

CLUSTAL 2.1 multiple sequence alignment

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foundBP1col5      CNANATGATTTNNTTGTACTGATAGTGACCTGTTTCGTTGCAACAAATTGATGAGCAATGC 60
expected_1_VF36  -----

foundBP1col5      TTTTTTATAATGCCAACTTTGTACAAAAAAGTTGGCACCAGATCTTAAGGCTAGAGTACTA 120
expected_1_VF36  -----

foundBP1col5      ATACGACTCACTATAGGGAATACAAGCTACTTGTCTTTTTTGCCTCGAGAATTCGCCAT 180
expected_1_VF36  -----

foundBP1col5      CATGTCAGATTAGATAAAAAGTAAAGTAAATTAACAGCGCATTAGAGCTGCTTAATGAGGT 240
expected_1_VF36  -ATGTCAGATTAGATAAAAAGTAAAGTAAATTAACAGCGCATTAGAGCTGCTTAATGAGGT 59
*****

foundBP1col5      CGGAATCGAAGGTTTAAACAACCCGTAAGTAACTCGCCAGAAAGCTAGGTTTCGAGCAGCCTAC 300
expected_1_VF36  CGGAATCGAAGGTTTAAACAACCCGTAAGTAACTCGCCAGAAAGCTAGGTNNGAGCAGCCTAC 119
*****

foundBP1col5      ATTGTATTTCGCATGTAAAAAATAAGCGGGCTTTGCTCGACGCCTTAGCCATTGAGATGTT 360
expected_1_VF36  ATTGTATTTCGCATGTAAAAAATAAGCGGGCTTTGCTCGACGCCTTAGCCATTGAGATGTT 179
*****

foundBP1col5      AGATAGGCACCATACTCACTTTGCCCTTTAGAAGGGGAAAGCTGGCAAGATTTTTTACG 420
expected_1_VF36  AGATAGGCACCATACTCACTTTGCCCTTTAGAAGGGGAAAGCTGGCAAGATTTTTTACG 239
*****

foundBP1col5      TAATAACGCTAAAGTTTTAGATGTGCTTTACTAAGTCATCGCGATGGAGCAAAAGTACA 480
expected_1_VF36  TAATAACGCTAAAGTTTTAGATGTGCTTTACTAAGTCATCGCGATGGAGCAAAAGTACA 299
*****

foundBP1col5      TTTAGGTACACGGCCTACAGAAAAACAGTATGAAACTCTCGAAATCAATTAGCCTTTTT 540
expected_1_VF36  TTTAGGTACACGGCCTACAGAAAAACAGTATGAAACTCTCGAAATCAATTAGCCTTTTT 359
*****

foundBP1col5      ATGCCAACAAAGGTTTTTCACTAGAGAATGCATTATATGCACTCAGCGCTGTGGGCATTT 600
expected_1_VF36  ATGCCAACAAAGGTTTTTCACTAGAGAATGCATTATATGCACTCAGCGCTGTGGGCATTT 419
*****

foundBP1col5      TACTTTAGGTTGCGTATTGGAAGATCAAGAGCATCAAGTCGCTAAAGAAGAAAGGAAAC 660
expected_1_VF36  TACTTTAGGTTGCGTATTGGAAGATCAAGAGCATCAAGTCGCTAAAGAAGAAAGGAAAC 479
*****

foundBP1col5      ACCTACTACTGATAGTATGCGCCATTATTACGACAAGCTATCGAATTATTTGATCACCA 720
expected_1_VF36  ACCTACTACTGATAGTATGCGCCATTATTACGACAAGCTATCGAATTATTTGATCACCA 539
*****

foundBP1col5      AGGTGCAGAGCCAGCCTTCTTATTCGGCCTTGAATTGATCATATGCGGATTAGAAAAACA 780
expected_1_VF36  AGGTGCAGAGCCAGCCTTCTTATTCGGCCTTGAATTGATCATATGCGGATTAGAAAAACA 599
*****

foundBP1col5      ACTTANATGTGAAAGTGGGTCTGGGGTCTCATCATCATTAATAACGACTCAGGCT 840
expected_1_VF36  ACTTAAATGTGAAAGTGGGTCT----- 621
*****

foundBP1col5      GCTACAANAAAAAAAAAAAAAAAAAAAAAAAACTAGCATAACCCCTTGGGCCTCTAA 900
expected_1_VF36  -----

foundBP1col5      ACGGGTCTTGAGGGTTTTTGTGCAACCTTCTTGTACAAAGTTGGCATTATAANAAA 960
expected_1_VF36  -----

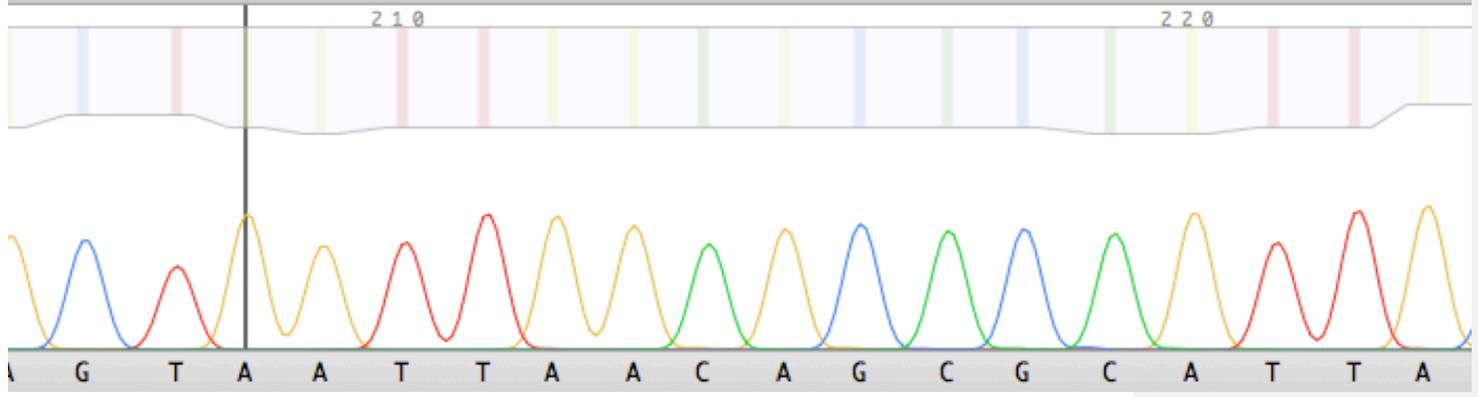
foundBP1col5      GCATTGCTTATCAATTTGTTGCAACGAACAGGTCATATCAGTCAAATAAA 1012
expected_1_VF36  -----

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Lilia S 16.8.11 21:10  
**Commentaire [1]:** Codes for serine instead of tryptophane

BP1col5\_1579314.ab1

208 Zoom:



BP1col5\_1579314.ab1

309 Zoom:

