCCATGACTACGTTCCCAAGAT
GCCAAATCAGACAGAATTAGATTTGATATTTGATACAAGCTTGCCAGATGTGCAACCATACTTATTCAGG
ATATCCCATCAGACTACGGGTCTTCCAGCTATCTGTCTGGAACCACCATGAGGAAGTTCATCAAGGACA
CACTGGCCCTATGATGCTGCCACAGGGACTGGATCAAAGTCTCTCAGAGGTGGATCCAAGTCCATCAAG
GTGAATCAAGGCCCTCCTTGGTGGATCAAATCCTTGAGGGGTGGGGATTTATTCAATATAACTAATG
CAGCACCAGTGAATGGTCAGCTTCGCTTCTACTTGTGTCTTTTACATTGAATTACATGTATTGAATCTGT
ATGTGTCCATTTTGAATATAGCATAACAGTACTAAATTTGTCATTTATTCTATATGTGAGCAGTTGTAATAG
CTTTTTTCTGTGTTATAAACGTAAGAATGGTTTTTGGAGTAGTTAAGTAGTACATGTTTCAATGAACACTA
CAGTCATTTTTTTTATTGATTTCAGAAATTTTAATACACATTGAAATGCTGTATGTCCAATGAAAAAAGT
TTTTTTTATAAGAATTTAAAGATCAATTATCAAAAAGTTGTTGTTTTAATAGCAGAACATTTGAAAAGTTG
AAATAGTATTAATAAATGTTAAAATGCAACCCCATTCATTACTCCTGCGAAAGAATTTTATAAATGTACAT
GTTGTCAAGAAATAAAGCTGGAAAATGGTAACTATTAATCAATACCCTTTTTTAAATAAGTACCTGGTAC
GGGATAAATTTATAGCAATGATCTTTATTTCTAGTGAAACATCATCTAAAGTAGTTAGAAAAAACCCCA
GTAATATATATGGATGTCTTTCATGTCAACAGAAATGTGAAGATAACAGAGAGAGAGAGAGAAAGAGAGA
GAAAGAACACGTACAGCAATATTTTATAATGGAACATGCTCATTGATTTTGATACATTACTGTCAATTT
TATGGTAAGAATCAATCTTCCAATTTTATGGTATTAGTACATTGTACATTTTGTATATTACTGTACG
TTTTGTTTCTTGGAAATCTTGCATAAAAATTTGATCACCTTATTTTTGTCAACTCATAAACACCATAGTGT
TATATAATCATCATCTACTTATAATTGCTAATTATACTCATATTTTCAACAGCAAAAATATACATACAT
GACATATTCACCAAATCAATTGTGTGCTATATAATGTCTTGTATTTTTTCCACGGAAAATATGTTGCTG
TAAGTCAGAATAAATTTTGTATAAACCACA

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

9. 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
MNSFSSAQSDHSQHSSIPDICLSAGNEMSSLEAQLAESIIDLNDPYDNIGDEDEFIKKLD
CDSNEHVKVVSIFGNTGDGKSFTLNHTFFGGKEVFKTSSHQSSCTVGVWAAAFDPKEKVIV
IDTEGLLGITSNQNQRMRLLLKILGISDIIYRTRAERLHNDMYQFLCESSAYTKHFS
ELEATAKRCNKGVDLTPAVIIFQETVNTNVLGSSGTDSAEKFIWNTFRQLECPMHFKDL
TYVGIRTGRPPTDFTQFQRTMSQHLQDKSNRAARQPAIVYKTLKLNLDKFNGEVEKPLYG
TFPDQLFSCSMKCLSCGEGCTRSMNHDTDSKAHETDKRCKYQHOFENKVFLCKSCYLSGK
EHVVIKPTSESRDSAWSGLIKYVWAGEVLECPSCGVIFRSRQNWYGNKEVEEIVHTEIRH
VWPDGYKMLQGTNNAARKVIDGFHYIADSITSVSGSKPTKMSIDWMNDRIAPEYWVPNSQI
SHCHQCSKELETEQKHHCRACGKGFCDCCSSSHRRRVPERGWGEMEVVCDKCYGGKKMSD
SNDSTGNSNSQVTARKVGEVVTSAISVAASTLNYPIDMIKDTARPGYWTPEQIKACYVCE
ELFGPKLRIHHCACGQGVCECSPNKRVPVPLRGWDYPVIRICRKCINKPDRL

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

ACTCCGATCAGCTGATCCCAACTGACAACAGGAGAGGAGGAAGCCCGGGAGGCAACGAAGGAGGAGGGTG
GCGGAGATGGAGATGAGGATGGATCTGCCGGTGTCTGAGGAATAGCCTCTGCCCCACTGGCGCCCTGC
GGCCCCCGACGCCGCCTTGCTGCGGCCGAGCTTCTCAGTGGTATCCCCTGAAATACTGACTTCAGGTTCG
AATTATATTGAAAAGCTCCTGACCACTTTCTTTTATTACCAAACTTTGTAGCTGATGTCCAACCGATGA
ACCCACCACCGTGAACCCATCAGACCTCTCTCAGATAGCCATAAAAAGACCCTTCCAAGTCAATTTTGACC
ACATCTTTGCTTGCACCTTTATGGAGGATGAAACCATCAAACCAAATCAACGTTGCTGCTAATACAAGAGT
CTTAGAGGCAGCAAATTAATAATTTGAACATTTGTTTGTGAAGAACTATAACAGGACATGAAAGGTGTTTC
TTTTTTAAAGTGTTGAGAACCCTGTGGAAGTTTCGTGCAGTCTTCAGACTCAAATCTTCGTCTTCACCCC
CGGGGCAAGCTCAGTGACTATTATATGGTGGGTGTGTTTCTTACCAGCGTGAGTATGAGTGCCAGACT
TCCCCAGCAGAGAAGGGCCTGAATCCGGGGCTGATGTGCCAGGAAAAGTTACGCTTGCAGCGGGACTGATG
AAGCTATCTTTGAGTGTGATGAGTGTGCAGTCTGCAGTGTCTCCGCTGCGAGGAGGAGCTCCATCGGCA
GGAGCGCCTGAGAAACCATGAGCGGATAAGACTCAAACCTGGCCATGTCCCTTACTGTGACCTCTGCAAG
GGTCTCAGTGGGCATTTACCAGGTGTTAGGCAGAGGGCAATAGTGAGGTGCCAGACCTGCAAAAATTA
TGTGCCTGGAGTGCCAGAAGAGGACTCATTCTGGGGGTAACAAAAGGAGACACCCCTGTACTGTGTACAA
TGTCAAGTAACTCCAGGAGTCACTGGAGGCAGAAGAGATGGATGAGGAGACCAAGAGGAAGAAGATGACT
GAGAAGGTTGTGAGTTTCTCCTAGTAGACGAAAATGAAGAAATTCAGGTAACAAAATGAAGAAGACTTTA
TTAGAAAATTGGACTGCAACCTGATCAGCATCTGAAAGTGGTTTCCATTTTTGGAAAATACTGGTGATGG
AAAGTCTCATACTCTCAACCACACTTTCTTTTTATGGTTCGTGAAGTCTTTAAAACCTCCCCGACCCAGGAG
TCCTGCACTGTGGGAGTGTGGGCAGCCTATGACCCAGTTACAAAAGTAGCAGTGATCGATACGGAAAGGC
TCCTGGGGGCCACCGTGAATCTAAGCCAGAGAACACGGCTGCTGCTTAAGGTCTGGCCATCTCAGACCT
CGTCATCTATCGAACTCATGCAGACCGGCTGCATAACGACCTCTTCAAATTCCTTGGGGATGCCCTCAGAA
GCTTATCTGAAGCACTTACCAAGGAGCTCAAGGCCACCACTGCTCGCTGTGGCCTGGATGTCCCTTTAT
CCACACTGGGCCCTGCAGTTATCATCTTCCATGAGACCGTGCACACCCAGCTACTGGGCTCTGATCATCC
CTCAGAGGTGCCAGAGAAGCTCATCCAGGACCGGTTCCGGAAGCTGGGCCGTTTCCCTGAAGCCTTTAGT
TCCATTCACTACAAGGGAACGAGGACTTACAACCCCTCCCACGGACTTTTCTGGGCTTCGGCGTCTTTGG
AGCAGCTACTAGAGAATAACACCACCCGTTCTCCCCGGCACCCGGGAGTCATCTTCAAAGCCCTGAAGGC
ACTAAGTGACCGCTTACGCGGTGAGATCCCCGATGACCAGATGGCGCACAGCTCCTTTTTTTCCAGATGAG
TATTTACCTGCTCCTCCTTGTGCCTCAGCTGTGGGGTTGGATGTAAGAAAAGCATGAATCATGGGAAGG
AAGGAGTGCCTCATGAAGCCAAGAGCCGCTGCAGATACTCCCACCAGTATGACAACCGAGTGTATACCTG
CAAGGCCTGCTATGAGAGAGGGCGAGGAAGTCAGTGTAGTGCCAAAACATCTGCTTCCACTGACTCCCC
TGGATGGGTCTCGCAAAATATGCCTGGTCTGGGTATGTGATCGAATGTCTTAACTGTGGCGTGGTCTATC
GTAGTCGGCAGTACTGGTTTGGAAACCAAGATCCTGTGGATACGGTGGTGGGACAGAGATTGTGCATGT
GTGGCCTGGAAGTACTGGGTTTCTGAAGGACAACAACAATGCTGCCAGCGCCTGTTGGACGGGATGAAC
TTCATGGCTCAGTCGGTGTCCGAGCTTAGCCTTGGACCCACCAAGGCTGTGACTTCTGGCTGCAGACCC
AGATCGCCCCCTGCCTACTGGAGGCCAACTCCCAGATTCTGAGCTGCAACAAGTGTGCGACGTCCTTTAA
AGATAACGACACTAAGCATCACTGCCGAGCCTGTGGGGAGGGCTTCTGTGACAGCTGTTTATCAAAGACT
CGGCCAGTGCCTGAGCGGGGCTGGGGCCCTGCGCCAGTGCGGGTCTGTGACAAGTGTACGAAGCCAGGA
ACGTCCAGTTAGCTGTTACCGAGGCACAAGTGGACGATGAAGGTGGAACGCTCATTGCTCGGAAGGTGGG
CGAGGCCGTGCAGAACACTCTGGGAGCCGTGGTGCAGCCATTGACATACCACTAGGTCTGGTAAAGGAC
GCGGCCAGGCCTGCGTACTGGGTGCCTGACCACGAAATCCTCCACTGCCACAAGTGTCCGGAAGGAGTTCA
GCATCAAGCTCTCAAGCACCCTGCCGGGCCCTGCGGACAGGGCTTCTGTGATGAGTGTCCCATGACCG
CCGGGCTGTTCTTCTCGTGGCTGGGACCATCCCCTCCGAGTCTGCTTCAACTGCAATAAAAAGCCCGGT
GACCTTTAACCCAGCCCCCTCTCCGAGTCTTACAATTCCTTAGGTTCTCAGGGTTAGAAAACAGTCTT
GCGAGGTAGGCCCTCCTCCCAGTACCTGCTGTGGTGTGTGCTCTCCTCTCCGCATCCAGGGCCACTT
TCCCTCAGTGGGGGTGAGCCTGGCGGCAGGCCCGAAGGTGTGGACCCCTCAGGGCAGGGGACCTTGCAAC
TTATCGCAAAGGGGAATGAACCTGAATCCGTTGCATTTATTTTCAAGTAAAAATAATGAATATATATGTGT
ATATCTCTCTCATATATACATATGAAAGGCACTCGGGGCGTATCGAGGCTGCTGCTGGCTGTGAAGAC
TTCGCACAGTCTCCTCCGCACAGGGTGGAGTGGCAGTGGCAGCACGCTTCTCATGAGCCGAGCCAGGT
CCATGGCCACCACGTGGCTGGCCCCCTTCTCTGCTGCTTGGAGCCTTGGAAAGCCTCTCCTGTCTTGG
CTCTTCCCTCCATGCCTGTGAGTGCCTGGGGAGTGGAGCTCCCTGGTCCCTTCTGCTGCTGAAACAGCCTG
AAGGGAATTCTCCCTAGGTCTCCTGGGAGTCGAGTCCCAATTCCTGGCTTAAGCCTGTTTTAGTCAGAGA
CCACCCAACTTAGCGTGCAGGTACCGGAGTGGGTGGAGGGTCAGAGGTCCGGTCTTCGGCCCTGAGAAG
TAGAAATGCAGGGGCCGTGCTGTCCCTGGTCCCCAGGGAACAGCAAGGAAGGAAGTGAAGCCTTCTCCAG
CAGGGCTTCTGTCCCAGTGTCTGTCTCCACTCGGCTTTCCAAAAGGCGGCACCCAGCTCCTCAATC
GAAGCATCTGCCTCCCACCCCTCGGCCCCCTCAAGCCCACCATCTGCTTCTGAGTGTGCGACTAGGATTT
TCATTGCTTATTTTTAAAGTGTCTTAATCCTTTGTTCCAGACACACAACCCCTCTAGCTCTCGGAGGGGC
GATCATGAGAAACCTTCCAGGGAACTGAGCACAGGATGAACTGTAGTTGTTTTTAAAGTCTATATAA
ATATTTCAACAGATCGTAAAGAAAAAATTTATCTCTTTGGTCCCTTGAAGAGAAGTCAAAGGAAGTCTTTG
TTTCTCCTCAAGAGCCTGGACATCTCTGTCTGTGATGACTGGAAAGGGCCCGTTGTGCTGAAATCCTATC
ATCATGGTGGATTTGATCTTCAGTGGCCAAACACGAATTAAGTATAAATTCCTTAACTGAACTGGTGGGTG
GGTTGAGCTTTAGGGAAGTATATGGCGGTCAATTCCTGGTGCCTATCGGTGTGACATGAGCCCTGGAGT
GTGTCGTCCCTCTCAGCCCTGCTCCTCCTGCCTCCTGGGGTCCAGTGAAGTGGGACCCCTACTCTAGAAGT
TGTACCATCCAATTCGCCATCATAAAGGAATCTTCTGCA

10. ATG9A (autophagy related 9A)

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

```
GAACTCACAGAACTGGACATATACCACTGGATACTCAGGTTCAAAAACTACATGATTGCCATGGAGAGGT
AATCCTTACTTCCATTTAAACATAGCATTCCCTTAATGGGAGAATGTGCTTTCTACAGCATTGGATTGAA
ATGCAATCAGGATTTCTTGCTCTTCTGGGGTCCTTGGTCACCTTTTGAAGAATTACTGGAAGTTGAAGGAT
GAATTCAAAATTTATCATAAAAGAAAACAATTGGCAGAAGAGTTGTCTAAGAAAGTTCTATGGATCGGCA
TTGCAAACCTTTGCCCTTAGTCCACTCATTCTACTATGGCAGATCTTATACTCCTTCTTTAGATATGCAGA
TACACTTAAAAGAGAACCTTCAATGTTAGGATCAAGAAGATGGTCAAATTATGCGAGACTTTATTTACGG
CATTATAATGAGCTTGATCATGAATTTGATGCAAGGCTGAATAGAGGCTATAGATTAGCCAACAAATACA
TGGATATCTTTACTTCACAACCTTATAGTTATATTAGCCAAGAATGTGGCATTCTTTGCTGGTTCTGTGCT
GGCTGTGCTGGTTGTGCTGACTGTGATTGATGAGGATGTGCTGGCTGTGGAGCACGTGCTGACCTCCATG
ACAGTTGCTGGTCTGATTGTGACAGCATGTAAAGTCTTTTATACCAGATGAGCATTAAAGTGTACTGCCCTG
AGATTCTGATGAGGAACATCTTGGCCCATGTCCACTACATGCCTCCTGATTGGTCAGGCAATGCCACAC
ATCGAAAGTCCGCAATGAATTCTCCATATTTTTCCAATACAAAGTTGCATACTTATTCGAGGAGCTTTTA
AGTCCCCTTGTACCCTTATAGTACTCTGCTTTTCCCTGCGTCACAAATCGATGGAGATTGTGGATTTTT
TCCGTAACCTTTACGGTCGATGTTGTGCGGAGTGGGGGATGTGTGTTTCTTTGCACAACCTGGATGTCCGCA
GCGAGACAACAAAATGGATGATAGGGAGGAGGAGGAAGAGCCTCAACCATCCCTGAGGACCAACATGTTT
ACTCCAGACCAGGCCCTCACAGGAGGGCAAGATCCAGATGTCCCTCATGCACTTCCACCTTACAAACC
CAGAGTGGAAACCTCCAAAGGAATGCAGTCTGTTTCAATGACATCAAAGAAAAAGCCAATAGAAACAC
TACTTCTCTAAGCATCTTTAACCTGTGACCCAGAATATGGTGTGATGTCATCTCAGGGGTCCCTTACAGGG
TATCTTTCTGGACTACAGCCAGCGGAGCAGGAGCCCTGGGGGAAAGTGCAACAGACCAGTACACCAGCC
TAGCGTCAAGCATCGCCATACAGAGTGGCATGTACCCCCAGTCTACTCAAGTGTCCATGGCCCCCAGTGT
GAGTGGGGTTCACCACAGGCTCCGGGGGGCCATATCCACCCTGAAGGACCCCTGGAACGGTCCATCGGT
GGACCAGTGGGAACCATGCAGGGCTCGACCAGCATGATCGGCAGTGGGTGGGGGGATACCACTCCATAG
GAAGCTCCAAGCCGAGTGTGGACGAGGGCTCACTTGAAGTGTGTCACATGACATGAGTGTGACGCGCT
GTACCTACACGACCTTCAGTCTCGCAAACAGAGAGGTCAAAGTCAAATGGGATATGAAAATATAGAGGAA
ATGCGGGCTAGGAACCTGTGGCAGAGACAGGACAGTAACCAAGGCCAGTGCATGCTGGGATGCCTAATA
TACAGGAGAAGAGGGGAAGAGGAGGAGAAAGATAGTGAAACACCGAAACCATTGCTAAATCTGTCTAGTG
CCAACAAAAACTCCCACAATGCATAGCTTTTTTGTGTCAGCCAGTTATTGTAACTAACATCTCTTTGTGC
TGAGTGTGTGTCTGTGACTTATATATATACCAGCTATCTGTATTGTGCTATATCATGTGGCATTACATGT
ACTTTCACCATGTGTTAATCTCATGAACCTGTTGGATTTTTATTTATTGACATTTACTTTGTTTTATTGCA
TTCAGATAGACATGTACGTACACATGATGTATAATATAAGGCACATTAACCAAAAAATACATGTATAATG
TGTATTTTGTCTCTAAAGAGGACATGAGGTACTTTTTCATGTAACAAAAGCTGAATTGTTTATCTTGATAT
GTAGAATTGATCAGATGTGCTTTGTGTCAGTATCAGTTATCAGTATGAACCGAATGAATGATCAGATCTCG
GGAGGTTTTTTTTTGGCTTTTTTTGTTTACATACACATGTACATGTATTATGAAGTATATAGATACTTCAA
ATAAACCTGAATAATTGTAGAAAGTAGAAGAACATTATTTAAGCAC
```

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

```
MAQFDTEYQRLEASYSDSPGEEEDLLVHVAEGSKSPWHHIENLDLFFSRVYNLHQKNGFT
CMLIGEIFELMQFLFVVAFTTFLVSCVDYDILFANKMVNHSLHPTEPVKVTLPD AFLPAQ
VCSARIQENGLITILVIAGVFWIHRLIKFIYNICCYWEIHSFYLLHALRIPMSALPYCTW
QEVQARIVQTQKEHQICIHKRELTELDIYHRILRFQNYMVALVNKSLPLRFRPLGLGEA
VFFTRGLKYNFELILFWGPGSLFLNEWSLKAHEYKRGGQRLELAQRLSNRILWIGIANFLL
CPLILIWQILYAFFSYAEVLKREP GALGARCWSLYGRCYLRHFNELEHELQSRLNRYKYP
ASKYMNCFLSPLLTL LAKNGAFFAGSILAVLIALT IYDEDVLAVEHVLT TVTLLGVTVTV
CRSFI PDQHMVFCPEQLLRVILAHIHYPDHWQGNHR SQTRDEFAQLFQYKAVF ILEEL
LSPIVTP LILIFCLRPRALEIIDFFRNFTVEVVGVGDTCSFAQMDVRQHGHPQWLSAGQT
EASVYQQAEDGKTELSLMHFAITNPGWQPPRESTAFLGFLKEQVQRDGAASLAQGGLLP
ENALFTSIQSLQSESEPLSLIANVVAGSSCRGPPLPRDLQSRHRAEVASALRSFSPLOP
GQAPTGRAHSTMTGSGVDARTASSGSSVWEGQLQSLV LSEYASTEMSLHALYMHQLHKQQ
QAQAEPERHVHRRRESDESSESAPDEGEGGARAPQSI PRSASYPCAAPRPGAPETTALHGG
FQRRYGGITDPGTVPRVPSHFSRLPLGGWAEDGQSASRHPEPVPEEGSEDELPPQVHKV
```

>sp|Q12142|ATG9_YEAST Autophagy-related protein 9 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG9 PE=1 SV=1
MERDEYQLPN SHGKNTFLSRIFGLQSDEVNPSLNSQEMSNFPLPDIERGSSLLHSTNDSR
EDVDENDLRVPESDQGTSTEEDEVEDEEQVQAYAPQISDGLDGDHQLNSVTSKENVLETE
KSNLERLVEGSTDDSVPKVQQLSSEEEEDNEFINNDGFD DDTPLFQKSKIHEFSSKKSNT

IEDGKRPLFFRHILQNNRPQRDTQKLFSSNAIHHDKDKSANNGPRNINGNQKHGTYFG
SATQPRFTGSPLNNTNRFTKLFPLRKNLNSISVLNNTPEDRINTLSVKERALWKWANV
ENLDIFLQDVYNYLGNFYCIILEKILNICTLLFVVFVSTYMGHCVDYSKLPTSHRVS
IIIDKCYNSITGFTKFFLWMFYFFVILKIVQLYFDVQKLSLQNFYKYLNNISDDELQ
LPWQNVIIQQLMYLKDQAMTANVVEVKAKNRIDAHDVANRIMRRENYLIALYNSDILNLS
LPIPLFRNTVLTKTLEWNINLCVMGFVFNESGFIKQSILKPSQREFTREELQKRFLAGF
LNIILAPFLVTVYFVLLYFFRYFNEYKTSPPSIGARQYTPIAEWKRFREYNELYHIFKKRIS
LSTTLANKYVDQFPKEKTNLFLKFVSFICGSEFVAILAFLTVFDPENFLNFEITSDRSVIF
YITILGAIWSVSRNTITQEYHVFDPEETLKELYEYTHYLPKEWEGRYHKEEIKLEFCKLY
NLRIVILLRELTSLMITPFVLWFLSPSSAGRIVDFFRENSEYVDGLGYVCKYAMFNMKNI
DGEDTHSMDEDSLTKKIAVNGSHTLNSKRRSKFTAEDHSDKDLANNKMLQSYVYFMDAYS
NSENLTGKYQLPAKKGYPNNEGDSFLNNKYSWRKQFQPGQKPELFRIGKHALGPGHNI
AIYSTRNPGKNWDDNNNGDDIKNGTNNATAKNDDNNGNDHEYVLTESFLDLSGAFPNHDV
IDHNKMLNSNYNGNGLLNKGGVGLVKEYYKSDVGR

11. ATG9B (autophagy related 9B)

>sp|Q674R7|ATG9B_HUMAN Autophagy-related protein 9B OS=Homo sapiens OX=9606
GN=ATG9B PE=2 SV=1

MVSRMGWGGRRRLGRWDLGPGSVPLLPMLPPPPPPSCRGPGGGRISIFSLSPAPHTR
SSPSSFSPTAGPPCSVLQGTGASQSCHSALPIPATPPTQAQPAMTPASASPSWGSHTP
PLAPATPTPSQQCPQDSPGLRVGGLIPEQDYERLEDCDPEGSQDSPIHGEEQQPLLHVPE
GLRGSWHHIQNLDSFFTKIYSYHQRNQGFACILLEDFVQLGQFIFIVTFTTFLLRCDYV
LFANQPSNHTRPGPFHSHKVTLSDAILPSAQCAERIRSSPLLVLVLLVLAAGFWLVQLLRSV
CNLFSYWDIQVFYREALHIPPEELSSVPWAEVQSRLALQRSGLCVQPRPLTELDIHR
ILRYTNYQVALANKGLLPARCPLPWGSSAAFLSRGLALNVDLLLFRGPFSLFRGGWELPH
AYKRSQDQALAAARWGRVTLVLLAALNLALSPLVLAWQVLHVYSHVELLRREP GALGARG
WSRLARLQLRHFNELPHELRLARLARAYRPAFLRTAAPPAPLRTLARQLVFFAGALFA
ALLVLTVYDEVDLAVEHVLTAAMTALGVTATVARSFIPPEEQCQGRAPQLLLQTALAHMHYL
PEEPGPGGRDRAYRQMAQLLQYRAVSLLEELLSPLLTPLFLLFWFRPRALEIIDFFHHFT
VDVAGVGDICSFALMDVVRHGHQPWLSAGQTEASLSQRAEDGKTELSLMRFSLAHPLWRP
PGHSSKFLGHLWGRVQQDAAAWGATSARGPSTPGVLSNCTSPLEAFLANLHVHPLPPR
DLSPTAPCPAAATASLLASISRIAQDPSSVSPGGTGGQKLAQLPELASAEMSLHVIYHLQ
LHQQQQQQEPWGEAAASILSRPCSSPSQPPSPDEEKPSWSSDGS SPASSPRQQWGTQKAR
NLFPPGGFQVTTDTQKEPDRASCTD

12. 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

MEAEAADAPPGGVESALSCFSFNQDCTSLATGKAGYKLFSLSSVEQLDQVHGSNEIPDV
YIVERLFSSSLVVVVSHTKPRQMNVYHFKKGTEICNYSYSSNILSIRLNQRLLVCLLEES
IYIHNKIDMKLLKTLLEDIPANPTGLCAL SINHSNSYLAYPGSLTSGEIVLYDGNLSKTVC
TIAAHEGTLAAITFNASGSKLASASEKGTVIRVFSVPDQKLYEFRRGMKRYVTISSLVF
SMDSQFLCASSNTETVHIFKLEQVTNSRPEEPSTWSGYMGKMFMAATNYLPTQVSDMMHQ
DRAFATARLNFSGQRNICTLSTIQKLPRLLVASSSGHLYMYNLDPODGGECVLIKTHSLL
GSGTTEENKENDLRPSLPQSYAATVARPSASSASTVPGYSEDGGALRGEVIPEHEFATGP
VCLDDENEFPPIILCRGNQKGTKQS

>sp|P43601|ATG18_YEAST Autophagy-related protein 18 OS=Saccharomyces
cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATG18 PE=1 SV=1

MSDSSPTINFNFNQTGTICISLGTSGKFKIFNCEPFKGFYSEDSGGYAIVEMLFSTSLLA
LVGIGDQPALSPRLRIINTKKHSIIICEVTFPTSILSVKMNKSRLVLLQEQIYIYDINT
MRLHHTIETNP NPRGLMAMSPSVANSYLVPSPPKVINSEIKAHATTNNITLSVGGNTET
SFKRDDQDAGHSDISDLQYSSFTKRDDADPTSSNGGNSSIIKNGDVIVFNLETLOPTMV
IEAHKGEIAAMAI SFDGTLMATASDKGTIIRVFDIETGDKIYQFRRGTYATRIYSISFSE
DSQYLAVTGSSKTVHIFKLGHSMSNNKLDSDDSNMEEAAADSSLDTTSIDALSDEENPT
RLAREPYVDASRKT MGRMIRYSSQKLSRRAARTLGQIFPIKVTSLLESSRHFASLKL PVE
TNSHVMTISSIGSPIDIDTSEYPELFETGNSASTESYHEPVMKMVPIRVVSSDGYLYNFV
MDPERGGDCLILSQYSILMD

13. 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
MNLATKTGDEQSDLLFVNFNQDCTSLAVGTRTGYKFLSLSVVKLEQIYDNESEDICIVE
RLFSSSLVAIVSLSSPRKLVKVFHFKKGTICNYSYSNSILAVRLNRQRLIVCLEESLYIH
NIRDMKVLHTIRDTPPNPHGLCAL SINNDNCFLAYPGSNQIGEVQIFDTINLRVAMIPA
HDNPLASLAFNAQGTGLATASEKGTVIRVFSIPDGQKMFERRGVKRCVSIYSMAFSADS
LFLSASSNTETVHIFKLEVPKDRPAEQEPQGWMGYFGQALKSSATYLP SQMTEMFNQGRA
FATARLPNSGMHNVCALATI QKVPRLVVSQDGYLYIYNLDPNEGGE CMLLRQHRLDGRA
GDSPVPEVTPTRPLTHPTSGTSYASSVKKPESSVVPESQPYQEQSTGEGEGTGLG
HLRLDDDNFPMTHTKSD

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

GTACCGGGTGCCCCGGCTCTGGAGCATAAACAAGAGCGGGGACGGGATGAGGCGGCGGTTGATCCCAGGG
TGGCGAGTGGCGGCGACCGAGGCGGCGAGCGGGGCCCCGGCGCCGACCCTGAGTGCAGCCTGACCCGCCCT
CGCGCGCGCCCTCCCCGGCCGGGCCACTCGCCGCGCGCCAGCCATGAACCTGGCGAGCCAGAGCGG
GGAGGCGCGCGCCGGCCAGCTGCTCTTCGCCAACTCAACACAGGACAACACAGAAGTGAAGGGGGCATCA
AGAGCAGCTGGTCTTGGCCGTGCGCTGTTGTCTGGTCCCTAGCTGTTGGTAGTAAGTCCGGTTATAAAT
TTTTCTCCCTTCTTCTGTGGATAAGCTGGAACAGATCTATGAATGCACCGATACGGAAGATGTGTCAT
TGTAGAGAGATTGTTCTCCAGCAGCCTAGTGGCCATCGTCAGCCTTAAAGCACCAAGGAAGCTAAAGGTT
TGCCACTTTAAGAAGGGAAGTCTGCAACTACAGCTACTCCAACACGATTCTGGCTGTGAAGCTCA
ACAGGCAGAGGCTGATAGTATGCCTGGAGGAGTCCCTGTACATCCACAACATTCGGGACATGAAGGTGCT
GCATACGATCAGGGAGACGCCTCCAAACCCTGCAGGCCTGTGTGCGCTGTCAATCAACAACGACAACCTGC
TACTTGGCGTACCCAGGGAGCGGACCATCGGAGAGGTGCAGGTCTTCGATACCATTAATTTGAGAGCTG
CAAACATGATTCCGGCTCACGACAGTCCCTTAGCGGCACTGGCCTTTGACGCAAGTGGAACTAAACTTGC
CACGGCTTCGGAGAAGGGGACCGTGATTAGGGTATTTTCCATTCCAGAAGGACAAAACTCTTTGAGTTT
CGGAGAGGAGTAAAGAGGTGCGTGAGCATCTGCTCCCTGGCCTTCAGCATGGACGGCATGTTCTCTCCG
CCTCCAGCAACACTGAGACCGTGCACATCTCAAACCTCGAGACTGTGAAAGAAAAACCCCCAGAGGAGCC
CACCACCTGGACCGGGTACTTCGGGAAAGTGCTCATGGCCTCCACCAGCTACCTGCCTTCCCAAGTGACA
GAAATGTTCAACCAGGGCAGAGCCTTCGCCACGGTCCGCTGCCATTCTGCGGCCACAAAAACATCTGCT
CGTAGCCACAATTCAGAAGATCCCGCGGTTGTTGGTGGGTGCCGCCGACGGGTACCTGTACATGTACAA
CCTGGACCCCCAGGAGGGCGGCGAGTGTGCCCTGATGAAGCAGCACC GGCTGGACGGCAGTCTGGAAACG
ACCAATGAGATCTTGGACTCTGCCTCTCACGACTGCCCTTAGTCACTCAGACATACGGCGCAGCTGCAG
GAAAAGCCTACACAGACGACCTGGGTGCTGTGGTGGCGCCTGCCTGGAGGACGAGGCCAGCGCCCTGCG
CCTGGATGAGGACAGCAGCACC CGCCATGATTCTTCGACTGACTGAACTTGACCTGTGACCTTGAC
CCGGGGAGCAGAGAACACTGGCTTCACAGAGGACTTTGTGCATTGCTGCTATGAACTTTGACCTGAGTCG
GGGGAGAGGATGGCAGAGACTTTATTAATAAAAAAAAAAAAAAGATTGTAGTGGTAGTCTAACTCCATAACGCT
GAGGAAATACATCATTTTTCACTTCAGTGGCTTTTTAAATCCTGCTTATGAATTTTAGCTTTTTTGTGTTT
GTTTTCTTTTTTGCCAAAATTAAGTGTGTTGGTGAAGCCCGCAAAACCTCCTCGCTTTGCATGCATGAAC
GTGCCAAGCCAGCATAGGGGAGCTAGAAGCCACTTTCCAGCCACCTGCCGTTGGGTTTTTTCATATCTGT
ACATAATGCCGAGTGCCTAAGGAAACCGTGGCGTCCGCGCACAGTGGGTCTGCTTGTCAAGGCCAGTTCTG
CAGTGACAGGCCCAGGGGCTGCCACCAGGTGTGCTGGGCAGACTTCAGCTGGGACAGAAGTCCGATCTC
CCTAGGGCCCCACCTGGACCATTTTCCCTCCGTTTTATTTTGTAAATTAATTTCTTCCAAATTTGGATCG
CTCTGGGATTTCTTCCATGGTGGACTTTTGTCTGATCTTGTCTTCCCTGTGGATATTGGAGGACAGCG
AGGTTCTTTCTGATACTAAAAACCTTTCTTTCAGGCAGCAAATGAACTTGAAAGGTTGCCCTGGACTCGCT
GGAGCAAAGGAAAGCGATTTTGTGTTGATAATTAATGATCTGTTCTTCTACTTCACTCTTCTGTTGAA
AACTGTGTGATTTTTTTTTTTTTTTTTAAGTAAAGTTTGTAGCTCCTCCCATGCCAGGAAAGCACAGAAC
TCAAGTGTGGTGGCCGTCTGAGCTGTCTTTTCGCTGGCCCCGCTGTCCGCAGGGGCTTCTACCTGTGTG
AGAGGTCGTAGCGGGAGACAGCAACAGAGAGTAGGCGGCTGGGCCACGTCCTTACAGGGCGTCATGTGC
CTTTCTATTTTCATCTTAGAAAATTTCTCAGCAAACCGATGAGAGATTGTGGTTGCAAGCTTCAGTATT
TGCCTCGCTTCCCTTCCCTTTTCATATTTACAGAAATTAACAACCTCAAGTACCTCAGACTCTGCATTC
CAAACCAAGGCCACCCAGCCAGCAAGTGTGCGAGGCAATTAAGTGGCATTAAATGGCAGGAGAGATGTTT
TAGAATCTATGGAGTGGTGAAGTTACGGATAGAAGGAAAAGGCAAAAACCTATTTACCTGCCCTTTGCA
GGCTGGGGTTTTTGAACCGAGGAAGGCTGGGACGCTGTTTCCAGATGGTTGTCATGGTCACGCTGGGCG
AAGAGCTGGAGGGGAGTTGTCCCTCAGCTGAGCGGCTGCCGTGAAATGCCCCAGTGTTCCTGGGTTGGC
TTTACGGCAAACATAATGCAGGGGACGCTGGAGTCCGACTCACCTACACCGGCTTCTCCAGCCGCTGG
TGTGCGGCACACACAACATCTGCATTAGGCAGAGGTGCAAGTGGGCTGATTGAACTTTTCTTCAAACC
TGCTTGTCTGTCTGGACCTTTGATGAAATGGGATCCCGGTCACGCAGGCTGAGACAGTGGGGACCGCCG
AGGCCAGAGTGGGCTATGCTTGAGCAGGGATGAGAAGGGCCGCGGCAGCACGCAGCCTTGACCCACGCCT
GCGTCTTGTGGTGAAGGCCAGAGGGCTCTCTCTAGAACCTGACCGTGCCTCATCTCTGGGAGCCAC

TTTTGGCAAGAGTGAGTGTGGGGGAAAAAGTGTGCACAAGAGATACGGAACCCCTGAGCTAGGGTTTCCT
GTCACCAAAGAGTGAGCTGCATTTCCAGTTCTGCGTTAAAGTATCGTTTGTCTGGTGCCTGCCTGTGGT
GGTGATTTGGAGACTCAAATTTCCCTTTGCCAGGTCTCTTTTGTCTTTCTTTGGGATTGGTAGTATAGAAG
ATGCTGGGAATTGTCTTCCCTCGCTCAGCCTCGGCTTCCCGCACTGTAAGATGAGGCAGTTGCAGAGGAGG
CCTCGGACGTCTGTGACCCTCGGCCCACACTCCCCCTTGGGTGGCCCTGGCAGGGCTGGCTAGGTGCGT
TCCCTGCAGACCACGGGAAGCCCTGTGCTTGCCTGGGTGAGGGCTAAGCTGTGCGCCCTAGAGGAGGGAG
GAGGACTGCAGATTCTTGGTCGAGAAGAATGAAGAGGATTTCTGTGTTTGTGAGCAGCCATTGTGGAGG
GTTACCCGCTCCACTTTCCCGTTGCCATTTCACTGCCACCAGCTCCTCTTCTCTGCTCGAACCTATG
AGTCCCAGCCTCACTGGCGGCCTCAGACATGCTCAGGAGTGACGGGGACAGAGGGAGGCCGCTGAGTTGC
CCGTTAGAACTCTTACTGCTGCGCCAGTGACCCAGGTGGAGAGGGACCCCTGAACCAAACAGAACGTGTGC
TAATTTTCCGAACTCCAAACTGTACACTCATATTCATTTTTAAATTTGTATTTTTTCCAAACTTCAAAAAGG
ACGATGAGCGTGGGGGATAGGAAACAAAACCTGTAAACGTTGTGAATGGGCTCAGTGGACTCTGGGACCA
AACCTTCTGTAATCTCTAAAACAATGGGACCAAGAGCTGGATGGAACCTGGAGTCAAAAAGAACTGCTTC
AGTCCCCGCTGTACCGCCTGCCTAGCTGTGGGAGCAGGCAGGGCGCCTGGGAGCCTGCGTTTTCTGGACC
GTTCCATGGGACTCATCCCTACCTCACAGGGCTGTTGTGAGGTGTTGTGTGACTGCGTGTCTGCAAACG
CCCAGCTCGGTGCCAGCCAGCGGTGGGCACCCAATAAACGCTACAACATAAATGTGTCTTCTGCAATTA
AA

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

ATGTCTGATTCATCACCTACTATCAACTTTATTAATTTCAATCAAACCCGGAACGTGTATTTCCCTTGAA
CGTCGAAAGGTTTCAAATATTCAATTGTGAGCCCTTCGAAAATTTTATTCAGAGGACAGTGGGGGCTA
TGCTATCGTCGAGATGTTGTTCTCCACCTCGTTACTAGCCCTCGTTGGGATAGGCGATCAACCTGCGCTT
TCACCAAGGAGATTGCGTATAATCAACACAAAAAACATTCTATTATCTGTGAGGTGACTTTCCCTACTT
CTATTCTGAGTGTGAAAATGAATAAGTCTCGATTGGTGGTACTTTTACAAGAGCAGATTTATATTTATGA
TATCAACACCATGAGACTATTGCATACTATAGAAACAAACCCTAACCCACGTGGCCTTATGGCTATGTCT
CCTTCGGTAGCCAACAGCTATTTAGTGTATCCATCACCACAAAAGTTATTAACCTCCGAAATTTAAAGCTC
ATGCCACCACAAACAATATCACATTGTGAGTTGGTGGCAACACAGAGACCAGTTTCAAGAGAGATCAGCA
AGATGCTGGCCATAGTGACATTAGCGACTTGGATCAGTATTTCGAGCTTTACTAAGAGGGATGATGCGGAT
CCAACAAGCAGTAACGGCGGTAACAGCAGTATAATAAGAATGGTGTGATGATCGTATTCAACTTGGAAA
CATTACAGCCAACCATGGTTCATCGAAGCTCATAAGGGCGAGATTGCTGCAATGGCAATTAGTTTTGATGG
GACACTAATGGCTACCGCCTCTGATAAAGGTACTATCATCAGGGTCTTTGACATTGAAACGGGTGATAAG
ATCTACCAATTCAGGAGAGGGACGTACGCGACAAGAATTTACTCCATATCATTGAGTGAAGATAGCCAGT
ACTTGGCGGTTACCGGCTCTTCCAAAACCGTGCATATCTTCAAATTTGGGGCATTCAATGAGCAACAATAA
ACTAGACAGCGATGATAGCAACATGGAAGAAGCTGCAGCCGATGATTTCATCGCTCGATAACCACAGTATC
GATGCGCTGAGTGACGAGGAAAACCCGACAAGACTCGCAAGAGAACCATATGTGGATGCATCAAGAAAAGA
CAATGGGTAGGATGATACGTTACTTCTTCAAAGCTATCCCGAAGAGCTGCCAGAACATTGGGTGAGAT
TTTCCCCATCAAAGTTACATCGTTGTTGGAATCCTCGCGCCATTTTTCGCTCTTTGAAACTTCCCGTTGAA
ACCAATTCCCATGTAATGACCATATCAAGTATAGGCTCTCCAATAGATATAGACACATCCGAGTATCCGG
AACTCTTCAAAGTGGCAATTCCGCAAGTACAGAGTCTACCATGAGCCTGTTATGAAGATGGTCCCAT
CAGGGTCGTTTCCCTCGGATGGATACCTATACAACTTTGTTATGGACCCGGAGAGAGGCGCGATTGCTTA
ATATTGTCACAGTATTCATCTTGGATGGATTGA

14. 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
FRCNYLALVGGGKPNPKYPPTKVMVWDDLKKKPVIELEFSTEVRSVRLRRDRIVVVLDTLI
KVYFTFTQNPQQLHVFETCPNPKGLCVLCPNSNNSLLTFPGRKSGHVQIVDLANTEKSATD
IPAHEAPLSCIAMNLQGTRLATSSEKGLTIRVFDTHSGLQLHELRRGANSAAHIYCINFNQ
DSSLKCVASDHGTVHIFSTEDLKKNKQLGIGSASFLPKYFSSWTFKQVPPGGARICA
FGADPNSVIVICADGSYYKVFVFNQKGECTRDVYAQFLEMTDDRS

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

TCCTAATCACTCAAATGTTTATCATCGTATGGGGGTGTGTTGTCTAGTAGCTGAAAATAATGTCACATTT
TGCTCCAAAATGAATGCAAATATTCATCGATAGCAACAACAAGTAAAAAATGGATTTATCCCTCGGTAA
TTCGTATGGCAACGGCTTGTGTGATGCGGGTTGGAACCAGGATCAAGGATGTTTTGCTTGTGGTATGGAG
ACGGGGTCCGGGTTTATAACTCAGATCCACTGAAAGAGAAGGAACGACAAGATTTTGTGATGGTGGCA
TTCATCACATTGAGATGTTGTTTCAAGTGCATTAACCTGGCATTGGTGGGAGGGGGTAAAAATCCAAAGTA
CCCACCTACAAAAGTAATGGTGTGGGATGACCTGAAGAAGAAACCTGTGATAGAAGTGGAGTTTTCCACA

GAAGTCCGCAGCGTTTCGACTGCGACGAGACAGAATTGTGGTGGTGCCTTGATACCCCTCATCAAAGTGTACA
CGTTTACGCAGAATCCACAGCAGCTTTCACGTATTCGAAACTTGCCTCAATCTAAAGGACTGTGTGTGTT
GTGTCCAAACAGTAACAACCTCGCTCTTGACTTTTCTGGGAGGAAGTCCGGCCATGTCCAGATAGTGGAC
CTGGCCAACACCGAAAAATCGGCCACCGATATTCCAGCTCATGAGGCCCGCTAAGTTGTATTGCCATGA
ATCTGCAGGGGACCAGGTTAGCAACAAGCTCAGAGAAGGGTACTCTTATCCGTGTATTTGATACTCATTC
AGGGCTCCAGTTACATGAACTACGGAGAGGTGCTAATAGTGTCTACATTTACTGCATCAATTTCAACCAG
GATTCCAGTCTTCTATGTGTGGCCAGTGACCATGGCCACTGTACATATCTTCTCTACAGAGGATCTTAAAA
AGAACAACAGTTAGGGATTGGGTCCGGCCAGCTTCTACCCAAGTACTTCAGCTCTACGTGGAGTTCTC
CAAGTTCAGGTTCCAGGAGGGGCACGGTGCATCTGTGCCTTTGGGGCTGACCCAACTCTGTGCATAGTT
ATCTGTGCTGATGGCAGCTACTACAAGTTTTGTGTTCAACCAGAAGGGCGAGTGTACGAGAGATGTGTATG
CCCAGTTTCTGGAAATGACGGACGACAGATCCTAAATCATTGTCATAATTTGTCACCGCGACATGAGCAT
GCAATTATAGAATCAATGTTTTTCACAATTTTTCTCACCACCAGTGTGCAAGTAGCGCATGAAATGCAGC
TTATGCCAGGTTCTTTTGCAATATTTTATGTTGATATAACATTGTTACGTTGGTTGATTATTATATTTTT
TTTTAAACATCTTCTCATTAGAGAGTTTATTTATGAAGTCATATGATTCTTTATTATGTGCATGGAAC
AATATGCCTGTAATATCGGGAGAAGCAACCCTCATGGATTTTGTATATCTTGTCTTTAATTTTCATATAGT
TTTGAACATATAAAAATTATAACAAAAAACTGGTGCCTGTAATGTGCATAGGCCTATTCTTGATACAAAAT
AGTGAATCAGGGGAATTTAAACGTACTCATGTAAAATAA

>KX434429.1 Homo sapiens WIPI3 long variant (WIPI3) mRNA, complete cds
ATGGATTCCGGCGCCATGAACCTCCTGCCGTGTAACCCTCACGGCAACGGGCTGCTCTACGCCGGCTTCA
ACCAGGACCACGGATGCTTTGCGTGTGGGATGGAAAATGGATTCCGAGTCTATAAACTGATCCACTAAA
AGAAAAAGAGAAACAAGAATTTCTAGAAGGAGGAGTTGGCCATGTTGAAATGTTATTTGCTGCAACTAT
TTAGCTTTAGTTGGTGGTGGAAAAAGCCGAAATACCCTCCCAACAAAGTAATGATCTGGGATGACCTGA
AGAAGAAGACTGTTATTGAAATAGAATTTTCTACAGAAGTCAAGGCAGTCAAGCTGCGGCGAGATAGAAT
TGTGGTGGTTTTGGACTCCATGATTAAGGTGTTTACATTCACACACAATCCCCATCAGTTGCACGTCTTC
GAAACCTGCTATAACCCCAAAGGCCTCTGTGTCTTTGTCCCAATAGTAACAACCTCCCTCCTGGCCTTTC
CGGGCACGCACACGGGCCATGTGCAGCTTGTGGACCTGGCCAGCACGGAGAAGCCACCCGTGGACATTCC
TGCACACGAGGGTGTCTGAGCTGCATTGCACTCAACCTGCAGGGAACAAGAATTGCAACTGCATCCGAG
AAAGGGACGCTTATAAGAATATTTGATACTTCATCAGGGCATTAAATCCAGGAACTGCGAAGAGGATCTC
AAGCAGCCAATATTTACTGCATCAACTTCAATCAGGATGCGTCCCTCATCTGCGTATCCAGCGACCGCGG
CACAGTGCATATTTTGCAGCTGAAGATCCAAAAAGGAATAAACAGTCCAGTTTGGCCTCAGCCAGTTTC
CTTCCAAAATACTTCAGTTCCAAGTGGAGTTTCTCCAAGTTTTCAGGTTCCCTCAGGCTCTCCGTGCATTT
GTGCCTTTGGAACAGAGCCAAACGCCGTCATTGCAATTTGTGCAGACGGCAGCTACTACAAATTCCTGTT
CAACCCCAAGGGGAGTGCATCCGAGATGTCTACGCGCAGTTTCTAGAGCTGACCGATGACAAGCTGTGA

>sp|P43601|ATG18_YEAST Autophagy-related protein 18 OS=Saccharomyces
cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATG18 PE=1 SV=1
MSDSSPTINFNFQGTGTCISLGTSGKFKIFNCEPFGKIFYSEDSGGYAIVEMLFSTSLLA
LVGIGDQPALSPRRLRIINTKKHSIIICEVTFPTSILSVKMNKSRLVLLQEQIYIYDINT
MRLLLHTIETNPNRGLMAMSPSVANSYLVYSPPKVINSEIKAHATTNNITLSVGGNTEF
SFKRDQQDAGHSDISDLDOYSSFTKRDDADPTSSNGGNSSIIKNGDVIVFNLETLPQPTMV
IEAHKGEIAAMAI SFDGTLMATASDKGTIIIRVFDIETGDKIYQFRRGTYATRIYSISFSE
DSQYLAVTGSSKTVHIFKLGHSMSNNKLSDSDSNMEEAAADDSLDTTSIDALSDEENPT
RLAREPYVDASRKTMRMIRYSSQKLSRRAARTLGQIFPIKVTSLESSRHFASLKLPE
TNSHVMTISSIGSPIDIDTSEYPELFETGNSASTESYHEPVMKMPVIRVVSSDGYLYNFV
MDPERGGDCLILSQYSILMD

15. WDR45/WIPI4 (WD repeat domain 45)

>XM_011455938.2 PREDICTED: Crassostrea gigas WD repeat domain
phosphoinositide-interacting protein 4-like (LOC105347054), mRNA
AAAACGTAATTTAGACATTTGCTAATAAGTTATTAACACCACATACTTTCACTTTATAAAAATGTCAACAA
AAATGTTACGCCACAAGACTGAACAATAATTGTATCTTACCAAGTTACCAATGCTGTCAGGGGACGTC
AAGAATGTCAAGAGGTGTACTTTCTTAAGATTCAACCAAGATCATGGTTGTTTCACTTGTGCAACAGA
AACTGGGCTAAAAATCTACAATGTTGAGCCATTGACCCAAAAAACTTACCCTAGGGCAAGATGTGGTGGGA
AGTATTGCATCTGCAGAGATGTTGTTTTCGCTCAAACCTTAGTTGCAATGGTTGGAGGGGGGAACCTCACCAA
AATATGACGAGAAAGCAGCGTTGATATGGGATGATACAGCAAAAAAAGTAGTCATGGATGTTTCGTTTAA
CCAGCCAGTGGTGTCAATCAAACCTCAAGTATGACAGATTAATTGTGGTGTGAGAAATCAAATCCATGTC
TTTAGTTTTCCCAATAATCCTACCTTGTGTCATTCATTTGATACAAGGGATAATCCGAAAGGGCTGTGTG
ATGTCAGTCTTTTTGGACAAGTGTAGCTTTTTCTGGACGAAAATGTGGCAGTGTGCAAAATGCTGACCT
AGAAACCACCCAGCCAGGGCAGTCCACGTCCCCCATACAATCAGTGCCCACCAGGGGGAGTTAGCGTAT

ATTACAGTGAATCAACAGGGCACATTACTGGCTACAGCTTCCAAGAAGGGAACATTGATTTCGTGTCTTTG
ACACAACCACAAAGAAGTTGGTGGTGGAGCTACGCAGAGGTGCTGACCCAGCCACACTCTACTGCATTAC
CTTCAGCCATGATTCTCATTCTTTTGTGTGCCTCCAGTGATAAAGGAACATTCATATTTTTGCTGTGAAA
GACACGAGTCTGAACAGGAGATCGACATTTAAGAAGATGGGGTTTCTGGGCACTTACGTAGAGTCTCAGT
GGGGCTTGGCCAGCTTCACTGTGGCTGCAGAGTGTGCATGTATCTGTGCCTTCGGACCAGGGCATTGAGT
GATAGCTGTCTGTGTTGATGGGACCTTTTACAAGTATGTGTTCACTACTGATGGTAACTGCAATAGGGAA
GCCTATGATGTGTACTIONTGGACATTGGGGATGACTTTGAATGAGAGAACTAAGTTGATGTACATGTCCAG
TCTATTATTTAACATGTTGTTATAGAAAATCAATTTCTATCAAATTTCTGTTTAAATGCATGTACATGTA
CAATGTATATGTGGAATAATTTTTAAATGTTTGGAGGGTGTACAATGTACACATATTTTTATGTTTTATTGG
TGTAACCTTTAAGCAATGGCTGAGGAATTTGGTACATTTGAAGTTATTTAGCCAGTTTTGCCTTGCCAGT
AAGGTACCAGCATAACAGTACATGCAATTTGAACATTTTGAAGGATTTTCAATGTACATTTGTCTCATCTGTG
TATACATACTTTTCAATATCATTGCTTATTTTGCACCTTTTAAAAAAAATATATTTAAGTACATGCAAATGT
AAAGTTCAATTTTAAATCTGAATGTAAAAATCAACACAATAAGCATAAAGAGATCTGATTTTATTTATATG
TGATATAAATAAACACAACAATTGTCAA

>sp|Q9Y484|WIPI4_HUMAN WD repeat domain phosphoinositide-interacting
protein 4 OS=Homo sapiens OX=9606 GN=WDR45 PE=1 SV=1
MTQQPLRGVTSRFRNQDQSCFCCAMETGVRIYNVEPLMEKGLHDHEQVGSMLGVEMLHRS
NLLALVGGGSSPKFSEISVLIWDDAREGKDSKEKLVLEFTFTKPVLSVRMRHDKIVIVLK
NRIYVYSFPDNPRLFEFDRDNPGLCLDPCSLEKQLLVFPGHKCSLQLVDLASTKPG
TSSAPFTINAHQSDIACVSLNQPSTVVASASQKGLIRLFDTSKEKLVLRGTDPATL
YCINFSHSDSSFLCASSDKGTVHIFALKDTRLNRRSALARVGVKVGPMIGQYVDSQWLSASF
TVPAESACICAFGRNTSKNVNSVIAICVDGTFHKYVFTPDGNCNREAFDVYLDICDDDDF

>sp|P43601|ATG18_YEAST Autophagy-related protein 18 OS=Saccharomyces
cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATG18 PE=1 SV=1
MSDSSPTINFINFNQTGTCISLGTSGKFKIFNCEPFGKIFYSEDSGGYAIIVEMLFSTSLLA
LVGIGDQPALSPRRLRIINTKKHSIIICEVTFPTSILSVKMNKSRLVLLQEQIYIYDINT
MRLHHTIETNPNRGLMAMSPSVANSYLVPSPPKVINSEIKAHATTNITLSVGGNTET
SFKRDQDAGHSDISDLQYSSFTKRDDADPTSSNNGNSSIIKNGDVIVFNLETLOPTMV
IEAHKGEIAAMAI SFDGTLMATASDKGTIIIRVFDIETGDKIYQFRRGTYATRIYSISFSE
DSQYLAVTGSSKTVHIFKLGHSMSNNKLDSDSNMEEAAAADSSLDTTSIDALSDEENPT
RLAREPYVDASRKTMGMRIMYSSQKLSRRAARTLQIIFPIKVTSLLESSRHFASLKLPE
TNSHVMTIISSPIDIDTSEYPELFEETGNSASTESYHEPVMKMPVIRVVS SDGYLYNFV
MDPERGGDCLILSQYSILMD

16. 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
MSNFWKISGEELKAGIWRPHTLMFLLLWVPTVSQILVFPDVKQGHMYSSMHSGAPA
LKAHVKSQVQNKRSQRSSGGPRTEISVNLAKLECELDGPLYFSQTMEDESASDETKIDL
SVNCPVVKLTLRFPIPDLRNGSEVTKLPWWQKNLRDELLILDLEQARFQTSFLSNQPIQQ
VEVSSRNVLGSFRIDPNQSAVPPFAFVSCGIDGQEGFNFPQIIKFTQETISVLDEENPD
SDNSIPMDSLNGACEFAKQDTSPPFSTKHKHMYGKGEMSDQATQHVSDVMVPGNREDMADF
QERASANCLTLVQLVPLINLYIPDQKFYEVLYNRI SNDLLLWEPMA PAPIPTQEVGPGS
IQPFDLSCYTHAEDCHGEVMGVVKDANL FVASSYQGNPLLQYICFYCNKATLYHNAAVPD
KKEEFEIENLDFETI PAHLEKSCI IDRSEPGVLCHQSADVESTVRDMVSVAVRIKLDSTP
LSDLTRDEKIKEFTVAVGVTGATLRHKMAETDMSWISQILNFLDVKDYDILGYVTPKILT
ELHVHLWDCAVDYRPLHLPTKGVVAANYFSSISSNIVANSQTSLLRFVLEDAGMYLSQKKG
RESTVDLKKDYVCVLDVESFELELRSDGKDPKFPKMDLRLR TNKINMRTCTDSCKALFE
LIRYFANDGDLVEYEEPTNKRQSLDLEMNKEEASSDEDSKKKELSESRLNLSHLED
AMQESGSGSDNDGSESSKQSPNKTEVFFVAQGERDAQVPPAGVMRP I VITASADSVTSS
AVSERTDIFSDEEEEEEDFCIIDDAGLGITPRDGKPEVKIFTDEPIEIKDNYFSQPHGKT
DLLKAPDHFPNAEYRYTLKELTIVVHMYGGSDFSPTVQKQKPVETEVMVSRKMKDYGEYV
TETSVRFAASKGSSVDRI PWTQRGGVGRDHTLMELQLTKVRFQHERYPGHTEQASRQVLI
ISDAEIRDRLSDSKINKFLYQYSSENLPKQTNNSNMVYIKALHKRPDP SVKTEEC SLRVSL
QPLRLNIDQDSLFFLKKFFTEITGGNVNDNPSDPDPKQRARSVSGASGAPAPVITVGQPEC
PGEERTPQELLMKFDEMQQSLASQGSMMSSASVASSSDRTEQSQPVF IKNFMFSPDVPI
RLDYHGKKWVDREHGTLAGVLVGLASLNCSELKLRNLNYKHGLLGMDKLQAYCINEWITD
ILKKQLPSILGGVGPMSFVQIAQGIRD LFWLPVEQYKRDGRFVIRGIRGATSFSSTAM
AMLELTNRAVQSVQYVAEVTYDMVTPG PSCRVRRLRGP PADVREGVENAYIAITEVQG

TAQYDLLPANDRKMDHIELFPAPREKFRVY

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

AGTGAACAGCGGAGCCGGACGGGGATCGCCGGCGGGCGGCAAGCGGAGGGCGGCCAGGCCGGCGGTCTC
CGAGATGTCACGATGGCTGTGGCCATGGTCAAACCTGTGTGAAAGAGCGGGTCTGCCGCTACTTGCTGCAC
CACTACTTAGGTCACTTCTTCCAAGAGCACCTCAGCCTGGACCAGCTCAGCCTCGATCTGTACAAGGGCA
GCGTTGCCCTGCGAGACATCCACCTGGAAATCTGGTCTGTGAACGAGGTGCTGGAGTCAATGGAGTCACC
GCTGGAGCTGGTGGAAAGGCTTCGTGGGCTCCATCGAGGTGGCCGTGCCCTGGGCTGCTCTGCTCACCAC
CACTGCACAGTGCAGCTGTCCGGCCTCCAGCTCACCTTGCAGCCCCGCGGGGTCCAGCGCCAGGGGCTG
CCGACTCACAGAGCTGGGCCTCATGCATGACCACAAGCCTGCAGCTGGCCAGGAGTGTCTGCGGGATGG
GCTACCGGAGCCCTCTGAGCCACCACAGCCCTGGAGGGGCTGGAGATGTTTGGCCAGACCATTGAGACT
GTGCTTCGGAGGATCAAAGTGACCTTCTGGACACTGTCTGTGAGGGTGGAGCACTCTCCGGGTGATGGGG
AACGTGGTGTGGCCGTGAGGTCCGTGTGCAGAGACTGGAGTACTGTGATGAGGCAGTGCGGGACCCAAG
CCAGGCGCCGCGGTGGACGTGCATCAGCCGCTGCCTTCCAGACAAGCTGTGCAGACTGGCAGGGGTC
CGCCTGCACACTCAGAGGAGCTCCCGGCACAGGAAGAGCCTCCAGAGCCCCCTTGCAGATCGGCAGCTGCT
CAGGGTACATGGAGCTGATGGTGAAGTTGAAGCAAAATGAGGCCTTCCCTGGCCCCAAGTTGGAGGTGGC
GGGACAGCTGGGCTCCCTGCACCTGCTCCTGACCCCCGAGGCAGCTCCAGCAACTTCAGGAACTGCTCAGC
GCCGTGAGCCTTACAGACCACGAGGGCCTGGCTGACAAGCTGAACAAGAGCCGCCCGCTAGGTGCCGAAG
ACCTGTGGCTGATTGAGCAGGACCTGAACCAGCAGCTGCAGGCAGGGGCAGTGGCTGAGCCCCCTCAGCCC
AGACCCCTTACCAACCCCTTCTCAACCTGGATAACACTGACCTCTTCTTCTCCATGGCTGGCCTCACA
AGCAGTGTGGCCTCAGCCCTCTCTGAGCTCTCCCTCTCCGATGTAGACCTGGCCTCCTCTGTGCGCAGCG
ACATGGCCTCCCGCCGGCTCTCTGCCCAGGCCCCACCCAGCTGGCAAGATGGCCCCAACCCCTCTGGA
CACCATGCGCCCTGACTCGCTGCTGAAGATGACCTTGGGGGGTGTGACCCTGACCTTGCTTCAGACGTCT
GCCCCATCTTCCGGACCACCTGACCTCGCCACGCACTTTTTACCGAGTTTGATGCCACCAAGGATGGGC
CCTTCGGTTCCCGAGACTTCCATCACCTTCGACCACGCTTCCAGAGGGCCTGTCCCTGTAGCCATGTTTCG
GCTAACGGGCACAGCCGTGCAGCTGTCTGGGAGCTGCGGACGGGCAGTCCGGGGCCGGCGGACAACCAGC
ATGGAAGTGCACCTTCGGGCAGCTGGAGGTGCTGGAGTGTCTGTGGCCCCGGGGCACCTCTGAGCCTGAGT
ACACGGAGATCCTGACCTTTCCTGGTACGCTGGGCTCCCAGGCCTCAGCTCGGCCCTGCGCCCATCTGCG
CCACACACAGATCCTGCGCCGTGTGCCTAAGAGCCGACCCCGGCCTCAGTTGCCTGCCATTGCCACTCA
GAACTGGCCCTGGACCTGGCCAACCTCCAGGCGGACGTGGAGCTGGGGGCCCTGGACCGGCTGGCCGCC
TACTGCGCCTGGCACCTGCTGAGCCTCCAGCCGCGCTGCTGACAGAGCCCCCTGCCGGCGATGGA
GCAGCAGCAGGATTTTCGGCTCTCTGCACCCCGGCCACGCTGCGGCTGCGCTTCCCCATTCGCCACTG
CGGCCTGAGCCGACCCCTGGGCGGGCCAGGCCGTGCGGGCTGAGCAGCTTCGGCTGGAGTGGAGTGGC
CCCAGTTCCGGTCAGAGCTTAGCAGTGGGCTGGTCCCCCAGTCCCCACCCACCTGGAACCTCACCTGCTC
CGACCTACATGGTATCTATGAAGATGGAGGGAAGCCACCTGTCCCTTGCTGCGTGTCTCCAAAAGCCCTG
GACCCCAAGAGCACTGGGCGCAAGTACTTCCCTGCCCCAGGTAGTGGTACTGTGAACCCCCAGTCCAGCA
GCACACAGTGGGAGGTGGCCCCGGAGAAGGGAGAGGAAGTGGAGCTGTGAGTGGAGAGTCCCTGTGAGCT
GCGGGAACCTGAGCCCTCGCCCTTCTCCTTAAGAGGACCATGTATGAGACAGAGGAGATGGTGTATCCCT
GGAGACCCTGAGGAGATGAGGACGTTCCAGAGCCGACCCCTGGCACTGTCCCGCTGCAGCCTGGAAGTGA
TCCTGCCCAGTGTCCACATCTTTCTGCCCAGCAAGGAGGTCTACGAGAGCATCTACAACAGGATCAACAA
CGACCTGCTCATGTGGGAGCCTGCAGATCTGCTTCCACCCCCGACCCCGCCGCCAGCCCTCGGGCTTC
CCCGGCCCTCAGGCTTCTGGCACGACAGCTTTAAGATGTGCAAGTCAGCCTTCAAGCTGGCCAACCTGCT
TTGATCTACCCAGACTCGGACTCGGATGACGAGGATGCCCACTTCTTCTCAGTGGGGGCATCAGGTGG
CCCACAGGCCGCTGCCCTGAGGCCCAAGTCTTCACTTGCAGAGCACCTTCTCTACACTGGTGACAGTG
CTGAAGGGGCGGATCACAGCCCTCTGTGAGACCAAGGATGAGGGTGGGAAGCGGCTGGAGGCTGTGCACG
GGGAGCTGGTGTGACATGGAGCACGGTACCCTCTCAGCGTCTCCAGTACTGTGGCCAGCCAGGACT
TGGTACTTCTGTCTGGAAGCTGAAAAGGCAACACTTACCACCGAGCGGCCGTGGATGACTACCCGCTG
CCCAGTACCTGGACCTTCCCAGTTTCGCTCCCCCGCTCAGCTGGCCCCAACCATCTACCCATCGGAGG
AAGGGGTGACCGAGCCGGGAGCCTCGGGCCGCAAGGGCCAGGGCCGGGACCCACATGTTGTCCACTGC
TGTGCGCATCCACCTGGACCCCCACAAGAATGTGAAGGAGTTCTGGTGCAGACTGCGGTTGCACAAAGCC
ACCTTGGCGCCACTACATGGCCCTGCCCGAGCAGAGCTGGCATTCCCAGTTGTTGGAGTTTCTAGACGTGC
TGGATGACCCTGTGCTGGGCTACCTGCCCCGACGGTCATCACCATCCTGCACACACACCTGTTCTCCTG
CTCTGTGGACTATAGGCCACTCTACCTCCCAGTGGTGTCTCATCACCAGGAGACCTTCACTCTCTCC
AGCAACATCATCATGGACACCTCCACCTTCCCTGCTCAGGTTTCTCCTCGATGACTCCGCTTGTACCTGT
CCGACAAGTGTGAGGTGGAGACCCTGGACCTGCGGCGAGATTATGTCTGTGTTTTGGATGTTGACCTCTT
GGAACCTGTGATTAACCTGGAAAGGGAGCACCGAGGGCAAACCTGAGCCAGCCACTATTCGAGCTGCGC
TGCTCCAACAATGTGGTACACGTGCACAGCTGTGCCGACTCCTGTGCCCTGCTGGTCAACCTGCTCCAGT
ACGTAATGAGCACAGGCGATCTGCACCCCCACCCCGGCCCCCCAGCCCCACGGAGATCGCCGGCCAGAA
GCTCTCGGAGAGTCTGCCTCTCTGCCCTCGTGGCCCCAGTGGAGACGGCCCTCATCAACCAGCGTGAC
CTGGCCGACGCCCTCCTGGACACCGAGCGCAGCCTACGGGAGCTGGCCAGCCTTCCAGGTGGCCACCTCC
CTCAGGCGTGCACCATCTCCGTCTACCTATTCCCAGGTGAACGGAGTGGGGCCCCACCCCTTACCACC
TGTCGGGGGCCCTGCTGGCAGCTTAGGGTCATGCTCAGAGGAGAAGGAAGATGAAAGGGGAAGAGGAGGGC

GATGGAGACACCCTGGACAGTGATGAGTTCTGCATCCTTGATGCTCCCGGCTGGGCATCCCGCCCCGAG
ATGGGGAGCCTGTGGTGACACAGCTGCATCCCGGCCCATCGTTGTGAGGGACGGTTACTTCTCACGGCC
GATCGGCAGCACGGACTTGCTGCGGGCACCTGCCATTTCCAGTGCCAGCACTCGGGTGGTGCTACGT
GAGGTCTCCCTCGTCTGGCACCTCTATGGGGGCCGAGACTTTGGCCCCACCCCGGCCACAGGGCAAGAA
CTGGCCTCTCAGGTCCCAGGAGCTCCCCTTCCCGCTGCTCTGGCCCCAACCGCCCCAGAACTCATGGCG
CACGCAGGGGGGCGAGCGGGGGCAGCACCATGTCTCATGGAGATCCAGCTGAGCAAGGTAAGCTTCCAG
CACGAGGTGTACCCAGCGGAGCCAGCCACAGGGCCCTGCGGCCCCAGCCAGGAGCTGGAGGAGCGACCGC
TGTCCCGTCAGGTGTTTCATCGTGCAGGAGCTGGAGGTCCGAGACCGGCTCGCCTCCTCCCAGATCAACAA
GTTTCTGTACCTACACACGAGTGAGCGGATGCCGCGACGTGCCCACTCTAACATGCTCACCATCAAAGCG
CTGCATGTGGCCCCACTACCAACCTGGGTGGGCCTGAGTGCTGTCTCCGCGTCTCGCTGATGCCCTGC
GGCTCAATGTGGACCAGGATGCCCTCTTCTTCTCAAGGACTTCTTCACTAGTCTGGTGGCCGGCATCAA
CCCCGTGGTCCCAGGGGAGACCTCCGCTGAGGCTCGCCCCGAGACTCGAGCCAGCCAGCAGCCCCCTG
GAAGGGCAGGCCGAAGGCGTAGAGACCACTGGTTCGAGGAGGGCCCCAGGAGGTGGACACAGCCCCCTCC
CTCCTGACCAGCAGCCCATCTACTTCAGAGAGTTCCGCTTACAGTCTGAGGTCCCATCTGGCTGGATTA
CCATGGCAAGCACGTACGATGGACCAGGTGGGCACTTTTGCTGGCCTCCTCATCGGCTGGCCAACTG
AACTGCTCCGAGCTGAAGCTAAAGCGGCTCTGTTGCAGGCACGGGCTCCTGGGTGTGGACAAGGTGCTGG
GCTATGCCCTCAACGAGTGGCTGCAGGACATCCGCAAGAACCAGCTGCCCGGCTGCTGGGAGCGTGGG
CCCCATGCACTCGGTTGTCCAGCTCTTCCAAGGGTTCCGGGACCTGCTGTGGCTGCCCATGAGCAGTAC
AGGAAGGATGGCCGCTCATGCGGGGGCTGCAGCGAGGGGCTGCCTCCTTTGGCTCATCCACAGCCTCTG
CCGCCCTGGAACCTAGCAACCGGTTGGTACAGGCTATCCAGGCCACAGCTGAGACCGTGTATGACATCCT
GTCCCCGGCAGCCCCCGTCTCCCGCTCCCTGCAGGATAAGCGCTCTGCGCGGAGGCTGCGCAGGGGCCAG
CAGCCTGCCGACCTGCGGGAGGGTGTGGCCAAGGCCTACGACACAGTGCAGAGGGGCATCTTGATACAG
CTCAGACCATCTGTGACGTGGCATCGCGGGCCATGAGCAGAAGGGGCTGACGGGCGCCGTGGGGGGCGT
GATCCGCCAGCTGCCCGGACTGTGGTGAAGCCGCTCATCCTGGCCACGGAGGCCACGTCCAGCCTGCTC
GGGGGCATGCGCAACCAGATTGTCCCCGACGCCACAAGGACCACGCCCTCAAGTGGCGCTCGGACAGTG
CCCAAGACTGAGCCTGGGGTGCCCGGCACCCAGAGGGTGTGCCACCATGCTCCTGAGCCTCCCAAGAG
CTGCAGCCCACGGGCCCCGGCCCCGGCCTGGCCCTTCAGGGGATGGCCACTGTGAAGGACGCCTTCCCAGCC
TGCCCGTTGCCAATCTGCTGTGAGAGGGGGGCTCCCTGCCTTGGGGCCTTAGCCCTGGCTCTGCACTTT
TCCTCCGGGGAGAAAGGACACTGCCCTCCCCCGACCTGGGCCACACTGCTGCCTTCTCCAGGACGGA
GGCTTTTGGACCCTCGGACCCCATCCCACTCAGCCAAGTGTCTTTCTGTGTCTGGGGGGAGGAGGGGATG
ATATCCGTGTGGTTCGATGTATTATTTTTAAGCTCCGTGAGTGGTGGGTCAGTGTCTGCATGAAGTGA
ATAAAGTGGCCACCGCCA

>NM_001183080.1 *Saccharomyces cerevisiae* S288C Atg2p (ATG2), partial mRNA
ATGGCATTGTTGGTTACCTCAAAATATACAAAAGCGGCTGCTTCTTTACGTCCCTCAGCAAATTTTCGCTGT
TCTCCAATATAGATTTATCTAAGTGGACGTTTCTATAGGGTCTAAGTACATTTCTCGTTCCATGATGT
GAATCTGTCACTTGATGATCTCAACATTTCAAACGTGCAAATAAACGAAGGCATAGTTGACGAGCTTGTG
TTAAAATTAACAGTTTCTGGCGGTGTGGAAATCGATGGGTCTGGTTAAGATTTATCATGACACCTTTAT
ATTCCAGTGGCTCACAGGAACCTTCACTCAGATTTTTTGGTTAAAAGCATCCAAGATCTTACGAATTCGAT
GTTACAATTTAGTGATCCATTGACCACATATAATAGGTACAAAGAAGATGACATTAGCTCTTCAGACAGT
AGTAGTGATCTCAACTCTAATATAGAAGCTTCAAACCAGCCGCAAATGGTCTTATACTCTTCAAAATA
TGCGGAACAAGGCCCTTAATGTAGCCTTAGCGAAATTGAAAATAGCATTAAAGGACGTTACCATACGTTT
CATAGTGAATGATAGAGATCCTTCCGATAACATTGTGGAGGTTTCATCTAGAAAAGCATACAACCTTACT
ACAGACGCAAATTTACGACATATAAACATTGAAAATATCACCATTTCTCAATACAAAAACAAGCTGTAC
CCGACTCTCCTGTGCATCCTTTCAATAATGACGATCTGTCAAAAGCGTTTATTTATCAAAAAATGGAGGC
TACTTCACTTTATATGAGCGCCATGGAAGAGCAATCAAATGAAGACCCAGTGAACCCCAAGTTACACAA
GAAGAACAAGAGAATGATAAGTGAAGGAATCTTTAATGGAATAAATAATTTGAACATAGCTTTTAAAG
GTTTATCATCGGTCAATGATCTCAGAATGTCTAATATTGTTATTGATATTCAGGATGTTTATTTAGCGAT
ACACAAAATTTGTCGAAATCAAAAACCTCCACTTTGAAGAATATTATAGATATCATTGTTACACATTTGGAT
GCCAATGAAAGCTTTTCTTCCAGGATTTCCCAAAGTCTTACCTGACAAGCAGGAACCATCAGCTCTTT
CTTCTGTTGATATCAAATGTATATACTTAAACTTAGGCCAAGATATCACAGTAATTTGAAGAGCTTTAA
ATTAGAGCAAAGGAAAATAATTCATTGGCATTCTTTAGGCTCATTATTTCTAATTCGAGTCCATTG
ACAATTAGCCATAAAACTAAGCCATTGCTCACTGGAGAACAACCCCTCAAAGCATCGCATTAATATG
GCGACGAACTAGATATTATTATCAGTCATGATGGCATTGCGCATTCTTTAAAATCTTTCAGTTTGTTC
AAAATGTATGTCCTTTTATCAGAATAAGTCAAAGGGATGATGCCTCAAATAGCATCGGATACTAAAAG
ACCGTACAACCTTACCTCAAAGCAGTGAAGTTGTGCTTAAAGTTCCATATTTTTTATTATGTTCCAGG
TTTACCCTTCAATTCAGACTCTAACCCTGAGTTGTACATTGAGCTTGTAGACGTAATTAACAACTACC
TTCTCGGTGCACGAAAATATTGACAATGTGAGCATTACGATCTCGAACTTGCAATCCCCCTTACAACCTG
GGTTCATATGACGATACTTTGAAAGAAGCGCTAATTTATAGTTCTGTCCATGCAATCATCAAAGAAGTGA
TATTTAACGAAGAATATTCTGGAATAGTACAATTAGTCAAGATATTTCTGCGTTTGGAAAACCTTTTAC
GGATTCAAAGAACAGTGAATGTACAGGAAAGTCTAAAAGCAAGAGAGGCTCCTTTTTTGCAGAGAAGTGT
AGAGTACTTAATTTCCAGGTTTCGTTTACAAGCAGAGTTTATCCGCTAATTTTTCTCTCAAGATAGATT
CCATGAAGTTAAAAGTATCAGAAATATAGGGCCGCAATTTGGTTCTGTGGAAGCATTACTATCAAATAA

TTTCTTTGCGATTACGGATGACTCTCAAATTTGTATATTTTACAAAAGAACTTAAAGGTAGAAAAGAAAGACA
CCGTCATTATTAGAGCCACAAGAAATCATGTTCAGTAGTTTTGAATAAAGCAGTTAACGAACCTGTACTAT
ATGTTTCATAGAAGGGCGAATGGAAAGTTAAAAGTCATTTTTAACAACATTCGCATACATTACTATGCAAG
GTGGTTAGAAATACTAAAGAAAAACATCGGCCCGGATAATGCCAGTTCAAAGATGAACCTGTTTCACAA
AAGCTTAGTAAAAACAACCGACTTCAGGATTTCCCTGGGAACCTCAAATGTCTGGACTGCTCTCTAATTC
TGCACCCTTTTCAGATTA AAAAGTGTAAATGGTTCATTGTACTTGACAATCTAACAACCTGGTGGAAAGTTCATT
TATCCCGCAGGCAAAGCTTCTTTCAAAGGCGAATACACTCTTCTTAATAGATGACTATCAGAATTTCAA
ATTCAAAAAGATAAGAAGTGGCCTAGTTTGATAAATTTTTATGCTGGTCAAGGTTTCTCTGCAATCGGTA
AAATAGATACTTTGAATTTTTTAATAAACAAATCCGATGGTGCCTTTTTATTGGATTGTAAAAATAGAACA
AGTTGGTCTTTTCATTATGCGCGGATTCTTTTTCAAACCTTTTTGTTCAGCTTTGTATTGATTTAAAAATATCCT
CAGACGTTTCTGATGAGGAAAAATTTAGAACGCAGTTGAAAAATCCTATCGATGTATTCAAAGACATCG
ATTGTGATCTTTTCAATTCTGCCTTCATCCGGGAGAACAATCATCAAAATGATTACGACTCAGTGCATTT
GGTAGACAGTTTTCTCGACAAAACCTCACGAGTTCAACAATGGTGGCAGAAGTAAACTATCCTCTCAAGGT
TCATATGAAATGGACAGTTCTCTGGAAGTCCACAGGTGGTATTTTACTTCCCCATGAGAGTTATCTAG
ACTCTGCTCAGCCAAAAGAAGAAGATACTCCACCAATCGCTCAAAGAGCAAGAAAGGATGTGGATAT
AAGGGGTAGTATAGATGTGAAAAAGTTGTTATAAAAACCTATTTCGATGGGTATGATTGGAAATATACGCGG
AAATTTATCGCTAATACTGTTGAAAAACTGGATAAAGAGCTCAGTAAAGCGGAAGCAAGCAGTTTCGAAAT
CAAATGTACCCCAATCAGAGGCAAATATTTTTGACTCTATTTATATATCTGCTAACAAAAACAATGTAC
AGATTTGAGAAGAAATCTTGATGGTGGAGATCCAGGGGTTTCAAGAATTCCTTCTCTGATGTCTCTAAAGTT
AATTTGCGACCTTCTAAGCATTACAAAGCCCTGATTCAATTGAACAAAGTACATGTCAATTTGAAGAATT
ATCGAGTAGATGAACCCGATGAGTCTAACTCTGATAATTCCACAGATGTTTTGAACCGATGTGTAGTTTC
CATTTACGAATTTGAAATTTATCGATAATGTTCCCACGTCCACCTGGAATAAATTTGTAACCTTTGCTAAAG
CACGAACCGTGGCCACACAGTTCTCCGATGTTTCTTCTGGACCTGGAATTTATCCGGCCGATCGACTTTT
TGCAAGCAGTGGAAATTAGTCATGCAATTAATGTTGCGCCTTTACGCTTTCACGTGGATCAAGACACTTT
AGAGTTTCTAATAAGGTTCTTAGGGTTCAAAGATAAAGATTTGAATTAATTGATGAGTATCCAGATATT
GTATTTATTCAAAATTTAGCACTAATTCAAATTAAGTTAAGATTAGATTATAAGCCGAAAAAAGTTGATT
ATGCGGGTTTTAAGATCGGGCCAAACTTCTGAATTTGATGAATTTTTTTTACCCTTGATGGATCCAAGATTAT
TTTGAAGAGCGTAGTCTGTATGGATTAAATGGATTTCGATGAATTAATAAATAAACTGAAAGCCATTTGG
ACGCCGGATATTACAAAAAGCAGCTGCCTGGCGTTTTTGAAGGACTGGCTCCTGTGATCGTFTTATGG
CGATTGGGTGAGGGGTGAAGACCCTAGTCACAGTACTAATGTGAGAATACAGGCAAGAAGGGCATTTGGG
AAGGAGTCTGAAAAAGGGTGGCAATGTCTTCTTGA AAAACGACAACCGGAGATTTTGTGAAATTTGGGAGTT
AAATTAACCTCAGGGACACAGGCGATATTGGAGAACACCGGAGAACTATTCCGGTGGTGTGGTTCCAATG
GCAGGGTGTACGATGCATCGAAATTTGGCTCCGCTGATGGTGCAGACAGTGCAGTGCAGTGCATGATTTAGA
CTTGATACTTTTATTCGAGGAGGATCAGTTAGTTGGTAGTAAATATTCCAGGATAAGAGATCATGAGCCC
ACGGCAGTAGTCATCGATATGTCTTACCAGGGAGATCACAACGAACCCACAATAGTGAGTCTGTACGCAG
ATCAGCCCCCTCGACCTGCCACGGGTTTTGAAGGAGGCGTATAGTTTCATTAGAAAAGCATATGCATATTGC
GTACGATGCGGTATGGAGGGCAAAGGGACAGATGAAGGATGATAAACGGGGAGGGCCGAGCGCCGAGCA
GTTTTATGTTGCTAGAGCTGCACCTGTGGCAATTTATTCGGCCGTTAATTGGGGCCACTGAGGCAGTGTCTA
AGACTTTACAGGGAATAGCTAATCAAGTGGATAAGACGCATAACGAGCAAATCAATGATAAGTACAAGTC
CAATCGGACTGATTCTGTA

17. 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
MPWTFPWFTEFLKKRACRYLLQHLYLGQFLKEKLSLDQLSVDLYNRRGSIKDLELDVEALNE
ALDSSSVPLEIVDGFINQISVSVPWNTLIQSSTEMEIQGLEITVQPKQRMENVGGLETMF
NSMCSMTSSLQIAEDCLKSTSDADQGGDLGTFEFGVQKFAQTIDSVLCRVKVTLLIDTVVR
VEHLPDSAEGVALEIKIKRIEYFDDMAKEEGSPVDDSSRTTWEPAIAHKNLLIDGMQI
LCDEFSRPTHQTPSRMFSSDSYQQTTFMSTTSSPSTPVDNQQGTVPVSEVFSDFVQIAGFT
GKSSLKVKLKQEEGVQGPKEIELEVGGLHLLSPTQFHAVLDLVNGLFSPKSSNEGRER
ARSKSKPMNEEDYRKVETELQRQLHSDRFHPSHMDTLTATDLQDIMTHSIGDEQYFSLAP
DPMESSVNSNFSLASGRSGSTVTTTRSGPRKDGKAAKDSIQRFLDDPSAELCRYHLRAVF
FSVALLHENPSQKVDLSSAKANNKNQMKDIAAQYFQKMHFSFAASGGEVKALRAAFAEA
LPQDHLRLIGKPVNIEIVERTAPTHHCLTVDVDTAGFLDVVECLFNRTLQTIIEPDYTELAA
QLAHQGSQDKFNRTVCEISHF

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

TTTTGAAAGAGAAACTGTCTCTAGATCAACTGAGTGTGGATCTGTACAATGGAAGAGGCTCGATCAAAGA
TTTGGAGCTGGATGTGGAGGCTTTGAATGAAGCCTTGGATTCCAGCAGTGTACCACTAGAGATAGTGGAT
GGCTTCATTAACCAAATCTCCGTGTCTGTTCCCTGGACCAATCTGATCCAGAGCAGCACAGAGATGGAGA
TCCAGGGACTAGAGATCACAGTACAGCCAAACAGCGCATGGAAAATGTGGGGGGCCTGGAGACCATGTT
CAACAGCATGTGCAGCATGACCAGCAGTCTACAGATAGCGGAGGACTGCCTCAAGTCCACATCAGACGCA
GACCAGGGCCAGGACCTGGGCACACCTTTTGGAGGGCGTGCAGAAGTTTGGCCAGACCATTGATTCTGTGC
TGTGCAGGGTTAAGGTACCTTGATTGACACAGTTGTGAGGGTGGAGCACCTCCCTGACTCAGCAGAGAA
GGGCGTGGCACTTGAAATCAAATCAAACGAATAGAGTACTTTGACGACATGGCGAAGGAGGAGGGCAGT
CCCGTGGATGATTCCCTCCAGAACCACGTGGGAGCCAGCAGCCATCGCCCAAGAACCTGCTGATAGACG
GCATGCAGATTCTGTGTGACGAGTTTCTGTCGCCCCACTCATCAGACCCCTCCAGAATGTTCTCGTCTGA
CTCGTACCAACAGACTTTTCTGTCCACTACAAGTTCCCCATCCACCCCACTGGACAATCAAGGTGGGACG
GTCCCGGTATCCGAGGTCTTCTGTGACCCGGTACAGATTGCCGGATTACAGGAAAAGTCCAGTCTGAAAAG
TCAAACCTCAAACAGGAGGAAGGCGTGCAGGGGCCAAAGGTGGAGATTGAGCTAGAAGTTGGAGGACTCCA
TTTGTGTCTCAGTCCCACACAGTTCATGCTGTCTTGGACCTTGCAATGGCTTCTGTGCCCCAAAATCC
AGCAACGAGGGCAGGGAGCGGGCAAGGAGTAAAAGTAAGCCAATGAATGAGGAGGATTACAGAAAGTGG
AGACGGAGTTACAGAGACAGTCCACTCGGACCGCTCCACCCAGCCACATGGACACACTGACTGCCAC
GGATCTCCAAGACATCATGACACATTCCATTGGGGATGAGCAGTATTTTTACTAGCTCCTGACCCAAATG
GAATCATCAGTCAACAGTAACTTTAGCTTGGCTTTCAGGCAGATCTGGAAGCACTGTAACCACCACACGAT
CAGGGCCAAGAAAAGATGGGAAAAGCTGCAAAAAGATTCTATTAGCGTTCCTTGACGACCTTTCAGCAGA
GCTCTGTAGGTATCACCTAAGGGCAGTCTTCTTCTGTGTTGCTTCTCCACGAAAACCCGTCCCAAAAA
GTGGACCTATCTTCCAGTGCCAAAGCCAACAACAAGAATCAGATGAAGGACATTGCAGCCAGTACTTCC
AGAAGATGCACTCTTTTGTGCGGGCAGTGGAGGAGAGGTGAAGGCCTTACGTGCTGCCTTCGACAGGGC
ATTGCCTCAGGACCATCTCAGGTTGATAGGTAAACCGGTGAATATAGAGATTGTTGAGAGAACAGCCCT
ACCCACCATGTTTGTGACGGTAGACGTAAGTCTGCTGGTTTTCTAGATGTGGTAGAATGTCTGTTCAACAGAA
CTCTTCAGACTATTGAGCCAGACTACACTGAGATTCTGGTATTCCCCCGAGATGTCTCAACCAAACAGGG
GCACATGTACAGTAGCATGCACTCAGGTGCACCTGCACTCAAGGCCCATGTCAAGTCAGTGCAGCAAAAC
AAGAGATCACAGAGGTCTTTCAGGTGGACCCAGGACAGAGATTAGCGTCAATTTGGCCAAAACCTGGAGTGTG
AATTGGATGTGACAATTATAGACAGGATAGGAAGCCTGATAAAGCCCTCTCCTCACCAGCCATACAATGG
CAGCACTGCAGCCTCACAGGGGGGTCCATTGTACAGTTTCTCCAGACGATGGAGGATGAGTCTGCTTCA
GACGAGACAAAGATCGATCTCAGTGTCAACTGTCTGAGGTCAAACCTCACACTCAGATTTCCAATCCCTG
ACCTGAGGAATTGGGTGAGAGGTCAGTCAAGCTGCCCTGGTGGCAGAAGAACCCTGAGGGACGAGCTGCTGAT
CTTGGATTACAGGAGGGCCGGTCCAGACTTCTTCTCTAACCAGCCTATCCAGCAAGTCTGAGGTTGTTA
TCCAGCAGAAATGTGCTAGGTTCTTTCCGTATTCTTCCAAACCAGAGTGCAGTCCCTTTGATTTGTTA
GCTGTGAGGGAATTGATGGACAAGAGGGCTTCAACTTCCACAGATAATAATTAAGTTTACAGAACAGAC
CATCTCTGTTCTGGATGAAGAAAATCCAGACTCAGATAACAGTATTCTATGGACTCGTTGAATGGTGCT
TGTGAATTTGCCAAACAAGACACGTACCTTTTTTCTACAAAAGAAAACACATGTATGGGAAGGGGGAGATGT
CGGACCAAGCTACTCAGCATGTGAGTGTGAGATGGTGTGCTGGCAACAGAGAGGACATGGCCGACTT
CCAGGAGAGAGCCTCGGCCAACTGCCTGACCCTGGTCCAGCTAGTCTTACCCTCATCAACCTCTACATT
CCAGACCAGAAGTTCTATGAAGTTCTGTACAATAGGATTAGCAATGATCTGTTGCTATGGGAACCAATGG
CACCTGCTCCAATTCGACCCAGGAAGTTGGGCCTGGGTCTATCCAGCCATTTGATCTGAGCTGTTATAC
TCATGCTCTGCAGGAAAATTTTAGTATGGCAAAGTCAGCAATACAGTATGACTCTTCAGATGAGGAGGAA
GATAGTAGTTTTGGTTACTACAGTATTCATGACAACAAGCATCCACGCAGGACATTTGACCAGAAGTCAA
GGCCAAGTAAGATGTGTCTGCTCAAGATAGACAAAAGGGAAAATCACAGCAAGGACCGACTCAAAGGC
TGAGGATTGCCATGGGGAAGTTATGGGTGTGGTCAAGGATGCCAATCTGTTTGTGGCCTCCAGTTACCAA
GGAAACCCACTGCTTCAGTATATCTGCTTCTATTGCAATAAAGCAACTTTATATCATAATGCTGCAGTTC
CAGATAAAAAGGAAGAATTTGAGATAGAGAATTTGGACTTTGAGACAATCCCTGCCACCTGGAGAAGAG
TTGTATTATAGATAGGTCTGAGCCTGGGGTCTGTGTACCAGTCAGCTGATGTCGAGTCCACGGTTCAGG
GACATGGTGTGAGTGGCGGTGAGAATCAAGCTCGACTCCACCCCTCAGTGACCTAACACGGGATGAGA
AAATCAAGGAGTTTACAGTAGCAGTTGGTGTCACTGGAGCAACTTAAGACACAAGATGGCCGAAACAGA
TATGAGCTGGATATCTCAAATTTTGAACTTTTGAGTGTGAAGGACTACGACATCCTTGGATATGCTACT
CCAAAATCCTGACCAGCTACACGTACATCTCTGGGACTGCGCTGTGGATTACAGACCATTCATCTAC
CAACCAAAGGAGTAGTAGCAGCCAATTACTTCAGTATTTCCAGTAACATAGTGGCCAACCTCCAGACCTC
GCTGCTAAGGTTTGTCTTGGAGGATGCTGGGATGATTTGTCTCAAAAAGAAAAGGGAGAGAATCCACTGTC
GACCTCAAAAAGATTATGTATGTGTCCTTGATGTGGAAAAGTTTTGAATTGGAATTGCGTACAAGTGCAG
GAAAAGATCCAAAGTTTCCAAAGATGGACTTGGCGCTCCGAACCAACAAGATCAACATGAGGACGTGTAC
CGACTCTTGTAAAGGCTCTGTTTGTAGTTAATTCGATACTTTGCTAACGATGGCGACCTCGTGGAGTATGAG
GAGGAGCCCAATAAACGCCAGAGTCTGGACCTAGAGATGATGAATAAGGAGGAGGCTCTAGTGTATG
AGGACTCAAAGAAGAAAGAGTTGAGTGTGAGTCCAGATTGGAAAACCTTTCTCTCATCTGGAGGATGCCAT
GCAGGAATCTGGATCCGGATCAGATAATGATGGAAGTGAAGCTCCAAAACAAGTCCCTAACAAAACAGAA
GTGTTCTTTGTGGCCAGGGGGAGAGGACGGATGCCAGGTGCCCCCTGCAGGGGTGATGCGACCTATTG
TGATAACAGCCAGTGGCGACTCGGTAACCAGTAGTGCTGTGTGTCAGAGAGAACTGATATCTTCAGCGATGA
GGAGGAGGAGGAAGAGGACTTCTGTATCATTGACGATGCAGGGCTGGGCATCACTCCAAGAGATGGAAAAG
CCAGAGGTAAGATATTCACCGATGAGCCGATAGAGATCAAAGACAACCTACTTCAGTGCAGCTCATGGTA

AAACGGATCTCCTGAAAGCCCCGACCCTTCCCTAACGCCGAGTACAGGTACACCCTAAAGGAGCTGAC
CATCGTCTGGCATATGTATGGAGGGAGCGACTTCTCCGATACACCCGTCCAACAGAAAACCGGTGGAAAACA
GAAGTGGTCATGTCTAGAAAAATGAAGGATTATGGAGAATATGTAACAGAGACCTCCGTACGATTTGCTT
CCAAAGGGTTCGTAGTGGACCGTATCCCATGGACACAGCGTGGAGGGGTGGGGAGGGACCACGACTCT
GATGGAGCTCCAGCTCACCAAGGTGAGATTTTACGATGAGAGGTACCCTGGTACACAGAGCAGGCCTCT
AGACAGGTGCTGATTATCAGTGTGCGGAAATCAGGGACCGACTGTCTGACTCCAAGATCAACAAGTTTC
TGTACCAGTACTCCTCTGAAAACCTTGCCAAAACAACCAACTCCAACATGGTGTACATAAAAAGCATTACA
CAAGAGACCAGATCCCAGTGTAAAGACTGAGGAGTGTCTATTGAGAGTTTCTCTACAGCCACTGAGACTC
AATATTGACCAGGACTCCTTGTCTTCCCTAAAGAAATTCTTACAGAAAATAACCGGTGGTAATGTAGATA
ATCCCTCTGACCCTGACCCCAAACAAGGGCAAGGTGAGTATCTGGAGCCAGTGGAGCTCCAGCCCCCTGT
GATAACAGTTGGTCAACCAGAGTGCCTCCGGGGAGGAAAGAACCCCAAGAACTATTGATGAAGTTTGGT
GAGATGCAGCAGAGCTTAGCCAGTCAAGGATCGATGATGTCGTCTGCCTCTGTTGCCAGTAGTGACTCAG
ATCGCACGGAGCAGTCTCAACCAGTGTTCATCAAAAACCTTCATGTTTTCTCCTGATGTGCCAATCAGACT
TGACTACCATGGAAGAAGTGGGTTCGACAGAGAACATGGGACCCTGGCGGGTGTGTTGGTGGGACTGGCC
AGTCTTAACTGTTCTGAGCTGAAGTTGAAGAGGCTAAATTATAAACATGGGCTTCTAGGGATGGATAAGC
TTCAGGCTTACTGTATCAATGAGTGGATCAGCGACATCCTGAAGAAAACAGCTTCCCAGCATCTGGGTGG
TGTAGGACCAATGCACTCATTTGTACAAATAGCACAAAGGAATTCGAGATCTCTTTTGGCTGCCTGTGGAG
CAATACAAGAGAGATGGCCGATTTGTTCCGGGGATCCAGAGAGGGGCGACCTCCTTCTCCACCTCCACTG
CCATGGCGATGTTAGAAGTACCAACCGAGCCGTCCAATCTGTTGAGTACGTTGCTGAAGTGACCTATGA
CATGGTGCAGCCTGGACCCAGCTGTGAGTTTACGCGACGACACTGAGGGGTCTCCAGCTGATGTCAGA
GAGGGTGTGGAGAATGCTTACATTGCCATAACAGAGGGCTTACGTAACACAGCATATAACATTTGGAGG
TGGCAACAAAAGAACACCAGCAGAAAGGAATGACAGGGGCGGTGGGGGAGCCATTAGACTGGTTCCCTCC
AACAGTTCTCTCCCTGTTCATCATAGCCACAGAGGCCACCTCCAATGTCTTAGGGGGCATGAGAAATCAG
CTGCAGCCAGATGCTAGAAAAGAAGATGAAGAGAAGTGGAAAGGGAACCAGACTTAAGGGACTAGTCAAG
ACTGTTACTGTTGACTTTTTTAAAAATATATTA

>XM 006720187.2 PREDICTED: Homo sapiens autophagy related 2B (ATG2B),
transcript variant X1, mRNA

ACAGCCGGGAACGCGCCTCGCGGATGACAACAAATTCGTGCGCGGGCGGCAGTGGCGGTGGCTGCCTCAG
CCCCTGCCGCCTCCTCTCGCGCTCTCTTGCCTCTCTCCGAGCCGGTTGGGACCCCTCCTCGGAAGTCCCC
TGGCCTGGGGCCAGGAGGACCCCTCTGCGTCTTGCCTCCGCCAGGCCAGCGCGAGCGGTGCGGCGCCGG
CGATGGGGTCTCCTTGAAGGACTCCCGGCACCAATAGGGATGGAGGGGCGCCAGGCTTAGGCCCCG
CCGCGGGCTGGAGCCGGAGTTCGCTACCCCGAGCCGGAGCCGTCGCAACCCGAGCCAGTGCAGCCAG
CTGCCAGCAGTCACTATGCCTTGGCCGTTTTTCGGAGTCCATCAAGAAGAGGGCCTGCCGTTACTCCTGC
AGAGGTACCTGGGCCACTTTCTGCAGGAGAAGCTGAGCCTGGAGCAGCTCAGCCTGGACCTGTACCAAGG
CACCGGGTCCCTCGCCAGGTCCCCTTGGACAAATGGTGTCTCAATGAGATCTTGGAGTCAAGCAGATGCA
CCCTTAGAAGTCACTGAAGGATTCATTCAGTCAATTTCCCTGTGAGTTCATGGGGCTCTTTACTGCAGG
ATAATTGTGCACTGGAAGTGAAGGATTAGAAATGGTCTTCCGGCCTAGACCTCGCCAGCAACTGGTTC
TGAGCCTATGTATTGGTCAAGTTTTATGACCAGCAGTATGCAATTGGCAAAAAGATGTCTTAGCCAGAAA
CTAACAGATGAACAAGGAGAAGGATCCCAGCCTTTTGAAGGACTTGAAAAGTTTGTGAAACCATTTGAAA
CAGTACTAAGAAGAGTAAAAGTCACTTTTATAGATACTGTTTTGAGAATTGAACATGTGCCAGAAAATTC
CAAACTGGAAGTGCCTTGAATTCGAATAGAAAAGACTGTGTACTGTGATGAAACTGCTGACGAATCC
TCAGGAATTAATGTGCATCAACCCACTGCTTTTGTGCTCACAAGTACTTCAGCTCTCTGGAGTGTCTCTCT
TCTGGGATGAGTTTTCTGCATCAGCCAAATCTTCCCCAGTGTGTTCAACTGCACCAGTGGAAAAGTGGCC
AAAGCTCTCACCTAGCTGGAACCCCAAATTTATTTATGAGCCACACCCACAGCTAACTAGAAAATTTACCA
GAGATAGCACCTTCTGACCCAGTGCAGATTGGACGGTTAATTGGTAGGTTGGAGTTGAGTCTCACGTTGA
AACAGAATGAAGTGTCTTCTGGAGCTAAGTTGGATGTTGATGGACAGATAGACTCTATTCATCTACTCCT
GTCACCAAGACAGGTGCCTTGTCTTTGGATATGTTGGCAGCTATTGCTGGACCAGAAAATTTCTAGCAAA
ATAGGGTTAGCTAATAAAGATAGGAAAAATCGACCCATGCAGCAGGAAGACGAGTATCGAATTCAGATGG
AATTAACCGGTATTATTTGAGAAAAGATTTCCCTCTCTGTGGGTGTATCTTCAGAGCAAAGCTTTTATGA
GACAGAAAACAGCTCGTACACCTTCTAGCCGTGAAGAAGTATTCTTCTCCATGGCTGATATGGACATGTC
CATAGTCTCTCTCTCTTCCACCCCTTGGGGACCCCCCAAACATGGACCTTGAGTTATCATTAAGTATGTA
CATATACAAATACCCAGCAGGATCTCCATTAAGTGTACTGTGCTTCCAGCCACTTGGGGAGAGTTTCTT
TGATCATCATAAAGAACAGCCAGTAAGAGGGTCAACATTTCCATCCAACCTAGTTTACCCAAACCTTTA
CAGAAGACATCTCTCCATCTAGATCTGTTTTCAGTGGATGAATCAAGGCCTGAACTTATTTTTAGACTAG
CTGTGGGAACTTTTTCAATCTCTGTGCTTACATTTGATCCTTTATCTCCACCTGAAACGTCACAGAACCT
TAATCCATTGACACCTATGGCAGTAGCTTTCTTTACTTGTATAGAAAAGATTGATCCAGCAAGATTTTCA
ACAGAAGATTTTAAGTCTTTCCGAGCAGTGTGTTGCAGAAGCTTGCTCACACGATCACCTTAGATTTATAG
GTACTGGCATTAAAGTATCCTATGAACAAAGACAAAGATCAGCTTCCCAGATTTTTAGTACTGATATGTC
CATTGGGCAAATGGAATTTTTGGAGTGCCTATTTCCAACCTGATTTTCACTTCTGTTTCTCTCACTATACA
GAGCTTTTTAACGTTCCATTCCAAGAAGAACTGGTTCCCATTTCCCTGTGTGCTTTCAGCTTCAATTATA
AGCATTCTGAGAATAGAGGGCCCCAGGGTAATCAAGCAAGACTTAGTTTCAAGTTCCTCACAAGGCAGAAAT
GCAAATTAATTAATCCAGTGTGTTGTGAGCTGGATATCAGTATTGTGGACAGGTTAAATTCCTTGTCTT

CAACCACAGAACTTGCCACAGTAGAGATGATGGCATCCCACATGTATACTTCATATAATAAACATATTA
GTCTGCACAAGGCTTTCACTGAAGTGTTTCTAGATGATTACATAGTCCTGCAAATGTGCGGATATCAGT
ACAAGTTGCCACACCAGCATTAAACCTTTCTGTTGCTTCCCAATACCTGATCTTCGATCTGATCAAGAA
AGAGGACCATGGTTTAAAGAAGTCACTTCAGAAGGAGATCCTTTATTTAGCCTTCACAGATCTAGAATTTA
AGACTGAATTTATAGGAGGATCAACCCCAGAACAAATTAATTTGGAACCTTACCTTTAGAGAACTAATTTG
ATCGTTCCAGGAAGAGAAAGGAGATCCATCTATTAAGTTTTTCCATGTGTCTAGTGGAGTAGATGGAGAT
ACAACATCGTCAGATGACTTTGACTGGCCACGAATTGTACTGAAAATAAATCCACCAGCCATGCATTTCCA
TTTTGGAGAGAATTGCAGCTGAAGAAGAAGAGGAGAATGATGGTCACTACCAGGAGGAAGAGGAAGGAG
TGCTCATTCCTTGAAAGATGTTTGTGATCTAAGAAGACCAGCCCCATCTCCTTTTTCTTCTCGTAGAGTA
ATGTTTGAATGAACAGATGGTGATGCCAGGAGACCCTGTAGAAATGACAGAATTTTCAAGGATAAAGCAA
TCAGCAATTTCACTATGTGCTGGAACCTTACGTTACCAATATTTATGTAACACTACCTAATAAGAGCTT
TTATGAGAAGCTTTATAATAGGATCTTTAATGACTTGCTACTGTGGAAACCAACAGCTCCTTCACCAGTG
GAGACATTCGAGAATATTTCCATGTCATTGGGCTTTTCACTAGCCAGTCAGCTCATTAATACTTTCAACA
AAGATAGTTTTAGTGCATTTAAATCTGCAGTTCACATGATGAGGAAAGTGGATCTGAGGAGGAGACTTT
GCAGTATTTTTCCACTGTTGATCCCAACTATCGTTCTCGCAGGAAAAAAAATAGACTTCTCAGAACAAG
AACTCTCAGAGTTTTCTCTCAGTTCCTTCTGAATATTAATCATGGATTAATAGCAGTGTTCACAGATGTGA
AGCAAGATAATGGAGATCTGTTGGAAAACAAGCATGGTGAATTTCTGGTTAGAGTTCAATAGGTTTCATT
ATTTTTGTGTGACAAAATATGAAGGTTTTGATGACAAGCACTACATTTGCCTTCATTCTAGCAGTTTTCAGT
CTGTACCATAAAGGCATAGTGAATGGAGTGATTCTCCCGACAGAAAACAGACTTCCAGCTCAACCCGCC
CACACTGGTTGGAACCTACTATTTATTCCTCTGAAGAAGATGGCCTCAGTAAAACTTCTTCAGATGGAGT
TGGAGGAGACAGTTTTGAATATGCTGTCTGTTGCCGTTAAAATATTGTCTGATAAATCAGAGTCCAATACA
AAGGAATTTCTCATTGCCGTAGGACTGAAAGGAGCCACTCTCCAGCATAGAATGCTTCCTTCTGGGCTTA
GCTGGCATGAGCAGATTTTATACTTCTTGAATATTGCTGATGAACCTGTTTTGGGATATAATCTCCAAC
TTCATTTACAACCTTTTCATGTTTCATCTTTGGAGCTGTGCACCTTGATTATAGACCCCTTTATTTGCCAATC
CGATCTCTTCTTACCGTGGAAACATTCAGTGTTCAGTAGCGTTGCATTGGATAAATCTTCTCTACTC
TCAGAATAATCTTGGATGAAGCTGCTTTACATCTATCTGACAAAATGCAATACTGTCACTATAAATCTGAG
TAGAGATTATGTTTCGTGTGATGGATATGGGGCTTTTTGGAGTTAACCATAACTGCAGTGAAGTCTGATTCT
GATGGAGAGCAAACCTGAGCCCGCTTTGAGTTACACTGTTCCAGCGATGTTGTCCATATCAGAACGTGCT
CAGACTCTTGTGCTGCGTTAATGAATCTCATTAGTACATTGCAAGCTATGGTGACTTGCAGACACCTAA
CAAGGCAGATATGAAGCCTGGAGCCTTTCAAAGAAGGTCTAAGGTAGATTCCAGTGGTTCGATCATCCTCA
CGTGGTCCAGTACTTCTGAAGCAGATCAACAAATGTTACGAGATCTGATGAGTGTATGATGAGGAGAGA
TCGACATGCAACAAGGCACCTCGTCAGTAAACCAACAGGCTAATGGTGTTTTTGGATGAAAAATCTCAAAT
TCAGGAGCCATGTTGTTTCCAGCCTCTTCTGTTTCTGACGAGAGTGGGAATGTATCCCAGGATCCGGC
CCCACCTATGCCTCATTCTCTCACCATTTTATCAGTGTGCAATGACAGGTGTGCCACTGAGAATGATG
ACTTTTTGCATTCTTTTTGCACCAAAAAGCAGCCATGCAGGAGAAGGAAGAAGAACAGTTATAAAAAATCAT
GGTTGATGATGCAATTTGTGATAAGAGACAATTTATTTTCACTGCTGCCCGTTAATAAGACCATACGAGCAAA
GCCCCCTTACACTTTCCCATTCCTGTGATTGCTATGTGGTGAAGGAGGTCTCTCTTGTCTGGCATCTTT
ATGGAGGAAAGGATTTTGAATAGTCCCTCCCCTTCTCCGGCTAAAAGTTATATTAGTCCCCACAGTTC
GCCTTCTCACACACCCACGAGACATGGACGTAATACAGTATGTGGGGGAAAAGGAAGGAACCATGACTTT
TTAATGGAATACAGCTAAGCAAGGTGAAGTTTTCAGCATGAAGTCTACCCGCCATGCAAACTGATTGTG
ATTCCAGCCTCTCAGAACACCCAGTCTCCCGGCAGGTGTTTATTGTTTTCAGGATCTTGAGATTCGAGATCG
TTTGGCAACATCACAAATGAATAAATTTTTTATACCTGTATTGCAGTAAAGAAATGCCTCGAAAAGCTCAC
TCCAACATGTTGACAGTGAAGCCTTACACGTGTGTCCAGAATCTGGCAGGTCCCCACAGGAGTGTGCT
TGAGAGTGTGCTGATGCCGCTCCGCCTCAATATTGACCAGGATGCTTTGTTCTTCTTGAAGGATTTCTT
CACAAGTCTTTCTGCAGAAGTAGAGCTTCAAATGACTCCAGATCCAGAAGTTAAAAAGTCTCCTGGAGCT
GATGTCACCTGCAGTTTGCCAAGGCATTTGAGTACCTCAAAGGAGCCAAATCTGGTTATTTCTTCTCTG
GGCAAAAACAGCCTTCCCAAAATGATAGTGCCAATTCAGTGAAGTGGTAAATGGCATGGAAGAGAAGAA
CTTCTCTGCTGAAGAAGCATCTTTTAGGGATCAGCCTGTGTTTTTTAGAGAATTTAGATTCACGTCAGAA
TTGCCATTCGACTTGATTATCATGGCAAACATGTATCAATGGATCAGGGTACGCTAGCTGGGATTTTGA
TTGGTCTGGCTCAGTTAAACTGCTCTGAACATAAGTCTCAAGAGGCTTTTCTATCGACATGGTTTACTAG
CGTTGACAAAATTTCTCATATGCAATCACTGAGTGGCTTAATGACATTAAGAAGAACCAGCTACCAGGA
ATCCTGGGAGGTGTTGGACCTATGCATTCAGTACATAATAGTACAAGGCCTAAAAGACTTGGTCTGGC
TCCCAATAGAGCAGTACCGGAAGGATGGCCGATTTGTCAGAGGGTTTTCAGAGAGGCGCTGCTTCTTTGG
TACCTCGACAGCGATGGCTGCTCTAGAACTCACAAACAGAATGGTTCAAACCATACAGGCAGCTGCAGAG
ACTGCTTATGATATGGTGTCTCCTGGTACCCTTTCTATCGAGCCAAAGAAGACCAAAAAGGTTTCTCATC
ACCGGTTAGCCCACCAGCCAGTAGACCTGAGGGAAAGGTGTGGCAAGGCCTACAGTGTGTGAAAGAGGG
AATCACAGACACGGCTCAGACCATTTATGAAACTGCGGCTCGAGAACACGAGAGCAGAGGGGTGACTGGT
GCCGTGGGCGAGGTTCTGCGCCAGATTTCTCCGGCAGTGGTGAACCTCTGATTGTTGCCACAGAAGCAA
CGTCAAACGTGCTGGGTGGCATGAGAAACCAAAATTAGGCCAGATGTCCGGCAAGACGAGTCAAGAAATG
GCGCCACGGGGATGACTGATGGCTTGAACCTGACAGTGTGAAGATAAGGAGAGTGAACACCAGGAGCTCAG
AGTCTGACAGCAGCTTTCAGAGGAAGCTCGTTTTAATTTTTATTGTGCTCATCTCAGGAACAAAAGCATTTT
TTAGTTAAATAATTTAACATCAAAAACAACATGCAACCAAAAACCTTCTGACATTTATAGTTGATACTTGCC
TATAGAAATGTTTGGTGGCTGGTGTCAAAGGTCTTAAAGCATTTGCTGCCAAGTTAGTGAAGGCTCAC

TTTTGTTAAGATGACTGTAATTCTCCTTGTTACCGACGAGAGATCATTGGAAGCTGCCTTCTAACACTTT
GTGTAGCTCTGTGGAGTTGGATTTTCTTAAGGTTTAAAAAGAATCACAGCTTCGGAACTTTTAACTGAAA
ATGAGAGACAGAAGCCACAGGGGAAGCAAAGCAAATAGGATTTTCAATATAAATATCAGTGTGAAAAAT
AACCTATTCTGTTGAATTTAGTGTTCATGCACTTGAGAACAACATTATTTCCATTTACTCCGAAAAATCCT
TCTGTGGGGGTTTGAGAAAGTGAATGTTGCAGACATGTTCTGTTGTGTTGCACTTTATCCTGTGTTTATG
TGTATGTGTTTTTAGATTAATTCAAGTTGTGTGCTATATTTCTTGTATAATTTACAAAGTTACACAAAAT
ATAAAGAGCAGTAACTTGTCTGAAAGTTTTTGGCAAAGGAAGGTAACCTCAATGTAATAGCTTCCTTTA
AGAGTACAGGAAAATGCATTCTGTAATGAAGTGGGGCCCATGTAATTGTTTATATTTTCAGTTTTAAGCA
GGTATAGTGCAGGCTTGTTAGGAATGTGTGGAAGGGAAGATTGGAAGTGATTTTTCTCTTTTTAAAAGTA
AACAAAATTCTTCAAATATGCCCTAGTTAACTATTTTCAGCATACCATTTTTTACTTGGTTAACAGTGTACA
TTTTGATAACCTATCAGGAATGAATAAAGTATTTTTATTTAAAGGTGATATTGTTTTATGCTTCCATGAA
TATTTTGCTTTTCTTAGAGCATATTCATAGATGCAGTACTGTGATTTACCACAAGATAATTGGGAACACT
TTCTCAAATCGATTTTGGTTAATATCAGGTAAATCATTACCTAGGAGTAAGAGGGAAATGTTGTCAAT
TCCTGACTTTAGATTTGATCCAGCAGAAAGAAAAGGTGGAACCTTGTATATATCCACTGTTGAAAGTTGCA
TGACCTGACTTCTGTTTTCTAAAGTTGGGGGAATATTATTGAACTTCAATTTCAGAACTGCATTTCAAT
TTGGGGCTTGAAAATGTAGTTAAATCAATTTTCGTTCTCTAAATTTTCTAAGCAGGAAAGCAATGTAAC
CAAAAATCAAATGTTTAGAATTTATAAAAAATGGGGTTATATAGCTTTTAATTTTAGTTTTCTTTTACT
GCCAAAAAAGTTAAAAGACAACAGCGTAACCACCTGTTTAAAGCACCCTGGGACCATCTCTTATTCGGGT
AGAGCCTGGTCTGGCGACACACTAACAGGAAGGCGTGCTGTGTTACCGGGAAGGCGCCTCTGGCTGTGG
GGTGCCTTCTGACCACCCGCTCAGATGCCAGCATTTTCCATTTGCCCTTAAAGGAACTTGCTATGTGTG
TTAACCCAGTTATGATTAGTCAAACCTGGAAAACACTTGATCAAACCTAAAATTTGAAAATCTGTCTAACT
TTTAAATATACTTTCCACAGTTGTACTTAAAGTTCAATTAACCTACAGTATAGAGAAAAATAATTATCTCT
TCTTTGCACCCGGAGTTGCAAACAAATTAAGTTTACAAATCTCATTTAAACATATATCTTTGTAATGTAA
TCTCCGCGTTCTTTCTTTGTTCTACCCTCCTGCACCTGTTGTCGATGTAATCATTTTGGGAACAGAAAC
GTTGTGTCTCAAAAAGATTGTTGTCAGTTGAGCAAGATGTTCTTTACCTGAGATTCTGAAAAGATGTT
TATCTATATCGGAACACTTCTACATTATTAATGTCTTAAAGCTTTTTCTTTTTTA

>sp|P53855|ATG2_YEAST Autophagy-related protein 2 OS=Saccharomyces
cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATG2 PE=1 SV=1
MAFWLPQNIQKRLLLYLVLQQLSFLSNIDLSNLDVSIKSKSHFSFHDVNLSDLDDLNIQVQ
INEGIVDELVLKLTVSGGVEIDGSLRFIMTPLYSSGSQELHSDFLVKS IQDLTNSMLQF
SDPLTTYNYRKEDDISSDSSDLNSNIEASKPAANGSYTLQNMNRKALNVALAKLIAL
KDVTIRFIVNRDPSDNIVEVHLESIQILITTDANLRHINENITISSIQKQAVPDPVHP
FNNDLDSQSVYLSKMEATSLYMSAMEEQSNEDPSEPQVTQEEQENDKCKESLMEINLNI
AFKGLSSVNDLRMSNIVIDIQDVHLAIHKIVEIKNSTLKNIIIDIIVTHLDANESFSCQDS
QSPSPDKQEPSALSSVDIKCIYLNLGQDITVILKSFKLEQKENNSLAFSLGSFYNSSSPL
TISHKTKPLLTGEQTPQSIALNMGDELIIISHDGHIAHFFKIFQFVSKCMSFYQNKSKGM
MPQIASDTRKTVQLTSKAVKLSLKFPYFLLCFQVSPFIYDSNRELYIELVDVFKKLPSRC
TKILTMSSITISNLQSPQLGSDYDDLKEALIIYSSVHAIKEVIFNEEYSGIVQLVEDIS
AFGKLFDTSKNSECTGKSKSKRGSFLQRSVRVLNSSRFVYKQSLSANFSLKIDSMKLVKVS
EIIIGPQFGSVEALLSNNFFAITDSDQIVYFTKNLKVVERKTPSLEPQEIMSVVLNKAVNE
PVLYVHRRANGKLVIFNNIRIHYYARWLEILKKNIGPDNASSKDEPVSQKLSKKQPTSG
FPWELKCLDCSLILHPFRLKSVMVIVLDNLTGGSSFIQAKLLSKANTLFLIDDYQNFK
IQKDKNWPSLINFYAGQGFSAIGKIDTLNFLINKSDGALLLDCKIEQVGLSLCADSFQTF
CQLCIDLKYPTFPDEEKFRQTKLNPIDVFKDIDCDLNFSAFIRENNHQNDYDSVHLVDS
FLDKTHEFNNGARSKLSSQGSYEMDSSSGTATGGILLPHESYLDSAQPKEEDTPPIASKE
QERDVDIRGSDIDVEKVVIKLFDGYDWKYTRKFIANTVEKLDKELSKAEASSSKSNVPQSE
ANIFDSIYISANKNNVTDLRRNLDGEIQGVQNSFSDVSKVNLRPSKHYKALIQLNKVHVN
LKNYRVDEPDESNSDNSTDVLRNRCVVSIEFEIINDVPTSTWNKFVTLKHEPWPWPHSSPM
FLLDLEFIRPIDFLQAVELVMQLNVAPLRLRHVDQDTLEFLIRFLGFKDKRFELIDEYPDI
VFIQKFFSTNSIKLRLDYKPKKVDYAGLRSGQTSSELMNFFTLDGSKIILKSVVLYGLNGFD
ELNNKLIKAIWTPDITKKQLPGVLEGLAPVRSFMAIGSGVKTTLVTVLMSEYRQEGHLGRSL
KKGGNVFLKTTTGDFVKLVKLTSGTQAILENTEELFGGVGSGNRVYDASKFGSADGADS
DTAAVLDLDTLFEEDQLVGSKYSRIRDHEPTAVVIDMSSPGDHNEPTIVSLYADQPLDLP
TGLKEAYSLEKHMHIAYDAVWRKAGQMKDDKRGGPSAAAVYVARAAPVAIRPLIGATE
AVSKTLQGIANQVDKTHNEQINDKYKSNRTDS

18. 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
MGEMSDRFHYVYSCDLVNLQIKIGTLEGERQRPDYKELLDDPMLKFSGVYGEECSDLYV

TCQVFADGHPLSLSMSTSYKAFSTRWNWNEWITLPVKYSDLPRNAILSLTIWDIYGTNKS
IPVGSTVIPLFGKRGTYRQGMHDLKVPDMLPDPSSNSTTPGKSKDHKQMSKLAKLKSKK
HRDGHMLKVDWLDRLTFREIEMINEKQKRDSKFMYLMI EFPLIHYEDIEYSVVYFEKDGD
EPLVYKTI PDLVQVPDPEIDMENLVESKHHRLARSLRSGPTDRDMKPD AKTRNLLHEIVR
YPPTKTLTSEEDLVWKFRFYLCNQKKALTKFLKCVNWKQPQESRQGI ELLTRWSPMDVE
DALELLSPAFSHPTVRKYAVSRLRQADDQDLLLYLLQLVQALKYEDFEEIMRYNDSIVDR
KDSVSDTSAPEKTRTTSVLSRASSNESILHALGGSSPSQSESPESKLEREMDLASFLISR
ACNNTSLANYFYWYLSVECVDPNGLDVKDSKVTKMYQHVLKRF SQALFKESNESRQRSM
IARQQT FIDRLVDLVKIVTRESGNRKKKIERLQALLHDQEACKFDFSNFEPLSLPLDPI
KICGIIPEKATLFKSNLMPCKFVFKMVEGGEY MAMYKHGDDL RQDNLILQIITLMDKLLM
RDNLDLKLTYPYKVLATSCKHGFVQFVESVAVAEVLNQHTGIQSFFKICAPCENTPYGFQP
EVMDFVFKSCAGYCVITYVLGVGDRHFDNLLLTKTGKLFHVDGFFILGRDPKLLPPLMKL
TTEMIDGMGGPNSEHFHDFKLCYTAFLAIRRSSNLILNLF TLMVNANIPI DIAIEPDKSV
KKVQDKFVLLHTDEEAVQYMQNVIDGSV SAMMPV LVERFHTIAQASTSQTLYIKYTL

>NM_002647.4 Homo sapiens phosphatidylinositol 3-kinase catalytic subunit
type 3 (PIK3C3), transcript variant 1, mRNA

ATGTTGTTTTTTCCTGTACCTAAGTTCCTCCGCTGTAGGTGGTACCTTTGCAGACGGTGCATGGGGGAAGCA
GAGAAGTTTCTACTACATCTATAGTTGTGACCTGGATATCAACGTCAGCTTAAGATAGGAAGCTTGAAG
GGAAGAGAGAACAAGAGATTATAAAGCTGTCCTGGAAGACCAATGTTGAAGTTCTCAGGACTATATCA
AGAGACATGCTCTGATCTTTATGTTACTTGTCAAGTTTTTGCAGAAGGGAAGCCTTTGGCCTTGCCAGTG
AGAACATCCTACAAAGCATTTAGTACAAGATGGAAGTGAATGAATGGCTGAAAACCTACCAGTAAAAATACC
CTGACCTGCCCAGGAATGCCCAAGTGGCCCTCACCATATGGGATGTGTATGGTCCCGGAAAAGCAGTGCC
TGTAGGAGGAACAACGGTTTTCGCTCTTTGGAAAATACGGCATGTTTTCGCAAGGGATGCATGACTTGAAA
GTCTGGCCTAATGTAGAAGCAGATGGATCAGAACCACAAAACTCCTGGCAGAACAAGTAGCACTCTCT
CAGAAGATCAGATGAGCCGTCTTGCCAAGCTCACCAAAGCTCATCGACAAGGACACATGGTGAAAGTAGA
TTGGCTGGATAGATTGACATTTAGAGAAATAGAAATGATAAATGAGAGTGAAAAACGAAGTTCTAATTTTC
ATGTACCTGATGGTTGAATTTTCGATGTGTCAAGTGTGATGATAAGGAATATGGTATTGTTTATTATGAAA
AGGACGGTGTGATGAATCATCTCCAATTTTAACAAGTTTTGAATTAGTGAAAAGTTTCTGACCCCCAGATGTC
TATGGAGAATTTAGTTGAGAGCAAACACCACAAGCTTGCCCGGAGTTTTAAGAAGTGACCTTCTGACCAC
GATCTGAAACCCAATGCTGCCACGAGAGATCAGTTAAATATTATTGTGAGTTATCCACCAACCAAGCAAC
TTACATATGAAGAACAAGATCTTGTGTTGGAAGTTTAGATATTATCTTACGAATCAAGAAAAAGCCTTGAC
AAAATTTCTGAAATGTGTTAATTGGGATCTACCTCAAGAGGCCAAACAGGCCTTGGAACTTCTGGGAAAA
TGGAAGCCGATGGATGTAGAGGACTCCTTGAGCTGTTATCCTCTCATTACACCAACCAACTGTGAGGC
GTTATGCTGATTTGCCCGTTGCGACAGGCCGATGATGAGGATTTGTTGATGTACCTATTACAATTTGGTCCA
GGCTCTCAAATATGAAATTTTGTATGATATAAAGAAATGGATTGGAACCTACCAAGAAGGATAGTCAGAT
TCAGTGT CAGAAAATGTGTCAAATTTCTGGAATAAATTTGCGAGAAAATAGATAGCTCCCAAATTTATAACCA
GCCCCCTTCTTTCAGTCTCTTACCTCCTCCTGCATCAAAAAACAAAAGAAGTTCCAGATGGCGAAAAATCT
GGAACAAGATCTCTGTACCTTCTTGATATCGAGAGCCTGCAAAAACTCAACACTGGCTAATTTATTTATAC
TGGTATGTGATAGTGAATGTGAAGATCAAGATACTCAGCAGAGAGATCCAAAGACCCATGAGATGTACT
TGAACGTAATGAGAAGATTCAGCCAAGCATTGTTGAAGGGTGATAAGTCTGTGAGAGTTATGCGTTCTTT
GCTGGCTGCACAACAGACATTTGTAGATCGGTTGGTGCATCTAATGAAGGCAGTACAACCGGAAAGTGGA
AATCGTAAGAAAAAGAATGAGAGACTACAGGCATTGCTTGAGATAATGAAAAGATGAATTTGTCAGATG
TGGAACCTTATCCCGTTGCCTTTAGAACCCCAAGTAAAATTAGAGGAATAATTCCGAAAACAGCTACACT
GTTTTAAAAGTGCCCTTATGCCTGCACAGTTGTTTTTTAAGACGGAAGATGGAGGCAAATATCCAGTTATA
TTTTAAGCATGGAGATGATTTACGTCAAGATCAACTTATTCTTCAAATCATTTCACCTCATGGACAAGCTGT
TACGGAAAGAAAATCTGGACTTGAAATTTGACACCTTATAAGGTGTTAGCCACCAGTACAAAACATGGCTT
CATGCAGTTTTATCCAGTCAGTTCTGTGGCTGAAGTTCTTGATACAGAGGGGAAGCATTCAGAACTTTTTT
AGAAAATATGCACCAAGTGAGAATGGGCCAAATGGGATTAGTGCTGAGGTCATGGACACTTACGTTAAAA
GCTGTGCTGGATATTGCGTGATCACCTATATACTTGGAGTTGGAGACAGGCACCTGGATAACCTTTTGCT
AACAAAAACAGGCAAACCTTCCACATAGACTTTGGATATATTTTTGGGTCGGGATCCAAAGCCTCTTCCT
CCACCAATGAAGCTGAATAAAGAAATGGTAGAAGGAATGGGGGACACAGAGTGAGCAGTACCAAGAGT
TCCGTAACAGTGTTACACGGCTTTCCCTCCACCTGCGAAGGTATTCTAATCTGATTTGAACTGTGTTTCT
CTTGATGGTTGATGCAAAACATTCAGATATTGCACTTGAACCCAGATAAAAACCTGTGAAAAGGTTTCAGGAT
AAATTCGCTTAGACCTGTGCGATGAAGAGGCTGTGCATTACATGCAGAGTCTGATTGATGAGAGTGTC
ATGCTCTTTTTGCTGCAGTGGTGAACAGATTACAAGTTTGCCAGTACTGGAGAAAATGAACTGGGA
TTGACCCATCAAGATGCTTGGCTCAATAAGAAAACCAGTTAGGAGCAACCTTTGTATATTGGAGACTTC
AGAGTAACCAGCAAGGAAGAGAAATCTTAATCTTCAAGTTACCATATTTTCCAAATATTACATGGTACCT
GAGTTCTGCTTCTTGGATGTCATTGCTTAAATATAGTCTTGAAGGGCTTGTGTTGAAATATTGTATATA
TTTTTTCAAATGTATACATTGTTAATAAATTAAGAAATGAGAAAACATTTCTTATTTATGTACATGTTATGA
GAGTTCTGGAGGAAGTAATATGTTGAAATAGTAAAACATTTTAGTTTTTGTGTTTTGAGTTTTAAAATGTTATTTTT
CCTCTTATATCTTCATATCAGGACAGCAGTAACCTGAATTTAGATTGTCACAGTTTACAAGTTTTTGTGTT

GTTCCCTTCTTTCCCTCTCTCTCTCCCACTCACTTTTTGTGTGTTGTTTGTTTTTGCCTAATTTACATGTTTT
AAAGTTCTACTTAAAATTTTTCTTCAAGTTTTACATGTGATGGCTCATTCTTCTGCAGTTCAAGAATTGC
TTATATTTTTAGAAATACTCATTCTCTTACAAATAATTAATTTTTGTAAACTACAGTTAATAGTTC
TTCTAGCTTGTAAAGTGTGTAAGTAGAATATGAAAATGTGGCTATTTAGATAACTGGCCAAAAGGTCATA
TGACCACCAGTTTTAGTATTGAGCATAAGATATTTTTACATATTCATGTAAGACAATGAAAATGTCTTT
CTGCAATAAATTTTTGGATGCAAATTTAGATTTCAAAGCTTTTTGATGTTATAAAGGAGTTGAGGAAC
AAAAAGCTCTTTGAAATAGCTCACCTAGACCTGTTAATGTAATATATTCTTTCTGAATTAAGCAAAATTT
TTTTTGTCTTTTAAAGACTAGAACTAATCCCTCTAGCTTTTTTACTGGAACCTTGGGGAAAAAGAACAAT
ACAAATATACAAATGATATGAACAATATGGTAATAATCTTTTTGCAACTTAATATGTTACATAGTCATATG
ACTTGGTCTTGGAAAGAAAAGAATTGTTTTGGTGTCTGAATAAATATTAGAAAATCAAGTGACAGAGAAGAT
GAAGGTAATAATTGTGGCACAGTTTCAGAGAATGCCGTTAATGATAACGTGTTATTTGTCTCAAAATCTTA
GCCCTGGGCTTGCCTCTTCAGAGTGGGGTTACCGGCGAGAGGGCAAGCATGTAATTAAGAGACACTCTAG
AGGCATATGGAATATAGTTTTGTATAAAACATACTGCTGATTAGAAAAATGGTAAAAATGAAAATACCTT
TGTACATCATCTTAAGAGAGCTTATATATAAACTAAATGGGCAGGCTCCATCGTCTACCTTCTTTTTCT
TTTTCTCACATGTTTTATGTCTTTTTTGTATTAGTCAGACATTTTTAGCCCTCTGTATGCTCATCTTTCT
AGTTCTATTTCTATTGAACTTCTCCAAAACCTTTCTCTGAATTACCTTGTGAACTGACCTTTCTT
CCGTGTGAACCTTACACTTGCATCTCCTATTTTCCAGGATTTGGCATACTTTTTCTTTAATGGGCTAAGAA
AGTAAATATCTTCAGCTTTGGGGGGCATATGATCCCAATAGCATCAACTTAACTCTGCTAACTGGAAGGC
AAAAGTGTATCATCTTACTCGTCTTTATAAACTCCACAGCACTCTGCATAGATATGACCATGTTTATAAG
GAACTCAATAAATAATTTTGACACAAACATGAAATTTCTAGAAGGGCAGACACTGACAACCTAGTAAGGAAG
TTGATCATGAGTAACTTTGTATTAGTGCCACCTTAACAAGAATTGTAAGAGGATAAACTTTCTAGGA
AGGTTGATGCGTGTGGGTGAGGAAGGAGCATCTCTCAGGAGGGTAAACAGTAGCTGTGGTTTTGCTGAG
AGATTTTGGCTGTGAGTGACAAGCCTATATCAAAAAGAAAAGTGGCTTATCAATCTCAGTTTTTATTGCT
CAAAGCAATTTCTTACTCCTATTTTTTCCAAATTCATTGTTTTTACTCTTTAGAGCTCTATCCTCAGAG
TGTAGTCTGCATATTTCTTTATTATCATTGCCATGTGACTTCTTTGGTGACAAGTTCAGTGATATTTCAA
GCATGATGTTTTGAGTTTTGAGAAATGATTTGTGAGGACACATCACTTTAATTAAGGAGTGAGTACT
ATGGTCATTAAGTTATTTCAGAGTGAGATTTCTGAGAGGAGAAGAGAGAATGTAGATGGCAGTTATTGAGA
GTGGGGCTATAGGACAAAAAGAAGAAAAGTATGGTTAACATTTGCCAAAATAAGGGTCATACAGCCTTGCT
TTTTGCTGGAGTTAGCAAAAATCATTCTCCATATGATAGTTTTAGATGTTCCCAGCTCATTTGTATTAT
TGAGTTTTTCAGCTGGGTATATATTATAAACAGTCAACATGATGTAGGGGCTCAGTATTACATGGCAGG
GCTATACTAATTGCTTCATATGCCTTATCTCATTATTCTGTGAGATAGAATTGCTCTCCTCATTTTTTGT
TGAATAACTGAAGTTTTAAAGCAATTGAATCTGCCAAGGATAAGCTGCTGGTGAGAGCAGAGTTGG
GATTTGAAGTGCAGTTAGACCCAGTGATCAGCTTTGACGATTAATTTCTCCAGCTTCATTTTTCA
CTGAGATAATGGTAGTGATAGTACTGACCTCTAATGTGTGCATTTGTGGGTATGTGGTCCATTCAGCTTT
AATCCCCAGAAGACAAGGCTTATTCTTTTTCTTATTTTTTGGTCATGTTTTATTTTTTCCATTGCTTTTTAAC
AGGATTACCAAAGGCACACTCAGTAGTCAGTAAACACATTTCTAGGAAAAGGTGTTGTGTGCATCATGCCAC
ATATTCATACTTTTCTTGGGTTGGAAAATAGATCATTTCAGTAAAAACATACAGGAAAAATGAATCTTGCC
AATGCAATTTGTTAACCTACAACCATAATATACCTTAAGTATATTTTTGCACATAAGTATAACATTTGCGAT
TTAAAACAATAAACCAGATTGAGATTCTAAGGAGCATTTTGTAAGTAATTACTAATGTTTATTTTAGAGA
GATCACACAACCTCAAATAAAAACCTGACATAGATTGAACACCTTGAATAAACTTTAGTGCCAAAATGGA
AAATAATTTTTTACAAGTAAATTTGAAGAACAATGTGAACCTTTCTATAATTATATACAGAAAAATATACTG
ATTTGCCAAAATGAGTAATTTTTGATATATTAATATTTCACTTATAAGAATGCATACCACCTGATCCAGGA
TGGGATCCAGGAACAGAAAAAGAACATTAGGTAAAAATGACAGAAATCTGAATATAGTATAGAGTAGCTA
AAAACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAGGAAAAACAGAATAAGCCTCAGAAGATAGTGAGCATCCC
ACCTGGGTGACCACTTAGAGAAGCTGAGGTGGGACCCCTGCATCCGATAAGTGGCTGCACTAGACCACAG
GAACCAGACTCCACTGTAAGAACTAGAGTGGGAATGGACATGTCAAAACCTCCTGGGAACCTTATTAAT
GTGCACATTTCCCAATCCCCACTCCTGAGCAGCCAAATCAATCTGCAGGTGGGCTTGTGAGTTTTCCAG
GGGATTCGGATGCCTGTAGATTTAACAGTAGATGAGATGTTAAGTTATCCTGTAGTCCAGAGATTTCA
CAGGCCAGTGTCAAGGAACAGGGGCCAGGGCTGGGAAGGCATAAGAACAGAAGATAAATTTGAGGCTCTG
TTACGCTGGTCACTCAACCCAACCAGGTATCTCTTGTATATGCTAACTTCAATTTCCCTTTCTTGTCCA
TAGTGGGAAAAATAATTTTTAACTGGCTATGTAGTTAAAAAACCTAACAAAAAGCACTTTTCTATATAA
TGAGTGGTTTTATATTAAGAATAGGTACAATGTAAATACTGGTAAGTGAAAGTTCATTTTTGTTTCAGTGCTA
TGGGCTGGTACATTTGCATTTCAACACTAGTTTTTTACTTTTTATCTACCCTGAGGGTAGATAAACCATATT
CCAAAATACAGTATTATTTTTCATTTGCTGTAACATTTTAAAGAAATATGTAGTTTCTAAAACTTCATATAC
TTTATATGGAATATGAACAACCTTAAATATGAATAAATAGTCTAGAAAAAATTTAGGAAAAATTTGCCATG
AAATCATGAGCTAAGTCAATGGTTATTTTTAAACCCTTAATTTTGGACTAGTATTTTACATACAGAAAAAG
CTAATACTGATATCACACACTAATTGTGTATAAAACACTAGGAATGTCAAAATAGAACATAAGAAAAATGA
GTCTAGTGGACCCACTGCATAGTGAACCTTTGGGATGAATTTAAAAGAATATTTAAGTCAAGTCAATTT
TCTGTTGGTCTAATTTTACCAAATAACCCCTAAATAAGAAGTCTGATTTATCTAAAATAGAAGTTAACA
TAGCATCCAGTATTGCCATTCTAAAACCTCTGGCATGTAAATGGGAGAAATGGAAATAAGCTCAAAATGG
GTAGAGTAACCCATTTCTGCATGAACCATAGAATTTAACTAGAATTTGGCTGGCTCATGCCTGTAATGCC
AGCACTTTGGGAGGCCAAGGCAGGCAGATCACTTGGACCCAGGAGTTTGGAGACCAGCCGGGCAACATGG
TGAAACTCCATCTCTTCAAAAATATATATTTGTGTGTGTGTGTGTGTGTATGTGCGTGACAAAAATTAG

CTGAGTGTGGTGGTTACACTTGTAAATCACAGCTACCTGGGAGGCTGAGGCAGGAGGATTGCTTGAGCCT
GGGAGGCAGAGGTTGCAGTGAGCTGAGATTGCACCATTGCACTGCAGCCTGGGTAATAGAGCGAGACAAC
TCTATCTCAAAAAAAAAAGAATTTCACTAGAAATTTATATCTTCAGTGTTCATTAGATTGTCACCAGCACT
ATCTGCCTTGTGACTGTCAGGACTAATCCTTATATCATTATCTTATGTCTTTACCTCAGTTTATGTCT
GTCACCACAAGAAACCCAGACCTCCCTAATCATACCATATGCCCTGGTCTTACCCACATACAGCTCGGTA
CAACTGCATTTCCCCAAACCTCAGAACTCCTTGGGCCATCACTGTCAGAGACATTTGAACTAGAGCAACT
CCATCTTGAGTAGGGACTGGGTATAATGAAGCTGAGACCCACTGGGCTGCATTCCCAGGAAGTTAGGCAT
TCTTAGTCACAGGATGAGATAGGAGATTGGCTCAAGATAAGGTCACAAAGACCTTGCTGATAAAACAGTC
TGTGGTAAAGAAGCCAGCCAAAACCCACAAAACCAAGACGGGAATGAAAAGTGACCTCCGGTCATCCTCA
CTGCTCATTATACGCTAGTTATAATGCATTGACATGCTAAGAGACACTCCCACCAGCACCATGACAGTTT
ACAAATGCCATAACAACATCAGGAAGTTACCCTATATGGTCTAAAAAGGGGAGGAACCCCTCAGTTCTGAG
AATTTCCCTTGAAAATTCATGAATAATCCACCCCTTGTTTAGCATATGATCAAGAAAATAATCATTAAAAA
TAGCCAACCAGCAGCTCATGCTGCTGGTCTGCCTATGGAGTAGCCATCCTTTCTTTATTAACCTGCTTTC
ACTTTATGGACTCCCCTGAATTCCTTCTGCAGGAGATCCAAGAACCCTCTCTTGGAGTCTTAACCAGGATC
CCTTTCCAGTAACCTCAGCAGGATCTGTGAGTGCCAGTTTCCTTCTGTGGTGCAAAACTAGGTGCTAAGT
ACACTTTTTTCCCCCTTTCCCTCTATTTTTTAAAAGAAGCTTTTCCAGCCCTTTTGAAGTGCGGTACATTGCTGG
AGTACATACCCTGGGGTTCATTGTTATAGGAGAATTTAGGACACAGACACACAGGAGTTTAGGAGCAGA
GGTTTAATAGGTAGAAGAGAAGGGAAAGAGAAAACAGCTTCCCTCTATAGATGTCTGCACTGACACCGTGGC
TTTAAGGCATGGCCCATGATGTGTCTCCGAGTGGAAAAGACTGGTTGGTGGTGAATGCGCCAAAATTTTAT
AGTCCGGTTTGAGGAGGTGGTTTCTGATTGGTTGCATCATGTATGACGTTTGCAAGGTGCATGTGGAAGG
CTGGTCGCCCCACCCTAATCTTATGCAAATGGGCTTTCCAGTTGATTGGGTCCATCTTGTGTAACACGTG
GCTGGCAGAGAAGGGAAGATGAAGCCACCATCTTAAAATGTCTAGTCCTTAGTTTCTGCTGGCATTAC
CCATGCAAGCTGCCAGCTTGTCTATGTCTGCAGCTCAACTTTACAGGCTGCTCTTTGTAGCAAATGATT
TGGAGCTTCTTTTCATTAAGAAAAAAGCCTTACCGAGGACTCCCATACCCTTGCTTCTGCTTAAGTGA
TTTCTTCTTAACCTCTATGTCAATTTTATACAGCATGAAATAATGATGTATCTATAAATGAGCCTTTGCA
AGATTACCATTTATCAAGAAAACCAGTGATGTTTAGTTAACTGTTTGTAAAAATAAATGGTTAGTAGAA
TGTCTAATTCATAAATGTTTCATAAATGAGTAAA

>NM_001182127.1 *Saccharomyces cerevisiae* S288C phosphatidylinositol 3-
kinase VPS34 (VPS34), partial mRNA
ATGTCACTGAGACAACATAACACTTCTGTGCTCACAGGATCTGGATGTTCCCTGAAAGTGAAAAATCAAGT
CATTGGAAGGACATAAGCCACTGTTGAAGCCATCTCAAAAAATCCTGAACCCCTGAATTAATGCTGATAGG
GTCAAATGTATTTCCCTCTAGTGATCTAATTTGATATCCTTACAGGTATTTGATAAAGAGAGAAAACAGAAAT
TTAACTCTTCCGATATACACGCCGTATATTCCTTTTCCAGAACTCTAGAACCCTGGGATTATTGGTTGACTT
TGCCCATACGTATCAAACAGCTTACCTTTAGCAGTCATTTACGCATTATTTTTGTGGGAATACAATGGATC
CAAGCAAATTCCTTTTTCAATCTAGAAAACGAGCATCTTTAACTTAAAAGACTGTACTTTAAAAAGAGGG
TTTGAATCCTTAAAATTTTCGTTATGATGTGATTGACCCTGTGAAAGTGGTCACTGATAACAAAAGATCAAG
AAAATTTGAATAAATATTTTTCAGGGTGAATTCACGAGACTCCCTTGGCTTGACGAAATCACTATAAGCAA
ATTAAGGAAACAACGGGAAAATAGGACTTGGCCTCAGGGCACCTTTGTCTTAACTTAGAATTTCCAATG
TTAGAGCTTCCCTGTTGTGTTTCATCGAAAGGGAAATATGAATACTCAAATGAATATTCCAACCTTTGAAGA
ACAATCCTGGACTAAGCACAGACTTACGAGAACCGAATAGGAATGATCCTCAAATCAAAAATTTCTTTGGG
GGACAAATATCACTCCACATTGAAGTTTTACGATCCTGACCAACCAACAATGATCCAATAGAGGAAAAG
TATAGGAGATTGGAAAGAGCATCTAAAAATGCAAACCTTGACAAAGCAAGTGAAGCCGGACATTAAAAAGA
GGGACTACTTGAATAAAATCATCAACTACCCCCCTGGCACTAAATTAACAGCACATGAAAAGGGTTCAAT
ATGGAATATAGGTATTATTTGATGAACAATAAAAAAGCTCTTACAAAGTTATTACAGAGTACAAAATTTG
AGAGAAGAATCGGAAAGAGTAGAGGTTTTAGAATAATGGACTCATGGGCAGAAAATGATATAGACGACG
CATTAGAATATTAGGCTCAACTTTTTAAAACCTTTTCCAGTGAGATCGTACGCCGTAAATAGGCTGAAGAA
GGCATCAGACAAGGAGCTGGAATTGTACTTATTACAGTTGGTAGAAGCTGTCTGTTTTGAGAACCTGTCC
ACTTTTTCCGACAAATCTAACAGTGAATTCACTATTGTGGATGCCGTATCTTCGAAAAGCTTTTCGGGTG
ATTCTATGTTACTATCTACATCGCATGCCAACCAAAAATTTAAAGTCCATCTCGAGTGAATCGGAAAC
TTCCGGGACAGAATCGTACCAATCGTCATTTCTCCCTTGGCTGAGTTTTTTGATTAGGAGACACTGGTTC
AACCCAAGGTTAGGAAGTTTTTTCTATTGGTATTTAAAGTCCGAGTCTGAGGACAAGCCATATTTAGACC
AGATTTTTAAGTTCCTTTTGGAGTAGACTGGATAAAAAATCTCGGAATATACTGAACGATCAAGTCAGGCT
AATAAATGTGCTCAGGGAATGTTGTGAAACAATTAAGAGGCTGAAAGATACTACAGCCAAAAAGATGGAA
TTACTAGTGCATTTATTGGAGACGAAAGTCAGGCCTCTTGTCAAAGTACGACCAATTGCTTTACCACTAG
ACCCTGATGTGTTGATATGCGACGTTTGTCTGAAACTTCGAAGGTATTTAAAAGCTCTTTATCGCCACT
AAAAATAACATTCAAAACGACCTTAAACCAACCATATCACTTAATGTTTAAAGGTTGGCGATGATTTGAGA
CAAGATCAACTGGTAGTACAGATCATAAGTTTAAATGAATGAGTTATTAAAAAATGAAAACGTGGACTTGA
AATTGACACCATACAAAAATTTTGGCAACAGGACCACAAGAAGGTGCCATTGAATTTATCCCTAATGACAC
ATTAGCTAGCATACTAAGCAAATATCACGGTATCTTGGCTACCTTAAACTCCACTATCCTGATGAGAAC
GCGACATTAGGCGTACAAGGCTGGGTTTTAGATAATTTTGTCAAATCTTGTGCTGGCTATTGTGTTATTA
CATACATCTTAGGTGTGCGCGATAGGCATTTAGACAACCTTACTAGTCACGCCAGATGGGCACTTTTTTCA
CGCAGACTTTGGTTATATCTTGGGTGAGGACCCCAACCTTTTCCGCCATTAATGAAATGCCCCCTCAA

ATTATAGAGGCGTTTGGGGGTGCAGAATCATCAAATTATGATAAAATTCGCAGCTACTGTTTTGTGGCAT
ATTTCGATTTTAAGAAGGAATGCAGGCTTAATCTTAAACCTGTTTGAATTAATGAAGACTTCGAACATACC
TGATATCAGAATAGATCCCAATGGTGCTATATTACGTGTAAGAGAGAGATTTAATTTGAATATGTCCGAA
GAAGATGCCACAGTGCATTTTTCAGAATCTAATCAATGATAGTGTAATGCTTTGCTGCCTATCGTGATTG
ATCATTTACATAATCTGGCACAATACTGGCGGACCTGA

19. 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
RIEKKWLAFLQLLCALNQCHKIKVCHGDIKAENVMITSWNWLILLTDFASFKPTYLPEDNPS
DFSYYFFDTSRRRCCYIAPERFVESGLKNQEGAGQIDLTNSNEVKSGDITPPMDIFSAGC
VICELFTEGTPPFDFSQLLAYRNGEYSPWKVLEKIDDNIRDLVRHMIKKDPSHRLSAEE
YMIQQRGKAFPEYFYTFCLKIYLLQFVSTPLTPPDDRINKIKRDFPRIVKSI CPQEERSED
NIGLVLIISLIISSSRKLHLCNTKLTALQLLLEASKFVTTDII LDRIIPYMLSFANDQFP
RVRAEVIHVVTQCLLDVDSIPRSDANVFPEYIFPNITHLTQDPVVMVRAAYAENIAKLAE
TALRVLEMTQRIDLEETEETEEESVDGLLYQANYDIELLTLQETIQQKVVTLSSDPDNSVKR
TLLNGITKLCVFFGRQKANDVLLSHMITFNLNDKTDWHLRGSFFDNIVGVAAYVWGQSCS
ILKPLLDQGLSDPEEFVVKHTLGLALTALTELGLIQKSMLEFLQEVVFFLAHPGIWIRCS
AIGFISALTRMFNIADVHCKVLPALQPCLKRVLQIDKEIFLLNALQSPIPRPVFDYILR
VSQPDRLFDILRERQYMRISRSRSHRTTYSELDEAMSQVFKKLN SFGMDESHEDKILAMK
DYVMKLRSRAGSVETKHELGDSPGRFCIVGAGKAITRRHAELIKQKDPKQQGADQTTSS
RSSKKVQSKEQSVNMNSEWKS MFGS NESDSSNASLSPKARTLQKTAESLEKKLNTSQTVS
QTSSSSGSFVTMSQSQVSSEGSIRSVTEKGS DKNPITKYHNCKIALRNIVHKKRELYSAE
SKDLLEIAWERRPPPSNWKPKGLLV AHLQEHRAAINRIQVSHDHAFASASNDGTVKLWE
SEKLEGNSVANRSKQTLKNTSLPGEKVKGLVFCEASGPSLSLATFTDLGAINIFK IETGK
ASWNKDLRVDKPDYGNIVDMTYFDTGAQSVLSYATVNGFLVGHDLRTNKEVWKL RNDPKA
GLITSFVHHSQCWLAVGTSSGTHICWDMRFQLPINSIVHPTGARVRRLIMHPQEQSWLI
SATQGNNEVSIWDVETGARQKVLWASPTPTLSLNQASHHSVYGLHMAVTD TNVFMLTGG
DMRARFWDLSYPANSFILAGAASDPVQQTG VNYRAKLV DGVVEVIQELYTKKPV TND DAPR
RGPEAPPQGHRDII SDINLCQASQCMVITGSRDGVIKVWK

>NM_014602.3 Homo sapiens phosphoinositide-3-kinase regulatory subunit 4
(PIK3R4), mRNA
GAGGTCAGACCGGTTGCTTTCCCGGGAGTTCGGCGTTTGTCTGGGGCTGCAGCAGCTGAAGTG TAGTGT
TCTTGGGACTGGCGGTCTGCACTTCTCTCCCGGGTTCATCTCCCCCGCCCGGTGGTGAGCCCTCGAG
GAGGGCTCGGACGGGTGTAGCGATCCGCGCTAGAGGAAGACGAGGCCCGGGAACGCATGTCCCCAGGGC
AGGTTAGGGGGCTGGAGGGGTCAAATCCCGGGTACTTGTGGAGACTCTTTAGCGTGGCTTCTTCTCTCT
GCTGAGACCCCGAGAGCTTTCCAGTTCCTCCAGGACCACCGGGGTTCCTGAAGATCGGGACTTTTC
TGCGCCCTCCACCAACAGCCCATCTCCTGTCTATGAAGAAAGACCCTTCGTAGAAAACA ACTTCCCGCT
GCTGACGCGTTTTCCCGTCCCGTCCCGAAGTAGTCTACTATGACCTCGTTGTGAGCCTCTGAACGATTT
TGACACTTTCCCGAGGCCTAGGGTATTATATCCTAACCTTACTAAAGACCACAGAGGTGCTTGCCATTAT
GGGAAATCAGCTTGCTGGCATTGCTCCCTCCAGATCCTTTCTGTAGAGAGTTATTTTTCAGATATTCAT
GACTTTGAATATGATAAAAGCCTGGGGAGTACTCGGTTTTTTAAAGTTGCTCGAGCCAAGCACCAGAA
GCCTGGTCTGTGTAAGGTTTTTGCAATTCAGGATCCCACATTGCCTTTAACCAGCTATAAACAAGAGCT
GGAGGAAC TGAAATCAGGCTTAATTCTGCACAGAATTGTCTACCTTTCCAGAAAAGCATCAGAAAAAGCA
TCTGAGAAAAGCAGCTATGCTCTTTAGGCAGTATGTGCGAGACAATCTCTATGATCGCATCAGTACCCGTC
CATTCTTGAATAACATTGAGAAGCGCTGGATTGCTTTCCAGATCCTGACAGCTGTGGACCAAGCACACAA
ATCTGGAGTTCGT CATGGGGACATCAAGACTGAGAATGTGATGGTACCAGTTGGAATGGGTTCTTCTA
ACTGATTTTGCCAGTTTTAAGCCCACTTATCTTCCAGAAGACAACCCGGCAGATTTCAATTATTTCTTTG
ACACATACCGGAGGAGA ACTTGCTATATTGCTCTCTAGACGTTTTGTTGATGGTGGGATGTTTGCCACTGA
GTTAGAATATATGAGAGATCTTTCAACTCCGCTTGTAGACTTAAATAGCAATCAGAGAACAAGAGGAGAG
TTGAAGAGACAAATGGACATCTTTTCAGCAGGTTGTGTGATAGCTGAGCTTTTTTACAGAAGGTGTACCAT
TATTTGATCTCTCTCAACTTTTGGCTTATAGAAATGGACATTTTTTCCCTGAACAAGTCTAAATAAAAT
TGAAGATCACAGTATCAGAGAATTGGTAACTCAGATGATTCACCGTGAGCCAGATAAACGTTT TAGAGGCA
GAAGATTACTTAAAACAGCAGCGTGGCAATGCCTTTCTGAAATATTTTACACTTTTCTTCAGCCCTACA
TGGCCCAGTTTGCCAAGGAAACGTTTCTTTCTGCAGATGAGCGTATTCTGGTTATACGGAAGGATTTGGG
CAACATTATTCACAATCTCTGTGGACATGATCTGCCAGAAAAGCCGAAGGAGAGCCTAAGGAAAATGGG
CTGGTTATCTTGGTATCTGTTATAACATCTGCCTACAGACCCTTAAATACTGTGATTCAAAAC TAGCTG
CTTTGGAAC TATTCTTCAATTTGGCTCCAAGATTAAGTGTGAAATCCTTTTGGATCGTATTACTCCATA

TCTTTTGCATTTTCAGCAATGACTCTGTTCTAGGGTGAGGGCTGAAGCCTTGAGGACGTTGACCAAAGTT
CTTGCTCTCGTCAAAGAGGTTTCTCGTAATGATATCAATATTTATCCGGAATACATTCTGCCAGGCATAG
CCCCTTAGCCCAAGATGATGCTACTATCGTTAGACTAGCCTATGCTGAAAACATAGCTCTGCTGGCAGA
AACAGCTCTGAGATTCCTGGAATTAGTACAGTTAAAAAATCTTAATATGGAAAATGACCCCAATAATGAA
GAAATAGATGAGGTTACACATCCAAATGGAAATTATGACACAGAGCTCCAAGCCTTACATGAAATGGTCC
AGCAGAAAGTTGTTACTTTGCTAAGTGACCCTGAAAATATTGTAAAACAAACCTTGATGGAAAATGGAAT
AACACGGCTGTGTGATTCTTTGGACGTCAGAAAGCCAACGATGTTTTGTTGTCCCACATGATTACTTTC
CTAAATGATAAGAATGATTGGCATCTACGTGGAGCATTTTTTGTATAGTATAGTTGGTGTGCTGCTATG
TTGGCTGGCAAAGCTCCTCAATTCTCAAGCCTCTGCTGCAACAAGGTCTTAGTGATGCTGAGGAATTTGT
CATTGTGAAAGCTCTTTATGCCCTTACTTGTATGTGCCAGTTAGGACTGCTACAAAAACCCCATGTTTAC
GAATTTGCCAGTGATATTGCCCTTCTCTGTGTCATCCCAATTTATGGATACGTTATGGTGCCGTGGGAT
TTATCACAGTGGTAGCTCGTCAAATAAGTACAGCTGATGTCTACTGTAAACTGATGCCTTATCTTGACCC
ATATATTACCCAACCAATAATACAGATTGAAAGAAAACCTTGTCTGCTCAGTGTTTTAAAGGAACCAGTA
AGTCGTTCTATATTTGATTATGCTTTGAGGTCTAAAGATATTACTAGCTTGTTCAGACATCTTCACATGC
GTCAGAAGAAACGAAATGGTTCTCTCCGACTGCCCTCCGCCAGAGGATCCTGCCATAGCAGACTTCT
GAAGAAGTTGCTCTCACAGGGAATGACAGAGGAAGGAAGCAAACTTCTGGCACTGAAAGACTTCATG
ATGAAATCTAATAAAGCAAAGGCCAATATAGTGGACCAGAGCCATCTTCATGATAGTAGTCAGAAAGGTG
TAATTGACTTGGCAGCTTTAGGCATAACTGGGAGACAAGTTGATCTTGTAAAACCAAACAAGAACCAGA
TGACAAACGGGCCAGAAAACATGTAAAACAAGACTCAAATGTAAATGAAGAATGGAAAAGCATGTTTGGG
TCACTGGACCCACCAAACATGCCACAGGCCCTACCTAAAGGGAGTGATCAGGAGGTGATTCAGACTGGGA
AACCTCCTCGTTCGAGTCTCTGCTGGCATTGTGTCCCTTTGTCAACTTCTTCACAGGTTCCAGAAGT
GACAACGTCCAAAATAAAAAACCAGTAATACCGTTTTAAGTAGTACAATCTTACCATCCACCTATCAG
ATTTCGAATTACAACCTGTAAAACCTGAACTTCAGCAACTCATCCAGCAAAAAGCGGGAGCAGTGCAATGCTG
AGAGAATAGCTAAGCAGATGATGGAAAATGCTGAATGGGAGAGTAAACCACCACCCTGGATGGCGTCC
TAAAGGGCTGTTAGTTGCCCATCTTCATGAGCATAAATCTGCTGTGAATCGAATTAGAGTCTCTGATGAA
CACTCACTTTTTGCAACATGTTCAAATGATGGCACAGTGAAAATCTGGAACAGTCAAAAAGATGGAGGGGA
AGACCACCCTACCAGATCTATTCTTACATACAGCCGAATTGGAGGACGAGTCAAGACGCTCACATTTCTG
CCAAGGCTCCCCTATTTAGCCATAGCATCTGATAATGGTGCTGTCCAGCTTCTTGGAAATGAGGCTTCT
AAGCTGCCCAAGTCTCCTAAAATCCATCCTCTACAAAGCAGAATTCTAGATCAGAAGGAGGACGGTTGTG
TTGTGGATATGCATCACTTCAACTCTGGAGCACAGTCTGTTCTTGCCTATGCCACTGTGAATGGCTCTCT
GGTTGGCTGGGACCTTAGGTCTTCAAGCAATGCGTGGACTTTAAAGCATGATTTAAAGTGGGCTCATC
ACTTCTTTGCTGTGGACATCCCAATGCTGGCTCTGCATTGGTACAAGCAGTGGTACCATTGGCTTGT
GGACATGAGGTTCCAGTTGCCAATTTCAAGTCACTGCTGCATCTTCCAGGGCTCGAATCAGACGCCCTC
AATGCACCCTCTGTATCAGTCTGGGTGATTGAGCTGTTTCCAGGGCAACAACGAAGTGTCCATGTGGGAC
ATGGAGACTGGTGACAGAAGATTTACTCTCTGGGCCAGCAGTGCACCACCCTTTCTGAATTACAGCCTT
CTCCTCATAGCGTCCATGGTATCTACTGTAGTCTGCAGATGGAAAATCCTATCCTACTAACAGCTGGCTC
AGATATGAAAATAAGGTTTTGGGACTTGGCTTACCCAGAAAGGCTCTATGTTGTTGAGGAAAGTACTAGT
TCCCCATCTGTGCTCTACTACAGGAAAATAAATTGAAGGCACTGAAGTTGTCCAGGAAATTCAGAATAAGC
AGAAAGTAGGACCAAGTATGACACCCCTCGAAGGGGCCAGAGTCCCTGCCCGTGGGACATCATGACAT
CATCACTGATGTCGCCACATTCCAGACCACACAGGGCTTCATCGTAACTGCTTCTAGAGATGGGATTTGTG
AAGGTGTGAAATAAAACCTACTGATTTGTATAAATTTAATAGTTATAAATAAATACTATAAATCGAG
AAAAGGCATTTCTAGAGAACAGATTCATTTGCTTAATTTTCAAATTTATGTCTCCATATTACTGTTTCAT
GACTGACTGACTAAATGACACCCAAAATGGTTAAGATGTACTTGACTAGTTTACTTATGCATCTCTTTGC
AAGAATCAGCCAGCCAACAATGTCTGGGATTTTTATTGTATATGTTATAGAGGTGAGAAAATGTAATAAT
GAAAATGAATATGTTTATTTTGTATTGAAAAGATGGTTGAAAAGATGGTTGTAAGCTATTATAGTATAA
ACACATTTTTGCTATTTAAAATGCTATTCAAAGCAGTTAAACTGTA

>NM_001178445.2 *Saccharomyces cerevisiae* S288C ubiquitin-binding
serine/threonine protein kinase VPS15 (VPS15), partial mRNA
ATGGGGGCACAATTATCACTAGTGGTCCAAGCATCACCTTCCATAGCCATTTTTTTCATATATCGATGTCT
TAGAGGAAGTACACTACGTTTACAGTTAAACTCATCAAGATTCTTAAAAACATGCAAGGCACTGGACCC
TAACGGCGAAATTGTTATCAAAGTGTTTATTAACCAAAGACCAATATAGCTTACGACCTTTTCTCCAA
CGTATAAGGGCTCAATCGTTTAAAGTTGGGACAACCTACCGCACGTTTTTAAACTACAGTAAAATTGATCGAGA
CAAATAGAGCCGGCTACATGATACGGCAGCACTTAAAAAATAATTTATATGACAGATTGAGTTTGGAGACC
TTACTTACAAGACATTGAACTGAAATTCATTGCTTTCCAGTTGTTAAATGCATTAAGGACATTCATAAT
CTGAATATTGTCCATGGTATATAAAGACAGAAAATATCCTAGTAACAAGTTGGAATTTGGTGTATATTGA
CAGATTTTGTGCTGATTTATCAAACCCGTATATTTGCCTGAAGATAATCCAGGTGAATTTTTTATTCTACTT
CGACACCTCGAAGAGAAGAACCTGTTATCTAGCCCCGGAGAGGTTTAACTCTAAACTTTACCAAGATGGA
AAATCTAACAATGGTAGGCTAACTAAAGAAATGGACATATTTAGTCTTGGATGTGTTATTGCAGAAAATAT
TTGCTGAAGGAAGACCCATCTTCAACTTATCACAGCTATTCAAATATAAAAAGTAATTCATATGACGTAAA
CAGGGAATTTCTCATGGAGGAAATGAATTTACCGATTTAAGGAACTTGGTTCTAGACATGATTCAACTA
GATCCATCCAAAAGACTTTTCATGTGATGAACTACTGAATAAATATCGTGGCATTTTTCTTCCCGATTATT
TCTACACTTTTCATTTATGATTATTTTCAAGAAATTTGGTTACTATGACAACAAGCACACCGATATCAGATAA

CACTTGCACCAATAGTACCTTGGGAAGACAATGTAAAACTTTTAGATGAAACTACGGAAAAAATATACAGA
GATTTTTCCCAAATATGTCATTGTTTGGACTTTCCTTTAATAAAAAGACGGGGGTGAGATTGGTTCAGACC
CCCCAATTTTGGAACTTTACAAAATAGAGATAGAAATTAGTCGGTTTTTAAACACAAACTTATATTTCCC
CCAAAATTACCATTTAGTCTTACAGCAGTTTACCAAAGTATCCGAAAAGATAAAAATCAGTTAAAGAGGAA
TGTGCCTTACTCTTTATCTCTTATTTGTCTCATAGTATAAGAAGTATTGTTTCGACTGCTACGAACTTA
AAAATTTAGAACTATTAGCAGTATTTGCACAATTCGTTTCTGATGAAAATAAAAATTGATCGAGTCGTACC
TTATTTTCGTATGTTGTTTTGAAGATAGTGACCAGGACGTCCAGGCCCTATCTTTGTTAACATTAATCCAG
GTACTCACCTCTGTAAGAAAATTGAATCAATTGAACGAGAATATATTTGTGGACTACTTACTTCCGAGAC
TGAAAAGATTACTTATTTCCAATAGGCAGAATACCAATTATTTAAGGATTGTGTTTTGCTAATTGTTTGGAG
CGACTTGGCCATTATCATTAAATAGATTTCAAGAATTTACATTTGCTCAGCACTGCAATGATAACTCAATG
GATAACAACACGGAAATCATGGAAAGCAGTACCAAGTATTGATCCAAAAGTGTGGAAGATT
TAACTGTCTCTTTTTTAACAGATAATGATACTTATGTAAAGATGGCACTTTTGCAAAACATTTCTTCCACT
TTGTAATTTTTTTGGTAGGAAAGAACAACGATATTATACTGAGTCATTTAATAACCTACCTTAATGAT
AAGGACCCAGCATTGCGAGTTTCCCTTAATTCAAACAATATCCGGAATATCAATTCCTTTGGGTACCGTTA
CATTAGAACAGTATATTTTACCATTGTTAATCCAGACCATCACTGATTCGGAAGAATTAGTAGTGATCAG
TGTTTTTACAAAGCTTAAAATCTTTGTTCAAGACTGGGTTGATTAGGAAAAAATATTATATTGATATATCA
AAAACAACATCTCCCTTGTGTTGCATCCTAATAATTGGATAAGACAGTTTACTTTGATGATAATTATAG
AAATTATTAATAAGTTATCAAAGCCGAAGTGTACTGCATTCTCTATCCAATAATAAGGCCTTTCTTCGA
ATTTGACGTTGAGTTCAACTTCAAATCAATGATAAGCTGTTGCAAGCAACCAGTGTCAAGATCGGTTTAC
AATCTATTGTGTAGTTGGTCTGTTAGAGCGTCAAATCTTTATTTTGGAAAAAATCATCACAAATCATG
TAGATTCATTCGAAATAATAGAATCGAATTTATAACAAAAAATTACTCAAGTAAAAATATGGATTTAA
TAAAAGAGATACGAAATCAAGTTCCCTCGCTGAAGGGTATTAAAAACATCATCCACCGTCTATTCACATGAC
AACAAGGAAATTCCTTAACTGCTGAAGACAGAAATTGGATTGATAAGTTCCACATTAATGGGCTAACAG
AAAAAGATATTTGGAAAATTGTGGCTTTGAGGGGTTATGTAATAAGGACAGCGAGAGTTATGGCAGCGAA
CCCTGATTTTCCATATAATAATAGTAATTACCGTCCATTAGTACAGAACTCACCACCTAACCTAACCTT
ACGAATATTATGCCAAGAAACATTTTCTTTGATGTAGAGTTTGTGGAAGAGTCGACAAGTGAGGGACAAG
ATTCTAACTTAGAGAACCAACAGATATATAAATATGATGAAAAGTGAAGAGATAGCAATAAGCTAAATAT
TAACGGTAGCAAACAGCTATCTACCGTCATGGACATAAATGGATCACTAATATTCAAAAATAAGTCCATT
GCCACTACTACTTCTAATTTGAAGAACGTTTTTGTTCAGTTAGAACCAACGTCTATCACATGCATTTCTC
CAAATCATGGCTTGAAGATAATGCAAATGTTAAACCAGAAAGGAAGGTAGTCGTCAGCAACAGCTATGA
AGGCGACGTTGAAAGCATAGAAAAATTCCTATCGACTTTCAAAATTTTACCTCCTCTGAGAGATTATAAG
GAGTTTGGGCCTATTCAAGAGATTGTACGGAGTCCAAACATGGGTAATTTGAGGGGCAAGTTGATAGCTA
CTTTGATGGAAAACGAACCCAAATTTACTATTACGCTTCTGCTGTTTCTCCAGGAGAAAACACCCATTTAAT
AACAGGTTTCAGATCAAGGTGTAATCAAGATTTGGAACCTGAAAGAGATTATCGTGGGCGAGGTTTACTCT
TCTTCTTTAACTTATGACTGCTCCTCTACCGTAACTCAGATAACCATGATTCCCTAACTTTGACGCGTTT
CCGTTTTCCAGTAAAGATGGACAAAATAATTGTATTAAGGTTAATCATTACCAACAAGAAAGTGAAGTCAA
ATTTTTGAATTGCGAATGCATCAGGAAAATTAACCTGAAGAATTTTGGTAAAAATGAATACGCAGTGAGA
ATGAGAGCATTGTGAATGAGGAAAATCTCTACTAGTAGCATTGACGAATTTGTCAAGGGTTATATATAT
TTGATATTAGAACCCTGGAGAGGTTACAAATATAGAGAATTTCTCCAAGGCATGGTGCCGTTTCAAGCAT
CTGTATCGATGAAGAGTGTGTGTCCTAATTTTGGGGACGACTAGAGGTATTATTGATATATGGGATATC
CGTTTCAACGTGCTGATAAGGAGTTGGTCCCTTTGGGGACCACGCACCAATCACGCATGTGGAGGTTTGT
AGTTTTATGGAAAGAATTTCTGTAATTTGTTGTAGGAGGTAGTTCAAAAACATTTCTAACAATATGGAATTT
TGTTAAGGGGCATTGTGAGTATGCTTTTCATAAATTTCTGATGAACAGCCATCTATGGAGCACTTTTTACCA
ATTGAGAAAGGCTTAGAAGAATTAATTTTTTGTGGAATCAGGTCTTTAAACGCACTAAGCACTATCTCAG
TATCTAATGATAAAATTTCTTCTTACCGATGAAGCAACAAGTTCATTGTTATGTTTAGCCTAAATGAGCT
TTCTTCTTCTAAAGCAGTAATAAGTCCTTCAAGATTCAGTGACGTTTTTATTCTTACACAAGTTACGGCA
AATCTCACAATGTTATTGAGAAAAATGAAACGTAAGTACTAGCACTCATTGATGATGATCTCTATATCATC
ATGATATTATAAATTTCTATATCTACATGTGAAGTTGATGAGACACCTTTGCTGGTTGCTTGTGATAACTC
AGGGCTTATTGGAATCTTCCAATAA

20. BECN1 (beclin 1)

>tr|K1QHY7|K1QHY7_CRAGI Beclin-1 OS=Crassostrea gigas OX=29159
GN=CGI_10027731 PE=4 SV=1
MATIKVESKSGTTHVSFVCQRQRQPLKLDHSFNTLDRQLLAELSAGPFLTGFSSLLDDV
EVDENYSKRDIITSTPEPEDAGDFLLGGETSPGNMNDLSHRIRVSSALFDVMSGQSEIDH
PLCEECTDNLDDQLDNQLKITEDECKDYREFLENLDSNHTEEDGSNLDVELQQQLQAEEQS
LRQQLQNLLETEQEHEALKEKEREISQKLQDEEDKYWKEYNEYKRQVQELEDEQRSVDNQ
LKYAQTQLDKLKKTNVFNNTTFHIWHSGHFGTINNFRGLRPLSVPVDWNEINAAWGQTVLL
LNSLAKKMNLTFRYRLVPPGNHSYIESLSDKSKELPLYGSGGFRFFWDTKFDQAMVAFL
DCLQQFKEEVEKGDGTGFLPYKMEKGIKIEDSSTGTSYSIKIQFNSEEQWTKALKYMLTNL
KWGLAWVSSQFANK

>AF139131.1 Homo sapiens beclin 1 (BECN1) mRNA, complete cds
CGGGAAGTCGCTGAAGACAGAGCGATGGTAGTTCTGGAGGCTCGCTCCGGGGCCGACCCGAGGCCACAG
TGCCTCCGCGGTAGACCGGACTTGGGTGACGGGCTCCGGGCTCCCGAGGGATGGAAGGGTCTAAGACGTC
CAACAACAGCACCATGCAGGTGAGCTTCGTGTGCCAGCGCTGCAGCCAGCCCCTGAAACTGGACACGAGT
TTCAAGATCCTGGACCGTGTCAACCATCCAGGAACACAGCTCCATTACTTACCACAGCCAGGCGAAAC
CAGGAGAGACCCAGGAGGAAGAGACTAACTCAGGAGAGGAGCCATTTATTGAAACTCCTCGCCAGGATGG
TGTCTCTCGCAGATTTCATCCCCCAGCCAGGATGATGTCCACAGAAAAGTGCCAACAGCTTCACTCTGATT
GGGGAGGTATCTGATGGCGGCACCATGGAGAACCTCAGCCGAAGACTGAAGGTCCTGGGGACCTTTTTTG
ACATCATGTGGGGCCAGACAGATGTGGATCACCCACTCTGTGAGGAATGCACAGATACTCTTTTTAGACCA
GCTGGACACTCAGCTCAACGTCCTGAAAATGAGTGTGAGAACTACAAACGCTGTTTGGAGATCTTAGAG
CAAATGAATGAGGATGACAGTGAACAGTTACAGATGGAGCTAAAGGAGCTGGCACTAGAGGAGGAGAGGC
TGATCCAGGAGCTGGAAGACGTGGAAAAGAACCGCAAGATAGTGGCAGAAAATCTCGAGAAGGTCCAGGC
TGAGGCTGAGAGACTGGATCAGGAGGAAGCTCAGTATCAGAGAGAATACAGTGAATTTAAACGACAGCAG
CTGGAGCTGGATGATGAGCTGAAGAGTGTGAAAACAGATGCGTTATGCCAGACGCTGGACAGTTTGGCACAATCAATA
CTTCAGGCTGGGTGCCTGCCAGTGTTCCTGGAATGGAATGAGATTAATGCTGCTTGGGGCCAGACT
GTGTTGCTGCTCCATGCTCTGGCCAATAAGATGGGTCTGAAATTTTCCAGAGATACCGACTTGTTCCTTACG
GAAACCATTTCATATCTGGAGTCTCTGACAGACAAATCTAAGGAGCTGCCGTTATACTGTTCTGGGGGGT
GCGGTTTTTCTGGGACAACAAGTTTGACCATGCAATGGTGGCTTTTCTGGACTGTGTGCAGCAGTTCAAAA
GAAGAGTTTGGAAAAGGCGAGACACGTTTTTGTCTTCCCTACAGGATGGATGTGGAGAAAAGGCAAGATTG
AAGACACAGGAGGCAGTGGCGGCTCCTATTCCATCAAAAACCCAGTTTAACTCTGAGGAGCAGTGGACAAA
AGCTCTCAAGTTCATGCTGACGAATCTTAAGTGGGGTCTTGCTTGGGTGTCTCACAATTTTATAACAAA
TGACTTTTTTCTTAGGGGGAGGTTTGCCTTAAAGGCTTTTTAATTTTGTGTTTGTGCAACATGTTTT
AAATTAATTCGGGTAATATTAACAGTACATGTTTACAATACCAAAAAAGAAAAAATCCACAAAAGCCA
CTTTATTTTAAAATATCATGTGACAGATACTTTCCAGAGCTACAACATGCCATCTATAGTTGCCAGCCCT
GGTCAGTTTTGATTCTTAACCCCATGGACTCCTTTCCCTTTCTTCTCTGAAAAAACTAATTTAAATTTG
CTTTTCTTTTTTTAACTGAGTTGAATTGAGATTGATGTGTTTTCACTGGATTTTTATCTCTCTCAACTT
CCTGCACCTAACAAATATGAAATAGAACTTTTTGTCTTTACTGAGATGAGGATATGTTTGGATGCACAGT
TGGGATAATGTGGGAAAATGACATCTAAGCTTTACCTGGTCACCATGTGATGTGATCAGATGCTTGAAT
TTAACACTTTTCACTTGGTTCTTATACTGAATGCCGACTCTGCTCTGTGTTAGAGATATGAAATGGTGT
TGATACTGTTTGGAGACATTATGGAGAGATTTAATTATTTGTAATAAAAAGATTTGCTGCAGTCTGAAAA

>NM_001183934.1 Saccharomyces cerevisiae S288C beclin 1 (VPS30), partial mRNA

ATGAAGTGCCAAACATGTCACCTTACCCTGCAACTAGACCCATCTTTAGAAGGTCTTAGTTTAAACCCAAA
GAAATTTGCTACTTTCAAATAATTCAATTATCACTGCAACGAATGAAAATGTCATCAGCAACAAGGGCAT
CGAAGCCGAGATAATTGTGGGCCTCAAATACCGAAGGAGAGGCTGAGGCGATTAGGGGAGATTCAGAAC
ATAAAAGACTTGAATTTAAAAGATGATAAATTAATCACTGATTTCGTTTGTGTTTTCTTAATCAGATGATG
ATGATAATGCTAATATTACGAGTAATAGCAGAGAGGACCAGCGTTATGGAAATGCCAACGAAAATGATAA
TAAAAAAGCTAATAGTGATACTTCCGATGGAACCAAGTACCTTTCCGAGATCATGACGAAGAGGAACAAGAA
GCTACGGATGAGGACGAAAACCAACAATAACAATTGAATTCGAAGACTTTGTCCACACAAGTCAACGCAA
TGACTAATGTATTTAACATTCTATCTTCTCAAACAAACATAGACTTTTCTATCTGTGAGGACTGCTGTAA
CATCTTGATAAACAGACTAAAAAGTGAGTATGATGATGCAATAAAAAGAGAGAGATACTTACGCTCAATTT
TTATCGAAGTTAGAGAGTCAAAAACAAAGAAATATCAGAAAGCAATAAAGAAAAAGCAGTATTTCCATAATC
TTTCGGAAAAAGAAAATTTGAAAAAGGAAGAGGAAAGACTCTTGGATCAATTATTACGTTTGGAAAATGAC
AGATGATGACTTAGATGGAGAAGTTCGTTTACAAGAAAAGAAAGTTCAACTGGAAAATGAGAAAATC
CAAAAACCTGAGTGCAGAAATTTAATGGATTTAAATAACATTCAATTCAACAAAAATTTACAGTCATTAA
AACTGCAATACGAATTTATCCTTGAATCAATTAGATAAGTTGAGGAAAATCAATATTTCAATGCTACATT
CAAAATCTCACATAGCGGCCCTTTGCCACTATAAATGGATTGAGATTAGGCAGTATACCAGAATCAGTG
GTACCTTGAAGGAAAATCAATGCAGCACTGGGCCAATTGATTCTTTTACTGGCTACCATAAACAAAAACC
TGAAGATAAATTTAGTAGACTACGAATTACAACCGATGGGTTCAATTTTCCAAAATCAAGAAAAGAAATGGT
TAACAGTGTGCAATATAATAATTCACACTACGAACGCTCCCGGTGATTGGTTGATTCTGCCTGTCTACTAT
GATGAGAATTTCAATTTGGGGAGAATCTTCCGCAAGGAAACGAAGTTTGAATAAATCATTAGAAAACAACAT
TAGAAATAATAAGCGAAAATCACTCGGCAGCTTTCTACGATAGCGTCATCATATTCATCTCAAAACTCAC
AACAAGCCAAGATGAATCTTCAATGAATAACGCAATGACGTTGAAAATAGTACTTCCATTCTCGAGCTA
CCCTATATCATGAATAAGGACAAGATTAATGGATTATCCGTCAAATTCATGGTAGCAGTCCCAACCTTG
AATGGACAACGGCTATGAAATTTTTATTAACCAATGTAAAGTGGTTGTTAGCGTTTTCTTCCAATTTACT
ATCCAAGTCAATTACCTTAAGCCCTACAGTGAATTACAATGATAAGACCATCAGCGGAAACTAA

21. ATG14 (autophagy related 14)

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

CTTTTAGAAAACCAATTACGTCATTTCCATTTTTATTATAATGGCGACCTCCAGTTCTTGTGAAAGCAAC
TTAGCTCCAACAGAATTTAACTTGACCAGTTTCGATAGAAAGTTCCCCTGGTCTCACTGTGCGCATAGAAC
GATGCCCTTATGCGATGGAAGTAGGCGGTCAATTTTCATTGCAGAAAATGTGTCAACGAAGGACTCTTTGT
TCACACGAAAGGAAGCCATCCTGAAAGATACAAAGAAAAGAGATTCAAGCTTGATCATTGCAAAAAGAA
AGACAAGGAAGGTTGGAGAGGGTACAAGATGCACTGAAACAGCACATGCAAAGAGACAAAACAAATCGGGG
AAATTGAAAATGCAGAGAGAGGATAAACCTGTTAAAAATGGCTCTCACAGCAGCAAAAAGAAAAGAGAG
GAAAAGTAAAGAAATTTTCGACAAGAAAAGAGAGAAAACCTATCTACGGGTTGTGAAAAGTTCGAAAACAT
GAAGAAAAGAAAAGCGCATTATTTCTACATTGAAAACAGTGAGAATGTCAAATGAAGAGAAAAAGAGC
TTTGTTTACAGAAAAGAGGCAACTAGCTGCAGAGAGGAAGATACAGGTCCAGAGATTGGTGGAGTTTAT
CTTTCAGGTGGAGGAAGTGGCTCTTATTAGTGAGTCACTCGATGGCTGTGAGCACAGTGAGTGCCCTG
CGAGATGCGAGTCACACGGCCTATGTGAGAGGGCAGTGGGTGTACACTGATGGTAGTGGCGAGGCCAGT
ACAGGATCGTGGAGCCCACCTTACCCTGCAGTGGGGACTACTCAGCCTATAATCTGTGGGTGGCTGCTAG
TCAGGAAAATGGTGGTAACCCAGACAACAGTTTAAGGAACCCAGGTCACAGAATCAGTGCGGGTTTGTGC
TACGCTAGTCAGATGACAGCCATCCTCAGTCATATACTGGACATCCGCTGCCAAGAAAACAGCCTTATA
GCGAGTTTTGTACTAATGAGATCACAGAGCGGCAGTTCAAGCACAGTGTGGCCTCTCTCAACCAGAACAT
CCTGTATCTGTGCTTCTCCAGAGTGTGCCAATCCCGAGCGGCTTGACCCCCGCAACACCCTCCAGAAC
ATCGTGGTGTACTCTCCTGTCTTTATTGGGAAGGAACTCCAATTTGAAAATGACAAAAGACCTGATGG
CATCCATTGAAGACTCTATCATATTTCAAGAGGAAGATTTCGGATACTGGAGGAATGGAGGATGAAATGAT
CAATGATTGGGAACAGGTGTGAGAGGATGTGACCTATGTGACAGACGTTCCAGCCCAGTCTGGATATAGC
AGCACTCTATCCAACATCCAGACAATGTCGTATCCAGGTCAGCCTCCGGAACAACACTGACTGCCAGTGGTT
TTGTTACATCTGCAGCCACATCTTTCATGTCAATTATTCAGGGGAGGAGATCACAAAAGCTGACATCAGAG
AATTCTCGAGAAAGATATTAGGAAACGCATTTAAAATAAATCAGTATTTTTTATCCATCCCAATCACACAT
GTAAAGAGATAGTACCATAGTGAATAATTTTTTTTTTTTTTCAAAGTGAATAATTTTTTTCATGCCAACCAAT
ATTTTTGAACGATGTTTTGACTTCTAAGATCAGCAATTTGGATGCATATTGTTTTTGTATTGCTTGAAT
AAACCTTAATGAATTCAACTTAAGTCTTCTACCAATATTTTTGAAGAAAAAACATAACCCTAAAAATAT
TCTTGAAGGGTGGCCTGTTATCCCATGGTCATAAGTAGTTGACTGTTACATTTCAAGGTTATTCATGGAG
TTCAAGGTCAAATTTATCAGAGTTAAATGTATTATGATACAGTTTGAACCTGATTTATTGTATGGGATTT
TAAAAGTTCTCTATCATGCTACAAATCCATTTATTGTTAATAACTCCAATTCTAAAGATAACTCAGAAAA
CCATAGCTGTATTAGATAGTGCCTCAATATGCCTTGTGCAATCATTCTTATGATTAAGGACTGTGAT
ATGAGCTTTAGTGCATTGTTTATAGCATTGCATGGTGTCTAGCTTCTACTGCAGAGATTAGATAATGCC
ATTATTTTATGGTAAAATTTAAATTTATACATGTATTATGTTATTTTTTTTTTGTGGTGAATAATGATTA
TTAAATTTTTTTTTTAAATTTGCTTACCTCAAATCACAAAATCATGAATTTTTTAAATGATGCTAAGAAA
ATACCAAATGCATGTCTATTTTTTGGTCTCCAGCTGTTCTCAGGGTTTGTTTATTTGTTAATGAATGTA
TGTTAACGATTGTATGTTGATATTACTTTTTTTTTTCACTAAATTTGGCAAGGCATCCTCCTTGAAATGTTT
AAGAAAAATGTAACATGTTATTGGATGCAATTTTAAATATTGGATTTTTTTTTTACTAAAAGAGATAAAGA
ATCATTCTTTGAGTATTATGAAGTATCAAGAAAGAATAAATGAAGAATGAAATGATAATATTATAAGAC
AGAAATGTATATAAAATTTTGTATTAGTAAATGTTTTTCAAGTCTCCTGAAAACCTGTTAATCATCTCA
TATTGCCCTATATCTTTTCGATAAATTTGTGCTAAAATTTATGTTTCTGAAACGTTTTTGGTACAACCTT
GATATGTGGTTCACTTTTTGCATTCAGTTAAATGGTGTCTGCTTTTTTATTGCTTATTAGGTACAGTTGG
TTTTAGTGTTCGAAAATCTATTCTGACTTTTTCAATGAGCTTTACCTTGCCATTTCCAAGACAATATGC
AATATTTTTAGCAGATTCCTGTATGGTTACTTTTACCTGTAGTTTTGTTTTATTTTTTCCATTGATAA
ATATATTTATTTACTATATCAGTTTTATATATTTTTTTTTGATTTTCTGTGTCCATTAATAGTCGAAAGGA
AGATATATTTTTAATTATCATGACATACAAGTTTTGCCGTTATAGAAGTCCGAGACGATTTAAAAATATTT
TTCTCCTACAAAGAACAACCTTTAGCTTAAAAAGAGCTGTTAATTTTTAAAAATATAAAATTTAAAAAATAG
CTTAAGAAAAGGATGAACAAGTTAATCAATAAAATCCAGTGAAGTATTAACATTTGTTTTATGGTGTCTGA
CTTCACTTTTTTGGATTTGATTATTCATGAATTATTTTGCAGCTGATTGAAAAACTCAGCTAGTGTATAT
TAGCCACGGAATGCATGAACCTGATGTCAGAATCCATGTTTTTTTTTACTTCTATATAACAATTAATTGTT
AATTATTTTTAAATCAGCTACCAAATGTTTCGTTTTGATGTTAGTAAAATGCCTTATGGCTATATGAAA
AAAATTGAGAAGACGTTTTTATGAAATTTTACCCTTTGAGGACCATTCCATGAAACTAAAATATTTATTA
TTCGAATTTTTTTAAAGCAGCAGTAGGCTTATGTTTGAATAAGATACCTTTTCTAACGGTTCAAATTTCA
AGAGTTTTTACATTTGTATGAACGTCATTGTGATGTCTACAATTCAGACCAATAAAGAAGGAACGGAT

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

MASPSGK GARALEAPGCGPRPLARDLVDSVDDAEGLYVAVERCPLCNTTRRRRLTCAKCVQ
SGDFVYFDGRDRERFIDKKERLSRLKSKQEEFQKEVLKAMEGKWI TDQLRWKIMSCKMRI
EQLKQTI CKGNEEMEKNSEGLLKTKEKNQKLYSRAQRHQEKKEKIQRHNRKLGDLVEKKT
IDLRSHYERLANLRSHILELTSVIFPIEEVKTGVRDPADVSSSESDSMTSSTVSKLAEA
RRTTYLSGRWVCDHNGDTSISITGPWISLPNNGDYSAYYSWVEEKKTTQGPDMEQSNPA
YTISAALCYATQLVNILSHILDVNLPKKLCNSEFCGENLSKQKFTRAVKKNANILYLCF
SQHVNL DQLQPLHLRLNMLVSPSSEHLGRSGPFEVRADLEESMEFVDPGVAGESDESG

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
DIKRMEKKKDPMLNSMLMKLDVLRMKNNNLIHRHRIEQLNERIYSKRNIHSELKVEIDNYK
CYKVGTTGDKLREQVEISDAKNKLAQVSKICESARDYKLNLLNNWFVIQKLQDNFQIPFA
IAFQPLISLKNFRILPLAITNDSINIMWKYISFFSDILMIKLPYTNKICEQPMFEFSDSI
QTVVQRLIKLIINILQICRHLKLVLPSTPMDIPWLLDQYDVGDLFYNMVKNKMKCRSVSL
YWTFGMLYSMVLDMNNPQRGHPARRTAPPPTVTGPHDRWYVVG

22. 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
DGTKVASTHGHDHTVRVSDVATGKCLHILRGHPRTPWCFIAFHPTSNQILASGCLGGEVRIW
DLHGFGTEVWRSKDNYEITSLTFHPTDHVLFVSVTNHIYFWDWSQPEPFVVKTNYEYEK
IRWVKFDPLGQFLYTGIANNTTVRPPSRVSVFISGNTHPNTVFNASRTQQLSNVYDSLVEC
FQASRRDRVLRNTEAGQDPQSVSNTQHGASNHQSPVHEEGLSLARQYASHITQSSQRSM
QGMSQRPEIPSGASNSSSSPDTMDGISSPANPVLAMQPPRGASADNDVSGESPPSIVSV
DGESSQTRAVSNHPRSERVPGTLIVTERSPEQTSPPFQSLDTSSGVRIVSEAQSVRGILN
DQVHASTTAFIAPEEEPAEEVISLSELTSRGLSEEHLHHSNTDCDRLNCPVCGNFDT
THIRRVCESEMFTQLRARRRSLQNSMNNVSARSASFSPYTYNRHGSLVRPEIHSIQDPSQ
LGEMHEIRRVENPNAGASNMDHVSSNNSAPSNTTEGDARLTQVGDNIDICASIENFATIT
ARIEREMNELDRRINNLNRTFNESLRRLQHHRVSFLSAREGDVNGRRPSFIVARHTQQAE
GASSSRPEDSTHSLDRGQHLLLETALRSSRPDRGTGSHSHVPRELDS SHAWQSLERHHLHP
HYSVSILDNTINRPNDPIQTAINRAIADAFMGRGEPAVATNI INHTYRIQAWDFSRCNIP
DLTDTKSNIVVQHCKLHNDASCNLSQDGTMLATFVPSHRGFPDDNIMAVYSLEPKTRGQC
LFTKSFNPNAISVLSLSPGSGYVMVGLAAKQLSWVFTPNQHITDVMHPCMDDIRTHVSVNS
ARWMPGSGEGIVYGTNRGDLHVCRPGTKKSVAGDNSDDRSIRRNLMHMLRMSGEQDVPRI
NTSTQTPGVRRSASTQTDTDSDM

>DQ870924.1 Homo sapiens activating molecule in beclin-1-regulated
autophagy (AMBRA1) mRNA, complete cds
ATGAAGGTTGTCAGAAAAGAATGCTGTCCGGATACTCTGGGGCGAGAACGGGGTGCTCGGGCCATGG
GAGCTCAGCGCTTCTGCAGGAGCTGGTAGAAGATAAAACCCGGTGGATGAAATGGGAGGGCAAGAGAGT
AGAAGTCCCGATAGTCCACGCTCTACCTTCTTATTGGCCTTCAGCCCAGACAGGACTCTCTTAGCCTCC
ACCCATGTGAACCATAATATCTATATTACGGAGGTGAAGACTGGCAAGTGTGTTTCAATCCCTGATTGGAC
ACCGCCGACTCCATGGTGTGTCACTTTTCATCCACCATCTCAGGCCTTATTGCTTCTGGCTGCCTAGA
TGGGGAGGTTAGGATTTGGGATTTACACGGTGGCAGTGAAAGCTGGTTCACAGATAGCAACAATGCCATT
GCCTCCCTGGCTTTCCACCCTACGGCTCAGCTCCTGCTGATTGCCACTGCCAATGAGATCCACTTCTGGG
ACTGGAGTCGACGGGAACCCCTTTGCTGTGGTGAAGACAGCTAGTGAGATGGAACGGGTCCGCTCTGGTGAG
ATTTGATCCACTTGGACACTACTTACTCACAGCAATTGTTAACCCCTCTAATCAACAGGGTGATGACGAA
CCAGAGATCCCATAGATGGAACAGAATTATCCCACTACCGTCAGCGTGCCCTCCTGCAATCACAGCCAG
TTCGCCGACGCCTCTCCTCCACAATTTCTGACATGCTGTCTCCCGCTCTTCTGGCATCCAGGTGGG
AGAGCAAAGCACAGTGCAAGATTCTGCTACCCCTCACCCACCAGCCTCCCCCTCAGCCCTCCACGGAG
CGCCCCAGGACTTCCGCTTACATCAGGCTCCGACAGCGGGTACAGTTACCCACAGCTGAGTGCTGCCAGC
ACCTTGGGATCCTGTGCCTTTGCAGCCGCTGCTCTGGCACTCGAGTTTCTTCCCTTCTGCCACACCAGGA
CAGTGTCCCCCTGCTTCTGCCAGAGCTACTACCCCTTCTTTTCTTTGTACAGACCGAGCCCTTCCAT
CCCCCGGAGCAGGCCTCGTCAACGCAGCAGGACCAGGGCCTCCTGAACCGCCGCTCTGCCTTCAGTACAG
TCCAGAGCAGCACTGCCGGCAACACGCTCCGCCAACCTCAGTCTGGGTCTACCCGCGCTCTTTGGGAGG
GCCTCTGTCTAGCCACCTTCTAGGTATCAGGAGAAATAGCTCCTGGGTTGACAGGATCTGAGTGGACC
CCCACTGACTCAGTCTGAATCCCGCTCTGAGGCGGAATCCATGCCCCCGCCAGAACCACTGCCCTT
CGGTGAGTTTGTCTGTGCTGAGACAGCAGGAAGGTGGCTCTCAGGCATCTGTGTACACTTCAGCCAC
AGAAGGGAGGGGTTTTCCGGCATCAGGGTTGGCAACTGAGTCAGATGGAGGGAATGGCTCCAGCCAAAAC
AACTCGGGCAGCATTGCCATGAGCTTCACTGTGACCTGAGACGCTTCTTTCTGGAGTATGACCGGCTTC
AGGAGCTGGATCAGAGCCTGAGTGGGGAAGCTCCCCAGACCAACAGGCCAGGAAATGCTCAACAATAA
CATTGAATCTGAGAGGCCAGGCCCTTCCCACCAGCCACCCACACAGCAGTGAGAACAACCTCAACCTG
TCCCGTGGCCACCTGAATCGCTGTCTGCTTGGCACAATCTCCTGACCTTCAACAACGATAACCTGCGCT
GGGAAAGAACCACACCTAACTACTCTCTGGCGAGGCTAGTTCCTTCTGGCAGGTCCCAGCTCCTTGA

GAGTGTGCCATCAAGTGGCAGCCAGTTGCCACCTCTCGAGCGGACTGAGGGCCAAAACGCCAGCTCCAGC
AGGCTGGAGTTGAGCAGCTCTGCTAGTCCGCAGGAGGAGAGGACTGTGGGGGTGGCCTTTAACCCAGGAGA
CAGGCCACTGGGAAAGAATTTACACCCAGTCCAGCAGATCTGGAACGTGTGTACAGGAGGCCCTTACATCA
GGATATGCCTGAGGAGAGCTCTGAGGAGGATTCACTCAGGAGATTATCTCCTGCTGCATACTACGCCAG
AGGATGATCCAGTATCTCTCACGGAGAGACAGTATTCGCCAGCGCTCCATGCGCTACCAACAGAACCCTC
TCCGTTCTTCCACCTCCTCCTCTTCTCAGACAACCAGGGTCCATCAGTAGAGGGAACCGACTTGAATT
TGAGGACTTTGAGGACAATGGTGCAGATCCAGGCACCGAGCTCCACGCAATGCCCCGATGTCTGCACCT
TCGCTTGGACGCTTTGTCCCAAGGCGTTTCTTGCTGCCTGAGTACTTGCCCTATGCTGGGATTTTCATG
AACGTGGACAGCCTGGCTTGGCTACTCACTCTTCTGTAAACAGGGTCTTGGCAGGGGCAGTGATCGGTGA
TGGACAGTCTGCTGTGGCCAGTAACATTGCCAATACTACCTACCGGCTCCAGTGGTGGGACTTCACTAAG
TTTGACCTCCCTGAAATCAGTAATGCTTCCGTGAATGTGCTGGTGCAGAACTGCAAGATCTACAATGATG
CCAGCTGTGACATTTCTGCAGATGGCCAGCTCCTGGCAGCTTTCATCCCAGCAGCCAGAGGGGCTTTC
TGATGAAGGCATCCTGGCAGTGTACTCCCTGGCCCCCATAACCTGGGCGAAATGCTCTACACCAAGCGA
TTTGGTCCCAATGCCATTTCCGTGAGCCTGTCCCCAATGGGCAGATATGTAATGGTGGGCTTGGCCTCAC
GAAGGATCCTGCTGCACCCCTCCACAGAGCACATGGTGGCCAGGCTTTCAGGCTGCAACAGGCCCATGG
TGGAGAGACCTCCATGAGGAGAGTTTTCAACGTCTTTTATCCCATGCCTGCCGACCAGCGGAGACATGTC
AGTATCAACTCTGCCCGTTGGCTGCCTGAGCCAGGGCTTGGCTTGGCCTATGGTACTAACAAAGGAGACC
TGGTGTACTGCCGACCAGAGGCCTTAAACTCTGGTGTGAGTACTACTGGGACCAGCTGAACGAGACGGT
CTTCACTGTCCATTCCAACAGCAGGAGCAGCGAGCGGCCTGGAACCAGCAGAGCCACATGGAGGACAGAC
AGAGACATGGGGCTGATGAATGCCATTGGGCTTTCAGCCCCGAAACCCTGCCACCTCAGTGACATCTCAGG
GCACCCAGACTCTGGCCCTTTCAGCTGCAGAATGCCGAAACACAGACTGAGAGGGAGGTGCCGGAGCCAGG
GACAGCCGCTCAGGTCTTGGTGAAGGTGAGGGTTTCAGAGTATGGTGCAGTGGAGAAGATGCGCTCAGC
AGGATCCAGAGGCTGATGGCGGAGGGCGGCATGACAGCCGTGGTGCAGCGGGAGCAGAGCACCACCATGG
CCTCCATGGGCGGCTTCGGCAACAACATCATCGTCAGCCACCGCATTACCCGAGCTCTCAGACGGGCAC
TGAACCTGGTGGCGCCACACCTCCTCACCCAGCCCTCCACCTCTCGGGGACTGCTCCCAGAGCCGGG
CAACTGGCAGAGCGAGGCCTAAGCCCCCGACAGCTTCTGGGACCAGCCTGGTACCCCTGGGCGGGGAC
CAACCCAGCCAACCCTGCCCTCTTCTCCCTGTCCCCATTCTGTTTTCCCTTCCCAGCGCTGAGGGGACC
AACCTCCACTGCGAGTTGACCAATAACAACCACCTTCTGGATGGTGGCAGCAGCAGGGGGGACGCTGCA
GGCCCTAGGGGAGAACCACGGAACAGGTAG

23. UVRAG (UV radiation resistance-associated)

>XM_020069853.1 PREDICTED: *Crassostrea gigas* UV radiation resistance associated protein (LOC105334521), mRNA
ATGGGATCTCTCTGTGAGAATTATGTTCTTGTGTTATCATGCAGCTGGTCTCTGCTGGTACGAGTCTGGG
TAAAGAACAAGACAAGTACCCGCCTCCTCTTGGACTGGATGGTGGACCTAAACGCCCTGGAATATCTCGC
AGACAAGCTCCAGCAGGATAAAGGCATTAAGTATGCTCCAAACACTCTCATCTTTGGAATGTTTGATCAA
TTCTTTCAGAGCCCTGAAGTGAAGCCTGTGGGAGTGGGTGTTGGAGACCCAGGAGTTGAGCAGAGAATG
ATAAATCCAGTAAGTCACAATCTGTGAGCACACAGTCTTCTCAAGGTGGAAATAGCCAGCACCAGAA
GTCTTACACAGCCAGTTCTTTGTCCAGAATATACACCGTCTTAAAGCAATCAAGCAAACTCAAGCCTCG
GTACATAAAGTTCGAAGGTCAATTGAGGACAAATTATTGTCTCACAAGAGACAACAAGGAAAAGGGCAG
AGCATGAGGACCTGCTCCTCAAGAGGGAACAACACTGTGTGCAGAAGTGACGTGGAGGACAGCCTCCGTCAA
CAAGATGAAGGACCAGGCAGATCAACTCCACAGGTCCAACCAAGAACAAGAAACAGCAATGAAAAAGAA
AAAGAGAAATTGGAAGAGAAACAGAGAGAACAGGCAGAAAAGAAGAAGGATTATGACCAAACAAGAGAAA
AGCTAATTAAGAGAGTGTCTCAACTTTTTCATCAGAAGGAAACAGCTGATCCGTGAATTAGCCACCTACAT
TTATCCAATTAAGAGAGTGTCTCAACTTTTTCATCAGAAGGAAACAGCTGATCCGTGAATTAGCCACCTACAT
CAAGGCAAGGATGACAACATGATAGGAGTTTTCCCTGGGCTACACCTGTCATCTGTTGTTGATGATTTCTG
GTATTCTGGACATTTCACTCCGGTACAGCATGACTCATCTAGTGTCCAAATCAGTCATCCGTGACGACAT
CCACAGCAGACTGGAGGACAAAGAAAGGGACTTCCCTTTTATATTCCAAGGGCAAGGAACAAAATTTATTC
CGATATGGAGTGTTCACCCTGAACAAAATATCAGTCAGATGCGGTTTTATTTGGGGATGGGAACGGTGG
ACCTGAGAACCCTCTGATGAATATAAAGACGTTGCTGGAGAATAGACTAGGCTTGAAACCAGAGAGTCA
GACTGCACAACCTTCGTCCAGCGAGTGAACCGGGTGCAGACAATACAGTACTTTGACAGAACAGACACG
CGAAGTTCTCTGGCGTCTATGGTAGGATGGCAGTGGACTTCCGGAGGGAACCTTCTGTGCCGCCACGG
AAGAATCTTCTAGACAACCTCGCCAAATCTCAGCAGGTTGGAGGAAAAGGAGATTTTCCATCCAAGCAG
TGATGACAATTTCTTCAAATTTCAAACCTGTGTGCGAGAGATTGGCAGATTTTGAGAGTGAATCAAT
GGATGTGCACAGGACACAGTGAATTTTATAAGCCTTTCGACAATCGCCGGCAGACTTGTGGAACGGTG
TAGGAAGCAATGACTTTAATGCTGGTGTGATCAGCCTGAGGAGGACCATATATATGAAACTGTTAATGTGAG
AAAGACAGCCAGTGAAGTTTATGATAAATCACCGAGTCCATCAAATATTTCTATCATCTGATGAGTGTG
AATGTTAGATGTGTGAAAATTTATATACCTACTGTATACTCGATGATGAACTTACTCCTTTGGCCTCAACC
CGCAAGTCTTTGCTTACTCAAAAAGACACGTGATTTTAAATCTGAAAACCTGACAGGAATGATTTCAAAA
CATGTCCAAATGCTTTTTCAGTGGAAAACAATTTGGGTGAATTCATCCTTGTATACAGTAATGTTTAT
TGAAGAATCAAATTTGTGCAATATAGTTATTAATATTTGAAATGATTAAGAATATTTCAAAGTATTAAGG

GACAGGTTTGGATGTTTTGACACAAGGACAGAAATGATATCAAAAAGTTAACTTTTTGTCATAAAGGTATCCA
TTTGATAATTTCCATAATTATTATTTTTAAATTTAATTTCAATGTATGTAGTACATGTATTTATTTAATA
CAGATACCAATAGTTGCATCAACTTGAGGCAGAATGTCCTGATGATTGAGTTTTTAAAAAGAAATGTCCTT
ATGTTGACAACTTGAAGGAAAGTGTGTATTTGAAGTTGAAATATTTTGAACAACTAAAAACATGCATAT
ATCATGTGGACTGATCTTGAATAGAAAAGTCAATAAATGATCTAGAAATCTTTCAA

>sp|Q9P2Y5|UVRAG_HUMAN UV radiation resistance-associated gene protein
OS=Homo sapiens OX=9606 GN=UVRAG PE=1 SV=1

MSASASVGGPVPQPPPGPAAALPPGSAARALHVELPSQQRRRLRHLRNIAARNIVNRNGHQ
LLDITYFTLHLCSTEKIYKEFYRSEVIKNSLNPTWRSDFGIMPDRDLTSSVSCFVVKIWWG
KENIYQLLIEWKVLCDGLKYLGGQIHARNQNEIIFGLNDGYYGAPFEHKGYSNAQKTILL
QVDQNCVRNSYDVFSLRLHRAQCAIKQTQVTVQKIGKEIEEKLRLLTSTSNEKLLKSECL
QLKILVLQNELERQKKALGREVALLHKQOIALQDKGSAFSAEHLKQLQKESLNELRKEC
TAKRELFLKTNALQITIRCRQLLSELSYIYPIDLNEHKDYFVCGVKLPNSDFQAKDDGSI
AVALGYTAHLVSMISFFLQVPLRYPPIHKGSRSTIKDNINDKLTEKEREFFLYPKGGEKL
QFDYGVYLLNKNIAQLRYQHGLGTPDLRQTLPLNKNFMEHGLMVRCDRHHTSSAIPVPKR
QSSIFGGADVGFSGGIPSPDKGHRKRASSENERLQYKTPPPSYNSALAQPVTTVPVSMGET
ERKITSLSSSLDTSDFSKENKKKGEDLVGSLNNGGHANVHPSQEQQEALSghRATVNGTL
LPSEQAGSASVQLPGEFHPVSEAELECCVEQAEEIIGLEATGFASGDQLEAFNCIPVDSA
VAVECDEQVLGEFEFFSRRIYALNENVSSFRPRRSSDK

>sp|Q05919|VPS38_YEAST Vacuolar protein sorting-associated protein 38
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VPS38
PE=1 SV=1

MKRFLLSRRQRHLRMICFHNISLFRANGDSKLIKEYGDGFIPCFFILESIRGELLYVSEV
QSGSLRKLFSQELPKLTGASTMIVLKLVLGSLVPSDILCTISSDKNGIIDDKWCVLCTYITID
LNKLQPINEDTVLITGTNAPVLDLIDGSYTLAAEKIKPLKGLVSSHKNISQVKIKFSLA
YSSLLKLNKLLYSSQVHEEINEISSKIEDDFLSLKNQNHWMRTVQKSIETLEKEVLR
KKSCKNIEMAQLESNDTINHSTELSLMSQDESINDDYGSYSRFVQIKDRDLQLRFKKL
YQLIGIFHSTDLFNSDRGYIYFEKPSVNDVINRLKPLNIEILLRQAGESTKHREYVN
SQLGYLLFLHLTAIQIFKAPLRYRLMYGSTSVIDSQYPLYFTDQMIKHKQAKLIKAIH
YFNADILQFKQILENYRPT

24. RUBCN (rubicon autophagy regulator)

>XM_011421238.2 PREDICTED: Crassostrea gigas run domain Beclin-1-
interacting and cysteine-rich domain-containing protein (LOC105322496),
transcript variant X3, mRNA

ACGCTTTGATAACCAAGGAGCTTCATTTTGGACACATGACAAAATTCGGGCAGTCAAGATGTAAACAAGACG
AATATTTGTTTTGAGGAGTTTTAAAGAAGGACATAGCCTCTTGGATCATAAAAAGATGTCTGATGAAGTA
AACGCGGATCATAATTACAGGTCAGAACGTCAAAGCCTACTGTTTGGATTGAAGGCAGTTACAGAGGGGC
TTTTATCCGGACAGAGCAGCAATGTTTGAACATCCATGGAGGACTTAACAGAATGTGTGTTCAACTGGA
ACACATTATGTATCATGGTTTGAAGAGTATCAAGGGAAATTTTTGGATAGAGTTGGATTTCTGGCCATTT
GTGTACAGTCTTAAGATGTTGAACCCAGTCTTGGCCCTGCCTTAGACAAGGTCAACCGATCAGGAGGAA
ATAAAGGGTCAATGTGGCTGAGAGAAAGTTTAAAGGGATCACACCCTGTCTCGCAGTTGTCTACCTTGGT
GTGCAACAAATCACTGATGAAAAGGTTTTACGGTGACTTGGCATTCTGAATGATGCACAATACTTCAA
GCTCTTTGTGTTTGCTTAAAAGCTATTGAACTCAACCAAATTTCTTGTGGCTGAACTAGACCTAAAAC
TGCTTAGTAATAACCATGAACCTAACATGAGGGGGTTCGAGGAGTAGATCTTGGGCTGTACCAGAAAAGAA
ACATCACTTATCGACAGTGAGGGAAAATCAAGCTCCCATGGTGCCATGGCTTTGGCACCACCATTTGCA
TCTCCAAAAAAGGAGAGTATCTTGTGTATGTGAGATGAGCATGCTGTCCCTTCTTCAATCAGAGCAAGCA
CAAGCCCTGAGGACACAAAGAACATGGCTCGTGAATCTTTGAGAACAGTTCTACGGAAATCTGGTTCGGA
CTCCCAACTGGGGATGCCCTGACTTTAGTTTCTATGACAACCTCAACAGTGACCCATTATGAATATA
GAGTTTAGTGAATAACGGCCACTGATAGTGAAGATTCACATGCAGAAGTGGGATCCGGTGAACGCATTG
TCAATTCAGTCAAAGAAGCCATAGTGAGGAGCCAGTCAGATACAGGGATGTCAAACACTTTAACTGT
GATTAATAATATATACAAAGCAACAGGAGACTTTGAGCCCGAAAGTCAAGGACTGTGAACAGGCTCGAG
GATATTTTTTCTGACTCTGAGTGCCCCAAAAGGGGGAAGAAGAAAATGTCAAGGTCAAAGCAAAATCAA
AAGGGCATAAAAAGGTCAAGGTGAGATCATGGAGGTATAAAAAGTGGAGAAAAGGACCCAGAAAAGAAAAG
AAAAGTGCCAAATAAACTCAGAGAGAAGATTCTATCTGAACCAGCAAGTAAAGATATACCAGGGGAGACA
ACTTTCAGGCAGCCTGTACATGGTCAGTCCCTCATCAACTACCTGTCTTCTCAGGATTTTAAACCTGTG
CCAATCTAGACAAGGAGAATGCACATTTAGCATATCTGAGGCATTGATAGCAGCCATAGAACAATGAA
GTGGAACCACGTATAAGTCCGAAGGACCGTGAGGATCCTGAGGAGGAAGACTCGGACGAGGAAATCAAC
AAACTGAAGCAGCGAATCCGCATCCGCAACAGCAGAACTAAGGGAGAAAGCCAAATTTTTCCCTACAT

CCAGTGATGGACTTACTGAAACGGCTACAACCTAGCAAGAGTCCCTCTTCAGTGTTAAATTTCTTCCTGTCA
AGATAACACAGATAGCAGTAATTCAGACATTGAGGTGGATGAAATCAATCTAACAAATGCAGATTTACAG
AAAGTGAAGCCAGATAGACAAAGCTCTATGGAGATATCTGACCAATCTGGCATGTCAGCAGAGTCGGTAG
CCATTTTGTGTTAAAGAAATTTCTCGGAAAAGCAGCTTCCAAAGGCATCCGAGCTGGAGTGGCTGGTACC
TATATCTGAGGCTCCACAGGAGTTACTTCCCTTACCAAAGTCATATCCAGTATCTCCAGATGATATTGAA
AATGAGATTGGAGGATTACAAACTCGCTGTTTGGGACATTGAGATTGAGAGGGAACAATGAATGGGCTC
CTCCAGATCACAGATCATCTTTGACATCCATCCATATCAAAGAGAGCTGTTGTTATGGCAAAGCAAAA
TTTCCGGTGTGCTGGATGTGGAACCCGAGTTGAACCAGCCTATATTAAGATTCGGATACTGTGAATAT
CTAGGGAAATACTTTTGTTCAGTGTTGTCATAGAAACGAAATCAACTACATTCCGGGGCATATAATCAGGA
AGTGGGATTTTAAACAGTATCCAGTGTCCAATTTCTCTTGGAGATTACTTTCAAGGATTTTAAATGAACC
TTATTTTAAACCTAAGTACAATTAATCCATCACTGTTCAAACGAGTGAAGTTGTTGGAGACAGTCCATGCT
TTTAGAGTGCAGCTCATGTATCTGTGTAATTTCTCAGGATTTGTAATATTCAGAAAGGTGAGTTGAAA
CCATTGGTTTACTTTTCATGTCTCTAATGCCTTTCATCATCTTTAATAACAAATGCATAGCTGGTGCTTC
TCATCTAAATACATGTATGTAGATGATAAAAAATCTTCCCTATTGGCCTACTATAAAATTAACAAGACCA
CTTTAGCCTCTTGAACCTGACTTAGATTATATAGACATAAGTATAATTTGATTTCCACATGCAGTTC
ACATCCCTAAATAGCTACATGTAAAGCATTATTACATGTAAGTTAGGAAAATAGAAAATAGACATGAT
AAGGGTATAGGTTTGTATGCACTGATGAAGATGGAGAGTGCATATGGAAAAATAATTTAGATGAGGTAT
GGGGGAAAATTATTGTTTGCATATATTAACATGTGATTAATGCTGAAGCTCTTTACTTTTAAATCAGAT
TGGACTTAAAAATTGTCTTGTGAATTTTTCTTGCATCTGTTTGTTTTAAAGATGGAAAAGATTGCCATATAA
TCTTTTCTTCAGAAAGATAGATCTATGAGTCTTATTATATTTTAAATAATATATTGTTTGGCTGATTTAG
CACAAGTACATATCGTGAATTTGTACTCTGAAAACTGCATGTTTATTGGTCACAACCTTATAAGGTATG
ATACTGAAATATACAAATGATTATATAAATAGGGGTAACAATTGAATTGACAACCTGTGAAAACCATTG
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
MQSILYHGLIRDQACRRQTDYWQFVKDIRWLSPHSALHVEKFISVHENDQSSADGASERA
VAELWLQHSLOQHLSAQLRPLLGDRQYIRKFYTDAAFLLSDAHVTAMLQCLEAVEQNNP
RLLAQIDASMFARKHESPLLVTKSQSLTALPSSTYTPPNSYAQHSYFGSFFSLHQSVPNP
GSERRSTSFPLSGPPRKPQESRGHVSPAEDQTIQAPPVSVSALARDSPLTPNEMSSSTLT
SPIEASWVSSQNDSPGDASEGPEYLAIGNLDPRGRTASCQSHSSNAESSSSNLFFSSSSSQ
KPDASAASSLGDQEGGGESQLSSVLRSSSFSEGTTLTVTSGAKKSHIRSHSDTSIASRGAP
ESCNDKAKLRGPLPYSQOSSEVSTPSSLYMEYEGGRYLCSEGMFRRPSEGQSLISYLSE
QDFGSCADLEKENAHFISISLIIAIELMKCNMMSQCLEEEEEVEEEDSDREIQELKQKIR
LRRQQIRTKNLLPMYQEAHGSFRVTSSSSQFSSRDSAQLSDSGSADEVDEFEIQDADIR
RNTASSSKSFVSSQSFHCFHSTSAEAVAMGLLKQFEGMQLPAASELEWLVPHEHAPQK
LLPIPDSPISPDDGQHADIYKLRIRVRGNLEWAPPRPQIIFNVHPAPTRKIAVAKQNYR
CAGCGIRTDPDYIKRLRYCEYLGKYFCQCHENAQMAIPSRVLRKWDFSKYYVSNFSDKL
LIKIWNDFLNVQDINSALYRKVLLNQVRLLRVQLCHMKNMFKTCRLAKELLDSDFTVP
GHLTEDLHLYSLNDLTATRKGELGPRLAELTRAGATHVERCMLCQAKGFICEFCQNEDDI
IFPFELHKCRTCEECKACYHKACFKSGSCPRCERLQARREALARQSLESYLSDYEEEPAE
ALALEAAVLEAT

25. 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
MDANTGLFKMKKFVSDASTVFNRAVQFTEEKLGSAEKTELDHAFENLLQRADKTKAWTEK
ILKQTESVLQPNPNIRMEDFVYEKLDKKKRDRVNHHEVLGHVLDVGGNDFGPGTTYGNAL
VKCGQAQLRIGNAEREFIQTTSNNFLQPLHNFLEGDMKTIQKEKKILETKRLDLDAASKNR
LRKAKSTSQPQSSQNSPQNVLMVVEAEADLRVAQAEFDRQAEITKLLLEGVSSAHAHHLR
CLNDFIEAQLTYAQCNQYISELQQQLGYSYHSTSGVGNSSNSGAGISSGIPSSVPLQP
SAPPQINVIATPNIEKKQARVLYDYDAADSELTLLELITVYKTPGLDPDWLMAERG
PQKGVPTTYLEVLE

>AF263293.1 Homo sapiens endophilin B1 mRNA, complete cds
CTAGGATGAATATCATGGACTTCAACGTGAAGAAGCTGGCGGCCGACGCAGGCACCTTCTCAGTCGCGC
CGTGCAGTTCACAGAAGAAAAGCTTGGCCAGGCTGAGAAGACAGAATTGGATGCTCACTTAGAGAACCCTC
CTTAGCAAAGCTGAATGTACCAAAATATGGACAGAAAAATAATGAAACAAACTGAAGTGTATTGCAGC
CAAATCCAAATGCCAGGATAGAAGAATTTGTTTATGAGAACTGGATAGAAAAGCTCCAAGTCGTATAAA
CAACCCAGAACTTTTGGGACAATATATGATTGATGCAGGGACTGAGTTTGGCCCAGGAACAGCTTATGGT

AATGCCCTTATTAAATGTGGAGAAACCCAAAAAGAATTGGAACAGCAGACAGAGAAGTATTCAAACGT
CAGCCTTAAATTTTCTTACTCCTTTAAGAACTTTATAGAAGGAGATTACAAAAAATGCTAAAAGAAAG
GAACTATTGCAAATAAGAGACTGGATTTGGATGCTGCAAAAACGAGACTAAAAAAGGCCAAAAGCTGCA
GAACTAGAAATTCACAATAAAGTAACTCAGCTCGCCTTGAAGGAGATAACATTATGATTTGGGCAGAGGAG
TGACAAAATCTGAACAGGAATTAAGAATAAAGTAAAGTGAATTTGATCGTCAAGCAGAGATTACCAGACT
TCTGCTAGAGGGAATCAGCAGTACACATGCCCATCACCTTCGCTGTCTGAATGACTTTGTAGAAGCCCAG
ATGACTTACTATGCACAGTGTACCAGTATATGTTGGACCTCCAGAAACAAGTGGGAAGTTTCCATCCA
ATTATCTTAGTAACAACAATCAGACTTCTGTGACACCTGTACCATCAGTTTTACCAAATGCGATTGGTTC
TTCTGCCATGGCTTCAACAAGTGGCCTAGTAATCACCTCTCCTTCCAACCTTAGTGACCTTAAGGAGTGT
AGTGGCAGCAGAAAGGCCAGGGTTCTCTATGATTATGATGCAGCAAAACAGTACTGAATTATCACTTCTGG
CAGATGAGGTGATCACTGTGTTTCAAGTGTGTTGGAATGGATTGAGACTGGCTAATGGGGGAAAAGGGGAAA
CCAGAAGGGCAAGGTGCCAATTACCTACTTAGAACTGCTCAATTAAGTAGGTGGACTATGGAAAAGGTTGC
CCATCATGA

26. ATG12 (autophagy related 12)

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

GTGCTGTCTAATTTGACAGGAAGTAAACAAACATGTCTGATGACGGAAATGAAAGTAGAGACAGTAAAAA
CAGAGAAGCTGAAGAGAAGAGCACACCAGCAAGTCCAAGTCATGTCGCCGAAACAAAAATGATGTACTT
TTAAACCAGCTGGAGATGCTCCAATTATGAAGAAAAAGAAGTGGGCTGTAGACAGGAATAAACGGATTG
GCTGGGTGGGAGAGTTCATCAAGAAGTACCTAAAGCTTACTGCTCAGGATTCTTTGTTCTTGTATGTAAA
CCAGTCTTTTGTCTACACCTGACACAGAAATTTGGCTCTATATTTGATTGCTTTGGGAGTGATGGAAAA
CTTGTGTTACATTACTGTAAAACACAGGCCTGGGGTTAACCACAAGAAGCAGTAGCTGGTGTCTTTAAAA
CTGTCTAAGTTATGTAAAAGAAGAAAGGGGGTACTTTTTGTTTTTTGTGATGGGATCAACATTGTGAGCTA
GTGCCTCAACCAAAGGATCAGTACAAAGTATTTATGTAAACATATGGGCACAGACATGTTAATGTGGTT
GATGGATGGCTCTTGGTACAAGGTGGTAGTAATAGAAGAAAATCAACCCAACCATCCTGTAGAGTTTAA
CTTGTACCTTAAACTTTATAGGTCTTTTTTGGAGGGGGGATTTCTAGCTTATTGACCACATGTAGTTGAT
GTTTAAGGGTAATTTACAGGATTA AAAACTTTTACAAAACAGATTGAACATTTATTAGAAAAAACCCAGAT
TCATTTAAATGTACTATAAAATGCAACATGTACCTGGCATCAGACTTTTGAATTTTAAACCAGATTTAAC
ACAGTATCATTATGTACATGTGTTAATTCTTACATGATCATCACATTTGATGTGAAATGTACTGTTTGT
TTATTTCCAAGTTCATGAAAAAGTAAAGAATGAAAATTGG

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

MAEEPQSVLQLPTSIAAGGEGLTDVSPETTTPEPPSSAAVSPGTEEPAGDTKKKIDILLK
AVGDTPIMKTKKWAVERTRTIQGLIDFIKKFLKLVASEQLFYIVNQSFAPSPDQEVGTLTY
ECFGSDGKLVLHYCKSQAWG

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

MSRILESENETESDESSIISTNNGTAMERSRNNQELRSSPHTVQNRLELFSRRLSQLGLA
SDISVDQQVEDSSSGTYEQEETIKTNAQTSKQKSHKDEKNIQKIQIKFQPIGSIGQLKPS
VCKISMSQSFAMVILFLKRLKMDHVYCYINNSFAPSPQONIGELWMOFKTNDDELIVSYC
ASVAFG

27. ATG5 (autophagy related 5)

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

MLLPKILISGRRKLNHMGENREIQKGVWEGRIPVAFRLSEEDTDGERPEPVYLMVPRISY
FPLHTEKINKHFLKYASEKESEEIWLHDNQPLKWHYPVGLLFDLYGSETSLPWTITVHF
KDFPEEELLHCVSKDAVESHFMSSIKEADSLKHRGQVINSMQKRDHKQLWTGLLHDKFDQ
FWSVNKKLMESSGDETFKYIPFRLYMVDRHYMTNLFRLPTEEGHHQSLKHLLLSAVPQFF
NEEEEFQKHVRIHGTEPLLDTPILWLSENFSFPDNFLHLVISDK

>EU283339.1 Homo sapiens ATG5 autophagy related 5-like (ATG5) mRNA,
complete cds, alternatively spliced

ATGACAGATGACAAAGATGTGCTTCGAGATGTGTGGTTTGGACGAATTCCAACCTGTTTACGCTATATC
AGGATGAGATAACTGAAAGGGAAGCAGAACCATACTATTTGCTTTTGGCAAGAGTAAGTTATTTGACGTT
GGTAACTGACAAAGTGA AAAAGCACTTTT CAGAAGTTATGAGACAAGAAGACATTAGTGAGATATGGTTT
GAATATGAAGGCACACCCTGAAATGGCATTATCCAATTGGTTTGTCTATTTGATCTTCTTGCATCAAGTT

CAGCTCTTCCTTGGAACATCACAGTACATTTTTAAGAGTTTTCCAGAAAAAGACCTTCTGCACTGTCCATC
TAAGGATGCAATTGAAGCTCATTATATGTCATGTATGAAAGAAGCTGATGCTTTAAAAACATAAAAGTCAA
GTAATCAATGAAATGCAGAAAAAGATCACAAGCAACTCTGGATGGGATTGCAAAATGACAGATTTGACC
AGTTTTGGGCCATCAATCGGAAACTCATGGAATATCCTGCAGAAGAAAATGGATTTCTGTTATATCCCCTT
TAGAATATATCAGACAACGACTGAAAGACCTTTTCATTGAGAAGCTGTTTCGTCTGTGGCTGCAGATGGA
CAGTTGCACACACTAGGAGATCTCCTCAAAGAAGTTTGTCTTCTGCTATTGATCCTGAAGATGGGGAAA
AAAAGAATCAAGTATGATTCATGGAATTGAGCCAATGTTGGAAACACCTCTGCAGTGGCTGAGTGAACA
TCTGAGCTACCCGGATAATTTTCTTCATATTAGTATCATCCCACAGCCAACAGATTGA

>NM_001183963.1 *Saccharomyces cerevisiae* S288C Atg5p (ATG5), partial mRNA
ATGAATGACATTAACAATTACTTTTGGAAATGGTGAGCTTAATGTGCTGGTATCGATCGATCCTTCATTTT
TGATGAAAGGAAGTCCAAGAGAAATTGCGGTGCTACGAATAAGGGTACCAAGGGAAACATATTTAGTCAA
TTATATGCCCTCATTGGAAACAAGATTAAGGCTTTCTTTCTTTTACCATTGACCGACAGTGAGAAG
TATTTCTGGTTTGGCATAATAAGACGCCTATTCGGTGAATACCCAGTAGGTGTTTGTGACTGCC
TAGCCGGAAAAAGCGTACTTTTACCACCTCTTTTGGAAACCAGGTAAAGGATGTTCTCACTTTTGTGAG
AATTCACTTGGTTATGGGCGATTTCGTTGCCACCAACTATCATTCCCATCGCATCTAGCAAAACGCAAGCG
GAAAAGTTTTGGTTTACCAATGGAAACAAGTTTGTCTCATACTGAATGGTTCTCAAAGCTATTATGT
CTTTATCGGTCAACGAAGCTCGAAAATTTTGGGGCAGTGTTATTACGAGAAAATTTCCAAGATTTTCAATGA
AATATCTAACAAGATAAGTTCATCAAGACCGCGACATATACCGCTCATCATTCAAACCTCAAGGACATCA
GGAACCTTTTGAATATCACAACCAACTATCAGTATGACTGGAGTCAATCCTACGTTGAAGGATATTGAAG
GCGATATTCTGGACGTAAAGGAAGGAATCAATGGTAATGATGTCATGGTTATTTGTCAAGGAATTGAAAT
TCCTTGGCATATGCTCCTGTATGATTTGTATTCTAAATTGCGAAGTTTTGATGGCTTTTGTACATAACT
CTTGTTCTATAAAAGGCGGCGATAAAGCTTCTCTGAGCTCTAA

28. 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
MDPKDLHWKHSLLLEQLRQRDKKEKEPFESLISSHWKHFASQSLKSKNTQLTWEAEKLKE
ENLGLQIKVEQGGSGNSQALEQKLFKLQEEVTELRHRRGENTQQIIDLNNALQDKEKEL
QGRDARLNLLANELALKMEIKNLESTIMELEATNQMLKDEHQALQLTYTGLEEKYRKVE
QDNQQLLERWIKQQAQMADQLNAENDQFMAVRQKLRQDLEDAARENIQILPENQAGVYV
PTSIPICLSASLPTKAQYKFDHGDVNAVRSWSPSGSLFATGGADRKIKLWEVINGKCEC
KGILTGSNAGIMALDFDLEENTILGASNDFASRVWSLTDHRVRHRTLGHSGKVLAAKFLG
DSFKVVSQSHDRTLKIWDLHSRSCVKTI FAGSSCNDLVTIHGNTIVSGHFDKRVRFWDSR
VDSNTNEILLQGRLLSLDLSDPKMSLLCCTRDRTLKVLDLRMNQISTTLAHDHDFKVGCDW
SRAVFRHSVIACSWHPVGSYVLSCEKQRKTVLWSDI

>JQ924062.1 *Homo sapiens* autophagy-related protein 16-1 isoform 2 (ATG16L1)
mRNA, complete cds
ATGTCGTCGGGCTCCGCGCCGCTGACTTCCCCCGCTGGAAGCGCCACATCTCGGAGCAACTGAGGCGCC
GGGACCGGCTGCAGAGACAGGCGTTTCGAGGAGATCATCCTGCAGTATAACAAATTGCTGGAAAAGTCAGA
TCTTCATTCAGTGTTGGCCCAGAACTACAGGCTGAAAAGCATGACGTACCAAACAGGCACGAGATAAGT
CCCGGACATGATGGCACATGGAATGACAATCAGCTACAAGAAATGGCCCAACTGAGGATTAAGCACCAAG
AGGAAGTACTGAATTACACAAGAAACGTGGGGAGTTAGCTCAACTGGTGATTGACCTGAATAACCAAAT
GCAGCGGAAGGACAGGGAGATGCAGATGAATGAAGCAAAAATTCAGAATGTTTGCAGACTATCTCTGAC
CTGGAGACGGAGTGCCTAGACCTGCGCACTAAGCTTTGTGACCTTGAAAGAGCCAACCAGACCTGAAGG
ATGAATATGATGCCCTGCAGATCACTTTTACTGCCTTGGAGGGAAAAGTACTGAGGAAAAGTACGGAAGAGAA
CCAGGAGCTGGTACCAGATGGATGGCTGAGAAAAGCCAGGAAGCCAATCGGCTTAATGCAGAGAATGAA
AAAGACTCCAGGAGGCGGCAAGCCCGGCTGCAGAAAAGAGCTTGCAGAAGCAGCAAAGGAACCTCTACCAG
TCGAACAGGATGATGACATTGAGGTCAATTGTGGATGAAACTTCTGATCACACAGAAGAGACCTCTCCTGT
GCGAGCCATCAGCAGAGCAGCCACGAGACGCTCTGTCTCTTCTTCCCAGTCCCCCAGGACAATGTGGAT
GCTCATCTCGTTCTGGTAAAGAAGTGAAGGTACAGGCTACTGCCTTGTGTGTCTTCGATGCACATGATG
GGGAAGTCAACGCTGTGCAGTTTCAGTCCAGGTTCCCGGTTACTGGCCACTGGAGCATGGACCGCAGGGT
TAAGCTTTGGGAAGTATTTGGAGAAAAATGTGAGTTC AAGGGTTCCTATCTGGCAGTAATGCAGAAAT
ACAAGCATTGAATTTGATAGTGTGATCTTACCTCTTAGCAGCTTCAAATGATTTTGCAGCCGAATCT
GGACTGTGGATGATTATCGATTACGGCACACACTCACGGGACACAGTGGGAAAAGTGTCTGTCTGCTAAGTT
CCTGCTGGACAATGCGCGGATTGTCTCAGGAAGTACAGACCGGACTCTCAAACCTCTGGGATCTACGCAGC
AAAGTCTGCATAAAGACAGTGTTCAGGATCCAGTTGCAATGATATTGTCTGCACAGAGCAATGTGTAA
TGAGTGGACATTTTGCAGAAAATTCGTTTCTGGGACATTTCGATCAGAGAGCATAGTTTCGAGAGATGGA
GCTGTTGGGAAAGATTACTGCCCTGGACTTAAACCCAGAAAGGACTGAGCTCCTGAGCTGCTCCCGTGAT
GACTTGCTAAAAGTTATTGATCTCCGAACAAATGCTATCAAGCAGACATTCAGTGCACCTGGGTTCAAGT

CGGGCTCTGACTGGACCAGAGTTGTCTTCAGCCCTGATGGCAGTTACGTGGCGGCAGGCTCTGCTGAGGG
CTCTCTGTATATCTGGAGTGTGCTCACAGGGAAAGTGGAAAAGGTTCTTTCAAAGCAGCACAGCTCATCC
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

29. 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
MAGPGVPGAPAARWKRHIVRQLRLDRDRTQKALFLELVPAYNHLLLEKAELLDKFSKKLQPE
PNSVTPPTHQGPWESEELSDSQVPSLVALRVKQEEEEGLRLVCGEMAYQVVEKGAALGT
LESELQQRQSRLAALARVAQLREARAQQAQVVEEWRAQNAVQRAAYEALRAHVGLREAA
LRRLQEEARDLLERLVQRKARAAAERNLNRNERRERAKQARVSQELKKAARKRTVSI SEGPD
TLGDGMREERRETLALAPEPEPLEKEACEKWKRPFRSASATSLTSLSHCVDDVVKGLLDFKKR
RGHSIGGAPEQRYQIIPVCVAARLPTRAQDVLDAHLSEVNAVRFGNPSSLLATGGADRLI
HLWNVVGSRLEANQTLLEGAGGSITSVDFDPSGYQVLAATYNQAAQLWKVGEAQSKETLSG
HKDKVTAAKFKLTRHQAVTGSRDRTVKEWDLGRAYCSRTINVLSYCNDVVCGDHI IISGH
NDQKIRFWDSRGPHTQVIVPQGRVTSLSLSDQLHLLSRSRDNLTQKVIDLRVSNIRQVF
RADGFKCGSDWTKAVFSPDRSYALAGSCDGALYIWDVDTGKLESRLQGPCHCAAVNAVAWC
YSGSHMVSVDQGRKVVWLWQ

30. ATG10 (autophagy related 10)

>tr|K1PT50|K1PT50_CRAGI Autophagy-related protein 10 OS=Crassostrea gigas
OX=29159 GN=CGI_10025434 PE=4 SV=1
MAAGSISEDEYWDSIIFFLTLSSKIDSKWTIVDTKDGRRFAKKTEVFILSTENKESTMND
DVIRNTELMEEQEEDTAAAFQVRGNSDVEVVTYEYHILYSPSYGVPVLYFNAHTQGGKLLA
LEEIWKRPVDPAYKERLSEERWTFITQQEHPLLGRPFYYLHPCHTADLMKNSPVLTDKRHY
IVSWLSAVGPPVGLKLPLEYGKLCVS

>XM_005248611.5 PREDICTED: Homo sapiens autophagy related 10 (ATG10),
transcript variant X1, mRNA
CGGTCATAGCTCACTGCAACCTTGAATTCCTAGCCTCAAGTGATCCTCCTACCTCGGCCTTGCAAAGTGT
ACATCAGTTTGTGTAAGAAGGTCCAAGAAGTGAACAGGCCTGAAAGTTGAAGAAAGTTATCATTTAACA
TGGAAGAAGATGAGTTTCATTGGAGAAAAACATTCACCGTTATTGTGCAGAATTCATTAACATTCACA
ACAGATAGGTGATAGTTGGGAATGGAGACCATCAAAGGACTGTTCTGATGGCTACATGTGCAAAATACAC
TTTCAAATTAAGAATGGGTCTGTGATGTCACATCTAGGAGCATCTACCCATGGACAGACATGTCTTCCCA
TGGAGGAGGCTTTTCGAGCTACCCTTGGATGATTGTGAAGTGATTGAAACTGCAGCAGCGTCCGAAGTGAT
TAAATATGAGTATCATGTCTTATATTCCTGTAGCTACCAAGTGCCTGTACTTTACTTTAGGGCAAGCTTT
TTAGATGGGAGACCTTTAACTCTGAAGGACATATGGGAAGGAGTTCATGAGTGCTATAAGATGCGACTGC
TACAGGGACCATGGGACACTATTACGCAACAGGAACATCCAATACTTGGGCAACCTTTTTTGTACTTCA
TCCCTGCAAGACGAATGAATTCATGACTCCTGTATTAAGAATTCTCAGAAAATCAATAAGAATGTCAAC
TATATCACATCATGGCTGAGCATTGTAGGGCCAGTTGTTGGGCTGAATCTACCTCTGAGTTATGCCAAG
CAACGTCTCAGGATGAACGAAATGTCCCTTAACAAGATTCTTCTATTGAGTTTAGGAATTGCGGCACGAA
GAATGCCAAGAGTTTACCTGGCCAGCCCTGGCTTTAATAGGACTGATACCATGGAATATTTTCATCTCACC
AAGATGTGACATGGATTATTTTTCCCTTGGACACAAATGTCTACAGCAACTGGTGTGTTGATAGGCTGAAT
GTTTAGAAGAAACACTTCAAAGGGATACATCATGGCCAGGCATGGTGGCTCACACCTGTAATCCAAGCAC
TTTGGGAGGCCAAGGTGGGAGCATCACTTGATCCTGGGAGTTCGAGACCAGCCTGGGCAACATGGTGAAA
CCCTGTCCGTACAAAAAATAAAAAATTTGCCTGTTTATGGTGGTGTGTTTCTGTAGTCCCAGCTCCCC
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
NHIELYLTYSKVYNEPLLLLRIWEEKSIDGIPMTKMLPTDIESLLDVQGKFQLGLDTII
NLEGSVWYSFHPCDTSCIVGDQAEFMSTYLRRWVSIFIFSWLGYEDS

31. 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
MEMQKPFKERRSLTQRLKDVESIRTQHMDKIPVIIERYNGEKSLPMLDKTKFLVPDNNM
SELVKIIRRRQLHPSQAFYLVNRRSMVSNTPPIAEVYEQEKDEDEGFLYIVYASQETFG
GSCH

>BT007452.1 Homo sapiens microtubule-associated protein 1 light chain 3
alpha mRNA, complete cds
ATGCCCTCAGACCGGCCTTTCAAGCAGCGGGCGGAGCTTCGCCGACCGCTGTAAGGAGGTACAGCAGATCC
GCGACCAGCACCCCAGCAAAATCCCGGTGATCATCGAGCGCTACAAGGGTGAGAAGCAGCTGCCCGTCCT
GGACAAGACCAAGTTTTTGGTCCCGGACCATGTCAACATGAGCGAGTTGGTCAAGATCATCCGGCGCCGC
CTGCAGCTGAACCCACGCAGGCCTTCTTCTGCTGGTGAACCAGCACAGCATGGTGTGTGTCCACGC
CCATCGCGGACATCTACGAGCAGGAGAAAGACGAGGACGGCTTCTCTATATGGTCTACGCCTCCAGGA
AACCTTCGGCTTCTAG

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

32. 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
MPSEKTFKQRRTEQRVEDVRLIREQHPTKIPVIIERYKGEKQLPVLDKTKFLVPDHNMM
SELIKIIRRRQLNANQAFFLLVNGHSMVSVSTPISEVYESEKDEDEGFLYVMVYASQETFG
MKLSV

33. 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
MPEKGGDITYKTFKQRKSFVAVRKEEVVGIIRSKFPTKVPVIVERYKQQLPMLDKTKFLVP
QELSMSQFASIIIRNRMSLNSNQAFYLVNKNKSISSMSMTLAEVYRDEKDEDEGFLYMTYAS
QEMFGGC

>XM_005273139.3 PREDICTED: Homo sapiens microtubule associated protein 1
light chain 3 gamma (MAP1LC3C), transcript variant X1, mRNA
GATCTGCCACCTCCGCCTCCTAAAGTACTGGGATTACAGGTGTGAGCCACTGCACCTGGTGGAAATCCTT
GGAATTTTTCAAAGTGACACAGCTACTGAGTGCAATGCCGCTCCACAGAAAATCCCAAGCGTCAGACCCT
TCAAGCAGAGGAAAAGCTTGGCAATCAGACAAGAGGAAGTTGCTGGAATCCGGGCAAAGTTCCCAACAA
AATCCCGGTGGTAGTGGAGCGCTACCCCAGGGAGACGTTTCTGCCCCGCTGGACAAAACCAAGTTCTCTG
GTCCCGCAGGAGCTGACCATGACCCAGTTTCTCAGCATCATCCGAGCCGCATGGTCTGAGAGCCACGG
AAGCCTTTTACTTGGTGGTGAACAACAAGAGCCTGGTGCAGCATGAGCGCAACCATGGCAGAGATCTACAG
AGACTACAAGGATGAGGATGGCTTCGTGTACATGACCTACGCCTCCAGGAGACATTTGGCTGCCTGGAG
TCAGCAGCCCCAGGGATGGGAGCAGCCTTGAGGACAGACCCTGCAATCCTCTCTAGCCCATGTCGGGAA
GGATGTGTGCTCTGACAGACGTGTGAGATGCTGGCAGAAGGGATTGGTTTTCTCCTGTGTATACAGTGA
GGAGTCTGAGAAGCAGGGATGCCTGGGGTGATCAGCTCCAACCAGTGGCAGCAGAGTGGTGGCTCTTCTCT
AGTTTAGTTTTTGTGCTCCGTGTTCTTGTGTCCTTCTAAGAAAAATGTGGGCTGCTCTTGAAGTTATAT
AATTATCATTTTTTTTTTTTTTGAACAGGGTCTTGTCTATTGCCTAGGCTGGAGCACAGTGGCATGATC
TTGGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGTGATTCTTCTGCCTCCACCCCCGAGTGGCTGGTA
TTACAAGCACATGCCACCACACCAGGCTAATTTTTGTATTTTTTAGTAGAGACGGGGTTTACCATGTTGG

CCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCACCCACCTCGGCCTCCCAAAGTGCTGGGATTACA
GGCGTGAGCCACTGCATCCAGCCATATAACCGTATTCTAAATAAGAAATGGTTGGCTTGTGTGATGGTTT
TGTGTAATGAGCTAGAGATAATATTTAAGTGTCTTCTGTGGTATATGTGGGAGGGCCATTAAGGAGTGG
GTTTCACTCCCTGCATGTGGGCAGGTGTCCCATCTAGGGCTCGGTAAGTACTAGAGAATCTCTGGCCTGTAGGC
TGTCTCTGTGGAACCCAGTGAAGCCAGCGTGAACAATGGTAAGCTCATCTGGAGGTGCTCTTATCTGTGT
CATTAGAGAGATTATTCGATTTCCCCAGCATTCACTCTATTTAGTTATTTTCTGTCACTCTCTTTTGTGTC
TTTCTATACCATACATATTTATGCCAAAGCTGTAACCTTCTCAACATGAAGTCATTTAAACCATGTGCATG
TTTACTATGTGCCAAGCTGTATTCTAAATAAATATTTCTTTATTTT

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

ATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAAAGGAAGGCGGAGTCCGAGAGGATTGCTGACA
GGTTCAAGAATAGGATACCTGTGATTTGCGAAAAAGCTGAAAAGTCAGATATTCCAGAGATTGATAAGCG
TAAATATCTAGTTCCTGCTGACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAGAGAATTATGCTA
CCCCCTGAGAAGGCCATCTTCATTTTTGTCAATGATACTTTGCCACCTACTGCGGCGTTGATGTCTGCCA
TATATCAAGAACAACAAGGATAAGGACGGGTTTTTGTATGTCACTTACTCAGGAGAAAATACATTTGGCAG
GTAG

34. 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

MKWEYKEEHSFEKRRAEGEKIRKKYPDRVPVIVEKAPKARVGDLDKPKYLVPDLTVGQF
YFLIRKRIHLRPEDALFFVNNVIPPTSATMGSLYQEHHEEDFFLYIAYSDESUYGA

>AF161586.1 *Homo sapiens* GABA-A receptor-associated protein (GABARAP) mRNA,
complete cds

CGACCGGCCCCGTCGCGGCCCCCTGGGTTCCCTCAGCCCAGCCCTGTCCAGCCCGGTTCCCGGGAGGAT
GAAGTTCGTGTACAAAGAAGAGCATCCGTTTCGAGAAGCGCCGCTCTGAGGGCGAGAAGATCCGAAAGAAA
TACCCGGACCGGGTGCCTGGTATAGTAGAAAAGGCTCCCAAAGCTCGGATAGGAGACCTGGACAAAAAGA
AATACCTGGTGCCTTCTGATCTCACAGTTGGTTCAGTTTCTACTTCTTGATCCGGAAGCGAATTCATCTCCG
AGCTGAGGATGCCTTGTTTTTCTTTGTCAACAATGTCATTCCACCCACCAGTCCACAATGGGTCAGCTG
TACCAGGAACACCATGAAGAAGACTTCTTTCTCTACATTGCCTACAGTGACGAAAGTGTCTACGGTCTGT
GAAGCTGCTGCCCCTGAGCTGGAGGGGGTCTCATTCTACAAAGAGAGAGGTTGGCCCCCTTTCTTGACC
TCCTCCTCCTTCAAGCTCAAACACCACCTCCCTTATTTCAGGACCGGCACTTCTTAATGTTTGTGGCTTTC
TCTCCAGCTCTCTTAGGAGGGGTAATGGTGGAGTTGGCAACTTGTAACCTCTCCTTTCTCCTTTCTTCCC
CTTTCTGCTCCCTTTCCCATCTCTGCTGTAGACTTCTTGATTGTCAGTCTGTGTGCATCCAGTGATT
GTTTTGGTTTTCTGTTCCCTTTCTGACTCCGTCAGGGGCTCAGAACCAGCAATCCCTTCTTCTACTAC
CTTCTTTTTTGGGGTAGTTGGAAGGGACTGAAATTGTGGGGGAAGGTAGGAGGCACATCAATAAAGAG
GAAACCACCAAGCTG

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

ATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAAAGGAAGGCGGAGTCCGAGAGGATTGCTGACA
GGTTCAAGAATAGGATACCTGTGATTTGCGAAAAAGCTGAAAAGTCAGATATTCCAGAGATTGATAAGCG
TAAATATCTAGTTCCTGCTGACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAGAGAATTATGCTA
CCCCCTGAGAAGGCCATCTTCATTTTTGTCAATGATACTTTGCCACCTACTGCGGCGTTGATGTCTGCCA
TATATCAAGAACAACAAGGATAAGGACGGGTTTTTGTATGTCACTTACTCAGGAGAAAATACATTTGGCAG
GTAG

35. 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

MKFQYKEDHDPFEYRKEGEKIRKKYPDRVPVIVEKAPKARVPLDKRKYLVPSDLTVGQF
YFLIRKRIHLRPEDALFFVNNVIPPTSATMGQLYEDNHEEDYFLYVAYSDESUYGK

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

MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRYLVPADLTVGQF
VYVIRKRIMLPPEKAIFFVNDLPTAALMSAIYQEHKDKDGFYVVTYSGENTFGR

36. 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 MWIIRKRIQLPSEKAIIFLVGVKVLQSSASMGQVYEEHKDEDEGFLYIAYSAGENTFGQ

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

AGTCGCCGCCGCTCGCTGCCGCTGCCGCTGCCGCGCTCGTTGTTGTTGTGCTCGGTGCGCTGAGCTCCGCG GCTCCGCGAGCCGGTCCCGTCCCCTTCCC GCCCGCCGCCATGAAGTGGATGTTCAAGGAGGACCACTCGCT GGAACACAGATGCGTGGAGTCCGCGAAGATTTCGAGCGAAATATCCC GACAGGGTTCCGGTGATTGTGGAA AAGGTCTCAGGCTCTCAGATTGTTGACATTGACAAACGGAAGTACTTGGTTCCATCTGATATCACTGTGG CTCAGTTCATGTGGATCATCAGGAAAAGGATCCAGCTTCTTCTGAAAAGGCGATCTTCTGTGTTGTGGA TAAGACAGTCCCACAGTCCAGCCTAACTATGGGACAGCTTTACGAGAAGGAAAAAGATGAAGATGGATTC TTATATGTGGCCTACAGCGGAGAGAACACTTTTGGCTTCTGAGGGCCATTGCTGGGCTAGGTGCACCGTA ACTGCTTGTGTATCTTGTAAATAGCCAGCCATTTTTCAGTTATTATAACCAGAACCTCTTCACATAGACCTA TTAGTGCATTTGTAAGTGGATTTATTTCTTAATATATTGGAAGGTTTTGTTTCTTAGACTAGTAAATTA TCATACAGAGTTTTATTTTGGAGTTTTTCTTTTTGTGCATTGTCTCATGCCTGTATTCTCCAGGAACTT GTCCTTCTGAAATCATATTGAATGATATTTCTATATCGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG GGAAGGTGATGCATTTATTTCTGGGTTATGCTTGAAGTGTAGATGGCTAAGTATTAATAATATCCAAAT AAATCCTTAGCAGTCAGAACAACCTTGCTTCACTAGAATATGCCAACTGCCAATCATGTTGGACTGAGCTAA TTTGTTCTCTTTCTGAAACTATTAAGGTAAATAATTAACAATAAAAAATTCTCTTATAAAGGCA

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

ATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAAAGGAAGGCGGAGTCCGAGAGGATTGCTGACA GGTTCAGAATAGGATACCTGTGATTTGCGAAAAAGCTGAAAAGTCAGATATTCCAGAGATTGATAAGCG TAAATATCTAGTTCCTGCTGACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAGAGAATTATGCTA CCCCCTGAGAAGGCCATCTTCATTTTTGTCAATGATACTTTGCCACCTACTGCGGCGTTGATGTCTGCCA TATATCAAGAACACAAGGATAAGGACGGGTTTTTGTATGTCACTTACTCAGGAGAAAATACATTTGGCAG GTAG

37. 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 YLLIRKRIHLRPEDALFFFVNNITPPTSATMGQLYEDSHEEDDFLYVAYSNESVY GK

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

38. ATG7 (autophagy related 7)

>XM_011419559.2 PREDICTED: Crassostrea gigas ubiquitin-like modifier-activating enzyme ATG7 (LOC105321294), transcript variant X1, mRNA CACGTGATATTCAAATGTCTGCGCCCTTGTAAACAAAATGGAACGTAAACAACACTACAGTTTGTGGCAT TTAATAGTTTTTTAGACTCAGGATTTTGGCATAAGCTCTCCGAAAATAAACTTGATGTTTATGGTTTAGA TGAAAGCCAAAAGGAGATAAAAGGATTTTACTTCAATGGTACCCTGTTGGAATGCCTTGCAGAATGAAT GTTGAGTTTTCTGCATTTGACCAAGATGCCAAAACGCCACAGCGATGCCTGCCCATGCTGGGAGAGTTAC ATAACACCAATACAGTGGACAAATTCAAGGAGTGTGATAAAAAAGAGATGATCAGTGAAGCCGGGAAAAA GATATGGGACTCCGTTGTAAGTGGTAAAGCACTGGACACCCCTGAACTTCTGGCTACTTCTCTCTTTTG ACCTTTGCAGACTTAAAGAAGTACCATTACTATTACTGGTTCTGTTTTCCCTGTCTCTGTCCATCAACTG ACATCACCTTTGACCAAGAACCAAAGAACTCAAGTACAGTTGACTGCAGAGGAGATGGAACAGTTTCT ACAAGCTTATGACACATTTCAAGATGCTCATCCAACATATCAGGGTTTCTTTGTTGCTGTCTTTCTAAA GGGAACATTGTAATCGAGGATGTAATAATATGAACAAGTTTAAAAATACTCAGGAGGTGTAATTTGGAT TCTGTGATCCCAGTAATATTGAGGACTATCCAGGCTGGCCTCTTAGGAATTTCTGATGTTGATATCCTA TCATTGGAAGGGAGACCTGCGAGGTGTAATGTACTGTGTTTGCAGATAGGAGTCGAGACGGGACACGA GATATATCACACAGTCTTCTGCTGTCCCTTTGTGTCCCGATATTAAGAATGTGCTAGAATGTCCAAAGT

GTGTGGGTTGGGAGAAAAATGAAAAACAAAAGCTGGCTCCAAGATTTGTAAATCTCAGTGCTAGCATGGA
CCCCACAAGACTGGCAGCCTCAGCTGTTGACCTCAATCTAAAGCTGATGAGATGGAGGCTGCTCCCAGAG
CTTGACCTTGACCTTATATCAAAGACAAAATGTCTGCTGCTAGGAGCCGGGACTCTTGGATGCAATGTGG
CAAAGTGCCTGATGGGCTGGGGAGTAAGAACCATAACTCTGGTGGACAATGGCCGCGTGTCTTACTCTAA
CCCAGTACGCCAGCCCTTGTTCAGTTTTGAAGACTGTGTAAAGGGAGGTAAGCCAAAAGCGGAGGCTGCT
GCAGAGGCCATGAAGAAGATATTCCCTGGAGTGAATGCAAAAAGGGTTGAGTTTATCCATTCTATGCCTG
GACATGCAGTACCTGAGAGTGAATAGAGGGTGTGAAGAAAGACGTTGAAACCCCTCCAGGATCTGGTGAA
TTCTCACGATGCAGTGTCTTACTGTTGGATACGCGGGAGAGCCGTTGGCTTCTTACATTGATGGCAGCA
GAAAAACAAAAGATAGTGATATGCTCTGCACTGGGCTTTGACACATATCTAGAGATGCGCCACGGCGTAA
GGTCAGACACAGAGGGAGCTGACCTCGCCCCCTCTGTCTCTTACAGCTCCATCCCCAGGGATCAGCTAGG
CTGCTACTTCTGCAATGATGTAGTGGCACCAGGGAATCTTTGAAGGACCGTACTCTGGACCAGCAGTGT
ACAGTATCCAGGCCGGGCATCTCTACATGGCGTCCGCGCTCGCCGTAGAACTCCTTGTGTCCATGCTCC
AACATCCAGAAGTGGGAAAGCCCCGGCGGATATAAGTGTAGTATGAGCACCTGAGTAAAGACTTTGT
CTGCCCCCTAGGGCTGGTCCCTCACCAGGTGAGGTCATTGTACTGCTGTCTCCAATGTCAATGAAATGTC
ATACTGGTTCCCTCTGTTTAAATTTACTGATTGAAGTAACTGGAATCTTATGAAGCATGTGATTTTGTAGCTA
ACCTGAGCTGCTGAAACCATGCCTTTTTGCAAAGGTAGTGTAGATTCAAAGTTGTGAAAATAATGA

>XM_020072211.1 PREDICTED: Crassostrea gigas ubiquitin-like modifier-
activating enzyme ATG7 (LOC105340241), mRNA
TTTCTTTCCCTCTAGATGGAACAGTTTCTGCAAGCTTATGACACATTCCAAGATGCTCATCCAACATATC
AGGGTTTCTTTGTTGCTGTCTTTCTAAAGGGAACATTGTAATTGAGGATGTAAAACATATGAACAAGTT
TGAAAATACTCAGGAGGTGTACTTTGGATTCTGTGATCCCAGTAATATTGAGGACTATCCAGGCTGGCCT
CTTAGGAATTTCTGATGTTGATATCCTATCATTGGAAGGGAGACCTGCGAGGTGTAAATGTACTGTGTT
TGCGAGATAGGAGTCGAGACGGGACTCGAGATATATCACACAGTCTTCTGCTTTCCCTTAAATGTCCCGGA
TATTAGGAATGTGCCAGAATGTCCAAAGTGTGTGGGTTGGGAGAAAAATGAAAAACAAAAGCTGGCTCCA
AGATTTGTTAATCTCAGTGCTAGCATGGACCCACAAGACTGGCAGCCTCAGCTGTTGACCTCAATCTAA
AGCTTATGAGATGGAGGCTTCTCCCAGAGCTTGACCTTGACCTTATATCAAGGACAAAATGTCTGCTGCT
AGGAGCTGGAACCTTTGGATGTAATGTGGCAAGGTGTCTGATGGGCTGGGGAGTAAGAACCATAACTCTG
GTGGACAATGGCCGCGTGTCTTACTCTAACCAGTACGCCAGTCTTGTTCAGTTTGAAGACTGTGTAA
AGGGAGGTAAGCCAAAAGCGGAGGCTGCTGCAGAGGCCATGAAGAAGATATCCCTGGAGTGAATGCAAA
AGGGTTGAGTTTATCCATTCCCTATGCCTGGACATGCAGTACCTGAGAGTGAATAGAGGGTGTGAAGAAA
GACGTTGAAACCCCTCCAGGATCTGGTGAATCTCATTGATGACAGTGTCTTACTGTTGGATACGCGGGAGA
GCCGTTGGCTTCTTACATTGATGGCAGCAGAAAAACAAAAGATAGTATGCTCTGCCCTGGGCTTTGA
CACATATCTAGTATGCGCCACGGCGTGAGGTGAGACACAGAGGGAGCTGACCTGCCCCCTGTCTCTCT
TACAGCTCCATCCCCGGGGATCAGCTAGGCTGCTACTTCTGCAATGATGTAGTGGCACCAGGGAATTTCTT
TGAAGGACCGTACTCTGGACCAGCAGTGTACAGTATCCAGGCCGGGCATCTCCTACATGGCGTCCGCGCT
CGCCGTAGAACTCCTTGTGTCCGTGCTCCAGCATCCAGAACTAGGGAAAGCCCCGGCGGATACAAGCGCT
AGTGATGAGCACCTGAGTAAAGACTTTGTCTGCCCCCTAGGGCTGGTCCCTCACCAGATTCGATGCTTTG
TGTCCCCTTCCAGCAAGTGTACCAGGCTGTAAAGCATTTGATAAATGTACAGCTTGTTCAAAGACTGT
GATAGAACAGTTCGACGGGACGGCTTTGACTTCCCTGAGGCGGGCGTTCAATGACCCGTCCTACCTGGAG
GATCTTACAGGGCTCACACAGATGCATCAGGAAACCCCTCGACGCTGAGGTGTGGGGGTTTCAAGTATGACG
AGGAATGTAGCAGCATGGAAGTCTCCAGCTCTTGACCCAGTTTTAAATTTGTGACCCAACTGAAGACTTTC
ATTTTTATTTTATTTATTTACCAATCAGACATTTATCAGTGTATAAGCTTTTCATGGTATTACATGTAA
TGTACTTTTGTATTACATGTAATAAGTACATTGTAGCGTAAATTTGTGATATTCCGATTCAGGTTATGAA
TCATTATATTATACAATGAATAATATGACATTAATAATGCTTTAACTCTGTT

>sp|O95352|ATG7_HUMAN Ubiquitin-like modifier-activating enzyme ATG7
OS=Homo sapiens OX=9606 GN=ATG7 PE=1 SV=1
MAAATGDPGLSKLQFAPFSSALDVGFWHELQKLLNEYRLDEAPKDIKGYYYNGDSAGLP
ARLTLEFSAFDMSAPTARCCPAIGTLYNTNTLESFKTADKLLLEQAANEIWESI KSGT
ALENPVLLNKFLLLTFADLKKYHFYYWFCYPALCLPESLPLIQGPVGLDQRFSLKQIEAL
ECAYDNLQTEGVTAALPYFLIKYDENMVLVSLKHYSDFFQGGQRTKITIGVYDPCNLAQY
PGWPLRNFLVLAHRWSSSFQSVVEVVCFRDRMTMQGARDVAHSIIFEVKLPEMAFSPDCPK
AVGWENKQKGGMGRMVNLSECMDPKRLAESSVDLNLKLMCWRLVPTLDLTKVSVKCLL
LGAGTLGCNVARTLMGWGVRHITFVDNAKISYSNPVRQPLYEFEDCLGGGKPKALAAADR
LQKIFPGVNRGFNMSI PMPGHPVNFSSVTLEQARRDVEQLEQLIESHDVVFLMDTRES
RWLPVAVIAASKRKLVINAAALGFDTFVVMRHGLKKPKQQGAGDLCPNHPVASADLLGSSLF
ANIPGYKLGICYFCNDVVAPGDSTRDRTLDQQCTVSRPGLAVIAGALAVELMVSVLQHPGEG
GYAIASSSDDRMNEPPTSLGLVPHQIRGFLSRFDNVLVPSLAFDKCTACSSKVLVDQYERE
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
MSSERVLSYAPAFKSFLDTSFFQELSRLKLDVLDKLDSTCQPLTVNLDLHNI PKSADQVPL
FLTNRSEFKHNNKRTNEVPLQGSIFNFNVLDEFKNDKQLFLHQRALECWEDGIKDINKC
VSFVVIISFADLKKYRFYYWLVGVPFCQRPSSSTVLHVRPEPSLKGLFSKCQKWFVNYSKWV
CILDADDEIVNYDKCIIRKTKVLAIRDSTSTMENVPSALTKNFLSVLQYDVPDLIDFKLLI
IRQNEGSFALNATFASIDPQSSSNPDMKVSGWERNVQGLAPRVVDLSSLLDPLKIADQ
SVDLNLKLMKWRILPDLNLDIIKNTKVLVLLGAGTLGCVSRALIAWGVKITFVDNGTVS
YSNPVRQALYNFEDCGKPKAELAAASLKRIFFPLMDATGVKLSIPMIGHKLVNEEAQHDKF
DRLRALIKEHDIIFLLVDSRESRWLPSLLSNIENKTVINAALGFDSYLVMRHGHRDEQSS
KQLGCFYCHDVVAPTDSLTDRTLDQMCTVTRPGVAMMASSLAVELMSTLLQTKYSGSETT
VLGDIHQIRGFLHNFSILKLETPAYEHC PACSPKVIEAFTDLGWFEVFKALEHPLYLEE
ISGLSVIKQEVERLGNDFEWEDESDEIA

39. ATG3 (autophagy related 3)

>tr|K1R934|K1R934_CRAGI Autophagy-related protein 3 OS=Crassostrea gigas
OX=29159 GN=CGI_10024759 PE=3 SV=1
MQNVINAVKGTALNVAEKFTPVLEKSKFKETGVITPEEFVAAGDHLVHHCPTWQWSTGDE
SKVKPYLPKEKQYLITRNVPCYKRVKQVDSHKEEQEKVIEADDEDGGWVDTHHFPDPGTT
SLQDAVQEMTLDGKGDKRSSEEVKRS GDDDDDDDDDDDEEAMDMEAFFEQSGMLDEEDD
AALDPSTLGRQDSESAATESGILQTRTYDLNITYDKYYQTPRLWLFYDENRKLPTVEQM
YEDFSQDHAKKTVTMEAHPLPGPPLASVHPCRHADVMKKIIQMVAEGGGDLGVHVYLM I
FLKFVQAVIPTIEYDFTRDFTM

>AB079384.1 Homo sapiens mRNA for Apg3p, complete cds
ATGCAGAATGTGATTAATACTGTGAAGGGAAAGGC ACTGGAAGTGGCTGAGTACCTGACCCCGGTCCTCA
AGGAATCAAAGTTTAAAGGAAACAGGTGTAATTACCC CAGAAGAGTTTGTGGCAGCTGGAGATCACCTAGT
CCACC ACTGTCCAACATGGCAATGGGCTACAGGGGAAGAATTGAAAGTGAAGGCATACCTACCAACAGGC
AAACAATTTTTGGTAACCAAAAATGTGCCGTGCTATAAGCGGTGCAAACAGATGGAATATTCAGATGAAT
TGGAAGCTATCATTGAAGAAGATGATGGTGATGGCGGATGGGTAGATACATATCACAAACACAGGTATTAC
AGGAATAACGGAAGCCGTTAAAGAGATCACACTGGAAAATAAGGACAATATAAGGCTTCAAGATTGCTCA
GCACTATGTGAAGAGGAAGAAGATGAAGATGAAGGAGAAGCTGCAGATATGGAAGAATATGAAGAGAGTG
GATTGTTGGAACAGATGAGGCTACCCTAGATACAAGGAAAATAGTAGAAGCTTGTAAGCCAAAACCTGA
TGCTGGCGGTGAAGATGCTATTTTTGCAAAC CAGA ACTTATGACCTTTACATCACTTATGATAAATATTAC
CAGACTCCACGATTATGGTTGTTTTGGCTATGATGAGCAACGGCAGCCTTTAACAGTTGAGCACATGTATG
AAGACATCAGTCAGGATCATGTGAAGAAAACAGT GACCATTGAAAATCACCCCTCATCTGCCACCACCTCC
CATGTGTTTCAGTTCACCCATGCAGGCATGCTGAGGTGATGAAGAAAATCATTGAGACTGTTGCAGAAGGA
GGGGGAGA ACTTGGAGTTCATATGTATCTTCTTATTTTTCTTGAAATTTGTACAAGCTGTCATTCCAACAA
TAGAATATGACTACACAAGACACTTCACAATGTAATGA

>NM_001183184.3 Saccharomyces cerevisiae S288C Atg3p (ATG3), partial mRNA
ATGATTAGATCTACTAAGTAGTTGGAGAGAATATCTTACCC CATAACGCACAAATCTACCTTTTTAA
CCACAGGTCAAATAACTCCTGAGGAGTTTGTACAAGCAGGTGATTATTTATGTCATATGTTTCCACCTG
GAAGTGAACGAAGAGTCGTCAGATATTAGTTACAGAGATTTTTTACC GAAGAATAAGCAGTTTCTGATA
ATTAGAAAAGTTCCTGTGATAAACGTGCCGAGCAATGTGTGCGAAGTTGAAGGGCCAGATGTAATCATGA
AAGGTTTTGCAGAAGATGGAGATGAAGATGATGTTCTGGAATACATAGGATCTGAAACTGAACATGTGCA
AAGTACGCCTGCGGGGGGGACCAAGGACTCATCTATCGATGATATTGATGAGCTAATACAAGACATGGAA
ATAAAAGAGGAGGATGAAAATGACGATACAGAAGAATTTAATGCTAAAGGTGGCCTAGCCAAAAGATATGG
CGCAAGAAAGGTATTACGACCTTTATATTGCGTACTCGACATCTTATAGGGTCCCTAAAATGTATATAGT
GGGTTTTAATTCTAATGGTTCAACCTAAGCCCTGAGCAGATGTTCGAAGATATATCAGCAGATTATAGA
ACAAAGACAGCCACCATTGAAAAGCTACCTTTTTACAAGAATTCAGTGTTATCTGTTTCCATTCATCCAT
GTAAGCATGCTAATGTAATGAAAATATTGCTAGATAAGGTTTCGTGTGGTTAGACAACGAAGAAGGAAAGA
GCTGCAGGAAGAACAAGAGCTGGACGGTGTGCGGAGACTGGGAGGATTTACAAGACGATATTGATGATTCG
TTACGGGTAGACCAATACTTGATTGTTTTCTTAAAGTTTATTACTAGTGTTACACCGAGTATACAACATG
ACTTACCATGGAAGGTTGGTAA

40. ATG4 (autophagy related 4 cysteine peptidase)

>tr|K1QKP1|K1QKP1_CRAGI Cysteine protease OS=Crassostrea gigas OX=29159
GN=CGI_10023225 PE=3 SV=1

MDMTNDVGTGTCMVTYESAALGYVDFPLTEEPVYLLGIKYSALYDRDELKGFDFLSKIWCTYR
KNFPAIGGTGPTCDGGWGCMLRCGQMMMLAQALVVRHLGRDWKWNKNCQDQTYKRILQMFA
DKKSANYSIQQIASMGVSEGKPVGSWFGPNTVAQVLKKLAVYDEWSSIVIHIAMDNTVIE
NDIKSVCKDDGKSTCDIIGVRQLKHESAATGRSKKSSQDSSKQDKNKQNAVDVKSWKPLL
LVIPLRLGLTEINSVYVQSLKACLSPQSVGIIIGGKPNHAHWVFGYMSDKLIYLDPHTTQ
LCEDLDSPNFSDESYHCPYPSTMNVMELDPSIALGFYCGTEKEFDDLTQSVQKFFVVGSSK
TPMFELYKDRPPHPPPYESYTGQTTASAGVMTMTGGQDTDEEFELV

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

GGAGATTTGTCATGTGAAAGAGAACTTGACGGATGTCACGGATATGTTAATGTTCCGACGTTTCGTACAA
ATTTTGGTTAAAAATGAATTAAGATGAATCGAAAACTCCCAAGAGTTACTCTCGTCGAGTATCTGAGGA
TGTGGCTTCTTTAGATTTCATGGAGTGAAGCTCTGAGTGTGATGTGTCAACTATAACGGTAAATGATAAA
GGCCATCACTAACTCCTGTAGATTTAAAAGCGAGGAAAACTCTTCTAATAACCAGCTTTTATTGAATC
CAGCAAAGTTGGTTTCTCAATCCTCATCGCGAAATGCTGTTTCGGAACAGAAACGAAGAAGTGGGAGAAG
ATTTCGAAGCGAGTAGTTCTCGGACCAAGGCGAAATCCTTCAGAACAACAGGTGTGAAGTTGACATCTCT
ACAAGCGATCCCTTTGATATTGACGATGGATCATTTCGATAATATCAACAGTGTGTATTTATCATTGCCTG
AAGGACATGGGGCTTGTCTAAAGGAGTCATATTCCACCATCAGTACCTCGGAAAAATAACCTGGACTATAA
TGACTGTAGTGATTTTCATAGCCTCCAGATTTAACTGCGGTTAATTCAAAAGACACGGACGTATCCCCCT
CACTATGTACACCCAAAATCTTTGCAATATCCAACACAGGGTGAACCTTCGGAAAAAGTGAAAAACAAGT
TAATGTCCATGTGGAACAATGTGAAATATGGATGGACGTTGAAGACAAAGACCAGCTTTAGATTTGACAG
TCCAGTCTGGCTTTTGGGAAAATTTTACCATATAAAGCCAAGTGATCTCATAGATGATGATATTCAGAGA
GGAAAAAGAACAAGAGTTGTGCCAAACATTGAAAAGTTCAAACAGGATTTCTCGAGCCTGCTGTGGTTTA
CGTATAGACAAGACTTCCCGGCTATCCCGGGGACCAAGCTGACCTCGGACTGTGGGTGGGGGTGCATGTT
AAGGAGTGGTCAGATGATGCTTGCTAAGGCTCTCACATTACATTACTTAGGACCAGAATGGAATGTGTTT
AGTGACCAACAAGAGAACAGGAAACGTACAGGAAGCAGATAATCCGCTGGTTTTGGAGATTACCTCTGTG
ACGAGTCACCGTTCTCTATGCACCGATTGGTGGAGGTCGGGAAAAATCTTGGCAACAGCCAGGGGAGTG
GTTTTGGTCCCGCCTCAGTCGCTCACATACTCAAGGAAACAATGGTGAAAGGACAGAAGACACAGACAGTT
CTGTGATCTCTGTGTATATGTCTCTCAGGACTGCACTGTCTACAAACAGGACATATATGAGCTCTGTT
GTACGCGACCGAGGGCGGATACAAAGTTCACCAACTCCACGGAGTCGGAGCATGAATCCAGTCAGGATGC
TTCTCCATGGACTGGAAGCGGGCTGTCTGTATCCTTATTCCGGTTAGACTAGGAGGGGAGCAGCTTAAT
CCAGTCTACATTCCTTGTGTGAAAGGGCTTCTACTCAGGACTCCTGTATCGGCATCATCGGAGGGAAGC
CCAAACATTCCTACTCTACTTTGTAGGATGGCAAGAGGCAAACTGATATATTTAGATCCACACTGTCA
GGATGTGGTTGACACAAGGGGAGAGACACTTTCCAATCCAGTCTTACTGTATGTGCGCCAGAAAGGTC
TCCATTGACAAAATAGACCCTAGCTGTACCATTGGCTTCTACTGCAGAAACCAGAAAAGATTTGAAAAGT
TTGTACAGCAACAGAGGAGATGGTGGCACCACAAAACAAAGGCTTTCTTACCCAATGTTTTGTGTTTCAG
TGATGGACATAGTAATGAGGTCAAGATAGACACGGCTGAAAAGGACCGCCTCCTTCGAGTCAAGCACGTT
CGCCTGGACGAATATGGTTCGATTCGTTCCAGACACTGGATTCTGAGGAATTTGTAGTTTATAAACAC
TATTTATTTGTTGACTTAGCCTTATTATATAATGGAGTGCAGTAGTACAAATTAGCATGTACATGTATGT
TTCTCCTTCTTGAGAGCTATGTTTAACTTCTATACTATGTTAACAATCTTCTAGCATAATGAAGCATAT
CAGTTCTTTGATATCTGAGGCATTACCTTAGCCACTATCTGGAGCATATATTTATAGGGTGTAGTTAAA
ATCCCTGTAAAAGAAAATCTGAGGGAAGGTGATATCTGAGGCATTACCTTAGCAACTATCTGGAGCATAT
ATTTATAGTGTGTTAGTAACATCTGTCCATCTTGTTTAGAAGTGATATAAAGCTCAAATGGATTTGTGTC
CTAACCTTATTTTTCGATACGACATATTTACTCCTAGTTGTGTGAAGTTAATCCCAAGCAGTTAAAAAGT
TCAGATTTCAAAGACATCAAAGGGATATGGATCGCGCTTATTTTTTCAGCCTAGAATAAATACCAGACGTA
CCATACATGTAAAACCTTGACGACAAAAATCCAGATGTCTAAGTTATGACAATCAATTACACTTCATTGAG
AGTCTTTCCCTGTAAGAAGTGTTCGTCTACATGTATAACAACCTGCTCTACTTTCTTGGTAAATGCACAC
TGTAAGTTCATCATATTAACCTTACCATGTTTTTCATCTGTCTTGTGCAATAGCGAGACTTGCATAAAC
TGTCCCAAAATTGATTGGCAATGTTAATTTTTGTGTGAACCTCTCTCAAACATCCCGAGTTTATTTTGGCGT
GTTAATTTTTGATTTGGAATTTGAACCTATTTGGCAAGTTGAACAATGTCAAATAATTTGACACTTTAACTT
AATGTGGTGACTTAAGTCTGTACTTCAGTTAGTACGTGATGTTGGTAAATTCAGGTTCTGAGGATTCAC
ATTTTACTGTATCTCGTATATTCATGATTAATAATTAATTACCATTGGGCACTAGAATGATTGCTCACATCA
AAGAGTAAAGAGAATTCTCTGGTTACTTTGCATCTTGATATGTAGTATTGGAAAATTTGTTTTGCCAAATG
AAGGAATTTAATTTAGAATTTACACTATTTTTGGTGAATTTTTAATCTGCCAGTTTTTCGGTACAGGTA
TTTGAGAATAAGAATTCAAAGAATGTTTTTCATAAGATTACCTCCATGTACATATATATATATTAACAAC
TGATTTAGGAGAATAACCAGGATGCATCAAAGAAATCTTAGATAACCTTGAAGAGATCAGCCAAAATTA
CGAACTCTGTACAATGTATACATATGATTTCCAAGCTACATGCTTGTCTTTAAACAAAATAGATGGCTGT
ACATATGAAGAAAGATGTACTGTTATAAAGCAGTTCAGACCTATTTTATTTGTACAAGAATATACATGTA
TGTATATTTTTATTGTTAATGTTAATTTGTACATAATGGTTAATCATGTACCGTACATTATTTTTGATTTGC
AATATTTGTATATTATGTTAATTTATTTTTTGTCTGTACGATATGAATCAGATGGCAGTAAATGGGAAAT
ATACAAGTGTGTTTTACAAATTTGTCTTAGCATAATTTTTCGGTCAAGTATGTGATTTGTTTTGGGTGACCT
ATTTCTTGAATGTTGTTGTTAATGAATATGAAATAAAAATATTGAATTTTACCAAAAAAAAAAAAA

>sp|Q8WYN0|ATG4A_HUMAN Cysteine protease ATG4A OS=Homo sapiens OX=9606
GN=ATG4A PE=1 SV=1
MESVLSKYEDQITIFTDYLEEYPDTDELVWILGKQHLLKTEKSKLLSDISARLWFTYRRK
FSPIGGTGPSSDAGWGCMLRCGQMMMLAQALICRHLGRDWSWEKQKEQPKEYQRILQCFLD
RKDCCYSIHQMAQMGVGEKSGIGEWFGPNTVAQVLKLLALFDEWNSLAVYVSMNDTVVIE
DIKKMCRVLPASDTAGDRPPDSLASNQSKGTSAYCSAWKPLLLIVPLRLGINQINPVY
VDAFKECFKMPQSLGALGGKPNNAYYFIFGLGDELIFLDPHTTQTFVDTEENGTVNDQTF
HCLQSPQRMNILNLDPSVALGFFCKEEKDFDNWCSLVQKEILKENLRMFELVQKHPSHWP
PFVPPAKPEVTTTGAEFIDSTEQLLEEFDLEEDFEILSV

>XM_017003638.1 PREDICTED: Homo sapiens autophagy related 4B cysteine
peptidase (ATG4B), transcript variant X3, mRNA
TTGTTTGTGATGCAGGATTTTTCTCAGCCACTCTGGCAGCCAGAGACCTCCGGCTGGCGAGGCCCTGCC
CAGGCCTTGCTTGGGTCCAGGCTCGCCGAGGAGATACCCCATCTACTTGGTCCACCGGTGGGCACCTGG
TTTGCACTATGGCACGGATACCATGGCCACCATGACTGTATGCTCAGCCCTGGCGGGAGTGGGTGTGTG
GCTACTCTGACCTACGACACTCTCCGGTTTGTGAGTTTGAAGATTTTCTGAGACCTCAGAGCCCGTTT
GGATACTGGGTAGAAAATACAGCATTTTTACAGAAAAGGACGAGATCTTGTCTGATGTGGCATCTAGACT
TTGGTTTACATACAGGAAAACCTTTCCAGCCATTGGGGGGACAGCCCCACCTCGGACACAGGCTGGGGC
TGCATGCTGCGGTGTGGACAGATGATCTTTGCCAAAGCCCTGGTGTGCCGGCACCTAGGCCGAGATTGGA
GGTGGACACAAAGGAAGAGGCAGCCAGACAGCTACTTCAGCGTCCTCAACGCATTCATCGACAGGAAGGA
CAGTTACTACTCCATTACCAGATAGCGCAAATGGGAGTTGGCGAAGGCAAGTCCATAGGCCAGTGGTAC
GGGCCAACACTGTCGCCCAGGTCCTGAAGAAGCTTGTGTCTTCGATACGTGGAGCTCCTTGGCGGTCC
ACATTGCAATGGACAACACTGTTGTGATGGAGGAAATCAGAAGGTTGTGCAGGACCAGCGTTCCTGTGC
AGGCGCCACTGCGTTTCTGTCAGATTCCGACCGGCCTGCAACGGATTCCCTGCCGGAGCTGAGGTACC
AACAGGCCGTCGCCATGGAGACCCCTGGTACTTCTCATTCCCCTGCGCCTGGGGCTCACGGACATCAACG
AGGCCTACGTGGAGACGCTGAAGCACTGCTTCATGATGCCCCAGTCCCTGGGCGTCATCGGAGGGAAGCC
CAACAGCGCCCACTACTTCATCGGCTACGTTGGTGTGAGGAGCTCATCTACCTGGACCCCCACACCACGCAG
CCAGCCGTGGAGCCCACTGATGGCTGCTTCATCCCGGACGAGAGCTTCCACTGCCAGCACCCGCCGTGCC
GCATGAGCATCGCGGAGCTTGACCCGTCATCGCTGTGGGGTTTTTCTGTAAGACTGAAGATGACTTCAA
TGATTGGTGGCAGCAAGTCAAAAAGCTGTCTCTGCTTGGAGGTGCCCTGCCCATGTTTGTGAGCTGGTGGAG
CTGCAGCCTTACATCTGGCCTGCCCCGACGTCCTGAACCTGTCCCTAGATTCTTCTGATGTAGAGCGAC
TGGAAAGATTCTTGCAGTCAAGAATGAAGACTTTGAAATCCTGTCCCTTTGAAAATCCTGGGGTGGGG
GTGGCAGCTGTGAGAGCCTGGGGCTCCTGGGCTCGCTGCGTTTTCATCCATCCCGCCGCTCGCCTGCCGA
GGGCTGCGCCCCGTGCTGCTCCCCCAGAGGGCCACCCGCTGTGCTCGTGGACTGAGGCTGCGCTGCC
GGGAGGCCTTACTGCTTGGTGTGACTGCCCAGCTCAGAGTGGCCGTCAGGGCCTGTGCATCCGCACGC
GGAGCCGTCTGTTAGGAGCTTCCAGAGTGTCTCTCGACACTGCCAGCCCCGTGTTAGCACCTGGGCCCTC
AGTCCCCTTGTCTCCAGGCGCCGTTTCTGTGGTTGGTTTTGGAATTAAGTCTGTTTGAAGTTGTCAGA

>sp|Q96DT6|ATG4C_HUMAN Cysteine protease ATG4C OS=Homo sapiens OX=9606
GN=ATG4C PE=1 SV=1
MEATGTDEVDKLLKTKFISAWNNMKYSWVLKTKTYFSRNSPVLGKCYHFKYEDEDKTLF
AESGCTIEDHVIAGNVEEFRKDFISRIWLTYREEFPQIEGSALTTDCGWGCTLRGTGQMLL
AQGLILHFLGRAWTWPDALNIENSDESWSHTVKKFTASFEASLSGEREFKPTISLKE
TIGKYSDDHEMRNEVYHRKIIISWFGDSPLALFGLHQLIEYGKKS GKAGDWYGPVVAHI
LRKAVEEARHPDLQGITIYVAQDCTVYNSDVIDKQSASMTSDNADKAVIILVPVRLGGE
RTNTDYLEFVKGILSLEYCVGIIGGKPKQSYFFAGFQDDSLIYMDPHYCQSFVDVSIKDF
PLETFHCPSPKKMSFRKMDPSCITGFYCRNVQDFKRASEEITKMLKFSSEKEYPLFTFVN
GHSRDYDFTSTTTNEEDLFSSEDEKKQLKRFSTEEFVLL

>sp|Q86TL0|ATG4D_HUMAN Cysteine protease ATG4D OS=Homo sapiens OX=9606
GN=ATG4D PE=1 SV=1
MNSVSPAAAQYRSSPEDARRRPEARRPRGPRGPDNGLGSPGASGPALGSPGAGPSEPD
EVDKFKAKFLTAWNNVKYGWVVKSRFSFSKISSIHLGRRYRFEGEGDIQRFQRFVSR
WLTYYRRDFPPLPGGCLTSDCGWGCMLRSGQMMMLAQGLLLHFLPRDWTWAEGMGLGPPELS
GSASPSRYHGPARWMPRWAQGAPELEQERRHRQIVSWFADHPRAPFGLHRLVELGQSSG
KKAGDWYGPSLVAHILRKAVESCDVTRLVVYVSQDCTVYKADVARLVARPDPTAEWKS
VILVPVRLGGETLNPVYVPCVKELLRCELCLGIMGGKPRHSYFYGYQDDFLLYLDPHYC
QPTVDVVSQADFPLEFSFHTSPRKMAFAKMDPSCITVGFYAGDRKEFETLCELTRVLS
SSSS ATERYPMFTLAEGHAQDHSLLDLCSQLAQPTLRLPRTGRLLRAKRPSSEDFVFL

>sp|P53867|ATG4_YEAST Cysteine protease ATG4 OS=Saccharomyces cerevisiae
(strain ATCC 204508 / S288c) OX=559292 GN=ATG4 PE=1 SV=2
MQRWLQLWKMDLVQKVSHGVFEGSSEPAALMNHDIIVLGEVYPERDEESGAEQCEQDCR

YRGEAVSDGFLSSFLGREISSYTKFLLLDVQSRVNFTYRTRFVPIARAPDGPSPLSLNL
VRTNPISTIEDYIANPDCFNNDIGWGCMI RTGQSLLGNALQILHLGRDFRVNGNESL
ERESKFFVNWFDNTPPEAPFSLHNFVSAGTELSDKRPGWFGPAATARS IQSLIYGF
PECGIDDCIVSVSSGDIYENEVEKVFENPNSRILFLLGVKLGINAVNESYRESIC
GILSSTQSVGIA GGRPSSSLYFFGYQGNFLHFDPHIPQPAVEDS FVESCHTSK
FVKLQLSEMDPSMLIGIL IKGEKDWQWKLEVAESAI INVLAKRMDDFDVSC
SMDDVESVSSNSMKK DASNNENLGVLEGDYVDIGAI FPHTTNTEDVDEYDC
FQDIHCKKQKIVVMGNHTHTVNANLTDYEVEGV LVEKETVGIHSPIDEKC

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

ATGCAGAGGTGGCTACAAC TGTGGAAAATGGATTTGGTACAAAAAGTGTCTCATGGCGT
TTTTGAAGGCTCGTCCGAAGAACCGGCTGCTCTTATGAATCATGATTATATAGTATTAG
GGGAAGTATATCCTGAGCGAGA CGAAGAATCTGGCGCTGAACAATGTGAACAAGACT
GTTCGATATCGCGGTGAAGCGGT TAGTGACGGGTTT TAAAGCTCTCTTTTTGGT
TAGGGAAATTTCTTCTTACACAAAGGAATTTCTTTTGGATGTACAATCAAGGCT
CAACTTTACATATCGGACAAGATTTGTTCTTATAGCAAGGGCCAGATGGGCCCT
CACCTTAAAGTAAATTTATTAGTACGTACAAATCCGATCAGTACAATAGAGGACT
ATATAGCAAATCCTGATTGCTTTAAC ACTGATATTGGGTGGGGTGTATGATAAGG
ACAGGACAAAGTTTGTGGGGAATGCCTTACAAATCCTTCATTTGGGCAGAGATTT
CAGGGTAAATGGTAACGAAAGTCTGGAAAGAGAATCAAAATTTGTAAATTTGGTT
TAATGACACGCCTGAGGCTCCATTTTCGTTACATAACTTTGTTTCTGCAGGTACAG
AACTCTCTGATAAAAGACCAGGTGAATGGTTTTGGTCCCAGCTACGGCAAGGAGT
ATAACAATCTTTAATATATGGCTTCCCGAATGTGGCATCGATGATTGTATAGTATCT
GTTTCATCCGGCGATATCTATGAAAATGAAGTTGAAAAAGTATTTGCTGAGAAT
CCAAATAGTAGAATATTGTTCTTGTGGGCGTGAAGCTCGGGATTAATGCGGTAAAT
GAGAGCTATAGAGAAAGTATATGTGGTATCTTAAGTTCAACACAGTCAGTAGGC
ATTGCCGGCTAGGC CGTCTTCATCGTTGTATTTTTTTGGTTATCAAGGAAATGA
ATTTTTTACATTTTCGATCCTCATATTCCTCA ACCGGCAGTAGAAGATTCATTT
GTAGAGTCGTGCCATAACCAGTAAATTTGGTAAATTGCAACTATCGGAAATGG
ATCCCTCGATGCTCATTGGTATTTTGTAAAGGGCGAAAAAGACTGGCAACAAT
GGAAAGCTAGAAGTTGCAGAATCTGCTATTATCAATGTTCTTGCTAAGAGAAT
GGATGACTTTTGATGTGAGTTGTAGTATGGA TGACGTGGAAAGTGAAGTTCT
AACTCAATGAAGAAAGATGCAAGCAATAATGAAAATCTCGGAGTACTA
GAGGGAGACTACGTAGATATTGGTGAATATTTCCACACACAACAATA
CAGAAGATGTAGACGAATATGATTGTTTTCAAGATATTCATTGCAAGAAAC
AGAAGATTGTTGTTATGGGAAACACACACTGTTAATGC GAATTTAACAGAT
TATGAAGTAGAAGGCGTCTTGTAGAGAAGGAAACGGTAGGTATTCACAGT
CCTATTGATGAAAAATGCTAG

41. SQSTM1 (sequestosome 1)

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

TTGGTTATGCAAAGTCACATGACCATGATGTTGTGAATTTGACAGGTCCTATA
AAAAGCCAGACTAAGCCA TTTGCAACCATTATTGGCCATTTTTGAGATAGAAGGA
AGGAAGCTACAAGACAAACGAATATTTTCCCGA AAAGTACATTAGTTGTCA
ACTAATTTATTTTCGAAAAGTACGAGATCCAAGATGTCACCTACTGTAAAAGC
ATTTTTGGTGAAGGAGGGAATGAGAAGGCCGAAATTCGACGCTTACAGTGCCT
CAAGATGTATCCGCAAGTTTTGATTACCTGCAGAAGAAGATCGCTGACATCTTT
CCAGGACTTGCTCGAGGCAACTTTAATTTGT TTTGGAAAGATGAGGATGGT
GATCTTATTGCCTTCTCAACTGGAGAGGAGTTGCTTGAGGCTTTGGGATT
TGTGGACAATGGACTTTTCAGAGTTTTTTGTTAAACCAACATCTCAGTCAAGT
GGTGACAAACCAGCAGGA AATACTCCCATGCAGGAGCATCCTGGAATCATCT
GCGATGGATGCGAGGGTAAAGTGATCGGAAGACGGTACAAGTGTACTGAGT
GTCCAGATTATGACCTGTGTGAGAGCTGCGAGTCCAAAGGAATCCACTCGG
AGCA TAACTTTATGATGTATGACACCCCTGTCCACCCTGGATATGGATT
CCCCCTTCTCCTGGCCCCCAAGACCC CAGTGTCCCCCTGGGCCCGTGGAC
CTAGTGGCCAAGGACAACCCCATGTGCCCTCCCCACTTTTTTCC GTTGGAT
GGAGAGAATGGCAAGGAGACAGCAAAAACAGAGATAATGCTGGCTGTCCC
AGGAGTGGCCAAAGGAACGCTGAAGATCAAGGGTCAAATGACACCAGTGG
AGAGGGTGCCTACAATCCCGAGGAATTCCTGCAG AATGTTGGCCAGAGT
GTGGCTGCTATGCTTGATCCATTAGGAATTGATGTTCAAGTGGATGTT
GAACATG GAGGACGTAGATGCCAGCTTGGGGACAGGGTGGAGGATGCAAG
GGAAAGAGAAGTGGAAAGTGTGGACA AAGAAAATGTGGAAACAAAGG
AGAACAGGAGGAAAATGGAGTCTGACAAAGTGGAGACTGAACAGATG
AAGACCCAGAGGAGGCCACTCCAATGGCCACCAGCAATGCCGACAAGCT
GCAGACAGATGGACATCCA CAAGCGCAGAAAATGCCCAAACCCATCTG
AAAAGGTCACCAAGGACTTTGAAACCTGGACCTTCATGGA GGATGGCAAT
TAGATCTGGGAGA ACTCCCTCTCCCCCTGCTCCTACCCCAGTACAG
CCCCCTCCCACCCAG CTGATCTATCCCCCACAGATCCAAGAATTGCAGA
AGCCCTGCAGCAGATGCTCGGAATGGGATTT CACAATGAGGGAGGAT
GGCTACAGAACCTGTTGGAGCAGAAGGAGGGAAACATCAGCCAGGTGTT
GGACGCCATCCAGACCAGAGCCAAGACCACCCCTGATGGCGGCTTCAT
GGCCTAAACCCATGGGAAAGATGGAAATATA TAGAACTGGAGACAGAT
TTGGACTTTGTCTTGACTTTTAATTTTTTGGTGGATGTTGTAATTTTT
TGTAGTTTGGTAACTTTTCTTATTAATATGAATCACTACCTATAGTGT
GTGCTTATTCTGTTTGTGTTGAAATGTTT

TTTATTCTAGTATTTTGGAAACATGACTTGTGTATTTTATTTTTTTAACCATGTAAACATTGAAATCAAT
CTTGCTTAACACAGACATTATGATTTTAAAAATGTATATTTAAAAATTGTTAAACCTGTTAACGATAATT
GTGGTACTGCTTTCCCAAAATGATAAAATATTTAATTTATAATCAAATAAATGACATAAATGAAACAATT
GCTGTTTCATATTTAACCATATTATGCATGGGTAACCTTGCTTCATCCTGCAAAAAAGTAGTACTGCGGTTA
TAGTGAAGCAGTTTTTATGTCAAATTGCTTTATGAATACATGTAACATCAGTCGGATTTCCTGTGTGTGG
GCTGGTTCTAATTAGACTTACAATTTAGAGTTATTTCAAAGATCATGTATGATAACAAGAAGGGATGACC
TATTATTATTTTAGACAAATTGGGAATTGTTGAATCTTTGATATTTTATTTAGTAAATTGTCTATTTTA
ATTTTTTGATCTTACTTAGAACCTACTACATGAAAAATTTTTGTTATGTTATTGTCTTGCCTACTTTTA
ATGACCAAAATTCATAAAAAAAAAATCATCAAAATAATA

>sp|Q13501|SQSTM_HUMAN Sequestosome-1 OS=Homo sapiens OX=9606 GN=SQSTM1
PE=1 SV=1

MASLTVKAYLLGKEDAAREIRRFSFCCSPEPEAEAEAAAGPGPCERLLSRVAALFPALRP
GGFQAHYRDEGDGLVAFSSDEELTMAMSYVKDDIFRIYIKEKKECRRDHRPPCAQEAPRN
MVHPNVICDGCNGPVGTRYKCSVCPDYDLCVCEGKGLHRGHTKLAFFSPFGHLESGFS
HSRWLRKVKHGHFVPGWPGWMPGNWSPRPPRAGEARPGPTAESASGPSSEDPVSVNFKNV
GESVAAALSPLGIEVDIDVEHGGKRSRLTPVSPSSSTEKSSSQPSSCCSDPSKPGGNV
EGATQSLAEQMRKIALESEGRPEEQMESDNCSGGDDDWTHLSSKEVDPSTGELQSLQMP
SEGPSLLDPSQEGPTGLKEAALYPLPPEADPRLIESLSQMLSMGFSDEGGWLRLLQTK
NYDIGAALDTIQYSKHPPL

42. 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
MIMNSTNTVVYIKVKGRRPQGFLDPPKFEWNGTKERQLWTMVSNLNYSQDQIDWQNLSKI
FETPEFFLKKRKYKLF AEHLELLQLQLEKKRDLEKYSNDQVNEGMSDLIHKYTPTLQNDN
LLNVSASPLTTERQDSEEVETEVTNEALQHLQTSKILNIHKKTSSENKPNDKLKDGIN
KEMECGSSDDDLSSSLSVSKSALEALMDRLQF

43. 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
MNVTVTVYDKNVKYRLEENIKNNKGPSNDDQPAYNNEKSTDGSDYAMFPTNIKYIFEDN
NDELVDSSDAALTAGIDKVGDELENNIIVQLDESGSLEDITLISDQYELLSHRTNSLSLE
ENQMRTLSSHGDDKSNDEEEELSVDSDRFRVSDIELDVISQFCDLSPFLRDLSLNDLIK
LYVTQNEQLQMLNSV

44. 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
MSDLNDVQENAKLNSETRNTGKAEPPHGTTEYVAEAEISKNGVSGPKKSPKKGKVGKGDN
NKVETELVHTALLEKDNPFMEEGPTGFTKSALLEIPGMRSHNLKPNEDYEDDSEGLLPL
NQESNAETCRTSLSGSINSMNGETSASEEPSVSNRKKSAIRIHILEAKRVSEGOGRAYIAY
VIQFENSTVQRRYSDFESLRSILIRLFPMTLIPPIPEKQSIKNYGKSITGSSSKYLLPSE
GSGSVDLSLSVIHASVNSNDEKLIRHRIRMLTEFLNKLLTNEEITKTSIITDFLDPNNHN
WHEFVNSSSTFSSLPKSILQCNPLDPTNTTRIHAMLPPIPGSSQLLLNKESNDKMDKER
SKSFTNIEQDYKQYENLLDNGIYKYNRRTTKTYHDLKSDYNEIGEVFAQFAHEQAQVQV
AEQLSYLSNAFSGSSISLEKLVGRLYNINEPLNESVHMATSARELIKRYRKLKYLQNEMI
KKSLSNKRAQLEKLEAQNNEYKDVKIIDNEMSKSHTINLERPNNTGSGGKSYGGKLFN
GFNKLASMVKDSVKYQETDPHTASINLKKEIEQLSESLVTEVDLEVISKVIKNDQLPKF
SKEREVDLSEILKHYSRYMRNYARQNLIEWKEVKRHQDFA

45. 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
MTDKGKNDLTSKAKDKARGNPEKPPYWFEEIIVSDPQKRTGDPGSSSGYVSYQISTKTNT
SFYDNRGDPESIIIVHRRYSLLLLLDILLNRFPCTIIPPLPDKKVFQYIAGDRFSQRFT

QKRCHSLQNFLRRVSLHPDLSQSKVFKTFLVSKDWESHKRVLQDSLQPNKDEVTDAFMNA
FKTVHKQNEEFTEIREKSDKLDRTVTKIDKLFHKVVKKNDMSSEDTKLGSNLQELQELV
TGENEELAALKLIFNEGVTSYGLQDLTKYLDYEYIVDLKDLEHYIDSMRQLIKLKDQK
QIDYEELSDYLTRSIEKNNLISGYGGSNFFANKLEELAGINQEASRREKINKLEGKITS
LTGELENAKKVADGFEQECLKEIDHFESVKTAIEIKKSLGSLADHHIEFYERILEAWEKVD
DSL

46. 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
EIIIRLETLLRDFKKNKFIIEELKRQSGRIRSEMGNIDFHLSKIEESKHQLMKRIGFESP
LTQEKLSEKIFNLRLSSADEDYNERQTIMKNFVHMKDLIELKIEDLQEQLMRNKNESS
TVLTQRELWLDCKQKVGDLSEKLTITKLRSSNSKIIPPSEMSEMINSTIYLNLLDSSDE
KLTTTLISNERDVLKACEELHSESTTAQDGSSALPSKPIDIHKSHKGSNASSNLKQPST
PSFLVASKSPPKIGISESVVNANKNDIAISKKVE

47. 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
MVSKTWICGFISIIITVVQALSCEKHDVLLKQVGVKFSSTLSTERDTPPSTTIEKWWINVC
EEHNVEPPEECKNDMLCGLTDVILPGKDAITQIIDFDKNIGFNVEETESALTTLTKGA
TWGANSFDKLEFQCNDNMKQDELTSHTWADKSIQLTLKGPSGLCKSKDDDKKNGDGDNG
KGDGSEGGKPAKKAGGTSWFTWFLYALLFTLIYLMVVSFLNTRGGSFQDFRAEFIQRST
QFLTSLPEFCKEVVSRI LGRSTAQRGGYSAV

48. 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
MNNSKTNQMMNTSMGYPLTVYDECNKFLQIVPTLDANIMLWCIGQLSLLNDSNGCKHLFW
QPNDKSNVRILLNNDYDGHFLFKYLQCKQKCSVYIIGEGTLKKNLTISTSFDFDLTPSE
EKESLCREDAHEDPVPKAGSEEEISPSTSNVVVSRECLDNFMKQLLKLEESLNKLELE
QKVTNKEPNHRISGTIDIPEDRSELVNFTELKTVKQLEDVVFQRYHDIYERLSQECDSKTE
IASDHSKKEKIEVEPPNERSLQITMNRDNSLYFQLFNNTNSVLGNCKLKFTDAGDKP
TTQIIDMGPEIGIKEYKEYRFPYALDLEAGSTIEIENQYGEVIFLGKYGSSPMINLRP
PSRLSAESLQASQEPFYSFQIDTLPPELDDSSIIISTISISLSYDGDNEKALTWEEL

49. 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
MNEADVTKFVNNARKTLTDAQLLCSSANLRIVDIKKKLSWQLSISKLNFLIVGLRQQGK
FLYTILKEGIGTKLIQKQWNQAVLVVLDVEMKYWQYEITSKVQRLDGIVNELSISEKDDT
DPSKLGDIYISRDVNLNDKLEKVPVIERQIENIKLQYENMVRKVNKELIDTKLTDVTOK
FQSKFGIDNLMETNVAEQFSRELTDLKDLAEIMNSLTQHFDKTLQLQDKKIDNDEREEL
FKVVQGDDEKELYNIKTLHEVIDDVDTILNLGQFLQAKIKEKTELHSEVSEIINDFNRN
LEYLLIFKDISNLIDSFKNSCTQDIQTTELCEFYDNFEESYGNLVLEAKRRKDVANRMK
TILKDEKQLQNLDAQDQEERQNFIAENGTYLPETIWPBKIDDFSSLYTLNYNVKNP

50. 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
MADADEYSTAPTQOEITPLQTTATIINAISGECITTNVDFVSLDKFKQFIARKWKIPPD
QLLILLPYGNKPKSMFKELLINRSFTLNDFFVYDRRLFLVSKPTPTNLLTSKDSNPMN
SPNSNDLTETLEYLIKNSHISQYQGSDTIMIKPMPSPLEDADVDLSRLNYHSVTSLLTTN

LGWLSALEIDVHYFKSLIPDIIAHIKRIFDGLTVCSQYLKLYCFDVESLYNSNVQFLNQL
VDNGMTSKWEKCFNDTLSKLTALEGDSLQKFINIESLLENEKSVKILNHSINGKLNKIKR
EIDENASFRDIITVNIIDRLRQMFTPNESKFELEDQMAESFEVLVSEMRTSRNVLDKEEE
EFNSQEFLLKSMNVMLEKDKKESVKTFTISQALYSQIGELIDLKKSLOKHAVAILGNIAF
TQMEILGIKRLLLNECNKDLELYKKYEVEFAQVEDLPLIYGLYLIEKYRRLSWFQQILSF
ISNFNQDLELQNELRTRNKWVKNFGSIATVFCEDLLSSSDFKRLNEYHSHTSPPNEDE
EDENENSIANYRQDLVKVVSQAIDNYMTQIKETDVSEPIIDLLSKTLFETKRFHIIYSNFK
NNNNNSNGNSISPEGSIALKSDDVVKGYKTRIKKLESLLEHFQYSDIGHWPQGVLNTHL
KPFGRSATSINKKKFLGASVLLLEPANISEVNIDSVSQANNHQIQELESNVDDLLHQQLL
KEENNRKSMQISEMGKKISDLEVEKTAYRETLTNLNQELARLTNEEQSHRTEIFTLNASF
KKQLNDIISQDNEKIEKLTGDYDDVSKSRERLQMDLDESNNKHEQEVNLLKADIERLGKQ
IVTSEKSYAETNSSSMEKGEKFETIPLAEDPGRENQISAYTQTLQDRIFDIISTNIFILE
NIGLLLTFDNNNNIQIRRVKGLKKGTAQSNILDESTQMLDAHNSLIKSPVFQKLKDEYE
LIKSVANGSEKDTQOSIFLGNITQLYDNKLYEVAVIRRFKDIETLAKKLTKENKIKRTLL
ERFQREKVTLRNFQIGDLALFLPTRENVNSVGSMSSTSSLSSSFSSVDLSTPPPLDAMS
IQSSPSVIHSNVINQASISGRDKNKLMPWAAFTAFEESTRYFLKDEKGLTKGKEWFVGR
IVTLEHFVADSPSNNPFRLPKGSVWFQVTAVVVSYQGV

Figure S2.

1. ATG7

```
>MK173046|Ubiquitin-like modifier-activating enzyme ATG7
[organism=Crassostrea gigas] mRNA, complet cds
MSAPLVNKMESKQLQFVAFNSFLDSGFVHKLSENKLDVYGLDESQKEIKG
FYFNGDPVGMPCRMNVEFSAFDQDAKTPQRYLPMLGELHNTNTVDFKKEC
DKKEMISVAGKKIWDIVTGKALDTPPELLATFLLLTFFADLKKYHYWFC
FPCLCPSTDITFDQEPKLLKDKLTAEMEQLQAYDTFQDAYPTYQGFFV
AVLSKGNIVIEDVKHMNKFENTQEVYFGFCDPNSIEDYPGWPLRNFMLLI
SYHWKGDRLGVNVLCLDRSRDGTDRDISHSLLLSLNVDPDIKNVSECPKCV
GWEKNEKQKLAPRFVNLASMDPTRLAASAVDLNLKLMRWRLPELDL
ISRKCLLLGAGTLGCNVARCLMGWVVRTITLVDNGRVSYSNPVRQSLFQ
FEDCVKGGKPKAEAAEAAMKKIFPGVNAKGLSLSIPMPGHAVPESAIEGV
KKDVETLQDLVNSHDVAFLLLDTRSRWLPMLMAAEKQKIVICSAFGFDT
YLVMRHGVRSDEGADPAPLSSYSSIPGDQLGCYFCNDVVAPGNSLKDRT
LDQQCTVSRPGISYMASALAVELLVSVLQHPHELKAPADTSASDEHLSKD
FVCPLGLVPHQIRCFVSRFQQVLPACKAFDKCTACSKTVIEQFRRDGFDF
LRRAFNDPSYLEDLTGLTQMHQETLDAEVWGFSDDEECSSMEVSSS
```

```
>sp|O95352|ATG7_HUMAN Ubiquitin-like modifier-activating enzyme ATG7
OS=Homo sapiens OX=9606 GN=ATG7 PE=1 SV=1
MAAATGDPGLSKLQFAPFSSALDVGFWHELTQKKLNEYRLDEAPKDIKGYYYNGDSAGLP
ARLTLEFSAFDMSAPTARCCPAIGTLYNTNTLESFKTADKLLLEQAANEIWESIKSGT
ALENPVLLNKFLLLTFFADLKKYHFYYWFCYPALCLPESLPLIQGPVGLDQRFSLKQIEAL
ECAYDNLCQTEGVTALPYFLIKYDENMVLVSLKHYSDFFQGGQRTKITIGVYDPCNLAQY
PGWPLRNFVLAHRWSSSFQSVVEVCFRDRTMQGARDVAHSIIFEVKLPEMAFSPDCPK
AVGWENKQKGGMGPRMVNLSECMDPKRLAESSVDLNLKLMCWRLVPTLDLKDVKVSVKCLL
LGAGTLGCNVRTLMGWGVRHITFVDNAKISYSNPVRQPLYEFEDCLGGGKPKALAAADR
LQKIFPGVNARGFNMSIPMPGHPVNFSSVTLEQARRDVEQLEQLIESHDVVFLMDTRES
RWLPVAVIAASKRKLVINAAALGFDTFVVMRHGLKPKQGGAGDLCPNHPVASADLLGSSLF
ANIPGYKLGCFYFCNDVVAPGDSTRDRTLQDQCTVSRPGLAVIAGALAVELMVSVLQHP
GYAIASSSDRRMNEPPTSLGLVPHQIRGFLSRFDNVLVPSLAFDKCTACSSKVLQYERE
GFNFLAKVFNSSHSFLEDLTGLTLLHQETQAAEIWDMSDEETI
```

```
>sp|Q9D906|ATG7_MOUSE Ubiquitin-like modifier-activating enzyme ATG7 OS=Mus
musculus OX=10090 GN=Atg7 PE=1 SV=1
MGDPGLAKLQFAPFNSALDVGFWHELTQKKLNEYRLDEAPKDIKGYYYNGDSAGLPTRLT
LEFSAFDMSASTPAHCCPAMGTLHNTNTLEAFKTADKLLLEQSANEIWEAIKSGAALN
PMLLNKFLLLLTFFADLKKYHFYYWFCYALCLPESLPIRGPVSLDQRLSPKQIQALEHAY
DDL CRAEGVTALPYFLFKYDDDTVLVSLKHYSDFFQGGQRTKITVGVYDPCNLAQYPGWP
LRNFLVLAHRWSSSFQSVVEVLCFRDRTMQGARDVTHSIIFEVKLPEMAFSPDCPKAVGW
EKNQKGGMGPRMVNLSGCMDPKRLAESSVDLNLKLMCWRLVPTLDLKDVKVSVKCLLLGAG
TLGCNVRTLMGWGVRHVTFVDNAKISYSNPVRQPLYEFEDCLGGGKPKALAAAERLQKI
FPGVNARGFNMSIPMPGHPVNFSDVTMEQARRDVEQLEQLIDNHDIFFLLMDTRESRWLP
TVIAASKRKLVINAAALGFDTFVVMRHGLKPKQGGAGDLCPSHLVAPADLGSSLFANIPG
YKLGCFYFCNDVVAPGDSTRDRTLQDQCTVSRPGLAVIAGALAVELMVSVLQHP
GGYAIASSSDRRMNEPPTSLGLVPHQIRGFLSRFDNVLVPSLAFDKCTACSPKVLQYEREGFTFL
AKVFNSSHSFLEDLTGLTLLHQETQAAEIWDMSDEETV
```

```
>sp|Q5ZKY2|ATG7_CHICK Ubiquitin-like modifier-activating enzyme ATG7
OS=Gallus gallus OX=9031 GN=ATG7 PE=2 SV=1
MAAVSNESQNPVDPGSSKQLQFAPFSSALNVGFVHWTQKKLNEYRLDETPKVIKGYYYNG
DPSGFPARLTLEYSAFDINASIPARCCPAFGTLYNTNTFETFKSCDKKSLEKEANEIWE
SIKSGAALNPMLLNRFLLLTFFADLKKYHFYYWFCYPALCFDPDGIHVIQKPVCLGDRFSL
NQIQALQKAYDELQTEGVTAFPPYFLIKYHDNSVVVSPKKWDGFFQDQGGKVTGVYD
CNLSHYPGWPLRNFLLILASHKWGNILQSIIEVLCFRDRTMQGVRDITHSIIFEIKLPQGA
GPDCPKAVGWENKQKGGMGPRVVNLSECMDPKRLAESSVDLNLKLMCWRLVPTLDLEKIV
SAKCLLLGAGTLGCSVARTLMGWGVRKITFVDNARISYSNPVRQPLYEFEDCLSGGKPKA
LAAAERLQKIFPGVNSEGYNMSIPMPGHPVNFSEVTMAQARKDVATLEELIDAHDVVFL
MDTRESRWLPVAVIAASKRKLVINAAALGFDTFVVMRHGLKPKQQETGNACFSTAPGPSDL
```

LGSSLSFSNIPGYKLGICYFCNDVVAPGDSTRDRITLDQQCTVSRPGLAMIAGALAVELMVS
LQHPEGGYAVASSSDRRMNEPPTSLGLVPHQIRGFLSRFDNVLVSLAFDKCTACSPKVL
DQYEREGFNFLAKVFNSSSHFLLEDLTGLTLLHQETQAAEIWDMSDDET

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

MSTEKEIILQFAPWESFVSPTFWHKLAELKLDHDLSDSKRSITGHYTNRNASGCLLEVD
YTAYNRMAKPPKFSHSAIGTIYNKNTIEEFKALDKLQLLADEGKELLADMCSGGALRDP
LLTRFFVLSFADLKCHSYWFAFPCPLTPTLKLQGAQKLRDLNPNSSSYIMALKALPTE
SQNFFILYANVEKNIFEARSLSLDDKNVEFCYFGFADPSEYEHPAWIMRNYAAFLQOC
PSFVVGKPLKFLGLRHNQOMNIDDSLVWVKVIQTEACDLSQSENIKFGWELNKNKMGPRM
VCMRDSMDPAKLAENSVNLNKLKMKWRLVPLDNLLEIISQTKCLLFGAGTLGCAVARNLLS
WGFKHITLLDSGKVGFSNPVRQNLTYHADAVAGNRMKATTAOQLKEINPSAETAGYVLE
IPMPGHTIGESLLAQTKHEHLKVIKLVQDHDVIFLLTDSRESRWLPTLLGAAKEKIVINA
ALGFDSYLVMRHGTTTRKEAGDDGQEIIEGLKCCINGDQGLGICYFCNDVTAAPGNLKDRTLDQ
CTVTRPGVSNIAASYAVELLVALLQHPRELAPAYYAQSGRGRSEETEEKVPEGLLGILP
HSIRGMLCNYENILPATQKFAQCIACSAAVLNEYKKEGHAFLEFKTFETAKFLEDLTGISE
FKRLNSEIIFDDEEFDMSSDSD

>tr|G5EBK4|G5EBK4_CAEEEL AuTophagy (Yeast Atg homolog) OS=Caenorhabditis
elegans OX=6239 GN=atg-7 PE=1 SV=1

MATFVFPVTCCLDTGFWNEVNKKLNDWKLDETPKCISSQLSLHQTEGFKCHLSLSYDSLS
SLESTTGLSMSGTLNLYNTIESFKMVDKSDLRSEAEKIWESITTRKWLQNPRLLSQFFI
IAFADLKKFKYWWTCVPALVYPSEIKQEIITPLSSLGADHKILFDFYRKNFPFIPLYSKQ
SSKMLELSELENNTNPDEICVWVADPSPVAYSAGWMVRNVLAVAHLHPTWKHCHIIISLR
SADSIGIKYTWTLPSEACSDAGQNAVPAVGVWERNANDKLPISVDLSKEFDPKILMER
SVDLNLSLIKWRLHPDIQLERYSQKVLILGAGTLGCNIARCLIGWVRHISFLDNSTVS
YNNPVRQSLSEFEDARLGRGKAETAQAAIQRIFFSIQATAHRLTVMPGHSIDKDVPEL
EKDIAKLEQLVKDHDVFLALDSREARWLPTVLASRHKKIAISVAIGFDYVIIRHGIGS
RSESVSDVSSSDSVPYSQLSYFCSDVTAAPGNSTFDRTLDQCTVARPGTSMIASGIAVE
LLSSVLQYDPDKTPASHDDNTTVLGAAPHQIRGFLGRFQQILPSVKRFDQCVACGDAIA
AQFQQNGWKVFRDVMNSPGRLEEVTVGLDELQNSVNAIDIDFEDDEF

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

MASQEKTDSSQQLQFAPFSSALDVGFWHKLQKKLNEYKLDGPKDIYGYNGDPDGL
PCRLSLEFNADFQSETTPPHCFSSRGTLVNFNTLDAFKTCDDKALLDVTAEQWDDIRQG
SAIQDPSLLSRFRLTFADLKKYHYCYWFAFPALLAPEGKLIQPEKLDKAMDQDKITA
LQAAAYDLASQSLGQEPAFFLISTEDDKTVVPLTAWDQVTDKSKVMFGYADPCTLEQYPG
WPLRNFCLISCHWASQLDQVTVVCFRNRTREGIRNSSHSLILRLQVPSTSPETSCPKCV
GWEKNQRNKLARKVDLSSMDPTRLAETSVDLNLKLMRWRLPSLDLTKISQTRCLLLG
SGTLGCNVARCLLGWVVRTITFVDNSTVSFSNPVRQSLFEFEDSLGGGPKAQTAEEKIE
KIFPGVKTRGVLSIPMPGHAVGTSDEAIQQTRESVQKLEELIDEHDVVFLLMDTRESRW
LPTVICSSKRKIVMNAALGFDTYLVLRHGMKPARDQPPDQTPSSASSGAAGGAEGGAA
GGASCSTSSISLSHIPGDKLGCYFCNDVVAPGDSTRDRITLDQQCTVSRPGLSMVAAALVV
ELMVSILQHSQGAYAAAETSADKSHLTVDLTSPGLVPHQIRGFLARYHCVLPASLCFDK
CTACCDIVLASYEREGFDLLKVFNKPRFVEDLTGLSQLHLESELIEILDFSDDETMTS
SQ

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

RTPNIIISMAESSLKLQFAPFCSALEAGFWHQLTQKKLNEYRLDESPKNIKGYNGDAVG
LPARLTLEFSADFADGPTPARCCPASGTLYNTNTLEAFKSTDKKALLDKAANEIWSAIQS
GALEDSSILNKFILLTFADLKKYHFYWFPCFALCFVEGIQLLRAPLSLEQHFSDKQIS
SLQSAYDNLCASSGTTAVPHFLKYSSEESVEVAPLKEKLSFFPDLKRVYISTSHQCGLLP
QHPGWPLRNLVLLAKKWASQLDVVEVLCFRDRTLQGVRSVQHSIIFQLRLSDPAPSAAP
TTDINIHWKMIHSIQGNSAFFVSECQGVRLAESSVDLNLKLMRWRLVPLDLEKVVST
RCLLLGAGTLGCNVARTLMGWGVRHITFVDNAKISYSNPVRQPLYEFEDCLSGKSKALAA
VDRLLKIFPGVNAEGFNMSIPMPGHPVNFSDLTVAQAQQDVEQLKKLISEHDVVFLLMDT
RESRWLPTVIAASQRKLVNAAALGFDTFVVMRHGLKPRESEESSPMSASSSSSSSNTPA
ATVTAGSSLSFSNIPGHRLGCYFCNDVVAPGDSTRDRITLDQQCTVSRPGLAMIAGALAVEL
MVSVLQHPEGGYAVASSSDRRMNEPPTSLGLVPHQIVPLLSNVTNVLYEMFWRKDRCL

KKVLENYEREGFQFLAKVFNSSHSFLEDLTGLTLLHQETQAAEVRLTPSISI

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

MSEFVKFTKLRSTTDCTFWAKFVELKIDKFKLDEKSNLWGSYSLSQSLNEDNFNPLVLDF
TSFNEDLETINNKSSVICFGHMINTNTFEAFRQINPEQFIDSMGKDIINSIQDGTILQNP
WKLSLFLVLAYSDLKKYRFYYWVAHPTPLKLPemyyEEIPKSITEEFSEKHVEDLCNNFL
HLDCRTKNYFTVLI SKENKMCIVDLATGINVININNEKQSQDYTEIYFAFYDPTSSNPG
WPLRNLLCLLCWYCPTHYFSKI IKFISIRGNAQKSLVFKLKTKEYKKNYKNIRDNLFLSH
LVGWESNSNDKLGPTIADLSDTMDPTKLSDKAINLNLKLMKWRLVPLNDLEKICNLKCLL
LGAGTLGCSVARVLLGWGVNII FVDSSHVSHSNTVRSQSLYNHQDAIKHKYKAHAAKDAL
LNIRPSINTEGIVLHIPMPGHVVGQSMLESTKQSLKKLEELIEISDVVFLLLDSREARWL
PTVLC AAKNKITINAALGFDSYTVQRHGTRNFNNQISPDLVKNPRGMDLGCYFCNDVTQ
PGNSQTDRTLDQOCTVSRPGLSQIAAGLAVELLVALLQHPEGVEAEALVGNRDNINSND
AKLVGLLGCVPHITIRGSLWNYDTQLTITHRFTSCTACSVPI IEYKNRGLSFVLDACNIP
NYLEKLSGLEEILKRPDLDELALYALDNISDEDEDDQKM

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

MSAPMERKQLQFVPFSSFLDSGFWHKLSENKLDVYGLDES RKDIKGFYFNGDPVGMPCRMNVEFSAFDLD
AKTPQKCLPMLGELHNTNTIDKFKCEDKKEMMTEAGKKIWEAII SGRALVSPNLLASFLILTFADLKKYH
YYYWFCFPCLCLPTDVTNLNQEPIKMKDKFTKEQMDQFLT SYDTFQEEQPCYQGGFFVAAFSODKFMVKDVK
SLNNFDDTQEVYFGFCDPSTIEDYPGWPLRNFLMLISYHWKGSLENINVL CIRDRSRDGNRDISHSVLLS
LNVDPVKS LQECPKCVGW EKNEKQKLAPRFVNL SASMDPARLAASAVDLNLKLMRWRLPELDDLISRT
KCLLLGAGTLGCNVARCLLGWGVRTITLVDNGRISYSNPVRQSLFQFEDCVKGGKPKAEAAAESLKRIFP
GVNATGLSLSI PMPGHAVPDSAIDGVQKDVATLQSLVDSHDAIFLLLDTRESRWLPTLMAAEKQKIVICS
ALGFDTYLVMRHGKSDTEEEEDVPLSYHSIPGDQLGCYFCNDVVAPGNSLKDRTLDQOCTVSRPGISYM
ASALAVELLVSVLQHPQGGKAPADTSANDDHLSKDFVCPLGLVPHQIRCFVSRFQQVLPACKAFDKCTAC
SKTVIKEFRKEGFGFLRRAFNEPSYLEDLTGLTQM HQETLDAEVWGFSDDEECSSMEVS

2. ULK2

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

MEVVGDEYYSKKDLIGHGAFVVFKGRHRKRPNHVVAIKSITKKNLAKSQNLLSKEIKIL
KELSDLHHENVVALLDCKETTNNHVYLVMEYCNNGDLADYLQAKGTLSEDTIASFLRQIAA
AMQVMNGKGI VHRDLKQNILLCHDGPNTPSTEMRLKIADFGFARFLNDGVMAATLCGS
PMYMAPEVIMS LQYCAKADLWSIGTIVFQCLTGKAPFQAQTPQQLKHFYEKHAELKPNIP
KDTSPELRDLLLKMLKRNADRIEFASVPVPGRASQGCSSSPTPPRCVSASPLSGKAD
YSTPPSKVVQMVKQQEVAEAMQGSTHDEEFLKVDKGPTPRSNSPTEHDFVLVDPGMSDQS
DGS DKGRAPSTEDLQSLGERAQPQVVRVEPQVGSVAYKKDSGDVSSPSRPSLPMQSNNO
SEPIPVPTQVKAYERIRSSSSPLSSPRKCGTEPSPLDSAKLSSQNIKISPPQESKFSAPD
IGSFSPTVKFSVGTTPPNVSTPWRRGSIGSSQGGAIYHPPSNASNSPSRRASMGSSPSGF
NRNFSSPGSLPTILDASPHFELNQEPOFTDNMPTVPVRAPFGQSKPAIPEKSGTKRYHP
SEVDRVKLNLMECNTDPGAAGGMSMLSQOMKVAYMNQQGLNLLLEGQVVRYTSENENLVSP
NDNTVQMDTQRSGLRRTMSATTPPSNLMFAQSPNMEGPVAFVAPGLAEETLMGDNHN
EIMAKLSFVNDLADCVMEAMAKGAPLNTLSESVNWKQEGEPLHGDQMPKFI EAQRLLEQ
LVLYVRS LQLLSSSLQ LARREIKDERLQISNALKTLLKQMNERYHRCVSVCKHIQORLGI
TMQNALTPQVVIATADKLIYNYAIEMCQTAALDELFGNPQECFKRYNTAHILLHSLSQQA
RNSNDKQLLDKYKDAVERRLSHIQATQNYYPQFEIS

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

MEVVGDFEYSKRDLVGHGAFVVFGRHRQKTDWEVAIKSINKKNLSKSKQILLGKEIKIL
KELQHENIVALVDVQELPNSVFLVMEYCNNGDLADYLQAKGTLSEDTIRVFLHQIAAAMR
ILHSGKGI IHRDLKQNILLSYANRRKSSVSGIRIKIADFGFARYLHSNMMAATLCGSPMY
MAPEVIMS QHYDAKADLWSIGTVIYQCLVKGPPFQANSPQDLRMFYEKNRSLMPSIPRET
SPYLANLLLGLLQRNQKDRMDFEAFFSHPFLEQGPVKKSCPVPVPMYSGSVSGSSCGSSP
SCR FASPPSLPDMQHIQEENLSSPPLGPPNYLQVSKDSASTSSKNSSCDTDDFVLPVPHNI
SSDHSCDMPVGTAGRRASNEFLVCGGQCQPTVSPHSETAPIPVPTQIRNYQRIEQNLSTST
ASSGTNVHGS PRSAVVRNS TSPMGFLRPGSCSPVPADTAQTVGRRLSTGSSRPYSPSPL

VGTIPEQFSQCCCGHPQGHDSRSRNSGSPVPPQAQSPQSLLSGARLQSAPTLTDIYQNKQ
KLRKQHS DPVCP SHTGAGYSYSPQPSRPGSLGTSPTKHLGSSPRSSDWFFKTPLPTIIGS
PTKTTAPFKI PKTQASSNLLALVTRHGPAEEQSKDGNPRECAHCLLVQGSEQRAEQQS
KAVFGRSVSTGKLS DQOGKTPICRHQGSTDSLNTERPMDIAPAGACGGVLAPPAGTAASS
KAVLFTVGSPPHSAAAPTCTHMFRLRTRTTSVGPNSGGSLCAMSGRVCGVSPGPGFGSS
PPGAEAAPSLRYVPYGASPPSLEGLITFEAPELPEETLMEREHTDTLRHLNVMLMFTECV
LDLTAMRGGNPELCTSAVS LYQIQESVVDQISQLSKDWGRVEQLVLYMKAQAQLLAASLH
LAKAQIKSGKLS PSTAVKQVVKNLNERYKFCITMCKKLTEKLNRFSDKQRFIDEINSVT
AEKLIYNCAVEMVQSAALDEMFOQTEDIVYRYHKAALLLEGLSRILQDPADIENVHXYKC
SIERRLSALCHSTATV

>sp|Q9QY01|ULK2_MOUSE Serine/threonine-protein kinase ULK2 OS=Mus musculus
OX=10090 GN=Ulk2 PE=1 SV=1

MEVVGDFEYCKRDLVGHGAFVVFGRHRQKTDWEVAIKSINKKNLSKSKQILLGKEIKIL
KELQHENIVALYDVQELPNSVFLVMEYCNNGDLADYLQAKGTLSEDTIRVFLHQIAAAMR
ILHSGKIIHRDLKPQNILLSYANRRKSNVSGIRIKIADFGFARYLHSNTMAATLCGSPMY
MAPEVIMSQHYDAKADLWSIGTVIYQCLVGKPPFQANS PQDLRMFYEKNSLMPSPRET
SPYLANLLLGLLQRNQKDRMDFEAFFSHPFLEQVPVKKSCVPVPVYSGVPVPGSSCSSSP
SCRFASPPSLPDMQHIQEENLSSPPLGPPNYLQVSKDSASNSKNSSCDTDDFVLPVPHNI
SSDHSYDMPMGTARRASNEFFMCGGQCQPTVSPHSETAPIPVPTQVRNYQRIEQNLIST
ASSGTNPHGSPRSVAVRRSNTSPMGFLRVGSCSPVPGDTVQTGGRRLLSTGSSRPYSPSPL
VGTIPEQFSQCCCGHPQGHDSRSRNSGSPVPPQAQSPQSLLSGARLQSAPTLTDIYQNKQ
KLRKQHS DPVCP SHAGAGYSYSPQPSRPGSLGTSPTKHTGSSPRNSDWFFKTPLPTIIGS
PTKTTAPFKI PKTQASSNLLALVTRHGPAESQSKDGNPRECSHCLSVQSERHRSEQQQ
SKAVFGRSVSTGKLS EQQVKAPLGGHQGSTDSLNTERPMDVAPAGACGVMALPAGTAAS
ARAVLFTVGSPPHSATAPTCTHMLRTRTTSVGSSSSGSLCSASGRVCGVSPGPGPLGS
SPPGAEGAPSLRYVPYGASPPSLEGLITFEAPELPEETLMEREHTDTLRHLNMMLMFTEC
VLDLTA VRGGNPELCTSAVS LYQIQESVVDQISQLSKDWGRVEQLVLYMKAQAQLLAASL
HLAKAQVKSGLSPSMVAVKQVVKNLNERYKFCITMCKKLTEKLNRFSDKQRFIDEINSV
TAEKLIYNCAVEMVQSAALDEMFOQTEDIVYRYHKAALLLEGLSKILQDPTDVENVHXYK
CSIERRLSALCCSTATV

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

METVGD FEYSRKDLIGHGAFVVFGRHKKKTDWEVAIKSINKKNLSKSKQILLGKEIKIL
KELQHENIVALYDVQETPSSVFLVMEYCNNGDLADYLQAKGTLREDTLRVFLQQAIAAAMR
ILNSKGI IHRDLKPQNILLSYTGKSSINGIRIKIADFGFARYLQSNMMAATLCGSPMY
MAPEVIMSQNYDAKADLWSIGTVIYQCLVGKPPFQANS PQDLRMFYEKNSLVPNIPRET
SPQLEDLLLGLLQRNQKDRIDFDFFFHSHPFLEPISTIKKSCVPVPVPSGLVSDSTCGSS
PSCRYVSPPLPDMQTLPELVLSPPPLGPPNYLQLSKESGGSTSSKNSSCDTDDFVLPVPH
LSGEQSYDLPMAVAVRRPSSEFLLCGGSPQSTGQTPMVSPRSETTPIPVPTQVRNYQRI
KQNLSSSPTTTLYGSPRSGTVRRSNTSPMGFPKMVSASPSPADTVQTVGRRLLSTGSSRPY
SPSPLVGTIPEQLGHCCCGHPQSHEPRSRSSSGGSPVPSQLLGARLQSAPTLTDIYQSK
QKLHKQLSDPVHPTSSAYPSNHSPQLGRPANLGTSPTKHLGSSPRTSDWLTKSPLPTIIG
SPTKVTA PFKI PKTQASCNLMALADSPIPNKTLMDGRELCAHHTAYPSSRQPAPEASKT
SFGRSVSAGRLSEPPVRLITGGQPYQGSTDSLNTERPMDTAPAGMCALAAGGGSPRTVVF
TVGSPSSSTPPTCSHLASRPRATSVGSNSAGSLCSTSGKVYMGSPPGMTIGSSPPGAE
AGPSSLRYPYGTSPPSLDGFITFEAPELPEETLMEREHTDTLMYLRMMLSFTDCVLEIA
ALRAGGPD LGASAASLYPPQDSVVDQISQLSREWGQVEQLVLYMKAQAQLLASSLHLAKA
QIKSAKLN PSTAVKQVVKSLNERYKSCISLCRRLTDKLNHFFSDKQRFVDEINSVTAEKLI
YNHAVEMVQSAALDEMFOQTEDIA YRYNKASMLLEGLTKILQDPADIENVIKYKASVDR
RISALCYCTVTLYE

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

MESIGDFEYNKRDLIGHGAFVVFGRHKVTHDPVAIKSITKKNLAKSQNLLSKEIKILK
ELSDLHHENVALLDCKETTHHVYLVMEYCNNGDLADYLQAKGTLSEDTISGFLRQIAGA
MRALNGKGI VHRDLKPQNILLTHSGQSPNPQPSDLQLKIADFGFARFLNDGVMAATLCGS
PMYMAPEVIMSVQYDAKADLWSIGTIVFQCLTGKAPFQAQTPQQLKAFYEKNANLAPNIP
SGTSKELRDLLMKLLKRNADRIDFDEFFSHPFVCPAKASSVPVPPQRRARHPSDSPTLK
TVSSSPLSGNVYPVNTDVQRVQKQEDVSESPQEGADFKVVDKSKSGSPAEDFVLPVNNL
GGESEGSASSGRSKEKSPKHGRKDSQPSAQRVVRVDTTTEAASFRKGNAGSPSPQDQTS

TRPTSLPVIKQTSPPSQPIPVPTQVEAYQRIQKNSPSSPKEPRTKEAGTHVMSPQRELAS
QAVPIPRIASDRMVSVGSFPDIRSVSPSVQFHIGTPPSKNIRRNSIEVSPGRPNTATPP
NGSPLRKSQAQSNSSPFGSPASLPKPSVMSVAQRFTVTNYPAGGRDVVALARTRTVPEGV
QAMTTVAGAAYPDYATWPRRLDTTGLAPSQTEPSNLQRTTSSGGHLAPTRIGEQLMKAAFG
QTTRGLSNQIPANSVVPYRERNSQSESGQRERRDSFQKRDSFTREERQDSTGRERSGSSPP
NSLPYAQSPPNMEGPILFEAPELAEETLMDSEHNETVAKLTFVLALVETIIELAQKRSTP
LTQSISPPQRRDGGSEQVKFLSESQRRMEQLVLHVKALQLLSASLQLAKEEIKAGKLMPS
NTVKNILKEMNNHYHRCMGISKQLKSCNINDNELKSFSTADKLIYNYAIEMCQTAALDE
LFGNPQECFRMYKNAQIILLHALAHQAQHNKDKDMLNKYKEAVEKRLFSLSQSQGLNYFQYE
N

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

MEHIDEYEYNNKKDIIHGAFIVFRGRERKRPDQTVAIKCKINKKNLSKSKQTFPEKEIEILKELHHGNVVS
LLHFKEETSSLFMVMEFCNGGDLADYLLHIKGTLS EDTIRFFLGQIACAMKAIHEKGIHRDLKPNLLLS
HNSKHKVPHPNEIHLKIIDFGFARFLLEGDMMAATLCGSPLYMAPEVITSQHYDAKADLWSIGTII FQCLT
GSAPFKAANPPPELKKLYMKARTLDPNIPPGTSKALKDLLIRLLKRNQKDRIEFDKFFSHDFLGKNLKSTS
TSPMPVPSRTYSFSSDSPGERRSLSVSPLSGHMPISSEPEEPSVSGCGPRGYSISPLAAPPListDRPS
AAKGLQEKLRLLSSGMGSSDLVEDDFVIVQPSIVSELSYETSGASINVQTTDVTITRSNSSPIMSSSRGH
SAQPKSSTSPVSGRIMAAVVRKLPSPSERPSSLPISSSPSTSPNTGRHRVSPKQSPSSLI SPSRIHAQI
RHSYSSSGSPIGSPSQRRRLSPNQSPSLARHCILAQAGVDNKPPSPVQVTGLSSPGSQYNPGVVHKF
YKFHASPTSPSPSPPHI PRVSTDPMSCSQAGLYRGSSPQSQSGTSPTNIPSPARRKLSSPARSSPQFF
TGPSSLPTIAGSPTKKGFNEITFTIGTHGISPSEPLNMPFAKSRVRASSCCLEGGQDDISDSPGRDA
LIPRSASSRLLSEPLCLKAAFDNLAMNPGSSIEGIPGAI AASPPMHPTSFFIGSQRRNSVLTEGSPSSQ
GSLTFATSPPNMEGPISFVAPPELPEETLLAAEHTETVDRLNVILGIVEAIVEVAKRSRVP LAES IYNQGS
SIFSNSQVCFVSENYRLAEQLVLYTRSLLELLNAALTMAKEEFAARLKPSNAVRTVLQELNRYVHLCCLIK
SRQLCEGSPLQSLDIDLNSAMITADKLMYSYAI EQCQSAGMDEMFGNTQECLQRYRTAQMLLHGLCLQAG
TDHDRNLLLKFKNALDQRLFLERQQTPTVPMIGL

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

MEVVGDFEYSSKKDLIGHGAFVVFVKGRHRKKTDEVAIKSINKKNLSKSKQILLGKEIKILKELQHENIVA
LYDVQEMPSSVFLVMEYCNGGDLADYLQAKGTLS EDTIRVFLQQIAAAMRILHSGKGIHRDLKPNILLS
YASRRKSSVSGIRIKIADFGFARYLHSNMMAATLCGSPMYMAPEVIMSQHYDAKADLWSIGTVIYQCLVG
KPPFQANSPQDLRMFYEKNRNLIPIPIPRETSTYLADLLGLLQRNQKDRMDFEAFFNHPFLDQISTVKKS
CPVPVPTYAGSVSGSSCGSSPSCRFA SPPSLPDMQHIQEENLSSPPLGPPNYLQVSKDSASTSSKNSSCD
TDDFVLVPHNISSDHSYDMP LGAAGRASSEFLMCGQSPLTISGSSGTVQKPSSTSSRSTASGTTNRHC
QPSVSPRSETAPIPVPTQLRNYQRIEQNLSSTASPVSNPHGSPRAGVVRNNTSPMGFMKMGSCSPIPGD
TAQGVGRRLSTGSSRPYSPSPLVGTIPEQLGHCCCGQLQGHESSRNRFAGSPIPPSQSPQSLMGARLQS
APTLDIYQNKQKLRKQHS DPVCP SYAGYGYSHSPQPSRPGSLGTSPTKHMGS SPRSSDWLFKTP LPTII
GSPTKATTPFKI PKTQASSNLLALANRQGSIDAPLQPKDITEPRDFSHFHSTQGSEKHAGEQHSKATFGR
SVSTGKLS DQVKTTLGGQLYQGSTDSLNTERPMDTAPAGAYGIAVAPP SMGSGASSRAVMFTVGSPPSS
ATPPTCTHMVLRTRTTSVGSNSGGSLCSTSGRVYMGSPPGIYMGSSPPGAEAAPSLKYMPYGTSPPSLE
GFITFEAPELPEETLMEREHTDTLRHLNMMLTFTTECVLDTALRGGNPDLC T SAVSLYQIQESIVVDQIS
QLSKEWQVEQLVLYMKAQQLLASSLHLAKAQVKLGKLN PSTAVKHVVKSLNERYKFCIGMCKKLTEKLN
RFFSDKQRFIDEINSVTAEKLIYSCAVEMVQSAALDEMFOQTEDITYRYHKAALLLEGLTKILQDPADIE
NVHKYKSSIERRLSALCCSTVAVYEQ

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

MEVVGDIYEYSSKKDLIGHGAFVVFVKGRHRKRNPHVVAIKSITKKNLAKSQNLLSKEIKILKELSDLHHEN
VVALLDCKETT NHVYLVMEYCNGGDLADYLQAKGTLS EDTIAAFLRQIAAAMQVMNGKGI VHRDLKPN I
LLCHDGKPNTPSTEMRLKIADFGFARFLNDGVMAATLCGSPMYMAPEVIMSLQYCAKADLWSIGTIVFQC
LTGKAPFQAQTPQQLKH FYEKHAELKPNIPKDTSPELRDLLLKMLKRNKDRIEFEDFFKHPFLKPPGQS
AAASSSPVPVPGRTSQGCSSESPTPPRCVSASPLSGKAEYSTPPSKVVQMVKQOEVAEAMQGS SHDEEFL
KVDKGPTRSNSPTEHDFVLVPGGMSDQSDGSDKGRVPSS EDLPGLGERAQPVVRVPEQAGSVAFFKDT
VDVPSRSPSSLPMTQNTQNSEPIPVPTQVKAYERIRSSSSPLSSPRKFGAVEVSPVDPALSSQNIKMS P
QPESKFSAPDIGSFPPTGTLKFCVGTTPPNVSTPWRRSIGSSQGAQYHPPSNASNSP SRRASMGSSPL
GFNRNFTSPGSLPTILDASPHFELNQEPQITDNMPTVPVRAPFGQSKPKAIPESKGTKRYNPSEVDRVKV
NLMERCNTDGAAGGLSMLSQOMKVAYMNQOGLNQLEGGVMRYTSNEQLVSPNENTVQMDTQORSGNLRR
TMSATTPPSNLMFAQSPPNMEGPVAFVAPGLAEETLMGDNHNEIMAKLSFVNDLADCVME LAMAKGAPLN
TLSESVNWKQEGEPLQGEPM PKFIEAQRLLEQLVLYVRS LQLLSSSLQLARREIKDERLQISNALKTLLK

QMNERYHRCVSVCKHIQQRLGITMQNALTPQVVIATADKLIYNYAIEMCQTAALDELFGNPQECFKRYNT
AHILLHLSLQQARNSENDKQLLDKYKDAVERRLSHIQATQNYYPQFEIS

3. ATG12

>MK069431|Ubiquitin-like protein ATG12 [organism=Crassostrea gigas] mRNA,
complet cds
MSDDGNESRDSKNTETEEKSTPASPISHVAETKIDVLLKPAGDAPIMKKKK
WAVDRNKRIGWVGEFIKKYLKLTAQDSLFLYVNQSFAPTPDTEIGSIFDC
FGSDGKLVLYHCKTQAWG

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

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

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

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

>tr|Q10931|Q10931_CAEEL Ubiquitin-like protein ATG12 OS=Caenorhabditis
elegans OX=6239 GN=lgg-3 PE=1 SV=1
METETATPTGNTPEPTAAASAEPKSDKVTVRLRNIADAPVLKNNKMMVVNPTDTPVASFIL
KLRKLLNIQANNSLFLYIDNTFAPSPDTTFETLSRCYSVKITDKEILELQYSITPAYG

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

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

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

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

4. ATG9A

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

MADYQTQYQPLASCEEDTDENDVPIHESANLMMHVPESTRWNHIENLDD
FFTRVYHYHQGGFVCMVSDVLQLIQFIFVVGSTFLLCEVNYDILFAN
SKNDTHKVTIPEAVAPFGQCVQEFDFGITVCLLVAFVFWFRLIKVLYNI
FKYWEIRSFYLTALHITTTDLTNMTWHEVQRRLLEVQKEQQMC IHKQELT
ELDIYHRILRFKNYMIAMERKSLLPFKHSIPLMGECAFYSIGLKYNLDFL
LFWGWPSPFENYWKLKDEFKIIYHKRQLAEELSKKILWIGIANFALSPLI
LLWQILYSFFRYADTLKREPSMLGSRWSNYARLYLRHYNELDHEFDARL
NRGYRLANKYMDIFTSQLIVILAKNVAFFAGSVLAVLVVLTVIDEDVLAV
EHVLTMTVAGLIVTACKVFIPEHLVYCEILMRNILAHVHYMPPDWSG
NAHTSKVRNEFSIFFQYKVAYLFEELLSPLVTPIVLCFSLRHKSMEIVDF
FRNFTVDVVGVDVCSFAQLDVRKRDNKMDRRDDEEPPQPSLRTNMFTPD
QSPSQEGKIQMSLMHFHLTNPEWKPPKECSLFINDIKEKANRNTTSLSIF
NPVTQNMVMSSQGLTGYLSGLQPSGAGALGESATDQYTSLASSIAIQSG
MYPQSTQVSMAPSVSGVHRLRGAISTAEGPLERSIGGPVGTMQGSTSMI
GSLGGYHSIGSSKPSVDEGSLELLSHDMSVSALYLHDFQSRKQRGQGM
GYENIEEMRARNLWQRQDSNQGPPVHAGMPNIQEKREEEKDSGNTETIAK
SV

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

MAQFDTEYQRLEASYSPPGEEEDLLVHVAEGSKSPWHHIENLDFFSRVYNLHQKNGFT
CMLIGEIFELMQFLFVVAFTTFLVSCVDYDILFANKMVNHS LHPTEPVKVTLPDAFLPAQ
VCSARIQENGLITILVIAGVFWIHRLIKFIYNICCYWEIHSFYLHALRIPMSALPYCTW
QEVQARIVQTQKEHQIC IHKRELTELDIYHRILRFQNYMVALVNKSLPLRFRLPGLGEA
VFFTRGLKYNFELILFWGPGSLFLNEWSLKAEYKRGQRLELAQRLSNRILWIGIANFLL
CPLILIWQILYAFFSYAEVLKREPGALGARCWSLYGRCYLRFHNELEHELQSRNLNRYKYP
ASKYMNCFLSPLLLAKNGAFFAGSILAVLIAITTYDEDVLAVEHVLTVTLLGVTVTV
CRSFIIPDQHMVFCPEQLLRVILAHIHYPDHWQGNHRSQTRDEFAQLFQYKAVF ILEEL
LSPIVTPLILIFCLRPRALEIIDFFRNFTVEVVGVDTCFAQMDVRQHGHPQWLSAGQT
EASVYQQAEDGKTELSLMHFAITNPGWQPPRESTAFLGFLKEQVQRDGAASLAQGGLLP
ENALFTSIQSLQSESEPLSLIANVVAGSSCRGPPLPRDLQGSRHRAEVASALRSFSPLOP
GQAPTGRAHSTMTGSGVDARTASSGSSVWEGQLQSLVSEYASTEMSLHALYMHQLHKQQ
AQAEPERHVHRRRESDESGESAPDEGEGGARAPQSI PRSASYPCAAPRPGAPETTALHGG
FQRRYGGITDPGTVPRVPSHFSRLPLGGWAEDGQSASRHPEPVPEEGSEDELPPQVHKV

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

MAQFDTEYQRLEASYSPPGEEEDLLVHVAEGSKSPWHHIENLDFFSRVYNLHQKNGFT
CMLIGEMFELMQFLFVVAFTTFLVSCVDYDILFANKMVNHS LHPTEPVKVTLPDAFLPAQ
VCSARIQENGLITILVIAGVFWIHRLIKFIYNICCYWEIHSFYLHALRIPMSALPYCTW
QEVQARIVQTQKEHQIC IHKRELTELDIYHRILRFQNYMVALVNKSLPLRFRLPGLGEV
VFFTRGLKYNFELILFWGPGSLFLNEWSLKAEYKRGQRLELAQRLSNRILWIGIANFLL
CPLILIWQILYAFFSYAEVLKREPGALGARCWSLYGRCYLRFHNELEHELQSRNLNRYKYP
ASKYMNCFLSPLLLAKNGAFFAGSILAVLIAITTYDEDVLAVEHVLTVTLLGVTVTV
CRSFIIPDQHMVFCPEQLLRVILAHIHYPDHWQGVHLGGVAESHRHTPHSHLLPPPSGPG
DHRLLPQLYGRGRGCRHLLLCSDGRSPAWPSSVAVWRADRLSVPASRGREDRVVAHAL
CHHQSRLAAPS

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

MAHFDTEYQRLEASYSPPGEEENLLVHVPEGSKSPWHHIENLDFQQRVYNLHQKNGFT
CMLLGEIFELVQLVVAFTVFLANCVDYDILFANKFVNHTDSLKVTLPAFLPVDVCSA
RIRDSVPVIFILVISGVFWLHRLVKFIYNICCYWEIRSFIYINALKISMADLPYFTWQEVQ
ARIVEIQKEHQIC IHKKESELDIYHRILRFKNYMVAMVNKSLPVRFRPLVLDGTVFYT
RGLKYNFELIFFWPGSLFENEWSLKSEYKRGGRLELADRLSSRILWIGIANLLLCPIVI
LIWQILYAFFSYTEVIKREPGSLGARCWSLYGRFYLRHFNELDHELMSRLSKGYKASSKY
MNCFMSPLLTVAVKNAFFAGSILAVLIAITTYDEDVLAVEHVLSITLLGVCITVCRSF

IPDKHMVFCPEQLLKVILAHIHYPMDHWQGNHRYETRDEFAQLFQYKAVFILEELLSPV
ITPFILIFCLRRKSLEIIDFFRNFTVDVVGVDTC SFAQMDVRQHGHPAWMSAGKTEASI
YQQAEDGKTELSLMHFAITNPHWQPPRESTHFI SLLKEKVHRDAAVGQQGI IAENAGFTS
THSLHNDSEPRSLIANLLMGPPSLASHLGREGSINHVSIGVSEGASALRSLSPVSTSLH
LRGSYPSARLPRSDHPAVVAGRGMAGSGTDARTISSGSSAWEGQLTSMILSEYASTEMSI
HALYMHMHKQQRGELSRHTWHRQESDESSES VNEDEVAARNFPRSSTFPCTTTSHQEG
AAAQQSGSQRQGGTSDPSSGSRVQRTPRMAMGGWSEENQTSRHHDVPVEEGSEDELPP
HIHKVT

>tr|A0A0B4KF86|A0A0B4KF86_DROME Autophagy-related protein 9 OS=Drosophila
melanogaster OX=7227 GN=Atg9 PE=1 SV=1
MSSPHINYSRLAEAAAPFLEHHPSTGQGPSKTQDAKANAAAAHLDPGEHGLEQPLDEH
DTEHEGEDTPRNSGVMIHMPETGRARWNHIEDLDSFFSRMYQYQKKGFTVIIVVDEMLQ
VLEFGFVWLLAFVMHCVRFDVLFGDTPPGGLNPNKTTLSDVMYPTGECLANFTWVYTLV
VFIAAIYLGIRLLKMYVHITQYADIKRFYNSALHIEDSDLNFTWHEVQQRIRRVQAEQH
MCIDKESLTELDIYHRVLRFKNYLVALMNKQLLPVRFHIPLEGEVVSLSRGMFLNIDFIL
FRGPGSPFQNNWQLRDEFVRSNQTELAQRLSKLILGVALLNLVLPVIFVWQLIYFSFS
YANILRKEPGALGLRTWSNYGRLYLRHFNELDHELDARLNRAYDYADRYLNSFSPLAAV
IAKNLLFISGGLLLLILALGIYEEHVQVEHLLAILAGLGAIGVVCRTLIPDENLVWCPE
QLMTAILAHVHYLPSEWRQQAHTTKVRQEFNSFFQFKAGYLLSEIFSPFVTPFVLI FVFR
PKAIELVRRFFRTFTVSVRGVGNVCSFAQMDVRKHGNPDWQLTSELEEMTRATAQQPQQEP
QQQSLAGGKTEMSLLRFTLNNPEWQMPKEAKQFLRGVREHAVGELVQAKTSMVQENPLTN
SLISFGTMGADYCSIANSVLTAQVTPQQLEISQSLRPLGVPVSGGFVAASDFRQMLQQN
LSASVGPLDSMRRLRLSRAEGRLEGPTDTLLYGLCGVDPVVGSTPLNVGVADMCLSALYL
HELNQQKRQARQSRIDEAEDERPGETSHWPPRPPAAPSADTGFGSRHTVITSKAAESTPLL
GSIRSXQRPEWI

>tr|E1BVB2|E1BVB2_CHICK Autophagy-related protein 9 OS=Gallus gallus
OX=9031 GN=ATG9A PE=3 SV=2
MAHLETQYQRLESSTESPPGGDLLVHVPEGAKSPWHHIENLDLFFSRVYNLHQKNGFT
CMLIGEIFELMQFIFVVAFTTFLISCVDYDILFANKAVNHSQHPSEPIKVTLPDFAFLPPN
VCSARIQANSFICILVIAGVFWIHRLVKFIYNICCYWEIHSFYINALRIPMSNLPYYTW
QEVQARIVQIQKEHQICIHKKELTELDIYHRILRKFKNYVMAMVNKSLLPPIRFRPLPLGDT
VFYTRGLKYNFELIFFWPGSLFENESLKAHEYKRAGNRLELAEKLSTRILWIGIANFLL
CPLILIWQILYAFFSYTEILKREPGLGARCWSLYGRCYLRFNELDHELQSRLSKGYKP
ASKYMNCFISPLLTIVAKNVAFFAGSILAVLIALTIYDEDVLAVEHVLTVTLLGVGITV
CRSFIIPDQHLVFCPEQLLRVILAHIHYPMDHWQGNHRYETRDEFAQLFQYKAVFILEEL
LSPITPLILIIICLRPKSLDIVDFRNFTVEVVGVDTC SFAQMDVRQHGHPAWMSAGKT
EASIQQAEDGKTELSLMHFAITNPKWQPPRESTAFIGFLKERVHRDSSVALAQAVLPE
NALFSSIQSLQSESEPHSLIANVIAGSSVLGFHMGRDQASRHLSEVASALRSFSPLQSA
QQPSGGFQTAGSSAMTASGADARTMSSGSSAWEGQLQSMILSEYASTEMSLHALYMHHELH
KQHAQLEPERHTWHRRESDESSESTHEELDAQRGAPVPLPRSASYPFSSRQPAEETATLQ
TGFQRRYGGITDPGTVHRAPSHFSRLPLGGWAEDGQSARHPEVPVEESSEDELPPQIHKV

>tr|Q3T903|Q3T903_CAEL Autophagy-related protein 9 OS=Caenorhabditis
elegans OX=6239 GN=atg9 PE=2 SV=1
MAETQNLQKIDNSSINLIFFQKKTHQMFNSSQSKRAYQQIDDDFDDEVLRNSTCTSRFMQ
GWGSSTRSLLFGGASNDEQRNLIASSSSHSHSYHDS PAEEPETHYEQFTATHNHGPPTMA
SSSQLNRRWDHVLNLDEFFTHIYEHQNGGYLCIVLQKVFSLLOQIFVMSFTTFFFTQCV
NYQFLFANTNVTSHGTVNQGRHFGDAVVDNCPAHISIWMIFAILAAIVYWITRVIKHAQ
YIMKMSIEIQFYAHELKIADDQLPNLTWHAIVKRICEAQKKLRLSIHQDNITSIYIYHRI
LRYKNYMTGMINKRILHPVFDVPFLGPIAYLPNNLKHEIERILFTSSTSAWTNGPNLREE
YKHHEQLDMAAKMKEDVINLFLQILRISVARPDASTAPIPDYGIVLLTDGAHKKTTTRWA
WNEKIQYLLRHFNELDHELSARLNRSIYAAAYMDQFFSPVLEIAAKNITFIAAAVFGVL
TILSAWDEDVLQVEHVITVLTICGIVVLVCRGMIPDENLVWQPEILMTHVTSELHYLPST
WKGKAHTTGVREHFDQLFQMKWMMFFVLELTSPIFTFVLLFWLRPRCSQLANFFHDYTER
VDGLGDVCSFAVMDVGKHGDPKWNHIKELKAIVEDQEDQQAQSVVTSLNRRARDGKTELS
ILHFKTTNPEWQPPKASEKFLRKFNRNLGQEA SMLAPLTSMHLGQMDRQQQQGKIGRNI
LLESVHSIVPTTSGGISASQVAPGRHPLIGDGLHRIDGPVGNAFQGIQGAKLGGGGVLAS
LYQEQPRAAESLSNSLRASGVDIDGAGAEMRINALFLRGLHDESIHSSSRNYGGTTSSF
NMHPTAMQSVFAMPDGFQPAVAESSLIDIETPTYHRESVQRSAAEHKMEHETPEPLAE
LPDLPGSSSEHQQRSLVPNTQHRQINEEEEEEEEEEDNTPPLSFSS

>tr|A0A087ZP33|A0A087ZP33_APIME Autophagy-related protein 9 OS=Apis mellifera OX=7460 GN=Atg9 PE=3 SV=1
MKRETVITCVEPNRRAKTMTTVDGSGYQRMPEYDGEEDGEDDDEHEETPQESGVMIHVV
PEGNKARWNHVEDLDSFFTRMYHYHQKHGFACMILQEALGQFIFVVFSTFLFHCINY
SLLFKNGKERRKISISDVLISKSECIASMGITWICILVAAIFWILRLVKVLYHCTQFWDI
KLFFNTALKIEDCDLNLTWHEIQKRVREVQKEQEMCIHKRELTELDIYHRILRFKNYMV
AMINKSLLPIRLKVPIIGEIIIFLTRGLKYNMELLLFWGWPSPFENNWHLKEDYKKNLKRQ
ELARALSKHILWVGIVNLLCPLILLWQILYSFFNYGEI IKREPGLGTRMWSLYGRLLYL
RHFNELDHELNARLNARYPASKYMSMFTSPIIMTVIAKNVAFVAGSILAVLLILTIVYDED
VLTVEHVLTITITILGAI VAGARAFIPDENLVWCPETLLTAVLAHTHYRPSWRGHAHTQT
TRAEVAQLFQYRAVHLLLEELISPLITPFILCFMRQRALDIVDFYRNFTIEVTGVDVCS
FAQMDVRKHGNPMWQTATQIPVQDRAAKYDNQYATDPEKLQIPISDQYTAEDGKTELSL
IHFTLTNPEWKPPSHAENFVTALRERVKKDVHGGGHEINPLLASLNSLSGLGPGYNDIIS
NIIRSTMINQASGPSTSTMFTNQPCCTTSVCTSGNEMLNMKSDIFPHAVQCGLSKAEGPVH
NEKGLLYGLQQEISNQSLGASVFSHEFSTDLSIPVELIAADMSLSTLYLHELHHRQVR
RRGYQELAMRSVWQRSVPQELATLPEVRQERAPLLHHQDSSIRNNREFKYNLNTRLDSI

>tr|A0A1S3JC03|A0A1S3JC03_LINUN Autophagy-related protein 9 OS=Lingula unguis OX=7574 GN=LOC106171792 PE=3 SV=1
MSEFTTSYQPLPASGYEEDVDTPHMETDVLIHVVPEESSKSRWNHIENLDEFFARVYQY
HQRNQFFCMVLEDVLQQLQFVVFVILFSSYLIECVKYDVVFDEIYRNNTGHKKVTIAESV
IPLDQCVSSVRPFVAICLLVAAVFVWLRLIKVVYNVLYWEIRAFYLTALKISADELPNL
TWHEVQKRVVEVQEQQMC I HKKELTELDIYNRILRFKNYQVAMVNKSLPLKYRIPFVG
DYVFLSTGLKYNLEMILFWGWPAPFENYWHLKQDFKNYHKRRELADYVVSQRILWLGLANL
ILSPLIFLWQILYSFFRYAEI IKRQPGSLGARRWSLYGRLLYLRHFNELDHEFEARLNRY
KPAEYMNIFTSPVLVILAKNVVFFAGAVLAVLIILTLIDEDTLQVENILRMMTILGAVV
AVCRAVIPAHEMVFCEFLMTHILKEVHYIPDSWKGNATHKVRQEFQQLFQYKALYLLE
ELISPLVTPILCF SIRHKAYDIVDFYRNFTVEVTGVDVCSFAQMDIRKHGNPQWVKEE
QTQADLYHQAEDGKAELSLMHFALTNPEWKPPENC SVFLNDIKDQAVNDANA AVVAPGDN
ALFTSLHTFALS PGGVYNSINISSVVPGPSMASAHSMRPLGTVPGPMSPPGGSHLRGA
GVAHAEGPLQSGGKILASLHSSGALSGSATGLGSGPTSLDTGHFLSSEVSQELSSAEMS
FSALYIHELHRRRRRQGGHRLEYLDFDGRPHVELQELGTRLTDFDLDPMPGHGGVVRGHMSNI
VESPQEEKSEEMSNEDAITFVSFDERVTKST

>XP_022310215.1 autophagy-related protein 9A-like isoform X1 [Crassostrea virginica]
MSGAMADYQTQYQALGSCDEDDTDETDAPTHESANLMIHVVPSTRWNHIENLDDFFTRVYHYHQGGF
LCMMVSDVLQLVQFLFVVGSTFLLECVNYDILFANSKNDTHKVTISEAVTPFGQCQVQEFDFGITVCLLV
ALAFWIFRTIKVLYNIFKYSEIRSFYLTALHISTAELSNMTWHEVQRRLLLEVQKEQQMC I HKQELTELDI
YHRILRFKNYMIAMERKSLPLKHKVPCLGECAFYSIGLKYNLDFLLFWGWPSPFENYWKLDKEYKVYHK
RKQLADELSKILWIGVANFALSPLILLWQILYSFFRYADTLKREPSMLGSRWSNYARLYLRHYNELDH
EFDARLNRYRLANKYMDIFTSELIVILAKNVAFFAGSVLAVLVVLTVIDEDVLAVEHVLTITMTVAGLIV
TACKVFI PDEHLVYCEPILMRNILAHVHYMPDPWTGNAHTSKVRNEFSMFFQYKVAYLFEELLSP IITPL
ILCFYLRHKSMEIVDFFRNFTVDVVGVDVCSFAQLDVRKRDKKTGEVEQEEEEDEPESLRTNMFTPVQS
PSQEGKIEMSLMHFHLTNPEWKPPKECSLFLNDVKEKAQRNTASLSIFHPVTQNMVNSSQGS LTGYLSGL
QPSGAGGLGESSTEQYTS LASSIAIQSGMYPQSTQVSMAPSVSGVHRLRGAISTAEGPLERSVSGNLGT
LTNMQASSTASMGVSGVMGYHSLGNSKPSVDEGSLELMSQDMSVSALYLHDLQSRRRRQGGHLYENLED
LRARNLWQRQDSNNPPPGASAGMYNIQEKKEEEEGGREGETSETITKTA