

Fig. 1 Suppl. The nucleotide sequence and deduced amino acid sequence of *GmMS*.

1 **ATGGCATCTCACATCGTTGGATACCCCCGTATGGGTCCCAAGAGAGAGGTCAAGTTTCGCT**
 M A S H I V G Y P R M G P K R E V K F A
61 **CTCGAGTCTTTCTGGGATGGCAAGAGCAGCGCCGAGGATTTGCAGAAGGTGTCTTCTGAT**
 L E S F W D G K S S A E D L Q K V S S D
121 **CTCAGGGCATCCATCTGGAAGCAGATGGCTGATGCTGGGATCAAGTACATCCCCAGCAAC**
 L R A S I W K Q M A D A G I K Y I P S N
181 **ACTTTCTCTCACTATGACCAGGTTCTCGACGCCACCGCCACCCTCGGTGCCGTTCCACCA**
 T F S H Y D Q V L D A T A T L G A V P P
241 **AGGTACGGCTGGACCGGCGGCGAGACTGGGTTTGATACCTACTTCTCCATGGCCAGAGGT**
 R Y G W T G G E T G F D T Y F S M A R G
301 **AATGCTACCGTGCCAGCTATGGAGATGACCAAGTGGTTCGACACCAACTACCACCTTTATT**
 N A T V P A M E M T K W F D T N Y H F I
361 **GTCCCTGAATTGGGCCCTGATGTGAACCTTACCTATGCTTCTCACAAGGCTGTTGATGAA**
 V P E L G P D V N F T Y A S H K A V D E
421 **TACAAGGAGGCCAAGGCGCTTGGAGTGGATACCGTTCCGGTCTCGTTGGCCCTGTTACA**
 Y K E A K A L G V D T V P V L V G P V T
481 **TACCTGTTGCTCTCCAAGCCTGCCAAGGGAGTTGAGAAATCCTTTTCTCTCTCTCTCTC**
 Y L L L S K P A K G V E K S F S L L S L
541 **CTTCCCAAGGTTCTTGCTGTCTACAAGGAAGTTATTGCTGACCTTAAGGCAGCTGGTGCT**
 L P K V L A V Y K E V I A D L K A A G A
601 **TCATGGATTCAAGTTTGATGAGCCTACCCTTGTCTTGGACCTTGAGTCTCACAAGTTGCAA**
 S W I Q F D E P T L V L D L E S H K L Q
661 **GCATTCACTGACGCATATGCAGAAGCTTGCACCTGCTTTGTCTGGTTTGAATGTTCTTGTT**
 A F T D A Y A E L A P A L S G L N V L V
721 **GAGACCTACTTTGCTGACATCCCTGCTGAGGCATACAAGACCCTCACATCTCTGAATGGC**
 E T Y F A D I P A E A Y K T L T S L N G
781 **GTCACCTGCATATGGATTTGATTTGGTCCGTGGAACCAACACTCTTGATTTGATCAAGGGT**
 V T A Y G F D L V R G T N T L D L I K G
841 **GGATTTCCAGCGGAAAATACCTCTTTGCTGGAGTGGTTGATGGAAGGAACATCTGGGCC**
 G F P S G K Y L F A G V V D G R N I W A
901 **AATGACCTTGCTGCTTCTCTCACTACCTTGACAGGGTCTTGAGGGCATTGTGGGCAAAGAT**
 N D L A A S L T T L Q G L E G I V G K D
961 **AAGCTTGTTGTGTCCACCTCCTCCTCCCTTCTTCACACTGCTGTTGATCTAGTTAACGAG**
 K L V V S T S S S L L H T A V D L V N E
1021 **ACCAAGTTGGATGATGAGATCAAGTCATGGCTAGCTTTTGCTGCCCAAAAAATGTTGAA**
 T K L D D E I K S W L A F A A Q K I V E
1081 **GTTAACGCATTGGCTAAAGCATTGTCTGGCCACAAGGATGAGGCCTTCTTCTCTGGTAAT**
 V N A L A K A L S G H K D E A F F S G N
1141 **GCTGCTGCTCTGGCTTCAAGGAAGTCTTCTCCAAGAGTGACCAACGAGGCTGTTTCAAG**
 A A A L A S R K S S P R V T N E A V Q K
1201 **GCTGCTGCTGCATTGAAGGGTTCAGATCATCGCCGTGCAACAAATGTCAGTGCCAGACTG**
 A A A A L K G S D H R R A T N V S A R L

1261 **GATTCTCAACAAAAGAAGCTCAACCTTCCAATCCTGCCAACCACCCTATTGGATCCTTC**
D S Q Q K K L N L P I L P T T T I G S F

1321 **CCTCAGACTGTAGAACTGAGGAGGGTACGCCGTGAATTCAAGGCTAACAAGATCTCCGAG**
P Q T V E L R R V R R E F K A N K I S E

1381 **GAAGAGTATGTAAAGTCAATTAAGGAGGAAATTCGCAAAGTTGTTGAGCTTCAAGAAGAG**
E E Y V K S I K E E I R K V V E L Q E E

1441 **CTTGATATTGATGTTCTTGTTTCATGGAGAACCAGAGAGAAATGATATGGTTGAGTACTTC**
L D I D V L V H G E P E R N D M V E Y F

1501 **GGTGAACAATTGTCAGGCTTTGCCTTCACCGTTAATGGGTGGGTGCAATCCTATGGTTCC**
G E Q L S G F A F T V N G W V Q S Y G S

1561 **CGTTGCGTGAAGCCACCGATCATCTATGGTGATGTGAGCCGCCCAAAGCCAATGACCGTC**
R C V K P P I I Y G D V S R P K P M T V

1621 **TTCTGGTCATCTCTGGCTCAGAGCTTTACCAAGCGCCCAATGAAGGGAATGCTTACCGGT**
F W S S L A Q S F T K R P M K G M L T G

1681 **CCTGTTACCATTCTCAACTGGTCCCTTTGTTAGAAATGACCAACCTAGATCTGAGACCACC**
P V T I L N W S F V R N D Q P R S E T T

1741 **TACCAGATTGCTTTGTCTATCAAGGACGAAGTGGAAGACCTTGAAAAGGCTGGCATCACT**
Y Q I A L S I K D E V E D L E K A G I T

1801 **GTTATCCAAATTGATGAAGCTGCTTTGAGAGAGGGTCTTCCACTGAGGAAATCAGAGCAA**
V I Q I D E A A L R E G L P L R K S E Q

1861 **GCTCACTACTTGGACTGGGCTGTCCATGCCTTCAGAATCACCAATGTTGGTGTCCAGGAT**
A H Y L D W A V H A F R I T N V G V Q D

1921 **ACCACCCAGATCCACACTCACATGTGCTACTCGAACTTCAACGACATCATCCACTCCATC**
T T Q I H T H M C Y S N F N D I I H S I

1981 **ATCGACATGGACGCCGATGTTATCACCATTGAGAACTCTCGCTCCGACGAGAAGCTTCTG**
I D M D A D V I T I E N S R S D E K L L

2041 **TCAGTCTTCCGCGAAGGTGTGAAGTATGGTGCTGGAATTGGCCCTGGTGTCTATGACATC**
S V F R E G V K Y G A G I G P G V Y D I

2101 **CACTCCCCAAGAATACCACCAACTGAAGAAATTGCTGACAGAATCAACAAGATGCTGGCA**
H S P R I P P T E E I A D R I N K M L A

2161 **GTGCTCGAGAAGAACATCTTGTGGGTGAACCCTGACTGTGGGCTCAAGACCCGTAAGTAC**
V L E K N I L W V N P D C G L K T R K Y

2221 **ACTGAGGTGAAGCCAGCCCTCACAAACATGGTTGCCGCAGCAAACTCATCCGCAACGAA**
T E V K P A L T N M V A A A K L I R N E

2281 **CTTGCCAAGTGA**
L A K *