**ID: sp|Q6IQ55-3|TTBK2\_HUMAN Peptide: AATEEENSHGQANGLLNAPSLGS#PIR  
Scan Number: 1635 Charge: 3**

|  |  |
| --- | --- |
| Seq # b y +1   A 1 72.0 - 26   A 2 143.1 2642.2 25   T 3 244.1 2571.2 24   E 4 373.2 2470.1 23   E 5 502.2 2341.1 22   E 6 631.2 2212.0 21   N 7 745.3 2083.0 20   S 8 832.3 1969.0 19   H 9 969.4 1881.9 18   G 10 1026.4 1744.9 17   Q 11 1154.5 1687.8 16   A 12 1225.5 1559.8 15   N 13 1339.5 1488.7 14   G 14 1396.6 1374.7 13   L 15 1509.6 1317.7 12   L 16 1622.7 1204.6 11   N 17 1736.8 1091.5 10   A 18 1807.8 977.5\* 9   P 19 1904.9 906.4 8   S 20 1991.9 809.4 7   L 21 2105.0 722.3 6   G 22 2162.0 609.3 5   #S 23 2329.0 552.2 4   P 24 2426.1 385.2\* 3   I 25 2539.1 288.2 2   R 26 - 175.1\* 1     Seq # b y +2   A 1 36.5 - 26   A 2 72.0 1321.6 25   T 3 122.6 1286.1 24   E 4 187.1 1235.6 23   E 5 251.6 1171.0 22   E 6 316.1 1106.5 21   N 7 373.2 1042.0\* 20   S 8 416.7 985.0 19   H 9 485.2 941.5 18   G 10 513.7 872.9 17   Q 11 577.7\* 844.4 16   A 12 613.3 780.4 15   N 13 670.3\* 744.9 14   G 14 698.8 687.9 13   L 15 755.3 659.3 12   L 16 811.9 602.8\* 11   N 17 868.9 546.3 10   A 18 904.4 489.2\* 9   P 19 952.9 453.7 8   S 20 996.5 405.2 7   L 21 1053.0 361.7 6   G 22 1081.5 305.1\* 5   #S 23 1165.0 276.6 4   P 24 1213.5 193.1 3   I 25 1270.1 144.6 2   R 26 - 88.1 1    \* Ion Match, # Phosphorylated | **JUMPvms2_Output_20200814/Intermediate/IMG/P175.1635.1.3.dta.gif** |

**ID: sp|Q6IQ55-3|TTBK2\_HUMAN Peptide: AATEEENSHGQANGLLNAPSLGS#PIR  
Scan Number: 2211 Charge: 3**

|  |  |
| --- | --- |
| Seq # b y +1   A 1 72.0 - 26   A 2 143.1 2642.2 25   T 3 244.1 2571.2 24   E 4 373.2\* 2470.1 23   E 5 502.2 2341.1 22   E 6 631.2 2212.0 21   N 7 745.3 2083.0 20   S 8 832.3 1969.0 19   H 9 969.4 1881.9 18   G 10 1026.4 1744.9 17   Q 11 1154.5 1687.8 16   A 12 1225.5 1559.8 15   N 13 1339.5 1488.7 14   G 14 1396.6 1374.7 13   L 15 1509.6 1317.7 12   L 16 1622.7 1204.6 11   N 17 1736.8 1091.5 10   A 18 1807.8 977.5 9   P 19 1904.9 906.4 8   S 20 1991.9 809.4 7   L 21 2105.0 722.3 6   G 22 2162.0 609.3 5   #S 23 2329.0 552.2 4   P 24 2426.1 385.2\* 3   I 25 2539.1 288.2 2   R 26 - 175.1\* 1     Seq # b y +2   A 1 36.5 - 26   A 2 72.0 1321.6 25   T 3 122.6 1286.1 24   E 4 187.1\* 1235.6 23   E 5 251.6 1171.0 22   E 6 316.1 1106.5 21   N 7 373.2\* 1042.0\* 20   S 8 416.7 985.0 19   H 9 485.2 941.5 18   G 10 513.7 872.9 17   Q 11 577.7\* 844.4 16   A 12 613.3 780.4 15   N 13 670.3\* 744.9 14   G 14 698.8 687.9 13   L 15 755.3 659.3 12   L 16 811.9 602.8\* 11   N 17 868.9 546.3 10   A 18 904.4 489.2 9   P 19 952.9 453.7 8   S 20 996.5 405.2 7   L 21 1053.0 361.7 6   G 22 1081.5 305.1\* 5   #S 23 1165.0 276.6 4   P 24 1213.5 193.1 3   I 25 1270.1 144.6 2   R 26 - 88.1 1    \* Ion Match, # Phosphorylated | **JUMPvms2_Output_20200814/Intermediate/IMG/P175.2211.1.3.dta.gif** |