

CLUSTAL 2.1 multiple sequence alignment

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foundBP2col5      NNGGCNANATGATTTTATTTTGACTGATAGTGACCNNTTCGTTGCAACAAATTNNTGAGC  60
expected_2_EA37   -----

foundBP2col5      AATGCTTTTTTATAATGCCAACTTTGTACAAAAAAGTTGGCACCAGATCTTAAGGCTAGAG  120
expected_2_EA37   -----

foundBP2col5      TACTAATACGACTCACNNTAGGGAATACAAGCTACTTGTCTTTTTGCACTCGAGAATTC  180
expected_2_EA37   -----

foundBP2col5      GCCACCATGTCCAGATTAGATAAAAGTAAAGTGATTAACAGCGCATTAGAGCTGCTTAAT  240
expected_2_EA37   -----ATGTCCAGATTAGATAAAAGTAAAGTGATTAACAGCGCATTAGAGCTGCTTAAT  54
                  *****

foundBP2col5      GAGGTCGGAATCGAAGGTTTAAACAACCCGTAAACTCGCCAGAAGCTAGGTGTAGCGCAG  300
expected_2_EA37   GAGGTCGGAATCGAAGGTTTAAACAACCCGTAAACTCGCCAGAAGCTAGGTGTANNNCAG  114
                  *****

foundBP2col5      CCTACATTGTATTGCGCATGTAAAAAATAAGCGGGCTTTGCTCGACGCCTTAGCCATTGAG  360
expected_2_EA37   CCTACATTGTATTGCGCATGTAAAAAATAAGCGGGCTTTGCTCGACGCCTTAGCCATTGAG  174
                  *****

foundBP2col5      ATGTTAGATAGGCACCATACTCACTTTTGCCCTTTAGAAGGGGAAAGTTGGCAAGATTTT  420
expected_2_EA37   ATGTTAGATAGGCACCATACTCACTTTTGCCCTTTAGAAGGGGAAAGCTGGCAAGATTTT  234
                  *****

foundBP2col5      TTACGTAATAACGCTAAAGTTTTGGAATGTGCTTTACTAAGTCATCGCGATGGAGCAAAA  480
expected_2_EA37   TTACGTAATAACGCTAAAGTTTTAGATGTGCTTTACTAAGTCATCGCGATGGAGCAAAA  294
                  *****

foundBP2col5      GTACATTTAGGTACACGGCCTACAGAAAAACAGTATGAAACTCTCGAAAATCAATTAGCC  540
expected_2_EA37   GTACATTTAGGTACACGGCCTACAGAAAAACAGTATGAAACTCTCGAAAATCAATTAGCC  354
                  *****

foundBP2col5      TTTTATGCCAACAAAGGTTTTTCACTAGAGAAATGCATTATATGCACTCAGCGCTGTGGGG  600
expected_2_EA37   TTTTATGCCAACAAAGGTTTTTCACTAGAGAAATGCATTATATGCACTCAGCGCTGTGGGG  414
                  *****

foundBP2col5      CATTTTACTTTAGGTTGCGTATTGGAAGATCAAGAGCATCAAGTCGCTAAAGAAGAAAGG  660
expected_2_EA37   CATTTTACTTTAGGTTGCGTATTGGAAGATCAAGAGCATCAAGTCGCTAAAGAAGAAAGG  474
                  *****

foundBP2col5      GAAACACCTACTACTGATAGTATGCCGCCATTATTACGACAAGCTATCGAATTATTGAT  720
expected_2_EA37   GAAACACCTACTACTGATAGTATGCCGCCATTATTACGACAAGCTATCGAATTATTGAT  534
                  *****

foundBP2col5      CACCAAGGTGCAGAGCCAGCCTTCTTATTCGGCCTTGAATTGATCATATGCGGATTAGAA  780
expected_2_EA37   CACCAAGGTGCAGAGCCAGCCTTCTTATTCGGCCTTGAATTGATCATATGCGGATTAGAA  594
                  *****

foundBP2col5      AAACAACCTTANATGTGAAAGTGGGTCTGGGGGTCTCATCATCTCATCATTAATAAC  840
expected_2_EA37   AAACAACCTTAAATGTGAAAGTGGGTCT-----  621
                  *****

foundBP2col5      GACTCAGGCTGTACAAAANAANNNAANAAAAAATACTAGCATAACCCCTT  900
expected_2_EA37   -----

foundBP2col5      GGGGCCTCTAAACGGGTCTTGAGGGGTTTTTGTGTGCAACTTTCTTGTACAAAGTTGGC  960
expected_2_EA37   -----

foundBP2col5      ATTATAANNAAGCATTGCTTTATCAATTTGTGTGCAACGAANNGGGTC  1009
expected_2_EA37   -----
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Lilia S 17.8.11 14:35

Commentaire [1]: Serine instead of tryptophane position 43

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Commentaire [2]: Silent mutation (serine position 74)

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Commentaire [3]: Glycine instead of Arginine at position 87

