

CLUSTAL 2.1 multiple sequence alignment

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foundBP4col3      CNNATGATTTNNTTGTACTGATAGTGACCNGTTCGTTGCAACAAATTGATGAGCAATGC 60
expected_4_YF42  -----

foundBP4col3      TTTTTTATAATGCCAACTTTGTACAAAAAAGTTGGCACCAGATCTTAAGGCTAGAGTACTA 120
expected_4_YF42  -----

foundBP4col3      ATACGACTCACTATAGGGAATACAAGCTACTTGTCTTTTTTGCCTCGAGAATTCGCCAC 180
expected_4_YF42  -----

foundBP4col3      CATGTCAGATTAGATAAAAAGTAAAGTATTAAACAGCGCATTAGAGCTGCTTAATGAGGT 240
expected_4_YF42  -ATGTCAGATTAGATAAAAAGTAAAGTATTAAACAGCGCATTAGAGCTGCTTAATGAGGT 59
*****

foundBP4col3      CGGAATCGAAGGTTTAAACAACCCGTAAGTAACTCGCCAGAAAGCTAGGTGTAGAGCAGCCTAC 300
expected_4_YF42  CGGAATCGAAGGTTTAAACAACCCGTAAGTAACTCGCCAGAAAGCTAGGTGTAGAGCAGCCTAC 119
*****

foundBP4col3      ATTGTTTGGCATGTAAAAATAAGCGGGCTTTGCTCGACGCTTGGCCATTGAGATGTT 360
expected_4_YF42  ATTTNNNTGGCATGTAAAAATAAGCGGGCTTTGCTCGACGCTTGGCCATTGAGATGTT 179
****.*****

foundBP4col3      AGATAGGCACCATACTCACTTTTGCCTTTTGAAGGGGAAAGCTGGCAAGATTTTTTACG 420
expected_4_YF42  AGATAGGCACCATACTCACTTTTGCCTTTTGAAGGGGAAAGCTGGCAAGATTTTTTACG 239
*****

foundBP4col3      TAATAACGCTAAAAGTTTGTAGATGTGCTTTACTAAGTCATCGCGATGGAGCAAGGTACA 480
expected_4_YF42  TAATAACGCTAAAAGTTTGTAGATGTGCTTTACTAAGTCATCGCGATGGAGCAAGGTACA 299
*****

foundBP4col3      TTTAGGTACACGGCTACAGAAAAACAGTATGAACTCTCGAAAATCAATTAGCCTCTTT 539
expected_4_YF42  TTTAGGTACACGGCTACAGAAAAACAGTATGAACTCTCGAAAATCAATTAGCCTCTTT 359
*****

foundBP4col3      ATGCCAACAAAGGTTTTTCACTAGAGAATGCATTATATGCCTCAGCGCTGTGGGGCATT 599
expected_4_YF42  ATGCCAACAAAGGTTTTTCACTAGAGAATGCATTATATGCCTCAGCGCTGTGGGGCATT 419
*****

foundBP4col3      TACTTTAGGTTGCGTATTGGAAGATCAAGAGCATCAAGTCGCTAAAGAAGAAAGGGAAC 659
expected_4_YF42  TACTTTAGGTTGCGTATTGGAAGATCAAGAGCATCAAGTCGCTAAAGAAGAAAGGGAAC 479
*****

foundBP4col3      ACCTACTACTGATAGTATGCGGCCATTATTACGACAAGCTATCGAATTATTTGATCACCA 719
expected_4_YF42  ACCTACTACTGATAGTATGCGGCCATTATTACGACAAGCTATCGAATTATTTGATCACCA 539
*****

foundBP4col3      AGGTGCAGAGCCAGCCTTCTTATTCGGCCTTGAATTGATCATATGCGGATTAGAAAACA 779
expected_4_YF42  AGGTGCAGAGCCAGCCTTCTTATTCGGCCTTGAATTGATCATATGCGGATTAGAAAACA 599
*****

foundBP4col3      ACTTANATGTGAAAGTGGGTCTGGGGTCTCATCATCATCATCATTAATAACGACT 839
expected_4_YF42  ACTTAAATGTGAAAGTGGGTCT----- 621
*****

foundBP4col3      CAGGCTGTACAAAAANANAANAAAAANNAANAAAAACTAGCATAACCCCTTGGGGC 899
expected_4_YF42  -----

foundBP4col3      CTCATAACGGGCTTGTAGGGTTTTTGTGTTGCCAATTTCTTGTACAAATTGGCATTAT 959
expected_4_YF42  -----

foundBP4col3      AANAAAGCATTGCTTATCAATTTGTTGCAACGAACAGGCTACTATCAGTCAA 1012
expected_4_YF42  -----

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Lilia S 17.8.11 14:54
Commentaire [1]: Silent mutation position 55 Leucine

Lilia S 17.8.11 14:57
Commentaire [2]: Silent mutation lysine position 98

Lilia S 17.8.11 14:58
Commentaire [3]: DELETION position E107

Lilia S 17.8.11 14:59
Commentaire [4]: Mutation Threonine to Alanine position 112

Lilia S 17.8.11 15:01
Commentaire [5]: Position 119 serine instead of phenylalanine

