Human GP1BA: Published Nucleotide sequence and predicted amino acid sequence

Reported GP1BA Mutations and Polymorphisms highlighted. References listed below

The sequence numbering is according to the GP1BA sequence of Lopez et al "Cloning of the alpha chain of human platelet glycoprotein Ib: a transmembrane protein with homology to leucine-rich alpha 2-glycoprotein." Proc Natl Acad Sci U S A. 1987 84(16):5615-5619.

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                                    M  P  L  L  L  L  L  L  L  L  P  S  P  L  H  P    -1
                          (-5T/C)(1)
GACGCTCTGTGCCTTCGGAGGTCTTTCTGCCTGCCTGTCCTCATGCCTCTCCTCCTCTTGCTGCTCCTGCTGCCAAGCCCCTTACACCCC   90

 H  P  I  C  E  V  S  K  V  A  S  H  L  E  V  N  C  D  K  R  N  L  T  A  L  P  P  D  L  P    30
CACCCCATCTGTGAGGTCTCCAAAGTGGCCAGCCACCTAGAAGTGAACTGTGACAAGAGGAATCTGACAGCGCTGCCTCCAGACCTGCCG  180

 K  D  T  T  I  L  H  L  S  E  N  L  L  Y  T  F  S  L  A  T  L  M  P  Y  T  R  L  T  Q  L    60
AAAGACACAACCATCCTCCACCTGAGTGAGAACCTCCTGTACACCTTCTCCCTGGCAACCCTGATGCCTTACACTCGCCTCACTCAGCTG  270

                    (Leu70Phe)(2)
 N  L  D  R  C  E  L  T  K  L  Q  V  D  G  T  L  P  V  L  G  T  L  D  L  S  H  N  Q  L  Q   120
AACCTAGATAGGTGCGAGCTCACCAAGCTCCAGGTCGATGGGACGCTGCCAGTGCTGGGGACCCTGGATCTATCCCACAATCAGCTGCAA  360

 S  L  P  L  L  G  Q  T  L  P  A  L  T  V  L  D  V  S  F  N  R  L  T  S  L  P  L  G  A  L   120
AGCCTGCCCTTGCTAGGGCAGACACTGCCTGCTCTCACCGTCCTGGACGTCTCCTTCAACCGGCTGACCTCGCTGCCTCTTGGTGCCCTG  450

                                                                  (Thr145Met)(3)
 R  G  L  G  E  L  Q  E  L  Y  L  K  G  N  E  L  K  T  L  P  P  G  L  L  T  P  T  P  K  L   150
CGTGGTCTTGGCGAACTCCAAGAGCTCTACCTGAAAGGCAATGAGCTGAAGACCCTGCCCCCAGGGCTCCTGACGCCCACACCCAAGCTG  540

 E  K  L  S  L  A  N  N  N  L  T  E  L  P  A  G  L  L  N  G  L  E  N  L  D  T  L  L  L  Q   180
GAGAAGCTCAGTCTGGCTAACAACAACTTGACTGAGCTCCCCGCTGGGCTCCTGAATGGGCTGGAGAATCTCGACACCCTTCTCCTCCAA  630

 E  N  S  L  Y  T  I  P  K  G  F  F  G  S  H  L  L  P  F  A  F  L  H  G  N  P  W  L  C  N   210
GAGAACTCGCTGTATACAATACCAAAGGGCTTTTTTGGGTCCCACCTCCTGCCTTTTGCTTTTCTCCACGGGAACCCCTGGTTATGCAAC  720
                                                                (Gly233Ser)(5,6)
                                                                (Gly233Val)(4)  (Met239Val)(7,8)
 C  E  I  L  Y  F  R  R  W  L  Q  D  N  A  E  N  V  Y  V  W  K  Q  G  V  D  V  K  A  M  T   240
TGTGAGATCCTCTATTTTCGTCGCTGGCTGCAGGACAATGCTGAAAATGTCTACGTATGGAAGCAAGGTGTGGACGTCAAGGCCATGACC  810

 S  N  V  A  S  V  Q  C  D  N  S  D  K  F  P  V  Y  K  Y  P  G  K  G  C  P  T  L  G  D  E   270
TCTAACGTGGCCAGTGTGCAGTGTGACAATTCAGACAAGTTTCCCGTCTACAAATACCCAGGAAAGGGGTGCCCCACCCTTGGTGATGAA  900

 G  D  T  D  L  Y  D  Y  Y  P  E  E  D  T  E  G  D  K  V  R  A  T  R  T  V  V  K  F  P  T   300
GGTGACACAGACCTATATGATTACTACCCAGAAGAGGACACTGAGGGCGATAAGGTGCGTGCCACAAGGACTGTGGTCAAGTTCCCCACC  990

 K  A  H  T  T  P  W  G  L  F  Y  S  W  S  T  A  S  L  D  S  Q  M  P  S  S  L  H  P  T  Q   330
AAAGCCCATACAACCCCCTGGGGTCTATTCTACTCATGGTCCACTGCTTCTCTAGACAGCCAAATGCCCTCCTCCTTGCATCCAACACAA 1080

 E  S  T  K  E  Q  T  T  F  P  P  R  W  T  P  N  F  T  L  H  M  E  S  I  T  F  S  K  T  P   360
GAATCCACTAAGGAGCAGACCACATTCCCACCTAGATGGACCCCAAATTTCACACTTCACATGGAATCCATCACATTCTCCAAAACTCCA 1170

 M  E  S  I  T  F  S  K  T  P  T  T  S  E  P  V  P  E  P  A  P  N  M  T  T  L  E  P  T  P   390
AAATCCACTACTGAACCAACCCCAAGCCCGACCACCTCAGAGCCCGTCCCGGAGCCCGCCCCAAACATGACCACCCTGGAGCCCACTCCA 1260

                    (399)   (VNTR length polymorphism) (411) (9)            (27 bp del)(10)
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 S  P  T  T  P  E  P  T  S  E  P  A  P  S  P  T  T  P  E  P  T  P  I  P  T  I  A  T  S  P   420
AGCCCGACCACCCCAGAGCCCACCTCAGAGCCCGCCCCCAGCCCGACCACCCCGGAGCCCACCCCAATCCCGACCATCGCCACAAGCCCG 1350

 T  I  L  V  S  A  T  S  L  I  T  P  K  S  T  F  L  T  T  T  K  P  V  S  L  L  E  S  T  K   450
ACCATCCTGGTGTCTGCCACAAGCCTGATCACTCCAAAAAGCACATTTTTAACTACCACAAAACCCGTATCACTCTTAGAATCCACCAAA 1440

 K  T  I  P  E  L  D  Q  P  P  K  L  R  G  V  L  Q  G  H  L  E  S  S  R  N  D  P  F  L  H   480
AAAACCATCCCTGAACTTGATCAGCCACCAAAGCTCCGTGGGGTGCTCCAAGGGCATTTGGAGAGCTCCAGAAATGACCCTTTTCTCCAC 1530

 P  D  F  C  C  L  L  P  L  G  F  Y  V  L  G  L  F  W  L  L  F  A  S  V  V  L  I  L  L  L   510
CCCGACTTTTGCTGCCTCCTCCCCCTGGGCTTCTATGTCTTGGGTCTCTTCTGGCTGCTCTTTGCCTCTGTGGTCCTCATCCTGCTGCTG 1620

 S  W  V  G  H  V  K  P  Q  A  L  D  S  G  Q  G  A  A  L  T  T  A  T  Q  T  T  H  L  E  L   540
AGCTGGGTTGGGCATGTGAAACCACAGGCCCTGGACTCTGGCCAAGGTGCTGCTCTGACCACAGCCACACAAACCACACACCTGGAGCTG 1710

 Q  R  G  R  Q  V  T  V  P  R  A  W  L  L  F  L  R  G  S  L  P  T  F  R  S  S  L  F  L  W   570
CAGAGGGGACGGCAAGTGACAGTGCCCCGGGCCTGGCTGCTCTTCCTTCGAGGTTCGCTTCCCACTTTCCGCTCCAGCCTCTTCCTGTGG 1800

 V  R  P  N  G  R  V  G  P  L  V  A  G  R  R  P  S  A  L  S  Q  G  R  G  Q  D  L  L  S  T   600
GTACGGCCTAATGGCCGTGTGGGGCCTCTAGTGGCAGGAAGGAGGCCCTCAGCTCTGAGTCAGGGTCGTGGTCAGGACCTGCTGAGCACA 1890

 V  S  I  R  Y  S  G  H  S  L STOP
GTGAGCATTAGGTACTCTGGCCACAGCCTCTGA
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