



INK2S00114_ANXA11_G38R_A01_AB
 22,345 bp

5'
3'

TACCTCTGAGGTGGGAGAACAGGCCAGAGGGCGCACTGCACCTTGGCCAGCAGAGGCAGGAGCAAAGCTTCAGTGAGAGGGCCTT
ATGGAGACTCCACCCTCTTGTCCGGGTCTCCGCGTGACGTGGGAACGGTCTGCTCCGTCCTCGTTTCGAAGTCACTCTCCCGGAA

85

ANXA11

ANXA11-203

TCAAGGAAACTGGCTCATGGGGAGTGAATCCTGTCACTGTGGGTGGGGCCGGGGGTGTGGCCCTGGCCCAGAAGTCAGGCAGCAT
AGTTCCTTTGACCGAGTACCCCTCACTTAGGACAGTGACACCCACCCCGGCCCCACACCCGGGACCGGGTCTTCAGTCCGTCGTA

170

ANXA11

ANXA11-203

GCTGGTGGGTACTGTTTCTAGCTGGAGGCACCAGCAGGAGACAGTGAAC TGGTCTGCGACAAGCAGGGCAGATGCAGCAGTTTCT
CGACCACCCATGACAAAGATCGACCTCCGTGGTCTGCTGCTCACTTGACCAGACGCTGTTTCGTCCCGTCTACGTCGTCAAAGA

255

ANXA11

ANXA11-203

TCTGCAGGGTCCCAAGTTGTGGTGGTGGCTGCCCTTTCAGGAAGCTGGGTCCACGGGCCAGCAGGGGGCTCTCAGGCAGAGCCTGA
AGACGTCCCAGGGTCAACACCACCACCGACGGGAAAGTCTTCGACCCAGGGTGCCTCCGTCGTCCTCCCGAGAGTCCGTCCTCGGACT

340

ANXA11

ANXA11-203

ATGTGCTTTCGTCTTCTCTTCCAGATCTAACCATGAGCTACCCTGGCTATCCCCGCCCCAGGTGGCTACCCACCAGCTGCACC
TACACGAAAGCAGAAGAGAAGGTCTAGATTGGTACTCGATGGGACCGATAGGGGGCGGGGGTCCACCGATGGGTGGTTCGACGTGG

425

ANXA11

ANXA11-203

1 5 10 15
M S Y P G Y P P P P G G Y P P A A P
ENSE00003531093
ANXA11-203

AGGTAAGAGGGTCTGGGGTGGGGAGGAGAGTGAATGCTGCCTCTGTACAGTGGCTGGGAGTGGAGAGGGGAGAACAGTAGTTTCC
TCCATTCTCCAGACCCACCCCTCCTCTCACTTACGACGGAGACATGTCACCGACCCCTCACCTCTCCCTCTTGTTCATCAAAGG

510

ANXA11

ANXA11-203

TCACTCCCTCCTCCCTCACAGCACGGCCCAGCAGGGGAGGAGAGGACAACAGGAGTAGTGGGACAGCCAGCCGAGGCAGGGGC
AGTGAGGGGAGGAGGGGAGTGTGCTGTCGGGTGCTCCCTCCTCTCTGTTGTCTCATCACCTGTTCGGTTCGGCTCCGTCCTCCG

595

ANXA11

ANXA11-203

TGGAGAAGAGCATGACACTAAGGCCATCGGAGGCCTAGGTTTGAAC TGCCTCCAGAAAGCCCTGGACCAGGCCAGGGCTGGGT
ACCTCTTCTCGTACTGTGATTCCGGTAGCCTCCGGATCCAAACTTTGACGGAGGTCTTTTCGGGACCTGGTCCGGGTCCCGACCCA

680

ANXA11

ANXA11-203

ANXA11-203

CTCTTGCCTTACTCTCTAGTAACAGTGGGCAAATGCTGTCACTTTGAGACTCAGTTTTCTTCTCCGCAAAATTGCTTCAAGGATT
GAGAACGGAATGAGAGATCATTGTACCCCGTTTACGACAGTGAAACTCTGAGTCAAAAAGAAGAGGGCGTTTTAACGAAGTTCCTAA

765

ANXA11

ANXA11-203

ANXA11-203

TCTCCCTCATTAGGTGGTCCTGGATACTGATGAGATAGGCAGGCAGAGCGACACGGTGTCTCCAAAGCATTGCTAGGTGATGGT
AGAGGGGAGTAATCCACCAGGACCTATGACTACTCTATCCGTCCGTCTCGCTGTGCCACAGGAGGTTTTCGTAACGATCCACTACCA

850

ANXA11

ANXA11-203

ANXA11-203

TGCCCCCTTACCACCTCTCCTACCCTCTGCTCAAGGTGTGTGGGTTTGCAGCAACAAGATCCCCCTTGCCAAGAGAGGAAGTGGAG
ACGGGGGAATGGTGGAGAGGATGGGAGACGAGTTCACACACCCAAACGTCGTTGTTCTAGGGGGGAACGGTTCTCTCCTTCACCTC

935

ANXA11

ANXA11-203

ANXA11-203

GCAGATGCTAAGGGTCAAAGGTCACCTCCCTGTTTTCTGCAGGAGCTGTGGGTAGTCACATGGAGAAGTCGTCTTCTCTGGCCCTG
CGTCTACGATTCCCAGTTTTCCAGTGAGGGACAAAAGACGTCCTCGACACCCATCAGTGTACCTCTTCAGCAGAAGAGACCGGGAC

1020

ANXA11

ANXA11-203

ANXA11-203

GCCCCTTTTGGTCCTCAAATGAGATTTGGTCCCCACTGTGGGAAAGGAAATATGAGGGCTCATGAGACCAAGGGGAGAAAAGGGT
CGGGGAAAACCAGGAGTTTACTCTAAACCAGGGGTGACACCCTTTTCTTTATACTCCCGAGTACTCTGGTTCCCCTCTTTTTCCCA

1105

ANXA11

ANXA11-203

ANXA11-203

CATTCCAAGGCTGGTTCATCCTGAGGGTGCCTGAGCCGCTGCCCTCTCCCCAGGGGACTCCTAGGCATCATTGATTTCTTTGGAG
GTAAGGTTCCGACCAGTAGGACTCCACGGACTCGGCACGGGGAGAGGGGTCCCCTGAGGATCCGTAGTAACCTAAAGAAACCTC

1190

ANXA11

ANXA11-203

ANXA11-203

CTGAGGTCTGTGGTTTTGAACACCCCAGACCTGCAGGCCATTTACCTTCCCTCCCATTTCAGCAGGTGAAGAACAGACTCAGACCT
GACTCCAGGACACCAAACCTTGTGGGGTCTGGACGTCCGGTAAATGGAAGGGAGGGTAAGTCGTCCACTTCTTGTCTGAGTCTGGA

1275

ANXA11

ANXA11-203

ANXA11-203

AGAGGTGGCTCAGCTGCTGTCCCAGGGCATGTTAGGGGCTGAGCTGGGCCACTGCCCTCTGAATGAGCCCACCCAGGTTGGCTG
TCTCCACCGAGTCGACGACAGGGTCCCCTACAATCCCCGACTCGACCCGGTGACGGGAGACTTACTCGGGTGGGGTCCAACCGAC

1360

ANXA11

ANXA11-203

ANXA11-203

GCACTGGCCTGGGTTCTCTCTATAGTAGAAATCCTGCCATCCAGATCCTGCCACTGCCACCTTTGCTAGCACAGCTGAGCAGC
CGTGACCCGGACCCAAGAGAGAGATATCATCTTTAGGACGGTAGGTCTAGGACGGTGACGGTGGAAACGATCGTGTCGACTCGTCCG

1445

ANXA11

ANXA11-203

ANXA11-203

CTCTGAGCAGCAAGAGAGGGAGGAGGCAGGAAATTTAGGGAAGGTTCTTCCTGGAGGGTCTGGAGCCCTGGAGATGAAGAGCCGAT
GAGACTCGTCGTTCTCTCCTCCTCCGTCCCTTTAAATCCCTTCCAAGAAGGACCTCCCAGACCTCGGGACCTCTACTTCTCGGCTA

1530

ANXA11

ANXA11-203

ANXA11-203

CCGAAGCTGCCATGTAGAGGAAAGCATCTAACAGGCCAGAGGCCCATGATGATGTGGAATGCCCATCGGGCACCCAGCTGAGCC
GGCTTCGACGGTACATCTCCTTTTCGTAGATTGTCCGGTCTCCGGGGTACTACTACAGCTTACGGGTAGCCCGTGGGTTCGACTCGG

1615

ANXA11

ANXA11-203

ANXA11-203

CTGCAGGTGTTAACTCAGTCTTCGTACAGCAGTCTAGGCATACACTCACCATTAGCCCATTTGTAAGCTGAGGAAACAAGCCTA
GACGTCCACAATTGAGTCAGAAGCAGTGTCTGTCAGATCCGTATGTGAGTGGTAATCGGGTAAACATTCGACTCCTTTGTTTCGGAT

1700

ANXA11

ANXA11-203

ANXA11-203

AGGAGGGTGAAAGCCTTGCCCCAGGGCACATACCGGTCTGCTGGTTTCAGAGCGGGCTTTTCACCTCTGTTTCTTCCTGTCTC
TCCTCCCCTTTTCGGAACGGGGTCCCCTGTATGGCCAGGACGACCAAAGTCTCGCCCCGAAAAGTGGAGACAAAAGAAGGACAGGAG

1785

ANXA11

ANXA11-203

ANXA11-203

TTGTGGACTGGTATCTGTGTTTACCATGACCCAGCCCCATGTCCCTCCAGCCTCTTATCCTGCTTCTCCCTGCCTTTTACAGACT
AACACCTGACCATAGACACAAATGGTACTGGGTTCGGGGTACAGGGAGGTTCGGAGAATAGGACGAAGAGGGACGGAAAATGTCTGA

1870

ANXA11

ANXA11-203

ANXA11-203

TGTAATAGCAAACAGCCAAACCCCTCCCGCCAGTGCCTTCGCATTACTGAAATCTCAGAGCTCCCTATGGTCACCTCTGTCATG
ACATTATCGTTTGTCTGGTTTGGGGGAGGGCGGTCACGGAAGCGTAATGACTTTAGAGTCTCGAGGGATACCAGTGAGACAGTAC

1955

ANXA11

ANXA11-203

ANXA11-203

GGCTCAGCATGGTGTCCACAAACAGTCTGTCCTTGTCTGTCCTCTGCTCCATGATGGTGAACCTTGGGAGGGCAGAGCCTGCCTG
CCGAGTCTGACACAGGGTGTGTCAGACAGGAACAGACAGGAGGACGAGGTACTACCACTTGAACCCCTCCCGTCTCGGACGGAC

2040

ANXA11

ANXA11-203

ANXA11-203

GGCTCTCCCAGCCTCCTTAATACCCACAGAGGGTCTTGGGAGTGTGGGGAACCTCCACCTTCTCCCTGGGAAGAGGGGAAGG
CCGAGAGGGTCGGAGGAATTATGGGGTGTCTCCAGAACCCTCACAAACCCCTTGAGGTGGAAGGAGGGACCTTCTCCCTTCC

2125

ANXA11

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PCR Reverse
TCATGTGGTCTGTGGTGTCC

TTTCCCTCCTCTGCCAGTGGGATAGGGGGAGACTTTCTCCTGGTGTTCATGTGGTCTGTGGTGTCCCGAGGCTCGAGGCTC
AAAGGGGAGGAGACGGTCACCTATCCCCCTCTGAAAGGAGGACCACAAAAGTACACCAGACACCACAGGGCTCCGAGCTCCGAG

2210

ANXA11

ANXA11-203

ANXA11-203

GAGGCTTTACTGGGCCTCCCTTTCTGACCACCTGGGAGCTCTCATCTCTGCCTTTCCCGTGTGGTGGGGGACTGGCAGGGGGCT
CTCCGAAATGACCCGGAGGGAAAAGACTGGTGGACCCTCGAGAGTAGAGACGGAAAAGGGGCACACCACCCCTGACCGTCCCCCGA

2295

ANXA11

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ANXA11-203

AAAGGGCTTGGTGTGCTTTACAGGTGGTGGTCCCTGGGGAGGTGCTGCCTACCCTCCTCCGCCAGCATGCCCCCATCGGGCTG
TTTCCCGAACCAACGAAAAGTCCACCACCAGGGACCCCTCCACGACGGATGGGAGGAGGGCGGGTTCGTACGGGGGGTAGCCCGAC

2380

ANXA11

ANXA11-203

G G G P W G G A A Y P P P P S M P P I G L
ENSE00003646683

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Donor Template WT -> SNV

PAM
Protospacer Sequence

SNV

GATGGGAGGAGGCGGGTTCGTACGGGGGGTAGCCGAC
Donor Template WT -> SNV

AGCCCGAC
gRNA Protospacer

GATAACGTGGCCACCTATGCGGGGCAAGTTCAACCAGGACTATCTCTCGGGAATGGTGAGTCCAGCTCTCCTGCTGAGGCAGCCCT
CTATTGCACCGGTGGATACGCCCCGTCAAGTTGGTCTGTATAGAGAGCCCTTACCACTCAGGTCGAGAGGACGACTCCGTCGGGA

ANXA11

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40 N V A T Y A G Q F N Q D Y L S G M

ENSE00003646683

ANXA11-203

Donor Template WT -> SNV

Protospacer Sequence

CTATTGCACCGGTGGATACGCCCCGT

Donor Template WT -> SNV

CTATTGCACCGG

gRNA Protospacer

GGGGCCACACCTGCGTGGCCAGAGGAATCAAAGCTGCTGGCCTCTGGGGCTCCAGAGTTGTCTATGTGTGTGTTGCTGTGGTGTG
CCCCGGTGTGGACGCACCGGTCTCCTTAGTTTCGACGACCGGAGACCCCGAGGTCTCAACAGATACACACACAACGACACCCACAC

ANXA11

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ANXA11-203

TAGTGTGTTGAGCTGTACCTTAGAACAGGGTTTTTCATCAGGCTTCTGCCACCTGCTCTCTGCCCTCTCTGGGTCTCACTTTTTCC
ATCACACAACCTCGACATGGAATCTTGTCCAAAAGTAGTCCGAAGACGGTGGACGAGAGACGGGGAGAGACCCAGAGTGAAAAGG

ANXA11

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CCCAAAAGTAGTCCGAAGACG

PCR Forward

CCCAAAAGTAGTCCGAAGACG

Sanger Sequencing

CATCTGTAAATGAGGGGAAGGGGACCAGATGATCTCACAGGTCCCTTTACGCCCTGAGGGGTTAGGGTTGGGAAGGTGGCGAGG
GTAGACATTTTACTCCCTTCCCTGGTCTACTAGAGTGTCCAGGGAAAGTCGGGACTCCCAATCCCAACCTTCCACCGCTCC

ANXA11

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ANXA11-203

GTATCTGCATGAGTGTGCATGCACGTGCTATGTATGAGTATCCACATTCATATACCTGCATGTGCATGTGTGTACATATGGAGGG
CATAGACGTACTCACACGTACGTGCACGATACATACTCATAGGTGTAAGTATATGGACGTACACGTACACACATGTATACCTCCC

ANXA11

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ANXA11-203

CTCTTCTGGTTAGGCCTTGGTGGGTGTGTGGCAGGTATCTTGGGCAGACATGCTACTTTTTAAATTTGTTGTTTCACTTTTTAAA
GAGAAGACCAATCCGGAACCACCCACACACCGTCCATAGAACCCGCTGTACGATGAAAAATTTAAACAACAAAGTGAAAAATTTT

ANXA11

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ANXA11-203

TAATACATTTTATGATTTGAAAAACAAACGTATGCTTAGTTTATGATTTGAAAAACAAACGTATGCTTAGAGGAAATTATGCAACCA
ATTATGTAAAATACTAAACTTTTGTTCATACGAATCAAATACTAAACTTTTGTTCATACGAATCTCCTTTAATACGTTGGT

2975

ANXA11

ANXA11-203

ANXA11-203

ATACACACCCTAATTTGTGCCAGGCCAGTTCTAGGCACTGGGGATATGTGAATAAAACAAACAAAAATCTCAGCCGTGCTGCAC
TATGTGTGGGATTAACACGGTCCGGGTCAAGATCCGTGACCCCTATACACTTATTTTGTTCATACGAATCTCCTTTAATACGTTGGT

3060

ANXA11

ANXA11-203

ANXA11-203

TTATCATCTATGGGGAAAAGACAGGCAGTACCTTAAGTCAACGATGTGATGTTATTGAAAGTGTAGGTGCCATAGGAACAAGTTG
AATAGTAGATACCCCTTTTCTGTCCGTCATGGAATTCAGTTGCTACACTACAATAACTTTCACATCCACGGTATCCTTGTTC AAC

3145

ANXA11

ANXA11-203

ANXA11-203

ACCAGGGTAAAGGGGTCAGGAGTGGGGGTGGGGTGATGTAAGGATAATGATTTTAAAGTTAGCAGTAAGGTGGGTCTGGCTGAAAA
TGGTCCCATTTCAGTCCCTCACCCCCACCCCACTACATTCTATTACTAAAATTCAATCGTCATTCCACCCAGACCGACTTTT

3230

ANXA11

ANXA11-203

ANXA11-203

GAGGATGTGTGAGCAAAGACCTGCATCAGGGGAAGGAAGTGCTGTATGGATGTCTAGGGAATGCCGGTGCCCTGAGGTGCCAAGG
CTCCTACACACTCGTTTTCTGGACGTAGTCCCTTCTTTCACGACATACCTACAGATCCCTTACGGCCACGGGACTCCACGGTTCC

3315

ANXA11

ANXA11-203

ANXA11-203

GGTGTGAGGTGCTCAGGGACAGGGAGGAGAGGCCAGTGTGGCTAAAGTGGAAAGGCGAGGGGGTGAGATGGGAAATGAAGTCTGG
CCACACTCCACGAGTCCCTGTCCCTCCTCTCCGGTCACACCGATTTACCTTTCCGCTCCCCCACTCTACCCTTTACTTCAGACC

3400

ANXA11

ANXA11-203

ANXA11-203

GGGTCTAGCTCTTGCAGGGTGTAGGAGGCTATCCATCCTAAGGATTTAGGTTTTTATTCTGGTGAGTGCAGATTCACCTGAACA
CCCAGATCGAGAACGTCCCACATCCTCCGATAGGTAGGATTCCTAAATCCAAAAATAAGGACCACTCACGTCTAAGTGGACTTGT

3485

ANXA11

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TGCCTGCCAGAGGTGTCTGTGGGTAGCAGGCTGATGTGATGGGGATGCCCCCAACCTGCATATGGGACCCACGCACCTTCTTGG
ACGGACGGTCTCCACAGACACCCATCGTCCGACTACACTACCCCTACGGGGGTTGGGACGTATACCCCTGGGTGCGTGGAAGAACC

3570

ANXA11

ANXA11-203

ANXA11-203

GCAGTGAGCTCTTAACCTTCACCCAGGTGGTCTGGGATGGGAGGAGCAACCATGTGGAGAGGGGAAGGCATCTCCCCTGCAGAAGG
CGTCACTCGAGAATTGGAAGTGGGTCCACCAGACCCCTACCCTCCTCGTTGGTACACCTCTCCCTTCCGTAGAGGGGACGTCTTCC

3655

ANXA11

ANXA11-203

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GGATGAGGATCTCTGGTTTGGATCGAGTCGCACTGTTCACTGGCTGTGTAACCTTTGAGCAAGTAAACTCATTCTGTGGTCTGTGA
CCTACTCCTAGAGACCAAACCTAGCTCAGCGTGACAAGTGACCGACACATTGAAACTCGTTTCATTTGAGTAAGACACCAGACACT

3740

ANXA11

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AATGGGTATAACGGTACTTTCATATTCACAAAGCGGAGATGCTGTGAGGACTGACTTGGCTTAGGTATGAAAAAGGGTGGAGGGAC
TTACCCATATTGCCATGAAGTATAAGGTGTTTCGCTCTACGACACTCCTGACTGAACCGAATCCATACTTTTTCCACCTCCCTG

3825

ANXA11

ANXA11-203

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GGAGTGCAGCAGGGCCCATTTGGCCTCAGGCTCTGCTTTGTGTCCTTGCAAGCGCCCAACATGTCTGGGACATTTGGAGGAGCCAA
CCTCACGTCGTCCCGGGTAACCGGAGTCCGAGACGAAACACAGGAACGTCCGCCGGTTGTACAGACCCTGTAAACCTCCTCGGTT

3910

ANXA11

ANXA11-203

ANXA11-203

A A N M S G T F G G A N
ENSE00002518768

CATGCCCAACCTGTACCCTGGGGCCCTGGGGCTGGCTACCCACCAGTGCCCCCTGGCGGCTTTGGGCAGCCCCCTCTGCCAG
GTACGGGTTGGACATGGGACCCCGGGGACCCGACCGATGGGTGGTCACGGGGGACCGCCGAAACCCGTCGGGGGGAGACGGGTC

3995

ANXA11

ANXA11-203

ANXA11-203

M P N L Y P G A P G A G Y P P V P P G G F G Q P P S A Q

ENSE00002518768

CAGCCTGTTCCCTCCCTATGGGATGTATCCACCCCAAGGAGGAAACCCACCCCTCCAGGATGCCCTCATATCCGCCATACCCAGGGG
GTCGGACAAGGAGGGATACCCTACATAGGTGGGGGTCCTCCTTTGGGTGGGAGGTCTACGGGAGTATAGGCGGTATGGGTCCCC

4080

ANXA11

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ANXA11-203

Q P V P P Y G M Y P P P G G N P P S R M P S Y P P Y P G

ENSE00002518768

CCCCTGTGCCGGGGCCAGCCCATGCCACCCCCCGGACAGCAGCCCCAGGGGGCTACCCCTGGGCAGCCACCAGTGACCTACCCCTGG
GGGGACACGGCCCCGGTCGGGTACGGTGGGGGGCCTGTCTGTCGGGGGTCCCCGGATGGGACCCGTCGGTGGTCACTGGATGGGACC

4165

ANXA11

ANXA11-203

A P V P G Q P M P P P G Q Q P P G A Y P G Q P P V T Y P G

ENSE00002518768

ANXA11-203

TCAGCCTCCAGTGCCACTCCCTGGGCAGCAGCAGCCAGTGCCGAGCTACCCAGGATACCCGGGGTCTGGGACTGTACCCCCGCT
AGTCGGAGGTCACGGTGAGGGACCCGTCGTCGTCGGTTCACGGCTCGATGGGTCCCTATGGGCCCCAGACCCCTGACAGTGGGGGCGA

4250

ANXA11

ANXA11-203

Q P P V P L P G Q Q Q P V P S Y P G Y P G S G T V T P A

ENSE00002518768

ANXA11-203

GTGCCCCAACCAGGTGAGTGTGACGCCACTGCCTCCCTTGGTCCAGGCCTGGGCCCCAAAGGCTGGAGACACATGGCTCAGTA
CACGGGGGTTGGGTCCACTCACAGTCGGGTGACGGAGGGAACCAGGTCCGGACCCGGGGTTTCCGACCTCTGTGTACCGAGTCAT

4335

ANXA11

ANXA11-203

V P P T Q

ENSE00002518768

ANXA11-203

GATGGGGAGACAGGGAAAGGCGCAGGCCTCCAGCTGCACTTCTTGTTTTAAACAAATAGTGTGGCCGGGTGCAGTGACTCATGCC
CTACCCCTCTGTCCCTTTCCGCGTCCGGAGGTGACAGTGAAGAACAAATTTGTTTATCACAGCCGGGCCACGTCACTGAGTACGG

4420

ANXA11

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ANXA11-203

TGTAATCCCAGCACTTTGGGAAGCTGAGGTGGGCAGATCGCTTGAGCCCAGGAGTTCAAGACCAACCTGGGCGAAATGGTGAAC
ACATTAGGGTTCGTGAAACCCTTCGACTCCACCCGTCTAGCGAACTCGGGTCTCAAGTTCTGGTTGGACCCGCTTTACCACTTTG

4505

ANXA11

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ANXA11-203

CCTATCTCTACTAAAAATAGAAAAAAATTAGCTGGGCATGGTGGTGCATACCTGTAGGCCAGCTACTCGGGAGGCTGAGGTGG
GGATAGAGATGATTTTTATCTTTTTTTAATCGACCCGTACCACCACGTATGGACATCCGGGTCGATGAGCCCTCCGACTCCACC

4590

ANXA11

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ANXA11-203

GAGGATCACCTCAGCCCAGGAGACAGAGGTTGCAGTGAGCCGGGATCATGCCGCTGCACTCACTCCAGCCTAGGTGACAGAGTAA
CTCCTAGTGGAGTCGGGTCTCTGTCTCCAACGTCCTCGGCCCTAGTACGGCGACGTGAGTGAGGTCGGATCCACTGTCTCATT

4675

ANXA11

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ANXA11-203

GACCCAGTTTTTAAAAACAAAAACAAAAACAAAAAAGACAAACAAAGAGCGTCACCTTCTTGCAGACTCCCCACCTCTGGGTTGT
CTGGGTCAAAAATTTTGTTTTTGTTTTGTTTTTCTGTTTGTCTCGCAGTGGAAGAACGTCTGAGGGGTGGAGACCCAACA

4760

ANXA11

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ANXA11-203

GTTGCTTAAGGCCCAAGGGAGCTGTCCTGTTTCTCCTGGTGTGATGAGACGCTCCACATCCGAGTTGGGTCAGAACACCCCTGGC
CAACGAATTCGGGTTCCCTCGACAGGACAAAGAGGACCACACTACTCTGCGAGGTGTAGGCTCAACCCAGTCTTGTGGGGACCG

4845

ANXA11

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ANXA11-203

GAGTACTCCTTATTCTCTGTGTCATTTACTGCCTGGGCTGTGTGTTTTGTAAGAACTGCCAGGCCACCTGTCTCAAGGCTTTG
CTCATGAGGAATAAGGAGACACAGTAAATGACGGACCCGACACACAAAACATTCTTGACGGGTCCGGTGGACAGAGTTCCGAAAC

4930

ANXA11

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ANXA11-203

TGCTCAACAGCTGTCTTCGGTCCCTTGATATGCACCACCCCGCCCCCGGGCACAGACAGGTTTTGGAGGATTATTAATAATTC
ACGAGTTGTGACAGAAGCCAGGGAACATACGTGGTGGGGGCGGGGGGGCCGTGTCTGTCCAAAACCTCCTAATAATTTAAG

5015

ANXA11

ANXA11-203

ANXA11-203

CCTTTGGGTAGGGAGAATGTTGGCAGTTCCCTCCAGGGTTGATCTTGGCTCATTTTGGAGAACAGTTTCGTGTTTGCAGAGCCTAGA
GGAAACCCATCCCTCTTACAACCGTCAAGGAGGTCCCAACTAGAACCGAGTAAAACCTCTTGTCAAGCACAAAACGTCTCGGATCT

5100

ANXA11

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ANXA11-203

ATTCGTTGTCATGGTTCTGTGGCCCAACCAGCCAGCACAGGGGTAGTGGTATGTGCTCAATGACTATTTTTAGACAGAGGGTCTC
TAAGCAACAGTACCAAGACACCGGGTTGGTCGGTCTGTCCCCATCACCATACACGAGTTACTGATAAAAATCTGTCTCCCAGAG

5185

ANXA11

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ANXA11-203

CTTTCCTCCTTCCCTTCCATACCCACACGTTCCCCACCCTGTGCCATCCTCCAGCCTCCCTCCCTTATCTTTTCCCTGAGCTGC
GAAAGGAGGAAGGGAAGGTATGGGTGTGCAAGGGGGTGGGACACGGTAGGAGGTCTGGAGGGAGGGAATAGAAAAGGGACTCGACG

5270

ANXA11

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ANXA11-203

CCTCTTAATTGTGTTATAACCAGTTTGTACCAGCCCCTAGGAAGACAATCCACTGGGAGACAGTTTAGCCTGGAAAGTTCCAGTT
GGAGAATTAACACAATATTGGTCAAACATGGTTCGGGGATCCTTCTGTAGGTGACCCCTCTGTCAAATCGGACCTTTCAAGGTCAA

5355

ANXA11

ANXA11-203

ANXA11-203

TGCGGGTTTTGTGCAGCTATCAGGGTCTGGAGGAAGTCCGGCAGATGCTAGTCTAGAGAACAGTGCGAGGGAAACCAGTGCTAGATC
ACGCCCAAACACGTCGATAGTCCCAGACCTCCTTCAGGCCGTCTACGATCAGATCTCTTGTACGCTCCCTTGGTCCACGATCTAG

5440

ANXA11

ANXA11-203

ANXA11-203

AAGAGGTCATCAGGCTGCCATGCACAGTTGTGGAGGCTCAATACCTGCATCCACTGGAGGGGACACATGGGCTAGCCAGCCCTGT
TTCTCCAGTAGTCCGACGGTACGTGTCAACACCTCCGAGTTATGGACGTAGGTGACCTCCCCTGTGTACCCGATCGGTCGGGACA

5525

ANXA11

ANXA11-203

ANXA11-203

TAGGAGTACCCATGTGTGCTCACATGTGCTGTGGAGGCCAGGCATCGATGAGAGAGGCCACAGCCCCTGCTCCCGAGACCTGCCC
ATCCTCATGGGTACACACGAGTGTACACGACACCTCCGGTCCGTAGCTACTCTCTCCGGTGTTCGGGGACGAGGGCTCTGGACGGG

5610

ANXA11

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ANXA11-203

TTCATCAGGAGCCTGAGCCCCAGCCCTGGAGGACCTGGGCACTGGGCAGATTTTCAGCATCAGGACTCAGCTATAGGTGAGCTCC
AAGTAGTCCTCGGACTCGGGGTCGGGACCTCCTGGACCCGTGACCCGTCTAAAAGTCGTAGTCCTGAGTCGATATCCACTCGAGG

5695

ANXA11

ANXA11-203

ANXA11-203

CAGCCACTGGAGCCAGGAAAAAGCTTCAGTACTAGAACAAGGCCAGATAACAGTCAAGTTAGGTAGACGCGGCGTAAAGTCCT
GTCGGTGACCTCGGTCTTTTTCGAAGTCATGATCTTGTGTTCCGGTCTATTGTCAAGTTCAATCCATCTGCGCCGCATTTTCAGGA

5780

ANXA11

ANXA11-203

ANXA11-203

CTGCATTGTTGACTGTGGACTCCTTTAGATACTCCAACCTTTAGAGAAAGGGCTGTTCCAGAGTCTAGGGGTGGAGCAGCCTTG
GACGTAACAACCTGACACCTGAGGAAATCTATGAGGTTGAGAATCTCTTTCCGACAAGGGTCTCAGATCCCCACCTCGTCCGGAAC

5865

ANXA11

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ANXA11-203

AATGTGGGGAAGGCGGCATGCACGACATCTTACCTGAGACTGTTTGTCCGAGTAGTTTGGAAAGCCGAGGCACCATCACTGATGCT
TTACACCCCTTCCGCGGTACGTGCTGTAGAAATGGACTCTGACAAACAGGCTCATCAAACCTTCGGCTCCGTGGTAGTGACTACGA

5950

ANXA11

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F G S R G T I T D A
ENSE00003585307

ANXA11-203

CCCGGCTTTGACCCCTGCGAGATGCCGAGGTCCTGCGGAAGGCCATGAAAGGCTTCGGTAAGAGACCTGGGTGGCTCAAATCC
GGGCCGAAACTGGGGGACGCTCTACGGCTCCAGGACGCCCTCCGGTACTTTCCGAAGCCATTCTCTGGGACCCACCGAGTTTAGG

6035

ANXA11

ANXA11-203

P G F D P L R D A E V L R K A M K G F
ENSE00003585307

ANXA11-203

TACTCCCTGCCCCCTATTTCCAGGCAGTTTCACTGTGGCTCTGTGGGCTGGGGTAGCTGGGGGACGCTGACCTGGCCCCAGTGG
ATGAGGGACGGGGGATAAAGGGTCCGTCAAAGTGACACCGAGACACCCGACCCCATCGACCCCTGCGACTGGACCGGGGTCAAC

6120

ANXA11

ANXA11-203

ANXA11-203

TGATAGAAGGTGGATGTGGGGTATGGCTAGCATGCCAGAACAGTTGAGGGGGCCAGGCCAGGGAAGTCTCAGCTGCAGAGCAT
ACTATCTTCCACCTACACCCCATACCGATCGTACGGGTCTTGTCAACTCCCCGGGTCCGGTCCCTTCAGAGTCGACGTCTCGTA

6205

ANXA11

ANXA11-203

ANXA11-203

CTCATGACCCCTACCCGACCCACCCCTGCTGCCTCTTCTCCAGGGACGGATGAGCAGGCCATCATTGACTGCCTGGGGAGTCGC
GAGTACTGGGGATGGGCTGGGTGGGGACGACGGAGAAGGAGGTCCCTGCCTACTCGTCCGGTAGTAAGTACGCGGACCCCTCAGCG

6290

ANXA11

ANXA11-203

G T D E Q A I I D C L G S R
ENSE00002509632

ANXA11-203

TCCAACAAGCAGCGGCAGCAGATCTACTTTCTTCAAGACGGCTTACGGCAAGGCGAGCTGCGGGGTGGGGGCGCGGGACAGTG
AGGTTGTTTCGTCGCCGTCGTCTAGGATGAAAGGAAGTTCTGCCGAATGCCGTTCCGCTCGACGCCACCCCGCGCCCTGTCAC

6375

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S N K Q R Q Q I L S F K T A Y G K
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AGGCGTGTCTGGGCTCAGCACAGCCCTGCTCTCCCTGCTTTTCTTGGGTGGGCGCGGATCTCCCGGATGGACAGTAAGGAGC
TCCGCACAGGACCCGAGTCGTGTCGGGACGAGAGGGGACGAAAAGGAACCCACCCGGGCTTAGAGGGCCTACCTGTCATTCTCG

6460

ANXA11

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AGGAGGGCATTTCCTTCTGCCCATCCAGCTGGTGGCATCGTTGGGAGGTGAAGGATGCCACCGGGTGCTGAGGTTTGGCTGAGAGG
TCCTCCCGTAAAGGAAGACGGGTAGGTCGACCACCGTAGCAACCTCCACTTCCTACGGTGGCCACGACTCCAAACGACTCTCC

6545

ANXA11

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CTCCAGACATCTATCCCTGGGTTCTAGCCCTTGCTCTGCCACATCTCACTGAGGTTGTGGCCACATCATTTTTCTTCCCCTGCC
GAGGTCTGTAGATAGGGACCCAAGATCGGGAACGAGACGGTGTAGAGTGACTCCAACACCGGTGTAGTAAAAGGAAGGGGACGGG

6630

ANXA11

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TCTTCATGACCACCTGGGGGGTTTAGCTGATGTAAGAGCTTTCAGGGAAAGGCTGTGAGTGCTGCCCAAGTACGAGGGGCGTG
AGAAGTACTGGTGGGACCCCAAAATCGACTACATTCTCGAAACGTCCCTTTCGACACTCACGACGGGTTTCATGCTCCCCGCAC

6715

ANXA11

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TATGAGCATATTTTGAACCTTCTGGGGTTTTGAATCTTAGAAAGATAAAAATTCGGTAAATATTGATTAGATTCGTGTTCTAGCCC
ATACTCGTATAAACTTGAAGACCCCAAACTTAGAATCTTCTATTTTTAAGCCATTTATAACTAATCTAAGCACAAGATCGGG

6800

ANXA11

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AGTGCTTCTCAAACCTCATTGTGTCACCGATCCCTGGGCATCTTGGTAAAATGTGGTCTCTGATTTGGGAGGTTTGGGGCAGGG
TCACGAAGAGTTTGAAGTAACACAGTGGCTAGGGGACCCGTAGAACCATTTTACACCAGAGACTAAACCTCCAAACCCCGTCCC

6885

ANXA11

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CTGAGAGCAGGCTTTTCTCTCAGGCCCTGGGGGATGTCCATGCTGCTGTTCTCAAATCTGGGATATGGCTCTTATTAGTCACT
GACTCTCGTCCGAAAAGAGAGTCCGGGGACCCCTACAGGTACGACGACAAGGAGTTTAGACCCTATACCGAGAATAATCAGTGA

6970

ANXA11

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TCCTGTGGATTTTTTAAATAGACTTGTTTTTTTTTTGTTGGTTGTTTGAATATCCAATCAGGATTTGATCAAAGATCTGA
AGGACACCTAAAAATTTATCTGAACAAAAAACAACCAACAACAACTTATAGGTTAGTCTAAACTAGTTTCTAGACT

7055

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250
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TTCTGTGCTTCTCCTACCATGGCTGCTTCATGTGGGGTGGGAGAGGGGGCCTGTCGACCACTCTCCGCATAACTATGAGACCCAG
AAGACACGAAGAGGATGGTACCGACGAAGTACACCCACCCCTCTCCCCGGACAGCTGGTGAGAGGCGTATTGATACTCTGGGTC

7735

ANXA11

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CTCCAGAAGAGACCAGCAGGGTCTCCAAACGGGCAGGTTCTGACGGGCCCGGCTTGGACTCACTGTTCCCTCCAGTCCTGCGGGT
GAGGTCTTCTCTGGTCGTCCCAGAGGTTTGCCTGTCGAAGACTGCCCGGGCCGAACCTGAGTGACAAGGGGAGGTCAGGACGCCCA

7820

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TTTGACTGAGGGTTGGGTCCTGTCCATTCTGTGCAGTCCCACAGCTCTGTGTGCACCCTGCAGGCAGGGGCAGGCAGCTCCCTTG
AAACTGACTCCCAACCCAGGACAGGTAAGACACGTCAGGGTGTTCGAGACACACGTTGGGACGTCCTGTCCTCCCGTCCGTCGAGGGAAC

7905

ANXA11

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GAAAGGGGAATCCCATGAGTCAGGCTGGAGCCCAGAAGGAGCCTGTCACCTCAGAGGCCTGATAAGCACAGTGAATGTTCCCTCCTT
CTTTCCCTTAGGGTACTCAGTCCGACCTCGGGTCTTCTCGGACAGTGAGTCTCCGGACTATTCTGTCCTTACAAGGGAGGAA

7990

ANXA11

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CAGGAGAAGCAGAGACTTCAGTGTGGTGGCCTGGAAAGGAGAGGGGTCTCCGCTGAAACACATCTACATGTGTTATTCTAGGGAG
GTCCTCTTCGTCTCTGAAGTCACACCACCGGACCTTTCTCTCCCCAGAGGGCGACTTTGTGTAGATGTACACAATAAGATCCCTC

8075

ANXA11

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GGGGTCAGGAGGCCATCAGGCAGGGCGATGGCCCGGGGCCCCAGGGAGTGGACCCAGACATCTCCCTGGCCCCCGTCTTCAGCCG
CCCCAGTCTCCGGTAGTCCGTCCCGCTACCGGGCCCCGGGGTCCCTCACCTGGGTCTGTAGAGGGACCGGGGGCAGAAAGTCGGC

8160

ANXA11

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GAGTCATGAGCTGGTGGTTGTGGAGTGTAGAAACCACACAGGTTTGGGGCAGCTGTCACTCACCAGCTGTGTGTCCTTGAGCAC
CTCAGTACTCGACCACCAACACCTCACAATCTTTGGTGTGTCCAAACCCGTCGACAGTGAGTGGTCGACACACAGGAACCTCGTG

8245

ANXA11

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CTGTGAAATGGGGACAGTGGATGCTGTCTCAGGACATGCTGGGAATACTGGGTGAGGGGGCTAACGTGTAGTAACCCAATAGTAGC
GACACTTTACCCCTGTACCTACGACAGAGTCTGTACGACCCCTTATGACCCCACTCCCCGATTGCACATCATTGGGTTATCATCG

8330

ANXA11

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TGTAGCAGGAAACAGCTGACACAATGTCGCACGTCCTGCCTGACAGGCCCTAAGTGCTCTACGTACATTAACCTCACTTAATCCTC
ACATCGTCCCTTGTGCGACTGTGTTACAGCGTGCAGGACGGACTGTCCGGGATTCACGAGATGCATGTAATTGAGTGAATTAGGAG

8415

ANXA11

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ATGACTTTTCCTGTGAGGTAGGTCCTAGTATCACTCCCATCTTACAGACAAGGAACTGGAAGCACAGAGAGGTTAAGTAATGTGCC
TACTGAAAGGACACTCCATCCAGGATCATAGTGAGGGTAGAATGTCTGTTCCCTTGACCTTCGTGTCTCTCCAATTCATTACACGG

8500

ANXA11

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CGAGGTCACACAGCTGGTAAGCTGCAGAGCCAGGATTCAAACCAACATACAAGCCAGGCTGCCCAGCCTGTCCTCTATGGTCTTA
GCTCCAGTGTGTCGACCATTTCGACGTCTCGGTCCCTAAGTTTGGTTGTATGTTTCGGTCCGACGGGTCGGACAGGAGATACCAGAAT

8585

ANXA11

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CTGTCCCTGGCGTGGTTGTCCGATTCATCCTTGTGTTCCCTACCTTTTCTAGTTGTTTTTCAGACATTCCACCATCCCCTCTAGG
GACAGGGACCGCACCAACAGGCTAAGTAGGAACAACAAGGATGGAAAAGGATCAACAAAAGTCTGTAAGGTGGTAGGGGAGATCC

8670

ANXA11

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ACCAGGGTTTCGTATGTCCACTTGGATCTCTCTTGTCTTTTACCCATTTTTTTCAGTTGTTGTTCATCTCGCTTCCGGCTGAACTC
TGGTCCCAAAGCATACAGGTGAACCTAGAGAGAACGAAAAATGGGTAAAAAAAAGTCAACAACAGTAGAGCGAAGGCCGACTTGAG

8755

ANXA11

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TGAATAAAGCAGGCCTCGGTCCACATTTTAACCCAACCATTTACTGTGTGGCCTCGGACCAGCCAGTACCCCTCTCTGATGCTCA
ACTTATTTTCGTCCGGAGCCAGGTGTAATAATTGGGTTGGTAAATGACACACCGGAGCCTGGTCGGTCATGGGGAGAGACTACGAGT

8840

ANXA11

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GTTTTCTGATCCATGGGGATGCCCTTTGTGTGAGCCCTACTCATCACCCTGCCACTGTCATTGTGCTTGCCCGGGCTGTGGAG
CAAAAAGACTAGGTACCCCTACGGGGAAACACACTCGGGATGAGTAGTGGTGACGGTGACAGTAACACGAACGGGCCCGACACCTC

8925

ANXA11

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AAGAGCTGATGCCCTCGAGCCTGGGAGTGGCTGGAGGGTGTGTCTCTGTGTCAAGGGCCTCTGTTGCTGGGATTAAGGCAGCAGC
TTCTCGACTACGGGAGCTCGGACCCTCACCGACCTCCACACAGAGACACAGTCCCCGGAGACAACGACCCTAATTCCGTCGTCG

9010

ANXA11

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GTAGCCCCACCCCTTCTTCCCGAGTGTCTGGTGAGGCTGTCTGGAACAAGCACATGGTTGGTTGTATTCTCTGCCCTGCAGGGGGT
CATCGGGGGTGGGAAGAAGGGCTCACGACCACTCCGACGACCTTGTTCTGTACCAACCAACATAAGAGACGGGGACGTCCCCCA

9095

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TGGCACTGATGAAGCCTGCCTGATTGAGATCCTCGCTTCCCGCAGCAATGAGCACATCCGAGAATTAACAGAGCCTACAAAGCA
ACCGTGACTACTTCGGACGGACTAACTCTAGGAGCGAAGGGCGTCTTACTCGTGTAGGCTCTTAATTTGTCTCGGATGTTTCGT

9180

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290 295 300 305 310 315
G T D E A C L I E I L A S R S N E H I R E L N R A Y K A

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GGTGAGGCCGCTCCCTCTGCCCTCTGCCCTCTGCAGATCCCTGTGCTCTTGGGGCTGTGGCCTCATTCTCTCCTAGGG
CCACTCCGGCGAGGGAGACGGGAGACGGGAGACGGGAGACGCTTAGGGACACGAGAACCCTCGACACCGGAGTAAGAGAGGATCCC

9265

ANXA11

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CCTTTTACTCCTTCCTGGCCTTCTTATCAACCCATCTTCTGCCACCCCAATACTTTGGGCTTTGACCCAAGACCCAGCCCTTCC
GGAAAATGAGGAAGGACCGGAAGAATAGTTGGGTAGAAGACGGTGGGGGTTATGAAACCCGAAACTGGGTTCTGGGTCGGGAAGG

9350

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TTCTGTTTATACATGGTGCAAATGACTAATGTAAGGGAGAGGCAGGGAAAACCTGGATGTGGTTTGGGCCAAGGCTGACTAGAGG
AAGACAAATATGTACCACGTTTACTGATTACATTCCCTCTCCGTCCCTTTTGGACCTACACCAAACCCGGTTCCGACTGATCTCC

9435

ANXA11

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CCAGGTCAGCCTGGAGGGTCACAGGCTTGTATATCCCTGGAGGGCCATATGGGCTATTTGTTCTCTTGAGCCCGAGCCAAGACCTC
GGTCCAGTCGGACCTCCAGTGTCCGAACATATAGGGACCTCCCGGTATACCCGATAAACAAGAGAAGCTCGGGCTCGGTTCTGGAG

9520

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CAGCCTTTTTCTCCCCAGTACCCACTTTTTGATAGTGTGTTTGAATGGGCAGCTCCATAAAGAGAGCTACAGGATGGACCTTCCTT
GTCGGAAAAAGAGGGGTTCATGGGTGAAAACTATCACAAAACGTTACCCGTCGAGGTATTTCTCTCGATGTCCTACCTGGAAGGAA

9605

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GCTTCTCCCTTTTCAGAAATTCAAAAAGACCCTGGAAGAGGGCCATTGGAAGCGACACATCAGGGCACTTCCAGCGGCTCCTCATCTC
CGAAGAGGGAAAGTCTTAAGTTTTCTGGGACCTTCTCCGGTAAGCTTCGCTGTGTAGTCCCGTGAAGGTCGCCGAGGAGTAGAG

9690

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E F K K T L E E A I R S D T S G H F Q R L L I S
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TCTCTCAGGTACTTTTTCCACGACAGGGCTCGGGGCCCCCAAGCCATGGAAGTCAAAGAGATGGGATCCCCGCAATGAGGAAA
AGAGAGAGTCCATGAAAAGGGTGCTGTCCCGAGCCCCGGGGTTTCGGTACCTTCAGTTTTCTTACCCTAGGGGGCGTTACTCCTTT

9775

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ENSE0000246...

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GGGAAAATAAATGGGGAAGGAGTGGGCATGACCATACACCTGCTTCCTTTCAGGGAAACCGTGATGAAAGCACAAACGTGGACAT
CCCTTTTATTTACCCCTTCTCACCCGTAAGTGTGGACGAAGGAAAGTCCCTTTGGCACTACTTTCGTGTTTGCACCTGTA

9860

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GCTCACTCGCCCAGAGAGATGCCAGGTGAGTGTGATGGCCAAGCCCTGGACTTCTAAAGCAGGGATGCACCCCGCTTTCTTTCG
CAGTGAGCGGGTCTCTCTACGGGTCCACTCACACTACCGTTTCGGGGACCTGAAGGATTTTCGTCCCTACGTGGGGCGAAAGAACG

9945

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S L A Q R D A Q
ENSE00002521933

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TTCTGAGAGAGGTACCCTAGGGTGGAAAAGAACAATAGATAAGCAGTGGGTTGCAGATGCTGTGAGTTTCAGACGCGCTGAACTG
AAGGACTCTCTCCATGGGATCCCACCTTTCTTGTATCTATTTCGTACCCAACGTCTACGACACTCAAAGTCTGCGCGACTTGAC

10,030

ANXA11

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TTCAACTGTATGACCTAGAACAGGTAATCTGACCTCCAGGGCTTCAGCTTCCCCACCTATAGGAGGGGAACATGTGAGATAATTAG
AAGTTGACATACTGGATCTTGTCCATTAGACTGGAGGTCCCGAAGTCGAAGGGGTGGATATCCTCCCTTGTACTCTATTAATC

10,115

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TATTTTCGATAGTTGATAGATCATGGTTTTGGACGTGGGATTTTGTGTGACAGCGTACTTTCCCATGTTTAGTTGCACATAGCAT
ATAAAAGCTATCAACTATCTAGTACCAAAACCTGCACCCTAAAACACACTGTCGCATGAAAGGGGTACAAATCAACGTGTATCGTA

10,200

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TATGTTTGC AAAGGGGCAA AATTTGC ACTTGCTTATTAAGTTTTT GAGGATTTGAGCCTAGAAACCAGCTGCCACATTAGTTGAG
ATACAAACGTTTCCCGTTTTAAACGTGAACGAATAATTCAAAACCTCCTAAACTCGGATCTTTGGTCGACGGTGTAATCAACTC

10,285

ANXA11

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CACCCTTAGAATTCTGTCGTTGTCCCTCTTGTGAGTTGCAGACAAAAGGGGAAAAGTCCAAGCAAAGTCCAGGCATCTGAGCTAC
GTGGGAATCTTAAGACAGCAACAGGGAGAACACTCAACGTCTGTTTTCCCTTTTTCAGGTTTCGTTTCAGGTCCGTAGACTCGATG

10,370

ANXA11

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TCTCTCGAAAAGTTTGGGTTTCCCACTAATGAATTTCAACCGTAGTATTATGGCAGGGCAGAGCCATTACTTCTGGTGGGGTGG
AGAGAGCTTTTTCAAACCCAAAGGGTGATTACTTAAAGTTGGCATCATAATACCGTCCCGTCTCGGTAATGAAGGACCACCCACC

10,455

ANXA11

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AGTTGGCCATACCTCTCTGTCTCCCTTCACTGCTCTTGTTCATCCACGGCAGGGCATTACCAGGAGCTGCCAGTGGTCTAAATTA
TCAACCGGTATGGAGAGACAGAGGGAAGTGACGAGAACAGTAGGTGCCGTCCCGTAAGTGTTCTCGACGGTCACCAGATTTAAT

10,540

ANXA11

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TCTCTACCATCTGCGGGATTGGAATGAGACCTCAAGGAATGCCCCCTTGTTAGGGCTGGAGGAGAGCTACTCCTCTGGTCTGGTC
AGAGATGGTAGACGCCCTAACCTTACTCTGGAGTTCTTACGGGGGAACAATCCCGACCTCCTCTCGATGAGGAGACCAGACCAG

10,625

ANXA11

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CTTTTGCTGGTCTCCTTTTCCGGAGGAGGAAACTGAGGCTCAAAAAGGTTGAGCACTGTTCCCAACTGAAAAGCTAGAAGCAGAG
GAAAACGACCAGGAGGAAAAGGCCTCCTCCTTTGACTCCGAGTTTTTCCAACCTCGTGACAAGGGTTGACTTTTCGATCTTCGTCTC

10,710

ANXA11

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CCCGGACAAGGGCCTATACTCCTGGCTCGGTCTTCTGTGCCAGTCAGCACTTGCCTCTGCCCTGGTCTCAGACCTGCTGCTCCT
GGGCCTGTTCCCGGATATGAGGACCGAGCCAGAAGACACGGGTCAAGTCGTGAACGGAGACGGGACCAGAGTCTGGACGACGAGGA

10,795

ANXA11

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GCAGGGTCTGCCTTATTCAGTGTCTCTCTGGCTGGTAACATCCATTCCCATTCTGGGAGTCAGGGCTGGACACGCCTGGGGCTCA
CGTCCCAGACGGAATAAGTCACAGAGAGACCGACCATTGTAGGTAAGGGTAAGACCCTCAGTCCCAGACCTGTGCGGACCCCGAGT

10,880

ANXA11

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GGGCTCTGGCTTTTGGCTCCAGCGAGAGTTTTGCATGCCACTTTTAGCGGGGCAAAAATTGTCTCATGCTCTGCCTTCTCAGTCCA
CCCGAGACCGAAAACGAGGTCGCTCTCAAAACGTACGGTGAAAATCGCCCCGTTTTTAACAGAGTACGAGACGGAAGAGTCAGGT

10,965

ANXA11

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GAGCTGCTTTGGCCTCATCTTGACCTGTGGGATCTCAGCCCCTGATTGCTGCTTTCTGCTCTTTTTTCAGGGCTGCTACCTGAGGC
CTCGACGAAAACCGGAGTAGAACTGGACACCCTAGAGTCGGGGACTAACGACGAAAAGACGAGAAAAAGTCCCAGACGATGGACTCCG

11,050

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CTAGCAGGCACTTTAGAGGCCATCTAGTTCAGAGGTTGCAAATTGGCAAATACTTTAGGCTCAAACCTTCAGAAGTTTACCAGGC
GATCGTCCGTGAAATCTCCGGTAGATCAAGTCTCCAACGTTTAACCGTTTATGAAATCCGAGTTTGGAAAGTCTTCAAATGGTCCG

11,135

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TCTCCTGGGTGACCTGGGCCTGGGGTCTGGGTGTGGCCTGTGCCACATGTGCGTCTTCTCCTCTCTCCAGGAGCTGTATGCGGCC
AGAGGACCCACTGGACCCGGACCCAGACCCACACCGGACACGGTGTACACGCAGAAGGAGAGAGAGGTCTCTCGACATACGCCGG

11,220

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GGGGAGAACC CGCTGGGAACAGACGAGTCCAAGTTCAATGCGGTTCTGTGCTCCCGGAGCCGGGCCACCTGGTAGCAGGTAAGG
CCCCCTCTTGCGGGACCCCTTGTCTGCTCAGGTTCAAGTTACGCCAAGACACGAGGGCCTCGGGCCGGGTGGACCATCGTCCATTCC

11,305

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370 375 380 385 390
G E N R L G T D E S K F N A V L C S R S R A H L V A

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CAGGCTGGGGTCCCTCAGAGGCCAGTTAGATGAGGGCAGTCAGGGGATTGTGGGGAAACAAAGCTATGGGAACACTTGGTCGTTCC
GTCCGACCCCGAGGGAGTCTCCGGTCAATCTACTCCCGTCAGTCCCCCTAACACCCCTTTGTTTTCGATACCCCTTGTGAACCAAGCAAG

11,390

ANXA11

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CTCCCTGCGTGGGGCTTTTCGCCTCCTCAAAAGAGCCCCCTGGTGGGAATTTAAAAGACACTGTCAGAGGGTTTTCTGAGTTCTGG
GAGGGACGCACCCCGAAAGCGGAGGAGTTTTCTCGGGGGACCACCCCTTAAATTTTTCTGTGACAGTCTCCCAAAGGACTCAAGACC

11,475

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CAAACATCCAGTTCTGGAGGTTCTACCGGTGTAGAAACCTGGTGTCTTTGTACGTGGGAATGTGGAACGTCAGAGTTGGGAGGGT
GTTTGTAGGTCAAGACCTCCAAGATGGCCACATCTTTGGACCACAGAAACATGCACCCTTACACCTTGCAGTCTCAACCCTCCCA

11,560

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CCTTCGGGAGCACCCAATCCAGTGTTCCTCCAAAGCCTGGCATAAGAAACAGTCATAACAATAAAACTGGGTGCCATTCAATTTACT
GGAAGCCCTCGTGGGTTAGGTCACAAAAGGTTTCGGACCCTATTCTTTGTGTCAGTATTGTTATTTTGACCCACGGTAAGTAAATGA

11,645

ANXA11

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CATTCATTCAACAGATGTAAATCGCGCTCCCGCATGGGTTCAGTCTGTCAGGTGGTGGAGCAGGTGTGGGGCCACGGTGGGGGGCA
GTAAGTAAGTTGTCTACATTTAGCGCGAGGGCGTACCCAGTCAGACAGTCCACCACCTCGTCCACACCCCGGTGCCACCCCCCGT

11,730

ANXA11

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GGGCACTGCAGAGTGTGTTCCATGGGCTGCACTTTCTCATTTGGGGAGACAGACAGTAAACAACAATGAAATAAAATCTGTATCA
CCCGTGACGTCTCACACAAGGTACCCGACGTGAAAGAGTAAACCCCTCTGTCTGTCAATTTGTTGTTACTTTATTTTAGACATAGT

11,815

ANXA11

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GATGGGAAATCCTGTAGAGGAAAATCAAGCTGGAAACAGGTAGGGAGTGATGGTAGGGTCCACCGGGAGGTGCTTGGGCCAGTCC
CTACCCTTTAGGACATCTCCTTTTAGTTTCGACCTTTGTCCATCCCTCACTACCATCCCAGGTGGCCCTCCACGAACCCGGTCAAG

11,900

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CCACTGAGGTCGTGACATTTGATTTAAAAACCTAAAGGGAGATGCAGGGGCAGAGGCCTGCCTGGGGCTCCCAGCACGACTGAGA
GGTGACTCCAGCACTGTAAACTAAATTTTTGGATTTCCCTCTACGTCCCCGTCTCCGGACGGACCCCGAGGGTCTGTGCTGACTCT

11,985

ANXA11

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ACAGTGAAGGGGGACCATGTGGAGCAGGTGGAGTGAGCAAGAGGAGTGAGGGTGGAGGGCAGAGAGGGGAGAGGGCCCTGCTGAT
TGTCACTTCCCCCTGGTACACCTCGTCCACCTCACTCGTTCTCCTCACCTCCACTCCCGTCTCTCCCTCTCCCGGGACGACTA

12,070

ANXA11

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GACTTCCCGGAGCTGGGTATTTATCCTGAGCAAAAAGAGGAAGCCAGTGGAGGGCCCTGAGCAGAGGAGGCTGTGCAGAATCCCTG
CTGAAGGGCCTCGACCCATAAATAGGACTCGTTTTCTCCTTCGGTCACTCCCGGGACTCGTCTCCTCCGACACGTCTTAGGGAC

12,155

ANXA11

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GCTGTGGTGCCGAGAATGGAGTGAAGGGTGCAAGGCCAAGCAGCGAAGCCTGTCTGGGAGGCTGCTGCAGGGACCCGGGGAGGAAT
CGACACCACGGCTCTTACCTCACTTCCCACGTTCCGGTTCGTTCGCTTCGGACAGCCCTCCGACGACGTCCCTGGGCCCTCCTTA

12,240

ANXA11

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GGTGGTAATAGGGGCTTGTGGTGAGGAGGTGTCAGGTTCCGGCCATGTTTGCTGATGAATTGGACACGTGACGTGTGGGAGAGAG
CCACCATTATCCCCGAACACCACTCCTCCACAGTCCAAGGCCGGTACAAACGACTACTTAACCTGTGCACTGCACACCCTCTCTC

12,325

ANXA11

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AGGGTTCGAGGATTATACAGGGTTTCTTTAGGCCAAGCAGTGGGAGAATGGCCCTCAACTGAGACAGGGGGACTGTAGGTGGAGC
TCCCAAGCTCCTAATATGTCCCAAAGAAATCCGGTTCGTCAACCCTCTTACCGGGAGTTGACTCTGTCCCCCTGACATCCACCTCG

12,410

ANXA11

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TGGCTTTAGGTGCCTGTAGGGTGGAGCTGCAGGGAGGGCTGCTGGGTTGCTGAGTGTGGAGGTCAGGAGAGGTCTGGCCTGGTTGT
ACCGAAATCCACGGACATCCCACCTCGACGTCCCTCCGACGACCCAACGACTCACACCTCCAGTCCTCTCCAGACCGGACCAACA

12,495

ANXA11

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GGAAGGTAAGGGAGCTATGGGTAGTTGAAGTTATCTGAGGCTCTGGGACTGCAGGAGGTCCCTCAGGAGGGAGACTGTGGGGAG
CCTTCCATTCCCTCGATACCCATCAACTTCAATAGACTCCGAGACCCTGACGTCTCCAGGGGAGTCCTCCCTCTGACACCCCTC

12,580

ANXA11

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CCCACCGGTGTGAGGAGACTAAGAAGGAGCAGCTAGGGAGGGAGGAGGACGCAGAGGAAGGGGGTCTGGAGGCCAGTGTGAGGT
GGGTGGCCACACTCCTCTGATTCTTCTCGTCGATCCCTCCCTCCTCCTGCGTCTCCTTCCCCAGGACCTCCGGTCACACTCCA

12,665

ANXA11

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GGCAGGCAAGGACTGAGGATGGTGACCACACGGAGCAACTGGTGGGCTGTGGCCAGGGCTGCTCCAGTGGGCAGTGAGGGTGAAA
CCGTCCGTTCTGACTCCTACCACTGGTGTGCCTCGTTGACCACCCGACACCGGTCCCGACGAGGTCACCCGTCACTCCCACCTT

12,750

ANXA11

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ACCCAGCGACCGCTCTGTGCTGCACACAGAGACAGGCGCTGTGGCTCTCCCATTCGCAGCTGTGAAAGCAGGCACAGGGTGTTA
TGGGTCGCTGGCGAGACACGACGTGTGTCTCTGTCCGCGACACCGAGAGGGGTAAGCGTCGACACTTTTCGTCCGTGTCCCACCAT

12,835

ANXA11

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GAGGAAGTAGGGGTGCACAGCTAGTAACAGCTGAGCTGGGATTTGAACCCAGACCACCCGACCCCAGAGCACACTTTTTAACCTC
CTCCTTCATCCCCACGTGTGATCATTGTGACTCGACCCTAAACTTGGGTCTGGTGGGCTGGGGTCTCGTGTGAAAAATTGGAG

12,920

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TGCACTATCCTGTAATGGAGCCTGAGTGAAAGCATTTCATCTTAATCATTATTTCTTTTAAATGAGTACAGAACATGTAAGTAGT
ACGTGATAGGACATTACCTCGGACTCACTTTTCGTAAGTAGAATTAGTAATAAAGAAAATTACTCATGTCTTGTACATTTCATCA

13,005

ANXA11

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GCATCAAGCCCATGGCTTCACAAACATTATTACTTAGGAGAAAAGAGTAGCTGATTGGAAGAAGATATTAATTGAGACAGATACA
CGTAGTTCGGGTACCGAAGTGTTTGTAATAATGAATCCTCTTTTCTCATCGACTAACCTTCTTCTATAATTAECTCTGTCTATGT

13,090

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CACAGAGCAGAAATCACAACCTTTAAAATGCAAATGGTAGCTGAGACTCAGGCTGGGGAAGGAGAGTTTTATGTCCTGGGTCAGAA
GTGTCTCGTCTTTAGTGTTGAAATTTTACGTTTACCATCGACTCTGAGTCCGACCCCTTCTCTCAAAAATACAGGACCCAGTCTT

13,175

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CTGGAGTCAGGACCAAGGTCTCCATCATGCCACCTGTCTCTCTAGGAGCCAGCCATCCACTCCTGTGGGTGCTTAGCGTGTCTTA
GACCTCAGTCTTGGTTCCAGAGGTAGTACGGTGGACAGAGAGATCCTCGGTCGGTAGGTGAGGACACCCACGAATCGCACAGGAT

13,260

ANXA11

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GGTCGAGGTGAGCAGCAAGAAGCCAGGCTGGCTGGGGCAGGCTGGGCCTCAGCTCACAGGCAGGCTGAGGAAGACAGATGGATGC
CCAGCTCCACTCGTTCGTTCTTCGGTCCGACCCCGTCCGACCCGGAGTCGAGTGTCCGTCGGACTCCTTCTGTCTACCTACG

13,345

ANXA11

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ANXA11-203

ATGAATAAAGCCAAGGAATGGCAGAGACTGGAGGTGTGGAGGATTTGAGAAGAGGGGACACTGTCTTGGAGTACATGGGAGTGGG
TACTTATTTTCGGTTCCTTACCGTCTCTGACCTCCACACCTCCTAAACTCTTCTCCCTGTGACAGAACCTCATGTACCCTCACCC

13,430

ANXA11

ANXA11-203

ANXA11-203

CCCTGGAGGGGTATTAAGGTGCGATTTGGTTAAGCAGATTGGCAGTCCTGAGAAAAGGGACCACACAGGGAGGGACATCAGGTGGT
GGGACCTCCCCATAATTCCACGCTAAACCAATTCGTCTAACCGTCAGGACTCTTTCCTGGTGTGTCCCTCCCTGTAGTCCACCA

13,515

ANXA11

ANXA11-203

ANXA11-203

GCATGTAACCTTGTGACGAAGACTCTGACTTCCTTGAGCGCTAGCAGGCCTGGGGACGTGCAGGGTGTGGGAGCAGAGTGGCAGGT
CGTACATTGAACACTGCTTCTGAGACTGAAGGAACCTCGCATCGTCCGGACCCCTGCACGTCCCACACCCCTCGTCTCACCGTCCA

13,600

ANXA11

ANXA11-203

ANXA11-203

GGGAGATTTTGGGGCAGAGGCCACCTCATGTGAGTCCTCTGTTAGTCTGCTCATGCTGCCATGACAAAATACCACAGACTGGGTG
CCCTCTAAAACCCCGTCTCCGGTGGAGTACACTCAGGAGACAATCAGACGAGTACGACGGTACTGTTTTATGGTGTCTGACCCAC

13,685

ANXA11

ANXA11-203

ANXA11-203

GCTTAAGCAGCAGATACTCATTTTTGTTACAGTTTTGAAGGCCAGATATCCAAGAGTGGGGTGCCGGTTTTCTCCCGTGGCCTCTTC
CGAATTCGTCTATGAGTAAAACAATGTCAAAACTTCCGGTCTATAGGTTCTCACCCACGGCCAAAAGAGGGGCACCGGAGAAG

13,770

ANXA11

ANXA11-203

ANXA11-203

GTGACAATCACTGTGCTCACATGGTCTTTCTCTGCATGTGCACATCCCTGGGATCTCTGTGTGTGTCTTAATCTTCTTTCTTC
CACTGTTAGTGACACGAGTGTACCAGAAAGGAGACGTACACGTGTAGGGACCCTAGAGACACACACAGGATTAGAAGAGAAGAAG

13,855

ANXA11

ANXA11-203

ANXA11-203

TAAGGAGACCAGGCGAATTGGATTAGGGTACACCCTAGCAGCATGTTTTAACTTAATTACCTCTTTAAAGATCTTATCTCCAAAC
ATTCTCTGGTCCGCTTAACCTAATCCCATGTGGGATCGTCTGACAAAATTGAATTAATGGAGAAATTTCTAGAATAGAGGTTTG

13,940

ANXA11

ANXA11-203

ANXA11-203

ACGGTTATATTCTGAAGTCTGGGAGTTGGGACTTCCACATATGAACTTTGGGGAGACACATTTTCAGTTCATAATATAAGCCTCT
TGCCAATATAAGACTTCAGGACCCTCAACCCTGAAGGTGTATACTTGAAACCCCTCTGTGTAAAGTCAAGTATTATATTCTGGGAGA

14,025

ANXA11

ANXA11-203

ANXA11-203

GTCATCCCATAGTTTTCAATGAGTACCAGAGAATGACAGGCCGGGACATTGAGAAGAGCATCTGCCGGGAGATGTCGGGGGACC
CAGTAGGGGTATCAAAAAGTTACTCATGGTCTCTTACTGTCCGGCCCTGTAACCTCTTCTCGTAGACGGCCCTCTACAGGCCCTG

14,110

ANXA11

ANXA11-203

V F N E Y Q R M T G R D I E K S I C R E M S G D
ENSE00000909278

ANXA11-203

TGGAGGAGGGCATGCTGGCCGTGGGTAAAGTGTCTCAGGTTTGGCGCCACCTGCCAGGGGCTAACGTGTATCGTGAGTGTTCAGG
ACCTCCTCCCGTACGACCGGCACCCATTACAGAGTCCAACCGGCGGGTGGACGGTCCCGATTGCACATAGCACTCACAAAGTCC

14,195

ANXA11

ANXA11-203

L E E G M L A V
ENSE00000909278

ANXA11-203

CTGCTCGCCTGTCCCTCCAGCTGATGGGTGACACCGTGAAGGGACCACAGGATCCAAGATCGCTCAGCCCAGAGTGTCCAGATGCT
GACGAGCGGACAGGAGGTGCGACTACCCACTGTGGCACTTCCCTGGTGTCTTAGGTTCTAGCGAGTCTCGGGTCTCACAGGTCTACGA

14,280

ANXA11

ANXA11-203

ANXA11-203

GGGAAGTCATGCTGCTTCCCGGTTCCCTGTGCAGTTGAACCCCTAGCTGTCCTGGAGGTGTCTTGTGTGTGTTTGCGGTGCAGCT
CCCTTCAGTACGACGAAGGGCCAAGGGACACGTCAACTTGGGGATCGACAGGACCTCCACAGAACACACACAAACGCCACGTCGA

14,365

ANXA11

ANXA11-203

ANXA11-203

CTGGAGTAGGGAACCTGCAGTGTGGGTATTAGTGGGAGGGCATCCAACCTGCGCTCCCGGAGGAGTATGACTCATATCCTGCCACGT
GACCTCATCCCTTGACGTCACACCCATAATCACCTCCCGTAGGTTGACGCGAGGGCCTCCTCATACTGAGTATAGGACGGTGCA

14,450

ANXA11

ANXA11-203

ANXA11-203

TTCCTCTAAAAATACATCCCTGCAGGCAGTTGTCAGATGTTTGTGATGGAAACACGTGGAAAGATTTTTACTTGCAGCAGCGAAA
AAGGAGATTTTTATGTAGGGACGTCCGTCAACAGTCTACAAACACTACCTTTGTGCACCTTTCTAAAAATGAACGTCGTCGCTTT

14,535

ANXA11

ANXA11-203

ANXA11-203

CAGGCCCATGCTGAGGAAAAGCTGGCTTGGCTCCAGGATGGTGGTGTGCCTCTTACATTGCCCATGTCTCTAGCAGGGCCCTCCC
GTCCGGGTACGACTCCTTTGACCGAACCGAGGTCTACCACCACACGGAGAATGTAACGGGTACAGGAGATCGTCCCGGGAGGG

14,620

ANXA11

ANXA11-203

ANXA11-203

ACTGTGCAGAGTTGGGTCCCTGCCCTGAGGCCCTCACAAACCCCTCTTTCTACTCACTTGGGAAAATCAGTCTGCCCTTTTTTCA
TGACACGTCTCAACCCAGGGACGGGACTCCGGGAGTGTGGGGAGAAAAGATGAGTGAACCCCTTTTAGTCAGACGGGGAAAAAAGT

14,705

ANXA11

ANXA11-203

ANXA11-203

TTATGCTTTTTTTGGAGCTTTCTGGATGGGAGAGATGGAAAATCCTCATTTCCCTGCCTGTCCCCCATAGTAGGTCTCATGGCCT
AATACGAAAAAACCTCGAAAGACCTACCCTCTCTACCTTTTAGGAGTAAAGGGACGGACAGGGGGTATCATCCAGAGTACCGGA

14,790

ANXA11

ANXA11-203

ANXA11-203

GGGAAGCCTAGGGAGATGCACATTCCACTCAGCCACGGTTTTCTCCATGACGGTCATGGCCTCTCCAGTCTGCCCTCCTGCCTGA
CCCTTCGGATCCCTCTACGTGTAAGGTGAGTCGGTGCCAAAGAGGTA CTGCCAGTACCGGAGAGGTCAGACGGGGAGGACGGACT

14,875

ANXA11

ANXA11-203

ANXA11-203

GCAGCAGCACAGTTCTCATCACCATCCACATTGCTTCCCTGTGTAGCTCCTAGCCCCACTAAGACCCCCGCCCTCTGACTCTT
CGTCGTCGTGTCAAGGAGTAGTGGTAGGTGTAACGAAGGGACACATCGAGGATCGGGGTGATTCTGGGGGCGGGGAGACTGAGAA

14,960

ANXA11

ANXA11-203

ANXA11-203

GGTCCTTTCACCGCAGTGGTTGCCAGGAAAGAGGGTGGGTTGGTTTCCAGGCTTTGCGTGTCTTCTGTTCCAAATAGCTGGAGCCA
CCAGGAAAGTGGCGTCACCAACGGTCTTTCTCCCACCCAACCAAAGGTCCGAAACGCACAAAGACAAGGTTTATCGACCTCGGT

15,045

ANXA11

ANXA11-203

ANXA11-203

AGATCATGGGATAGTTGAGCCTGGAACAGAAGGAGGAGGAGAAAAGATGGATGCAGTGATGGGTTTGACATCTGGGCCTCTAAGA
TCTAGTACCCTATCAACTCGGACCTTGTCTTCTCCTCCTCTTTTCTACCTACGTCACTACCCAAACTGTAGACCCGGAGATTCT

15,130

ANXA11

ANXA11-203

ANXA11-203

GGACACTTGTAGACTCCATGCCCTGCTTGGGCTGAGAATTTTCTGCAGATCTGGTTATGCCGAGTTTCTCTCTTCTAGTGAAATG
CCTGTGAACATCTGAGGTACGGGACGAACCCGACTCTTAAAAGACGTCTAGACCAATACGGCTCAAAGAGAGAAAGATCACTTTAC

15,215

ANXA11

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ENSE000...

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TCTCAAGAATACCCCAGCCTTCTTTGCGGAGAGGCTCAACAAGGCCATGAGGGTATGTAAC TTCCATGTGCAGGTTGCGATGGAA
AGAGTTCTTATGGGGTCGGAAGAAACGCCCTCTCCGAGTTGTTCCGGTACTCCCATACATTGAAGGTACACGTCCAACGCTACCTT

15,300

ANXA11

ANXA11-203

430 435 440 445
L K N T P A F F A E R L N K A M R

ENSE00000909277

ANXA11-203

CCTTAGCCTCGCCTGTGCCTGGGACCAAGGGCTGAGGGCAGAAGGCCCTGGGGAGAGCTAAATCTCAGCTGAGAGTTCCGAGGACC
GGAATCGGAGCGGACACGGACCTGGTTCCCGACTCCCGTCTTCCGGACCCCTCTCGATTTAGAGTCGACTCTCAAGGCTCCTGG

15,385

ANXA11

ANXA11-203

ANXA11-203

TGGGTAGGGAGGGGACTGGAGGGCCAGGGCAGGTGGGAAGGTGAGGAGGCCTGGTGTCTCATGCTCTTGGGTGGACTCTCTTTAG
ACCCATCCCTCCCCTGACCTCCCAGGGTCCCGTCCACCCTTCCACTCCTCCGGACCACGAGTACGAGAACCCACCTGAGAGAAATC

15,470

ANXA11

ANXA11-203

ANXA11-203

GGGGCAGGAACAAAGGACCGGACCCTGATTTCGCATCATGGTGTCTCGCAGCGAGACCGACCTCCTGGACATCAGATCAGAGTATA
CCCCGTCTTTGTTTCTGGCCTGGGACTAAGCGTAGTACCACAGAGCGTTCGCTCTGGCTGGAGGACCTGTAGTCTAGTCTCATAT

15,555

ANXA11

ANXA11-203

G A G T K D R T L I R I M V S R S E T D L L D I R S E Y

ENSE00000909276

ANXA11-203

AGCGGATGTACGGCAAGTCGCTGTACCACGACATCTCGGTACGGGCCTGCTGCAGGCCAACTGGGCTCCCTTTTGGCATCTCAGT
TCGCCATACATGCCGTTTACGCGACATGGTGTCTGTAGAGCCATGCCCGGACGACGTCGCGTTGACCCGAGGGAAAACCGTAGAGTCA

15,640

ANXA11

ANXA11-203

K R M Y G K S L Y H D I S

ENSE00000909276

ANXA11-203

CACCTGTGGAACCTCCCTCCTTGGAGTGGCCATATGCTTGGCCTCTGTGCTGTGTGTGGGCATCTTGATTATGGACCTCGGACTT
GTGGACACCTTGGAGGGAGGAACCTCACCGGTATACGAACCGGAGACACGACACACCCGTAAGAACTAATACCTGGAGCCTGAA

15,725

ANXA11

ANXA11-203

ANXA11-203

GTTTCATCCCCTTGCCCTTAAACAGATTATAAATTTCTGAGGGCAGGTGGATCATGACCTTGCTGTGCGCCCCACCTTGCATCCCC
CAAGTAGGGGAACGGGAATTTGTCTAATATTTAAAGACTCCCGTCCACCTAGTACTGGAACGACAGCGGGGGTGGAACTGAGGGG

15,810

ANXA11

ANXA11-203

ANXA11-203

CAGCAGCATCAGAGAACACTCGGGACCTCCCAACCTTGACCGTGACCTTCAGCGTTCGGATCACCGTGTGATTCCCTTGATCTGT
GTCGTCGTAGTCTCTTGTGAGCCCTGGAGGGGTTGGAACCTGGCACTGGAAGTCGCAAGGCTAGTGGCACACTAAGGAACTAGACA

15,895

ANXA11

ANXA11-203

ANXA11-203

CAGTGAGAACTCATGTCCCAAAGGCTCTGTGGAGCTCTGCTGTCACTCCCTGACAAAGCACTTCTGCACTCAGCTTTATGGCGT
GTCACCTTGTAGTACAGGGTTTCCGAGACACCTCGAGACGACAGTGAGGGACTGTTTCGTGAAGGACGTGAGTCGAAATACCGCA

15,980

ANXA11

ANXA11-203

ANXA11-203

AGGCCACATAGTAAGGCCGTTTCAGAGCGAGGGCCCTGGGGGTCACGCCACTTGGAGTCCAGCTTTTCTACTTGCTAACTGTGTGA
TCCGGTGTATCATTCCGGCAAGTCTCGCTCCCGGGACCCCAAGTGCGGTGAACCTCAGGTCGAAAAGATGAACGATTGACACACT

16,065

ANXA11

ANXA11-203

ANXA11-203

CCTTGAATGGCTCCCTTAAATCTCCCTGAACCCAGCTCCATTGTCTTTAAGATGAGAAAATAATCGTTCCTTCCTGGGAATGTT
GGAACCTACCGAGGGAATTTAGAGGGACTTGGGGTCGAGGTAACAGAAATCTACTCTTTTATTAGCAAGGAAGGACCCCTTACAA

16,150

ANXA11

ANXA11-203

ANXA11-203

GTGAGTATTGAGTGAGGCAGTGCAGGTCAAGTGTCTATTAACACTAGCCACAGTTGTATCGCTGTGTGGCAGAGCCAGTCTGAC
CACTCATAACTCACTCCGTCACGTCCAGTTCACAGATAATTTGTGATCGGTGTCAACATAGCGACACACCGTCTCGGTCAGACTG

16,235

ANXA11

ANXA11-203

ANXA11-203

AAAATACATTCTCAGCTGTGTGGTCTAACGCTCAAATTTCTGAACTCACATGAGCCTTGCAATTGCACCATGGGGACCACGTCTCTC
TTTTATGTAAGAGTCGACACACCAGATTGCGAGTTTAAGACTTGAGTGTACTCGGAACGTTAACGTGGTACCCCTGGTGCAGGAG

16,320

ANXA11

ANXA11-203

ANXA11-203

CCACCTTAGACTCAGTAGCATTTGATGATGGTGGGCATGTCATCACAGGAACTCACTGTGTTTCCTTGGCTGTATGAATGAAGC
GGTGGAACTCTGAGTCATCGTAAACTACTACCACCCGTACAGTAGTGTCTTTGAGTGACACAAAGGAACCGACATACTTACTTCG

16,405

ANXA11

ANXA11-203

ANXA11-203

TGTTGTTAGAGAATTAGTGATTCTAGGCTGGGCACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCAGGTGGA
ACAACAATCTCTTAATCACTAAGATCCGACCCGTGTCACCGAGTGCGGACATTAGGGTCGTGAAACCCTCCGACTCCGTCCACCT

16,490

ANXA11

ANXA11-203

ANXA11-203

TCATTTGAGGTCAGGAGTTTCGAGACCAGCCTGGCCAACAAGGTAAAACCCTGTCTCTACTAAAAATACAAAATTAGCTGGGCTTG
AGTAAACTCCAGTCTCAAGCTCTGGTCGGACCGGTTGTTCCATTTTGGGACAGAGATGATTTTATGTTTTAATCGACCCGAAC

16,575

ANXA11

ANXA11-203

ANXA11-203

CCTGTAATCCCAGCTAATTAGGTAGGCTGCGGCAGGAGAATTGCTTGAACCCGGGAGACAGAGGTTGCAGTGAGCTGGGATCACG
GGACATTAGGGTTCGATTAATCCATCCGACGCCGTCTCTTAACGAACCTTGGGCCCTCTGTCTCCAACGTCACTCGACCCTAGTGC

16,660

ANXA11

ANXA11-203

ANXA11-203

CCATTCCACTTCAGTCTTGGTGACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGAGAGTTAATAATTCATTACAGAGTATCTCCT
GGTAAGGTGAAGTCAGAACCCTGTCTCACTCTGAAGCAGAGTTTTTTTTTTCTCTCAATTATTAAGTAATGTCTCATAGAGGA

16,745

ANXA11

ANXA11-203

ANXA11-203

GCATGCCAGCAAGCTATGGACATCTGGAAGAAGCCACATGCCTTGCCCTCAAGTTGCTTAGGGTGAAGGAAATGATTAGAAATG
CGTACGGTTCGTTTCGATACCTGTAGACCTTCTTCGGTGTACGGAACGGGAGTTCAACGAATCCCACCTTCTTTACTAATCTTTAC

16,830

ANXA11

ANXA11-203

ANXA11-203

AGCCAAGCCGAGCCTGCACTCTTAGAGTAAGTGTAGTGGCCTCAGACAGAGGAGAGATCCCTGGGACCTGGGCAGTCTGAGCCTT
TCGGTTCGGCTCGGACGTGAGAATCTCATTACATCACCGGAGTCTGTCTCCTCTCTAGGGACCTGGACCCGTCAGACTCGGAA

16,915

ANXA11

ANXA11-203

ANXA11-203

CCACTGGACAGTCATGTGTGAGGAGATTGCATTTCTGAGCAGGACACTGTGTTGCGTTACATTGGTAACCCCAATTTAAGGCAG
GGTGACCTGTCAGTACACACTCCTCTAACGTAAAGGACTCGTCTGTGACACAACGCAATGTAACCATTGGGGTTAAATTCGTC

17,000

ANXA11

ANXA11-203

ANXA11-203

CATAAATGCACTGGGAAAACAGCAATATTGGTTAGCCCTGGGAAGTGGTTTTTAGGATGATTATAATTTTTTTTTGTGGGTATTC
GTATTTACGTGACCCTTTTGTGCGTTATAACCAATCGGGACCTTCACCAAAAATCCTACTAATATTAACCAAAAACACCCATAAG

17,085

ANXA11

ANXA11-203

ANXA11-203

ATTTGATGTGGATAGCTGGGGTGAGTGCTGCTTTCCGTCTTCTGATGGGGGCCTGGAGAAGGCTGAACTGCATTTTTTAAGGTCT
TAAACTACACCTATCGACCCCACTCACGACGAAAGGCAGAAGACTACCCCGGACCTCTCCGACTTGACGTAAAAAATTCAGA

17,170

ANXA11

ANXA11-203

ANXA11-203

GTGACGCCTGCTGCAGGACCTGCAGTGGGAGAAAATTCCCCAGGGTGGGGCTTTCTCCCTATAAGGGTGCTCAGGGCTGAATATC
CACTGCGGACGACGTCTCTGGACGTCAACCTCTTTTAAGGGGTCCCACCCCGAAAGAGGGATATTTCCACGAGTCCCGACTTATAG

17,255

ANXA11

ANXA11-203

ANXA11-203

AGGACCCAGAAGGCTGAAAAGTGACTGTCCCTCCCTTAACGGATGTCTTCCTTGTCTTCTGTGGCCAGGGAGATACTTCAGGGGATT
TCCTGGGTCTTCCGACTTTCACTGACAGGGAGGGAATTGCCTACAGAAGGAACAAAGACACCGGTCCCTCTATGAAGTCCCCTAA

17,340

ANXA11

ANXA11-203

490
G D T S G D
ENSE00001457270

ANXA11-203

ACCGGAAGATTCTGCTGAAGATCTGTGGTGGCAATGACTGAACAGTGACTGGTGGCTCACTTCTGCCACCTGCCGGCAACACCA
TGGCCTTCTAAGACGACTTCTAGACACCACCGTTACTGACTTGTCACTGACCACCGAGTGAAGACGGGTGGACGGCCGTTGTGGT

17,425

ANXA11

ANXA11-203

495 500 505
Y R K I L L K I C G G N D
ENSE00001457270
ANXA11-203

GTGCCAGGAAAAGGCCAAAAGAATGTCTGTTTCTAACAAATCCACAAATAGCCCCGAGATTCACCGTCTAGAGCTTAGGCCTGT
CACGGTCTTTTTCCGGTTTTCTTACAGACAAAGATTGTTTAGGTGTTTATCGGGGCTCTAAGTGCCAGGATCTCGAATCCGGACA

17,510

ANXA11

ANXA11-203

CTTCCACCCCTCCTGACCCGTATAGTGTGCCACAGGACCTGGGTCCGGTCTAGAACTCTCTCAGGATGCCTTTTTCTACCCCATCCC
GAAGGTGGGGAGGACTGGGCATATCACACGGTGTCTTGGACCCAGCCAGATCTTGAGAGAGTCTACGGAAAAGATGGGGTAGGG

17,595

ANXA11

ANXA11-203

TCACAGCCTCTTGCTGCTAAAATAGATGTTTTCATTTTTCTGACTCATGCAATCATTCCCCTTTGCCTGTGGCTAAGACTTGGCTT
AGTGTCGGAGAACGACGATTTTATCTACAAAGTAAAAAGACTGAGTACGTTAGTAAGGGGAAACGGACACCGATTCTGAACCGAA

17,680

ANXA11

ANXA11-203

CATTTTCGTCATGTAATTGTATATTTTTATTTGGAGGCATATTTTCTTTTCTTACAGTCATTGCCAGACAGAGGCATACAAGTCTG
GTAAAGCAGTACATTAACATATAAAAAATAAACCTCCGTATAAAAAGAAAAGAATGTCAGTAACGGTCTGTCTCCGTATGTTTCAGAC

17,765

ANXA11

ANXA11-203

TTTGCTGCATACACATTTCTGGTGGGGCGACTGGGTGGGTGAAGCACCGTGTCTCTCGCTGAGGAGAGAAAAGGGAGGCGTGCCTG
AAACGACGTATGTGTAAGACCACTCCCGCTGACCCACCACTTCGTGGCACAGGAGCGACTCCTCTCTTTCCCTCCGCACGGAC

17,850

ANXA11

ANXA11-203

AGAAGGTAGCCTGTGCATCTGGTGAGTGTGTGCACGAGCTTTGTTACTGCCAAACTCACTCCTTTTTAGAAAAACAAAAAAG
TCTTCCATCGGACACGTAGACCACTCACACAGTGCTCGAAACAATGACGGTTTGAGTGAGGAAAAATCTTTTTTGTTTTTTTTC

17,935

ANXA11

ANXA11-203

GGCCAGAAAGTCATTCTTCCATCTTCTTGCAGAAACCACGAGAACAAGCCAGTTCCCTGTCAGTGACAGGGCTTCTTGTAA
CCGGTCTTTCAGTAAGGAAGGTAGAAGGAACGTCTTGGTGCTCTTGTTCGGTCAAGGGACAGTCACTGTCCCGAAGAACATTA

18,020

ANXA11

ANXA11-203

TTGTGGTATGTGCCTTAAACCTGAATGTCTGTAGCCAAAACCTGTTTCCACATTAAGAGTCAGCCAGCTCTGGAATGGTCTGGAA
AACACCATACACGGAATTTGGACTTACAGACATCGGTTTTGAACAAAGGTGTAATTCAGTCGGTCGAGACCTTACCAGACCTT

18,105

ANXA11

ANXA11-203

ATGTCTTCTGGTACCAACTTGTCTTCTGCTTGATTCTGCCCTGTGGCTCAGAGGTCTGGCCTTATCAGCCAGTGAAAAGTTC
TACAGAAGGACCATGGTTGAACAAAAGAAGACGAACTAAGACGGGACACCGAGTCTCCAGACCGGAATAGTCGGTCACTTTCAAG

18,190

ANXA11

ANXA11-203

ATGTAACCTTACGTAGAGATTTGTGTGCAGGAAACCCTGAGCATACTAGTTTGCAGGGACTCGTAAGGACATGGGAAGGGAGG
TACATTGGAATGCATCTCTAAACACACGTCTTTGGGACTCGTATGTGATCAAACGTCCCTGAGCATTCTGTACCCTTCCCTCC

18,275

ANXA11

ANXA11-203

TTCCCGAAATCCAGGCAGGAGGCCAGACACCTGAAAGGCAAAGGGATCTTGGTTGGTTGCAGGTGCAGTGAAGTCCACTGAAGG
AAGGGCTTTAGGTCCGTCTCCGGGTCTGTGGACTTTCGTTTTCCCTAGAACCAACCAACGTCCACGTCACTTCAGGTGACTTCC

18,360

ANXA11

ANXA11-203

TGTGGTGCGAAGAATGCAGTCCTTACCCAGGTCCCAGGAGGGAAGAAGGGTGTGTGCTAATTCCTGGTGGCCCTCGGCGGGGGC
ACACCACGCTTCTTACGTACAGGAAGTGGGTCCAGGGTCTCCCTTCTTCCCACACACGATTAAGGACCACGGGGAGCCGCCCCCG

18,445

ANXA11

ANXA11-203

CAGAGAGAAGGATGGGGACAACCCAGAGAGTCAACAAGACCAGTGCCTCCCTCAGGGTGCCTCCAGGCTGAAAAGGGGCTCTGGC
GTCTCTTCTTCTACCCCTGTTGGGTCTCTCAGTGTCTGGTACCGGAGGGGAGTCCCACGGAGGTCCGACTTTCCTCCGAGGACCG

18,530

ANXA11

ANXA11-203

TCTGGTCTCTGGGGACCCTGTGCCCGTTGGTTGGTGGTGTGAGGGGAAGAGAATCCATAAGAGAGTTTCTGAGAATTATGGTGTCA
AGACCAGAGACCCCTGGGACACGGGCAACCAACCACACTCCCTTCTCTTAGGTATTCTCTCAAAGACTCTTAATACCACAGT

18,615

ANXA11

ANXA11-203

TGTCCAGAAGCTAGAGCTTACCTTGCATCAGGGGTCTCCACCCACTCCTTTTCCAACCTCCTGCGTTGAGGTTTAGAAAAGAGAG
ACAGGTCTTCGATCTCGAATGGAACGTAGTCCCCAGAGGTGGGTGAGGAAAAGGTTGGAGGACGCAACTCCAAATCTTTTCTCTC

18,700

ANXA11

ANXA11-203

AATCGACTAGGCACATATGGCTCACGCCTGTAATCCAAGGACTTTGGGAAGCTGAGGTGAGAGGATCACTTGAGCTCAGGAGTTCA
TTAGCTGATCCGTGATACCGAGTGCGGACATTAGGTTCTGAAACCCCTTCGACTCCACTCTCCTAGTGAACCTCGAGTCTCAAGT

18,785

ANXA11

ANXA11-203

AGACTAGCCTAGCCAACAGCGAGACCCCTGTCTCTACTAAAAAATTTGGCCAGGCGTGGTGGCTCACGGCTGTAATCCCAGCACT
TCTGATCGGATCGGTTGTGCTCTGGGGACAGAGATGATTTTTTAAACCGGTCCGCACCACCGAGTGCCGACATTAGGGTCGTGA

18,870

ANXA11

ANXA11-203

TTGGGAGGTGAGGCGGGCAGATCACCTGAGGTCAGGAGTTTCGAGACCCAGCCTGGCCAACATGGTGAACCCCATCTCTACTAAA
AACCCCTCCACTCCGCCCGTCTAGTGGACTCCAGTCTCAAGCTCTGGGTGCGACCGGTTGTACCACCTTTGGGGTAGAGATGATTT

18,955

ANXA11

ANXA11-203

AATACAAAAATTAGCCAGGCATGGTGGCACATTCCTGTAATCCCAGCTACACAGGATGCTGAGGCAGGAGAATCACTTGAACCCA
TTATGTTTTTAATCGGTCCGTACCACCGTGAAGGACATTAGGGTCGATGTGTCTACGACTCCGTCTCTTAGTGAACCTTGGGT

19,040

ANXA11

ANXA11-203

GGAGGCAGAGGTTGTAGTGAGCTGAGATCACACCATTGCACTTCAACCTGGGTGGACAGAGTGAGACTCTGTCTCAAAAAAAAAA
CCTCCGTCTCCAACATCACTCGACTCTAGTGTGGTAACGTGAAGTTGGACCCACCTGTCTCACTCTGAGACAGAGTTTTTTTTTTT

19,125

ANXA11

ANXA11-203

AAAAATTTACCTGGCATTGTAGTGCATTCCCTATAGTCGGCTACTCTGGAGGCTGAGGCAGGAAGATCCTTAGAGCCCAAGAAAT
TTTTTAAATGGACCGTAACATCACGTAAGGGATATCAGCCGATGAGACCTCCGACTCCGTCTCTAGGAATCTCGGGTTCTTTA

19,210

ANXA11

ANXA11-203

TGAGGCCGTAGTAAGCTGTGATTACACCACTGCACTCCAGCCTGGACAACAGAGCGAGACCTTGTCTCAAATGAGAAAAAAACAA
ACTCCGGCATCATTGACACTAATGTGGTGACGTGAGGTCGGACCTGTTGTCTCGCTCTGGAACAGAGTTTACTCTTTTTTTTGT

19,295

ANXA11

ANXA11-203

AAAGAAATGGGAGAATCCAGAGAGACTAGGCTAGATCAAGCCTGCTGGGTCTGGCAGGAGCCCCAGGGAGTAGCTCATCTGCAG
TTTCTTTACCCTCTTAGGTCTCTCTGATCCGATCTAGTTCGGACGACCCAGGACCGTCTCGGGGTCCCTCATCGAGTAGACGTC

19,380

ANXA11

ANXA11-203

ACATTTGCTTGAGGACTACCCCTAAACATAAAGGAAGAATGACATCCGAAGGGTGTGGAGCAGCCATGAGCTGAGAACTAGCCT
TGTA AACGAACTCCTGATGGGGGATTTGTATTTCTTCTTACTGTAGGCTTCCACACCTCGTCTGGTACTCGACTCTTGATCGGA

19,465

ANXA11

ANXA11-203

GGTCTACCTGAGATTGATGGCAGGTCCTGGTCAACACGTGACCTCTGCGTCAGAGTCCATGCCTCAAGCCCAAGCTGAAGCCCCA
CCAGATGGACTCTAACTACCGTCCAGGACCAGTTGTGCAGTCGAGACGCAGTCTCAGGTACGGAGTTCGGGTTCGACTTCGGGGT

19,550

ANXA11

ANXA11-203

TCCCTGCTGCTCTCCCAAGAACTCCTCTGCTAGGGCAGGCCCTTGCCTTGGGTGCCAGGTGGGACCTGCCTGATGGGATGGGG
AGGGACGACGAGAGGGTTCTTGAGGAGACGATCCCGTCCGGGGAACGGGAACCCACGGTCCACCCTGGACGGACTACCCTACCCC

19,635

ANXA11

ANXA11-203

TGCTTGGCATATACAACCTTGCCATGAACTCAAGGTGACCCTGGGGGCTCCTGAATTGTGATGGGGCCTAGAACCAATGTGCTCT
ACGAACCGTATATGTTGAACGGTACTTGAGTTCCACTGGGACCCCCGGAGGACTTAACACTACCCCGGATCTTGGTTACACGAGA

19,720

ANXA11

ANXA11-203

GATGTGACCATATTCTGTGACATTACCTTGCCTGTTTACTCCAAAGTTCCAGCCTGGTGCCAGCAGGCAATATTGCACCTAC
CTACACTGGTATAAGACACTGTAATGGAACGGGACAAATGAGGTTTCAAGGGTCGGACCACGGGTCGTCCGTTATAACGTGGATG

19,805

ANXA11

ANXA11-203

AGACACATTTACTTTGGTTTCCAAAGTGTTTTTAGACATTTGAATTTGTTGCCAACATTTAAACATTGAGAGATTTTCATATTTTT
TCTGTGTAAATGAAACCAAAGGTTTCCAAAAATCTGTAAACTTAAACAACGGTTGTAAATTTGTAACCTCTCTAAAGTATAAAAA

19,890

ANXA11

ANXA11-203

AAAAATCTGGAATTCTGGCTTCTCTTGAAAACTCAGAAATTTCTGGCACTATGGGGCTTGCAATTCCTGCATGGCTGGAGCTGAGTT
TTTTTAGACCTTAAGACCGAAGAGAACTTTTTGAGTCTTTAAGACCGTGATACCCCGAACGTAAGGACGTACCGACCTCGACTCAA

19,975

ANXA11

ANXA11-203

GCAGCTGCCCTTTAGGCCTGTA CTCTTATTTGCTATAGGCTCCGTCTTGTATTACACTAAGCCCATGTCACCCATTTGGCTCC
CGTCGACGGGGAAATCCGGACATGAGGAATAAACGATATCCGAGGCAGAACATAATGTGATTCCGGGTACAGTGGGTAAACCGAGG

20,060

ANXA11

ANXA11-203

TGCAGGCCTTTGGGTTTGAGACCCTGGTCTACACACTTGAGAGACCACCTGTTGTAAAGTACATGGATGTGCTTTGGTCAAGGAAT
ACGTCCGGAAACCCAAACTCTGGGACCAGATGTGTGAACCTCTGGTGGACAACATTTTCATGTACCTACACGAAACAGTTTCCTTA

20,145

ANXA11

ANXA11-203

AGACCAAGGTGGATATCCAGGCCAGAGTGACTCAGCGAGTTTAGGTCACAGGCGTATACTCCACTTGTATATAACCTGCTTGTG
TCTGGTTCCACCTATAGGTCCGGTCTCACTGAGTCGCTCAAATCCAGTGTCCGCATATGAGGTGAACAATATATTGGACGAACAC

20,230

ANXA11

ANXA11-203

TAAGTTCACTACTTGGCTCAAAGCCACTATTGTTTGGAAAAGGTATAACTGCCCTGCTGACGCTGTACAGATGTTCTTGGGCTCGG
ATTCAAGTATGAACCGAGTTTTCGGTGATAACAAACCTTTTCCATATTGACGGGACGACTGCGACATGTCTACAAGAACCCGAGCC

20,315

ANXA11

ANXA11-203

ATGGGCATGGCTCCACGTGGTGTGCACTAGCACCCAGAGAGAGTGAAGCTATTGACCCCTGTAAGGGAGAGTGACCATCTGGCAG
TACCCGTACCGAGGTGCACCACACGTGATCGTGGGTCTCTCACTTCGATAACTGGGGACATTCCCTCTCACTGGTAGACCGTC

20,400

ANXA11

ANXA11-203

ATAGATAGAGGGGAGCCAGGACATGGCTCAGCTTGTGCCAGAGGGGAGAGTTAAGCCGCTGACCCTGTAGCCAGGGAGTGCACCT
TATCTATCTCCCTCGGTCTGTACCGAGTCGAACACGGGTCTCCCTCTCAATTCGGCGACTGGGACATCGGTCCCTCACGTGGA

20,485

ANXA11

ANXA11-203

GCAAGCATGGGGGTGGCAGGAGCCACAGAGCTGGCTGCTGAGAGGAGCTGCAGATCTGGAGAAGACAGCCTAGGTAAAGGTGGAC
CGTTCGTACCCCAACCGTCTCGGTGTCTCGACCGACGACTCTCCTCGACGTCTAGACCTCTTCTGTCTGGATCCATTTCCACCTG

20,570

ANXA11

ANXA11-203

AGTGTGAGAGCTGCTGATGAGATAGCTGCTGAATAAACTACATTTTACCTGCCTATGGCCCGCCAGGTTTTCTTTTCAGCTATCG
TCACACTCTCGACGACTACTCTATCGACGACTTATTTTGATGTAATAATGGACGGATACCGGGCGGTCCAAAAGAAAGTTCGATAGC

20,655

ANXA11

ANXA11-203

CCCATCCACCCAGTCCCTCGAACCTCAGCATGGGCTGGAACCTGACCCTGGGCATGACATTTGGCATAAGTTGTGGACCTGACAC
GGGTAGGTGGGTCAGGGGAGCTTGGAGTCGTACCCGACCTTGGACTGGGACCCGTACTGTAAACCGTATCAACACCTGGACTGTG

20,740

ANXA11

ANXA11-203

CTGTGTTTGTCTAGTCCTGTTTCTCCCTGCCTTCTGTTTCTCTCGCTGCCCTCATGGTCACTCCCAAGAGATCCAACCCATGT
GACACAAACAGGATCAGGACAAAGAGGGACGGAAGGACAAGGAGAGCGACGGGAGTACCAGTGAGGGTTCTCTAGGTTGGGTACA

20,825

ANXA11

ANXA11-203

TAAGTATGGGCTGGAGGACTGCATGAATGCCTCATGATCTTCCCAGAGGCAAAGGCACCTACTGCCTTCCAAGGTCAGTGGGAGG
ATTCATACCCGACCTCTGACGTACTTACGGAGTACTAGAAGGGTCTCCGTTTCCGTGGATGACGGAAGGTTCCAGTCACCCCTCC

20,910

ANXA11

ANXA11-203

TTGGGATCAACACTGTTTATTATGCTTAGGACAAAAAGATAGGGAGAAAGATGTGCAACCTTACAGGTCATCTTTCTGGGATAG
AACCCTAGTTGTGACAAATAATACGAATCCTGTTTTTCTATCCCTCTTTCTACACGTTGGAATGTCCAGTAGAAAGACCCTATC

20,995

ANXA11

ANXA11-203

AACACAATGGGTCTTCTCCTGCCTCCTGGATATGTTAGTCAAGGCCAGTCCATGCTACACATCTAGTCTGACTTCTAAAAATAGAA
TTGTGTTACCCAGAAGAGGACGGAGGACCTATACAATCAGTTCCGGTCAGGTACGATGTGTAGATCAGACTGAAGATTTTATCTT

21,080

ANXA11

ANXA11-203

GCACCAGATGAATTCAGCCCTGAGAGAATTTTCAGCAGCTGTGGGGGCGCTGGAGGAAACACTATTAATAGTTTTGACCTGAG
CGTGGTCTACTTAAGTCGGGACTCTCTTAAAAGTCGTGACACCCCGCGACCTCCTTTGTGATAATTTATCAAAACGTGGACTC

21,165

ANXA11

ANXA11-203

ACAGATAGCCTCACTCGCCTCACCTAGTCTGGTGGCATTGTTCTCAGGTGCAAAATTTAAGAAAGAAACCTTGGAGTGCTCAC
TGTCTATCGGAGTGAGCGGAGTGGGATCAGGACCACCGTAAACAGAGTCCACGTTTTAAATCTTTCTTTGGAACCTCACGAGTG

21,250

ANXA11

ANXA11-203

CCTGTGGCTGGGTAGATGGTCCTAAAAGTGGTGGTTTTCAAGCCTGAGTGTGTATCAGGATCATCAGGGGAGCTTGCTAAAAGAGCA
GGACACCGACCCATCTACCAGGATTTACCACCAAAAAGTTTCGGACTCACACATAGTCCTAGTAGTCCCTCGAACGATTTCTCGT

21,335

ANXA11

ANXA11-203

GTTCTGCGGTCAGACCCTCATGCATTTTGGAGAGGTGTGGGGACTGGGAAACTGCATCTGTAACCTGCTGTAATCTAACGCTTA
CAAGGACGCCAGTCTGGGAGTACGTAAAACCTCGTCCACACCCCTGACCCTTTGACGTAGACATTGGACGACATTAGATTGCGAAT

21,420

ANXA11

ANXA11-203

TCTAAATACTACTGTGCTCACACAGAGAACACCGCAAAAAGTAGAGGTGTTTCCTCCAGAGGGCAGGTGAGCAGATGGCACAGTCTG
AGATTTATGATGACACGAGTGTGTCTTGTGGCGTTTTTCATCTCCACAAGGAGGTCTCCCGTCCACTCGTCTACCGTGTGACAGC

21,505

ANXA11

ANXA11-203

CTTGGAAATTCAGTCAGGTGATGAGAGATGAGATGAGGCACCTCTAGCTTTGGGAAGAGGGAGCTGAAAGATGAACCTTTGCAGGT
GAACCTTAAGTCAGTCCACTACTCTCTACTCTACTCCGTGAGGATCGAAACCTTCTCCCTCGACTTTCTACTTTGGAAACGTCCA

21,590

ANXA11

ANXA11-203

GCCACGGTCAAAGTGGTGGTTAATGCCATGCCATGCCATTTTCTGTTGGCCTTGGCAGGGAGTTACAGCCCTACCTTAGGAC
CGGGTGCCAGTTTTACCACCAAATTACGGTACGGTACGGGTAAAAGACAACCGGAACCGTCCCTCAATGTCGGGATGGAATCCTG

21,675

ANXA11

ANXA11-203

CTGGCTCCTTATTTCTGCTGTAGGCTCTTTCCTGCCCTGGCCGAGATGGAGTGAATGAGACCTAGAAAACATCAAGCTAAATACA
GACCGAGGAATAAAGACGACATCCGAGAAAAGGACGGGACCGGCTCTACCTCACCTTACTCTGGATCTTTGTAGTTCGATTTATGT

21,760

ANXA11

ANXA11-203

TGTCCTCAGAAAGATAAAGGTTTACATTTTACCCCCATCAAATCTGAAAGCTCTCTGCCTGTGTTTTTCTAAGGGATAGGGACA
ACAGGAGTCTTTCTATTTCCAAATGTAAGTGGGGGTAGTTTAGACTTTTCGAGAGACGGACACAAAAGATTCCCTATCCCTGT

21,845

ANXA11

ANXA11-203

TCATTACTCAGTCCACAACCTGGACTCATGTAGGGTCCCTGTGTCAGTAAAGGAGTCAGTCAAGCCACCAGGTATACCAAGGACT
AGTAATGAGTCAGGTGTTGGACCTGAGTACATCCCAGGGGACAGTCAATTTCTCAGTCAGTTCGGGTGGTCCATATGGTTCCCTGA

21,930

ANXA11

ANXA11-203

CTTACCCTCAGCCCCTACTCCTTGGAAAAGCTGCCCTTGGCCTAATATTGGTGTTTAGCTTGAGCCTGACTCCTTCTCAACACTA
GAATGGGAGTCGGGGATGAGGAACCTTTTCGACGGGGAAACCGGATTATAACCACAAATCGAACTCGGACTGAGGAAGAGTTGTGAT

22,015

ANXA11

ANXA11-203

AGAGCTGATGAAGTCTGAAGCAGAAAGAGCTCTGACCTGAGAGTCAAACATCCTTATTCTGATCTCAGCTCAGCCCCTGATTTG
TCTCGACTACTTCAGGACTTCGTCTTTCTCGAGACTGGACTCTCAGTTTGTAGGAATAAGACTAGAGTCGAGTCGGGGACTAAAC

22,100

ANXA11

ANXA11-203

TTGTGTGACCCTGGATATGTCACCTCCTGTCTTTTTGACTTTTTAAAAATGAAGGGTAGACTAGAGGAGAGCTTCTAAAACTTTAA
AACACACTGGGACCTATACAGTGAAGGACAGAAAAACTGAAAAATTTTACTTCCCATCTGATCTCCTCTCGAAGATTTTGAAATT

22,185

ANXA11

ANXA11-203

TGTGGTCAACGAAATGGAATAGGAAATTCCACAAGTCTGTCTTCCACAAAAGCAGCAAATAAGGTGGCAAAAACCTCAAATTTAT
ACACCAGTTGCTTTACCTTATCCTTTAAGGTGTTTCAGACAGGAAGGTGTTTTTCGTCGTTTATTCCACCGTTTTTGAGTTTAAATA

22,270

ANXA11

ANXA11-203

GGGAACTCTGGAAACGAATTGAAAGTTTACAGCAATCAGGTGAATACCTAAGAATAAAAAGCTGGATTTAGTAAGA
CCCTTGAGACCTTTGCTTAACTTTCAAATGTCGTTAGTCCACTTATGGATTCTTATTTTCGACCTAAATCATTCT

3'

22,345

5'

ANXA11

ANXA11-203

Feature	Location	Size	Type
✓ ANXA11	1 .. 22,345	22,345 bp	gene
/note	= gene ENSG00000122359 Protein coding		
ANXA11-202	1 .. 22,345	22,345 bp	prim_transcript
/note	= primary transcript ENST00000372231		
✓ ANXA11-203	1 .. 22,345	22,345 bp	prim_transcript
/note	= primary transcript ENST00000422982		
ANXA11-205	1 .. 22,345	22,345 bp	prim_transcript
/note	= primary transcript ENST00000438331		
ANXA11-208	1 .. 400	400 bp	prim_transcript
/note	= primary transcript ENST00000463657 protein_coding_CDS_not_defined		
ANXA11-204	213 .. 4154	3942 bp	prim_transcript
/note	= primary transcript ENST00000437799		
ANXA11-201	363 .. 18,110	17,748 bp	prim_transcript
/note	= primary transcript ENST00000265447		
ANXA11-202	373 .. 17,381	17,009 bp	CDS
▶ 14 segments = 1518 bp			
/note	= coding sequence ENSP00000361305		
/translation	= MSYPGYPPPPGGYPPAAP,,GGGPWGGAAAYPPPPSMPPIGLDNVATYAGQFNQDYLSGM,,AANMSGTFGGANMPNLYPGAPGAGYPPVPPG GFGQPPSAQQPVPPYGMYPGGNPPSRMPSYPPYPGAPVPGQPMPPPQQPPGAYPGQPPVTPYGGQPPVPLPGQQQPVPSYPGYPGS GTVTPAVPPTQ,,FGSRGTITDAPGFDPLRDAEVLKAMKGF,,GTDEQAIIDCLGSRSNKQRQQILLSFKTAYGK,,DLIKDLKSELSGNFEKTIL ALMKTPLVLDIYEIKEAIK,,GVGTDEACLIIEILASRSNEHIRELNRAYKA,,EFKKTLEEAIKSDTSGHFQRLILISLSQ,,GNRDESTNVDMSLAQR DAQ,,ELYAAGENRLGTDESKFNAVLCRSRAHLVA,,VFNEYQRMTGRDIEKSICREMSGDLEEGMLAV,,VKCLKNTPAFFAERLNKAMR,,GA GAGTKDRTLIRIMVRSSETDLLDIRSEYKRMYGKSLYHDIS,,GDTSGDYRKILLKICGGND*		
✓ ANXA11-203	373 .. 17,381	17,009 bp	CDS
▶ 14 segments = 1518 bp			
/note	= coding sequence ENSP00000404412		
/translation	= MSYPGYPPPPGGYPPAAP,,GGGPWGGAAAYPPPPSMPPIGLDNVATYAGQFNQDYLSGM,,AANMSGTFGGANMPNLYPGAPGAGYPPVPPG GFGQPPSAQQPVPPYGMYPGGNPPSRMPSYPPYPGAPVPGQPMPPPQQPPGAYPGQPPVTPYGGQPPVPLPGQQQPVPSYPGYPGS GTVTPAVPPTQ,,FGSRGTITDAPGFDPLRDAEVLKAMKGF,,GTDEQAIIDCLGSRSNKQRQQILLSFKTAYGK,,DLIKDLKSELSGNFEKTIL ALMKTPLVLDIYEIKEAIK,,GVGTDEACLIIEILASRSNEHIRELNRAYKA,,EFKKTLEEAIKSDTSGHFQRLILISLSQ,,GNRDESTNVDMSLAQR DAQ,,ELYAAGENRLGTDESKFNAVLCRSRAHLVA,,VFNEYQRMTGRDIEKSICREMSGDLEEGMLAV,,VKCLKNTPAFFAERLNKAMR,,GA GAGTKDRTLIRIMVRSSETDLLDIRSEYKRMYGKSLYHDIS,,GDTSGDYRKILLKICGGND*		
ANXA11-205	373 .. 17,381	17,009 bp	CDS
▶ 14 segments = 1518 bp			
/note	= coding sequence ENSP00000398610		
/translation	= MSYPGYPPPPGGYPPAAP,,GGGPWGGAAAYPPPPSMPPIGLDNVATYAGQFNQDYLSGM,,AANMSGTFGGANMPNLYPGAPGAGYPPVPPG GFGQPPSAQQPVPPYGMYPGGNPPSRMPSYPPYPGAPVPGQPMPPPQQPPGAYPGQPPVTPYGGQPPVPLPGQQQPVPSYPGYPGS GTVTPAVPPTQ,,FGSRGTITDAPGFDPLRDAEVLKAMKGF,,GTDEQAIIDCLGSRSNKQRQQILLSFKTAYGK,,DLIKDLKSELSGNFEKTIL ALMKTPLVLDIYEIKEAIK,,GVGTDEACLIIEILASRSNEHIRELNRAYKA,,EFKKTLEEAIKSDTSGHFQRLILISLSQ,,GNRDESTNVDMSLAQR DAQ,,ELYAAGENRLGTDESKFNAVLCRSRAHLVA,,VFNEYQRMTGRDIEKSICREMSGDLEEGMLAV,,VKCLKNTPAFFAERLNKAMR,,GA GAGTKDRTLIRIMVRSSETDLLDIRSEYKRMYGKSLYHDIS,,GDTSGDYRKILLKICGGND*		
ANXA11-204	373 .. 4154	3782 bp	CDS
▶ 3 segments = 450 bp			
/note	= coding sequence ENSP00000414642		
/translation	= MSYPGYPPPPGGYPPAAP,,GGGPWGGAAAYPPPPSMPPIGLDNVATYAGQFNQDYLSGM,,AANMSGTFGGANMPNLYPGAPGAGYPPVPPG GFGQPPSAQQPVPPYGMYPGGNPPSRMPSYPPYPGAPVPGQPMPPPQQPPGAYPGQPPV 150 amino acids = 15.0 kDa		
✓ Donor Template WT -> SNV	2344 .. 2406	63 bp	misc_feature
ANXA11-201	2363 .. 17,381	15,019 bp	CDS
▶ 13 segments = 1419 bp			
/note	= coding sequence ENSP00000265447		
/translation	= MPPIGLDNVATYAGQFNQDYLSGM,,AANMSGTFGGANMPNLYPGAPGAGYPPVPPGGFQPPSAQQPVPPYGMYPGGNPPSRMPSYPP PYPGAPVPGQPMPPPQQPPGAYPGQPPVTPYGGQPPVPLPGQQQPVPSYPGYPGSGTVTPAVPPTQ,,FGSRGTITDAPGFDPLRDAEVL KAMKGF,,GTDEQAIIDCLGSRSNKQRQQILLSFKTAYGK,,DLIKDLKSELSGNFEKTILALMKTPLVLDIYEIKEAIK,,GVGTDEACLIIEILASRS NEHIRELNRAYKA,,EFKKTLEEAIKSDTSGHFQRLILISLSQ,,GNRDESTNVDMSLAQRDAQ,,ELYAAGENRLGTDESKFNAVLCRSRAHLVA ,,VFNEYQRMTGRDIEKSICREMSGDLEEGMLAV,,VKCLKNTPAFFAERLNKAMR,,GAGTKDRTLIRIMVRSSETDLLDIRSEYKRMYGKSLYH DIS,,GDTSGDYRKILLKICGGND*		
✓ PAM	2370 .. 2372	3 bp	misc_feature
✓ Protospacer Sequence	2373 .. 2392	20 bp	misc_feature

Feature	Location	Size			Type
✓ SNV	2375 .. 2375	1 bp			misc_feature
/note	= WT = G SNV = A				
ANXA11-210	4147 .. 6835	2689 bp			prim_transcript
/note	= primary transcript ENST00000481805 Retained intron				
ANXA11-206	11,222 .. 17,594	6373 bp			prim_transcript
/note	= primary transcript ENST00000447489				
ANXA11-206	11,222 .. 16,825	5604 bp			CDS
▶ 5 segments = 446 bp					
/note	= coding sequence ENSP00000405009				
/translation	= GRTAWEQTSPPSMRFCAPGAGPTW*Q,,FSMSTRE*QAGTLRRASAGRCPGTWRRACWPW,,*NVSRIQPSLRRGSTRP*G,,GQEQRTGP* FASWCLAARPTSWTSDQSIGCTASRCTTTSR,,VSPACQQA MDIWKKPHALPSSCLGWKEMI 148 codons (5 internal stop codons)				
ANXA11-207	15,216 .. 17,646	2431 bp			prim_transcript
/note	= primary transcript ENST00000463340 protein_coding_CDS_not_defined				

Primer	Length		Binding Sites		Tm	Date Added
✓ PCR Reverse	20-mer		2176 .. 2195		59°C	Jan 10, 2023
/sequence	= TCATGTGGTCTGTGGTGTCC 55% GC / 6146.0 Da					
✓ Donor Template WT -> SNV	63-mer		2344 .. 2406		81°C	Jan 10, 2023
/sequence	= TGCCCCGCATAGGTGGCCACGTTATCCAGCCTGATGGGGGGCATGCTGGGCCGGAGGAGGGTAG 67% GC / 19,642.7 Da					
✓ gRNA Protospacer	20-mer		2373 .. 2392		65°C	Jan 10, 2023
/sequence	= GGCCACGTTATCCAGCCCGA 65% GC / 6063.0 Da					
✓ PCR Forward	21-mer		2578 .. 2598		58°C	Jan 10, 2023
/sequence	= GCAGAAGCCTGATGAAAACCC 52% GC / 6433.3 Da					
✓ Sanger Sequencing	21-mer		2578 .. 2598		58°C	Jan 10, 2023
/sequence	= GCAGAAGCCTGATGAAAACCC 52% GC / 6433.3 Da					