```
WT: 1   ATGGCGGCCTCAGGGCTGTTTCGATGCTTGCCTGTGCCATGCCCGGAGGACCTGCTGGTGGAGGAATTGGTGGACGGGCTATTATCCTTGGAGGAAGAGT 100
        ::::: ::    ::  : ::  : ::  : :: :: :: :: :: :: ::  :  : :: :: ::  : :: :: ::  :  :     : :: :: ::
SM: 1   ATGGCAGCAAGCGGATTATTCAGGTGTCTTCCGGTACCCTGTCCAGAAGATTTATTAGTAGAAGAGCTTGTAGATGGATTGCTCAGTCTTGAAGAGGAAC 100

WT: 101 TAAAGGACAAGGAGGAGGAGGAAGCTGTGCTTGACGGTTTGCTATCCTTAGAAGAGGAAAGCCGCGGCCGGCTGCGACGGGGCCCTCCAGGGGAGAAAGC 200
        : :: :: :: :: :: :: :: :: :: ::  : :: ::  :  :     : :: :: ::     : ::  :  :  :  : :: :: :: :: :: :: ::
SM: 101 TGAAAGATAAAGAAGAAGAAGAGGCCGTATTGGATGGCCTTTTGAGTCTCGAGGAAGAGTCAAGAGGAAGATTAAGGAGAGGACCCCCGGGAGAAAAGGC 200

WT: 201 GCCACCTCGCGGGGAAACGCATCGTGATCGGCAGCGACGGGCTGAGGAGAAGAGGAAGCGAAAAAAAGAGCGGGAGAAAGAGGAGGAAAAGCAGATTGCT 300
         :: ::  : :: :: :: ::  : ::  : ::  :  : :: :: :: ::  : ::  : :: :: ::  : :: :: :: :: :: :: :: :: ::
SM: 201 ACCGCCGAGAGGTGAGACACACAGGGACAGACAAAGGAGAGCCGAAGAAAAACGAAAAAGGAAGAAGGAAAGAGAAAAGGAAGAAGAGAAACAAATCGCG 300

WT: 301 GAGTATTTGAAAAGGAAGGAAGAGGAGAAGGCACGGCGCAGGAGGCGGGCGGAGAAGAAGGCCGCTGACGTCGCCCGGAGAAAGCAGGAAGAGCAGGAGC 400
        :: ::  : ::  : :: :: :: :: :: ::  :  :  :  :  : :: :: :: :: :: :: :: :: :: ::  :::: :: :: :: :: ::
SM: 301 GAATACCTTAAGCGTAAAGAGGAAGAAAAAGCGAGAAGACGACGTAGAGCAGAAAAAAAAGCAGCGGATGTAGCACGTCGAAAACAAGAGGAACAAGAAA 400

WT: 401 GCCGTGAGCGCAAGTGGAGACAAGGGGCTGAGAAGGCGAAACAGCATAGTGCTAGGAAAGAAAAAATGCAGGAGTTGGGGATTGATGGCTATACTAGACA 500
        :  : ::  : :: ::: : :: :: :: :: :: :: :: :: ::    ::  : :: :: :: ::::: ::  : :: :: :: :: :: ::  : ::
SM: 401 GAAGGGAAAGAAAATGGCGCCAGGGAGCCGAAAAAGCTAAGCAACACTCCGCCCGTAAGGAGAAGATGCAAGAACTAGGTATCGACGGATACACCCGGCA 500

WT: 501 GTTGGAAGGCGAGGTGGAGTCCTTGGAGGCTGAACGGAGGAAGTTGCTGCAGGAGAAGGAGGATTTAATGGGAGAGGTTAATTATTGGCAGGGGAGGCTG 600
          : :: :: :: :: ::     : :: :: ::  :  : ::  :  : :: :: :: :: ::  : ::::: :: :: :: :: ::::: ::  :: :
SM: 501 ACTTGAGGGTGAAGTTGAAAGTCTAGAAGCCGAGAGACGTAAACTATTACAAGAAAAAGAAGACCTTATGGGTGAAGTCAACTACTGGCAAGGTCGGTTA 600

WT: 601 GAGGCGATGTGGTTGCAATAA 621
        :: :: :::::: : :: :::
SM: 601 GAAGCTATGTGGCTTCAGTAA 621
```