

1 gaccacaaacttgtcaacatggccagcagtgactgggaagaagtgaacggcttgcggca  
**D H K L V N M A S S D W E E V K R L A A** 20  
61 gatttcaagcgagcacagttaacgctcgtcatcacagagattatcagaaagaactgtgtg  
**D F K R A Q L T S S S Q R L S E R N C V** 40  
121 gagatactatccaaactcattgaagaaaaacaaattgaagtcatttactcactagacggc  
**E I L S K L I E E K Q I E V I Y S L D G** 60  
181 aaagaatatgtcacaccttcccagctatttaaagaatacagagatgaacttatagtacat  
**K E Y V T P S Q L F K E I R D E L I V H** 80  
241 ggaggaagagtaaacttggtagatcttcaacaaaccattgggatcgagctctcccaaatc  
**G G R V N L V D L Q Q T I G I E L S Q I** 100  
301 gaaaccaaggctgccgagatcgtcaggtccgaccagtcctggttagtgtaggacag  
**E T K A A E I V R S D Q S V S L V L G Q** 120  
361 cttatagcagattctttagctatctgdcggaagaataaacgaacagcttcaagag  
**L I D D S Y L D H L A E E I N E Q L Q E** 140  
421 aacggccaagttactattccagcacttaccagtcgctcgatcttctgccgacttttta  
**N G Q V T I P A L T Q S L D L P A D F L** 160  
481 tcagaggctattgaatcacgtattggctcggtaataatggggagatcgatccatacagc  
**S E A I E S R I G R L I N G E I D P Y D** 180  
541 agggacgtcatcttccaccaggcctttgtcgcagaggaatacagcaaaggcagaggtgtc  
**R D V I F T Q A F V E R N T A K V R G V** 200  
601 ttcagtgctataactaggccaacatctgtacaaagtatcttgaacaagtacaaattccct  
**F S A I T R P T S V Q S I L N K Y K F P** 220  
661 gaaaaactctttatagtgcttagaaaagcttgcactctggctcgttgaatggtgac  
**E K L F Y S V L E K L V N S G R L N G D** 240  
721 atcatcgggtggcgtcaagacaaagcttcttaccgtcccagagatattttctaaaacgcag  
**I I G G R Q D K A S Y V P E I F S K T Q** 260  
801 aataactgggtcgtattcttctacaaacaaatggatacttggaaatgatagcttgtca  
**N N W V D S F Y K Q N G Y L E Y D T L S** 280  
861 agacttgggtgacagaccctaaaggttacatcaagagggcgttcaaggcggagaaattc  
**R L G V T D P K G Y I K R R F K A E K F** 300  
921 atccacctgaaggctgcatccatcgggaagatactgcaggaccaagtagatgctaccatc  
**I H L K A A S I G K I L Q D Q V D A T I** 320  
981 gatgaagctgtgagaacatcaagttgggtggatgtcatgcctatcctgccatcgccctc  
**D E A V R T S S W V D V M P I L P S S L** 340  
1041 tccagacaagacgtaaccaactcattcaagatattttgaaaccgaagagtaaactcggg  
**S R Q D V N Q L I Q D I L K P K S K L G** 360  
1101 attaagctcttcaacgcacattctcgcagcaaagccttctcgcagcagtgcttgacg  
**I K V F N D T I I C S K A F L D E C L T** 380  
1161 atctttgaaccggtcatgaaggagaaggctcaaaaggatgctgtgactcatcgcgacttt  
**I F E P V M K E K A Q K D A V T H R D F** 400  
1221 ttcctacacaaagataagaaagcgggtggcagcattcagcggctcggacggaaaacaagac  
**F L H K D K K A V A A F S G S D G K Q D** 420  
1281 aagaaggatgagagaaggaaaaagctgcaggtggcgggtggcagcagtgaggaaatccggc  
**K K D E R R K K A A G G G G S S G K S G** 440  
1341 gttgccagcacaagtcgagaggtcaagactaagaaggtaagaaggccggaacaaagac  
**V A S T S R E V K T K K V K K G R N K D** 460  
1401 ccggtagaaccggttagaagaagaatcgtcgcagcagcagcagaggtcaaagccaggagttg  
**P V E P L E E E S S T S S R G Q S Q E L** 480  
1461 gagttctatccggtggagaaaatagagggatattaagaccaactacgggattgccca  
**E F Y P V E K I E G I L K T K L R D C P** 500  
1521 gaagagttgcacacagaattagcggaggatttattaagaccttgaccagacgatataca  
**E E L H T E L A E D L L R P L T R R Y Q** 520  
1581 gaaacagccaaggaggcttacatggcgttagcaggggttctctgctgcagagaggaga  
**E T A K E A Y M A L A G G S S A A E R R** 540  
1641 aagaccacagagaatgtccaggagaaggtaactcactctggaccaacgtcaaactcttt  
**K T H E N V Q E K V N S L W T N V K L F** 560  
1681 gagaaggggattaatcaatttacagatgaagatgtgggtcagccaactgaacaagtacc  
**E K G I N Q F T D E D V V S Q L N K Y** 579

**Figure S2.**

Putative protein from which the peptide GYI is derived. The sequence of isotig 09011 is shown (lowercase, 1738 bases) with the partial sequence of the protein that it encodes shown underneath in bold uppercase (579 amino acid residues). The GYI sequence is shown in red. Submission of this protein sequence as a query in a BLAST search of the GenBank protein database indicates that it is an *A. stichopus* homolog of human UFM1-specific ligase 1 (see text in results section).