



E Alignment of nucleotide acid sequences for *Cystatin 11* alternate transcripts

1 20 40 60 80 100 120
CST11 TCTCCCCACAGTCATTGGGCTGCAGCTCGAGAGCCGAGGAGACGCCGCTGCTGCTGCTGGGCTGCCTTAAACCCACAGGAGCCGACCCCTCGGGGGCTTCCTCCCCAGCT
CST11A TCTCCCCACAGTCATTGGGCTGCAGCTCGAGAGCCGAGGAGACGCCGCTGCTGCTGCTGGGCTGCCTTAAACCCACAGGAGCCGACCCCTCGGGGGCTTCCTCCCCAGCT

121 140 160 180 200 220 240
CST11 GAGCAGCCATGGCCAGACCCAGCAGGGCCCCGGCTGCTGCTGGCCATCGTAGGGGCCCTGGTGGCCCTCAGCTACCAAAAGAAAGAGCTTCATCCAGCTCCAGGAGCTGCCCG
CST11A GAGCAGCCATGGCCAGACCCAGCAGGGCCCCGGCTGCTGCTGGCCATCGTAGGGGCCCTGGTGGCCCTCAGCTACCAAAAGAAAGAGCTTCATCCAGCTCCAGGAGCTGCCCG

241 260 280 300 320 340 360
CST11 TGTCAGATCCTTTCTGGTGCACCAACCTGGATTTTGTGAGTAAGAGTTCAACAAGAGAGTGGAGACAAGTACAATTTCCGAGTCGCTGCTGCTTAAAGGCCGTGCAAGTGGTGACCA
CST11A TGTCAGATCCTTTCTGGTGCACCAACCTGGATTTTGTGAGTAAGAGTTCAACAAGAGAGTGGAGACAAGTACAATTTCCGAGTCGCTGCTGCTTAAAGGCCGTGCAAGTGGTGACCA

361 380 400 420 440 460 480
CST11 ACCACTTAGAGTACCGCTGAACCTGGAGATGCAGAGGAGCGTCTGCCCAAGGCAGAGAGAACACTGCACCTTCAGGAAGGGAGCTGTACAAGAAATCGATTGCTTCTTCTCAG
CST11A ACCACTTAGAGTACCGCTGAACCTGGAGATGCAGAGGAGCGTCTGCCCAAGGCAGAGAGAACACTGCACCTTCAGGAAGGGAGCTGTACAAGAAATCGATTGCTTCTTCTCAG

481 500 520 540 560 580 600
CST11 GTTTTGCTGCTCCCTGGTTTGAAGATATAAAATCTGACCAAAACTGCACCGATGGCTAGGTGTCCCGAGCTCGCGGGCAGTCACCGCTGTGTACAGTGTCTGTCACCAAGAGGG
CST11A GTTTTGCTGCTCCCTGGTTTGAAGATATAAAATCTGACCAAAACTGCACCGATGGCTAGGTGTCCCGAGCTCGCGGGCAGTCACCGCTGTGTACAGTGTCTGTCACCAAGAGGG

601 620 640
CST11 GCTCTCCATGTAAAAAATAAATGTTAGTCAGTTTCTCTCTTAA-----
CST11A GCTCTCCATGTAAAAAATAAATGTTAGTCAGTTTCTCTCTTAAAAA

F Alignment of acid amino sequences for *Cystatin 11* isoforms

1 20 40 60 80 100 120

G Alignment of nucleotide acid sequences for *Eg627821* alternate transcripts

1 20 40 60 80 100 120
Eg627821 GGAATCTGGGAGAAGAGTGGGTGACCAGAGTCTCTGTGTCTCTGGAAGAGATCGTCCACCCCAAGTCCCGCCCCCGCATGCACACATCAGGGCCCTTTGGAAGATGCTCTGCTGAT
Eg627821A GGAATCTGGGAGAAGAGTGGGTGACCAGAGTCTCTGTGTCTCTGGAAGAGATCGTCCACCCCAAGTCCCGCCCCCGCATGCACACATCAGGGCCCTTTGGAAGATGCTCTGCTGAT

121 140 160 180 200 220 240
Eg627821 ACTGTCTTCTCTGGGACTGGCAGGAGCTGCATTCCCGAGGAAGTCGCCACAGAAGAAAAATCAAATGCTGAAGGAATCGTGGGAATGATGAGCAGGCTCTCTTCAGATGGTCTCAG
Eg627821A ACTGTCTTCTCTGGGACTGGCAGGAGCTGCATTCCCGAGGAAGTCGCCACAGAAGAAAAATCAAATGCTGAAGGAATCGTGGGAATGATGAGCAGGCTCTCTTCAGATGGTCTCAG

241 260 280 300 320 340 360
Eg627821 ACTCAGTGGCAATCCCTCAAGAGGCCCTCCCTGGCACCACCCACAAGATAGGACCGAAGAGAGATCAAAATATTGAACAGATCCTAGGTTTCTGAGCCTGCAGGTGTTAAATGAAGA
Eg627821A ACTCAGTGGCAATCCCTCAAGAGGCCCTCCCTGGCACCACCCACAAGATAGGACCGAAGAGAGATCAAAATATTGAACAGATCCTAGGTTTCTGAGCCTGCAGGTGTTAAATGAAGA

361 380 400 420 440 460 480
Eg627821 AAAAAATGGCTGCAAGGAAGAGTGAAGTTTCTCCCAACCCCCATCCCGACCAAGAGGCACTGAAGAAAGAACAGATGGAGCTCTCTTGAGATGGCTACATGATCCTCACTTCTCT
Eg627821A AAAAAATGGCTGCAAGGAAGAGTGAAGTTTCTCCCAACCCCCATCCCGACCAAGAGGCACTGAAGAAAGAACAGATGGAGCTCTCTTGAGATGGCTACATGATCCTCACTTCTCT

481 500 520 540 560 580 600
Eg627821 GTTCGTGCTCTACACAAAGGCGACTGG-----GTGTTACTGCCATTACTGTATACCCAGAAGTGACACAGCAAGTGAACCCCTGCTGTGCTTTCTAGCAGCCCTGCTGCACCTCCACTCCGCGCTC
Eg627821A GTTCGTGCTCTACACAAAGGCGACTGG-----GTGTTACTGCCATTACTGTATACCCAGAAGTGACACAGCAAGTGAACCCCTGCTGTGCTTTCTAGCAGCCCTGCTGCACCTCCACTCCGCGCTC

601 620 640 660 680 700 720
Eg627821 ACAACTCTCCGCTCCAGGCAGACAGTCTCACTCTCCGAGAAACTCTGTCCTTACGATGACCGATTGGAGGGTAAAGCGCTTGGTCTTTAGAGAAAGCGCCTGTCTGCTCAGA
Eg627821A ACAACTCTCCGCTCCAGGCAGACAGTCTCACTCTCCGAGAAACTCTGTCCTTACGATGACCGATTGGAGGGTAAAGCGCTTGGTCTTTAGAGAAAGCGCCTGTCTGCTCAGA

721 740 760 780 800 820 840
Eg627821 AGCGTGGCAGAAAGGTGCTCTGAGAAGATGCCGCCAGAGAGTCACTAGAGCAGGCTCTGACGGGGTCTCCCCACACCTCTCTTAGTCTTCTCAGACTTCCCGCGGTAGCGCTAAT
Eg627821A AGCGTGGCAGAAAGGTGCTCTGAGAAGATGCCGCCAGAGAGTCACTAGAGCAGGCTCTGACGGGGTCTCCCCACACCTCTCTTAGTCTTCTCAGACTTCCCGCGGTAGCGCTAAT

841
Eg627821 AAAATGTGCACTTGTGG
Eg627821A AAAATGTGCACTTGTGG