

CLUSTAL 2.1 multiple sequence alignment

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foundBP4col1      NNGCNANATGATTTATTTTGACTGATAGTGACCTGNTCGTTGCAACAAATTGATGAGCAA 60
expected_4_YF42  -----

foundBP4col1      TGCTTTTTTATAATGCCAACTTTGTACAAAAAAGTTGGCACCGATCTTAAGGCTAGAGTA 120
expected_4_YF42  -----

foundBP4col1      CTAATACGACTCACTATAGGGAATACAAGCTACTTGTCTCTTTTGCACCTCGAGAATTTCGC 180
expected_4_YF42  -----

foundBP4col1      CGCCAN[NG]TCCAGATTAGATAAAAAGTAAAGTGATTAACAGCGCATTAGAGCTGCTTAATGA 240
expected_4_YF42  ----ATGTCAGATTAGATAAAAAGTAAAGTGATTAACAGCGCATTAGAGCTGCTTAATGA 56
                * *****

foundBP4col1      GGTGCGAATCGAAGGTTTAAACAACCCGTAAACTCGCCCGAAGCTAGGTGTAGAGCAGCC 300
expected_4_YF42  GGTGCGAATCGAAGGTTTAAACAACCCGTAAACTCGCCCGAAGCTAGGTGTAGAGCAGCC 116
                *****

foundBP4col1      TACATTGTTT[TT]TGGCATGTAAAAATAAGCGGGCTTTGCTCGACGCCTTAGCCATTGAGAT 360
expected_4_YF42  TACATTGNNNTGGCATGTAAAAATAAGCGGGCTTTGCTCGACGCCTTAGCCATTGAGAT 176
                *****

foundBP4col1      GTTAGATAGGCACCATACTCACTTTTGCCTTTTGAAGGGGAAAGCTGGCAAGATTTTTT 420
expected_4_YF42  GTTAGATAGGCACCATACTCACTTTTGCCTTTTGAAGGGGAAAGCTGGCAAGATTTTTT 236
                *****

foundBP4col1      ACGTAATAACGCTAAAAGTTTGTAGTGTGCTTTACTAAGTCATCGCGATGGAGCAAAAGT 480
expected_4_YF42  ACGTAATAACGCTAAAAGTTTGTAGTGTGCTTTACTAAGTCATCGCGATGGAGCAAAAGT 296
                *****

foundBP4col1      ACATTTAGGTACACGGCTACAGAAAAACAGTATGAAACTCTCGAAAATCAATTAGCCTT 540
expected_4_YF42  ACATTTAGGTACACGGCTACAGAAAAACAGTATGAAACTCTCGAAAATCAATTAGCCTT 356
                *****

foundBP4col1      TTTATGCCAACAAAGGTTTTCCTAGAGAATGCATTATATGCGCTCAGCGCTGTGGGGCA 600
expected_4_YF42  TTTATGCCAACAAAGGTTTTCCTAGAGAATGCATTATATGCGCTCAGCGCTGTGGGGCA 416
                *****

foundBP4col1      TTTTACTTTAGGTTGCGTATTGGAAGATCAAGAGCATCAAGTCGCTAAAGAAGAAAGGGA 660
expected_4_YF42  TTTTACTTTAGGTTGCGTATTGGAAGATCAAGAGCATCAAGTCGCTAAAGAAGAAAGGGA 476
                *****

foundBP4col1      AACACCTACTACTGATAGTATGCCGCCATTATTACGACAAGCTATCGAATTATTTGATCA 720
expected_4_YF42  AACACCTACTACTGATAGTATGCCGCCATTATTACGACAAGCTATCGAATTATTTGATCA 536
                *****

foundBP4col1      CCAAGGTGCAGAGCCAGCCTTCTTATTCGGCCTTGAATTGATCATATGCGGATTGGAAAA 780
expected_4_YF42  CCAAGGTGCAGAGCCAGCCTTCTTATTCGGCCTTGAATTGATCATATGCGGATTAGAAAA 596
                *****

foundBP4col1      ACAACTTANATGTGAAAGTGGGTCTGGGGTCTCATCATCATCATCATTAATAACG 840
expected_4_YF42  ACAACTTAAATGTGAAAGTGGGTCT----- 621
                *****

foundBP4col1      ACTCAGCTGCTACAAAAAANAAAAANAAAAANAAAAANCTAGCATAACCCCTTGG 900
expected_4_YF42  -----

foundBP4col1      GGCCTCTAAACGGGCTTGAGGGGTTTTTGTGTGCCAACTTCTTGTACAAAGTTGGCAT 960
expected_4_YF42  -----

foundBP4col1      TATAANAAGCATTGCTTATCAATTGTGTGCAACGAANAGGTCATATCAGTCAAATAA 1020
expected_4_YF42  -----

foundBP4col1      AA 1022
expected_4_YF42  --
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Lilia S 19.8.11 10:53

Commentaire [1]: ab1 file shows T as expected

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Commentaire [2]: Position 132 silent mutation alanine

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Commentaire [3]: Position 197 silent mutation leucine

