Gene: GJB2 - Sequence: NG_008358.1
Transcript: NM_004004.5 - Protein: NP_003995.2
Date : February 26, 2015

1^{st} line: Base numbering. Full stops for intronic +/- 5, 10, 15...
2^{nd} line: Base sequence. lower case Introns, upper case Exons
3^{rd} line: Amino acid sequence. Printed on FIRST base of codon
4^{th} line: Amino acid numbering. Numbered on 1^{st} and increments of 10

```
Exon 1 | Start: 5001 | End: 5193 | Length: 192

.    .    .    .    .    .    .    .    .    .    .    .
ctgggggtcccgactctcagccgcccccgcttcacccgggccgccaaggggctgggggga

.    .    .    .    .    .    .    .    .    .    .    .
ggcggcgctcggggtaaccgggggagactcagggcgctgggggcacttggggaactcatg

.    .    .    .    .    .    .    .    .    .    .    .
ggggctcaaaggaactaggagatcgggacctcgaaggggacttgggggttcggggcttt

.    .    .    .    .    .    .    .    .    .    .    .
cgggggcggtcgggggttcgcggacccgggaagctctgaggacccagaggccgggcgcgc

.    .    .    .    .    .    .    .    .    .    .    .
tccgcccgcggcgccgccccctccgtaactttcccagtctccgagggaagaggcggggtg

      |-209     |-199     |-189     |-179     |-169     |-159
GGGGTGCGGTTAAAAGGCGCCACGGCGGGAGACAGGTGTTGCGGCCCCGCAGCGCCCGCG

      |-149     |-139     |-129     |-119     |-109     |-99
CGCTCCTCTCCCCGACTCGGAGCCCCTCGGCGGCGCCCGGCCCAGGACCCGCCTAGGAGC

      |-89      |-79      |-69      |-59      |-49      |-39
GCAGGAGCCCCAGCGCAGAGACCCCAACGCCGAGACCCCCGCCCCGGCCCCGCCGCGCTT

      |-29       .    .    .    .    .    .    .    .    .
CCTCCCGACGCAGgtgagcccgccggcccccggactgcccggccaggaacctggcgcgggg

  .    .    .    .    .    .    .    .    .    .    .    .
agggaccgcgagacccagagcggttgcccggccgcgtgggtctcggggaaccgggggggct

  .    .    .    .    .    .    .    .    .    .    .    .
ggaccaacacacgtccttgggccgggggggcgggggccgccttctggagcgggcgtttctg

  .    .    .    .    .    .    .    .    .    .    .    .
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cggccgagctccggagctggaatggggcggccggggaagtggacgcgatggcaccgcccg

  .    .    .    .    .    .    .    .    .    .    .    .
gggtgcgagtggggccgggcgcgcgcgggaggggaaaaaggcgcgggcgagccgccagcg

  .    .    .
cgaggtttgtggt
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Exon 2 | Start: 8373 | End: 10513 | Length: 2140

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.    .    .    .    .    .    .    .    .    .    .    .
gacactccccagcacagcaaatttttatgatgtgtttaaagattgggtgaattactcagg

.    .    .    .    .    .    .    .    .    .    .    .
tgaacaagctacttttttatcagagaacacctaaaaacacgttcaagagggtttgggaact

.    .    .    .    .    .    .    .    .    .    .    .
atacatttaatcctatgacaaactaagttggttctgtcttcacctgttttggtgaggttg

.    .    .    .    .    .    .    .    .    .    .    .
tgtaagagttggtgtttgctcaggaagagatttaagcatgcttgcttacccagactcaga

.    .    .    .    .    .    .    .    .    .    .    .
gaagtctccctgttctgtcctagctagtgattcctgtgttgtgtgcattcgtctttcca

   |-19      |-9       |1        |11       |21       |31
AGCAAACCGCCCAGAGTAGAAGATGGATTGGGGCACGCTGCAGACGATCCTGGGGGGTGT
                      M  D  W  G  T  L  Q  T  I  L  G  G  V
                      |1                          |11

  |41       |51       |61       |71       |81       |91
GAACAAACACTCCACCAGCATTGGAAAGATCTGGCTCACCGTCCTCTTCATTTTTCGCAT
 N  K  H  S  T  S  I  G  K  I  W  L  T  V  L  F  I  F  R  I
                      |21                         |31

  |101      |111      |121      |131      |141      |151
TATGATCCTCGTTGTGGCTGCAAAGGAGGTGTGGGGAGATGAGCAGGCCGACTTTGTCTG
 M  I  L  V  V  A  A  K  E  V  W  G  D  E  Q  A  D  F  V  C
                      |41                         |51

  |161      |171      |181      |191      |201      |211
CAACACCCTGCAGCCAGGCTGCAAGAACGTGTGCTACGATCACTACTTCCCCATCTCCCA
 N  T  L  Q  P  G  C  K  N  V  C  Y  D  H  Y  F  P  I  S  H
                      |61                         |71

  |221      |231      |241      |251      |261      |271
CATCCGGCTATGGGCCCTGCAGCTGATCTTCGTGTCCACGCCAGCGCTCCTAGTGGCCAT
 I  R  L  W  A  L  Q  L  I  F  V  S  T  P  A  L  L  V  A  M
                      |81                         |91

  |281      |291      |301      |311      |321      |331
GCACGTGGCCTACCGGAGACATGAGAAGAAGAGGAAGTTCATCAAGGGGGAGATAAAGAG
 H  V  A  Y  R  R  H  E  K  K  R  K  F  I  K  G  E  I  K  S
                      |101                        |111
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  |341       |351       |361       |371       |381       |391
TGAATTTAAGGACATCGAGGAGATCAAAACCCAGAAGGTCCGCATCGAAGGCTCCCTGTG
 E  F  K  D  I  E  E  I  K  T  Q  K  V  R  I  E  G  S  L  W
                     |121                       |131

  |401       |411       |421       |431       |441       |451
GTGGACCTACACAAGCAGCATCTTCTTCCGGGTCATCTTCGAAGCCGCCTTCATGTACGT
 W  T  Y  T  S  S  I  F  F  R  V  I  F  E  A  A  F  M  Y  V
                     |141                       |151

  |461       |471       |481       |491       |501       |511
CTTCTATGTCATGTACGACGGCTTCTCCATGCAGCGGCTGGTGAAGTGCAACGCCTGGCC
 F  Y  V  M  Y  D  G  F  S  M  Q  R  L  V  K  C  N  A  W  P
                     |161                       |171

  |521       |531       |541       |551       |561       |571
TTGTCCCAACACTGTGGACTGCTTTGTGTCCCGGCCCACGGAGAAGACTGTCTTCACAGT
 C  P  N  T  V  D  C  F  V  S  R  P  T  E  K  T  V  F  T  V
                     |181                       |191

  |581       |591       |601       |611       |621       |631
GTTCATGATTGCAGTGTCTGGAATTTGCATCCTGCTGAATGTCACTGAATTGTGTTATTT
 F  M  I  A  V  S  G  I  C  I  L  L  N  V  T  E  L  C  Y  L
                     |201                       |211

  |641       |651       |661       |671       |681       |*11
GCTAATTAGATATTGTTCTGGGAAGTCAAAAAAGCCAGTTTAACGCATTGCCCAGTTGTT
 L  I  R  Y  C  S  G  K  S  K  K  P  V  *
                     |221

   |*21       |*31       |*41       |*51       |*61       |*71
AGATTAAGAAATAGACAGCATGAGAGGGATGAGGCAACCCGTGCTCAGCTGTCAAGGCTC

   |*81       |*91       |*101      |*111      |*121      |*131
AGTCGCTAGCATTTCCCAACACAAAGATTCTGACCTTAAATGCAACCATTTGAAACCCCT

   |*141      |*151      |*161      |*171      |*181      |*191
GTAGGCCTCAGGTGAAACTCCAGATGCCACAATGGAGCTCTGCTCCCCTAAAGCCTCAAA

   |*201      |*211      |*221      |*231      |*241      |*251
ACAAAGGCCTAATTCTATGCCTGTCTTAATTTTCTTTCACTTAAGTTAGTTCCACTGAGA

   |*261      |*271      |*281      |*291      |*301      |*311
CCCCAGGCTGTTAGGGGTTATTGGTGTAAGGTACTTTCATATTTTAAACAGAGGATATCG
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   |*321      |*331      |*341      |*351      |*361      |*371
GCATTTGTTTCTTTCTCTGAGGACAAGAGAAAAAAGCCAGGTTCCACAGAGGACACAGAG

   |*381      |*391      |*401      |*411      |*421      |*431
AAGGTTTGGGTGTCCTCCTGGGGTTCTTTTTGCCAACTTTCCCCACGTTAAAGGTGAACA

   |*441      |*451      |*461      |*471      |*481      |*491
TTGGTTCTTTCATTTGCTTTGGAAGTTTTAATCTCTAACAGTGGACAAAGTTACCAGTGC

   |*501      |*511      |*521      |*531      |*541      |*551
CTTAAACTCTGTTACACTTTTTGGAAGTGAAAACTTTGTAGTATGATAGGTTATTTTGAT

   |*561      |*571      |*581      |*591      |*601      |*611
GTAAAGATGTTCTGGATACCATTATATGTTCCCCCTGTTTCAGAGGCTCAGATTGTAATA

   |*621      |*631      |*641      |*651      |*661      |*671
TGTAAATGGTATGTCATTCGCTACTATGATTTAATTTGAAATATGGTCTTTTGGTTATGA

   |*681      |*691      |*701      |*711      |*721      |*731
ATACTTTGCAGCACAGCTGAGAGGCTGTCTGTTGTATTCATTGTGGTCATAGCACCTAAC

   |*741      |*751      |*761      |*771      |*781      |*791
AACATTGTAGCCTCAATCGAGTGAGACAGACTAGAAGTTCCTAGTGATGGCTTATGATAG

   |*801      |*811      |*821      |*831      |*841      |*851
CAAATGGCCTCATGTCAAATATTTAGATGTAATTTTGTGTAAGAAATACAGACTGGATGT

   |*861      |*871      |*881      |*891      |*901      |*911
ACCACCAACTACTACCTGTAATGACAGGCCTGTCCAACACATCTCCCTTTTCCATGACTG

   |*921      |*931      |*941      |*951      |*961      |*971
TGGTAGCCAGCATCGGAAAGAACGCTGATTTAAAGAGGTCGCTTGGGAATTTTATTGACA

   |*981      |*991      |*1001     |*1011     |*1021     |*1031
CAGTACCATTTAATGGGGAGGACAAAATGGGGCAGGGGAGGGAGAAGTTTCTGTCGTTAA

   |*1041     |*1051     |*1061     |*1071     |*1081     |*1091
AAACAGATTTGGAAAGACTGGACTCTAAAGTCTGTTGATTAAAGATGAGCTTTGTCTACT

   |*1101     |*1111     |*1121     |*1131     |*1141     |*1151
TCAAAAGTTTGTTTGCTTACCCCTTCAGCCTCCAATTTTTTAAGTGAAAATATAGCTAAT

   |*1161     |*1171     |*1181     |*1191     |*1201     |*1211
AACATGTGAAAAGAATAGAAGCTAAGGTTTAGATAAATATTGAGCAGATCTATAGGAAGA

   |*1221     |*1231     |*1241     |*1251     |*1261     |*1271
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TTGAACCTGAATATTGCCATTATGCTTGACATGGTTTCCAAAAAATGGTACTCCACATAT

   |*1281     |*1291     |*1301     |*1311     |*1321     |*1331
TTCAGTGAGGGTAAGTATTTTCCTGTTGTCAAGAATAGCATTGTAAAAGCATTTTGTAAT

   |*1341     |*1351     |*1361     |*1371     |*1381     |*1391
AATAAAGAATAGCTTTAATGATATGCTTGTAACTAAAATAATTTTGTAATGTATCAAATA

   |*1401     |*1411     |*1421     |*1431       .     .     .
CATTTAAAACATTAAAATATAATCTCTATAATAATTTAAAAtctaatatggttttaatag

.    .    .    .    .    .    .    .    .    .    .    .
aacagcaaattttaatttcatctatcacttttatataaatacattaatgttttatattt

.    .    .    .    .    .    .    .    .    .    .    .
cataacaccaatgggtaagttgccagagtgtctgaccccattctgccccagttacagaaa

.    .    .    .    .    .    .    .    .    .    .    .
agcttctgtcaccagaaagtttggtggggaaggaagggaggaagatgatttctacctaac

.    .    .    .    .    .    .    .    .    .    .    .
cccgtgcccacctctaccaggtttttgaggcatatcagtctatggacaatgtggtgtttg

.    .    .    .    .    .    .    .    .
gtctggaaacgtaccttggtgaatgctgagttggctggaca
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GBK Parser: Version: 1.1, Version Date: 11/02/2015
Reader: Version: 1, Version Date: 11/02/2015
Writer: Version: 1, Version Date: 11/02/2015
Control: Version: 1, Version Date: 11/02/2015
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