```
        V  Y  Q  *  M  A  T  T  V  Y  T  T  E  E  V  E  L  Q  D  G  T  T  V  T  L  K  P  L  T  I  K  N  L
       R  F  T  N  K  W  Q  L  Q  Y  I  Q  P  K  R  S  S  F  R  T  A  Q  R  L  H  L  S  H  S  Q  L  R  I  S
        G  L  P  I  N  G  N  Y  S  I  Y  N  R  R  G  R  A  S  G  R  H  N  G  Y  T  *  A  T  H  N  *  E  S
22601  AGGTTTACCAATAAATGGCAACTACAGTATATACAACCGAAGAGGTCGAGCTTCAGGACGGCACAACGGTTACACTTAAGCCACTCACAATTAAGAATCT
       ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
       TCCAAATGGTTATTTACCGTTGATGTCATATATGTTGGCTTCTCCAGCTCGAAGTCCTGCCGTGTTGCCAATGTGAATTCGGTGAGTGTTAATTCTTAGA
       F  T  *  W  Y  I  A  V  V  T  Y  V  V  S  S  T  S  S  *  S  P  V  V  T  V  S  L  G  S  V  I  L  F  R
        L  N  V  L  L  H  C  S  C  Y  I  C  G  F  L  D  L  K  L  V  A  C  R  N  C  K  L  W  E  C  N  L  I
         P  K  G  I  F  P  L  *  L  I  Y  L  R  L  P  R  A  E  P  R  C  L  P  *  V  *  A  V  *  L  *  S  D

        R  K  F  M  K  T  M  E  A  F  A  E  A  E  T  E  E  D  G  L  E  V  M  L  D  S  A  A  L  C  L  K  S
         E  S  L  *  R  R  W  R  L  L  L  R  Q  R  Q  K  R  M  A  L  R  S  C  L  I  Q  P  L  F  V  *  S  L
       P  K  V  Y  E  D  D  G  G  F  C  *  G  R  D  R  R  G  W  P  *  G  H  A  *  F  S  R  S  L  F  E  V  S
22701  CCGAAAGTTTATGAAGACGATGGAGGCTTTTGCTGAGGCAGAGACAGAAGAGGATGGCCTTGAGGTCATGCTTGATTCAGCCGCTCTTTGTTTGAAGTCT
       ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
       GGCTTTCAAATACTTCTGCTACCTCCGAAAACGACTCCGTCTCTGTCTTCTCCTACCGGAACTCCAGTACGAACTAAGTCGGCGAGAAACAAACTTCAGA
         R  F  N  I  F  V  I  S  A  K  A  S  A  S  V  S  S  S  P  R  S  T  M  S  S  E  A  A  R  Q  K  F  D
       E  S  L  K  H  L  R  H  L  S  K  S  L  C  L  C  F  L  I  A  K  L  D  H  K  I  *  G  S  K  T  Q  L  R
        G  F  T  *  S  S  S  P  P  K  Q  Q  P  L  S  L  L  P  H  G  Q  P  *  A  Q  N  L  R  E  K  N  S  T

       Q  R  P  E  F  W  D  E  K  T  N  K  H  A  E  D  F  E  D  A  I  D  I  P  T  I  Y  K  V  L  D  V  C  G
        S  V  Q  S  S  G  T  R  R  Q  T  S  T  L  R  I  S  R  M  Q  L  T  F  Q  Q  F  T  R  F  S  M  S  A
         A  S  R  V  L  G  R  E  D  K  Q  A  R  *  G  F  R  G  C  N  *  H  S  N  N  L  Q  G  S  R  C  L  R
22801  CAGCGTCCAGAGTTCTGGGACGAGAAGACAAACAAGCACGCTGAGGATTTCGAGGATGCAATTGACATTCCAACAATTTACAAGGTTCTCGATGTCTGCG
       ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
       GTCGCAGGTCTCAAGACCCTGCTCTTCTGTTTGTTCGTGCGACTCCTAAAGCTCCTACGTTAACTGTAAGGTTGTTAAATGTTCCAAGAGCTACAGACGC
        *  R  G  S  N  Q  S  S  F  V  F  L  C  A  S  S  K  S  S  A  I  S  M  G  V  I  *  L  T  R  S  T  Q
         L  T  W  L  E  P  V  L  L  C  V  L  V  S  L  I  E  L  I  C  N  V  N  W  C  N  V  L  N  E  I  D  A
       E  A  D  L  T  R  P  R  S  S  L  C  A  R  Q  P  N  R  P  H  L  Q  C  E  L  L  K  C  P  E  R  H  R  R

        G  I  K  L  N  D  P  N  L  L  A  A  A  A  E  A  L  G  R  N  *  T  S  P  N  *  R  Q  R  L  F  F  *
       E  V  L  S  *  M  T  Q  I  F  *  R  R  Q  R  R  L  L  G  G  T  E  P  R  P  T  R  G  R  G  F  S  S  R
        R  Y  *  V  E  *  P  K  S  S  S  G  G  S  G  G  S  W  E  E  L  N  L  A  Q  L  E  A  E  A  F  L  L
22901  GAGGTATTAAGTTGAATGACCCAAATCTTCTAGCGGCGGCAGCGGAGGCTCTTGGGAGGAACTGAACCTCGCCCAACTAGAGGCAGAGGCTTTTCTTCTA
       ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
       CTCCATAATTCAACTTACTGGGTTTAGAAGATCGCCGCCGTCGCCTCCGAGAACCCTCCTTGACTTGGAGCGGGTTGATCTCCGTCTCCGAAAAGAAGAT
       P  P  I  L  N  F  S  G  F  R  R  A  A  A  A  S  A  R  P  L  F  Q  V  E  G  L  *  L  C  L  S  K  K  *
        S  T  N  L  Q  I  V  W  I  K  *  R  R  C  R  L  S  K  P  P  V  S  G  R  G  V  L  P  L  P  K  E  E
         L  Y  *  T  S  H  G  L  D  E  L  P  P  L  P  P  E  Q  S  S  S  F  R  A  W  S  S  A  S  A  K  R  R

        V  T  G  K  T  S  M  R  L  R  T  P  S  V  *  K  S  F  K  L  F  L  K  P  Q  E  R  K  N  I  E  D  K
         S  L  E  K  L  R  *  D  *  G  L  P  Q  S  R  R  A  S  S  Y  S  *  S  R  K  R  E  R  I  *  R  T  K
       G  H  W  K  N  F  D  E  I  E  D  S  L  S  L  E  E  L  Q  A  I  L  E  A  A  R  E  K  E  Y  R  G  Q  K
23001  GGTCACTGGAAAAACTTCGATGAGATTGAGGACTCCCTCAGTCTAGAAGAGCTTCAAGCTATTCTTGAAGCCGCAAGAGAGAAAGAATATAGAGGACAAA
       ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
       CCAGTGACCTTTTTGAAGCTACTCTAACTCCTGAGGGAGTCAGATCTTCTCGAAGTTCGATAAGAACTTCGGCGTTCTCTCTTTCTTATATCTCCTGTTT
         T  V  P  F  V  E  I  L  N  L  V  G  E  T  *  F  L  K  L  S  N  K  F  G  C  S  L  F  F  I  S  S  L
       L  D  S  S  F  S  R  H  S  Q  P  S  G  *  D  L  L  A  E  L  *  E  Q  L  R  L  L  S  L  I  Y  L  V  F
        P  *  Q  F  F  K  S  S  I  S  S  E  R  L  R  S  S  S  *  A  I  R  S  A  A  L  S  F  S  Y  L  P  C

       N  L  Q  Q  L  *  R  V  L  T  L  M  K  R  L  V  K  Q  I  P  H  L  M  M  *  S  A  E  Q  R  R  N  C  T
        I  C  S  S  S  K  G  Y  *  P  *  *  K  G  W  *  N  R  Y  L  I  *  *  C  E  A  P  S  R  G  E  I  A
         F  A  A  A  L  K  G  I  D  L  D  E  K  V  G  K  T  D  T  S  F  D  D  V  K  R  R  A  E  A  K  L  H
23101  AATTTGCAGCAGCTCTAAAGGGTATTGACCTTGATGAAAAGGTTGGTAAAACAGATACCTCATTTGATGATGTGAAGCGCCGAGCAGAGGCGAAATTGCA
       ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
       TTAAACGTCGTCGAGATTTCCCATAACTGGAACTACTTTTCCAACCATTTTGTCTATGGAGTAAACTACTACACTTCGCGGCTCGTCTCCGCTTTAACGT
        F  K  C  C  S  *  L  T  N  V  K  I  F  L  N  T  F  C  I  G  *  K  I  I  H  L  A  S  C  L  R  F  Q
         I  Q  L  L  E  L  P  Y  Q  G  Q  H  F  P  Q  Y  F  L  Y  R  M  Q  H  H  S  A  G  L  L  P  S  I  A
       F  N  A  A  A  R  F  P  I  S  R  S  S  F  T  P  L  V  S  V  E  N  S  S  T  F  R  R  A  S  A  F  N  C

        G  Y  P  K  K  S  W  S  L  L  T  S  A  L  Q  *  L  K  N  K  D  *  L  K  *  K  I  S  R  F  A  L  V
       R  G  I  R  R  R  V  G  V  C  *  H  R  H  C  S  N  *  R  I  R  T  D  *  N  R  K  Y  P  D  S  L  *  W
        G  V  S  E  E  E  L  E  F  A  D  I  G  I  A  V  I  E  E  *  G  L  I  E  I  E  N  I  Q  I  R  F  S
23201  CGGGGTATCCGAAGAAGAGTTGGAGTTTGCTGACATCGGCATTGCAGTAATTGAAGAATAAGGACTGATTGAAATAGAAAATATCCAGATTCGCTTTAGT
       ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
       GCCCCATAGGCTTCTTCTCAACCTCAAACGACTGTAGCCGTAACGTCATTAACTTCTTATTCCTGACTAACTTTATCTTTTATAGGTCTAAGCGAAATCA
       V  P  Y  G  F  F  L  Q  L  K  S  V  D  A  N  C  Y  N  F  F  L  S  Q  N  F  Y  F  I  D  L  N  A  K  T
        R  P  I  R  L  L  T  P  T  Q  Q  C  R  C  Q  L  L  Q  L  I  L  V  S  Q  F  L  F  Y  G  S  E  S  *
         P  T  D  S  S  S  N  S  N  A  S  M  P  M  A  T  I  S  S  Y  P  S  I  S  I  S  F  I  W  I  R  K  L
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