

Gene: ENST00000448314 - Sequence: chromo-  
some:GRCh38:CHR\_HSCHR6\_MHC\_SSTO\_CTG1:32030453:32034790:1  
Transcript: ENST00000448314 - Protein: ENSP00000398594  
Date : February 24, 2015

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

Exon 1 | Start: 500 | End: 824 | Length: 324  
BE AWARE: Flanking intron is shared with the following exon

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. . . . .
ttgttcttcaggcgattcaggaaggcctattaggcagggactgccattttctctctgaga

. . . . .
caaacatcatgccagtaaaactggcccacggtgggggtggcagagggagagggcccaggtgg

. . . . .
gggcggaactattgcctgcacagttgatgtggaaccagaaagctgactctggatgcagg

. . . . .
aaaaaggtcagggttgcatttcccttccttgcttcttgatgggtgatcaatTTTTTgaa

. . . . .
atacggacgtcccaaggccaatgagactggtgtcattccagaaaagggccactctgtggg

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

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

      |1          |11          |21          |31          |41          |51
TCGCCATGCTGCTCCTGGGCCTGCTGCTGCTGCCCCCTGCTGGCTGGCGCCCGCCTGCTGT
      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
GGAAGTGGTGGAAGCTCCGGAGCCTCCACCTCCCGCCTCTTGCCCCGGGCTTCTTGCACT
      N  W  W  K  L  R  S  L  H  L  P  P  L  A  P  G  F  L  H  L
      |21                                |31

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

Exon 2 | Start: 921 | End: 1011 | Length: 90  
BE AWARE: Flanking intron is shared with both adjacent exons

TGAACTCCAAGAGGACCATTGAGGAAGCCATGGTCAAAAAGTGGGCAGACTTTGCTGGCA  
N S K R T I E E A M V K K W A D F A G R

|221 |231 |241 |251 |261 |271  
|81 |91

atcctccacctcagcctcaagtgtgagccacctttgg

ggcatccccaatccaggtccctggaagctcttgggggggcatatctggtggggagaaagc

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. . . . .
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

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Exon 4 | Start: 1555 | End: 1657 | Length: 102  
 BE AWARE: Flanking intron is shared with both adjacent exons

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. . . . .
ccccgcctgccccgtgcacagcggcctgctgaactcacactgtttctccacaCGCATG
                                     R M

|451      |461      |471      |481      |491      |501
AGAGCCCAGCCCGGCACCCCTGTGGCCATTGAGGAGGAATTCTCTCTCCTCACCTGCAGC
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

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Exon 5 | Start: 1745 | End: 1847 | Length: 102  
 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 S I Q
      |191                      |201

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

. . . . .
taggggagaggctgggg

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Exon 6 | Start: 1948 | End: 2035 | Length: 87  
 BE AWARE: Flanking intron is shared with both adjacent exons

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. . . . . |651
tggagggagaggctccttcccacagctgcattctcatgcttcctgccgcaTTCTTCCCA
                                     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

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Exon 7 | Start: 2204 | End: 2405 | Length: 201  
 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: 2605 | End: 2784 | Length: 179  
 BE AWARE: Flanking intron is shared with both adjacent exons

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. . . . .
cttgcctcaccggcactcaggctcactgggttgctgaggagcggtggaggctgggcag

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

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      |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
GTGCACGGCTGCCCTTGCTCAATGCCACCATCGCCGAGGTGCTGCGCCTGCGGCCCGTTG
  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      .      .      .
TGCCCTTAGCCTTGCCCCACCGCACACAGGCCAGCAGgtgactcccagggttgggg
  P  L  A  L  P  H  R  T  T  R  P  S  S
      |361                      |371

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      .      .      .      .
atgagtgaggaaagcccgag

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Exon 9 | Start: 2867 | End: 2971 | Length: 104  
 BE AWARE: Flanking intron is shared with the previous exon

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

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      |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

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

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      .      .      .      .      .      .      .      .      .      .
tggtggaggctggtccccgctgccgctgaacgcctccccacccacctgtccacccgcccg

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      .      .      .      .      .      .      .      .      .      .
cagatcgcttcctggagccaggcaagaactccagagctctggccttcggctgcggtgccc

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      .      .      .      .      .      .      .      .      .      .
gcgtgtgcctgggcgagccgctggcgcgccctggagctcttcgtggtgctgacccgactgc

```

. . . . .  
 tgcaggccttcacgctgctgccctccggggacgccctgccctccctgcagcccctgcccc  
 . . . . .  
 actgcagtgtcatcctcaagatgcag

Exon 10 | Start: 3068 | End: 3838 | Length: 770  
 BE AWARE: Flanking intron is shared with the previous exon

. . . . . |1221 |1231  
 ccccgctgccgctgaacgcctccccacccacctgtccacccgcccgcgaATCGCTTCCTGG  
 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  
 TGCTGCCCTCCGGGACGCCCTGCCCTCCCTGCAGCCCCTGCCCACTGCAGTGTATCC  
 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  
 TCAAGATGCAGCCTTTCCAAGTGCGGCTGCAGCCCCGGGGGATGGGGGCCACAGCCCAG  
 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

AGAAGGCTTCCTCCAGCGGCTGGGTGGTGAAGGACCCTGGCTCTTCTCTCGGGGCGACCC

*171	*181	*191	*201	*211	*221
CTCAGTGCTCGGCAGTCATACTGGGGTGCGAGAGAGGTGGGCAGCAGCTCAGCCTCCCCC					
*231	*241	*251	*261	*271	*281
CGCTGGGGAGCGAAAGTTTCTTGGTCTCAGCTTCATTTCCGTGAAGGGCACCGAGAACTC					
*291	*301	*311	*321	*331	*341
GAAGCCCTTCCAGTGGTACCAGCTCACTCCCTGGGAAAGGGGTTGTCAAGAGAGAGTCAA					
*351	*361	*371	*381	*391	*401
AGCCGGATGTCCCATCTGCTCTTCCCGTTCCCTTAAGGAGGTAGCTCCCAGCACTCAAC					
*411	*421	*431	*441	*451	*461
CAACCTCCCCGCAGAGCTCCCTTCTGACCCTCCGCTGCAGAGGATTGAGGCTTAATTCT					
*471	*481	*491	*501	.	.
GAGCTGGCCCTTTCCAGCCAATAAATCAACTCCAGCTC	cctctgcgaggctggcatgatt				
.	.	.	.	.	.
gttccatttcacccagccgctcagtccttgctgttacactgtggggctgaaacctagg					
.	.	.	.	.	.
caggccgagccccagccaccccagctctgagccgctccccacccctcacctgatggtcc					
.	.	.	.	.	.
actgtgctcccgtagagcccgttgagggtggcgtagtggcagttcctgtaccaccaggcc					
.	.	.	.	.	.
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