

Gene: CYP21A2 - Sequence: ENST00000448314
Transcript: NM_000500.7 - Protein: ENSP00000398594
Date : February 26, 2015

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

Exon 1 | Start: 501 | End: 824 | Length: 323
BE AWARE: Flanking intron is shared with the following exon

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. . . . .
ttgttcttcaggcgattcaggaaggcctattaggcagggactgccattttctctctgaga

. . . . .
caaacatcatgccagtaaactggcccacggtgggggtggcagagggagagggcccaggtgg

. . . . .
gggcggaactattgcctgcacagttgatgtggaaccagaaagctgactctggatgcagg

. . . . .
aaaaaggtcagggttgcatcttccttccttgcttcttgatgggtgatcaatTTTTTgaa

. . . . .
atacggacgtcccaaggccaatgagactggtgtcattccagaaaagggccactctgtggg

      |-119      |-109      |-99      |-89      |-79      |-69
GGGTGCGTGGGAGGGTACCTGAAGGTGGGGTCAAGGGAGGCCCAAAACAGTCTACACAG

      |-59      |-49      |-39      |-29      |-19      |-9
CAGGAGGGATGGCTGGGGCTCTTGAGCTATAAGTGGCACCTCAGGGCCCTGACGGGCGTC

      |1          |11          |21          |31          |41          |51
TGC CATGCTGCTCCTGGGCCTGCTGCTGCTGCCCTGCTGGCTGGCGCCCGCCTGCTGT
  M  L  L  L  G  L  L  L  L  P  L  L  A  G  A  R  L  L  W
      |1                      |11

      |61          |71          |81          |91          |101         |111
GGA ACTGGTGGAAGCTCCGGAGCCTCCACCTCCCGCCTCTTGCCCCGGGCTTCTTGCACT
  N  W  W  K  L  R  S  L  H  L  P  P  L  A  P  G  F  L  H  L
      |21                      |31

      |121         |131         |141         |151         |161         |171
TGCTGCAGCCCGACCTCCCAATCTATCTGCTTGGCCTGACTCAGAAATTCGGGCCCATCT

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L Q P D L P I Y L L G L T Q K F G P I Y
|41                                     |51

|181      |191      . . . . .
ACAGGCTCCACCTTGGGCTGCAAGgtgagaggctgatctcgctctggccctcaccatagg
R L H L G L Q D
|61

. .
agggggcgaggagg

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Exon 2 | Start: 922 | End: 1011 | Length: 89
 BE AWARE: Flanking intron is shared with both adjacent exons

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. . . . . |201 |211
tgacggagagggctcctctctccgctgacgctgctttggctgtctcccaATGTGGTGGTGC
                                     V V V L
                                     |71

      |221      |231      |241      |251      |261      |271
TGAACTCCAAGAGGACCATTGAGGAAGCCATGGTCAAAAAGTGGGCAGACTTTGCTGGCA
  N S K R T I E E A M V K K W A D F A G R
                        |81                        |91

      |281
GACCTGAGCCACTTACCTgtaagggtgggggcattttttctttcttaacaaatttttt
  P E P L T Y

. . . . .
ttaaagagatgggttcttgctatgttgcccaggctggtcttaaattcctagctctcaaag

. . . . .
atcctcccacctcagcctcaagtgtgagccacctttgg

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Exon 3 | Start: 1294 | End: 1448 | Length: 154
BE AWARE: Flanking intron is shared with both adjacent exons

.
ggcatccccaatccaggtccctggaagctcttgggggggcatatctggtggggagaaagc

.
aggggttggggaggccgaagaaggtcaggccctcagctgccttcacagttcccaccctc

. |291 |301 |311 |321
cagcccccaactcctcctgcaACAAGCTGGTGTCTAAGAACTACCCGGACCTGTCCTTGG
K L V S K N Y P D L S L G
|101

|331 |341 |351 |361 |371 |381
GAGACTACTCCCTGCTCTGGAAAGCCCACAAGAAGCTCACCCGCTCAGCCCTGCTGCTGG
D Y S L L W K A H K K L T R S A L L L G
|111 |121

|391 |401 |411 |421 |431 |441
GCATCCGTGACTCCATGGAGCCAGTGGTGGAGCAGCTGACCCAGGAGTTCTGTGAGgtaa
I R D S M E P V V E Q L T Q E F C E
|131 |141

.
ggctgggctcctgaggccacctcgggtcagcctcgcctctcacagtag

Exon 4 | Start: 1556 | End: 1657 | Length: 101
BE AWARE: Flanking intron is shared with both adjacent exons

.
ccccgccctgcccgctgcacagcggcctgctgaactcacactgtttctccacaCGCATG
R M

|451 |461 |471 |481 |491 |501
AGAGCCCAGCCCGGCACCCCTGTGGCCATTGAGGAGGAATTCTCTCCTCACCTGCAGC
R A Q P G T P V A I E E E F S L L T C S
|151 |161

|511 |521 |531 |541
ATCATCTGTTACCTCACCTTCGGAGACAAGATCAAGgtgcctcacagcccctcaggccca
I I C Y L T F G D K I K
|171 |181

. . . .
ccccagcccctccctga

Exon 5 | Start: 1746 | End: 1847 | Length: 101
 BE AWARE: Flanking intron is shared with both adjacent exons

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. . . . . |551 |561
gcctctccttgctcctgaactgaaagtactccctccttttctggcaGACGACAACTTAATG
                                     D D N L M

      |571      |581      |591      |601      |611      |621
CCTGCCTATTACAAATGTATCCAGGAGGTGTTAAAAACCTGGAGCCACTGGTCCATCCAA
P A Y Y K C I Q E V L K T W S H W S I Q
      |191                      |201

      |631      |641      . . . . .
ATTGTGGACGTGATTCCCTTTCTCAGGgtgaggacctggagcctagacacccctggggttg
I V D V I P F L R
      |211

. . . . .
taggggagaggctgggg

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Exon 6 | Start: 1949 | End: 2035 | Length: 86
BE AWARE: Flanking intron is shared with both adjacent exons

. |651
tggaggaggaggctccttcccacagctgcattctcatgcttcctgccgcaTTCTTCCCCA
F F P N

|661 |671 |681 |691 |701 |711
ATCCAGGTCTCCGGAGGCTGAAGCAGGCCATAGAGAAGAGGGATCACATCGTGGAGATGC
P G L R R L K Q A I E K R D H I V E M Q
|221 |231

|721 |731
AGCTGAGGCAGCACAAAGgtggggactgtacgtggacggcctcccctcggcccacagccag
L R Q H K
|241

.
tgatgctaccggcctcagcattgctatgaggcgggttcttt

Exon 7 | Start: 2205 | End: 2405 | Length: 200
 BE AWARE: Flanking intron is shared with both adjacent exons

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. . . . .
tgcataccccagttatgggcctgttgccactctgtactcctctccccaggccagccgctc

. . . . . |741 |751 |761 |771
agcccgctcctttcaccctctgcaGAGAGCCTCGTGGCAGGCCAGTGGAGGGACATGATG
                        E S L V A G Q W R D M M
                        |251

|781 |791 |801 |811 |821 |831
GACTACATGCTCCAAGGGGTGGCGCAGCCGAGCATGGAAGAGGGCTCTGGACAGCTCCTG
D Y M L Q G V A Q P S M E E G S G Q L L
|261 |271

|841 |851 |861 |871 |881 |891
GAAGGGCACGTGCACATGGCTGCAGTGGACCTCCTGATCGGTGGCACTGAGACCACAGCA
E G H V H M A A V D L L I G G T E T T A
|281 |291

|901 |911 |921 |931 . . .
AACACCCTCTCCTGGGCCGTGGTTTTTTTGCTTCACCACCCTGAGgtgcgtcctggggac
N T L S W A V V F L L H H P E
|301 |311

. . . . .
aagcaaaaggctccttcccagcaacctggccagggcggtgggcaccctcactcagctctg

. . . . .
agcactgtgcggctggggctgtg

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Exon 8 | Start: 2606 | End: 2784 | Length: 178
 BE AWARE: Flanking intron is shared with both adjacent exons

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. . . . .
cttgccctcaccggcactcaggctcactgggttgctgaggagcggctggaggctgggcag

. . . . . |941 |951
ctgtgggctgctggggcaggactccacccgatcattccccaATTCAGCAGCGACTGCAGG
                                I Q Q R L Q E

|961 |971 |981 |991 |1001 |1011
AGGAGCTAGACCACGAACTGGGCCCTGGTGCCTCCAGCTCCCGGGTCCCCTACAAGGACC
E L D H E L G P G A S S S R V P Y K D R
|321 |331

|1021 |1031 |1041 |1051 |1061 |1071
GTGCACGGCTGCCCTTGCTCAATGCCACCATCGCCGAGGTGCTGCGCCTGCGGCCCCGTG
A R L P L L N A T I A E V L R L R P V V
|341 |351

|1081 |1091 |1101 |1111 . . . .
TGCCCTTAGCCTTGCCCCACCGCACACACGGCCAGCAGgtgactcccgagggttgggg
P L A L P H R T T R P S S
|361 |371

. . . .
atgagtgaggaaagcccag

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Exon 9 | Start: 2868 | End: 2971 | Length: 103
 BE AWARE: Flanking intron is shared with the previous exon

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. . . . . |1121 |1131
cccagggaggctcctggccagcctctaactccagcccccttcaCATCTCCGGCTACGACAT
                                     I S G Y D I

      |1141      |1151      |1161      |1171      |1181      |1191
CCCTGAGGGCACAGTCATCATTCCGAACCTCCAAGGCGCCACCTGGATGAGACGGTCTG
P E G T V I I P N L Q G A H L D E T V W
|381                                |391

      |1201      |1211      . . . . .
GGAGAGGCCACATGAGTTCTGGCCTGgtatgtggggggccgggggcctgccgtgaaaatg
E R P H E F W P D
|401

. . . . .
tgggtggaggctggtccccgctgccgctgaacgcctccccaccacactgtccaccgccccg

. . . . .
cagatcgcttcctggagccaggcaagaactccagagctctggccttcggctgcggtgccc

. . . . .
gcgtgtgcctgggcgagccgctggcgcgcctggagctcttcgtggtgctgacccgactgc

. . . . .
tgcaggccttcacgctgctgccctccggggacgccctgccctccctgcagcccctgcccc

. . . . .
actgcagtgtcatcctcaagatgcag

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Exon 10 | Start: 3069 | End: 3838 | Length: 769
 BE AWARE: Flanking intron is shared with the previous exon

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. . . . . |1221 |1231
ccccgctgccgctgaacgcctccccaccacctgtccacccgccgcaATCGCTTCCTGG
                                     R F L E
                                     |411

      |1241      |1251      |1261      |1271      |1281      |1291
AGCCAGGCAAGAACTCCAGAGCTCTGGCCTTCGGCTGCGGTGCCCCGCGTGTGCCTGGGCG
  P G K N S R A L A F G C G A R V C L G E
                        |421                        |431

      |1301      |1311      |1321      |1331      |1341      |1351
AGCCGCTGGCGCGCCTGGAGCTCTTCGTGGTGTGACCCGACTGCTGCAGGCCTTCACGC
  P L A R L E L F V V L T R L L Q A F T L
                        |441                        |451

      |1361      |1371      |1381      |1391      |1401      |1411
TGCTGCCCTCCGGGGACGCCCTGCCCTCCCTGCAGCCCCTGCCCCACTGCAGTGTCAATCC
  L P S G D A L P S L Q P L P H C S V I L
                        |461                        |471

      |1421      |1431      |1441      |1451      |1461      |1471
TCAAGATGCAGCCTTTCCAAGTGGGCTGCAGCCCCGGGGGATGGGGGCCACAGCCCAG
  K M Q P F Q V R L Q P R G M G A H S P G
                        |481                        |491

      |1481|*1      |*11      |*21      |*31      |*41
GCCAGAACCAGTGATGGGGCAGGACCGATGCCAGCCGGGTACCTCAGTTTCTCCTTTATT
  Q N Q *

      |*51      |*61      |*71      |*81      |*91      |*101
GCTCCCGTACGAACCCCTCCCCTCCCCCTGTAAACACAGTGCTGCGAGATCGCTGGCAG

      |*111      |*121      |*131      |*141      |*151      |*161
AGAAGGCTTCTCCAGCGGCTGGGTGGTGAAGGACCCTGGCTCTTCTCTCGGGGCGACCC

      |*171      |*181      |*191      |*201      |*211      |*221
CTCAGTGCTCGGCAGTCATACTGGGGTGCGAGAGAGGTGGGCAGCAGCTCAGCCTCCCCC

      |*231      |*241      |*251      |*261      |*271      |*281
CGCTGGGGGAGCGAAAGTTTCTTGGTCTCAGCTTCATTTCCGTGAAGGGCACCGAGAACTC

      |*291      |*301      |*311      |*321      |*331      |*341
GAAGCCCTTCCAGTGGTACCAGCTCACTCCCTGGGAAAGGGGTTGTCAAGAGAGAGTCAA

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*351	*361	*371	*381	*391	*401
AGCCGGATGTCCCATCTGCTCTTCCCGTTCCCTTAAGGAGGTAGCTCCCAGCACTCAAC					
*411	*421	*431	*441	*451	*461
CAACCTCCCCGCAGAGCTCCCTTCCTGACCCTCCGCTGCAGAGGATTGAGGCTTAATTCT					
*471	*481	*491	*501	.	.
GAGCTGGCCCTTTCCAGCCAATAAATCAACTCCAGCTCcctctgcgaggctggcatgatt					
.
gttccatttcacccagccgctcagtccttgccctgttacactgtggggctgaaacctagg					
.
caggccgagccccagccaccccagctctgagccgcctccccacccctcacctgatggtcc					
.
actgtgctcccgtagagcccgttgaggttggcgtagtggcagttcctgtaccaccaggcc					
.
cctcggtaggagacagcgcaggagatgagcaagctggtggggtcccgatcacgggcagag					
.
aagacactgccgctgtggtagctcatggagtcccctgg					

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