

INK2S00114R_ANXA11_G38R_A07_AA
 22,312 bp

5'

3'

CACTGCACCCTTGCCAGCAGAGGGCAGGAGCAAAGCTTTCAGTGAGAGGGCCTTTCAAGGAAACTGGCTCATGGGGAGTGAATCCTG
GTGACGTGGGAACGGTTCGTCTCCGTCTCGTTTCGAAGTCACTCTCCCGGAAAAGTTCTTTGACCGAGTACCCCTCACTTAGGAC

85

ANXA11

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TCACTGTGGGTGGGGCCGGGGGTGTGGCCCTGGCCCAAGAAGTCAGGCAGCATGCTGGTGGGTACTGTTTCTAGCTGGAGGCACCA
AGTGACACCCACCCCGGGCCCCACACCGGGACCGGGTCTTTCAGTCCGTTCGTACGACCACCCATGACAAAAGATCGACCTCCGTGGT

170

ANXA11

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GCAGGAGACAGTGAAGTGGTCTGCGACAAGCAGGGCAGATGCAGCAGTTTCTTCTGCAGGGTCCCAGTTGTGGTGGTGGCTGCCC
CGTCCCTCTGTCACTTGACCAGACGCTGTTTCGTCCCGTCTACGTCGTCAAAGAAGACGTCCCAGGGTCAACACCACCACCGACGGG

255

ANXA11

ANXA11-203

TTTCAAGAAGCTGGGTCCCACGGGCCAGCAGGGGCTCTCAGGCAGAGCCTGAATGTGCTTTTCGTCTTCTCTTCCAGATCTAACCA
AAAGTTCTTCGACCCAGGGTGCCCGGTTCGTCCCGAGAGTCCGTCTCGGACTTACACGAAAGCAGAAGAGAAGGTCTAGATTGGT

340

ANXA11

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TGAGCTACCCTGGCTATCCCCGCCCCAGGTGGCTACCCACCAGCTGCACCAGGTAAGAGGGTCTGGGGTGGGGAGGAGAGTGA
ACTCGATGGGACCGATAGGGGGCGGGGGTCCACCGATGGGTGGTGCAGCTGGTCCATTCTCCCAGACCCACCCCTCCTCTCACT

425

ANXA11

ANXA11-203

1 5 10 15
M S Y P G Y P P P G G Y P P A A P

ENSE00003531093

ANXA11-203

ATGCTGCCTCTGTACAGTGGCTGGGAGTGGAGAGGGGAGAACAGTAGTTTCTCACTCCCCTCCTCCCCTCACAGCACGGCCCCAG
TACGACGGAGACATGTCACCGACCTCACCTCTCCCCTCTTGTCAATCAAAGGAGTGAGGGGAGGAGGGGAGTGTGCTGCCGGGTC

510

ANXA11

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ANXA11-203

CAGGGGAGGAGAGGACAAACAGGAGTAGTGGGACAGCCAGCCGAGGCAGGGGCTGGAGAAGAGCATGACACTAAGGCCATCGGAGG
GTCCCCTCCTCTCCTGTTGTCTCATCACCTGTTCGGTTCGGTCCCGTCCCGACCTCTTCTCGTACTGTGATTCCGGTAGCCTCC

595

ANXA11

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CCTAGGTTTGAAGTGCCTCCAGAAAGCCCTGGACCAGGCCAGGGCTGGGTCTTTCCTTACTCTCTAGTAACAGTGGGCAAA
GGATCCAAACTTTGACGGAGGTCTTTCGGGACCTGGTCCGGGTCCCGACCCAGAGAACCGGAATGAGAGATCATTGTACCCGTTT

680

ANXA11

ANXA11-203

ANXA11-203

TGCTGTCACTTTGAGACTCAGTTTTTCTTCTCCGCAAAATTGCTTCAAGGATTTCTCCCTCATTAGGTGGTCTGGATACTGATGA
ACGACAGTGAAACTCTGAGTCAAAAAGAAGAGGCGTTTTAACGAAGTTCTTAAAGAGGGGAGTAATCCACCAGGACCTATGACTACT

765

ANXA11

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GATAGGCAGGCAGAGCGACACGGTGTCTCCAAAGCATTGCTAGGTGATGGTTGCCCTTACCACCTCTCCTACCCTCTGCTCAA
CTATCCGTCCGTCTCGCTGTGCCACAGGAGGTTTCGTAACGATCCACTACCAACGGGGAATGGTGGAGAGGATGGGAGACGAGTT

850

ANXA11

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GGTGTGTGGGTTTGCAGCAACAAGATCCCCCTTGCCAAGAGAGGAAGTGGAGGCAGATGCTAAGGGTCAAAGGTCCTCCCTGTT
CCACACACCCAAACGTCGTTGTTCTAGGGGGAACGGTTCTCTCCTTACCTCCGTCTACGATTCCAGTTTCCAGTGAGGGACAA

935

ANXA11

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TTCTGCAGGAGCTGTGGGTAGTCACATGGAGAAGTCGTCTTCTCTGGCCCTGGCCCTTTTGGTCTCAAATGAGATTTGGTCCC
AAGACGTCTCGACACCCATCAGTGTACCTCTTCAGCAGAAGAGACCGGGACCGGGGAAAACAGGAGTTTACTCTAAACCAGGG

1020

ANXA11

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CACTGTGGGAAAGGAAATATGAGGGCTCATGAGACCAAGGGGAGAAAAGGGTCATTCCAAGGCTGGTTCATCCTGAGGGTGCCTGA
GTGACACCCTTTCTTTATACTCCCGAGTACTCTGGTTCCCTCTTTTCCCAGTAAGGTTCCGACCAGTAGGACTCCCACGGACT

1105

ANXA11

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GCCGCTGCCCTCTCCCAAGGGGACTCCTAGGCATCATTGATTTCTTTGGAGCTGAGGTCTGTGGTTTTGAACACCCAGACCTG
CGGCGACGGGGAGAGGGGTCCCTGAGGATCCGTAGTAACTAAAGAAACCTCGACTCCAGGACACCAAACCTGTGGGGTCTGGAC

1190

ANXA11

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CAGGCCATTTACCTTCCCTCCCATTCAGCAGGTGAAGAACAGACTCAGACCTAGAGGTGGCTCAGCTGCTGTCCCAGGGCATGTT
GTCCGGTAAATGGAAGGGAGGGTAAGTCGTCCACTTCTTGTCTGAGTCTGGATCTCCACCGAGTCGACGACAGGGTCCCGTACAA

1275

ANXA11

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AGGGGCTGAGCTGGGCCACTGCCCTCTGAATGAGGCCACCCAGGTTGGCTGGCACTGGCCTGGGTTCTCTCTATAGTAGAAA
TCCCCGACTCGACCCGGTGACGGGAGACTTACTCGGGTGGGGTCCAACCGACCGTGACCCGGACCCAAGAGAGAGATATCATCTTT

1360

ANXA11

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TCCTGCCATCCAGATCCTGCCACTGCCACCTTTGCTAGCACAGCTGAGCAGCCTCTGAGCAGCAAGAGAGGAGGGAGGCAGGAAAT
AGGACGGTAGGTCTAGGACGGTGACGGTGGAAACGATCGTGTGCGACTCGTCGGAGACTCGTCGTTCTCTCCTCCTCCGTCTTTA

1445

ANXA11

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TTAGGGAAGGTTCTTCTGAGGGTCTGGAGCCCTGGAGATGAAGAGCCGATCCGAAGCTGCCATGTAGAGGAAAGCATCTAACA
AATCCCTTCCAAGAAGGACCTCCAGACCTCGGGACCTCTACTTCTCGGCTAGGCTTCGACGGTACATCTCCTTTTCGTAGATTGT

1530

ANXA11

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GGCCAGAGGCCCCATGATGATGTCGAATGCCCATCGGGCACCCAGCTGAGCCCTGCAGGTGTTAACTCAGTCTTCGTACAGCAG
CCGGTCTCCGGGGTACTACTACAGCTTACGGGTAGCCCGTGGGTGCGACTCGGGACGTCCACAATTGAGTCAGAAGCAGTGTGTC

1615

ANXA11

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TCTAGGCATACACTCACCATTAGCCATTTGTAAGCTGAGGAAACAAGCCTAAGGAGGGTGAAAGCCTTGCCCCAGGGCACATAC
AGATCCGTATGTGAGTGGTAATCGGGTAAACATTGCGACTCCTTTGTTTCGGATTCTCCCACTTTTCGGAACGGGGTCCCGTGTATG

1700

ANXA11

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CGGTCTGCTGGTTTTAGAGCGGGCTTTTACCTCTGTTTCTTCTGTCCTCTTGTGGACTGGTATCTGTGTTTACCATGACCCA
GCCAGGACGACCAAAGTCTCGCCGAAAAGTGGAGACAAAGAAGGACAGGAGAACACCTGACCATAGACACAAATGGTACTGGGT

1785

ANXA11

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GCCCCATGTCCCTCCAGCCTCTTATCCTGCTTCTCCCTGCCTTTTACAGACTTGTAAATAGCAAACAGCCAAACCCCTCCCGCCA
CGGGGTACAGGGAGGTTCGGAGAATAGGACGAAGAGGGACGGAAAATGTCTGAACATTATCGTTTGTGCGTTTGGGGGAGGGCGGT

1870

ANXA11

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GTGCCTTCGCATTACTGAAATCTCAGAGCTCCCTATGGTACCTCTGTTCATGGGCTCAGCATGGTGTCCCACAACAGTCTGTCTCT
CACGGAAGCGTAATGACTTTAGAGTCTCGAGGGATACCAGTGGAGACAGTACCCGAGTCTGTACCACAGGGTGTGTGTCAGACAGGA

1955

ANXA11

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TGTCTGTCTCCTGCTCCATGATGGTGAACCTTGGGAGGGCAGAGCCTGCCTGGGCTCTCCCAGCCTCCTTAATACCCACAGAGG
ACAGACAGGAGGACGAGGTACTACCACTTGAACCTCCCGTCTCGGACGGACCCGAGAGGGTCTGGAGGAATTATGGGGTGTCTCC

2040

ANXA11

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GTCTTGGGAGTGTGTTGGGGAACCTCCACCTTCCCTCCCTGGGAAGAGGGGAAGGTTTCCCTCCTCTGCCAGTGGGATAGGGGGAGA
CAGAACCTCACAAACCCCTTGAGGTGGAAGGAGGGACCTTCTCCCTTCCAAAGGGGAGGAGACGGTCAACCTATCCCCCTCT

2125

ANXA11

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PCR Reverse
TCATGTGGTCTGTGGTGTCC

CTTTCCTCCTGGTGTGTTTTCATGTGGTCTGTGGTGTCCCGAGGCTCGAGGCTCGAGGCTTTACTGGGCCTCCCTTTCTGACCACCT
GAAAGGAGGACCACAAAAGTACACCAGACACCACAGGGCTCCGAGCTCCGAGCTCCGAAATGACCCGGAGGGAAAGACTGGTGGGA

2210

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Donor Template SNV -> REV

gctttcagGTGGTGGTCC

GGGAGCTCTCATCTCTGCCTTTCCCGTGTGGTGGGGGACTGGCAGGGGGCTAAAGGGCTTGGTGTGCTTTTCAGGTGGTGGTCC
CCCTCGAGAGTAGAGACGGAAAGGGGCACACCACCCCTGACCGTCCCCCGATTTCCCGAACCAACGAAAGTCCACCACCAAGG

2295

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20
G G G P
ENSE0000364...

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Donor Template SNV -> REV

Donor Template SNV -> REV

CTGGGGAGGTGCTGCCTACCTCCTCCGCCCAGCATGCCCCCATCGGGCTGGATAACGTGGCCACCTATGCGGGGCAGTTC

CTGGGGAGGTGCTGCCTACCTCCTCCGCCCAGCATGCCCCCATCGGGCTGGATAACGTGGCCACCTATGCGGGGCAGTTC AAC
GACCCCTCCACGACGGATGGGAGGAGGGCGGGTCTGTACGGGGGGTAGCCGACCTATTGCACCGGTGGATACGCCCCGTCAAGTTG

2380

ANXA11

ANXA11-203

W G G A A Y P P P S M P P I G L D N V A T Y A G Q F N

ENSE0003646683

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Donor Template SNV -> REV



CAGGACTATCTCTCGGGAATGGTGAGTCCAGCTCTCCTGCTGAGGCAGCCCTGGGGCCACACCTGCGTGGCCAGAGGAATCAAAG
GTCCTGATAGAGAGCCCTTACCACCTCAGGTCGAGAGGACGACTCCGTCGGGACCCCGGTGTGGACGCACCGGTCTCCTTAGTTTC

2465

ANXA11

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Q D Y L S G M

ENSE0003646683

ANXA11-203

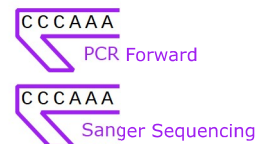
CTGCTGGCCTCTGGGGCTCCAGAGTTGTCTATGTGTGTGTTGCTGTGGTGTGTAGTGTGTTGAGCTGTACCTTAGAACAGGGTTT
GACGACCGGAGACCCCGAGGTCTCAACAGATACACACACAACGACACCACACATCACACAACCTCGACATGGAATCTTGTCCCAA

2550

ANXA11

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TCATCAGGCTTCTGCCACCTGCTCTCTGCCCTCTCTGGGTCTCACTTTTCCCATCTGTAAAATGAGGGGAAGGGGACCAGATGA
AGTAGTCCGAAGACGGTGGACGAGAGACGGGGAGAGACCCAGAGTGAAAAGGGTAGACATTTTACTCCCTTCCCCTGGTCTACT

2635

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AGTAGTCCGAAGACG

PCR Forward

AGTAGTCCGAAGACG

Sanger Sequencing

TCTCACAGGTCCCTTTCAGCCCTGAGGGGTTAGGGTTGGGAAAGTGGCGAGGGTATCTGCATGAGTGTGCATGCACGTGCTATGT
AGAGTGTCCAGGAAAGTCCGGACTCCCAATCCCAACCCTTCCACCGCTCCCATAGACGTACTCACACGTACGTGCACGATACA

2720

ANXA11

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ATGAGTATCCACATTCATATACCTGCATGTGCATGTGTGTACATATGGAGGGCTCTTCTGGTTAGGCCTTGGTGGGTGTGTGGCA
TACTCATAGGTGTAAGTATATGGACGTACACGTACACACATGTATACCTCCCGAGAAGACCAATCCGGAACCACCCACACACCGT

2805

ANXA11

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GGTATCTTGGGCAGACATGCTACTTTTTAAATTTGTTGTTTCACTTTTAAAATAATACATTTTATGATTTGAAAACAAACGTATG
CCATAGAACCCGTCTGTACGATGAAAAATTTAAACAACAAAGTGAAAAATTTATTATGTAAAAATACTAAACTTTTGTGTTGCATAC

2890

ANXA11

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CTTAGTTTATGATTTGAAAACAAACGTATGCTTAGAGGAAATTATGCAACCAATACACACCCTAATTTGTGCCAGGCCAGTTCT
GAATCAAATACTAAACTTTTGTGTTGCATACGAATCTCCTTTAATACGTTGGTTATGTGTGGGATTAACACGGTCCGGGTCAAGA

2975

ANXA11

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AGGCACTGGGGATATGTGAATAAAACAAACAAAAATCTCAGCCGTGCTGCACTTATCATCTATGGGGAAAAGACAGGCAGTACCT
TCCGTGACCCCTATACACTTATTTTGTGTTTGTGTTTGTAGAGTCGGCACGACGTGAATAGTAGATACCCCTTTTCTGTCCGTCATGGA

3060

ANXA11

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TAAGTCAACGATGTGATGTTATTGAAAAGTGTAGGTGCCATAGGAACAAGTTGACCAGGGTAAAGGGGTTCAGGAGTGGGGGTGGGG
ATTCAGTTGCTACACTACAATAACTTTTCATCCACGGTATCCTTGTTCAACTGGTCCCATTTCACCCAGTCCCTCACCCCCACCCC

3145

ANXA11

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TGATGTAAGGATAATGATTTTAAAGTTAGCAGTAAGGTGGGTCTGGCTGAAAAGAGGATGTGTGAGCAAAGACCTGCATCAGGGGA
ACTACATTCCTATTACTAAAATTCAATCGTCATTCCACCCAGACCGACTTTTCTCCTACACACTCGTTTCTGGACGTAAGTCCCCT

3230

ANXA11

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AGGAAGTGCTGTATGGATGTCTAGGGAATGCCGGTGCCCTGAGGTGCCAAGGGGTGTGAGGTGCTCAGGGACAGGGAGGAGAGGC
TCCTTCACGACATACCTACAGATCCCTTACGGCCACGGGACTCCACGGTTCCCCACACTCCACGAGTCCCTGTCCCTCCTCTCCG

3315

ANXA11

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CAGTGTGGCTAAAAGTGGAAAGGCGAGGGGGTGTAGATGGGAAATGAAGTCTGGGGGTCTAGCTCTTGCAGGGTGTAGGAGGCTATC
GTCACACCGATTTACACCTTTCCGCTCCCCCACTCTACCCTTTACTTCAGACCCCCAGATCGAGAACGTCCCACATCTCCGATAG

3400

ANXA11

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CATCCTAAGGATTTAGGTTTTTATTCTGGTGTAGTGCAGATTCACCTGAACATGCCTGCCAGAGGTGTCTGTGGGTAGCAGGCTG
GTAGGATTCCTAAATCCAAAAATAAGGACCACTCACGTCTAAGTGGACTTGTACGGACGGTCTCCACAGACACCCATCGTCCGAC

3485

ANXA11

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ATGTGATGGGGATGCCCCAACCCCTGCATATGGGACCCACGCACCTTCTTGGGCAGTGAGCTCTTAACCTTCACCCAGGTGGTCT
TACACTACCCCTACGGGGGTTGGGACGTATACCCTGGGTGCGTGGAAGAACCCGTCACCTCGAGAATTGGAAGTGGGTCCACCAGA

3570

ANXA11

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GGGATGGGAGGAGCAACCATGTGGAGAGGGAAGGCATCTCCCCTGCAGAAGGGGATGAGGATCTCTGGTTTGGATCGAGTCGCAC
CCCTACCCCTCCTCGTTGGTACACCTCTCCCTTCCGTAGAGGGGACGTCTTCCCCTACTCCTAGAGACCAAACCTAGCTCAGCGTG

3655

ANXA11

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TGTTCACTGGCTGTGTAACCTTTGAGCAAGTAAACTCATTCTGTGGTCTGTGAAATGGGTATAACGGTACTTCATATTCCACAAGC
ACAAGTGACCGACACATTGAAACTCGTTTCATTTGAGTAAGACACCAGACACTTTACCCATATTGCCATGAAGTATAAGGTGTTTCG

3740

ANXA11

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GGAGATGCTGTGAGGACTGACTTGGCTTAGGTATGAAAAAGGGTGGAGGGACGGAGTGCAGCAGGGCCCATTTGCCCTCAGGCTCT
CCTCTACGACACTCCTGACTGAACCGAATCCATACTTTTTCCACCTCCCTGCCTCACGTGCTCCGGGTAACCGGAGTCCGAGA

3825

ANXA11

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GCTTTGTGTCCTTGCAGGCGGCCAACATGTCTGGGACATTTGGAGGAGCCAACATGCCAACCTGTACCCTGGGGCCCTGGGGC
CGAAACACAGGAACGTCCGCCGGTTGTACAGACCCTGTAAACCTCCTCGGTTGTACGGGTTGGACATGGGACCCCGGGGACCCCG

3910

ANXA11

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A A N M S G T F G G A N M P N L Y P G A P G A

ENSE00002518768

ANXA11-203

TGGCTACCCACCAAGTGCCTCCCTGGCGGCTTTGGGCAGCCCCCTCTGCCAGCAGCCTGTTCCCTCCCTATGGGATGTATCCACCC
ACCGATGGGTGGTACAGGGGGACCGCCGAAACCCGTCGGGGGGAGACGGGTCGTCGGACAAGGAGGGGATACCTACATAGGTGGG

3995

ANXA11

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

ENSE00002518768

ANXA11-203

CCAGGAGGAAACCCACCTCCAGGATGCCCTCATATCCGCCATACCCAGGGGCCCTGTGCCGGGGCCAGCCATGCCACCCCCCG
GGTCTCCTTTGGGTGGGAGGTCTTACGGGAGTATAGGCGGTATGGGTCCCCGGGGACACGGCCCGGTCGGGTACGGTGGGGGGC

4080

ANXA11

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

ENSE00002518768

ANXA11-203

GACAGCAGCCCCAGGGGCTACCCTGGGCAGCCACCAAGTGACCTACCCTGGTCAGCCTCCAGTGCCACTCCCTGGGCAGCAGCA
CTGTCGTCGGGGGGTCCCCGGATGGGACCCGTCGGTGGTCACTGGATGGGACCAGTCGGAGGTCACGGTGAGGGACCCGTCGTCGT

4165

ANXA11

ANXA11-203

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

ENSE00002518768

ANXA11-203

GCCAGTGCCGAGCTACCCAGGATACCCGGGGTCTGGGACTGTCAACCCCGCTGTGCCCCCAACCCAGGTGAGTGTGAGCCCACTG
CGGTACAGGCTCGATGGGTCTTATGGGCCCCAGACCTGACAGTGGGGGGCAGACGGGGGTTGGGTCCACTCACAGTCGGGTGAC

4250

ANXA11

ANXA11-203

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

ENSE00002518768

ANXA11-203

CCTCCCTTGGTCCAGGCCTGGGCCCCAAAGGCTGGAGACACATGGCTCAGTAGATGGGGAGACAGGGAAAGGCAGGCCTCCAG
GGAGGGAACCAAGTCCGGACCCGGGGTTTCCGACCTCTGTGTACCGAGTCATCTACCCCTCTGTCCCTTTCCGCGTCCGGAGGTC

4335

ANXA11

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ANXA11-203

CTGCACTTCTTGTTTTAAACAAATAGTGTGGCCGGGTGCAGTGACTCATGCCTGTAATCCCAGCACTTTGGGAAGCTGAGGTGGG
GACGTGAAGAACAATAATTGTTTATCACAGCCGGCCACGTCAGTACGGACATTAGGGTCGTGAAACCCCTTCGACTCCACCC

4420

ANXA11

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ANXA11-203

CAGATCGCTTGAGCCAGGAGTTCAAGACCAACCTGGGCGAAATGGTGAAACCCCTATCTCTACTAAAAATAGAAAAAAATTAGC
GTCTAGCGAACTCGGGTCTCAAGTTCTGGTTGGACCCGCTTTACCACTTTGGGATAGAGATGATTTTTTATCTTTTTTTTAAATCG

4505

ANXA11

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TGGGCATGGTGGTGCATACCTGTAGGCCAGCTACTCGGGAGGCTGAGGTGGGAGGATCACCTCAGCCCAGGAGACAGAGGTTGC
ACCCGTACCACCACGTATGGACATCCGGGTCGATGAGCCCTCCGACTCCACCCTCCTAGTGGAGTCGGGTCCTCTGTCTCCAACG

4590

ANXA11

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AGTGAGCCGGGATCATGCCGCTGCACTCACTCCAGCCTAGGTGACAGAGTAAGACCCAGTTTTTAAAACAAAAACAAAAACAAA
TCACTCGGCCCTAGTACGGCGACGTGAGTGAGGTGGATCCACTGTCTCATTCTGGGTCAAAAATTTTGTTTTTGTTTTGTTTT

4675

ANXA11

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AAAGACAAACAAAGAGCGTACCTTCTTGCAGACTCCCCACCTCTGGGTTGTGTTGCTTAAGGCCCAAGGGAGCTGTCTCTGTTTC
TTTCTGTTTGTCTCGCAGTGGAAGAACGTCTGAGGGGTGGAGACCCAACACAACGAATTCGGGTTCCCTCGACAGGACAAAG

4760

ANXA11

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TCCTGGTGTGATGAGACGCTCCACATCCGAGTTGGGTCAGAACACCCCTGGCGAGTACTCCTTATTCCTCTGTGTCAATTTACTGC
AGGACCACACTACTCTGCGAGGTGTAGGCTCAACCCAGTCTTGTGGGGACCCTCATGAGGAATAAGGAGACACAGTAAATGACG

4845

ANXA11

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ANXA11-203

CTGGGCTGTGTGTTTTGTAAGAACTGCCAGGCCACCTGTCTCAAGGCTTTGTGCTCAACAGCTGTCTTCGGTCCCTTGATATGC
GACCCGACACACAAAACATTCTTGACGGGTCCGGTGGACAGAGTTCGAAACACGAGTTGTGACAGAAGCCAGGGAACTATACG

4930

ANXA11

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ANXA11-203

ACCACCCCGCCCCCCCCGGGCACAGACAGGTTTTGGAGGATTATTAATAATTCCTTTGGGTAGGGAGAATGTTGGCAGTTCCTCC
TGGTGGGGGGCGGGGGGGCCGTGTCTGTCCAAAACCTCCTAATAATTTAAGGGAAACCCATCCCTCTTACAACCGTCAAGGAGG

5015

ANXA11

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AGGGTTGATCTTGGCTCATTTTGGAGAACAGTTCGTGTTTGCAGAGCCTAGAATTCGTTGTCATGGTTCTGTGGCCCAACCAGCC
TCCCAACTAGAACCGAGTAAAACCTCTTGTCAAGCACAAACGTCTCGGATCTTAAGCAACAGTACCAAGACACCGGGTTGGTCGG

5100

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ANXA11-203

AGCACAGGGGTAGTGGTATGTGCTCAATGACTATTTTTAGACAGAGGGTCTCCTTTCCCTCCTTCCATACCCACACGTTCC
TCGTGTCCCATCACCATAACAGGAGTTACTGATAAAAAATCTGTCTCCAGAGGAAAGGAGGAAGGGAAGGTATGGGTGTGCAAGG

5185

ANXA11

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ANXA11-203

CCCACCCTGTGCCATCCTCCAGCCTCCCTCCCTTATCTTTTTCCCTGAGCTGCCCTCTTAATTGTGTTATAACCAGTTTGTACCAG
GGGTGGGACACGGTAGGAGGTTCGGAGGGAGGGAATAGAAAAGGGACTCGACGGGAGAATTAACACAATATTGGTCAAACATGGTC

5270

ANXA11

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CCCCTAGGAAGACAATCCACTGGGAGACAGTTTTAGCCTGGAAAGTTCCAGTTTGCGGGTTTGTGCAGCTATCAGGGTCTGGAGGA
GGGGATCCTTCTGTTAGGTGACCCTCTGTCAAATCGGACCTTTCAAGGTCAAACGCCCAAACACGTCGATAGTCCCAGACCTCCT

5355

ANXA11

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ANXA11-203

AGTCCGGCAGATGCTAGTCTAGAGAACAGTGCGAGGGGAACCAAGTCTAGATCAAGAGGTCATCAGGCTGCCATGCACAGTTGTGG
TCAGGCCGTCTACGATCAGATCTCTTGTACGCTCCCTTGGTACGATCTAGTTCTCCAGTAGTCCGACGGTACGTGTCAACACC

5440

ANXA11

ANXA11-203

ANXA11-203

AGGCTCAATACCTGCATCCACTGGAGGGGACACATGGGCTAGCCAGCCCTGTTAGGAGTACCCATGTGTGCTCACATGTGCTGTG
TCCGAGTTATGGACGTAGGTGACCTCCCTTGTGTACCCGATCGGTGGGACAATCCTCATGGGTACACACGAGTGTACACGACAC

5525

ANXA11

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ANXA11-203

GAGGCCAGGCATCGATGAGAGAGGCCACAGCCCCTGCTCCCGAGACCTGCCCTTCATCAGGAGCCTGAGCCCCAGCCCTGGAGGA
CTCCGGTCCGTAGCTACTCTCTCCGGTGTGCGGGACGAGGGCTCTGGACGGGAAGTAGTCTCGGACTCGGGGTGCGGGACCTCCT

5610

ANXA11

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ANXA11-203

CCTGGGCACTGGGCAGATTTTCAGCATCAGGACTCAGCTATAGGTGAGCTCCCAGCCACTGGAGCCAGGAAAAAGCTTCAGTACT
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5695

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ANXA11-203

AGAACACAAGGCCAGATAACAGTCAAGTTAGGTAGACGCGGGCGTAAAGTCTCTGCATTGTTGACTGTGGACTCCTTTAGATACT
TCTTGTGTTCCGGTCTATTGTCAGTTCAATCCATCTGCGCCGCATTTTCAGGAGACGTAACAACCTGACACCTGAGGAAATCTATGA

5780

ANXA11

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ANXA11-203

CCAACTCTTAGAGAAAGGGCTGTTCCAGAGTCTAGGGGTGGAGCAGCCTTGAATGTGGGGAAGGCGGCATGCACGACATCTTAC
GGTTGAGAATCTCTTTCCCGACAAGGGTCTCAGATCCCCACCTCGTCGGAACCTTACACCCCTTCCGCCGTACGTGCTGTAGAATG

5865

ANXA11

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ANXA11-203

CTGAGACTGTTTGTCCGAGTAGTTTGGAAAGCCGAGGCACCATCACTGATGCTCCCGGCTTTGACCCCTGCGAGATGCCGAGGTC
GACTCTGACAAACAGGCTCATCAAACCTTCGGCTCCGTGGTAGTGACTACGAGGGCCGAAACTGGGGGACGCTCTACGGCTCCAG

5950

ANXA11

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F G S R G T I T D A P G F D P L R D A E V
ENSE00003585307

ANXA11-203

CTGCGGAAGGCCATGAAAGGCTTCGGTAAGAGACCCTGGGTGGCTCAAATCCTACTCCCTGCCCCCTATTTCCAGGCAGTTTCA
GACGCCTTCGGTACTTTCCGAAGCCATTCTCTGGGACCCACCGAGTTTAGGATGAGGGGACGGGGGATAAAGGGTCCGTCAAAAGT

6035

ANXA11

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L R K A M K G F
ENSE00003585307

ANXA11-203

CTGTGGCTCTGTGGGCTGGGGTAGCTGGGGGACGCTGACCTGGCCCCAGTGGTGATAGAAGGTGGATGTGGGGGTATGGCTAGCA
GACACCGAGACACCCGACCCCATCGACCCCTGCGACTGGACCGGGGTCACCACTATCTTCCACCTACACCCCATACCGATCGT

6120

ANXA11

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ANXA11-203

TGCCCAGAACAGTTGAGGGGCCAGGCCAGGGAAGTCTCAGCTGCAGAGCATCTCATGACCCCTACCCGACCCACCCCTGCTGCC
ACGGGTCTTGTCAACTCCCCGGGTCCGGTCCCTTCAGAGTCGACGTCTCGTAGAGTACTGGGGATGGGCTGGGTGGGGACGACGG

6205

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ANXA11-203

TCTTCTCCAGGGACGGATGAGCAGGCCATCATTGACTGCCTGGGGAGTCGCTCCAACAAGCAGCGGCAGCAGATCCTACTTTCC
AGAAGGAGGTCCCTGCCTACTCGTCCGGTAGTAACTGACGGACCCCTCAGCGAGGTTGTTTCGTCGCCGTCGTCTAGGATGAAAGG

6290

ANXA11

ANXA11-203

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

ANXA11-203

TTC AAGACGGCTTACGGCAAGGCGAGCTGCGGGGTGGGGGCGCGGGACAGTGAGGGCGTGTCTCTGGGCTCAGCACAGCCCTGCTCT
AAGTTCTGCGGAATGCCGTTCCGCTCGACGCCCCACCCCGCGCCCTGTCACTCCGCACAGGACCCGAGTCGTGTCTGGGACGAGA

6375

ANXA11

ANXA11-203

245
F K T A Y G K
ENSE00002509632

ANXA11-203

CCCCTGCTTTTCTTGGGTGGGCCCGGATCTCCCGGATGGACAGTAAGGAGCAGGAGGGCATTTCCTTCTGCCCATCCAGCTGGT
GGGGACGAAAAGGAACCCACCCGGGCTAGAGGGCCTACCTGTCAATTCTCGTCTCCCGTAAAGGAAGACGGGTAGGTCGACCA

6460

ANXA11

ANXA11-203

ANXA11-203

GGCATCGTTGGGAGGTGAAGGATGCCACCGGGTGCTGAGGTTTGTGAGAGGCTCCAGACATCTATCCCTGGGTTCTAGCCCTTG
CCGTAGCAACCCTCCACTTCTACGGTGGCCACGACTCCAACGACTCTCCGAGGTCTGTAGATAGGGACCCAAGATCGGGAAC

6545

ANXA11

ANXA11-203

ANXA11-203

CTCTGCCACATCTCACTGAGGTTGTGGCCACATCATTTTCTTCCCTGCCCTCTTCATGACCACCCTGGGGGGTTTAGCTGATG
GAGACGGTGTAGAGTGACTCCAACACCGGTGTAGTAAAAGGAAGGGGACGGGAGAAGTACTGGTGGGACCCCCAAATCGACTAC

6630

ANXA11

ANXA11-203

ANXA11-203

TAAGAGCTTTGCAAGGAAAGGCTGTGAGTGCTGCCAAGTACGAGGGGCGTGTATGAGCATATTTTGAACCTTCTGGGGTTTTGAA
ATTCTCGAAACGTCCCTTTCCGACACTCACGACGGGTTTCATGCTCCCGCACATACTCGTATAAACTTGAAGACCCCAAACTT

6715

ANXA11

ANXA11-203

ANXA11-203

TCTTAGAAAAGATAAAAATTCGGTAAATATTGATTAGATTCGTGTTCTAGCCCAGTGCTTCTCAAACCTTCATTGTGTCACCGATCC
AGAATCTTTCTATTTTAAAGCCATTTATACTAATCTAAGCACAAAGATCGGGTCACGAAGAGTTTGAAGTAACACAGTGGCTAGG

6800

ANXA11

ANXA11-203

ANXA11-203

CCTGGGCATCTTGGTAAATGTGGTCTCTGATTTGGGAGGTTTGGGGCAGGGCTGAGAGCAGGCTTTTCTCTCAGGCCCTGGGG
GGACCCGTAGAACCATTTTACACCAGAGACTAAACCTCCAACCCCGTCCCGACTCTCGTCCGAAAAGAGAGTCCGGGGACCCC

6885

ANXA11

ANXA11-203

ANXA11-203

GATGTCCATGCTGCTGTTTCCTCAAATCTGGGATATGGCTCTTATTAGTCACTTCCTGTGGATTTTTTAAATAGACTTGTTTTTTTT
CTACAGGTACGACGACAAGGAGTTTAGACCCATACCGAGAATAATCAGTGAAGGACACCTAAAAAATTTATCTGAACAAAAAAA

6970

ANXA11

ANXA11-203

ANXA11-203

TTTTGTTGGTTGTTTGAATATCCAATCAGGATTTGATCAAAGATCTGAAATCTGAACTGTCAGGAACTTTGAGAAGACAA
AAAAACAACCAACAAACAAACTTATAGGTTAGTCCTAAACTAGTTTCTAGACTTTAGACTTGACAGTCCTTTGAAACTCTTCTGTT

7055

ANXA11

ANXA11-203

250 255 260 265
D L I K D L K S E L S G N F E K T
ENSE00002494992

ANXA11-203

TCTTGGCTCTGATGAAGACCCAGTCCTCTTTGACATTTATGAGATAAAGGAAGCCATCAAGGTGTGTACGTGTGTGTGTGTG
AGAACCAGACTACTTCTGGGGTCAGGAGAACTGTAATACTCTATTTCTTCGGTAGTTCCACACATGCACACACACACACAC

7140

ANXA11

ANXA11-203

270 275 280 285
I L A L M K T P V L F D I Y E I K E A I K
ENSE00002494992

ANXA11-203

TGTGTGTGTGTGTGTGTGCGCGCGTGTGTGCGCACGCGCGCATGCGTGTGGACACACAGCCAGAAAGGAGGCCTGGATGGCGTGC
ACACACACACACACACGCGCGCACACACGCGTGTGCGCGGTACGCACACCTGTGTGTGCGGGTCTTCTCCGGACCTACCGCACG

7225

ANXA11

ANXA11-203

ANXA11-203

TGTGTTCTAGCCCACTCATTAGCTGCTGTTGTCAGTATGGCTCCCAGGCCTTCTGGGTTGGAGTCCACATGCTATAGAAAAGGG
ACACAAGATCGGGTGAGTAATCGACGACAACAGTCATACCGAGGGTCCGGAAGGACCCAACCTCAGGTGTACGATATCTTTTCCC

7310

ANXA11

ANXA11-203

ANXA11-203

AACTCCCTGTGATTTCCCAAGAGGGCAAATGACGCACCAAGTCATCATCAGGGAGGGCTTAAGTCTCTCTCCATCTTAAAGAAAAGG
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7395

ANXA11

ANXA11-203

ANXA11-203

GGGAGCTCGGGTTTGAAGGTTGCGATTCTGTGGTAAGAAGAGGGGTAGGAGGCCATGGTTGGTATCGTTCTCATTCTTTAGGACT
CCCTCGAGCCCAAACTTCCAACGCTAAGACACCATTCTTCTCCCATCTCCGGTACCAACCATAGCAAGAGTAAGAAATCCTGA

7480

ANXA11

ANXA11-203

ANXA11-203

CTGTTACTAGCAAATGACAGAAACACACTTCGGTTTAAAGAACAACAAAAGTGGAGAATCAGTCATGTGGGTAAAGAGGGGCCAGG
GACAATGATCGTTTACTGTCTTTGTGTGAAGCCAAATTCTTGTGTGTTTTACCTCTTAGTCAGTACACCCATTTCTCCCGGGTCC

7565

ANXA11

ANXA11-203

ANXA11-203

CCAGACGTCTCTCTGGTCTCTGTCTCTCCTGAGCGCCCGCTTTTCTGTTCAGTTTCTGTGCTTCTCCTACCATGGCTGCTTCATGT
GGTCTGCAGAGAGACCAGAGACAGAGAGGACTCGCGGGCGAAAAGACAGTCAAAGACACGAAGAGGATGGTACCGACGAAGTACA

7650

ANXA11

ANXA11-203

ANXA11-203

GGGGTGGGAGAGGGGGCCTGTCGACCACTCTCCGCATAACTATGAGACCCAGCTCCAGAAGAGACCAGCAGGGTCTCCAAACGGG
CCCCACCCTCTCCCCCGGACAGCTGGTGAGAGGCGTATTGATACTCTGGGTCGAGGTCTTCTCTGGTCGTCCCAGAGGTTTGCC

7735

ANXA11

ANXA11-203

ANXA11-203

CAGGTTCTGACGGGCCCCGGCTTGGACTCACTGTTCCCTCCAGTCCTGCGGGTTTTGACTGAGGGTTGGGTCCTGTCCATTCTGTG
GTCCAAGACTGCCCGGGCCGAACCTGAGTGACAAGGGAGGTCAGGACGCCCAAACCTGACTCCCAACCCAGGACAGGTAAGACAC

7820

ANXA11

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ANXA11-203

CAGTCCCACAGCTCTGTGTGCACCCTGCAGGCAGGGGCGAGGCAGCTCCCTTGGAAAAGGGAATCCCATGAGTCAGGCTGGAGCCCA
GTCAGGGTGTGCGAGACACACGTGGGACGTCCGTCCCCGTCCGTGAGGGGAACCTTTCCCTTAGGGTACTCAGTCCGACCTCGGGT

7905

ANXA11

ANXA11-203

ANXA11-203

GAAGGAGCCTGTCACTCAGAGGCCTGATAAGCACAGTGAATGTTCCCTCCTTCAGGAGAAGCAGAGACTTCAGTGTGGTGGCCTG
CTTCCTCGGACAGTGAGTCTCCGGACTATTTCGTGTCACTTACAAGGGAGGAAGTCCTCTTCGTCTCTGAAGTCACACCACCGGAC

7990

ANXA11

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ANXA11-203

GAAAGGAGAGGGGTCTCCGCTGAAACACATCTACATGTGTTATTCTAGGGAGGGGGTTCAGGAGGCCATCAGGCAGGGCGATGGCC
CTTTCCTCTCCCCAGAGGCGACTTTGTGTAGATGTACACAATAAGATCCCTCCCCAGTCTCCGGTAGTCCGTCCCGCTACCGG

8075

ANXA11

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CGGGGCCCCAGGGAGTGGACCCAGACATCTCCCTGGCCCCCGTCTTCAGCCGGAGTCATGAGCTGGTGGTTGTGGAGTGTTAGAA
GCCCCGGGGTCCCTCACCTGGGTCTGTAGAGGGACCGGGGGCAGAAGTCGGCCTCAGTACTCGACCACCAACACCTCACAATCTT

8160

ANXA11

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ANXA11-203

ACCACACAGGTTTTGGGGCAGCTGTCACTCACCAGCTGTGTGTCCTTGAGCACCTGTGAAATGGGGACAGTGGATGCTGTCTCAGG
TGGTGTGTCCAAACCCCGTCGACAGTGAGTGGTCGACACACAGGAACCTCGTGGACACTTTACCCCTGTACCTACGACAGAGTCC

8245

ANXA11

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ACATGCTGGGAATACTGGGTGAGGGGCTAACGTGTAGTAACCCAAATAGTAGCTGTAGCAGGAAACAGCTGACACAATGTGCGCACG
TGTACGACCCTTATGACCCACTCCCCGATTGCACATCATTGGGTTATCATCGACATCGTCTTTGTGCGACTGTGTTACAGCGTGC

8330

ANXA11

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TCCTGCCTGACAGGCCCTAAGTGCTCTACGTACATTAACCTCACTTAATCCTCATGACTTTCCTGTGAGGTAGGTCCTAGTATCAC
AGGACGGACTGTCCGGGATTACGAGATGCATGTAATTGAGTGAATTAGGAGTACTGAAAGGACACTCCATCCAGGATCATAGTG

8415

ANXA11

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TCCATCTTACAGACAAGGAACTGGAAGCACAGAGAGGTTAAGTAATGTGCCCGAGGTCACACAGCTGGTAAGCTGCAGAGCCAG
AGGGTAGAATGTCTGTTCCCTTGACCTTCGTGTCTCTCCAATTCATTACACGGGCTCCAGTGTGTGCGACCATTGACGCTCTCGGTC

8500

ANXA11

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GATTCAAACCAACATACAAGCCAGGCTGCCAGCCTGTCTCTATGGTCTTACTGTCCCTGGCGTGGTTGTCCGATTCATCCTTG
CTAAGTTTGGTTGTATGTTCCGGTCCGACGGGTCGGACAGGAGATACCAGAATGACAGGGACCGCACCAACAGGCTAAGTAGGAAC

8585

ANXA11

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TTGTTCCCTACCTTTTCCTAGTTGTTTTTCAGACATTCCACCATCCCCTCTAGGACCAGGGTTTTCGTATGTCCACTTGGATCTCTCT
AACAAAGGATGGAAAAGGATCAACAAAAGTCTGTAAGGTGGTAGGGGAGATCCTGGTCCCAAAGCATAACAGGTGAACCTAGAGAGA

8670

ANXA11

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TGCTTTTACCCATTTTTTTCAGTTGTTGTCATCTCGCTTCCGGCTGAACTCTGAATAAAGCAGGCCTCGGTCCACATTTTAACC
ACGAAAAATGGGTAAAAAAGTCAACAACAGTAGAGCGAAGGCCGACTTGAGACTTATTTTCGTCCGGAGCCAGGTGTAAATTGG

8755

ANXA11

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CAACCATTTACTGTGTGGCCTCGGACCAGCCAGTACCCCTCTCTGATGCTCAGTTTTCTGATCCATGGGGATGCCCTTTGTGTG
GTTGGTAAATGACACACCGGAGCCTGGTCGGTCATGGGGAGAGACTACGAGTCAAAAAGACTAGGTACCCCTACGGGGAAACACAC

8840

ANXA11

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AGCCCTACTCATCACCCTGCCACTGTCATTGTGCTTGCCCGGGCTGTGGAGAAGAGCTGATGCCCTCGAGCCTGGGAGTGGCTG
TCGGGATGAGTAGTGGTGACGGTGACAGTAACACGAACGGGCCCGACACCTCTTCTCGACTACGGGAGCTCGGACCCTCACCGAC

8925

ANXA11

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GAGGGTGTGTCTCTGTGTCAGGGGCCTCTGTTGCTGGGATTAAGGCAGCAGCGTAGCCCCACCCCTTCTTCCCGAGTGCTGGTGA
CTCCACACAGAGACACAGTCCCCGGAGACAACGACCCTAATTCCGTCGTCGCATCGGGGGTGGGAAGAAGGGCTCACGACCACT

9010

ANXA11

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GGCTGCTGGAACAAGCACATGGTTGGTTGTATTCTCTGCCCTGCAGGGGGTTGGCACTGATGAAGCCTGCCTGATTGAGATCCT
CCGACGACCTTGTTCGTGTACCAACCAACATAAGAGACGGGGACGTCCCCAACCGTGACTACTTCGGACGGACTAACTCTAGGA

9095

ANXA11

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G V G T D E A C L I E I L
ENSE00002448092

ANXA11-203

CGCTTCCCGCAGCAATGAGCACATCCGAGAATTAACAGAGCCTACAAAGCAGGTGAGGCCGCTCCCTCTGCCCTCTGCCCTCTG
GCGAAGGGCGTCGTTACTCGTGTAGGCTCTTAATTTGTCTCGGATGTTTCGTCCACTCCGGCGAGGGAGACGGGAGACGGGAGAC

9180

ANXA11

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A S R S N E H I R E L N R A Y K A

ENSE00002448092

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CCCTCTGCAGATCCCTGTGCTCTTGGGGCTGTGGCCTCATTCTCTCCTAGGGCCTTTTACTCCTTCTGTCCTTCTTATCAACCC
GGGAGACGTCTAGGGACACGAGAACCCGACACCGGAGTAAGAGAGGATCCCGAAAAATGAGGAAGGACCGGAAGAATAGTTGGG

9265

ANXA11

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ATCTTCTGCCACCCCAATACTTTGGGCTTTGACCCAAGACCCAGCCCTTCTTCTGTTTATACATGGTGCAAATGACTAATGTA
TAGAAGACGGTGGGGGTTATGAAACCCGAAACTGGGTTCTGGGTGCGGAAGGAAGACAAATATGTACCACGTTTACTGATTACAT

9350

ANXA11

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AGGGAGAGGCAGGGAAAACCTGGATGTGGTTTTGGGCCAAGGCTGACTAGAGGCCAGGTCAGCCTGGAGGTCACAGGCTTGTATAT
TCCCTCTCCGTCCCTTTTGGACCTACACCAAACCCGGTTCGACTGATCTCCGGTCCAGTCGGACCTCCAGTGTCCGAACATATA

9435

ANXA11

ANXA11-203

ANXA11-203

CCCTGGAGGGCCATATGGGCTATTTGTTCTCTTGAGCCCCGAGCCAAGACCTCCAGCCTTTTTCTCCCCAGTACCCACTTTTGATA
GGGACCTCCCGGTATACCCGATAAACAAGAGAAGCTCGGGCTCGGTTCTGGAGGTCGGAAAAAGAGGGGTCATGGGTGAAAACATAT

9520

ANXA11

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GTGTTTTGCAATGGGCAGCTCCATAAAGAGAGCTACAGGATGGACCTTCCTTGCTTCTCCCTTTCAGAATTCAAAAAGACCCTGG
CACAAAACGTTACCCGTCGAGGTATTTCTCTCGATGTCTACCTGGAAGGAACGAAGAGGGAAAGTCTTAAGTTTTTCTGGGACC

9605

ANXA11

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E F K K T L
ENSE00002460881

AAGAGGCCATTGGAAGCGACACATCAGGGCACTTCCAGCGGCTCCTCATCTCTCTCTCAGGTACTTTTCCCACGACAGGGCTC
TTCTCCGGTAAGCTTCGCTGTGTAGTCCCGTGAAGGTCGCCGAGGAGTAGAGAGAGAGAGTCCATGAAAAGGGTGCTGTCCCGAG

9690

ANXA11

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E E A I R S D T S G H F Q R L L I S L S Q
ENSE00002460881

GGGGCCCCAAGCCATGGAAGTCAAAGAGATGGGATCCCCGCAATGAGGAAAGGGAAAAATAAATGGGGAAGGAGTGGGCATGACC
CCCCGGGGGTTCCGGTACCTTCAGTTTCTTACCCTAGGGGCGTTACTCCTTTCCCTTTTATTTACCCCTTCCCTCACCCGTA

9775

ANXA11

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ATACACCTGCTTCCTTTTCAGGGAAACCGTGATGAAAGCACAAACGTGGACATGTCACTCGCCCAGAGAGATGCCCAGGTGAGTGT
TATGTGGACGAAGGAAAAGTCCCTTTGGCACTACTTTCGTGTTTGCACCTGTACAGTGAGCGGGTCTCTCTACGGGTCCACTCACA

9860

ANXA11

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G N R D E S T N V D M S L A Q R D A Q
ENSE00002521933

GATGGCCAAGCCCCTGGACTTCCTAAAGCAGGGATGCACCCCGCTTTCTTGCTTCCTGAGAGAGGTACCCTAGGGTGGAAAGAAC
CTACCGGTTTCGGGGACCTGAAGGATTTTCGTCCCTACGTGGGGCGAAAGAACGAAGGACTCTCTCCATGGGATCCCACCTTTCTTG

9945

ANXA11

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AATAGATAAGCAGTGGGTTGCAGATGCTGTGAGTTTCAGACGCGCTGAACTGTTCAACTGTATGACCTAGAACAGGTAATCTGAC
TTATCTATTCGTCACCCAACGTCTACGACACTCAAAGTCTGCGCGACTTGACAAGTTGACATACTGGATCTTGTCCATTAGACTG

10,030

ANXA11

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CTCCAGGGCTTCAGCTTCCCCACCTATAGGAGGGGAACATGTGAGATAATTAGTATTTTCGATAGTTGATAGATCATGGTTTTGGAC
GAGGTCCCGAAGTCGAAGGGGTGGATATCCTCCCTTGTACACTCTATTAATCATAAAGCTATCAACTATCTAGTACCAAAACCTG

10,115

ANXA11

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GTGGGATTTTGTGTGACAGCGTACTTTCCCATGTTTAGTTGCACATAGCATTATGTTTGC AAAGGGGCAAAATTTGCACTTGCT
CACCC TAAAACACACTGTCGCATGAAAGGGGTACAAATCAACGTGTATCGTAATACAAACGTTTCCCGTTTTAAACGTGAACGA

10,200

ANXA11

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TATTAAGTTTTTGGAGGATTTGAGCCTAGAAACCAGCTGCCACATTAGTTGAGCACCCCTTAGAATTCTGTCGTTGTCCCTCTTG
ATAATTCAAAACACTCCTAAACTCGGATCTTTGGTCGACGGTGTAAATCAACTCGTGGGAATCTTAAGACAGCAACAGGGGAGAACAC

10,285

ANXA11

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AGTTGCAGACAAAAGGGGAAAAGTCCAAGCAAAGTCCAGGCATCTGAGCTACTCTCTCGAAAAGTTTTGGGTTTTCCCACTAATGAA
TCAACGTCTGTTTTCCCTTTTCAGGTTTCGTTTCAGGTCCGTAGACTCGATGAGAGAGCTTTTCAAACCCAAAGGGTGATTACTT

10,370

ANXA11

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TTTCAACCGTAGTATTATGGCAGGGCAGAGCCATTACTTCCTGGTGGGGTGGAGTTGGCCATACCTCTCTGTCTCCCTTCACTGC
AAAGTTGGCATCATAATACCGTCCCGTCTCGGTAATGAAGGACCACCCACCTCAACCGGTATGGAGAGACAGAGGGAAGTGACG

10,455

ANXA11

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TCTTGTTCATCCACGGCAGGGCATTACCCAGGAGCTGCCAGTGGTCTAAATTATCTCTACCATCTGCGGGATTGGAATGAGACCTC
AGAACAGTAGGTGCCGTCCCGTAAGTGGTCTCTCGACGGTACCAGATTTAATAGAGATGGTAGACGCCCTAACCTTACTCTGGAG

10,540

ANXA11

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AAGGAATGCCCCCTTGTAGGGCTGGAGGAGAGCTACTCCTCTGGTCTGGTCTCTTTTGGTGGTCTCCTTTTCCGGAGGAGGAAA
TTCCTTACGGGGGAACAATCCCGACCTCCTCTCGATGAGGAGACCAGACCAGGAAAAACGACCAGGAGGAAAAAGGCCTCCTCCTTT

10,625

ANXA11

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CTGAGGCTCAAAAAGGTTGAGCACTGTTCCCAACTGAAAGCTAGAAGCAGAGCCCCGGACAAGGGCCTATACTCCTGGCTCGGTCT
GACTCCGAGTTTTTCCAACCTCGTGACAAGGGTTGACTTTCGATCTTCGTCTCGGGCCTGTTCCCGGATATGAGGACCGAGCCAGA

10,710

ANXA11

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TCTGTGCCCAGTCAGCACTTGCCTCTGCCCTGGTCTCAGACCTGCTGCTCCTGCAGGGTCTGCCTTATTCAGTGTCTCTCTGGCT
AGACACGGGTCAGTCGTGAACGGAGACGGGACCAGAGTCTGGACGACGAGGACGTCCAGACGGAATAAGTCACAGAGAGACCGA

10,795

ANXA11

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GGTAACATCCATTCCATTCTGGGAGTCAGGGCTGGACACGCCTGGGGCTCAGGGCTCTGGCTTTTGGCTCCAGCGAGAGTTTTGC
CCATTGTAGGTAAGGGTAAGACCCTCAGTCCCGACCTGTGCGGACCCCGAGTCCCAGACCGAAAACGAGGTCGCTCTCAAAACG

10,880

ANXA11

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ATGCCACTTTTAGCGGGGCAAAAATTGTCTCATGCTCTGCCTTCTCAGTCCAGAGCTGCTTTGGCCTCATCTTGACCTGTGGGAT
TACGGTGAAAATCGCCCCGTTTTTAACAGAGTACGAGACGGAAGAGTCAGGTCTCGACGAAACCGGAGTAGAACTGGACACCCTA

10,965

ANXA11

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CTCAGCCCCTGATTGCTGCTTTCTGCTCTTTTTTCAGGGCTGCTACCTGAGGCCTAGCAGGCACTTTAGAGGCCATCTAGTTCAGA
GAGTCGGGGACTAACGACGAAAGACGAGAAAAAGTCCCGACGATGGACTCCGGATCGTCCGTGAAATCTCCGGTAGATCAAGTCT

11,050

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GGTTGCAAATTTGGCAAATACTTTAGGCTCAAACCTTCAGAAGTTTACCAGGCTCTCCTGGGTGACCTGGGCCTGGGGTCTGGGTG
CCAACGTTTTAACCGTTTTATGAAATCCGAGTTTGGAAAGTCTTCAAATGGTCCGAGAGGACCCACTGGACCCGGACCCAGACCCAC

11,135

ANXA11

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TGGCCTGTGCCACATGTGCGTCTTCTCTCTCTCCAGGAGCTGTATGCGGCCGGGGAGAACCAGCCTGGGAACAGACGAGTCCAAG
ACCGGACACGGTGTACACGCAGAAAGGAGAGAGAGGTCCTCGACATACGCCGGCCCTCTTGGCGGACCCCTTGTCTGCTCAGGTTTC

11,220

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E L Y A A G E N R L G T D E S K
ENSE00000909279

ANXA11-203

TTCAATGCGGTTCTGTGCTCCCGGAGCCGGGCCACCTGGTAGCAGGTAAGGCAGGCTGGGGTCCCTCAGAGGCCAGTTAGATGA
AAGTTACGCCAAGACACGAGGGCCTCGGCCCGGGTGGACCATCGTCCATTCCGTCCGACCCAGGGAGTCTCCGGTCAATCTACT

11,305

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F N A V L C S R S R A H L V A
ENSE00000909279

ANXA11-203

GGGCAGTCAGGGGATTGTGGGGAAACAAAGCTATGGGAACACTTGGTTCGTTCTCCCTGCGTGGGGCTTTTCGCCTCCTCAAAAAGA
CCCGTCAGTCCCTAACACCCCTTTGTTTTGATACCTTGTGAACCAGCAAGGAGGGACGCACCCCGAAAGCGGAGGAGTTTTCT

11,390

ANXA11

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GCCCCCTGGTGGGAATTTAAAAGACACTGTCAGAGGGTTTCTGAGTTCTGGCAAACATCCAGTTCTGGAGGTTCTACCGGTGTA
CGGGGGACCACCCTTAAATTTCTGTGACAGTCTCCCAAAGGACTCAAGACCGTTTGTAGGTCAAGACCTCCAAGATGGCCACAT

11,475

ANXA11

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GAAACCTGGTGTCTTTGTACGTGGGAATGTGGAACGTGAGAGTTGGGAGGGTCTTCGGGAGCACCCAATCCAGTGTTTTCCAAA
CTTTGGACCACAGAAACATGCACCCTTACACCTTGCAGTCTCAACCCTCCCAGGAAGCCCTCGTGGGTTAGGTACAAAAAGGTTT

11,560

ANXA11

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GCCTGGCATAAGAAACAGTCATAACAATAAACTGGGTGCCATTCACTTACTCATTCAATCAACAGATGTAAATCGCGCTCCCGC
CGGACCGTATTCTTTGTGAGTATTGTTATTTGACCCACGGTAAGTAAATGAGTAAGTAAGTTGTCTACATTTAGCGCGAGGGCG

11,645

ANXA11

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ATGGGTCAGTCTGTTCAGGTGGTGGAGCAGGTGTGGGGCCACGGTGGGGGGCAGGGCACTGCAGAGTGTGTTCCATGGGCTGCACT
TACCCAGTCAGACAGTCCACCACCTCGTCCACACCCCCGGTGCCACCCCCCGTCCCCTGACGTCTCACACAAGGTACCCGACGTGA

11,730

ANXA11

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TTCTCATTTGGGGAGACAGACAGTAAACAACAATGAAATAAAATCTGTATCAGATGGGAAATCCTGTAGAGGAAAATCAAGCTGG
AAGAGTAAACCCCTCTGTCTGTTCATTTGTTGTTACTTTATTTTAGACATAGTCTACCCTTTAGGACATCTCCTTTTAGTTTCGACC

11,815

ANXA11

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ANXA11-203

AAACAGGTAGGGAGTGATGGTAGGGTCCACCAGGAGGTGCTTGGGCCAGTCCCCACTGAGGTCGTGACATTTGATTTAAAAACCT
TTTGTCCATCCCTCACTACCATCCCAGGTGGCCCTCCACGAACCCGGTCAGGGGTGACTCCAGCACTGTAAACTAAATTTTTGGA

11,900

ANXA11

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ANXA11-203

AAAGGGAGATGCAGGGGCAGAGGCCTGCCTGGGGCTCCCAGCACGACTGAGAACAGTGAAGGGGGACCATGTGGAGCAGGTGGAG
TTTCCCTCTACGTCCCCGTCTCCGGACGGACCCCGAGGGTCTGTCTGACTCTTGTCACTTCCCCCTGGTACACCTCGTCCACCTC

11,985

ANXA11

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TGAGCAAGAGGAGTGGGAGGTGAGGGCAGAGAGGGGAGAGGGCCCTGCTGATGACTTCCCGGAGCTGGGTATTTATCCTGAGCAA
ACTCGTTCTCCTCACCTCCACTCCCGTCTCTCCCTCTCCCGGGACGACTACTGAAGGGCCTCGACCCATAAATAGGACTCGTT

12,070

ANXA11

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AAGAGGAAGCCAGTGGAGGGCCCTGAGCAGAGGAGGCTGTGCAGAATCCCTGGCTGTGGTGCCGAGAATGGAGTGAAGGGTGCAA
TTCTCCTTCGGTCACTCCCGGGACTCGTCTCCTCCGACACGTCTTAGGGACCGACACCACGGCTCTTACCTCACTTCCCACGTT

12,155

ANXA11

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GGCCAAGCAGCGAAGCCTGTCGGGAGGCTGCTGCAGGGACCCGGGGAGGAATGGTGGTAATAGGGGCTTGTGGTGAGGAGGTGTC
CCGGTTCGTGCTTCGGACAGCCCTCCGACGACGTCCCTGGGCCCTCCTTACCACATTATCCCCGAACACCACTCCTCCACAG

12,240

ANXA11

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AGGTTCCGGCCATGTTTGGCTGATGAATTGGACACGTGACGTGTGGGAGAGAGAGGGTTTCGAGGATTATACAGGGTTTCTTTAGGC
TCCAAGGCCGGTACAAACGACTACTTAACCTGTGCACTGCACACCCTCTCTCTCCCAAGCTCCTAATATGTCCCAAAGAAATCCG

12,325

ANXA11

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CAAGCAGTGGGAGAATGGCCCTCAACTGAGACAGGGGGACTGTAGGTGGAGCTGGCTTTAGGTGCCTGTAGGGTGGAGCTGCAGG
GTTCGTCACCCTCTTACCGGGAGTTGACTCTGTCCCCCTGACATCCACCTCGACCGAAATCCACGGACATCCCACCTCGACGTCC

12,410

ANXA11

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GAGGCTGCTGGGTTGCTGAGTGTGGAGGTCAGGAGAGGTCTGGCCTGGTTGTGGAAGGTAAGGGAGCTATGGGTAGTTGAAGTTA
CTCCGACGACCCAACGACTCACACCTCCAGTCTCTCCAGACCGGACCAACACCTTCCATTCCCTCGATACCCATCAACTTCAAT

12,495

ANXA11

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TCTGAGGCTCTGGGACTGCAGGAGGTTCCCTCAGGAGGGAGACTGTGGGGAGCCACCGGTGTGAGGAGACTAAGAAGGAGCAGC
AGACTCCGAGACCCTGACGTCTCCAGGGGAGTCTCCCTCTGACACCCCTCGGGTGGCCACACTCCTCTGATTCTTCTCGTCCG

12,580

ANXA11

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TAGGGAGGGAGGAGGACGCAGAGGAAGGGGGTCTGGAGGCCAGTGTGAGGTGGCAGGCAAGGACTGAGGATGGTGACCACACGG
ATCCCTCCCTCCTCCTGCGTCTCCTTCCCCCAGGACCTCCGGTCACTCCACCGTCCGTTCCCTGACTCCTACCACTGGTGTGCC

12,665

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AGCAACTGGTGGGCTGTGGCCAGGGCTGCTCCAGTGGGCAGTGAGGGTGAAAACCCAGCGACCGCTCTGTGCTGCACACAGAGAC
TCGTTGACCACCCGACACCGGTCCCAGAGGTCACCCGTCCTCCACTTTTGGGTCGCTGGCGAGACACGACGTGTGTCTCTG

12,750

ANXA11

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ANXA11-203

AGGCGCTGTGGCTCTCCCCATTTCGCAGCTGTGAAAGCAGGCACAGGGTGGTAGAGGAAGTAGGGGTGCACAGCTAGTAACAGCTG
TCCGCGACACCGAGAGGGGTAAGCGTCGACACTTTCGTCCGTGTCCACCATCTCCTTCATCCCCACGTGTGATCATTGTGCGAC

12,835

ANXA11

ANXA11-203

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AGCTGGGATTTGAACCCAGACCACCCGACCCAGAGCACACTTTTTAACCTCTGCACTATCCTGTAATGGAGCCTGAGTGAAAAGC
TCGACCCCTAAACTTGGGTCTGGTGGGCTGGGGTCTCGTGTGAAAAATTGGAGACGTGATAGGACATTACCTCGGACTCACTTTTCG

12,920

ANXA11

ANXA11-203

ANXA11-203

ATTTTCATCTTAATCATTATTTCTTTTAATGAGTACAGAACATGTAAGTAGTGCATCAAGCCCATGGCTTCACAAACATTATTAC
TAAAAGTAGAATTAGTAATAAAGAAAATTACTCATGTCTTGTACATTCATCACGTAGTTCGGGTACCGAAGTGTTTGTAAATAATG

13,005

ANXA11

ANXA11-203

ANXA11-203

TTAGGAGAAAAGAGTAGCTGATTGGAAGAAGATATTAATTGAGACAGATACACACAGAGCAGAAAATCACAACTTTAAAATGCAAA
AATCCTCTTTTCTCATCGACTAACCTTCTTCTATAATTAACCTCTGTCTATGTGTGTCTCGTCTTTAGTGTTGAAAATTTTACGTTT

13,090

ANXA11

ANXA11-203

ANXA11-203

TGGTAGCTGAGACTCAGGCTGGGGAAGGAGAGTTTTATGTCTGGGTGAGAACTGGAGTCAGGACCAAGGTCTCCATCATGCCAC
ACCATCGACTCTGAGTCCGACCCCTTCTCTCAAATACAGGACCCAGTCTTGACCTCAGTCTCGGTTCCAGAGGTAGTACGGTG

13,175

ANXA11

ANXA11-203

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CTGTCTCTCTAGGAGCCAGCCATCCACTCCTGTGGGTGCTTAGCGTGTCTTAGGTCGAGGTGAGCAGCAAGAAGCCAGGCTGGCT
GACAGAGAGATCCTCGGTCGGTAGGTTGAGGACACCCACGAATCGCACAGGATCCAGCTCCACTCGTCTGTTCTTCGGTCCGACCGA

13,260

ANXA11

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GGGGCAGGCTGGGCCTCAGCTCACAGGCAGGCTGAGGAAGACAGATGGATGCATGAATAAAGCCAAGGAATGGCAGAGACTGGAG
CCCCGTCCGACCCGGAGTCGAGTGTCCGTCCGACTCCTTCTGTCTACCTACGTACTTATTTTCGGTTCCTTACCGTCTCTGACCTC

13,345

ANXA11

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GTGTGGAGGATTTGAGAAGAGGGGACACTGTCTTGGAGTACATGGGAGTGGGCCCTGGAGGGGTATTAAGGTGCGATTTGGTTAA
CACACCTCCTAAACTCTTCTCCCCTGTGACAGAACCTCATGTACCCTCACCCGGGACCTCCCATAATTCCACGCTAAACCAATT

13,430

ANXA11

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GCAGATTGGCAGTCTCTGAGAAAAGGGACCACACAGGGAGGGGACATCAGGTGGTGCATGTAACCTTGTGACGAAGACTCTGACTTCCT
CGTCTAACCGTCAAGGACTCTTTCCCTGGTGTGTCCCTCCCTGTAGTCCACCACGTACATTGAACACTGCTTCTGAGACTGAAGGA

13,515

ANXA11

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TGAGCGCTAGCAGGCCTGGGGACGTGCAGGGTGTGGGAGCAGAGTGGCAGGTGGGAGATTTTGGGGCAGAGGCCACCTCATGTGA
ACTCGCGATCGTCCGGACCCCTGCACGTCCCACACCCTCGTCTCACCGTCCACCCTCTAAAACCCCGTCTCCGGTGGAGTACACT

13,600

ANXA11

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GTCCTCTGTTAGTCTGCTCATGCTGCCATGACAAAATACCACAGACTGGGTGGCTTAAGCAGCAGATACTCATTTTGTACAGTT
CAGGAGACAATCAGACGAGTACGACGGTACTGTTTTATGGTGTCTGACCCACCGAATTCGTCTATGAGTAAAACAATGTCAA

13,685

ANXA11

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TTGAAGGCCAGATATCCAAGAGTGGGGTGCCGGTTTCTCCCGTGGCCTCTTCGTGACAATCACTGTGCTCACATGGTCTTTCCCTC
AACTTCCGGTCTATAGGTTCTCACCCACGGCCAAAGAGGGCACCGGAGAAGCACTGTTAGTGACACGAGTGTACCAGAAAGGAG

13,770

ANXA11

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TGCATGTGCACATCCCTGGGATCTCTGTGTGTGTCCTAATCTTCTCTTCTTAAGGAGACCAGGCGAATTGGATTAGGGTACAC
ACGTACACGTGTAGGGACCCCTAGAGACACACACAGGATTAGAAGAGAAGAAGATTCCTCTGGTCCGCTTAACCTAATCCCATGTG

13,855

ANXA11

ANXA11-203

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CCTAGCAGCATGTTTTAACTTAATTACCTCTTTAAAGATCTTATCTCCAACACGGTTATATTCTGAAGTCCTGGGAGTTGGGAC
GGATCGTCTGTACAAAATTGAATTAATGGAGAAATTTCTAGAATAGAGGTTTGTGCCAATATAAGACTTCAGGACCCTCAACCCTG

13,940

ANXA11

ANXA11-203

ANXA11-203

TTCCACATATGAACTTTGGGGAGACACATTTAGTTCATAATATAAGCCTCTGTCATCCCCATAGTTTTCAATGAGTACCAGAGA
AAGGTGTATACTTGAAACCCCTCTGTGTAAAGTCAAGTATTATATTCGGAGACAGTAGGGGTATCAAAGTTACTCATGGTCTCT

14,025

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ATGACAGGCCCGGGACATTGAGAAGAGCATCTGCCGGGAGATGTCCGGGGACCTGGAGGAGGGCATGCTGGCCGTGGGTAAAGTGTCT
TACTGTCCGGCCCTGTAACCTCTTCTCGTAGACGGCCCTCTACAGGCCCTGGACCTCCTCCCCTACGACCGGCACCCATTACAG

14,110

ANXA11

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

ENSE00000909278

ANXA11-203

TCAGGTTTGGCCGCCACCTGCCAGGGGCTAACGTGTATCGTGAGTGTTCAGGCTGCTCGCCTGTCTCCAGCTGATGGGTGACAC
AGTCCAAACGGCGGGTGGACGGTCCCCGATTGCACATAGCACTACAAGTCCGACGAGCGGACAGGAGGTCGACTACCCACTGTG

14,195

ANXA11

ANXA11-203

ANXA11-203

CGTGAAGGGACCACAGGATCCAAGATCGCTCAGCCCAGAGTGTCCAGATGCTGGGAAGTCATGCTGCTTCCCGGTTCCCTGTGCA
GCACTTCCCTGGTGTCTTAGGTTCTAGCGAGTCGGGTCTCACAGGTCTACGACCCCTTCAGTACGACGAAGGGCCAAGGGACACGT

14,280

ANXA11

ANXA11-203

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GTTGAACCCCTAGCTGTCTGGAGGTGTCTTGTGTGTGTTTGGGGTGCAGCTCTGGAGTAGGGAAGTGCAGTGTGGGTATTAGTG
CAACTTGGGGATCGACAGGACCTCCACAGAACACACACAAACGCCACGTGAGACCTCATCCCTTGACGTACACCCATAATCAC

14,365

ANXA11

ANXA11-203

ANXA11-203

GGAGGGCATCCAACCTGCGCTCCCGGAGGAGTATGACTCATATCCTGCCACGTTTCTCTAAAAATACATCCCTGCAGGCAGTTGT
CCTCCCCTAGGTTGACGCGAGGGCCCTCCTCATACTGAGTATAGGACGGTGCAAAGGAGATTTTTATGTAGGGACGTCCGTCAACA

14,450

ANXA11

ANXA11-203

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CAGATGTTTGTGATGGAAACACGTGGAAAGATTTTTACTTGCAGCAGCGAAACAGGCCCATGCTGAGGAAAGCTGGCTTGGCTCC
GTCTACAAACACTACCTTTGTGCACCTTTCTAAAAATGAACGTCGTCGCTTTGTCCGGGTACGACTCCTTTTCGACCGAACCAGG

14,535

ANXA11

ANXA11-203

ANXA11-203

AGGATGGTGGTGTGCCTCTTACATTGCCCATGTCTCTAGCAGGGCCCTCCCACTGTGCAGAGTTGGGTCCCTGCCCTGAGGCC
TCTACCACCACACGGAGAATGTAACGGGTACAGGAGATCGTCCCGGGAGGGTGACACGTCTCAACCCAGGGACGGGACTCCGGG

14,620

ANXA11

ANXA11-203

ANXA11-203

TCACAACCCCTCTTTCTACTCACTTGGGAAAATCAGTCTGCCCTTTTTTTCATTATGCTTTTTTTGGAGCTTTCTGGATGGGAGA
AGTGTGGGGGAGAAAAGATGAGTGAACCCTTTTAGTCAGACGGGGAAAAAAGTAATACGAAAAAACCTCGAAAGACCTACCCTCT

14,705

ANXA11

ANXA11-203

ANXA11-203

GATGGAAAATCCTCATTTCCTGCCTGTCCCCATAGTAGGTCTCATGGCCTGGGAAGCCTAGGGAGATGCACATTCCACTCAGC
CTACCTTTTAGGAGTAAAGGGACGGACAGGGGGTATCATCCAGAGTACCGGACCCTTCGGATCCCTCTACGTGTAAGGTGAGTCG

14,790

ANXA11

ANXA11-203

ANXA11-203

CACGGTTTCTCCATGACGGTCATGGCCTCTCCAGTCTGCCCTCCTGCCTGAGCAGCAGCACAGTTCTCATCACCATCCACATT
GTGCCAAAGAGGTACTGCCAGTACCGGAGAGGTCAGACGGGGAGGACGGACTCGTCGTCGTGCAAGGAGTAGTGGTAGGTGTAA

14,875

ANXA11

ANXA11-203

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GCTTCCTGTGTAGCTCCTAGCCCCACTAAGACCCCCGCCCTCTGACTCTTGGTCCTTTCACCGCAGTGGTTGCCAGGAAAGAG
CGAAGGGACACATCGAGGATCGGGGTGATTCTGGGGGCGGGGAGACTGAGAACCAGGAAAGTGGCGTCAACCAACGGTCTTTCTC

14,960

ANXA11

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GGTGGGTTGGTTTCCAGGCTTTGCGTGTCTGTTCCAAATAGCTGGAGCCAAGATCATGGGATAGTTGAGCCTGGAACAGAAGG
CCACCCAACCAAAGGTCCGAAACGCACAAAGACAAGGTTTATCGACCTCGGTTCTAGTACCCTATCAACTCGGACCTTGTCTTCC

15,045

ANXA11

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ANXA11-203

AGGAGGAGAAAAGATGGATGCAGTGATGGGTTTGACATCTGGGCCTCTAAGAGGACACTTGTAGACTCCATGCCCTGCTTGGGCT
TCCTCCTCTTTTCTACCTACGTCACTACCCAAACTGTAGACCCGGAGATTCTCCTGTGAACATCTGAGGTACGGGACGAACCCGA

15,130

ANXA11

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GAGAATTTTCTGCAGATCTGGTTATGCCGAGTTTCTCTCTTCTAGTGAAATGTCTCAAGAATACCCCAGCCTTCTTTGCGGAGAG
CTCTTAAAAGACGTCTAGACCAATACGGCTCAAAGAGAGAAGATCACTTTACAGAGTTCTTATGGGGTCGGAAGAAACGCCTCTC

15,215

ANXA11

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V K C L K N T P A F F A E R
ENSE00000909277

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GCTCAACAAGGCCATGAGGGTATGTAACCTCCATGTGCAGGTTGCGATGGAACCTTAGCCTCGCCTGTGCCTGGGACCAAGGGCT
CGAGTTGTTCCGGTACTCCCATACATTGAAGGTACACGTCCAACGCTACCTTGAATCGGAGCGGACACGGACCTTGGTTCCCGA

15,300

ANXA11

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440 445
L N K A M R

ENSE00000909277

ANXA11-203

GAGGGCAGAAGGCCTGGGGAGAGCTAAATCTCAGCTGAGAGTTCCGAGGACCTGGGTAGGGAGGGGACTGGAGGGCCAGGGCAG
CTCCCGTCTTCCGGACCCCTCTCGATTTAGAGTTCGACTCTCAAGGCTCCTGGACCCATCCCTCCCTGACCTCCC66GTCCCGTC

15,385

ANXA11

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GTGGGAAGGTGAGGAGGCCTGGTGCTCATGCTCTTGGGTGGACTCTCTTTAGGGGGCAGGAACAAAGGACCGGACCTGATTTCGC
CACCTTCCACTCCTCCGGACCACGAGTACGAGAACCACCTGAGAGAAATCCCCCGTCTTGTTCCTGGCCTGGGACTAAGCG

15,470

ANXA11

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450 455
G A G T K D R T L I R
ENSE00000909276

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ATCATGGTGTCTCGCAGCGAGACCGACCTCCTGGACATCAGATCAGAGTATAAGCGGATGTACGGCAAGTCGCTGTACCACGACA
TAGTACCACAGAGCGTCGCTCTGGCTGGAGGACCTGTAGTCTAGTCTCATATTCGCCTACATGCCGTTTCAGCGACATGGTGTCTGT

15,555

ANXA11

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

ENSE00000909276

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TCTCGGTACGGCCTGCTGCAGGCCAACTGGGCTCCCTTTTGGCATCTCAGTCACCTGTGGAACCTCCCTCCTTGGAGTGGCCAT
AGAGCCATGCCCGGACGACGTCCGGTTGACCCGAGGGAAAACCGTAGAGTCACTGGACACCTTGGAGGGAGGAACCTCACCGGTA

15,640

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ATGCTTGGCCTCTGTGCTGTGTGTGGGCATCTTGATTATGGACCTCGGACTTGTTCATCCCCTTGCCTTAAACAGATTATAAAT
TACGAACCGGAGACACGACACACCCGTAAGACTAATACCTGGAGCCTGAACAAGTAGGGGAACGGGAATTTGTCTAATATTTA

15,725

ANXA11

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TTCTGAGGGCAGGTGGATCATGACCTTGCTGTCGCCCCACCTTGCATCCCCAGCAGCATCAGAGAACAACCTCGGGACCTCCCCA
AAGACTCCCCTCCACCTAGTACTGGAACGACAGCGGGGGTGAACGTAGGGGGTTCGTCGTAGTCTCTTGTGAGCCCTGGAGGGGT

15,810

ANXA11

ANXA11-203

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ACCTTGACCGTGACCTTCAGCGTTCCGATCACCGTGTGATTCTTGATCTGTTCAGTGAGAACTCATGTCCCAAAGGCTCTGTGGA
TGGAACTGGCACTGGAAGTCGCAAGGCTAGTGGCACACTAAGGAACTAGACAGTCACTCTTGAGTACAGGGTTTCCGAGACACCT

15,895

ANXA11

ANXA11-203

ANXA11-203

GCTCTGCTGTCACTCCCTGACAAAGCACTTCCTGCACTCAGCTTTATGGCGTAGGCCACATAGTAAGGCCGTTTCAGAGCGAGGGC
CGAGACGACAGTGAGGGACTGTTTCGTGAAGGACGTGAGTCGAAATACCGCATCCGGTGTATCATTCCGGCAAGTCTCGCTCCCG

15,980

ANXA11

ANXA11-203

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CCTGGGGGTACGCCACTTGGAGTCCAGCTTTTCTACTTGCTAACTGTGTGACCTTGAATGGCTCCCTTAAATCTCCCTGAACCC
GGACCCCCAGTGCGGTGAACCTCAGGTCGAAAAGATGAACGATTGACACACTGGAACCTTACCGAGGGAATTTAGAGGGACTTGGG

16,065

ANXA11

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CAGCTCCATTGTCTTTAAGATGAGAAAATAATCGTTCCCTTCCCTGGGAATGTTGTGAGTATTGAGTGAGGCAGTGCAGGTCAAGTG
GTCGAGGTAACAGAAATTCTACTCTTTTATTAGCAAGGAAGGACCTTACAACACTCATAACTCACTCCGTCAAGTCCAGTTCAC

16,150

ANXA11

ANXA11-203

ANXA11-203

TCTATTAACACTAGCCACAGTTGTATCGCTGTGTGGCAGAGCCAGTCTGACAAAATACATTCTCAGCTGTGTGGTCTAACGCTC
AGATAATTTGTGATCGGTGTCAACATAGCGACACACCGTCTCGGTCAAGTCTGTTTTATGTAAGAGTCGACACACCAGATTGCGAG

16,235

ANXA11

ANXA11-203

ANXA11-203

AAATTCTGAACTCACATGAGCCTTGCAATTGCACCATGGGGACCACGTCCTCCCACCTTAGACTCAGTAGCATTGATGATGGTG
TTTAAGACTTGAGTGTACTCGGAACGTTAACGTGGTACCCTGGTGCAGGAGGGTGGAACTCTGAGTCATCGTAAACTACTACCAC

16,320

ANXA11

ANXA11-203

ANXA11-203

GGCATGTCATCACAGGAAACTCACTGTGTTTTCTTGGCTGTATGAATGAAGCTGTTGTTAGAGAATTAGTGATTCTAGGCTGGGC
CCGTACAGTAGTGTCTTTGAGTGACACAAAGGAACCGACATACTTACTTCGACAACAATCTCTTAATCACTAAGATCCGACCCG

16,405

ANXA11

ANXA11-203

ANXA11-203

ACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGGCTGAGGCAGGTGGATCATTGAGGTCAGGAGTTTCGAGACCAGCCTGG
TGTCAACCGAGTGC GGACATTAGGGTTCGTGAAACCTCCGACTCCGTCCACCTAGTAAACTCCAGTCTCTCAAGCTCTGGTTCGGACC

16,490

ANXA11

ANXA11-203

ANXA11-203

CCAACAAGGTAAAACCTGTCTCTACTAAAAATACAAAATTAGCTGGGCTTGCCTGTAATCCCAGCTAATTAGGTAGGCTGCGGC
GGTTGTTCCATTTTGGGACAGAGATGATTTTTATGTTTTAATCGACCCGAACGGACATTAGGGTTCGATTAATCCATCCGACGCCG

16,575

ANXA11

ANXA11-203

ANXA11-203

AGGAGAATTGCTTGAACCCGGGAGACAGAGGTTGCAGTGAGCTGGGATCACGCCATTCCACTTCAGTCTTGGTGACAGAGTGAGA
TCCTCTTAACGAACTTGGGCCCTCTGTCTCCAACGTCCTCGACCCAGTGC GGTAAGGTGAAGTCAGAACCCTGTCTCACTCT

16,660

ANXA11

ANXA11-203

ANXA11-203

CTTCGTCTCAAAAAAAAAAAGAGAGTTAATAATTCATTACAGAGTATCTCCTGCATGCCAGCAAGCTATGGACATCTGGAAGAAG
GAAGCAGAGTTTTTTTTTCTCTCAATTATTAAGTAATGTCTCATAGAGGACGTACGGTTCGATACCTGTAGACCTTCTTC

16,745

ANXA11

ANXA11-203

ANXA11-203

CCACATGCCTTGCCCTCAAGTTGCTTAGGGTGGAAAGGAAATGATTAGAAATGAGCCAAGCCGAGCCTGCACTCTTAGAGTAAGTG
GGTGTACGGAACGGGAGTTCAACGAATCCACCTTCCTTTACTAATCTTTACTCGGTTCCGGCTCGGACGTGAGAATCTCATTAC

16,830

ANXA11

ANXA11-203

ANXA11-203

TAGTGGCCTCAGACAGAGGAGAGATCCCTGGGACCTGGGCAGTCTGAGCCTTCCACTGGACAGTCATGTGTGAGGAGATTGCATT
ATCACC GGAGTCTGTCTCCTCTTAGGGACCTGGACCCGTCAGACTCGGAAGGTGACCTGTCAGTACACACTCCTCTAACGTAA

16,915

ANXA11

ANXA11-203

ANXA11-203

TCCTGAGCAGGACACTGTGTTGCGTTACATTGGTAACCCCAATTTAAGGCAGCATAAATGCACTGGGAAAACAGCAATATTGGTT
AGGACTCGTCTGTGACACAACGCAATGTAACCATTGGGGTTAAATTCCGTTCGTATTTACGTGACCCTTTTGTTCGTTATAACCAA

17,000

ANXA11

ANXA11-203

ANXA11-203

AGCCCTGGGAAGTGGTTTTTTAGGATGATTATAATTTTTTTTTTGTGGGTATTCATTTGATGTGGATAGCTGGGGTGAAGTGCTGCTT
TCGGGACCCCTTACCAAAAAATCCTACTAATATTAAAAAAAAAAACCCATAAGTAAACTACACCTATCGACCCCACTCACGACGAA

17,085

ANXA11

ANXA11-203

ANXA11-203

TCCGTCTTCTGATGGGGGCCTGGAGAAGGCTGAACTGCATTTTTTAAGGTCTGTGACGCCTGCTGCAGGACCTGCAGTGGGAGAA
AGGCAGAAGACTACCCCGGACCTCTTCCGACTTGACGTAATAAATCCAGACACTGCGGACGACGTCTTGGACGTCACCCTCTT

17,170

ANXA11

ANXA11-203

ANXA11-203

AATTCCCAGGGTGGGGCTTTCTCCCTATAAGGGTGTCTAGGGCTGAATATCAGGACCCAGAAGGCTGAAAGTGAAGTGTCCCTCC
TTAAGGGGTCCACCCCGAAAGAGGGATATTCCACGAGTCCCGACTTATAGTCTGGGTCTTCCGACTTTCACTGACAGGGAGG

17,255

ANXA11

ANXA11-203

ANXA11-203

CTTAACGGATGTCTTCTTCTTCTGTGGCCAGGGAGATACTTCAGGGGATTACCGGAAGATTCTGCTGAAGATCTGTGGTGGCA
GAATTGCCTACAGAAGGAACAAAGACACCGGTCCCTCTATGAAGTCCCTAATGGCTTCTAAGACGACTTCTAGACACCACCGT

17,340

ANXA11

ANXA11-203

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ANXA11-203

ATGACTGAACAGTGAAGTGGTGGCTCACTTCTGCCACCTGCCGGCAACACCAAGTGCCAGGAAAAAGGCCAAAAGAATGTCTGTTTC
TACTGACTTGTCACTGACCACCGAGTGAAGACGGGTGGACGGCGTTGTGGTCACGGTCTTTTCCGGTTTTCTTACAGACAAAG

17,425

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TAACAAATCCACAAATAGCCCCGAGATTCACCGTCTAGAGCTTAGGCCTGTCTTCCACCCCTCTGACCCGTATAGTGTGCCAC
ATTGTTTAGGTGTTTATCGGGGCTCTAAGTGGCAGGATCTCGAATCCGGACAGAAGGTGGGGAGGACTGGGCATATCACACGGTG

17,510

ANXA11

ANXA11-203

AGGACCTGGGTCTGGTCTAGAACTCTCTCAGGATGCCTTTTTCTACCCCATCCCTCACAGCCTCTTGCTGCTAAAATAGATGTTTCA
TCCTGGACCCAGCCAGATCTTGAGAGAGTCTTACGGAAAAAGATGGGGTAGGGAGTGTCTGGAGAACGACGATTTTATCTACAAAAGT

17,595

ANXA11

ANXA11-203

TTTTTCTGACTCATGCAATCATTCCCTTTGCCTGTGGCTAAGACTTGGCTTCATTTTCGTCATGTAATTGTATATTTTTATTTGG
AAAAAGACTGAGTACGTTAGTAAGGGGAAACGGACACCGATTCTGAACCGAAGTAAAGCAGTACATTAACATATAAAAAATAAAC

17,680

ANXA11

ANXA11-203

AGGCATATTTTCTTTTCTTACAGTCATTGCCAGACAGAGGCATACAAGTCTGTTTGTCTGCATACACATTTCTGGTGAGGGCGACT
TCCGTATAAAAAGAAAAGAATGTCAGTAACGGTCTGTCTCCGTATGTTTCAGACAAAACGACGTATGTGTAAGACCCTCCCGCTGA

17,765

ANXA11

ANXA11-203

GGGTGGGTGAAGCACCGTGTCTCGCTGAGGAGAGAAAAGGGAGGCGTGCCTGAGAAGGTAGCCTGTGCATCTGGTGAGTGTGTCA
CCCACCCACTTCGTGGCACAGGAGCGACTCCTCTCTTTCCCTCCGCACGGACTCTTCCATCGGACACGTAGACCCTCACACAGT

17,850

ANXA11

ANXA11-203

CGAGCTTTGTTACTGCCAACTCACTCCTTTTTAGAAAAACAACAAAAAAGGGCCAGAAAAGTCATTCTTCCATCTTCCCTTGCA
GCTCGAAACAATGACGGTTTGAGTGAGGAAAAATCTTTTTTGTTTTTTTTTTCCCGGTCTTTCAGTAAGGAAGGTAGAAGGAACGT

17,935

ANXA11

ANXA11-203

GAAACCACGAGAACAAGCCAGTTCCTGTCAAGTGCAGGGCTTCTTGTAAATTTGTGGTATGTGCCTTAAACCTGAATGTCTGTA
CTTTGGTGTCTTTGTTTCGGTCAAGGGACAGTCACTGTCCCGAAGAACATTAACACCATACACGGAATTTGGACTTACAGACAT

18,020

ANXA11

ANXA11-203

GCCAAAACCTGTTTCCACATTAAGAGTCAGCCAGCTCTGGAATGGTCTGGAATGTCTTCTGGTACCAACTTGTTTTCTTCTGC
CGGTTTTGAACAAAAGGTGTAATTCTCAGTCGGTTCGAGACCTTACCAGACCTTTACAGAAGGACCATGGTTGAACAAAAGAAGACG

18,105

ANXA11

ANXA11-203

TTGATTCTGCCCTGTGGCTCAGAGGTCTGGCCTTATCAGCCAGTGAAAGTTCATGTAACCTTACGTAGAGATTTGTGTGCAGGAA
AACTAAGACGGGACACCGAGTCTCCAGACCGGAATAGTCGGTCACTTTCAAGTACATTGGAATGCATCTCTAAACACACGTCTTT

18,190

ANXA11

ANXA11-203

ACCCTGAGCATACACTAGTTTGCAGGGACTCGTAAGGACATGGGAAGGGAGGTTCCCGAAATCCAGGCAGGAGGCCAGACACCT
TGGGACTCGTATGTGATCAAACGTCCCTGAGCATTCTGTACCCTTCCCTCCAAGGGCTTTAGGTCCGTCTCCGGGTCTGTGGA

18,275

ANXA11

ANXA11-203

GAAAGGCAAAGGGATCTTGGTTGGTTGCAGGTGCAGTGAAGTCCACTGAAGGTGTGGTGCGAAGAATGCAGTCCTTACCCAGGT
CTTTCCGTTTCCCTAGAACCAACCAACGTCCACGTCACTTCAGGTGACTTCCACACCACGCTTCTTACGTACAGGAAGTGGGTCCA

18,360

ANXA11

ANXA11-203

CCCAGGAGGGAAGAAGGGTGTGTGCTAATTCCTGGTGCCCTCGGCAGGGGGCCAGAGAGAAGGATGGGGACAACCCAGAGAGTCA
GGGTCTCTCCCTTCTTCCACACACGATTAAGGACCACGGGGAGCCGCCCCCGGTCTCTCTTCTTACCCTGTTGGGTCTCTCAGT

18,445

ANXA11

ANXA11-203

CAAGACCAGTGCCTCCCTCAGGGTGCCTCCAGGCTGAAAGGGGCTCCTGGCTCTGGTCTCTGGGGACCCTGTGCCCGTTGGTTG
GTTCTGGTACGGAGGGGAGTCCACGGAGGTCCGACTTTCCCGAGGACCGAGACCAGAGACCCCTGGGACACGGGGCAACCAAC

18,530

ANXA11

ANXA11-203

GTGGTGTGAGGGGAAGAGAATCCATAAGAGAGTCTTCTGAGAATTATGGTGTGCATGTCCAGAAGCTAGAGCTTACCTTGCATCAGGG
CACCACACTCCCTTCTCTTAGGTATTCTCTCAAAGACTCTTAATACCACAGTACAGGTCTTCGATCTCGAATGGAACGTAGTCCC

18,615

ANXA11

ANXA11-203

GTCTCCACCCACTCCTTTTCCAACCTCCTGCGTTGAGGTTTGTAGAAAAGAGAGAATCGACTAGGCACTATGGCTCACGCCTGTAAT
CAGAGGTGGGTGAGGAAAAGGTTGGAGGACGCAACTCCAAATCTTTTCTCTCTTAGCTGATCCGTGATACCGAGTGCGGACATTA

18,700

ANXA11

ANXA11-203

CCAAGGACTTTGGGAAGCTGAGGTGAGAGGATCACTTGAGCTCAGGAGTTCAAGACTAGCCTAGCCAACAGCGAGACCCCTGTCT
GGTTCCTGAAACCCTTCGACTCCACTCTCCTAGTGAACCTCGAGTCTCAAGTTCTGATCGGATCGGTTGTCGCTCTGGGGACAGA

18,785

ANXA11

ANXA11-203

CTACTAAAAAATTTGGCCAGGCGTGGTGGCTCACGGCTGTAATCCCAGCACTTTGGGAGGTGAGGCGGGCAGATCACCTGAGGTC
GATGATTTTTTAAACCAGGTCGACACCAGAGTCCGACATTAGGGTCGTGAAACCCTCCACTCCGCCCGTCTAGTGGACTCCAG

18,870

ANXA11

ANXA11-203

AGGAGTTCGAGACCCAGCCTGGCCAACATGGTGAAACCCATCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGGCACATT
TCCTCAAGCTCTGGGTCGGACCGGTTGTACCACTTTGGGGTAGAGATGATTTTTTATGTTTTTAATCGGTCCGTACCACCGTGTA

18,955

ANXA11

ANXA11-203

CCTGTAATCCCAGCTACACAGGATGCTGAGGCAGGAGAATCACTTGAACCCAGGAGGCAGAGGTTGTAGTGAGCTGAGATCACAC
GGACATTAGGGTCGATGTGTCTACGACTCCGTCTCTTAGTGAACCTGGGTCCTCCGTCTCCAACATCACTCGACTCTAGTGTG

19,040

ANXA11

ANXA11-203

CATTGCACTTCAACCTGGGTGGACAGAGTGAGACTCTGTCTCAAAAAAAAAAAAAAAAAATTTACCTGGCATTGTAGTGCATTCCCTA
GTAACGTGAAGTTGGACCCACCTGTCTCACTCTGAGACAGAGTTTTTTTTTTTTTAAATGGACCGTAACATCACGTAAGGGAT

19,125

ANXA11

ANXA11-203

TAGTCGGCTACTCTGGAGGCTGAGGCAGGAAGATCCTTAGAGCCCAAGAAATTGAGGCCGTAGTAAGCTGTGATTACACCACTGC
ATCAGCCGATGAGACCTCCGACTCCGTCTTCTAGGAATCTCGGGTCTTTAACTCCGGCATCATTGACACTAATGTGGTGACG

19,210

ANXA11

ANXA11-203

ACTCCAGCCTGGACAACAGAGCGAGACCTTGTCTCAAATGAGAAAAAAAAACAAAAAGAAATGGGAGAATCCAGAGAGACTAGGCTA
TGAGGTCGGACCTGTTGTCTCGCTCTGGAACAGAGTTACTCTTTTTTTGTTTTTCTTTACCCTCTTAGGTCTCTCTGATCCGAT

19,295

ANXA11

ANXA11-203

GATCAAGCCTGCTGGGTCCTGGCAGGAGCCCCAGGGAGTAGCTCATCTGCAGACATTTGCTTGAGGACTACCCCTAAACATAAA
CTAGTTCGGACGACCCAGGACCGTCTCGGGTCCCTCATCGAGTAGACGTCTGTAAACGAACTCCTGATGGGGGATTTGTATTT

19,380

ANXA11

ANXA11-203

GGAAGAATGACATCCGAAGGGTGTGGAGCAGCCATGAGCTGAGAAGCTAGCCTGGTCTACCTGAGATTGATGGCAGGTCTCTGGTCA
CCTTCTTACTGTAGGCTTCCACACCTCGTCGGTACTCGACTCTTGATCGGACCAGATGGACTCTAACTACCGTCCAGGACCAAGT

19,465

ANXA11

ANXA11-203

ACACGTCAGCTCTGCGTCAGAGTCCATGCCTCAAGCCCAAGCTGAAGCCCCATCCCTGCTGCTCTCCCAAGAACTCCTCTGCTAG
TGTGCAGTCGAGACGCAGTCTCAGGTACGGAGTTCGGGTTTCGACTTCGGGGTAGGGACGACGAGAGGGTTCTTGAGGAGACGATC

19,550

ANXA11

ANXA11-203

GGCAGGCCCTTGCCCTTGGGTGCCAGGTGGGACCTGCCTGATGGGATGGGGTGCTTGGCATATACAACCTTGCCATGAACTCAAG
CCGTCCGGGGAACGGGAACCCACGGTCCACCCTGGACGGACTACCCTACCCACGAACCGTATATGTTGAACGGTACTTGAGTTTC

19,635

ANXA11

ANXA11-203

GTGACCCTGGGGGCCTCCTGAATTGTGATGGGGCCTAGAACCAATGTGCTCTGATGTGACCATATTCTGTGACATTACCTTGCCC
CACTGGGACCCCCGGAGGACTTAACACTACCCCGGATCTTGGTTACACGAGACTACACTGGTATAAGACACTGTAATGGAACGGG

19,720

ANXA11

ANXA11-203

TGTTTACTCCAAAAGTTCAGCCTGGTGCCAGCAGGCAATATTGCACCTACAGACACATTTACTTTGGTTTCCAAAAGTGTTTTT
ACAAATGAGGTTTTCAAGGGTCGGACCACGGGTTCGTCGGTTATAACGTGGATGTCTGTGTAATGAAACCAAAGTTTTACAAAAA

19,805

ANXA11

ANXA11-203

AGACATTTGAATTTGTTGCCAACATTTAAACATTGAGAGATTTTCATATTTTTAAAAATCTGGAATTTCTGGCTTCTCTTGAAA
TCTGTAAACTTAAACAACGGTTGTAATTTGTAACCTCTCTAAAGTATAAAAAATTTTTAGACCTTAAGACCGAAGAGAAGCTTTTGA

19,890

ANXA11

ANXA11-203

CAGAAATCTGGCACTATGGGGCTTGCATTCCCTGCATGGCTGGAGCTGAGTTGCAGCTGCCCTTTAGGCCTGTACTCCTTATTT
GTCTTTAAGACCGTGATACCCGAACGTAAGGACGTACCGACCTCGACTCAACGTGACGGGGAAATCCGGACATGAGGAATAAA

19,975

ANXA11

ANXA11-203

GCTATAGGCTCCGTCTTGTATTACACTAAGCCCATGTCACCCATTTGGCTCCTGCAGGCCTTTGGGTTTGGAGACCCTGGTCTACA
CGATATCCGAGGCAGAACATAATGTGATTTCGGGTACAGTGGGTAACCGAGGACGTCCGGAAACCCAAACTCTGGGACCAGATGT

20,060

ANXA11

ANXA11-203

CACTTGGAGACCACCTGTTGTAAGTACATGGATGTGCTTTGGTCAAGGAATAGACCAAGGTGGATATCCAGGCCAGAGTGACTC
GTGAACCTCTGGTGGACAACATTTTCATGTACCTACACGAAACAGTTCCCTTATCTGGTTCCACCTATAGGTCCGGTCTCACTGAG

20,145

ANXA11

ANXA11-203

AGCGAGTTTGGTTCACAGGCGTATACTCCACTTGTATATAACCTGCTTGTGTAAGTTTCATACTTGGCTCAAAGCCACTATTGTT
TCGCTCAAATCCAGTGTCCGCATATGAGGTGAACAATATATTGGACGAACACATTCAAGTATGAACCGAGTTTCGGTGATAACAA

20,230

ANXA11

ANXA11-203

TGGAAAAGGTATAACTGCCCTGCTGACGCTGTACAGATGTTCTTGGGCTCGGATGGGCATGGCTCCACGTGGTGTGCACTAGCAC
ACCTTTTCCATATTGACGGGACGACTGCGACATGTCTACAAGAACCCGAGCCTACCCGTACCGAGGTGCACCACACGTGATCGTG

20,315

ANXA11

ANXA11-203

CCAGAGAGAGTGAAGCTATTGACCCCTGTAAGGGAGAGTGACCATCTGGCAGATAGATAGAGGGGAGCCAGGACATGGCTCAGCT
GGTCTCTCTCACTTCGATAACTGGGGACATTCCCTCTCACTGGTAGACCGTCTATCTATCTCCCCTCGGTCTGTACCGAGTCTCGA

20,400

ANXA11

ANXA11-203

TGTGCCCCAGAGGGAGAGTTAAGCCGCTGACCCTGTAGCCAGGGAGTGACCTGCAAGCATGGGGGTGGCAGGAGCCACAGAGCTG
ACACGGGTCTCCCTCTCAATTCGGCGACTGGGACATCGGTCCCTCACGTGGACGTTTCGTACCCCCACCGTCTCTCGGTGTCTCGAC

20,485

ANXA11

ANXA11-203

GCTGCTGAGAGGAGCTGCAGATCTGGAGAAGACAGCCTAGGTAAAGGTGGACAGTGTGAGAGCTGCTGATGAGATAGCTGCTGAA
CGACGACTCTCCTCGACGTCTAGACCTCTTCTGTCTGGATCCATTTCCACCTGTACACTCTCTGACGACTACTCTATCGACGACTT

20,570

ANXA11

ANXA11-203

TAAAACACTACATTTTACCTGCCTATGGCCCGCCAGGTTTTCTTTCAAGTATCGCCCATCCACCCAGTCCCCTCGAACCTCAGCATG
ATTTTGTATGTAATAATGGACGGATACCGGGCGGTCCAAAAGAAAGTCGATAGCGGGTAGGTGGGTGAGGGGAGCTTGGAGTCTGATC

20,655

ANXA11

ANXA11-203

GGCTGGAACCTGACCCTGGGCATGACATTTGGCATAGTTGTGGACCTGACACCTGTGTTTGTCTAGTCTCTTTCTCCCTGCCT
CCGACCTTGGACTGGGACCCGTAAGTAAACCGTATCAACACCTGGACTGTGGACACAAACAGGATCAGGACAAAGAGGGACGGA

20,740

ANXA11

ANXA11-203

TCCTGTTCTCTCGCTGCCCTCATGGTCACTCCCAAGAGATCCAACCCATGTTAAGTATGGGCTGGAGGACTGCATGAATGCCTC
AGGACAAGGAGAGCGACGGGAGTACCAGTGAGGGTTCTCTAGGTTGGGTACAATTCATACCCGACCTCCTGACGTACTTACGGAG

20,825

ANXA11

ANXA11-203

ATGATCTTCCCAGAGGCAAAGGCACCTACTGCCTTCCAAGGTGAGTGGGAGGTTGGGATCAACACTGTTTATTATGCTTAGGACA
TACTAGAAGGGTCTCCGTTTCCGTGGATGACGGAAGGTTCCAGTCAACCTCCAACCTAGTTGTGACAAATAATACGAATCCTGT

20,910

ANXA11

ANXA11-203

AAAAAGATAGGGAGAAAAGATGTGCAACCTTACAGGTCATCTTTCTGGGATAGAACACAATGGGTCTTCTCCTGCCTCCTGGATAT
TTTTTCTATCCCTCTTTCTACACGTTGGAATGTCCAGTAGAAAAGACCCTATCTTGTGTTACCCAGAAGAGGACGGAGGACCTATA

20,995

ANXA11

ANXA11-203

GTTAGTCAAGGCCAGTCCATGCTACACATCTAGTCTGACTTCTAAAATAGAAGCACCAGATGAATTCAGCCCTGAGAGAATTTTC
CAATCAGTTCGGTTCAGGTACGATGTGTAGATCAGACTGAAGATTTTATCTTCGTGGTCTACTTAAGTCGGGACTCTCTTAAAAG

21,080

ANXA11

ANXA11-203

AGCAGCTGTGGGGGCGCTGGAGGAAACACTATTAATAAGTTTTTGCACCTGAGACAGATAGCCTCACTCGCCTCACCCCTAGTCCTG
TCGTCGACACCCCCGCGACCTCCTTTGTGATAATTTATCAAAACGTGGACTCTGTCTATCGGAGTGAGCGGAGTGGGATCAGGAC

21,165

ANXA11

ANXA11-203

GTGGCATTGTCTCAGGTGCAAAATTTAAGAAAGAAACCTTGGAGTGCTCACCCCTGTGGCTGGGTAGATGGTCCTAAAGTGGTGG
CACCGTAAACAGAGTCCACGTTTTAAATTCTTTCTTTGGAACCTCACGAGTGGGACACCGACCCATCTACCAGGATTTACCACC

21,250

ANXA11

ANXA11-203

TTTTCAAGCCTGAGTGTGTATCAGGATCATCAGGGGAGCTTGCTAAAGAGCAGTTCCTGCGGTCAGACCCTCATGCATTTTGAGC
AAAAGTTCGGACTCACACATAGTCCCTAGTAGTCCCCTCGAACGATTTCTCGTCAAGGACGCCAGTCTGGGAGTACGTAACACTCG

21,335

ANXA11

ANXA11-203

AGGTGTGGGGACTGGGAAACTGCATCTGTAACCTGCTGTAATCTAACGCTTATCTAAATACTACTGTGCTCACACAGAGAACACC
TCCACACCCCTGACCCCTTGACGTAGACATTGGACGACATTAGATTGCGAATAGATTTATGATGACACGAGTGTGTCTCTTGTGG

21,420

ANXA11

ANXA11-203

GCAAAAGTAGAGGTGTTCCCTCCAGAGGGCAGGTGAGCAGATGGCACAGTCTGCTTGGAAATTCAGTCAGGTGATGAGAGATGAGAT
CGTTTTTCATCTCCACAAGGAGGTCTCCCGTCCACTCGTCTACCGTGTGACACGAACTTAAGTCAGTCCACTACTCTCTACTCTA

21,505

ANXA11

ANXA11-203

GAGGCACTCCTAGCTTTGGGAAGAGGGAGCTGAAAGATGAACCTTTGCAGGTGCCACGGTCAAAGTGGTGGTTTTAATGCCATGC
CTCCGTGAGGATCGAAACCCTTCTCCCTCGACTTTCTACTTGGAAACGTCCACGGGTGCCAGTTTTACCACCAAATTACGGTACG

21,590

ANXA11

ANXA11-203

CATGCCCATTTTCTGTTGGCCTTGGCAGGGAGTTACAGCCCTACCTTAGGACCTGGCTCCTTATTTCTGCTGTAGGCTCTTTCT
GTACGGGTAAAAGACAACCGGAACCGTCCCTCAATGTGCGGATGGAATCCTGGACCGAGGAATAAAGACGACATCCGAGAAAGGA

21,675

ANXA11

ANXA11-203

GCCCTGGCCGAGATGGAGTGGAATGAGACCTAGAAACATCAAGCTAAATACATGTCTCAGAAAGATAAAGTTTTACATTTTAC
CGGGACCGGCTCTACCTCACCTTACTCTGGATCTTTGTAGTTTCGATTTATGTACAGGAGTCTTTCTATTTCCAATGTAAGGATG

21,760

ANXA11

ANXA11-203

CCCCATCAAATCTGAAAGCTCTCTGCCTGTGTTTTCTAAGGGATAGGGACATCATTACTCAGTCCACAACCTGGACTCATGTAG
GGGGTAGTTTAGACTTTTCGAGAGACGGACACAAAAGATTCCCTATCCCTGTAGTAATGAGTCAGGTGTTGGACCTGAGTACATC

21,845

ANXA11

ANXA11-203

GGTCCCTGTGTCAGTAAAGGAGTCAGTCAAGCCCACAGGTATACCAAGGACTCTTACCCTCAGCCCTACTCCTTGGAAAGCTGC
CCAGGGGACAGTCATTTCTCAGTCAGTTCGGGTGGTCCATATGGTTCCTGAGAATGGGAGTCGGGGATGAGGAACCTTTTCGACG

21,930

ANXA11

ANXA11-203

CCCTTGGCCTAATATTGGTGTTTAGCTTGAGCCTGACTCCTTCTCAACACTAAGAGCTGATGAAGTCCTGAAGCAGAAAAGAGCTC
GGGAACCGGATTATAACCACAAATCGAACTCGGACTGAGGAAGAGTTGTGATTCTCGACTACTTCAGGACTTCGTCTTTCTCGAG

22,015

ANXA11

ANXA11-203

TGACCTGAGAGTCAAACATCCTTATTCTGATCTCAGCTCAGCCCCTGATTTGTTGTGTGACCCTGGATATGTCACTTCCTGTCTT
ACTGGACTCTCAGTTTGTAGGAATAAGACTAGAGTCGAGTCGGGGACTAAACAACACACTGGGACCTATACAGTGAAGGACAGAA

22,100

ANXA11

ANXA11-203

TTTGACTTTTTAAAATGAAGGGTAGACTAGAGGAGAGCTTCTAAAACCTTTAATGTGGTCAACGAAATGGAATAGGAAATCCACA
AAACTGAAAAATTTTACTTCCCATCTGATCTCCTCTCGAAGATTTTGAAATTACACCAGTTGCTTTACCTTATCCTTTAAGGTGT

22,185

ANXA11

ANXA11-203

AGTCTGTCCTTCCACAAAAGCAGCAAATAAGGTGGCAAAAACCTCAAATTTATGGGAACTCTGGAAACGAATTGAAAGTTTACAGC
TCAGACAGGAAGGTGTTTTCGTCGTTTTATTCCACCGTTTTTGAGTTTAAATACCCTTGAGACCTTTGCTTAACTTTCAAATGTCG

22,270

ANXA11

ANXA11-203

AATCAGGTGAATACCTAAGAATAAAAAGCTGGATTTAGTAAGA
TTAGTCCACTTATGGATTCTTATTTTCGACCTAAATCATTCT

3'

22,312

5'

ANXA11

ANXA11-203

Feature	Location	Size	Type
✓ ANXA11	1 .. 22,312	22,312 bp	gene
/note	= gene ENSG00000122359 Protein coding		
ANXA11-202	1 .. 22,312	22,312 bp	prim_transcript
/note	= primary transcript ENST00000372231		
✓ ANXA11-203	1 .. 22,312	22,312 bp	prim_transcript
/note	= primary transcript ENST00000422982		
ANXA11-205	1 .. 22,312	22,312 bp	prim_transcript
/note	= primary transcript ENST00000438331		
ANXA11-208	1 .. 367	367 bp	prim_transcript
/note	= primary transcript ENST00000463657 protein_coding_CDS_not_defined		
ANXA11-204	180 .. 4121	3942 bp	prim_transcript
/note	= primary transcript ENST00000437799		
ANXA11-201	330 .. 18,077	17,748 bp	prim_transcript
/note	= primary transcript ENST00000265447		
ANXA11-202	340 .. 17,348	17,009 bp	CDS
▶ 14 segments = 1518 bp			
/note	= coding sequence ENSP00000361305		
/translation	= MSYPGYPPPPGGYPPAAP,,GGGPWGGAAAYPPPPSMPPIGLDNVATYAGQFNQDYLSGM,,AANMSGTFGGANMPNLYPGAPGAGYPPVPPG GFGQPPSAQQPVPPYGMYPGGNPPSRMPSYPPYPGAPVPGQPMPPPQQPPGAYPGQPPVTPYGGQPPVPLPGQQQPVPSYPGYPGS GTVTPAVPPTQ,,FGSRGTITDAPGFDPLRDAEVLKAMKGF,,GTDEQAIIDCLGSRSNKQRQQILLSFKTAYGK,,DLIKDLKSELSGNFEKTIL ALMKTPLVLDIYEIKEAIK,,GVGTDEACLIIEILASRSNEHIRELNRAKYA,,EFKKTLEEAIKSDTSGHFQRLILSLSQ,,GMRDESTNVDMSLAQR DAQ,,ELYAAGENRLGTDESKFNAVLCRSRAHLVA,,VFNEYQRMTGRDIEKSICREMSGDLEEGMLAV,,VKCLKNTPAFFAERLNKAMR,,GA GAGTKDRTLIRIMVSRSETDLLDIRSEYKRMYGKSLYHDIS,,GDTSGDYRKILLKICGGND*		
✓ ANXA11-203	340 .. 17,348	17,009 bp	CDS
▶ 14 segments = 1518 bp			
/note	= coding sequence ENSP00000404412		
/translation	= MSYPGYPPPPGGYPPAAP,,GGGPWGGAAAYPPPPSMPPIGLDNVATYAGQFNQDYLSGM,,AANMSGTFGGANMPNLYPGAPGAGYPPVPPG GFGQPPSAQQPVPPYGMYPGGNPPSRMPSYPPYPGAPVPGQPMPPPQQPPGAYPGQPPVTPYGGQPPVPLPGQQQPVPSYPGYPGS GTVTPAVPPTQ,,FGSRGTITDAPGFDPLRDAEVLKAMKGF,,GTDEQAIIDCLGSRSNKQRQQILLSFKTAYGK,,DLIKDLKSELSGNFEKTIL ALMKTPLVLDIYEIKEAIK,,GVGTDEACLIIEILASRSNEHIRELNRAKYA,,EFKKTLEEAIKSDTSGHFQRLILSLSQ,,GMRDESTNVDMSLAQR DAQ,,ELYAAGENRLGTDESKFNAVLCRSRAHLVA,,VFNEYQRMTGRDIEKSICREMSGDLEEGMLAV,,VKCLKNTPAFFAERLNKAMR,,GA GAGTKDRTLIRIMVSRSETDLLDIRSEYKRMYGKSLYHDIS,,GDTSGDYRKILLKICGGND*		
ANXA11-205	340 .. 17,348	17,009 bp	CDS
▶ 14 segments = 1518 bp			
/note	= coding sequence ENSP00000398610		
/translation	= MSYPGYPPPPGGYPPAAP,,GGGPWGGAAAYPPPPSMPPIGLDNVATYAGQFNQDYLSGM,,AANMSGTFGGANMPNLYPGAPGAGYPPVPPG GFGQPPSAQQPVPPYGMYPGGNPPSRMPSYPPYPGAPVPGQPMPPPQQPPGAYPGQPPVTPYGGQPPVPLPGQQQPVPSYPGYPGS GTVTPAVPPTQ,,FGSRGTITDAPGFDPLRDAEVLKAMKGF,,GTDEQAIIDCLGSRSNKQRQQILLSFKTAYGK,,DLIKDLKSELSGNFEKTIL ALMKTPLVLDIYEIKEAIK,,GVGTDEACLIIEILASRSNEHIRELNRAKYA,,EFKKTLEEAIKSDTSGHFQRLILSLSQ,,GMRDESTNVDMSLAQR DAQ,,ELYAAGENRLGTDESKFNAVLCRSRAHLVA,,VFNEYQRMTGRDIEKSICREMSGDLEEGMLAV,,VKCLKNTPAFFAERLNKAMR,,GA GAGTKDRTLIRIMVSRSETDLLDIRSEYKRMYGKSLYHDIS,,GDTSGDYRKILLKICGGND*		
ANXA11-204	340 .. 4121	3782 bp	CDS
▶ 3 segments = 450 bp			
/note	= coding sequence ENSP00000414642		
/translation	= MSYPGYPPPPGGYPPAAP,,GGGPWGGAAAYPPPPSMPPIGLDNVATYAGQFNQDYLSGM,,AANMSGTFGGANMPNLYPGAPGAGYPPVPPG GFGQPPSAQQPVPPYGMYPGGNPPSRMPSYPPYPGAPVPGQPMPPPQQPPGAYPGQPPV 150 amino acids = 15.0 kDa		
✓ Donor Template SNV -> REV	2278 .. 2377	100 bp	misc_feature
ANXA11-201	2330 .. 17,348	15,019 bp	CDS
▶ 13 segments = 1419 bp			
/note	= coding sequence ENSP00000265447		
/translation	= MPPIGLDNVATYAGQFNQDYLSGM,,AANMSGTFGGANMPNLYPGAPGAGYPPVPPGGFQPPSAQQPVPPYGMYPGGNPPSRMPSY PYPGAPVPGQPMPPPQQPPGAYPGQPPVTPYGGQPPVPLPGQQQPVPSYPGYPGSGTVTPAVPPTQ,,FGSRGTITDAPGFDPLRDAEVL KAMKGF,,GTDEQAIIDCLGSRSNKQRQQILLSFKTAYGK,,DLIKDLKSELSGNFEKTILALMKTPLVLDIYEIKEAIK,,GVGTDEACLIIEILAS NEHIRELNRAKYA,,EFKKTLEEAIKSDTSGHFQRLILSLSQ,,GMRDESTNVDMSLAQRDAQ,,ELYAAGENRLGTDESKFNAVLCRSRAHLVA ,,VFNEYQRMTGRDIEKSICREMSGDLEEGMLAV,,VKCLKNTPAFFAERLNKAMR,,GAGTKDRTLIRIMVSRSETDLLDIRSEYKRMYGKSLY HDIS,,GDTSGDYRKILLKICGGND*		
✓ PAM	2337 .. 2339	3 bp	misc_feature
✓ Protospacer Sequence	2340 .. 2359	20 bp	misc_feature

Feature	Location	Size			Type
✓ SNV	2342 .. 2342	1 bp			misc_feature
/note	= REV = G SNV = A				
ANXA11-210	4114 .. 6802	2689 bp			prim_transcript
/note	= primary transcript ENST00000481805 Retained intron				
ANXA11-206	11,189 .. 17,561	6373 bp			prim_transcript
/note	= primary transcript ENST00000447489				
ANXA11-206	11,189 .. 16,792	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	15,183 .. 17,613	2431 bp			prim_transcript
/note	= primary transcript ENST00000463340 protein_coding_CDS_not_defined				

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Reverse	20-mer	2143 .. 2162	59°C	Jan 10, 2023
/sequence = TCATGTGGTCTGTGGTGTCC 55% GC / 6146.0 Da				
✓ Donor Template SNV -> REV	100-mer	2278 .. 2377	85°C	Jan 10, 2023
/sequence = gctttcagGTGGTGGTCCCTGGGGAGGTGCTGCCTACCCTCCTCCGCCCAGCATGCCCCCATCGGGCTGGATAACGTGGCCACCTATG 65% GC / 31024.8 Da				
✓ gRNA Protospacer	20-mer	2343 .. 2359	57°C	Jan 10, 2023
/sequence = GGCCACGTTATCCAGCCTGA 60% GC / 6078.0 Da				
✓ PCR Forward	21-mer	2545 .. 2565	58°C	Jan 10, 2023
/sequence = GCAGAAGCCTGATGAAAACCC 52% GC / 6433.3 Da				
✓ Sanger Sequencing	21-mer	2545 .. 2565	58°C	Jan 10, 2023
/sequence = GCAGAAGCCTGATGAAAACCC 52% GC / 6433.3 Da				