```
     ATTCTTTGCCAGATATCAACCAAACACACAAACCCAGTTTAGCCACCAGTAGTAGTAG   -37
GAGGAACGATACGTCCTCAAACCAAAATAAAAAAAAATGACATCCTCAACAACGACGGACGCA    27
                                     M  T  S  S  T  T  T  D  A     9
ACCGATTCGGAGTTCGACCAGAGGAAGCTTCAATGCTTGGAAATGCTCAACGCAACCACCGAA    90
 T  D  S  E  F  D  Q  R  K  L  Q  Ⓒ  L  E  M  L  N  A  T  T  E     30

TTCACCACAACCCGGTCTGGACCTTTCTGCAGGGGAACCTGGGATGGTTGGCTCTGTTGGCCG    153
 F  T  T  T  R  S  G  P  F  Ⓒ  R  G  T  W  Ⓓ  G  W  L  Ⓒ  Ⓦ  Ⓟ     51

GATACTGCGGCTGGCGAATCTGCACTGCTACCCTGCCCAGATTTCATGGATGGATTCGATCCA    216
 D  T  A  A  G  E  S  A  L  L  P  Ⓒ  Ⓟ  D  F  M  D  G  F  D  P     72

ACAAGATTCGCACACAAAGACTGCGATGAGGACGGAGAATGGTTTAGGCATCCACTGACCAAC    279
 T  R  F  A  H  K  D  Ⓒ  D  E  D  G  E  Ⓦ  F  R  H  P  L  T  N     93

AGAACTTGGTCCAATTACACAACCTGCGTTAATTTGGATAAGCTCGAGTGGATGGAACAAGTG    342
 R  T  W  S  N  Y  T  T  Ⓒ  V  N  L  D  K  L  E  W  M  E  Q  V     114

AGAACGATATACGAAACGGGATACTCGATTTCGCTGATAGCCCTCATCTTATCGCTTGGTATT    405
 R  T  I  Y  E  T  G  Y  S  I  S  L  I  A  L  I  L  S  L  G  I     135

TTAAGTTACTTTAGGTCACTGAAATGCGCTCGCATTACGCTACATATGAACCTGTTTGCGTCG    468
 L  S  Y  F  R  S  L  K  C  A  R  I  T  L  H  M  N  L  F  A  S     156

TTTGCCTCAAACAACACACTCTGGCTGCTGTGGTACCGGATGGTGCTGGCAGATCCGGAAGTT    531
 F  A  S  N  N  T  L  W  L  L  W  Y  R  M  V  L  A  D  P  E  V     177

CTCAAGCACAATGGGGCGTCCTGCATCACACTGCACCTGGTGCTGCACTACTTCCTCATCACC    594
 L  K  H  N  G  A  S  C  I  T  L  H  L  V  L  H  Y  F  L  I  T     198

AACTACGCGTGGATGCTCTGCGAAGGATTCTATCTGCACACGGTCCTGGTGTCGGCATTCGTT    657
 N  Y  A  W  M  L  C  E  G  F  Y  L  H  T  V  L  V  S  A  F  V     219

TCGGAGAAAAAACTCGTCAACTGGCTTGTGGTCCTCGGATGGACCACACCGGGGATCGTGATC    720
 S  E  K  K  L  V  N  W  L  V  V  L  G  W  T  T  P  G  I  V  I     240

ATGGCGTATGGATTTCTGCGAGGATACGCCGGTACCCCGGAGGATACGATAGAGTGCTGGATG    783
 M  A  Y  G  F  L  R  G  Y  A  G  T  P  E  D  T  I  E  C  W  M     261

AACGAAAGCGTGTATGATAACGTTTTCAAGGCACCGGTGTGCATCTCGATGCTGCTCAATTTG    846
 N  E  S  V  Y  D  N  V  F  K  A  P  V  C  I  S  M  L  L  N  L     282

CTATTCCTGTGCAATATCATACGAGTAGTTCTGCTGAAGTTGAAAGCTCCTGCGGGACCGCAA    909
 L  F  L  C  N  I  I  R  V  V  L  L  K  L  K  A  P  A  G  P  Q     303

GGTACCGGGCCATCGAGAACCATACTGCAAGCGTTCAGAGCCACTCTGCTGCTAGTTCCGCTT    972
 G  T  G  P  S  R  T  I  L  Q  A  F  R  A  T  L  L  L  V  P  L     324

CTTGGCCTACAGTACATATTGACTCCGTTCCGACCCGATCCTGGACATTCTTATGAGCGAACG    1035
 L  G  L  Q  Y  I  L  T  P  F  R  P  D  P  G  H  S  Y  E  R  T     345

TACGAAATTATATCGGCGTTCACGGCATCATTCCAAGGTCTATTCGTAGCCGTCCTGTTCTGT    1098
 Y  E  I  I  S  A  F  T  A  S  F  Q  G  L  F  V  A  V  L  F  C     366

TTCTTCAACGGAGAGGTTATCGCACAAGTGAAACGGAAATGGCGCACCGTGTTCTTGCGGACT    1161
 F  F  N  G  E  V  I  A  Q  V  K  R  K  W  R  T  V  F  L  R  T     387
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CGAACCAATTCCTACACCGCAACGCAAGTGTCCTTCATTCGTAGCGGTCCGCCTATTCCCGGC    1224
 R  T  N  S  Y  T  A  T  Q  V  S  F  I  R  S  G  P  P  I  P  G     408

GAAGAGAAGGTCTGACTAAAAGAGTACGCCAGCGGCAATAGGTCTCCCCAGCCAACGAGCTTG    1287
 E  E  K  V  *                                                     412
AACCCCGTTAACGATCGGAGTTTTTCGGGAAATCCAACGACACCAACGGGTTTGGAAGGTAAG    1350
AGCAACGGTAATGGACCGGACTTATCGGTAGACGTGTCGAAAGATGACGCAATCTTTGGAGAC    1413
GCCAAAGCAAAGATCAATGGAGCTTCCGCCCATATCGAAGAACGGCTCGGCACATGGCGGAGA    1476
GGTTCAATTGAGTGTAGACATGTGAAGTTACCTCTTCTGGAAGCGCAACACAGGGAAAACGAT    1539
GGGGATCGTGAGGGAGAGGCTGAACAAGCTTCGCAACTTTTCGTTGAGCCGGCTCCGGCAGAT    1602
GAAGTGTTGTGAACTCTCGTTAGAACACAAATGTATCGAATTAATGATAGGTGAATTTATTAG    1665
CTTAAGGTTCAAAGAATTTCGAATATGTACAATGATGTAGTCATTCTAAGCTTAGTCTTACTA    1728
TTGTGACCGGTGGAAACCCACTTAACTACGCGTAGTTTTTATTTTAACGTTCTTAAACGCTTC    1791
AATTTTTTTGTAGCAAATACACAAACACACTCCACCTGTTAAGGGATAAATGTGATCATGGTG    1854
CAAAATAAAACTATCTGATTCGTGAAAAAAAAAAAAAAAAAAAAAA                     1901
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Figure S1. *AaegGPRcal1* full length cDNA cloned from MTs, and deduced amino acid sequence. The cDNA sequence is 1995 bp, encoding a 412 amino acid residue protein. Seven transmembrane regions are predicted by TMHMM and underlined (●—●). The highly conserved six cysteine (C21, C40, C49, C63, C80, C102), two tryptophan (W50, W86), two proline (P51, P64), and aspartic acid (D45) residues in Family B GPCRs are indicated with white letters in black circles (residues at the N terminus) [1,2]. Three predicted N-linked glycosylation sites are double-underlined. Black squares indicate prediction of potential phosphorylation sites by protein-kinase A, D, and G.

References

1. Harmar AJ (2001) Family-B G-protein-coupled receptors. Genome Biol 2: 3013.
2. Hoare SR (2005) Mechanisms of peptide and nonpeptide ligand binding to Class B G-protein coupled receptors. Drug Discov Today 10: 417-427.