

nrxn2a.ape
Alignment to
2A_TMR_F3_8R_210.txt-- Matches:188; Mismatches:14; Gaps:342; Unattempted:0

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      *      *      *      *      *      *      *      *      *      *
1>~~~~~CCTGGTGTAGGCAAAAGTGGCCACGGTGACCACCGTCCTCCAGTCCCTGCCCCGACCACCCATCCTAACCAGTCCACATC>81
222<TCCTGGTTAGCAAAAGGCTCCTGGTGTAGGCAAAAGTGGCCACGGTGACCACCGTCCTCCAGTCCCTGCCCCGACCACCCATCCTAACCAGTCCACATC<123

      *      *      *      *      *      *      *      *      *      *
82>CCAGCGGGCAAAATGAACACCCGCGACCAGGTGCTCCTGCCACCCGTCCCGTCCTCGCGCCACACTCCAGGTCTAACCTACCCGCCTGATTTCCTCCCATG>181
122<CCAGCGGGCAAAATGAACACCCGCGACCAGGTGCTCCTGCCACCCGTCCCGTCCTCGCGCC-----<62

      *      *      *      *      *      *      *      *      *      *
182>TGCCCAAGCTCATCCACCGACCTGATGGAGAAGGGCCGTCCAGGTGCCGTGGAGGTGATTCGAGAGTCCAGCAGCACCACAGGCATGGTGGTTGGCAT>281
62<-----<62

      *      *      *      *      *      *      *      *      *      *
282>CGTGCGGGTGCCGCCCTCTGCATCCTCATCTCTATACGCCATGTATAAATACCGCAATCGAGACGAAGGCTCTTATCAGGTGGATCAAAGCCGCAAC>381
62<-----<62

      *      *      *      *      *      *      *      *      *      *
382>TCCGGCTCTGAAAGCAACGGTGCCGTAGTGAAGGAGAAAACGCCGAGTACGACTGCCCGCGTGGCTAAAACCACCACCAAGGGCAAGAAGAACAAAGACA>481
61<-----ACCACCACCAAGGGCAAGAAACACACACAC<31

      *      *      *      *
482>AGGAGTATTACGTCTGAG-AAAGACAGAGGAGAAGGTACTGATG>524
30<AGCAACTA-----GAGCAATGACACACAGAGA-----GATG<1
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