

Gene: ENSG00000109501 - Sequence: ENST00000226760
 Transcript: ENST00000226760 - Protein: ENSP00000226760
 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: 502 | End: 666 | Length: 164

```

. . . . .
gaaggcgagcggcctcgctaagcaactggacgttccgcgggcggggcgggggcggggcccg

. . . . .
gggcccagagtcgctcggaaactttcgctgtgggcgagccggacccgccttctggccccct

. . . . .
cgggcccaccacgcagggggagtgccgggcccgcagctaggcgaggcgcacctgattgg

. . . . .
cggagatgtggagtgattggcggctacaccggccactcagcaggccgagctggcgccgca

. . . . .
tccggggggcgcgctctggagtgaggggaggccgaaggccccgcccctgccccgccccct

|-169      |-159      |-149      |-139      |-129      |-119
GTGCAGAAGGCCGCGCTAGCCGGCTCTTCAGCAGCGAGTGCAGATTGCTCCCCGCGGCC

|-109      |-99       |-89       |-79       |-69       |-59
GCAGATCTCCGTTTGCGCCGCGTTCAGCTGTCCCGAACAACTTTTCTGCCGGCCCAGA

|-49       |-39       |-29       |-19       |-9        .      .      .
GGCCCCAGGGCGTCGAGCGCCGCTGCGGCCCACTCACGGGCCGgtgagtacttcggcg

. . . . .
ctggggcagtgggcggtggctgtgggcagcgcgcaggaggcgggcaagagccctgaggc

. . . . .
actgtcctcttcgggcctcagtttccccttccgagctgatgggtggctggcccaaagtc

. . . . .
ccgacaaggtccccgaagttggagggccgggggtcccggccgctctgcaacgcgcaaggc

. . . . .

```

gacccctgttccggggcccgaacgggtcaccggggggcgcgccccggtccccgcgcgct

.
gtcgcctggagccccgccgcgggcgggacagcaggccccgagaggc

Exon 2 | Start: 8103 | End: 8339 | Length: 236

```
. . . . .
gaaggccagggttggtggctcatgcccagtgaggcagggactccaggcctcggcattgtg
. . . . .
caggctctgagattgtaagtgccatgccatctgtagagtcacgtgggtgagtgctctcca
. . . . .
tggtttcctccctggaagcgggtgctggcccatggggactgtactgagtgtcagcgagatc
. . . . .
ctgtatggagtgcttggcagctccacctgcctccctctgcttttctgtctccagcagac
. . . . .
actaagtgccagagcgggctctgccggtgctggatgtgcctgaccttgacttttcttcca

      |1      |11      |21      |31      |41      |51
GCAGGATGGACTCCAACACTGCTCCGCTGGGCCCTCCTGCCACAGCCCCCGCCAGCAC
      M D S N T A P L G P S C P Q P P P A P
      |1      |11
      |61      |71      |81      |91      |101      |111
CGCAGCCCCAGGCGCTTCCCGACTCAATGCCACAGCCTCGTTGGAGCAGGAGAGGAGCG
      Q P Q A R S R L N A T A S L E Q E R S E
      |21      |31
      |121      |131      |141      |151      |161      |171
AAAGGCCCCGAGCACCCGAGCCCCAGGCTGGCCCTGGCCCTGGTGTAGAGACGCAGCGG
      R P R A P G P Q A G P G P G V R D A A A
      |41      |51
      |181      |191      |201      |211      |221      |231
CCCCCGCTGAACCCAGGCCAGCATACCAGGAGCCGGGAAAGAGCAGACGGCACCGGta
      P A E P Q A Q H T R S R E R A D G T G
      |61      |71

. . . . .
agggagcaggctgggaagcccaggctggggatgttcagggatagctgggtgggaacgggg
. . . . .
ttcagccaccctggagggtcccccgccaggctcctctgcagttcagcattgtgcagctc
. . . . .
ccatgctgtgcacaggcgtccatccagtggggctaccacctcctcagagccttgccacct
```

.
gtcacctttgtggcaccactcgaggtggctgggtgccccactcctctgcagtccttc
.
tcttcccagggcctctgcagcacttcacagcttccatttgcaacagcgtccaaacat

Exon 3 | Start: 17745 | End: 17827 | Length: 82

```
. . . . .
cttggctctgtgctcgcctccttcccatgcctcccaccccgagcgctttgagttgctgtt

. . . . .
gaaccacctcaccgcatagagtttgctcatcttgctctggcgctgcttgtagccggaag

. . . . .
gcaaacagtggctttctgggcatcttccctgtctgtgtctgtgtctctctgtactcctgg

. . . . .
cctggatttgaaagtgacaagcagcagcagatctgaagaccctcatgccttgctccctcc

. . . . .
atcctgacaagtgacaaagtctggctttgtgacatgtgtgtttgtttcttctgtgttaa

      |241      |251      |261      |271      |281      |291
GGCCTACAAAGGGAGACATGGAAATCCCCTTTGAAGAAGTCCTGGAGAGGGCCAAGGCCG
 P T K G D M E I P F E E V L E R A K A G
      |81                      |91

      |301      |311      . . . . .
GGGACCCCAAGGCACAGACTGAGgtgaggactgcggtgccggcagggacttcgggacgcg
 D P K A Q T E
      |101

. . . . .
gccccggcacaacaggcctggccacgagctccacagcccacagagaagtgtcggtgcct

. . . . .
gagatcggggtcaggagccagcgtggtgcaccctacccacttgagccccatgttggtag

. . . . .
ggtgcccattgttactgtgccagttttcctcctggcactcctctggggagcagcgctcat

. . . . .
cccccttttgtccaactcacacctcatcttgggcatcacctcctccaggatgacctcctg

. . . . .
gcttcctgcagctgcctgctcag
```

Exon 4 | Start: 19639 | End: 19783 | Length: 144

```
. . . . .
tgagccttggcaggcaggagcaactcaaggaagagaacctgtaccagtaccagtcggagc

. . . . .
ccgtgtctccctcgccgtgtggatggggtggccacaccttcctcaccgtgttttgaggag

. . . . .
cgagtggccggaggctcagtagggcctagcctagtggacatgcctggtgtgacccattt

. . . . .
ctgccccttccttcctggcctgggtgacaaagggaagtgggtgaaaggaggtgggctggc

. . . . .
agggagcatggggtgggagagggtcggagaatctggaggctgactggtgtctggcttgca

      |321      |331      |341      |351      |361      |371
GTGGGGAAGCACTACCTGCAGTTGGCCGCGACACGGATGAAGAACTCAACAGCTGCACC
V  G  K  H  Y  L  Q  L  A  G  D  T  D  E  E  L  N  S  C  T
                |111                                |121

      |381      |391      |401      |411      |421      |431
GCTGTGGACTGGCTGGTCCTCGCCGCGAAGCAGGGCCGTCGCGAGGCTGTGAAGCTGCTT
A  V  D  W  L  V  L  A  A  K  Q  G  R  R  E  A  V  K  L  L
                |131                                |141

      |441      |451      . . . . .
CGCCGCTGCTTGGCGGACAGAAGAGGgtgggtctgtgtgaggcttagaacagcctctggag
R  R  C  L  A  D  R  R  G
                |151

. . . . .
ggttgagcagccttgtaatgctgcttgctaactgaacaactaaaatcttacaaacctaac

. . . . .
gctggtgatgctgttgggaaatttcagtttctgttttgctggtggccttctcattttaga

. . . . .
cactgtttctggacttaacatgggatatttaacagaccaagccattttcattctctttgg

. . . . .
cttggttggtatctccaagtggtaactatacatcctgcttcctgctgggttctgatcc

. . . . .
aaactgagacatcgatcctgggttc
```

Exon 5 | Start: 21849 | End: 22019 | Length: 170

```
. . . . .
gcctccgggtctgcacctctgagagaggggaggaacaggaagaggctgccttcttcccgc

. . . . .
cagcatgtagggggcacttgggggctgtgtgggagaccagtctggcctcccagctgga

. . . . .
gagtgggctggcgcatgtcctcttgagtcatgtccatgcatccttccttggttaacc

. . . . .
aagtctgacaccttctatgagtctcgctcgaagccttcaggcagagttggcagggtc

. . . . .
agagtggcacccgaaagcctaggcagggcacacaaggcctttgaccacatcctatccctca

|461      |471      |481      |491      |501      |511
GCATCACGTC CGAGAACGAACGGGAGGTGAGGCAGCTCTCCTCCGAGACCGACCTGGAGA
  I T S E N E R E V R Q L S S E T D L E R
      |161                      |171

|521      |531      |541      |551      |561      |571
GGGCCGTGCGCAAGGCAGCCCTGGTCATGTACTGGAAGCTCAACCCCAAGAAGAAGAAGC
  A V R K A A L V M Y W K L N P K K K K Q
      |181                      |191

|581      |591      |601      |611      |621      |631 .
AGGTGGCCGTGGCGGAGCTGCTGGAGAATGTCGCCAGGTCAACGAGCACGgtgagga
  V A V A E L L E N V G Q V N E H D
      |201                      |211

. . . . .
ttcaccctgggcaccagccttccctgggctggcagccttcccacaggagccaggaccttcc

. . . . .
cataggggctgggaccttccctcaggggctgggtcttcccacaggagccgggaccttccc

. . . . .
tgtgaggacagggcccttccctgtggggaccaggggaccagaaccttccctgtagagaccg

. . . . .
tgccctagtgggtgaggtgtgtgggtggcattttgacagcatctgccctggctcaagtgtc

. . . . .
cactcattgaataaaccagagggtattctgcccagtgctctgtgaccacgt
```

Exon 6 | Start: 22569 | End: 22649 | Length: 80

```
. . . . .
tcactcattgaataaaccagagggtattctgccagtgctctgtgaccacgtctaccaat

. . . . .
gggacggactgtgtccatcaccaagtgggagcacgctacgtggtgctgagtcaccccag

. . . . .
ctactggagggtacagagggtgtggccctgctctgcctgcctgggggcccctatgatcccc

. . . . .
agaacgtaggatgccctggaactggcgtgccctaggaacagtgcgccagtttctggtgg

. . . . .
gctgcagggcacgaggagatagtcaacttgtctgactgttaatccaccctgtcccctgca

      |641      |651      |661      |671      |681      |691
ATGGAGGGGCGCAGCCAGGCCCGTGCCCAAGTCCCTGCAGAAGCAGAGGCGCATGCTGG
  G  G  A  Q  P  G  P  V  P  K  S  L  Q  K  Q  R  R  M  L  E
                        |221                                |231

      |701      |711      . . . . .
AGCGCCTGGTCAGCAGCGAGTgtgagtgagccctgccccgtctcacccatgcctccca
  R  L  V  S  S  E  S

. . . . .
gcctgcacctgcaggcgacctctccttcctgtgagactccatcctggcctgccctatct

. . . . .
caccctgcctcccagcctgcgcctgcaggcgacctctccttcctgtgcgaccccatcc

. . . . .
tggccctgctaggatctcaggcggccggtttggggctcagtgttctggacgctgggagta

. . . . .
gaccctgcccacctggagcgacgcactggagggaaggcagaccaggacagaaacatg

. . . . .
atgtgccagtcctccttgac
```


Exon 7 | Start: 25693 | End: 25841 | Length: 148

```
. . . . .
tgggtgagtggccccaggcataaggagctaggcagagaggacacttgggggtgggggaca
. . . . .
gcacaccaggggccgggggcccaggagtggaggctggcacttggaacacctgcccccttc
. . . . .
ctcctcaccagcctggctcctcaaccctcaggccgcccagggaagggtttcctccacctg
. . . . .
aaccactcagctcctttcttagcttggccccacgccaccgtccccagcccattgctctg
. . . . .
tgtgagggtggcagtggggctgcagtgtggggcgcccatgctgttttctctcatgcttca
      |721      |731      |741      |751      |761      |771
CCAAGAACTACATCGCGCTGGATGACTTTGTGGAGATCACTAAGAAGTACGCCAAGGGCG
  K  N  Y  I  A  L  D  D  F  V  E  I  T  K  K  Y  A  K  G  V
      |241                        |251
      |781      |791      |801      |811      |821      |831
TCATCCCCAGCAGCCTGTTCTGTCAGGACGACGAAGATGATGACGAGCTGGCGGGGAAGA
  I  P  S  S  L  F  L  Q  D  D  E  D  D  D  E  L  A  G  K  S
      |261                        |271
      |841      |851      |861 . . . . .
GCCCTGAGGACCTGCCACTGCGTCTGAAGgtgagtgaccaagaccccggtcaggccggag
  P  E  D  L  P  L  R  L  K
      |281
. . . . .
cctgcctcccaaggactcgcgcacctcaggcagggcaccttccaggaagctgcaggtggg
. . . . .
gaggttcgcgctaacaagagtgtcttacagccgtgccgctggtacctttgggtcatca
. . . . .
tctatcgtcataaggatgtgtcctcgggagagaggcctttcttttctgcgccgtcaggct
. . . . .
cagaaaccaggggcggtgttgggcaggagtgctaggatggcaagcaaggggcccctgggt
. . . . .
ctttctgtgcagtgtagggggcagtgggg
```

Exon 8 | Start: 31309 | End: 33917 | Length: 2608

.
ggaggtcttgccagggagagaagcacacatgcatctagtcacgctggtagaagggtggggag

.
ccaggcacggggcagaggggggctccaggcccagaagaggaggggctcacaggggaccgcg

.
agcatggggagggccacctggagaaggggggagggaggaccactaggtggggctgggtga

.
tgggaaaacgcaagggtgcgggttccttttgcagaggcagggtggtcagaggggaggcg

.
tgagatggggagcagtgggggtcctgtcccagcctcgttcccacgtaccatctttcccca

871	881	891	901	911	921
GTGGTCAAGTACCCCCTGCACGCCATCATGGAGATCAAGGAGTACCTGATTGACATGGCC					
V V K Y P L H A I M E I K E Y L I D M A					
291			301		

931	941	951	961	971	981
TCCAGGGCAGGCATGCACTGGCTGTCCACCATCATCCCCACGCACCACATCAACGCGCTC					
S R A G M H W L S T I I P T H H I N A L					
311			321		

991	1001	1011	1021	1031	1041
ATCTTCTTCTTCATCGTCAGCAACCTCACCATCGACTTCTTCGCCTTCTTCATCCCGCTG					
I F F F I V S N L T I D F F A F F I P L					
331			341		

1051	1061	1071	1081	1091	1101
GTCATCTTCTACCTGTCCTTCATCTCCATGGTGATCTGCACCCTCAAGGTGTTCCAGGAC					
V I F Y L S F I S M V I C T L K V F Q D					
351			361		

1111	1121	1131	1141	1151	1161
AGCAAGCCTGGGAGAACTTCCGCACCCTCACCGACCTGCTGCTGCGCTTCGAGCCCAAC					
S K A W E N F R T L T D L L L R F E P N					
371			381		

1171	1181	1191	1201	1211	1221
CTGGATGTGGAGCAGGCCGAGGTCAACTTCGGCTGGAACCACCTGGAGCCCTATGCCCAT					
L D V E Q A E V N F G W N H L E P Y A H					
391			401		

1231	1241	1251	1261	1271	1281
TTCCTGCTCTCTGTCTTCTTCGTCATCTTCTCCTTCCCCATCGCCAGCAAGGACTGCATC					
F	L	L	S	V	F
F	V	I	F	S	F
P	I	A	S	K	D
C	I				
411			421		

1291	1301	1311	1321	1331	1341
CCCTGCTCGGAGCTGGCTGTCATCACCGGCTTCTTTACCGTGACCAGCTACCTGAGCCTG					
P	C	S	E	L	A
V	I	T	G	F	F
T	V	T	S	Y	L
S	L				
431			441		

1351	1361	1371	1381	1391	1401
AGCACCATGCAGAGCCCTACACGCGCAGGGCCCTGGCCACCGAGGTCACCGCCGGCCTG					
S	T	H	A	E	P
Y	T	R	R	A	L
A	T	E	V	T	A
G	L				
451			461		

1411	1421	1431	1441	1451	1461
CTATCGCTGCTGCCCTCCATGCCCTTGAATTGGCCCTACCTGAAGGTCCTTGGCCAGACC					
L	S	L	L	P	S
M	P	L	N	W	P
Y	L	K	V	L	G
Q	T				
471			481		

1471	1481	1491	1501	1511	1521
TTCATCACCGTGCCTGTCGGCCACCTGGTCGTCCTCAACGTCAGCGTCCCGTGCCTGCTC					
F	I	T	V	P	V
G	H	L	V	V	L
N	V	S	V	P	C
L	L				
491			501		

1531	1541	1551	1561	1571	1581
TATGTCTACCTGCTCTATCTTCTTCCGCATGGCACAGCTGAGGAATTCAAGGGCACC					
Y	V	Y	L	L	Y
L	F	F	R	M	A
Q	L	R	N	F	K
G	T				
511			521		

1591	1601	1611	1621	1631	1641
TACTGCTACCTTGTGCCCTACCTGGTGTGCTTCATGTGGTGTGAGCTCTCCGTGGTCATC					
Y	C	Y	L	V	P
Y	L	V	C	F	M
W	C	E	L	S	V
V	I				
531			541		

1651	1661	1671	1681	1691	1701
CTGCTGGAGTCCACCGGCCTGGGGCTGCTCCGCGCCTCCATCGGCTACTTCTCTTCCTC					
L	L	E	S	T	G
L	G	L	L	R	A
S	I	G	Y	F	L
F	L				
551			561		

1711	1721	1731	1741	1751	1761
TTTGCCCTCCCCATCCTGGTGGCCGGCCTGGCCCTGGTGGGCGTGCTGCAGTTCCGCCGG					
F	A	L	P	I	L
V	A	G	L	A	L
V	G	V	L	Q	F
A	R				
571			581		

1771	1781	1791	1801	1811	1821
TGGTTCACGTCTCTGGAGCTCACCAAGATCGCAGTCACCGTGGCGGTCTGTAGTGTGCC					
W	F	T	S	L	E
591			601		
1831	1841	1851	1861	1871	1881
CTGCTGTTGCGCTGGTGGACCAAGGCCAGCTTCTCTGTGGTGGGGATGGTGAAGTCCCTG					
L	L	L	R	W	T
611			621		
1891	1901	1911	1921	1931	1941
ACGCGGAGCTCCATGGTCAAGCTCATCCTGGTGTGGCTCACGGCCATCGTGTGTTCTGC					
T	R	S	S	M	V
631			641		
1951	1961	1971	1981	1991	2001
TGGTTCTATGTGTACCGCTCAGAGGGCATGAAGGTCTACAACCTCCACACTGACCTGGCAG					
W	F	Y	V	Y	R
651			661		
2011	2021	2031	2041	2051	2061
CAGTATGGTGCCTGTGCGGGCCACGCGCCTGGAAGGAGACCAACATGGCGCGCACCCAG					
Q	Y	G	A	L	C
671			681		
2071	2081	2091	2101	2111	2121
ATCCTCTGCAGCCACCTGGAGGGCCACAGGGTCACGTGGACCGGCCGCTCAAGTACGTC					
I	L	C	S	H	L
691			701		
2131	2141	2151	2161	2171	2181
CGCGTGA CTGACATCGACAACAGCGCGGAGTCTGCCATCAACATGCTCCCGTTCTTCATC					
R	V	T	D	I	D
711			721		
2191	2201	2211	2221	2231	2241
GGCGACTGGATGCGCTGCCTCTACGGCGAGGCCTACCCTGCCTGCAGCCCTGGCAACACC					
G	D	W	M	R	C
731			741		
2251	2261	2271	2281	2291	2301
TCCACGGCCGAGGAGGAGCTCTGTCGCCTTAAGCTGCTGGCCAAGCACCCCTGCCACATC					
S	T	A	E	E	E
751			761		
2311	2321	2331	2341	2351	2361

AAGAAGTTCGACCGCTACAAGTTTGAGATTACCGTGGGCATGCCATTTCAGCAGCGGCGCT
K K F D R Y K F E I T V G M P F S S G A
|771 |781
|2371 |2381 |2391 |2401 |2411 |2421
GACGGCTCGCGCAGCCGCGAGGAGGACGACGTCACCAAGGACATCGTGCTGCGGGCCAGC
D G S R S R E E D D V T K D I V L R A S
|791 |801
|2431 |2441 |2451 |2461 |2471 |2481
AGCGAGTTCAAGAGCGTGCTGCTCAGCCTGCGCCAGGGCAGCCTCATCGAGTTTCAGACC
S E F K S V L L S L R Q G S L I E F S T
|811 |821
|2491 |2501 |2511 |2521 |2531 |2541
ATCCTGGAGGGCCGCTGGGCAGCAAGTGGCCTGTCTTCGAGCTCAAGGCCATCAGCTGC
I L E G R L G S K W P V F E L K A I S C
|831 |841
|2551 |2561 |2571 |2581 |2591 |2601
CTCAACTGCATGGCCAGCTCTCACCCACCAGGCGGCACGTGAAGATCGAGCAGCTGG
L N C M A Q L S P T R R H V K I E H D W
|851 |861
|2611 |2621 |2631 |2641 |2651 |2661
CGCAGCACCGTGTCATGGCGCGTGAAGTTCGCCTTCGACTTCTTTTCTCCCATTCCTG
R S T V H G A V K F A F D F F F F P F L
|871 |881
|2671 |*11 |*21 |*31 |*41
TCGGCGGCCTGAGGATGGTCCGCCACGAGGAGCTTCCAGTGCATGTTGCCATGAGGCCTT
S A A *
|891
|*51 |*61 |*71 |*81 |*91 |*101
TCCCCAGTGTGGCCCCAGCCGACAGGCATGCACCAAGTCCGCGCTGTGCCACGTGTGCA
|*111 |*121 |*131 |*141 |*151 |*161
GACTGTGGCTGCAGAGACCTTGCGACCATGTGTAGATTGCGTGACCCCGACAAAGGGAA
|*171 |*181 |*191 |*201 |*211 |*221
GGCTGCTGTGTAGCTCTGTCCACTCTGAATACCAAGTGTGTTGGGAATTGCATGCCATCT
|*231 |*241 |*251 |*261 |*271 |*281
CCACCCTGAGCCTGACCTTTCTGAGTGACATGGGTGTGCCAGGCTAGACTAGGAGGTTCC

*291	*301	*311	*321	*331	*341
GGTGTCTGAAAAGCACTTTACAGATGAGATTCCCTCTCCTCCCCACCTTCAAGCACCC					
*351	*361	*371	*381	*391	*401
TGTTCCCTCTTTCTTTCTTTGTGTTGGATTGTTTAAAAACCAAATAAGCATCTGTGTA					
*411	*421	*431	*441	*451	*461
ACCTCCACAGTAGCATTCTTATTTGTTTGGTCACTGCTACACCTTAGCAGCTCTTCCCC					
*471	*481	*491	*501	*511	*521
TTTCCTGGGGGATGTGCACGGCAGCTTGAGCCTGTCACGTGGTCAAGGCCCGGCCCATC					
*531	*541	*551	*561	*571	*581
AGAGGCTGGGGGAGCGGCACATTGGCAGTGTGTCACACTGAGCTGGGCACCACAGGCTG					
*591	*601	*611	*621	*631	*641
CCTCATGACCCTCCTGTCCAGCAGGTAGTGGGTGAATGTGTGAAGTCTTGCCTGAATCC					
*651	*661	*671	*681	*691	*701
ATCAGGACTTGGGAAACAGAGAACCTGTGGGGGCGGCTGTGGGGGAGTCCCTGCCAGT					
*711	*721	*731	*741	*751	*761
GTTTAGAAGAGCCTGACTGTGTTCACTGCCTTGAGAGAGAAAGCCAGGGTCTGAGTGGC					
*771	*781	*791	.	.	.
TGAAATAAAAGCCTCTGGTGAACCTGCAGcgcttttccttcctttctttaccgaaaagaa					
.
gtctttctgtgtacgtgcgtgagaatcagcagagcctgcactcctgttgaaatgaaatgcaa					
.
gtgcaatttgagttataaaagagcaaggttgatgtttcacagttgatggcttcctgccac					
.
agcgagaccctggcttcatctccagctggagggggccctggggcatctgccgtaactgtg					
.
gggtggcctgggcatgggctgcctgtgcagagagacctgtgctgaaggtagccatggagt					
.
gtcagcccagccatcttcagatcttactg					

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