

Figure S1

1. Serine/threonine-protein kinase mTOR (mTOR)

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>tr|K1PYM7|K1PYM7_CRAGI Serine/threonine-protein kinase TOR OS=Crassostrea  
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LHKLLVVGITDTGELEEGVINIRTELEYSVGRNKEQAAKMLGHLVANAARLVRPYMEP  
ILNALIPKLKEPDPNPNVTISVLVAIGEQAQVSGTEMRKWMDPELLPILEMLQDSSSLQ  
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EKIPFRLTRMLINAMEVTGIDGNYKMTCESVMEVLRHKDSLMAVLEAFVYDPLLNR L M  
DTTAKGKTKTKDSYSGGSQE QADMLENV DINQTAHKRSAP EAASSVSGDNFQAEVINKKA  
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>sp|P42345|MTOR_HUMAN Serine/threonine-protein kinase mTOR OS=Homo sapiens  
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VVMEMASKAIGRLAMAGDTFTA EYVEFEVKRALEWLGADRNEGRRHA AVLVLRELAI SVP  
TFFFQVQV PFFDNIFVAVWDPKQAI REGAVAALRACLILTTQREP KEMQKQWYRHTFEE  
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VVGITDPDPDIRYCVLASLDERFDAHLAQ AENLQALFVALNDQVFEIRELAICTVGR LSS  
MNP AFVMPFLRKMLIQILTELEHSGIGRIKEQSARMLGHLVSNAPRLIRPYMEPILKALI  
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>sp|P35169|TOR1_YEAST Serine/threonine-protein kinase TOR1 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=TOR1 PE=1 SV=3

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TSCEYGFQVNTLECIHASLLVYKEILFLKDPFLNQVFDQMCLNCIAYENHKAKMIREKIY
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MRVLRDNKESLMAILEAFALDPLIHWGFDLPPQKLTEQTGIPLPLINPSELLRKGAITVE
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>sp|P32600|TOR2_YEAST Serine/threonine-protein kinase TOR2 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=TOR2 PE=1 SV=3

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LIPSSDIEVMRLAANTLGR LTVPGGTLTSD FVEFEVRTCIDWLT LTADNNSSSSKLEYRR
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LKVLGELS VVGKEMTRYLKELMPLIINTFQDQSN SFKRDAALTTLGQLAASSGYVVGPL
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2. Serine/threonine-protein kinase atg1 (ULK1)

>tr|K1QJ91|K1QJ91_CRAGI Serine/threonine-protein kinase atg1 OS=**Crassostrea gigas** OX=29159 GN=CGI_10022785 PE=4 SV=1
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>sp|075385|ULK1_HUMAN Serine/threonine-protein kinase ULK1 OS=**Homo sapiens**
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>sp|P53104|ATG1_YEAST Serine/threonine-protein kinase ATG1 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=ATG1 PE=1 SV=1
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3. Serine/threonine-protein kinase ULK2 (ULK2)

>tr|K1PNL8|K1PNL8_CRAGI Serine/threonine-protein kinase ULK2 OS=**Crassostrea gigas** OX=29159 GN=CGI_10015287 PE=4 SV=1
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PMYMAPEVIMSLQYCAKADLWSIGTIVFQCLTGKAPFQAQTPQQLKHFY EKHAELKPNIP
KDTSPELRDLLLKMLKRNADRIEFASPVVPGRASQGCSSSPTPPRCVSASPLSGKAD
YSTPPSKVVQMVKQQEVAEAMQGSTHDEEFLKVDKGPTPRSNSPTEHDFVLVDPGMSDQS
DGS DKGRAPSTEDLQSLGERAQPQVVRVEPQVGSVAYKKDSDGVSSPSRPSLPMQSNQ
SEPIPVPTQVKAYERIRSSSSPLSSPRKCGTEPSPLDSAKLSSQNIKIS PQPESKFSAPD
IGSFSPTVKFVSVGTPPNVSTPWR RGSIGSSQGGAIYHPPSNASNPSRRASMGSSPSGF
NRNFSSPGSLPTILDASPHFELNQEPQFTDNMPTVPVRAPFGQSKPKAIPESKGT KRYHP
SEVDRVKLNLME RCNTDPGAAGGMSMLSQQMKVAYMNQQGLNLLLEGQVVRYT SNENLVSP

NDNTVQMDTQRSGLRRTMSATTPPSNLMFAQSPPNMEGPVAFVAPGLAEETLMGDNHN
EIMAKLSFVNDLADCVMELAMAKGAPLNTLSESVNWKQEGEPLHGDQMPKFIEAQRLLLEQ
LVLYVRSLLQLSSSLQLARREIKDERLQISNALKTLKQMNERYHRCVSVCKHIQQRLGI
TMQNALTPQVVIATADKLIYNYAIEMCQTAALDELFGNPQECFKRYNTAHILLHSLSQQA
RNSNDKQLLDKYKDAVERRLSHIQATQNYYPQFEIS

>sp|Q8IYT8|ULK2_HUMAN Serine/threonine-protein kinase ULK2 OS=**Homo sapiens**
OX=9606 GN=ULK2 PE=1 SV=3
MEVVGDFEYSKRDLVGHGAFVFRGRHRQKTDEVAIKSINKKNLSKSKQILLGKEIKIL
KELQHENIVALYDVQELPNSVFLVMEYCNNGDLADYLQAKGTLS EDTIRVFLHQIAAAMR
ILHSGKGIHRDLKPQNILLSYANRRKSSVSGIRIKIADFGFARYLHSNMMAATLCGSPMY
MAPEVIMSQHYDAKADLWSIGTVIYQCLVKGPPFQANSQDLRMFYEKNRSLMPSIPRET
SPYLANLLLGLLQRNQKDRMDFEAFSSHFPFLEQGPVKKSCPVPVPMYSGSVSGSSCGSSP
SCRFA SPPLPDMQHIQEENLSSPPLGPPNYLQVSKDSASTSSKNSSCDTDDFVLPVPHNI
SSDHSCDMPVGTAGRRASNEFLVCGGQCQPTVSPHSETAPIPVPTQIRNYQRIEQNLST
ASSGTNVHGS PRSAVRRSNTSPMGFLRPGSCSPVPADTAQT VGRRLSTGSSRPYSPSPL
VGTIPEQFSQCCCGHPQGHDSRSRNSSGSPVQAQSPQSLLSGARLQSAPTLTDIYQNKQ
KLRKQHS DPVCP SHTGAGYSYSPQPSRPGSLGTSPTKHLGSSPRSSDWFFKTP LPTIIGS
PTKTTAPFKI PKTQASSNLLALVTRHGPAAEQSKDGNPRECAHCLLVQGSERQRAEQQS
KAVFGRSVSTGKLS DQQKTPICRHQGSTDSLNTERPMDIAPAGACGGVLAPPAGTAASS
KAVLFTVGSPPHSAAPTCTHMFLRTRTTSVGPSNSGSLCAMSGRVCVGSPPGPGFGSS
PPGAEAAPSLRYVPY GASPPSLEGLITFEAPELPEETLMEREHTD TLRHLNVMLMFTCEV
LDLTAMRGGNPELCTSAVSLYQIQESVVVDQISQLSKDWGRVEQLVLYMKAQAQLLAASLH
LAKAQIKSGKLS PSTAVKQVVKNLNERYKFCITMCKKLTEKLNRFSDKQRFIDEINSVT
AEKLIYNCAVEMVQSAALDEMFOQTEDIVYRYHKAALLLEGLSRILQDPADIENVHKKYC
SIERRLSALCHSTATV

4. serine/threonine-protein kinase ULK3 (ULK3)

>XP_011415026.1 PREDICTED: serine/threonine-protein kinase ULK3
[**Crassostrea gigas**]
MSRPTSGRPSTAKSVAVIVPKLSGFVFTEKLGSGTYAVVYKAYRKSGSRQVVAIKCVLKSSLNKASTENL
LTEIEILLKKNLHNENIVRLEDFQWDDQYIYLIMEYCSGGDLNFIIRSKRTL PENILKRFLQQIAKAMRYLR
EFNIAHMDLKPQNILLTSEYNPTLKIADFGFSKHLFKGDELHAMRGSPLYMAPEIICKGTYDSRVDLWSI
GVIIYECLFGRAPFASRTFKELENKIWDSKPV EIPYGVNVSENCRD LILRLLRRDPDERITFDEFNHPF
VDLEHCASNESLSKAVNIVANAVKKDQNGEYKEAIKLYCDSLGHFMPAIIHYEKDERKKEAIRAKVKDYMN
RAEELKMLKPKRPPPPVNGVKRTISEDPMEE TELCKDNEELTAAVTLIRAADTENSQEDYEQALKHYE
LALSTFIKFLKEEKPGHRKDLIGKLSRSWMDEAEKIKMFLDVQNLQTEDTSAKEEENEKKYLYTEKCGIQ

>sp|Q6PHR2|ULK3_HUMAN Serine/threonine-protein kinase ULK3 OS=**Homo sapiens**
OX=9606 GN=ULK3 PE=1 SV=2
MAGPGWGPPRLDGFILTERLGS GTYATVYKAYAKD TREVVAIKCVAKKSLNKASVENLL
TEIEILKGI RHPHIVQLKDFQWSDNIYLIMEFCAGGDLSRFIHTRRILPEKVARVFMQQ
LASALQFLHERNISHLDLMPQNILLSLEKPHLKLADF GFAQHMSPWDEKHVLRGSPLYM
APEMVCQRQYDARVDLWKGQVILYEALFGQPPFASRSFSELEEKIRSNRVIELPLRPLLS
RDCRDLLQRLLERDPSRRISFQDFFAHPVWDLEHMPSG ESLGRATALVVQAVKQDQEGDS
AAALSLYCKALDFFVPALHYEVDAQRKEAIKAKVGYVSRAEELKAI VSSNQALLRQGT
SARDLLREMARKPRLLAAL EVASAAMAKEEAAGGEQDALDLYQHSLGELLLLLLAAEPPG
RRRELLHTEVQNL MARAEYLKEQVKMRESRWEADTL DKEGLSESVRSSCTLQ

5. Serine/threonine-protein kinase ULK4 (ULK4)

>tr|K1QQA6|K1QQA6_CRAGI Serine/threonine-protein kinase ULK4 OS=**Crassostrea gigas**
OX=29159 GN=CGI_10017902 PE=4 SV=1
MENFVLYEELGRGDNSIIYKGRRKGTINFVAIHCI EKCRPEVTNTV RMT HDISHPNVVK
FYEWYETS NHLWLVLV LCTGGSLATLITQDRNL PESSIRSF GIDLVTGIHYI HSLGILFC
DLRPTKILLDGSGLTKYADFGLSRVEGEILEELFEKFADAGEMWSNEADLDDNPLSKKYK
TTGAPTYMSPEGFQSQEITILSDLWLSLGC VLYEMFTGHPPFLAESFQQLKEKILHKELPP
PKVKGSRFSSKPSDFHNLLEGLLQKDPDKRMGWPGLVNH SFWQGRLSHLAKDLVTSQEV
RSSIVNTTRSSVLVEGTASALGRIKTVDLKKSMDR PVSTLETEGTRPGSTMGDYMRPKTA
PGNEGGSTLFTLSTRPPTAVPPDEKLAPTQKPTQSPLSTRETVRETIGTTGGESQADETKN
EAELEIYHHSDFHITPIVDNTKI QKPGA AKFDAKILVPP PFTA EKMANMSEKELSKHIKA

IIDGLSINEKGPPSQKRIHLLHYLTGLSTNPQVATALTRNNVLSVLAKVVKETQHLDVKT
KAARVVGLIAGNAEDLDESVTISESIATLTEVIRENVKNGKLGQVLPVAVGELLYFVAQQ
EVKHGKTCDNWSVTSMTYTVITRCCREGEDAVVNHIAAKTVENVVATQSTHAQKFSNEM
GQSLWYIFKHSTVDSLRI TALNALCRITHHNPTVFQSVIDTVGMTTILSALSFGITRIQQ
SIVTMFGALIASGQSLNRVVQDKDFLOKLI RLLDSPSVVIRAKAFVVIHEVVKNNDLLL
NSCQSRVLMYIERDSRRQTPREGKAPENNGSESVEYLMQCLDLLINHMVDVVPRLFKEIV
TSLDAV MGRKHPNAVQAKQLRSSPLIHVFLHLVTSQVFRPKIVNEEFIKNLSSVLSHIK
SIELGETNIEGASGISPSDFVTTTMSVLEGISQHPMIVA EYHQVILESVLP IADLVVS
QNGETRALSRLRFSEIASVYLNQEYAAAGEKMMNVAGLHKI IITERLLPQFEQILLDQEPL
PSYGLKLLLLDQNGGFVKQFEQQGLVSVIFQVMMDHQSNPLNSSMQSIAGILNCLVAH
KDTNMKDLYEQGLIDYFTTFFDVTTACLDTEDHADNKIAHSMQLNLLD TLHSMFKYVSE
VVRKALQNKKAGGEGGNREAEAEQ LLLTNKSLD LTTILTQLLCFEDTDIQDFSTKCLS
LLVQLFGGENKDSMTPENMEYYSKALKKSDAKKQKVLLRI IKRLLSTERVHVESMKQHGE
TLANTIRNLVQTASSHADVAISSLAADILKMTVPQEYYSKALKKADAKKQKVLLRI IKRL
LSTERVHVESMKQHGETLANTIRNLVQTASSHADVAISSLAADILKMTDIVLPGMEAF TM
ADQNDIRVKNQDFVGCYMDQEPRTLNEKMTVSTTMTVDS CRKTC TDLKFKYYGVEYSAQC
FCGNQPLNVRKMRREGDCLKPCAGDRTQACGGSWRIAVYENPQNI PKFVGCYMDQQARTLN
EKMTVSTTMTVDS CRKTC TDLKFKYYGVEYSSQCF CGNQLMNVRKMRREGDCLKPCDGDRT
QACGGNWR IAVYENPLYIPKFVGCYVDQTYRTLGEKMTVSTTMTVDS CRKTC TDLKFKYY
GVEYSSQCF CGYDLIHAIKVSEEDCLRPCSGDRTQACGGSWRIAVYENPRYISREYEEEN
NVEFVGCYVDQARTLNGKMTTSTTMTVYNCRKTCTDLKFMFYGVEVKKAGRKGGNQKAE
HMFPTKSLTDMTTILTSWELLFEFCFCGNKLTITTKMRDGDCLKPCTGDKTQACGGDWRI
AVYENPYITPPKFVGCYMDQQARTLNEKKT VSTTMTVDS CRKTC TDLKFKYYGVEVNICR
ICWLLHGSTSQNLERKDDCLYNNDSGQLPKNVYGVSEV

>sp|Q96C45|ULK4_HUMAN Serine/threonine-protein kinase ULK4 OS=**Homo sapiens**
OX=9606 GN=ULK4 PE=1 SV=2

MENFILYEEIIGRSKTVVYKGRRKGTINFAVAILCTDKCKRPEITNWVRLTREIKHKNIVT
FHEWYETS NHLWLVLVVELCTGGSLKTVIAQDENLPEDVVREFGIDLISGLHHLHKLGLIFC
DISPRKILLEGPGTLKFSNFCLAKVEGENLEEFFALVAEEGGGDNGENVLKKSMSKSRVK
GSPVYTAPEVVVRGADFSISSDLWSLGLL YEMFSGKPPFFSESISELTEKILCEDPLPPI
PKDSSRPKASSDFINLLDGLLQRDPQKRLTWT RLLQHSFWKKA FAGADQESSVEDLSLSR
NTMECSGPQDSKELLQNSQSRQAKGHKSGQPLGHSFRLENPTEFRPKSTLEGQLNESMFL
LSSRPTPRTSTAVEVSPGEDMTHCSPQKTSPLTKITSGHLSQODLESQMRELIYTDSDLV
VTPIIDNPKIMKQPPVKF DAKILHLPTYSVDKLLFLKDQDWNDFLQQVCSQIDSTEKSMG
ASRAKLNLLCYLCVAVAGHQEVATRLLHSPFLQLLIQHLRIAPNWDIRAKVAHVIGLLASH
TAE LQENTPVVEAIVLLTELIRENFRNSKLLKQCLLPTLGLIYL VATQEEKKNPRECWA
VPLAAYTVLMRCLREGEERVVNHMAAKI IENVCTTFSAQSGFITGEIGPILWYLF RHST
ADSLRITAVSALCRITRHSPTAFQNVIEKVLNSVINSLASAI CKVQYMLTLFAAMLSC
GIHLQRLIQEKGFVSTIIRLLDSPSTCIRAKAFLVLLYIL IYNREMLLLSCQARLVMI E
RDSRKTTPGKEQQSGNEYLSKCLDLLICHIVQELPRILGDILNSLANVSGRKH PSTVQVK
QLKLCPLMPVVLHLVTSQVFRPQVVTEEFLFSYGTILSHIKSVDSGETNIDGAIGLTAS
EEFIKITLSAFEAI IQYPILLKDYRSTVV DYLPLVSLVQSQNVEWRLFSRLRLSETTS
LLVNQEFQDGKEKASVDSNLLALIRDVLLPQYEHILLEPDPVPAYALKLLVAMTEHNP
TFTRLVEESKLIPLIFEVTLHQESILGNTMQSVIALLSNLVACKDSNMELLYEQGLVSH
ICNLLTETATLCLDVDNKNNNEMAAPLLFSLLDILHSMLTYTSGIVRLALQAQKSGSGED
PQAAEDLLLLNRPLTDLISLLIPLLPNEDPEIFDVSSKCLSILVQLYGGENPDSLSPENV
EIFAHLT SKEDPKQKLLLRILRRMITSNEKHLES LKNAGSLLRALERLAPGSGSFADS
AVAPLALEILQAVGH

6. Autophagy-related protein 13 (ATG13)

>tr|K1QIF8|K1QIF8_CRAGI Autophagy-related protein 13 OS=**Crassostrea gigas**
OX=29159 GN=CGI_10016010 PE=3 SV=1

MSKLSQQDRKDLEKFTKFLIYKSLQIIVQSRLGEKIQA KSKPFFSSGADWFNLAIKDIVEV
HNETKKALVSQTALLSQNVCEISLKTSEGDSMVLETWYIGLNKETCDVNARISYTVYNR
MGIALKTLFSISRVTPAYKLSRQQGANADEYVICYRFYQGDQPFFMLGDNYQTIKVGSV P
TPVGTIYINLAYRTKLLITPQKSCAIP IEVKDDHFKKDNSPRRPTTPKPCSLGFRRNST
SEDLFGDGVGDQDL CSTTFD NSPGEAFL LGMTQHGLVPPNIQQKTALKTDNRENNEAPKK
QENVEKQLSFTSYQKVGAFQAQNRNSKEINNTDLEDVFPFLNLLQAE GKSEVKMTVQRELQ N
DIESNEQVSSNKSEEEKSLEQALSPSESISSNTSAPDDFVMVELKTPFAGADPNQDLGKF
YRECQGAPQLTMCSGETNVTEALAEISSQIQMFESNIEGFDDFVTSITESVTVE

>sp|075143|ATG13_HUMAN Autophagy-related protein 13 OS=**Homo sapiens** OX=9606
GN=ATG13 PE=1 SV=1

METDLNSQDRKDLDFKFKFFALKTVQVIVQARLGEKICTRSSSSPTGSDWFNLAIKDIPE
VTHEAKKALAGQLPAVGRSMCVEISLKTSEGDSELEIWCLEMNEKCDKEIKVSYTVYNR
LSLLKSLLAITRVTPAYRLSRKQGHEYVILYRIYFGEVQLSGLGEGFQTVRVGTVPV
GTITLSCAYRINLAFMSTRQFERTPPIMGIIIDHFVDRPYSSSPMHPCNYRTAGEDTGV
IYPSVEDSQEVCTTSFSTSPPSQLSSSRLSYQPAALGVGSADLAYPVVFAAGLNATHPHQ
LMVPGKEGGVPLAPNQPVHGTQADQERLATCTPSDRTHCAATPSSSEDTETVSNSSSEGRA
SPHDVLETIFVRKVGAFVNKPINQVTLTSLDIPFAMFAPKNLELEDTPMVNPPDSPETE
SPLQGSLSHSDGSSGGSSGNTHDDFVMIDFKPAFSKDDILPMDLGTFFYREFQNPPLSSLS
IDIGAQSMAEDLDSLPEKLAVHEKNVREFDAFVETLQ

>sp|Q06628|ATG13_YEAST Autophagy-related protein 13 OS=**Saccharomyces
cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=ATG13 PE=1 SV=1

MVAEEDIEKQVLQLIDSFFLKTLLICSTESSRYQSSTENIFLFDDTWFEDHSELVSELP
EIIISKWSHYDGRKELPPLVVETYLDLRQLNSSHLVRLKDHEGHLWNVCKGTTKQEIWMER
WLIELDNSSPTFKSYSEDETVDNELSKQLVLLFRYLLTLIQLLPTTELYQLLIKSYNGPQ
NEGSSNPITSTGPLVSIKTCVLDGSKPILSKGRIGLSKPIINTYSNALNESNLPAHLQK
KITPVWTKFGLLRVSVSYRRDWKFEINNTNDELFSARHASVSHNSQGPQNPQEQEGQSDQ
DIGKRQPQFQQQQQQPQQQQQQQQQQQQRQHQVOTQQQRQIPDRRSLSLSPCTRANSFEPQS
WQKKVYPISRVPQPFKVGSGISQSASRNPSNSSFFNQPPVHRPSMSSNYGPMNIEGTSV
GSTSKYSSSFGNIRRHSSVKTTENAEKVSKAVKSPLOPQESQEDLMDDFVKLLLEEKPDLT
KKTSGNPPNINISDSLIRYQNLKPSNDLLSEDLVSLSMDPNHTYHRGRSDSHSPLPSI
SPSMHYGSLNSRMSQGANASHLIARGGNSSTSALNSRRNSLDKSSNKQGMGLPPIFGG
ESTSYHHDNKIQKYNQLGVEEDDDENDRLLNQMGNSATKFKSSISPRSIDSISSSFIKS
RIPIRQPYHYSQPTTAPFQAQAKFHKPANKLIDNGNRSNSNNNNHNGNDAVGMHNDEDD
QDDDLVFFMSDMNLSKEG

7. RB1-inducible coiled-coil protein 1

>tr|K1QSI9|K1QSI9_CRAGI RB1-inducible coiled-coil protein 1 OS=**Crassostrea
gigas** OX=29159 GN=CGI_10019938 PE=4 SV=1

MELKLMKSLTVSQALIELKRKHEKEISEMISKLEKEKSDSLTAIHNSLQAEKQVAFNEA
VTKLSQDKDKVIEDLRAKEKDLLEQLSTDQETILKLNEEKSKLEDIKTRAMSHLSDKERE
YNAARRQLEDDLALTRQQLSQYQSQLQAMSTISVPSVMEISQIEDSSRIASLEDELKSKS
EKIAELQQKMEISMTTSTRHIAEDKVSITSCNVGDALFCLDDRHDQYVVFTIGSTLHF
LHTDCQDTLGLKPNPGETKKSWSVLAEITEKEYCQAKKPQNRFKVPVGTGFYRVKAKPWRP
ESGARGTSSTAST

>sp|Q8TDY2|RBCC1_HUMAN RB1-inducible coiled-coil protein 1 OS=**Homo sapiens**
OX=9606 GN=RB1CC1 PE=1 SV=3

MKLYVFLVNTGTTLTFDELTVQTVADLKHAIQSKYKIAIQHQVLLVNGGECMAADDRVC
TYSAGTDTNPIFLFNKEMILCDRPPAIPKTTTFSTENDMEIKVEESLMPAVFHTVASRTQ
LALEMYEVAKKLCSEGLVHDEHLQHGWAAIMANLEDCSNSYQKLLFKFESIYSNYLQ
SIEDIKLKLTHLGTAVSVMKIPLELCLTRHSYRECLGRDLDSLPEHEDSEKAEMKRSTEL
VLSPPDMPRTTNESSLTSFPKSVHEVSPDTADAESGKEIRESCQSTVHQDETTIDTKDGD
LPPFNVSLLDWINVQDRPNQDVESELVLRKCFDSMSRLDPRIIRPFIAECRQTIAKLDNQNMK
AIKGLEDRLYALDQMIASCGRLVNEQKELAQGFANQKRAENLKDASVLPDLCLSHANQL
MIMLQNHKLLDIKQKCTTAKQELANNLHVRLKWCFCVMLHADQDGEKQLALLRLVIELL
ERVKIVEALSTVPQMYCLAVEVVRKMFIKHYREWAGALVKDGKRLYEAEKSKRESFGK
LFRKSFLRNRLFRGLDSWPPSFCTQKPRKFDCELPDISLKDQLQFLQSFCEVQPFLLRVP
LLCDFEPLHQHVLALHNLVKAQAQSLDEMSQITDLLSEQKASVSQTSPPQSASSPRMESTA
GITTTTSPRTPPPLTVQDPLCPAVCPLEELSPDSIDAHTFDFETIPHPNIEQTIHQVSLD
LDSLAESEDFMSAVNEFVIEENLSSPNPISDPQSPPEMMVESLYSSVINAIDSRRMQDT
NVCGKEDFGDHTSLNVQLERCVRVAQDSHFSIQTIKEDLCHFRTFVQKEQCDFSNLKTCT
AVEIRNIIKVKCSLEITLKEKHQKELLSLKNEYEGKLDGLIKETEENENKIKKLGELV
CLEEVLQNKDNEFALVKHEKEAVICLQNEKDQKLEMEMIMHSQNCIEIKELKQSREIVLE
DLKKLHVENDEKLQLLRAELQSLEQSHLKELEDTLQVRHIQEFKVMTDHRVSLEELKKE
NQQIINQIQESHAEIIQEKEKQLQELKLVSDLSDRCKLEVELALKEAETDEIKILLEE
SRAQQKETLKSLEQETENLRTEISKLNQKIQDNENYQVGLAELRTLMTIEKDQCISEL
ISRHEEESNILKAELNKVTSLHNQAFEIEKNLKEQIIEQLSKLDSELSALERQKDEKITQ

QEEKYEAI IQNLEKDRQKLVSSQE QDREQLIQKLNCEKDEAIQTALKEFKLEREVVEKEL
LEKVKHLENQIAKSPAIDSTRGDSSSLVAELQEKLQEEKAKFLEQLLEEQEKRNNEEMQNV
RTSLIAEQQTNFNTVLTRKMRKENIINDLSDKLNKSTMQQQERDKDLIESLSEDRARLLE
EKKKLEEEVSKLRSSSFVPSYPVATAPELYGACAPELPGESDRSAVETADEGRVDSAMET
SMMSVQENIHMLSEEKQRIMLLERTLQLKEEENKRLNQRMSQSMSSVSSRHSEKIAIRD
FQVGDVLVLIILDERHDNYVLFVTSPTLYFLHSESLPALDLKPGEGASGASRRPWVLGKVM
EKEYCQAKKAQNRFKVPLGTFYRVKAVSWNKKV

>sp|Q12527|ATG11_YEAST Autophagy-related protein 11 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=ATG11 PE=1 SV=1
MADADEYSTAPTQOEITPLQTTATIINAISGECITTNVDFVSLDKFKQFIARKWKIPPD
QLLILLPYGNKLPSPMFKELLINRSFTLNDFYVYDRRLFSLVSKPTPTNLLTSKDSNPMN
SPNSNDLTETLEYLIKNSHISQYQGSDTIMIKPMPSPLEDADVDLSRLNYHSVTSLLTTN
LGWLSALEIDVHYFKSLIPDIIAHIKRIFDGLTVCSQYLKLYCFDVESLYNSNVQFLNQL
VDNGMTSKWEKCFNDTSLKLTALEGDSLQKFINIESLLENEKSVKILNHSINGKLNKIKR
EIDENASFRDIITVNIIDRLRQMFTPNESKFELEDQMAESFEVLVSEMRTRSRNVLDKEEE
EFNSQEFKLSMNVMLEKDKKESVKTLFTISQALYSQIGELIDLKKSLOKHAVAILGNIAF
TQMEILGIKRLLLNECNKDLLEYKKEVEFAQVEDLPLIYGLYLIIEKYRRLSWFQQILSF
ISNFNQDLELQKQNELRTRNKVKNFGSIATVFCEDLLSSSDFKRLNEYHSHTSPNDE
EDENENSIANYRQDLVKVSAIDNYMTQIKETDVSEPIIDLKSKTLFETKRFHIIYSNFK
NNNNNSNGNSISPEGSIALKSDDVVKGYKTRIKKLESLLHEFQYSDIGHWPQGVNLNTHL
KPFGRSATSINKKFLGASVLEPANISEVNIIDSVSQANHQIQELESNVDDLHQLQLL
KEENNRKSMQISEMGKKISDLEVEKTAYRETLTNLNQELARLTNEEQSHRTEIFTLNASF
KKQLNDIISQDNEKIEKLTGDYDDVSKSRERLQMDLDESNNKHEQEVNLLKADIERLGKQ
IVTSEKSYAETNSSSMEKGEKFETIPLAEDPGRENQISAYTQTLQDRIFDIISTNIFILE
NIGLLLTDFNNNNIQRVVKGLKKGTAQSNILDESTQMLDAHDNSLIKSPVFQKLKDEYE
LIKSVANGSEKDTQQSIFLGNITQLYDNKLYEVAVIRRFKDIETLAKKLTKENKIKRTLL
ERFQREKVTLRNFQIGDLALFLPTRENVNSVSGSMSSSTSSLSSSFSSVDLSTPPPLDAMS
IQSSPSVIHSNVINQASISGRDKNKLMRPWAAFTAFAEESTRYFLKDEKGLTKGKEWVGR
IVTLEHFVADSPSNPFRLPKGSVWFQVTAVVVSYQGV

8. Autophagy-related protein 101 (ATG101)

>XP_011447317.1 PREDICTED: autophagy-related protein 101 [**Crassostrea gigas**]
MNARSQVFELSVEGRQIEETVSSIFHTLLLQRTVGVKGFHYKQEGTYSIGTVGVEDVDCDFVDFTYVRVAD
TLDHMIKKDIALFRDTRLRSMNPGSGQISLEFYQKKRGRWPFPEPICPWEVWTVKLDILTLNNESESRQIC
REKLGEMLGERVITIAIDLNRHDYVPKMPNQTELDLIFDTSLPDVQPYLFRISHQTTGPSQSSVGTMRK
FIKDTLAL

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

9. Zinc finger FYVE domain-containing protein 1 (DFCP 1)

>EKC37743.1 Zinc finger FYVE domain-containing protein 1 [**Crassostrea gigas**]
MNSFSSAQSDHSQHSSIPDICLSAGNEMSSLEAQLAESIIDLNPDYDNI GDEDEFIKKLDSCSNEHVKV
SIFGNTGDGKSFTLNHTFFGGKEVFKTSSHQSSCTVGVWAAAFDPKEKVIIVIDTEGLLGITSNQNRMLL
LKILGISDIIYRTRAERLHNDMYQFLCESSAYTKHFSDELEATAKRCNKGVGDLTPAVIIFQETVNTN
VLGSSGTDSAEKFIWNTFRQLECPMHFKDLTYVGIRTGRPPTDFTQFQRTMSQHLQDKSNRAARQPAIVY
KTLKLNLDKFNGEVEKPLYGTFPDQLFSCSMKCLSCGEGCTRSNMHDTDSKAHETDKRCKYQHGFENKVF
LCKSCYLSGKEHVVIPKTSESRDSAWSGLIKYVWAGEVLECPSCGVIFRSRQNWYGNKEVEEIVHTEIRH
VWPDGYKMLQGTNNAARKVIDGFHYIADSITSVSGSKPTKMI SDWMNDRIAPEYWV PNSQISHCHQCSKEL
ETEQKHHCRACGKGFCDCCSSHRRRVPERGWGEMEVVCDKCYGGKKMSDSNDSTGSNSQVTARKVGEVV
TSAISVAASTLNYPIDMIKDTARPGYWTPDEQIKACYVCEELFGPKLRIHHCACGQGVCESCSPNKRPV
PLRGWDYPVIRICRCKINPKDRL

>sp|Q9HBF4|ZFYV1_HUMAN Zinc finger FYVE domain-containing protein 1 OS=**Homo sapiens** OX=9606 GN=ZFYVE1 PE=1 SV=1
MSAQTSPAEEKLNPLMCQESYACSGTDEAIFECDECCSLQCLRCEEELHRQERLRNHER
IRLKPGLVHPYCDLCKGLSGHLPGVRQRAIVRCQTCKINLCLECQKRTHSGGNKRRHPVTV
YNVSNLQESLEAEEMDEETKRKKMTEKVVVSLLDVENEIEIQVTNEEDFIRKLDCKPDQHL
KVVSIFGNTGDGKSHTLNHTFFYGREVFKTSPTQESCTVGVWAAYDPVHKVAVIDTEGLL
GATVNLSQRTRLLLLKVLAIISDLVIYRTHADRLHNDLFKFLGDASEAYLKHFTELKATTA
RCGLDVPLSTLGPAAVIFHETVHTQLLGSDDHPSEVPEKLIQDRFRKLGRFPFAFSSIHK
GTRTYNPPDFSGLRRALEQLLENNTTRSPRHPGVIFKALKALSDRFSGEIPDDQMAHSS
FFPDEYFTCSSLCLSCGVGCKKSMNHGKEGVPHEAKSRCRYSHQYDNRVYTCKACYERGE
EVSVPKTSASTDSPWMGLAKYAWSGYVIECPNCGVVYRSRQYWFNGQDPVDTVVVRTEIV
HVWPGTDGFLKDNNAQRLLDGMNFMAQSVSELSLGPTKAVTSWLTQIAPAYWRPNSQ
ILSCNKCATSFKDNDTKHHCRCACGEGFCDCSSKTRPVPERGWGPAPVVRVCDNCEARNV
QLAVTEAQVDDEGGTLIARKVGEAVQNTLGAVVTAIDIPGLVKDAARPAYWVPDHEILH
CHNCRKEFSIKLSKHHCRACGQGFCDCECSDRRRAVPSRGWDHPVVRVCFNCNKKPGDL

10. Autophagy-related protein 9A (ATG9A)

>tr|K1PLJ3|K1PLJ3_CRAGI Autophagy-related protein 9 OS=**Crassostrea gigas**
OX=29159 GN=CGI_10002035 PE=3 SV=1
MESNVTLRFDFGITVCLLVAFAIWFVRLIKVLYNIFKYWEIRSFYLTAVHITTTDLTNMT
WHEVQRRLLLEVQKEQMCIHKQELTELDIYHRILRFKNYMIAMERKSLLPFKHSIPLMGE

>tr|K1Q6P8|K1Q6P8_CRAGI Autophagy-related protein 9 OS=**Crassostrea gigas**
OX=29159 GN=CGI_10007875 PE=3 SV=1
MEIVDFFRNFTVDVVGVDVCSFAQLDVRKRDNKMDREEEEEEPQPSLRTNMFTPDQSPS
QEGKIQMSLMHFHLTNPEWKPPKECSLFINDIKEKANRNTTSLSIFNPVTQNMVSSQGS
LTGYLSGLQPSGAGALGYTSLASSIAIQSGMYPQSTQVSMAPSVSGVHRLRGAISTAEG
PLERSIGGPVGTMQGSTSMIGSGLGGYHSIGSSKPSVDEGSLELLSHDMSVSALYLHDLQ
SRKQRGQGMGYENIEEMRARNLWQRQDSNQGPPVHAGMPNIQEKREEEEEKDSGNTETIAK
SV

>tr|K1RCA8|K1RCA8_CRAGI Autophagy-related protein 9 OS=**Crassostrea gigas**
OX=29159 GN=CGI_10005289 PE=3 SV=1
MERLIVTVCKVFISDEHLVYCPEILMRNILAHVHYMPPDWSGNAHTSKVRNKLSPYFPNT
KFTLLFPASQIDGRGYFFRNFTVDVVGVDVCSFVQLDVRKRDNKMDRDEEKEHQPSL
RTNMFTLDQSPSQEGKIQMSLMHFHLTNPEWKPPKECSLFINDIKEKANRNTTSLSIFNP
VTQNMVSSQGS LTGYLSGLQPSGAGALGYTSLASSIAIQSGMYPQSTQVSMAPSVSGVH
HRLRGAISTAEGPLERSISGPVGTMQGSTSMIGSGLGGYHSVGS SKPSVDEGSLELLSHD
MSVSALYLHDLQSRKQRGQGMGYENVEDMRARNLLQRQDSNQGPPVHAGMPNIQEKREEE
EKDSGNTETIAKSV

>tr|K1QIH2|K1QIH2_CRAGI Autophagy-related protein 9 OS=**Crassostrea gigas**
OX=29159 GN=CGI_10003880 PE=3 SV=1
MEIVDFFRNFTVDVVGVDVCSFAQLDVRKRDNKMDDRYTSLASSIAIQSGMYPQSTQVS
MAPSVSGVHRLRGAISTAEGPLERSIGGPVGTMQGSTSMIGSGLGGYHSIGSSKPSVDE
GSPELLSHDMSVSALYLHDLQSRKQRLGQGMGYENIEEMRAKNLWQRQDSNQGPPVHAGMP
NIQEKREEEEEKDNSSAVMFIKAIYEGGVDFPSTGQTGVHAIIV

>sp|Q7Z3C6|ATG9A_HUMAN Autophagy-related protein 9A OS=**Homo sapiens** OX=9606
GN=ATG9A PE=1 SV=3
MAQFDTEYQRLEASYS DSPGEEEDLVHVAEGSKSPWHH IENLDLFFSRVYNLHQKNGFT
CMLIGE I FELMQFLVVAFTTFLVSCVDYDILFANKMVNHS LHPTEPVKVTLPDAFLPAQ
VCSARIQENGLITILVIAGVFWIHRLIKFIYNICCYWEIHSFYLHALRIPMSALPYCTW
QEVQARIVQTQKEHQIC IHKRELTELDIYHRILRFQNYMVALVNKSLPLRFRLPGLGEA
VFFTRGLKYNFELILFWGPGSLFLNEWSLKA EYKRGQRLELAQR LSNRILWIGIANFLL
CPLILIWQILYAFFSYAEVLKREPGALGARCWSLYGR CYLRHFNELEHELQSR LN RGYKP
ASKYMNCFLSPLLTLLAKNGAFFAGSILAVLIALT IYDEDVLAVEHVLT TTVTLLGVTVTV
CRSFIPDQHMVFCPEQLLRVILAHIHYPDHWQGN AHRSQTRDEFAQLFQYKAVFILEEL
LSPIVTPLILIFCLRPRALEIIDFFRNFTVEVVGVDTC SFAQMDVRQHGHPQWLSAGQT

EASVYQQAEDGKTELSLMHFAITNPGWQPPRESTAFLGFLKEQVQRDGAASLAQGGLLP
ENALFTSIQSLQSESEPLSLIANVVAGSSCRGPPLPRDLQGSRHRAEVASALRSFSPLQP
GQAPTGRAHSTMTGSGVDARTASSGSSVWEGQLQSLVLSEYASTEMSLHALYMHQLHKQQ
AQAEPERHVHRRRESDESGESAPDEGGEGARAPQSI PRSASYPCAAPRPGAPETTALHGG
FQRRYGGITDPGTVPRVPSHFSRLPLGGWAEDGQSASRHPEVPVEEGSEDELPPQVHKV

>sp|Q12142|ATG9_YEAST Autophagy-related protein 9 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=ATG9 PE=1 SV=1
MERDEYQLPNSHGKNTFLSRIFGLQSDEVNPSLNSQEMSNFPLPDIERGSSLLHSTNDSR
EDVDENDLRVPESDQGTSTEEEDVDEEQVQAYAPQISDGLDGDHQLNSVTSKENVLETE
KSNLERLVEGSTDDSVPKVQLSSEEEEDNEFINNDGFDDDTPLFQKSKIHEFSSKKSNT
IEDGKRPLFFRHILQNNRPQRDTQKLFSTSSNAIHDKDKSANNGPRNINGNQKHGTYFG
SATQPRFTGSPLNNTNRFTKLFPLRKNLLSNISVLNNTPEDRINTLSVKERALWKWANV
ENLDIFLQDVYNYLNGFYCIILEKILNICTLLFVVFVSTYMGHCVDYSKLPSTHRVSD
I I I DKCYSNSITGFTKFFLWMFYFFVILKIVQLYFDVQKLSLQNFYKYLNI S DDELQT
LPWQNVIIQQLMYLKDQAMTANVVEVKAKNRIDAHDVANRIMRENYLIALYNSDILNLS
LPIPLFRNTVLTKTLEWNINLCVMGFVFNESGFIKQSIKPSQREFTREELQKRFMLAGF
LNIILAPFLVTVYFVLLYFFRYFNEYKTSFGSIGARQYTPIAEWKFREYNELYHIFKKRIS
LSTTLANKYVDQFPKEKTNLFLKFVSFICGSFVAILAFLTVFDPENFLNFEITSDRSVIF
YITILGAIWSVSRNTITQEYHVFDPEETLKELYEYTHYLPKEWEGRYHKEEIKLEFCKLY
NLRIVILLRELTSLMITPFVLWFLPSSAGRIVDFFRENEYVDGLGYVCKYAMFNMKNI
DGEDTHSMDEDSLTKKIAVNGSHTLNSKRRSKFTAEDHSDKDLANNKMLQSYVYFMDDYS
NSENLTGKYQLPAKKGYPNNEGDSFLNNKYSWRKQFQPGQKPELFRIGKHALGPGHNI SP
AIYSTRNPGKNWDDNNNGDDIKNGTNNATAKNDDNNGNNDHEYVLTESFLDSGAFPNHDV
IDHNKMLNSNYNGNGLNKGGLVGLVKEYYKSDVGR

11. Autophagy-related protein 9B (ATG9B)

>sp|Q674R7|ATG9B_HUMAN Autophagy-related protein 9B OS=**Homo sapiens** OX=9606
GN=ATG9B PE=2 SV=1
MVSRMGWGRRRRLGRWGD LGPGSVPLLPMLPPPPPPSCRGPGGGRISIFSLSPAPHTR
SSPSSFSPTAGPPCSVLQGTGASQSCHSALPIPATPPTQAQPAMTPASASPSWGSHTP
PLAPATPTPSQQCPQD SPGLRVGPLIPEQDYERLEDCDPEGSQD SPIHGEEQQPLLHVPE
GLRGSWHHIQNLDSFFTKIYSYHQRN GFACILLEDV FQLGQFIFIVTFTTFLLRCDYINV
LFANQPSNHTRPGPFHSHKVTLSDAILPSAQCAERIRSSPLLVLVLAAGFWLVQLLSV
CNLFSYWDIQVFYREALHIPPEELSSVPWAEVQSRL LALQRSGGLCVQPRPLTELDIHR
ILRYTNYQVALANKGLLPARCLPWGGSAAFLSRGLALNVDLLFRGPFSLFRGGWELPH
AYKRS DQRGALAA RWGRTVLLAALNLALSPLVLAWQVLHV FYSHVELLRREPGALGARG
WSRLARLQLRHFNELPHELRLARLARAYRPA AAF LR TAAPPAPLR TLLARQLVFFAGALFA
ALLVLT VYDEEDVLAVEHVLTAMTALGVTATVAR SFIPEEQCQGRAPQLLQTALAHMHYL
PEEPGPGGRDRAYRQMAQLLQYRAVSLLEELLSPLLTPLFLLFWFRPRALEIIDFFHHFT
VDVAGVGDICSFALMDVKRHGHPQWLSAGQTEASLSQRAEDGKTELSLMRFSLAHPLWRP
PGHSSKFLGHLWGRVQQDAAAWGATSARGPSTPGVLSNCTSPLEAF LANLFVHPLLPPR
DLSPTAPCPAAATASLLASISRIAQDPSSVSPGGTGGQKLAQLPELASAEMSLHVIYLHQ
LHQQQQQQEPWGEAAASILSRPCSSPSQPPSPDEEKPSWSSDGS SPASSPRQQWGTQKAR
NLFPGGFQVTTDTQKEPDRASCTD

12. WD repeat domain phosphoinositide-interacting protein 1 (WIPI1)

>sp|Q5MNZ9|WIPI1_HUMAN WD repeat domain phosphoinositide-interacting
protein 1 OS=**Homo sapiens** OX=9606 GN=WIPI1 PE=1 SV=3
MEAEAADAPGGVESALSCFSFNQDCTSLATGTKAGYKLFSLSSVEQLDQVHGSNEIPDV
YIVERL FSSSLVVVVSHTKPRQMN VYHFKKGTEICNYSYSSNILSIRLNRQRLLVCLEES
IYIHNIKDMKLLKTL LDI PANPTGLCAL SINHSNSYLAYPGSLTSGEIVLYDGN SLKTVC
TIAAHEGTLAAITFNASGSKLASASEKGTVIRVFSVPDQKLYEFRRGMKRYVTISSLVF
SMDSQFLCASSNTETVHIFKLEQVTNSRPEEPSTWSGYMGKMFMAATNYLPTQVSDMMHQ
DRAFATARLNFSGQRNICTLSTIQKLPRLLVASSGHLYMYNLDPQDGGECVLIKTHSLL
GSGTTEENKENDLRPSLPQSYAATVARPSASSASTVPGYSEDGGALRGEVIPEHEFATGP
VCLDDENEFPPIILCRGNQKGTKQS

>EGA79032.1 Atg18p [**Saccharomyces cerevisiae** Vin13]

MSDSSPTINFNFNQTGTICISLGTSGKFKIFNCEPFGKIFYSEDSGGYAIVEMLFSTSLALVIGDQPAL
SPRRLRIINTKKHSIIICEVTFXTSILSVKMNKSRLVLLQEIQIYIDINTMRLLLHTIETNPNPRGLMAMS
PSVANSYLVPSPPKVINSEIKAHATTNNITLSVGGNTETSFKRDQQDAGHSDISDLDDQYSSFTKRDDAD
PTSSNGGNSSIIKNGDVIVFNLETLOPTMVEIAHKGIEAAMAI SFDGTLMATASDKGTIIRVFDIETGDK
IYQFRRTYATRIYSISFSEDSQYLAVTGSSKTVHIFKLGHSMSNNKLDSDSDSNMEEAAAADDSSLDTTSI
DALSDEENPTLAREPYVDASRKTMRMIRYSSQKLSRRAARTLGQIFPIKVTSLLESSRHFASLKLPE
TNSHVMTISSIGSPIDIDTSEYPELFETGNSASTESYHEPVMKMPVIRVSSDGYLYNFVMDPERGGDCL
ILSQYSILMD

13. WD repeat domain phosphoinositide-interacting protein 2 (WIPI2)

>tr|K1QZR2|K1QZR2_CRAGI WD repeat domain phosphoinositide-interacting
protein 2 OS=**Crassostrea gigas** OX=29159 GN=CGI_10011163 PE=4 SV=1
MNLATKTGDEQSDLLFVNFNDCTSLAVGTRTGYKLFSLSSVDKLEQIYDNESEIDICIVE
RLFSSSLVAIVSLSSPRKLKLVCHFVKKGTICNYSYSNSILAVRLNRQRLIVCLEESLYIH
NIRDMKVLHTIRDTPPNPHGLCAL SINNDNCFLAYPGSNQIGEVQIFDTINLRAVAMIPA
HDNPLASLAFNAQGTKLATASEKGTVIRVFSIPDGQKMFERRGVKRCVSIYSMAFSADS
LFLSASSNTETVHIFKLEVPKDRPAEQEPQGWGMYFGQALKSSATYLP SQMTEMFNQGRA
FATARLPNSGMHNVCALATI QKVPRQLVVSQDGYLYIYNLDPNEGGECLLRQHRLDGRA
GDSVPVEVTPDRPLTHPTSGTSYASSVKKPESSVPPESQPYQELEQGSTGEGEGTGLG
HLRLDDDNEFPMPMTHKSD

>sp|Q9Y4P8|WIPI2_HUMAN WD repeat domain phosphoinositide-interacting
protein 2 OS=**Homo sapiens** OX=9606 GN=WIPI2 PE=1 SV=1
MNLASQSGEAGAGQLLFANFNQDNTEVKGASRAAGLGRRAVVWSLAVGSKSGYKFFSLSS
VDKLEQIYECTDTEVCIVERLRFSSSLVAIVSLKAPRKLKLVCHFVKKGTICNYSYSNTIL
AVKLNQRQLIVCLEESLYIHNIRDMKVLHTIRETPPNPAGLCAL SINNDNCFLAYPGSAT
IGEVQVFDTINLRAANMIPAHDSPALAFDASGTKLATASEKGTVIRVFSIPEGQKLF
FRRGVKRCVSI CSLAFSMDGMFLSASSNTETVHIFKLETVKEKPPEEPTTWTGYFGKVL
ASTSYLPSQVTEMFNQGRA FATVRLPFCGHKNICSLATI QKI PRLLVGAADGYLYMYNLD
PQEGGECALMKQHRLDGSLETTNEILDSASHDCPLVTQTYGAAAGKGTYPSSPTRLAYT
DDLGA VGGACLEDEASALRLDEDESEHPPMILRTD

>AJV23610.1 Atg18p [**Saccharomyces cerevisiae** YJM1399]
MSDSSPTINFNFNQTGTICISLGTSGKFKIFNCEPFGKIFYSEDSGGYAIVEMLFSTSLALVIGDQPAL
SPRRLRIINTKKHSIIICEVTFPTSILSVKMNKSRLVLLQEIQIYIDINTMRLLLHTIDTNPNPRGLMAMS
PSVANSYLVPSPPKVINSEIKAHATTNNITLSVGGNTETSFKRDQQDAGHSDINDLDQYSSFTKRDDAD
PTSSNGGNSSIIKNGDVIVFNLETLOPTMVEIAHKGIEAAMAI SFDGTLMATASDKGTIIRVFDIETGDK
IYQFRRTYATRIYSISFSEDSQYLAVTGSSKTVHIFKLGHSMSNNKLDSDSDSNMEEAAAADDSSLDTTSI
DALSDEENPTLAREPYVDASRKTMRMIRYSSQKLSRRAARTLGQIFPIKVTSLLESSRHFASLKLPE
TNSHVMTISSIGSPIDIDTSEYPELFETGNSASTESYHEPVMKMPVIRVSSDGYLYNFVMDPERGGDCL
ILSQYSILMD

14. WD repeat domain phosphoinositide-interacting protein 3 (WIPI3)

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

>sp|Q5MNZ6|WIPI3_HUMAN WD repeat domain phosphoinositide-interacting
protein 3 OS=**Homo sapiens** OX=9606 GN=WDR45B PE=2 SV=2
MNLPCNPHGNGLLYAGFNQDHGCFACGMENGFVYNTDPLKEKEKQEFLEGGVGHVEML
FRCNYLALVGGGKPKYPNPKVMIWDDLKPKVIEIEFSTEVKAVKLRRDRIVVVLDSMI
KVFTFTHNPHQLHVFETCYNPKGLCVLCPNSNNSLLAFPGTHTGHVQLVDLASTEKPPVD
IPAHEGVLSCIALNLQGTRIATASEKGTIRIFDTSSGHLIQELRRGSQAANIYCINFNQ
DASLICVSSDHGTVHIFAAEDPKRNKQSSLASASFLPKYFSSKWSFSKQVPPSGSPICA

FGTEPNAVIAICADGSYYKFLFNPKGECIRDVYAQFLEMTDDKL

>EGA79032.1 Atg18p [*Saccharomyces cerevisiae* Vin13]
MSDSSPTINFNFNQTGTCISLGTSGKFKIFNCEPFGKIFYSEDSGGYAIIVEMLFSTSLALVIGDQPAL
SPRRLRIINTKKHSIICEVTFXTSILSVKMNKSRLVLLQEQIYIYDINTMRLLLHTIETNPNRGLMAMS
PSVANSYLVPSPPKVINSEIKAHATTNNITLSVGGNTETSFKRDQQDAGHSDISDLQYSSFTKRDDAD
PTSSNGGNSSIIKNGDVIVFNLETLOPTMVEAHKGEIAAMASFDGTLMATASDKGTIIRVFDIETGDK
IYQFRRTYATRIYSISFSEDSQYLAVTGSSKTVHIFKLGHSMSNNKLDSDSNMEEAAAADDSSLDTTSI
DALSDDEENPTRLAREPYVDASRKTMRMIRYSSQKLSRRAARTLGQIFPIKVTSLLESSRHFASLKLPE
TNSHVMTISSIGSPIDIDTSEYPELFETGNSASTESYHEPVMKMVPIRVVSSDGLYNFVMDPERGGDCL
ILSQYSILMD

15. WD repeat domain phosphoinositide-interacting protein 4 (WIPI4)

>sp|Q9Y484|WIPI4_HUMAN WD repeat domain phosphoinositide-interacting
protein 4 OS=*Homo sapiens* OX=9606 GN=WDR45 PE=1 SV=1
MTQQPLRGVTSRFRNQDQSCFCAMETGVRIYNVEPLMEKGLDHEQVGSMLVEMLHRS
NLLALVGGGSSPKFSEISVLIWDDAREGKDSKEKLVLEFTFTKPVLSVRMRHDKIVIVLK
NRIYVYSFPDNPRLKLEFEDTRDNPGLCDLCPKLEKQLLVFPGHKCGSLQLVDLASTKPG
TSSAPFTINAHQSDIACVSLNQPPTVVASASQKGTILRLFDTSKEKLVLELRRTDPATL
YCINFSHSDSSFLCASSDKGTVHIFALKDTRLNRRSALARVGVKVGPMIGQYVDSQWSLASF
TVPAESACICAFGRNTSKNVNSVIAICVDGTFHKYVFTPDGNCNREAFDVYLDICDDDDF

>XP_011454240.1 PREDICTED: WD repeat domain phosphoinositide-interacting
protein 4-like [*Crassostrea gigas*]
MSRGVLSLRFNQHGCFTCATETGLKIYNVEPLTQKLTGQDVVGSIASAEMLFRSNLVAMVGGGTSPKY
DEKAALIWDDTAKKVVMDVSNQPVVSIKLYDRLIVVLRNQIHVFSFPNNPTLLHSFDTRDNPGLCDV
SPFGQVIAFPGRKCGSVQIADLETTQPGQSTSPITISAHQGELAYITVNQQGTLATASKKGTIRVFDT
TTKLVLELRGADPATLYCITFSHSDSSFLCASSDKGTIHFVAVKDTSLNRRSTFKKMGFLGTYVESQWG
LASFTVAEACACICAFGPGHVSIAVCVDGTFHKYVFTPDGNCNREAYDVYLDIGDDFE

>sp|P43601|ATG18_YEAST Autophagy-related protein 18 OS=*Saccharomyces
cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=ATG18 PE=1 SV=1
MSDSSPTINFNFNQTGTCISLGTSGKFKIFNCEPFGKIFYSEDSGGYAIIVEMLFSTSLLA
LVGIGDQPALSPRRLRIINTKKHSIICEVTFPTSILSVKMNKSRLVLLQEQIYIYDINT
MRLLLHTIETNPNRGLMAMSPSVANSYLVPSPPKVINSEIKAHATTNNITLSVGGNTET
SFKRDQQDAGHSDISDLQYSSFTKRDDADPTSSNGGNSSIIKNGDVIVFNLETLOPTMV
IEAHKGEIAAMASFDGTLMATASDKGTIIRVFDIETGDKIYQFRRTYATRIYSISFSE
DSQYLAVTGSSKTVHIFKLGHSMSNNKLDSDSNMEEAAAADDSSLDTTSIDALSDEENPT
RLAREPYVDASRKTMRMIRYSSQKLSRRAARTLGQIFPIKVTSLLESSRHFASLKLPE
TNSHVMTISSIGSPIDIDTSEYPELFETGNSASTESYHEPVMKMVPIRVVSSDGLYNFV
MDPERGGDCLILSQYSILMD

16. Autophagy-related protein 2-like protein A (ATG2A)

>tr|K1RSP2|K1RSP2_CRAGI Autophagy-related protein 2-like protein A
OS=*Crassostrea gigas* OX=29159 GN=CGI_10022068 PE=4 SV=1
MSNFWKISGEELKAGIWRPHTLMFLLLWPVTVSQILVFPDVPSTKQGHMYSMHSYGAPA
LKAHVKSQVQNKRSQRS SGGPRTEISVNLAKLECELDGPLYSFQSTMEDESASDETKIDL
SVNCPVEVTLTRFPIPDRLNGSEVTKLPWWQKNLRDELLILDLEQEARFQTSFSLNQPIQQ
VEVSSRNVLGSFRIDPNQSAVPPAFVVSCEGIDGQEGFNFPQIIKIFTEQTSVLDDEENPD
SDNSIPMDSLNGACEFAKQDTPFSTKHKMYGKGGEMSDQATQHVSDMVMVPGNREDMADF
QERASANCLTLVQLVPLINLYIPDQKFYEVLYNRI SNDLLLWEPMAPIPTQEVGPGS
IQPFDLSCYTHAEDCHGEVVMGVKDNANL FVASSYQGNPLLOQYICFYCNKATLYHNAAVDP
KKEEFEIENLDFETIPAHLEKSCIIDRSEPGVLCHQSADVESTVRDMVSVAVRIKLDSTP
LSDLTRDEKIFETVAVGVGTGATLRHKMAETDMSWISQILNFDLVKDYDILGYVTPKILT
ELHVHLWDCAVDPRPLHPTKGVVAANYAETSISSNIVANSQTSLLRFVLEADAGMYLSQKKG
RESTVDLKKDYVCVLDVESFELELRSDGKDPKPKMDLRLRRTNKINMRTCTDCKALFE
LIRYFANDGDLVEYEEPTNKRQSLDLEMNKEEASSDEDSKKKELSESRLNLSHLED
AMQESGSGSDNDGSESSKQSPNKTEVFFVAQGERTDAQVPPAGVMRPIVITASADSVTSS
AVSERTDIFSDEEEEEEDFCIIDDAGLGITPRDGKPEVKIFTDEPIEIKDNYFSQPHGKT

DLLKAPDHFHPNAEYRYTLKELTIVVHMYGGSDFSDFTPVQQKPVETEVMMSRKMMDYGEYV
TETSVRFAASKSSVDRI PWTQRGGVGRDHDITLMELQLTKVRFQHERYPGHTEQASRQVLI
ISDAEIRDRLSDSKINKFLYQYSSENLPKQTNNSNMVYIKALHKRPDPSVKTEECSLRVSL
QPLRLNIDQDSLFFLKKFFTEITGGNVNDNPSDPDPKQRARSVSGASGAPAVITVQPEC
PGEERTPQELLMKFDEMQQSASQGSMMSSASVASSSDRTEQSQPVF IKNFMFSPDVPI
RLDYHGKKVVDREHGTLAGVLVGLASLNCSELKLRKLNKHLGMDKLGAYCINEWITD
ILKKQLPSILGGVGPMSFVQIAQGIRDLEFWLPVEQYKRDGRFVIRGIQRGATSFSTSTAM
AMLELTNRAVQSVQYVAEVTYDMVTPGPGSCRVRQRRRLRGPADVREGVENAYIAITEVQG
TAQYDLLPDANDRKMDHIELFPAPREKFRVY

>sp|Q2TAZ0|ATG2A_HUMAN Autophagy-related protein 2 homolog A OS=**Homo sapiens** OX=9606 GN=ATG2A PE=1 SV=3

MSRWLWPNVNCVKEKRYLLHHLGHFFQEHLSLDQSLDLYKGSVALRDIHLEIWSVN
EVLESMEAPLELVEGFVGSIEVAVPWAALLTDHCTVVRVSGLQTLQPRRGPAPGAADSQS
WASCMTTSLQLAQECLRDGLPEPSEPPQPLEGLEMFQAQTIETVLRRIKVTFLDTVVRVEH
SPGDGERGVAVEVRVQRLEYCDEAVRDPSQAPPVDVHQPPAFHLKLLQLAGVRLHYEELP
AQEPEPEPPLQIGSCSGYMEMLVKLQNEAFPGPKLEVAGQLGSLHLLLTFRQLQQQLQEL
LSAVSLTDHEGLADKLNKSRPLGAEDLWLEIQDLNQQQLQAGAVAELSPDPLTNPLLNLD
NTDLFFSMAGLTSSVASALSELSDVDLASSVRSDMASRRLSAQAHPAGKMAPNPLLDL
MRPDSLLKMTLGGVTLTLLQTSAPSSGPPDLATHFFTEFDATKDGPFGRDFHHLRPRFQ
RACPCSHVRLTGTAVQLSWELRTGSRGRRTTSMEVHFGQLEVLVLECLWPRGTSEPEYTEIL
TFPGTLGSQASARPCAHLRHTQILRRVPKSRPRRSVACHCHSELALDLANFQADVELGAL
DRLAALLRLATVPAEPPAGLLTEPLPAMEQQTVFRLSAPRATLRLRFP IADLRPEPDPWA
GQAVRAEQLRLELSEPPQFRSELSSGPGPPVPTHLELTCSDLHGIYEDGGKPPVPCLRVSK
ALDPKSTGRKYFLPQVVVTVNPSQSSSTQWEVAPEKGEELSVESPCELREPEPSPFSSK
RTMYETEEMVPIPGDPEEMRTFQSRTLALSRCSEVILPSVHIFLPSKEVYESIYNRINND
LLMWEPADLLPTPDAAQPSGFGPSPGFHDSFKMCKSAFKLANCFDLTPDSDSDEDAH
FFSVGASGGPQAAPEAPSLHLQSTFSTLVTVLKGRI TALCETKDEGGKRLEAVHGELVL
DMEHGTLSVSVSYCGQPGLGYFCLEAEKATLYHRAAVDDYPLPSHLDLPSFAPPAQLAPT
IYPSEEGVTERGASGRKGGQGRGPHMLSTAVRIHLDPHKNVKEFLVTLRLHKATLRHYMAL
PEQSWHSQLEFLDVLDDPVLGYPPTVITILHHLFSCSVDIRPPLYLPVRLVITAEFT
LSSNIIMDTSTFLRLRFLDSDSALYSDSKCEVETLDRRDYVCVLDVDLLELVIKTWKGST
EGKLSQPLFELRCSNNVHVHSCADSCALLVNLQYVMSTGDLHPPRPPSPTEIAGQKL
SESPALPSCPPVETALINQRDLADALLDTERSRLRELAQPSGGHLPQASPI SVYLFPGER
SGAPPPSPVGGPAGSLGSCSEEEKEDEREEEGDGTLDSEFCILDAPGLGIPPRDGEPV
VTQLHPGPIVVRDGYFSRPIGSTDLLRAPAHFPVPSTRVVLREVSLVWHLYGGRDFGPH
GHRARTGLSGPRSSPSRCSGPNRPQNSWRTQGGSGRQHHLVMEIQLSKVSFQHEVYPAEP
ATGPAAPSQEEERPLSRQVFIVQEELEVRDRLASSQINKFLYLHTSERMPRAHSNMLTI
KALHVAPTTLGGPECCLRVSLMPLRLNVDQDALFFLKDFFTSLVAGINPVVPGETSAEA
RPETRAQPSPLEGQAEGVETTGSGEAPGGHSPSPDQOPIYFREFRFTSEVP IWL DYH
GKHVTMDQVGTGAGLLIGLAQLNCSSELKLRKLCRHLGGLGVDKVLGYALNEWLQDIRKNQ
LPGLLGGVGPMSVQVLFQGFRLDLWLP IEQYRKDGRLMRGLQGAASFGSSTASAALEL
SNRLVQAIQATAETVYDILSPAAPVSRSLQDKRSARRLRGQQPADLREGVAKAYDTVRE
GILDTAQTI CDVASRGHEQKGLTGAVGGVIRQLPPTVVKPLILATEATSSLLGGMNRQIV
PDAHKDHALKWRSDSAQD

>sp|P53855|ATG2_YEAST Autophagy-related protein 2 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=ATG2 PE=1 SV=1

MAFWLPQNIQKRLLLYVLQQLISLFSNIDLSNLDVSIKSKSHFSFHDVNLSLDDLNI PNQ
INEGIVDELVLKLLTVGGVEIDGSGLRFIMTPLYSSGSQELHSDFLVKS IQDLTNSMLQF
SDPLTTYNRYKEDDISSDSSDLNSNIEASKPAANGSYTLQNMNRKALNVALAKLKIAL
KDVTIRFIVNDRDPSDNIVEVHLESIQLITTDANLRHINIENITISSIQKQAVPDSVHP
FNNDLDSQSVYLSKMEATSLYMSAMEEQSNEDPSEPQVTQEEQENDKCKESLMEINNLNI
AFKGLSSVNDLRMSNIVIDIQDVHLAIHKIVEIKNSTLKNIIDIVTHLDANESFSCQDS
QSPSPDKQEPSALSSVDIKCIYLNLGQDITVILKSFKLEQKENNSLAFSLGSFYNSNSPL
TISHKTKPLLTGEQTPQSIALNMGDELIIISHDGHAFHFKIFQFVSKCMSFYQNKSKGM
MPQIASDTRKRVQLTSKAVKLSLKFYFLLCFQVSPFIYDSNRELYIELVDVFKKLP SRC
TKILTMSSITISNLQSPQLGSDYDITLKEALIIYSSVHAIKEVIFNEEYSGIVQLVEDIS
AFGKLF TDSKNSECTGKSKSKRGSFLQRSVRVLSNRSRFVYKQSLSANFSLKIDSMKLV S
EIIIGPQFGSVEALLSNFFAITDSDQIVYFTKNLVERKTPSLLPEQEI MSVVLNKAVNE
PVLYVHRRANGKLVIFNNIRIHYYARWLEILKKNIGPDNASSKDEPVSQKLSKKQPTSG
FPWELKCLDCSLILHPFRLKSVMI VLDNLTGGSSFI PQAKLLSKANTLFLIDDYQNFK
IQKDKNWPSLINFYAGQGFSAIGKIDTLNFLINKSDGALLLDCKIEQVGLSLCADSFQTF

CQLCIDLKYPQTFPDEEKFRITQLKNPIDVFKDIDCDLNFSAFIRENNHQNDYDSVHLVDS
FLDKTHEFNNGARSKLSSQGSYEMDSSSGTATGGILLPHESYLDSAQPKEEDTPPIASKE
QERDVIDRGSIDVEKVVIKLFDGYDWKYTRKFIANTVEKLDKELSKAEASSSKSNVPQSE
ANIFDSIYISANKNNVTDLRRNLDGEIQGVQNSFSDVSKVNLRPSKHYKALIQLNKVHVN
LKNYRVDEPDESNSDNSTDVLRNRCVVSIEFEIINDVPTSTWKNKFTLLKHEPWPWPHSSPM
FLLDLEFIRPIDFLQAVELVMQLNVAPLRLHVDQDTLEFLIRFLGFKDKRFELIDEYPDI
VFIQKFSTNSIKLRLDYKPKKVDYAGLRSGQTSSELMNFFTLDGSKIILKSVVLYGLNGFD
ELNNKLKAIWTPDITKKQLPGVLEGLAPVRSFMAIGSGVKTLLVTMLMSEYRQEGHLGRSL
KKGGNVFLKTTTGDFVVLGKLTSGTQAILENTEELFGGVGSGNRVYDASKFGSADGADS
DTAAVLDDLTLFEEDQLVGSKYSRIRDHEPTAVVIDMSSPGDHNEPTIVSLYADQPLDLP
TGLKEAYSSLEKHMHIAYDAVWRAGQMKDDKRGGPSAAAVYVARAAPVAIIRPLIGATE
AVSKTLQGIANQVDKTHNEQINDKYKSNRTDS

17. Autophagy-related protein 2-like protein B (ATG2B)

>tr|K1QL77|K1QL77_CRAGI Autophagy-related protein 2-like protein B
OS=**Crassostrea gigas** OX=29159 GN=CGI_10022070 PE=4 SV=1
MPWTFPWFTEFLKCRACRYLLQHYLGQFLKEKLSLDQLSVDLYNGRGSIKDLELDVEALNE
ALDSSSVPLIEVDGFINQISVSVPWNTLIQSSTEMEIQGLEITVQPKQRMENVGGLETMF
NSMCSMTSSLQIAEDCLKSTSDADQGDLTGTFEGVQKFAQTIDSVLCRVKVTLIDTVVR
VEHLPDSAEGKVALEIKIKRIEYFDDMAKEEGSPVDDSSRRTTWEPAIAHKNLLIDGMQI
LCDEFSRPTHQTPSRMFSSDSYQQTFMSTTSSPSTPVDNQGGTVPVSEVFSDFVQIAGFT
GKSSLKVKLQEEGVQGPKEIELEVGGLHLLLSPTQFHAVLDLVNGFLSPKSSNEGRER
ARSKSKPMNEEDYRKVETELQRQLHSDRFHPSHMDTLTATDLQDIMTHSIGDEQYFSLAP
DPMESSVNSNFSLASGRSGSTVTTTRSGPRKDGKAAKDSIQRFLLDDPSAELCRYHLRAVF
FSVALLHENPSQKVDLSSAKANNKNQMKDIAAQYFQKMHSFSAASGGEVKALRAAFAEA
LPQDHLRLIGKPVNIEIVERTAPTHHCLTVDVTAGFLDVVECLFNRTLQTIIEPDYTELAA
QLAHQSGGDKFNRVTVCEISHF

>sp|Q96BY7|ATG2B_HUMAN Autophagy-related protein 2 homolog B OS=**Homo sapiens**
OX=9606 GN=ATG2B PE=1 SV=5
MPWPFSESIIKCRACRYLLQRYLGHFLQEKLSLEQLSLDLYQGTGSLAQVPLDKWCLNEIL
ESADAPLEVTEGFIQSISLSPWGSLLQDNCALVVRGLEMVFRPRPRPATGSEPMYWSSF
MTSSMLAKECLSQKLTDEQGEQSPPFEGLEKFAETIETVLRVVKVTFIDTVLRIEHVPE
NSKTGTALEIRIERTVYCYDETADESSGINVHQPTAFAHKLLQLSGVSLFWDEFSSASAKSS
PVCSTAPVETEPKLSPSWNPKIIEYHPQLTRNLPEIAPSDPVQIGRLIGRLELSLTLKQ
NEVLPGAKLDVDGQIDSIHLLLSPRQVHLLLDMLAAIAGPENSSKIGLANKDRKNRPMQQ
EDEYRIQMELNRYLKRKDSLSVGVSSSEQSFYETETARTPSSREEEVFFSMADMMSHLS
SLPPLGDPNMDLELSLTSTYTNTPAGSPLSATVLQPTWGEFLDHHKEQPVRGSTFPSNL
VHPTPLQKTSLSRVSVDSESRPELIFRLAVGTFSISVLHIDPLSPPETSQNLNPLTPMA
VAFFTCIEKIDPARFSTDEDFKSFRAVFAEACSHDHLRFITGTIKVSYEQQRSASRYFST
DMSIGQMEFLECLFPTDFHSVPPHYTELLTFHSKEETGSHSPVCLQLHYKHSNRPQGN
QARLSSVPHKAELQIKLNPVCCELDISISVDRNLNLLQPQKLATVEMMASHMYTSYNKHIS
LHKAFTTEVFLDDSHSPANCRI SVQVATPALNLSVRFPIPDLRSDQERGPWFKKSQKEIL
YLAFTDLEFKTEFIGGSTPEQIKLELTFRELIGSFQEEKGDPKIKFFHVSSGVDGDTTSS
DDFDWPRIVLKINPPAMHSILERIAAEENDDGHYQEEEGGAHSLKDVCDLRRPAPSP
FSSRRVMFENEQMVMPGDPVEMTEFQDKAISNSHYVLELTLPNIVVTLPNKSFYEKLYNR
IFNDLLLWEPTAPSPVETFENISYGIGLSVASQLINTFNKDSFSAFKSAVHYDEESGSEE
ETLQYFSTVDPNYSRRKKKLDSONKNSQSFLSVLLNINHGLIAVFTDVKQDNGDLLENK
HGEFWLEFNSGSLFCVTKYEGFDDKHYICLHSSSFSLYHKGIVNGVILPTETRLPSSTRP
HWLEPTIYSSEEDGLSKTSSDGVGGDSLNLMSVAVKILSDKSESNTKEFLIAVGLKGATL
QHRMLPSGLSWHEQIILYFLNIADEPVLGYNPPTSFTTFHVHLWSCALDYRPLYLP IRSLL
TVETFSVSSSVALDKSSSTLRIILDEAALHLSDKCNTVTINLSRDYVRVMDMGLLELTIT
AVKSDSDGEQTEPRFELHCSSDVVHIRTCSDSCAALMNLIQYIASYGDLQTPNKADMKPG
AFQRRSKVDSSGRSSSRGPVLPEADQOQLRDLMSDAMEEIDMQQGTSSVKPQANGVLDEK
SQIQEPCCSDLFLFPDESIGNVSQESGPTYASFHHFISDAMTGVPTENDDFCILFAPKAA
MQEKEEEPVIKIMVDDAIVIRDNYFSLPVNKTDTSKAPLHFPPIPVIRYVVKEVSLVWHLY
GGKDFGIVPPTSAPKSYISPHSSPSTPTRHGRNTVCGGKGRNHDFLMEIQLSKVKFQHE
VYPKFCIPDCDSSLSEHPVSRQVFIQDLEIRDRLATSQMNKFLYLYCSKEMPRKAHNSML
TVKALHVCPEGRSPQECCLRVSLMPLRLNIDQDALFFLKDFFTSLSAEVELQMTDPDEV
KKSPGADVTCSLPRHLSTSKEPNLVISFSGPKQPSQNSANSVEVVNGMEEKNFSAEEAS
FRDQPVFFREFRFTSEVP IRLDYHGKHVSMQGTLAGILIGLAQLNCSELKLRLSYRHG

LLGVDKLFSYAITEWLNLDIKKNQLPGILGGVGPMSLVQLVQGLKDLVWLPVIEQYRKDGR
IVRGFQRGAASFSTAMAALLETNRMVQTIQAAAETAYDMVSPGTLSIEPKKTKRFPHH
RLAHQPVDLREGVAKAYSVVKEGITDTAQTIIYETAAREHESRGVTVGAVGEVLRQIPPAVV
KPLIVATEATSNVLGGMRNQIRPDVRQDESQKWRHGDD

>sp|P53855|ATG2_YEAST Autophagy-related protein 2 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=ATG2 PE=1 SV=1
MAFWLPQNIQKRLLLLYVLQQLSFLSNIDLSNLDVSIKSHSFSFHDVNLSDDDLNIQVQ
INEGIVDELVLKLTVSGGVEIDGSGLRFIMTPLYSSGSQELHSDFLVKSIIQDLTNSMLQF
SDPLTTYNRYKEDDISSSDSSDLNSNIEASKPAANGSYTLQNMNRKALNVALAKLKIAL
KDVTIRFIVNDRDPSDNIVEVHLESIQILITTDANLRHININENITISSIQKQAVPDSVHP
FNNDLDSQSVYLSKMEATSLYMSAMEEQSNEDPSEPQVTQEEQENDKCKESLMEINNLNI
AFKGLSSVNDLRMSNIVIDIQDVHLAIHKIVEIKNSTLKNIIIDIIVTHLDANESFSCQDS
QSPSPDKQEPSALSSVDIKCIYLNLGQDITVILKSFKLEQKENNSLAFSLGSFYNSSSPL
TISHKTKPLLTGEQTPQSIALNMGDELIIISHDGHIAHFFKIFQFVSKCMSFYQNKSKGM
MPQIASDTKRTVQLTSKAVKLSLKFPYFLLCFQVSPFIYDSNRELYIELVDVFKKLPSRC
TKILTMSSITISNLQSPQLGSDYDDLKEALIIYSSVHAIKEVIFNEEYSGIVQLVEDIS
AFGKLFRTDSKNSECTGKSKSKRGSFQLQSVRVNLSSRFVYKQSLSANFSLKIDSMKLVKVS
EIIIGPQFGSVEALLSNFFAITDDSQIVYFTKNLKVVERKTPSLLEPQEIMSVVNLKAVNE
PVLYVHRRANGKLVIFNNIRIHYARWLEILKKNIGPDNASSKDEPVSQKLSKKQPTSG
FPWELKCLDCSLILHPFRLKSMVIVLDNLTGGSSFIQAKLLSKANTLFLIDDYQNFK
IQKDKNWPSLINFYAGQGFSAIGKIDTLNLFINKSDGALLLDCKIEQVGLSLCADSFQTF
CQLCIDLKYPTFPDEEKFRQKLNPIQVFKDIDCDLNFSAFIRENNHQNDYDSVHLVDS
FLDKTHEFNNGARSKLSSQGSYEMDSSSGTATGGILLPHESYLDSAQPKEDTPIIASKE
QERDVIDRGSIDVEKVVIKLFDGYDWKYTRKFIANTVEKLDKELSKAEASSSKSNVPQSE
ANIFDSIYISANKNNVTDLRNLDGEIQGVQNSFSDVSKVNLRPSKHYKALIQLNKVHVN
LKNYRVDEPDESNSDNSTDVNLNRCVVSIIYEFEEIIDNVPTSTWNKRVTLKHEPWPSSPM
FLLDLEFIRPIDFLQAVELVMQLNVAPLRLHVDQDTLEFLIRFLGFKDKRFELIDEYPTDI
VFIQKFSTNSIKLRLDYKPKKVDYAGLRSGQTSSELMNFFTLDGSKIILKSVVLYGLNGFD
ELNNKKAIIWTPDITTKQLPGVLEGLAPVRSFMAIGSGVKTIVTVLMSEYRQEGHLGRSL
KKGGNVFLKTTTGDFVVKLVKLTSGTQAILENTEELFGGVGSGNRVYDASKFSGSADGADS
DTAAVLDLDTLFEEDQLVGSKYSRIRDHEPTAVVIDMSSPGDHNEPTIVSLYADQPLDLP
TGLKEAYSSLEKHMHIAYDAVWRAGQMKDDKRGGPSAAAVYVARAAPVAIRPLIGATE
AVSKTLQGIANQVDKTHNEQINDKYKSNRTDS

18. Phosphatidylinositol 3-kinase catalytic subunit type 3 (PI3KC3)

>tr|K1PVC2|K1PVC2 CRAGI Phosphatidylinositol 3-kinase catalytic subunit
type 3 OS=**Crassostrea gigas** OX=29159 GN=CGI_10006484 PE=3 SV=1
MGEMSDRFHYVYSCDLVDNLQIKIGTLEGERQRPDYKELLDDPMLKFSGVYGEECSDLYV
TCQVFADGHPLSLMSMSTSYKAFSTRWNWNEWITLQVYKSDLPNAILSLTIWDIYGTNKS
IPVGSTVPIPLFGKRGTYRQGMHDLKVVDPMLPDPSSNSTTPGKSKDHDQMSKLAKLKSK
HRDGHMLKVDWLDRLTFREIEMINEKQKRDSKFMYLMIIEFPLIHYEDIEYSVVYFEKDG
EPLVYKTIIDPLVQVPDPEIDMENLVEKHHRLARSLRSGPTDRDMKPAKTRNLLHEIVR
YPPTKTLTSEEDLVWKFYFLCNQKADTKFLKCVNWKQPQESRQGIELLTRWSPMDVE
DALELLSPAFSHPTVRKYAVSRLRQAKALDQDLLLYLLQLVQALKYEDFEEIMRYNDSIVDR
KDSVSDTSAPEKTRTTSVLSRASSNESILHALGGSSPSQSESPESKLEREMDLASFLISR
ACNNTSLANYFYWYLSVECVDPNGLDVKDSKVTKMYQHVLKRFQALFKESNESRQRSM
IARQQTIFIDRLVDLVKIVTRESGNRKKKIERLQALLHDQEAACKFDFSNFEPLSLPLDPI
KICGIIPEKATLFKSNLMPCKFVFKMVEGGEYMYKHGDDLQDNLILQIITLMDKLLM
RDNLDLKLTYPYKVLATSCKHGFVQFVESVAVAEVLNQHGTGQSFFKICAPCENTPYGFQ
EVMDNFKVSCAGYCVITYVLGVGDRHFDNLLLTGTGKLFHVDVGFILGRDPKLLPPLMKL
TTEMIDGMGGPNSEHFHDFKLCYTAFLAIRSSNLILNLFITLMVNANIPIAIEPDKSV
KKVQDKFVLHLTDEEAVQYMQNVIDGVSAMMPVVERFHTIAQASTSQTLIYKYTL

>sp|Q8NEB9|PK3C3 HUMAN Phosphatidylinositol 3-kinase catalytic subunit type
3 OS=**Homo sapiens** OX=9606 GN=PIK3C3 PE=1 SV=1
MGEAEKFHYIYSCDLIDINVQLKIGSLEGKREQKSYKAVLEDPMLKFSGLYQETCSLDLYVT
CQVFAEGKPLALPVRTSYKAFSTRWNWNEWLKLQVYKYPDLPRNAQVALTIWVYGPYKAV
PVGTTVSLFGKYGMFRQGMHDLKVVNPVEADGSEPTKTPGRTSSTLSEDQMSRLAKLTK
AHRQGHMVKVDWLDRLTFREIEMINESEKRSSNFMYLMVEFRCVKCDDKEYGIVYVEKDG
DESSPILTSFELVKVPDPQMSMENLVEKHHKLARSLRSGPSDHDLPNAATRDLNIIIV

SYPPTKQLTYEEQDLVWVKFRYYLTNQEKALTKFLKCVNWDLPQEAKQALELLGKWKPMDV
EDSLELLSSHYTNPTVRRYAVARLRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKK
DSQSSVSENVSNNGINSAEIDSSQIITSPLPSVSSPPPASKTKEVPDGENLEQDLCTFLI
SRACKNSTLANLYLYWYVIVECEDQDTQORDPKTHEMYLNMRRFSQALLKGDKSVRVMRS
LLAAQQTTFVDRVLVHLMKAVQRESGNRKKKNERLQALLGDNEKMNLSDELIPLEPQVK
IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLQDQLILQIISLMDKLLRK
ENLDLKLTPYKVLATSTKHGFMQFIQSVPVAEVLDTESIQNFFRKYAPSENGPNGISAE
VMDTYVKSCAGYCVITYILGVGDRHLDNLLLTKTGKLFHIDFGYILGRDPKPLPPPMKLN
KEMVEGMGGTQSEQYQEFRKQCYTAFLHLRYSNLILNLFSLMVDANIPDIALEPDKTVK
KVQDKFRLDLSDEEAVHYMQSLIDESVHALFAAVVEQIHKFAQYWRK

>sp|P22543|VPS34_YEAST Phosphatidylinositol 3-kinase VPS34 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=VPS34 PE=1 SV=1
MSLNNITFCVSQDLVPLKVKIKSLEGHKPLLKPSQKILNPELMLIGSNVFPSSDLIVSL
QVFDKERNRNLTLPIYTPYIPFRNSRTWDYWLTLPIRIKQLTFSSHLRIILWEYNGSKQI
PFFNLETSIFNLKDCITLKRGFESLKFYDVIDHCEVVTDNKKDQENLNKYFQGEFTRLPWL
DEITISKLRKQRENRTWPQGTFFVLNLEFPMLELPVVFIEREIMNTQMNIPITLKNPGLST
DLREPNRNDPQIKISLGDKYHSTLKFYDQPNNDPIEEKYRRLERASKNANLDKQVKPD
IKKRDYLNKIINYPGKTLTAHEKGSIWKYRYLLMNNKKALTKLLQSTNLREESEERVEVL
ELMDSWAEIDIDDALELLGSTFKNLSVRSYAVNRLKASDKELELYLLQLVEAVCFENLS
TFSDKSNSEFTIVDAVSSQKLSGDSMLLSTSHANQKLLKSISSESETSGTESLPVIVISPL
AEFLIRRALVNPRLGSFFYWLKSESEDKPYLDQILSSFWRLDKKSRNINLDQVRLINV
LRECCETIKRLKDTTAKKMEILLVHLETKVRPLVKVRPIALPLDPDLICDVCPEPETSQV
KSSLSPLKITFKTTLNQPYHLMFKVGGDDLQDQLVQIISLMNELLKNENVDLKLTYPYKI
LATGPQEGAIEFIPNDTLASILSKYHGILGYLKLHYPDENATLGVQGWVLDNFVKSCAGY
CVITYILGVGDRHLDNLLVTPDGHFFHADFGYILGQDPKFPPLMKLPPQIEAFGGAES
SNYDKFRSYCFVAYSILRRNAGLILNLFELMKTSNIPDIRIDPNGAILRVRERFNLNMSE
EDATVHFQNLINDSVNALLPIVIDHLHNLAQYWRK

19. Phosphoinositide 3-kinase regulatory subunit 4 (PIK3R4)

>tr|K1R976|K1R976_CRAGI Phosphoinositide 3-kinase regulatory subunit 4
OS=**Crassostrea gigas** OX=29159 GN=CGI_10027844 PE=4 SV=1
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SLPLTSHRNKLEDIHIRLQGSTSNCLPFQKAIHSDKAALLFRQYVKDSLYDRISTRPFLN
RIEKKWLAFLQLLCALNQCHKIKVCHGDIKAENVMITSWNWLLTDFASFKPTYLPEDNPS
DFSYYFDTSRRCYIAPERFVESGLKNQEGAGQTIDLTNSDEVKSGDITPPMDIFSAGC
VICELFTEGTPPFDFSQLLAYRNGEYSPWKVLEKIDDNIRDLVRHMIKKDPHRLSAEE
YMIQQRGKAFPEYFYTFCLKIYLLQFVSTPLTPDDRINKIKRDFPRIVKSIQPEERSED
NIGLVLIISLISSSRKLHLKNTKLTALQLLLEASKFVTTDIIIDRIIPYMLSFANDQFP
RVRAEVIHVVTQCLLDVDSIPRSDANVFPEYIFPNITHLTQDPVVMVRAAYAENIAKLAE
TALRVLEMTQRIDLEETEEEEESVDGLLYQANYDIELLTLOETIQQKVVTTLLSDPDNSVKR
TLLNGITKLCVFFGRQKANDVLLSHMITFLNDKTDWHLRGSFFDNIVGVAAYVWGQSCS
ILKPLLDQGLSDPEEFVHVHKTALGALTALTELKGLIQKSMLEFLQEVVFPFLAHPGIWIRQG
AIGFISALTRMFNIADVHCKVLPALQPCLEKRVLQIDKEIFLLNALQSPIPRPVFDYILR
VSQPDRFLDILRERQYMRISRSSSHRTTYSELDEAMSQVFKKLNSEFGMDESHEDKILAMK
DYVMKLHRSRAGSVETKHELGDSPGRFCIVGAGKAITRRHAELIKQKDPKQGGADQTTSS
RSSKKVQSKEQSVNMNSEWKSMEFSGNESDSSNASLSPKARTLQKTAESLEKKNLTSQTVS
QTSSSSGSFVTMSQSQSVSSEGSIRSVTEKGS DKNPITKYHNCKIALRNIVHKKRELYSAE
SKDLLEIAWERRPPPSNWKPKGLLV AHLQEHRAAINRIQVSHDHAFASASNDGTVKLWE
SEKLEGNSVANRSKQTLKNTSLPGEKVKGLVFCEASGPSLSLATFTDLGAINIFKIEETGK
ASWNKDLRVDKPDYGNIVDMTYFDTGASVLSYATVNGFLVGHDLRTNKEVWKL RNDPKA
GLITSFVHHSQCWLAVGTSSGTHICWDMRFQLPINSIVHPTGARVRRIMHPQEQSWLI
SATQGNNEVSIWVETGARQKVLWASPTPTLSLNQASHHSVYGLHMAVTDTNVFMILTGG
DMRARFWDLSYPANSFILAGAASDPVQQTGVNYRAKLV DGVVEVIQELYTKKPV TND DAPR
RGPEAPPQGHRIISDINLCQASQCMVITGSRDGVIKVWK

>sp|Q99570|PI3R4_HUMAN Phosphoinositide 3-kinase regulatory subunit 4
OS=**Homo sapiens** OX=9606 GN=PIK3R4 PE=1 SV=3
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NNIEKRWIAFQILTAVDQAHKSGVRHGDIKTENVMVTSWNWLLTDFASFKPTYLPEDNP

ADFNFFDTSRRRTCYIAPERFVDGGMFATELEYMRDPSTPLVDLNSNQRTRGELKRAMD
IFSAGCVIAELFTEGVPLFDLSQLLAYRNGHFFPEQVLNKKIEDHSIRELVTQMIHREPDK
RLEAEDYLKQQRGNAPPEIFYTFLQPYMAQFAKETFLSADERILVIRKDLGNI IHNLCGH
DLPEKAEGEPKENGVLIVSVITSCLOTLKYCDSKLALELILHLAPRLSVEILLDRITP
YLLHFSNDSVPRVRAEALRTLTKVLALVKEVPRNDINIYPEYILPGIAHLAQDDATIVRL
AYAENIALLAETALRFLELVQLKLNLMENDPNNEEIDEVTHPNGNYDELQALHEMVQOK
VVTLLSDPENIVKQTLMEGITRLCVFFGRQKANDVLLSHMITFLNDKNDWHLRGAFFDS
IVGVAAYVGVQSSSILKPLLQOGLSDAEFVIVKALYALTCMCQLGLLQKPHVYEFASDI
APFLCHPNLWIRYGAVGITVVARQISTADVYCKLMPYLDPYITQPIIQIERKLVLLSVL
KEPVRSRIFDYALRSKIDITSLFRHLHMRQKRNGLPDCPPPEDPAIAQQLLKKLLSQGMT
EEEEEDKLLALKDFMMKSNKAKANIVDQSHLHDSQKGVIDLAAALGITGRQVDLVKTKQEP
DDKRARKHVQKDSNVNEEWSMFGSLDPPNMPQALPKGSDQEVITGKPPRSESSAGICV
PLSTSSQVPEVTTVQNKPKVIPVLSSTILPSTYQIRITTTCKTELQQLIQOKREQCNAERI
AKQMMENAWEWESKPPPPGWRPKGLLVAHLHEHKSAVNRIRVSDHSLFATCSNDGTVKIW
NSQKMEGKTTTTTRSILTYSRIGGRVKTFTFCQGSHYLAIASDNGAVQLLIGIEASKLPKSP
KIHPQLSRILDQKEDGCVDMHHFNSGAQSVLAYATVNGSLVGVWDLRSSSNATLKHDLK
SGLITSAVDIHQCWLCIGTSSGTMACWDMRFQLPISSHCHPSRARIRRLSMHPLYQSWV
IAAVQGNNEVSMWDMETGDRRFTLWASSAPPLSELQSPHVSVHGIYCSPADGNPILLTAG
SDMKIRFWDLAYPERSYVAVGSTSSPSVSYRKIIEGTEVVQEIQNKQKVGPSDDTPRRG
PESLPVGHHDIIITDVATFQTTQGFIVTASRDGIVKVWK

>sp|P22219|VPS15_YEAST Serine/threonine-protein kinase VPS15
OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=VPS15
PE=1 SV=4

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DQYSLRPFQIRIRAQSFKLGQLPHVLNYSKLIETNRAGYMIROHLKNNLYDRLSLRPYLQ
DIELKFIAFQLLNALKDIHNLNIVHGDIKTENILVTSWNWCILTDFAAFIKPVYLPEDNP
GEFLFYFDTSKRRTCYLAPERFNSKLYQDGKSNNGRLTKEMDIFSLGCVIAEIFAEGRPI
FNLSQLFKYKNSYDVNREFLMEEMNSTDLRNLVLDMIQLDPSKRLSCDELLNKYRGIFF
PDYFYTFIYDYFRNLVMTTSTPISDNTCTNSTLEDNVKLLDETTEKIYRDFSQICHCLD
FPLIKDGGEGISDPPILESYKIEIEISRFLNTNLYFPQNYHLVLQOFTKVSEKIKSVKEE
CALLFISYLSHSIRSIVSTATKLNLELLAVFAQFVSDENKIDRVVPYFVCCFEDSDQDV
QALSLLTLIQVLTSVRKLNLNENIFVDYLLPRLKRLNISNRQNTNYLRIVFANCLSDLA
IIINRFQEFQHCNDNSMDNNTIMESSTKYSAKLIQSVEDLTVSFLTDNDTYVKMAL
LQNILPLCKFFGRERTNDIILSHLITYLNDKDPALRVSLIQTISGISILLGTVTLEQYIL
PLLIQTITDSEELVVISVLQSLKSLFKTLIRKKYYIDISKTTSPLLLHPNNWIRQFTLM
IIIEIINKLSKAEVYICILYPIIRPFVEFDVEFNFKSMISCKQPVRSRVYNLLCSWSVRA
SKSLFWKKIITNHVDSFGNNRIEFITKNYSKNYGFNKRDTKSSSSLKGIKTSSTVYSHD
NKEIPLTAEDRNWIDKFHIIIGLTEKDIWKIVALRGYVIRTARVMAANPDFPYNNSNYRPL
VQNSPPNLNLTNIMPRNIFFDVEFAEESTSEGQDSNLENQOIYKYDESEKDSNKLINGS
KQLSTVMDINGSLIFKNKSIATTTSNLKNVQLEPTSYHMSPNHGLKDNANVKPERKV
VVSNSYEGDVESIEKFLSTFKILPPLRDYKEFGPIQEIIVRSPNMGNLRGKLIATLMENEP
NSITSSAVSPGETPYLITGSDQGVIKIWNLKEIIVGEVYSSSLTYDCSSTVTQITMIPNF
DAFAVSSKDGQIIVLKVNHYYQSEVVKFLNCECIRKINLKNFGKNEYAVRMRAFVNEEKS
LLVALTNLSRVIIIFDIRTLERLQIENS PRHGAVSSICIDECCVLILGTTRGIIDIWDI
RFNVLIRSWSFGDHAPITHVEVCQFYGKNSVIVVGGSSKFTLTIWNFVKGHCQYAFINS
EQPSMEHFLPIEKGLEELNFCGIRSLNALSTISVSNKILLTDEATSSIVMFSLNELSSS
KAVISPSRFSDFIPTQVTANLTMLLRKMKRTSTHSVDDSLYHHDIIINSISTCEVDETPL
LVACDNSGLIGIFQ

20. Beclin-1 (BECN1)

>tr|K1QHY7|K1QHY7_CRAGI Beclin-1 OS=**Crassostrea gigas** OX=29159
GN=CGI_10027731 PE=4 SV=1

MATIKVESKSGTTHVSFVCQRCRQPLKLDHSFNTLDRQLLAELSAGPFLTGFSSLLDDV
EVDENYSKRDIITSTPEPEDAGDFLLLGGETSPGNMDNLSHRIRVSSALFDVMSGQSEIDH
PLCEECTDNLLDQLDNQLKITEDECKDYREFLENLDSNHTEEDGSNLDVLELQQLQAEEQS
LRQQLQNLETEQEHEALLEKEREISQKLQDEEDKYWKEYNEYKRQVQELEDEQRSVDNQ
LKYAQTQLDKLKKTNVFNNTTFHIWHSGHFGTINNFRGLRPLSPVPVDWNEINAAWQTVLL
LNSLAKKMNLTFRYRLVPPFGNHSYIESLSDKSKELPLYGSGGFRFFWDTKFDQAMVAFL
DCLQQFKEEVEKGDTFGLCPYKMEKGIEDSSTGTSYSIKIQFNSEEQWTKALKYMLTNL
KWGLAWVSSQFANK

>sp|Q14457|BECN1_HUMAN Beclin-1 OS=**Homo sapiens** OX=9606 GN=BECN1 PE=1 SV=2
MEGSKTSNNSTMQVSVFCQRCQSQPLKLDTSFKILDRVTIQELTAPLLTTAQAKPGETQEE
ETNSGEEPFIETPRQDGVSRRFIPPARMMSTESANSFTLIGEASDGGTMENLSRRLKVTG
DLFDIMSGQTDVDHPLCEECDTLLDQLDQLNVTENECQNYKRCLEILEQMNEDDSEQL
QMELKELALEEERLIQELEDVEKNRKIVAENLEKVQAEAERLDQEEAQYQREYSEFKRQQ
LELDDELKSVENQMRYAQTQLDKLKKTNVFNATFHIWHSQGFGTINNFRLGRLPSVPVEW
NEINAAWGQTVLLLHALANKMGLKFQRYRLVPYGNHSYLESLTDKSKELPLYCSGGLRFF
WDNKFDHAMVAFLDCVQQFKEEVEKGETRFCLPYRMDVEKGIKIEDTGGSGGSYSIKTQFN
SEEQWTKALKFMLTNLKWGLAWVSSQFYNK

>sp|Q02948|BECN1_YEAST Vacuolar protein sorting-associated protein 30
OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=VPS30
PE=1 SV=1
MKCQTCHLPLQLDPSLEGLSLTQRNLLLSNNSIITATNENVISNKGIEAADNCGPQIPKE
RLRRLGEIQNIKDLNLKDDKLIITDSFVFLNHDDDDNANITSNREDQRYGNANGNDNKKA
NSDTS DGTSTFRDHDEEEQEATDEDEDENQQIQLNSKTLSTQVAMTNVFNILSSQTNIDFP
ICQDCCNILINRLKSEYDDAIKERDTYAQFLSKLESQNKIEISESNKEKQYSHNLSEKENL
KKEEERLLDQLLRLEMTDDDLGELVRLQEKKVQLENEKLQKLSQNLMDLNNIQFNKNL
QSLKLQYELSLNQLDKLRKINIFNATFKISHSGPFATINGLRLGSIPESSVVPWKEINAAL
GQLILLLATINKNLKINLVYELQPMGSFSKIKKRMVNSVEYNNSTTNAPGDWLILPVYY
DENFNLGRIFRKETKFDKSLETTLEIIEITRQLSTIASSYSSQTLTTSQDESSMNAND
VENSTSILELPYIMNKDKINGLSVKLHGSSPNLEWTTAMKFLLTNVKWLAFSSNLLSKS
ITLSPTVNYNDKTISGN

21. Beclin 1-associated autophagy-related key regulator (ATG14)

>tr|K1QJY6|K1QJY6_CRAGI Uncharacterized protein OS=**Crassostrea gigas**
OX=29159 GN=CGI_10002920 PE=4 SV=1
MGSLCENYVLVLSCSWSLLVRVWVKNKTSTRLLLDWMVDLNALEYLADKLQDDKGIKYP
NTLIFGMFDQFFRAPEVKPVGVGVDPGVEAEDDKSSKSQSVSTQCFLKVEIASTKKSYP
ASSLSRIYTVLRAIKQTQASVHKVRRSIEDKLLSSQETTRKRAEHEDLLLKREQLCAEVT
WRTASVNKMKDQADQLHRSNQEQTAMKKNKEKLEEKQREQAEEKKDYDQTRYSSKDDNM
IGVSLGYTCHLLLMISGILDIPLRYSMTHLVSKSVIRDDIHSRLEDKERDFPLYSGKKEQ
NLFYRGVFTLNKNISQMRFYLGMGTVDLRRTLMNIKTLLNRLGLKPESQTAQLRPASEP
GDRQYSDFDRDTRSSLASYGMAVDFRRELSVPPTTESSRQSSPNLHEVEEKEIFHPSS
DDNFFKISNPVSERLADFESEINGCAQDVTNHFHKPSDNRRQTCWNGVGSNDFNAGDQPEE
DHIYETPLPVQNIITNNLEHKFFVFMHDGVYPVVPSPAVIMNRKQELAE

>tr|K1QSF1|K1QSF1_CRAGI Uncharacterized protein OS=**Crassostrea gigas**
OX=29159 GN=CGI_10025388 PE=4 SV=1
MYFRYKEKRFLDLHLQKERQGRLERVQDALKQHMQRDQKQIGEIEKCRERINLLKMALTA
KEKKRKSKEIFDKKKRENYLRVVKGRKHEEKKRIYSYIETVRMSNEEKELCLOKQRQL
AAERKIQVQRLVEFIFQVEEVALISESDMAVSTVSALRDASHTAYVRGQWVYTDGSGEA
QYRIVEPTLPCSGDYSAYNLWVAASQENGGNPDNSLRNPGHRISAGLCYASQMTAILSHI
LDIRLPRKQPYSEFCTNEITERQFKHSVASLNQNILYLCSFSQVSNPERLDPRNTLQNI
VLLSCPLLGRNSNFEIDKDLMASIEDSIIIFQEEDSDTGGMEDEMINDWEQVSEDVTVYTD
VPARGYSSTLSNIQTMSYPGPPEQLTASGFVTSAAATSFIESLYQYIFYIETHSFLDVY
IGTMWQLSYMPFVDKENILQMFPPKVFVAVAFPLAIGVIGLLVIGLFTSVTMSQRKGVNV
SKKS

>sp|Q6ZNE5|BAKOR_HUMAN Beclin 1-associated autophagy-related key regulator
OS=**Homo sapiens** OX=9606 GN=ATG14 PE=1 SV=1
MASPSGKGARALEAPGCGPRPLARDLVDSVDDAEGLYVAVERCPLCNTTTRRRRLTCAKCVQ
SGDFVLYDGRDRERFIKDKERLSRLKSKQEEFQKEVLKAMEGKWI TDQLRWKIMSCKMRI
EQLKQYITCKGNEEMKNSSEGLLKTKEKNQKLYSRAQRHQEKKEKIQRHNRKLGDLVEKKT
IDLRSHYERLANLRRSHILELTSVIFPIEEVKTGVRDPADVSSSESDSAMSSTVSKLAEA
RRTTYLSGRWVCDHNGDTSISITGPWISLPNNGDYSAYYSWVEEKKTTQGPDMESNPA
YTISAALCYATQLVNILSHILDVNLPKKLCNSEFCGENLSKQKFTRAVKLNANILYLCF
SQHVNLDQLQPLHLTLRNLMLVSPSSEHLGRSGPFVEVRADLEESMEFVDPGVAGESDESG
DERVSDEETDLGTDWENLPSPRFCDIPQSVEVSQSQSTQASPPIASSSAGGMISAAAAS

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
DIKRMEKKKDPMLNSMLKLDVLRMKNKNNLIRHRIEQLNERIYSKRNIHSELKVEIDNYK
CYKVGTTGDKLREQVEISDAKNKLAQVSKICESARDYKLNLLNNWFVIQKLQDNFQIPFA
IAFQPLISLKNFRILPLAITNDSINIMWKYISFFSDILMIKLPYTNKICEQPMFEFSDSI
QTVVQRLIKLIINILQICRHLKLVSTPMDIPWLLDQYDVGDLFYNMVKNKMKCRSVSL
YWTFGMLYSMVLDMNNPQRGHPARRTAPPPTVTGPHDRWYVVG

22. Activating molecule in BECN1-regulated autophagy protein 1 (AMBRA1)

>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
DGTKVASTHGDHTVRVSDVATGKCLHILRGHPRTWCIAFHPTSNQILASGCLGGEVRIW
DLHGFGTEVWRSKDNYEITSLTFHPTDHVLFVSVTNHIYFWDWSQPEPFVVKTNYEYEK
IRVVKFDPGQFLYTGIANNTTVRPPSRVSFISGNTHPNTVFNASRTQQLSNVYDSLVEC
FQASRRDRVLRNTEAGQDPQSVSNTQHGASNHQHSVPVHEEGLSLARQYASHITQSSQRSM
QGMSQRPEIPSGASNSSSSPDTDMDGISSPANPVLAMQPPRGASADNDVSGESPPSIVSV
DGESSQTRAVSNHPRSERVPGTLIVTERSPEQTSPPFQSLDTSSGVRIVSEAQSVRGILN
DQVHASTTAFIAPEEEPAEEVVISLSELTSRGLSEEHLHSSNTDCDRLNCPVCGNFDT
THIRRVCESEMFTQLRARRRSLQNSMNNVSARSASFSPYTYNRHGSLVRPEIHSIQDPSQ
LGEMHEIRRVENPNAGASNMDHVSNNNSAPSNTTEGDARLTQVGDNDIDICASIHENFATIT
ARIEREMNELDRRINNLNRTFNESLRLQHHRVSFLSAREGDVNGRRPSFIVARHTQQAE
GASSSRPEDSTHSLDRGQHLLLETALRSSRPDRTGSHSHSVPRELDSSHAWQSLERHHLHP
HYSVSILDNTINRPNDPIQTAINRAIADAFMGRGEPAVATNIINHTYRIQAWDFSRCNIP
DLTDTKSNIVVQHCKLHNDASCNLSQDGTMLATFVPSHRGFPDDNIMAVYSLEPKTRGQC
LFTKSFNPNAISVLSLPGSGYVMVGLAAKQLSWVFTPNQHITDVMHPCDMDIRTHVSVNS
ARWMPGSGEGIVYGTNRGDLHVCRPGTKKSVAGDNSDDRSIRRNLMHMLRMSGEQDVPRI
NTSTQTPGVRRSASTQTDTDSDM

>sp|Q9C0C7|AMRA1_HUMAN Activating molecule in BECN1-regulated autophagy protein 1 OS=**Homo sapiens** OX=9606 GN=AMBRA1 PE=1 SV=2
MKVVPEKNAVRIWGRERGARANGAQRLLQELVEDKTRWMKWEGKRVELPDSRSTFLLA
FSPDRLLASTHVNHNIYITEVKTGKCVHSLIGHRRTPWCVTFHPTISGLIASGCLDGEV
RIWDLHGGSSESWFTDSNNAIASLAFHPTAQLLLIATANEIHFWDWSRREPFAVVKTASEM
ERVRLVRFDPGLGHYLLTAIVNPSNQGDDEPEIPIIDGTELSHYRQRALLQSQPVRRTPLL
HNFLHMLSSRSSGIQVGEQSTVQDSATPSPPPPPPQPSTERPRTSAYIRLRQRVSYPTAE
CCQHLGILCLCSRCGTRVPSLLPHQDSVPPASARATTPSFSFVQTEPFHPPEQASSTQQ
DQGLLNRPASFASTVQSSTAGNTRLNLSLGPTRRSLGGPLSSHPSRYHREIAPGLTGSEWT
RTVLSLNSRSEAEASMPPTSSASSVLSLVLRLQOEGGSQASVYTSATEGRGFASGLATE
SDGGNGSSQNNSGSIRHELQCDLRRFFLEYDRLQELDQSLSGEAPQTQQAQEMLNNNIES
ERPGPSHQPTPHSSENNLSRGHLNRCRACHNLLTFNNDTLRWERTTPNYSSGEASSW
QVPSSFESVPSSGSQLPPLERTEGQTPSSSRLELSSASPQEERTVGVAFNQETGHWERI
YTQSSRSGTVSQEALHQDMPEESSEEDSLRRRLLESSLISLSRYDGAGSREHPIYPDPAR
LSPAAYYAQRMIQYLSRRDSIRQRSMRYQQNRLRSSTSSSSSDNQGPSVEGTDLEFEDFE
DNGDRSRHRAPRNARMSAPSLGRFVPRRFLPEYLPYAGIFHERGQPLATHSSVNRVLA
GAVIGDQSAVASNIANTTYRLQWDFTKFDLPEISNASVNVLVQNCKIYNDASCDISAD
GQLLAAFIPSSQRGFPDEGILAVYSLAPHNLGEMLYTKRFGPNAISVLSLSPMGRYVMVGL
ASRRILLHPSTEHMVAQVFRLLQQAAGGETSMRRVFNVLYPMPADQRRHVSINSARWLPEP
GLGLAYGTNKGDLVICRPEALNSGVEYYWDQLNETVFTVHSNSRSRSPGTSRATWRTRDR
DMGLMNAIGLQPRNPATSVTSQGTQTLALQLQNAETQTEREVPEPGTAASGPGESEY
GASGEDALSRIQRLMAEGGMTAVVQREQSTTMASMGGFNNIIVSHRIHRSSQTGTEPGA
AHTSSPQPSTSRGLLPEAGQLAERGLSPRTASWDQPGTPGREPTQPTLPSSSPVPPIPVSL
PSAEGPTLHCELTNNHLLDGGSSRGDAAGPRGEPNR

23. UV radiation resistance associated protein (UVRAG)

>XP_019925412.1 PREDICTED: UV radiation resistance associated protein
[Crassostrea gigas]
MGSLCENYVVLVLSCSWSLLVRVWVKNKTSTRLLLLDWMVDLNALEYLADKLLQDDKGIKYAPNTLIFGMFDQ
FFRAPEVVKVGVGVDGPGVEAEDDKSSKSQSVSTQCFLKVEIASTKKSYSYASSLSRIYTVLRAIKQTQAS
VHKVRRSIEDKLLSSQETTRKRAEHEDLLLKREQLCAEVTWRTASVNMKMDQADQLHRSNQEQETAMKKN
KEKLEEKQREQAEEKKKDYDQTREKLIKESAQLFIRRKQLIRELATYIYPIITEKKGLYYIANVYLPNSEDF
QGGDDNMIGVSLGYTCHLLLLMISGILDIPLYSMTHLVSKSVIRDDIHSRLEDKERDFPLYSKGKEQNLF
RYGVFTLNKNISQMRFYLGMGTVDLRRTTLMNIKTLLNRLGLKPESTQAQLRPASEPGDRQYSDFDRTDT
RSSLASVGRMAVDFRRELSVPPTEESSRQSSPNLHEVEEKEIFHPSSDDNFFKISNPVSERLADFESEIN
GCAQDVTNFHKPSDNRRTQTCWNGVGSNDFNAGDQPEEDHIYETVNVNRKTASESLDKSPSPSNILSS

>sp|Q9P2Y5|UVRAG_HUMAN UV radiation resistance-associated gene protein
OS=Homo sapiens OX=9606 GN=UVRAG PE=1 SV=1
MSASASVGGPVPQPPPGPAAALPPGSAARALHVELPSQQRRLRHLRNIAARNIVNRNGHQ
LLDITYFTLHLCSTEKIYKEFYRSEVIKNSLNPTWRSDFGIMPDRDLTSSVSCFVVKIWWG
KENIYQLLIEWKVLCDGLKYLGGQIHARNQNEIIFGLNDGYYGAPFEHKGYSNAQKTILL
QVDQNCVRNSYDVFSLRLHRAQCAIKQTQVTVQKIGKEIEEKLRLTSTSNELKKKSECL
QLKILVLQNELERQKKALGREVALLHKQIADLQDKGSAFSAEHLKQLQKESLNELRKEC
TAKRELFLKTNAQTLIRCRQLLSELSYIYPIIDLNEHKDYFVCGVKLPNSEDFQAKDDGSI
AVALGTYAHLVSMISFFLQVPLRYPIIHKGSRSTIKDNINDKLTAKEREFPLYPKGGEKL
QFDYGVYLLNKNIAQLRYQHGLGTPDLRQTLPNLKNFMEHGLMVRCDRHHTSSAIPVPKR
QSSIFGGADVGFSGGIPSPDKGHRKRASSENERLQYKTPPPSYNSALAQPVTTVPSMGET
ERKITSLSSSLDTSDFSKENKKKGEDLVGSLNGGHANVHPSQEQQEALSGHRATVNGTL
LPSEQAGSASVQLPGEFHPVSEAELECCCTVEQAEEIIGLEATGFASGDQLEAFNCIPVDSA
VAVECDEQVLGEFEFEFSRRIYALNENVSFRPRRSDK

>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
QSGSLRKLKSFQELPKLTGASTMIVLKLVLGSLVPSDILCTISSDKNGIIDDKWCVLCTYTID
LNKLQPINEDTVLITGTNAPVLDLIDGSYTLAAEKIKPLKGLVSSHKRNISQVKIKFSLA
YSSLLKLNKLLLEYSSQVHEEINEISSKIEDDFLSLKNQNHWMRTVQKSIETLEKEVLQR
KKSCKNIEMAQLESNDTINHSTELSLMSQDESINDDYGSYISRFVQIKDRLDQLRFKFL
YQLIGIFHSTDLFNSDRGYIYFEKPSVNDVINRLKPLNIEILLRQAGESTKHREYVN
SQLGYLLFLHLTAIQIFKAPLPYRLMYYGSTSVIDSQYPLYFTDQMISKHQAKLIKAIH
YFNADILQFKQILENYRPT

24. run domain Beclin-1-interacting and cysteine-rich domain-containing protein (RUBICON)

>XP_011419540.1 PREDICTED: run domain Beclin-1-interacting and cysteine-rich domain-containing protein isoform X3 [Crassostrea gigas]
MSDEVNADHNYSRERQSLLFGLKAVTEGLLSGQSSNVWNIHGGLNRMVCVQLEHIMYHGLKSIKGNFWIEL
DFWPFVYSLKMLNPVLAPALDKVNRSGGNGKSMWLRSLRDHTLSSQLSTLVCNKSMLKRFYGDALFLND
AQYFKALCVCLKAIELNQISLLAELDLKLLSNHEPNMRGSRSRSWAVPERKHHLSSTSEGKSSSHGAMAL
APPFASPKKESILCMSDEHAVPSSIRASTSPEDTKNMARESLRTVLRKSGSDSPTGDAPDFSFYDNLNSD
PLLNIEFSENAATDSENSHAEVGSGERIVNSSPKKAIVRSQSDTGMSKTLTVIKNIYKDNEDFEPGKSGT
VNRLEDIFSDSECPKKGEEENVKVKAKSKGHKRSRSDHGGIKVEKGPQKEKGVNPKTQREDSSEPASKD
IPGETTFRQPVHGQSLINYLSSQDFNTCANLDKENAHSISEALIAAIEQMKWNHVISPKDREDPEEEDS
DEEINKLQKQIRIRKQKQKLEKAKFFPTSSDGLTETATTSKSPSSVNLSSQDNTDSSNSDIEVDEINLT
NADLQKVKPDRQSSMESISDQSGMSAESVAILLKFKFSEKQLPKASELEWLVPISEAPQELLPLPKSYVPS
PDDIENEIGGFTNSLFGTLRLRGNNEWAPPRSQIIFDIHPYQKRAVVMKQNFRCAGCGTRVEPAYIKRF
RYCEYLKGYFCQCCHRNEINYIPGHIIRKWDFKQYPVSNFVSWRLLSRIFNEPYFNLSTINPSLFKRVKLL
ETVHAFRVQLMYLCKFLRICKYSER

>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
MRPEGAGMELGGGEERLPEESRREHWQLLGNLKTVEGLVSTNSPNVWSKYGGGLERLCRD
MQSILYHGLIRDQACRRQTDYWFVKDIRWLSPHSALHVEKFI SVHENDQSSADGASERA
VAELWLQHSLLQYHCLSAQLRPLLGDRQYIRKFYTDAAFLLSDAHVTAMLQCLEAVEQNNP

RLLAQIDASMFARKHESPLLVTKSQSLTALPSSTYTPPNSYAQHSYFGSFSSLHQSVPNNGSERRSTSFPLSGPPRKPQESRGHVSPAEDQTIQAPPVSVSALARDSPLTPNEMSSSTLTSPIEASWVSSQNDSPGDASEGPEYLAIGNLDPRGRTASCQSHSSNAESSSSNLFSSSSSQKPDSAASSLGDQEGGGESQLSSVLRSSFSSEGQTLTVTSGAKKSHIRSHSDTSIASRGAPESCNDKAKLRGPLPYSGQSSEVSTPSSLYMEYEGGRYLCSEGMFRRPSEGQSLISYLSEQDFGSCADLEKENAHFSISESLIAAIELMKCNMMSQCLEEEEEVEEEDSDREIQELKQKIRLRRQQIRTKNLLPMYQEAHGSFRVTSSSSQFSSRDSAQLSDSGSADEVDEFEIQDADIRNTASSSKSFVSSQSFHCFLHSTSAEAVAMGLLKQFEGMQLPAASELEWLVPEDHAPQKLLPIPDSLPISPDDGQHADIYKLRIRVRGNLEWAPPRPQIIFNVHPAPTRKIAVAKQNYRCAGCGIRTDPDYIKRLRYCEYLKGYFCQCCHENAQMAIPSRVLRKWDFSKYVVSNFSSKDLLIKIWNDPLFNVQDINSALYRKVKLLNQVRLLRVQLCHMKNMFKTCRLAKELLDSDFTVPGHLTEDLHLYSLNDLTATRKGELGPRLAELTRAGATHVERCMLCQAKGFICEFCQNEDDIIFPFELHKCRTCEECKACYHKACFKSGSCPRCERLQARREALARQSLESYLSDYEEEPAEALALEAAVLEAT

25. Endophilin-B1

>tr|K1Q963|K1Q963_CRAGI Endophilin-B1 OS=**Crassostrea gigas** OX=29159
GN=CGI_10012647 PE=4 SV=1
MDANTGLFKMKKFVSDASTVFNRAVQFTEEKLGSAEKTELDAHFENLLQRADKTKAWTEKILKQTESVLQPNPNIRMEDFVYEKLDKDKKRDVNHHEVLGHVLDVGGNDFGPGTTYGNALVKCGQAQLRIGNAEREFIQTTSNNFLOPLHNFLEGDMKTIQKEKKILETKRLDLDAASKNRLRKAKSTSQPQSSQNSPQNVLMVVEAEADLRVAQAEFDRQAEITKLLLEGVSSAHAHLRCLNDFIEAQLTYAQCQNYISELQQQLGSYSHTSGVGNSSNSGAGISSGIPSSVPLQPSAPPQINVIAATPNIEKKQARVLYDYDAADSELTLLEDELITVYKTPGLDPDWLMAERGPOKGVPTTYLEVEL

>sp|Q9Y371|SHLB1_HUMAN Endophilin-B1 OS=**Homo sapiens** OX=9606 GN=SH3GLB1
PE=1 SV=1
MNIMDFNVKLAADAGTFLSRAVQFTEEKLGQAEKTELDAHLENLLSKAECTKIWTEKIMKQTEVLLQPNPNARIEEFVYEKLDKDRKAPSRINNPELLGQYIMIDAGTEFGPGTAYGNALIKCGETQKRIGTADRELIQTSALNFLTPLRNFIIEGDYKTIAKERKLLQNKRLDLDAKTRLKAKAAETRNSSEQELRITQSEFDRQAEITRLLLEGISSTHAHHLRCLNDFVEAQMTYYAQCYQYMLDLQKQLGSFSPSNYLSNNNQTSVTPVPSVLPNAIGSSAMASTSGLVITSPSNLSDLKECSGSRKARVLYDYDAANSTELSLLADEVITVFSVVGMDSDWLMGERGNQKGVPIITYLELLN

26. ubiquitin-like protein ATG12 (ATG12)

>XP_011416102.1 PREDICTED: ubiquitin-like protein ATG12 [**Crassostrea gigas**]
MSDDGNESRDSKNTETEEKSTPASPISHVAETKIDVLLKPADAPIMKKKKWAVDRNKRIGWVGEFIKKYL
KLTAQDSLFLYVNVQSFAPTPDTEIGSIFDCFGSDGKLVLYHYCKTQAWG

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

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

27. Autophagy protein 5 (ATG5)

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

FPLHTEKINKHFLKYASEKESEEIWLHEDNQPLKWHYPVGLLFDLYGSETSLPWTITVHF
KDFPEEELLHCVSKDAVESHFMSI KEADSLKHRGQVINSMQKRDHKQLWTGLLHDKFDQ
FWSVNKKLMESSGDETFKYIPFRLYMVDRHYMTNLFRLPTEEGHHQSLKHLLLSAVPQFF
NEEEEFQKHVRIHGTEPLLDTPILWLSENFSFPDNFLHLVISDK

>sp|Q9H1Y0|ATG5_HUMAN Autophagy protein 5 OS=**Homo sapiens** OX=9606 GN=ATG5
PE=1 SV=2

MTDDKDVLRDVFGRIPTCFTLYQDEITEREAEPYLLLPVSYLTLVTDKVKKHFQKVM
RQEDISEIWFYEGTPLKWHYPIGLLFDLLASSALPWNITVHFKSFPEKDLLHCPSKDA
IEAHFMSCMEADALKHKSQVINEMQKKDHKQLWMGLQNDRFDFWAINRKLMEYPAEEN
GFRYIPFRIYQTTTTERPFIQKLFPRVAADGQLHTLGDLLKEVCPSAIDPEDGEKKNQVMI
HGIEPMLETPLQLWSEHLSYDPDNFLHISIIPQPTD

>sp|Q12380|ATG5_YEAST Autophagy protein 5 OS=**Saccharomyces cerevisiae**
(strain ATCC 204508 / S288c) OX=559292 GN=ATG5 PE=1 SV=1

MNDIKQLLWNGELNVLVSIDPSFLMKGSPREIAVLRIRVPRETYLVNYMPLIWNKIKSFL
SFDPLTDSEKYFWFEHNKTPIPWNYPVGVLFDFCLAGKSATFTTSFENQVKDVLTFRLIHL
VMGDSLPPITIIPIASSKTQAEKFWFHQWQVCFILNGSSKAIMSLSVNEARKFWGSVITR
NFQDFIEISNKISSRPRHIPLIIQTSRTSGTFRISQPTISMTGVNPTLKDIEGDILDVK
EGINGNDVMVICQIEIPWHMLLDLYSKLRSFDGFLYITLVPIKGGDKASSEL

28. Autophagy-related protein 16-1 (ATG16 L1)

>tr|K1RWG6|K1RWG6_CRAGI Autophagy-related protein 16-1 OS=**Crassostrea gigas**
OX=29159 GN=CGI_10012629 PE=4 SV=1

MDPKDLHWKHSLLLEQLRQRDKKEKEPFESLISHWKHFEASQSLKSKNTQLTWEAEKLKE
ENLGLQIKVEQGGSGNSQALEQKLFKLQEEVTELHRRRGENTQQIIDLNNALQDKEKEL
QGRDARLNDLLANELALKMEIKNLESTIMELEATNQMLKDEHQALQLTYYTGLEEKYRKVE
QDNQQLLERWIKQQAQMADQLNAENDQFMAVRQOKLRQDLEDAARENIQILPENQAGVYV
PTSIPICLSASLPTKAQYKFDADHDGDVNAVRSWSPSGSLFATGGADRKIKLWEVINGKCEC
KGILTGSNAGIMALDFDLEENTILGASNDFASRVWSLTDHRVVRHTLTGHSGKVLAAKFLG
DSFKVVS GSHDRTLKIWDLHSRSCVKTI FAGSSCNDLVTIHGTNIVSGHFDKRVRFWDSR
VDSNTNEILLQGRLTSLDLSPKMSLLCCTRDDTLKVLDLRMNQISTTLAHDHDFKVGCDW
SRAVFRHSVIACSWHPVGSYVLSCEKQRKTVLWSDI

>sp|Q676U5|A16L1_HUMAN Autophagy-related protein 16-1 OS=**Homo sapiens**
OX=9606 GN=ATG16L1 PE=1 SV=2

MSSGLRAADFPRWKRHISEQLRRRDLRQRAFEEIILQYNKLEKSDLHSVLAQKLQAEK
HDVPNRHEISPGHDGTWNDNQLQEMAQLRIKHQEELTELHKKRGELAQLVIDLNNQMQRK
DREMOMNEAKIAECLQTI SDLETECLDLRKTCLCDLERANQTLKDEYDALQITFTALEGKL
RKTTEENQELVTRWMAEKAQEANRLNAENKDSRRRQARLQKELAEAAKEPLPVEQDDDI
EVIVDETS DHTEETSPVRAISRAATKRLSQPAGGLLDSITNIFGRRSVSSFPVPQDNVDT
HPGSGKEVRVPATALCVFADHDGEVNAVQFSPGSRLLATGGMDRRVKLWEVFGKCEFKG
SLSGSNAGITSIEFDSAGSYLLAASNDFASRIWTVDYRLRHTLTGHSGKVL SAKFLLDN
ARIVSGSHDRTLKLWDLRSKVCIKTVFAGSSCNDIVCTEQCVMSGHFDKKIRFWDIRSES
IVREMELLGKITALDLNPERTELLSCSRDILLKVIDLRTNAIKQTF SAPGFKCGSDWTRV
VFSPDGSYVAAGSAEGSLYIWSVLTGKVEKVL SKQHSSINAVAWSPSGSHVVSVDKGCK
AVLWAQY

29. Autophagy-related protein 10 (ATG10)

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

MAAGSISEDEYWDSEIIFFLTSSKIDSKWTIVDTKDGRRFAKKTVEVFILSTENKESTMND
DVIRNTELMEEQEEDTAAAFQVRGNSDVEVVTYEYHILYSPSYGVPVLYFNAHTQGGKLLA
LEEIWKRVDPDAYKERLSEERWTFITQQEHPLLGRPFYLLHPCHTADLMKNSPVLTDKRHY
IVSWLSAVGPVVGLKLPLEYGKLCVS

>sp|Q9H0Y0|ATG10_HUMAN Ubiquitin-like-conjugating enzyme ATG10 OS=**Homo sapiens**
OX=9606 GN=ATG10 PE=1 SV=1

MEEDEFI G E K T F Q R Y C A E F I K H S Q Q I G D S W E W R P S K D C S D G Y M C K I H F Q I K N G S V M S H L G

ASTHGQTCLPMEEAFELPLDDCEVIETAAASEVIKYEYHVLYSCSYQVPVLYFRASFLDG
RPLTLKDIWEGVHECYKMRLQLQGPWDTITQQEHPILGQPFVVLHPCKTNEFMTPVLKNSQ
KINKNVNYITSWLSIVGPVVGLNLPLSYAKATSQDERNVP

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

30. Microtubule-associated proteins 1A/1B light chain 3A (MAP1LC3A)

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

>sp|Q9H492|MLP3A_HUMAN Microtubule-associated proteins 1A/1B light chain 3A
OS=*Homo sapiens* OX=9606 GN=MAP1LC3A PE=1 SV=2
MPSDRPFKQRRSFADRCKEVQQIRDQHPISKIPVIIERYKGEKQLPVLDKTKFLVPDHNVM
SELVKIIRRRRLQLNPTQAFFLLVNQHSMVSVSTPIADIYEQEKDEDDGFLYIMVYASQETFG
F

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

31. Microtubule-associated proteins 1A/1B light chain 3B (MAP1LC3B)

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

>sp|A6NCE7|MP3B2_HUMAN Microtubule-associated proteins 1A/1B light chain 3
beta 2 OS=*Homo sapiens* OX=9606 GN=MAP1LC3B2 PE=2 SV=1
MPSEKTFKQRRTFEQRVEDVRLIREQHPTKIPVIIERYKGEKQLPVLDKTKFLVPDHNVM
SELIKIIRRRRLQLNANQAFFLLVNGHSMVSVSTPISEVYESEKDEDDGFLYIMVCASQETFG
MKLSV

>NP_009475.1 ubiquitin-like protein ATG8 [*Saccharomyces cerevisiae* S288C]
MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQFVYVIRKRIML
PPEKAIFFVNDTLPPTAALMSAIYQEHKDKDGFLYVTYSGENTFGR

32. Microtubule-associated proteins 1A/1B light chain 3C (MAP1LC3C)

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

>sp|Q9BXW4|MLP3C_HUMAN Microtubule-associated proteins 1A/1B light chain 3C
OS=*Homo sapiens* OX=9606 GN=MAP1LC3C PE=1 SV=1
MPPPQKIPSVRPFKQRKSLAIRQEEVAGIRAKFPNKIPVVVERYPRETFLPPLDKTKFLV
PQELTMTQFLSIIIRSRMVLRAEAFYLLVNNKSLVSMASATMAEIIYRDYKDEDDGFLYMTYA

SQETFGCLESAAPRDGSSLEDRPCNPL

>NP_009475.1 ubiquitin-like protein ATG8 [*Saccharomyces cerevisiae* S288C]
MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQFVYVIRKRIML
PPEKAIFIFVNDLPTAALMSAIYQEHKDKDGLYVVTYSGENTFGR

33. Gamma-aminobutyric acid receptor-associated protein (GABARAP)

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

>sp|O95166|GBRAP_HUMAN Gamma-aminobutyric acid receptor-associated protein
OS=*Homo sapiens* OX=9606 GN=GABARAP PE=1 SV=1
MKFVYKEEHPFEKRRSEGEKIRKKYPDRVPVIVEKAPKARIGDLDKDKKYLVPDLTVGQF
YFLIRKRIHLRAEDALFFVNNVIPPTSATMGQLYQEHHEEDFFLYIAYSDESVEYGL

>NP_009475.1 ubiquitin-like protein ATG8 [*Saccharomyces cerevisiae* S288C]
MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQFVYVIRKRIML
PPEKAIFIFVNDLPTAALMSAIYQEHKDKDGLYVVTYSGENTFGR

34. Gamma-aminobutyric acid receptor-associated protein-like 1 (GABARAP L1)

>XP_011437796.1 PREDICTED: gamma-aminobutyric acid receptor-associated
protein [*Crassostrea gigas*]
MKWEYKEEHSFEKRRAEAGEKIRKKYPDRVPVIVEKAPKARVGDLDKDKKYLVPDLTVGQFYFLIRKRIHL
RPEDALFFVNNVIPPTSATMGSLYQEHHEEDFFLYIAYSDESVEYGA

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

>NP_009475.1 ubiquitin-like protein ATG8 [*Saccharomyces cerevisiae* S288C]
MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQFVYVIRKRIML
PPEKAIFIFVNDLPTAALMSAIYQEHKDKDGLYVVTYSGENTFGR

35. Gamma-aminobutyric acid receptor-associated protein-like 2 (GABARAP L2)

>sp|P60520|GBRL2_HUMAN Gamma-aminobutyric acid receptor-associated protein-
like 2 OS=*Homo sapiens* OX=9606 GN=GABARAPL2 PE=1 SV=1
MKWMFKEDHSLEHRCVESAKIRAKYPDRVPVIVEKVSQSQIVDIDKRKYLVPDLTVGQF
MWIIRKRIQLPSEKAIFLFDVKTVPQSSLTMGQLYEKEKDEDGFLYVAYSSENTFGF

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

>NP_009475.1 ubiquitin-like protein ATG8 [*Saccharomyces cerevisiae* S288C]
MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQFVYVIRKRIML
PPEKAIFIFVNDLPTAALMSAIYQEHKDKDGLYVVTYSGENTFGR

36. Gamma-aminobutyric acid receptor-associated protein-like 3 (GABARAP L3)

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

>NP_009475.1 ubiquitin-like protein ATG8 [*Saccharomyces cerevisiae* S288C]
MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQFVYVIRKRIML
PPEKAIFIFVNDTLPPTAALMSAIYQEHEKDKDGLYVVTYSAGENTFGR

37. Autophagy-related protein 7 (ATG7)

>tr|K1RAF7|K1RAF7_CRAGI Autophagy-related protein 7 OS=*Crassostrea gigas*
OX=29159 GN=CGI_10025698 PE=4 SV=1
MSFQQVYFGFCDPSNIEDYPGWPLRNFLMLISYHWKGDLRGVNVLCLRDRSRDGTDRDISH
SLLLSLNVDPDIRNVPECPKCVGWKNEKQKLAAPRFVNLSASMDPTRLAASAVDLNLKLMR
WRLLELDLISRTKCLLLGAGTLGCNVARCLMGWGVRTITLVDNGRVSYSNPVRQSLF
QFEDCVKGGKPKAEAAAEAMKKIFPGVNAKGLSLSIPMPGHAVPESAIEGVKKDVTQLQD
LVNSHDAVFLLLDTRESRWLPTLMAAEKQKIVICISALGFDTYLVMRHGVRSDTEGADPAP
LSSYSSIPGDQLGCYFCNDVVAPGNSLKDRTLDQQCTVSRPGISYMASALAVELLVSVLQ
HPELGKAPADTSASDEHLSKDFVCPLGLVPHQQIRCFVSRFQQVLPACKAFDKCTACSKT
VIEQFRRDGFDFLRRAFNDPSYLEDLTGLTQMHOETLDAEVWGFSDDEECSSMEVSSS

>tr|K1QKL2|K1QKL2_CRAGI Autophagy-related protein 7 OS=*Crassostrea gigas*
OX=29159 GN=CGI_10002553 PE=4 SV=1
MSAPLVNKMERKQLQFVAFNSFLDSGFWHKLSENKLDVYGLDESQKEIKGFYFNGDPVGM
PCRMNVEFSAFDQDAKTPQRCLPMLGELHNTNTVDKFKCEDKEMISEAGKKIWDSDIVSG
KALDTPPELLATFLLLTAFADLKKYHYFYWFPCPLCPSTDITFDQEPKPKLYRLTAEEMEQ
FLQAYDTFQDAHPTYQGGFFAVLSKGNIVIEDVKYMNKFENTQEVYFGFCDPSNIEDYPG
WPLRNFLMLISYHWKGDLRGVNVLCLRDRSRDGTDRDISHSLLLSLVCVPDIKNVLECPKCV
GWKNEKQKLAAPRFVNLSASMDPTRLAASAVDLNLKLMRWRLLELDLISRTKCLLLG
AGTLGCNVAKCLMGWGVRTITLVDNGRVSYSNPVRQPLFQFEDCVKGGKPKAEAAAEAMK
KIFPGVNAKGLSLSIPMPGHAVPEGVKKDVTQLQDLVNSHDAVFLLLDTRESRWLPTLMA
AEKQKIVICISALGFDTYLEMRHGVRSDTEGADLAPLSSYSSIPRDQLGCYFCNDVVAPGN
SLKDRTLDQQCTVSRPGISYMASALAVELLVSMQLQHPELYLVLFKFSMKNKAENYINYGS
TELQQRCLPTKQNRMAKGIHKTCLHKNRQOS

>sp|O95352|ATG7_HUMAN Ubiquitin-like modifier-activating enzyme ATG7
OS=*Homo sapiens* OX=9606 GN=ATG7 PE=1 SV=1
MAAATGDPGLSKLQFAPFSSALDVGFWHELTQKKLNEYRLDEAPKDIKGYYYNGDSAGLP
ARLTLEFSAFDMSAPTARCCPAIGTLYNTNTLESFKTADKLLLEQAANEIWESIKSGT
ALENPVLLNKFLLLTAFADLKKYHFYWFPCPALCLPESLPLIQGPVGLDQRFSLKQIEAL
ECAYDNLCQTEGVTALPYFLIKYDENMVLVSLKHYSDFFQQRKTIITIGVYDPCNLAQY
PGWPLRNFLVLAHRWSSSFQSVVEVVCFRDRTMQGARDVAHSIIFEVKLPMAFSPDCPK
AVGWKQKGGMGRPMVNLSECMDPKRLAESSVDLNLKLMCWRLVPTLDLTKVSVKCLL
LGAGTLGCNVARTLMGWGVRHITFVDNAKISYSNPVRQPLYEFEDCLGGGKPKALAAADR
LQKIFPGVNAARGFNMSIPMPGHPVNFSSVTLEQARRDVEQLEQLIESHDVVFLLMDTRES
RWLPAVIAASKRKLVINAAALGFDTFVVMRHGLKPKQAGDLCNHPVASADLLGSSLF
ANIPGYKLGCYFCNDVVAPGDSTRDRTLDQQCTVSRPGLAVIAGALAVELMVSVLQHPG
GYAIASSSDDRMNEPPTSLGLVPHQIRGFLSRFDNVLPVSLAFDKCTACSSKVLQYERE
GFNFLAKVFNSSHSFLEDLTGLTLLHQETQAAEIWDMSSDETI

>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
MSSERVLSYAPAFKSFLDTSFFQELSRLKLDVLKLDSTCQPLTVNLDLHNI PKSADQVPL
FLTNRSEFKHNNKRTNEVPLQGSIFNFNVLDEFKNLQFLHQRALCEWEDGKIDINKC
VSFVIIISFADLKRYFYWLGVPFCQRPSSTVLHVRPEPSLKGLFSKCQKWFVNYSKWV
CILDADDEIVNYDKCIIKTKVLAIRDSTSTMENVPALTKNFLSVLQYDVPDLIDFKLLI
IRQNEGSFALNATFASIDPQSSSNPDMKVSQWERNVQKLAAPRVVDLSSLLDPLKIADQ
SVDLNLKLMKWIRLPDLNLDIKNKTKVLLLGAGTLGCYVSRALIAWGVKRIITFVDNGTVS
YSNPVRQALYNFEDCGKPKAEALAAASLKRIIFPLMDATGVKLSIPMIGHKLVNEEAQHDKF
DRLRALIKEHDIIFLLVDSRESRWLPSLLSNIENKTVINAALGFDSYLVMRHGVRDEQSS
KQLGCYFCHDVVAPTDSLTDRTLDQMCTVTRPGVAMMASSLAVELMTSLLQTKYSGSETT
VLGDIHQIRGFLHNFSLKLETPAYEHCSPKVIIEAFTDLGWVFKKALEHPLYLEE
ISGLSVIKQEVERLGNDVFEWEDDESDEIA

38. Ubiquitin-like-conjugating enzyme ATG3 (ATG3)

>sp|Q9NT62|ATG3_HUMAN Ubiquitin-like-conjugating enzyme ATG3 OS=**Homo sapiens** OX=9606 GN=ATG3 PE=1 SV=1
MQNVINTVKGKALEVAEYLTPVLKESKFKETGVITPEEFVAAGDHLVHHCPTWQWATGEE
LKVKAYLPTGKQFLVTKNVPCKYKRCCKQMEYSDELEAIIIEEDDGGWVDTYHNTGITGIT
EAVKEITLENKDNIRLQDCSALCEEEEEDEDEGEAADMEEYEESGLLETDEATLDTRKIVE
ACKAKTDAGGEDAILQTRTYDLYITYDKYYQTPRLWLFGYDEQRQPLTVEHMYEDISQDH
VKKTVTIENHPLPPPPMCSVHPCRHAEMVKKI IETVAEGGGELGVHMYLLIFLKFVQAV
IPTIEYDYTRHFTM

>tr|K1R934|K1R934_CRAGI Autophagy-related protein 3 OS=**Crassostrea gigas**
OX=29159 GN=CGI_10024759 PE=3 SV=1
MQNVINAVKGTALNVAEKFTPVVKESKFKETGVITPEEFVAAGDHLVHHCPTWQWSTGDE
SKVKPYLPKEKQYLITRNVPCKYKRVKQVDSHKEEQEKVIEADDEDGGWVDTHHFDPDGT
SLQDAVQEMTLDGKGDKRSSEEVKRSGLDDDDDDDDDEEAMDMEAQESGMLDEEDD
AALDPSTLGRQDSESAATESGILQTRTYDLNITYDKYYQTPRLWLFGYDENRKLPTVEQM
YEDFSQDHAKKTVTMEAHPLPGPPLASVHPCRHADVMKKI IQMVAEGGGDLGVHVYLM
FLKFKVQAVIPTIEYDFTRDFTM

>sp|P40344|ATG3_YEAST Autophagy-related protein 3 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=ATG3 PE=1 SV=1
MIRSTLSSWREYLTPIHKTSTFLTGTQITPEEFVQAGDYLCHMFPTWKWNEESSDISYRD
FLPKNKQFLIIRKVPCKRAEQCVEVEGPDVIMKGFAEDGDEDDVLEYIGSETEHVQSTP
AGGTKDSSIDDIDELIQDMEIKEEDENDDTEEFNAKGLAKDMAQERYDLYIAYSTSYR
VPKMYIVGFNSNGSPLSPEQMFEDISADYRKTATIEKLPFYKNSVLSVSIHPCKHANVM
KILLDKVRVVRQRRRRELQEEQELDGVGDWEDLQDDIDDSLVRVDQYLIVFLKFKITSVTPS
IQHDYTMEGW

39. Cysteine protease ATG4 (ATG4)

>tr|K1QKP1|K1QKP1_CRAGI Cysteine protease OS=**Crassostrea gigas** OX=29159
GN=CGI_10023225 PE=3 SV=1
MDMTNDVGTGMVITYESAALGYVDFPLTEEPVYLLGIKYSALYDRDELKGFDSKIWCTYR
KNFPAIGGTGPTCDGGWGCMLRCGQMMMLAQALVVRHLGRDWWKWNKNCQDQTYKRILQMFA
DKKSANYSIQQIASMGVSEGKPVGSWFGPNTVAQVLKKLAVYDEWSSIVIHAMDNVTVE
NDIKSVCKDDGKSTCDIIGVRQLKHESAATGRSKSSQDSSKQDKNKQNAVVDKSWKPLL
LVIPLRLGLTEINSYVQSLKACLSPQSVGIIGGKPNHAHWFGYMSDKLIYLDPHHTQ
LCEDLSPNFSEDSYVHCYPSTMNVMELDPSIALGFYCGTEKEFDLDTQSVQKFFVVGSSK
TPMFELYKDRPPHWPPEYESTGQTTASASGVTMTGGQDTDEEFELV

>sp|Q8WYN0|ATG4A_HUMAN Cysteine protease ATG4A OS=**Homo sapiens** OX=9606
GN=ATG4A PE=1 SV=1
MESVLSKYEDQITIFTDYLEEYPTDELVWILGKQHLLKTEKSKLLSDISARLWFTYRRK
FSPIGGTGSSDAGWGCMLRCGQMMMLAQALICRHLGRDWSWEKQKEQPKEYQRILQCFLD
RKDCCYSIHQMAQMGVGEKSGIGEWFGPNTVAQVLKKLALFDEWNSLAVYVSMNDTVVIE
DIKKMCRVPLSADTAGDRPPDSLTAASQSKGTSAYCSAWKPLLLIPLRLGINQINPVY
VDAFKECFKMPQSLGALGGKPNNAFFIGFLGDELIFLDPHTTQTFVDTEENGTVDNQTF
HCLQSPQRMNINLNDPSVALGFFCKEEKDFDNWCSLVQKEILKENLRMFELVQKHP SHWP
PFVPPAKPEVTTTGAEFIDSTEQLLEEFDLEEDFEILSV

>sp|Q9Y4P1|ATG4B_HUMAN Cysteine protease ATG4B OS=**Homo sapiens** OX=9606
GN=ATG4B PE=1 SV=2
MDAATLTYDTLRFAEFEDFPETSEPVWILGRKYSIFTEKDEILSDVASRLWFTYRKNFPA
IGGTGPTSDTGWGCMLRCGQMIFAQALVCRHLGRDWRWTQRKRQPD SYF SVLNAF IDRKD
SYYSIHQIAQMGVGEKSGIQWYGPNTVAQVLKKLAVFDTWSSLAVHIAMDNVTVMEEIR
RLCRTSVPCAGATAFPADSDRHCNGFPAGAEVTNRPSRPLVLLIPLRLGLTDINEAYV
ETLKHCFMMPQSLGVIGGKPNNAHYFIGYVGEELIYLDPHHTTQPAVEPTDGC FIPDES
CQHPPCRMSIAELDPSIAVGFFCKTEDDFNDWCQVKKLSLLGGALPMFELVELQPSHLA
CPDVLNLSLDSSDVERLERFFDSEDEDFEILSL

>sp|Q96DT6|ATG4C_HUMAN Cysteine protease ATG4C OS=**Homo sapiens** OX=9606
GN=ATG4C PE=1 SV=1
MEATGTDEVDKDKTKFISAWNNMKYSWVLTCTKYFNRNSPVLGKCYHFKYEDDKTLP
AESGCTIEDHVIAGNVEEFRKDFISRIWLTYREEFPQIEGSALTTDCGWGCTLRGTGQMLL
AQGLLILHFLGRAWTWPDALNIENSDESWSHTVKKFTASFEASLSGEREFKPTPTISLKE
TIGKYSDDHEMRNEVYHRKIIISWFGDSPLALFGLHQLIEYGKKSCKKAGDWYGPVVAHI
LRKAVEEARHPDLQGITIYVAQDCTVYNSDVIDKQASMTSDNADDKAVIILVVPVRLGGE
RTNTDYLEFVKGILSLEYCVGIIGGKPKQSYFFAGFQDDSLIYMDPHYCQSFVDVSIKDF
PLETFHCPSPKKMSFRKMDPSCITIGFYCRNVQDFKRASEEITKMLKFSSEKEYPLFTFVN
GHSRDYDFTSTTTNEEDLFSSEDEKKQLKRFSTEEFVLL

>sp|Q86TL0|ATG4D_HUMAN Cysteine protease ATG4D OS=**Homo sapiens** OX=9606
GN=ATG4D PE=1 SV=1
MNSVSPAAAQYRSSSPEDARRRPEARRPRGPRGPDNGLGSPGASGPALGSPGAGPSEPD
EVDKFKAKFLTAWNNVYKGVVKSRTSFSKISSIHLGRRYRFELEGEDIQRFRQDFVSR
WLTYYRRDFPLPGGCLTSDCGWGCMLRSGQMMLAQGLLLHFLPRDWTWAEGLGPPPELS
GSASPSRYHGPARWMPRWAQGAPELEQERRHRQIVSWFADHPRAPFGLHRLVELGQSSG
KKAGDWYGPSLVAHILRKAVESCDVTRLVVYVSQDCTVYKADVARLVARPDPTAEWKS
VILVVPVRLGGETLNPVYVPCVKELLRCELCLGIMGGKPRHSLYFIGYQDDFLLYLDPHYC
QPTVDVVSQADFPLESFHCTSPRKMAFAKMDPSCITVGFYAGDRKEFETLCSELTRVLS
SSSS ATERYPMFTLAEGHAQDHSDDLCSQLAQPTLRLPRTGRLLRAKRPSSEDFVFL

>sp|P53867|ATG4_YEAST Cysteine protease ATG4 OS=**Saccharomyces cerevisiae**
(strain ATCC 204508 / S288c) OX=559292 GN=ATG4 PE=1 SV=2
MQRWLQWKMDLVQKVSHGVFEGSSEEPALMNHDIIVLGEVYPERDEESGAEQCEQDCR
YRGEAVSDGFLSSLFGREISSYTKFLLDVQSRVNFTYRTRFVPIARAPDGPSPLSLNL
VRTNPSTIEDYIANPDCFNFDIGWGCMI RTGQSLLGNALQILHLGRDFRVNGNESLERE
SKFVNWFNDTPEAPFSLHNFVSAGTELSDKRPGWFGPAATARSIQSLIYGFPECGIDDC
IVSVSSGDIYENEVEKVFENPNSRILFLLGVKLGINAVNESYRESICGILSSTQSVGIA
GGRPSSSLYFFGYQGNFLHFDPHIPQPAVEDSFVESCHTSKFGKQLQSEMDPMLIGIL
IKGEKDWQWKLEVAESAIINVLAKRMDDFDVSCSMDDVESVSSNSMKK DASNNENLGV
L EGDYVDIGAIFPHTTNTEDVDEYDCFQDIHCKKQKIVVMGNTHTVNANLTDYEVEGVLVE
KETVGIHSPIDEKC

40. Sequestosome-1 (SQSTM1)

>tr|K1QI43|K1QI43_CRAGI Sequestosome-1 OS=**Crassostrea gigas** OX=29159
GN=CGI_10004110 PE=4 SV=1
MSLTVKÄFLVKGGNEKAEIRRFTVPQDVSAFSDYLQKKIADIFPGLARGNFNLFWKDEDG
DLIAFSTGEELLEALGFVDNGLFRVFKPTSQSSGDKPAGNTPMQEHPGII CDGCEGKVI
GRRYKCTECPDYDLCSCESKGIHSEHNFMMYDTPVHPGYGFPFSWPPRPQCPPGPRGPS
GQGQPPCAPPHFFRWMERMARRQNRDNAGCPRSQRNAEDQGSNDTSGEGAYNPEEFLO
NVGQSVAAMLDPLGIDVQVDVEHGRRCPAWGQGGGCKGKRSKCGQKCGNKGEQEEKM
ESDKVETE QMKTPEEATPMATDNADKLQTDGPSTSAENAPNPSEKVTKDFETWTFMEDGN
RSGRTPSPAPTVPQPPPTQLIYPPTDPRIAEALQQMLGMGFHNEGGWLQNLLEQKEGNI
SQVLDAIQTRAKTTPDGGFMA

>tr|K1PXV3|K1PXV3_CRAGI Sequestosome-1 OS=**Crassostrea gigas** OX=29159
GN=CGI_10004109 PE=4 SV=1
MACWSVKAHLGDDGKTSEIRRVSVPVSATYNQLYDKTKTVFPDLHNEEISLSWKDGDGD
LVFSFSSDAEMLEFTRTAEDEFLRIFIKVRAPKSNKSTPKTPTGAEWVNPWIEKMSDLS
EEFSQSVLAGMRTVFQYIAGAETFHDKDRKIVDKSDVTNKEEREPSVCNNADHLHRDVTE
VRGTHKIEEAELEKLLAMGFHNEEGWLYRLIEEKEGRIDEVLESILPDENRAGIYGAQSSS
YQKHEASKPKSRDPVNRASYPYPSCKNNRKTSHPETGGKPDIEDGPVTRDSDPKNGESWT
LVEDDTS LAETKADQNLEEGGSTQGGGAERKSHNARPTIPPIDPKIASALAEEMMSMGFQ
N DDGWLCLLQENNGNIEKVLDI IQGSDGKIYSK

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

GGFQAHYRDEGDGLVAFSSDEELTMAMSYVKDDIFRIYIKEKKECRRDHRPPCAQEAPRN
MVHPNVICDGCNGPVVGTTRYKCSVCPDYDLCSVCEGKGLHRGHTKLAFFSPFGHLSEGFS
HSRWLRKVKHGHFGWPGWEMGPPGNWSPRPPRAGEARPGPTAESASGSPSEDPSVNFKNV
GESVAAALSPLGIEVDIDVEHGGKRSRLTPVSPESSTEEKSSSQSSCCSDPSKPGGNV
EGATQSLAEQMRKIALESEGRPEEQMESDNCSGGDDWTHLSSKEVDPSTGELQSLQMP
SEGPSLLDPSQEGPTGLKEAALYPHLPPEADPRLIESLSQMLSMGFSDDEGGWLRLLQTK
NYDIGAALDTIQYSKHPPPL

41. Autophagy-related protein 29 (Atg29)

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

42. Autophagy-related protein 31 (Atg 31)

>sp|Q12421|ATG31_YEAST Autophagy-related protein 31 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=ATG31 PE=1 SV=1
MNVTVTVYDKNVKYRLEENIKNNKGPSNDDQPAYNNEKSTDGSYAMFPTNIKIYIFEDN
NDELVDSSDAALTAGIDKVGDELENVIIVQLDESGSLEDITLISDQYELLSHRTNSLSLE
ENQMRTLSSHGDDKSNDEEEELSVDSDRFRVSDIELDVISQFCDLSPFLRDLSLNDLIK
LYVTQNEQLQMLNSV

43. Autophagy-related protein 20 (Atg20)

>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
NQESNAETCRTLSGINSMNETSASEEPSVSNRKK SARIHILEAKRVSEGOGRAYIAY
VIQFENSTVQRRYSDFESLRSILIRLFPMTLIPPIPEKQSIKNYGKSITGSSSKYLLPSE
GSGSVDLSLSVIHASVNSDEKLIRHRIRMLTEFLNKLLTNEEITKTSIITDFLDPNNHN
WHEFVNSSSTFSSLPKSILQCNPLDPTNTTRIHAMLPPIPGSSQLLLNKESNDKMDKER
SKSFTNIEQDYKQYENLLDNGIYKYNRRRTTKTYHDLKSDYNEIGEVFAQFAHEQAQV
GELAEQLSYLSNAFSGSSISLEKLVGRLYNINEPLNESVHMATSARELIKRYRKLKYLQ
NEMI KKSLSNKRQLEKLEAQNNEYKDVDKIIDNEMSKSHTINLERPNNNTGSGGKSY
GGKLFN GFNKLASMVKDSVKYQETDPHTASINLKKEIEQLSESLVETENDLEVISKVI
KNDQLPKF SKEREVDLSEILKHYSRYMRNYARQNLIEWKEVKRHQDFA

44. Sorting nexin-4 (Atg24)

>sp|P47057|SNX4_YEAST Sorting nexin-4 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=SNX4 PE=1 SV=1
MTDKGKNDLTSKAKDKARGNPEKPPYWFEEIIVSDPQKRTGDPGSSSGYVSYQISTKT
NNT SFYDNRGDPESIIIVHRRYSLLLLHDILLNRFPPTCIIPPLPKKVFQYIAGDRFS
QRFT QKRCHSLQNFLLRRVSLHPDLSQSKVFKTFLVSKDWESHKVLQDSLQPNKDEV
TDAFMNA FKTVHKQNEEFTEIREKSDKLDRTVTVKIDKLFHKVVKKNDMSSE
DYTKLGSNLQELQELV TGENEELAALKKIFNEGVTQLSYGLQDLTKYLDYEYIVDLK
DLEHYIDSMRQLIKLKDQK QIDYEELS DYLTRSIKEKNNLISGYGGSNFFANKLEEL
AGINQEASRREKINKLEGKITS LTGELENAKKVADGFEQECLKEIDHFESVKTAEIKK
SLGSLADHHIEFYERILEAWEKVD DSL

45. Autophagy-related protein 23 (Atg23)

>sp|Q06671|ATG23_YEAST Autophagy-related protein 23 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=ATG23 PE=1 SV=1
MELNQVLEKKEQILQYLGTLVGLHEKALSDVNSASQVTSIRK DITICLNDLCRINDLLVS
HDGLLKR EIGSLLRDKQELLELNEREQLLWKERKSWHIKQETDAAPADYVIDKDAIITIS

SHHRTSLNKYIESVGAENTILSNTDDSDAMIEEVQNAESSADQMIRNYKLLQLSHKQAKS
EIIIRLETLLRDFKKNKFIEEELKRQSGRIRSEMGNIDFHLSKIEESKHQLMKRIGFESP
LTQEKSLSEKIFNLRLSSADEDYNERQTINMKNFVHMKDLIELKIEDLQEQLMRNKNESS
TVLTQRELWLDCQKQVGDLESKLITKLRSSNSKIIPNEMSEMINSTIQYLNNLLDSSDE
KLTTTLISNERDVLKACEELHSESTTAQDGSSALPSKPIDIHKSHKGSNASSNLKQPST
PSFLVASKSPPKIGISESVVNANKNDIAISKKVE

46. Autophagy-related protein 27 (Atg27)

>tr|K1QA43|K1QA43_CRAGI Uncharacterized protein OS=**Crassostrea gigas**
OX=29159 GN=CGI_10013150 PE=4 SV=1
MKGVSELPLVFVIFLSAFVTAVFGQCTYRDQCSCSLSDGSIIDLSTLGNQDQTPAFPDSF
ATDGYFYSYNPCYSFIEGSCMNAAACQISGDQSTQYQIGDATSVTYSYDGTNVHALYSST
DSQGLTSLTTKACPNCGCAGPPPTNPTNPPGPPGSPSESDSGISTGTILCIAVLAI
AVVYLVAGTVFTMGVRKSKGKEAIPNVSFWTSPLGLIKDGFKFTFSKIRPGYSSVK

>sp|P46989|ATG27_YEAST Autophagy-related protein 27 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=ATG27 PE=1 SV=2
MVSKTWICGFISIIITVVQALSCEKHDVLLKKYQVQVGFSSLTSTERDTPPSTTIEKWWINVC
EEHNVEPPEECKKNDMLCGLTDVILPGKDAITQIIDFDKNIGFNVEETESALTLTLKGA
TWGANSFDKLEFQCNDNMKQDELTSHTWADKSIQLTLKGPSGLKSKDDDKKNGDGDNG
KGDSEGGKPAKKAGGTSWFTWLFYALLFTLIYLMVVSFLNTRGGSFQDFRAEFIQRST
QFLTSLPEFCKEVVSRIILGRSTAQRGGYSAV

47. Autophagy-related protein 19 (Atg19)

>sp|P35193|ATG19_YEAST Autophagy-related protein 19 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=ATG19 PE=1 SV=1
MNNSKTNQQMNTSMGYPLTVYDECNKFQLIVPTLDANIMLWCIGQLSLLNDSNGCKHLFW
QPNDKSNVRILLNNDYDGHFLFKYLQCQRKCSVYIIGEGTLKKNLTISTSFDFNFDLTPSE
EKESLCREDAHEDPVPKAGSEEEISPSTSNVVVSRECLDNFMKQLLKLEESLNKLELE
QKVTNKEPNHRISGTIDIPEDRSELVNFTELKTVKQLEDVVFQRYHDYERLSQECDSKTE
IASDHSSKTKIEVEPPNERSLQITMNQRDNSLYFQLFNNTNSVLAGNCKLKFTDAGDKP
TTQIIDMGPHEIGIKEYKEYRYFPYALDLEAGSTIEIENQYGEVIFLGKYGSSPMINLRP
PSRLSAESLQASQEPFYSFQIDTLPPELDDSSIIISTSIISLSYDGDNEKALTWEEL

48. Autophagy-related protein 17 (Atg17)

>sp|Q06410|ATG17_YEAST Autophagy-related protein 17 OS=**Saccharomyces cerevisiae** (strain ATCC 204508 / S288c) OX=559292 GN=ATG17 PE=1 SV=1
MNEADVTKFVNNARKTLTDAQLLCSSANLRIVDIKKKLSSWQLSISKLNFLIVGLRQQGK
FLYTILKEGIGTKLIQKQWNQAVLVVLVDEMKYWQYEITSKVQRDLGIVNELSISEKDDT
DPSKLGDIYSRDNVLLNDKLEVPVIERQIENIKLQYENMVRKVNKELIDTKLTDVDTQK
FQSKFGIDNLMETNVAEQFSRELTDLKDLAEIMNSLTQHFDKTLQLLQDKKIDNDEREEL
FKVVQGGDKELYNIFKTLHEVIDDVKTIILNLGQFLQAKIKEKTELHSEVSEIINDFNRN
LEYLLIFKDISNLIIDFSKNSCTQDIQTTKELCEFYDNFEESYGNLVLEAKRRKDVANRMK
TILKDCQKQLQNLDAQDQEQNFIAENGYLTPETIWPBKIDDFSSLYTLNYNVKNP

Figure S2

1. ATG7

```
>MK173046|Ubiquitin-like modifier-activating enzyme ATG7  
[organism=Crassostrea gigas] mRNA, complet cds  
MSAPLVNKMESKQLQFVAFNSFLDSGFVHKLSENKLDVYGLDESQKEIKG  
FYFNGDPVGMPCRMNVEFSAFDQDAKTPQRYLPLMLGELHNTNTVDFKKEC  
DKKEMISVAGKKIWDIVTGKALDTPPELLATFLLLTFFADLKKYHYWFC  
FPCLCPSTDITFDQEPKLLKDKLTAEMEQLQAYDTFQDAYPTYQGFFV  
AVLSKGNIVIEDVKHMNFENTQEVYFGFCDPNSIEDYPGWPLRNFMLLI  
SYHWKGDRLRGNVNLCLDRSRDGTDRDISHSLLLSLNVDPDIKNVSECPKCV  
GWEKNEKQKLAPRFVNLASMDPTRLAASAVDLNLKLMRWRLPELDL  
ISRKCLLLGAGTLGCNVARCLMGWVVRTITLVDNGRVSYSNPVRQSLFQ  
FEDCVKGGKPKAEAAEAMKKIFPGVNAKGLSLSIPMPGHAVPESAIEGV  
KKDVETLQDLVNSHDAVFLLLDTRESRWLPTLMAAEKQKIVICSALGFDT  
YLVMRHGVRSDEGADPAPLSSYSSIPGDQLGCYFCNDVVAPGNSLKDRT  
LDQQCTVSRPGISYMASALAVELLVSVLQHPHELKAPADTSASDEHLSKD  
FVCPLGLVPHQIRCFVSRFQQVLPACKAFDKCTACSKTVIEQFRRDGFDF  
LRRAFNDPSYLEDLTGLTQMHEQLDAEVWGFSDDEECSSMEVSSS
```

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>sp|O95352|ATG7_HUMAN Ubiquitin-like modifier-activating enzyme ATG7  
OS=Homo sapiens OX=9606 GN=ATG7 PE=1 SV=1  
MAAATGDPGLSKLQFAPFSSALDVGFWHELTQKKLNEYRLDEAPKDIKGYYYNGDSAGLP  
ARLTLEFSAFDMSAPTARCCPAIGTLYNTNTLESFKTADKKLLEQAANEIWESIKSGT  
ALENPVLLNKFLLLTFADLKKYHFYYWFCYPALCLPESLPLIQGPVGLDQRFSLKQIEAL  
ECAYDNLCQTEGVTALPYFLIKYDENMVLVSLKHYSDFFQQRKTIIGVYDPCNLAQY  
PGWPLRNFVLAHRWSSSFQSVVEVCFRDRTMQGARDVAHSIIFEVKLPEMAFSPDCPK  
AVGWENKQKGGMGPRMVNLSECMDPKRLAESVLDNLKLMCWRLVPTLDLKDVKVSVKCLL  
LGAGTLGCNVRTLMGWGVRHITFVDNAKISYSNPVRQPLYEFEDCLGGGKPKALAAADR  
LQKIFPGVNARGFNMSIPMPGHPVNFSSVTLEQARRDVEQLEQLIESHDVVFLMDTRES  
RWLPAVIAASKRKLVINAAALGFDTFVVMRHGLKPKQAGDLCPNHPVASADLLGSSLF  
ANIPGYKLCYFCNDVVAPGDSTRDRTLQDQCTVSRPGLAVIAGALAVELMVSVLQHP  
GYAIASSSDRRMNEPPTSLGLVPHQIRGFLSRFDNVLVPSLAFDKCTACSSKVLQYERE  
GFNFLAKVFNSSSHFLLEDLTGLTLLHQETQAAEIWDMSDEETI
```

```
>sp|Q9D906|ATG7_MOUSE Ubiquitin-like modifier-activating enzyme ATG7 OS=Mus  
musculus OX=10090 GN=Atg7 PE=1 SV=1  
MGDPGLAKLQFAPFNSALDVGFWHELTQKKLNEYRLDEAPKDIKGYYYNGDSAGLPTRLT  
LEFSAFDMSASTPAHCCPAMGTLHNTNTLEAFKTADKKLLEQSANEIWEAIKSGAALN  
PMLLNKFLLLTFADLKKYHFYYWFCYALCLPESLPIRGPVSLDQRLSPKQIQALEHAY  
DDLRCRAEGVTALPYFLFKYDDDTVLVSLKHYSDFFQQRKTIIVGVYDPCNLAQYPGWP  
LRNFLVLAHRWSSSFQSVVEVLCFRDRTMQGARDVTHSIIFEVKLPEMAFSPDCPKAVGW  
EKNQKGGMGPRMVNLSGCMDPKRLAESVLDNLKLMCWRLVPTLDLKDVKVSVKCLLLGAG  
TLGCNVRTLMGWGVRHVTFVDNAKISYSNPVRQPLYEFEDCLGGGKPKALAAAERLQKI  
FPGVNARGFNMSIPMPGHPVNFSDVTMEQARRDVEQLEQLIDNHDIIVFLMDTRESRWL  
TVIAASKRKLVINAAALGFDTFVVMRHGLKPKQAGDLCPSHLVAPADLGSSLFANIPG  
YKLCYFCNDVVAPGDSTRDRTLQDQCTVSRPGLAVIAGALAVELMVSVLQHP  
GGYAIASSSDRRMNEPPTSLGLVPHQIRGFLSRFDNVLVPSLAFDKCTACSPKVLQYERE  
GFTFLAKVFNSSSHFLLEDLTGLTLLHQETQAAEIWDMSDEETV
```

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>sp|Q5ZKY2|ATG7_CHICK Ubiquitin-like modifier-activating enzyme ATG7  
OS=Gallus gallus OX=9031 GN=ATG7 PE=2 SV=1  
MAAVSNESQNPVDPGSSKQLQFAPFSSALNVGFWEHLETPKVIKGYYYNG  
DPSGFPARLTLEYSAFDINASIPARCCPAFGTLYNTNTFETFKSCDKKSLEKEANEIWE  
SIKSGAALNPMLLNRFLLTFADLKKYHFYYWFCYALCFDPDGIHVIQKPVCLGDRFSL  
NQIQALQKAYDELQTEGVTAFPPYFLIKYHDNSVVVSPKKWDGFFQDQGGKVTGVYD  
CNLSHYPGWPLRNFLLILASHKWGNILQSIIEVLCFRDRTMQGVRDITHSIIFEIKLPQGA  
F  
GPDCPKAVGWENKQKGGMGPRVVNLSECMDPKRLAESVLDNLKLMCWRLVPTLDLEKIV  
SAKCLLLGAGTLGCSVARTLMGWGVRKITFVDNARISYSNPVRQPLYEFEDCLSGGKPKA  
LAAAERLQKIFPGVNSEGYNMSIPMPGHPVNFSEVTMAQARKDVATLEELIDAHDVVFL  
LMDTRESRWLPAVIAASKRKLVINAAALGFDTFVVMRHGLKPKQOETGNACFSTAPGPSDL
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LGSSLSFNSIPGYKLGICYFCNDVVAPGDSTRDRITLDQQCTVSRPGLAMIAGALAVELMVS
LQHPEGGYAVASSSDRRMNEPPTSLGLVPHQIRGFLSRFDNVLVSLAFDKCTACSPKVL
DQYEREGFNFLAKVFNSSSHFLLEDLTGLTLLHQETQAAEIWDMSDDET

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

MSTEKEIILQFAPWESFVSPTFWHKLAELKLDHDLSDSKRSITGHYTNRNASGCLLEVD
YTAYNRMAKPPKFSHSAIGTIYNKNTIEEFKALDKLQLLADEGKELLADMCSGGALRDP
LLTRFFVLSFADLKCHSYWFAFPCPLTPTLKLQGAQKLRDLNPNSSYIMALKALPTE
SQNFFILYANVEKNIFEARSLSLDDKNVEFCYFGFADPSEYEHPAWIMRNYAAFLQOC
PSFVVGKPLKFLGLRHNQOMNIDDSLVWVKVIQTEACDLSQSENIKFGWELNKNKMGPRM
VCMRDSMDPAKLAENSVNLNKLKMKWRLVPLDNLLEIISQTKCLLFGAGTLGCAVARNLLS
WGFKHITLLDSGKVGFSNPVRQNLTYHADAVAGNRMKATTAAQRLKEINPSAETAGYVLE
IPMPGHTIGESLLAQTKHEHLKVIKLVQDHDVIFLLTDSRESRWLPTLLGAAKEKIVINA
ALGFDSYLVMRHGTTRKEAGDDGQIEIEGLKCIINGDQGLGICYFCNDVTAAPGNLKDRTLDQ
CTVTRPGVSNIAASYAVELLVALLQHPRKELAPAYYAQSGRGRSEETEEKVPEGLLGLIP
HSIRGMLCNYENILPATQKFAQCIACSAAVLNEYKKEGHAFLEFKTFETAKFLEDLTGISE
FKRLNSEIIFDDEEFDMSSDSD

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

MATFVFPVTCCLDTGFWNEVNKKLNDWKLDETPKCISSQLSLHQTEGFKCHLSLSYDSLS
SLESTTGLSMSGTLLEYNTIESFKMVDKSDLRSEAEKIWESITTRKWLQNPRLLSQFFI
IAFADLKKFKYWWTCVPALVYPSEIKQEIITPLSSLGADHKILFDFYRKNFPIFLYSKQ
SSKMLELSELENNTNPDEICVVDADPSPVAYSAGWMVRNVLAVAHLHPTWKHCHIIISLR
SADSIGIKYTWTLPSEACSDGAQNAVPAVGVWERNANDKLPISVDLSKEFDPKILMER
SVDLNLSLIKWRLHPDIQLERYSQLKVLILGAGTLGCNIARCLIGWVRHISFLDNSTVS
YNNPVRQSLSEFEDARLGRGKAETAQAAIQRIFFSIQATAHRLTVMPGHSIDKDVPEL
EKDIAKLEQLVKDHDVFLALDSREARWLPTVLASRHKKIAISVAIGFDYVIIRHGIGS
RSESVSDVSSSDSVPYSQSLSCYFCSDVTAAPGNSTFDRTLDQQCTVARPGTSMIASGIAVE
LLSSVLQYDPDKTPASHDDNTTVLGAAPHQIRGFLGRFQQILPSVKRFDQCVACGDAIA
AQFQQNGWKFVRDVMNSPGRLEEVTGLDELQNSVNAIDIDFEDDEF

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

MASQEKTDSSQQLQFAPFSSALDVGFWHKLQKKNLNEYKLDGPKDIYGYNGDPDGL
PCRLSLEFNADFQSETTPPHCFSSRGTLVNFNTLDAFKTCDKALLDVTAEQWLWDDIRQG
SAIQDPSLLSRFRLTFADLKKYHYCYWFAFPALLAPEGKLIQPEKLDKAMDQDKITA
LQAAAYDLASQSLGQEPAFFLISTEDDKTVVPLTAWDQVTDKSKVMFGYADPCTLEQYPG
WPLRNFCLISCHWASQLDQVTVVCFRNRTREGIRNSSHSLILRLQVPSTSPETSCPKCV
GWEKNQRNKLARKVDLSSMDPTRLAETSVDLNLKLMRWRLPSLDLTKISQTRCLLLG
SGTLGCNVARCLLGWVRTITFVDNSTVSFSNPVRQSLFEFEDSLGGGPKAQTAAEKIE
KIFPGVKTRGVSLIPMPGHAVGTSDEAIQQTRESVQKLEELIDEHDVVFLMDTRESRW
LPTVICSSKRKIVMNAALGFDTYLVLRHGMKPARDQPPDQTPSSASSGAAGGAEGGAA
GGASCSTSSISLSHIPGDKLGCYFCNDVVAPGDSTRDRITLDQQCTVSRPGLSMVAAALVV
ELMVSILQHSQAYAAAETSADKSHLTVDLTSPGLVPHQIRGFLARYHCVLPASLCFDK
CTACCDIVLASYEREGFDLLKVFNKPRFVEDLTGLSQLHLESELIEILDFSDDETMTS
SQ

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

RTPNIIISMAESSLKLQFAPFCSALEAGFWHQLTQKKNLNEYRLDESPKNIKGYNGDAVG
LPARLTLEFSAFDADGPTPARCCPASGTLTYNTNTLEAFKSTDKKALLDKAANEIWSAIQS
GAALEDSSILNKFILLTFADLKKYHFYWFCCFPALCFVEGIQLLRAPLSLEQHFSDKQIS
SLQSAYDNLCASSGTTAVPHFLKYSSEESVEVAPLKEKLSFFPDLKRVIYSTSHQCGLLP
QHPGWPLRNLVLLAKKWASQLDVVEVLCFRDRTLQGVRSVQHSIIFQLRLSDPAPSAAP
TTDINIHWKMIHSIQGNSAFFVSECQGVRLAESSVDLNLKLMRWRLVPLDLEKVVST
RCLLLGAGTLGCNVARTLMGWVVRHITFVDNAKISYSNPVRQPLYEFEDCLSGKSKALAA
VDRLLKIFPGVNAEGFNMSIPMPGHPVNFSDLTVAQAQQDVEQLKLI SEHDVVFLMDT
RESRWLPTVIAASQRKLI VNAALGFDTFVVMRHGLKPRESEESSPMSASSSSSSNTPA
ATVTAGSSLSFNSIPGHRLGCYFCNDVVAPGDSTRDRITLDQQCTVSRPGLAMIAGALAVEL
MVSVLQHPEGGYAVASSSDRRMNEPPTSLGLVPHQIVPLLSNVTNVLYEMFWRKDRCL

KKVLENYEREGFQFLAKVFNSSHSFLEDLTGLTLLHQETQAAEVRLTPSISI

>tr|A0A087ZSN9|A0A087ZSN9_APIME Uncharacterized protein OS=*Apis mellifera*
OX=7460 GN=LOC726637 PE=4 SV=1
MSEFVKFTKLRSTTDCTFWAKFVELKIDKFKLDEKSNLWGSYSLSQSLNEDNFNPLVLDLDF
TSFNEDLETINNKSSVICFGHMINTNTFEAFRQINPEQFIDSMGKDIINSIQDGTILQNP
WKLSLFLVLAYSDDLKRYFYVVAHPTPLKLPemyyEEIPKSITEEFSEKHVEDLcnnFL
HLDCRTKNYFTVLI SKENKMCIVDLATGINVININNEKQSQDYTEIYFAFYDPTSSNPG
WPLRNLLCLLCWYCPTHYFSKI IKFISIRGNAQKSLVFKLKTKEYKKNYKNIRDNLFLSH
LVGWESNSNDKLGPTIADLSDTMDPTKLSDKAINLNLKLMKWRLVPLNDLEKICNLKCLL
LGAGTLGCSVARVLLGWGVNNI IFVDSHSVSHSNTVQRSLYNHQDAIKHKYKAHAAKDAL
LNIRPSINTEGIVLHIPMPGHVVGQSMLESTKQSLKKEELIEISDVVFLLLDSREARWL
PTVLCAAKNKITINAALGFDSYTVQRHGTRNFNNQISPDLVKNPRGMDLGCYFCNDVTQ
PGNSQTDRTLDQOCTVSRPGLSQIAAGLAVELLVALLQHPEGVEAEALVGNRDNINSND
AKLVGLLGCVPHITIRGSLWNYDTQLTITHRFTSCTACSVPI IEYKNRGLSFVLDACNIP
NYLEKLSGLEEILKRPDLDELALYALDNISDEDEDDQKM

>XP_022296278.1 ubiquitin-like modifier-activating enzyme ATG7 [*Crassostrea virginica*]
MSAPMERKQLQFVPFSSFLDSGFWHKLSENKLDVYGLDES RKDIKGFYFNGDPVGMPCRMNVEFSAFDLD
AKTPQKCLPMLGELHNTNTIDKFKCEDKKEMMTEAGKKIWEAII SGRALVSPNLLASFLILTFADLKKYH
YYYWFCFPCLCLPTDVTNLNQEPIKMKDKFTKEQMDQFLT SYDTFQEEQPCYQGGFFVAAFSQDKFMVKDVK
SLNNFDDTQEVYFGFCDPSTIEDYPGWPLRNFLMLISYHWKGSLENINVL CIRDRSRDGNRDISHSVLLS
LNVDPVKS LQECPKCVGWKNEKQKLAPRFVNL SASMDPARLAASAVDLNLKLMRWRLPELDDLISRT
KCLLLGAGTLGCNVARCLLGWGVRTITLVDNGRISYSNPVRQSLFQFEDCVKGGKPKAEAAAESLKRIFP
GVNATGLSLSIPMPGHAVPDSAIDGVQKDVATLQSLVDSHDAIFLLLDTRESRWLPTLMAAEKQKIVICS
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
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KELSDLHENVVALLDCKETTNNHVYLVMEYCNNGDLADYLQAKGTLSEDTIASFLRQIAA
AMQVMNGKGI VHRDLKQNILLCHDGPNTPTSTEMRLKIADFGFARFLNDGVMAATLCGS
PMYMAPEVIMS LQYCAKADLWSIGTIVFQCLTGKAPFQAQTPQQLKHFYEKHAELKPNIP
KDTSPELRDLLLKMLKRNADRIEFASVPVPGRASQGCSSSPTPPRCVSASPLSGKAD
YSTPPSKVVQMVKQQEVAEAMQGSTHDEEFLKVDKGPTPRSNSPTEHDFVLVDPGMSDQS
DGS DKGRAPSTEDLQSLGERAQPQVVRVEPQVGSVAYKKDSGDVSSPSRPSLPMQSNNO
SEPIPVPTQVKAYERIRSSSSPLSSPRKCGTEPSPLDSAKLSSQNIKISPQPESKFSAPD
IGSFSPTVKFVSVGTPPNVSTPWRRGSIGSSQGGAIYHPPSNASNSPSRRASMGSSPSGF
NRNFSSPGSLPTILDASPHFELNQEPOFTDNMPTVPVRAPFGQSKPAIPEKSGTKRYHP
SEVDRVKLNLMECNTDPGAAGGMSMLSQOMKVAYMNQQGLNLLLEGQVVRYTSENENLVSP
NDNTVQMDTQRSGLRRTMSATTPPSNLMFAQSPPNMEGPVAFVAPGLAEETLMGDNHN
EIMAKLSFVNDLADCVMEAMAKGAPLNTLSESVNWKQEGEPLHGDQMPKFIEAQRLLAQ
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
KELQHENIVALYDVQELPNSVFLVMEYCNNGDLADYLQAKGTLSEDTIRVFLHQIAAAMR
ILHSGKGIHRDLKQNILLSYANRRKSSVSGIRIKIADFGFARYLHSNMMAATLCGSPMY
MAPEVIMS QHYDAKADLWSIGTVIYQCLVKGPPFQANSQDLRMFYEKNRSLMPSIPRET
SPYLANLLLGLLQRNQKDRMDFEAFFSHPFLEQGPVKKSCPVPVPMYSGSVSGSSCGSSP
SCRFA SPPSLPDMQHIQEENLSSPPLGPPNYLQVSKDSASTSSKNSSCDTDDFVLPVPHNI
SSDHSCDMPVGTAGRRASNEFLVCGGQCQPTVSPHSETAPIPVPTQIRNYQRIEQNLSTST
ASSGTNVHGS PRSAVVRNS TSPMGFLRPGSCSPVPADTAQTVGRRLSTGSSRPYSPSPL

VGTIPEQFSQCCCGHPQGHSRNRSSGSPVPPQAQSPQSLLSGARLQSAPTLTDIYQNKQ
KLRKQHS DPVCP SHTGAGYSYSPQPSRPGSLGTSPTKHLGSSPRSSDWFFKTPLPTIIGS
PTKTTAPFKI PKTQASSNLLALVTRHGPAEEQSKDGNPRECAHCLLVQGSRQRAEQQS
KAVFGRSVSTGKLS DQOGKTPICRHQGSTDSLNTERPMDIAPAGACGGVLAPPAGTAASS
KAVLFTVGSPPHSAAAPTCTHMFLRTRTTSVGPNSGGSLCAMSGRVCVGSPPGPGFGSS
PPGAEAAPSLRYVPYGASPPSLEGLITFEAPELPEETLMEREHTDTLRHLNVMLMFTECV
LDLTAMRGGNPELCTSAVSLYQIQESVVVDQISQLSKDWGRVEQLVLYMKAQAQLLAASLH
LAKAQIKSGKLS PSTAVKQVVKNLNERYKFCITMCKKLTEKLNRRFFSDKQRFIDEINSVT
AEKLIYNCAVEMVQSAALDEMFOQTEDIVYRYHKAALLLEGLSRILQDPADIENVHXYKC
SIERRLSALCHSTATV

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

MEVVGDFEYCKRDLVGHGAFVVFGRHRQKT DWEVAIKSINKKNLSKSKQILLGKEIKIL
KELQHENIVALYDVQELPNSVFLVMEYCNGGDLADYLQAKGTLSEDTIRVFLHQIAAAMR
ILHSGKGIHRDLKPNILLSYANRRKSNVSGIRIKIADFGFARYLHSNTMAATLCGSPMY
MAPEVIMSQHYDAKADLWSIGTVIYQCLVGKPPFQANS PQDLRMFYEKNSLMPSPRET
SPYLANLLLGLLQRNQKDRMDFEAFFSHPFLEQVPVKKSCVPVPVYSGPVPGSSCSP
SCRFASPPSLPDMQHIQEENLSSPPLGPPNYLQVSKDSANSSKNSSCDTDDFVLPVPHNI
SSDHSYDMPMGTARRASNEFFMCGGQCQPTVSPHSETAPIPVPTQVRNYQRIEQNLIST
ASSGTNPHGSPRS AVVRRSNTSPMGFLRVGSCSPVPGDTVQTGGRRLSTGSSRPYSPSPL
VGTIPEQFSQCCCGHPQGHEARSRHSSGSPVPPQAPQSLLLGARLQSAPTLTDIYQNKQ
KLRKQHS DPVCP SHAGAGYSYSPQPSRPGSLGTSPTKHTGSSPRNSDWFFKTPLPTIIGS
PTKTTAPFKI PKTQASSNLLALVTRHGPAESQSKDGNPRECSHCLSVQSRHRSEQQ
SKAVFGRSVSTGKLS EQQVKAPLGGHQGSTDSLNTERPMDVAPAGACGVMALPAGTAAS
ARAVLFTVGSPPHSATAPTCTHMVLRTRTTSVGSSSSGSLCSASGRVCVGSPPGPGGLGS
SPPGAEGAPSLRYVPYGASPPSLEGLITFEAPELPEETLMEREHTDTLRHLNMMLMFTEC
VLDLTAVRGGNPELCTSAVSLYQIQESVVVDQISQLSKDWGRVEQLVLYMKAQAQLLAASL
HLAKAQVKSGLSPSM AVKQVVKNLNERYKFCITMCKKLTEKLNRRFFSDKQRFIDEINSV
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 FEYSRKDLIGHGAFVVFGRHKKKT DWEVAIKSINKKNLSKSKQILLGKEIKIL
KELQHENIVALYDVQETPSSVFLVMEYCNGGDLADYLQAKGTLREDTLRVFLQQAIAAAMR
ILNSKGIHRDLKPNILLSYTGRKKSSINGIRIKIADFGFARYLQSNMMAATLCGSPMY
MAPEVIMSQNYDAKADLWSIGTVIYQCLVGKPPFQANS PQDLRMFYEKNSLVPNIPRET
SPQLEDLLLGLLQRNQKDRIDFDFFFHSHPFLEPISTIKKSCVPVPVPSGLVSDSTCGSS
PSCRYVSPPLPDMQTLPELVLSPPPLGPPNYLQLSKESGGSTSSKNSSCDTDDFVLPVPH
LSGEQSYDLPMAVAVRRPSSSEFLLCGGSPQSTGQTPMVSPRSETTPIPVPTQVRNYQRI
KQNLSSSPTTTLYGSPRSGTVRRSNTSPMGFPKMVSASPSPADTVQTVGRRLSTGSSRPY
SPSPLVGTIPEQLGHCCCGHPQSHEPRSRSSSGGSPVPSQLLGARLQSAPTLTDIYQSK
QKLHKQLSDPVHPTSSAYPSNHSPQLGRPANLGTSPTKHLGSSPRTSDWLTKSPLPTIIG
SPTKVTA PFKI PKTQASCNLMALADSPIPNKTLMDGRELCAHHTAYPSSRQPAPEASKT
SFGRSVSAGRLSEPPVRITLGGQPYQGSTDSLNTERPMDTAPAGMCALAAGGGSPRTVVF
TVGSPSSSTPPTCSHLASRPRATSVGSNSAGSLCSTSGKVYMGSPPGMTIGSSPPGAE
AGPSSLRYPYGTSPPSLDGFITFEAPELPEETLMEREHTDTLMYLRMMLSFTDCVLEIA
ALRAGGPD LGASAASLYPPQDSVVVDQISQLSREWGQVEQLVLYMKAQAQLLASSLHLAKA
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

MESIGDFEYKRD LIGHGAFVVFGRHKVTHDPVAIKSITKKNLAKSQNLLSKEIKILK
ELSDLHHENVALLDCKETTHHVYLVMEYCNGGDLADYLQAKGTLSEDTISGFLRQIAGA
MRALNGKGIHRDLKPNILLTHSGQSPNPQPSDLQLKIADFGFARFLNDGVMAATLCGS
PMYMAPEVIMSVQYDAKADLWSIGTIVFQCLTGKAPFQAQTPQQLKAFYEKNANLAPNIP
SGTSKELRDLLMKLLKRNADRIDFDEFFSHPFVCPAKASSPVPVPQQRARHPSDSPTLK
TVSSSPLSGNVPYSPVNTDVQRVQKQEDVSESPQEGADFKVVDKSGSPAEDFVLPVNNL
GGESEGSASSGRSKESPKHGRKDSQPSAQRVVRVDTTTEAASFRKGNAGSPSPQDQTS

TRPTSLPVIKQTSPPSQPIPVPTQVEAYQRIQKNSSPSPKEPRTKEAGTHVMSPQRELAS
QAVPIPRIASDRMVSVGSFPDIRSVSPSVQFHIGTPPSKNIRRNSIEVSPGRPNTATPP
NGSPLRKSQAQSNSSPFGSPASLPKPSVMSVAQRFTVTNYPAGGRDVVALARTRTVPEGV
QAMTTVAGAAYPDYATWPRRLDTTGLAPSQTEPSNLQRTTSSGGHLAPTRIGEQLMKAAFG
QTTRGLSNQIPANSVVPYRERNSQESGQRERRDSFQKRDSFTREERQDSTGRERSGSSPP
NSLPYAQSPPNMEGPILFEAPELAEETLMDSEHNETVAKLTFVLALVETIIELAQKRSTP
LTQSI SPQGRRDGGSEQVKFLSESQRRMEQLVLHVKALQLLSASLQLAKEEIKAGKLMPS
NTVKNILKEMNNHYHRCMGI SKQLKSCNINDNELKSFSTADKLIYNYAIEMCQTAALDE
LFGNPQECFRMYKNAQIILLHALAHQAQHNKDKDMLNKYKEAVEKRLFSLQSQGLNYFQYE
N

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

MEHIDEYEYNNKKDIIHGAFAVVFRGRERKRPDQTVAIKCKINKKNLSKSSQTFPEKEIEILKELHHGNVVS
LLHFKEITSSLFMVMEFCNGGDLADYLLHIKGTLS EDTIRFFLGQIACAMKAIHEKGIHRDLKQPONLLLS
HNSKHKVPHPNEIHLKIIDFGFARFLEGDMMAATLCGSPLYMAPEVITSQHYDAKADLWSIGTII FQCLT
GSAPFKAANPPELKKLYMKARTLDPNIPPGTSKALKDLLIRLLKRNQKDRIEFDKFFSHDFLGKNLKSTS
TSPMPVPSRTYSFSSDSPGERRSLSVSPLSGHMPISSEPEPSVSGCGPRGYSISPLAAPP LI STDRPS
AAKGLQEKLRLSSGMGSSDLVEDDFVIVQPSIVSELSYETSGASINVQTTDVTITRSNSSPIMSSSRGH
SAQPKSSTSPVSGRIMAAVVRKLPSPSERPSSLPISSSPSTSPNTGRHRVSPKQSPSSLI SPSRIHAQI
RHSYSSSGSPIGSPSQRRRLSPNQSPSLARHCILAQAGVDNKPPSPVQVTGLSSPGSQYNPGVVHKF
YKFHASPTSPSPSPPHI PRVSTDPMSCSQAGAGLYRGSSPQSQSGTSPTNIPSPARRKLSSPARSSPQFF
TGPSSLPTIAGSPTKKGFNEITFTIGTHGISPSEPLNMPFAKSRVRASSCCLEGGQDDISDSPGRDA
LIPRSASSRSLSEPLCLKAAFDNLAMNPGSSIEGIPGAI AASPPMHPTSFFIGSQRRNSVLTEGSPSSQ
GSLTFATSPPNMEGPI SFVAPELPEETLLAAEHTETVDRLNVILGIVEAIVEVAKRSRVP LAES IYNQGS
SIFSNSQVCFVSENYRLAEQLVLYTRSLLELLNAALTMAKEEFAARLKPSNAVRTVLQELNRYVHLCCLIK
SRQLCEGSPQLSLDIDLNSAMITADKLMYSYAI EQCQSAGMDEMFGNTQECLQRYRTAQMLLHGLCLQAG
TDHDRNLLLKFKNALDQRLFLERQQTPTVPMIGL

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

MEVVGDFEYSSKDLIGHGAFVVFVKGRHRKKTDEVAIKSINKKNLSKSSQILLGKEIKILKELQHENIVA
LYDVQEMPSSVFLVMEYCNNGDLADYLQAKGTLS EDTIRVFLQQIAAAMRILHSGKGIHRDLKQPONILLS
YASRRKSSVSGIRIKIADFGFARYLHSNMMAATLCGSPMYMAPEVIMSQHYDAKADLWSIGTVIYQCLVG
KPPFQANSPQDLRMFYEKNRNLIPIPIPRETSTYLADLLGLLQRNQKDRMDFEAFFNHPFLDQISTVKKK
CPVPVPTYAGSVSGSSCGSSPSCRFA SPPSLPDMQHIQEENLSSPPLGPPNYLQVSKDSASTSSKNSSCD
TDDFVLVPHNIISSDHSYDMPLGAAGRASSEFLMCGQSPLTISGSSGTVQKPSSTSSRSTASGTTNRHC
QPSVSPRSETAPIPVPTQLRNYQRIEQNLSSTASPVSNPHGSPRAGVVRNNTSPMGFMKMGSCSPIPGD
TAQGVGRRLSTGSSRPYSPSPLVGTIPEQLGHCCCGQLQGHESSRNRFAGSPIPPSQSPQSLLMGARLQS
APTLDIYQNKQKLRKQHS DPVCP SYAGYGYSHSPQSRPGLGTSPTKHMGS SPRSSDWLFKTPLP TII
GSPTKATTPFKI PKTQASSNLLALANRQGSIDAPLQPKDITEPRDFSHFHSTQGSEKHAGEQHSKATFGR
SVSTGKLS DQVKTTLGGQLYQGSTDSLNTERPMDTAPAGAYGIAVAPP SMGSGASSRAVMFTVGSPPSS
ATPPTCTHMVLRTRTTSVGSNSSGSLCSTSGRVYMGSPPGIYMGSPPGAEAAPSLKYMPYGTSPPSLE
GFITFEAPELPEETLMEREHTDTLRHLNMMLTFTTECVLDTALRGGNPDLC T SAVSLYQIQESIVVDQIS
QLSKEWQVEQLVLYMKAQQLASSLHLAKAQVKLGKLN PSTAVKHVVKSLNERYKFCIGMCKKLT EKL N
RFFSDKQRFIDEINSVTAEKLIYSCAVEMVQSAALDEMFOQTEDITYRYHKAALLLEGLTKILQDPADIE
NVHKYKSSIERRLSALCCSTVAVYEQ

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

MEVVGDIYEYSKDLIGHGAFVVFVKGRHRKRNHVVAIKSITKKNLAKSQNLLSKEIKILKELSDLHHEN
VVALLDCKETT NHVYLVMEYCNNGDLADYLQAKGTLS EDTIAAFLRQIAAAMQVMNGKGI VHRDLKQPONI
LLCHDGKPNTPSTEMRLKIADFGFARFLNDGVMAATLCGSPMYMAPEVIMSLQYCAKADLWSIGTIVFQC
LTGKAPFQAQTPQQLKH FYEKHAELKPNIPKDTSPELRDLLLKMLKRNKDRIEFEDFFKHPFLKPPGQS
AAASSPVPVPGRTSQGCSSESPTPPRCVSASPLSGKAEYSTPPSKVVQMVQQEVAEAMQGS SHDEEFL
KVDKGPTPRSNSPTEHDFVLVPGGMSDQSDGSDKGRVPSS E DLPGLGERAQPVVRVPEQAGSVAFKKDT
VDVPSRSPSSLPMTQNTQSEPIPVPTQVKAYERIRSSSSPLSSPRKFGAVEVSPVDPAKLSSQNIKMS P
QPESKFSAPDIGSFPPTGTLKFCVGTTPPNVSTPWRRSIGSSQGAQYHPPSNASNSP RRASMGSSPL
GFNRNFTSPGSLPTILDASPHFELNQEPQITDNMPTVPVRAPFGQSKPKAIPESKGTKRYNPSEVDRVKV
NLMERCNTDGAAGGLSMLSQOMKVAYMNQOGLNQLEGQVMRYTSNEQLVSPNENTVQMDTQ RSGSNLRR
TMSATTPPSNLMFAQSPPNMEGPVAFVAPGLAEETLMGDNHNE IMAKLSFVNDLADCVME LAMAKGAPLN
TLSESVNWKQEGEPLQGEPM PKFIEAQRLLEQLVLYVRS LQLLSSSLQLARREIKDERLQISNALKTLLK

QMNERVHRCVSVCKHIQQRLGITMQNALTPQVVIATADKLIYNYAIEMCQTAALDELFGNPQECFKRYNT
AHILLHLSLQQARNNDKQLLDKYKDAVERRLSHIQATQNYYPQFEIS

3. ATG12

>MK069431|Ubiquitin-like protein ATG12 [organism=**Crassostrea gigas**] mRNA,
complet cds
MSDDGNESRDSKNTETEEKSTPASPISHVAETKIDVLLKPAGDAPIMKKKK
WAVDRNKRIGWVGEFIKKYLKLTQAQDSLFLYVNVQSFAPTPDTEIGSIFDC
FGSDGKLVLYHYCKTQAWG

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

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

>sp|Q9VTU1|APG12_DROME Autophagy protein 12-like OS=**Drosophila melanogaster**
OX=7227 GN=atg12 PE=3 SV=3
MAETPESQAALSTSSSTPADKDGSKICILLNATGNVPIIKKRTWTVDPNKTVGWIQTFIH
KFLKLDASEQIFLYVNVQTFAPAPDQIIKKNLYECHGTNGKLVLYYCKNQAWG

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

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

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

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

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

>XP_022317492.1 ubiquitin-like protein ATG12 isoform X1 [**Crassostrea
virginica**]
MSDDGNESRDSKNTETEEKSSPTSPSHAVESKIDVLLKPAGDAPIMKKKKWAVDRNKRIGWVGEFIKKYL
KLTQAQDSVFLYVNVQSFAPTPDTEIGSVFDKVLQTSMKMTKITGGPWATSLT

4. ATG9A

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

MADYQTQYQPLASCEEDTDENDVPIHESANLMMHVPESTRWNHIENLDD
FFTRVYHYHQGGFVCMVSDVLQLIQFIFVVGSTFLLCEVNYDILFAN
SKNDTHKVTIPEAVAPFGQCVQEFDFGITVCLLVAFVFWFRLIKVLYNI
FKYWEIRSFYLTALHITTTDLTNMTWHEVQRRLLEVQKEQQMC IHKQELT
ELDIYHRILRFKNYMIAMERKSLLPFKHSIPLMGECAFYSIGLKYNLDFL
LFWGWPSPFENYWKLKDEFKIIYHKRKLAEELSKKILWIGIANFALSPLI
LLWQILYSFFRYADTLKREPSMLGSRRSNYARLYLRHYNELDHEFDARL
NRGYRLANKYMDIFTSQLIVILAKNVAFFAGSVLAVLVVLTVIDEDVLAV
EHVLTMTVAGLIVTACKVFIPEHLVYCPEILMRNILAHVHYMPPDWSG
NAHTSKVRNEFSIFFQYKVAYLFEELLSPLVTPIVLCFSLRHKSMEIVDF
FRNFTVDVVGVDVCSFAQLDVRKRDNKMDRDEEPEQPSLRTNMFTPD
QSPSQEGKIQMSLMHFHLTNPEWKPPKECSLFINDIKEKANRNTTSLSIF
NPVTQNMVMSSQGSALTGYLSGLQPSGAGALGESATDQYTSLASSIAIQSG
MYPQSTQVSMAPSVSGVHRLRGAISTAEGPLERSIGGPVGTMQGSTSMI
GSLGGYHSIGSSKPSVDEGSLELLSHDMSVSALYLHDFQSRKQRGQGM
GYENIEEMRARNLWQRQDSNQGPPVHAGMPNIQEKREEEKDSGNTETIAK
SV

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

MAQFDTEYQRLEASYSPPGEEEDLLVHVAEGSKSPWHHIENLDLFFSRVYNLHQKNGFT
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VCSARIQENGLITILVIAGVFWIHRLIKFIYNICCYWEIHSFYLHALRIPMSALPYCTW
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EASVYQQAEDGKTELSLMHFAITNPGWQPPRESTAFLGFLKEQVQRDGAASLAQGGLLP
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OX=10090 GN=Atg9a PE=1 SV=1

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VCSARIQENGLITILVIAGVFWIHRLIKFIYNICCYWEIHSFYLHALRIPMSALPYCTW
QEVQARIVQTQKEHQIC IHKRELTELDIYHRILRFQNYMVALVNKSLPLRFRPLPGLGEV
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CPLILIWQILYAFFSYAEVLKREPGALGARCWSLYGRCYLRFHNELEHELQSRNLNRYKYP
ASKYMNCFLSPLLTLLAKNGAFFAGSILAVLIALTIIYDEDVLAVEHVLTVTLLGVTVTV
CRSFIIPDQHMVFCPEQLLRVILAHIHYPDHWQGVHLGGVAESHRHTPHSHLLPPPSGPG
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>tr|F1QCA8|F1QCA8_DANRE Autophagy-related protein 9 OS=**Danio rerio** OX=7955
GN=atg9a PE=3 SV=1

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MNCFMSPLLTVVAKNVAFFAGSILAVLIALTIIYDEDVLAVEHVLSITLLGVCITVCRSF

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YQQAEDGKTELSLMHFAITNPHWQPPRESTHFI SLLKEKVHRDAAVGQQGI IAENAGFTS
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LRGSYPSARLPRSDHPAVVAGRGMAGSGTDARTISSGSSAWEGQLTSMILSEYASTEMSI
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HIHKVT

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QQQSLAGGKTEMSLLRFTLNNPEWQMPKEAKQFLRGVREHAVGELVQAKTSMVQENPLTN
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LSPIITPLILIIICLRPKSLDIVDFRNFTVEVVGVDTC SFAQMDVRQHGHPAWMSAGKT
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NALFSSIQSLQSESEPHSLIANVIAGSSVLGFHMGRDQASRHLSEVASALRSFSPLOSA
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elegans OX=6239 GN=atg9 PE=2 SV=1
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SSSQLNRRWDHVLNLDEFTHIYEHQNGGYLCIVLQKVFSLLOQIFVMSFTTFFFTQCV
NYQFLFANTNVTSHGTVNQGRHFGDAVVDNCPAHISIWMIFAILAAIVYWITRVIKHAQ
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LRYKNYMTGMINKRILHPVFDVPFLGPIAYLPNNLKHEIERILFTSSTSAWTNGPNLREE
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VDGLGDVCSFAVMDVGKHDGPKWNHIKELKAIVEDQEDQQAQSVVTSLNRRARDGKTELS
ILHFKTTNPEWQPPKASEKFLRKFNRNLGQEA SMLAPLTSMHLGQQMDRQQQQGKIGRNI
LLESVHSIVPTTSGGISASQVAPGRHPLIGDGLHRIDGPVGNAFQGIQGAKLGGGVLAS
LYQEQPRAAESLSNSLRASGVDIDGAGAEMRINALFLRGLHDESIHSSSRNYGGTTSSF
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>tr|A0A087ZP33|A0A087ZP33_APIME Autophagy-related protein 9 OS=**Apis mellifera** OX=7460 GN=Atg9 PE=3 SV=1
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PEGNKARWNHVEDLDSFFTRMYHYHQKHGFACMILQEALELGQFIFVVFSTFLFHCINY
SLLFKNGKERRKISISDVLISKSECIASMGLITWICILVAAIFWILRLVKVLYHCTQFWDI
KLFFNTALKIEDCDLNLTWHEIQKRVREVQKEQEMCIHKRELTELDIYHRILRFKNYMV
AMINKSLLPIRLKVPIIGEIIIFLTRGLKYNMELLLFWGWPSPFENNWHLKEDYKKNLKRQ
ELARALSKHILWVGIVNFLLCPLILLWQILYSFFNYGEI IKREPGLGTRMWSLYGRLYL
RHFNELDHELNARLNRAYRPASKYMSMFTSPIMTVIAKNVAFVAGSILAVLLILTIVYDED
VLTVEHVLTITITILGAI VAGARAFIPDENLVWCPETLLTAVLAHATHYRPSWRGHAHTQT
TRAEVAQLFQYRAVHLLLEELISPLITPFILCFMRQRALDIVDFYRNFTIEVTGVDVCS
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IHFTLTNPEWKPPSHAENFVTALRERVKKDVHGGGHEINPLLASLNSLSGLGPGYNDIIS
NIIRSTMINQASGPSTSTMFTNQPCCTTSVCTSGNEMLNMKSDIFPHAVQCGLSKAEGPVH
NEKGLLYGLQQEISNQSLGASVFSHEFSTDLSIPVELIAADMSLSTLYLHELHHRQVR
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>tr|A0A1S3JC03|A0A1S3JC03_LINUN Autophagy-related protein 9 OS=**Lingula unguis** OX=7574 GN=LOC106171792 PE=3 SV=1
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IPLDQCVSSVRPFVAICLLVAAVFVWLRLIKVVYNVLYWEIRAFYLTALKISADELPNL
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DYVFLSTGLKYNLEMILFWGWPAPFENYWHLKQDFKNYHKRRELADYVVSQRILWLGLANL
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KPAAEYMNIFTSPVLVILAKNVVFFAGAVLAVLIILTLIDEDTLQVENILRMMTILGAVV
AVCRAVIPAHEMVFCEFLMTHILKEVHYIPDSWKGNATHKVRQEFQQLFYKALYLLE
ELISPLVTPILCF SIRHKAYDIVDFYRNFTVEVTGVDVCSFAQMDIRKHGPNQWVKEE
QTQADLYHQAEDGKAELSLMHFALTNPEWKPPENC SVFLNDIKDQAVNDANA AVVAPGDN
ALFTSLHTFALS PGGVYNSINISSVVPGPSMASAHSMRPLGTVP GPMSPPGGSHLRGA
GVAAHEGPLQSGSGKILASLHSSGALSGSATGLGSGPTSLDTGHFLSSEVSQELSSAEMS
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>XP_022310215.1 autophagy-related protein 9A-like isoform X1 [**Crassostrea virginica**]
MSGAMADYQTQYQALGSCDEDDTDETDAPTHESANLMIHVVPSTRWNHIENLDDFFTRVYHYHQGGF
LCMMVSDVLQVLVQFLFVVGSTFLLECVNYDILFANSKNDTHKVTISEAVTPFGQCQVQEFDFGITVCLLV
ALAFWIFRTIKVLYNIFKYSEIRSFYLTALHISTAELSNMTWHEVQRRLLLEVQKEQQMC IHKQELTELDI
YHRILRFKNYMIAMERKSLPLKHXVPCLGECAFYSIGLKYNLDFLLFWGWPSPFENYWKLDKEYKVYHK
RKQLADELSKILWIGVANFALSPLILLWQILYSFFRYADTLKREPSMLGSRWSNYARLYLRHYNELDH
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TACKVFI PDEHLVYCEPILMRNILAHVHYMPPDWTGNAHTSKVRNEFSMFFQYKVAYLFEELLSP IITPL
ILCFYLRHKSMEIVDFFRNFTVDVVGVDVCSFAQLDVRKRDKKTGEVEQEEEEDEPESLRTNMFTPVQS
PSQEGKIEMSLMHFHLTNPEWKPPKECSLFLNDVKEKAQRNTASLSIFHPVTQNMVNSSQGLTGYSGL
QPSGAGGLGESSTEQYTSLASSIAIQSGMYPQSTQVSMAPSVSGVHRLRGAISTAEGPLERSVSGNLGT
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