

Thimet oligopeptidase (EC 3.4.24.15) key functions suggested by knockout mice phenotype characterization

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Running Title: THOP1 knockout mice

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#These two authors contributed equally

Keywords: THOP1; neurodegeneration; inflammation; sepsis; MHC-I; peptidome.

Organization of MS supplementary information

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 - 2.3 MS spectra from striatum peptides.....pages 179-219
 - 2.4 MS spectra from hippocampus peptides.....pages 220-268

Mascot Search Results

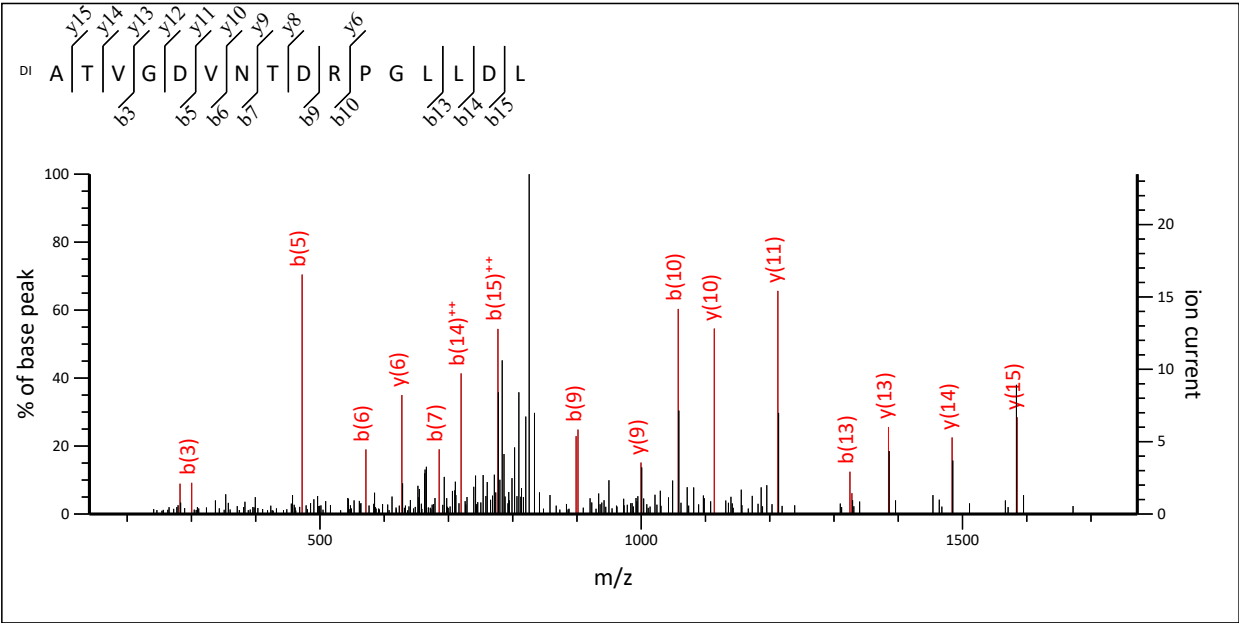
Peptide View

MS/MS Fragmentation of **ATVGDVNTDRPGLLDL**
Found in **ACBP_MOUSE** in **SwissProt**, Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=2

Match to Query 6508: 1682.897688 from(842.456120,2+) intensity(13946.9990) scans(9669) rawscans(sn9669) rtinseconds(3650.2103) index(7078)

Title: 7079: Scan 9669 (rt=3650.21) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]

Data file cortex_01.temp.mgf

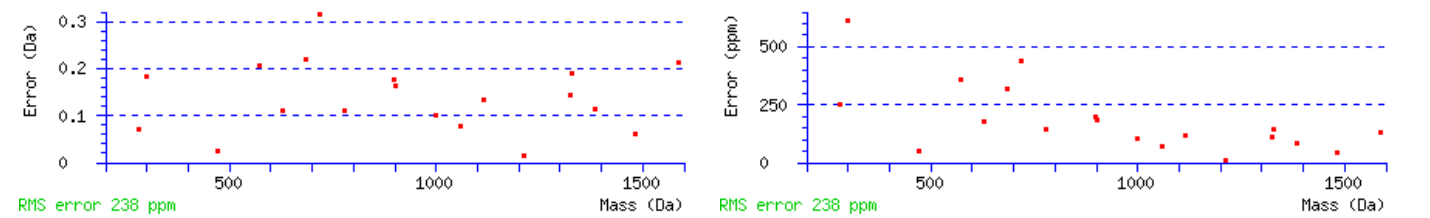


141.23 to 1772.07

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1682.8839
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 65 Expect: 0.01
Matches : 19/152 fragment ions using 29 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | | | A | | | | | | | 16 |
| 2 | 201.1234 | 101.0653 | | | 183.1128 | 92.0600 | T | 1584.8228 | 792.9150 | 1567.7962 | 784.4018 | 1566.8122 | 783.9097 | 15 |
| 3 | 300.1918 | 150.5995 | | | 282.1812 | 141.5942 | V | 1483.7751 | 742.3912 | 1466.7485 | 733.8779 | 1465.7645 | 733.3859 | 14 |
| 4 | 357.2132 | 179.1103 | | | 339.2027 | 170.1050 | G | 1384.7067 | 692.8570 | 1367.6801 | 684.3437 | 1366.6961 | 683.8517 | 13 |
| 5 | 472.2402 | 236.6237 | | | 454.2296 | 227.6185 | D | 1327.6852 | 664.3462 | 1310.6587 | 655.8330 | 1309.6747 | 655.3410 | 12 |
| 6 | 571.3086 | 286.1579 | | | 553.2980 | 277.1527 | V | 1212.6583 | 606.8328 | 1195.6317 | 598.3195 | 1194.6477 | 597.8275 | 11 |
| 7 | 685.3515 | 343.1794 | 668.3250 | 334.6661 | 667.3410 | 334.1741 | N | 1113.5899 | 557.2986 | 1096.5633 | 548.7853 | 1095.5793 | 548.2933 | 10 |
| 8 | 786.3992 | 393.7032 | 769.3727 | 385.1900 | 768.3886 | 384.6980 | T | 999.5469 | 500.2771 | 982.5204 | 491.7638 | 981.5364 | 491.2718 | 9 |
| 9 | 901.4262 | 451.2167 | 884.3996 | 442.7034 | 883.4156 | 442.2114 | D | 898.4993 | 449.7533 | 881.4727 | 441.2400 | 880.4887 | 440.7480 | 8 |
| 10 | 1057.5273 | 529.2673 | 1040.5007 | 520.7540 | 1039.5167 | 520.2620 | R | 783.4723 | 392.2398 | 766.4458 | 383.7265 | 765.4617 | 383.2345 | 7 |
| 11 | 1154.5800 | 577.7937 | 1137.5535 | 569.2804 | 1136.5695 | 568.7884 | P | 627.3712 | 314.1892 | | | 609.3606 | 305.1840 | 6 |
| 12 | 1211.6015 | 606.3044 | 1194.5749 | 597.7911 | 1193.5909 | 597.2991 | G | 530.3184 | 265.6629 | | | 512.3079 | 256.6576 | 5 |
| 13 | 1324.6856 | 662.8464 | 1307.6590 | 654.3331 | 1306.6750 | 653.8411 | L | 473.2970 | 237.1521 | | | 455.2864 | 228.1468 | 4 |
| 14 | 1437.7696 | 719.3884 | 1420.7431 | 710.8752 | 1419.7591 | 710.3832 | L | 360.2129 | 180.6101 | | | 342.2023 | 171.6048 | 3 |
| 15 | 1552.7966 | 776.9019 | 1535.7700 | 768.3886 | 1534.7860 | 767.8966 | D | 247.1288 | 124.0681 | | | 229.1183 | 115.0628 | 2 |
| 16 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI BLAST search of [ATVGDVNTDRPGLLDL](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|------------------------------------|
| 64.9 | 1682.8839 | 0.0138 | ATVGDVNTDRPGLLDL |
| 18.8 | 1682.9931 | -0.0954 | ATVPETGRKDTVVKV |
| 14.8 | 1682.9310 | -0.0333 | KVTAMIPLGHMGDPE |
| 12.9 | 1682.9203 | -0.0226 | DKNGKLEDEVLP SR |
| 12.2 | 1682.9138 | -0.0161 | ATVVAAVDMARVREPA |
| 10.6 | 1682.6485 | 0.2492 | CGCGNRGMQGNLDTCC |
| 10.6 | 1682.8927 | 0.0050 | ATVTQMHFLPGQGRL |
| 10.4 | 1682.8566 | 0.0411 | PLGGDHFAGGGDLASAPL |
| 10.3 | 1682.8841 | 0.0135 | SGTTTSGGGGRTRREAP |
| 10.1 | 1682.9167 | -0.0190 | LAMERDGSSGGVIRLA |

Mascot: <http://www.matrixscience.com/>

ATVGDVNTDRPGLLDL

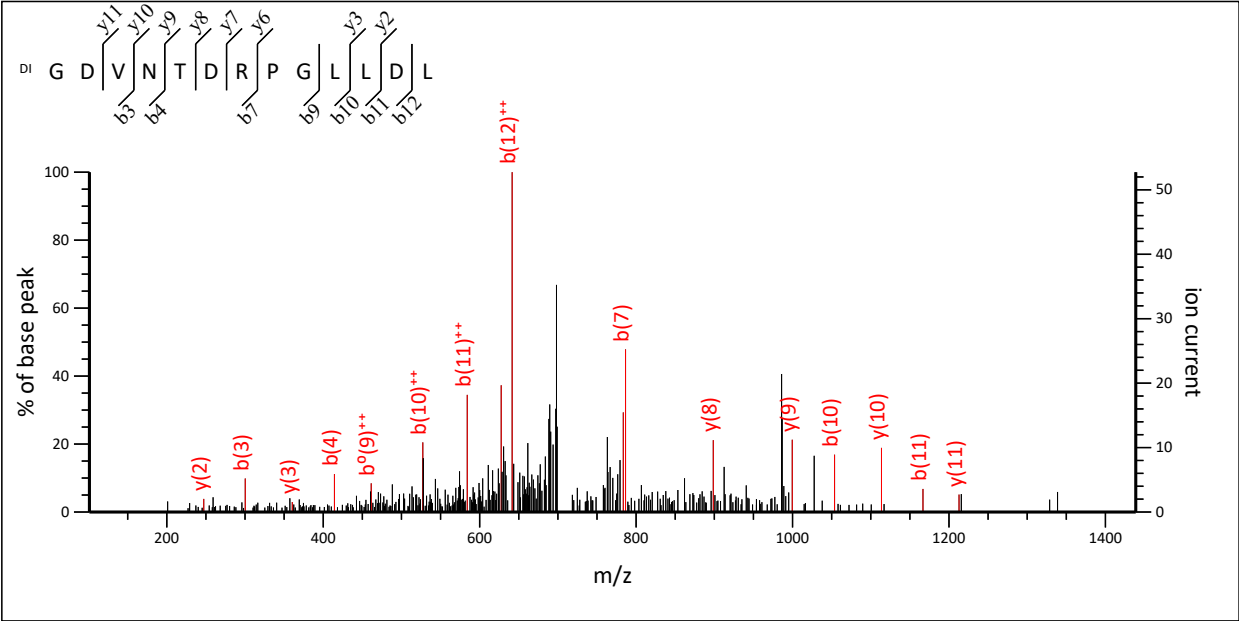
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDVNTDRPGLLDL**
Found in **ACBP_MOUSE** in **SwissProt**, Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=2

Match to Query 4471: 1411.736668 from(706.875610,2+) intensity(36356.2890) scans(8478) rawscans(sn8478) rtinseconds(3197.2789) index(6025)

Title: 6026: Scan 8478 (rt=3197.28) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf





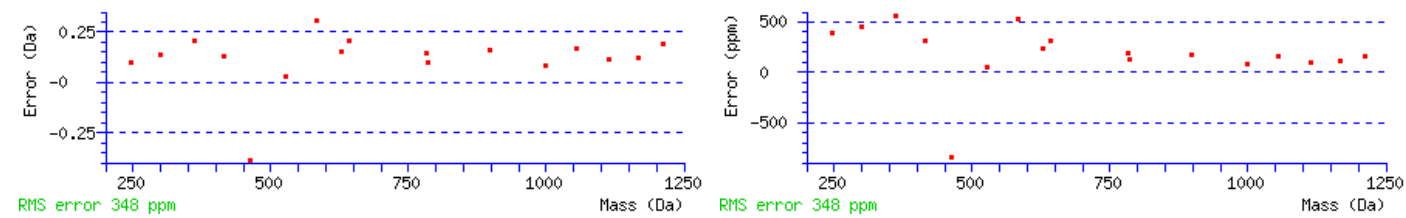
101.07 to 1438.8



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1411.7307
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 47 Expect: 0.67
Matches : 17/122 fragment ions using 34 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 86.0600 | 43.5337 | | | | | G | | | | | | | 13 |
| 2 | 201.0870 | 101.0471 | | | 183.0764 | 92.0418 | D | 1327.6852 | 664.3462 | 1310.6587 | 655.8330 | 1309.6747 | 655.3410 | 12 |
| 3 | 300.1554 | 150.5813 | | | 282.1448 | 141.5761 | V | 1212.6583 | 606.8328 | 1195.6317 | 598.3195 | 1194.6477 | 597.8275 | 11 |
| 4 | 414.1983 | 207.6028 | 397.1718 | 199.0895 | 396.1878 | 198.5975 | N | 1113.5899 | 557.2986 | 1096.5633 | 548.7853 | 1095.5793 | 548.2933 | 10 |
| 5 | 515.2460 | 258.1266 | 498.2195 | 249.6134 | 497.2354 | 249.1214 | T | 999.5469 | 500.2771 | 982.5204 | 491.7638 | 981.5364 | 491.2718 | 9 |
| 6 | 630.2729 | 315.6401 | 613.2464 | 307.1268 | 612.2624 | 306.6348 | D | 898.4993 | 449.7533 | 881.4727 | 441.2400 | 880.4887 | 440.7480 | 8 |
| 7 | 786.3741 | 393.6907 | 769.3475 | 385.1774 | 768.3635 | 384.6854 | R | 783.4723 | 392.2398 | 766.4458 | 383.7265 | 765.4618 | 383.2345 | 7 |
| 8 | 883.4268 | 442.2170 | 866.4003 | 433.7038 | 865.4163 | 433.2118 | P | 627.3712 | 314.1892 | | | 609.3606 | 305.1840 | 6 |
| 9 | 940.4483 | 470.7278 | 923.4217 | 462.2145 | 922.4377 | 461.7225 | G | 530.3184 | 265.6629 | | | 512.3079 | 256.6576 | 5 |
| 10 | 1053.5323 | 527.2698 | 1036.5058 | 518.7565 | 1035.5218 | 518.2645 | L | 473.2970 | 237.1521 | | | 455.2864 | 228.1468 | 4 |
| 11 | 1166.6164 | 583.8118 | 1149.5899 | 575.2986 | 1148.6058 | 574.8066 | L | 360.2129 | 180.6101 | | | 342.2023 | 171.6048 | 3 |
| 12 | 1281.6434 | 641.3253 | 1264.6168 | 632.8120 | 1263.6328 | 632.3200 | D | 247.1288 | 124.0681 | | | 229.1183 | 115.0628 | 2 |
| 13 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI BLAST search of [GDVNTDRPGLLDL](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

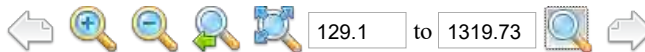
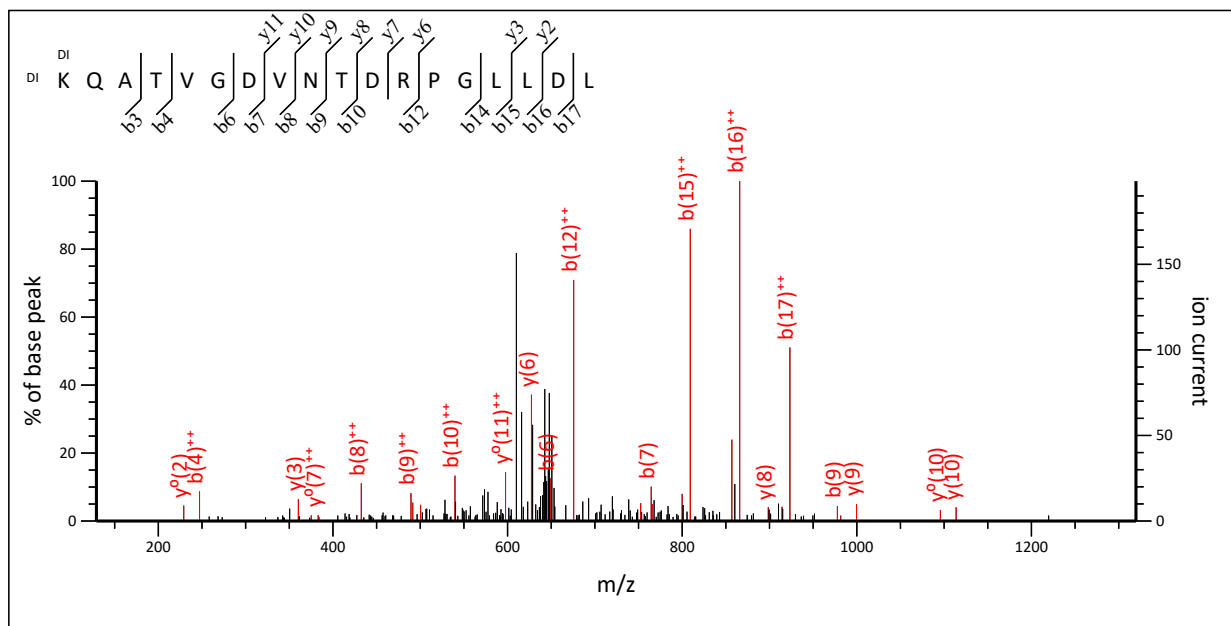
| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-----------------------------------|
| 46.6 | 1411.7307 | 0.0060 | GDVNTDRPGLLDL |
| 21.5 | 1411.7895 | -0.0529 | RDVAGGLRSLAQAA |
| 19.7 | 1411.8203 | -0.0836 | FPYKNLPIEDL |
| 19.7 | 1411.8333 | -0.0966 | ICRKDLLARNL |
| 19.7 | 1411.8973 | -0.1606 | KREADLVQLNL |
| 17.9 | 1411.7537 | -0.0170 | SFFIGDSGIPLEV |
| 16.2 | 1411.8224 | -0.0857 | SLASLPALASQPAL |
| 15.9 | 1411.7307 | 0.0059 | GTGLGLGGGSPGASTPV |
| 15.8 | 1411.5761 | 0.1605 | CPAGFHGVHCENN |
| 15.5 | 1411.9112 | -0.1745 | LDEKLLNIIDL |

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **ACBP_MOUSE** in **SwissProt**, Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=2

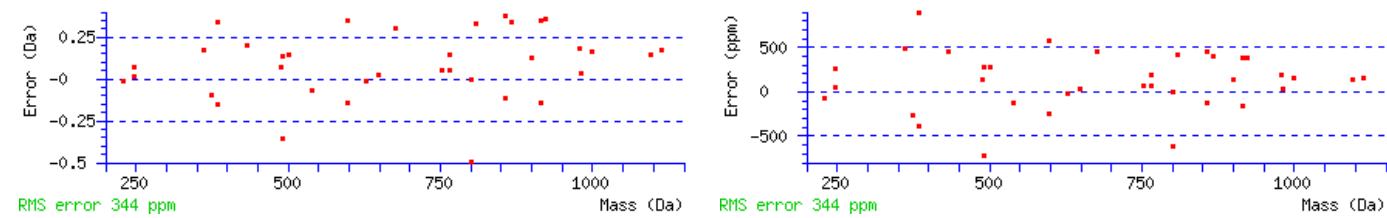
Title: 6402: Scan 11111 (rt=3418.99) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_04.raw]
Data file hipocampo_04.temp.mgf



Label all possible matches ☐ Label matches used for scoring ☒

Matches : 36/184 fragment ions using 58 most intense peaks ([help](#))

| # | b | b⁺⁺ | b[*] | b^{*++} | b⁰ | b⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ^{*++} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------------|----------------------|------------------------|----------------------|------------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 193.2151 | 97.1112 | 176.1885 | 88.5979 | | | K | | | | | | | 18 |
| 2 | 321.2736 | 161.1405 | 304.2471 | 152.6272 | | | Q | 1783.9185 | 892.4629 | 1766.8919 | 883.9496 | 1765.9079 | 883.4576 | 17 |
| 3 | 392.3107 | 196.6590 | 375.2842 | 188.1457 | | | A | 1655.8599 | 828.4336 | 1638.8333 | 819.9203 | 1637.8493 | 819.4283 | 16 |
| 4 | 493.3584 | 247.1829 | 476.3319 | 238.6696 | 475.3479 | 238.1776 | T | 1584.8228 | 792.9150 | 1567.7962 | 784.4018 | 1566.8122 | 783.9097 | 15 |
| 5 | 592.4268 | 296.7171 | 575.4003 | 288.2038 | 574.4163 | 287.7118 | V | 1483.7751 | 742.3912 | 1466.7485 | 733.8779 | 1465.7645 | 733.3859 | 14 |
| 6 | 649.4483 | 325.2278 | 632.4218 | 316.7145 | 631.4377 | 316.2225 | G | 1384.7067 | 692.8570 | 1367.6801 | 684.3437 | 1366.6961 | 683.8517 | 13 |
| 7 | 764.4752 | 382.7413 | 747.4487 | 374.2280 | 746.4647 | 373.7360 | D | 1327.6852 | 664.3462 | 1310.6587 | 655.8330 | 1309.6747 | 655.3410 | 12 |
| 8 | 863.5437 | 432.2755 | 846.5171 | 423.7622 | 845.5331 | 423.2702 | V | 1212.6583 | 606.8328 | 1195.6317 | 598.3195 | 1194.6477 | 597.8275 | 11 |
| 9 | 977.5866 | 489.2969 | 960.5600 | 480.7837 | 959.5760 | 480.2916 | N | 1113.5899 | 557.2986 | 1096.5633 | 548.7853 | 1095.5793 | 548.2933 | 10 |
| 10 | 1078.6343 | 539.8208 | 1061.6077 | 531.3075 | 1060.6237 | 530.8155 | T | 999.5469 | 500.2771 | 982.5204 | 491.7638 | 981.5364 | 491.2718 | 9 |
| 11 | 1193.6612 | 597.3342 | 1176.6347 | 588.8210 | 1175.6506 | 588.3290 | D | 898.4993 | 449.7533 | 881.4727 | 441.2400 | 880.4887 | 440.7480 | 8 |
| 12 | 1349.7623 | 675.3848 | 1332.7358 | 666.8715 | 1331.7518 | 666.3795 | R | 783.4723 | 392.2398 | 766.4458 | 383.7265 | 765.4617 | 383.2345 | 7 |
| 13 | 1446.8151 | 723.9112 | 1429.7885 | 715.3979 | 1428.8045 | 714.9059 | P | 627.3712 | 314.1892 | | | 609.3606 | 305.1840 | 6 |
| 14 | 1503.8365 | 752.4219 | 1486.8100 | 743.9086 | 1485.8260 | 743.4166 | G | 530.3184 | 265.6629 | | | 512.3079 | 256.6576 | 5 |
| 15 | 1616.9206 | 808.9639 | 1599.8941 | 800.4507 | 1598.9100 | 799.9587 | L | 473.2970 | 237.1521 | | | 455.2864 | 228.1468 | 4 |
| 16 | 1730.0047 | 865.5060 | 1712.9781 | 856.9927 | 1711.9941 | 856.5007 | L | 360.2129 | 180.6101 | | | 342.2023 | 171.6048 | 3 |
| 17 | 1845.0316 | 923.0194 | 1828.0051 | 914.5062 | 1827.0211 | 914.0142 | D | 247.1288 | 124.0681 | | | 229.1183 | 115.0628 | 2 |
| 18 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI **BLAST** search of [KQATVGDVNTDRPGLLDL](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|------------------------------------|
| 57.4 | 1975.1190 | 0.0028 | KQATVGDVNTDRPGLLDL |
| 35.0 | 1974.9839 | 0.1379 | RFQPTYPYVQHEIDL |
| 31.1 | 1974.9750 | 0.1468 | YTMNNGGSINSSTHLLDL |
| 23.7 | 1975.1367 | -0.0149 | FAKVFDAREIKQNAR |
| 22.0 | 1974.8663 | 0.2555 | CDLISDMGNLVHATNSEE |
| 22.0 | 1975.3664 | -0.2446 | TLAISAKGIADKLLLLDL |
| 21.2 | 1975.1106 | 0.0112 | CAQQQLLTRLHFILD |
| 21.1 | 1975.1171 | 0.0047 | PRDIERPLDILSDL |
| 21.1 | 1975.0900 | 0.0319 | TAIHEVMEQQTISIAKA |
| 20.9 | 1975.2070 | -0.0852 | PLTAFANLRKLERLDI |

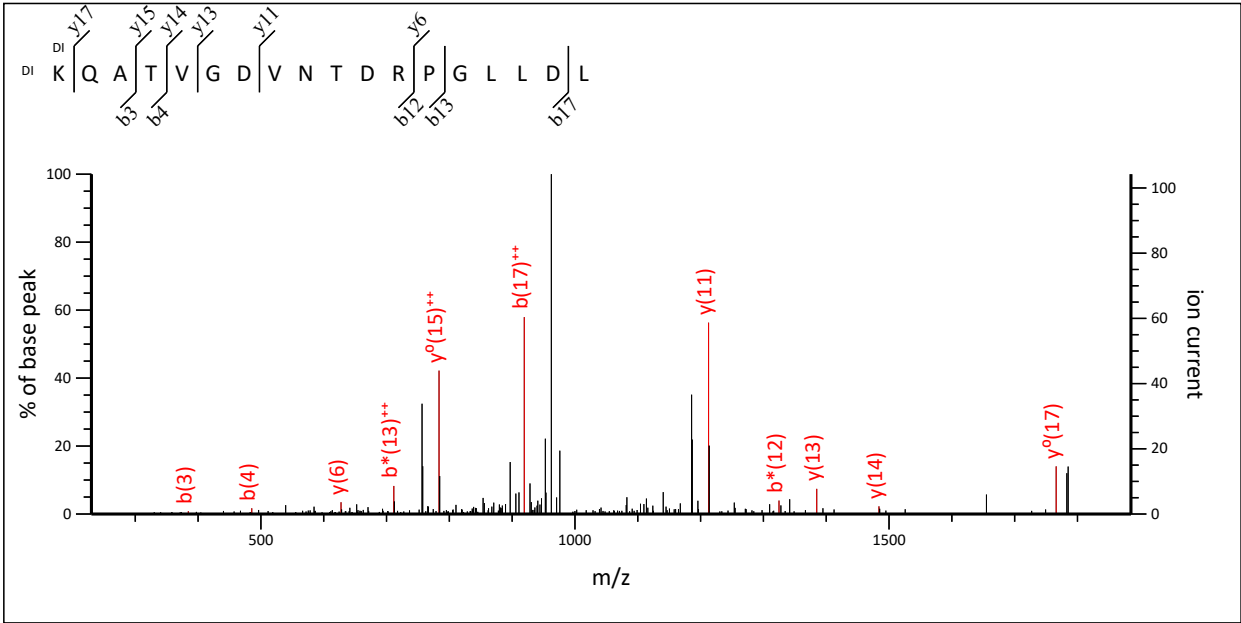
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **KQATVGDVNTDRPGLLDL**
Found in **ACBP_MOUSE** in **SwissProt**, Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=2

Match to Query 7527: 1967.069428 from(984.541990,2+) intensity(29598.1250) scans(7731) rawscans(sn7731) rtinseconds(2935.691) index(5420)
Title: 5421: Scan 7731 (rt=2935.69) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

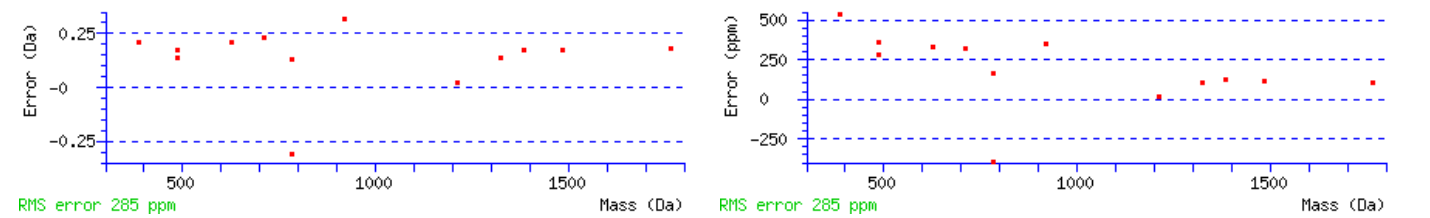


Navigation icons: ? (help), zoom in, zoom out, reset, and a range selector showing 230.2 to 1885.14.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1967.0688
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
Ions Score: 35 Expect: 10
Matches : 13/184 fragment ions using 14 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 185.1648 | 93.0861 | 168.1383 | 84.5728 | | | K | | | | | | | 18 |
| 2 | 313.2234 | 157.1153 | 296.1969 | 148.6021 | | | Q | 1783.9185 | 892.4629 | 1766.8919 | 883.9496 | 1765.9079 | 883.4576 | 17 |
| 3 | 384.2605 | 192.6339 | 367.2340 | 184.1206 | | | A | 1655.8599 | 828.4336 | 1638.8333 | 819.9203 | 1637.8493 | 819.4283 | 16 |
| 4 | 485.3082 | 243.1577 | 468.2817 | 234.6445 | 467.2976 | 234.1525 | T | 1584.8228 | 792.9150 | 1567.7962 | 784.4018 | 1566.8122 | 783.9097 | 15 |
| 5 | 584.3766 | 292.6920 | 567.3501 | 284.1787 | 566.3661 | 283.6867 | V | 1483.7751 | 742.3912 | 1466.7485 | 733.8779 | 1465.7645 | 733.3859 | 14 |
| 6 | 641.3981 | 321.2027 | 624.3715 | 312.6894 | 623.3875 | 312.1974 | G | 1384.7067 | 692.8570 | 1367.6801 | 684.3437 | 1366.6961 | 683.8517 | 13 |
| 7 | 756.4250 | 378.7162 | 739.3985 | 370.2029 | 738.4145 | 369.7109 | D | 1327.6852 | 664.3462 | 1310.6587 | 655.8330 | 1309.6747 | 655.3410 | 12 |
| 8 | 855.4934 | 428.2504 | 838.4669 | 419.7371 | 837.4829 | 419.2451 | V | 1212.6583 | 606.8328 | 1195.6317 | 598.3195 | 1194.6477 | 597.8275 | 11 |
| 9 | 969.5364 | 485.2718 | 952.5098 | 476.7585 | 951.5258 | 476.2665 | N | 1113.5899 | 557.2986 | 1096.5633 | 548.7853 | 1095.5793 | 548.2933 | 10 |
| 10 | 1070.5841 | 535.7957 | 1053.5575 | 527.2824 | 1052.5735 | 526.7904 | T | 999.5469 | 500.2771 | 982.5204 | 491.7638 | 981.5364 | 491.2718 | 9 |
| 11 | 1185.6110 | 593.3091 | 1168.5844 | 584.7959 | 1167.6004 | 584.3039 | D | 898.4993 | 449.7533 | 881.4727 | 441.2400 | 880.4887 | 440.7480 | 8 |
| 12 | 1341.7121 | 671.3597 | 1324.6856 | 662.8464 | 1323.7015 | 662.3544 | R | 783.4723 | 392.2398 | 766.4458 | 383.7265 | 765.4617 | 383.2345 | 7 |
| 13 | 1438.7649 | 719.8861 | 1421.7383 | 711.3728 | 1420.7543 | 710.8808 | P | 627.3712 | 314.1892 | | | 609.3606 | 305.1840 | 6 |
| 14 | 1495.7863 | 748.3968 | 1478.7598 | 739.8835 | 1477.7758 | 739.3915 | G | 530.3184 | 265.6629 | | | 512.3079 | 256.6576 | 5 |
| 15 | 1608.8704 | 804.9388 | 1591.8438 | 796.4256 | 1590.8598 | 795.9336 | L | 473.2970 | 237.1521 | | | 455.2864 | 228.1468 | 4 |
| 16 | 1721.9545 | 861.4809 | 1704.9279 | 852.9676 | 1703.9439 | 852.4756 | L | 360.2129 | 180.6101 | | | 342.2023 | 171.6048 | 3 |
| 17 | 1836.9814 | 918.9943 | 1819.9549 | 910.4811 | 1818.9708 | 909.9891 | D | 247.1288 | 124.0681 | | | 229.1183 | 115.0628 | 2 |
| 18 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI **BLAST** search of [KQATVGDVNTDRPGLLDL](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|---|
| 34.9 | 1967.0688 | 0.0007 | KQATVGDVNTDRPGLLDL |
| 19.9 | 1966.9133 | 0.1561 | RGGSGGSGAGPGTTGAAGEFAFA |
| 13.0 | 1967.0826 | -0.0132 | EFADSLGVPFLETSAKNA |
| 13.0 | 1967.2403 | -0.1709 | EVVLMKVLGGCKLLLRL |
| 12.7 | 1967.1237 | -0.0543 | REKLCESLGLRVADLPL |
| 12.0 | 1967.0404 | 0.0291 | EIIAELRYDLPALYNE |
| 11.8 | 1967.2281 | -0.1587 | SEAKILFLLQLLTDHI |
| 11.4 | 1967.0517 | 0.0178 | TIISIASNVAGHPLVWDF |
| 11.4 | 1966.9021 | 0.1674 | ISNNGATGTWLYRNESD |
| 11.2 | 1967.1826 | -0.1131 | LKGETRLNCIRIARKA |

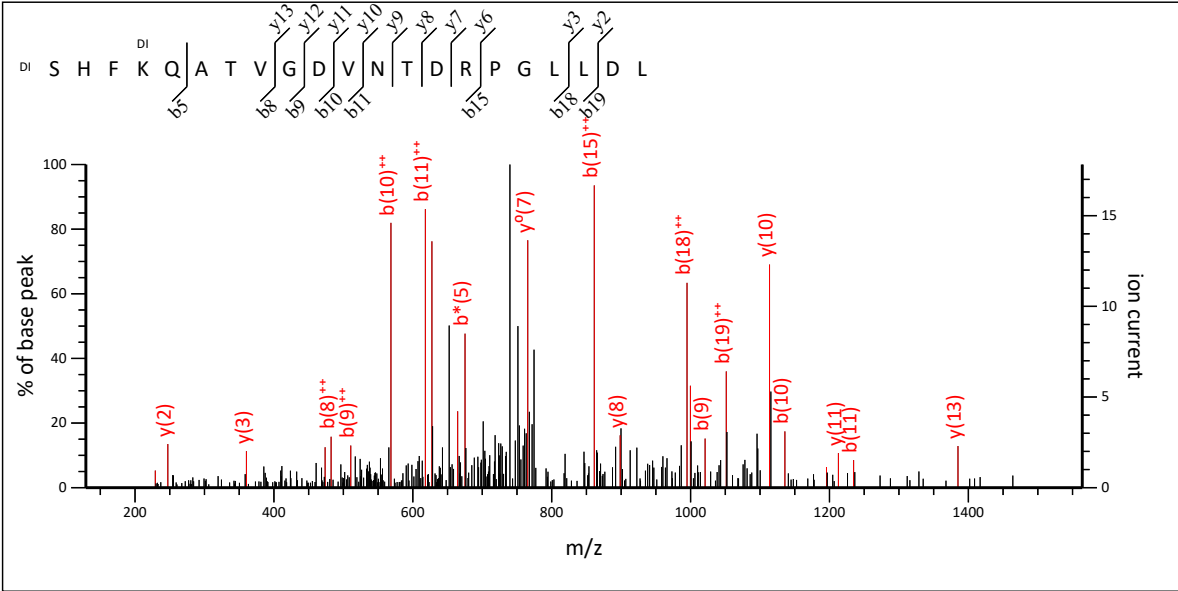
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SHFKQATVGDVNTDRPGLLDL**
Found in **ACBP_MOUSE** in **SwissProt**, Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=2

Match to Query 9570: 2346.289062 from(783.103630,3+) intensity(14550.9800) scans(7669) rawscans(sn7669) rtinseconds(2938.3815) index(5403)
Title: 5404: Scan 7669 (rt=2938.38) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR
NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf

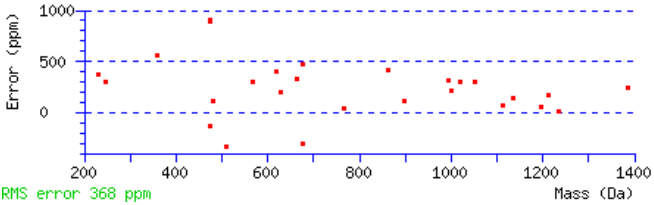
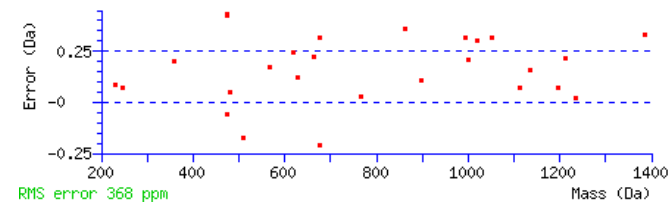


129.2 to 1564.02

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 2346.2784
Variable modifications:
N-term : Dimethyl:2H(4) (N-term)
K4 : Dimethyl:2H(4) (K)
Ions Score: 52 Expect: 0.2
Matches : 27/220 fragment ions using 37 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ^{*++} | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ^{*++} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 120.0957 | 60.5515 | | | 102.0851 | 51.5462 | S | | | | | | | 21 |
| 2 | 257.1546 | 129.0809 | | | 239.1441 | 120.0757 | H | 2228.1972 | 1114.6022 | 2211.1706 | 1106.0889 | 2210.1866 | 1105.5969 | 20 |
| 3 | 404.2230 | 202.6152 | | | 386.2125 | 193.6099 | F | 2091.1383 | 1046.0728 | 2074.1117 | 1037.5595 | 2073.1277 | 1037.0675 | 19 |
| 4 | 564.3744 | 282.6908 | 547.3479 | 274.1776 | 546.3638 | 273.6856 | K | 1944.0698 | 972.5386 | 1927.0433 | 964.0253 | 1926.0593 | 963.5333 | 18 |
| 5 | 692.4330 | 346.7201 | 675.4064 | 338.2069 | 674.4224 | 337.7148 | Q | 1783.9185 | 892.4629 | 1766.8919 | 883.9496 | 1765.9079 | 883.4576 | 17 |
| 6 | 763.4701 | 382.2387 | 746.4435 | 373.7254 | 745.4595 | 373.2334 | A | 1655.8599 | 828.4336 | 1638.8333 | 819.9203 | 1637.8493 | 819.4283 | 16 |
| 7 | 864.5178 | 432.7625 | 847.4912 | 424.2493 | 846.5072 | 423.7572 | T | 1584.8228 | 792.9150 | 1567.7962 | 784.4018 | 1566.8122 | 783.9097 | 15 |
| 8 | 963.5862 | 482.2967 | 946.5596 | 473.7835 | 945.5756 | 473.2915 | V | 1483.7751 | 742.3912 | 1466.7486 | 733.8779 | 1465.7645 | 733.3859 | 14 |
| 9 | 1020.6077 | 510.8075 | 1003.5811 | 502.2942 | 1002.5971 | 501.8022 | G | 1384.7067 | 692.8570 | 1367.6801 | 684.3437 | 1366.6961 | 683.8517 | 13 |
| 10 | 1135.6346 | 568.3209 | 1118.6081 | 559.8077 | 1117.6240 | 559.3157 | D | 1327.6852 | 664.3462 | 1310.6587 | 655.8330 | 1309.6747 | 655.3410 | 12 |
| 11 | 1234.7030 | 617.8551 | 1217.6765 | 609.3419 | 1216.6924 | 608.8499 | V | 1212.6583 | 606.8328 | 1195.6317 | 598.3195 | 1194.6477 | 597.8275 | 11 |
| 12 | 1348.7459 | 674.8766 | 1331.7194 | 666.3633 | 1330.7354 | 665.8713 | N | 1113.5899 | 557.2986 | 1096.5633 | 548.7853 | 1095.5793 | 548.2933 | 10 |
| 13 | 1449.7936 | 725.4004 | 1432.7671 | 716.8872 | 1431.7831 | 716.3952 | T | 999.5469 | 500.2771 | 982.5204 | 491.7638 | 981.5364 | 491.2718 | 9 |
| 14 | 1564.8206 | 782.9139 | 1547.7940 | 774.4006 | 1546.8100 | 773.9086 | D | 898.4993 | 449.7533 | 881.4727 | 441.2400 | 880.4887 | 440.7480 | 8 |
| 15 | 1720.9217 | 860.9645 | 1703.8951 | 852.4512 | 1702.9111 | 851.9592 | R | 783.4723 | 392.2398 | 766.4458 | 383.7265 | 765.4617 | 383.2345 | 7 |
| 16 | 1817.9744 | 909.4909 | 1800.9479 | 900.9776 | 1799.9639 | 900.4856 | P | 627.3712 | 314.1892 | | | 609.3606 | 305.1840 | 6 |
| 17 | 1874.9959 | 938.0016 | 1857.9694 | 929.4883 | 1856.9853 | 928.9963 | G | 530.3184 | 265.6629 | | | 512.3079 | 256.6576 | 5 |
| 18 | 1988.0800 | 994.5436 | 1971.0534 | 986.0303 | 1970.0694 | 985.5383 | L | 473.2970 | 237.1521 | | | 455.2864 | 228.1468 | 4 |
| 19 | 2101.1640 | 1051.0857 | 2084.1375 | 1042.5724 | 2083.1535 | 1042.0804 | L | 360.2129 | 180.6101 | | | 342.2023 | 171.6048 | 3 |
| 20 | 2216.1910 | 1108.5991 | 2199.1644 | 1100.0858 | 2198.1804 | 1099.5938 | D | 247.1288 | 124.0681 | | | 229.1183 | 115.0628 | 2 |
| 21 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI BLAST search of [SHFKQATVGDVNTDRPGLLDL](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--|
| 52.4 | 2346.2784 | 0.0107 | SHFKQATVGDVNTDRPGLLDL |
| 19.7 | 2346.2040 | 0.0851 | MVVQVVIGEQRGEGVFMAARC |
| 18.2 | 2346.1301 | 0.1590 | FDVLSSSEGGVATGTFSLEAMK |
| 17.2 | 2346.2563 | 0.0328 | LLRNMVGAGEVDEDELEVETK |
| 16.7 | 2346.3370 | -0.0480 | ATKKFRRSVLLSVDECEEV |
| 16.4 | 2346.5192 | -0.2302 | LLPKVLVQATVFARMAPEQK |
| 16.3 | 2346.2907 | -0.0016 | GTIHIQVTSEVLEQRIVQQV |
| 16.2 | 2346.1604 | 0.1286 | YQVHDRNATVDKLEDFINN |
| 15.9 | 2346.0798 | 0.2093 | CGNFDSVPGDDVNEHIASSKIS |
| 15.1 | 2346.2919 | -0.0028 | EPTPGLSREVIRFLLEQTVM |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

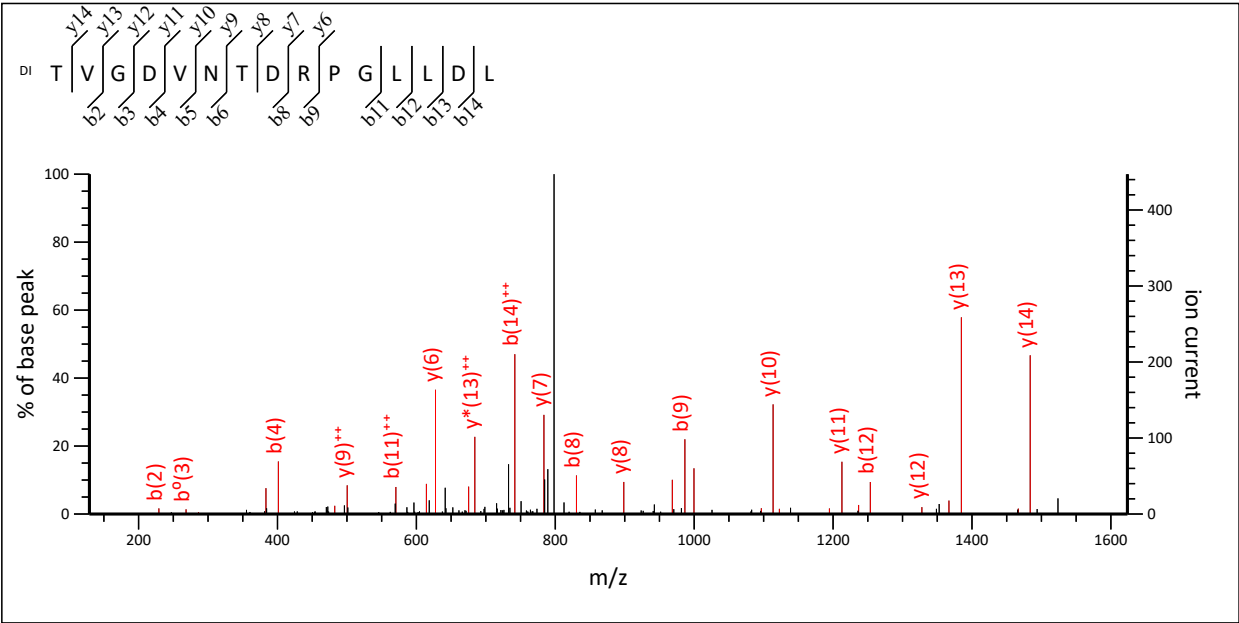
Peptide View

MS/MS Fragmentation of **TVGDVNTDRPGLLDL**
Found in **ACBP_MOUSE** in **SwissProt**, Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=2

Match to Query 5594: 1611.851988 from(806.933270,2+) intensity(92331.3520) scans(9395) rawscans(sn9395) rtinseconds(3525.0802) index(6752)

Title: 6753: Scan 9395 (rt=3525.08) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]

Data file hipocampo_01.temp.mgf

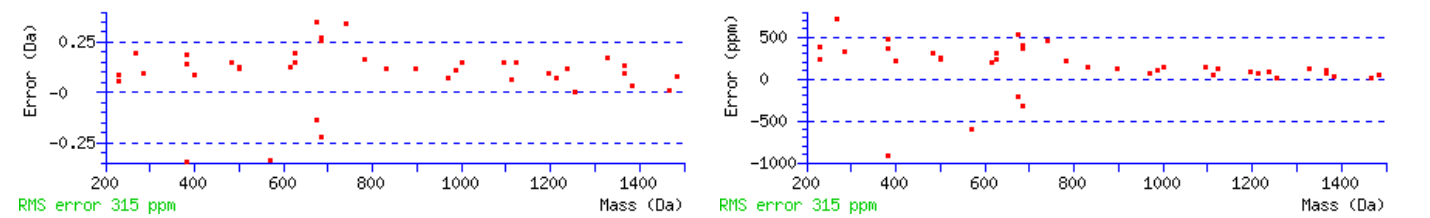


129.21 to 1623.82

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1611.8468
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 85 Expect: 0.0001
Matches : 40/144 fragment ions using 39 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 130.0863 | 65.5468 | | | 112.0757 | 56.5415 | T | | | | | | | 15 |
| 2 | 229.1547 | 115.0810 | | | 211.1441 | 106.0757 | V | 1483.7751 | 742.3912 | 1466.7485 | 733.8779 | 1465.7645 | 733.3859 | 14 |
| 3 | 286.1761 | 143.5917 | | | 268.1656 | 134.5864 | G | 1384.7067 | 692.8570 | 1367.6801 | 684.3437 | 1366.6961 | 683.8517 | 13 |
| 4 | 401.2031 | 201.1052 | | | 383.1925 | 192.0999 | D | 1327.6852 | 664.3462 | 1310.6587 | 655.8330 | 1309.6747 | 655.3410 | 12 |
| 5 | 500.2715 | 250.6394 | | | 482.2609 | 241.6341 | V | 1212.6583 | 606.8328 | 1195.6317 | 598.3195 | 1194.6477 | 597.8275 | 11 |
| 6 | 614.3144 | 307.6608 | 597.2879 | 299.1476 | 596.3039 | 298.6556 | N | 1113.5899 | 557.2986 | 1096.5633 | 548.7853 | 1095.5793 | 548.2933 | 10 |
| 7 | 715.3621 | 358.1847 | 698.3355 | 349.6714 | 697.3515 | 349.1794 | T | 999.5469 | 500.2771 | 982.5204 | 491.7638 | 981.5364 | 491.2718 | 9 |
| 8 | 830.3890 | 415.6982 | 813.3625 | 407.1849 | 812.3785 | 406.6929 | D | 898.4993 | 449.7533 | 881.4727 | 441.2400 | 880.4887 | 440.7480 | 8 |
| 9 | 986.4901 | 493.7487 | 969.4636 | 485.2354 | 968.4796 | 484.7434 | R | 783.4723 | 392.2398 | 766.4458 | 383.7265 | 765.4617 | 383.2345 | 7 |
| 10 | 1083.5429 | 542.2751 | 1066.5164 | 533.7618 | 1065.5323 | 533.2698 | P | 627.3712 | 314.1892 | | | 609.3606 | 305.1840 | 6 |
| 11 | 1140.5644 | 570.7858 | 1123.5378 | 562.2726 | 1122.5538 | 561.7805 | G | 530.3184 | 265.6629 | | | 512.3079 | 256.6576 | 5 |
| 12 | 1253.6484 | 627.3279 | 1236.6219 | 618.8146 | 1235.6379 | 618.3226 | L | 473.2970 | 237.1521 | | | 455.2864 | 228.1468 | 4 |
| 13 | 1366.7325 | 683.8699 | 1349.7060 | 675.3566 | 1348.7219 | 674.8646 | L | 360.2129 | 180.6101 | | | 342.2023 | 171.6048 | 3 |
| 14 | 1481.7594 | 741.3834 | 1464.7329 | 732.8701 | 1463.7489 | 732.3781 | D | 247.1288 | 124.0681 | | | 229.1183 | 115.0628 | 2 |
| 15 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI BLAST search of [TVGDVNTDRPGLLDL](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|------------------------------------|
| 84.9 | 1611.8468 | 0.0052 | TVGDVNTDRPGLLDL |
| 29.9 | 1611.8719 | -0.0200 | LSISASKSVPEVPEG |
| 29.6 | 1611.7678 | 0.0842 | GEQQPDTRPEDLPG |
| 28.2 | 1611.8658 | -0.0138 | PVTPTSQSVPSIPSIP |
| 28.2 | 1611.9147 | -0.0627 | RHLTSGNWEVIRI |
| 25.4 | 1611.7992 | 0.0528 | TLQGQELSTEPDGPL |
| 25.3 | 1611.9406 | -0.0887 | KEAVPSVAPSGLSGGGGA |
| 25.2 | 1611.9573 | -0.1053 | SLRELGVWRSLLR |
| 25.1 | 1611.9058 | -0.0538 | VLCGLIWASAALASLP |
| 24.9 | 1611.7127 | 0.1393 | EQDVQLYCDFPDI |

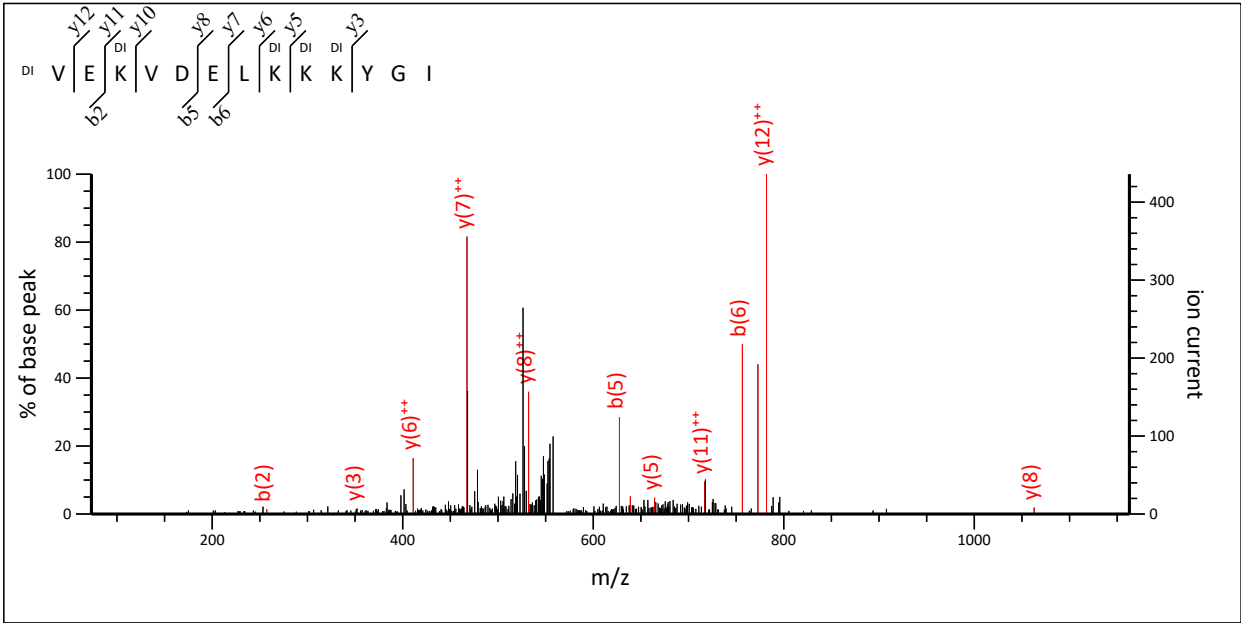
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEKVDELKKKYGI**
Found in **ACBP_MOUSE** in **SwissProt**, Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=2

Match to Query 6057: 1688.053872 from(563.691900,3+) intensity(158413.2800) scans(5190) rawscans(sn5190) rtinseconds(2058.7076) index(3181)
Title: 3182: Scan 5190 (rt=2058.71) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

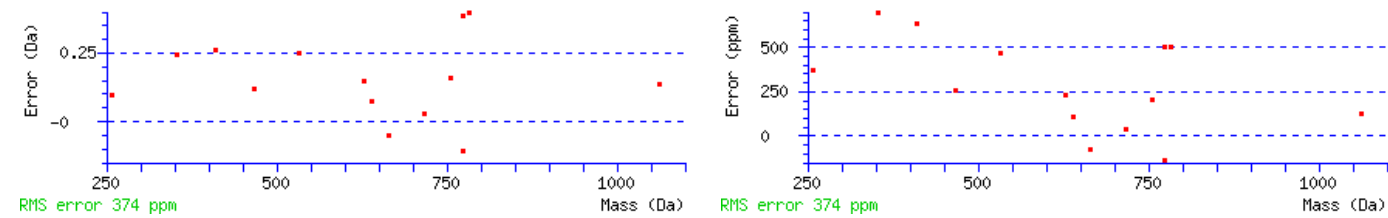


73.23 to 1162.83

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1688.0488
Variable modifications:
N-term : Dimethyl (N-term)
K3 : Dimethyl (K)
K8 : Dimethyl (K)
K9 : Dimethyl (K)
K10 : Dimethyl (K)
Ions Score: 23 Expect: 1.4e+002
Matches : 14/118 fragment ions using 31 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 128.1070 | 64.5571 | | | | | V | | | | | | | 13 |
| 2 | 257.1496 | 129.0784 | | | 239.1390 | 120.0731 | E | 1561.9564 | 781.4818 | 1544.9298 | 772.9685 | 1543.9458 | 772.4765 | 12 |
| 3 | 413.2758 | 207.1416 | 396.2493 | 198.6283 | 395.2653 | 198.1363 | K | 1432.9138 | 716.9605 | 1415.8872 | 708.4472 | 1414.9032 | 707.9552 | 11 |
| 4 | 512.3443 | 256.6758 | 495.3177 | 248.1625 | 494.3337 | 247.6705 | V | 1276.7875 | 638.8974 | 1259.7610 | 630.3841 | 1258.7769 | 629.8921 | 10 |
| 5 | 627.3712 | 314.1892 | 610.3447 | 305.6760 | 609.3606 | 305.1840 | D | 1177.7191 | 589.3632 | 1160.6925 | 580.8499 | 1159.7085 | 580.3579 | 9 |
| 6 | 756.4138 | 378.7105 | 739.3872 | 370.1973 | 738.4032 | 369.7053 | E | 1062.6921 | 531.8497 | 1045.6656 | 523.3364 | 1044.6816 | 522.8444 | 8 |
| 7 | 869.4979 | 435.2526 | 852.4713 | 426.7393 | 851.4873 | 426.2473 | L | 933.6496 | 467.3284 | 916.6230 | 458.8151 | | | 7 |
| 8 | 1025.6241 | 513.3157 | 1008.5976 | 504.8024 | 1007.6136 | 504.3104 | K | 820.5655 | 410.7864 | 803.5389 | 402.2731 | | | 6 |
| 9 | 1181.7504 | 591.3788 | 1164.7238 | 582.8656 | 1163.7398 | 582.3735 | K | 664.4392 | 332.7233 | 647.4127 | 324.2100 | | | 5 |
| 10 | 1337.8766 | 669.4420 | 1320.8501 | 660.9287 | 1319.8661 | 660.4367 | K | 508.3130 | 254.6601 | 491.2864 | 246.1468 | | | 4 |
| 11 | 1500.9400 | 750.9736 | 1483.9134 | 742.4604 | 1482.9294 | 741.9683 | Y | 352.1867 | 176.5970 | | | | | 3 |
| 12 | 1557.9614 | 779.4844 | 1540.9349 | 770.9711 | 1539.9509 | 770.4791 | G | 189.1234 | 95.0653 | | | | | 2 |
| 13 | | | | | | | I | 132.1019 | 66.5546 | | | | | 1 |



NCBI BLAST search of [VEKVDELKKKYGI](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|--------|----------------------------------|
| 23.4 | 1688.0488 | 0.0051 | VEKVDELKKKYGI |
| 18.9 | 1687.8927 | 0.1612 | GERLTQCREVLLTT |
| 17.2 | 1687.8570 | 0.1969 | FVFPRESETDHVK |
| 16.9 | 1687.8933 | 0.1605 | GSELGLELVFVWNR |
| 16.4 | 1687.9422 | 0.1117 | TQKSYSSSETLKAY |
| 15.7 | 1687.9719 | 0.0820 | LSAYEQKLQTVHAS |
| 15.4 | 1687.8967 | 0.1572 | ALLSGREMGPTLPGY |
| 15.4 | 1687.8516 | 0.2023 | KSVLTAGGVSGEELDE |
| 15.1 | 1688.0310 | 0.0228 | VELKIVGEKACKIF |
| 14.2 | 1687.7956 | 0.2582 | GELRTHVSRQVCM |

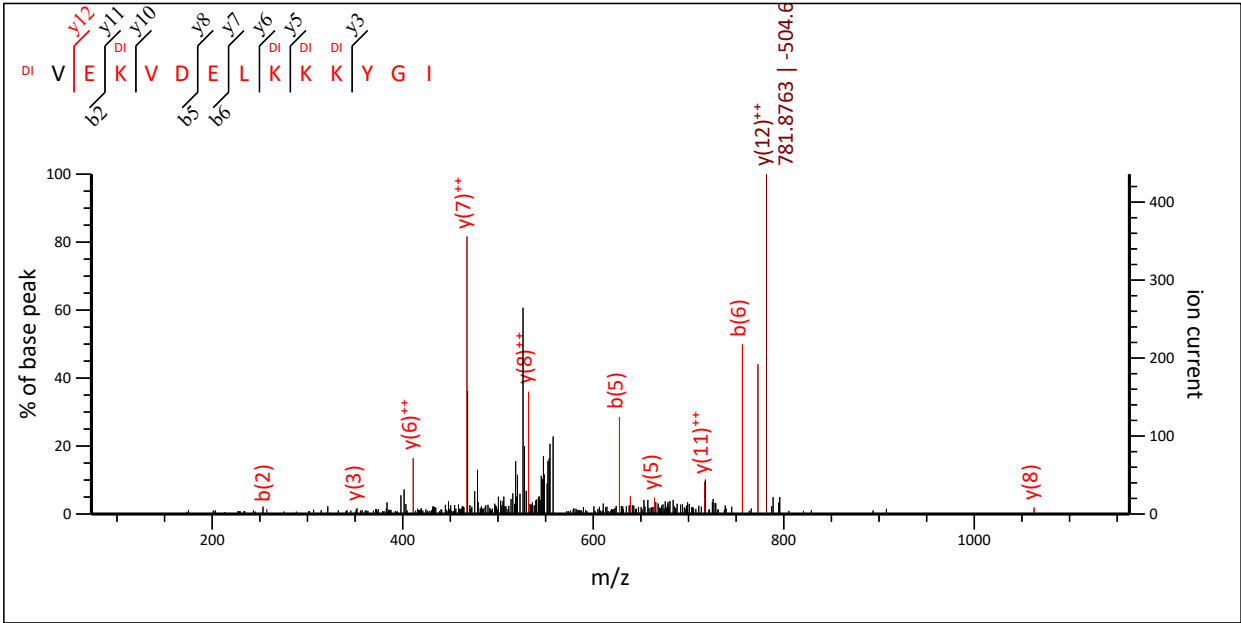
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEKVDELKKKYGI**
Found in **ACBP_MOUSE** in **SwissProt**, Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=2

Match to Query 6057: 1688.053872 from(563.691900,3+) intensity(158413.2800) scans(5190) rawscans(sn5190) rtinseconds(2058.7076) index(3181)
Title: 3182: Scan 5190 (rt=2058.71) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

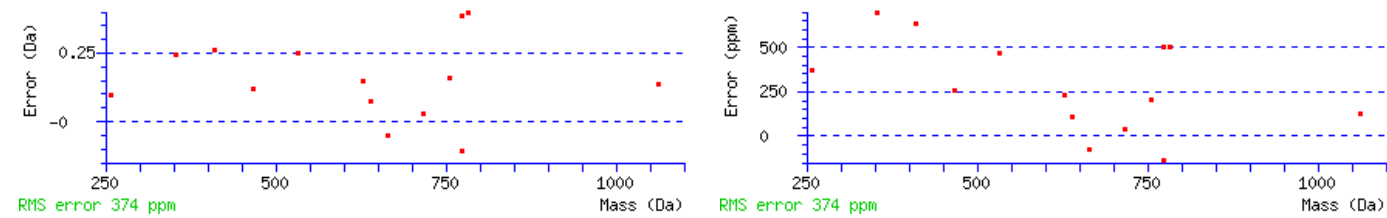


73.23 to 1162.83

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1688.0488
Variable modifications:
N-term : Dimethyl (N-term)
K3 : Dimethyl (K)
K8 : Dimethyl (K)
K9 : Dimethyl (K)
K10 : Dimethyl (K)
Ions Score: 23 Expect: 1.4e+002
Matches : 14/118 fragment ions using 31 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 128.1070 | 64.5571 | | | | | V | | | | | | | 13 |
| 2 | 257.1496 | 129.0784 | | | 239.1390 | 120.0731 | E | 1561.9564 | 781.4818 | 1544.9298 | 772.9685 | 1543.9458 | 772.4765 | 12 |
| 3 | 413.2758 | 207.1416 | 396.2493 | 198.6283 | 395.2653 | 198.1363 | K | 1432.9138 | 716.9605 | 1415.8872 | 708.4472 | 1414.9032 | 707.9552 | 11 |
| 4 | 512.3443 | 256.6758 | 495.3177 | 248.1625 | 494.3337 | 247.6705 | V | 1276.7875 | 638.8974 | 1259.7610 | 630.3841 | 1258.7769 | 629.8921 | 10 |
| 5 | 627.3712 | 314.1892 | 610.3447 | 305.6760 | 609.3606 | 305.1840 | D | 1177.7191 | 589.3632 | 1160.6925 | 580.8499 | 1159.7085 | 580.3579 | 9 |
| 6 | 756.4138 | 378.7105 | 739.3872 | 370.1973 | 738.4032 | 369.7053 | E | 1062.6921 | 531.8497 | 1045.6656 | 523.3364 | 1044.6816 | 522.8444 | 8 |
| 7 | 869.4979 | 435.2526 | 852.4713 | 426.7393 | 851.4873 | 426.2473 | L | 933.6496 | 467.3284 | 916.6230 | 458.8151 | | | 7 |
| 8 | 1025.6241 | 513.3157 | 1008.5976 | 504.8024 | 1007.6136 | 504.3104 | K | 820.5655 | 410.7864 | 803.5389 | 402.2731 | | | 6 |
| 9 | 1181.7504 | 591.3788 | 1164.7238 | 582.8656 | 1163.7398 | 582.3735 | K | 664.4392 | 332.7233 | 647.4127 | 324.2100 | | | 5 |
| 10 | 1337.8766 | 669.4420 | 1320.8501 | 660.9287 | 1319.8661 | 660.4367 | K | 508.3130 | 254.6601 | 491.2864 | 246.1468 | | | 4 |
| 11 | 1500.9400 | 750.9736 | 1483.9134 | 742.4604 | 1482.9294 | 741.9683 | Y | 352.1867 | 176.5970 | | | | | 3 |
| 12 | 1557.9614 | 779.4844 | 1540.9349 | 770.9711 | 1539.9509 | 770.4791 | G | 189.1234 | 95.0653 | | | | | 2 |
| 13 | | | | | | | I | 132.1019 | 66.5546 | | | | | 1 |



NCBI BLAST search of [VEKVDELKKKYGI](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

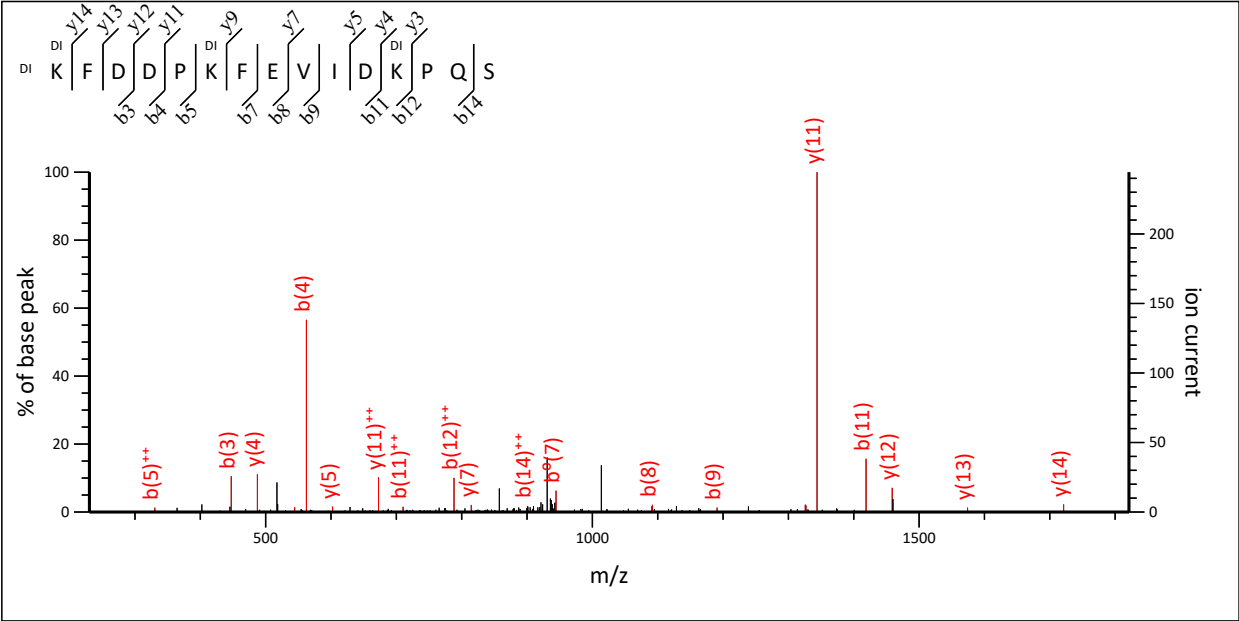
| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|--------|----------------------------------|
| 23.4 | 1688.0488 | 0.0051 | VEKVDELKKKYGI |
| 18.9 | 1687.8927 | 0.1612 | GERLTQCREVLLTT |
| 17.2 | 1687.8570 | 0.1969 | FVFPRESETDHVK |
| 16.9 | 1687.8933 | 0.1605 | GSELGLELVFVWNR |
| 16.4 | 1687.9422 | 0.1117 | TQKSYSSSETLKAY |
| 15.7 | 1687.9719 | 0.0820 | LSAYEQKLQTVHAS |
| 15.4 | 1687.8967 | 0.1572 | ALLSGREMGPTLPGY |
| 15.4 | 1687.8516 | 0.2023 | KSVLTAGGVSGEELDE |
| 15.1 | 1688.0310 | 0.0228 | VELKIVGEKACKIF |
| 14.2 | 1687.7956 | 0.2582 | GELRTHVSRQVCM |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **KFDDDPKFEVIDKPQS**
Found in **ATP5J_MOUSE** in **SwissProt**, ATP synthase-coupling factor 6, mitochondrial OS=Mus musculus GN=Atp5j PE=1 SV=1
Match to Query 7204: 1904.038388 from(953.026470,2+) intensity(32767.4570) scans(5862) rawscans(sn5862) rtinseconds(2278.4824) index(3776)
Title: 3777: Scan 5862 (rt=2278.48) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf



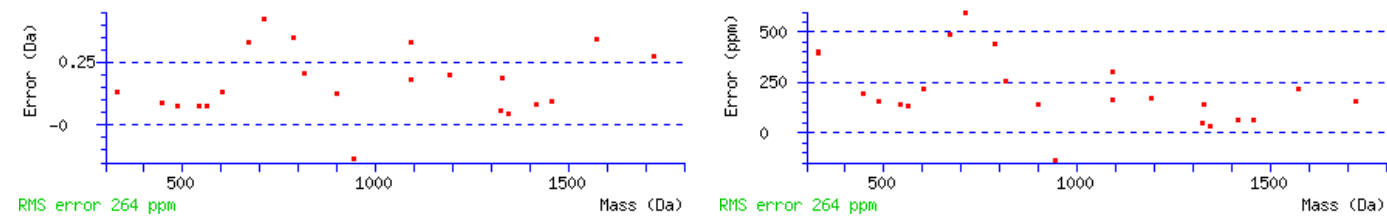


230.31 to 1821.15

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1904.0295
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
K6 : Dimethyl (K)
K12 : Dimethyl (K)
Ions Score: 45 Expect: 1
Matches : 23/162 fragment ions using 48 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 185.1648 | 93.0861 | 168.1383 | 84.5728 | | | K | | | | | | | 15 |
| 2 | 332.2333 | 166.6203 | 315.2067 | 158.1070 | | | F | 1720.8792 | 860.9433 | 1703.8527 | 852.4300 | 1702.8687 | 851.9380 | 14 |
| 3 | 447.2602 | 224.1337 | 430.2336 | 215.6205 | 429.2496 | 215.1285 | D | 1573.8108 | 787.4090 | 1556.7843 | 778.8958 | 1555.8003 | 778.4038 | 13 |
| 4 | 562.2871 | 281.6472 | 545.2606 | 273.1339 | 544.2766 | 272.6419 | D | 1458.7839 | 729.8956 | 1441.7573 | 721.3823 | 1440.7733 | 720.8903 | 12 |
| 5 | 659.3399 | 330.1736 | 642.3134 | 321.6603 | 641.3293 | 321.1683 | P | 1343.7569 | 672.3821 | 1326.7304 | 663.8688 | 1325.7464 | 663.3768 | 11 |
| 6 | 815.4662 | 408.2367 | 798.4396 | 399.7234 | 797.4556 | 399.2314 | K | 1246.7042 | 623.8557 | 1229.6776 | 615.3424 | 1228.6936 | 614.8504 | 10 |
| 7 | 962.5346 | 481.7709 | 945.5080 | 473.2577 | 944.5240 | 472.7656 | F | 1090.5779 | 545.7926 | 1073.5514 | 537.2793 | 1072.5673 | 536.7873 | 9 |
| 8 | 1091.5772 | 546.2922 | 1074.5506 | 537.7790 | 1073.5666 | 537.2869 | E | 943.5095 | 472.2584 | 926.4829 | 463.7451 | 925.4989 | 463.2531 | 8 |
| 9 | 1190.6456 | 595.8264 | 1173.6190 | 587.3132 | 1172.6350 | 586.8211 | V | 814.4669 | 407.7371 | 797.4403 | 399.2238 | 796.4563 | 398.7318 | 7 |
| 10 | 1303.7297 | 652.3685 | 1286.7031 | 643.8552 | 1285.7191 | 643.3632 | I | 715.3985 | 358.2029 | 698.3719 | 349.6896 | 697.3879 | 349.1976 | 6 |
| 11 | 1418.7566 | 709.8819 | 1401.7300 | 701.3687 | 1400.7460 | 700.8767 | D | 602.3144 | 301.6608 | 585.2879 | 293.1476 | 584.3039 | 292.6556 | 5 |
| 12 | 1574.8829 | 787.9451 | 1557.8563 | 779.4318 | 1556.8723 | 778.9398 | K | 487.2875 | 244.1474 | 470.2609 | 235.6341 | 469.2769 | 235.1421 | 4 |
| 13 | 1671.9356 | 836.4714 | 1654.9091 | 827.9582 | 1653.9251 | 827.4662 | P | 331.1612 | 166.0842 | 314.1347 | 157.5710 | 313.1506 | 157.0790 | 3 |
| 14 | 1799.9942 | 900.5007 | 1782.9677 | 891.9875 | 1781.9836 | 891.4955 | Q | 234.1084 | 117.5579 | 217.0819 | 109.0446 | 216.0979 | 108.5526 | 2 |
| 15 | | | | | | | S | 106.0499 | 53.5286 | | | 88.0393 | 44.5233 | 1 |



NCBI BLAST search of [KFDDPKFEVIDKPQS](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|------------------------------------|
| 44.9 | 1904.0295 | 0.0088 | KFDDPKFEVIDKPQS |
| 19.1 | 1903.9836 | 0.0548 | DPVSMPGSSRAVSDRRGV |
| 16.5 | 1903.9877 | 0.0506 | THHVLIRSTWDRRR |
| 16.4 | 1903.9965 | 0.0419 | MKDDPITLFVALSPQGT |
| 16.2 | 1903.8736 | 0.1648 | NFEFDQMYPVVALVML |
| 16.1 | 1904.0903 | -0.0520 | MKDDPITLFVALSPQGT |
| 15.2 | 1903.9164 | 0.1220 | GGDFDAKQSLVGDIGDVN |
| 14.2 | 1904.0458 | -0.0074 | ETSPPPRDELLDIARQ |
| 14.1 | 1903.8847 | 0.1537 | TLPEQGNATNRDHSSMT |
| 14.0 | 1904.0511 | -0.0127 | MFDGSVLAAYGNVIVVTL |

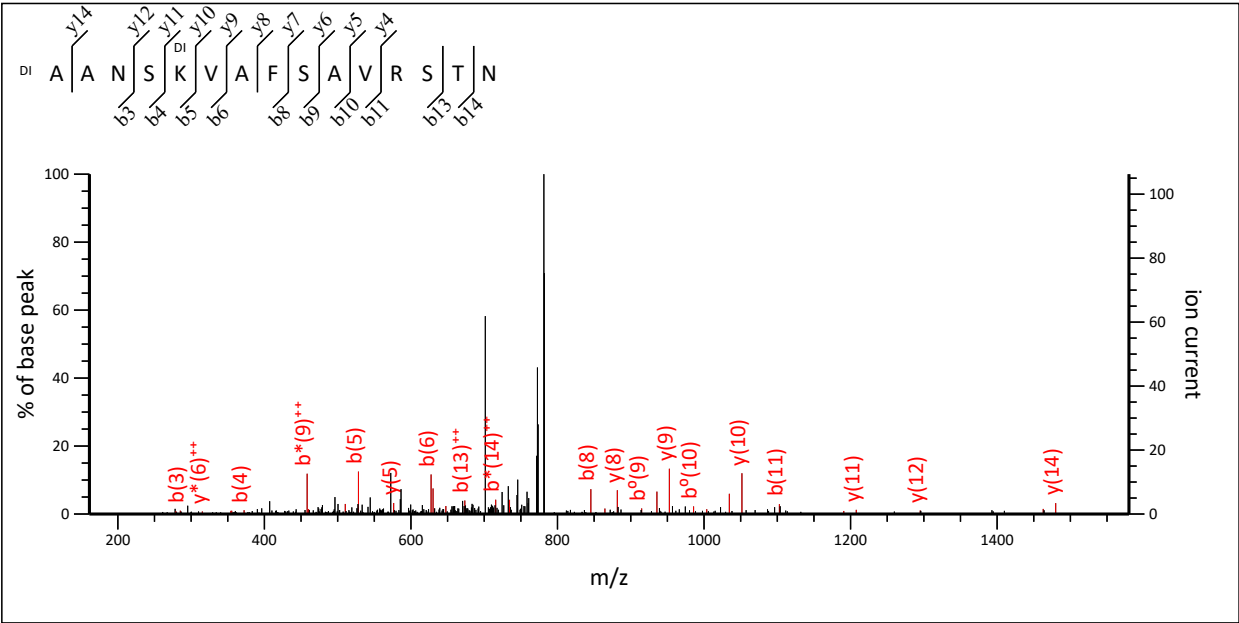
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AANSKVAFSAVRSTN**
Found in **CBLN4_MOUSE** in **SwissProt**, Cerebellin-4 OS=Mus musculus GN=Cbln4 PE=1 SV=1

Match to Query 5849: 1577.853468 from(789.934010,2+) intensity(26784.0980) scans(3621) rawscans(sn3621) rtinseconds(1555.4991) index(1881)
Title: 1882: Scan 3621 (rt=1555.5) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf

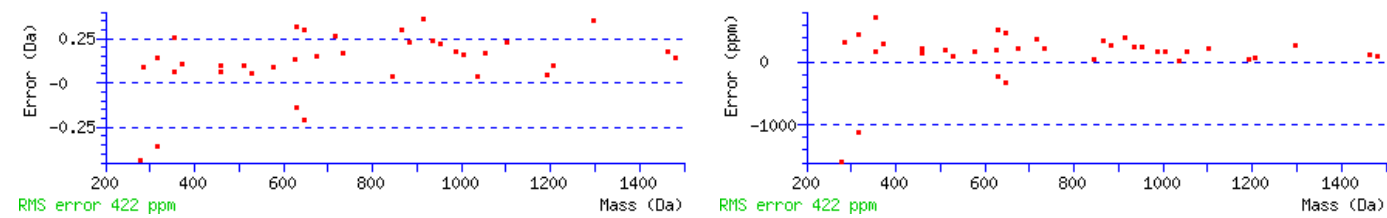


Navigation icons: ? (help), zoom in, zoom out, zoom reset, pan, and a range selector showing 161.21 to 1579.93.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1577.8525
Variable modifications:
N-term : Dimethyl (N-term)
K5 : Dimethyl (K)
Ions Score: 28 Expect: 50
Matches : 36/156 fragment ions using 100 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | | | A | | | | | | | 15 |
| 2 | 171.1128 | 86.0600 | | | | | A | 1479.7914 | 740.3993 | 1462.7649 | 731.8861 | 1461.7809 | 731.3941 | 14 |
| 3 | 285.1557 | 143.0815 | 268.1292 | 134.5682 | | | N | 1408.7543 | 704.8808 | 1391.7278 | 696.3675 | 1390.7437 | 695.8755 | 13 |
| 4 | 372.1878 | 186.5975 | 355.1612 | 178.0842 | 354.1772 | 177.5922 | S | 1294.7114 | 647.8593 | 1277.6848 | 639.3461 | 1276.7008 | 638.8540 | 12 |
| 5 | 528.3140 | 264.6606 | 511.2875 | 256.1474 | 510.3035 | 255.6554 | K | 1207.6793 | 604.3433 | 1190.6528 | 595.8300 | 1189.6688 | 595.3380 | 11 |
| 6 | 627.3824 | 314.1949 | 610.3559 | 305.6816 | 609.3719 | 305.1896 | V | 1051.5531 | 526.2802 | 1034.5265 | 517.7669 | 1033.5425 | 517.2749 | 10 |
| 7 | 698.4195 | 349.7134 | 681.3930 | 341.2001 | 680.4090 | 340.7081 | A | 952.4847 | 476.7460 | 935.4581 | 468.2327 | 934.4741 | 467.7407 | 9 |
| 8 | 845.4880 | 423.2476 | 828.4614 | 414.7343 | 827.4774 | 414.2423 | F | 881.4476 | 441.2274 | 864.4210 | 432.7141 | 863.4370 | 432.2221 | 8 |
| 9 | 932.5200 | 466.7636 | 915.4934 | 458.2504 | 914.5094 | 457.7584 | S | 734.3791 | 367.6932 | 717.3526 | 359.1799 | 716.3686 | 358.6879 | 7 |
| 10 | 1003.5571 | 502.2822 | 986.5306 | 493.7689 | 985.5465 | 493.2769 | A | 647.3471 | 324.1772 | 630.3206 | 315.6639 | 629.3365 | 315.1719 | 6 |
| 11 | 1102.6255 | 551.8164 | 1085.5990 | 543.3031 | 1084.6150 | 542.8111 | V | 576.3100 | 288.6586 | 559.2835 | 280.1454 | 558.2994 | 279.6534 | 5 |
| 12 | 1258.7266 | 629.8670 | 1241.7001 | 621.3537 | 1240.7161 | 620.8617 | R | 477.2416 | 239.1244 | 460.2150 | 230.6112 | 459.2310 | 230.1191 | 4 |
| 13 | 1345.7587 | 673.3830 | 1328.7321 | 664.8697 | 1327.7481 | 664.3777 | S | 321.1405 | 161.0739 | 304.1139 | 152.5606 | 303.1299 | 152.0686 | 3 |
| 14 | 1446.8063 | 723.9068 | 1429.7798 | 715.3935 | 1428.7958 | 714.9015 | T | 234.1084 | 117.5579 | 217.0819 | 109.0446 | 216.0979 | 108.5526 | 2 |
| 15 | | | | | | | N | 133.0608 | 67.0340 | 116.0342 | 58.5207 | | | 1 |



NCBI BLAST search of [AANSKVAFSAVRSTN](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|---------------------------------|
| 27.9 | 1577.8525 | 0.0009 | AANSKVAFSAVRSTN |
| 17.5 | 1577.8314 | 0.0220 | VTTRVWNRTEAAS |
| 16.4 | 1577.7435 | 0.1099 | ASLYVAMNGEGYLY |
| 14.5 | 1577.7825 | 0.0710 | VDEGGVFESLKAET |
| 13.9 | 1577.9323 | -0.0788 | GRHVAVLPEIDPV |
| 13.6 | 1577.9273 | -0.0738 | LISIKANCIDSTASA |
| 13.5 | 1577.9365 | -0.0830 | ASREHLKRSLALAA |
| 13.4 | 1577.8049 | 0.0486 | EDVPSQPPENVRAL |
| 13.0 | 1577.9029 | -0.0494 | KVEDVVETLLQLH |
| 12.9 | 1577.8161 | 0.0373 | LTENPQVAQRANAP |

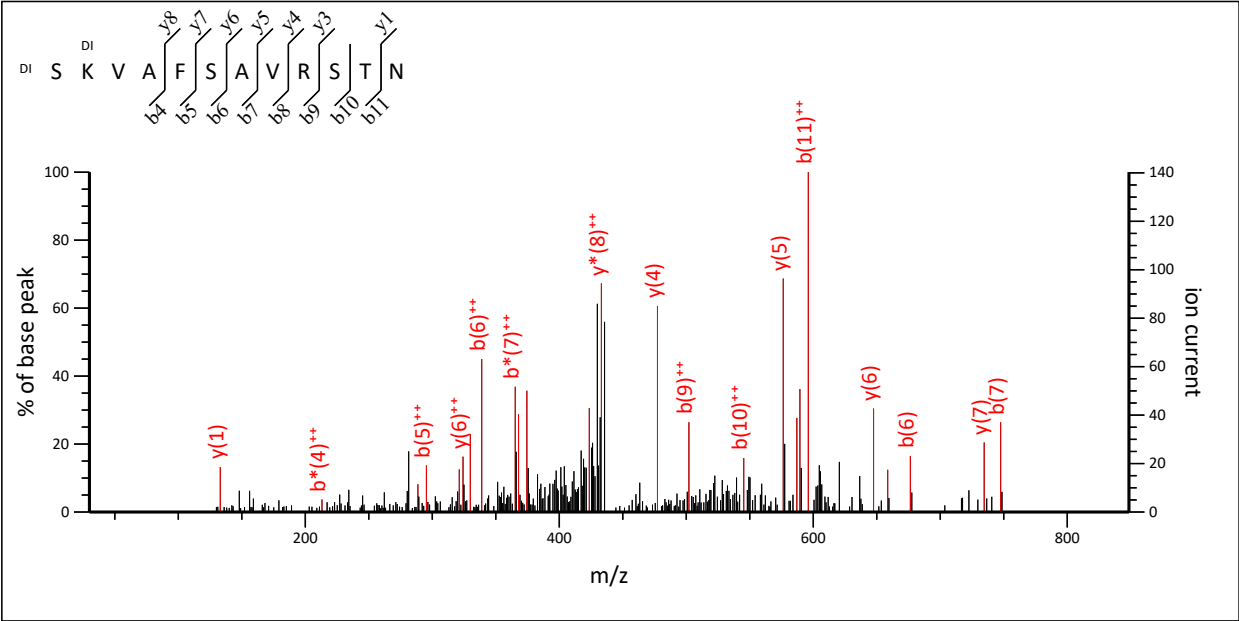
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SKVAFSAVRSTN**
Found in **CBLN4_MOUSE** in **SwissProt**, Cerebellin-4 OS=Mus musculus GN=Cbln4 PE=1 SV=1

Match to Query 3962: 1321.739472 from(441.587100,3+) intensity(89601.6020) scans(3471) rawscans(sn3471) rtinseconds(1502.291) index(1720)
Title: 1721: Scan 3471 (rt=1502.29) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

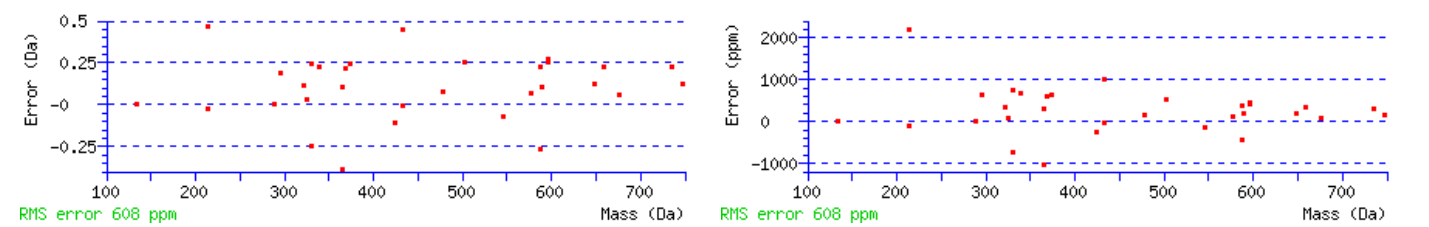


Navigation icons: ? (help), zoom in, zoom out, zoom reset, 30.01 to 848.6 (mass range), zoom in, zoom out, zoom reset.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1321.7354
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
Ions Score: 44 Expect: 1.3
Matches : 31/128 fragment ions using 41 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 116.0706 | 58.5389 | | | 98.0600 | 49.5337 | S | | | | | | | 12 |
| 2 | 272.1969 | 136.6021 | 255.1703 | 128.0888 | 254.1863 | 127.5968 | K | 1207.6793 | 604.3433 | 1190.6528 | 595.8300 | 1189.6688 | 595.3380 | 11 |
| 3 | 371.2653 | 186.1363 | 354.2387 | 177.6230 | 353.2547 | 177.1310 | V | 1051.5531 | 526.2802 | 1034.5265 | 517.7669 | 1033.5425 | 517.2749 | 10 |
| 4 | 442.3024 | 221.6548 | 425.2758 | 213.1416 | 424.2918 | 212.6496 | A | 952.4847 | 476.7460 | 935.4581 | 468.2327 | 934.4741 | 467.7407 | 9 |
| 5 | 589.3708 | 295.1890 | 572.3443 | 286.6758 | 571.3602 | 286.1838 | F | 881.4476 | 441.2274 | 864.4210 | 432.7141 | 863.4370 | 432.2221 | 8 |
| 6 | 676.4028 | 338.7051 | 659.3763 | 330.1918 | 658.3923 | 329.6998 | S | 734.3791 | 367.6932 | 717.3526 | 359.1799 | 716.3686 | 358.6879 | 7 |
| 7 | 747.4400 | 374.2236 | 730.4134 | 365.7103 | 729.4294 | 365.2183 | A | 647.3471 | 324.1772 | 630.3206 | 315.6639 | 629.3365 | 315.1719 | 6 |
| 8 | 846.5084 | 423.7578 | 829.4818 | 415.2445 | 828.4978 | 414.7525 | V | 576.3100 | 288.6586 | 559.2835 | 280.1454 | 558.2994 | 279.6534 | 5 |
| 9 | 1002.6095 | 501.8084 | 985.5829 | 493.2951 | 984.5989 | 492.8031 | R | 477.2416 | 239.1244 | 460.2150 | 230.6112 | 459.2310 | 230.1191 | 4 |
| 10 | 1089.6415 | 545.3244 | 1072.6150 | 536.8111 | 1071.6309 | 536.3191 | S | 321.1405 | 161.0739 | 304.1139 | 152.5606 | 303.1299 | 152.0686 | 3 |
| 11 | 1190.6892 | 595.8482 | 1173.6626 | 587.3350 | 1172.6786 | 586.8429 | T | 234.1084 | 117.5579 | 217.0819 | 109.0446 | 216.0979 | 108.5526 | 2 |
| 12 | | | | | | | N | 133.0608 | 67.0340 | 116.0342 | 58.5207 | | | 1 |



NCBI BLAST search of [SKVAFSAVRSTN](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--------------------------------|
| 43.7 | 1321.7354 | 0.0041 | SKVAFSAVRSTN |
| 32.1 | 1321.6700 | 0.0695 | RQESSALIDCL |
| 28.0 | 1321.6849 | 0.0545 | CQAALGASEASGLL |
| 25.8 | 1321.6048 | 0.1347 | REDENASAADV N |
| 25.6 | 1321.6664 | 0.0731 | VETTATGQQVTN |
| 25.6 | 1321.7486 | -0.0091 | GVTMKG TQDNSL |
| 25.4 | 1321.6486 | 0.0909 | GLLSMANSGPSTN |
| 24.3 | 1321.7242 | 0.0153 | FVTL SATNAKTN |
| 23.9 | 1321.7153 | 0.0242 | QSSQLANHIRH |
| 23.2 | 1321.7704 | -0.0309 | KDPYTGEQISL |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASKGLGSDLDSSLASL**

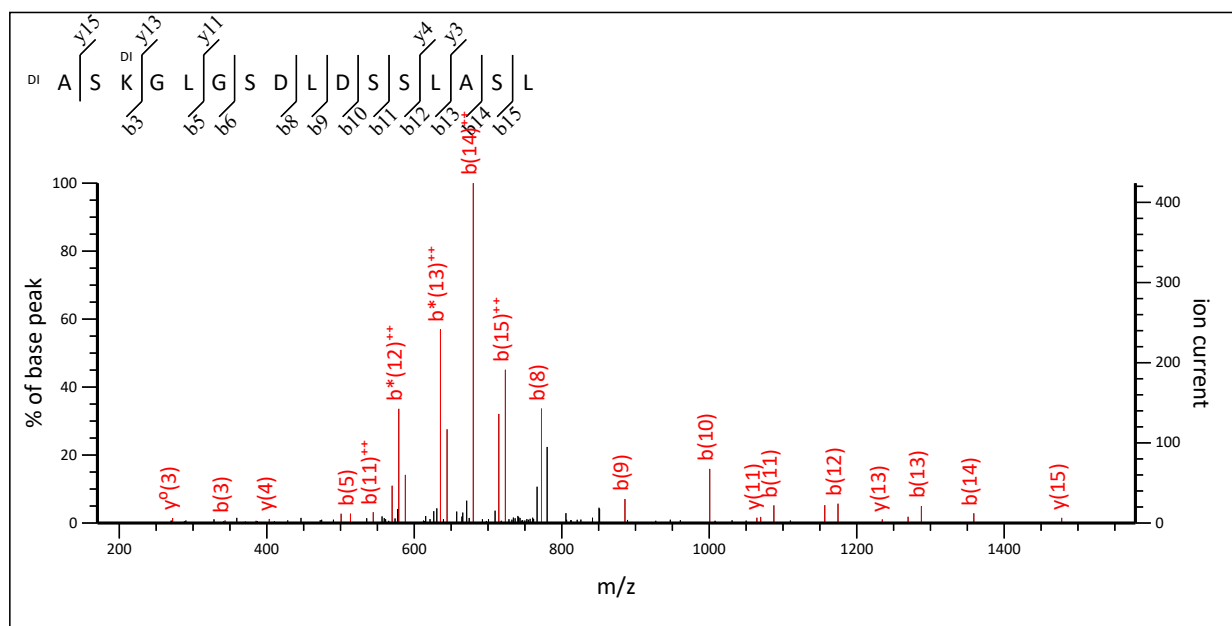
Found in **AP180 MOUSE** in **SwissProt**, Clathrin coat assembly protein AP180 OS=Mus musculus GN=Snap91 PE=1 SV=1

Match to Query 5405: 1575.841268 from(788.927910,2+) intensity(73989.8200) scans(9747) rawscans(sn9747) rtinseconds(3652.6788) index(7038)

Title: 7039: Scan 9747 (rt=3652.68) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR

NOVAMENTE\HIPOCAMPO\hipocampo 01.raw

Data file hipocampo 01.temp.mgf



| | | |
|--------|----|---------|
| 170.33 | to | 1577.92 |
|--------|----|---------|



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1575.8356

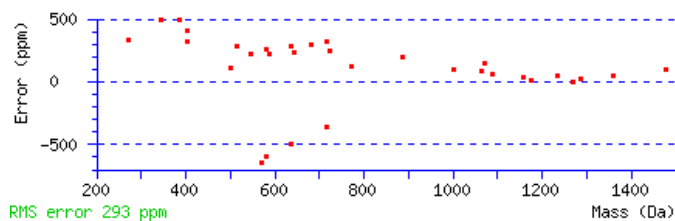
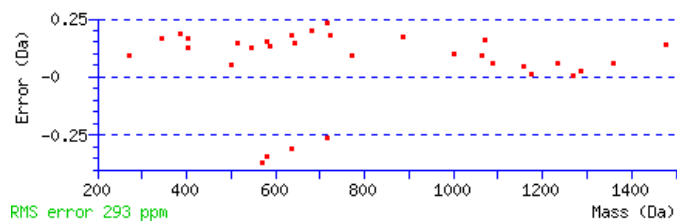
Variable modifications:

N-term : Dimethyl (N-term)

K3 : Dimethyl (K)
Ions Score: 77 Expect: 0.00063

Matches : 32/146 fragment ions using 41 most intense peaks ([help](#))

| # | b | b⁺⁺ | b[*] | b^{***} | b⁰ | b⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ^{***} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------------|----------------------|------------------------|----------------------|------------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | | | A | | | | | | | 16 |
| 2 | 187.1077 | 94.0575 | | | 169.0972 | 85.0522 | S | 1477.7744 | 739.3909 | 1460.7479 | 730.8776 | 1459.7639 | 730.3856 | 15 |
| 3 | 343.2340 | 172.1206 | 326.2074 | 163.6074 | 325.2234 | 163.1153 | K | 1390.7424 | 695.8748 | 1373.7159 | 687.3616 | 1372.7318 | 686.8696 | 14 |
| 4 | 400.2554 | 200.6314 | 383.2289 | 192.1181 | 382.2449 | 191.6261 | G | 1234.6161 | 617.8117 | | | 1216.6056 | 608.8064 | 13 |
| 5 | 513.3395 | 257.1734 | 496.3130 | 248.6601 | 495.3289 | 248.1681 | L | 1177.5947 | 589.3010 | | | 1159.5841 | 580.2957 | 12 |
| 6 | 570.3610 | 285.6841 | 553.3344 | 277.1709 | 552.3504 | 276.6788 | G | 1064.5106 | 532.7589 | | | 1046.5000 | 523.7537 | 11 |
| 7 | 657.3930 | 329.2001 | 640.3665 | 320.6869 | 639.3824 | 320.1949 | S | 1007.4891 | 504.2482 | | | 989.4786 | 495.2429 | 10 |
| 8 | 772.4199 | 386.7136 | 755.3934 | 378.2003 | 754.4094 | 377.7083 | D | 920.4571 | 460.7322 | | | 902.4466 | 451.7269 | 9 |
| 9 | 885.5040 | 443.2556 | 868.4775 | 434.7424 | 867.4934 | 434.2504 | L | 805.4302 | 403.2187 | | | 787.4196 | 394.2134 | 8 |
| 10 | 1000.5310 | 500.7691 | 983.5044 | 492.2558 | 982.5204 | 491.7638 | D | 692.3461 | 346.6767 | | | 674.3355 | 337.6714 | 7 |
| 11 | 1087.5630 | 544.2851 | 1070.5364 | 535.7719 | 1069.5524 | 535.2798 | S | 577.3192 | 289.1632 | | | 559.3086 | 280.1579 | 6 |
| 12 | 1174.5950 | 587.8011 | 1157.5685 | 579.2879 | 1156.5844 | 578.7959 | S | 490.2871 | 245.6472 | | | 472.2766 | 236.6419 | 5 |
| 13 | 1287.6791 | 644.3432 | 1270.6525 | 635.8299 | 1269.6685 | 635.3379 | L | 403.2551 | 202.1312 | | | 385.2445 | 193.1259 | 4 |
| 14 | 1358.7162 | 679.8617 | 1341.6896 | 671.3485 | 1340.7056 | 670.8564 | A | 290.1710 | 145.5892 | | | 272.1605 | 136.5839 | 3 |
| 15 | 1445.7482 | 723.3777 | 1428.7217 | 714.8645 | 1427.7376 | 714.3725 | S | 219.1339 | 110.0706 | | | 201.1234 | 101.0653 | 2 |
| 16 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI **BLAST** search of [ASKGLGSDLDSSLASL](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|----------------------------------|
| 76.9 | 1575.8356 | 0.0057 | ASKGLGSDLDSSLASL |
| 33.2 | 1575.8615 | -0.0203 | LAVMLAALMSSLASI |
| 31.9 | 1575.7613 | 0.0800 | AHRMDSLDSRDSI |
| 29.7 | 1575.8615 | -0.0203 | LAVMLAALMSSLASI |
| 28.0 | 1575.9021 | -0.0609 | VSALSSAGGTENLILL |
| 27.7 | 1575.9323 | -0.0911 | SVALSPTPTKSTPNI |
| 27.2 | 1575.7330 | 0.1083 | AGSLGPWGPMSSGPW |
| 26.7 | 1575.7450 | 0.0962 | NMLSSDVAQLSDPGV |
| 25.8 | 1576.1168 | -0.2755 | KPISVESSSKKVK |
| 25.8 | 1575.9134 | -0.0721 | LPLVSGRSASSSLASL |

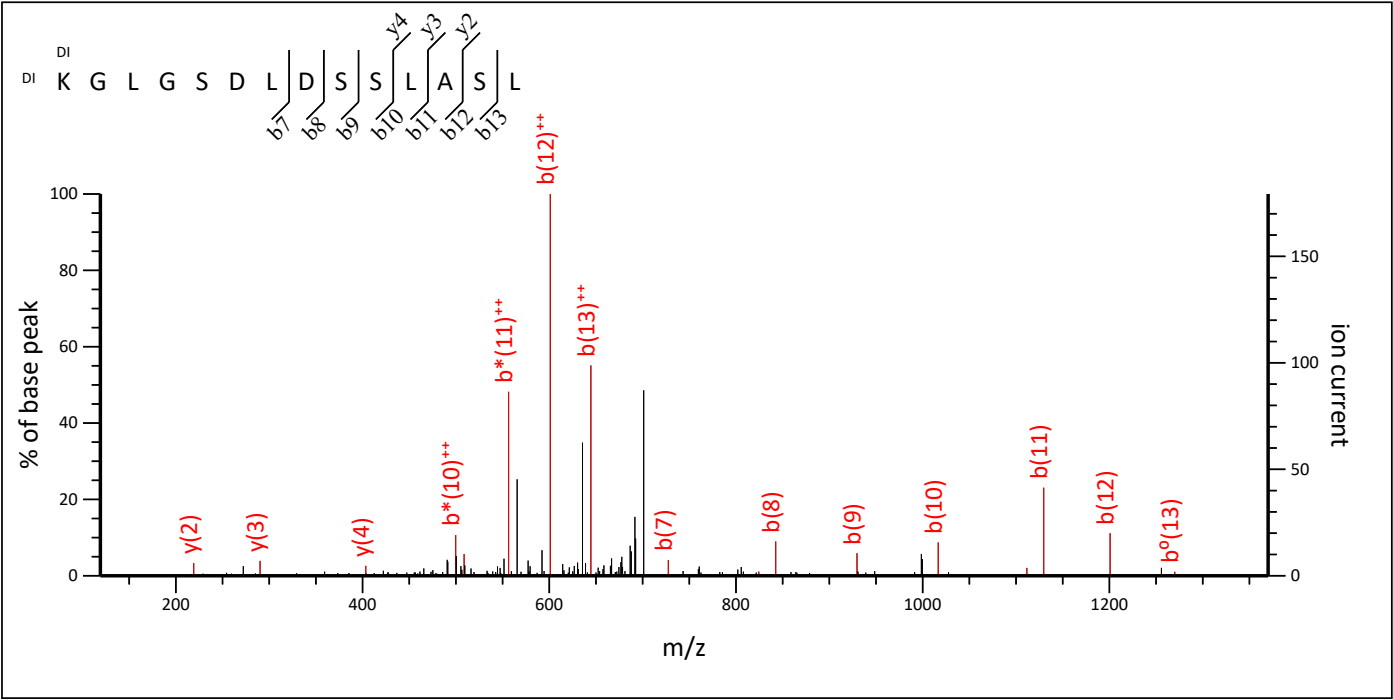
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGLGSDLSSLASL**
Found in **AP180_MOUSE** in **SwissProt**, Clathrin coat assembly protein AP180 OS=Mus musculus GN=Snap91 PE=1 SV=1

Match to Query 4749: 1417.773008 from(709.893780,2+) intensity(33636.4020) scans(9499) rawscans(sn9499)
rtinseconds(3590.1007) index(6933)
Title: 6934: Scan 9499 (rt=3590.1) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR
NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf



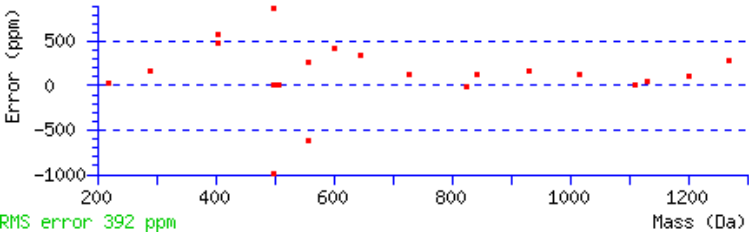
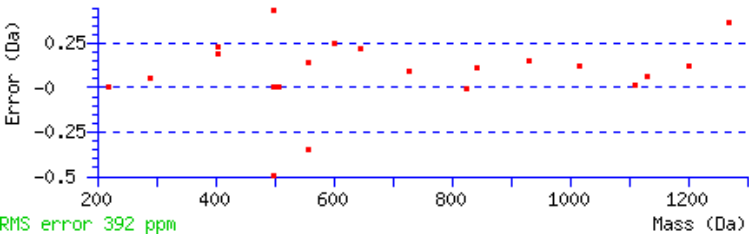
119.14 to 1370.03

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1417.7664
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
Ions Score: 57 Expect: 0.065
Matches : 21/120 fragment ions using 22 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ^{*++} | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y ^{*++} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|------------------|----------------|------------------|----|
| 1 | 185.1648 | 93.0861 | 168.1383 | 84.5728 | | | K | | | | | | 14 |
| 2 | 242.1863 | 121.5968 | 225.1598 | 113.0835 | | | G | 1234.6161 | 617.8117 | | 1216.6056 | 608.8064 | 13 |
| 3 | 355.2704 | 178.1388 | 338.2438 | 169.6255 | | | L | 1177.5947 | 589.3010 | | 1159.5841 | 580.2957 | 12 |
| 4 | 412.2918 | 206.6496 | 395.2653 | 198.1363 | | | G | 1064.5106 | 532.7589 | | 1046.5000 | 523.7537 | 11 |
| 5 | 499.3239 | 250.1656 | 482.2973 | 241.6523 | 481.3133 | 241.1603 | S | 1007.4891 | 504.2482 | | 989.4786 | 495.2429 | 10 |
| 6 | 614.3508 | 307.6790 | 597.3243 | 299.1658 | 596.3402 | 298.6738 | D | 920.4571 | 460.7322 | | 902.4466 | 451.7269 | 9 |
| 7 | 727.4349 | 364.2211 | 710.4083 | 355.7078 | 709.4243 | 355.2158 | L | 805.4302 | 403.2187 | | 787.4196 | 394.2134 | 8 |
| 8 | 842.4618 | 421.7345 | 825.4353 | 413.2213 | 824.4512 | 412.7293 | D | 692.3461 | 346.6767 | | 674.3355 | 337.6714 | 7 |
| 9 | 929.4938 | 465.2506 | 912.4673 | 456.7373 | 911.4833 | 456.2453 | S | 577.3192 | 289.1632 | | 559.3086 | 280.1579 | 6 |
| 10 | 1016.5259 | 508.7666 | 999.4993 | 500.2533 | 998.5153 | 499.7613 | S | 490.2871 | 245.6472 | | 472.2766 | 236.6419 | 5 |
| 11 | 1129.6099 | 565.3086 | 1112.5834 | 556.7953 | 1111.5994 | 556.3033 | L | 403.2551 | 202.1312 | | 385.2445 | 193.1259 | 4 |
| 12 | 1200.6470 | 600.8272 | 1183.6205 | 592.3139 | 1182.6365 | 591.8219 | A | 290.1710 | 145.5892 | | 272.1605 | 136.5839 | 3 |

| | | | | | | | | | | | | | |
|----|-----------|----------|-----------|----------|-----------|----------|---|----------|----------|--|----------|----------|---|
| 13 | 1287.6791 | 644.3432 | 1270.6525 | 635.8299 | 1269.6685 | 635.3379 | S | 219.1339 | 110.0706 | | 201.1234 | 101.0653 | 2 |
| 14 | | | | | | | L | 132.1019 | 66.5546 | | | | 1 |



NCBI **BLAST** search of [KGLGSDLDSSLASL](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

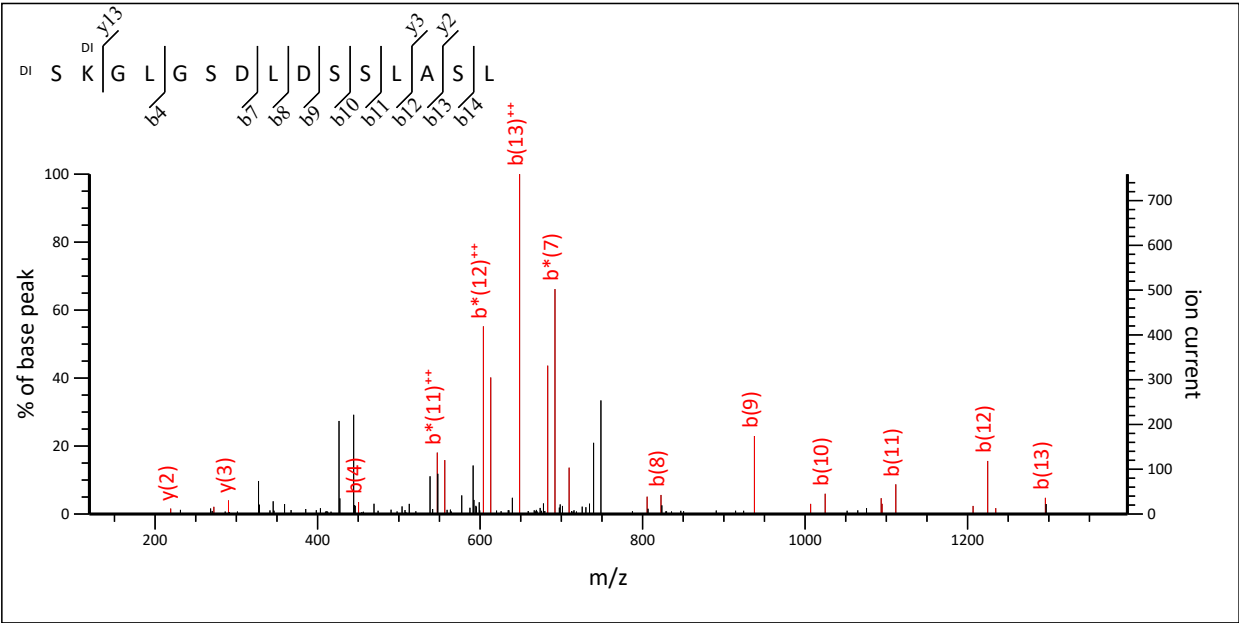
| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--------------------------------|
| 56.7 | 1417.7664 | 0.0066 | KGLGSDLDSSLASL |
| 46.6 | 1417.7010 | 0.0720 | MSLPDLSSLASI |
| 40.7 | 1417.7706 | 0.0024 | VNHADSRASLASL |
| 36.8 | 1417.6962 | 0.0768 | WALPGGSREPGEM |
| 36.1 | 1417.7920 | -0.0190 | LMDPVDGPILASL |
| 36.0 | 1417.7463 | 0.0267 | GQRHETTSSIASL |
| 35.8 | 1417.8788 | -0.1058 | AKLQMTEAALALS |
| 35.4 | 1417.7061 | 0.0670 | AEHMSDLSALASI |
| 35.2 | 1417.8079 | -0.0349 | GEALLDSGVRVTAV |
| 34.0 | 1417.7238 | 0.0492 | GSAISPDLLVDSNG |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SKGLGSDLSSLASL**
Found in **AP180_MOUSE** in **SwissProt**, Clathrin coat assembly protein AP180 OS=Mus musculus GN=Snap91 PE=1 SV=1
Match to Query 5450: 1512.856708 from(757.435630,2+) intensity(167512.9800) scans(9658) rawscans(sn9658) rtinseconds(3646.6755) index(7067)
Title: 7068: Scan 9658 (rt=3646.68) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf

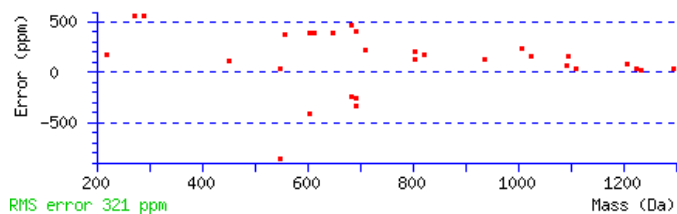
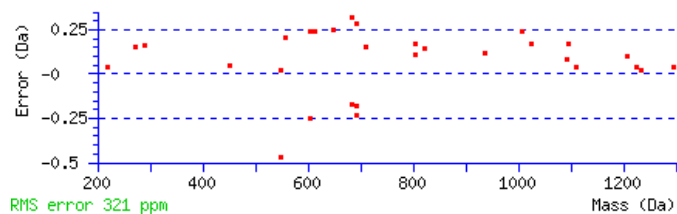


Navigation icons: ? (help), image (download), left arrow, zoom in, zoom out, zoom reset, 119.17 to 1396.72 (mass range), zoom in, right arrow.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1512.8487
Variable modifications:
N-term : Dimethyl:2H(4) (N-term)
K2 : Dimethyl:2H(4) (K)
Ions Score: 51 Expect: 0.25
Matches : 30/138 fragment ions using 40 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 120.0957 | 60.5515 | | | 102.0851 | 51.5462 | S | | | | | | | 15 |
| 2 | 280.2471 | 140.6272 | 263.2205 | 132.1139 | 262.2365 | 131.6219 | K | 1394.7675 | 697.8874 | 1377.7410 | 689.3741 | 1376.7569 | 688.8821 | 14 |
| 3 | 337.2685 | 169.1379 | 320.2420 | 160.6246 | 319.2580 | 160.1326 | G | 1234.6161 | 617.8117 | | | 1216.6056 | 608.8064 | 13 |
| 4 | 450.3526 | 225.6799 | 433.3261 | 217.1667 | 432.3420 | 216.6747 | L | 1177.5947 | 589.3010 | | | 1159.5841 | 580.2957 | 12 |
| 5 | 507.3741 | 254.1907 | 490.3475 | 245.6774 | 489.3635 | 245.1854 | G | 1064.5106 | 532.7589 | | | 1046.5000 | 523.7537 | 11 |
| 6 | 594.4061 | 297.7067 | 577.3796 | 289.1934 | 576.3955 | 288.7014 | S | 1007.4891 | 504.2482 | | | 989.4786 | 495.2429 | 10 |
| 7 | 709.4330 | 355.2202 | 692.4065 | 346.7069 | 691.4225 | 346.2149 | D | 920.4571 | 460.7322 | | | 902.4466 | 451.7269 | 9 |
| 8 | 822.5171 | 411.7622 | 805.4906 | 403.2489 | 804.5065 | 402.7569 | L | 805.4302 | 403.2187 | | | 787.4196 | 394.2134 | 8 |
| 9 | 937.5441 | 469.2757 | 920.5175 | 460.7624 | 919.5335 | 460.2704 | D | 692.3461 | 346.6767 | | | 674.3355 | 337.6714 | 7 |
| 10 | 1024.5761 | 512.7917 | 1007.5495 | 504.2784 | 1006.5655 | 503.7864 | S | 577.3192 | 289.1632 | | | 559.3086 | 280.1579 | 6 |
| 11 | 1111.6081 | 556.3077 | 1094.5816 | 547.7944 | 1093.5975 | 547.3024 | S | 490.2871 | 245.6472 | | | 472.2766 | 236.6419 | 5 |
| 12 | 1224.6922 | 612.8497 | 1207.6656 | 604.3364 | 1206.6816 | 603.8444 | L | 403.2551 | 202.1312 | | | 385.2445 | 193.1259 | 4 |
| 13 | 1295.7293 | 648.3683 | 1278.7027 | 639.8550 | 1277.7187 | 639.3630 | A | 290.1710 | 145.5892 | | | 272.1605 | 136.5839 | 3 |
| 14 | 1382.7613 | 691.8843 | 1365.7348 | 683.3710 | 1364.7507 | 682.8790 | S | 219.1339 | 110.0706 | | | 201.1234 | 101.0653 | 2 |
| 15 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI BLAST search of [SKGLGSDLDSSLASL](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|---------------------------------|
| 50.8 | 1512.8487 | 0.0080 | SKGLGSDLDSSLASL |
| 39.4 | 1512.8293 | 0.0274 | GGPHTKMGGSRDSL |
| 35.7 | 1512.9160 | -0.0593 | MTKPLVHSSLALS |
| 31.8 | 1513.0396 | -0.1829 | NFLTAIKKVIASL |
| 29.1 | 1512.7821 | 0.0746 | QSLSSSTATGTTVI |
| 28.8 | 1512.9037 | -0.0469 | VASLLNSMKSIASL |
| 28.3 | 1512.6878 | 0.1689 | NCDSSLNRTYAIS |
| 27.7 | 1512.8286 | 0.0281 | EPELLTALSISASL |
| 27.3 | 1512.8562 | 0.0005 | VSALAQDTHRATLV |
| 26.8 | 1512.8309 | 0.0258 | SQLSMKASLENSL |

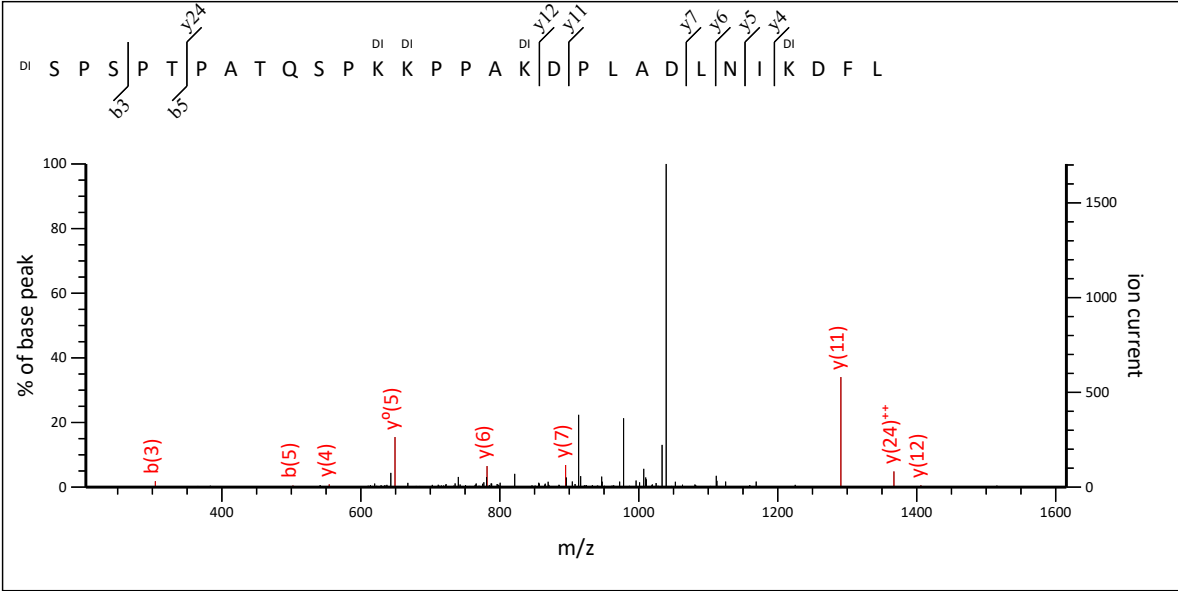
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPSPTPATQSPKKPPAKDPLADLNKDFL**
Found in **AP180_MOUSE** in **SwissProt**, Clathrin coat assembly protein AP180 OS=Mus musculus GN=Snap91 PE=1 SV=1

Match to Query 10492: 3232.944496 from(809.243400,4+) intensity(189922.9200) scans(10602) rawscans(sn10602) rtinseconds(3964.6895) index(7798)
Title: 7799: Scan 10602 (rt=3964.69) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf



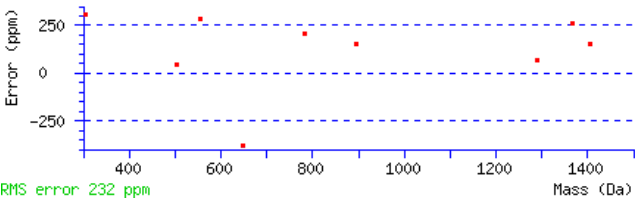
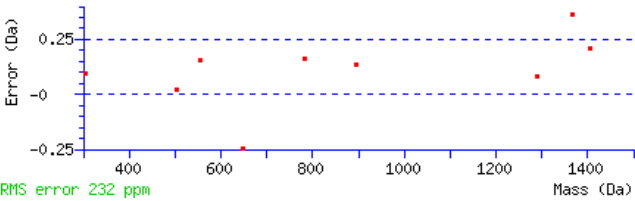
Navigation icons: ? (help), zoom in, zoom out, reset, and a range selector showing 204.27 to 1615.4.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 3232.9316
Variable modifications:
N-term : Dimethyl:2H(4) (N-term)
K12 : Dimethyl:2H(4) (K)
K13 : Dimethyl:2H(4) (K)
K17 : Dimethyl:2H(4) (K)
K26 : Dimethyl:2H(4) (K)
Ions Score: 20 Expect: 3.3e+002
Matches : 9/310 fragment ions using 13 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ^{*++} | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ^{*++} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 120.0957 | 60.5515 | | | 102.0851 | 51.5462 | S | | | | | | | 29 |
| 2 | 217.1485 | 109.0779 | | | 199.1379 | 100.0726 | P | 3114.8504 | 1557.9289 | 3097.8239 | 1549.4156 | 3096.8399 | 1548.9236 | 28 |
| 3 | 304.1805 | 152.5939 | | | 286.1699 | 143.5886 | S | 3017.7977 | 1509.4025 | 3000.7711 | 1500.8892 | 2999.7871 | 1500.3972 | 27 |
| 4 | 401.2333 | 201.1203 | | | 383.2227 | 192.1150 | P | 2930.7656 | 1465.8865 | 2913.7391 | 1457.3732 | 2912.7551 | 1456.8812 | 26 |
| 5 | 502.2809 | 251.6441 | | | 484.2704 | 242.6388 | T | 2833.7129 | 1417.3601 | 2816.6863 | 1408.8468 | 2815.7023 | 1408.3548 | 25 |
| 6 | 599.3337 | 300.1705 | | | 581.3231 | 291.1652 | P | 2732.6652 | 1366.8362 | 2715.6386 | 1358.3230 | 2714.6546 | 1357.8310 | 24 |
| 7 | 670.3708 | 335.6891 | | | 652.3603 | 326.6838 | A | 2635.6124 | 1318.3099 | 2618.5859 | 1309.7966 | 2617.6019 | 1309.3046 | 23 |
| 8 | 771.4185 | 386.2129 | | | 753.4079 | 377.2076 | T | 2564.5753 | 1282.7913 | 2547.5488 | 1274.2780 | 2546.5648 | 1273.7860 | 22 |
| 9 | 899.4771 | 450.2422 | 882.4505 | 441.7289 | 881.4665 | 441.2369 | Q | 2463.5276 | 1232.2675 | 2446.5011 | 1223.7542 | 2445.5171 | 1223.2622 | 21 |
| 10 | 986.5091 | 493.7582 | 969.4826 | 485.2449 | 968.4985 | 484.7529 | S | 2335.4691 | 1168.2382 | 2318.4425 | 1159.7249 | 2317.4585 | 1159.2329 | 20 |
| 11 | 1083.5619 | 542.2846 | 1066.5353 | 533.7713 | 1065.5513 | 533.2793 | P | 2248.4370 | 1124.7222 | 2231.4105 | 1116.2089 | 2230.4265 | 1115.7169 | 19 |
| 12 | 1243.7132 | 622.3603 | 1226.6867 | 613.8470 | 1225.7027 | 613.3550 | K | 2151.3843 | 1076.1958 | 2134.3577 | 1067.6825 | 2133.3737 | 1067.1905 | 18 |
| 13 | 1403.8646 | 702.4359 | 1386.8381 | 693.9227 | 1385.8540 | 693.4307 | K | 1991.2329 | 996.1201 | 1974.2063 | 987.6068 | 1973.2223 | 987.1148 | 17 |
| 14 | 1500.9174 | 750.9623 | 1483.8908 | 742.4491 | 1482.9068 | 741.9570 | P | 1831.0815 | 916.0444 | 1814.0550 | 907.5311 | 1813.0710 | 907.0391 | 16 |
| 15 | 1597.9701 | 799.4887 | 1580.9436 | 790.9754 | 1579.9596 | 790.4834 | P | 1734.0288 | 867.5180 | 1717.0022 | 859.0047 | 1716.0182 | 858.5127 | 15 |
| 16 | 1669.0073 | 835.0073 | 1651.9807 | 826.4940 | 1650.9967 | 826.0020 | A | 1636.9760 | 818.9916 | 1619.9495 | 810.4784 | 1618.9654 | 809.9864 | 14 |
| 17 | 1829.1586 | 915.0830 | 1812.1321 | 906.5697 | 1811.1481 | 906.0777 | K | 1565.9389 | 783.4731 | 1548.9123 | 774.9598 | 1547.9283 | 774.4678 | 13 |
| 18 | 1944.1856 | 972.5964 | 1927.1590 | 964.0831 | 1926.1750 | 963.5911 | D | 1405.7875 | 703.3974 | 1388.7610 | 694.8841 | 1387.7770 | 694.3921 | 12 |
| 19 | 2041.2383 | 1021.1228 | 2024.2118 | 1012.6095 | 2023.2278 | 1012.1175 | P | 1290.7606 | 645.8839 | 1273.7340 | 637.3706 | 1272.7500 | 636.8786 | 11 |

| | | | | | | | | | | | | | | |
|----|-----------|-----------|-----------|-----------|-----------|-----------|---|-----------|----------|-----------|----------|-----------|----------|----|
| 20 | 2154.3224 | 1077.6648 | 2137.2958 | 1069.1516 | 2136.3118 | 1068.6596 | L | 1193.7078 | 597.3575 | 1176.6813 | 588.8443 | 1175.6972 | 588.3523 | 10 |
| 21 | 2225.3595 | 1113.1834 | 2208.3330 | 1104.6701 | 2207.3489 | 1104.1781 | A | 1080.6237 | 540.8155 | 1063.5972 | 532.3022 | 1062.6132 | 531.8102 | 9 |
| 22 | 2340.3865 | 1170.6969 | 2323.3599 | 1162.1836 | 2322.3759 | 1161.6916 | D | 1009.5866 | 505.2970 | 992.5601 | 496.7837 | 991.5761 | 496.2917 | 8 |
| 23 | 2453.4705 | 1227.2389 | 2436.4440 | 1218.7256 | 2435.4600 | 1218.2336 | L | 894.5597 | 447.7835 | 877.5331 | 439.2702 | 876.5491 | 438.7782 | 7 |
| 24 | 2567.5134 | 1284.2604 | 2550.4869 | 1275.7471 | 2549.5029 | 1275.2551 | N | 781.4756 | 391.2414 | 764.4491 | 382.7282 | 763.4651 | 382.2362 | 6 |
| 25 | 2680.5975 | 1340.8024 | 2663.5710 | 1332.2891 | 2662.5869 | 1331.7971 | I | 667.4327 | 334.2200 | 650.4061 | 325.7067 | 649.4221 | 325.2147 | 5 |
| 26 | 2840.7489 | 1420.8781 | 2823.7223 | 1412.3648 | 2822.7383 | 1411.8728 | K | 554.3486 | 277.6780 | 537.3221 | 269.1647 | 536.3381 | 268.6727 | 4 |
| 27 | 2955.7758 | 1478.3915 | 2938.7493 | 1469.8783 | 2937.7653 | 1469.3863 | D | 394.1973 | 197.6023 | | | 376.1867 | 188.5970 | 3 |
| 28 | 3102.8442 | 1551.9258 | 3085.8177 | 1543.4125 | 3084.8337 | 1542.9205 | F | 279.1703 | 140.0888 | | | | | 2 |
| 29 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI BLAST search of [SPSPTPATQSPKKPPAKDPLADLNIKDFL](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|--------|---|
| 20.5 | 3232.9316 | 0.0129 | SPSPTPATQSPKKPPAKDPLADLNIKDFL |
| 18.7 | 3232.6049 | 0.3396 | FLRFIPTYTSRLAIISQSGQCQFCEPTG |
| 14.3 | 3232.6132 | 0.3313 | LMAIAHGSGPLMMIVFGEMTDKFVDNTG |
| 13.9 | 3232.6975 | 0.2470 | FLTDGASAMLIMSEDRALAMGYKPKAYL |
| 13.7 | 3232.6431 | 0.3014 | DKDIVMLQTGVSMMDPNHFLMIMLSRF |
| 13.6 | 3232.7254 | 0.2190 | SYLITTPCYSDAFKLL ESGDLSMNSIK |
| 13.6 | 3232.5079 | 0.4366 | NIDSDSILMSILDMSLHQMGSDRDLOS |
| 13.4 | 3232.7629 | 0.1816 | QSLEYLINDIRPPCIKEQMLGKGYETV |
| 12.7 | 3232.7576 | 0.1869 | CPNPKFINRSMATKGLLLPSRRSLASF |
| 11.8 | 3232.6950 | 0.2495 | PAHPTPFYIDDILGRGPAAPTPTPLSPNS |

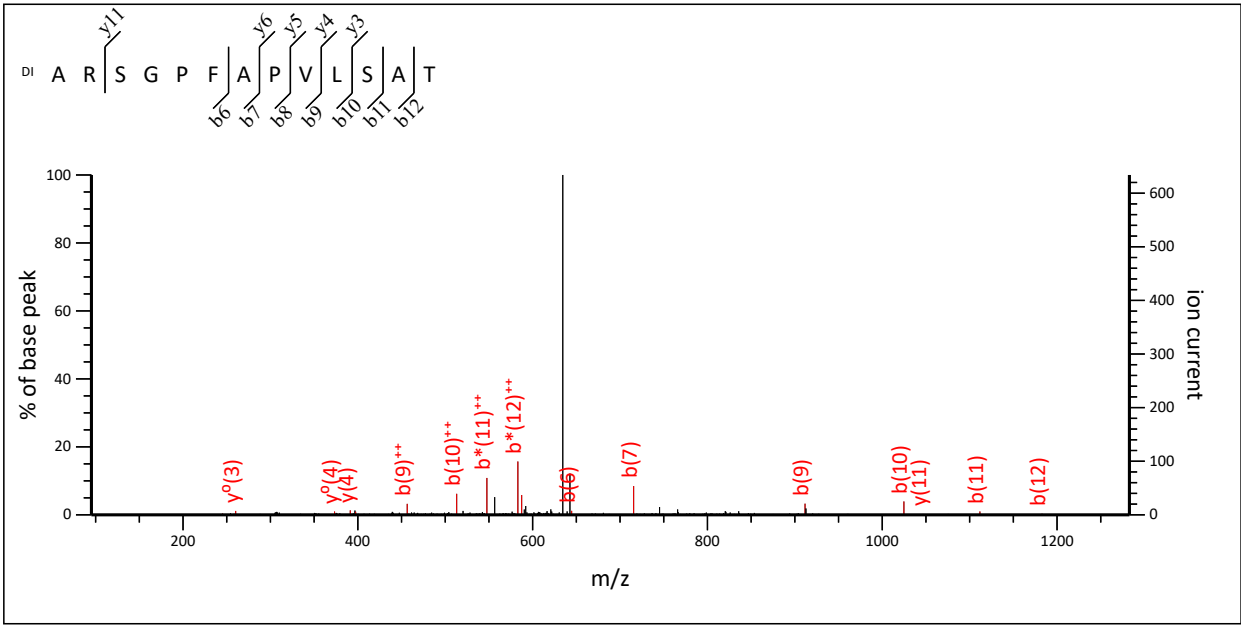
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ARSGPFAPVLSAT**
Found in **UCRI_MOUSE** in **SwissProt**, Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Mus musculus GN=Uqcrfs1 PE=1 SV=1

Match to Query 3942: 1300.719408 from(651.366980,2+) intensity(53800.7110) scans(7400) rawscans(sn7400) rtinseconds(2841.3764) index(5181)
Title: 5182: Scan 7400 (rt=2841.38) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf

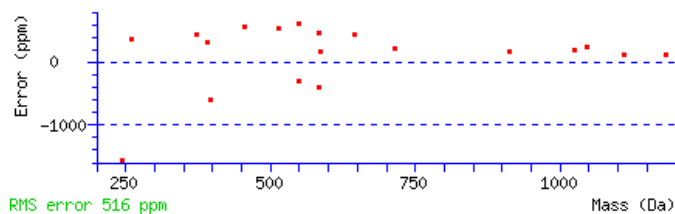
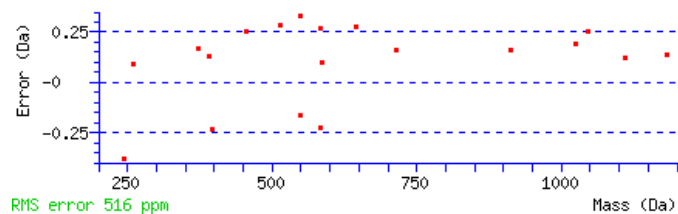


Navigation icons: ? (help), zoom in, zoom out, zoom reset, zoom full, zoom previous, zoom next, zoom home, zoom previous, zoom next, zoom home. Search range: 95.19 to 1282.8.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1300.7139
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 24 Expect: 1.2e+002
Matches : 19/116 fragment ions using 37 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ^{*++} | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ^{*++} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | | | A | | | | | | | 13 |
| 2 | 256.1768 | 128.5920 | 239.1503 | 120.0788 | | | R | 1202.6528 | 601.8300 | 1185.6263 | 593.3168 | 1184.6422 | 592.8248 | 12 |
| 3 | 343.2088 | 172.1081 | 326.1823 | 163.5948 | 325.1983 | 163.1028 | S | 1046.5517 | 523.7795 | | | 1028.5411 | 514.7742 | 11 |
| 4 | 400.2303 | 200.6188 | 383.2037 | 192.1055 | 382.2197 | 191.6135 | G | 959.5197 | 480.2635 | | | 941.5091 | 471.2582 | 10 |
| 5 | 497.2831 | 249.1452 | 480.2565 | 240.6319 | 479.2725 | 240.1399 | P | 902.4982 | 451.7527 | | | 884.4876 | 442.7475 | 9 |
| 6 | 644.3515 | 322.6794 | 627.3249 | 314.1661 | 626.3409 | 313.6741 | F | 805.4454 | 403.2264 | | | 787.4349 | 394.2211 | 8 |
| 7 | 715.3886 | 358.1979 | 698.3620 | 349.6847 | 697.3780 | 349.1926 | A | 658.3770 | 329.6921 | | | 640.3665 | 320.6869 | 7 |
| 8 | 812.4413 | 406.7243 | 795.4148 | 398.2110 | 794.4308 | 397.7190 | P | 587.3399 | 294.1736 | | | 569.3293 | 285.1683 | 6 |
| 9 | 911.5098 | 456.2585 | 894.4832 | 447.7452 | 893.4992 | 447.2532 | V | 490.2871 | 245.6472 | | | 472.2766 | 236.6419 | 5 |
| 10 | 1024.5938 | 512.8006 | 1007.5673 | 504.2873 | 1006.5833 | 503.7953 | L | 391.2187 | 196.1130 | | | 373.2082 | 187.1077 | 4 |
| 11 | 1111.6259 | 556.3166 | 1094.5993 | 547.8033 | 1093.6153 | 547.3113 | S | 278.1347 | 139.5710 | | | 260.1241 | 130.5657 | 3 |
| 12 | 1182.6630 | 591.8351 | 1165.6364 | 583.3218 | 1164.6524 | 582.8298 | A | 191.1026 | 96.0550 | | | 173.0921 | 87.0497 | 2 |
| 13 | | | | | | | T | 120.0655 | 60.5364 | | | 102.0550 | 51.5311 | 1 |



NCBI **BLAST** search of [ARSGPFAPVLSAT](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--------------------------------|
| 32.7 | 1300.8016 | -0.0822 | INITPLARLSAT |
| 32.6 | 1300.8380 | -0.1186 | SGTLRLVLGLLQ |
| 24.4 | 1300.7602 | -0.0408 | IGDKGVSKLSAT |
| 24.1 | 1300.7523 | -0.0329 | TYLGMSKISAT |
| 23.9 | 1300.7139 | 0.0055 | ARSGPFAPVLSAT |
| 23.6 | 1300.5964 | 0.1230 | HSEDYNLSTA |
| 22.9 | 1300.7420 | -0.0226 | GALAQPVPVPAEAT |
| 20.1 | 1300.6489 | 0.0705 | NSDYFIPISAT |
| 19.8 | 1300.7391 | -0.0197 | KYGTHLLISAT |
| 19.3 | 1300.6053 | 0.1141 | CSPVQSMRSSAT |

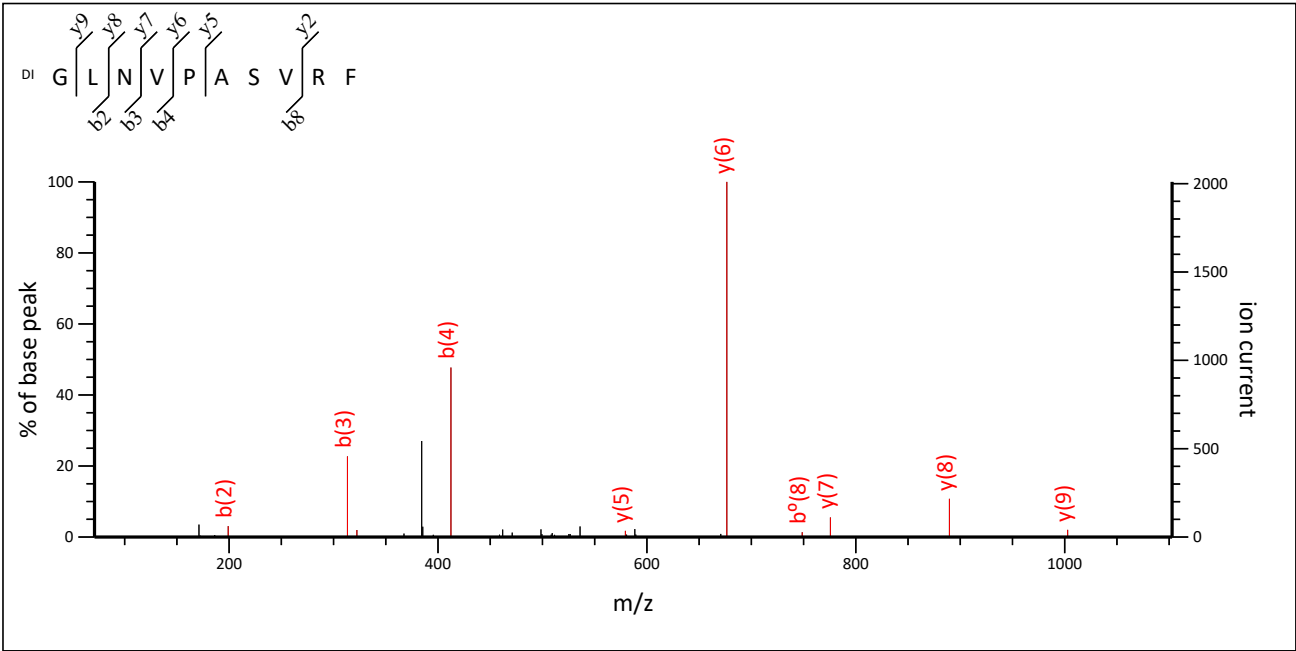
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLNVPASVRF**
Found in **UCRI_MOUSE** in **SwissProt**, Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Mus musculus GN=Uqcrfs1
PE=1 SV=1

Match to Query 2441: 1086.620988 from(544.317770,2+) intensity(154132.7200) scans(8139) rawscans(sn8139)
rtinseconds(3109.3608) index(5788)
Title: 5789: Scan 8139 (rt=3109.36) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR
NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf







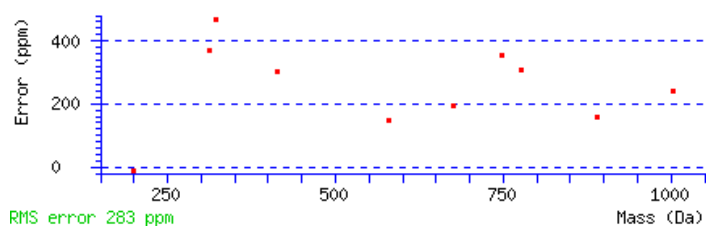
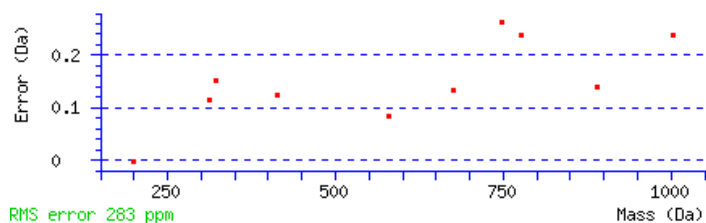
71.14 to 1102.81 



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1086.6186
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 48 Expect: 0.51
Matches : 10/84 fragment ions using 15 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ^{*++} | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ^{*++} | y ⁰ | y ⁰⁺⁺ | # |
|----|----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 86.0600 | 43.5337 | | | | | G | | | | | | | 10 |
| 2 | 199.1441 | 100.0757 | | | | | L | 1002.5731 | 501.7902 | 985.5465 | 493.2769 | 984.5625 | 492.7849 | 9 |
| 3 | 313.1870 | 157.0972 | 296.1605 | 148.5839 | | | N | 889.4890 | 445.2482 | 872.4625 | 436.7349 | 871.4785 | 436.2429 | 8 |
| 4 | 412.2554 | 206.6314 | 395.2289 | 198.1181 | | | V | 775.4461 | 388.2267 | 758.4196 | 379.7134 | 757.4355 | 379.2214 | 7 |
| 5 | 509.3082 | 255.1577 | 492.2817 | 246.6445 | | | P | 676.3777 | 338.6925 | 659.3511 | 330.1792 | 658.3671 | 329.6872 | 6 |
| 6 | 580.3453 | 290.6763 | 563.3188 | 282.1630 | | | A | 579.3249 | 290.1661 | 562.2984 | 281.6528 | 561.3144 | 281.1608 | 5 |
| 7 | 667.3774 | 334.1923 | 650.3508 | 325.6790 | 649.3668 | 325.1870 | S | 508.2878 | 254.6475 | 491.2613 | 246.1343 | 490.2772 | 245.6423 | 4 |
| 8 | 766.4458 | 383.7265 | 749.4192 | 375.2132 | 748.4352 | 374.7212 | V | 421.2558 | 211.1315 | 404.2292 | 202.6183 | | | 3 |
| 9 | 922.5469 | 461.7771 | 905.5203 | 453.2638 | 904.5363 | 452.7718 | R | 322.1874 | 161.5973 | 305.1608 | 153.0840 | | | 2 |
| 10 | | | | | | | F | 166.0863 | 83.5468 | | | | | 1 |



NCBI **BLAST** search of [GLNVPASVRE](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|--------|--------------------------------|
| 47.6 | 1086.6186 | 0.0024 | GLNVPASVRE |
| 27.5 | 1086.6107 | 0.0103 | GLGGVGLAVIMG |
| 27.5 | 1086.6107 | 0.0103 | GLGGVGLSVIMG |
| 24.8 | 1086.5380 | 0.0830 | QNVGTPVMVG |
| 22.3 | 1086.5305 | 0.0904 | GLAAAPGGSGAGSS |
| 22.0 | 1086.5896 | 0.0314 | GIKGPAGMPGE |
| 21.3 | 1086.5822 | 0.0388 | QNVPRYLQ |
| 21.0 | 1086.5669 | 0.0540 | QRVPGLSSDT |
| 19.6 | 1086.5557 | 0.0653 | QNVADSVEK |
| 19.6 | 1086.5532 | 0.0678 | QVHLGAVFM |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGQAAARPLVA**

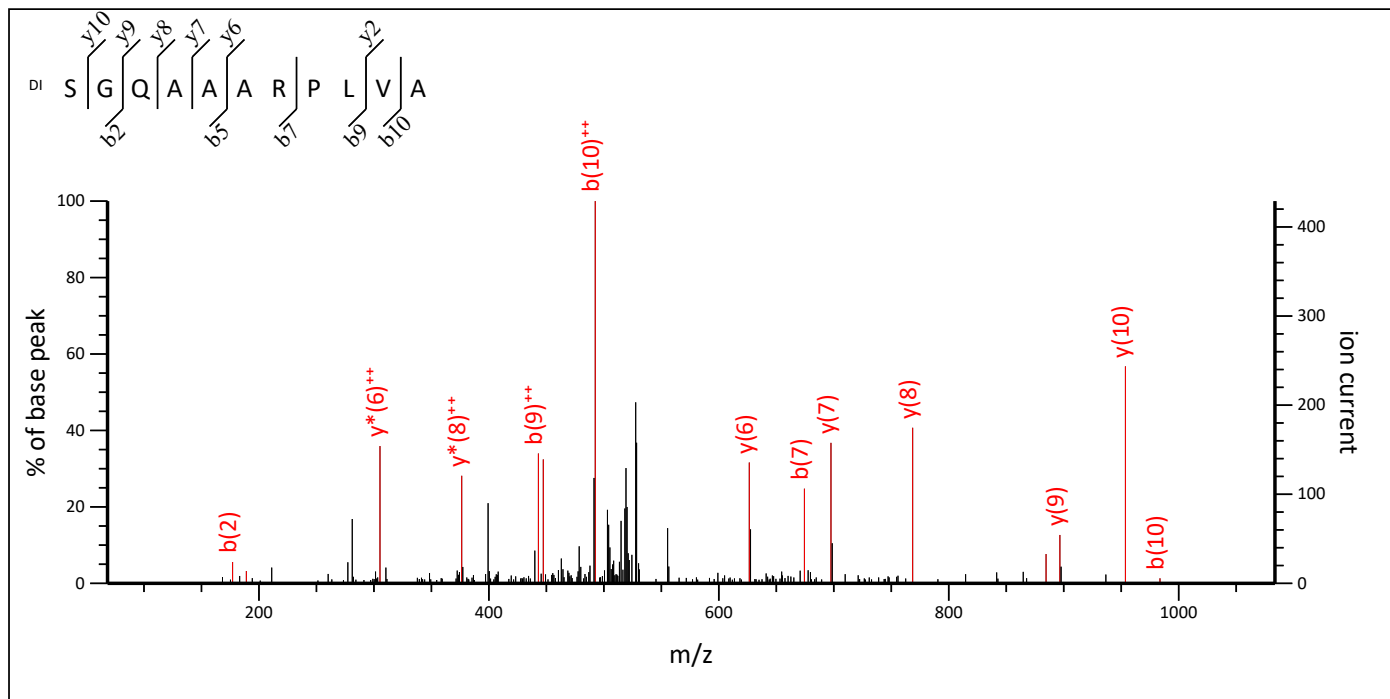
Found in **UCRI_MOUSE** in **SwissProt**, Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Mus musculus
GN=Uqcrfs1 PE=1 SV=1

Match to Query 2316: 1071.635948 from(536.825250,2+) intensity(150756.6900) scans(3397) rawscans(sn3397)

rtinseconds(1478.1366) index(1654)

Title: 1655: Scan 3397 (rt=1478.14) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]

Data file hipocampo_01.temp.mgf



68.29 to 1083.72



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1071.6338

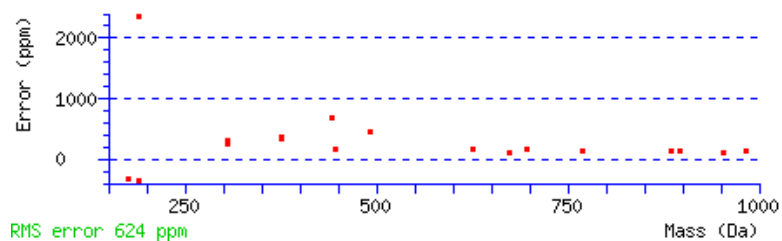
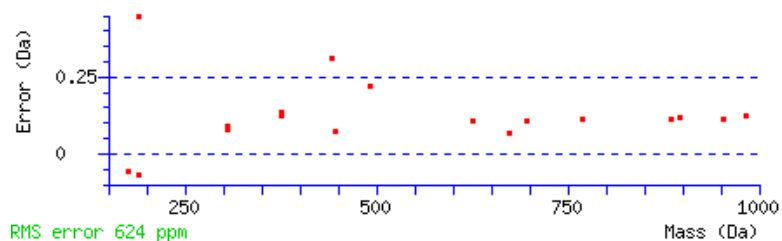
Variable modifications:

N-term : Dimethyl:2H(4) (N-term)

Ions Score: 51 Expect: 0.21

Matches : 18/88 fragment ions using 25 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ^{*++} | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ^{*++} | # |
|----|-----------------|-----------------|----------------|------------------|----------------|------------------|------|-----------------|-----------------|----------------|------------------|----|
| 1 | 120.0957 | 60.5515 | | | 102.0851 | 51.5462 | S | | | | | 11 |
| 2 | 177.1172 | 89.0622 | | | 159.1066 | 80.0569 | G | 953.5527 | 477.2800 | 936.5261 | 468.7667 | 10 |
| 3 | 305.1758 | 153.0915 | 288.1492 | 144.5782 | 287.1652 | 144.0862 | Q | 896.5312 | 448.7693 | 879.5047 | 440.2560 | 9 |
| 4 | 376.2129 | 188.6101 | 359.1863 | 180.0968 | 358.2023 | 179.6048 | A | 768.4727 | 384.7400 | 751.4461 | 376.2267 | 8 |
| 5 | 447.2500 | 224.1286 | 430.2234 | 215.6154 | 429.2394 | 215.1233 | A | 697.4355 | 349.2214 | 680.4090 | 340.7081 | 7 |
| 6 | 518.2871 | 259.6472 | 501.2605 | 251.1339 | 500.2765 | 250.6419 | A | 626.3984 | 313.7028 | 609.3719 | 305.1896 | 6 |
| 7 | 674.3882 | 337.6977 | 657.3617 | 329.1845 | 656.3776 | 328.6925 | R | 555.3613 | 278.1843 | 538.3348 | 269.6710 | 5 |
| 8 | 771.4410 | 386.2241 | 754.4144 | 377.7108 | 753.4304 | 377.2188 | P | 399.2602 | 200.1337 | | | 4 |
| 9 | 884.5250 | 442.7662 | 867.4985 | 434.2529 | 866.5145 | 433.7609 | L | 302.2074 | 151.6074 | | | 3 |
| 10 | 983.5934 | 492.3004 | 966.5669 | 483.7871 | 965.5829 | 483.2951 | V | 189.1234 | 95.0653 | | | 2 |
| 11 | | | | | | | A | 90.0550 | 45.5311 | | | 1 |



NCBI **BLAST** search of [SGQAAARPLVA](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-------------------------------|
| 51.5 | 1071.6338 | 0.0021 | SGQAAARPLVA |
| 31.0 | 1071.5812 | 0.0548 | DILLTAAQGT |
| 30.2 | 1071.4509 | 0.1851 | FDNYSAQSA |
| 27.2 | 1071.6338 | 0.0021 | GGLLRPAAQSA |
| 26.1 | 1071.5461 | 0.0898 | HYRIGAQGT |
| 25.2 | 1071.7226 | -0.0867 | KLLQAAAGASA |
| 25.2 | 1071.5993 | 0.0366 | YLIGTAAGASA |
| 24.1 | 1071.5825 | 0.0535 | IYALHRNSA |
| 23.7 | 1071.6338 | 0.0021 | ARAVPVAGAASA |
| 23.5 | 1071.5862 | 0.0497 | GVGAVPAAAAGSA |

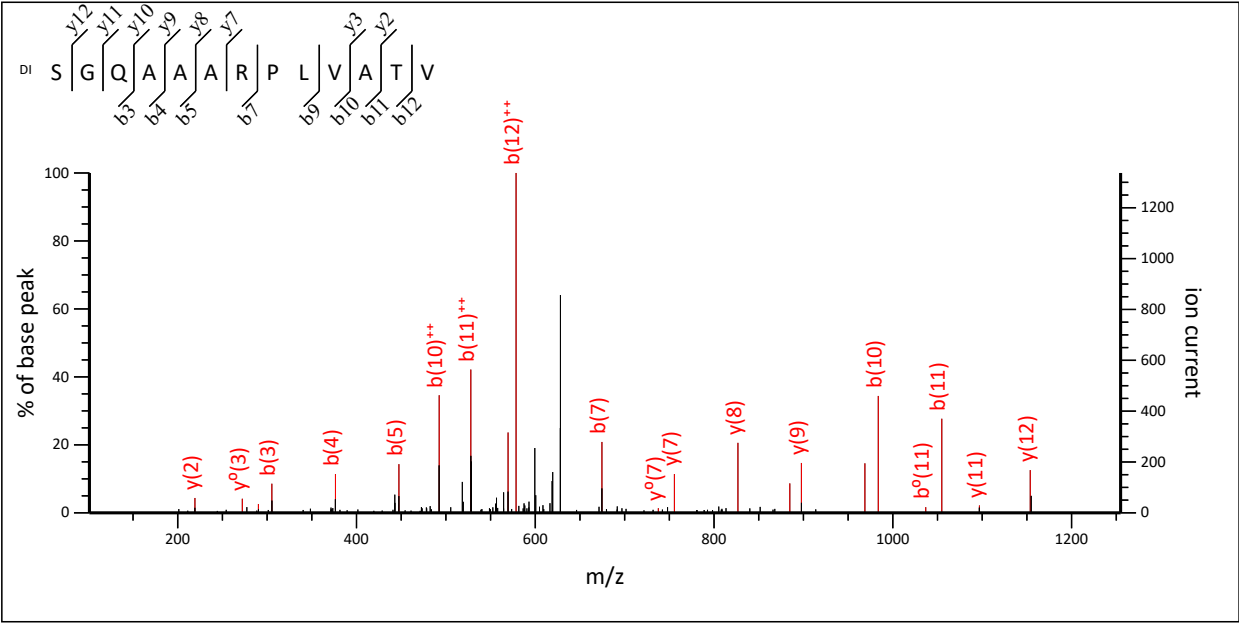
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGQAAARPLVATV**
Found in **UCRI_MOUSE** in **SwissProt**, Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Mus musculus GN=Uqcrfs1 PE=1 SV=1

Match to Query 3605: 1271.753708 from(636.884130,2+) intensity(369882.6500) scans(5065-5081) rawscans(sn5065:sn5081) rtinseconds(2018.9559-2024.242) index(3073)
Title: 3074: Sum of 2 scans in range 5065 (rt=2018.96) to 5081 (rt=2024.24) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

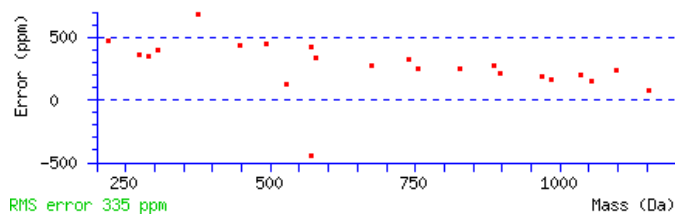
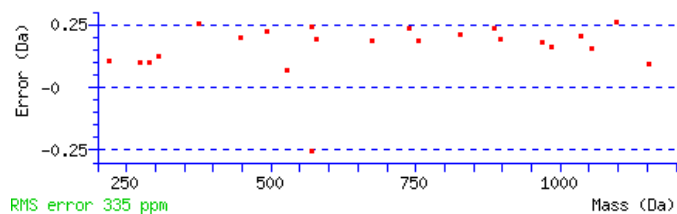


Navigation icons: ? (help), zoom in, zoom out, pan, and a search bar containing '101.21 to 1254.85'.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1271.7499
Variable modifications:
N-term : Dimethyl:2H(4) (N-term)
Ions Score: 83 Expect: 0.00014
Matches : 23/126 fragment ions using 29 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺ * | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺ * | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|-------------------|----------------|------------------|------|-----------|-----------------|----------------|-------------------|----------------|------------------|----|
| 1 | 120.0957 | 60.5515 | | | 102.0851 | 51.5462 | S | | | | | | | 13 |
| 2 | 177.1172 | 89.0622 | | | 159.1066 | 80.0569 | G | 1153.6688 | 577.3380 | 1136.6422 | 568.8248 | 1135.6582 | 568.3327 | 12 |
| 3 | 305.1758 | 153.0915 | 288.1492 | 144.5782 | 287.1652 | 144.0862 | Q | 1096.6473 | 548.8273 | 1079.6208 | 540.3140 | 1078.6368 | 539.8220 | 11 |
| 4 | 376.2129 | 188.6101 | 359.1863 | 180.0968 | 358.2023 | 179.6048 | A | 968.5887 | 484.7980 | 951.5622 | 476.2847 | 950.5782 | 475.7927 | 10 |
| 5 | 447.2500 | 224.1286 | 430.2234 | 215.6154 | 429.2394 | 215.1233 | A | 897.5516 | 449.2795 | 880.5251 | 440.7662 | 879.5411 | 440.2742 | 9 |
| 6 | 518.2871 | 259.6472 | 501.2605 | 251.1339 | 500.2765 | 250.6419 | A | 826.5145 | 413.7609 | 809.4880 | 405.2476 | 808.5040 | 404.7556 | 8 |
| 7 | 674.3882 | 337.6977 | 657.3617 | 329.1845 | 656.3776 | 328.6925 | R | 755.4774 | 378.2423 | 738.4509 | 369.7291 | 737.4668 | 369.2371 | 7 |
| 8 | 771.4410 | 386.2241 | 754.4144 | 377.7108 | 753.4304 | 377.2188 | P | 599.3763 | 300.1918 | | | 581.3657 | 291.1865 | 6 |
| 9 | 884.5250 | 442.7662 | 867.4985 | 434.2529 | 866.5145 | 433.7609 | L | 502.3235 | 251.6654 | | | 484.3130 | 242.6601 | 5 |
| 10 | 983.5934 | 492.3004 | 966.5669 | 483.7871 | 965.5829 | 483.2951 | V | 389.2395 | 195.1234 | | | 371.2289 | 186.1181 | 4 |
| 11 | 1054.6306 | 527.8189 | 1037.6040 | 519.3056 | 1036.6200 | 518.8136 | A | 290.1710 | 145.5892 | | | 272.1605 | 136.5839 | 3 |
| 12 | 1155.6782 | 578.3428 | 1138.6517 | 569.8295 | 1137.6677 | 569.3375 | T | 219.1339 | 110.0706 | | | 201.1234 | 101.0653 | 2 |
| 13 | | | | | | | V | 118.0863 | 59.5468 | | | | | 1 |



NCBI **BLAST** search of [SGQAAARPLVATV](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--------------------------------|
| 83.2 | 1271.7499 | 0.0038 | SGQAAARPLVATV |
| 31.2 | 1271.6510 | 0.1027 | PHLANGYTTAVT |
| 27.4 | 1271.6408 | 0.1129 | QELQHSAAAQSA |
| 27.3 | 1271.5414 | 0.2123 | FEESCMEVATV |
| 26.4 | 1271.6209 | 0.1328 | MSTSGAAAAAAGGT |
| 25.9 | 1271.7247 | 0.0290 | SVQEKTMVLGT |
| 25.1 | 1271.6469 | 0.1068 | TAAQAAAAAAGGTA |
| 24.8 | 1271.7159 | 0.0378 | VTMINAIPVASL |
| 24.2 | 1271.8135 | -0.0598 | EAKRREVLSA |
| 24.1 | 1271.7903 | -0.0366 | WSVLRLPVALS |

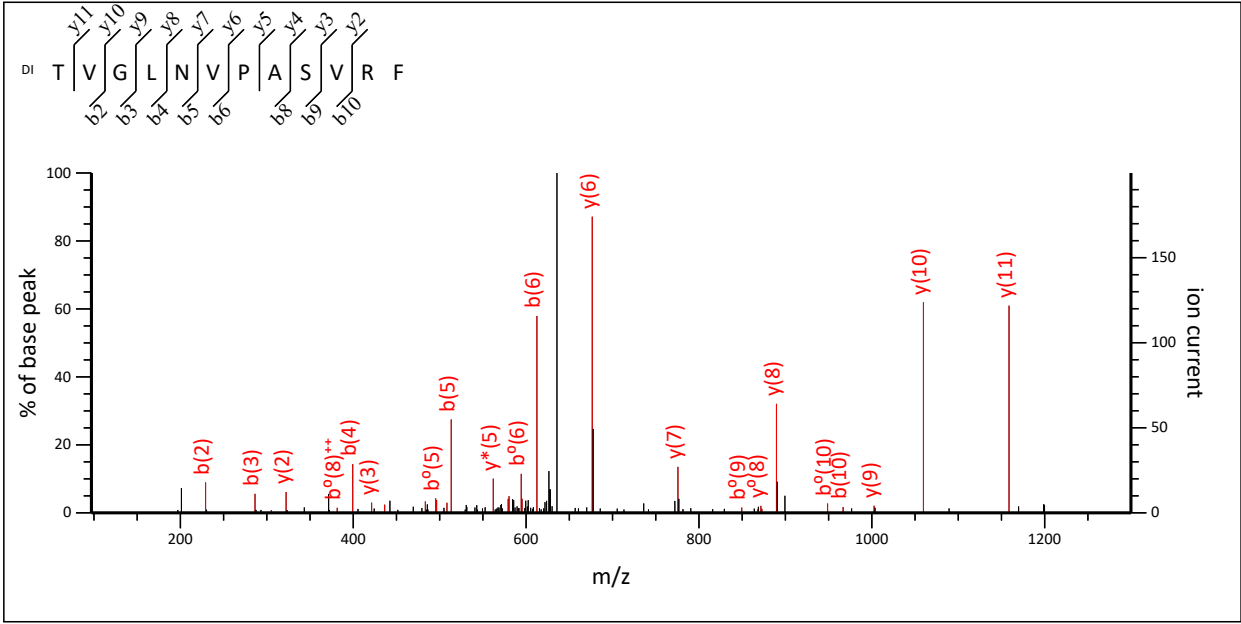
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVGLNVPASVRF**
Found in **UCRI_MOUSE** in **SwissProt**, Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Mus musculus GN=Uqcrfs1 PE=1 SV=1

Match to Query 3711: 1286.737948 from(644.376250,2+) intensity(47278.7850) scans(9142) rawscans(sn9142) rtinseconds(3433.9542) index(6546)
Title: 6547: Scan 9142 (rt=3433.95) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

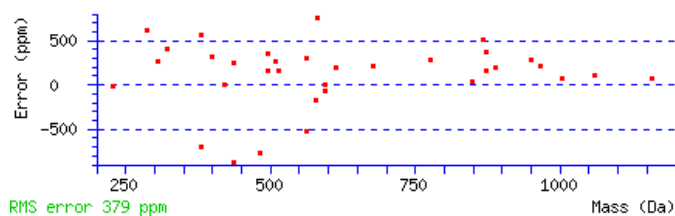
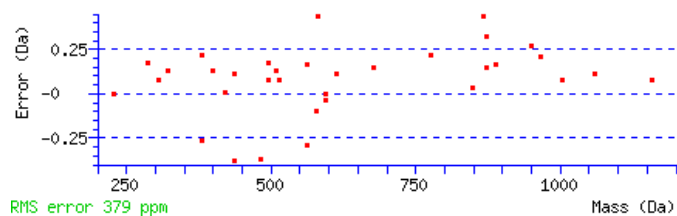


Navigation icons: ? (help), zoom in, zoom out, pan, and a range selector showing 97.07 to 1299.82.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1286.7347
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 55 Expect: 0.088
Matches : 34/116 fragment ions using 71 most intense peaks (help)

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 130.0863 | 65.5468 | | | 112.0757 | 56.5415 | T | | | | | | | 12 |
| 2 | 229.1547 | 115.0810 | | | 211.1441 | 106.0757 | V | 1158.6630 | 579.8351 | 1141.6364 | 571.3218 | 1140.6524 | 570.8298 | 11 |
| 3 | 286.1761 | 143.5917 | | | 268.1656 | 134.5864 | G | 1059.5946 | 530.3009 | 1042.5680 | 521.7876 | 1041.5840 | 521.2956 | 10 |
| 4 | 399.2602 | 200.1337 | | | 381.2496 | 191.1285 | L | 1002.5731 | 501.7902 | 985.5465 | 493.2769 | 984.5625 | 492.7849 | 9 |
| 5 | 513.3031 | 257.1552 | 496.2766 | 248.6419 | 495.2926 | 248.1499 | N | 889.4890 | 445.2482 | 872.4625 | 436.7349 | 871.4785 | 436.2429 | 8 |
| 6 | 612.3715 | 306.6894 | 595.3450 | 298.1761 | 594.3610 | 297.6841 | V | 775.4461 | 388.2267 | 758.4196 | 379.7134 | 757.4355 | 379.2214 | 7 |
| 7 | 709.4243 | 355.2158 | 692.3978 | 346.7025 | 691.4137 | 346.2105 | P | 676.3777 | 338.6925 | 659.3511 | 330.1792 | 658.3671 | 329.6872 | 6 |
| 8 | 780.4614 | 390.7343 | 763.4349 | 382.2211 | 762.4509 | 381.7291 | A | 579.3249 | 290.1661 | 562.2984 | 281.6528 | 561.3144 | 281.1608 | 5 |
| 9 | 867.4934 | 434.2504 | 850.4669 | 425.7371 | 849.4829 | 425.2451 | S | 508.2878 | 254.6475 | 491.2613 | 246.1343 | 490.2772 | 245.6423 | 4 |
| 10 | 966.5619 | 483.7846 | 949.5353 | 475.2713 | 948.5513 | 474.7793 | V | 421.2558 | 211.1315 | 404.2292 | 202.6183 | | | 3 |
| 11 | 1122.6630 | 561.8351 | 1105.6364 | 553.3218 | 1104.6524 | 552.8298 | R | 322.1874 | 161.5973 | 305.1608 | 153.0840 | | | 2 |
| 12 | | | | | | | F | 166.0863 | 83.5468 | | | | | 1 |



NCBI **BLAST** search of [TVGLNVPASVRF](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

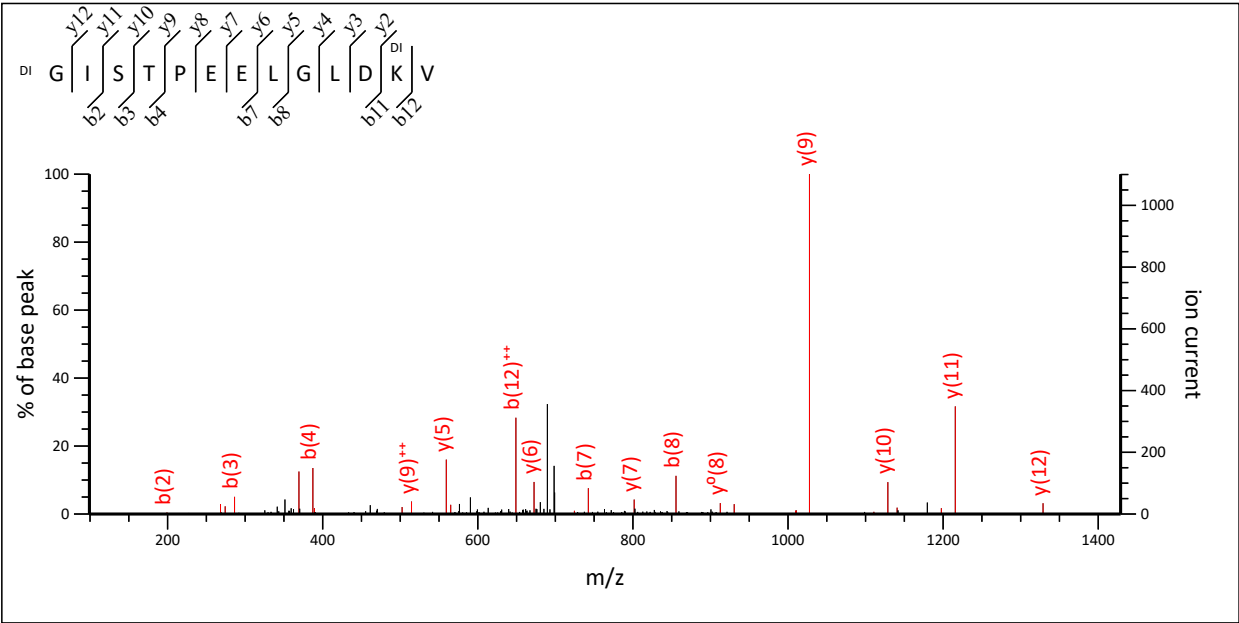
| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|------------------------------|
| 55.3 | 1286.7347 | 0.0033 | TVGLNVPASVRF |
| 23.7 | 1286.8351 | -0.0972 | PVVSLSKNGKY |
| 22.4 | 1286.8761 | -0.1382 | KLQHPVARGLP |
| 21.9 | 1286.7235 | 0.0145 | GISQVVFVSNPI |
| 21.9 | 1286.5965 | 0.1415 | SAGARVFEYMA |
| 19.8 | 1286.7995 | -0.0616 | KSCVWVNGLPL |
| 19.3 | 1286.7347 | 0.0033 | KTLNFDGRLPA |
| 19.3 | 1286.7950 | -0.0571 | LPRNKEPWIA |
| 18.6 | 1286.7234 | 0.0145 | VSAQKNYLGPI |
| 18.5 | 1286.7598 | -0.0219 | TVKQGQTLFIP |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GISTPEELGLDKV**
Found in **COX5A_MOUSE** in **SwissProt**, Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus musculus GN=Cox5a PE=1 SV=2
Match to Query 4478: 1412.778728 from(707.396640,2+) intensity(151348.6600) scans(8237) rawscans(sn8237) rtinseconds(3114.5524) index(5837)
Title: 5838: Scan 8237 (rt=3114.55) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

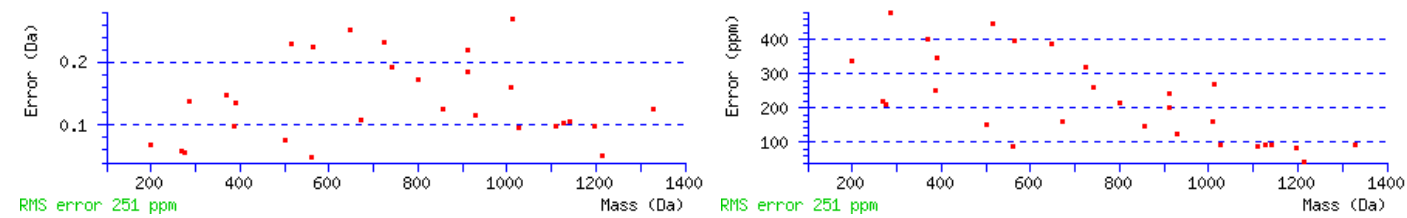


Navigation icons: ? (help), zoom in, zoom out, pan, and a range selector showing 99.21 to 1428.86.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1412.7763
Variable modifications:
N-term : Dimethyl (N-term)
K12 : Dimethyl (K)
Ions Score: 66 Expect: 0.007
Matches : 29/112 fragment ions using 60 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ^{*++} | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ^{*++} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 86.0600 | 43.5337 | | | | | G | | | | | | | 13 |
| 2 | 199.1441 | 100.0757 | | | | | I | 1328.7308 | 664.8690 | 1311.7042 | 656.3558 | 1310.7202 | 655.8637 | 12 |
| 3 | 286.1761 | 143.5917 | | | 268.1656 | 134.5864 | S | 1215.6467 | 608.3270 | 1198.6202 | 599.8137 | 1197.6361 | 599.3217 | 11 |
| 4 | 387.2238 | 194.1155 | | | 369.2132 | 185.1103 | T | 1128.6147 | 564.8110 | 1111.5881 | 556.2977 | 1110.6041 | 555.8057 | 10 |
| 5 | 484.2766 | 242.6419 | | | 466.2660 | 233.6366 | P | 1027.5670 | 514.2871 | 1010.5405 | 505.7739 | 1009.5564 | 505.2819 | 9 |
| 6 | 613.3192 | 307.1632 | | | 595.3086 | 298.1579 | E | 930.5142 | 465.7608 | 913.4877 | 457.2475 | 912.5037 | 456.7555 | 8 |
| 7 | 742.3618 | 371.6845 | | | 724.3512 | 362.6792 | E | 801.4716 | 401.2395 | 784.4451 | 392.7262 | 783.4611 | 392.2342 | 7 |
| 8 | 855.4458 | 428.2266 | | | 837.4353 | 419.2213 | L | 672.4291 | 336.7182 | 655.4025 | 328.2049 | 654.4185 | 327.7129 | 6 |
| 9 | 912.4673 | 456.7373 | | | 894.4567 | 447.7320 | G | 559.3450 | 280.1761 | 542.3184 | 271.6629 | 541.3344 | 271.1709 | 5 |
| 10 | 1025.5514 | 513.2793 | | | 1007.5408 | 504.2740 | L | 502.3235 | 251.6654 | 485.2970 | 243.1521 | 484.3130 | 242.6601 | 4 |
| 11 | 1140.5783 | 570.7928 | | | 1122.5677 | 561.7875 | D | 389.2395 | 195.1234 | 372.2129 | 186.6101 | 371.2289 | 186.1181 | 3 |
| 12 | 1296.7046 | 648.8559 | 1279.6780 | 640.3426 | 1278.6940 | 639.8506 | K | 274.2125 | 137.6099 | 257.1860 | 129.0966 | | | 2 |
| 13 | | | | | | | V | 118.0863 | 59.5468 | | | | | 1 |



NCBI **BLAST** search of [GISTPEELGLDKV](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

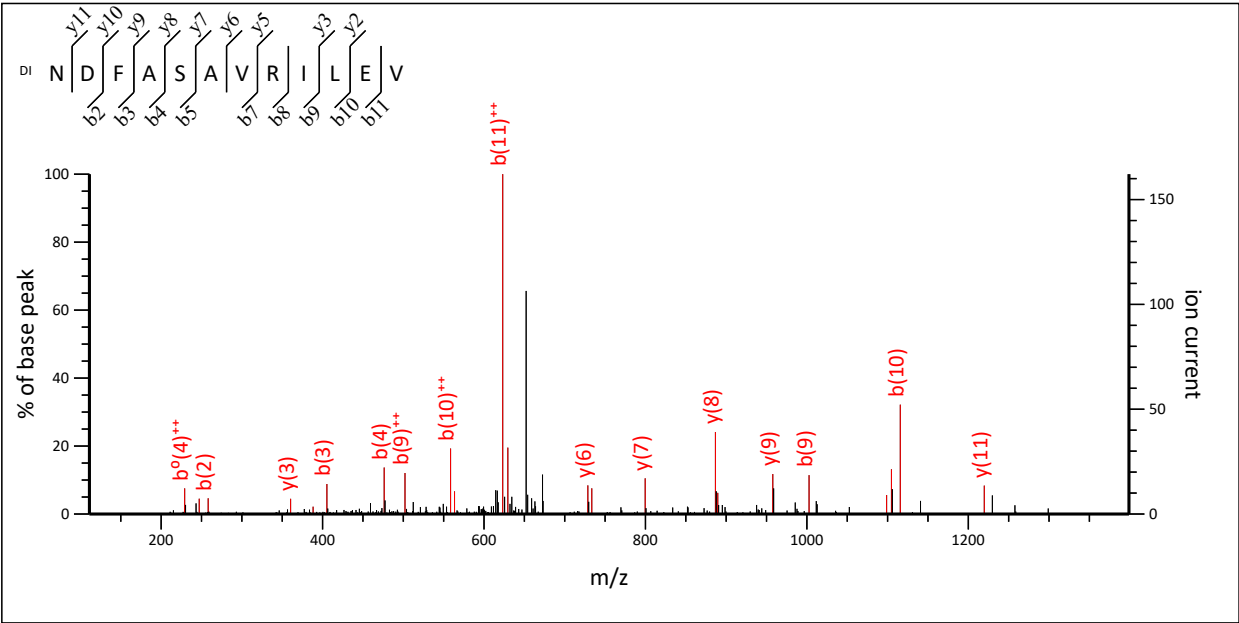
| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|---------------------------------|
| 66.4 | 1412.7763 | 0.0025 | GISTPEELGLDKV |
| 32.0 | 1412.8429 | -0.0641 | SPGLDGLLDLLLGV |
| 30.3 | 1412.8279 | -0.0492 | AVSTPAGLITPIVF |
| 25.7 | 1412.7925 | -0.0138 | RPTPVNSATAALPS |
| 25.0 | 1412.7623 | 0.0164 | LGTSGRAALGSVEPA |
| 24.9 | 1412.8239 | -0.0451 | GLSGLLKLDSLQN |
| 24.1 | 1412.7875 | -0.0088 | QSGSEGKVKPDK |
| 24.0 | 1412.6857 | 0.0930 | GIECQEELPAPSL |
| 23.6 | 1412.6969 | 0.0818 | QETLELIQHMQ |
| 23.6 | 1412.7299 | 0.0488 | TNTATLLRYYQ |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **NDFASAVRILEV**
Found in **COX5A_MOUSE** in **SwissProt**, Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus musculus GN=Cox5a PE=1 SV=2
Match to Query 4207: 1360.736888 from(681.375720,2+) intensity(31020.1310) scans(11202) rawscans(sn11202) rtinseconds(4184.7178) index(8301)
Title: 8302: Scan 11202 (rt=4184.72) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

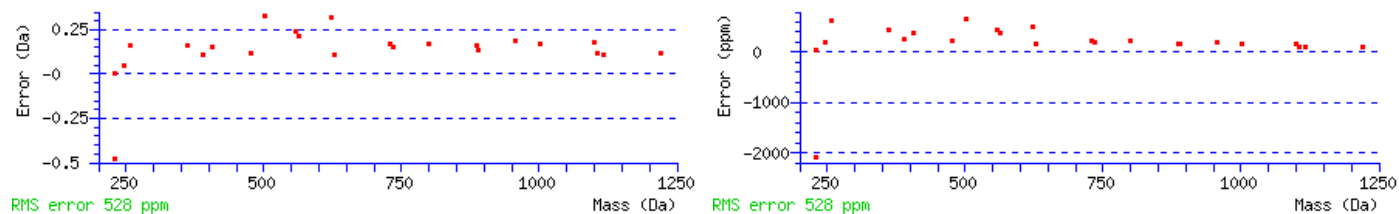


111.14 to 1399.02

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1360.7350
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 70 Expect: 0.0027
Matches : 24/120 fragment ions using 33 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 143.0815 | 72.0444 | 126.0550 | 63.5311 | | | N | | | | | | | 12 |
| 2 | 258.1084 | 129.5579 | 241.0819 | 121.0446 | 240.0979 | 120.5526 | D | 1219.6681 | 610.3377 | 1202.6416 | 601.8244 | 1201.6575 | 601.3324 | 11 |
| 3 | 405.1769 | 203.0921 | 388.1503 | 194.5788 | 387.1663 | 194.0868 | F | 1104.6412 | 552.8242 | 1087.6146 | 544.3109 | 1086.6306 | 543.8189 | 10 |
| 4 | 476.2140 | 238.6106 | 459.1874 | 230.0974 | 458.2034 | 229.6053 | A | 957.5728 | 479.2900 | 940.5462 | 470.7767 | 939.5622 | 470.2847 | 9 |
| 5 | 563.2460 | 282.1266 | 546.2195 | 273.6134 | 545.2354 | 273.1214 | S | 886.5356 | 443.7715 | 869.5091 | 435.2582 | 868.5251 | 434.7662 | 8 |
| 6 | 634.2831 | 317.6452 | 617.2566 | 309.1319 | 616.2726 | 308.6399 | A | 799.5036 | 400.2554 | 782.4771 | 391.7422 | 781.4931 | 391.2502 | 7 |
| 7 | 733.3515 | 367.1794 | 716.3250 | 358.6661 | 715.3410 | 358.1741 | V | 728.4665 | 364.7369 | 711.4400 | 356.2236 | 710.4559 | 355.7316 | 6 |
| 8 | 889.4526 | 445.2300 | 872.4261 | 436.7167 | 871.4421 | 436.2247 | R | 629.3981 | 315.2027 | 612.3715 | 306.6894 | 611.3875 | 306.1974 | 5 |
| 9 | 1002.5367 | 501.7720 | 985.5102 | 493.2587 | 984.5261 | 492.7667 | I | 473.2970 | 237.1521 | | | 455.2864 | 228.1468 | 4 |
| 10 | 1115.6208 | 558.3140 | 1098.5942 | 549.8007 | 1097.6102 | 549.3087 | L | 360.2129 | 180.6101 | | | 342.2023 | 171.6048 | 3 |
| 11 | 1244.6634 | 622.8353 | 1227.6368 | 614.3220 | 1226.6528 | 613.8300 | E | 247.1288 | 124.0681 | | | 229.1183 | 115.0628 | 2 |
| 12 | | | | | | | V | 118.0863 | 59.5468 | | | | | 1 |



NCBI **BLAST** search of [NDFASAVRILEV](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--------------------------------|
| 70.5 | 1360.7350 | 0.0018 | NDFASAVRILEV |
| 31.9 | 1360.8417 | -0.1048 | GPETVLQSAIKL |
| 27.8 | 1360.5825 | 0.1544 | NMMASIQSFSAM |
| 26.2 | 1360.7322 | 0.0047 | ATLAPTTRAMAPA |
| 26.1 | 1360.8417 | -0.1048 | KDNIGVAVVLEV |
| 23.8 | 1360.7380 | -0.0011 | VINAAPGAQGGTEV |
| 23.8 | 1360.6519 | 0.0849 | NPGPMVVFATPGM |
| 23.0 | 1360.6408 | 0.0960 | SQDASSRPDPEV |
| 22.6 | 1360.8166 | -0.0797 | APGVQKALGAGTEV |
| 22.4 | 1360.6097 | 0.1272 | TLDEMDSAASDL |

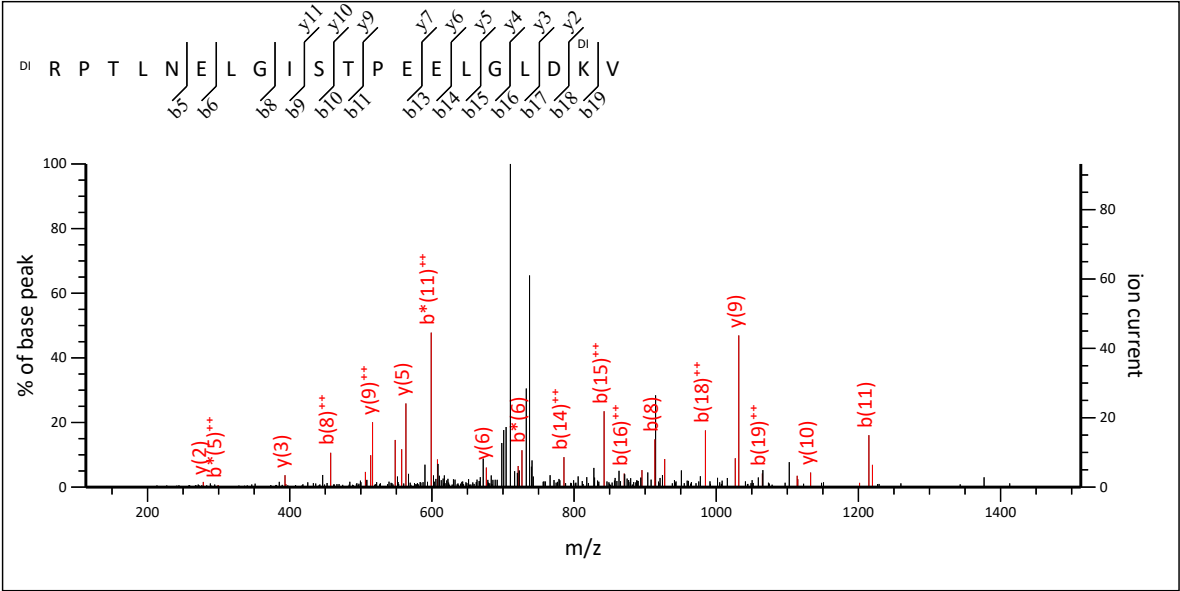
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPTLNELGISTPEELGLDKV**
Found in **COX5A_MOUSE** in **SwissProt**, Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus musculus GN=Cox5a PE=1 SV=2

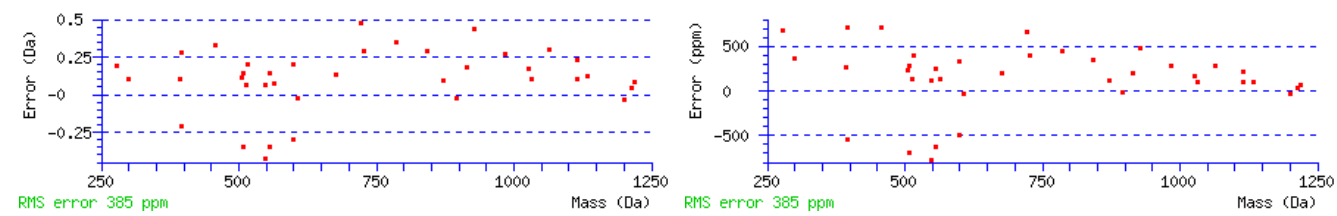
Match to Query 8645: 2244.298632 from(749.106820,3+) intensity(31536.9790) scans(10331) rawscans(sn10331) rtinseconds(3866.6548) index(7546)
Title: 7547: Scan 10331 (rt=3866.65) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 2244.2817
Variable modifications:
N-term : Dimethyl:2H(4) (N-term)
K19 : Dimethyl:2H(4) (K)
Ions Score: 42 Expect: 2.3
Matches : 38/218 fragment ions using 78 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺ * | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺ * | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|-------------------|----------------|------------------|------|-----------|-----------------|----------------|-------------------|----------------|------------------|----|
| 1 | 189.1648 | 95.0860 | 172.1382 | 86.5728 | | | R | | | | | | | 20 |
| 2 | 286.2176 | 143.6124 | 269.1910 | 135.0991 | | | P | 2057.1314 | 1029.0694 | 2040.1049 | 1020.5561 | 2039.1209 | 1020.0641 | 19 |
| 3 | 387.2652 | 194.1363 | 370.2387 | 185.6230 | 369.2547 | 185.1310 | T | 1960.0787 | 980.5430 | 1943.0521 | 972.0297 | 1942.0681 | 971.5377 | 18 |
| 4 | 500.3493 | 250.6783 | 483.3228 | 242.1650 | 482.3387 | 241.6730 | L | 1859.0310 | 930.0191 | 1842.0044 | 921.5059 | 1841.0204 | 921.0139 | 17 |
| 5 | 614.3922 | 307.6998 | 597.3657 | 299.1865 | 596.3817 | 298.6945 | N | 1745.9469 | 873.4771 | 1728.9204 | 864.9638 | 1727.9364 | 864.4718 | 16 |
| 6 | 743.4348 | 372.2210 | 726.4083 | 363.7078 | 725.4243 | 363.2158 | E | 1631.9040 | 816.4556 | 1614.8775 | 807.9424 | 1613.8934 | 807.4504 | 15 |
| 7 | 856.5189 | 428.7631 | 839.4923 | 420.2498 | 838.5083 | 419.7578 | L | 1502.8614 | 751.9343 | 1485.8349 | 743.4211 | 1484.8508 | 742.9291 | 14 |
| 8 | 913.5403 | 457.2738 | 896.5138 | 448.7605 | 895.5298 | 448.2685 | G | 1389.7773 | 695.3923 | 1372.7508 | 686.8790 | 1371.7668 | 686.3870 | 13 |
| 9 | 1026.6244 | 513.8158 | 1009.5979 | 505.3026 | 1008.6138 | 504.8106 | I | 1332.7559 | 666.8816 | 1315.7293 | 658.3683 | 1314.7453 | 657.8763 | 12 |
| 10 | 1113.6564 | 557.3319 | 1096.6299 | 548.8186 | 1095.6459 | 548.3266 | S | 1219.6718 | 610.3395 | 1202.6453 | 601.8263 | 1201.6613 | 601.3343 | 11 |
| 11 | 1214.7041 | 607.8557 | 1197.6776 | 599.3424 | 1196.6936 | 598.8504 | T | 1132.6398 | 566.8235 | 1115.6132 | 558.3103 | 1114.6292 | 557.8183 | 10 |
| 12 | 1311.7569 | 656.3821 | 1294.7303 | 647.8688 | 1293.7463 | 647.3768 | P | 1031.5921 | 516.2997 | 1014.5656 | 507.7864 | 1013.5815 | 507.2944 | 9 |
| 13 | 1440.7995 | 720.9034 | 1423.7729 | 712.3901 | 1422.7889 | 711.8981 | E | 934.5393 | 467.7733 | 917.5128 | 459.2600 | 916.5288 | 458.7680 | 8 |
| 14 | 1569.8421 | 785.4247 | 1552.8155 | 776.9114 | 1551.8315 | 776.4194 | E | 805.4968 | 403.2520 | 788.4702 | 394.7387 | 787.4862 | 394.2467 | 7 |
| 15 | 1682.9261 | 841.9667 | 1665.8996 | 833.4534 | 1664.9156 | 832.9614 | L | 676.4542 | 338.7307 | 659.4276 | 330.2174 | 658.4436 | 329.7254 | 6 |
| 16 | 1739.9476 | 870.4774 | 1722.9210 | 861.9642 | 1721.9370 | 861.4722 | G | 563.3701 | 282.1887 | 546.3435 | 273.6754 | 545.3595 | 273.1834 | 5 |
| 17 | 1853.0317 | 927.0195 | 1836.0051 | 918.5062 | 1835.0211 | 918.0142 | L | 506.3486 | 253.6780 | 489.3221 | 245.1647 | 488.3381 | 244.6727 | 4 |
| 18 | 1968.0586 | 984.5329 | 1951.0321 | 976.0197 | 1950.0480 | 975.5277 | D | 393.2646 | 197.1359 | 376.2380 | 188.6226 | 375.2540 | 188.1306 | 3 |
| 19 | 2128.2100 | 1064.6086 | 2111.1834 | 1056.0954 | 2110.1994 | 1055.6033 | K | 278.2376 | 139.6225 | 261.2111 | 131.1092 | | | 2 |
| 20 | | | | | | | V | 118.0863 | 59.5468 | | | | | 1 |



NCBI BLAST search of [RPTLNELGISTPEELGLDKV](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|---------------------------------------|
| 41.6 | 2244.2817 | 0.0170 | RPTLNELGISTPEELGLDKV |
| 18.0 | 2244.3293 | -0.0307 | LSAKGQLTNIVSPTAATTPRI |
| 17.3 | 2243.9274 | 0.3712 | MMESHSSNSNGTEMVSQPSH |
| 15.6 | 2244.1007 | 0.1979 | AENGHQMAAETAIQRPNVPH |
| 15.1 | 2244.1517 | 0.1469 | ARGFGLWEGALYEIGGLFGTG |
| 14.6 | 2244.1462 | 0.1524 | EDTMYPLIALVVIFFGMSL |
| 14.1 | 2244.2676 | 0.0310 | SLDATPSPETTSLSQTKKMTI |
| 13.6 | 2244.0580 | 0.2406 | VCPGIAADSPSSTDSPQNKEV |
| 12.8 | 2244.0220 | 0.2766 | LMSPMTSGEMSMPLMKTPS |
| 12.4 | 2244.0775 | 0.2211 | LVHGLTLVGTASNPCGVMMQM |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

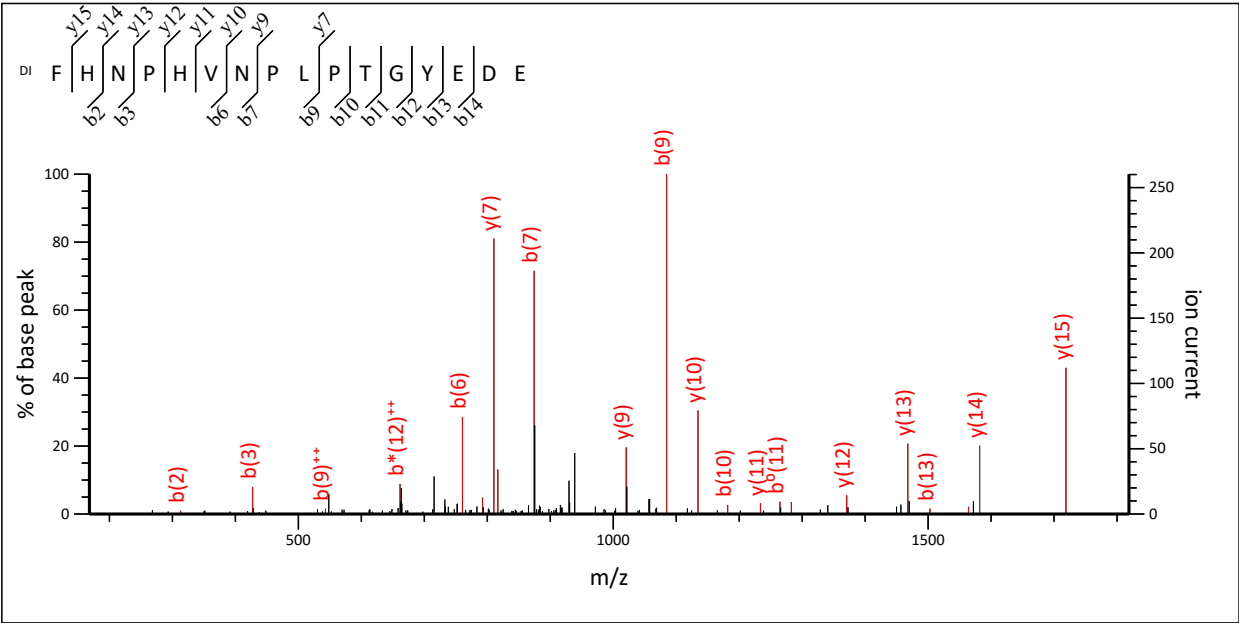
Peptide View

MS/MS Fragmentation of **FHNPHVNPLPTGYEDE**
Found in **CX6A1_MOUSE** in **SwissProt**, Cytochrome c oxidase subunit 6A1, mitochondrial OS=Mus musculus GN=Cox6a1 PE=1 SV=2

Match to Query 7128: 1892.874028 from(947.444290,2+) intensity(60708.2460) scans(5788) rawscans(sn5788) rtinseconds(2254.0558) index(3711)

Title: 3712: Scan 5788 (rt=2254.06) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]

Data file hipocampo_01.temp.mgf

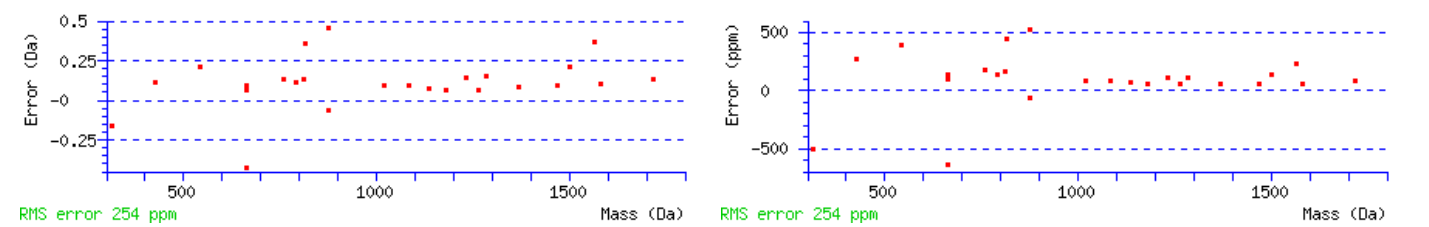


168.2 to 1818.91

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1892.8693
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 55 Expect: 0.11
Matches : 25/138 fragment ions using 42 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 176.1070 | 88.5571 | | | | | F | | | | | | | 16 |
| 2 | 313.1659 | 157.0866 | | | | | H | 1718.7769 | 859.8921 | 1701.7503 | 851.3788 | 1700.7663 | 850.8868 | 15 |
| 3 | 427.2088 | 214.1081 | 410.1823 | 205.5948 | | | N | 1581.7180 | 791.3626 | 1564.6914 | 782.8494 | 1563.7074 | 782.3573 | 14 |
| 4 | 524.2616 | 262.6344 | 507.2350 | 254.1212 | | | P | 1467.6751 | 734.3412 | 1450.6485 | 725.8279 | 1449.6645 | 725.3359 | 13 |
| 5 | 661.3205 | 331.1639 | 644.2940 | 322.6506 | | | H | 1370.6223 | 685.8148 | 1353.5957 | 677.3015 | 1352.6117 | 676.8095 | 12 |
| 6 | 760.3889 | 380.6981 | 743.3624 | 372.1848 | | | V | 1233.5634 | 617.2853 | 1216.5368 | 608.7721 | 1215.5528 | 608.2800 | 11 |
| 7 | 874.4318 | 437.7196 | 857.4053 | 429.2063 | | | N | 1134.4950 | 567.7511 | 1117.4684 | 559.2378 | 1116.4844 | 558.7458 | 10 |
| 8 | 971.4846 | 486.2459 | 954.4581 | 477.7327 | | | P | 1020.4520 | 510.7297 | | | 1002.4415 | 501.7244 | 9 |
| 9 | 1084.5687 | 542.7880 | 1067.5421 | 534.2747 | | | L | 923.3993 | 462.2033 | | | 905.3887 | 453.1980 | 8 |
| 10 | 1181.6214 | 591.3144 | 1164.5949 | 582.8011 | | | P | 810.3152 | 405.6612 | | | 792.3046 | 396.6560 | 7 |
| 11 | 1282.6691 | 641.8382 | 1265.6426 | 633.3249 | 1264.6586 | 632.8329 | T | 713.2624 | 357.1349 | | | 695.2519 | 348.1296 | 6 |
| 12 | 1339.6906 | 670.3489 | 1322.6640 | 661.8357 | 1321.6800 | 661.3436 | G | 612.2148 | 306.6110 | | | 594.2042 | 297.6057 | 5 |
| 13 | 1502.7539 | 751.8806 | 1485.7274 | 743.3673 | 1484.7433 | 742.8753 | Y | 555.1933 | 278.1003 | | | 537.1827 | 269.0950 | 4 |
| 14 | 1631.7965 | 816.4019 | 1614.7700 | 807.8886 | 1613.7859 | 807.3966 | E | 392.1300 | 196.5686 | | | 374.1194 | 187.5633 | 3 |
| 15 | 1746.8234 | 873.9154 | 1729.7969 | 865.4021 | 1728.8129 | 864.9101 | D | 263.0874 | 132.0473 | | | 245.0768 | 123.0420 | 2 |
| 16 | | | | | | | E | 148.0604 | 74.5339 | | | 130.0499 | 65.5286 | 1 |



NCBI **BLAST** search of [FHNPHVNPLPTGYEDE](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-----------------------------------|
| 54.7 | 1892.8693 | 0.0047 | FHNPHVNPLPTGYEDE |
| 16.7 | 1893.0683 | -0.1943 | LREIQELGQLIQAVQQ |
| 15.7 | 1892.8102 | 0.0638 | NEFYGLNFTCGGSNTSM |
| 15.1 | 1892.9576 | -0.0835 | TEREIVNDFREKMM |
| 14.9 | 1892.7746 | 0.0994 | NLMFGDYMNPDLEGDD |
| 14.6 | 1892.8549 | 0.0191 | EATHCTPLPAQHFQMP |
| 14.1 | 1893.1335 | -0.2594 | HVVLRRINNVHVKMD |
| 13.7 | 1892.7246 | 0.1494 | SEDEDEPDMKCDDMM |
| 13.5 | 1893.1222 | -0.2482 | KSMHLGRLPSRPPLPGS |
| 13.5 | 1892.7828 | 0.0912 | AGALAQDEYEEDSSDEE |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

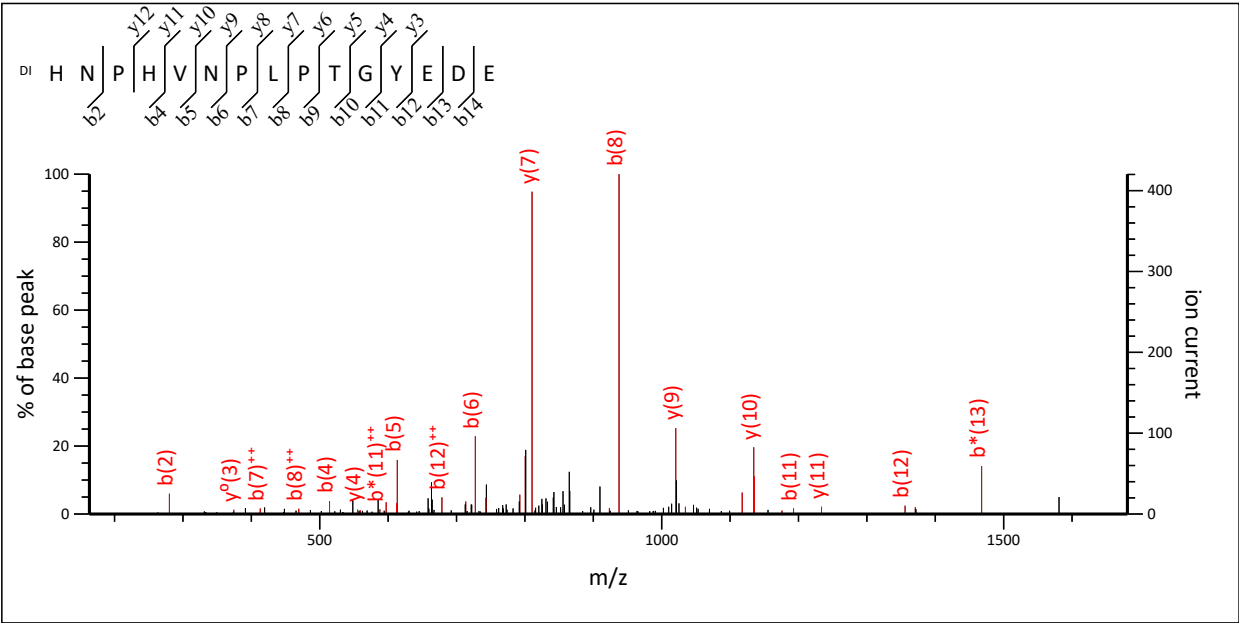
Peptide View

MS/MS Fragmentation of **HNP HVNPLPTGYEDE**
Found in **CX6A1_MOUSE** in **SwissProt**, Cytochrome c oxidase subunit 6A1, mitochondrial OS=Mus musculus GN=Cox6a1 PE=1 SV=2

Match to Query 6391: 1745.804808 from(873.909680,2+) intensity(84828.5230) scans(4888) rawscans(sn4888) rtinseconds(1960.3945) index(2914)

Title: 2915: Scan 4888 (rt=1960.39) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]

Data file hipocampo_01.temp.mgf

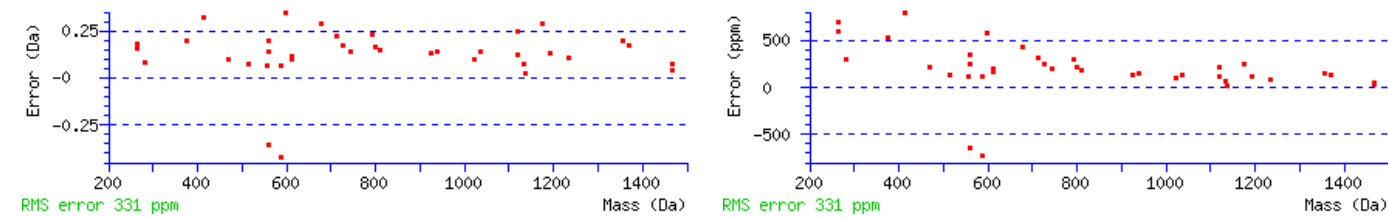


163.27 to 1680.94

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1745.8009
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 61 Expect: 0.023
Matches : 38/130 fragment ions using 69 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 166.0975 | 83.5524 | | | | | H | | | | | | | 15 |
| 2 | 280.1404 | 140.5738 | 263.1139 | 132.0606 | | | N | 1581.7180 | 791.3626 | 1564.6914 | 782.8494 | 1563.7074 | 782.3573 | 14 |
| 3 | 377.1932 | 189.1002 | 360.1666 | 180.5870 | | | P | 1467.6751 | 734.3412 | 1450.6485 | 725.8279 | 1449.6645 | 725.3359 | 13 |
| 4 | 514.2521 | 257.6297 | 497.2255 | 249.1164 | | | H | 1370.6223 | 685.8148 | 1353.5957 | 677.3015 | 1352.6117 | 676.8095 | 12 |
| 5 | 613.3205 | 307.1639 | 596.2940 | 298.6506 | | | V | 1233.5634 | 617.2853 | 1216.5368 | 608.7721 | 1215.5528 | 608.2800 | 11 |
| 6 | 727.3634 | 364.1854 | 710.3369 | 355.6721 | | | N | 1134.4950 | 567.7511 | 1117.4684 | 559.2378 | 1116.4844 | 558.7458 | 10 |
| 7 | 824.4162 | 412.7117 | 807.3896 | 404.1985 | | | P | 1020.4520 | 510.7297 | | | 1002.4415 | 501.7244 | 9 |
| 8 | 937.5003 | 469.2538 | 920.4737 | 460.7405 | | | L | 923.3993 | 462.2033 | | | 905.3887 | 453.1980 | 8 |
| 9 | 1034.5530 | 517.7802 | 1017.5265 | 509.2669 | | | P | 810.3152 | 405.6612 | | | 792.3046 | 396.6560 | 7 |
| 10 | 1135.6007 | 568.3040 | 1118.5742 | 559.7907 | 1117.5901 | 559.2987 | T | 713.2624 | 357.1349 | | | 695.2519 | 348.1296 | 6 |
| 11 | 1192.6222 | 596.8147 | 1175.5956 | 588.3014 | 1174.6116 | 587.8094 | G | 612.2148 | 306.6110 | | | 594.2042 | 297.6057 | 5 |
| 12 | 1355.6855 | 678.3464 | 1338.6589 | 669.8331 | 1337.6749 | 669.3411 | Y | 555.1933 | 278.1003 | | | 537.1827 | 269.0950 | 4 |
| 13 | 1484.7281 | 742.8677 | 1467.7015 | 734.3544 | 1466.7175 | 733.8624 | E | 392.1300 | 196.5686 | | | 374.1194 | 187.5633 | 3 |
| 14 | 1599.7550 | 800.3812 | 1582.7285 | 791.8679 | 1581.7445 | 791.3759 | D | 263.0874 | 132.0473 | | | 245.0768 | 123.0420 | 2 |
| 15 | | | | | | | E | 148.0604 | 74.5339 | | | 130.0499 | 65.5286 | 1 |



NCBI BLAST search of [HNPHVNPLPTYEDE](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-----------------------------------|
| 61.4 | 1745.8009 | 0.0039 | HNPHVNPLPTYEDE |
| 20.5 | 1745.9098 | -0.1050 | IGLHGGRPLQDMVGMGG |
| 17.4 | 1745.8723 | -0.0675 | KTGIDNPIFDTEEGI |
| 15.8 | 1745.9272 | -0.1224 | QAKYGDRHAMKQSD |
| 14.8 | 1746.0254 | -0.2206 | SHRMFDSTAKSFPK |
| 14.2 | 1745.8680 | -0.0632 | IFEVGKNGGSSCPECR |
| 14.1 | 1745.7171 | 0.0877 | DGMHQNLPPMERDM |
| 13.8 | 1745.8266 | -0.0218 | TMSEAELPLGFSRMN |
| 13.8 | 1745.9109 | -0.1061 | LDASDEFLKERVVN |
| 13.5 | 1745.8869 | -0.0821 | GKQLTRLRLMEEDE |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

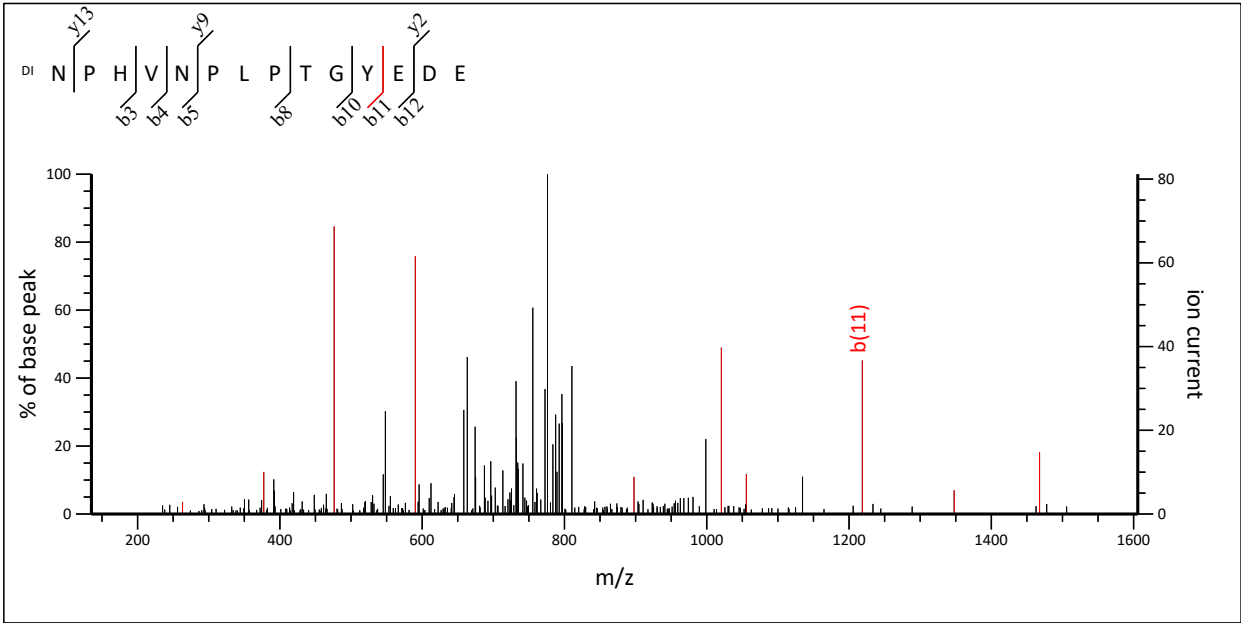
Peptide View

MS/MS Fragmentation of **NPHVNPLPTGYEDE**
Found in **CX6A1_MOUSE** in **SwissProt**, Cytochrome c oxidase subunit 6A1, mitochondrial OS=Mus musculus GN=Cox6a1 PE=1 SV=2

Match to Query 5578: 1608.746608 from(805.380580,2+) intensity(42224.8050) scans(5737) rawscans(sn5737) rtinseconds(2237.191) index(3665)

Title: 3666: Scan 5737 (rt=2237.19) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]

Data file hipocampo_01.temp.mgf

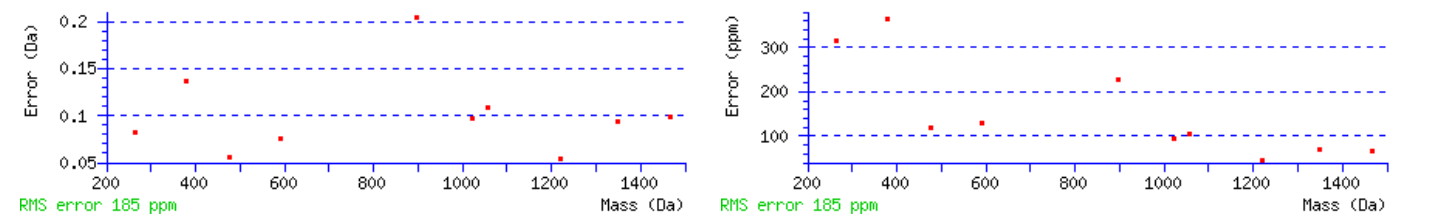


135.11 to 1605.82

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1608.7420
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 53 Expect: 0.17
Matches : 10/122 fragment ions using 13 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 143.0815 | 72.0444 | 126.0550 | 63.5311 | | | N | | | | | | | 14 |
| 2 | 240.1343 | 120.5708 | 223.1077 | 112.0575 | | | P | 1467.6751 | 734.3412 | 1450.6485 | 725.8279 | 1449.6645 | 725.3359 | 13 |
| 3 | 377.1932 | 189.1002 | 360.1666 | 180.5870 | | | H | 1370.6223 | 685.8148 | 1353.5957 | 677.3015 | 1352.6117 | 676.8095 | 12 |
| 4 | 476.2616 | 238.6344 | 459.2350 | 230.1212 | | | V | 1233.5634 | 617.2853 | 1216.5368 | 608.7721 | 1215.5528 | 608.2800 | 11 |
| 5 | 590.3045 | 295.6559 | 573.2780 | 287.1426 | | | N | 1134.4950 | 567.7511 | 1117.4684 | 559.2378 | 1116.4844 | 558.7458 | 10 |
| 6 | 687.3573 | 344.1823 | 670.3307 | 335.6690 | | | P | 1020.4520 | 510.7297 | | | 1002.4415 | 501.7244 | 9 |
| 7 | 800.4413 | 400.7243 | 783.4148 | 392.2110 | | | L | 923.3993 | 462.2033 | | | 905.3887 | 453.1980 | 8 |
| 8 | 897.4941 | 449.2507 | 880.4676 | 440.7374 | | | P | 810.3152 | 405.6612 | | | 792.3046 | 396.6560 | 7 |
| 9 | 998.5418 | 499.7745 | 981.5152 | 491.2613 | 980.5312 | 490.7693 | T | 713.2624 | 357.1349 | | | 695.2519 | 348.1296 | 6 |
| 10 | 1055.5633 | 528.2853 | 1038.5367 | 519.7720 | 1037.5527 | 519.2800 | G | 612.2148 | 306.6110 | | | 594.2042 | 297.6057 | 5 |
| 11 | 1218.6266 | 609.8169 | 1201.6000 | 601.3037 | 1200.6160 | 600.8116 | Y | 555.1933 | 278.1003 | | | 537.1827 | 269.0950 | 4 |
| 12 | 1347.6692 | 674.3382 | 1330.6426 | 665.8250 | 1329.6586 | 665.3329 | E | 392.1300 | 196.5686 | | | 374.1194 | 187.5633 | 3 |
| 13 | 1462.6961 | 731.8517 | 1445.6696 | 723.3384 | 1444.6856 | 722.8464 | D | 263.0874 | 132.0473 | | | 245.0768 | 123.0420 | 2 |
| 14 | | | | | | | E | 148.0604 | 74.5339 | | | 130.0499 | 65.5286 | 1 |



NCBI **BLAST** search of [NPHVNPLPTGYEDE](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|----------------------------------|
| 52.7 | 1608.7420 | 0.0046 | NPHVNPLPTGYEDE |
| 21.8 | 1608.8388 | -0.0922 | LIERGASLEEVNDE |
| 20.9 | 1608.8275 | -0.0809 | ALERDEVETLIDE |
| 19.1 | 1608.7885 | -0.0419 | EPGGRGGGASTRVEED |
| 18.9 | 1608.7197 | 0.0269 | SMDAPVMIMNGKDE |
| 18.0 | 1608.8589 | -0.1123 | EVSSIEPLTLGEPE |
| 17.3 | 1608.8235 | -0.0769 | NTSVSSKSTDPHFP |
| 17.3 | 1608.5923 | 0.1543 | TSCSYSEDSEDE |
| 16.1 | 1608.9483 | -0.2017 | PPTLRETKPVNMP |
| 13.9 | 1608.9169 | -0.1703 | LLEYRAGLVAGHGFA |

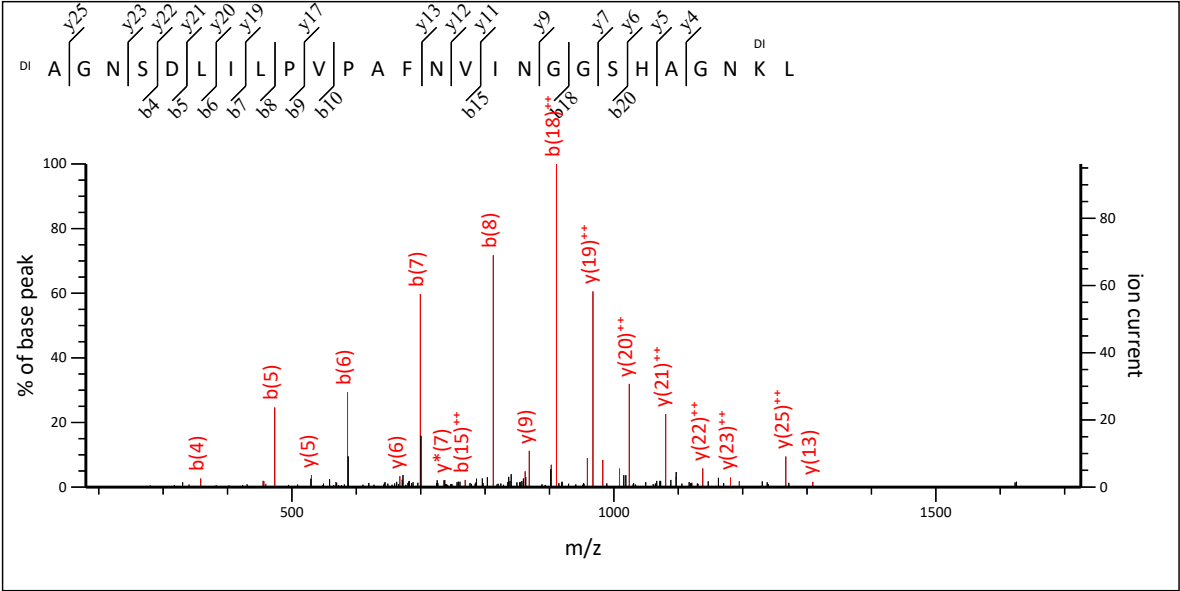
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGNSDLILVPAFNVINGGSHAGNKL**
Found in **ENOG_MOUSE** in **SwissProt**, Gamma-enolase OS=Mus musculus GN=Eno2 PE=1 SV=2

Match to Query 9603: 2630.429982 from(877.817270,3+) intensity(22324.3420) scans(11509) rawscans(sn11509) rtinseconds(4300.4458) index(8562)
Title: 8563: Scan 11509 (rt=4300.45) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf



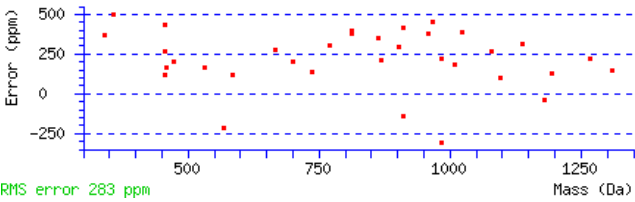
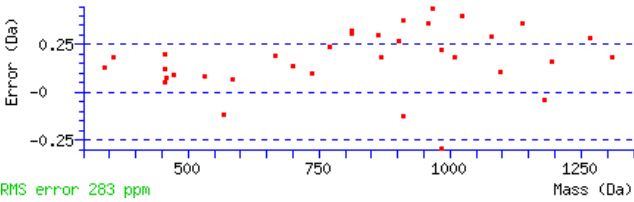
Navigation icons: ? (help), zoom in, zoom out, reset, and a search bar with the range 180.03 to 1725.12.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 2630.4180
Variable modifications:
N-term : Dimethyl (N-term)
K25 : Dimethyl (K)
Ions Score: 81 Expect: 0.00026
Matches : 34/276 fragment ions using 43 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | | | A | | | | | | | 26 |
| 2 | 157.0972 | 79.0522 | | | | | G | 2532.3569 | 1266.6821 | 2515.3303 | 1258.1688 | 2514.3463 | 1257.6768 | 25 |
| 3 | 271.1401 | 136.0737 | 254.1135 | 127.5604 | | | N | 2475.3354 | 1238.1714 | 2458.3089 | 1229.6581 | 2457.3249 | 1229.1661 | 24 |
| 4 | 358.1721 | 179.5897 | 341.1456 | 171.0764 | 340.1615 | 170.5844 | S | 2361.2925 | 1181.1499 | 2344.2660 | 1172.6366 | 2343.2819 | 1172.1446 | 23 |
| 5 | 473.1991 | 237.1032 | 456.1725 | 228.5899 | 455.1885 | 228.0979 | D | 2274.2605 | 1137.6339 | 2257.2339 | 1129.1206 | 2256.2499 | 1128.6286 | 22 |
| 6 | 586.2831 | 293.6452 | 569.2566 | 285.1319 | 568.2726 | 284.6399 | L | 2159.2335 | 1080.1204 | 2142.2070 | 1071.6071 | 2141.2230 | 1071.1151 | 21 |
| 7 | 699.3672 | 350.1872 | 682.3406 | 341.6740 | 681.3566 | 341.1819 | I | 2046.1495 | 1023.5784 | 2029.1229 | 1015.0651 | 2028.1389 | 1014.5731 | 20 |
| 8 | 812.4512 | 406.7293 | 795.4247 | 398.2160 | 794.4407 | 397.7240 | L | 1933.0654 | 967.0363 | 1916.0389 | 958.5231 | 1915.0548 | 958.0311 | 19 |
| 9 | 909.5040 | 455.2556 | 892.4775 | 446.7424 | 891.4934 | 446.2504 | P | 1819.9813 | 910.4943 | 1802.9548 | 901.9810 | 1801.9708 | 901.4890 | 18 |
| 10 | 1008.5724 | 504.7898 | 991.5459 | 496.2766 | 990.5619 | 495.7846 | V | 1722.9286 | 861.9679 | 1705.9020 | 853.4547 | 1704.9180 | 852.9626 | 17 |
| 11 | 1105.6252 | 553.3162 | 1088.5986 | 544.8030 | 1087.6146 | 544.3109 | P | 1623.8602 | 812.4337 | 1606.8336 | 803.9204 | 1605.8496 | 803.4284 | 16 |
| 12 | 1176.6623 | 588.8348 | 1159.6358 | 580.3215 | 1158.6517 | 579.8295 | A | 1526.8074 | 763.9073 | 1509.7809 | 755.3941 | 1508.7968 | 754.9021 | 15 |
| 13 | 1323.7307 | 662.3690 | 1306.7042 | 653.8557 | 1305.7201 | 653.3637 | F | 1455.7703 | 728.3888 | 1438.7437 | 719.8755 | 1437.7597 | 719.3835 | 14 |
| 14 | 1437.7736 | 719.3905 | 1420.7471 | 710.8772 | 1419.7631 | 710.3852 | N | 1308.7019 | 654.8546 | 1291.6753 | 646.3413 | 1290.6913 | 645.8493 | 13 |
| 15 | 1536.8421 | 768.9247 | 1519.8155 | 760.4114 | 1518.8315 | 759.9194 | V | 1194.6589 | 597.8331 | 1177.6324 | 589.3198 | 1176.6484 | 588.8278 | 12 |
| 16 | 1649.9261 | 825.4667 | 1632.8996 | 816.9534 | 1631.9156 | 816.4614 | I | 1095.5905 | 548.2989 | 1078.5640 | 539.7856 | 1077.5800 | 539.2936 | 11 |
| 17 | 1763.9690 | 882.4882 | 1746.9425 | 873.9749 | 1745.9585 | 873.4829 | N | 982.5065 | 491.7569 | 965.4799 | 483.2436 | 964.4959 | 482.7516 | 10 |
| 18 | 1820.9905 | 910.9989 | 1803.9640 | 902.4856 | 1802.9799 | 901.9936 | G | 868.4635 | 434.7354 | 851.4370 | 426.2221 | 850.4530 | 425.7301 | 9 |
| 19 | 1878.0120 | 939.5096 | 1860.9854 | 930.9964 | 1860.0014 | 930.5043 | G | 811.4421 | 406.2247 | 794.4155 | 397.7114 | 793.4315 | 397.2194 | 8 |
| 20 | 1965.0440 | 983.0256 | 1948.0175 | 974.5124 | 1947.0334 | 974.0204 | S | 754.4206 | 377.7139 | 737.3941 | 369.2007 | 736.4100 | 368.7087 | 7 |
| 21 | 2102.1029 | 1051.5551 | 2085.0764 | 1043.0418 | 2084.0923 | 1042.5498 | H | 667.3886 | 334.1979 | 650.3620 | 325.6847 | | | 6 |

| | | | | | | | | | | | | | | |
|----|-----------|-----------|-----------|-----------|-----------|-----------|---|----------|----------|----------|----------|--|--|---|
| 22 | 2173.1400 | 1087.0737 | 2156.1135 | 1078.5604 | 2155.1295 | 1078.0684 | A | 530.3297 | 265.6685 | 513.3031 | 257.1552 | | | 5 |
| 23 | 2230.1615 | 1115.5844 | 2213.1349 | 1107.0711 | 2212.1509 | 1106.5791 | G | 459.2926 | 230.1499 | 442.2660 | 221.6366 | | | 4 |
| 24 | 2344.2044 | 1172.6058 | 2327.1779 | 1164.0926 | 2326.1939 | 1163.6006 | N | 402.2711 | 201.6392 | 385.2445 | 193.1259 | | | 3 |
| 25 | 2500.3307 | 1250.6690 | 2483.3041 | 1242.1557 | 2482.3201 | 1241.6637 | K | 288.2282 | 144.6177 | 271.2016 | 136.1044 | | | 2 |
| 26 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI BLAST search of [AGNSDLILPVPAFNVINGGSHAGNKL](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--|
| 81.3 | 2630.4180 | 0.0120 | AGNSDLILPVPAFNVINGGSHAGNKL |
| 37.0 | 2630.4796 | -0.0496 | STSLLGQKKPGYHAPVALLNDIPQ |
| 27.7 | 2630.5195 | -0.0895 | MLLALILSMAVPTIIGLSLWKEF |
| 27.7 | 2630.6287 | -0.1987 | PVTFIILLNIIFLVITLCKMVK |
| 26.4 | 2630.4427 | -0.0127 | AIEMLDGHLyllldmgsGTIKIK |
| 25.6 | 2630.3262 | 0.1038 | MNVTVEGPTSILQNYQLIHTSE |
| 25.3 | 2630.4359 | -0.0059 | GTYDIEFYTAAKPGTYVIYVRFGG |
| 24.0 | 2630.3151 | 0.1148 | APPGALNLGLSSNNSTLSVAGAMGSHGG |
| 23.9 | 2630.5411 | -0.1111 | RQLQQLVLDPGFLGLEPLDLLL |
| 23.1 | 2630.5197 | -0.0897 | LTVLIPPEETRIDGGPVILLQAGTP |

Mascot: <http://www.matrixscience.com/>

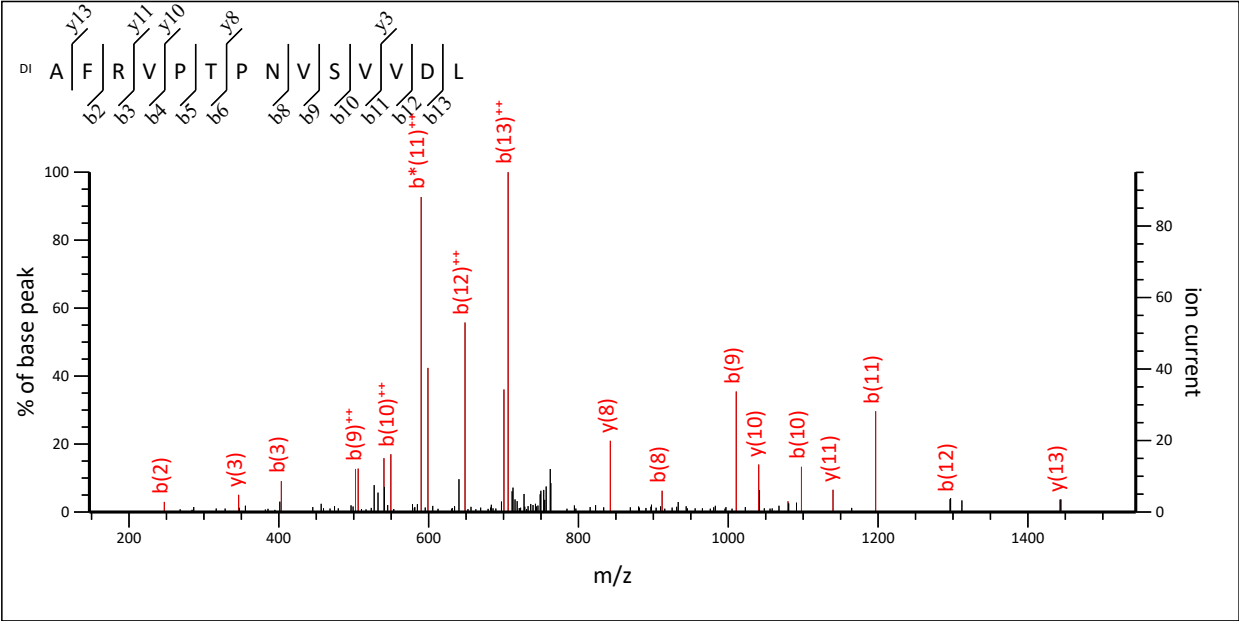
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFRVPTPNVSVVDL**
Found in **G3P_MOUSE** in **SwissProt**, Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2

Match to Query 5231: 1540.873148 from(771.443850,2+) intensity(23204.3850) scans(10746) rawscans(sn10746) rtinseconds(4016.6452) index(7908)

Title: 7909: Scan 10746 (rt=4016.65) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf





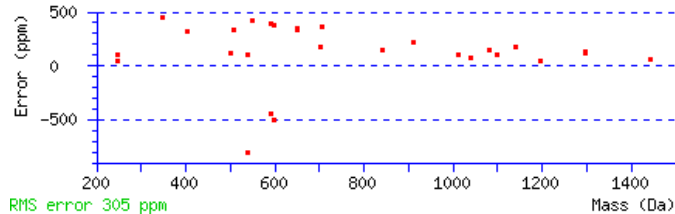
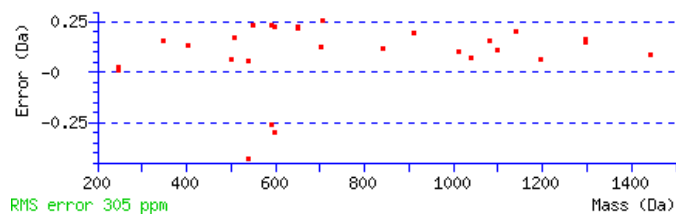
147.15 to 1544.02



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1540.8613
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 79 Expect: 0.00041
Matches : 28/128 fragment ions using 34 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | | | A | | | | | | | 14 |
| 2 | 247.1441 | 124.0757 | | | | | F | 1442.8002 | 721.9037 | 1425.7736 | 713.3905 | 1424.7896 | 712.8985 | 13 |
| 3 | 403.2452 | 202.1262 | 386.2187 | 193.6130 | | | R | 1295.7318 | 648.3695 | 1278.7052 | 639.8563 | 1277.7212 | 639.3642 | 12 |
| 4 | 502.3136 | 251.6605 | 485.2871 | 243.1472 | | | V | 1139.6307 | 570.3190 | 1122.6041 | 561.8057 | 1121.6201 | 561.3137 | 11 |
| 5 | 599.3664 | 300.1868 | 582.3398 | 291.6736 | | | P | 1040.5623 | 520.7848 | 1023.5357 | 512.2715 | 1022.5517 | 511.7795 | 10 |
| 6 | 700.4141 | 350.7107 | 683.3875 | 342.1974 | 682.4035 | 341.7054 | T | 943.5095 | 472.2584 | 926.4829 | 463.7451 | 925.4989 | 463.2531 | 9 |
| 7 | 797.4668 | 399.2371 | 780.4403 | 390.7238 | 779.4563 | 390.2318 | P | 842.4618 | 421.7345 | 825.4353 | 413.2213 | 824.4512 | 412.7293 | 8 |
| 8 | 911.5098 | 456.2585 | 894.4832 | 447.7452 | 893.4992 | 447.2532 | N | 745.4090 | 373.2082 | 728.3825 | 364.6949 | 727.3985 | 364.2029 | 7 |
| 9 | 1010.5782 | 505.7927 | 993.5516 | 497.2795 | 992.5676 | 496.7874 | V | 631.3661 | 316.1867 | | | 613.3556 | 307.1814 | 6 |
| 10 | 1097.6102 | 549.3087 | 1080.5837 | 540.7955 | 1079.5996 | 540.3035 | S | 532.2977 | 266.6525 | | | 514.2871 | 257.6472 | 5 |
| 11 | 1196.6786 | 598.8429 | 1179.6521 | 590.3297 | 1178.6681 | 589.8377 | V | 445.2657 | 223.1365 | | | 427.2551 | 214.1312 | 4 |
| 12 | 1295.7470 | 648.3772 | 1278.7205 | 639.8639 | 1277.7365 | 639.3719 | V | 346.1973 | 173.6023 | | | 328.1867 | 164.5970 | 3 |
| 13 | 1410.7740 | 705.8906 | 1393.7474 | 697.3774 | 1392.7634 | 696.8853 | D | 247.1288 | 124.0681 | | | 229.1183 | 115.0628 | 2 |
| 14 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI **BLAST** search of [AFRVPTPNVSVVDL](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

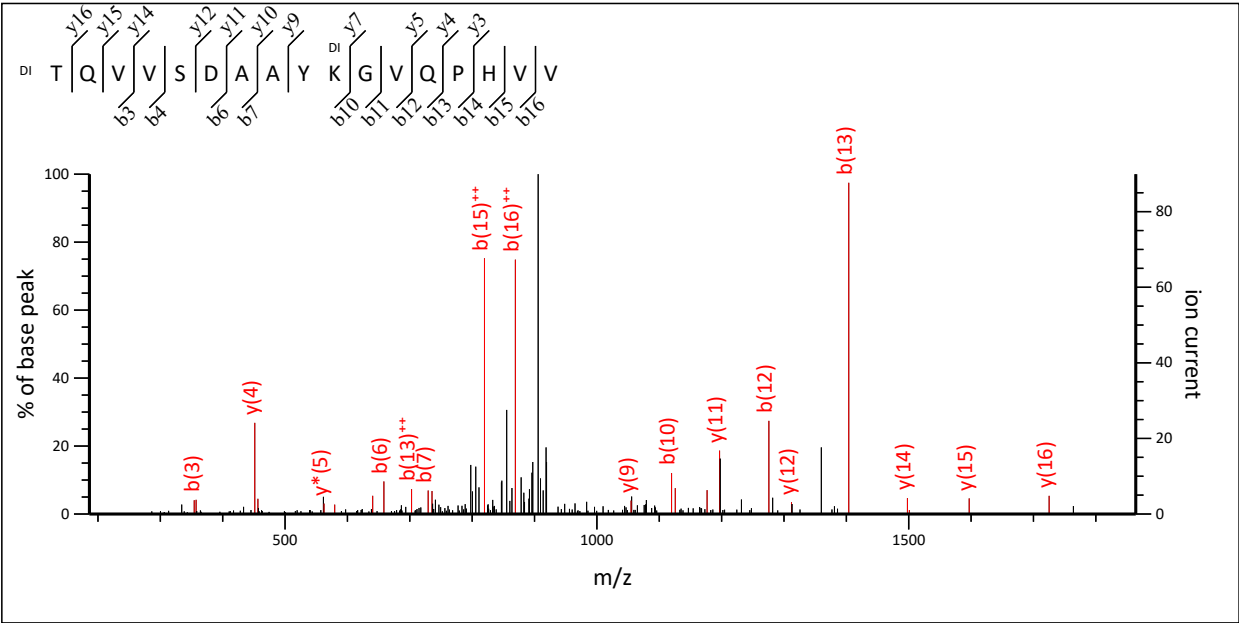
| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|---------------------------------|
| 78.8 | 1540.8613 | 0.0118 | AFRVPTPNVSVVDL |
| 30.7 | 1540.9287 | -0.0555 | SIVTGGEGKPGVVDL |
| 30.4 | 1540.8763 | -0.0031 | QLSVPLGQLREEV |
| 25.4 | 1540.7973 | 0.0758 | DLHHAKDSEGVDI |
| 24.4 | 1540.7820 | 0.0911 | QFVSLQTQHPRM |
| 24.1 | 1540.8622 | 0.0109 | ALKTQGSSMSVVDL |
| 23.8 | 1540.6939 | 0.1793 | MLDMAENEGVVDI |
| 23.8 | 1540.7415 | 0.1317 | MLDMAEREGVVDI |
| 23.7 | 1540.9127 | -0.0395 | ILSVVDLNPRGVDL |
| 23.0 | 1540.9127 | -0.0395 | LTIHQSAQVSVLLT |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TQVVSDAAYKGVQPHVV**
Found in **LNEBL_MOUSE** in **SwissProt**, LIM zinc-binding domain-containing Nebulette OS=Mus musculus GN=Nebi PE=1 SV=1
Match to Query 6921: 1853.007548 from(927.511050,2+) intensity(29419.5640) scans(5889) rawscans(sn5889) rtinseconds(2287.5838) index(3802)
Title: 3803: Scan 5889 (rt=2287.58) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf



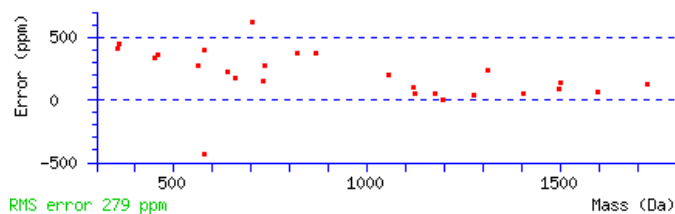
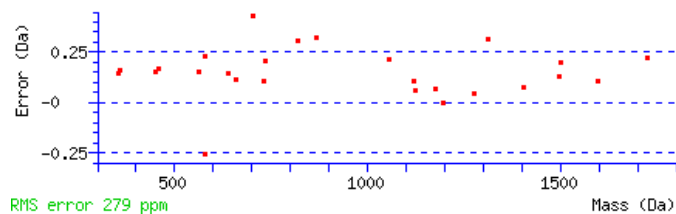


186.31 to 1864.04

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1853.0047
Variable modifications:
N-term : Dimethyl (N-term)
K10 : Dimethyl (K)
Ions Score: 83 Expect: 0.00018
Matches : 26/160 fragment ions using 39 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 130.0863 | 65.5468 | | | 112.0757 | 56.5415 | T | | | | | | | 17 |
| 2 | 258.1448 | 129.5761 | 241.1183 | 121.0628 | 240.1343 | 120.5708 | Q | 1724.9330 | 862.9701 | 1707.9064 | 854.4569 | 1706.9224 | 853.9649 | 16 |
| 3 | 357.2132 | 179.1103 | 340.1867 | 170.5970 | 339.2027 | 170.1050 | V | 1596.8744 | 798.9408 | 1579.8479 | 790.4276 | 1578.8639 | 789.9356 | 15 |
| 4 | 456.2817 | 228.6445 | 439.2551 | 220.1312 | 438.2711 | 219.6392 | V | 1497.8060 | 749.4066 | 1480.7795 | 740.8934 | 1479.7954 | 740.4014 | 14 |
| 5 | 543.3137 | 272.1605 | 526.2871 | 263.6472 | 525.3031 | 263.1552 | S | 1398.7376 | 699.8724 | 1381.7110 | 691.3592 | 1380.7270 | 690.8672 | 13 |
| 6 | 658.3406 | 329.6740 | 641.3141 | 321.1607 | 640.3301 | 320.6687 | D | 1311.7056 | 656.3564 | 1294.6790 | 647.8431 | 1293.6950 | 647.3511 | 12 |
| 7 | 729.3777 | 365.1925 | 712.3512 | 356.6792 | 711.3672 | 356.1872 | A | 1196.6786 | 598.8429 | 1179.6521 | 590.3297 | | | 11 |
| 8 | 800.4149 | 400.7111 | 783.3883 | 392.1978 | 782.4043 | 391.7058 | A | 1125.6415 | 563.3244 | 1108.6150 | 554.8111 | | | 10 |
| 9 | 963.4782 | 482.2427 | 946.4516 | 473.7295 | 945.4676 | 473.2375 | Y | 1054.6044 | 527.8058 | 1037.5778 | 519.2926 | | | 9 |
| 10 | 1119.6045 | 560.3059 | 1102.5779 | 551.7926 | 1101.5939 | 551.3006 | K | 891.5411 | 446.2742 | 874.5145 | 437.7609 | | | 8 |
| 11 | 1176.6259 | 588.8166 | 1159.5994 | 580.3033 | 1158.6154 | 579.8113 | G | 735.4148 | 368.2110 | 718.3883 | 359.6978 | | | 7 |
| 12 | 1275.6943 | 638.3508 | 1258.6678 | 629.8375 | 1257.6838 | 629.3455 | V | 678.3933 | 339.7003 | 661.3668 | 331.1870 | | | 6 |
| 13 | 1403.7529 | 702.3801 | 1386.7264 | 693.8668 | 1385.7423 | 693.3748 | Q | 579.3249 | 290.1661 | 562.2984 | 281.6528 | | | 5 |
| 14 | 1500.8057 | 750.9065 | 1483.7791 | 742.3932 | 1482.7951 | 741.9012 | P | 451.2663 | 226.1368 | | | | | 4 |
| 15 | 1637.8646 | 819.4359 | 1620.8380 | 810.9227 | 1619.8540 | 810.4306 | H | 354.2136 | 177.6104 | | | | | 3 |
| 16 | 1736.9330 | 868.9701 | 1719.9064 | 860.4569 | 1718.9224 | 859.9649 | V | 217.1547 | 109.0810 | | | | | 2 |
| 17 | | | | | | | V | 118.0863 | 59.5468 | | | | | 1 |



NCBI **BLAST** search of [TQVVSDAAYKGVQPHVV](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|------------------------------------|
| 82.6 | 1853.0047 | 0.0028 | TQVVSDAAYKGVQPHVV |
| 17.8 | 1852.9472 | 0.0603 | QTVFTIHPSHVQPAYT |
| 17.5 | 1852.8426 | 0.1649 | AGPVGEDMFHWQATIM |
| 16.4 | 1853.0168 | -0.0093 | MDTADGVPVNSRVSTKI |
| 15.0 | 1852.9117 | 0.0959 | VPPFFACSRQPCPHVV |
| 13.8 | 1852.8535 | 0.1540 | YCRFHKCLSVGMSHN |
| 12.2 | 1852.9291 | 0.0785 | LAHPASSNLDPSMQGLPA |
| 11.4 | 1853.0633 | -0.0558 | LSVRSVFFGVFQSEFVV |
| 11.3 | 1852.9046 | 0.1029 | PSHPPPPYPFGSQQASQ |
| 11.3 | 1852.9829 | 0.0247 | LGGMRTPAVKAPQERE |

Mascot: <http://www.matrixscience.com/>

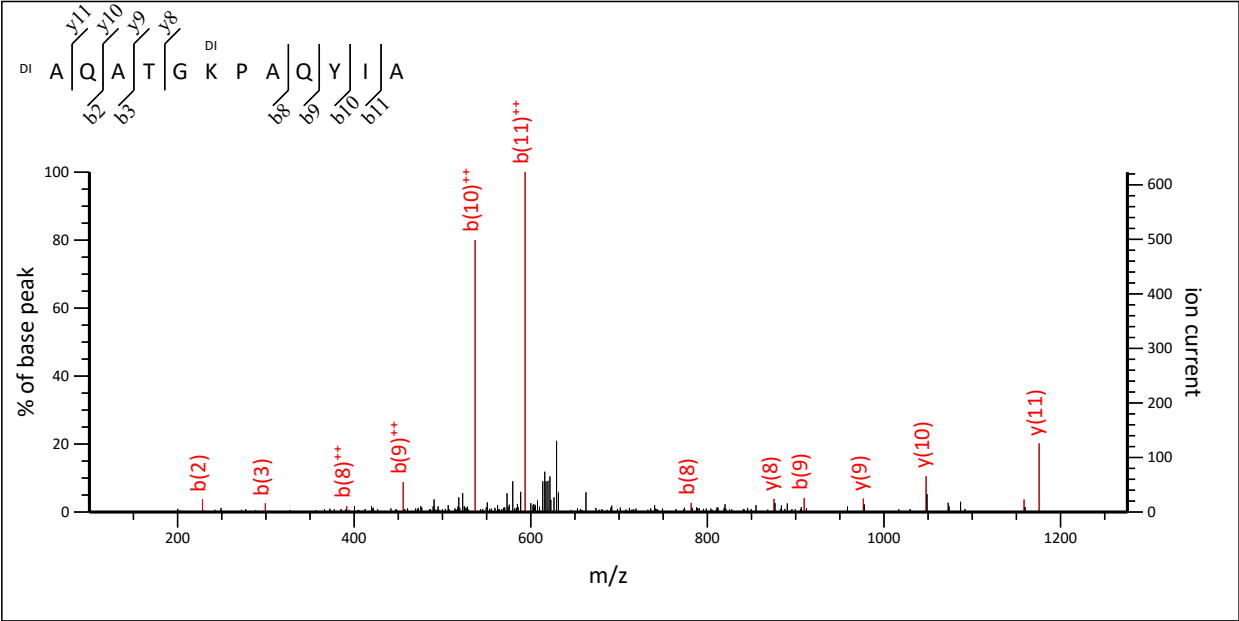
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AQATGKPAQYIA**
Found in **MIF_MOUSE** in **SwissProt**, Macrophage migration inhibitory factor OS=Mus musculus GN=Mif PE=1 SV=2

Match to Query 3619: 1273.707348 from(637.860950,2+) intensity(114164.7300) scans(3846) rawscans(sn3846) rtinseconds(1624.2138) index(2033)

Title: 2034: Scan 3846 (rt=1624.21) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

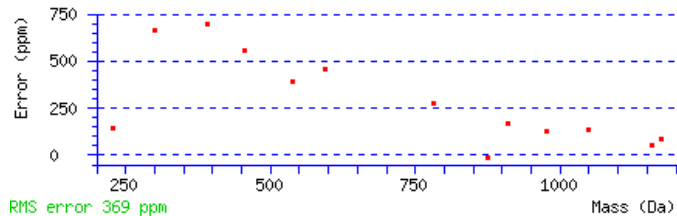
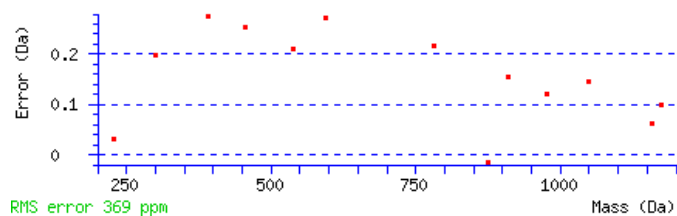


Navigation icons: ? (help), zoom in, zoom out, zoom reset, pan, 100.15 to 1275.74, zoom reset, pan.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1273.7030
Variable modifications:
N-term : Dimethyl (N-term)
K6 : Dimethyl (K)
Ions Score: 39 Expect: 3.4
Matches : 13/102 fragment ions using 20 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | | | A | | | | | | | 12 |
| 2 | 228.1343 | 114.5708 | 211.1077 | 106.0575 | | | Q | 1175.6419 | 588.3246 | 1158.6154 | 579.8113 | 1157.6313 | 579.3193 | 11 |
| 3 | 299.1714 | 150.0893 | 282.1448 | 141.5761 | | | A | 1047.5833 | 524.2953 | 1030.5568 | 515.7820 | 1029.5728 | 515.2900 | 10 |
| 4 | 400.2191 | 200.6132 | 383.1925 | 192.0999 | 382.2085 | 191.6079 | T | 976.5462 | 488.7767 | 959.5197 | 480.2635 | 958.5356 | 479.7715 | 9 |
| 5 | 457.2405 | 229.1239 | 440.2140 | 220.6106 | 439.2300 | 220.1186 | G | 875.4985 | 438.2529 | 858.4720 | 429.7396 | | | 8 |
| 6 | 613.3668 | 307.1870 | 596.3402 | 298.6738 | 595.3562 | 298.1817 | K | 818.4771 | 409.7422 | 801.4505 | 401.2289 | | | 7 |
| 7 | 710.4196 | 355.7134 | 693.3930 | 347.2001 | 692.4090 | 346.7081 | P | 662.3508 | 331.6790 | 645.3243 | 323.1658 | | | 6 |
| 8 | 781.4567 | 391.2320 | 764.4301 | 382.7187 | 763.4461 | 382.2267 | A | 565.2980 | 283.1527 | 548.2715 | 274.6394 | | | 5 |
| 9 | 909.5152 | 455.2613 | 892.4887 | 446.7480 | 891.5047 | 446.2560 | Q | 494.2609 | 247.6341 | 477.2344 | 239.1208 | | | 4 |
| 10 | 1072.5786 | 536.7929 | 1055.5520 | 528.2797 | 1054.5680 | 527.7876 | Y | 366.2023 | 183.6048 | | | | | 3 |
| 11 | 1185.6626 | 593.3350 | 1168.6361 | 584.8217 | 1167.6521 | 584.3297 | I | 203.1390 | 102.0731 | | | | | 2 |
| 12 | | | | | | | A | 90.0550 | 45.5311 | | | | | 1 |



NCBI **BLAST** search of [AQATGKPAQYIA](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--------------------------------|
| 39.5 | 1273.7030 | 0.0043 | AQATGKPAQYIA |
| 24.1 | 1273.6952 | 0.0122 | LKDLKGQMEA |
| 23.4 | 1273.5860 | 0.1213 | EGLGAPEVGAEMA |
| 22.1 | 1273.5319 | 0.1755 | AYCQSTMLDTN |
| 18.9 | 1273.6455 | 0.0618 | GAAQYYVAGHLP |
| 17.5 | 1273.5972 | 0.1101 | AGAAKCPGSEGSSP |
| 17.2 | 1273.7646 | -0.0572 | EAILKGLQSIF |
| 16.3 | 1273.8009 | -0.0936 | SGILGLSLFKLA |
| 15.9 | 1273.5826 | 0.1247 | DLETDHQYLA |
| 15.6 | 1273.5972 | 0.1101 | SSNHTVMIQET |

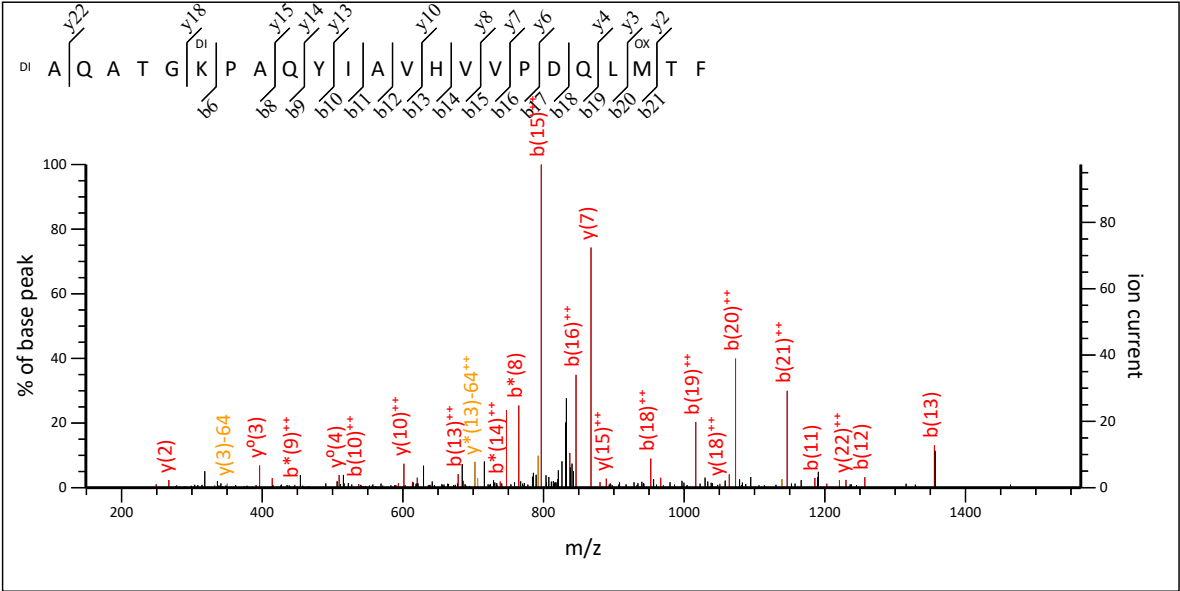
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AQATGKPAQYIAVHVVPDQLMTF**
Found in **MIF_MOUSE** in **SwissProt**, Macrophage migration inhibitory factor OS=Mus musculus GN=Mif PE=1 SV=2

Match to Query 9456: 2556.356622 from(853.126150,3+) intensity(25264.7190) scans(9989) rawscans(sn9989) rtinseconds(3740.7446) index(7248)
Title: 7249: Scan 9989 (rt=3740.74) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR
NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf



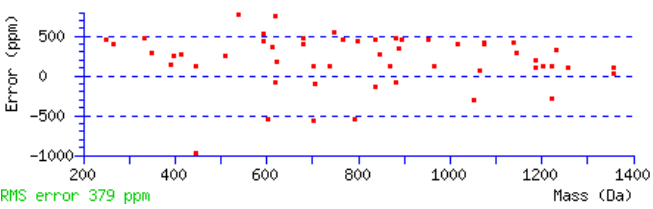
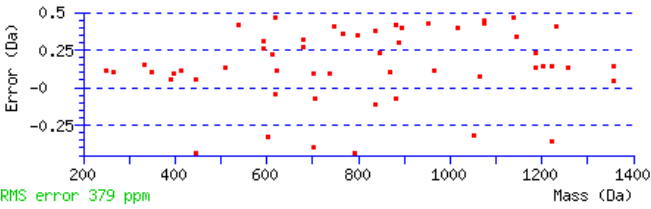
Navigation icons: ? (help), zoom in, zoom out, reset, and a range selector showing 149.24 to 1563.96.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 2556.3410
Variable modifications:
N-term : Dimethyl (N-term)
K6 : Dimethyl (K)
M21 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 45 Expect: 1.1
Matches : 55/374 fragment ions using 96 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | | | A | | | | | | | 23 |
| 2 | 228.1343 | 114.5708 | 211.1077 | 106.0575 | | | Q | 2458.2799 | 1229.6436 | 2441.2533 | 1221.1303 | 2440.2693 | 1220.6383 | 22 |
| 3 | 299.1714 | 150.0893 | 282.1448 | 141.5761 | | | A | 2330.2213 | 1165.6143 | 2313.1948 | 1157.1010 | 2312.2108 | 1156.6090 | 21 |
| 4 | 400.2191 | 200.6132 | 383.1925 | 192.0999 | 382.2085 | 191.6079 | T | 2259.1842 | 1130.0957 | 2242.1577 | 1121.5825 | 2241.1736 | 1121.0905 | 20 |
| 5 | 457.2405 | 229.1239 | 440.2140 | 220.6106 | 439.2300 | 220.1186 | G | 2158.1365 | 1079.5719 | 2141.1100 | 1071.0586 | 2140.1260 | 1070.5666 | 19 |
| 6 | 613.3668 | 307.1870 | 596.3402 | 298.6738 | 595.3562 | 298.1817 | K | 2101.1151 | 1051.0612 | 2084.0885 | 1042.5479 | 2083.1045 | 1042.0559 | 18 |
| 7 | 710.4196 | 355.7134 | 693.3930 | 347.2001 | 692.4090 | 346.7081 | P | 1944.9888 | 972.9980 | 1927.9623 | 964.4848 | 1926.9782 | 963.9928 | 17 |
| 8 | 781.4567 | 391.2320 | 764.4301 | 382.7187 | 763.4461 | 382.2267 | A | 1847.9360 | 924.4717 | 1830.9095 | 915.9584 | 1829.9255 | 915.4664 | 16 |
| 9 | 909.5152 | 455.2613 | 892.4887 | 446.7480 | 891.5047 | 446.2560 | Q | 1776.8989 | 888.9531 | 1759.8724 | 880.4398 | 1758.8884 | 879.9478 | 15 |
| 10 | 1072.5786 | 536.7929 | 1055.5520 | 528.2797 | 1054.5680 | 527.7876 | Y | 1648.8403 | 824.9238 | 1631.8138 | 816.4105 | 1630.8298 | 815.9185 | 14 |
| 11 | 1185.6626 | 593.3350 | 1168.6361 | 584.8217 | 1167.6521 | 584.3297 | I | 1485.7770 | 743.3921 | 1468.7505 | 734.8789 | 1467.7665 | 734.3869 | 13 |
| 12 | 1256.6998 | 628.8535 | 1239.6732 | 620.3402 | 1238.6892 | 619.8482 | A | 1372.6930 | 686.8501 | 1355.6664 | 678.3368 | 1354.6824 | 677.8448 | 12 |
| 13 | 1355.7682 | 678.3877 | 1338.7416 | 669.8744 | 1337.7576 | 669.3824 | V | 1301.6558 | 651.3316 | 1284.6293 | 642.8183 | 1283.6453 | 642.3263 | 11 |
| 14 | 1492.8271 | 746.9172 | 1475.8005 | 738.4039 | 1474.8165 | 737.9119 | H | 1202.5874 | 601.7973 | 1185.5609 | 593.2841 | 1184.5769 | 592.7921 | 10 |
| 15 | 1591.8955 | 796.4514 | 1574.8689 | 787.9381 | 1573.8849 | 787.4461 | V | 1065.5285 | 533.2679 | 1048.5020 | 524.7546 | 1047.5179 | 524.2626 | 9 |
| 16 | 1690.9639 | 845.9856 | 1673.9374 | 837.4723 | 1672.9533 | 836.9803 | V | 966.4601 | 483.7337 | 949.4335 | 475.2204 | 948.4495 | 474.7284 | 8 |
| 17 | 1788.0167 | 894.5120 | 1770.9901 | 885.9987 | 1770.0061 | 885.5067 | P | 867.3917 | 434.1995 | 850.3651 | 425.6862 | 849.3811 | 425.1942 | 7 |
| 18 | 1903.0436 | 952.0254 | 1886.0171 | 943.5122 | 1885.0330 | 943.0202 | D | 770.3389 | 385.6731 | 753.3124 | 377.1598 | 752.3284 | 376.6678 | 6 |
| 19 | 2031.1022 | 1016.0547 | 2014.0756 | 1007.5415 | 2013.0916 | 1007.0495 | Q | 655.3120 | 328.1596 | 638.2854 | 319.6464 | 637.3014 | 319.1543 | 5 |
| 20 | 2144.1863 | 1072.5968 | 2127.1597 | 1064.0835 | 2126.1757 | 1063.5915 | L | 527.2534 | 264.1303 | | | 509.2428 | 255.1251 | 4 |
| 21 | 2291.2217 | 1146.1145 | 2274.1951 | 1137.6012 | 2273.2111 | 1137.1092 | M | 414.1693 | 207.5883 | | | 396.1588 | 198.5830 | 3 |

| | | | | | | | | | | | | | | |
|----|-----------|-----------|-----------|-----------|-----------|-----------|---|----------|----------|--|--|----------|----------|---|
| 22 | 2392.2693 | 1196.6383 | 2375.2428 | 1188.1250 | 2374.2588 | 1187.6330 | T | 267.1339 | 134.0706 | | | 249.1234 | 125.0653 | 2 |
| 23 | | | | | | | F | 166.0863 | 83.5468 | | | | | 1 |



NCBI BLAST search of [AQATGKPAQYIAVHVVPDQLMTE](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|---|
| 45.0 | 2556.3410 | 0.0156 | AQATGKPAQYIAVHVVPDQLMTE |
| 14.7 | 2556.2868 | 0.0699 | MSMIQALAMTVAEIPVFLYTTE |
| 13.8 | 2556.2750 | 0.0816 | VGVDRADMESLKMMASKPLEEH |
| 13.4 | 2556.2572 | 0.0994 | PAVMQEFANGRMSKAITSCIMAL |
| 13.2 | 2556.4544 | -0.0978 | AVTRVHFPEALGHVALRLVPCPP |
| 12.8 | 2556.4818 | -0.1252 | ITELPKSLFEGLESLQLLLNA |
| 12.5 | 2556.2294 | 0.1273 | FSMLRDEDGKPYSPSEYSLOQ |
| 12.3 | 2556.4615 | -0.1049 | FSFLPTRALAALKCTCHHFKGI |
| 12.1 | 2556.4133 | -0.0567 | TSFILLNLTRAGLGSSAEHFVTV |
| 11.8 | 2556.5611 | -0.2044 | KMGVKKGDRVVGYPNSAHAVE |

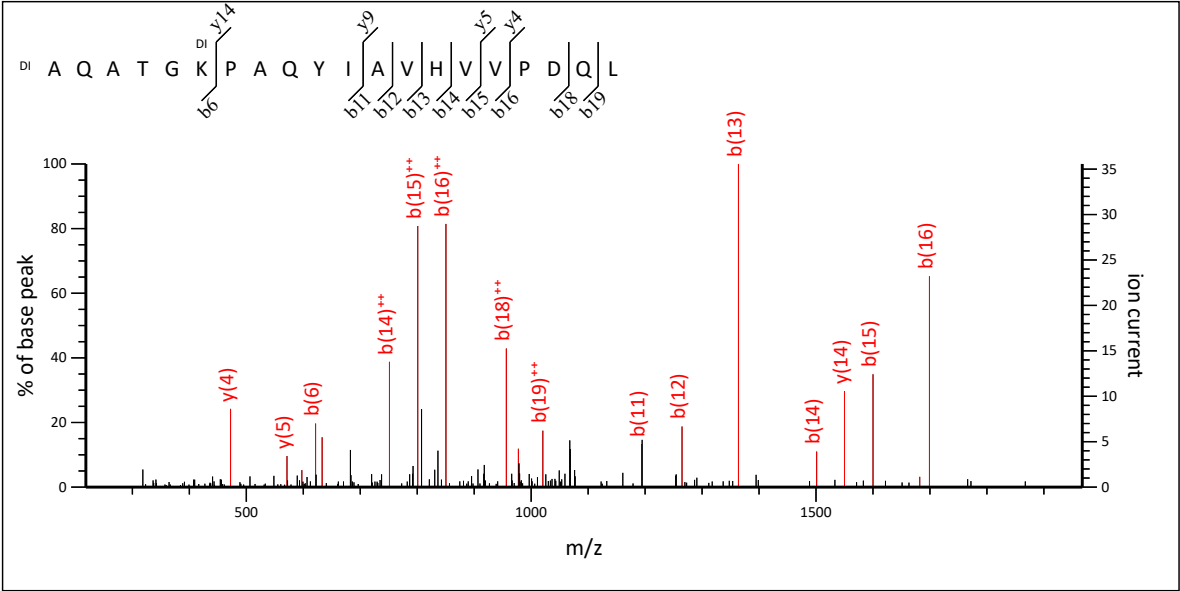
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AQATGKPAQYIAVHVVPDQL**
Found in **MIF_MOUSE** in **SwissProt**, Macrophage migration inhibitory factor OS=Mus musculus GN=Mif PE=1 SV=2

Match to Query 8410: 2169.248648 from(1085.631600,2+) intensity(11146.7990) scans(8075) rawscans(sn8075) rtinseconds(3057.8712) index(5696)
Title: 5697: Scan 8075 (rt=3057.87) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

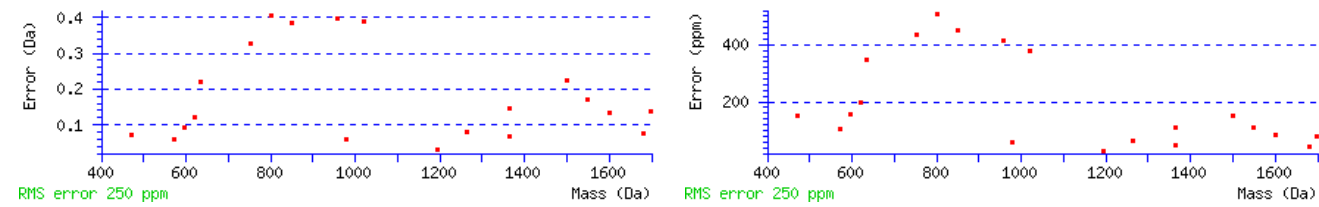


Navigation icons: ? (help), image (download), left arrow, magnifying glass (zoom in), magnifying glass (zoom out), magnifying glass (reset), input field with '218.35 to 1967.4', magnifying glass (search), right arrow.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 2169.2398
Variable modifications:
N-term : Dimethyl:2H(4) (N-term)
K6 : Dimethyl:2H(4) (K)
Ions Score: 47 Expect: 0.62
Matches : 20/214 fragment ions using 31 most intense peaks (help)

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 104.1008 | 52.5540 | | | | | A | | | | | | | 20 |
| 2 | 232.1594 | 116.5833 | 215.1328 | 108.0701 | | | Q | 2067.1535 | 1034.0804 | 2050.1270 | 1025.5671 | 2049.1429 | 1025.0751 | 19 |
| 3 | 303.1965 | 152.1019 | 286.1699 | 143.5886 | | | A | 1939.0949 | 970.0511 | 1922.0684 | 961.5378 | 1921.0844 | 961.0458 | 18 |
| 4 | 404.2442 | 202.6257 | 387.2176 | 194.1124 | 386.2336 | 193.6204 | T | 1868.0578 | 934.5325 | 1851.0313 | 926.0193 | 1850.0473 | 925.5273 | 17 |
| 5 | 461.2656 | 231.1365 | 444.2391 | 222.6232 | 443.2551 | 222.1312 | G | 1767.0101 | 884.0087 | 1749.9836 | 875.4954 | 1748.9996 | 875.0034 | 16 |
| 6 | 621.4170 | 311.2121 | 604.3905 | 302.6989 | 603.4064 | 302.2069 | K | 1709.9887 | 855.4980 | 1692.9621 | 846.9847 | 1691.9781 | 846.4927 | 15 |
| 7 | 718.4698 | 359.7385 | 701.4432 | 351.2252 | 700.4592 | 350.7332 | P | 1549.8373 | 775.4223 | 1532.8108 | 766.9090 | 1531.8267 | 766.4170 | 14 |
| 8 | 789.5069 | 395.2571 | 772.4803 | 386.7438 | 771.4963 | 386.2518 | A | 1452.7845 | 726.8959 | 1435.7580 | 718.3826 | 1434.7740 | 717.8906 | 13 |
| 9 | 917.5655 | 459.2864 | 900.5389 | 450.7731 | 899.5549 | 450.2811 | Q | 1381.7474 | 691.3774 | 1364.7209 | 682.8641 | 1363.7369 | 682.3721 | 12 |
| 10 | 1080.6288 | 540.8180 | 1063.6022 | 532.3048 | 1062.6182 | 531.8127 | Y | 1253.6889 | 627.3481 | 1236.6623 | 618.8348 | 1235.6783 | 618.3428 | 11 |
| 11 | 1193.7129 | 597.3601 | 1176.6863 | 588.8468 | 1175.7023 | 588.3548 | I | 1090.6255 | 545.8164 | 1073.5990 | 537.3031 | 1072.6150 | 536.8111 | 10 |
| 12 | 1264.7500 | 632.8786 | 1247.7234 | 624.3653 | 1246.7394 | 623.8733 | A | 977.5415 | 489.2744 | 960.5149 | 480.7611 | 959.5309 | 480.2691 | 9 |
| 13 | 1363.8184 | 682.4128 | 1346.7918 | 673.8996 | 1345.8078 | 673.4075 | V | 906.5043 | 453.7558 | 889.4778 | 445.2425 | 888.4938 | 444.7505 | 8 |
| 14 | 1500.8773 | 750.9423 | 1483.8507 | 742.4290 | 1482.8667 | 741.9370 | H | 807.4359 | 404.2216 | 790.4094 | 395.7083 | 789.4254 | 395.2163 | 7 |
| 15 | 1599.9457 | 800.4765 | 1582.9192 | 791.9632 | 1581.9351 | 791.4712 | V | 670.3770 | 335.6921 | 653.3505 | 327.1789 | 652.3665 | 326.6869 | 6 |
| 16 | 1699.0141 | 850.0107 | 1681.9876 | 841.4974 | 1681.0036 | 841.0054 | V | 571.3086 | 286.1579 | 554.2821 | 277.6447 | 553.2980 | 277.1527 | 5 |
| 17 | 1796.0669 | 898.5371 | 1779.0403 | 890.0238 | 1778.0563 | 889.5318 | P | 472.2402 | 236.6237 | 455.2136 | 228.1105 | 454.2296 | 227.6185 | 4 |
| 18 | 1911.0938 | 956.0506 | 1894.0673 | 947.5373 | 1893.0833 | 947.0453 | D | 375.1874 | 188.0974 | 358.1609 | 179.5841 | 357.1769 | 179.0921 | 3 |
| 19 | 2039.1524 | 1020.0798 | 2022.1259 | 1011.5666 | 2021.1418 | 1011.0746 | Q | 260.1605 | 130.5839 | 243.1339 | 122.0706 | | | 2 |
| 20 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI BLAST search of [AQATGKPAQYIAVHVVPDQL](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|--------|--------------------------------------|
| 47.3 | 2169.2398 | 0.0089 | AQATGKPAQYIAVHVVPDQL |
| 24.4 | 2169.2386 | 0.0100 | VGRVYRWMVDSRVALRI |
| 18.9 | 2169.2020 | 0.0466 | GQVLSTLKSEDVPYTAALTA |
| 18.4 | 2169.2207 | 0.0280 | GISGMVAATLTLPFDVVKTQ |
| 17.7 | 2169.1777 | 0.0709 | TIAAVNCPLYVVHVMSKSA |
| 17.3 | 2169.2021 | 0.0465 | VQIVVIVVVMMVMVVMITC |
| 17.3 | 2169.2021 | 0.0465 | VQIVVIVVVMMVMVVMITC |
| 17.3 | 2169.2021 | 0.0465 | VQIVVIVVVMMVMVVMITC |
| 17.3 | 2169.2021 | 0.0465 | VQIVVIVVVMMVMVVMITC |
| 17.1 | 2169.1336 | 0.1150 | RSMNHPTVALVRMVAPSPT |

Mascot: <http://www.matrixscience.com/>

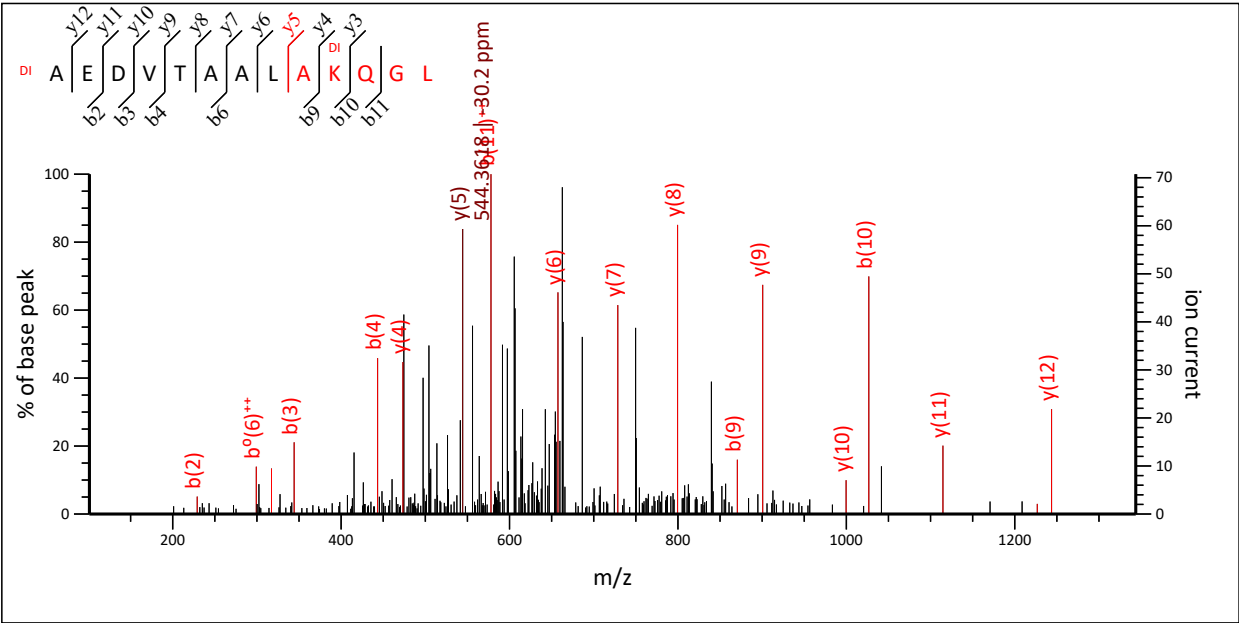
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEDVTAALAKQGL**
Found in **MTAP2_MOUSE** in **SwissProt**, Microtubule-associated protein 2 OS=Mus musculus GN=Map2 PE=1 SV=2

Match to Query 4065: 1341.747968 from(671.881260,2+) intensity(63764.9730) scans(7590) rawscans(sn7590) rtinseconds(2884.8337) index(5309)

Title: 5310: Scan 7590 (rt=2884.83) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

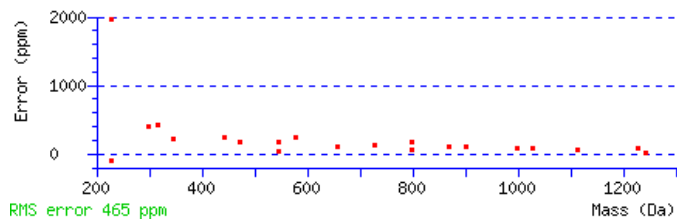
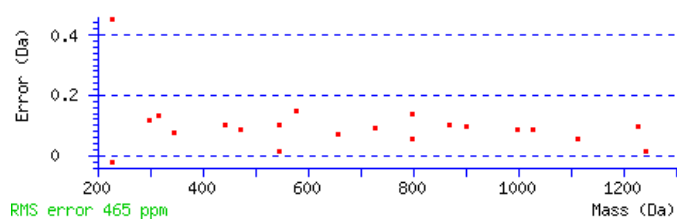


 to 

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1341.7504
Variable modifications:
N-term : Dimethyl (N-term)
K10 : Dimethyl (K)
Ions Score: 69 Expect: 0.0034
Matches : 21/104 fragment ions using 32 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺ * | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺ * | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|-------------------|----------------|------------------|------|-----------|-----------------|----------------|-------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | | | A | | | | | | | 13 |
| 2 | 229.1183 | 115.0628 | | | 211.1077 | 106.0575 | E | 1243.6892 | 622.3483 | 1226.6627 | 613.8350 | 1225.6787 | 613.3430 | 12 |
| 3 | 344.1452 | 172.5763 | | | 326.1347 | 163.5710 | D | 1114.6467 | 557.8270 | 1097.6201 | 549.3137 | 1096.6361 | 548.8217 | 11 |
| 4 | 443.2136 | 222.1105 | | | 425.2031 | 213.1052 | V | 999.6197 | 500.3135 | 982.5932 | 491.8002 | 981.6091 | 491.3082 | 10 |
| 5 | 544.2613 | 272.6343 | | | 526.2508 | 263.6290 | T | 900.5513 | 450.7793 | 883.5247 | 442.2660 | 882.5407 | 441.7740 | 9 |
| 6 | 615.2984 | 308.1529 | | | 597.2879 | 299.1476 | A | 799.5036 | 400.2554 | 782.4771 | 391.7422 | | | 8 |
| 7 | 686.3355 | 343.6714 | | | 668.3250 | 334.6661 | A | 728.4665 | 364.7369 | 711.4400 | 356.2236 | | | 7 |
| 8 | 799.4196 | 400.2134 | | | 781.4090 | 391.2082 | L | 657.4294 | 329.2183 | 640.4028 | 320.7051 | | | 6 |
| 9 | 870.4567 | 435.7320 | | | 852.4462 | 426.7267 | A | 544.3453 | 272.6763 | 527.3188 | 264.1630 | | | 5 |
| 10 | 1026.5830 | 513.7951 | 1009.5564 | 505.2819 | 1008.5724 | 504.7898 | K | 473.3082 | 237.1577 | 456.2817 | 228.6445 | | | 4 |
| 11 | 1154.6416 | 577.8244 | 1137.6150 | 569.3111 | 1136.6310 | 568.8191 | Q | 317.1819 | 159.0946 | 300.1554 | 150.5813 | | | 3 |
| 12 | 1211.6630 | 606.3352 | 1194.6365 | 597.8219 | 1193.6525 | 597.3299 | G | 189.1234 | 95.0653 | | | | | 2 |
| 13 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI **BLAST** search of [AEDVTAALAKQGL](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-------------------------------|
| 69.5 | 1341.7504 | -0.0024 | AEDVTAALAKQGL |
| 29.2 | 1341.6776 | 0.0704 | AEDVTAPLVDER |
| 23.3 | 1341.6776 | 0.0704 | AEGQEGQATTPI |
| 22.9 | 1341.6599 | 0.0881 | TGDNMGHVILLS |
| 21.6 | 1341.8909 | -0.1429 | KTVTAAIKVMD |
| 20.4 | 1341.8847 | -0.1367 | TTLSLVKTVVII |
| 20.0 | 1341.7343 | 0.0137 | LLWGSPAARGSPG |
| 20.0 | 1341.7798 | -0.0318 | IPPEAAATGQRVP |
| 20.0 | 1341.8785 | -0.1305 | LVVVLATAIALLD |
| 19.6 | 1341.7027 | 0.0452 | SVSESPAILPVSE |

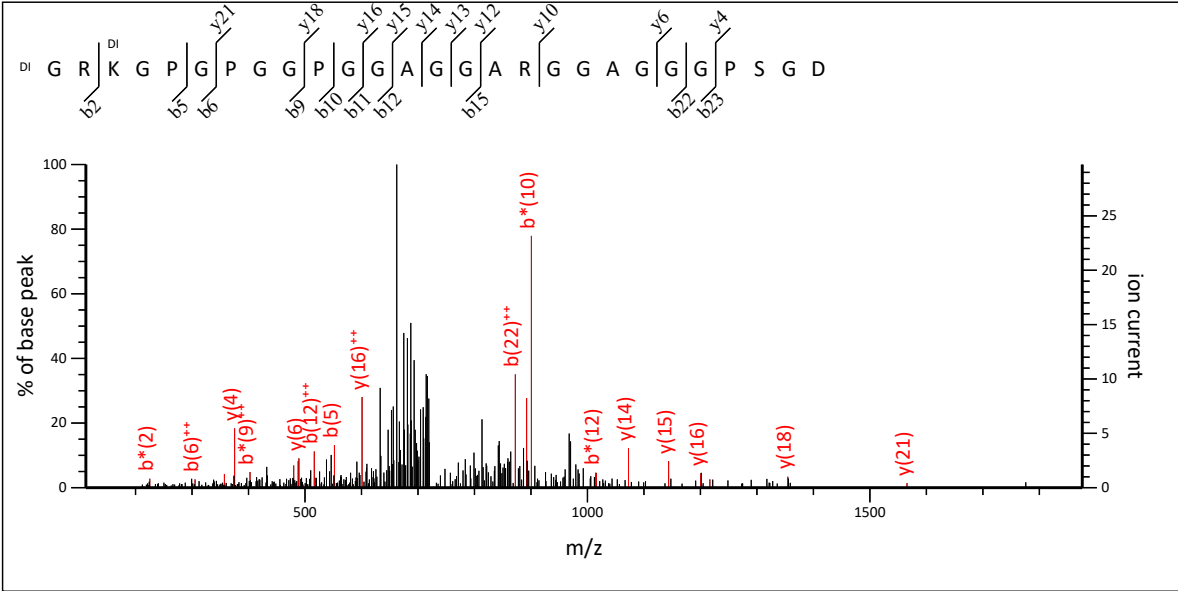
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GRKGPGGGPGGAGGARGGAGGGPSGD**
Found in **NEUG_MOUSE** in **SwissProt**, Neurogranin OS=Mus musculus GN=Nrgn PE=1 SV=1

Match to Query 8425: 2173.080372 from(725.367400,3+) intensity(17060.7050) scans(2144) rawscans(sn2144) rtinseconds(1045.6394) index(527)
Title: 528: Scan 2144 (rt=1045.64) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR
NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf



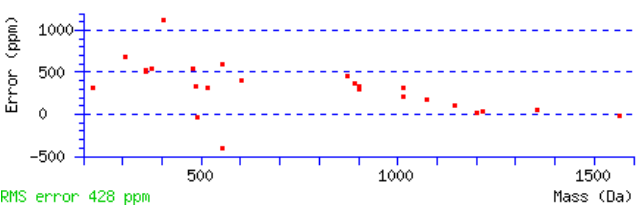
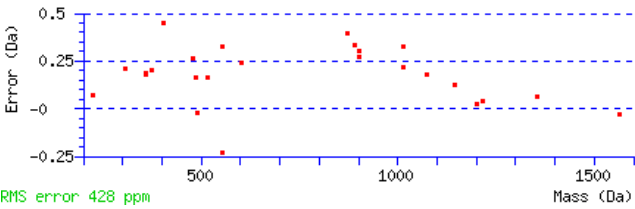
Navigation icons: ? (help), zoom in, zoom out, reset, and a range selector showing 112.08 to 1875.96.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 2173.0737
Variable modifications:
N-term : Dimethyl (N-term)
K3 : Dimethyl (K)
Ions Score: 33 Expect: 18
Matches : 25/242 fragment ions using 38 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ^{*++} | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ^{*++} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 86.0600 | 43.5337 | | | | | G | | | | | | | 27 |
| 2 | 242.1612 | 121.5842 | 225.1346 | 113.0709 | | | R | 2089.0282 | 1045.0177 | 2072.0016 | 1036.5045 | 2071.0176 | 1036.0125 | 26 |
| 3 | 398.2874 | 199.6473 | 381.2609 | 191.1341 | | | K | 1932.9271 | 966.9672 | 1915.9005 | 958.4539 | 1914.9165 | 957.9619 | 25 |
| 4 | 455.3089 | 228.1581 | 438.2823 | 219.6448 | | | G | 1776.8008 | 888.9040 | 1759.7743 | 880.3908 | 1758.7903 | 879.8988 | 24 |
| 5 | 552.3616 | 276.6845 | 535.3351 | 268.1712 | | | P | 1719.7794 | 860.3933 | 1702.7528 | 851.8800 | 1701.7688 | 851.3880 | 23 |
| 6 | 609.3831 | 305.1952 | 592.3566 | 296.6819 | | | G | 1622.7266 | 811.8669 | 1605.7000 | 803.3537 | 1604.7160 | 802.8616 | 22 |
| 7 | 706.4359 | 353.7216 | 689.4093 | 345.2083 | | | P | 1565.7051 | 783.3562 | 1548.6786 | 774.8429 | 1547.6946 | 774.3509 | 21 |
| 8 | 763.4573 | 382.2323 | 746.4308 | 373.7190 | | | G | 1468.6524 | 734.8298 | 1451.6258 | 726.3165 | 1450.6418 | 725.8245 | 20 |
| 9 | 820.4788 | 410.7430 | 803.4522 | 402.2298 | | | G | 1411.6309 | 706.3191 | 1394.6043 | 697.8058 | 1393.6203 | 697.3138 | 19 |
| 10 | 917.5316 | 459.2694 | 900.5050 | 450.7561 | | | P | 1354.6094 | 677.8084 | 1337.5829 | 669.2951 | 1336.5989 | 668.8031 | 18 |
| 11 | 974.5530 | 487.7802 | 957.5265 | 479.2669 | | | G | 1257.5567 | 629.2820 | 1240.5301 | 620.7687 | 1239.5461 | 620.2767 | 17 |
| 12 | 1031.5745 | 516.2909 | 1014.5479 | 507.7776 | | | G | 1200.5352 | 600.7712 | 1183.5087 | 592.2580 | 1182.5246 | 591.7660 | 16 |
| 13 | 1102.6116 | 551.8094 | 1085.5851 | 543.2962 | | | A | 1143.5137 | 572.2605 | 1126.4872 | 563.7472 | 1125.5032 | 563.2552 | 15 |
| 14 | 1159.6331 | 580.3202 | 1142.6065 | 571.8069 | | | G | 1072.4766 | 536.7420 | 1055.4501 | 528.2287 | 1054.4661 | 527.7367 | 14 |
| 15 | 1216.6545 | 608.8309 | 1199.6280 | 600.3176 | | | G | 1015.4552 | 508.2312 | 998.4286 | 499.7179 | 997.4446 | 499.2259 | 13 |
| 16 | 1287.6916 | 644.3495 | 1270.6651 | 635.8362 | | | A | 958.4337 | 479.7205 | 941.4071 | 471.2072 | 940.4231 | 470.7152 | 12 |
| 17 | 1443.7928 | 722.4000 | 1426.7662 | 713.8867 | | | R | 887.3966 | 444.2019 | 870.3700 | 435.6887 | 869.3860 | 435.1966 | 11 |
| 18 | 1500.8142 | 750.9107 | 1483.7877 | 742.3975 | | | G | 731.2955 | 366.1514 | | | 713.2849 | 357.1461 | 10 |
| 19 | 1557.8357 | 779.4215 | 1540.8091 | 770.9082 | | | G | 674.2740 | 337.6406 | | | 656.2634 | 328.6354 | 9 |
| 20 | 1628.8728 | 814.9400 | 1611.8463 | 806.4268 | | | A | 617.2525 | 309.1299 | | | 599.2420 | 300.1246 | 8 |
| 21 | 1685.8943 | 843.4508 | 1668.8677 | 834.9375 | | | G | 546.2154 | 273.6114 | | | 528.2049 | 264.6061 | 7 |
| 22 | 1742.9157 | 871.9615 | 1725.8892 | 863.4482 | | | G | 489.1940 | 245.1006 | | | 471.1834 | 236.0953 | 6 |

| | | | | | | | | | | | | | | |
|----|-----------|-----------|-----------|-----------|-----------|-----------|---|----------|----------|--|--|----------|----------|---|
| 23 | 1799.9372 | 900.4722 | 1782.9106 | 891.9590 | | | G | 432.1725 | 216.5899 | | | 414.1619 | 207.5846 | 5 |
| 24 | 1896.9900 | 948.9986 | 1879.9634 | 940.4853 | | | P | 375.1510 | 188.0792 | | | 357.1405 | 179.0739 | 4 |
| 25 | 1984.0220 | 992.5146 | 1966.9954 | 984.0014 | 1966.0114 | 983.5093 | S | 278.0983 | 139.5528 | | | 260.0877 | 130.5475 | 3 |
| 26 | 2041.0434 | 1021.0254 | 2024.0169 | 1012.5121 | 2023.0329 | 1012.0201 | G | 191.0662 | 96.0368 | | | 173.0557 | 87.0315 | 2 |
| 27 | | | | | | | D | 134.0448 | 67.5260 | | | 116.0342 | 58.5207 | 1 |



NCBI BLAST search of [GRKGPGGGPGGAGGARGGAGGGPSGD](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--|
| 32.7 | 2173.0737 | 0.0066 | GRKGPGGGPGGAGGARGGAGGGPSGD |
| 20.0 | 2173.3276 | -0.2472 | PGLVGLVLSYALSLTGLLSGLV |
| 15.5 | 2173.1793 | -0.0990 | VSRNWARAPLSPGVTTTLTD |
| 14.4 | 2173.1052 | -0.0248 | QYEYGS GK KYGGPCGGRNC |
| 13.3 | 2173.3988 | -0.3184 | LKMRI SRL VPWLILASVV |
| 12.1 | 2173.1565 | -0.0762 | TLRLSLWGMEALGTLGGQVQ |
| 11.4 | 2173.0184 | 0.0620 | DPSAPCFAPSTLLSPEASPCR |
| 11.0 | 2173.2793 | -0.1989 | EIAELLRAHSEPG RSLGPK |
| 10.9 | 2173.2371 | -0.1568 | KHLHTLIFNAARDLLINE |
| 10.8 | 2173.1467 | -0.0663 | AADGTGVVGGGAVGGGLPKDGLQD |

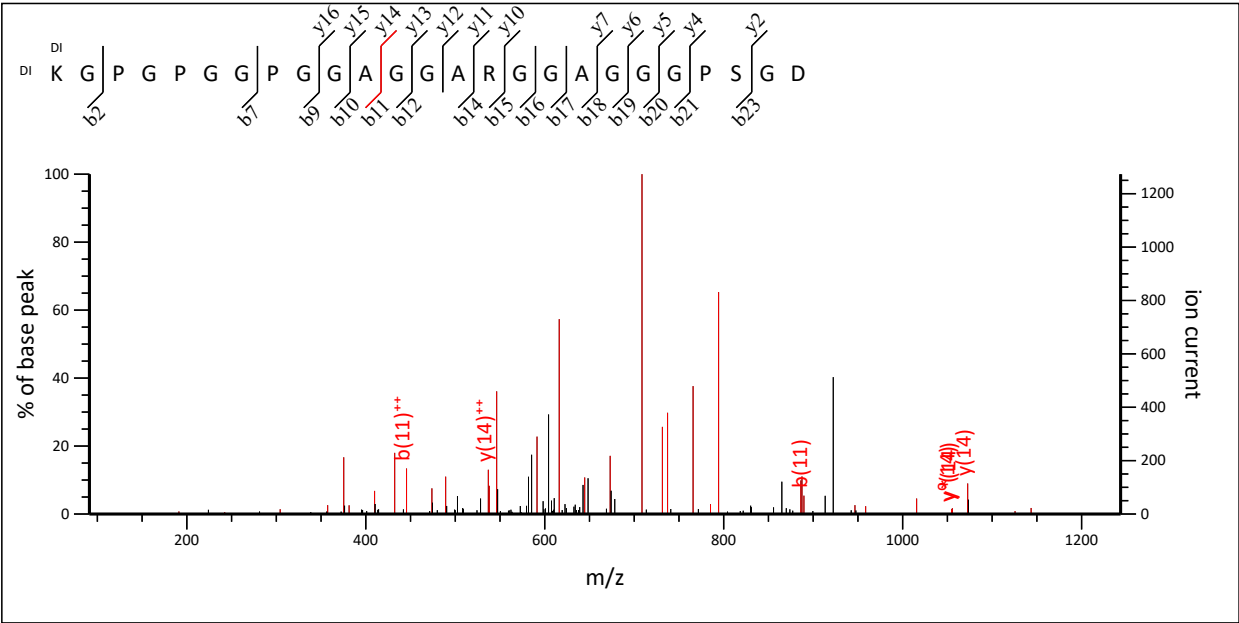
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGP GPGGPGAGGARGGAGGGPSGD**
Found in **NEUG_MOUSE** in **SwissProt**, Neurogranin OS=Mus musculus GN=Nrgn PE=1 SV=1

Match to Query 7492: 1959.958782 from(654.326870,3+) intensity(305028.6900) scans(2351) rawscans(sn2351) rtinseconds(1121.3576) index(719)
Title: 720: Scan 2351 (rt=1121.36) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf



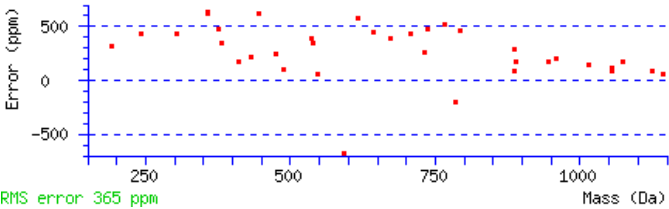
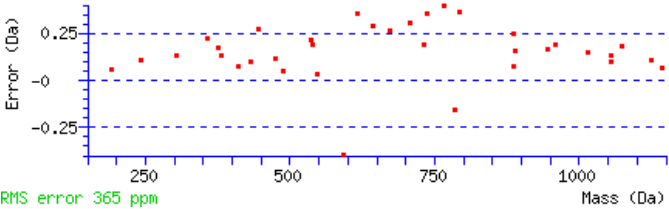
Navigation icons: ? (help), zoom in, zoom out, zoom reset, and a range selector showing 91.13 to 1243.58.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1959.9512
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
Ions Score: 106 Expect: 9.1e-007
Matches : 36/224 fragment ions using 46 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺ * | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺ * | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|-------------------|----------------|------------------|------|-----------|-----------------|----------------|-------------------|----------------|------------------|----|
| 1 | 185.1648 | 93.0861 | 168.1383 | 84.5728 | | | K | | | | | | | 25 |
| 2 | 242.1863 | 121.5968 | 225.1598 | 113.0835 | | | G | 1776.8008 | 888.9040 | 1759.7743 | 880.3908 | 1758.7903 | 879.8988 | 24 |
| 3 | 339.2391 | 170.1232 | 322.2125 | 161.6099 | | | P | 1719.7794 | 860.3933 | 1702.7528 | 851.8800 | 1701.7688 | 851.3880 | 23 |
| 4 | 396.2605 | 198.6339 | 379.2340 | 190.1206 | | | G | 1622.7266 | 811.8669 | 1605.7000 | 803.3537 | 1604.7160 | 802.8616 | 22 |
| 5 | 493.3133 | 247.1603 | 476.2867 | 238.6470 | | | P | 1565.7051 | 783.3562 | 1548.6786 | 774.8429 | 1547.6946 | 774.3509 | 21 |
| 6 | 550.3348 | 275.6710 | 533.3082 | 267.1577 | | | G | 1468.6524 | 734.8298 | 1451.6258 | 726.3165 | 1450.6418 | 725.8245 | 20 |
| 7 | 607.3562 | 304.1817 | 590.3297 | 295.6685 | | | G | 1411.6309 | 706.3191 | 1394.6043 | 697.8058 | 1393.6203 | 697.3138 | 19 |
| 8 | 704.4090 | 352.7081 | 687.3824 | 344.1949 | | | P | 1354.6094 | 677.8084 | 1337.5829 | 669.2951 | 1336.5989 | 668.8031 | 18 |
| 9 | 761.4305 | 381.2189 | 744.4039 | 372.7056 | | | G | 1257.5567 | 629.2820 | 1240.5301 | 620.7687 | 1239.5461 | 620.2767 | 17 |
| 10 | 818.4519 | 409.7296 | 801.4254 | 401.2163 | | | G | 1200.5352 | 600.7712 | 1183.5087 | 592.2580 | 1182.5246 | 591.7660 | 16 |
| 11 | 889.4890 | 445.2482 | 872.4625 | 436.7349 | | | A | 1143.5137 | 572.2605 | 1126.4872 | 563.7472 | 1125.5032 | 563.2552 | 15 |
| 12 | 946.5105 | 473.7589 | 929.4839 | 465.2456 | | | G | 1072.4766 | 536.7420 | 1055.4501 | 528.2287 | 1054.4661 | 527.7367 | 14 |
| 13 | 1003.5320 | 502.2696 | 986.5054 | 493.7563 | | | G | 1015.4552 | 508.2312 | 998.4286 | 499.7179 | 997.4446 | 499.2259 | 13 |
| 14 | 1074.5691 | 537.7882 | 1057.5425 | 529.2749 | | | A | 958.4337 | 479.7205 | 941.4071 | 471.2072 | 940.4231 | 470.7152 | 12 |
| 15 | 1230.6702 | 615.8387 | 1213.6436 | 607.3255 | | | R | 887.3966 | 444.2019 | 870.3700 | 435.6887 | 869.3860 | 435.1966 | 11 |
| 16 | 1287.6916 | 644.3495 | 1270.6651 | 635.8362 | | | G | 731.2955 | 366.1514 | | | 713.2849 | 357.1461 | 10 |
| 17 | 1344.7131 | 672.8602 | 1327.6866 | 664.3469 | | | G | 674.2740 | 337.6406 | | | 656.2634 | 328.6354 | 9 |
| 18 | 1415.7502 | 708.3788 | 1398.7237 | 699.8655 | | | A | 617.2525 | 309.1299 | | | 599.2420 | 300.1246 | 8 |

| | | | | | | | | | | | | | | |
|----|-----------|----------|-----------|----------|-----------|----------|---|----------|----------|--|--|----------|----------|---|
| 19 | 1472.7717 | 736.8895 | 1455.7451 | 728.3762 | | | G | 546.2154 | 273.6114 | | | 528.2049 | 264.6061 | 7 |
| 20 | 1529.7932 | 765.4002 | 1512.7666 | 756.8869 | | | G | 489.1940 | 245.1006 | | | 471.1834 | 236.0953 | 6 |
| 21 | 1586.8146 | 793.9109 | 1569.7881 | 785.3977 | | | G | 432.1725 | 216.5899 | | | 414.1619 | 207.5846 | 5 |
| 22 | 1683.8674 | 842.4373 | 1666.8408 | 833.9241 | | | P | 375.1510 | 188.0792 | | | 357.1405 | 179.0739 | 4 |
| 23 | 1770.8994 | 885.9533 | 1753.8729 | 877.4401 | 1752.8888 | 876.9481 | S | 278.0983 | 139.5528 | | | 260.0877 | 130.5475 | 3 |
| 24 | 1827.9209 | 914.4641 | 1810.8943 | 905.9508 | 1809.9103 | 905.4588 | G | 191.0662 | 96.0368 | | | 173.0557 | 87.0315 | 2 |
| 25 | | | | | | | D | 134.0448 | 67.5260 | | | 116.0342 | 58.5207 | 1 |



NCBI BLAST search of [KGPGPGGPGGAGGARGGAGGGPSGD](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|---|
| 105.5 | 1959.9512 | 0.0076 | KGPGPGGPGGAGGARGGAGGGPSGD |
| 30.4 | 1959.9185 | 0.0403 | TAIGGGGGPGGGGSGAIDEGGGRD |
| 29.3 | 1959.9212 | 0.0376 | VLFLMMSGAPDAGGQGGGGGGG |
| 25.2 | 1960.0757 | -0.1169 | WNGLLPDDTLQDLGLGK |
| 25.0 | 1960.0036 | -0.0448 | KHLNNMQNLQNGGGEQV |
| 24.1 | 1960.0030 | -0.0442 | LNDGNFEDNFADKDTVL |
| 22.6 | 1960.0955 | -0.1367 | GVKYLIVLINKMDDPT |
| 21.5 | 1960.0240 | -0.0653 | EENGPOKGGLEVADEALV |
| 21.3 | 1960.0683 | -0.1095 | YRWRAWLLGDAVAGVTV |
| 21.0 | 1959.8344 | 0.1243 | GEGGGGGGAANPAGGDSAVAGDE |

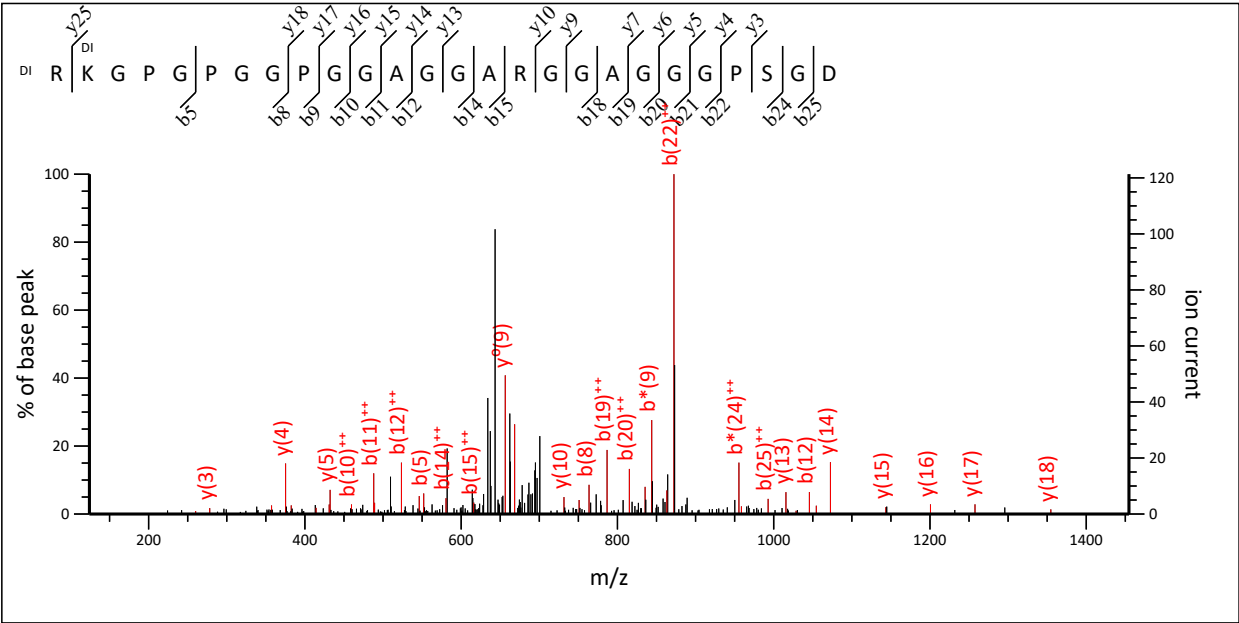
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **RKGPGGPGGAGGARGGGPSGD**
Found in **NEUG_MOUSE** in **SwissProt**, Neurogranin OS=Mus musculus GN=Nrgn PE=1 SV=1

Match to Query 8201: 2116.063242 from(706.361690,3+) intensity(39999.9770) scans(2066) rawscans(sn2066) rtinseconds(1016.7325) index(457)
Title: 458: Scan 2066 (rt=1016.73) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf



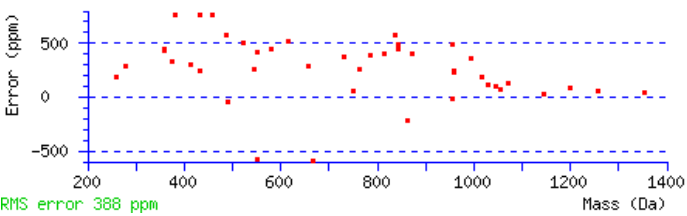
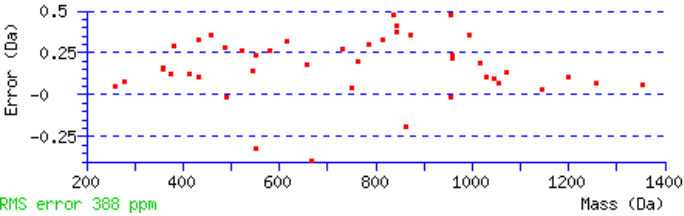
Navigation icons: ? (help), image (download), left arrow, zoom in, zoom out, right arrow, 124.22 to 1454.67 (range), zoom in, right arrow.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 2116.0523
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
Ions Score: 82 Expect: 0.00022
Matches : 44/234 fragment ions using 68 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 185.1397 | 93.0735 | 168.1131 | 84.5602 | | | R | | | | | | | 26 |
| 2 | 341.2659 | 171.1366 | 324.2394 | 162.6233 | | | K | 1932.9271 | 966.9672 | 1915.9005 | 958.4539 | 1914.9165 | 957.9619 | 25 |
| 3 | 398.2874 | 199.6473 | 381.2609 | 191.1341 | | | G | 1776.8008 | 888.9040 | 1759.7743 | 880.3908 | 1758.7903 | 879.8988 | 24 |
| 4 | 495.3402 | 248.1737 | 478.3136 | 239.6605 | | | P | 1719.7794 | 860.3933 | 1702.7528 | 851.8800 | 1701.7688 | 851.3880 | 23 |
| 5 | 552.3616 | 276.6845 | 535.3351 | 268.1712 | | | G | 1622.7266 | 811.8669 | 1605.7000 | 803.3537 | 1604.7160 | 802.8616 | 22 |
| 6 | 649.4144 | 325.2108 | 632.3879 | 316.6976 | | | P | 1565.7051 | 783.3562 | 1548.6786 | 774.8429 | 1547.6946 | 774.3509 | 21 |
| 7 | 706.4359 | 353.7216 | 689.4093 | 345.2083 | | | G | 1468.6524 | 734.8298 | 1451.6258 | 726.3165 | 1450.6418 | 725.8245 | 20 |
| 8 | 763.4573 | 382.2323 | 746.4308 | 373.7190 | | | G | 1411.6309 | 706.3191 | 1394.6043 | 697.8058 | 1393.6203 | 697.3138 | 19 |
| 9 | 860.5101 | 430.7587 | 843.4835 | 422.2454 | | | P | 1354.6094 | 677.8084 | 1337.5829 | 669.2951 | 1336.5989 | 668.8031 | 18 |
| 10 | 917.5316 | 459.2694 | 900.5050 | 450.7561 | | | G | 1257.5567 | 629.2820 | 1240.5301 | 620.7687 | 1239.5461 | 620.2767 | 17 |
| 11 | 974.5530 | 487.7802 | 957.5265 | 479.2669 | | | G | 1200.5352 | 600.7712 | 1183.5087 | 592.2580 | 1182.5246 | 591.7660 | 16 |
| 12 | 1045.5901 | 523.2987 | 1028.5636 | 514.7854 | | | A | 1143.5137 | 572.2605 | 1126.4872 | 563.7472 | 1125.5032 | 563.2552 | 15 |
| 13 | 1102.6116 | 551.8094 | 1085.5851 | 543.2962 | | | G | 1072.4766 | 536.7420 | 1055.4501 | 528.2287 | 1054.4661 | 527.7367 | 14 |
| 14 | 1159.6331 | 580.3202 | 1142.6065 | 571.8069 | | | G | 1015.4552 | 508.2312 | 998.4286 | 499.7179 | 997.4446 | 499.2259 | 13 |
| 15 | 1230.6702 | 615.8387 | 1213.6436 | 607.3255 | | | A | 958.4337 | 479.7205 | 941.4071 | 471.2072 | 940.4231 | 470.7152 | 12 |
| 16 | 1386.7713 | 693.8893 | 1369.7447 | 685.3760 | | | R | 887.3966 | 444.2019 | 870.3700 | 435.6887 | 869.3860 | 435.1966 | 11 |
| 17 | 1443.7928 | 722.4000 | 1426.7662 | 713.8867 | | | G | 731.2955 | 366.1514 | | | 713.2849 | 357.1461 | 10 |
| 18 | 1500.8142 | 750.9107 | 1483.7877 | 742.3975 | | | G | 674.2740 | 337.6406 | | | 656.2634 | 328.6354 | 9 |

| | | | | | | | | | | | | | | |
|----|-----------|----------|-----------|----------|-----------|----------|---|----------|----------|--|--|----------|----------|---|
| 19 | 1571.8513 | 786.4293 | 1554.8248 | 777.9160 | | | A | 617.2525 | 309.1299 | | | 599.2420 | 300.1246 | 8 |
| 20 | 1628.8728 | 814.9400 | 1611.8463 | 806.4268 | | | G | 546.2154 | 273.6114 | | | 528.2049 | 264.6061 | 7 |
| 21 | 1685.8943 | 843.4508 | 1668.8677 | 834.9375 | | | G | 489.1940 | 245.1006 | | | 471.1834 | 236.0953 | 6 |
| 22 | 1742.9157 | 871.9615 | 1725.8892 | 863.4482 | | | G | 432.1725 | 216.5899 | | | 414.1619 | 207.5846 | 5 |
| 23 | 1839.9685 | 920.4879 | 1822.9419 | 911.9746 | | | P | 375.1510 | 188.0792 | | | 357.1405 | 179.0739 | 4 |
| 24 | 1927.0005 | 964.0039 | 1909.9740 | 955.4906 | 1908.9900 | 954.9986 | S | 278.0983 | 139.5528 | | | 260.0877 | 130.5475 | 3 |
| 25 | 1984.0220 | 992.5146 | 1966.9954 | 984.0014 | 1966.0114 | 983.5093 | G | 191.0662 | 96.0368 | | | 173.0557 | 87.0315 | 2 |
| 26 | | | | | | | D | 134.0448 | 67.5260 | | | 116.0342 | 58.5207 | 1 |



NCBI BLAST search of [RKGP GPGGPGGAGGARGGAGGGPSGD](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|---|
| 81.8 | 2116.0523 | 0.0110 | RKGP GPGGPGGAGGARGGAGGGPSGD |
| 19.6 | 2116.0739 | -0.0106 | GDYVQQHGGVSLVEQLLQD |
| 18.7 | 2116.2255 | -0.1623 | GPKGSRGYIGLPGLFGLPGSD |
| 17.6 | 2116.0358 | 0.0274 | IGDGANDVSMIQVADIGIGVS |
| 17.4 | 2115.9780 | 0.0852 | LAGMSPGAGAMAGMSGSAGAAGVAG |
| 16.6 | 2116.0722 | -0.0089 | VTEMKALINADELANDVAGA |
| 16.0 | 2116.1503 | -0.0870 | FRGMTLLHLAAAQGYATLI |
| 15.7 | 2116.1056 | -0.0424 | LSGFSTAMGALAGGFALPDGLA |
| 15.6 | 2115.9495 | 0.1137 | GMKGVMEMMVALCGSERA |
| 14.6 | 2115.9495 | 0.1137 | GMKGVMEMMVALCGSERA |

Mascot: <http://www.matrixscience.com/>

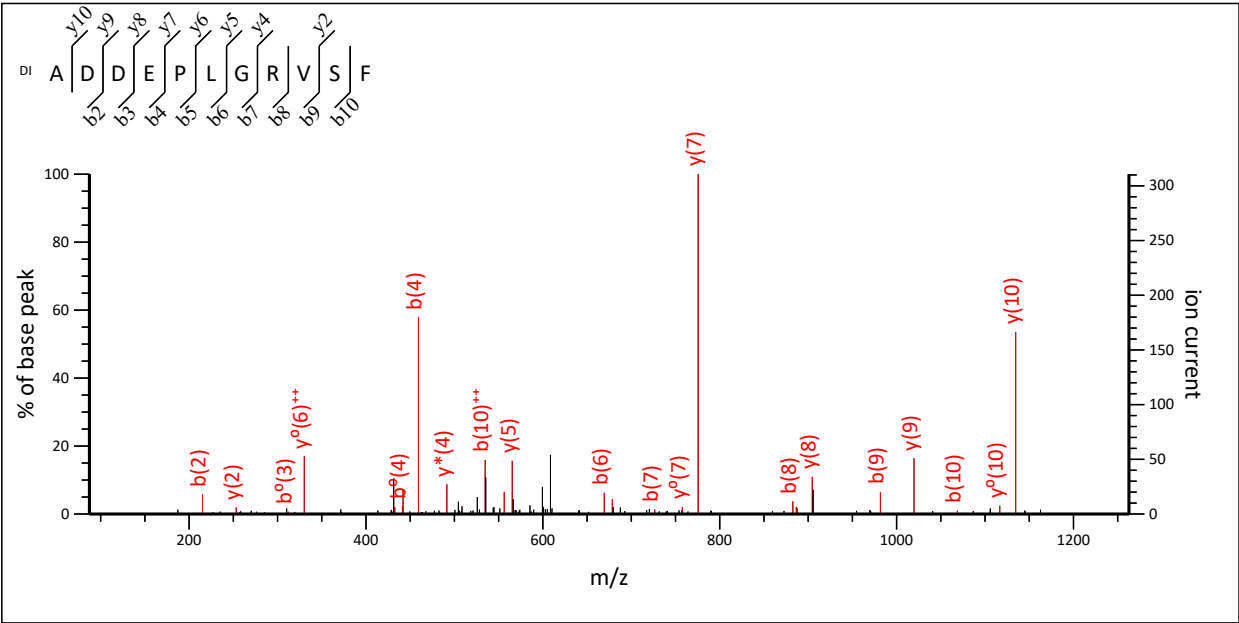
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADDEPLGRVSF**
Found in **PPIA_MOUSE** in **SwissProt**, Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2

Match to Query 3429: 1232.607428 from(617.310990,2+) intensity(48155.3950) scans(7430) rawscans(sn7430) rtinseconds(2852.3698) index(5207)

Title: 5208: Scan 7430 (rt=2852.37) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf

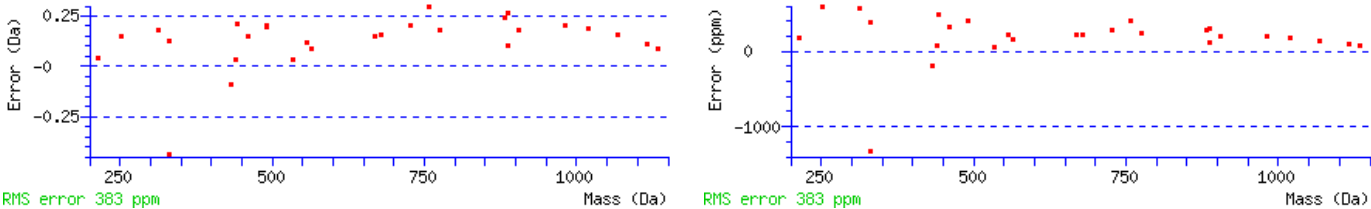


Navigation icons: ? (help), zoom in, zoom out, zoom reset, zoom to fit, zoom to selected, zoom to range. Range: 87.3 to 1262.73.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1232.6037
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 60 Expect: 0.029
Matches : 28/96 fragment ions using 49 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | | | A | | | | | | | 11 |
| 2 | 215.1026 | 108.0550 | | | 197.0921 | 99.0497 | D | 1134.5426 | 567.7749 | 1117.5160 | 559.2617 | 1116.5320 | 558.7696 | 10 |
| 3 | 330.1296 | 165.5684 | | | 312.1190 | 156.5631 | D | 1019.5156 | 510.2615 | 1002.4891 | 501.7482 | 1001.5051 | 501.2562 | 9 |
| 4 | 459.1722 | 230.0897 | | | 441.1616 | 221.0844 | E | 904.4887 | 452.7480 | 887.4621 | 444.2347 | 886.4781 | 443.7427 | 8 |
| 5 | 556.2249 | 278.6161 | | | 538.2144 | 269.6108 | P | 775.4461 | 388.2267 | 758.4196 | 379.7134 | 757.4355 | 379.2214 | 7 |
| 6 | 669.3090 | 335.1581 | | | 651.2984 | 326.1529 | L | 678.3933 | 339.7003 | 661.3668 | 331.1870 | 660.3828 | 330.6950 | 6 |
| 7 | 726.3305 | 363.6689 | | | 708.3199 | 354.6636 | G | 565.3093 | 283.1583 | 548.2827 | 274.6450 | 547.2987 | 274.1530 | 5 |
| 8 | 882.4316 | 441.7194 | 865.4050 | 433.2061 | 864.4210 | 432.7141 | R | 508.2878 | 254.6475 | 491.2613 | 246.1343 | 490.2772 | 245.6423 | 4 |
| 9 | 981.5000 | 491.2536 | 964.4734 | 482.7404 | 963.4894 | 482.2483 | V | 352.1867 | 176.5970 | | | 334.1761 | 167.5917 | 3 |
| 10 | 1068.5320 | 534.7696 | 1051.5055 | 526.2564 | 1050.5214 | 525.7644 | S | 253.1183 | 127.0628 | | | 235.1077 | 118.0575 | 2 |
| 11 | | | | | | | F | 166.0863 | 83.5468 | | | | | 1 |



NCBI **BLAST** search of [ADDEPLGRVSF](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-----------------------------|
| 60.1 | 1232.6037 | 0.0037 | ADDEPLGRVSF |
| 26.9 | 1232.7832 | -0.1757 | SVVLKALEDPV |
| 26.9 | 1232.5710 | 0.0364 | PSLESDENPV |
| 26.8 | 1232.5884 | 0.0190 | ADDEKSEDRI |
| 26.8 | 1232.6765 | -0.0691 | ADPKGHLETPI |
| 26.6 | 1232.6111 | -0.0037 | ALVFPNSDPVM |
| 25.9 | 1232.5781 | 0.0293 | EGMICNVELPT |
| 24.5 | 1232.7591 | -0.1517 | SKEPNLVVSF |
| 24.1 | 1232.6435 | -0.0360 | KTMRSTTDPV |
| 22.6 | 1232.5747 | 0.0327 | WNEADMEVIV |

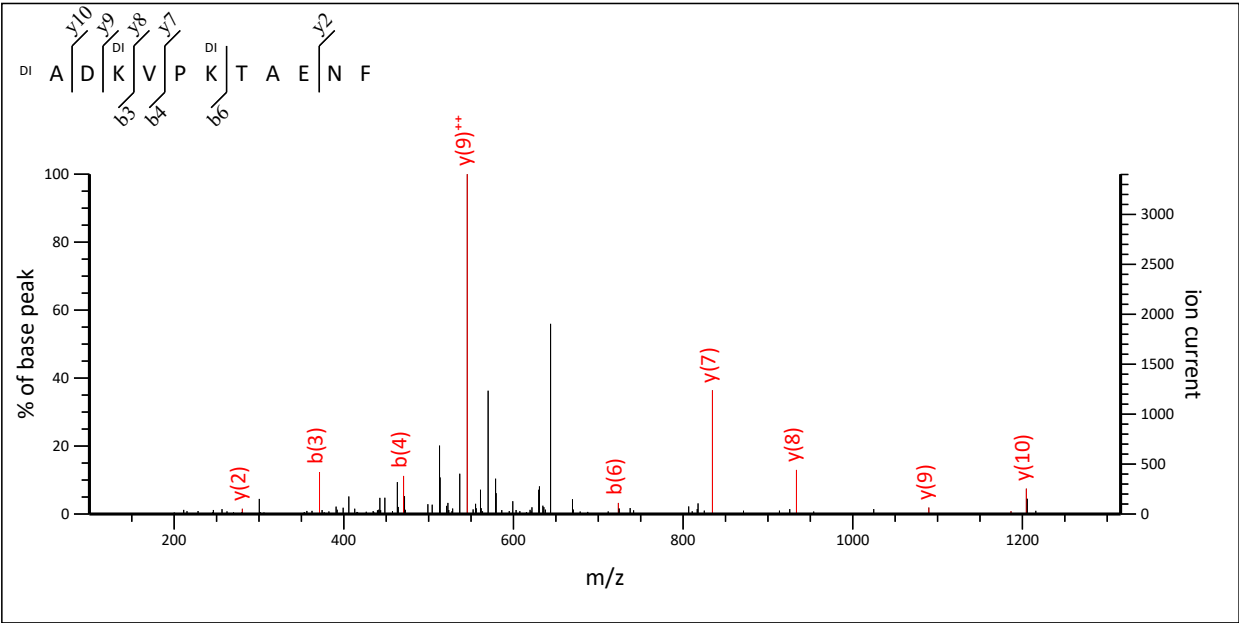
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADKVPKTAENF**
Found in **PPIA_MOUSE** in **SwissProt**, Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2

Match to Query 3953: 1302.721248 from(652.367900,2+) intensity(502996.7200) scans(3630) rawscans(sn3630) rtinseconds(1558.8044) index(1888)
Title: 1889: Scan 3630 (rt=1558.8) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf

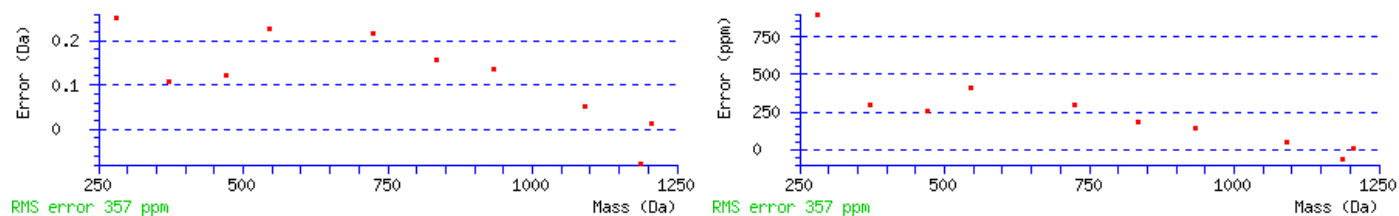


Navigation icons: ? (help), image (download), left arrow, zoom in, zoom out, zoom reset, 100.09 to 1315.79 (mass range), zoom in, right arrow.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1302.7184
Variable modifications:
N-term : Dimethyl (N-term)
K3 : Dimethyl (K)
K6 : Dimethyl (K)
Ions Score: 40 Expect: 3.1
Matches : 10/108 fragment ions using 11 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | | | A | | | | | | | 11 |
| 2 | 215.1026 | 108.0550 | | | 197.0921 | 99.0497 | D | 1204.6572 | 602.8322 | 1187.6307 | 594.3190 | 1186.6467 | 593.8270 | 10 |
| 3 | 371.2289 | 186.1181 | 354.2023 | 177.6048 | 353.2183 | 177.1128 | K | 1089.6303 | 545.3188 | 1072.6037 | 536.8055 | 1071.6197 | 536.3135 | 9 |
| 4 | 470.2973 | 235.6523 | 453.2708 | 227.1390 | 452.2867 | 226.6470 | V | 933.5040 | 467.2556 | 916.4775 | 458.7424 | 915.4934 | 458.2504 | 8 |
| 5 | 567.3501 | 284.1787 | 550.3235 | 275.6654 | 549.3395 | 275.1734 | P | 834.4356 | 417.7214 | 817.4090 | 409.2082 | 816.4250 | 408.7162 | 7 |
| 6 | 723.4763 | 362.2418 | 706.4498 | 353.7285 | 705.4658 | 353.2365 | K | 737.3828 | 369.1951 | 720.3563 | 360.6818 | 719.3723 | 360.1898 | 6 |
| 7 | 824.5240 | 412.7656 | 807.4975 | 404.2524 | 806.5135 | 403.7604 | T | 581.2566 | 291.1319 | 564.2300 | 282.6186 | 563.2460 | 282.1266 | 5 |
| 8 | 895.5611 | 448.2842 | 878.5346 | 439.7709 | 877.5506 | 439.2789 | A | 480.2089 | 240.6081 | 463.1823 | 232.0948 | 462.1983 | 231.6028 | 4 |
| 9 | 1024.6037 | 512.8055 | 1007.5772 | 504.2922 | 1006.5932 | 503.8002 | E | 409.1718 | 205.0895 | 392.1452 | 196.5763 | 391.1612 | 196.0842 | 3 |
| 10 | 1138.6467 | 569.8270 | 1121.6201 | 561.3137 | 1120.6361 | 560.8217 | N | 280.1292 | 140.5682 | 263.1026 | 132.0550 | | | 2 |
| 11 | | | | | | | F | 166.0863 | 83.5468 | | | | | 1 |



NCBI **BLAST** search of [ADKVPKTAENE](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-------------------------------|
| 39.8 | 1302.7184 | 0.0029 | ADKVPKTAENE |
| 33.6 | 1302.6905 | 0.0307 | ADRRGLHVQSH |
| 26.5 | 1302.7296 | -0.0083 | ADKVSSVRWIS |
| 26.1 | 1302.7395 | -0.0183 | ADKVESGKTSVV |
| 25.7 | 1302.6932 | 0.0280 | DGGLVSNAPHIPV |
| 24.1 | 1302.8163 | -0.0950 | ADKVLISILYI |
| 22.6 | 1302.8639 | -0.1427 | AKVPEVPKKPV |
| 21.7 | 1302.6213 | 0.1000 | GWGCMGRLAAPV |
| 21.7 | 1302.7953 | -0.0741 | HSIPLAHVRPV |
| 21.7 | 1302.9367 | -0.2154 | KPKVVVKVPV |

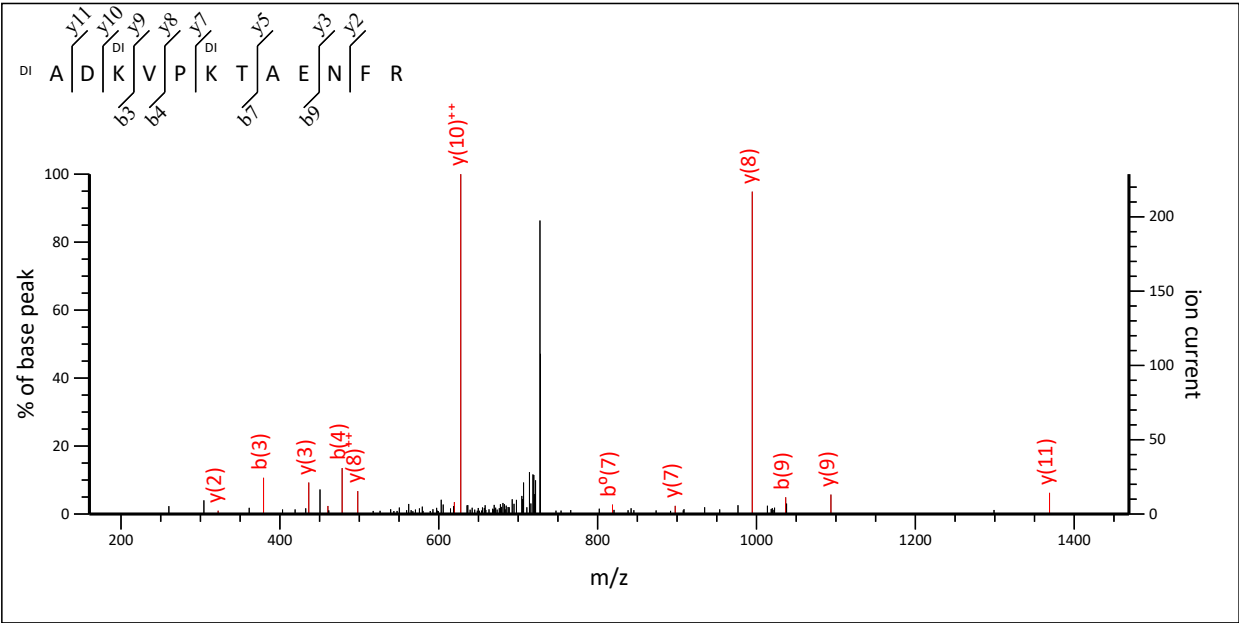
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADKVPKTAENFR**
Found in **PPIA_MOUSE** in **SwissProt**, Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2

Match to Query 5162: 1470.899548 from(736.457050,2+) intensity(51143.2770) scans(2908) rawscans(sn2908) rtinseconds(1323.3495) index(1267)
Title: 1268: Scan 2908 (rt=1323.35) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf







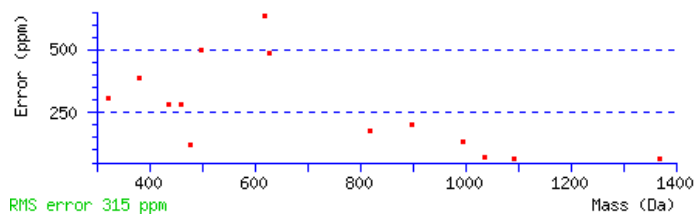
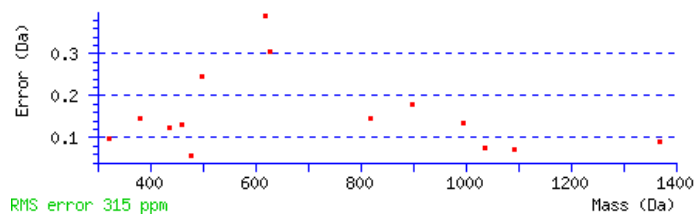
160.24 to 1468.9 



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1470.8948
Variable modifications:
N-term : Dimethyl:2H(4) (N-term)
K3 : Dimethyl:2H(4) (K)
K6 : Dimethyl:2H(4) (K)
Ions Score: 31 Expect: 25
Matches : 14/120 fragment ions using 27 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 104.1008 | 52.5540 | | | | | A | | | | | | | 12 |
| 2 | 219.1277 | 110.0675 | | | 201.1172 | 101.0622 | D | 1368.8085 | 684.9079 | 1351.7820 | 676.3946 | 1350.7980 | 675.9026 | 11 |
| 3 | 379.2791 | 190.1432 | 362.2526 | 181.6299 | 361.2685 | 181.1379 | K | 1253.7816 | 627.3944 | 1236.7550 | 618.8812 | 1235.7710 | 618.3892 | 10 |
| 4 | 478.3475 | 239.6774 | 461.3210 | 231.1641 | 460.3370 | 230.6721 | V | 1093.6302 | 547.3188 | 1076.6037 | 538.8055 | 1075.6197 | 538.3135 | 9 |
| 5 | 575.4003 | 288.2038 | 558.3737 | 279.6905 | 557.3897 | 279.1985 | P | 994.5618 | 497.7845 | 977.5353 | 489.2713 | 976.5512 | 488.7793 | 8 |
| 6 | 735.5517 | 368.2795 | 718.5251 | 359.7662 | 717.5411 | 359.2742 | K | 897.5090 | 449.2582 | 880.4825 | 440.7449 | 879.4985 | 440.2529 | 7 |
| 7 | 836.5993 | 418.8033 | 819.5728 | 410.2900 | 818.5888 | 409.7980 | T | 737.3577 | 369.1825 | 720.3311 | 360.6692 | 719.3471 | 360.1772 | 6 |
| 8 | 907.6365 | 454.3219 | 890.6099 | 445.8086 | 889.6259 | 445.3166 | A | 636.3100 | 318.6586 | 619.2835 | 310.1454 | 618.2994 | 309.6534 | 5 |
| 9 | 1036.6790 | 518.8432 | 1019.6525 | 510.3299 | 1018.6685 | 509.8379 | E | 565.2729 | 283.1401 | 548.2463 | 274.6268 | 547.2623 | 274.1348 | 4 |
| 10 | 1150.7220 | 575.8646 | 1133.6954 | 567.3513 | 1132.7114 | 566.8593 | N | 436.2303 | 218.6188 | 419.2037 | 210.1055 | | | 3 |
| 11 | 1297.7904 | 649.3988 | 1280.7638 | 640.8856 | 1279.7798 | 640.3935 | F | 322.1874 | 161.5973 | 305.1608 | 153.0840 | | | 2 |
| 12 | | | | | | | R | 175.1190 | 88.0631 | 158.0924 | 79.5498 | | | 1 |



NCBI **BLAST** search of [ADKVPKTAENFR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|---------------------------------|
| 30.8 | 1470.8948 | 0.0048 | ADKVPKTAENFR |
| 23.8 | 1470.7363 | 0.1632 | CSHLCLAVPVGGFV |
| 21.3 | 1470.8208 | 0.0787 | HRGVPKNIHFNP |
| 20.2 | 1470.8475 | 0.0520 | TQLVPPQPISTSA |
| 20.1 | 1470.8458 | 0.0537 | AIFSLGFIIVGSIC |
| 19.6 | 1470.7970 | 0.1026 | EILLDSKPVSSW |
| 19.1 | 1470.7719 | 0.1277 | GPPGVPGLDGPKGEP |
| 17.5 | 1470.9523 | -0.0528 | ATSSVADRKLVTK |
| 17.3 | 1470.8322 | 0.0673 | KSAVWSPSSQFLA |
| 17.0 | 1470.7261 | 0.1735 | AAFLAMRNGCADA |

Mascot: <http://www.matrixscience.com/>

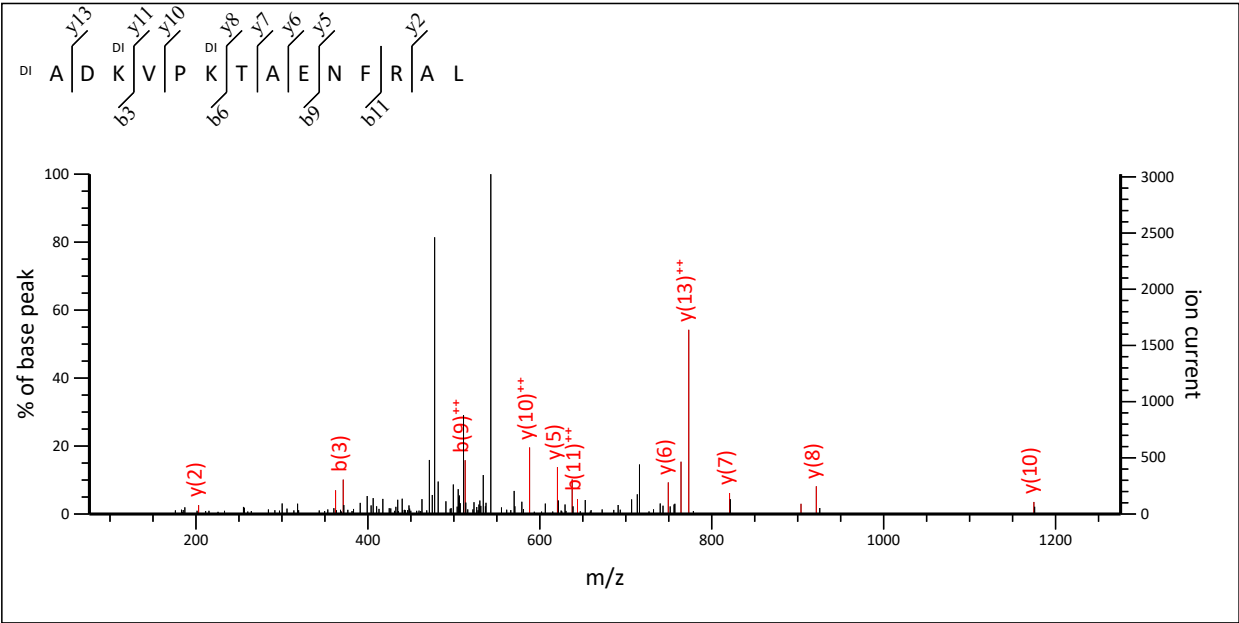
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADKVPKTAENFRAL**
Found in **PPIA_MOUSE** in **SwissProt**, Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2

Match to Query 6243: 1642.945362 from(548.655730,3+) intensity(616415.2500) scans(4642) rawscans(sn4642) rtinseconds(1883.5018) index(2746)

Title: 2747: Scan 4642 (rt=1883.5) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf



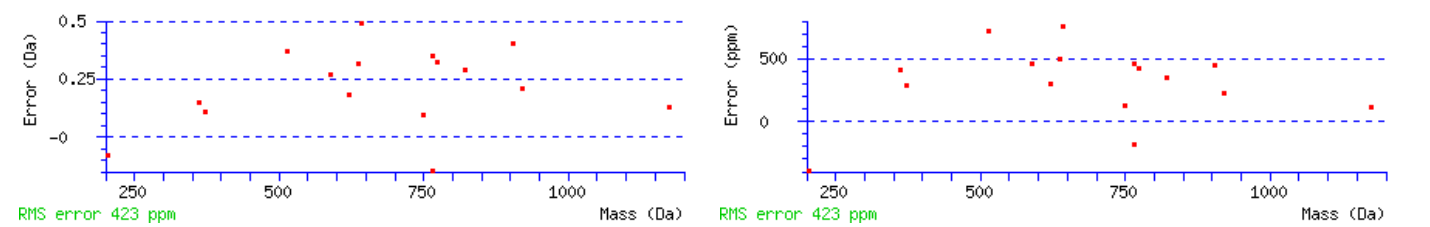


76.06 to 1275.66

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1642.9406
Variable modifications:
N-term : Dimethyl (N-term)
K3 : Dimethyl (K)
K6 : Dimethyl (K)
Ions Score: 22 Expect: 1.8e+002
Matches : 16/136 fragment ions using 32 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | | | A | | | | | | | 14 |
| 2 | 215.1026 | 108.0550 | | | 197.0921 | 99.0497 | D | 1544.8795 | 772.9434 | 1527.8530 | 764.4301 | 1526.8689 | 763.9381 | 13 |
| 3 | 371.2289 | 186.1181 | 354.2023 | 177.6048 | 353.2183 | 177.1128 | K | 1429.8526 | 715.4299 | 1412.8260 | 706.9166 | 1411.8420 | 706.4246 | 12 |
| 4 | 470.2973 | 235.6523 | 453.2708 | 227.1390 | 452.2867 | 226.6470 | V | 1273.7263 | 637.3668 | 1256.6997 | 628.8535 | 1255.7157 | 628.3615 | 11 |
| 5 | 567.3501 | 284.1787 | 550.3235 | 275.6654 | 549.3395 | 275.1734 | P | 1174.6579 | 587.8326 | 1157.6313 | 579.3193 | 1156.6473 | 578.8273 | 10 |
| 6 | 723.4763 | 362.2418 | 706.4498 | 353.7285 | 705.4658 | 353.2365 | K | 1077.6051 | 539.3062 | 1060.5786 | 530.7929 | 1059.5946 | 530.3009 | 9 |
| 7 | 824.5240 | 412.7656 | 807.4975 | 404.2524 | 806.5135 | 403.7604 | T | 921.4789 | 461.2431 | 904.4523 | 452.7298 | 903.4683 | 452.2378 | 8 |
| 8 | 895.5611 | 448.2842 | 878.5346 | 439.7709 | 877.5506 | 439.2789 | A | 820.4312 | 410.7192 | 803.4046 | 402.2060 | 802.4206 | 401.7139 | 7 |
| 9 | 1024.6037 | 512.8055 | 1007.5772 | 504.2922 | 1006.5932 | 503.8002 | E | 749.3941 | 375.2007 | 732.3675 | 366.6874 | 731.3835 | 366.1954 | 6 |
| 10 | 1138.6467 | 569.8270 | 1121.6201 | 561.3137 | 1120.6361 | 560.8217 | N | 620.3515 | 310.6794 | 603.3249 | 302.1661 | | | 5 |
| 11 | 1285.7151 | 643.3612 | 1268.6885 | 634.8479 | 1267.7045 | 634.3559 | F | 506.3085 | 253.6579 | 489.2820 | 245.1446 | | | 4 |
| 12 | 1441.8162 | 721.4117 | 1424.7896 | 712.8985 | 1423.8056 | 712.4064 | R | 359.2401 | 180.1237 | 342.2136 | 171.6104 | | | 3 |
| 13 | 1512.8533 | 756.9303 | 1495.8267 | 748.4170 | 1494.8427 | 747.9250 | A | 203.1390 | 102.0731 | | | | | 2 |
| 14 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI BLAST search of [ADKVPKTAENFRAL](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|--------|----------------------------------|
| 22.4 | 1642.9406 | 0.0047 | ADKVPKTAENFRAL |
| 15.5 | 1642.9082 | 0.0371 | ANKNYYGAAKLIFS |
| 13.1 | 1642.8501 | 0.0953 | CAPANHTPALPSINPL |
| 12.9 | 1642.7549 | 0.1905 | EFGKYCDDIVNTAA |
| 12.5 | 1642.8395 | 0.1058 | FFESLAAVNPNETV |
| 11.7 | 1642.7439 | 0.2015 | DHLPGGESQGCPCGQS |
| 11.4 | 1642.8463 | 0.0991 | LFGYGVLDAAGAMVKM |
| 11.1 | 1642.8342 | 0.1112 | PLTEVIEPLDFEDV |
| 11.1 | 1642.8050 | 0.1404 | ADPSAQSEGEKVADLA |
| 10.9 | 1642.7303 | 0.2151 | RMNMPISNEDMTV |

Mascot: <http://www.matrixscience.com/>

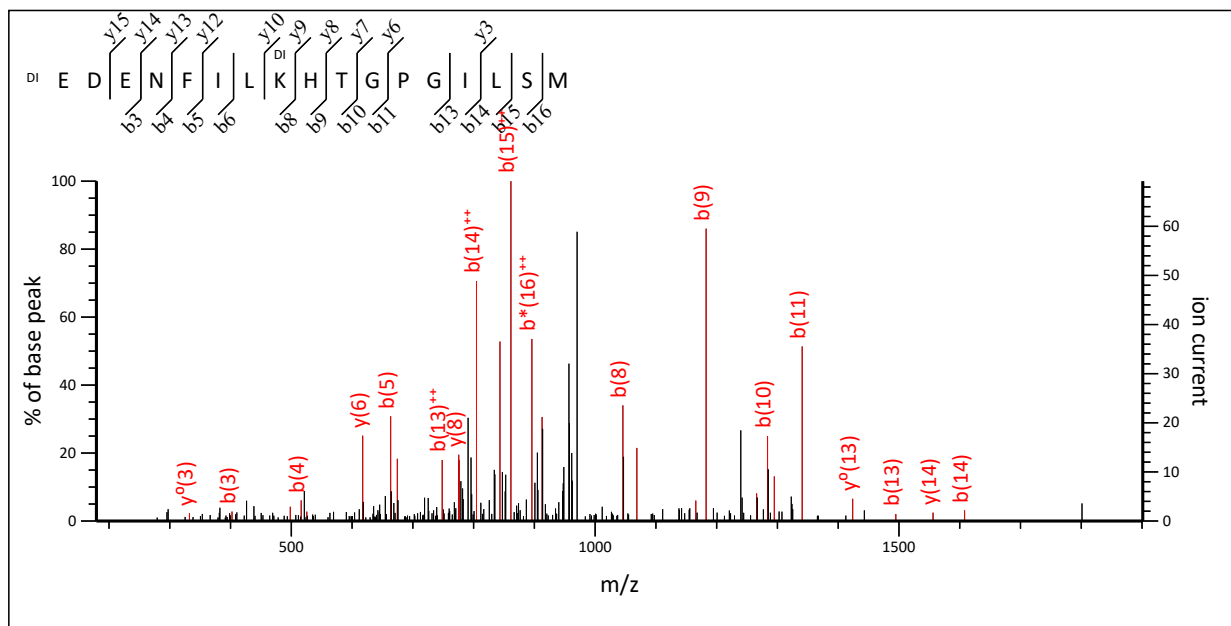
Peptide View

MS/MS Fragmentation of **EDENFILKHTGPGILSM**

Found in **PPIA MOUSE** in **SwissProt**, Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2

Match to Query 8035: 1956.012148 from(979.013350,2+) intensity(38344.8750) scans(10101) rawscans(sn10101) rtinseconds(3802.4217) index(7458)

Title: 7459: Scan 10101 (rt=3802.42) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf



179.29 to 1901.21



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1956.0026

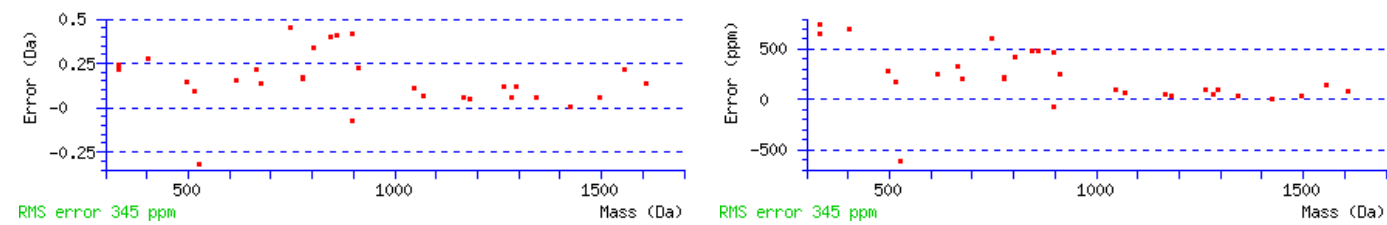
Variable modifications:

N-term : Dimethyl (N-term)

Ions Score: 57 Expect: 0.068

Matches : 30/166 fragment ions using 51 most intense peaks ([help](#))

| # | b | b⁺⁺ | b* | b^{***} | b⁰ | b⁰⁺⁺ | Seq. | y | y ⁺⁺ | y* | y ^{***} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------------|-----------|------------------------|----------------------|------------------------|------|-----------|-----------------|-----------|------------------|----------------|------------------|----|
| 1 | 158.0812 | 79.5442 | | | 140.0706 | 70.5389 | E | | | | | | | 17 |
| 2 | 273.1081 | 137.0577 | | | 255.0975 | 128.0524 | D | 1799.9360 | 900.4717 | 1782.9095 | 891.9584 | 1781.9255 | 891.4664 | 16 |
| 3 | 402.1507 | 201.5790 | | | 384.1401 | 192.5737 | E | 1684.9091 | 842.9582 | 1667.8825 | 834.4449 | 1666.8985 | 833.9529 | 15 |
| 4 | 516.1936 | 258.6005 | 499.1671 | 250.0872 | 498.1831 | 249.5952 | N | 1555.8665 | 778.4369 | 1538.8399 | 769.9236 | 1537.8559 | 769.4316 | 14 |
| 5 | 663.2620 | 332.1347 | 646.2355 | 323.6214 | 645.2515 | 323.1294 | F | 1441.8236 | 721.4154 | 1424.7970 | 712.9021 | 1423.8130 | 712.4101 | 13 |
| 6 | 776.3461 | 388.6767 | 759.3196 | 380.1634 | 758.3355 | 379.6714 | I | 1294.7552 | 647.8812 | 1277.7286 | 639.3679 | 1276.7446 | 638.8759 | 12 |
| 7 | 889.4302 | 445.2187 | 872.4036 | 436.7055 | 871.4196 | 436.2134 | L | 1181.6711 | 591.3392 | 1164.6445 | 582.8259 | 1163.6605 | 582.3339 | 11 |
| 8 | 1045.5564 | 523.2819 | 1028.5299 | 514.7686 | 1027.5459 | 514.2766 | K | 1068.5870 | 534.7972 | 1051.5605 | 526.2839 | 1050.5765 | 525.7919 | 10 |
| 9 | 1182.6153 | 591.8113 | 1165.5888 | 583.2980 | 1164.6048 | 582.8060 | H | 912.4608 | 456.7340 | | | 894.4502 | 447.7287 | 9 |
| 10 | 1283.6630 | 642.3352 | 1266.6365 | 633.8219 | 1265.6525 | 633.3299 | T | 775.4019 | 388.2046 | | | 757.3913 | 379.1993 | 8 |
| 11 | 1340.6845 | 670.8459 | 1323.6579 | 662.3326 | 1322.6739 | 661.8406 | G | 674.3542 | 337.6807 | | | 656.3436 | 328.6754 | 7 |
| 12 | 1437.7373 | 719.3723 | 1420.7107 | 710.8590 | 1419.7267 | 710.3670 | P | 617.3327 | 309.1700 | | | 599.3221 | 300.1647 | 6 |
| 13 | 1494.7587 | 747.8830 | 1477.7322 | 739.3697 | 1476.7482 | 738.8777 | G | 520.2799 | 260.6436 | | | 502.2694 | 251.6383 | 5 |
| 14 | 1607.8428 | 804.4250 | 1590.8162 | 795.9118 | 1589.8322 | 795.4197 | I | 463.2585 | 232.1329 | | | 445.2479 | 223.1276 | 4 |
| 15 | 1720.9268 | 860.9671 | 1703.9003 | 852.4538 | 1702.9163 | 851.9618 | L | 350.1744 | 175.5908 | | | 332.1639 | 166.5856 | 3 |
| 16 | 1807.9589 | 904.4831 | 1790.9323 | 895.9698 | 1789.9483 | 895.4778 | S | 237.0904 | 119.0488 | | | 219.0798 | 110.0435 | 2 |
| 17 | | | | | | | M | 150.0583 | 75.5328 | | | | | 1 |



NCBI **BLAST** search of [EDENFILKHTGPGILSM](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-------------------------------------|
| 56.8 | 1956.0026 | 0.0095 | EDENFILKHTGPGILSM |
| 20.0 | 1955.9375 | 0.0747 | CDVNHQNRAGYSALMLA |
| 18.3 | 1955.9741 | 0.0380 | WNSGSLSSGVHTFPAVLQ |
| 18.2 | 1956.0608 | -0.0487 | APLPAPGTSALFTFSPLTV |
| 17.3 | 1955.8801 | 0.1321 | DAREQEIRMGQMAMGGA |
| 14.1 | 1956.1913 | -0.1792 | TVLLAPRQPQSLIVTER |
| 13.3 | 1956.2739 | -0.2618 | PLPTATTGNVHTAKKISI |
| 12.7 | 1955.8306 | 0.1816 | LLEMDSESEDPRDTE |
| 12.3 | 1956.0793 | -0.0671 | FINATTGIVTVNRPLDR |
| 12.1 | 1955.9193 | 0.0928 | QASGNMGTPPTMTRVPGP |

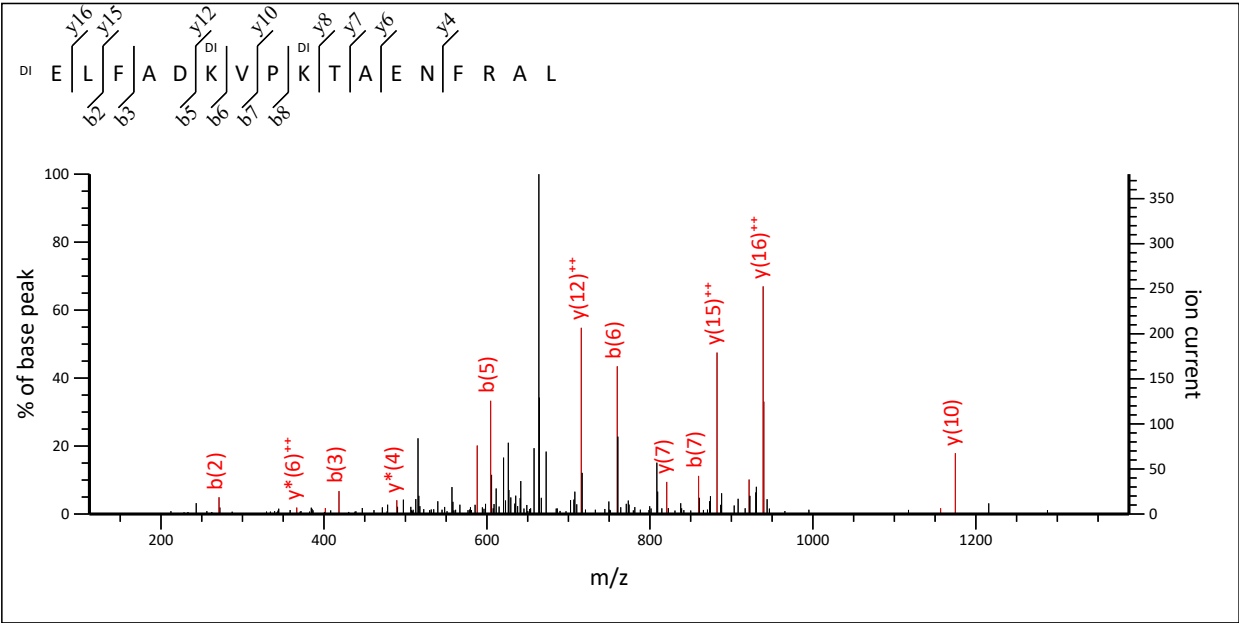
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELFADKVPKTAENFRAL**
Found in **PPIA_MOUSE** in **SwissProt**, Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2

Match to Query 8470: 2032.131582 from(678.384470,3+) intensity(105163.0900) scans(8156) rawscans(sn8156) rtinseconds(3115.0489) index(5804)
Title: 5805: Scan 8156 (rt=3115.05) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf

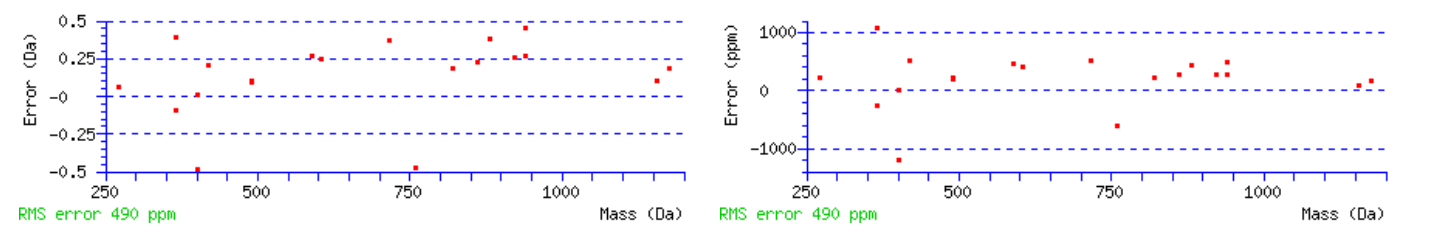


Navigation icons: ? (help), zoom in, zoom out, zoom reset, pan, and a range selector showing 112.17 to 1387.89.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 2032.1357
Variable modifications:
N-term : Dimethyl (N-term)
K6 : Dimethyl (K)
K9 : Dimethyl (K)
Ions Score: 29 Expect: 40
Matches : 21/168 fragment ions using 29 most intense peaks (help)

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 158.0812 | 79.5442 | | | 140.0706 | 70.5389 | E | | | | | | | 17 |
| 2 | 271.1652 | 136.0863 | | | 253.1547 | 127.0810 | L | 1876.0691 | 938.5382 | 1859.0425 | 930.0249 | 1858.0585 | 929.5329 | 16 |
| 3 | 418.2336 | 209.6205 | | | 400.2231 | 200.6152 | F | 1762.9850 | 881.9962 | 1745.9585 | 873.4829 | 1744.9745 | 872.9909 | 15 |
| 4 | 489.2708 | 245.1390 | | | 471.2602 | 236.1337 | A | 1615.9166 | 808.4619 | 1598.8901 | 799.9487 | 1597.9061 | 799.4567 | 14 |
| 5 | 604.2977 | 302.6525 | | | 586.2871 | 293.6472 | D | 1544.8795 | 772.9434 | 1527.8530 | 764.4301 | 1526.8689 | 763.9381 | 13 |
| 6 | 760.4240 | 380.7156 | 743.3974 | 372.2023 | 742.4134 | 371.7103 | K | 1429.8526 | 715.4299 | 1412.8260 | 706.9166 | 1411.8420 | 706.4246 | 12 |
| 7 | 859.4924 | 430.2498 | 842.4658 | 421.7366 | 841.4818 | 421.2445 | V | 1273.7263 | 637.3668 | 1256.6997 | 628.8535 | 1255.7157 | 628.3615 | 11 |
| 8 | 956.5451 | 478.7762 | 939.5186 | 470.2629 | 938.5346 | 469.7709 | P | 1174.6579 | 587.8326 | 1157.6313 | 579.3193 | 1156.6473 | 578.8273 | 10 |
| 9 | 1112.6714 | 556.8393 | 1095.6449 | 548.3261 | 1094.6608 | 547.8341 | K | 1077.6051 | 539.3062 | 1060.5786 | 530.7929 | 1059.5946 | 530.3009 | 9 |
| 10 | 1213.7191 | 607.3632 | 1196.6925 | 598.8499 | 1195.7085 | 598.3579 | T | 921.4789 | 461.2431 | 904.4523 | 452.7298 | 903.4683 | 452.2378 | 8 |
| 11 | 1284.7562 | 642.8817 | 1267.7297 | 634.3685 | 1266.7456 | 633.8765 | A | 820.4312 | 410.7192 | 803.4046 | 402.2060 | 802.4206 | 401.7139 | 7 |
| 12 | 1413.7988 | 707.4030 | 1396.7722 | 698.8898 | 1395.7882 | 698.3978 | E | 749.3941 | 375.2007 | 732.3675 | 366.6874 | 731.3835 | 366.1954 | 6 |
| 13 | 1527.8417 | 764.4245 | 1510.8152 | 755.9112 | 1509.8312 | 755.4192 | N | 620.3515 | 310.6794 | 603.3249 | 302.1661 | | | 5 |
| 14 | 1674.9101 | 837.9587 | 1657.8836 | 829.4454 | 1656.8996 | 828.9534 | F | 506.3085 | 253.6579 | 489.2820 | 245.1446 | | | 4 |
| 15 | 1831.0112 | 916.0093 | 1813.9847 | 907.4960 | 1813.0007 | 907.0040 | R | 359.2401 | 180.1237 | 342.2136 | 171.6104 | | | 3 |
| 16 | 1902.0484 | 951.5278 | 1885.0218 | 943.0145 | 1884.0378 | 942.5225 | A | 203.1390 | 102.0731 | | | | | 2 |
| 17 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI BLAST search of [ELFADKVPKTAENFRAL](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--|
| 29.1 | 2032.1357 | -0.0041 | ELFADKVPKTAENFRAL |
| 19.4 | 2032.1834 | -0.0518 | SLLHHGGFKVLQSLKGSV |
| 17.6 | 2032.0561 | 0.0755 | TQNADCVVVLDNTALNRI |
| 17.0 | 2032.0486 | 0.0830 | HSLLGPIILSCVAVCEVIDH |
| 17.0 | 2032.0661 | 0.0654 | SVSVARSSGNSGGLGRISGIGS |
| 16.6 | 2031.9935 | 0.1381 | EDVENLIHVQIEAMIDH |
| 15.7 | 2031.9281 | 0.2035 | EALLYCNIPSVAEHSMEG |
| 15.4 | 2032.0088 | 0.1228 | GANVSEQCETKGNPPPAIF |
| 14.9 | 2032.1066 | 0.0250 | EWGKDTARRLGSTTVGSK |
| 14.8 | 2032.0854 | 0.0462 | SLPVHVRNLWEVAGRT |

Mascot: <http://www.matrixscience.com/>

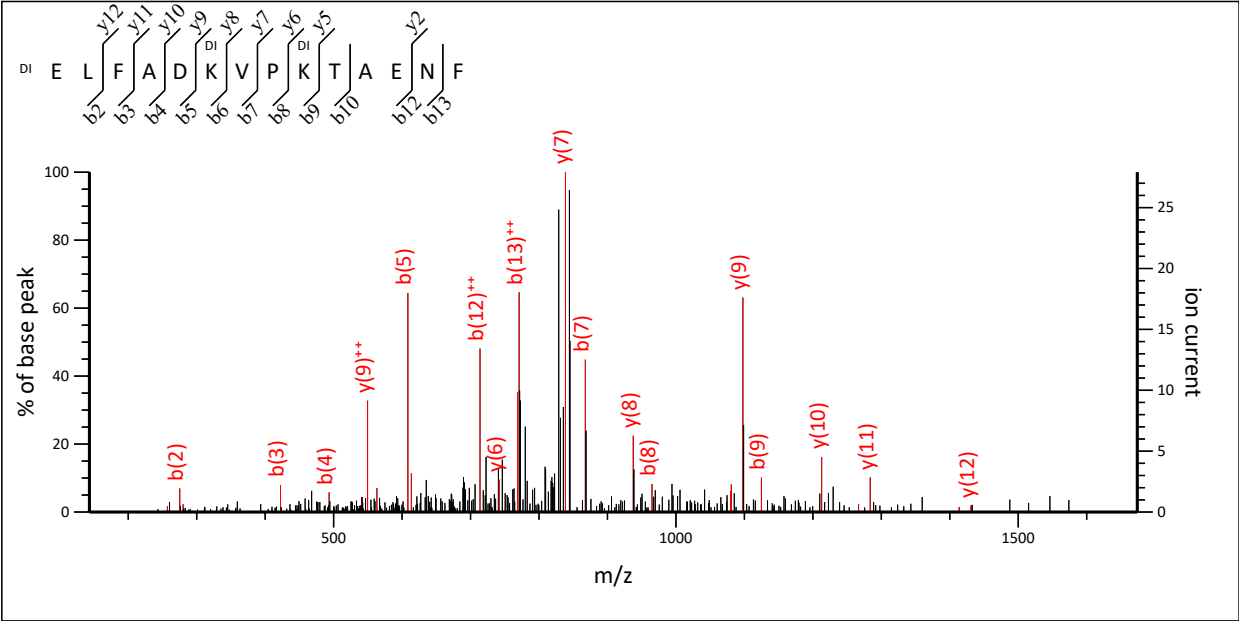
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELFADKVPKTAENF**
Found in **PPIA_MOUSE** in **SwissProt**, Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2

Match to Query 6637: 1703.953268 from(852.983910,2+) intensity(16920.4360) scans(7272) rawscans(sn7272) rtinseconds(2795.1865) index(5073)

Title: 5074: Scan 7272 (rt=2795.19) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf





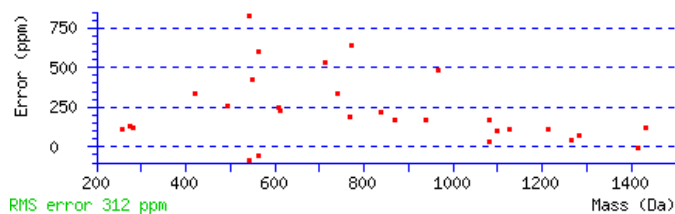
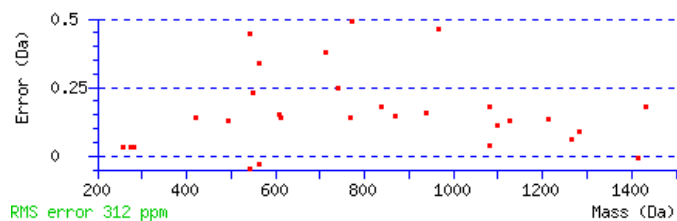
143.3 to 1673.93



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1703.9887
Variable modifications:
N-term : Dimethyl:2H(4) (N-term)
K6 : Dimethyl:2H(4) (K)
K9 : Dimethyl:2H(4) (K)
Ions Score: 34 Expect: 12
Matches : 29/140 fragment ions using 63 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 162.1063 | 81.5568 | | | 144.0957 | 72.5515 | E | | | | | | | 14 |
| 2 | 275.1903 | 138.0988 | | | 257.1798 | 129.0935 | L | 1543.8970 | 772.4521 | 1526.8705 | 763.9389 | 1525.8865 | 763.4469 | 13 |
| 3 | 422.2588 | 211.6330 | | | 404.2482 | 202.6277 | F | 1430.8130 | 715.9101 | 1413.7864 | 707.3968 | 1412.8024 | 706.9048 | 12 |
| 4 | 493.2959 | 247.1516 | | | 475.2853 | 238.1463 | A | 1283.7445 | 642.3759 | 1266.7180 | 633.8626 | 1265.7340 | 633.3706 | 11 |
| 5 | 608.3228 | 304.6650 | | | 590.3122 | 295.6598 | D | 1212.7074 | 606.8574 | 1195.6809 | 598.3441 | 1194.6969 | 597.8521 | 10 |
| 6 | 768.4742 | 384.7407 | 751.4476 | 376.2275 | 750.4636 | 375.7354 | K | 1097.6805 | 549.3439 | 1080.6539 | 540.8306 | 1079.6699 | 540.3386 | 9 |
| 7 | 867.5426 | 434.2749 | 850.5160 | 425.7617 | 849.5320 | 425.2697 | V | 937.5291 | 469.2682 | 920.5026 | 460.7549 | 919.5186 | 460.2629 | 8 |
| 8 | 964.5954 | 482.8013 | 947.5688 | 474.2880 | 946.5848 | 473.7960 | P | 838.4607 | 419.7340 | 821.4342 | 411.2207 | 820.4501 | 410.7287 | 7 |
| 9 | 1124.7467 | 562.8770 | 1107.7202 | 554.3637 | 1106.7362 | 553.8717 | K | 741.4079 | 371.2076 | 724.3814 | 362.6943 | 723.3974 | 362.2023 | 6 |
| 10 | 1225.7944 | 613.4008 | 1208.7679 | 604.8876 | 1207.7838 | 604.3956 | T | 581.2566 | 291.1319 | 564.2300 | 282.6186 | 563.2460 | 282.1266 | 5 |
| 11 | 1296.8315 | 648.9194 | 1279.8050 | 640.4061 | 1278.8210 | 639.9141 | A | 480.2089 | 240.6081 | 463.1823 | 232.0948 | 462.1983 | 231.6028 | 4 |
| 12 | 1425.8741 | 713.4407 | 1408.8476 | 704.9274 | 1407.8636 | 704.4354 | E | 409.1718 | 205.0895 | 392.1452 | 196.5763 | 391.1612 | 196.0842 | 3 |
| 13 | 1539.9170 | 770.4622 | 1522.8905 | 761.9489 | 1521.9065 | 761.4569 | N | 280.1292 | 140.5682 | 263.1026 | 132.0550 | | | 2 |
| 14 | | | | | | | F | 166.0863 | 83.5468 | | | | | 1 |



NCBI **BLAST** search of [ELFADKVPKTAENF](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|---------------------------------|
| 34.2 | 1703.9887 | -0.0355 | ELFADKVPKTAENF |
| 19.6 | 1703.8687 | 0.0846 | GQDFQCRETGRCLK |
| 17.5 | 1703.9375 | 0.0158 | VITFDKGGTWEFLQ |
| 17.4 | 1703.9959 | -0.0427 | EIAKEHDLPPAKSR |
| 16.4 | 1703.8565 | 0.0968 | SWSSQNVLMFMTLL |
| 15.7 | 1703.9591 | -0.0058 | QGCISKDKVDTLIM |
| 15.7 | 1703.8528 | 0.1005 | DLQKMSDAAGDFVDI |
| 15.0 | 1703.8930 | 0.0603 | SIAATDHEPTDARKS |
| 14.2 | 1703.9259 | 0.0274 | SFIINLFVMAVEGQA |
| 13.8 | 1703.8781 | 0.0752 | IFSADRPNVQDQLQ |

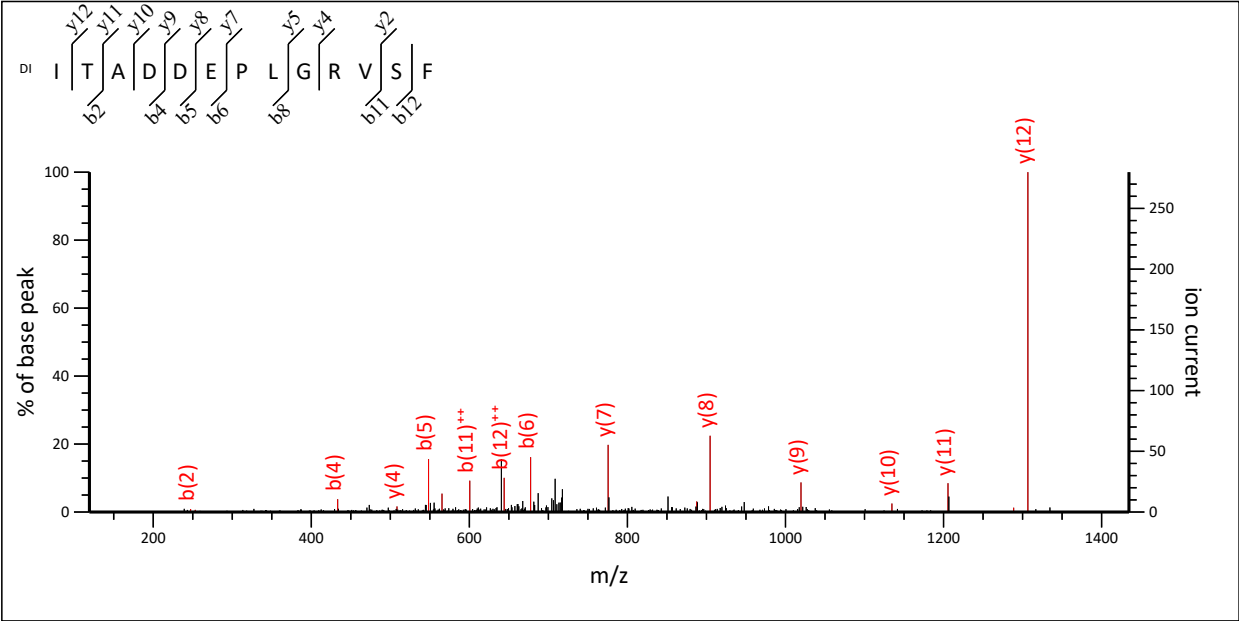
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITADDEPLGRVSF**
Found in **PPIA_MOUSE** in **SwissProt**, Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2

Match to Query 4721: 1450.766908 from(726.390730,2+) intensity(48205.5000) scans(8533) rawscans(sn8533) rtinseconds(3217.248) index(6069)
Title: 6070: Scan 8533 (rt=3217.25) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

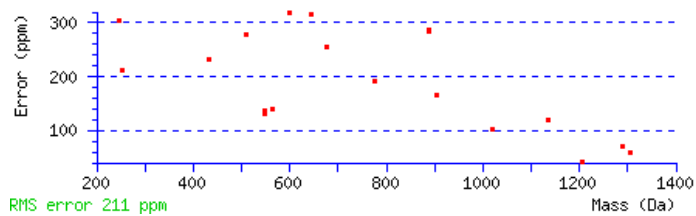
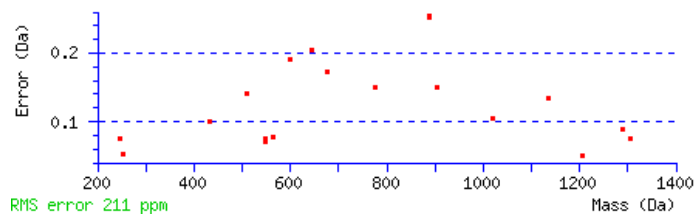


Navigation icons: ? (help), zoom in, zoom out, zoom reset, pan, 119.26 to 1434.61, zoom reset, pan.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1450.7606
Variable modifications:
N-term : Dimethyl:2H(4) (N-term)
Ions Score: 55 Expect: 0.098
Matches : 19/116 fragment ions using 34 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 146.1477 | 73.5775 | | | | | I | | | | | | | 13 |
| 2 | 247.1954 | 124.1014 | | | 229.1849 | 115.0961 | T | 1306.6274 | 653.8173 | 1289.6008 | 645.3040 | 1288.6168 | 644.8120 | 12 |
| 3 | 318.2325 | 159.6199 | | | 300.2220 | 150.6146 | A | 1205.5797 | 603.2935 | 1188.5531 | 594.7802 | 1187.5691 | 594.2882 | 11 |
| 4 | 433.2595 | 217.1334 | | | 415.2489 | 208.1281 | D | 1134.5426 | 567.7749 | 1117.5160 | 559.2617 | 1116.5320 | 558.7696 | 10 |
| 5 | 548.2864 | 274.6469 | | | 530.2759 | 265.6416 | D | 1019.5156 | 510.2615 | 1002.4891 | 501.7482 | 1001.5051 | 501.2562 | 9 |
| 6 | 677.3290 | 339.1681 | | | 659.3185 | 330.1629 | E | 904.4887 | 452.7480 | 887.4621 | 444.2347 | 886.4781 | 443.7427 | 8 |
| 7 | 774.3818 | 387.6945 | | | 756.3712 | 378.6892 | P | 775.4461 | 388.2267 | 758.4196 | 379.7134 | 757.4355 | 379.2214 | 7 |
| 8 | 887.4658 | 444.2366 | | | 869.4553 | 435.2313 | L | 678.3933 | 339.7003 | 661.3668 | 331.1870 | 660.3828 | 330.6950 | 6 |
| 9 | 944.4873 | 472.7473 | | | 926.4767 | 463.7420 | G | 565.3093 | 283.1583 | 548.2827 | 274.6450 | 547.2987 | 274.1530 | 5 |
| 10 | 1100.5884 | 550.7978 | 1083.5619 | 542.2846 | 1082.5779 | 541.7926 | R | 508.2878 | 254.6475 | 491.2613 | 246.1343 | 490.2772 | 245.6423 | 4 |
| 11 | 1199.6568 | 600.3321 | 1182.6303 | 591.8188 | 1181.6463 | 591.3268 | V | 352.1867 | 176.5970 | | | 334.1761 | 167.5917 | 3 |
| 12 | 1286.6889 | 643.8481 | 1269.6623 | 635.3348 | 1268.6783 | 634.8428 | S | 253.1183 | 127.0628 | | | 235.1077 | 118.0575 | 2 |
| 13 | | | | | | | F | 166.0863 | 83.5468 | | | | | 1 |



NCBI **BLAST** search of [ITADDEPLGRVSE](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--------------------------------|
| 54.9 | 1450.7606 | 0.0063 | ITADDEPLGRVSE |
| 29.0 | 1450.7672 | -0.0003 | MAGHDEAVLFVQV |
| 28.4 | 1450.8316 | -0.0647 | GCQLIKFDSVEV |
| 26.7 | 1450.7809 | -0.0140 | VIRTRAEDGDL |
| 25.3 | 1450.7250 | 0.0419 | LMWNREDALMV |
| 24.8 | 1450.7730 | -0.0061 | IFKANHPMDAEV |
| 22.9 | 1450.8119 | -0.0450 | LEGKANGGLVDSEV |
| 22.3 | 1450.7282 | 0.0387 | LTYPPGGWDEVSV |
| 21.1 | 1450.7765 | -0.0096 | AVRFRAMPRGNS |
| 21.1 | 1450.8231 | -0.0562 | LAESDEAKVQRAA |

Mascot: <http://www.matrixscience.com/>

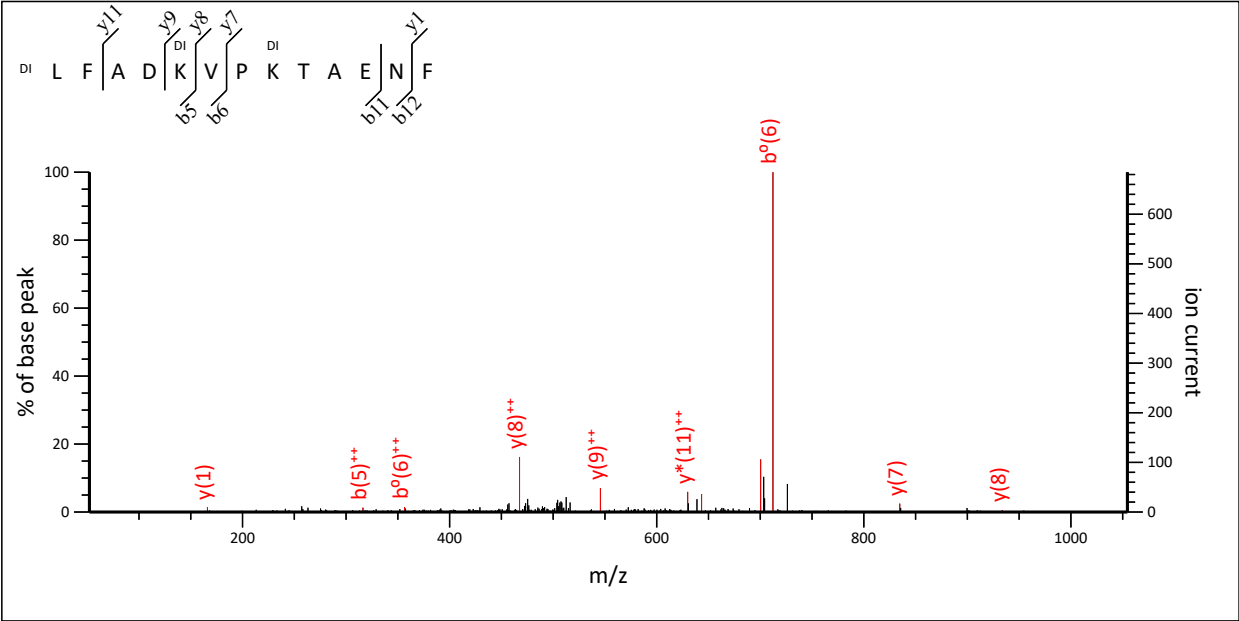
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFADKVPKTAENF**
Found in **PPIA_MOUSE** in **SwissProt**, Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2

Match to Query 5336: 1562.875962 from(521.965930,3+) intensity(66458.7810) scans(6289) rawscans(sn6289) rtinseconds(2422.4935) index(4162)

Title: 4163: Scan 6289 (rt=2422.49) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

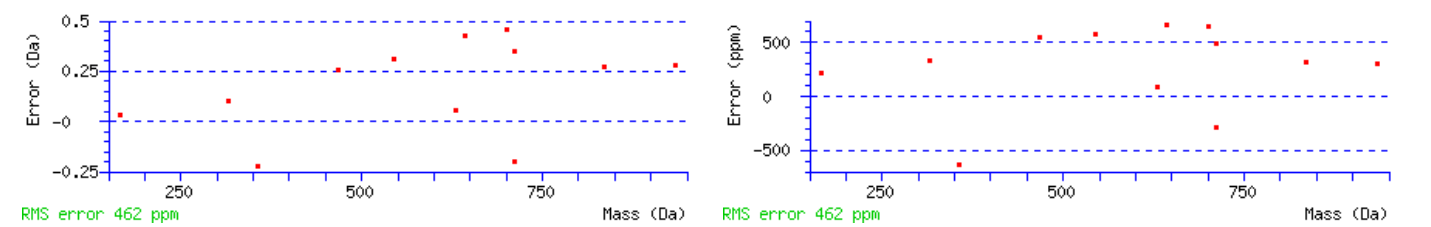


 to 

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1562.8708
Variable modifications:
N-term : Dimethyl (N-term)
K5 : Dimethyl (K)
K8 : Dimethyl (K)
Ions Score: 20 Expect: 2.9e+002
Matches : 12/124 fragment ions using 17 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 142.1226 | 71.5650 | | | | | L | | | | | | | 13 |
| 2 | 289.1911 | 145.0992 | | | | | F | 1422.7627 | 711.8850 | 1405.7362 | 703.3717 | 1404.7522 | 702.8797 | 12 |
| 3 | 360.2282 | 180.6177 | | | | | A | 1275.6943 | 638.3508 | 1258.6678 | 629.8375 | 1257.6838 | 629.3455 | 11 |
| 4 | 475.2551 | 238.1312 | | | 457.2445 | 229.1259 | D | 1204.6572 | 602.8322 | 1187.6307 | 594.3190 | 1186.6466 | 593.8270 | 10 |
| 5 | 631.3814 | 316.1943 | 614.3548 | 307.6811 | 613.3708 | 307.1890 | K | 1089.6303 | 545.3188 | 1072.6037 | 536.8055 | 1071.6197 | 536.3135 | 9 |
| 6 | 730.4498 | 365.7285 | 713.4232 | 357.2153 | 712.4392 | 356.7232 | V | 933.5040 | 467.2556 | 916.4775 | 458.7424 | 915.4934 | 458.2504 | 8 |
| 7 | 827.5026 | 414.2549 | 810.4760 | 405.7416 | 809.4920 | 405.2496 | P | 834.4356 | 417.7214 | 817.4090 | 409.2082 | 816.4250 | 408.7162 | 7 |
| 8 | 983.6288 | 492.3180 | 966.6023 | 483.8048 | 965.6182 | 483.3128 | K | 737.3828 | 369.1951 | 720.3563 | 360.6818 | 719.3723 | 360.1898 | 6 |
| 9 | 1084.6765 | 542.8419 | 1067.6499 | 534.3286 | 1066.6659 | 533.8366 | T | 581.2566 | 291.1319 | 564.2300 | 282.6186 | 563.2460 | 282.1266 | 5 |
| 10 | 1155.7136 | 578.3604 | 1138.6871 | 569.8472 | 1137.7030 | 569.3552 | A | 480.2089 | 240.6081 | 463.1823 | 232.0948 | 462.1983 | 231.6028 | 4 |
| 11 | 1284.7562 | 642.8817 | 1267.7297 | 634.3685 | 1266.7456 | 633.8765 | E | 409.1718 | 205.0895 | 392.1452 | 196.5763 | 391.1612 | 196.0842 | 3 |
| 12 | 1398.7991 | 699.9032 | 1381.7726 | 691.3899 | 1380.7886 | 690.8979 | N | 280.1292 | 140.5682 | 263.1026 | 132.0550 | | | 2 |
| 13 | | | | | | | F | 166.0863 | 83.5468 | | | | | 1 |



NCBI BLAST search of [LFADKVPKTAENF](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|---------------------------------|
| 20.2 | 1562.8708 | 0.0051 | LFADKVPKTAENF |
| 19.6 | 1562.8549 | 0.0211 | QGMLDDKGRVIED |
| 18.7 | 1562.7952 | 0.0807 | EPGANLDQPVTMIF |
| 18.5 | 1562.8273 | 0.0487 | AMDAKVGSLRRVM |
| 17.2 | 1563.0657 | -0.1897 | SPAGPSHKGKKAVN |
| 17.0 | 1562.7183 | 0.1577 | LLAAFSVDCCLAYM |
| 16.4 | 1562.7861 | 0.0898 | EKKAELTQTNM |
| 15.7 | 1562.9355 | -0.0595 | LFAGSSLGKRGVNAD |
| 15.4 | 1562.8966 | -0.0207 | LACLLTQYRVSLR |
| 15.0 | 1562.7974 | 0.0786 | LDDGSNMTELIRK |

Mascot: <http://www.matrixscience.com/>

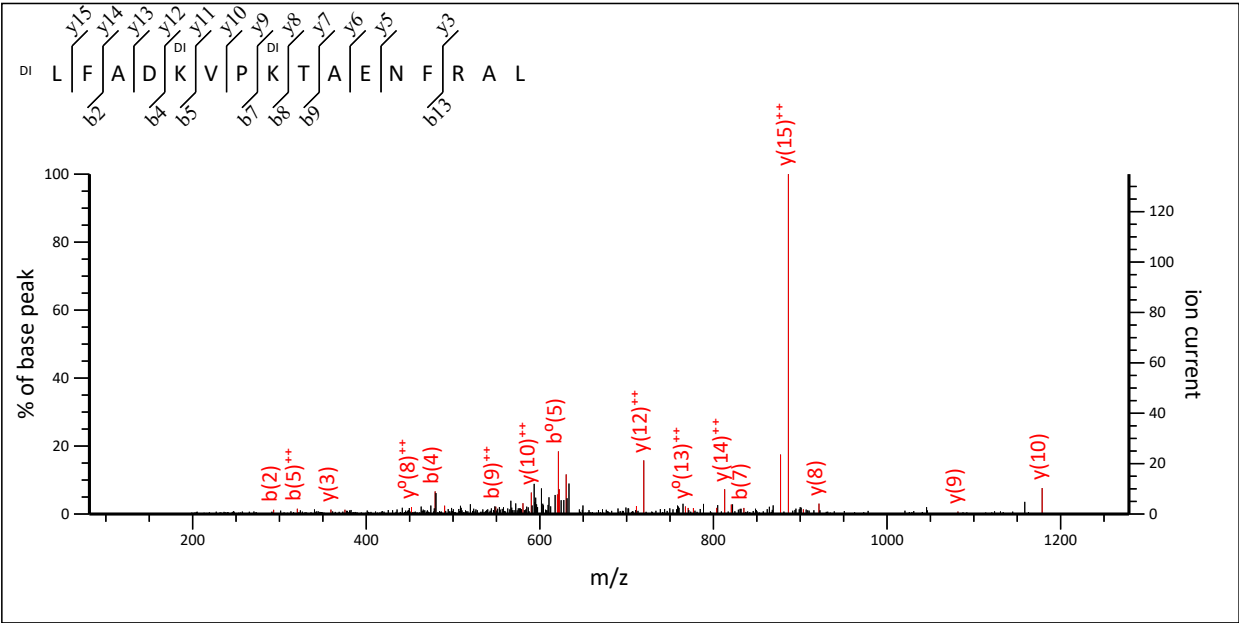
Mascot Search Results

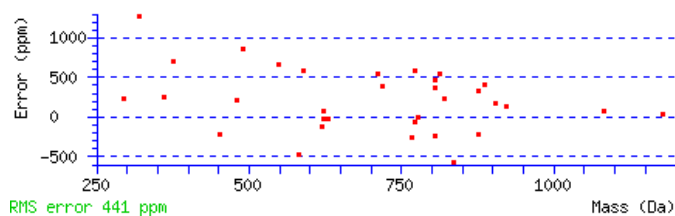
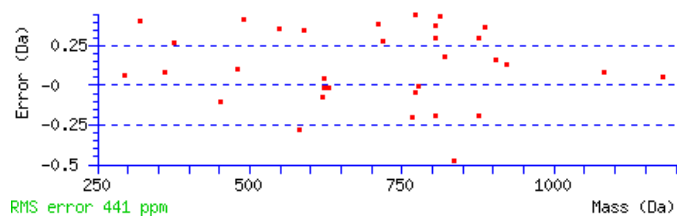
Peptide View

MS/MS Fragmentation of **LFADKVPKTAENFRAL**
Found in **PPIA_MOUSE** in **SwissProt**, Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2

Match to Query 7801: 1915.174002 from(639.398610,3+) intensity(25260.8220) scans(6886) rawscans(sn6886) rtinseconds(2655.6959) index(4749)

Title: 4750: Scan 6886 (rt=2655.7) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf





NCBI BLAST search of [LFADKVPKTAENFRAL](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|--------|-------------------------------------|
| 18.9 | 1915.1684 | 0.0056 | LFADKVPKTAENFRAL |
| 16.1 | 1915.0903 | 0.0837 | MRGTPVLVALGDFLGGPLA |
| 14.8 | 1915.1146 | 0.0594 | ADAFYKAKNEFAAKAT |
| 14.1 | 1915.0477 | 0.1263 | AEVLAARGYLTGMAGKW |
| 13.3 | 1915.0940 | 0.0800 | ADSTEMGDKATAGISKPL |
| 11.7 | 1914.8892 | 0.2848 | AFGEAALEQTLAEMCEL |
| 11.4 | 1915.0430 | 0.1310 | AIGYSETAVDPTLPKTF |
| 11.2 | 1914.9823 | 0.1917 | ATMTSHDLMKFVAPFN |
| 11.2 | 1915.0470 | 0.1270 | ITECSSLKRSLEQARM |
| 11.2 | 1914.9547 | 0.2193 | LTCESLEPVVVDLTHND |

Mascot: <http://www.matrixscience.com/>

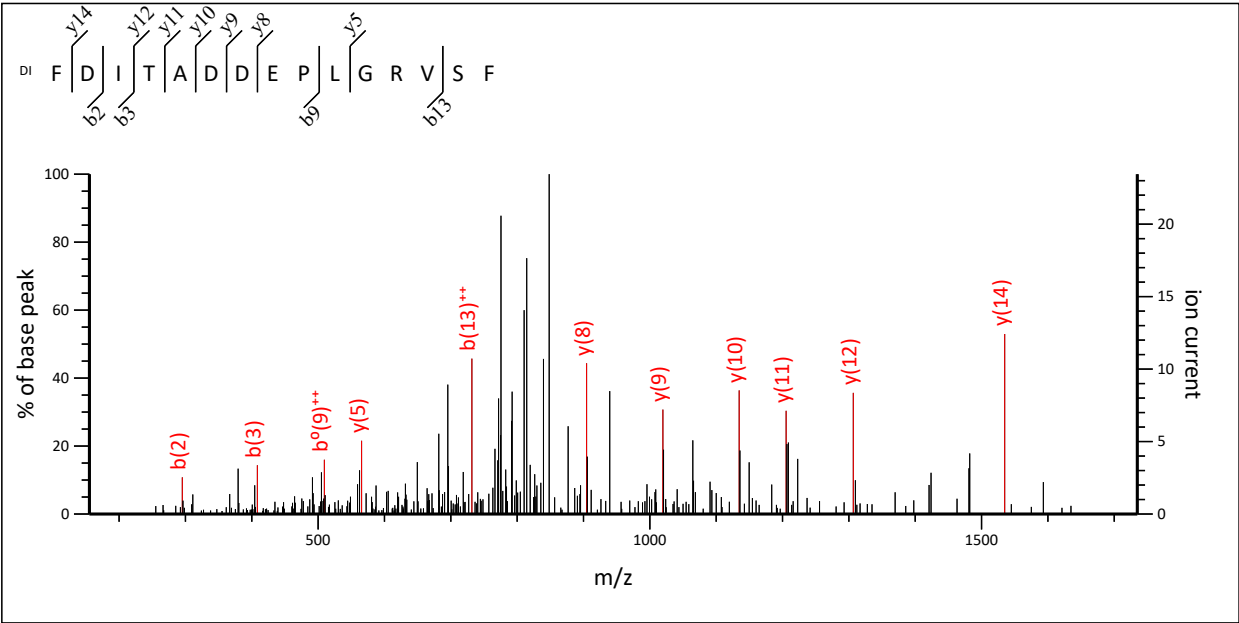
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FDITADDEPLGRVSF**
Found in **PPIA_MOUSE** in **SwissProt**, Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2

Match to Query 6309: 1712.868048 from(857.441300,2+) intensity(15595.4550) scans(10691) rawscans(sn10691) rtinseconds(4046.8744) index(7877)

Title: 7878: Scan 10691 (rt=4046.87) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_02.raw]
Data file hipocampo_02.temp.mgf



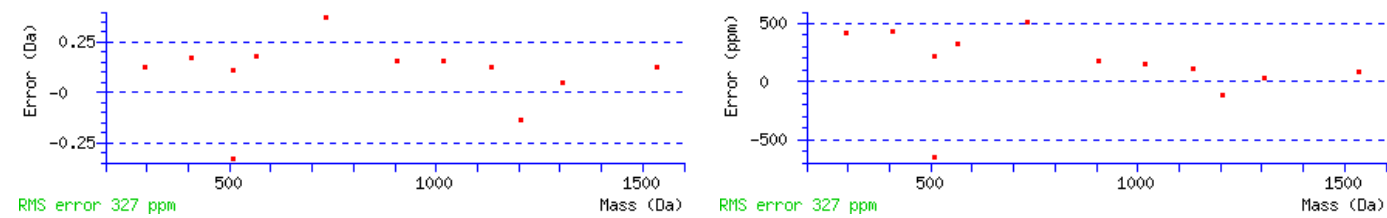


155.27 to 1734.77

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1712.8559
Variable modifications:
N-term : Dimethyl:2H(4) (N-term)
Ions Score: 49 Expect: 0.43
Matches : 12/136 fragment ions using 14 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 180.1321 | 90.5697 | | | | | F | | | | | | | 15 |
| 2 | 295.1590 | 148.0832 | | | 277.1485 | 139.0779 | D | 1534.7384 | 767.8728 | 1517.7118 | 759.3596 | 1516.7278 | 758.8675 | 14 |
| 3 | 408.2431 | 204.6252 | | | 390.2325 | 195.6199 | I | 1419.7114 | 710.3594 | 1402.6849 | 701.8461 | 1401.7009 | 701.3541 | 13 |
| 4 | 509.2908 | 255.1490 | | | 491.2802 | 246.1437 | T | 1306.6274 | 653.8173 | 1289.6008 | 645.3040 | 1288.6168 | 644.8120 | 12 |
| 5 | 580.3279 | 290.6676 | | | 562.3173 | 281.6623 | A | 1205.5797 | 603.2935 | 1188.5531 | 594.7802 | 1187.5691 | 594.2882 | 11 |
| 6 | 695.3548 | 348.1811 | | | 677.3443 | 339.1758 | D | 1134.5426 | 567.7749 | 1117.5160 | 559.2617 | 1116.5320 | 558.7696 | 10 |
| 7 | 810.3818 | 405.6945 | | | 792.3712 | 396.6892 | D | 1019.5156 | 510.2615 | 1002.4891 | 501.7482 | 1001.5051 | 501.2562 | 9 |
| 8 | 939.4244 | 470.2158 | | | 921.4138 | 461.2105 | E | 904.4887 | 452.7480 | 887.4621 | 444.2347 | 886.4781 | 443.7427 | 8 |
| 9 | 1036.4771 | 518.7422 | | | 1018.4666 | 509.7369 | P | 775.4461 | 388.2267 | 758.4196 | 379.7134 | 757.4355 | 379.2214 | 7 |
| 10 | 1149.5612 | 575.2842 | | | 1131.5506 | 566.2790 | L | 678.3933 | 339.7003 | 661.3668 | 331.1870 | 660.3828 | 330.6950 | 6 |
| 11 | 1206.5827 | 603.7950 | | | 1188.5721 | 594.7897 | G | 565.3093 | 283.1583 | 548.2827 | 274.6450 | 547.2987 | 274.1530 | 5 |
| 12 | 1362.6838 | 681.8455 | 1345.6572 | 673.3323 | 1344.6732 | 672.8402 | R | 508.2878 | 254.6475 | 491.2613 | 246.1343 | 490.2772 | 245.6423 | 4 |
| 13 | 1461.7522 | 731.3797 | 1444.7256 | 722.8665 | 1443.7416 | 722.3745 | V | 352.1867 | 176.5970 | | | 334.1761 | 167.5917 | 3 |
| 14 | 1548.7842 | 774.8957 | 1531.7577 | 766.3825 | 1530.7737 | 765.8905 | S | 253.1183 | 127.0628 | | | 235.1077 | 118.0575 | 2 |
| 15 | | | | | | | F | 166.0863 | 83.5468 | | | | | 1 |



NCBI **BLAST** search of [FDITADDEPLGRVSE](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-----------------------------------|
| 48.7 | 1712.8559 | 0.0121 | FDITADDEPLGRVSE |
| 25.4 | 1712.8052 | 0.0629 | SLLWCAGVDSVTTNAC |
| 22.4 | 1712.9083 | -0.0403 | TDLFEKGNADFTI |
| 21.1 | 1712.8791 | -0.0111 | MDITCYFLNKCGLL |
| 20.6 | 1712.9473 | -0.0793 | SEDSSDDEPLIKKL |
| 20.3 | 1712.8737 | -0.0057 | TELSWHSCRQLLY |
| 19.8 | 1712.9382 | -0.0701 | PDSREFGCAKTLI |
| 17.8 | 1712.8255 | 0.0426 | ASGGLSMAVEGPEGMER |
| 17.6 | 1713.0400 | -0.1719 | FSHTAGVGLIVSQKTP |
| 16.9 | 1712.8365 | 0.0316 | SLFEAKGDVMATLEM |

Mascot: <http://www.matrixscience.com/>

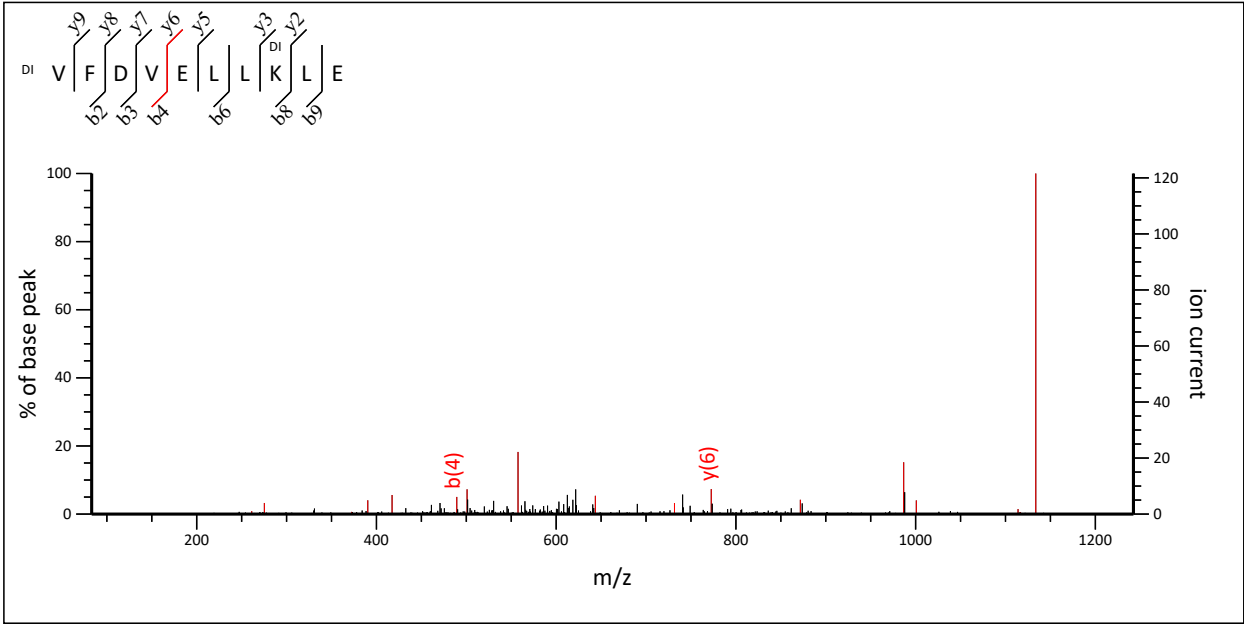
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFDVELLKLE**
Found in **FKB1A_MOUSE** in **SwissProt**, Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Mus musculus GN=Fkbp1a PE=1 SV=2

Match to Query 3517: 1259.744208 from(630.879380,2+) intensity(13627.6700) scans(11298) rawscans(sn11298) rtinseconds(4220.8133) index(8373)

Title: 8374: Scan 11298 (rt=4220.81) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

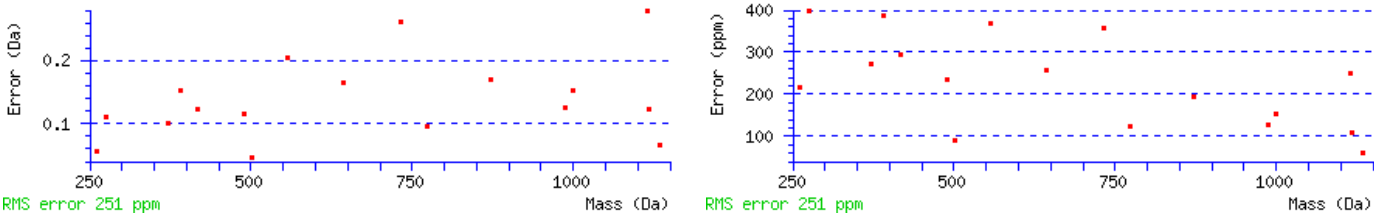


Navigation icons: ? (help), zoom in, zoom out, pan, and a range selector from 83.11 to 1242.39.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1259.7377
Variable modifications:
N-term : Dimethyl (N-term)
K8 : Dimethyl (K)
Ions Score: 53 Expect: 0.16
Matches : 17/86 fragment ions using 30 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 128.1070 | 64.5571 | | | | | V | | | | | | | 10 |
| 2 | 275.1754 | 138.0913 | | | | | F | 1133.6453 | 567.3263 | 1116.6187 | 558.8130 | 1115.6347 | 558.3210 | 9 |
| 3 | 390.2023 | 195.6048 | | | 372.1918 | 186.5995 | D | 986.5768 | 493.7921 | 969.5503 | 485.2788 | 968.5663 | 484.7868 | 8 |
| 4 | 489.2708 | 245.1390 | | | 471.2602 | 236.1337 | V | 871.5499 | 436.2786 | 854.5233 | 427.7653 | 853.5393 | 427.2733 | 7 |
| 5 | 618.3134 | 309.6603 | | | 600.3028 | 300.6550 | E | 772.4815 | 386.7444 | 755.4549 | 378.2311 | 754.4709 | 377.7391 | 6 |
| 6 | 731.3974 | 366.2023 | | | 713.3869 | 357.1971 | L | 643.4389 | 322.2231 | 626.4123 | 313.7098 | 625.4283 | 313.2178 | 5 |
| 7 | 844.4815 | 422.7444 | | | 826.4709 | 413.7391 | L | 530.3548 | 265.6811 | 513.3283 | 257.1678 | 512.3443 | 256.6758 | 4 |
| 8 | 1000.6077 | 500.8075 | 983.5812 | 492.2942 | 982.5972 | 491.8022 | K | 417.2708 | 209.1390 | 400.2442 | 200.6257 | 399.2602 | 200.1337 | 3 |
| 9 | 1113.6918 | 557.3495 | 1096.6653 | 548.8363 | 1095.6812 | 548.3443 | L | 261.1445 | 131.0759 | | | 243.1339 | 122.0706 | 2 |
| 10 | | | | | | | E | 148.0604 | 74.5339 | | | 130.0499 | 65.5286 | 1 |



NCBI **BLAST** search of [VFDVELLKLE](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|--------|-----------------------------|
| 52.5 | 1259.7377 | 0.0065 | VFDVELLKLE |
| 25.2 | 1259.6319 | 0.1123 | MQTVIEEVLE |
| 24.5 | 1259.6985 | 0.0457 | LEPLGTPMLIE |
| 24.1 | 1259.6584 | 0.0858 | VFPVQMSPIAQ |
| 23.8 | 1259.5769 | 0.1673 | GEDDATLEVIE |
| 21.9 | 1259.6659 | 0.0783 | ADRENIQVIE |
| 21.7 | 1259.6790 | 0.0652 | LLPEEAAEPQQ |
| 21.7 | 1259.5704 | 0.1739 | VMDVNDNAPEL |
| 20.9 | 1259.6961 | 0.0481 | IEKAHNNELE |
| 20.1 | 1259.6192 | 0.1250 | SETCLRMELE |

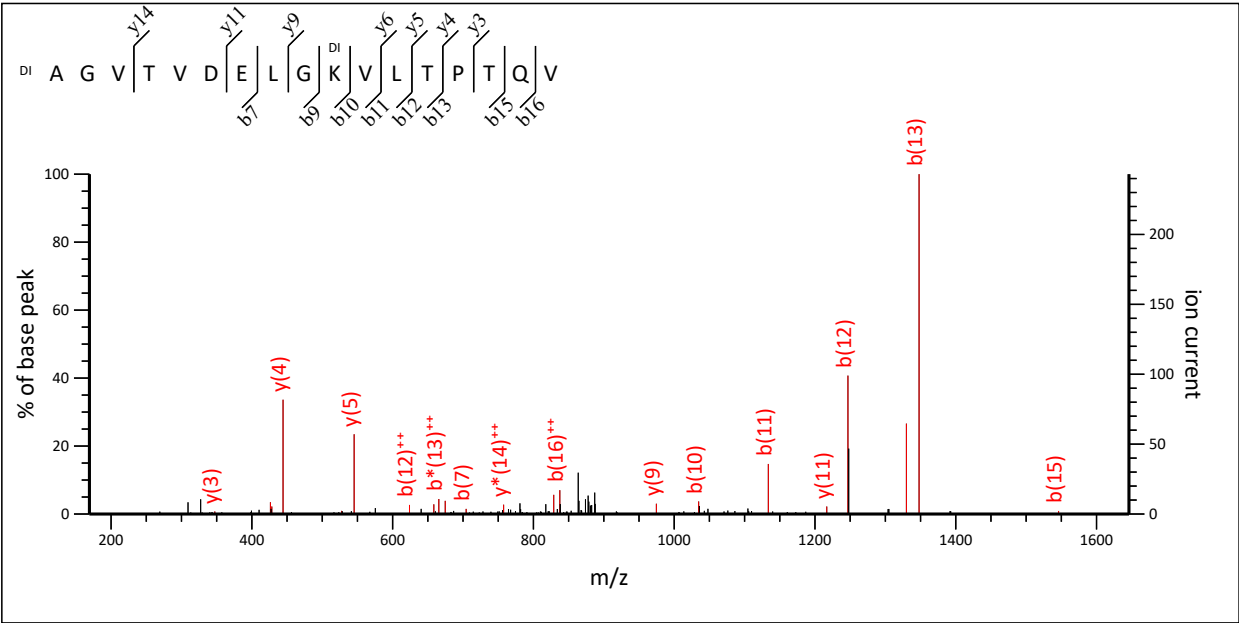
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGVTVDLGKVLTPQV**
Found in **PEBP1_MOUSE** in **SwissProt**, Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=3

Match to Query 6578: 1790.066948 from(896.040750,2+) intensity(33433.7420) scans(10412) rawscans(sn10412) rtinseconds(3896.0992) index(7621)
Title: 7622: Scan 10412 (rt=3896.1) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

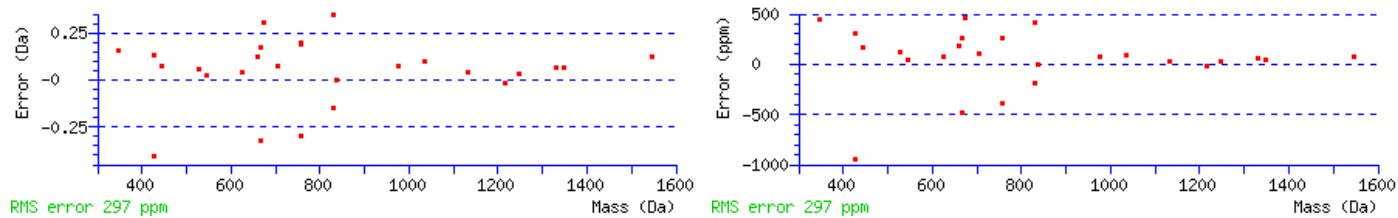


Navigation icons: ? (help), image (download), left arrow, zoom in, zoom out, right arrow, 169.23 to 1646.06 (mass range), image (download), right arrow.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1790.0641
Variable modifications:
N-term : Dimethyl:2H(4) (N-term)
K10 : Dimethyl:2H(4) (K)
Ions Score: 46 Expect: 0.72
Matches : 26/162 fragment ions using 36 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 104.1008 | 52.5540 | | | | | A | | | | | | | 17 |
| 2 | 161.1223 | 81.0648 | | | | | G | 1687.9778 | 844.4926 | 1670.9513 | 835.9793 | 1669.9673 | 835.4873 | 16 |
| 3 | 260.1907 | 130.5990 | | | | | V | 1630.9564 | 815.9818 | 1613.9298 | 807.4686 | 1612.9458 | 806.9765 | 15 |
| 4 | 361.2384 | 181.1228 | | | 343.2278 | 172.1175 | T | 1531.8880 | 766.4476 | 1514.8614 | 757.9343 | 1513.8774 | 757.4423 | 14 |
| 5 | 460.3068 | 230.6570 | | | 442.2962 | 221.6517 | V | 1430.8403 | 715.9238 | 1413.8137 | 707.4105 | 1412.8297 | 706.9185 | 13 |
| 6 | 575.3337 | 288.1705 | | | 557.3231 | 279.1652 | D | 1331.7719 | 666.3896 | 1314.7453 | 657.8763 | 1313.7613 | 657.3843 | 12 |
| 7 | 704.3763 | 352.6918 | | | 686.3657 | 343.6865 | E | 1216.7449 | 608.8761 | 1199.7184 | 600.3628 | 1198.7344 | 599.8708 | 11 |
| 8 | 817.4604 | 409.2338 | | | 799.4498 | 400.2285 | L | 1087.7023 | 544.3548 | 1070.6758 | 535.8415 | 1069.6918 | 535.3495 | 10 |
| 9 | 874.4818 | 437.7446 | | | 856.4713 | 428.7393 | G | 974.6183 | 487.8128 | 957.5917 | 479.2995 | 956.6077 | 478.8075 | 9 |
| 10 | 1034.6332 | 517.8202 | 1017.6067 | 509.3070 | 1016.6226 | 508.8150 | K | 917.5968 | 459.3020 | 900.5703 | 450.7888 | 899.5862 | 450.2968 | 8 |
| 11 | 1133.7016 | 567.3544 | 1116.6751 | 558.8412 | 1115.6911 | 558.3492 | V | 757.4454 | 379.2264 | 740.4189 | 370.7131 | 739.4349 | 370.2211 | 7 |
| 12 | 1246.7857 | 623.8965 | 1229.7591 | 615.3832 | 1228.7751 | 614.8912 | L | 658.3770 | 329.6921 | 641.3505 | 321.1789 | 640.3665 | 320.6869 | 6 |
| 13 | 1347.8334 | 674.4203 | 1330.8068 | 665.9070 | 1329.8228 | 665.4150 | T | 545.2930 | 273.1501 | 528.2664 | 264.6368 | 527.2824 | 264.1448 | 5 |
| 14 | 1444.8861 | 722.9467 | 1427.8596 | 714.4334 | 1426.8756 | 713.9414 | P | 444.2453 | 222.6263 | 427.2187 | 214.1130 | 426.2347 | 213.6210 | 4 |
| 15 | 1545.9338 | 773.4705 | 1528.9073 | 764.9573 | 1527.9232 | 764.4653 | T | 347.1925 | 174.0999 | 330.1660 | 165.5866 | 329.1819 | 165.0946 | 3 |
| 16 | 1673.9924 | 837.4998 | 1656.9658 | 828.9866 | 1655.9818 | 828.4945 | Q | 246.1448 | 123.5761 | 229.1183 | 115.0628 | | | 2 |
| 17 | | | | | | | V | 118.0863 | 59.5468 | | | | | 1 |



NCBI **BLAST** search of [AGVTVDELGKVLTPQV](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|--------|-----------------------------------|
| 46.4 | 1790.0641 | 0.0028 | AGVTVDELGKVLTPQV |
| 31.2 | 1789.8743 | 0.1927 | QLLSMGVFSRVTTYD |
| 24.4 | 1789.9798 | 0.0872 | ALANTLVALQMGVSVVD |
| 24.3 | 1789.8954 | 0.1716 | NGSLPCMESAVLTAAQI |
| 22.7 | 1789.9911 | 0.0759 | SNQHGIRRNLTAAALGL |
| 20.6 | 1789.7968 | 0.2701 | EPETMETKSVTDYE |
| 20.6 | 1790.0454 | 0.0215 | LPYTFGGGKLNRIK |
| 20.6 | 1789.9032 | 0.1637 | MPETITSRDAARFPI |
| 20.6 | 1789.9761 | 0.0909 | KCNTLFVVDVQTGRI |
| 20.4 | 1790.0275 | 0.0395 | REGLSRQHVLTIRIV |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DDYVPKLYEOLSGK**

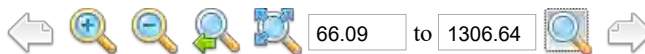
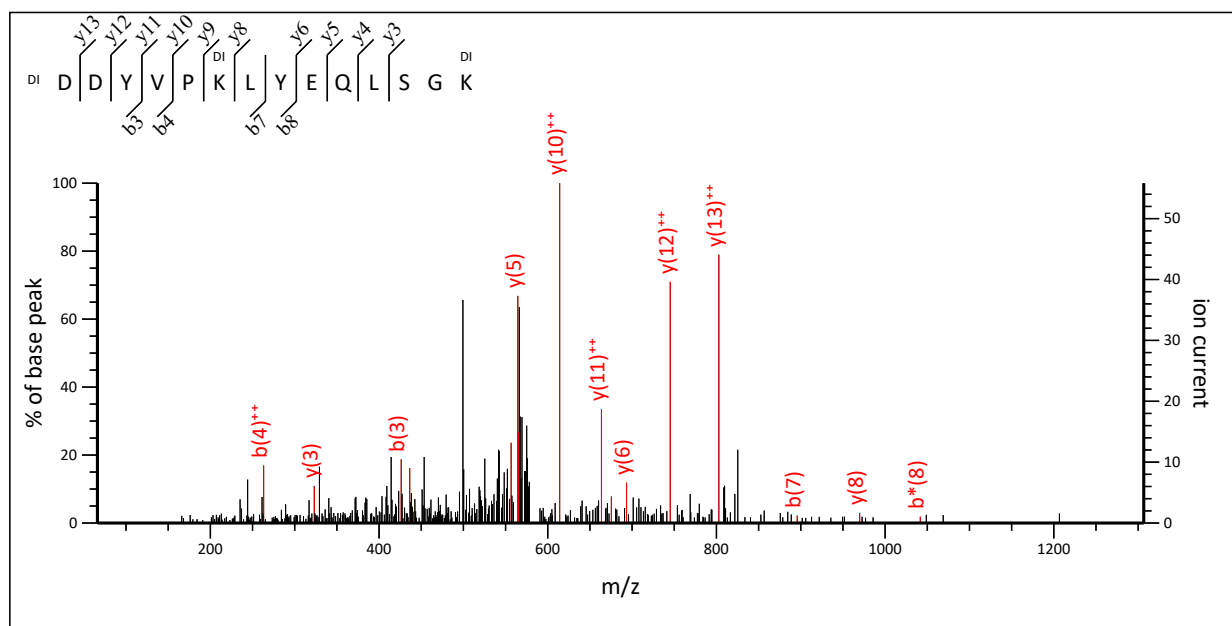
Found in **PEBP1 MOUSE** in **SwissProt**, Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=3

Match to Query 6409: 1750.006752 from(584.342860,3+) intensity(34890.2810) scans(8909) rawscans(sn8909) rtinseconds(3350.4485) index(6358)

Title: 6359: Scan 8909 (rt=3350.45) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR

NOVAMENTE\HIPOCAMPO\hipocampo 01.raw]

Data file hipocampo_01.temp.mgf



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1749.9942

Variable modifications:

N-term : Dimethyl:2H(4) (N-term)

K6 : Dimethyl:2H(4) (K)

```

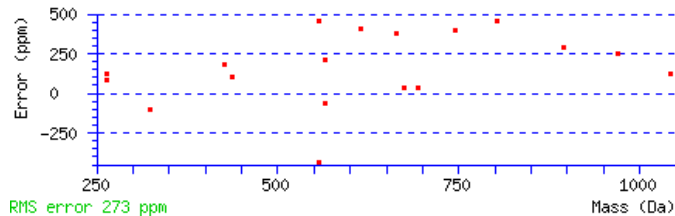
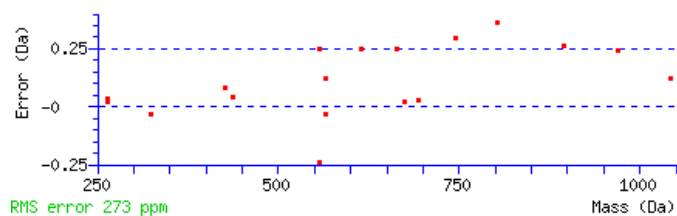
K14      : Dimethyl:2H(4) (K)

```

Ions Score: 28 Expect: 45

Matches : 18/142 fragment ions using 38 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b* | b ^{*++} | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y* | y ^{*++} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|-----------|------------------|----------------|------------------|------|-----------|-----------------|-----------|------------------|----------------|------------------|----|
| 1 | 148.0906 | 74.5490 | | | 130.0801 | 65.5437 | D | | | | | | | 14 |
| 2 | 263.1176 | 132.0624 | | | 245.1070 | 123.0571 | D | 1603.9182 | 802.4627 | 1586.8916 | 793.9494 | 1585.9076 | 793.4574 | 13 |
| 3 | 426.1809 | 213.5941 | | | 408.1703 | 204.5888 | Y | 1488.8912 | 744.9492 | 1471.8647 | 736.4360 | 1470.8806 | 735.9440 | 12 |
| 4 | 525.2493 | 263.1283 | | | 507.2387 | 254.1230 | V | 1325.8279 | 663.4176 | 1308.8013 | 654.9043 | 1307.8173 | 654.4123 | 11 |
| 5 | 622.3021 | 311.6547 | | | 604.2915 | 302.6494 | P | 1226.7595 | 613.8834 | 1209.7329 | 605.3701 | 1208.7489 | 604.8781 | 10 |
| 6 | 782.4534 | 391.7304 | 765.4269 | 383.2171 | 764.4429 | 382.7251 | K | 1129.7067 | 565.3570 | 1112.6802 | 556.8437 | 1111.6961 | 556.3517 | 9 |
| 7 | 895.5375 | 448.2724 | 878.5110 | 439.7591 | 877.5269 | 439.2671 | L | 969.5553 | 485.2813 | 952.5288 | 476.7680 | 951.5448 | 476.2760 | 8 |
| 8 | 1058.6008 | 529.8041 | 1041.5743 | 521.2908 | 1040.5903 | 520.7988 | Y | 856.4713 | 428.7393 | 839.4447 | 420.2260 | 838.4607 | 419.7340 | 7 |
| 9 | 1187.6434 | 594.3254 | 1170.6169 | 585.8121 | 1169.6329 | 585.3201 | E | 693.4079 | 347.2076 | 676.3814 | 338.6943 | 675.3974 | 338.2023 | 6 |
| 10 | 1315.7020 | 658.3546 | 1298.6755 | 649.8414 | 1297.6914 | 649.3494 | Q | 564.3653 | 282.6863 | 547.3388 | 274.1730 | 546.3548 | 273.6810 | 5 |
| 11 | 1428.7861 | 714.8967 | 1411.7595 | 706.3834 | 1410.7755 | 705.8914 | L | 436.3068 | 218.6570 | 419.2802 | 210.1437 | 418.2962 | 209.6517 | 4 |
| 12 | 1515.8181 | 758.4127 | 1498.7916 | 749.8994 | 1497.8075 | 749.4074 | S | 323.2227 | 162.1150 | 306.1962 | 153.6017 | 305.2121 | 153.1097 | 3 |
| 13 | 1572.8396 | 786.9234 | 1555.8130 | 778.4101 | 1554.8290 | 777.9181 | G | 236.1907 | 118.5990 | 219.1641 | 110.0857 | | | 2 |
| 14 | | | | | | | K | 179.1692 | 90.0882 | 162.1427 | 81.5750 | | | 1 |



NCBI **BLAST** search of [DDYVPKLYEQLSGK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-----------------------------------|
| 28.5 | 1749.9942 | 0.0125 | DDYVPKLYEQLSGK |
| 22.5 | 1749.8537 | 0.1531 | MLAKSAMPYVMMNE |
| 17.6 | 1749.9440 | 0.0627 | VVLSPYELKVYYED |
| 15.1 | 1749.9988 | 0.0079 | PRKAVPGNSFTYVNE |
| 14.9 | 1749.7377 | 0.2691 | HPSSSVSSSPSQMDHH |
| 14.4 | 1749.9245 | 0.0823 | KSTTVQVPMMHQL |
| 14.1 | 1749.7433 | 0.2635 | DDGAVFLAACSSGDTDE |
| 13.3 | 1750.0866 | -0.0799 | FLKAGTVCRKEKNE |
| 13.2 | 1749.6323 | 0.3745 | MSGMMMSHMSQASMQ |
| 13.2 | 1750.0792 | -0.0725 | AAHLGKKARGKEADE |

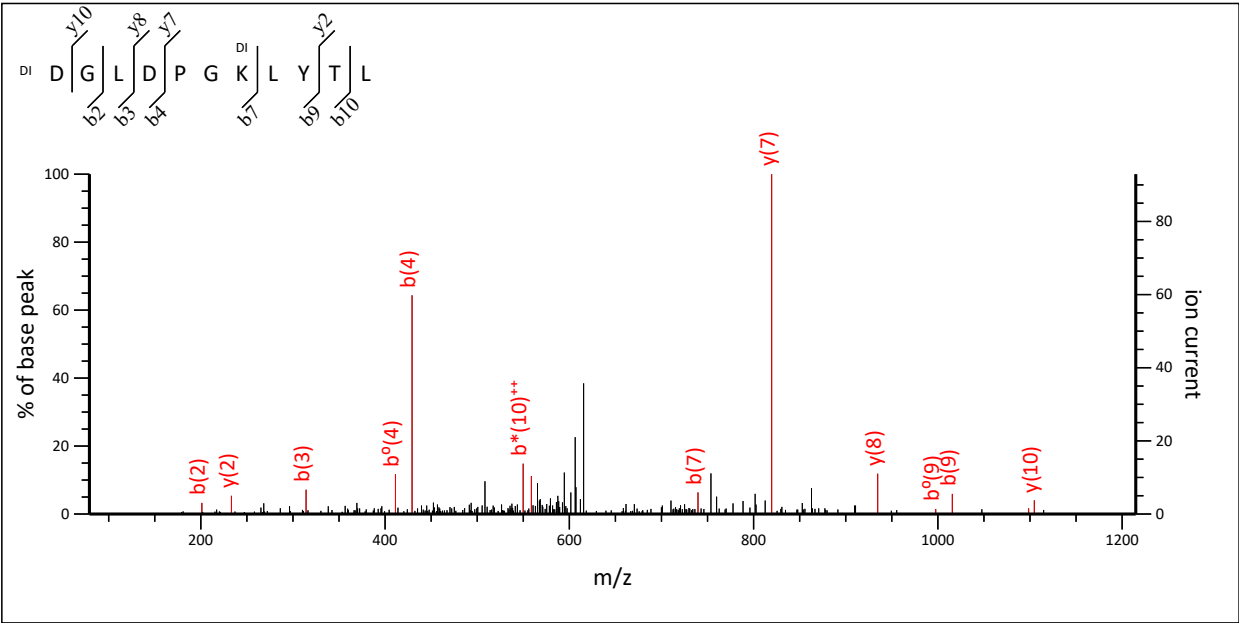
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DGLDPGKLYTL**
Found in **PEBP1_MOUSE** in **SwissProt**, Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=3

Match to Query 3369: 1246.687088 from(624.350820,2+) intensity(21610.6190) scans(9057) rawscans(sn9057) rtinseconds(3452.6934) index(6450)
Title: 6451: Scan 9057 (rt=3452.69) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_02.raw]
Data file hipocampo_02.temp.mgf

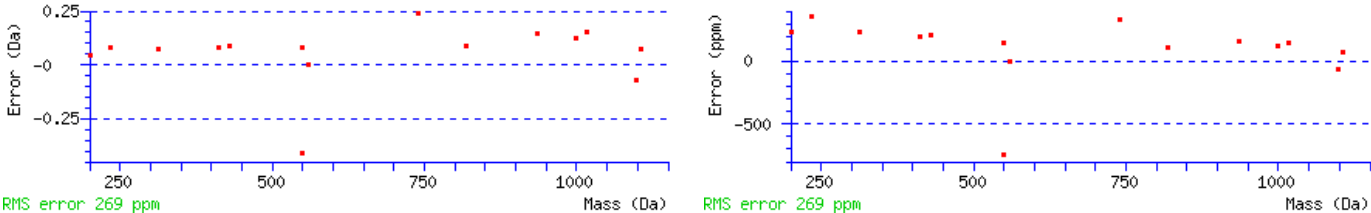


Navigation icons: ? (help), zoom in, zoom out, zoom reset, pan, 79.08 to 1214.8, zoom reset, pan.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1246.6809
Variable modifications:
N-term : Dimethyl (N-term)
K7 : Dimethyl (K)
Ions Score: 34 Expect: 11
Matches : 15/98 fragment ions using 20 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 144.0655 | 72.5364 | | | 126.0550 | 63.5311 | D | | | | | | | 11 |
| 2 | 201.0870 | 101.0471 | | | 183.0764 | 92.0418 | G | 1104.6299 | 552.8186 | 1087.6034 | 544.3053 | 1086.6194 | 543.8133 | 10 |
| 3 | 314.1710 | 157.5892 | | | 296.1605 | 148.5839 | L | 1047.6085 | 524.3079 | 1030.5819 | 515.7946 | 1029.5979 | 515.3026 | 9 |
| 4 | 429.1980 | 215.1026 | | | 411.1874 | 206.0974 | D | 934.5244 | 467.7658 | 917.4979 | 459.2526 | 916.5138 | 458.7606 | 8 |
| 5 | 526.2508 | 263.6290 | | | 508.2402 | 254.6237 | P | 819.4975 | 410.2524 | 802.4709 | 401.7391 | 801.4869 | 401.2471 | 7 |
| 6 | 583.2722 | 292.1397 | | | 565.2617 | 283.1345 | G | 722.4447 | 361.7260 | 705.4182 | 353.2127 | 704.4341 | 352.7207 | 6 |
| 7 | 739.3985 | 370.2029 | 722.3719 | 361.6896 | 721.3879 | 361.1976 | K | 665.4232 | 333.2153 | 648.3967 | 324.7020 | 647.4127 | 324.2100 | 5 |
| 8 | 852.4825 | 426.7449 | 835.4560 | 418.2316 | 834.4720 | 417.7396 | L | 509.2970 | 255.1521 | | | 491.2864 | 246.1468 | 4 |
| 9 | 1015.5459 | 508.2766 | 998.5193 | 499.7633 | 997.5353 | 499.2713 | Y | 396.2129 | 198.6101 | | | 378.2023 | 189.6048 | 3 |
| 10 | 1116.5936 | 558.8004 | 1099.5670 | 550.2871 | 1098.5830 | 549.7951 | T | 233.1496 | 117.0784 | | | 215.1390 | 108.0731 | 2 |
| 11 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI **BLAST** search of [DGLDPGKLYTL](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-------------------------------|
| 34.4 | 1246.6809 | 0.0062 | DGLDPGKLYTL |
| 28.9 | 1246.7529 | -0.0658 | AKDLRGEMTL |
| 28.8 | 1246.6670 | 0.0201 | RSDRPAYVTI |
| 27.1 | 1246.7716 | -0.0845 | VPVMAIRDKM |
| 25.1 | 1246.7781 | -0.0910 | KIDPSMGTLTI |
| 23.7 | 1246.7166 | -0.0295 | AKDMGGQLGGLA |
| 21.8 | 1246.6769 | 0.0102 | ATINTIGTGASTI |
| 21.5 | 1246.6115 | 0.0756 | GDIPVSGMLLS |
| 19.5 | 1246.6838 | 0.0033 | PVDVADVPEGTL |
| 19.0 | 1246.5717 | 0.1153 | DQDFPSSAPTL |

Mascot: <http://www.matrixscience.com/>

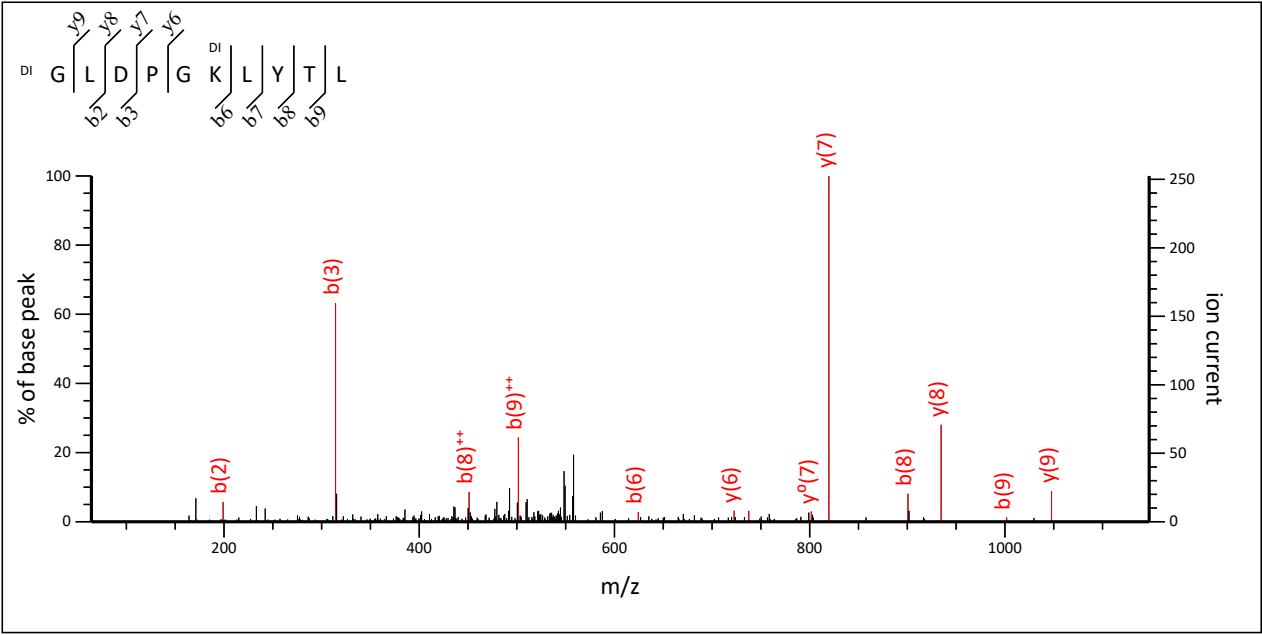
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLDPGKLYTL**
Found in **PEBP1_MOUSE** in **SwissProt**, Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=3

Match to Query 2711: 1131.658828 from(566.836690,2+) intensity(49904.5080) scans(8571) rawscans(sn8571) rtinseconds(3230.7918) index(6097)

Title: 6098: Scan 8571 (rt=3230.79) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

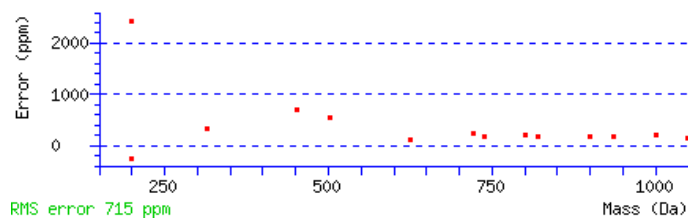
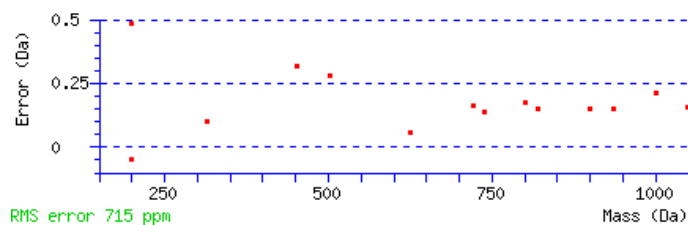


Navigation icons: ? (help), [back] (previous view), [zoom in] (magnifying glass), [zoom out] (magnifying glass), [reset] (circular arrow), [range] (input fields), [zoom in] (magnifying glass), [next] (arrow). Range: 64.16 to 1147.76.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1131.6540
Variable modifications:
N-term : Dimethyl (N-term)
K6 : Dimethyl (K)
Ions Score: 52 Expect: 0.18
Matches : 14/84 fragment ions using 18 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 86.0600 | 43.5337 | | | | | G | | | | | | | 10 |
| 2 | 199.1441 | 100.0757 | | | | | L | 1047.6085 | 524.3079 | 1030.5819 | 515.7946 | 1029.5979 | 515.3026 | 9 |
| 3 | 314.1710 | 157.5892 | | | 296.1605 | 148.5839 | D | 934.5244 | 467.7658 | 917.4979 | 459.2526 | 916.5138 | 458.7606 | 8 |
| 4 | 411.2238 | 206.1155 | | | 393.2132 | 197.1103 | P | 819.4975 | 410.2524 | 802.4709 | 401.7391 | 801.4869 | 401.2471 | 7 |
| 5 | 468.2453 | 234.6263 | | | 450.2347 | 225.6210 | G | 722.4447 | 361.7260 | 705.4182 | 353.2127 | 704.4341 | 352.7207 | 6 |
| 6 | 624.3715 | 312.6894 | 607.3450 | 304.1761 | 606.3610 | 303.6841 | K | 665.4232 | 333.2153 | 648.3967 | 324.7020 | 647.4127 | 324.2100 | 5 |
| 7 | 737.4556 | 369.2314 | 720.4291 | 360.7182 | 719.4450 | 360.2262 | L | 509.2970 | 255.1521 | | | 491.2864 | 246.1468 | 4 |
| 8 | 900.5189 | 450.7631 | 883.4924 | 442.2498 | 882.5084 | 441.7578 | Y | 396.2129 | 198.6101 | | | 378.2023 | 189.6048 | 3 |
| 9 | 1001.5666 | 501.2869 | 984.5401 | 492.7737 | 983.5560 | 492.2817 | T | 233.1496 | 117.0784 | | | 215.1390 | 108.0731 | 2 |
| 10 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI **BLAST** search of [GLDPGKLYTL](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

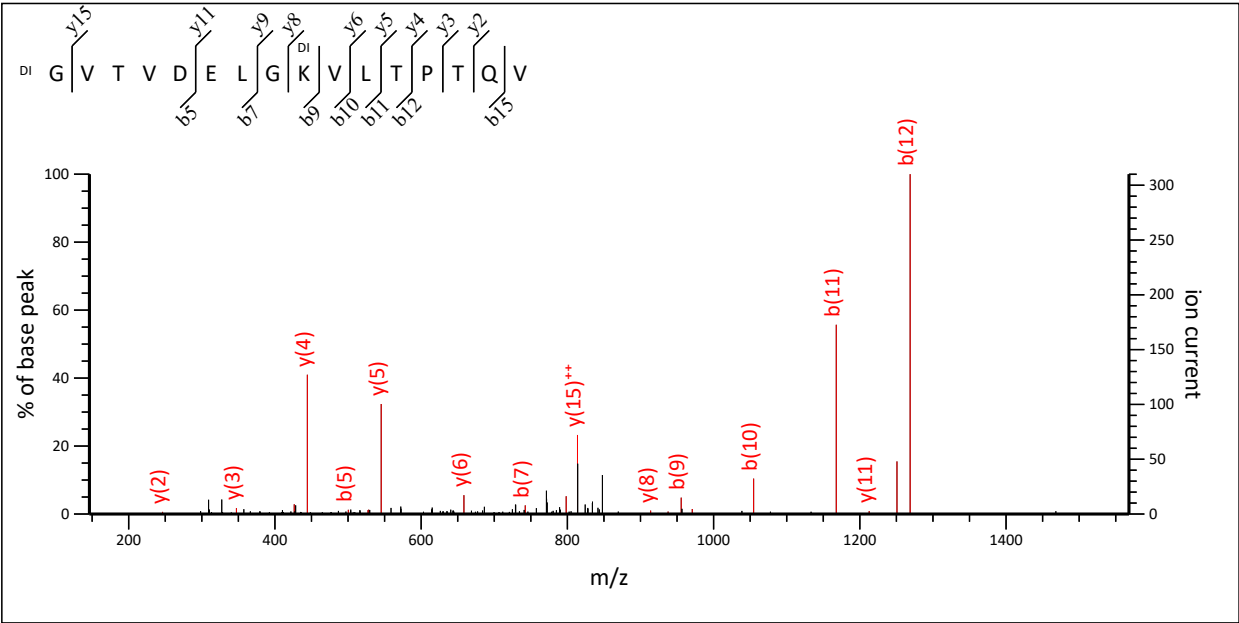
| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-----------------------------|
| 52.2 | 1131.6540 | 0.0049 | GLDPGKLYTL |
| 33.0 | 1131.4794 | 0.1794 | QDYMFETL |
| 29.4 | 1131.5448 | 0.1140 | QDFPSSAPTL |
| 24.9 | 1131.5772 | 0.0816 | ERVGDGVTTI |
| 24.9 | 1131.6135 | 0.0453 | GLDRSLETLT |
| 24.4 | 1131.5875 | 0.0714 | SMVSSGSSVTL |
| 23.6 | 1131.6023 | 0.0565 | EKVQEETTL |
| 23.3 | 1131.5295 | 0.1293 | QDSEGDVLSL |
| 21.9 | 1131.7355 | -0.0766 | ALPSPIEKTI |
| 21.8 | 1131.5560 | 0.1028 | GIPDDRDGLF |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVTVDLGKVLTPQV**
Found in **PEBP1_MOUSE** in **SwissProt**, Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=3
Match to Query 6673: 1710.997988 from(856.506270,2+) intensity(52410.6160) scans(10133-10239) rawscans(sn10133:sn10239)
rtinseconds(3813.7829-3851.1647) index(7485)
Title: 7486: Sum of 2 scans in range 10133 (rt=3813.78) to 10239 (rt=3851.16) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf





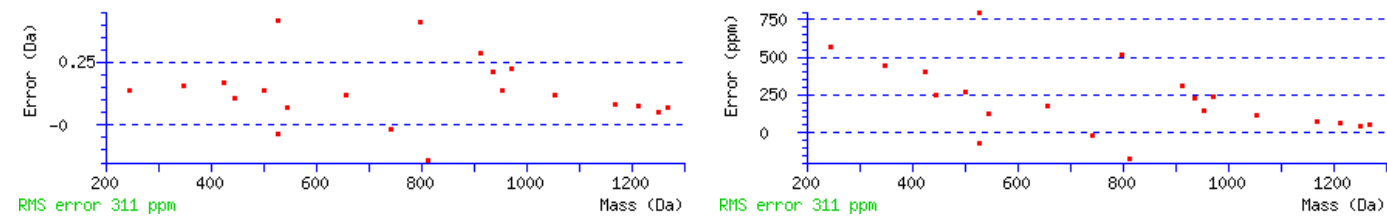
146.29 to 1568.09



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1710.9768
Variable modifications:
N-term : Dimethyl (N-term)
K9 : Dimethyl (K)
Ions Score: 34 Expect: 13
Matches : 21/154 fragment ions using 46 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 86.0600 | 43.5337 | | | | | G | | | | | | | 16 |
| 2 | 185.1285 | 93.0679 | | | | | V | 1626.9313 | 813.9693 | 1609.9047 | 805.4560 | 1608.9207 | 804.9640 | 15 |
| 3 | 286.1761 | 143.5917 | | | 268.1656 | 134.5864 | T | 1527.8629 | 764.4351 | 1510.8363 | 755.9218 | 1509.8523 | 755.4298 | 14 |
| 4 | 385.2445 | 193.1259 | | | 367.2340 | 184.1206 | V | 1426.8152 | 713.9112 | 1409.7886 | 705.3980 | 1408.8046 | 704.9059 | 13 |
| 5 | 500.2715 | 250.6394 | | | 482.2609 | 241.6341 | D | 1327.7468 | 664.3770 | 1310.7202 | 655.8637 | 1309.7362 | 655.3717 | 12 |
| 6 | 629.3141 | 315.1607 | | | 611.3035 | 306.1554 | E | 1212.7198 | 606.8635 | 1195.6933 | 598.3503 | 1194.7093 | 597.8583 | 11 |
| 7 | 742.3981 | 371.7027 | | | 724.3876 | 362.6974 | L | 1083.6772 | 542.3423 | 1066.6507 | 533.8290 | 1065.6667 | 533.3370 | 10 |
| 8 | 799.4196 | 400.2134 | | | 781.4090 | 391.2082 | G | 970.5932 | 485.8002 | 953.5666 | 477.2869 | 952.5826 | 476.7949 | 9 |
| 9 | 955.5459 | 478.2766 | 938.5193 | 469.7633 | 937.5353 | 469.2713 | K | 913.5717 | 457.2895 | 896.5451 | 448.7762 | 895.5611 | 448.2842 | 8 |
| 10 | 1054.6143 | 527.8108 | 1037.5877 | 519.2975 | 1036.6037 | 518.8055 | V | 757.4454 | 379.2264 | 740.4189 | 370.7131 | 739.4349 | 370.2211 | 7 |
| 11 | 1167.6984 | 584.3528 | 1150.6718 | 575.8395 | 1149.6878 | 575.3475 | L | 658.3770 | 329.6921 | 641.3505 | 321.1789 | 640.3665 | 320.6869 | 6 |
| 12 | 1268.7460 | 634.8767 | 1251.7195 | 626.3634 | 1250.7355 | 625.8714 | T | 545.2930 | 273.1501 | 528.2664 | 264.6368 | 527.2824 | 264.1448 | 5 |
| 13 | 1365.7988 | 683.4030 | 1348.7722 | 674.8898 | 1347.7882 | 674.3978 | P | 444.2453 | 222.6263 | 427.2187 | 214.1130 | 426.2347 | 213.6210 | 4 |
| 14 | 1466.8465 | 733.9269 | 1449.8199 | 725.4136 | 1448.8359 | 724.9216 | T | 347.1925 | 174.0999 | 330.1660 | 165.5866 | 329.1819 | 165.0946 | 3 |
| 15 | 1594.9051 | 797.9562 | 1577.8785 | 789.4429 | 1576.8945 | 788.9509 | Q | 246.1448 | 123.5761 | 229.1183 | 115.0628 | | | 2 |
| 16 | | | | | | | V | 118.0863 | 59.5468 | | | | | 1 |



NCBI BLAST search of [GVTVDELGKVLTPQTQV](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|------------------------------------|
| 33.9 | 1710.9768 | 0.0212 | GVTVDELGKVLTPQTQV |
| 29.5 | 1710.8788 | 0.1192 | SAQSSPQQAVLTIPSQ |
| 23.7 | 1710.9264 | 0.0716 | QLSSTLKRYTESSR |
| 22.0 | 1710.8611 | 0.1369 | LLGCENELGPITPGRD |
| 22.0 | 1711.0402 | -0.0422 | MRYHKAHLTRRL |
| 21.8 | 1710.7957 | 0.2023 | QLMQYDQCLTKGPD |
| 21.8 | 1711.0433 | -0.0454 | QLGLVDSLVLPLGILGSV |
| 21.1 | 1710.9930 | 0.0050 | GLGLATLVSETNRVLH |
| 21.1 | 1710.8976 | 0.1003 | ILMTLVLFPPDMLG |
| 21.1 | 1711.0535 | -0.0556 | LIFTIVVDILGNLLV |

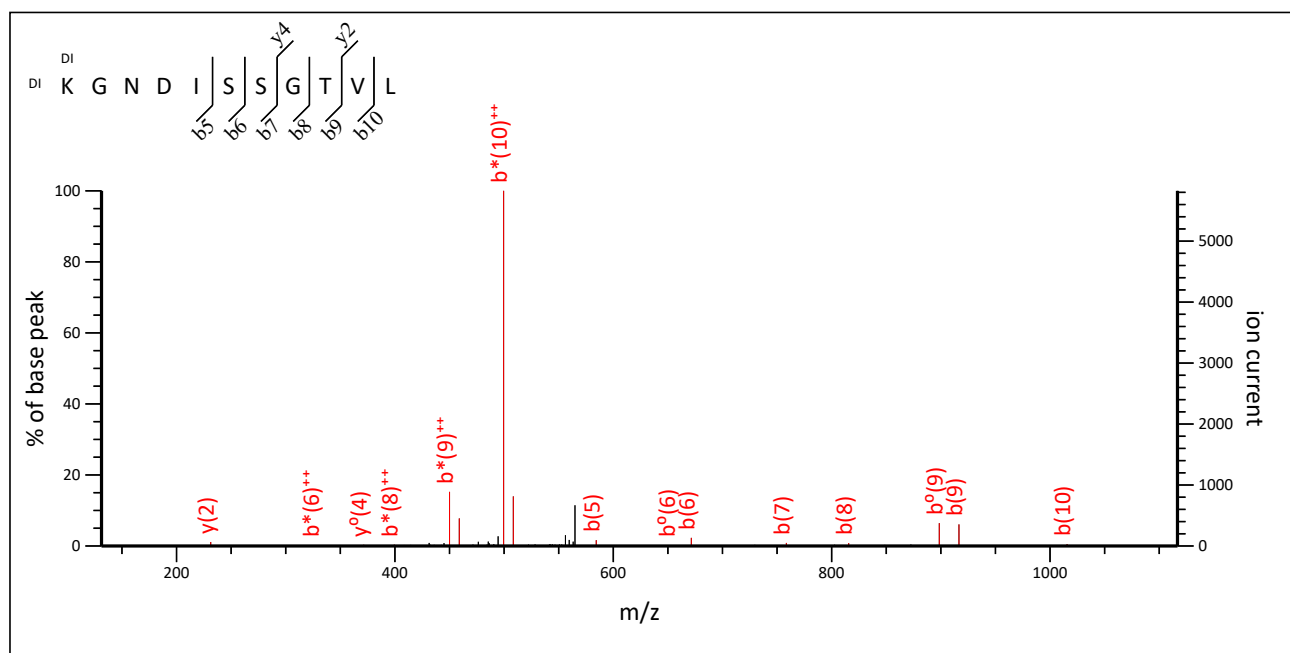
Mascot: <http://www.matrixscience.com/>

11/11/2019

MS/MS Fragmentation of **KGNDISSGTVL**

Found in **PEBP1 MOUSE** in **SwissProt**, Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=3

Title: 2986: Scan 6352 (rt=2247.29) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR
NOVAMENTE\HIPOCAMPO\hipocampo_04.raw]
Data file hipocampo_04.temp.mgf



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1145.6292

Variable modifications:

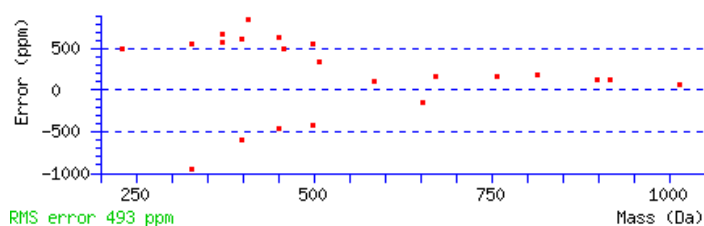
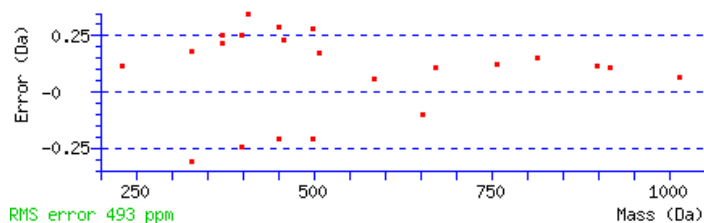
N-term : Dimethyl (N-term)

K1 : Dimethyl (K)

Ions Score: 38 Expect: 4.4

Matches : 22/94 fragment ions using 30 most intense peaks ([help](#))

| # | b | b⁺⁺ | b* | b^{*++} | b⁰ | b⁰⁺⁺ | Seq. | y | y ⁺⁺ | y* | y ^{*++} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------------|-----------|------------------------|----------------------|------------------------|------|----------|-----------------|----------|------------------|----------------|------------------|----|
| 1 | 185.1648 | 93.0861 | 168.1383 | 84.5728 | | | K | | | | | | | 11 |
| 2 | 242.1863 | 121.5968 | 225.1598 | 113.0835 | | | G | 962.4789 | 481.7431 | 945.4524 | 473.2298 | 944.4684 | 472.7378 | 10 |
| 3 | 356.2292 | 178.6183 | 339.2027 | 170.1050 | | | N | 905.4575 | 453.2324 | 888.4309 | 444.7191 | 887.4469 | 444.2271 | 9 |
| 4 | 471.2562 | 236.1317 | 454.2296 | 227.6185 | 453.2456 | 227.1264 | D | 791.4145 | 396.2109 | | | 773.4040 | 387.2056 | 8 |
| 5 | 584.3402 | 292.6738 | 567.3137 | 284.1605 | 566.3297 | 283.6685 | I | 676.3876 | 338.6974 | | | 658.3770 | 329.6921 | 7 |
| 6 | 671.3723 | 336.1898 | 654.3457 | 327.6765 | 653.3617 | 327.1845 | S | 563.3035 | 282.1554 | | | 545.2930 | 273.1501 | 6 |
| 7 | 758.4043 | 379.7058 | 741.3777 | 371.1925 | 740.3937 | 370.7005 | S | 476.2715 | 238.6394 | | | 458.2609 | 229.6341 | 5 |
| 8 | 815.4258 | 408.2165 | 798.3992 | 399.7032 | 797.4152 | 399.2112 | G | 389.2395 | 195.1234 | | | 371.2289 | 186.1181 | 4 |
| 9 | 916.4734 | 458.7404 | 899.4469 | 450.2271 | 898.4629 | 449.7351 | T | 332.2180 | 166.6126 | | | 314.2074 | 157.6074 | 3 |
| 10 | 1015.5419 | 508.2746 | 998.5153 | 499.7613 | 997.5313 | 499.2693 | V | 231.1703 | 116.0888 | | | | | 2 |
| 11 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI **BLAST** search of [KGNDISSGTVL](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-------------------------------|
| 49.1 | 1145.7383 | -0.0932 | YIHGKSGTVL |
| 38.3 | 1145.6292 | 0.0159 | KGNDISSGTVL |
| 36.7 | 1145.5746 | 0.0705 | GVPGSDGQPGTP |
| 35.8 | 1145.6366 | 0.0085 | DVLLCVSGTVI |
| 35.7 | 1145.7048 | -0.0597 | RGFYKGTVL |
| 33.6 | 1145.7008 | -0.0557 | HTQAKQGTVL |
| 31.7 | 1145.6416 | 0.0035 | VVSAAGGACPAVL |
| 29.4 | 1145.7372 | -0.0921 | NPRGGKVTVL |
| 28.1 | 1145.5564 | 0.0887 | SGVAALGSSGTD |
| 27.9 | 1145.6747 | -0.0295 | VPERPSSAVL |

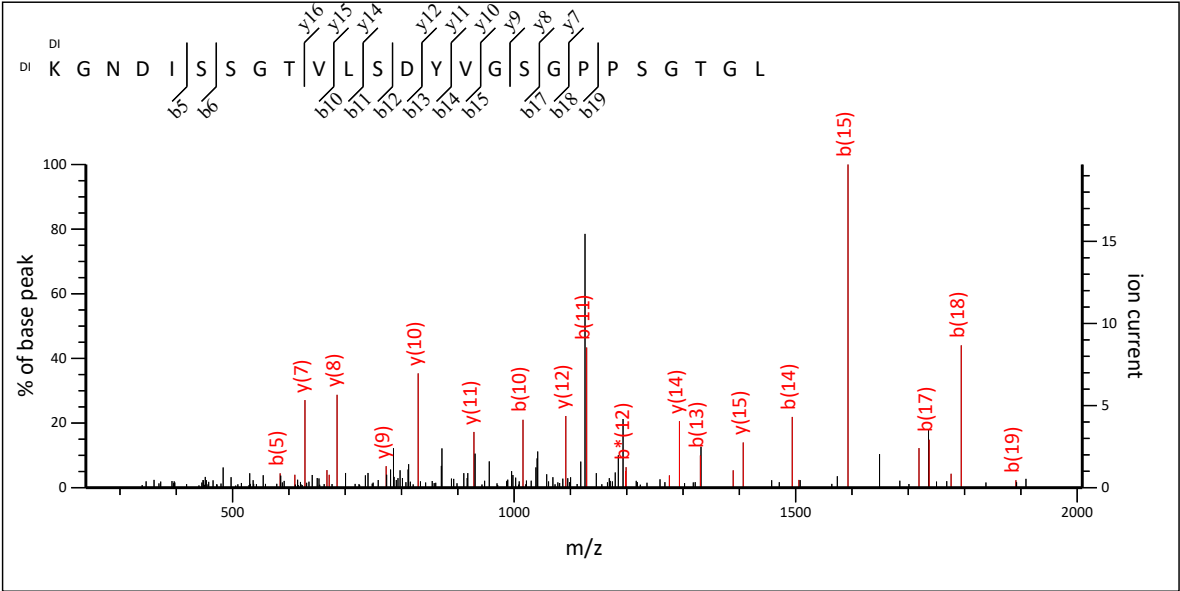
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGNDISSGTVLSDYVGSGPPSGTGL**
Found in **PEBP1_MOUSE** in **SwissProt**, Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=3

Match to Query 9731: 2420.222848 from(1211.118700,2+) intensity(5879.7676) scans(9689) rawscans(sn9689) rtinseconds(3685.0786) index(6733)
Title: 6734: Scan 9689 (rt=3685.08) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR
NOVAMENTE\ESTRIADO\estriado_01.raw]
Data file estriado_01.temp.mgf



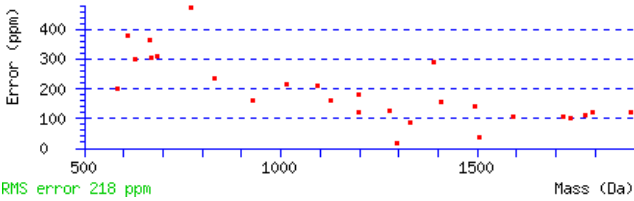
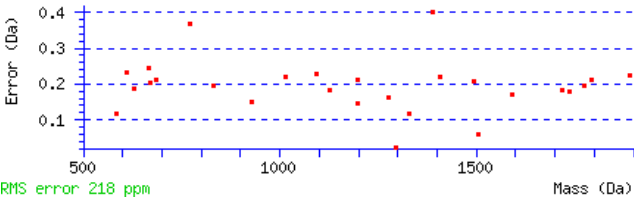
Navigation icons: ? (help), zoom in, zoom out, reset, and a range selector showing 239.42 to 2009.02.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 2420.2071
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
Ions Score: 43 Expect: 0.01
Matches : 27/234 fragment ions using 60 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺ * | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺ * | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|-------------------|----------------|------------------|------|-----------|-----------------|----------------|-------------------|----------------|------------------|----|
| 1 | 185.1648 | 93.0861 | 168.1383 | 84.5728 | | | K | | | | | | | 25 |
| 2 | 242.1863 | 121.5968 | 225.1598 | 113.0835 | | | G | 2237.0568 | 1119.0320 | 2220.0303 | 1110.5188 | 2219.0462 | 1110.0268 | 24 |
| 3 | 356.2292 | 178.6183 | 339.2027 | 170.1050 | | | N | 2180.0353 | 1090.5213 | 2163.0088 | 1082.0080 | 2162.0248 | 1081.5160 | 23 |
| 4 | 471.2562 | 236.1317 | 454.2296 | 227.6185 | 453.2456 | 227.1264 | D | 2065.9924 | 1033.4998 | | | 2047.9819 | 1024.4946 | 22 |
| 5 | 584.3402 | 292.6738 | 567.3137 | 284.1605 | 566.3297 | 283.6685 | I | 1950.9655 | 975.9864 | | | 1932.9549 | 966.9811 | 21 |
| 6 | 671.3723 | 336.1898 | 654.3457 | 327.6765 | 653.3617 | 327.1845 | S | 1837.8814 | 919.4443 | | | 1819.8709 | 910.4391 | 20 |
| 7 | 758.4043 | 379.7058 | 741.3777 | 371.1925 | 740.3937 | 370.7005 | S | 1750.8494 | 875.9283 | | | 1732.8388 | 866.9230 | 19 |
| 8 | 815.4258 | 408.2165 | 798.3992 | 399.7032 | 797.4152 | 399.2112 | G | 1663.8174 | 832.4123 | | | 1645.8068 | 823.4070 | 18 |
| 9 | 916.4734 | 458.7404 | 899.4469 | 450.2271 | 898.4629 | 449.7351 | T | 1606.7959 | 803.9016 | | | 1588.7853 | 794.8963 | 17 |
| 10 | 1015.5419 | 508.2746 | 998.5153 | 499.7613 | 997.5313 | 499.2693 | V | 1505.7482 | 753.3777 | | | 1487.7377 | 744.3725 | 16 |
| 11 | 1128.6259 | 564.8166 | 1111.5994 | 556.3033 | 1110.6153 | 555.8113 | L | 1406.6798 | 703.8435 | | | 1388.6692 | 694.8383 | 15 |
| 12 | 1215.6579 | 608.3326 | 1198.6314 | 599.8193 | 1197.6474 | 599.3273 | S | 1293.5957 | 647.3015 | | | 1275.5852 | 638.2962 | 14 |
| 13 | 1330.6849 | 665.8461 | 1313.6583 | 657.3328 | 1312.6743 | 656.8408 | D | 1206.5637 | 603.7855 | | | 1188.5531 | 594.7802 | 13 |
| 14 | 1493.7482 | 747.3777 | 1476.7217 | 738.8645 | 1475.7376 | 738.3725 | Y | 1091.5368 | 546.2720 | | | 1073.5262 | 537.2667 | 12 |
| 15 | 1592.8166 | 796.9120 | 1575.7901 | 788.3987 | 1574.8061 | 787.9067 | V | 928.4734 | 464.7404 | | | 910.4629 | 455.7351 | 11 |
| 16 | 1649.8381 | 825.4227 | 1632.8115 | 816.9094 | 1631.8275 | 816.4174 | G | 829.4050 | 415.2061 | | | 811.3945 | 406.2009 | 10 |
| 17 | 1736.8701 | 868.9387 | 1719.8436 | 860.4254 | 1718.8596 | 859.9334 | S | 772.3836 | 386.6954 | | | 754.3730 | 377.6901 | 9 |
| 18 | 1793.8916 | 897.4494 | 1776.8650 | 888.9362 | 1775.8810 | 888.4441 | G | 685.3515 | 343.1794 | | | 667.3410 | 334.1741 | 8 |
| 19 | 1890.9443 | 945.9758 | 1873.9178 | 937.4625 | 1872.9338 | 936.9705 | P | 628.3301 | 314.6687 | | | 610.3195 | 305.6634 | 7 |
| 20 | 1987.9971 | 994.5022 | 1970.9706 | 985.9889 | 1969.9865 | 985.4969 | P | 531.2773 | 266.1423 | | | 513.2667 | 257.1370 | 6 |
| 21 | 2075.0291 | 1038.0182 | 2058.0026 | 1029.5049 | 2057.0186 | 1029.0129 | S | 434.2245 | 217.6159 | | | 416.2140 | 208.6106 | 5 |
| 22 | 2132.0506 | 1066.5289 | 2115.0241 | 1058.0157 | 2114.0400 | 1057.5237 | G | 347.1925 | 174.0999 | | | 329.1819 | 165.0946 | 4 |

| | | | | | | | | | | | | | | |
|----|-----------|-----------|-----------|-----------|-----------|-----------|---|----------|----------|--|--|----------|----------|---|
| 23 | 2233.0983 | 1117.0528 | 2216.0717 | 1108.5395 | 2215.0877 | 1108.0475 | T | 290.1710 | 145.5892 | | | 272.1605 | 136.5839 | 3 |
| 24 | 2290.1197 | 1145.5635 | 2273.0932 | 1137.0502 | 2272.1092 | 1136.5582 | G | 189.1234 | 95.0653 | | | | | 2 |
| 25 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI BLAST search of [KGNDISSGTVLSDYVGSGPPSGTGL](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|---|
| 43.3 | 2420.2071 | 0.0157 | KGNDISSGTVLSDYVGSGPPSGTGL |
| 21.4 | 2420.0914 | 0.1314 | GTAMPPDDVTSLLHLGSGHDNDGA |
| 20.5 | 2420.4215 | -0.1987 | SVFLLCPWVIVLSVTTESKVE |
| 18.8 | 2420.3422 | -0.1194 | KSLVGASGGVYALMGGYFMNVIV |
| 17.3 | 2420.0910 | 0.1319 | CDTTHSNVSCLEMDVPIDLSK |
| 16.8 | 2420.2760 | -0.0532 | LLSLSTSGVLSIWDIDIITAMS |
| 16.2 | 2420.2226 | 0.0003 | QGGLVHGGSVGGLAQTNFEREGGSA |
| 16.0 | 2420.2329 | -0.0101 | RLANSTASVSRGSMQELDTLAGL |
| 15.9 | 2420.1642 | 0.0587 | KAMSSEESSNGSLSVFEFRHLQ |
| 15.7 | 2420.1244 | 0.0985 | AFPCGSDHTPSPMVSCVPLEATP |

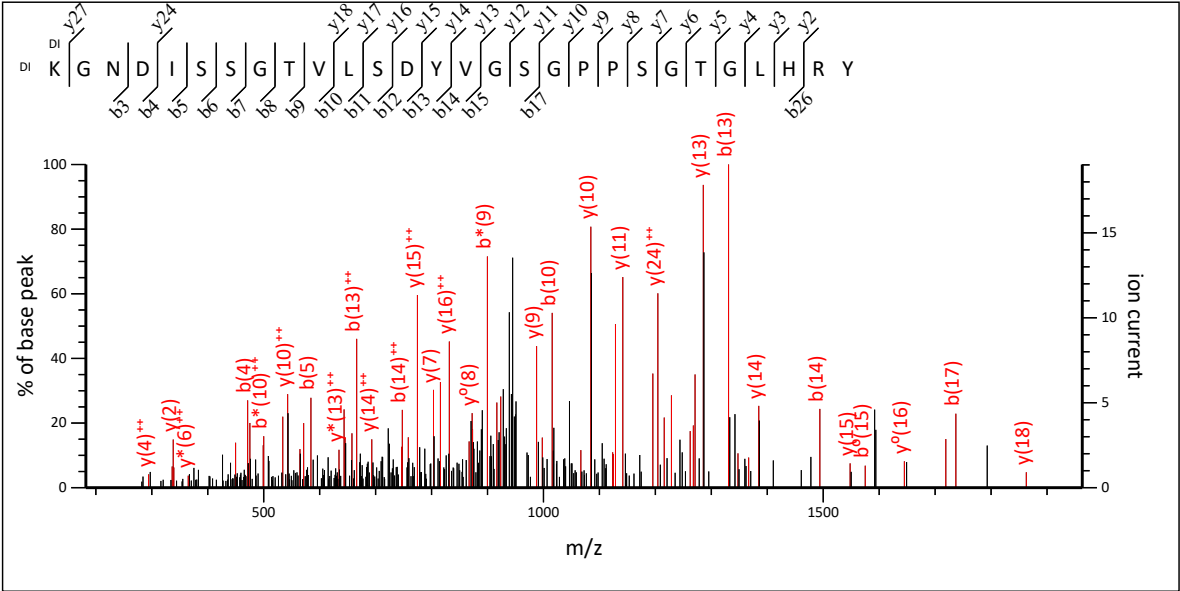
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGNDISSGTVLSDYVGSPPSGTGLHRY**
Found in **PEBP1_MOUSE** in **SwissProt**, Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=3

Match to Query 9997: 2876.458362 from(959.826730,3+) intensity(24883.7520) scans(7534) rawscans(sn7534) rtinseconds(2864.5721) index(5263)
Title: 5264: Scan 7534 (rt=2864.57) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR
NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf



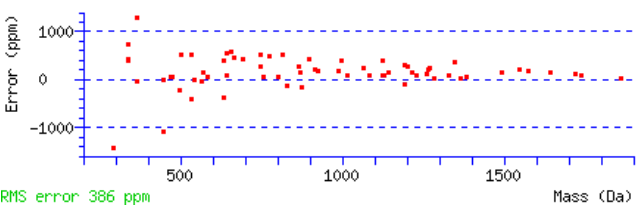
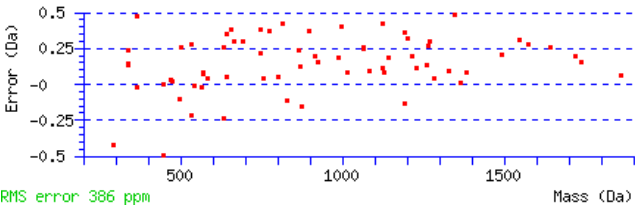
Navigation icons: ? (help), zoom in, zoom out, reset, and a range selector showing 182.18 to 1962.96.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 2876.4305
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
Ions Score: 81 Expect: 0.0003
Matches : 69/306 fragment ions using 105 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ^{*++} | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ^{*++} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 185.1648 | 93.0861 | 168.1383 | 84.5728 | | | K | | | | | | | 28 |
| 2 | 242.1863 | 121.5968 | 225.1598 | 113.0835 | | | G | 2693.2802 | 1347.1437 | 2676.2536 | 1338.6304 | 2675.2696 | 1338.1384 | 27 |
| 3 | 356.2292 | 178.6183 | 339.2027 | 170.1050 | | | N | 2636.2587 | 1318.6330 | 2619.2322 | 1310.1197 | 2618.2481 | 1309.6277 | 26 |
| 4 | 471.2562 | 236.1317 | 454.2296 | 227.6185 | 453.2456 | 227.1264 | D | 2522.2158 | 1261.6115 | 2505.1892 | 1253.0983 | 2504.2052 | 1252.6062 | 25 |
| 5 | 584.3402 | 292.6738 | 567.3137 | 284.1605 | 566.3297 | 283.6685 | I | 2407.1888 | 1204.0981 | 2390.1623 | 1195.5848 | 2389.1783 | 1195.0928 | 24 |
| 6 | 671.3723 | 336.1898 | 654.3457 | 327.6765 | 653.3617 | 327.1845 | S | 2294.1048 | 1147.5560 | 2277.0782 | 1139.0427 | 2276.0942 | 1138.5507 | 23 |
| 7 | 758.4043 | 379.7058 | 741.3777 | 371.1925 | 740.3937 | 370.7005 | S | 2207.0727 | 1104.0400 | 2190.0462 | 1095.5267 | 2189.0622 | 1095.0347 | 22 |
| 8 | 815.4258 | 408.2165 | 798.3992 | 399.7032 | 797.4152 | 399.2112 | G | 2120.0407 | 1060.5240 | 2103.0142 | 1052.0107 | 2102.0301 | 1051.5187 | 21 |
| 9 | 916.4734 | 458.7404 | 899.4469 | 450.2271 | 898.4629 | 449.7351 | T | 2063.0192 | 1032.0133 | 2045.9927 | 1023.5000 | 2045.0087 | 1023.0080 | 20 |
| 10 | 1015.5419 | 508.2746 | 998.5153 | 499.7613 | 997.5313 | 499.2693 | V | 1961.9716 | 981.4894 | 1944.9450 | 972.9761 | 1943.9610 | 972.4841 | 19 |
| 11 | 1128.6259 | 564.8166 | 1111.5994 | 556.3033 | 1110.6153 | 555.8113 | L | 1862.9032 | 931.9552 | 1845.8766 | 923.4419 | 1844.8926 | 922.9499 | 18 |
| 12 | 1215.6579 | 608.3326 | 1198.6314 | 599.8193 | 1197.6474 | 599.3273 | S | 1749.8191 | 875.4132 | 1732.7925 | 866.8999 | 1731.8085 | 866.4079 | 17 |
| 13 | 1330.6849 | 665.8461 | 1313.6583 | 657.3328 | 1312.6743 | 656.8408 | D | 1662.7871 | 831.8972 | 1645.7605 | 823.3839 | 1644.7765 | 822.8919 | 16 |
| 14 | 1493.7482 | 747.3777 | 1476.7217 | 738.8645 | 1475.7376 | 738.3725 | Y | 1547.7601 | 774.3837 | 1530.7336 | 765.8704 | 1529.7496 | 765.3784 | 15 |
| 15 | 1592.8166 | 796.9120 | 1575.7901 | 788.3987 | 1574.8061 | 787.9067 | V | 1384.6968 | 692.8520 | 1367.6702 | 684.3388 | 1366.6862 | 683.8468 | 14 |
| 16 | 1649.8381 | 825.4227 | 1632.8115 | 816.9094 | 1631.8275 | 816.4174 | G | 1285.6284 | 643.3178 | 1268.6018 | 634.8046 | 1267.6178 | 634.3125 | 13 |
| 17 | 1736.8701 | 868.9387 | 1719.8436 | 860.4254 | 1718.8596 | 859.9334 | S | 1228.6069 | 614.8071 | 1211.5804 | 606.2938 | 1210.5963 | 605.8018 | 12 |
| 18 | 1793.8916 | 897.4494 | 1776.8650 | 888.9362 | 1775.8810 | 888.4441 | G | 1141.5749 | 571.2911 | 1124.5483 | 562.7778 | 1123.5643 | 562.2858 | 11 |
| 19 | 1890.9443 | 945.9758 | 1873.9178 | 937.4625 | 1872.9338 | 936.9705 | P | 1084.5534 | 542.7803 | 1067.5269 | 534.2671 | 1066.5429 | 533.7751 | 10 |
| 20 | 1987.9971 | 994.5022 | 1970.9706 | 985.9889 | 1969.9865 | 985.4969 | P | 987.5007 | 494.2540 | 970.4741 | 485.7407 | 969.4901 | 485.2487 | 9 |
| 21 | 2075.0291 | 1038.0182 | 2058.0026 | 1029.5049 | 2057.0186 | 1029.0129 | S | 890.4479 | 445.7276 | 873.4213 | 437.2143 | 872.4373 | 436.7223 | 8 |
| 22 | 2132.0506 | 1066.5289 | 2115.0241 | 1058.0157 | 2114.0400 | 1057.5237 | G | 803.4159 | 402.2116 | 786.3893 | 393.6983 | 785.4053 | 393.2063 | 7 |

| | | | | | | | | | | | | | | |
|----|-----------|-----------|-----------|-----------|-----------|-----------|---|----------|----------|----------|----------|----------|----------|---|
| 23 | 2233.0983 | 1117.0528 | 2216.0717 | 1108.5395 | 2215.0877 | 1108.0475 | T | 746.3944 | 373.7008 | 729.3679 | 365.1876 | 728.3838 | 364.6956 | 6 |
| 24 | 2290.1197 | 1145.5635 | 2273.0932 | 1137.0502 | 2272.1092 | 1136.5582 | G | 645.3467 | 323.1770 | 628.3202 | 314.6637 | | | 5 |
| 25 | 2403.2038 | 1202.1055 | 2386.1773 | 1193.5923 | 2385.1932 | 1193.1003 | L | 588.3253 | 294.6663 | 571.2987 | 286.1530 | | | 4 |
| 26 | 2540.2627 | 1270.6350 | 2523.2362 | 1262.1217 | 2522.2522 | 1261.6297 | H | 475.2412 | 238.1242 | 458.2146 | 229.6110 | | | 3 |
| 27 | 2696.3638 | 1348.6856 | 2679.3373 | 1340.1723 | 2678.3533 | 1339.6803 | R | 338.1823 | 169.5948 | 321.1557 | 161.0815 | | | 2 |
| 28 | | | | | | | Y | 182.0812 | 91.5442 | | | | | 1 |



NCBI BLAST search of [KGNDISSGTVLSDYVGSPPSGTGLHRY](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--|
| 80.8 | 2876.4305 | 0.0279 | KGNDISSGTVLSDYVGSPPSGTGLHRY |
| 19.8 | 2876.4789 | -0.0205 | VGMLRGVGAGMRYLSDLGYIHRDLAA |
| 15.0 | 2876.4647 | -0.0063 | RSAQHPSSSDVVTYAPFTLFPSVPVPSA |
| 13.2 | 2876.3441 | 0.1143 | DLQSLCHDLGAVGGCYPEPHKHCHM |
| 13.2 | 2876.2574 | 0.2009 | GFVMDGQQHMGIRAPGMSGMGMMNMG |
| 13.2 | 2876.2574 | 0.2009 | GFVMDGQQHMGIRAPGMSGMGMMNMG |
| 11.5 | 2876.4010 | 0.0574 | DVGYRHVDTAYAYQVEEEIGQAIQS |
| 11.1 | 2876.6614 | -0.2030 | MLETYSNLVSVGYDIIKPDVIIKL |
| 11.0 | 2876.4436 | 0.0148 | TFEEKMQACDDLKTTEKLCES |
| 10.4 | 2876.5607 | -0.1023 | KGRAGESLGRNWYVTPEITITDNDL |

Mascot: <http://www.matrixscience.com/>

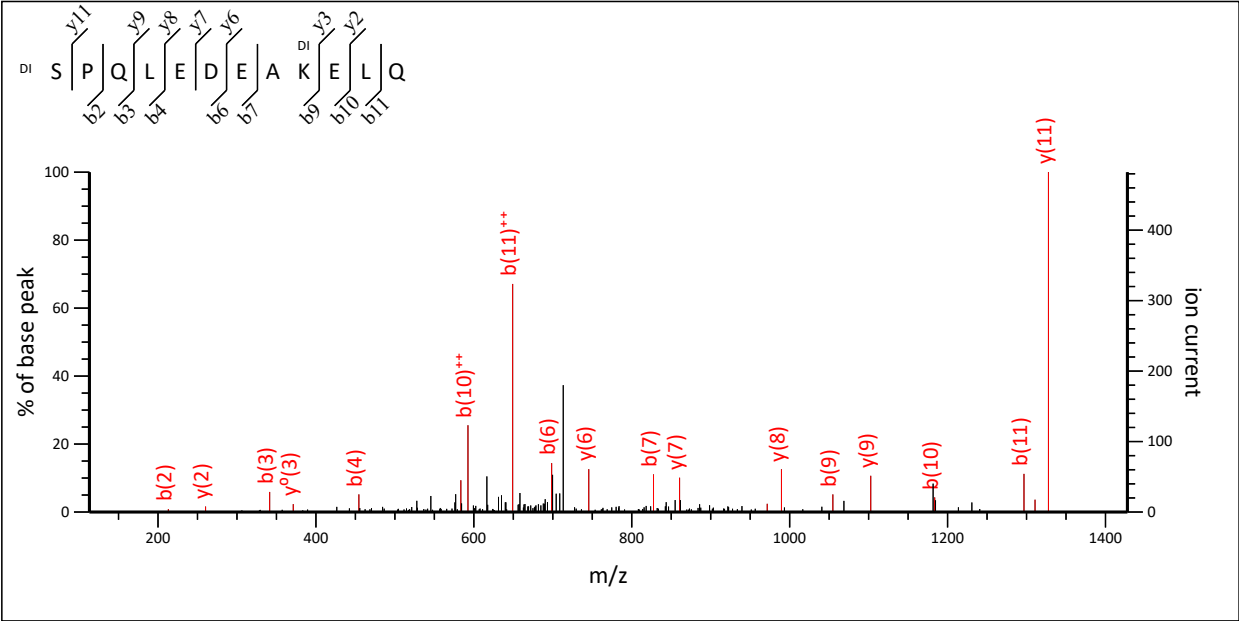
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPQLEDEAKELQ**
Found in **PENK_MOUSE** in **SwissProt**, Proenkephalin-A OS=Mus musculus GN=Penk PE=1 SV=2

Match to Query 4648: 1441.734468 from(721.874510,2+) intensity(97246.6800) scans(5703) rawscans(sn5703) rtinseconds(2225.6315) index(3634)

Title: 3635: Scan 5703 (rt=2225.63) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf





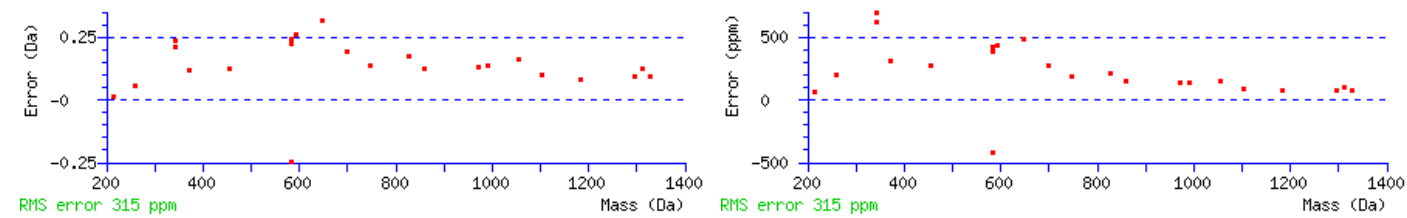
113.14 to 1427.77



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1441.7300
Variable modifications:
N-term : Dimethyl (N-term)
K9 : Dimethyl (K)
Ions Score: 91 Expect: 2.5e-005
Matches : 23/124 fragment ions using 23 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺ * | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺ * | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|-------------------|----------------|------------------|------|-----------|-----------------|----------------|-------------------|----------------|------------------|----|
| 1 | 116.0706 | 58.5389 | | | 98.0600 | 49.5337 | S | | | | | | | 12 |
| 2 | 213.1234 | 107.0653 | | | 195.1128 | 98.0600 | P | 1327.6740 | 664.3406 | 1310.6474 | 655.8274 | 1309.6634 | 655.3353 | 11 |
| 3 | 341.1819 | 171.0946 | 324.1554 | 162.5813 | 323.1714 | 162.0893 | Q | 1230.6212 | 615.8142 | 1213.5947 | 607.3010 | 1212.6107 | 606.8090 | 10 |
| 4 | 454.2660 | 227.6366 | 437.2395 | 219.1234 | 436.2554 | 218.6314 | L | 1102.5626 | 551.7850 | 1085.5361 | 543.2717 | 1084.5521 | 542.7797 | 9 |
| 5 | 583.3086 | 292.1579 | 566.2821 | 283.6447 | 565.2980 | 283.1527 | E | 989.4786 | 495.2429 | 972.4520 | 486.7297 | 971.4680 | 486.2376 | 8 |
| 6 | 698.3355 | 349.6714 | 681.3090 | 341.1581 | 680.3250 | 340.6661 | D | 860.4360 | 430.7216 | 843.4094 | 422.2084 | 842.4254 | 421.7163 | 7 |
| 7 | 827.3781 | 414.1927 | 810.3516 | 405.6794 | 809.3676 | 405.1874 | E | 745.4090 | 373.2082 | 728.3825 | 364.6949 | 727.3985 | 364.2029 | 6 |
| 8 | 898.4153 | 449.7113 | 881.3887 | 441.1980 | 880.4047 | 440.7060 | A | 616.3665 | 308.6869 | 599.3399 | 300.1736 | 598.3559 | 299.6816 | 5 |
| 9 | 1054.5415 | 527.7744 | 1037.5150 | 519.2611 | 1036.5310 | 518.7691 | K | 545.3293 | 273.1683 | 528.3028 | 264.6550 | 527.3188 | 264.1630 | 4 |
| 10 | 1183.5841 | 592.2957 | 1166.5576 | 583.7824 | 1165.5735 | 583.2904 | E | 389.2031 | 195.1052 | 372.1765 | 186.5919 | 371.1925 | 186.0999 | 3 |
| 11 | 1296.6682 | 648.8377 | 1279.6416 | 640.3245 | 1278.6576 | 639.8324 | L | 260.1605 | 130.5839 | 243.1339 | 122.0706 | | | 2 |
| 12 | | | | | | | Q | 147.0764 | 74.0418 | 130.0499 | 65.5286 | | | 1 |



NCBI **BLAST** search of [SPQLEDEAKELQ](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-------------------------------|
| 90.9 | 1441.7300 | 0.0045 | SPQLEDEAKELQ |
| 33.4 | 1441.7966 | -0.0621 | INIPLDEVGEALQ |
| 31.6 | 1441.7201 | 0.0143 | SWSRSIEDLQPP |
| 27.2 | 1441.7708 | -0.0364 | YVIPFSMGPLGSP |
| 26.2 | 1441.6333 | 0.1012 | YCNENEVGELIQ |
| 26.0 | 1441.8140 | -0.0795 | KAERDKSLELQ |
| 26.0 | 1441.8392 | -0.1047 | KLEKLSAAEEIQ |
| 26.0 | 1441.8252 | -0.0908 | RLKERSVEELQ |
| 25.8 | 1441.7235 | 0.0110 | NKLGTAMSHEIQ |
| 25.7 | 1441.6543 | 0.0802 | DYPEFPGSQNNP |

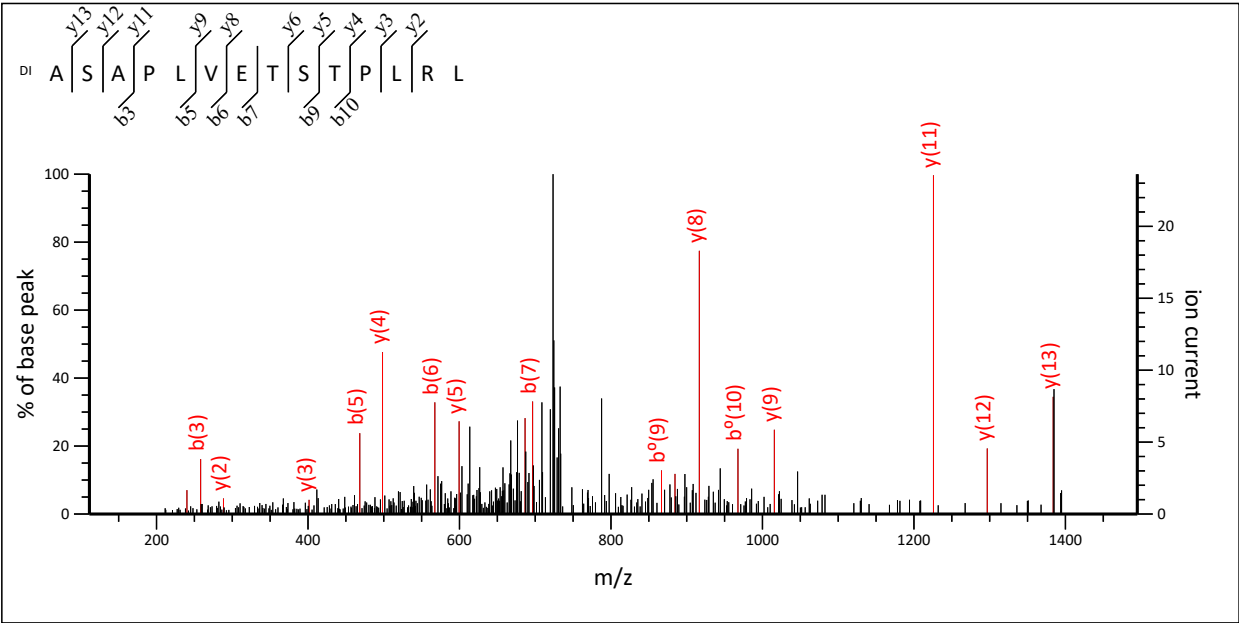
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAPLVETSTPLRL**
Found in **PCSK1_MOUSE** in **SwissProt**, ProSAAS OS=Mus musculus GN=Pcsk1n PE=1 SV=2

Match to Query 5247: 1481.858568 from(741.936560,2+) intensity(17465.0230) scans(9155) rawscans(sn9155) rtinseconds(3469.1442) index(6640)
Title: 6641: Scan 9155 (rt=3469.14) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf

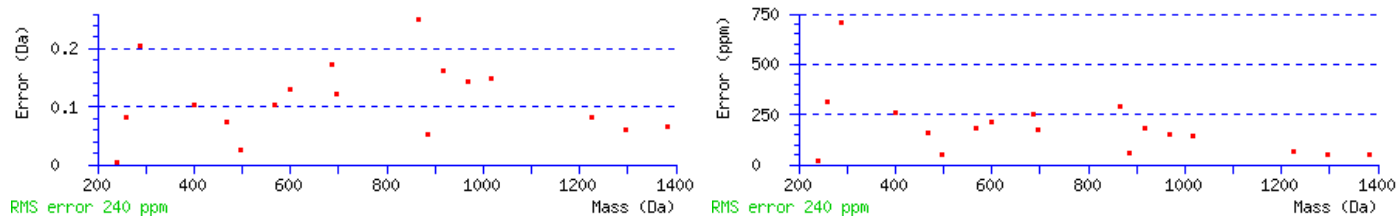


Navigation icons: ? (help), image (download), left arrow, zoom in, zoom out, zoom reset, 111.41 to 1494.92 (mass range), zoom in, right arrow.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1481.8453
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 67 Expect: 0.0056
Matches : 18/120 fragment ions using 36 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | | | A | | | | | | | 14 |
| 2 | 187.1077 | 94.0575 | | | 169.0972 | 85.0522 | S | 1383.7842 | 692.3957 | 1366.7577 | 683.8825 | 1365.7736 | 683.3905 | 13 |
| 3 | 258.1448 | 129.5761 | | | 240.1343 | 120.5708 | A | 1296.7522 | 648.8797 | 1279.7256 | 640.3665 | 1278.7416 | 639.8744 | 12 |
| 4 | 355.1976 | 178.1024 | | | 337.1870 | 169.0972 | P | 1225.7151 | 613.3612 | 1208.6885 | 604.8479 | 1207.7045 | 604.3559 | 11 |
| 5 | 468.2817 | 234.6445 | | | 450.2711 | 225.6392 | L | 1128.6623 | 564.8348 | 1111.6358 | 556.3215 | 1110.6517 | 555.8295 | 10 |
| 6 | 567.3501 | 284.1787 | | | 549.3395 | 275.1734 | V | 1015.5782 | 508.2928 | 998.5517 | 499.7795 | 997.5677 | 499.2875 | 9 |
| 7 | 696.3927 | 348.7000 | | | 678.3821 | 339.6947 | E | 916.5098 | 458.7585 | 899.4833 | 450.2453 | 898.4993 | 449.7533 | 8 |
| 8 | 797.4403 | 399.2238 | | | 779.4298 | 390.2185 | T | 787.4672 | 394.2373 | 770.4407 | 385.7240 | 769.4567 | 385.2320 | 7 |
| 9 | 884.4724 | 442.7398 | | | 866.4618 | 433.7345 | S | 686.4196 | 343.7134 | 669.3930 | 335.2001 | 668.4090 | 334.7081 | 6 |
| 10 | 985.5201 | 493.2637 | | | 967.5095 | 484.2584 | T | 599.3875 | 300.1974 | 582.3610 | 291.6841 | 581.3770 | 291.1921 | 5 |
| 11 | 1082.5728 | 541.7900 | | | 1064.5623 | 532.7848 | P | 498.3398 | 249.6736 | 481.3133 | 241.1603 | | | 4 |
| 12 | 1195.6569 | 598.3321 | | | 1177.6463 | 589.3268 | L | 401.2871 | 201.1472 | 384.2605 | 192.6339 | | | 3 |
| 13 | 1351.7580 | 676.3826 | 1334.7314 | 667.8694 | 1333.7474 | 667.3774 | R | 288.2030 | 144.6051 | 271.1765 | 136.0919 | | | 2 |
| 14 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI **BLAST** search of [ASAPLVETSTPLRL](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|---------------------------------|
| 67.4 | 1481.8453 | 0.0132 | ASAPLVETSTPLRL |
| 17.4 | 1481.6998 | 0.1588 | AGLPAEESDAQQAPA |
| 16.7 | 1481.6646 | 0.1939 | DGSLGSFTSTSNFM |
| 16.6 | 1481.8311 | 0.0274 | LPQVTWIVQYSA |
| 14.8 | 1481.7613 | 0.0972 | QVIEKTSGPEEPA |
| 14.0 | 1481.9983 | -0.1397 | AVKIMEKVVKII |
| 12.8 | 1481.6457 | 0.2129 | QPCGSQGTPTSFSSA |
| 12.8 | 1481.8541 | 0.0045 | SKSVTEGLLTQQQ |
| 12.3 | 1481.8326 | 0.0260 | RACGLLSPLSAHLA |
| 12.2 | 1481.7660 | 0.0926 | ASAPLMELLHSRN |

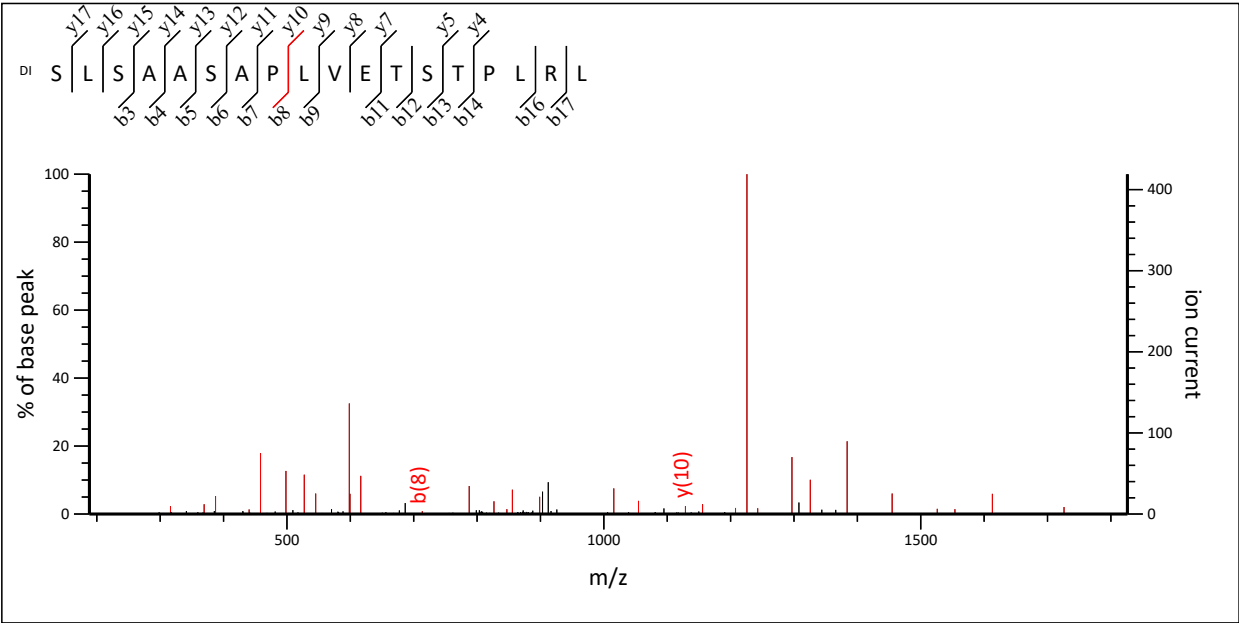
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLSAASAPLVETSTPLRL**
Found in **PCSK1_MOUSE** in **SwissProt**, ProSAAS OS=Mus musculus GN=Pcsk1n PE=1 SV=2

Match to Query 6853: 1840.034728 from(921.024640,2+) intensity(51618.4840) scans(10414) rawscans(sn10414) rtinseconds(3896.7859) index(7623)
Title: 7624: Scan 10414 (rt=3896.79) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

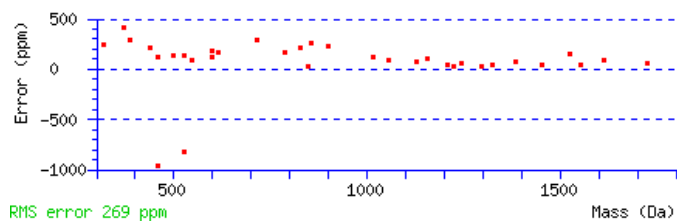
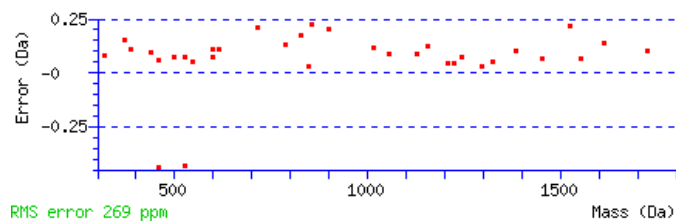


Navigation icons: ? (help), image (download), left arrow, zoom in, zoom out, zoom reset, 188.36 to 1826.08 (mass range), zoom in, right arrow.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1840.0305
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 125 Expect: 1e-008
Matches : 34/162 fragment ions using 38 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 116.0706 | 58.5389 | | | 98.0600 | 49.5337 | S | | | | | | | 18 |
| 2 | 229.1547 | 115.0810 | | | 211.1441 | 106.0757 | L | 1725.9745 | 863.4909 | 1708.9480 | 854.9776 | 1707.9640 | 854.4856 | 17 |
| 3 | 316.1867 | 158.5970 | | | 298.1761 | 149.5917 | S | 1612.8905 | 806.9489 | 1595.8639 | 798.4356 | 1594.8799 | 797.9436 | 16 |
| 4 | 387.2238 | 194.1155 | | | 369.2132 | 185.1103 | A | 1525.8584 | 763.4329 | 1508.8319 | 754.9196 | 1507.8479 | 754.4276 | 15 |
| 5 | 458.2609 | 229.6341 | | | 440.2504 | 220.6288 | A | 1454.8213 | 727.9143 | 1437.7948 | 719.4010 | 1436.8108 | 718.9090 | 14 |
| 6 | 545.2930 | 273.1501 | | | 527.2824 | 264.1448 | S | 1383.7842 | 692.3957 | 1366.7577 | 683.8825 | 1365.7736 | 683.3905 | 13 |
| 7 | 616.3301 | 308.6687 | | | 598.3195 | 299.6634 | A | 1296.7522 | 648.8797 | 1279.7256 | 640.3665 | 1278.7416 | 639.8744 | 12 |
| 8 | 713.3828 | 357.1951 | | | 695.3723 | 348.1898 | P | 1225.7151 | 613.3612 | 1208.6885 | 604.8479 | 1207.7045 | 604.3559 | 11 |
| 9 | 826.4669 | 413.7371 | | | 808.4563 | 404.7318 | L | 1128.6623 | 564.8348 | 1111.6358 | 556.3215 | 1110.6517 | 555.8295 | 10 |
| 10 | 925.5353 | 463.2713 | | | 907.5247 | 454.2660 | V | 1015.5782 | 508.2928 | 998.5517 | 499.7795 | 997.5677 | 499.2875 | 9 |
| 11 | 1054.5779 | 527.7926 | | | 1036.5673 | 518.7873 | E | 916.5098 | 458.7585 | 899.4833 | 450.2453 | 898.4993 | 449.7533 | 8 |
| 12 | 1155.6256 | 578.3164 | | | 1137.6150 | 569.3111 | T | 787.4672 | 394.2373 | 770.4407 | 385.7240 | 769.4567 | 385.2320 | 7 |
| 13 | 1242.6576 | 621.8324 | | | 1224.6470 | 612.8272 | S | 686.4196 | 343.7134 | 669.3930 | 335.2001 | 668.4090 | 334.7081 | 6 |
| 14 | 1343.7053 | 672.3563 | | | 1325.6947 | 663.3510 | T | 599.3875 | 300.1974 | 582.3610 | 291.6841 | 581.3770 | 291.1921 | 5 |
| 15 | 1440.7581 | 720.8827 | | | 1422.7475 | 711.8774 | P | 498.3398 | 249.6736 | 481.3133 | 241.1603 | | | 4 |
| 16 | 1553.8421 | 777.4247 | | | 1535.8315 | 768.4194 | L | 401.2871 | 201.1472 | 384.2605 | 192.6339 | | | 3 |
| 17 | 1709.9432 | 855.4753 | 1692.9167 | 846.9620 | 1691.9327 | 846.4700 | R | 288.2030 | 144.6051 | 271.1765 | 136.0919 | | | 2 |
| 18 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI **BLAST** search of [SLSAASAPLVETSTPLRL](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--------------------------------------|
| 124.9 | 1840.0305 | 0.0042 | SLSAASAPLVETSTPLRL |
| 30.1 | 1840.1246 | -0.0899 | PLGARRATKPLGTDRA |
| 29.4 | 1839.8879 | 0.1468 | SSSASSGPPGSSAASAPGIT |
| 27.4 | 1840.0495 | -0.0148 | PPLSATVTLTIAVSDNIP |
| 25.0 | 1840.1174 | -0.0827 | SFYVSPLKRQLVSRP |
| 24.1 | 1839.8859 | 0.1488 | QDEGPECIPPMQTVRI |
| 23.4 | 1839.9563 | 0.0784 | QLAASRGHGTCVQALTGP |
| 23.4 | 1840.1497 | -0.1149 | ASSAKMGLVETKLAIIP |
| 23.0 | 1839.9690 | 0.0657 | EAELNTRVNRQTVAASLP |
| 22.4 | 1839.9880 | 0.0467 | PGSSLPTSLTIPNPRET |

Mascot: <http://www.matrixscience.com/>

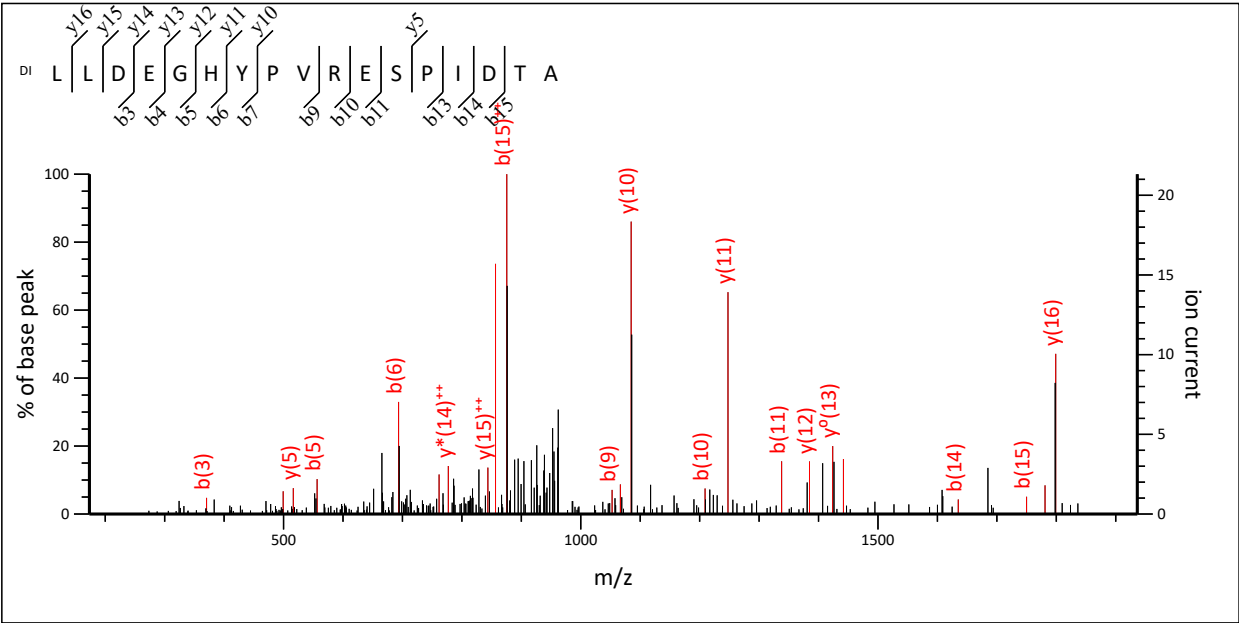
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLDEGHYPVRESPIDTA**
Found in **SCG1_MOUSE** in **SwissProt**, Secretogranin-1 OS=Mus musculus GN=Chgb PE=1 SV=2

Match to Query 7937: 1938.985088 from(970.499820,2+) intensity(10820.4620) scans(6117) rawscans(sn6117) rtinseconds(2384.1047) index(4055)

Title: 4056: Scan 6117 (rt=2384.1) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]
Data file cortex_01.temp.mgf

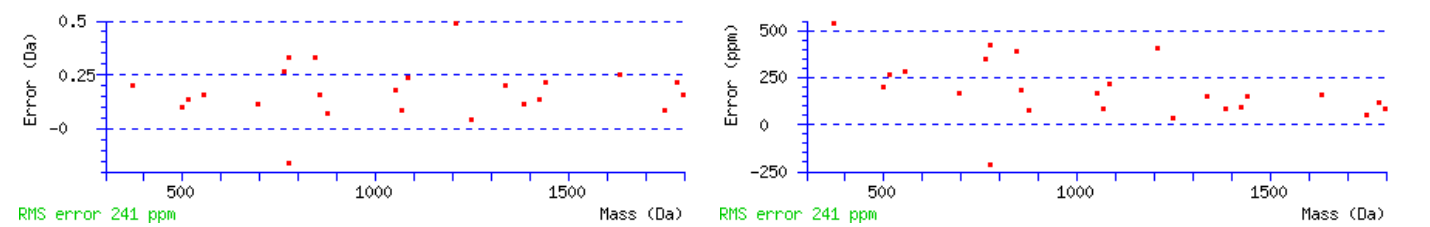


Navigation icons: ? (help), image (download), left arrow, zoom in, zoom out, zoom reset, 173.4 to 1936.29 (mass range), zoom in, right arrow.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1938.9687
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 46 Expect: 0.89
Matches : 24/154 fragment ions using 48 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 142.1226 | 71.5650 | | | | | L | | | | | | | 17 |
| 2 | 255.2067 | 128.1070 | | | | | L | 1798.8606 | 899.9339 | 1781.8341 | 891.4207 | 1780.8501 | 890.9287 | 16 |
| 3 | 370.2336 | 185.6205 | | | 352.2231 | 176.6152 | D | 1685.7766 | 843.3919 | 1668.7500 | 834.8786 | 1667.7660 | 834.3866 | 15 |
| 4 | 499.2762 | 250.1418 | | | 481.2657 | 241.1365 | E | 1570.7496 | 785.8784 | 1553.7231 | 777.3652 | 1552.7390 | 776.8732 | 14 |
| 5 | 556.2977 | 278.6525 | | | 538.2871 | 269.6472 | G | 1441.7070 | 721.3571 | 1424.6805 | 712.8439 | 1423.6965 | 712.3519 | 13 |
| 6 | 693.3566 | 347.1819 | | | 675.3461 | 338.1767 | H | 1384.6856 | 692.8464 | 1367.6590 | 684.3331 | 1366.6750 | 683.8411 | 12 |
| 7 | 856.4199 | 428.7136 | | | 838.4094 | 419.7083 | Y | 1247.6266 | 624.3170 | 1230.6001 | 615.8037 | 1229.6161 | 615.3117 | 11 |
| 8 | 953.4727 | 477.2400 | | | 935.4621 | 468.2347 | P | 1084.5633 | 542.7853 | 1067.5368 | 534.2720 | 1066.5528 | 533.7800 | 10 |
| 9 | 1052.5411 | 526.7742 | | | 1034.5306 | 517.7689 | V | 987.5106 | 494.2589 | 970.4840 | 485.7456 | 969.5000 | 485.2536 | 9 |
| 10 | 1208.6422 | 604.8248 | 1191.6157 | 596.3115 | 1190.6317 | 595.8195 | R | 888.4421 | 444.7247 | 871.4156 | 436.2114 | 870.4316 | 435.7194 | 8 |
| 11 | 1337.6848 | 669.3461 | 1320.6583 | 660.8328 | 1319.6743 | 660.3408 | E | 732.3410 | 366.6742 | | | 714.3305 | 357.6689 | 7 |
| 12 | 1424.7169 | 712.8621 | 1407.6903 | 704.3488 | 1406.7063 | 703.8568 | S | 603.2984 | 302.1529 | | | 585.2879 | 293.1476 | 6 |
| 13 | 1521.7696 | 761.3884 | 1504.7431 | 752.8752 | 1503.7591 | 752.3832 | P | 516.2664 | 258.6368 | | | 498.2558 | 249.6316 | 5 |
| 14 | 1634.8537 | 817.9305 | 1617.8271 | 809.4172 | 1616.8431 | 808.9252 | I | 419.2136 | 210.1105 | | | 401.2031 | 201.1052 | 4 |
| 15 | 1749.8806 | 875.4440 | 1732.8541 | 866.9307 | 1731.8701 | 866.4387 | D | 306.1296 | 153.5684 | | | 288.1190 | 144.5631 | 3 |
| 16 | 1850.9283 | 925.9678 | 1833.9018 | 917.4545 | 1832.9177 | 916.9625 | T | 191.1026 | 96.0550 | | | 173.0921 | 87.0497 | 2 |
| 17 | | | | | | | A | 90.0550 | 45.5311 | | | | | 1 |



NCBI BLAST search of [LLDEGHYPVRESPIDTA](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--------------------------------------|
| 45.6 | 1938.9687 | 0.0164 | LLDEGHYPVRESPIDTA |
| 10.7 | 1939.1393 | -0.1542 | TVPASAHKIDYSKRRD |
| 10.7 | 1938.9662 | 0.0189 | PPFMDGLQPGYRPVQPP |
| 10.1 | 1938.9981 | -0.0130 | ATLSHLMMPKPPNLIM |
| 9.9 | 1938.9850 | 0.0001 | SAASPAQQLPTSHPGPGPHA |
| 8.4 | 1938.8928 | 0.0923 | QVIEVACGSHHSMALAADG |
| 8.2 | 1938.9067 | 0.0784 | LNGPFTVVVKESCDGMGD |
| 7.8 | 1939.0163 | -0.0312 | QAPKASTGPHLANGYTTAV |
| 7.6 | 1938.8853 | 0.0998 | TMSGTHMVHMLCPSQVS |
| 7.2 | 1939.1583 | -0.1732 | EEIPPAVAPSIPLLLPLP |

Mascot: <http://www.matrixscience.com/>

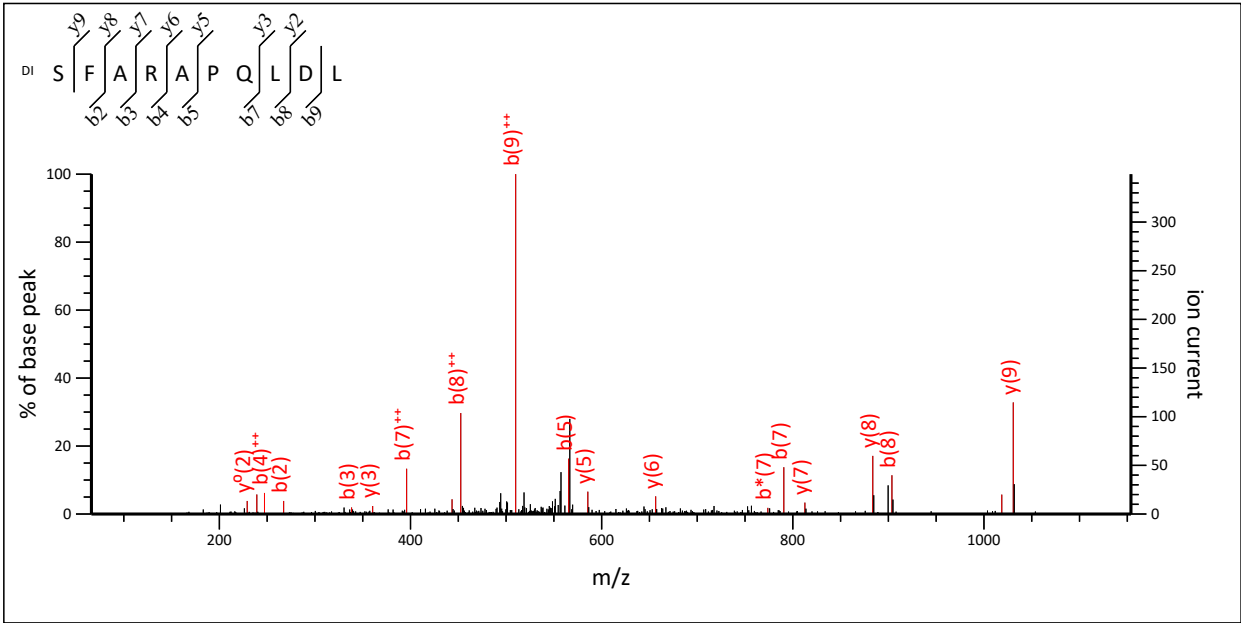
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFARAPQLDL**
Found in **SCG1_MOUSE** in **SwissProt**, Secretogranin-1 OS=Mus musculus GN=Chgb PE=1 SV=2

Match to Query 2758: 1148.654348 from(575.334450,2+) intensity(65289.3360) scans(7387) rawscans(sn7387) rtinseconds(2858.5866) index(5112)

Title: 5113: Scan 7387 (rt=2858.59) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_02.raw]
Data file hipocampo_02.temp.mgf

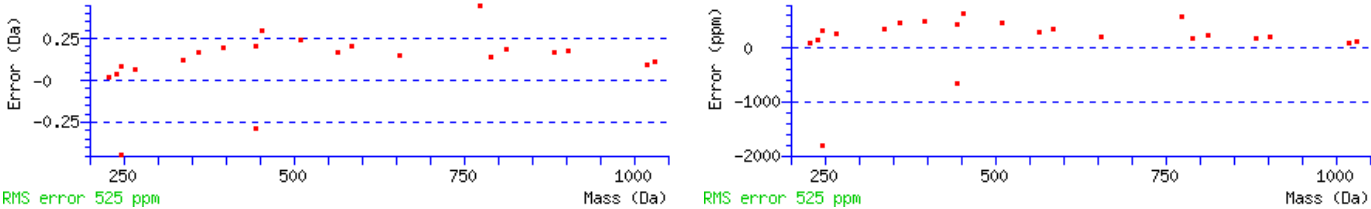


Navigation icons: ? (help), zoom in, zoom out, reset, and a range selector showing 66.13 to 1153.82.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1148.6492
Variable modifications:
N-term : Dimethyl:2H(4) (N-term)
Ions Score: 62 Expect: 0.019
Matches : 22/94 fragment ions using 27 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 120.0957 | 60.5515 | | | 102.0851 | 51.5462 | S | | | | | | | 10 |
| 2 | 267.1641 | 134.0857 | | | 249.1536 | 125.0804 | F | 1030.5680 | 515.7876 | 1013.5415 | 507.2744 | 1012.5574 | 506.7824 | 9 |
| 3 | 338.2012 | 169.6043 | | | 320.1907 | 160.5990 | A | 883.4996 | 442.2534 | 866.4730 | 433.7402 | 865.4890 | 433.2482 | 8 |
| 4 | 494.3023 | 247.6548 | 477.2758 | 239.1415 | 476.2918 | 238.6495 | R | 812.4625 | 406.7349 | 795.4359 | 398.2216 | 794.4519 | 397.7296 | 7 |
| 5 | 565.3395 | 283.1734 | 548.3129 | 274.6601 | 547.3289 | 274.1681 | A | 656.3614 | 328.6843 | 639.3348 | 320.1710 | 638.3508 | 319.6790 | 6 |
| 6 | 662.3922 | 331.6998 | 645.3657 | 323.1865 | 644.3817 | 322.6945 | P | 585.3243 | 293.1658 | 568.2977 | 284.6525 | 567.3137 | 284.1605 | 5 |
| 7 | 790.4508 | 395.7290 | 773.4243 | 387.2158 | 772.4402 | 386.7238 | Q | 488.2715 | 244.6394 | 471.2449 | 236.1261 | 470.2609 | 235.6341 | 4 |
| 8 | 903.5349 | 452.2711 | 886.5083 | 443.7578 | 885.5243 | 443.2658 | L | 360.2129 | 180.6101 | | | 342.2023 | 171.6048 | 3 |
| 9 | 1018.5618 | 509.7845 | 1001.5353 | 501.2713 | 1000.5512 | 500.7793 | D | 247.1288 | 124.0681 | | | 229.1183 | 115.0628 | 2 |
| 10 | | | | | | | L | 132.1019 | 66.5546 | | | | | 1 |



NCBI **BLAST** search of [SFARAPQLDL](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-----------------------------|
| 61.8 | 1148.6492 | 0.0052 | SFARAPQLDL |
| 28.6 | 1148.7117 | -0.0574 | RKQAQGGIDI |
| 28.6 | 1148.6331 | 0.0213 | RQNAQNLDL |
| 28.3 | 1148.5601 | 0.0943 | GEIYDAAIDL |
| 28.3 | 1148.6077 | 0.0466 | FGSSAIQALDL |
| 27.4 | 1148.6023 | 0.0520 | DDEDKDIDL |
| 26.4 | 1148.6946 | -0.0403 | VDARLQALDL |
| 25.9 | 1148.6569 | -0.0025 | VDLKEYVGY |
| 25.9 | 1148.6106 | 0.0437 | DSVDSHLLDL |
| 25.8 | 1148.6892 | -0.0349 | KGGALAADIDI |

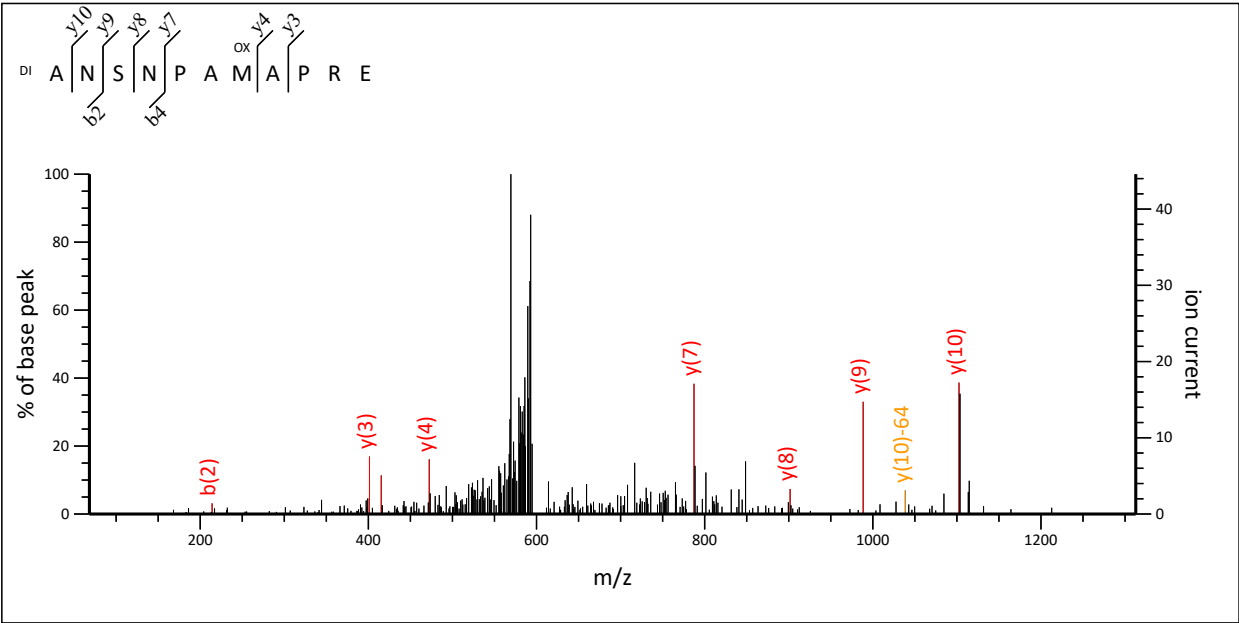
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANSNPAMPRE**
Found in **SMS_MOUSE** in **SwissProt**, Somatostatin OS=Mus musculus GN=Sst PE=3 SV=1

Match to Query 4543: 1200.559268 from(601.286910,2+) intensity(22792.0880) scans(2542) rawscans(sn2542) rtinseconds(1322.4824) index(413)
Title: 414: Scan 2542 (rt=1322.48) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_04.raw]
Data file hipocampo_04.temp.mgf

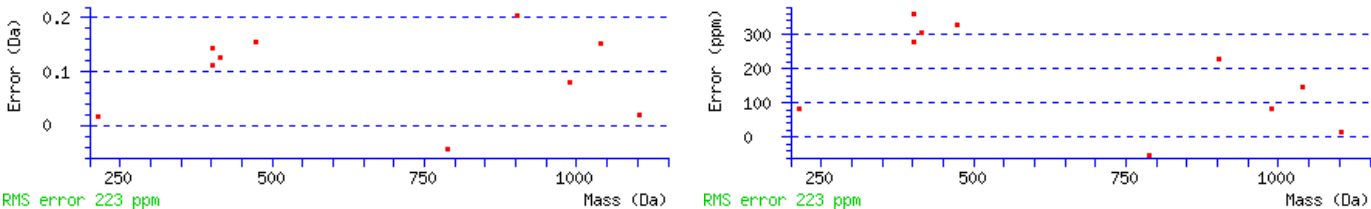


Navigation icons: ? (help), zoom in, zoom out, zoom reset, pan, and a range selector showing 68.23 to 1312.74.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1200.5557
Variable modifications:
N-term : Dimethyl (N-term)
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 28 Expect: 48
Matches : 10/172 fragment ions using 20 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | | | A | | | | | | | 11 |
| 2 | 214.1186 | 107.5629 | 197.0921 | 99.0497 | | | N | 1102.4946 | 551.7509 | 1085.4680 | 543.2377 | 1084.4840 | 542.7456 | 10 |
| 3 | 301.1506 | 151.0790 | 284.1241 | 142.5657 | 283.1401 | 142.0737 | S | 988.4517 | 494.7295 | 971.4251 | 486.2162 | 970.4411 | 485.7242 | 9 |
| 4 | 415.1936 | 208.1004 | 398.1670 | 199.5871 | 397.1830 | 199.0951 | N | 901.4196 | 451.2135 | 884.3931 | 442.7002 | 883.4091 | 442.2082 | 8 |
| 5 | 512.2463 | 256.6268 | 495.2198 | 248.1135 | 494.2358 | 247.6215 | P | 787.3767 | 394.1920 | 770.3502 | 385.6787 | 769.3661 | 385.1867 | 7 |
| 6 | 583.2835 | 292.1454 | 566.2569 | 283.6321 | 565.2729 | 283.1401 | A | 690.3239 | 345.6656 | 673.2974 | 337.1523 | 672.3134 | 336.6603 | 6 |
| 7 | 730.3189 | 365.6631 | 713.2923 | 357.1498 | 712.3083 | 356.6578 | M | 619.2868 | 310.1470 | 602.2603 | 301.6338 | 601.2763 | 301.1418 | 5 |
| 8 | 801.3560 | 401.1816 | 784.3294 | 392.6683 | 783.3454 | 392.1763 | A | 472.2514 | 236.6293 | 455.2249 | 228.1161 | 454.2409 | 227.6241 | 4 |
| 9 | 898.4087 | 449.7080 | 881.3822 | 441.1947 | 880.3982 | 440.7027 | P | 401.2143 | 201.1108 | 384.1878 | 192.5975 | 383.2037 | 192.1055 | 3 |
| 10 | 1054.5098 | 527.7586 | 1037.4833 | 519.2453 | 1036.4993 | 518.7533 | R | 304.1615 | 152.5844 | 287.1350 | 144.0711 | 286.1510 | 143.5791 | 2 |
| 11 | | | | | | | E | 148.0604 | 74.5339 | | | 130.0499 | 65.5286 | 1 |



NCBI **BLAST** search of [ANSNPAMAPRE](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|------------------------------|
| 27.9 | 1200.5557 | 0.0036 | ANSNPAMAPRE |
| 20.5 | 1200.5643 | -0.0050 | MPGPAMPGPAMP |
| 13.9 | 1200.7871 | -0.2278 | LLNAFTKKE |
| 13.9 | 1200.5411 | 0.0181 | PDGTQFANGPQ |
| 13.6 | 1200.6208 | -0.0615 | PGAPPAFASPPD |
| 13.1 | 1200.6176 | -0.0583 | PENGEEAVAVL |
| 13.0 | 1200.6362 | -0.0769 | ILCTQPAGVPE |
| 11.7 | 1200.5986 | -0.0394 | GAGSNPGDKTLE |
| 11.2 | 1200.6462 | -0.0870 | ANSAGGRIVISE |
| 10.6 | 1200.7566 | -0.1973 | LRGLCVAALVL |

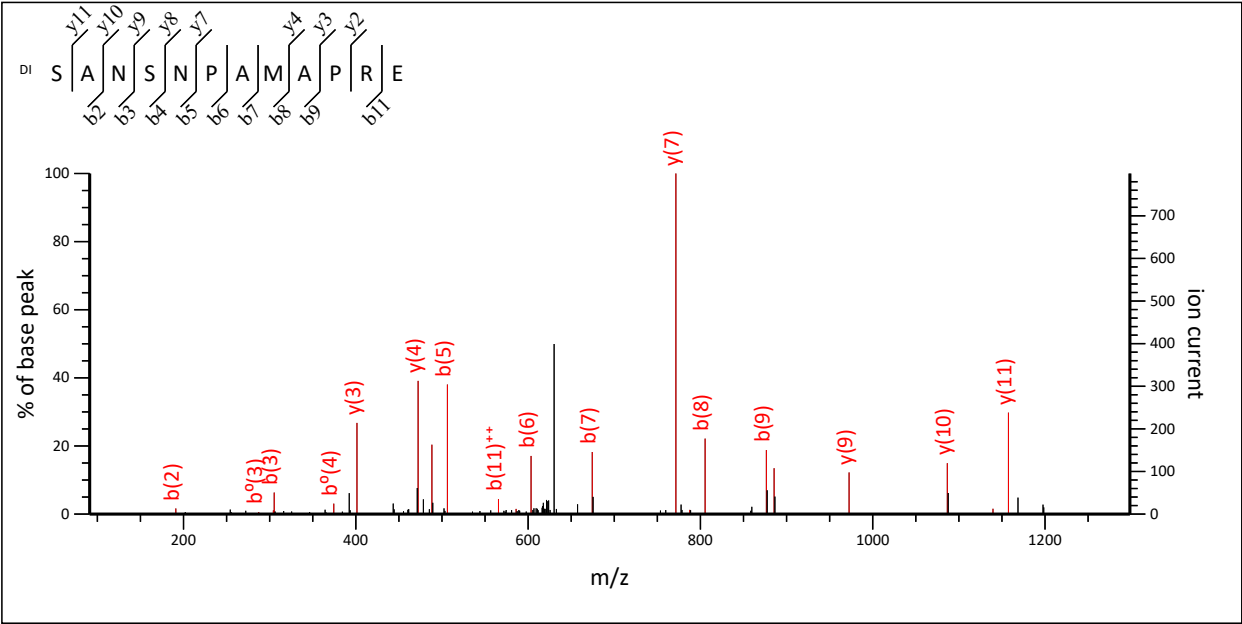
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SANSPAMAPRE**
Found in **SMS_MOUSE** in **SwissProt**, Somatostatin OS=Mus musculus GN=Sst PE=3 SV=1

Match to Query 3640: 1275.620628 from(638.817590,2+) intensity(145209.3100) scans(2791) rawscans(sn2791) rtinseconds(1276.3717) index(1116)
Title: 1117: Scan 2791 (rt=1276.37) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

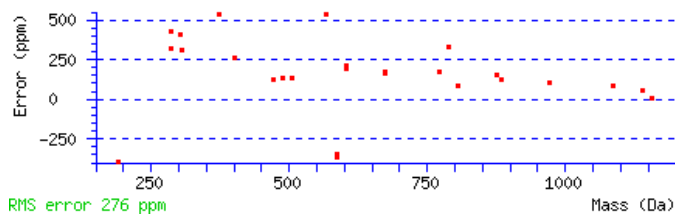
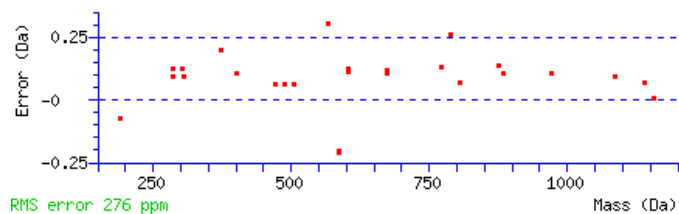


 to 

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1275.6179
Variable modifications:
N-term : Dimethyl:2H(4) (N-term)
Ions Score: 77 Expect: 0.00057
Matches : 26/126 fragment ions using 36 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 120.0957 | 60.5515 | | | 102.0851 | 51.5462 | S | | | | | | | 12 |
| 2 | 191.1328 | 96.0701 | | | 173.1223 | 87.0648 | A | 1157.5368 | 579.2720 | 1140.5102 | 570.7588 | 1139.5262 | 570.2667 | 11 |
| 3 | 305.1758 | 153.0915 | 288.1492 | 144.5782 | 287.1652 | 144.0862 | N | 1086.4997 | 543.7535 | 1069.4731 | 535.2402 | 1068.4891 | 534.7482 | 10 |
| 4 | 392.2078 | 196.6075 | 375.1812 | 188.0943 | 374.1972 | 187.6022 | S | 972.4567 | 486.7320 | 955.4302 | 478.2187 | 954.4462 | 477.7267 | 9 |
| 5 | 506.2507 | 253.6290 | 489.2242 | 245.1157 | 488.2401 | 244.6237 | N | 885.4247 | 443.2160 | 868.3982 | 434.7027 | 867.4141 | 434.2107 | 8 |
| 6 | 603.3035 | 302.1554 | 586.2769 | 293.6421 | 585.2929 | 293.1501 | P | 771.3818 | 386.1945 | 754.3552 | 377.6813 | 753.3712 | 377.1892 | 7 |
| 7 | 674.3406 | 337.6739 | 657.3140 | 329.1607 | 656.3300 | 328.6686 | A | 674.3290 | 337.6681 | 657.3025 | 329.1549 | 656.3185 | 328.6629 | 6 |
| 8 | 805.3811 | 403.1942 | 788.3545 | 394.6809 | 787.3705 | 394.1889 | M | 603.2919 | 302.1496 | 586.2654 | 293.6363 | 585.2813 | 293.1443 | 5 |
| 9 | 876.4182 | 438.7127 | 859.3916 | 430.1995 | 858.4076 | 429.7074 | A | 472.2514 | 236.6293 | 455.2249 | 228.1161 | 454.2409 | 227.6241 | 4 |
| 10 | 973.4709 | 487.2391 | 956.4444 | 478.7258 | 955.4604 | 478.2338 | P | 401.2143 | 201.1108 | 384.1878 | 192.5975 | 383.2037 | 192.1055 | 3 |
| 11 | 1129.5721 | 565.2897 | 1112.5455 | 556.7764 | 1111.5615 | 556.2844 | R | 304.1615 | 152.5844 | 287.1350 | 144.0711 | 286.1510 | 143.5791 | 2 |
| 12 | | | | | | | E | 148.0604 | 74.5339 | | | 130.0499 | 65.5286 | 1 |



NCBI **BLAST** search of [SANSNPAMAPRE](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-------------------------------|
| 77.2 | 1275.6179 | 0.0027 | SANSNPAMAPRE |
| 35.8 | 1275.6245 | -0.0038 | SANTHDIDSLAT |
| 29.6 | 1275.7237 | -0.1031 | SANSINWARLL |
| 29.2 | 1275.7972 | -0.1766 | KSLLGSLNSNAT |
| 24.4 | 1275.6319 | -0.0113 | DNLPPVCDTVAT |
| 24.3 | 1275.6964 | -0.0758 | RLTGLDAGHSAT |
| 23.8 | 1275.7150 | -0.0944 | ILNALGQNCPR |
| 23.7 | 1275.5475 | 0.0731 | CAAGVCVPGEEAT |
| 23.7 | 1275.6132 | 0.0074 | SAPSPLDASDGLD |
| 23.7 | 1275.6327 | -0.0121 | SAIAMPAPMMQP |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of SANSNPAMAPRE

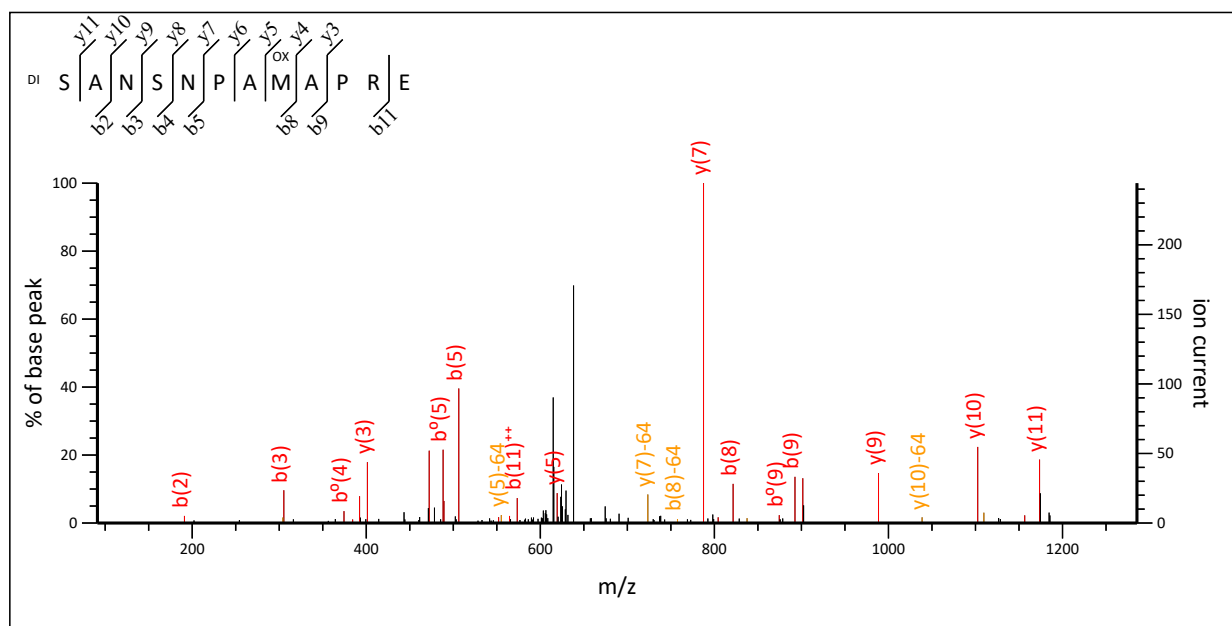
Found in **SMS MOUSE** in **SwissProt**, Somatostatin OS=Mus musculus GN=Sst PE=3 SV=1

Match to Query 3751: 1291.617208 from(646.815880,2+) intensity(53846.9410) scans(2268) rawscans(sn2268) rtinseconds(1091.4888)
index(642)

Title: 643: Scan 2268 (rt=1091.49) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR

NOVAMENTE\HIPOCAMPO\hipocampo 01.raw]

Data file hipocampo 01.temp.mgf



91.11

to



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1291.6128

Variable modifications:

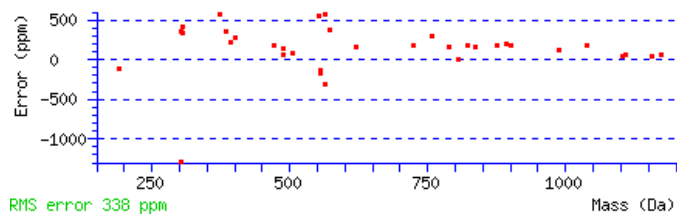
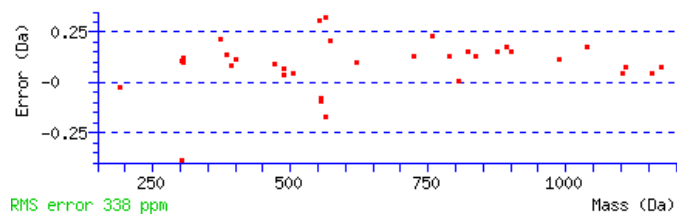
N-term : Dimethyl:2H(4) (N-term)

M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 61 Expect: 0.022

Matches : 35/192 fragment ions using 50 most intense peaks ([help](#))

| # | b | b⁺⁺ | b* | b^{***} | b⁰ | b⁰⁺⁺ | Seq. | y | y ⁺⁺ | y* | y ^{***} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------------|-----------|------------------------|----------------------|------------------------|------|-----------|-----------------|-----------|------------------|----------------|------------------|----|
| 1 | 120.0957 | 60.5515 | | | 102.0851 | 51.5462 | S | | | | | | | 12 |
| 2 | 191.1328 | 96.0701 | | | 173.1223 | 87.0648 | A | 1173.5317 | 587.2695 | 1156.5051 | 578.7562 | 1155.5211 | 578.2642 | 11 |
| 3 | 305.1758 | 153.0915 | 288.1492 | 144.5782 | 287.1652 | 144.0862 | N | 1102.4946 | 551.7509 | 1085.4680 | 543.2377 | 1084.4840 | 542.7456 | 10 |
| 4 | 392.2078 | 196.6075 | 375.1812 | 188.0943 | 374.1972 | 187.6022 | S | 988.4517 | 494.7295 | 971.4251 | 486.2162 | 970.4411 | 485.7242 | 9 |
| 5 | 506.2507 | 253.6290 | 489.2242 | 245.1157 | 488.2401 | 244.6237 | N | 901.4196 | 451.2135 | 884.3931 | 442.7002 | 883.4091 | 442.2082 | 8 |
| 6 | 603.3035 | 302.1554 | 586.2769 | 293.6421 | 585.2929 | 293.1501 | P | 787.3767 | 394.1920 | 770.3502 | 385.6787 | 769.3661 | 385.1867 | 7 |
| 7 | 674.3406 | 337.6739 | 657.3140 | 329.1607 | 656.3300 | 328.6686 | A | 690.3239 | 345.6656 | 673.2974 | 337.1523 | 672.3134 | 336.6603 | 6 |
| 8 | 821.3760 | 411.1916 | 804.3494 | 402.6784 | 803.3654 | 402.1863 | M | 619.2868 | 310.1470 | 602.2603 | 301.6338 | 601.2763 | 301.1418 | 5 |
| 9 | 892.4131 | 446.7102 | 875.3865 | 438.1969 | 874.4025 | 437.7049 | A | 472.2514 | 236.6293 | 455.2249 | 228.1161 | 454.2409 | 227.6241 | 4 |
| 10 | 989.4659 | 495.2366 | 972.4393 | 486.7233 | 971.4553 | 486.2313 | P | 401.2143 | 201.1108 | 384.1878 | 192.5975 | 383.2037 | 192.1055 | 3 |
| 11 | 1145.5670 | 573.2871 | 1128.5404 | 564.7739 | 1127.5564 | 564.2818 | R | 304.1615 | 152.5844 | 287.1350 | 144.0711 | 286.1510 | 143.5791 | 2 |
| 12 | | | | | | | E | 148.0604 | 74.5339 | | | 130.0499 | 65.5286 | |



NCBI **BLAST** search of [SANSNPAMAPRE](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|------------------------------|
| 61.3 | 1291.6128 | 0.0044 | SANSNPAMAPRE |
| 22.3 | 1291.6997 | -0.0825 | VVRFTRSGGNAT |
| 20.7 | 1291.5951 | 0.0221 | SGICINCQHNTA |
| 20.4 | 1291.5966 | 0.0207 | SENLCGLSDLAT |
| 20.0 | 1291.6053 | 0.0119 | QMPPGMTSPRF |
| 19.4 | 1291.4961 | 0.1211 | MYHGMNPSNGD |
| 18.9 | 1291.6521 | -0.0349 | FKDALRNSGGDG |
| 18.9 | 1291.6158 | 0.0014 | FSYYGVMALTA |
| 18.9 | 1291.8860 | -0.2688 | KEKSKSNNTA |
| 18.9 | 1291.6244 | -0.0072 | KGQTHENSNDG |

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGGPPHPQLNKS**

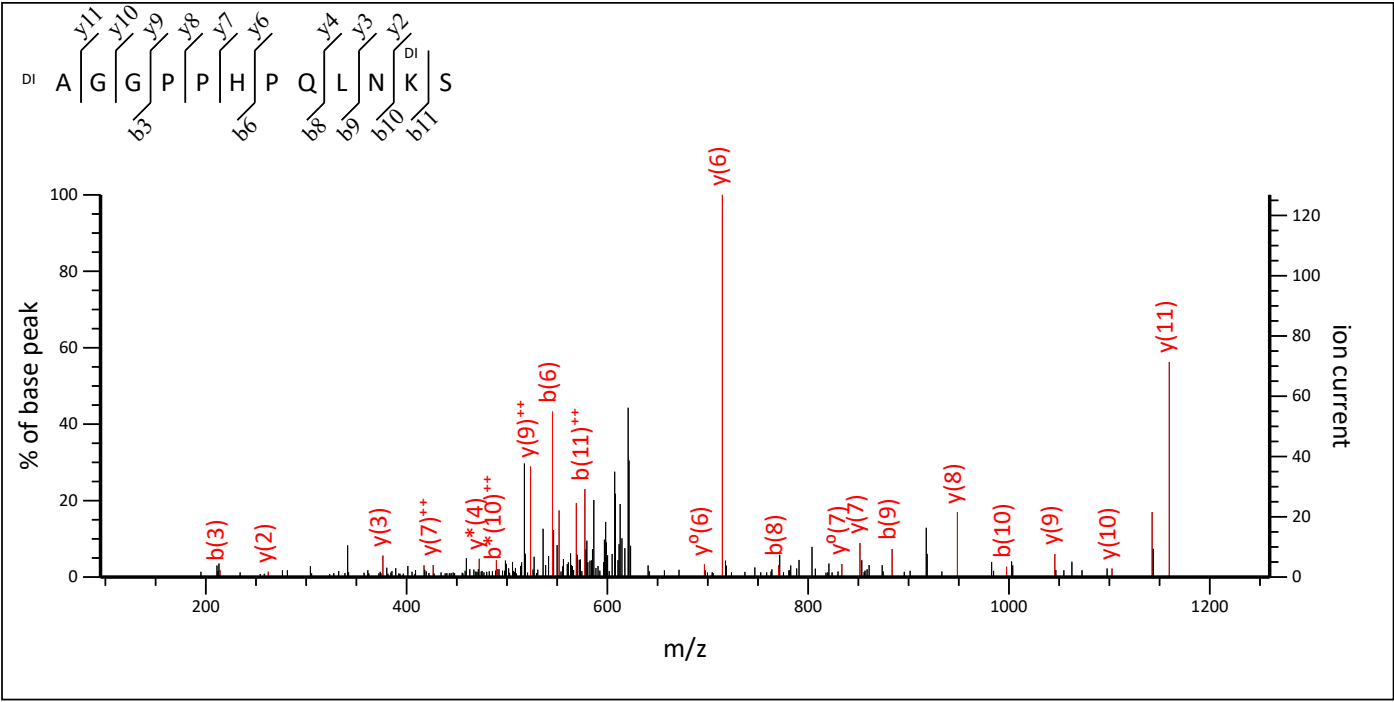
Found in **SYN1_MOUSE** in **SwissProt**, Synapsin-1 OS=Mus musculus GN=Syn1 PE=1 SV=2

Match to Query 3599: 1257.689248 from(629.851900,2+) intensity(45609.9800) scans(2659) rawscans(sn2659)

rtinseconds(1240.2501) index(1039)

Title: 1040: Scan 2659 (rt=1240.25) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\CORTEX\cortex_01.raw]

Data file cortex_01.temp.mgf



95.15

to

1259.69



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1257.6830

Variable modifications:

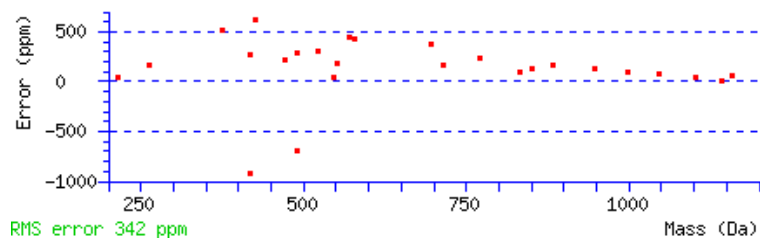
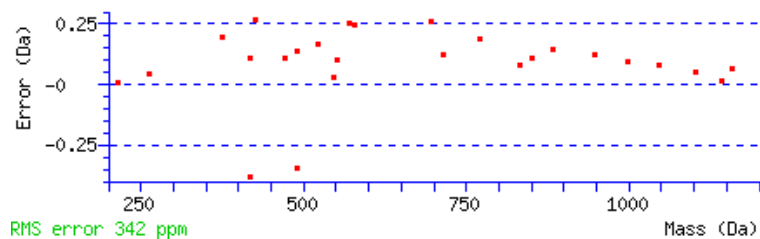
N-term : Dimethyl (N-term)

K11 : Dimethyl (K)

Ions Score: 42 Expect: 2

Matches : 26/94 fragment ions using 68 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ^{*++} | Seq. | y | y ⁺⁺ | y [*] | y ^{*++} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 100.0757 | 50.5415 | | | A | | | | | | | 12 |
| 2 | 157.0972 | 79.0522 | | | G | 1159.6218 | 580.3146 | 1142.5953 | 571.8013 | 1141.6113 | 571.3093 | 11 |
| 3 | 214.1186 | 107.5629 | | | G | 1102.6004 | 551.8038 | 1085.5738 | 543.2905 | 1084.5898 | 542.7985 | 10 |
| 4 | 311.1714 | 156.0893 | | | P | 1045.5789 | 523.2931 | 1028.5524 | 514.7798 | 1027.5683 | 514.2878 | 9 |
| 5 | 408.2241 | 204.6157 | | | P | 948.5261 | 474.7667 | 931.4996 | 466.2534 | 930.5156 | 465.7614 | 8 |
| 6 | 545.2831 | 273.1452 | | | H | 851.4734 | 426.2403 | 834.4468 | 417.7271 | 833.4628 | 417.2350 | 7 |
| 7 | 642.3358 | 321.6715 | | | P | 714.4145 | 357.7109 | 697.3879 | 349.1976 | 696.4039 | 348.7056 | 6 |
| 8 | 770.3944 | 385.7008 | 753.3679 | 377.1876 | Q | 617.3617 | 309.1845 | 600.3352 | 300.6712 | 599.3511 | 300.1792 | 5 |
| 9 | 883.4785 | 442.2429 | 866.4519 | 433.7296 | L | 489.3031 | 245.1552 | 472.2766 | 236.6419 | 471.2926 | 236.1499 | 4 |
| 10 | 997.5214 | 499.2643 | 980.4948 | 490.7511 | N | 376.2191 | 188.6132 | 359.1925 | 180.0999 | 358.2085 | 179.6079 | 3 |
| 11 | 1153.6477 | 577.3275 | 1136.6211 | 568.8142 | K | 262.1761 | 131.5917 | 245.1496 | 123.0784 | 244.1656 | 122.5864 | 2 |
| 12 | | | | | S | 106.0499 | 53.5286 | | | 88.0393 | 44.5233 | 1 |



NCBI **BLAST** search of [AGGPPHPQLNKS](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|--------------------------------|
| 41.9 | 1257.6830 | 0.0063 | AGGPPHPQLNKS |
| 18.9 | 1257.5949 | 0.0943 | AGGQEAEGSAPTR |
| 17.6 | 1257.6928 | -0.0036 | ALEESRKLADA |
| 17.4 | 1257.5858 | 0.1035 | PMQMNQALEM |
| 16.6 | 1257.5520 | 0.1372 | ANSRGLSDNCHG |
| 13.8 | 1257.7921 | -0.1029 | ANPPRLGPKKP |
| 13.7 | 1257.5877 | 0.1015 | ALQDVPGEWS |
| 13.5 | 1257.6288 | 0.0604 | APHGLPLCTGQH |
| 13.0 | 1257.6354 | 0.0539 | ANPPTTGAPPGPGP |
| 12.6 | 1257.6201 | 0.0692 | ALQDAASGLQEQ |

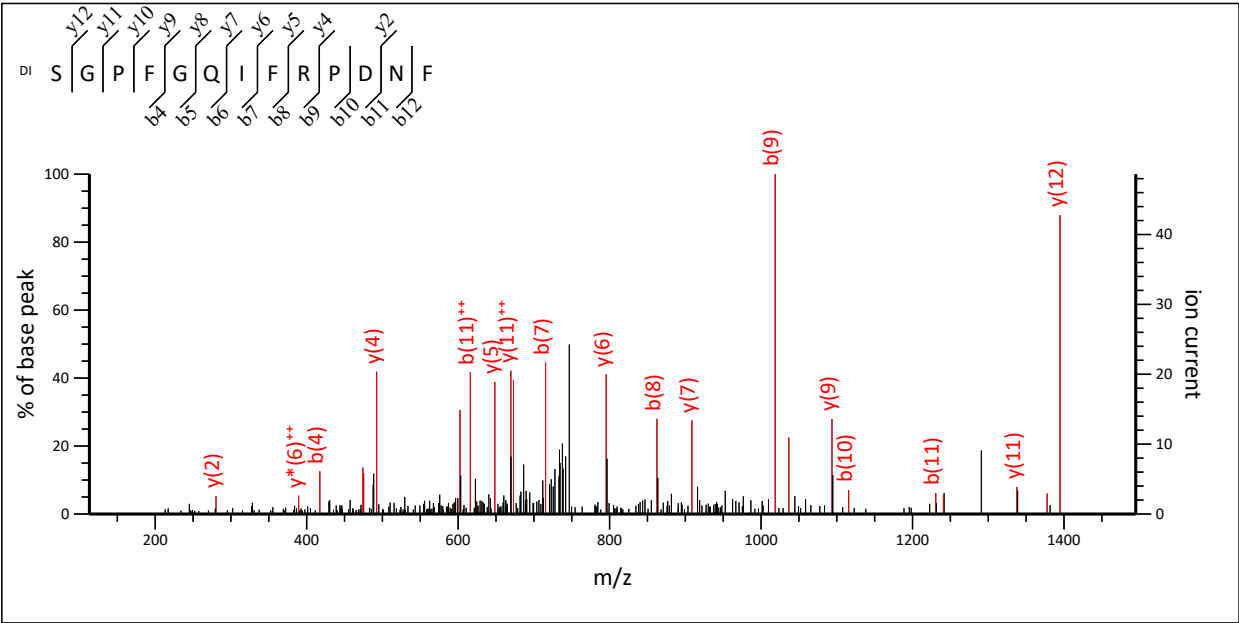
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGPFGQIFRPDNF**
Found in **TBB4B_MOUSE** in **SwissProt**, Tubulin beta-4B chain OS=Mus musculus GN=Tubb4b PE=1 SV=1

Match to Query 5040: 1508.746868 from(755.380710,2+) intensity(24802.6890) scans(10611) rawscans(sn10611) rtinseconds(3967.8521) index(7807)
Title: 7808: Scan 10611 (rt=3967.85) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

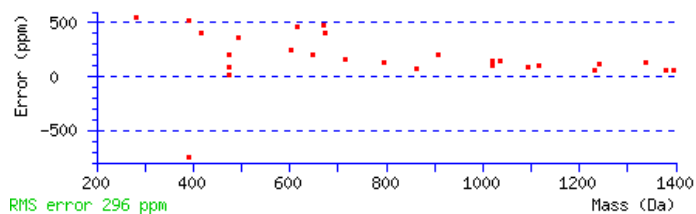
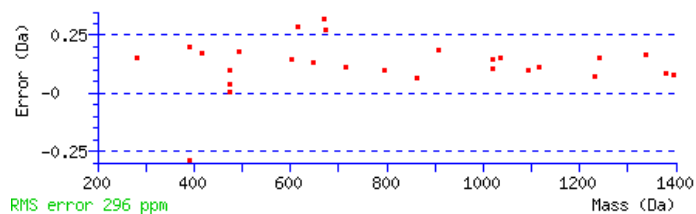


Navigation icons: ? (help), zoom in, zoom out, reset, and a range selector showing 113.14 to 1494.76.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1508.7412
Variable modifications:
N-term : Dimethyl (N-term)
Ions Score: 57 Expect: 0.055
Matches : 27/128 fragment ions using 48 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 116.0706 | 58.5389 | | | 98.0600 | 49.5337 | S | | | | | | | 13 |
| 2 | 173.0921 | 87.0497 | | | 155.0815 | 78.0444 | G | 1394.6852 | 697.8462 | 1377.6586 | 689.3329 | 1376.6746 | 688.8409 | 12 |
| 3 | 270.1448 | 135.5761 | | | 252.1343 | 126.5708 | P | 1337.6637 | 669.3355 | 1320.6371 | 660.8222 | 1319.6531 | 660.3302 | 11 |
| 4 | 417.2132 | 209.1103 | | | 399.2027 | 200.1050 | F | 1240.6109 | 620.8091 | 1223.5844 | 612.2958 | 1222.6004 | 611.8038 | 10 |
| 5 | 474.2347 | 237.6210 | | | 456.2241 | 228.6157 | G | 1093.5425 | 547.2749 | 1076.5160 | 538.7616 | 1075.5320 | 538.2696 | 9 |
| 6 | 602.2933 | 301.6503 | 585.2667 | 293.1370 | 584.2827 | 292.6450 | Q | 1036.5211 | 518.7642 | 1019.4945 | 510.2509 | 1018.5105 | 509.7589 | 8 |
| 7 | 715.3774 | 358.1923 | 698.3508 | 349.6790 | 697.3668 | 349.1870 | I | 908.4625 | 454.7349 | 891.4359 | 446.2216 | 890.4519 | 445.7296 | 7 |
| 8 | 862.4458 | 431.7265 | 845.4192 | 423.2132 | 844.4352 | 422.7212 | F | 795.3784 | 398.1928 | 778.3519 | 389.6796 | 777.3678 | 389.1876 | 6 |
| 9 | 1018.5469 | 509.7771 | 1001.5203 | 501.2638 | 1000.5363 | 500.7718 | R | 648.3100 | 324.6586 | 631.2835 | 316.1454 | 630.2994 | 315.6534 | 5 |
| 10 | 1115.5996 | 558.3035 | 1098.5731 | 549.7902 | 1097.5891 | 549.2982 | P | 492.2089 | 246.6081 | 475.1823 | 238.0948 | 474.1983 | 237.6028 | 4 |
| 11 | 1230.6266 | 615.8169 | 1213.6000 | 607.3037 | 1212.6160 | 606.8116 | D | 395.1561 | 198.0817 | 378.1296 | 189.5684 | 377.1456 | 189.0764 | 3 |
| 12 | 1344.6695 | 672.8384 | 1327.6430 | 664.3251 | 1326.6589 | 663.8331 | N | 280.1292 | 140.5682 | 263.1026 | 132.0550 | | | 2 |
| 13 | | | | | | | F | 166.0863 | 83.5468 | | | | | 1 |



NCBI **BLAST** search of [SGPFGQIFRPDNE](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|----------------------------------|
| 57.4 | 1508.7412 | 0.0056 | SGPFGQIFRPDNE |
| 57.4 | 1508.7412 | 0.0056 | SGPFGQLFRPDNE |
| 21.5 | 1508.7708 | -0.0239 | NNRG TIPGPPMGPGP |
| 20.8 | 1508.7694 | -0.0225 | IVTAGQLSLCSEEQ |
| 18.1 | 1508.9249 | -0.1781 | PRTTSRPSVPDKP |
| 18.1 | 1508.6631 | 0.0838 | TASSGYASVQGADEP |
| 17.7 | 1508.7657 | -0.0188 | TPQHNMGQLLSVY |
| 17.0 | 1508.8162 | -0.0694 | GRANGMGVIGQDGLL |
| 16.8 | 1508.7318 | 0.0150 | SSDSSRLVSASDDK |
| 16.5 | 1508.7475 | -0.0006 | DPWGT VVARCSEGP |

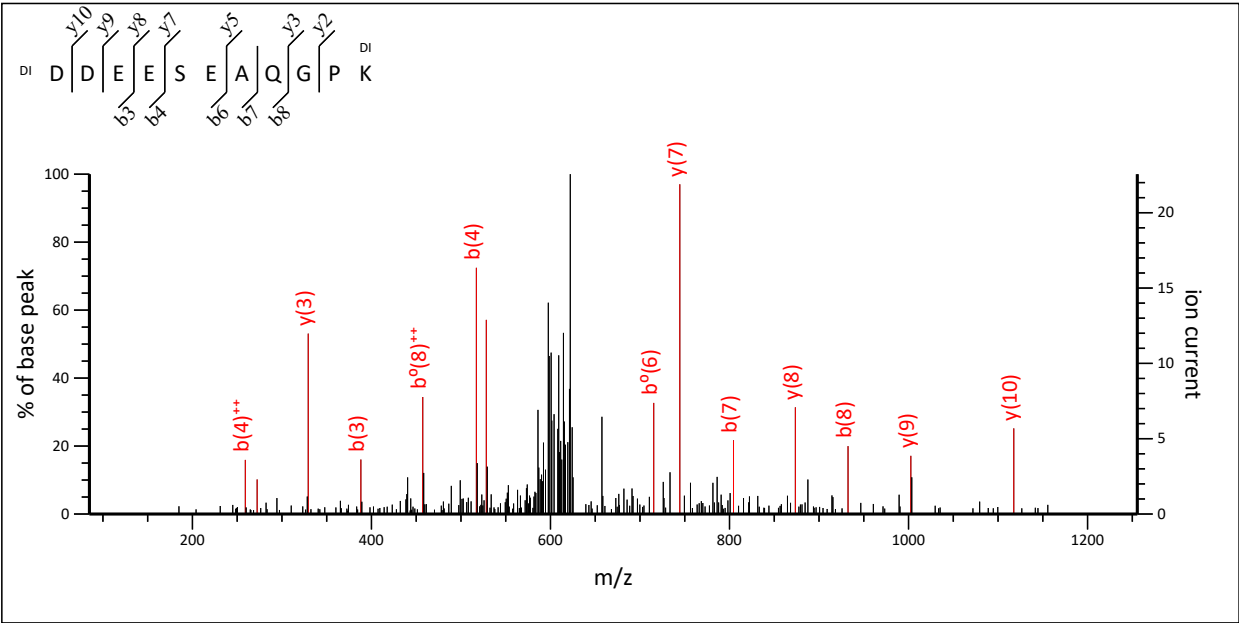
Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DDEESEAQGPK**
Found in **TBB3_MOUSE** in **SwissProt**, Tubulin beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1

Match to Query 3515: 1259.557768 from(630.786160,2+) intensity(12710.6270) scans(2116) rawscans(sn2116) rtinseconds(1035.1652) index(502)
Title: 503: Scan 2116 (rt=1035.17) [C:\Users\Administrador\Desktop\AMOSTRAS NO ORBITRAP LEANDRO RODAR NOVAMENTE\HIPOCAMPO\hipocampo_01.raw]
Data file hipocampo_01.temp.mgf

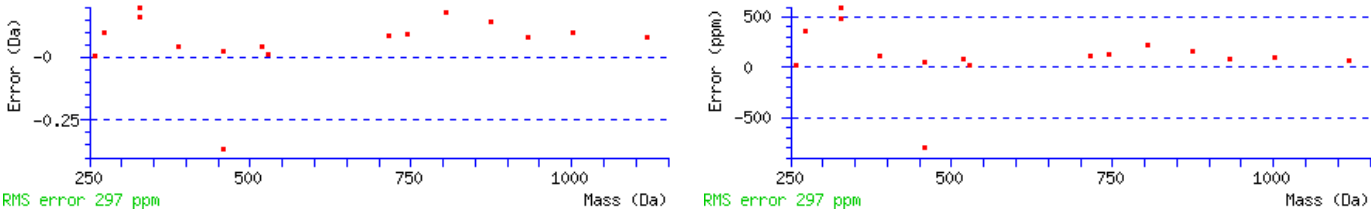


Navigation icons: ? (help), image (download), left arrow, zoom in, zoom out, zoom reset, 84.93 to 1255.58 (mass range), zoom in, right arrow.

Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1259.5517
Variable modifications:
N-term : Dimethyl (N-term)
K11 : Dimethyl (K)
Ions Score: 64 Expect: 0.011
Matches : 17/96 fragment ions using 20 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b [*] | b ⁺⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y [*] | y ⁺⁺⁺ | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|----------------|------------------|------|-----------|-----------------|----------------|------------------|----------------|------------------|----|
| 1 | 144.0655 | 72.5364 | | | 126.0550 | 63.5311 | D | | | | | | | 11 |
| 2 | 259.0925 | 130.0499 | | | 241.0819 | 121.0446 | D | 1117.5008 | 559.2540 | 1100.4742 | 550.7408 | 1099.4902 | 550.2487 | 10 |
| 3 | 388.1351 | 194.5712 | | | 370.1245 | 185.5659 | E | 1002.4738 | 501.7406 | 985.4473 | 493.2273 | 984.4633 | 492.7353 | 9 |
| 4 | 517.1776 | 259.0925 | | | 499.1671 | 250.0872 | E | 873.4312 | 437.2193 | 856.4047 | 428.7060 | 855.4207 | 428.2140 | 8 |
| 5 | 604.2097 | 302.6085 | | | 586.1991 | 293.6032 | S | 744.3886 | 372.6980 | 727.3621 | 364.1847 | 726.3781 | 363.6927 | 7 |
| 6 | 733.2523 | 367.1298 | | | 715.2417 | 358.1245 | E | 657.3566 | 329.1819 | 640.3301 | 320.6687 | 639.3461 | 320.1767 | 6 |
| 7 | 804.2894 | 402.6483 | | | 786.2788 | 393.6430 | A | 528.3140 | 264.6607 | 511.2875 | 256.1474 | | | 5 |
| 8 | 932.3480 | 466.6776 | 915.3214 | 458.1643 | 914.3374 | 457.6723 | Q | 457.2769 | 229.1421 | 440.2504 | 220.6288 | | | 4 |
| 9 | 989.3694 | 495.1884 | 972.3429 | 486.6751 | 971.3589 | 486.1831 | G | 329.2183 | 165.1128 | 312.1918 | 156.5995 | | | 3 |
| 10 | 1086.4222 | 543.7147 | 1069.3956 | 535.2015 | 1068.4116 | 534.7095 | P | 272.1969 | 136.6021 | 255.1703 | 128.0888 | | | 2 |
| 11 | | | | | | | K | 175.1441 | 88.0757 | 158.1176 | 79.5624 | | | 1 |



NCBI **BLAST** search of [DDEESEAQGPK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc) | Delta | Sequence |
|-------|-----------|---------|-------------------------------|
| 64.3 | 1259.5517 | 0.0060 | DDEESEAQGPK |
| 37.5 | 1259.6183 | -0.0605 | SPEESTVQVPN |
| 26.3 | 1259.7296 | -0.1718 | QKAGASEEQALG |
| 25.7 | 1259.6795 | -0.1218 | LVSEALCSTKGP |
| 25.3 | 1259.5266 | 0.0312 | EGGGQAEEQAAEG |
| 24.0 | 1259.5340 | 0.0238 | DDEEESHKCL |
| 23.8 | 1259.6357 | -0.0780 | DDEEEQKRK |
| 21.5 | 1259.6544 | -0.0966 | DNAMGKAVITAN |
| 21.5 | 1259.5266 | 0.0312 | DDEESVDGNRP |
| 21.3 | 1259.5380 | 0.0198 | DDEEMKEQE |

Mascot: <http://www.matrixscience.com/>

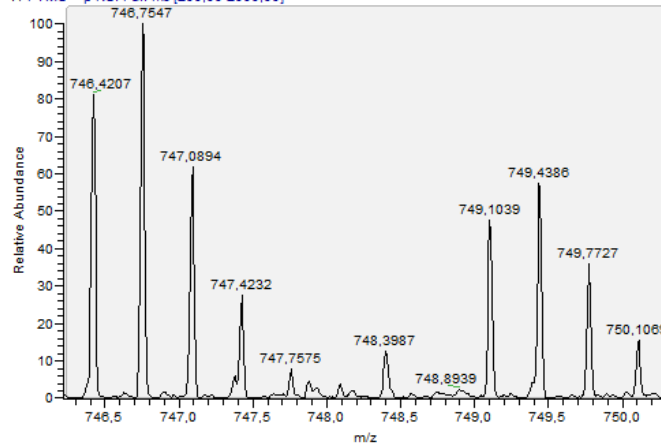
Diagram of Dimethyl labeling

| Samples | | Isotopic Labeling | | Liquid chromatography and mass spectrometry |
|---------------|---|---|---|--|
| | | H ₂ CO NaBH ₃ CN | D ₂ CO NaBH ₃ CN | |
| Cortex 1 | = | WT1 | + KO1 | LC/MS cortex run1 |
| Cortex 2 | = | WT2 | + KO2 | LC/MS cortex run2 |
| Cortex 3 | = | KO3 | + WT3 | LC/MS cortex run3 |
| Hippocampus 1 | = | WT1 | + KO1 | LC/MS hippocampus run1 |
| Hippocampus 2 | = | KO2 | + WT2 | LC/MS hippocampus run2 |
| Hippocampus 3 | = | KO3 | + WT3 | LC/MS hippocampus run3 |
| Striatum 1 | = | WT1 | + KO1 | LC/MS striatum run1 |
| Striatum 2 | = | KO2 | + WT2 | LC/MS striatum run2 |
| Striatum 3 | = | KO3 | + WT3 | LC/MS striatum run3 |

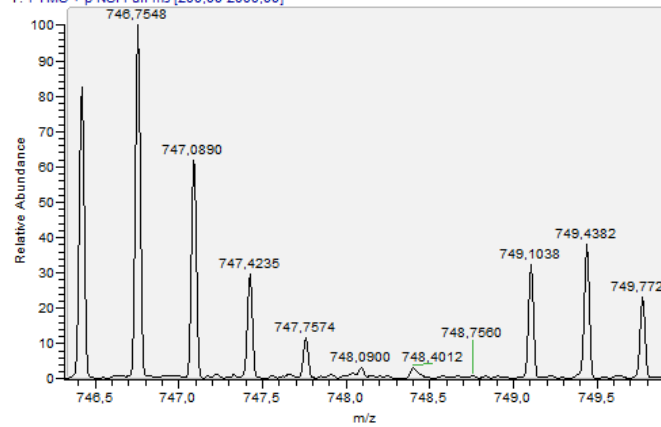
Dimethyl Isotopic labeling scheme used for relative quantification of peptides extracts from prefrontal cortex, striatum and hippocampus of THOP1^{-/-} mice and C57BL/69 wild type mice. For isotopic labeling with Formaldehyde tags were used two isotopic forms (H₂CO and D₂CO) plus NaBH₃CN and the final product of these reactions adds 28 or 32 Da to the final mass of peptides at each available (lysine or N-terminal) labeling site. Peptides extracted from each brain area (KO and WT samples) were labeled and pooled as indicated in three different runs. In some runs the labeling scheme was reverse.

RPTLNELGISTPEELGLDKV 3+

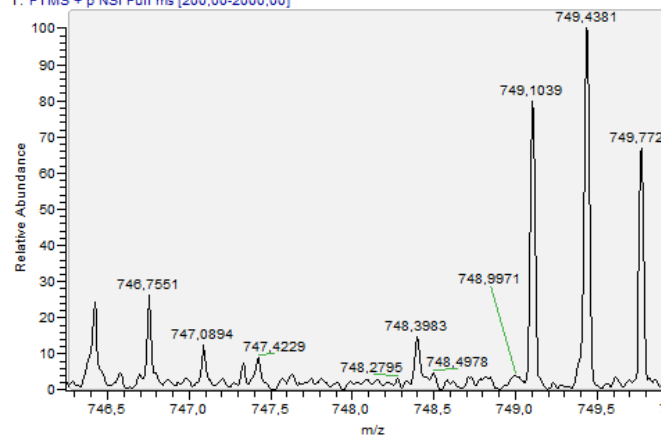
cortex_01 #10219-10410 RT: 64,16-65,14 AV: 9 NL: 9,58E4
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #12884-13159 RT: 65,94-67,03 AV: 40 NL: 9,40E4
T: FTMS + p NSI Full ms [200,00-2000,00]

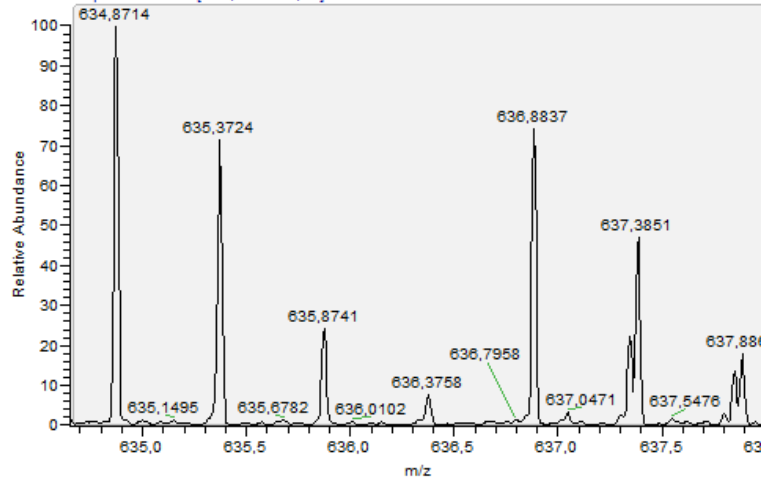


cortex_04 #12425-12595 RT: 65,56-66,27 AV: 31 NL: 1,90E4
T: FTMS + p NSI Full ms [200,00-2000,00]

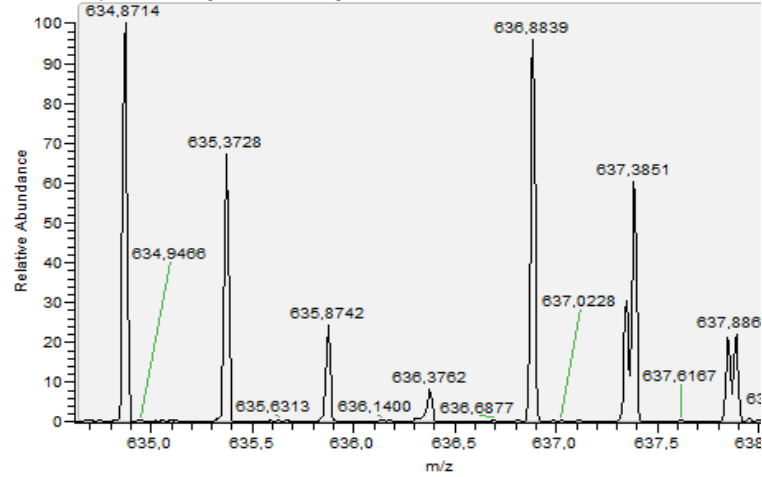


SGQAAARPLVATV 2+

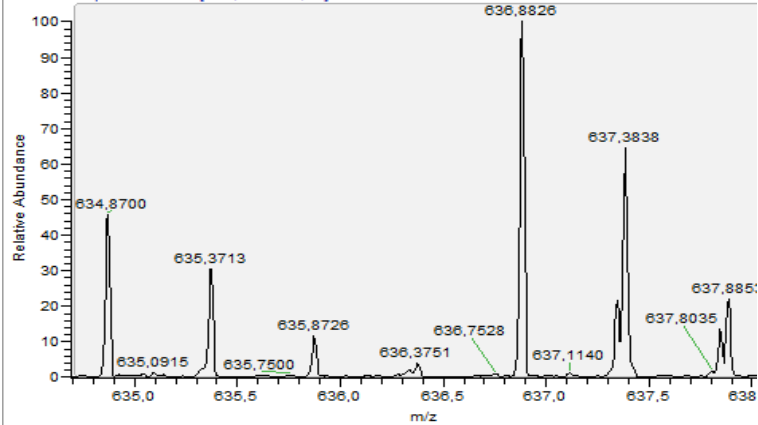
cortex_01 #4858-5248 RT: 32,64-34,73 AV: 21 NL: 2,54E5
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #6506-6691 RT: 40,37-41,11 AV: 33 NL: 7,10E4
T: FTMS + p NSI Full ms [200,00-2000,00]

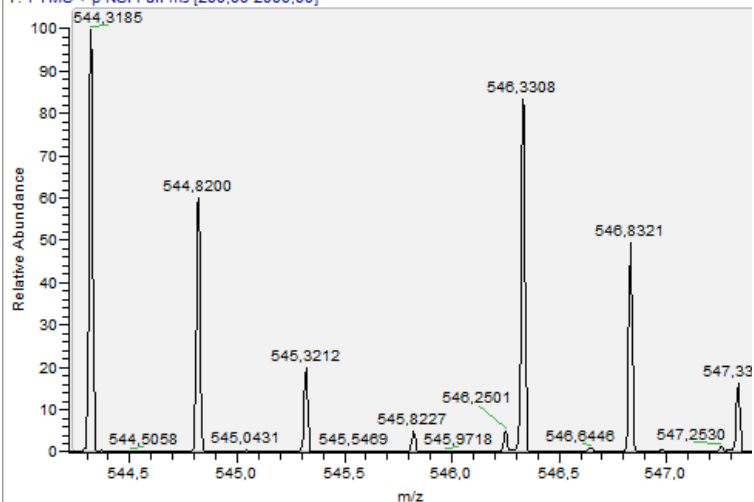


cortex_04 #6258-6599 RT: 38,89-40,37 AV: 94 NL: 6,39E4
T: FTMS + p NSI Full ms [200,00-2000,00]

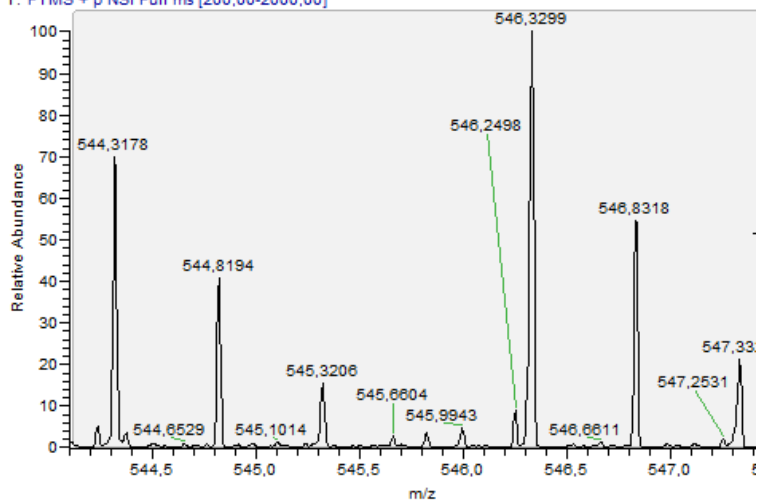


GLNVPSVRF 2+

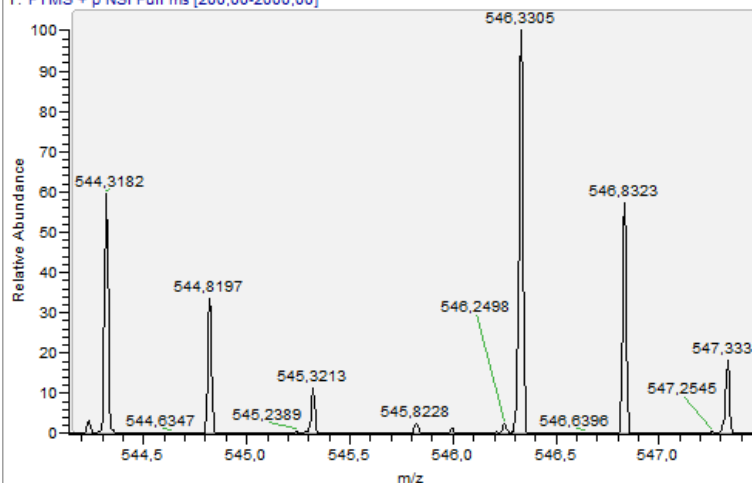
cortex_01 #8022-8210 RT: 51,12-52,20 AV: 16 NL: 5,04E5
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #10482-11136 RT: 56,31-58,89 AV: 100 NL: 6,23E4
T: FTMS + p NSI Full ms [200,00-2000,00]

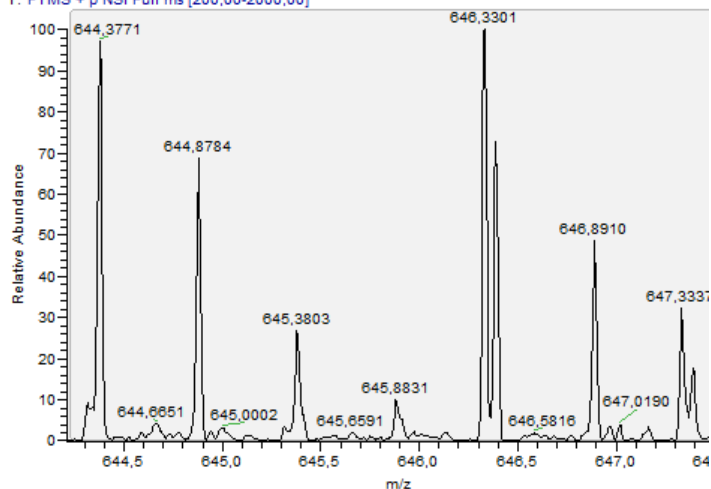


cortex_04 #10370-10624 RT: 56,67-57,76 AV: 60 NL: 1,26E5
T: FTMS + p NSI Full ms [200,00-2000,00]

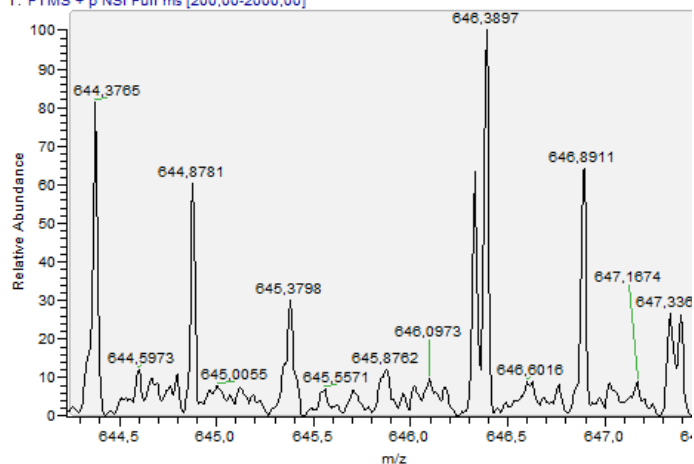


TVGLNVPASVRF 2+

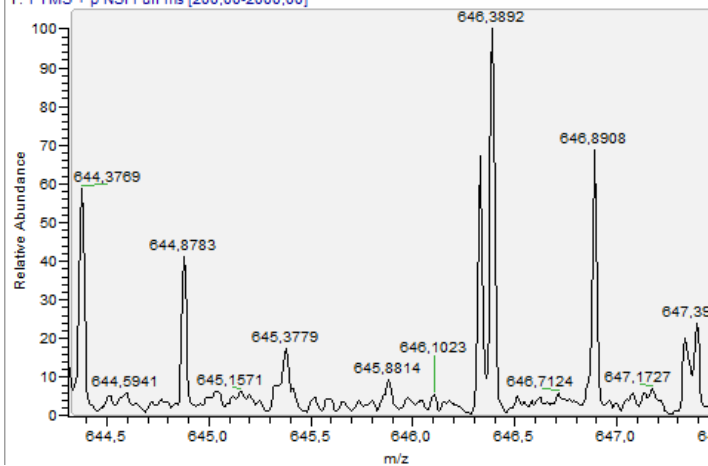
cortex_01 #9271-9526 RT: 58,53-59,94 AV: 15 NL: 5,71E4
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #11693-11971 RT: 61,11-62,20 AV: 44 NL: 1,57E4
T: FTMS + p NSI Full ms [200,00-2000,00]

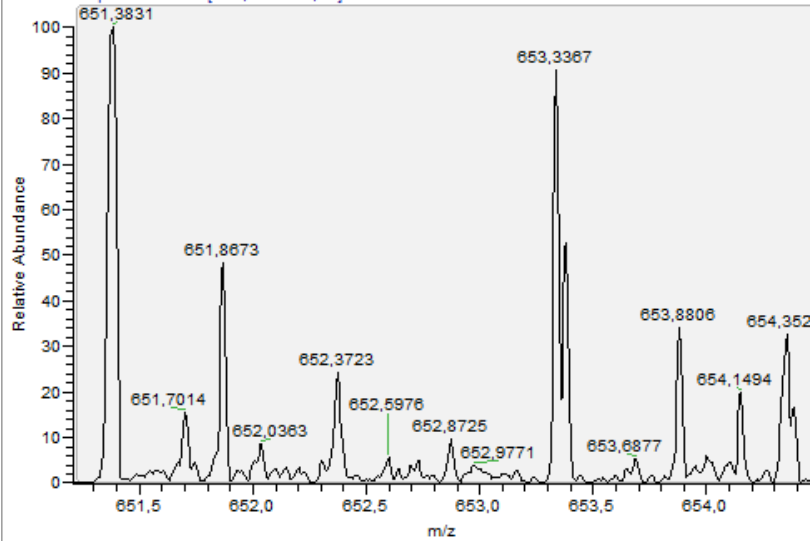


cortex_04 #11210-11461 RT: 60,38-61,48 AV: 61 NL: 1,84E4
T: FTMS + p NSI Full ms [200,00-2000,00]

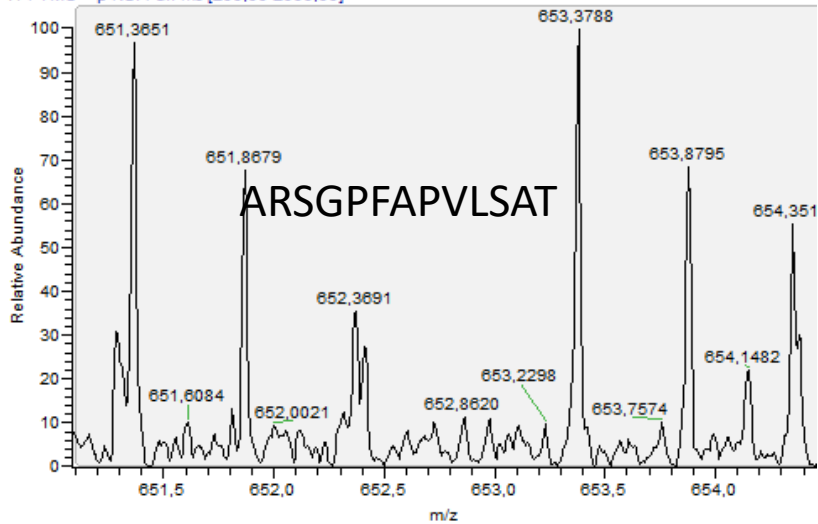


ARSGPFAPVLSAT 2+

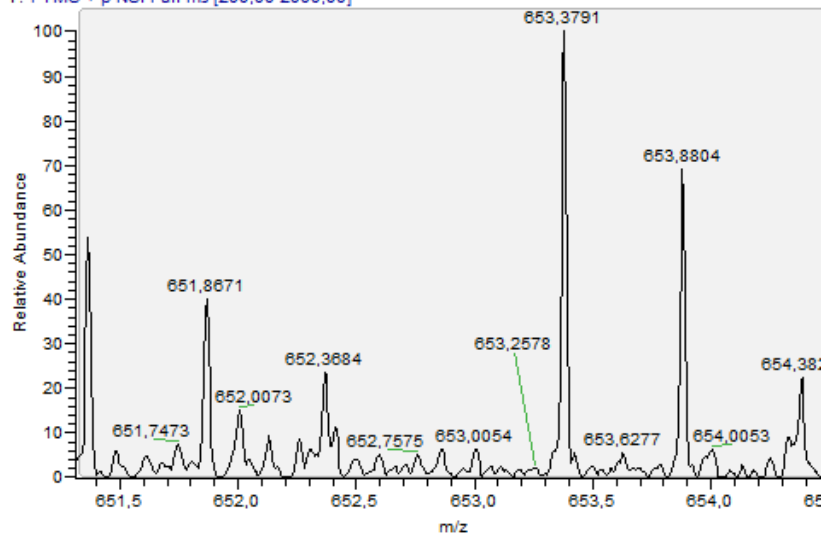
cortex_01 #7346-7533 RT: 47,13-48,11 AV: 11 NL: 5,39E4
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #9824-10014 RT: 53,73-54,43 AV: 30 NL: 1,43E4
T: FTMS + p NSI Full ms [200,00-2000,00]



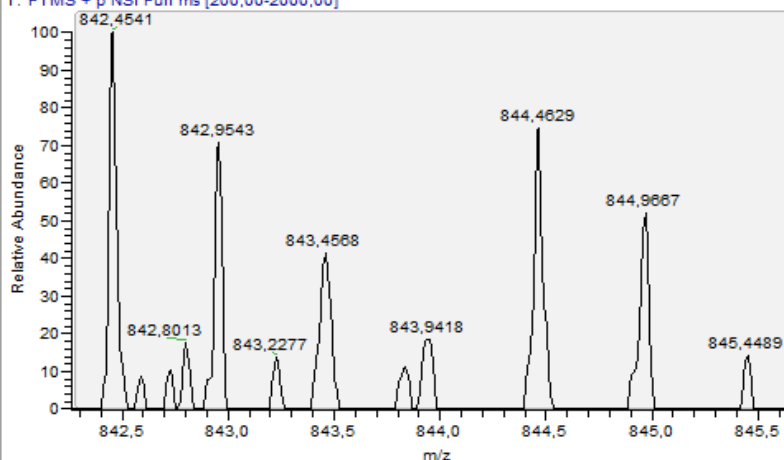
cortex_04 #9558-9617 RT: 53,18-53,41 AV: 13 NL: 1,83E4
T: FTMS + p NSI Full ms [200,00-2000,00]



ATVGDVNTDRPGLLDL 2+

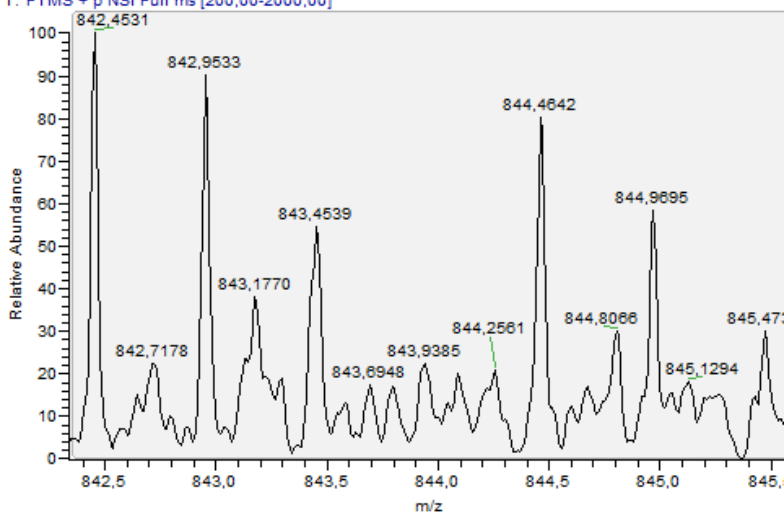
cortex_01 #9678 RT: 60.89 AV: 1 NL: 3,29E4

T: FTMS + p NSI Full ms [200,00-2000,00]



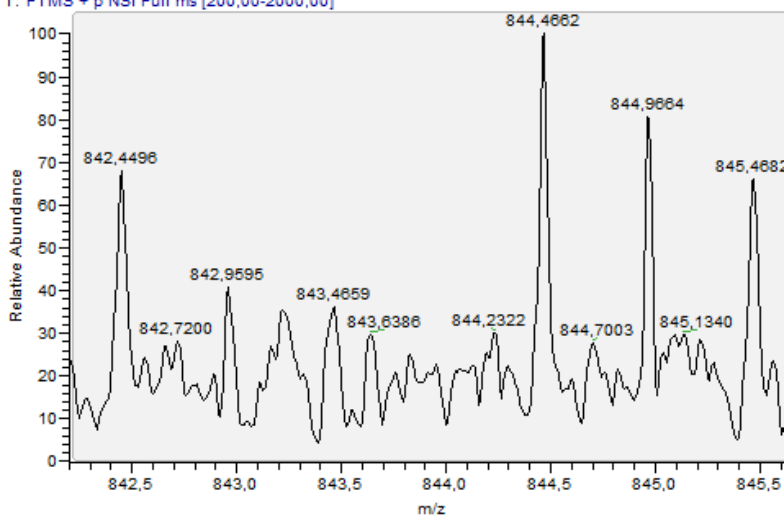
cortex_03 #12160-12337 RT: 62.99-63.69 AV: 28 NL: 6,06E3

T: FTMS + p NSI Full ms [200,00-2000,00]



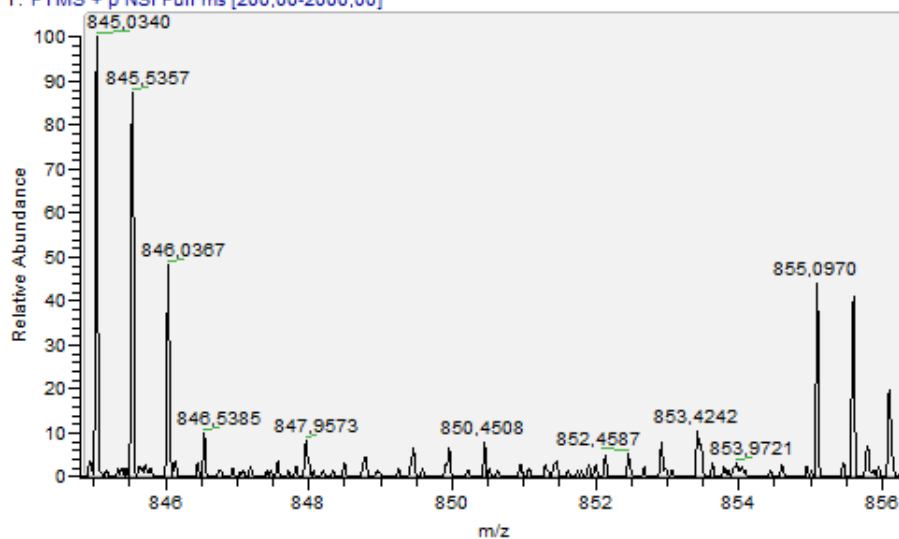
cortex_04 #11808-12155 RT: 62.96-64.44 AV: 73 NL: 3,21E3

T: FTMS + p NSI Full ms [200,00-2000,00]

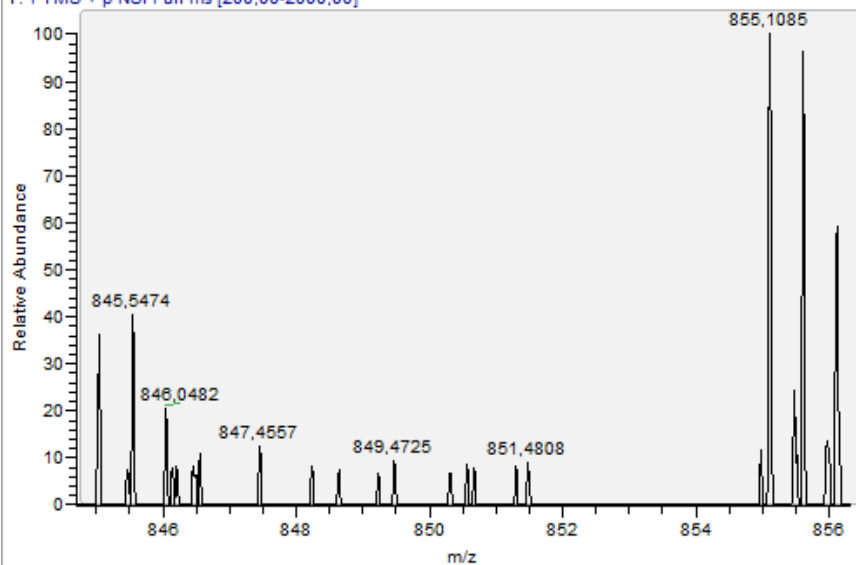


VEKVDELKKKYGI 2+

cortex_01 #6052-5183 RT: 33,71-34,44 AV: 8 NL: 6,33E4
T: FTMS + p NSI Full ms [200,00-2000,00]



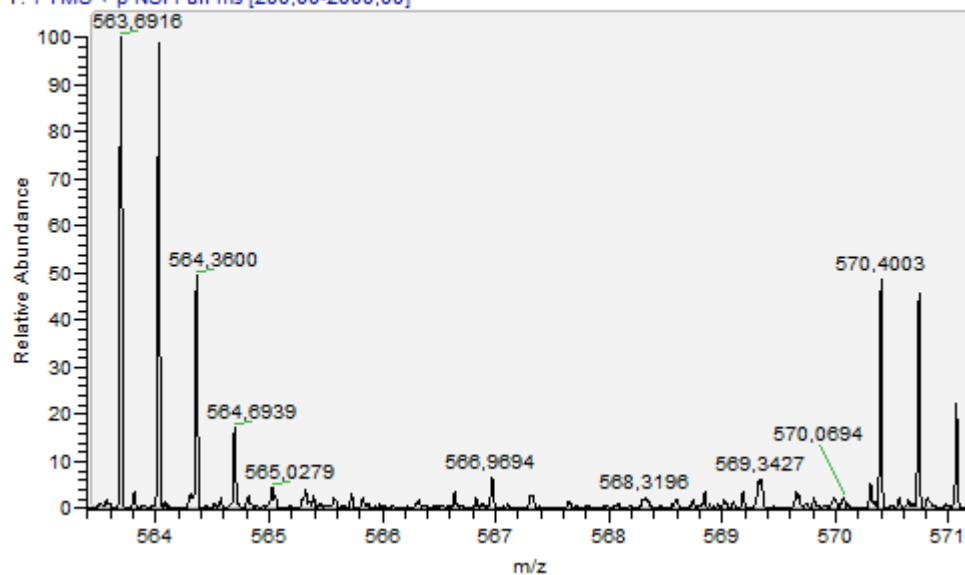
cortex_04 #6683 RT: 40,75 AV: 1 NL: 1,48E3
T: FTMS + p NSI Full ms [200,00-2000,00]



VEKVDLKKKYGI 3+

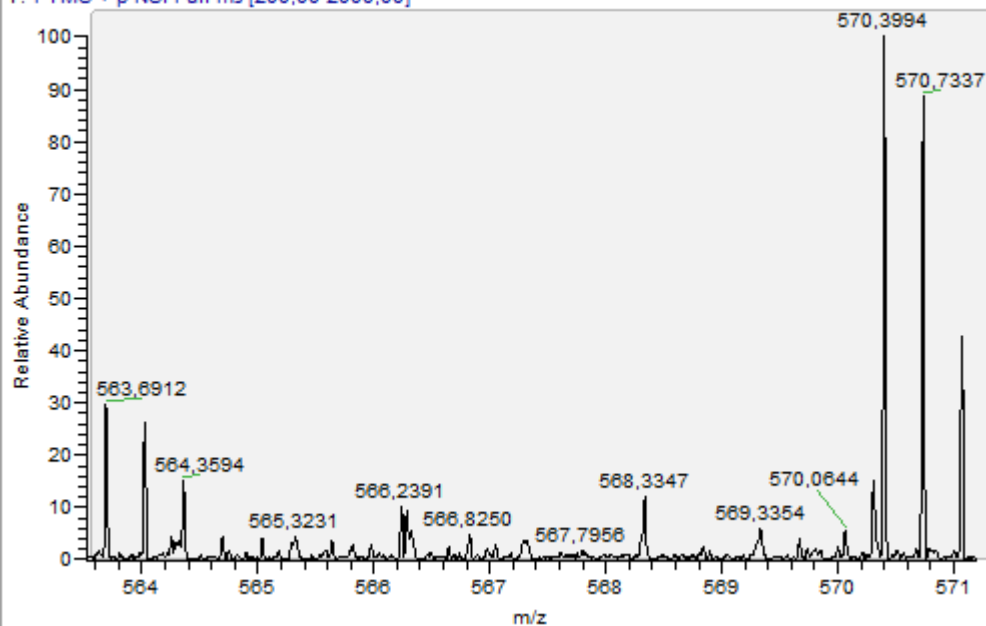
cortex_01 #5052-5183 RT: 33,71-34,44 AV: 8 NL: 3,16E5

T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_04 #6599-6943 RT: 40,37-41,84 AV: 79 NL: 3,62E4

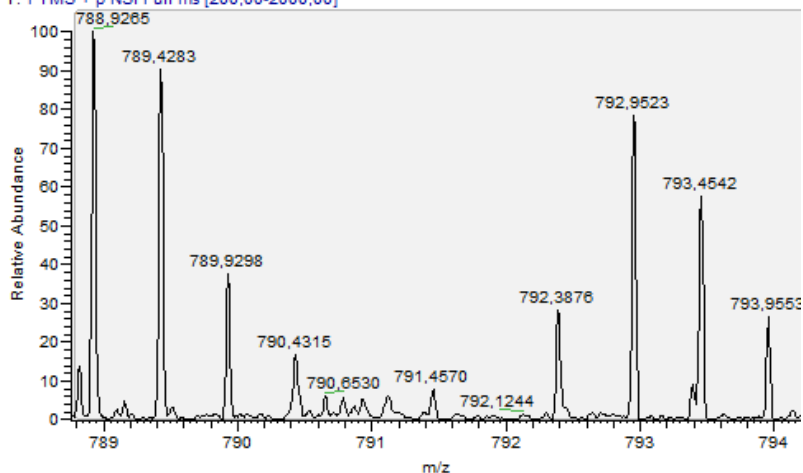
T: FTMS + p NSI Full ms [200,00-2000,00]



ASKGLGSDLDSSLASL 2+

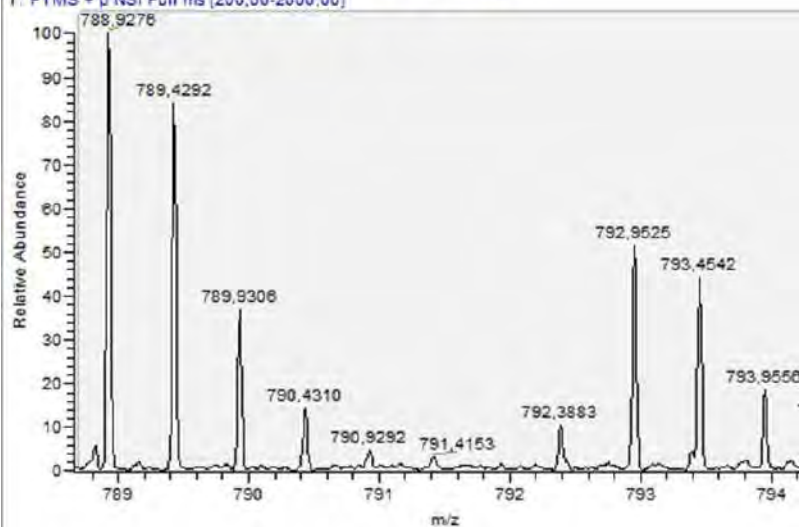
cortex_01 #9852-9778 RT: 60,77-61,39 AV: 8 NL: 9,45E4

T: FTMS + p NSI Full ms [200,00-2000,00]



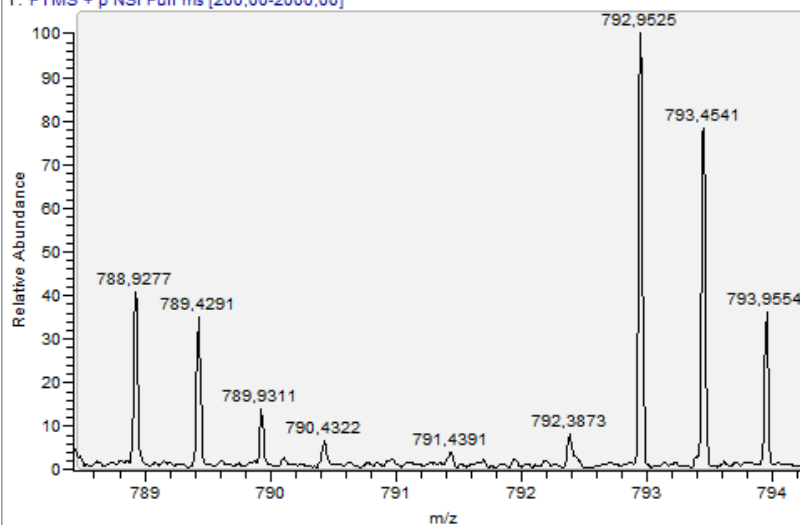
cortex_03 #12180-12521 RT: 62,99-64,43 AV: 56 NL: 8,99E4

T: FTMS + p NSI Full ms [200,00-2000,00]



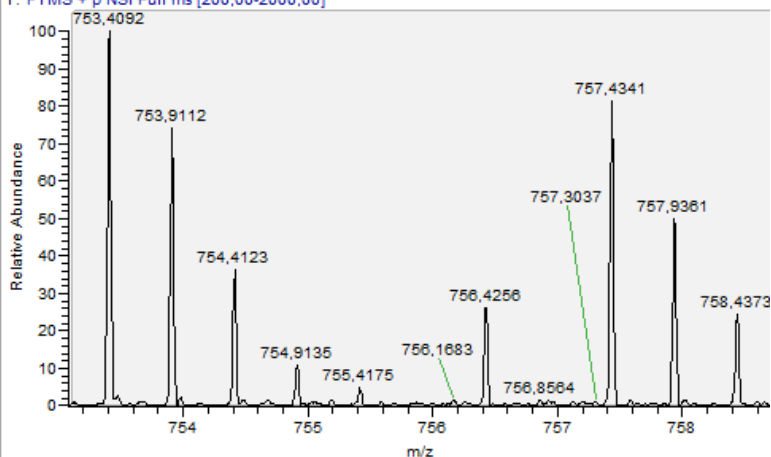
cortex_04 #11808-12155 RT: 62,96-64,44 AV: 73 NL: 5,50E4

T: FTMS + p NSI Full ms [200,00-2000,00]

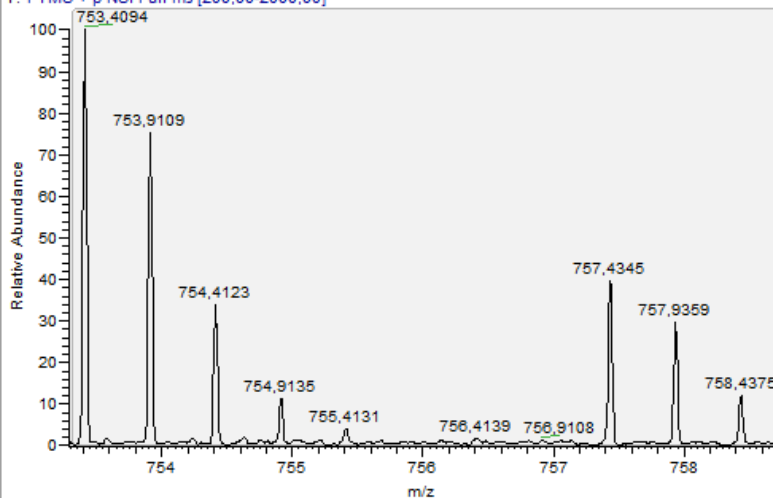


SKGLGSDLDSSLASL 2+

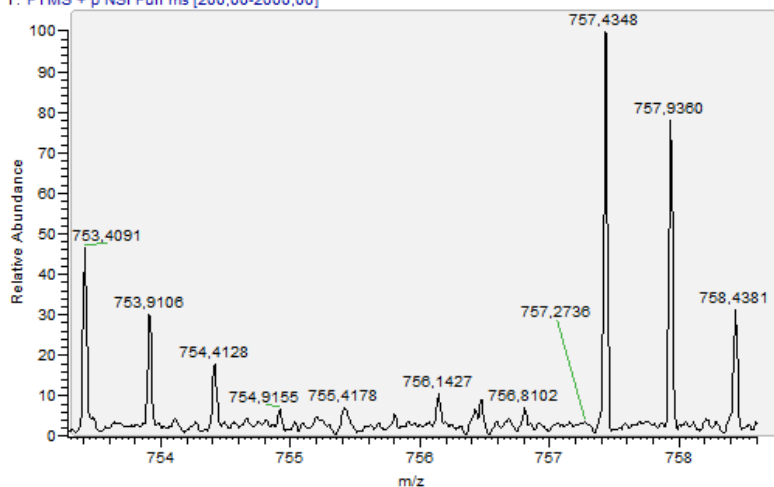
cortex_01 #9589-9716 RT: 60.43-61.01 AV: 6 NL: 1,92E5
T: FTMS + p NSI Full ms [200.00-2000.00]



cortex_03 #12160-12521 RT: 62.99-64.43 AV: 56 NL: 1,11E5
T: FTMS + p NSI Full ms [200.00-2000.00]

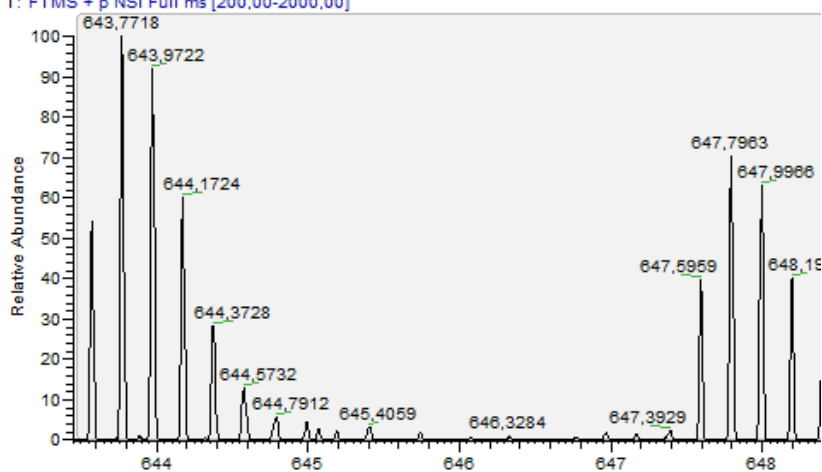


cortex_04 #11979-12244 RT: 63.70-64.82 AV: 50 NL: 3,01E4
T: FTMS + p NSI Full ms [200.00-2000.00]

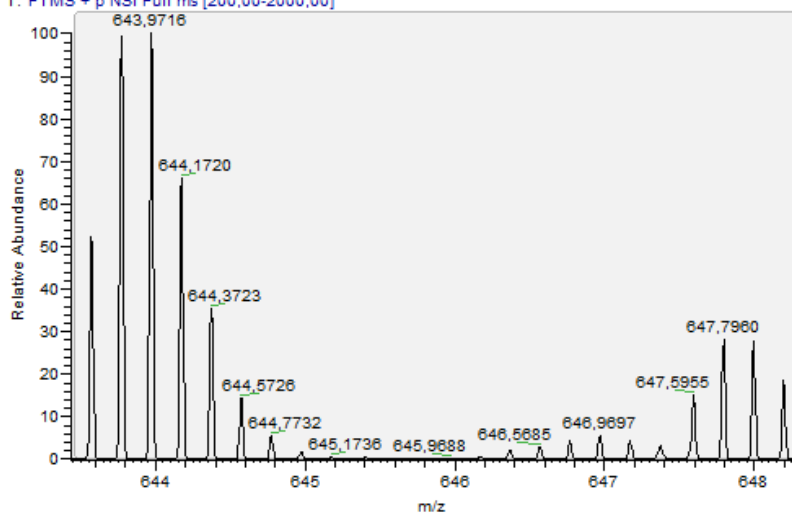


SPSPTPATQSPKKPPAKDPLADLNKDFL 4+

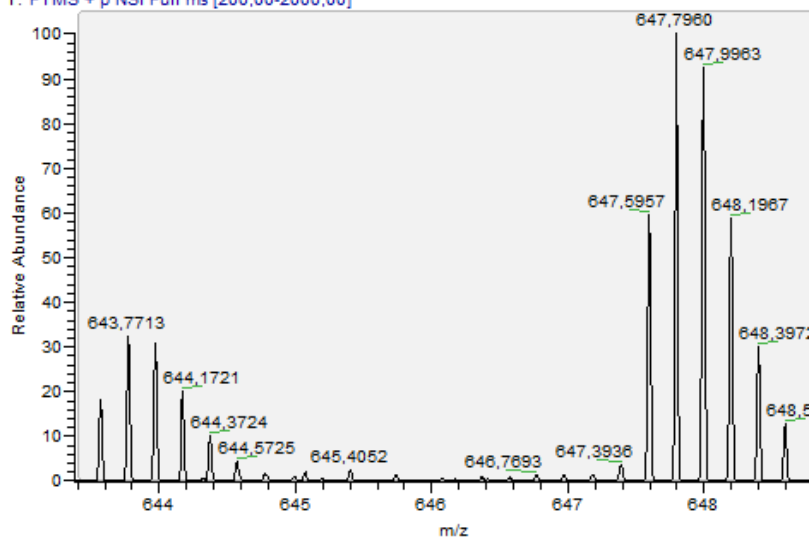
cortex_01 #10344-10537 RT: 64.91-65.83 AV: 9 NL: 8,01E5
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #13500-13858 RT: 68.52-70.00 AV: 55 NL: 3,83E5
T: FTMS + p NSI Full ms [200,00-2000,00]



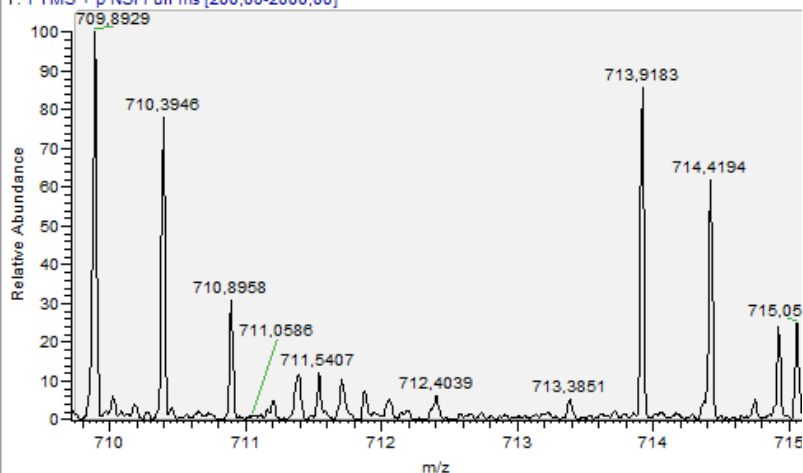
cortex_04 #12674-13019 RT: 66.67-68.13 AV: 65 NL: 5,79E5
T: FTMS + p NSI Full ms [200,00-2000,00]



KGLGSDLDSSLASL 2+

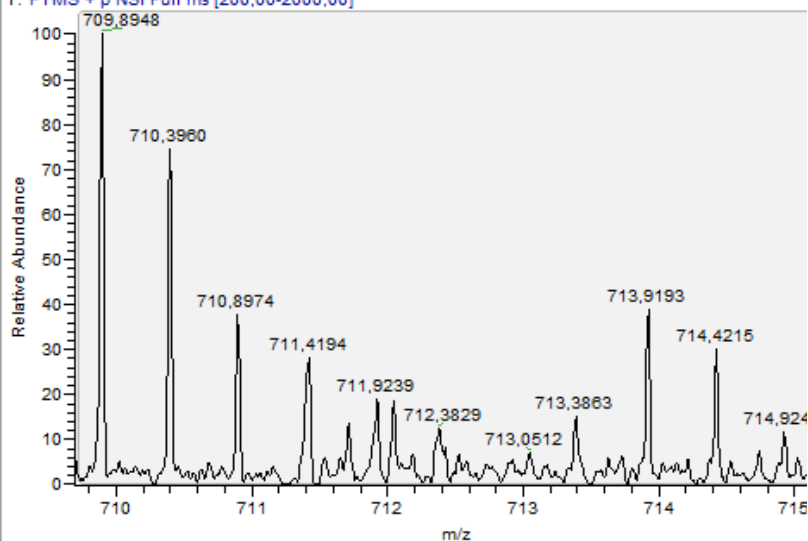
cortex_01 #9399-9716 RT: 59.27-61.01 AV: 17 NL: 6,79E4

T: FTMS + p NSI Full ms [200,00-2000,00]



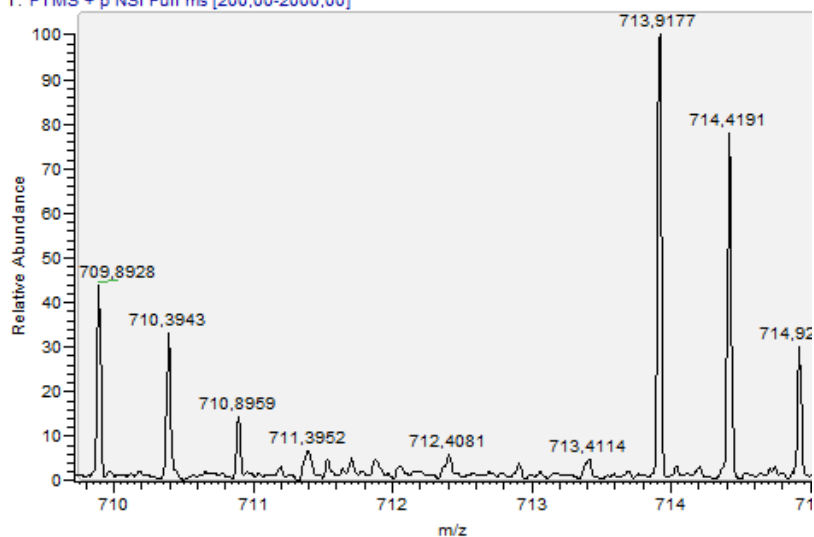
cortex_03 #12160-12337 RT: 62.99-63.69 AV: 28 NL: 2,13E4

T: FTMS + p NSI Full ms [200,00-2000,00]



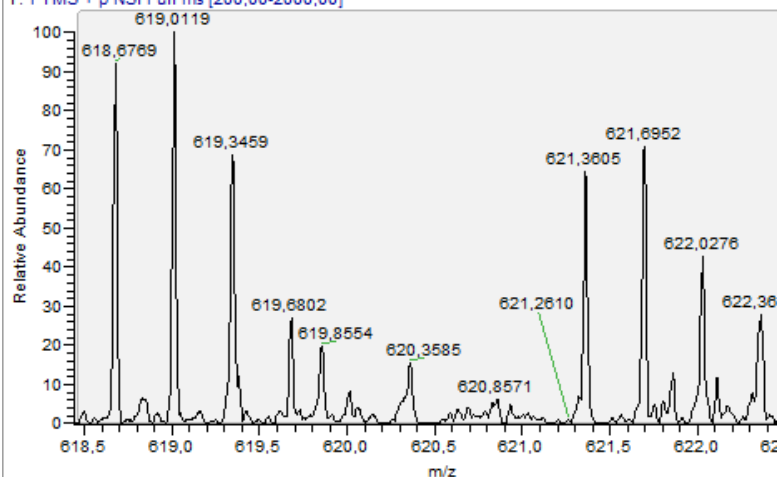
cortex_04 #11550-11894 RT: 61.85-63.33 AV: 73 NL: 4,62E4

T: FTMS + p NSI Full ms [200,00-2000,00]

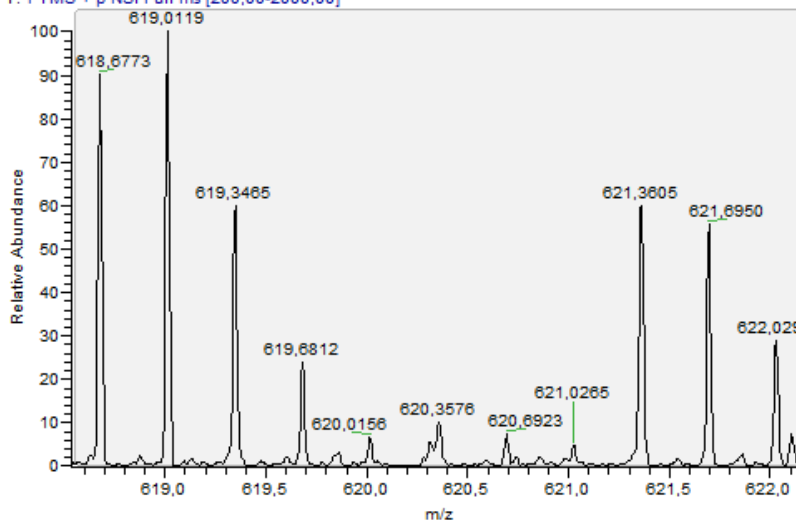


TQVVSDAAYKGVQPHVV 3+

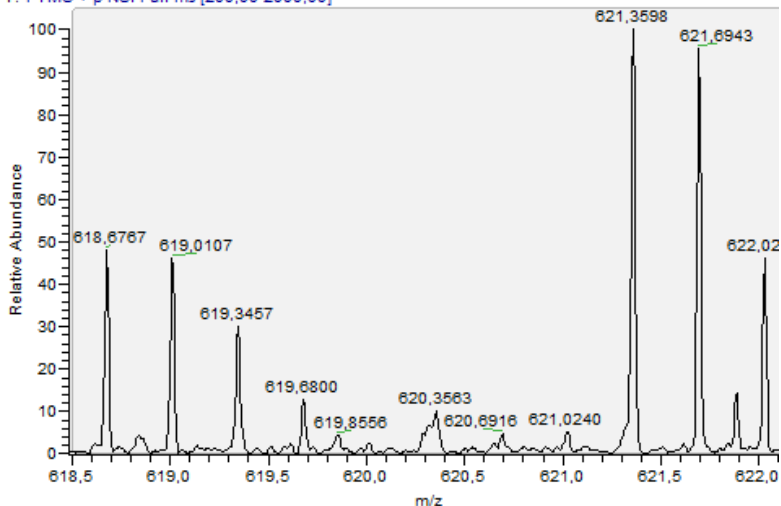
cortex_01 #5648-5838 RT: 37,11-38,03 AV: 11 NL: 6,88E4
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #7340-7522 RT: 43,72-44,44 AV: 35 NL: 3,13E4
T: FTMS + p NSI Full ms [200,00-2000,00]

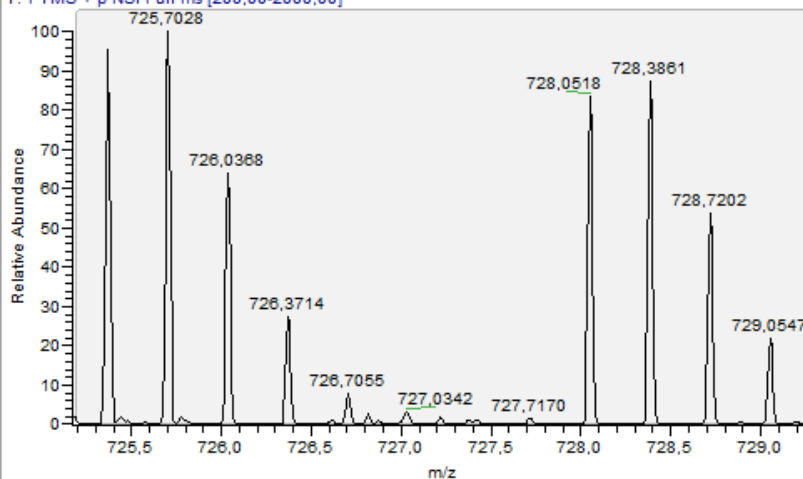


cortex_04 #7203-7459 RT: 42,98-44,06 AV: 57 NL: 1,90E4
T: FTMS + p NSI Full ms [200,00-2000,00]

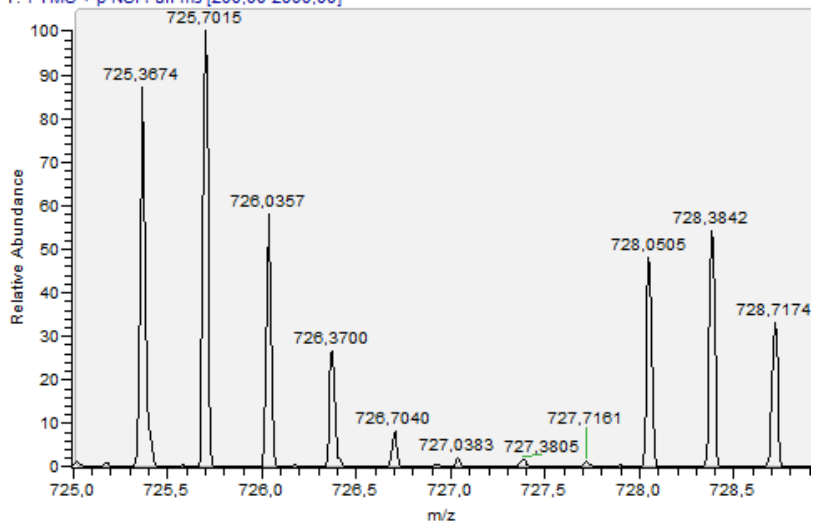


GRKGPGGGPGGAGGARGGAGGGPSGD 3+

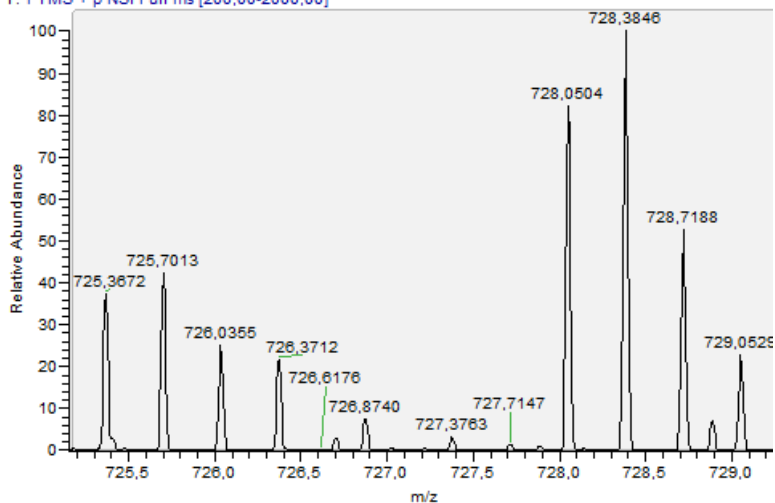
cortex_01 #1881-2115 RT: 15,92-17,31 AV: 13 NL: 5,16E4
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #2379-2599 RT: 22,59-23,70 AV: 83 NL: 7,27E3
T: FTMS + p NSI Full ms [200,00-2000,00]



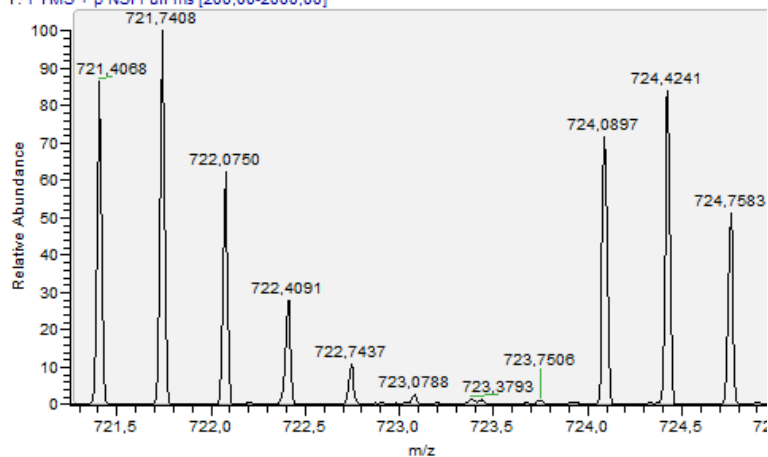
cortex_04 #1806-2250 RT: 19,63-21,85 AV: 152 NL: 4,13E3
T: FTMS + p NSI Full ms [200,00-2000,00]



AQATGKPAQYIAVHVVPDQL 3+

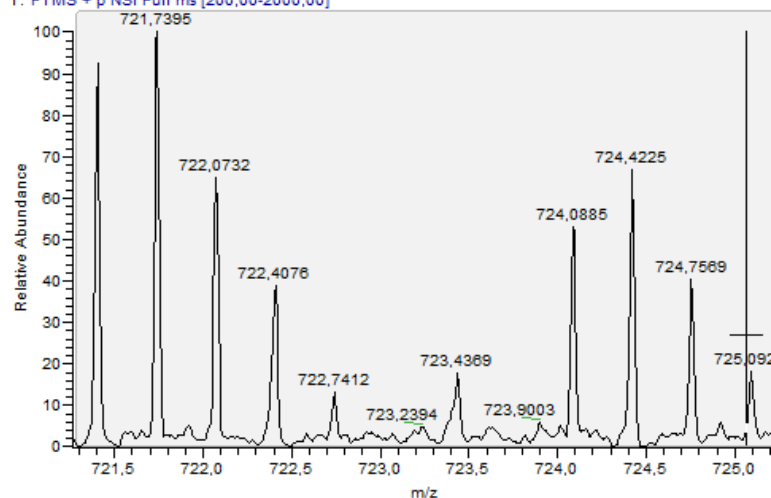
cortex_01 #8522-8649 RT: 54,10-54,77 AV: 10 NL: 3,29E5

T: FTMS + p NSI Full ms [200,00-2000,00]



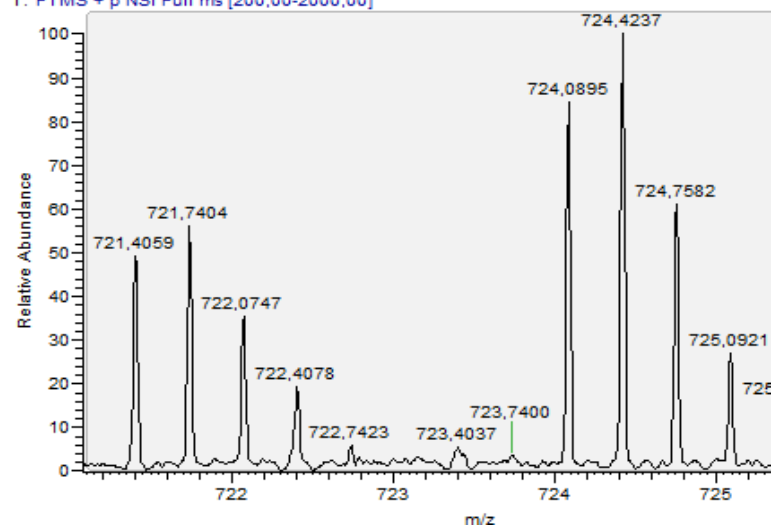
cortex_03 #10571-10853 RT: 56,67-57,78 AV: 43 NL: 3,38E4

T: FTMS + p NSI Full ms [200,00-2000,00]



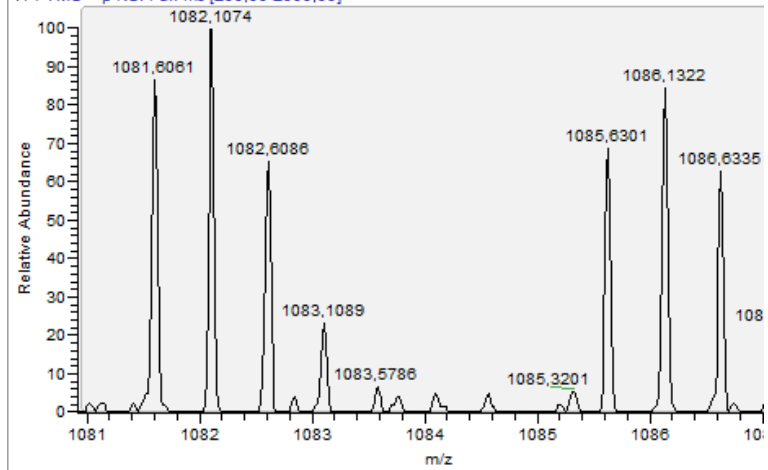
cortex_04 #10203-10539 RT: 55,93-57,40 AV: 80 NL: 3,65E4

T: FTMS + p NSI Full ms [200,00-2000,00]

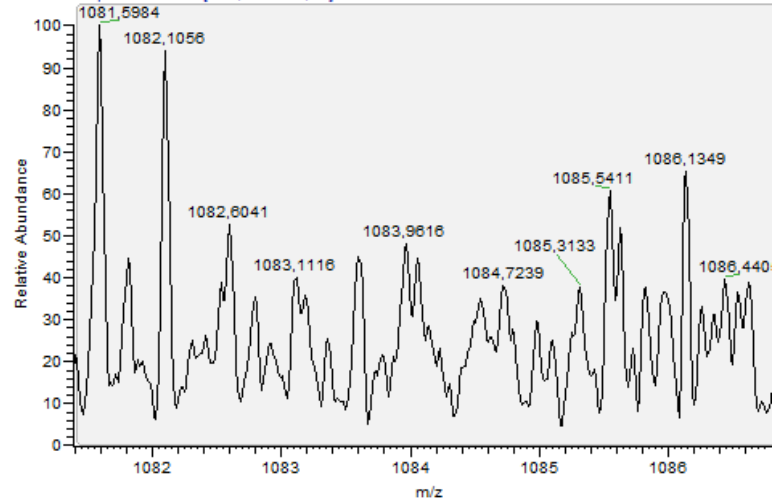


AQATGKPAQYIAVHVVPDQL 2+

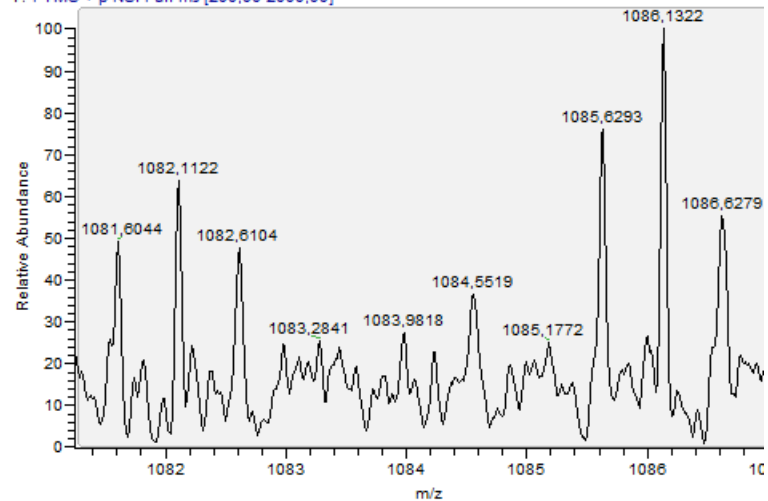
cortex_01 #8522-8649 RT: 54,10-54,77 AV: 10 NL: 2,18E4
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #10571-11042 RT: 56,67-58,52 AV: 70 NL: 2,18E3
T: FTMS + p NSI Full ms [200,00-2000,00]

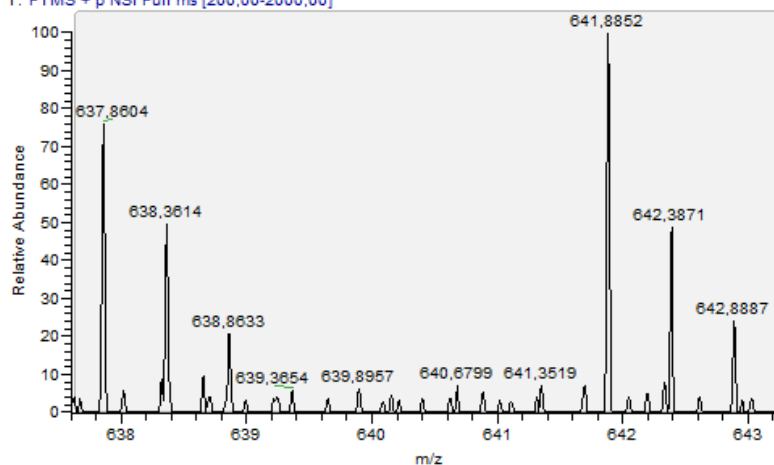


cortex_04 #10203-10539 RT: 55,93-57,40 AV: 80 NL: 2,50E3
T: FTMS + p NSI Full ms [200,00-2000,00]

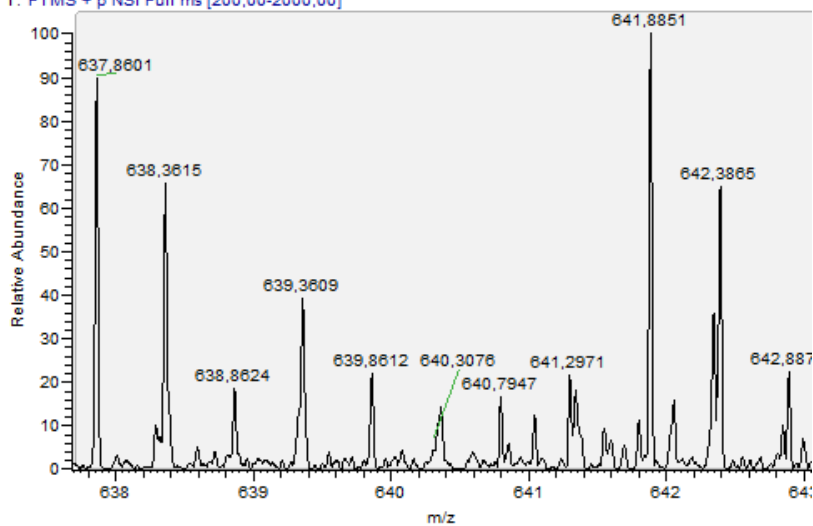


AQATGKPAQYIA 2+

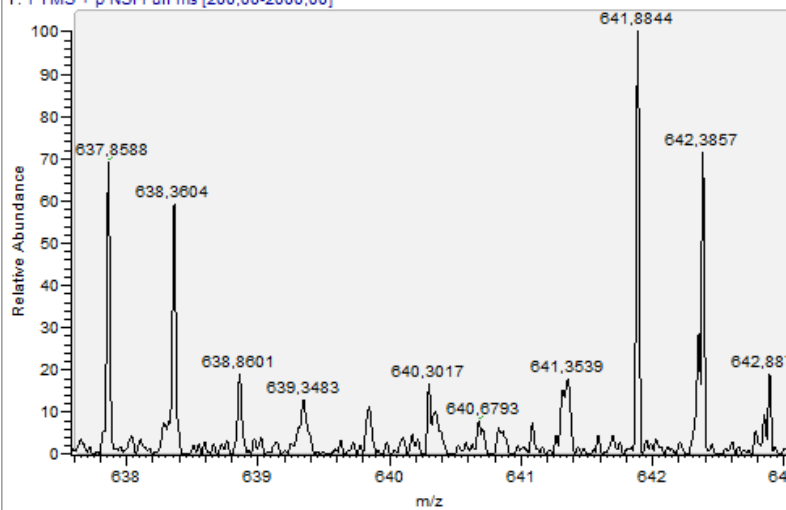
cortex_01 #3670 RT: 26.20 AV: 1 NL: 2,19E5
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #4811-5076 RT: 33.34-34.43 AV: 59 NL: 4,23E3
T: FTMS + p NSI Full ms [200,00-2000,00]



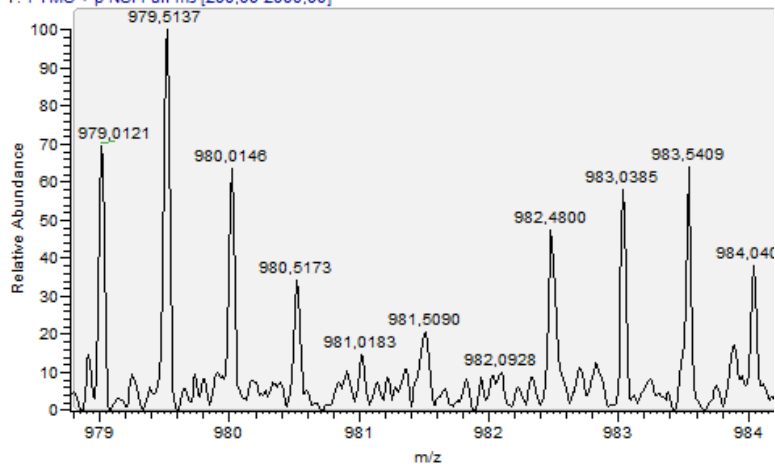
cortex_04 #4718-4894 RT: 32.23-32.94 AV: 45 NL: 9,63E3
T: FTMS + p NSI Full ms [200,00-2000,00]



EDENFILKHTGPGILSM 2+

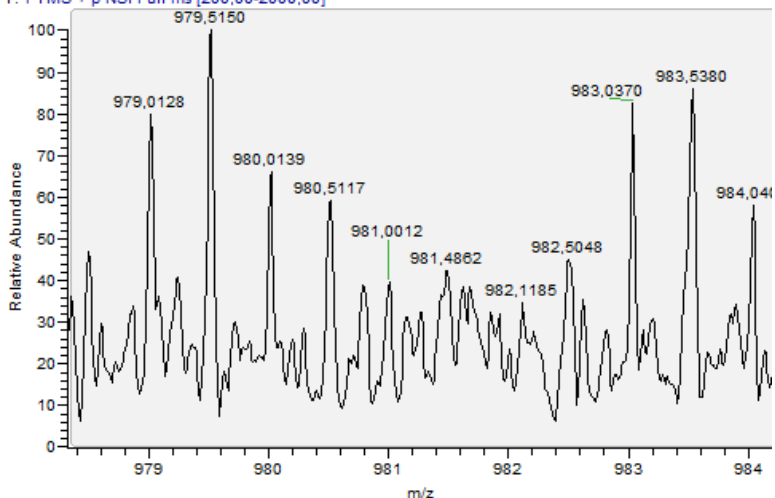
cortex_01 #10094-10282 RT: 63.36-64.41 AV: 10 NL: 1,54E4

T: FTMS + p NSI Full ms [200.00-2000.00]



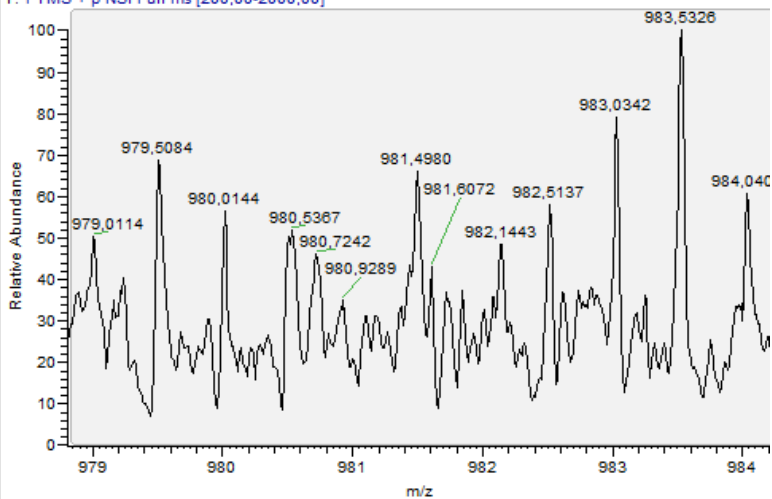
cortex_03 #12337-12793 RT: 63.73-65.55 AV: 72 NL: 2,68E3

T: FTMS + p NSI Full ms [200.00-2000.00]



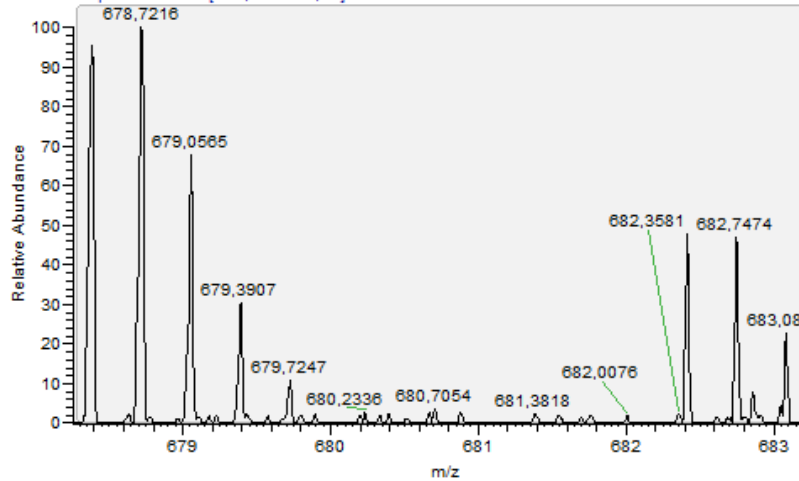
cortex_04 #12155-12595 RT: 64.44-66.27 AV: 78 NL: 2,15E3

T: FTMS + p NSI Full ms [200.00-2000.00]

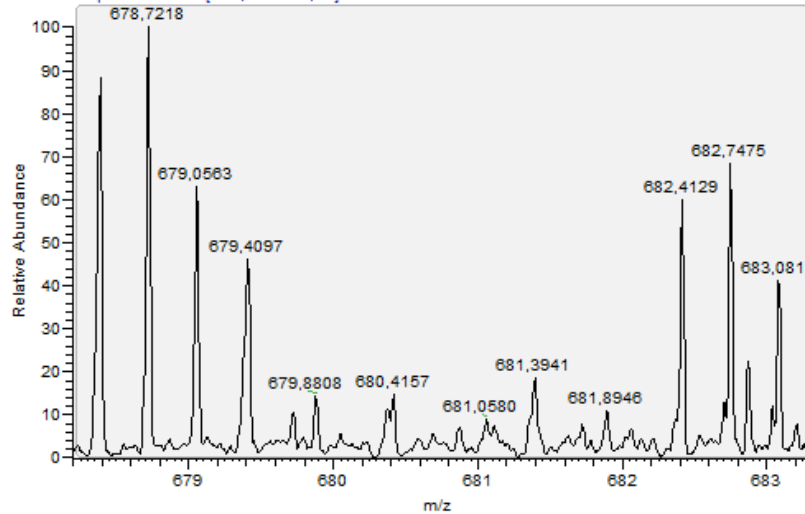


ELFADKVPKTAENFRAL 3+

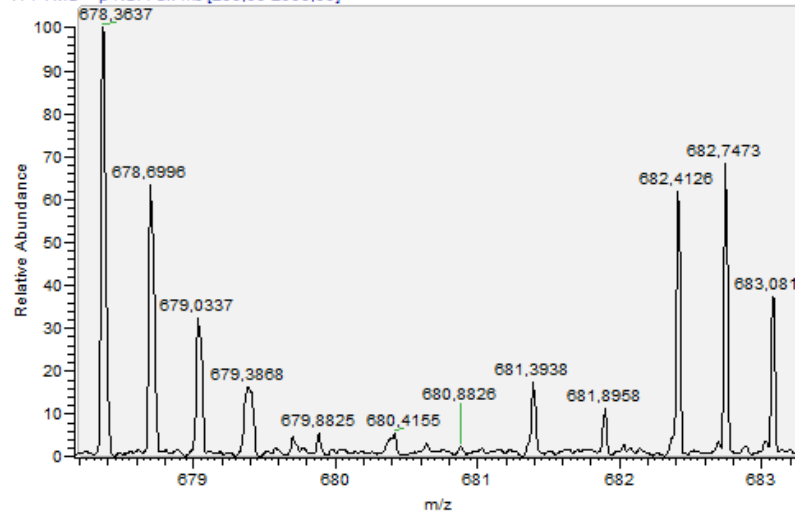
cortex_01 #8175 RT: 52.02 AV: 1 NL: 2,21E5
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #10200-10571 RT: 55.20-56.66 AV: 61 NL: 2,77E4
T: FTMS + p NSI Full ms [200,00-2000,00]

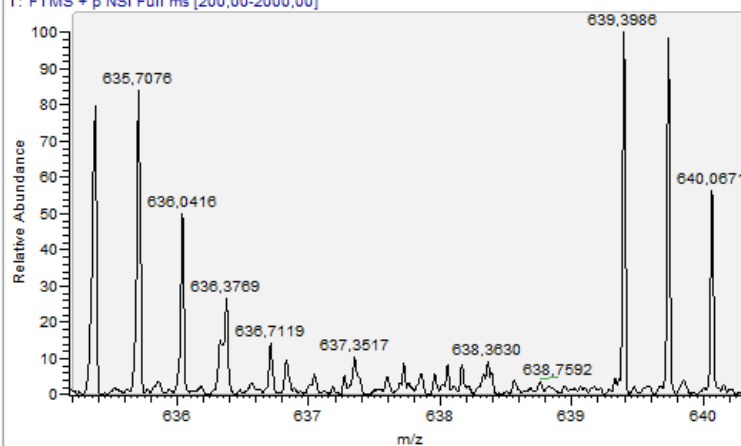


cortex_04 #9861-10203 RT: 54.46-55.93 AV: 78 NL: 4,43E4
T: FTMS + p NSI Full ms [200,00-2000,00]

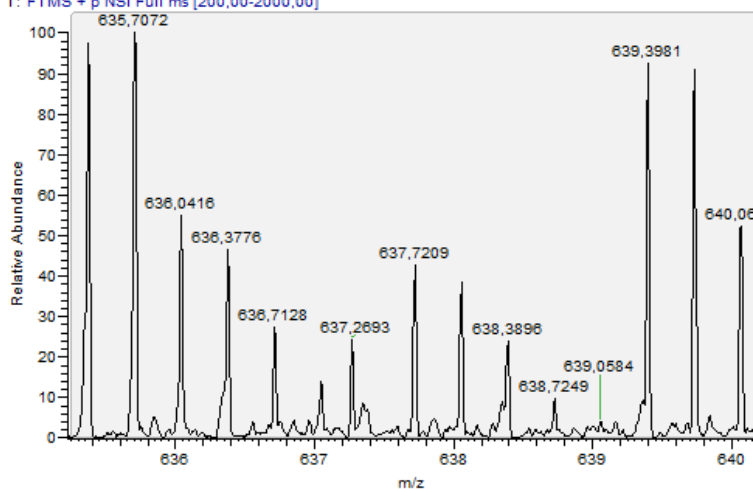


LFADKVPKTAENFRAL 3+

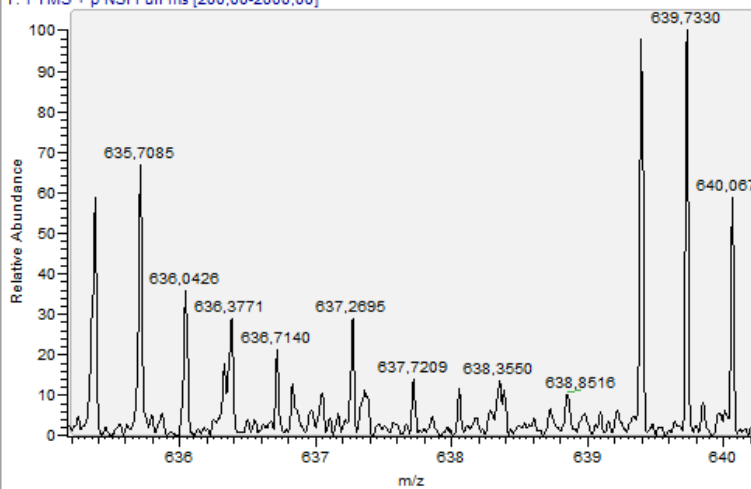
cortex_01 #6855-7102 RT: 44.15-45.55 AV: 26 NL: 7.43E4
T: FTMS + p NSI Full ms [200.00-2000.00]



cortex_03 #8901-9270 RT: 50.03-51.48 AV: 62 NL: 1.80E4
T: FTMS + p NSI Full ms [200.00-2000.00]

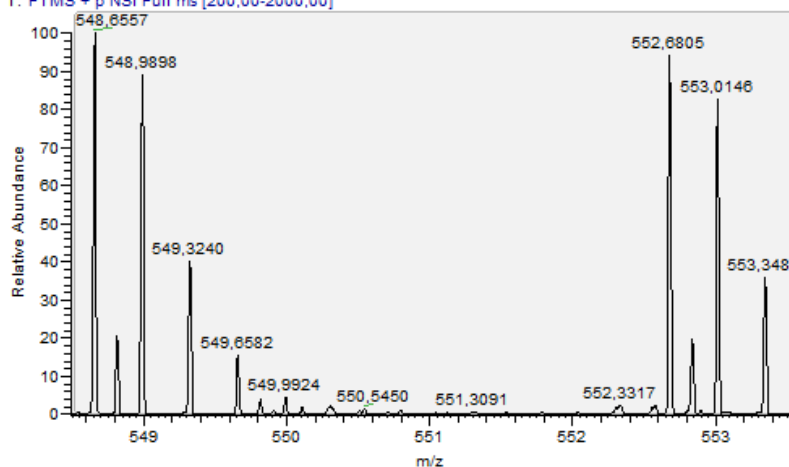


cortex_04 #8559-8732 RT: 48.89-49.61 AV: 35 NL: 1.40E4
T: FTMS + p NSI Full ms [200.00-2000.00]

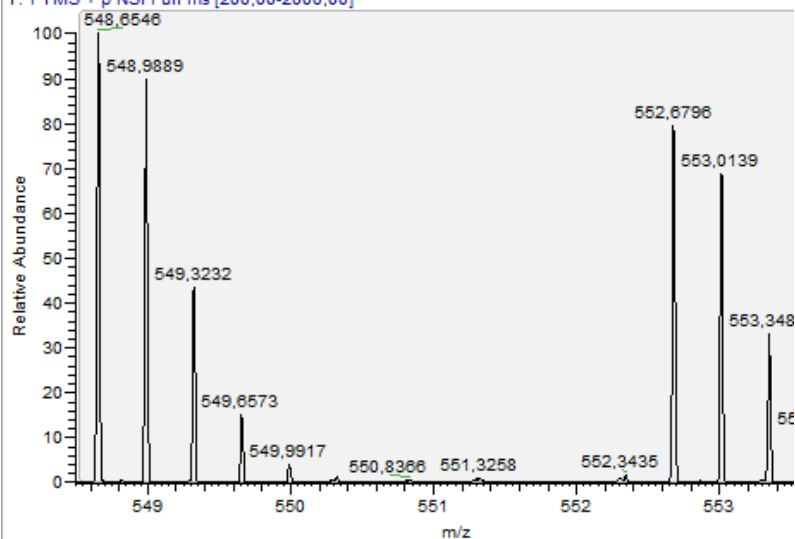


ADKVPKTAENFRAL 3+

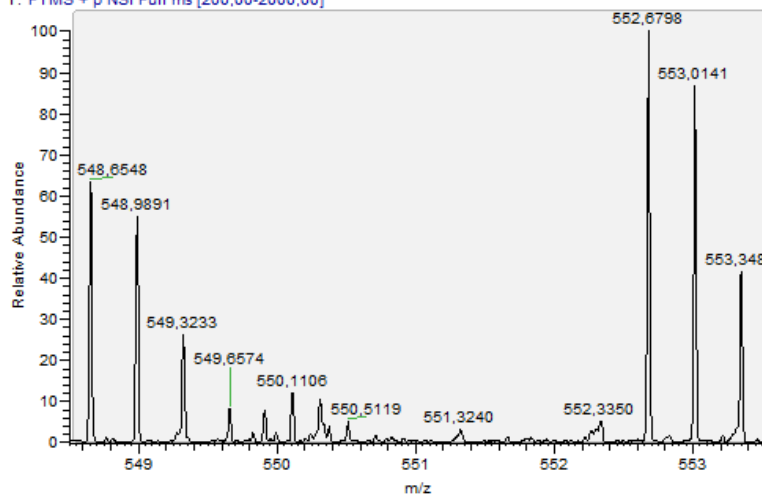
cortex_01 #4456-4724 RT: 30.43-31.85 AV: 15 NL: 1.01E6
T: FTMS + p NSI Full ms [200.00-2000.00]



cortex_03 #6147-6506 RT: 38.91-40.37 AV: 75 NL: 1.86E5
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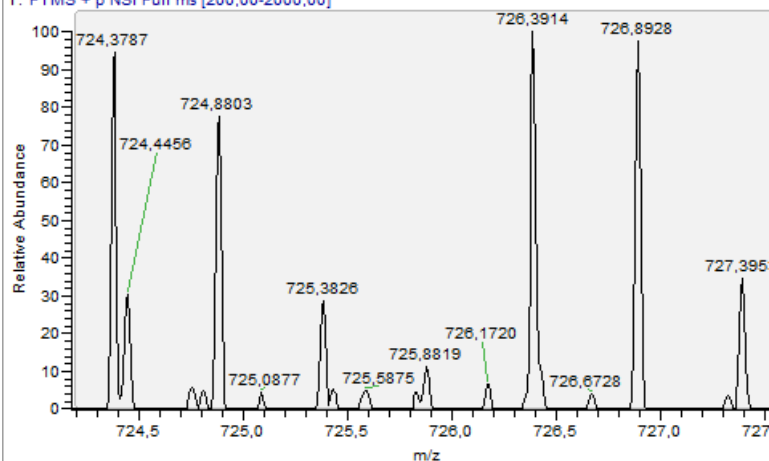


cortex_04 #6090-6434 RT: 38.15-39.60 AV: 90 NL: 4.96E4
T: FTMS + p NSI Full ms [200.00-2000.00]

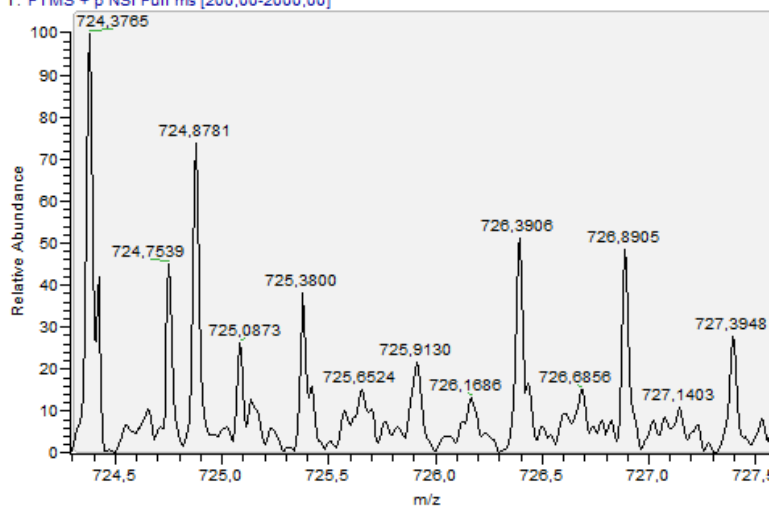


ITADDEPLGRVSF 2+

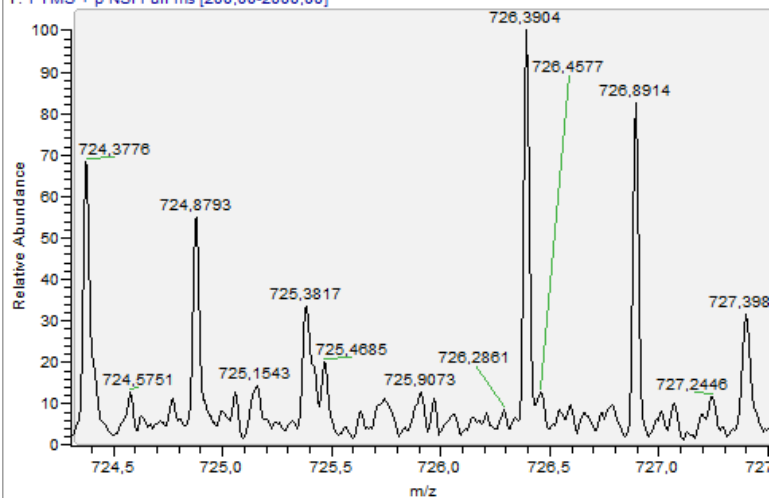
cortex_01 #8729 RT: 55,29 AV: 1 NL: 7,51E4
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #11136-11326 RT: 58,89-59,62 AV: 26 NL: 1,53E4
T: FTMS + p NSI Full ms [200,00-2000,00]



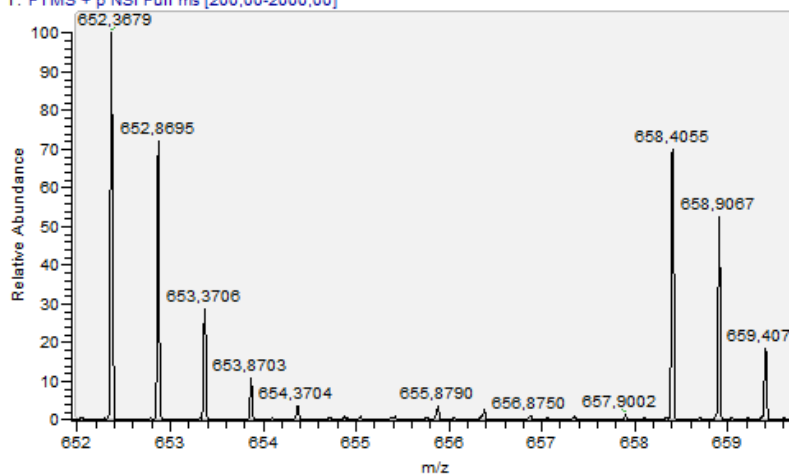
cortex_04 #10886-11051 RT: 58,89-59,63 AV: 42 NL: 8,23E3
T: FTMS + p NSI Full ms [200,00-2000,00]



ADKVPKTAENF 2+

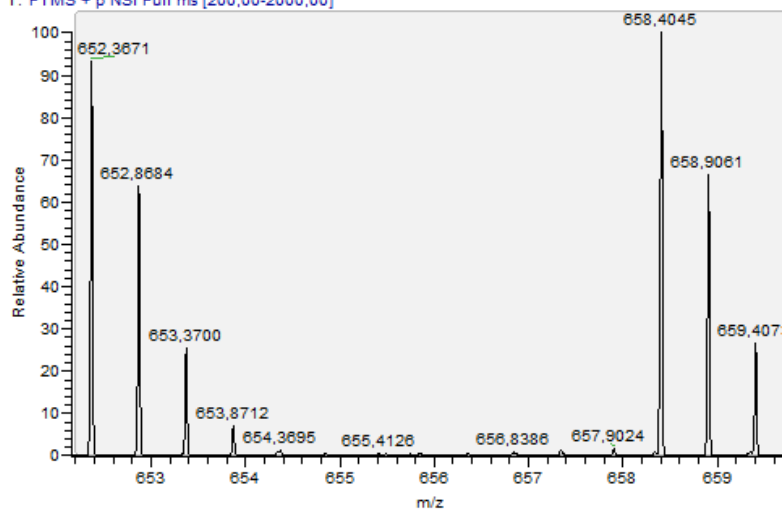
cortex_01 #3550-3760 RT: 25,64-26,64 AV: 10 NL: 7,20E5

T: FTMS + p NSI Full ms [200,00-2000,00]



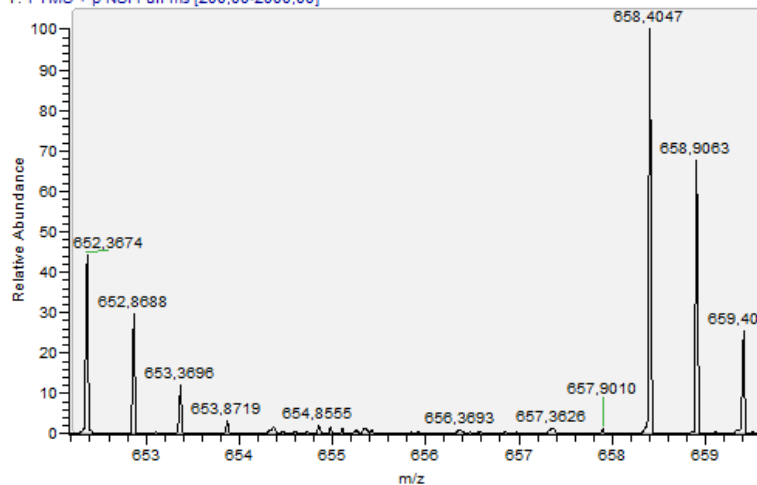
cortex_03 #4715-4900 RT: 32,98-33,70 AV: 34 NL: 1,09E5

T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_04 #4634-4807 RT: 31,86-32,59 AV: 48 NL: 1,18E5

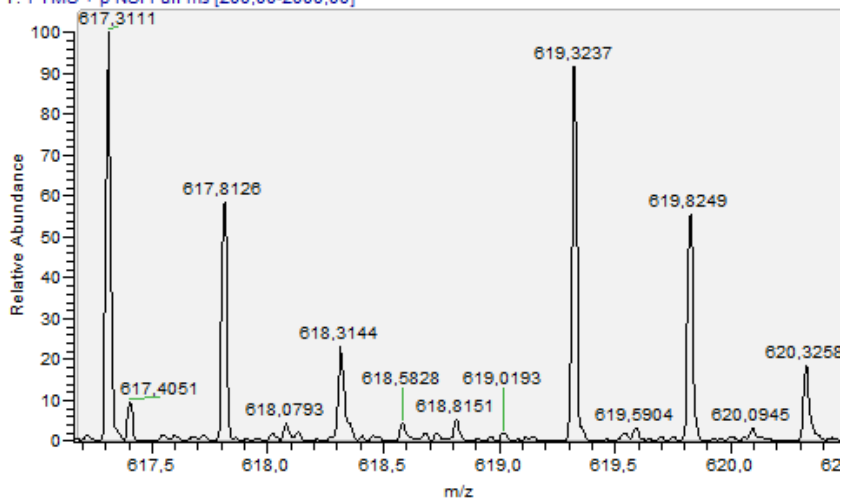
T: FTMS + p NSI Full ms [200,00-2000,00]



ADDEPLGRVSF 2+

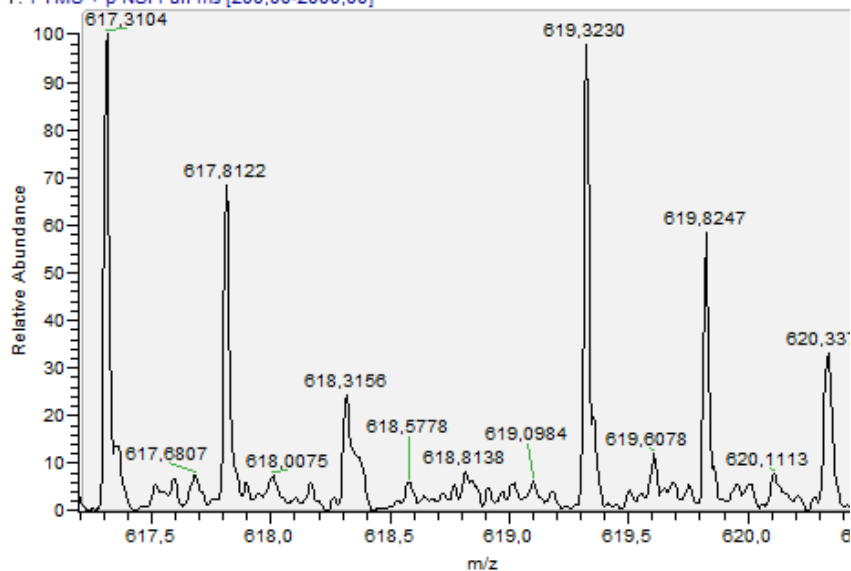
cortex_01 #7346-7470 RT: 47,13-47,76 AV: 7 NL: 1,16E5

T: FTMS + p NSI Full ms [200,00-2000,00]



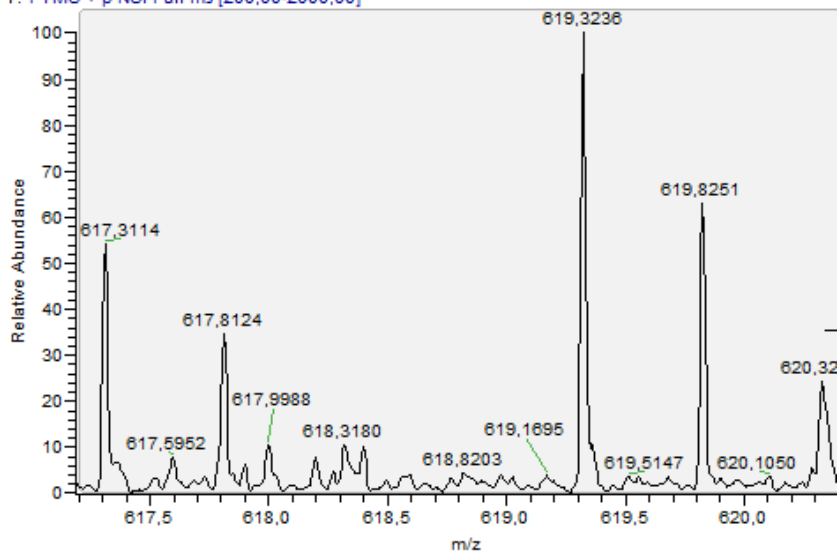
cortex_03 #9824-10291 RT: 53,73-55,54 AV: 76 NL: 1,49E4

T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_04 #9684-9943 RT: 53,70-54,80 AV: 58 NL: 1,95E4

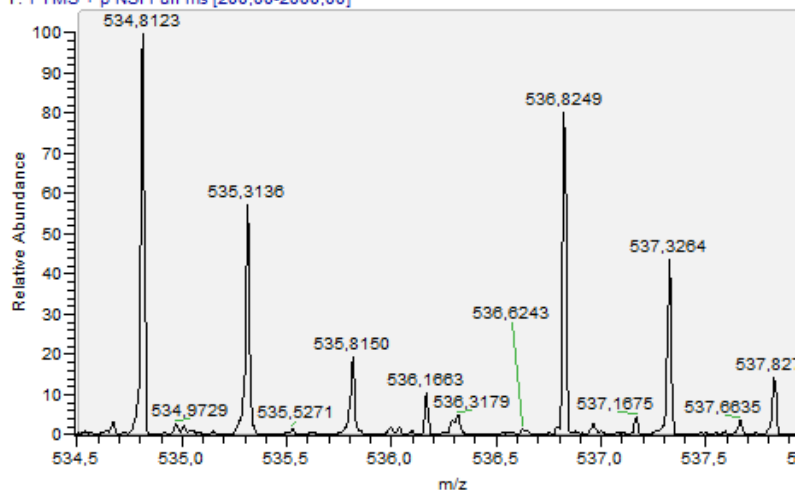
T: FTMS + p NSI Full ms [200,00-2000,00]



SGQAAARPLVA 2+

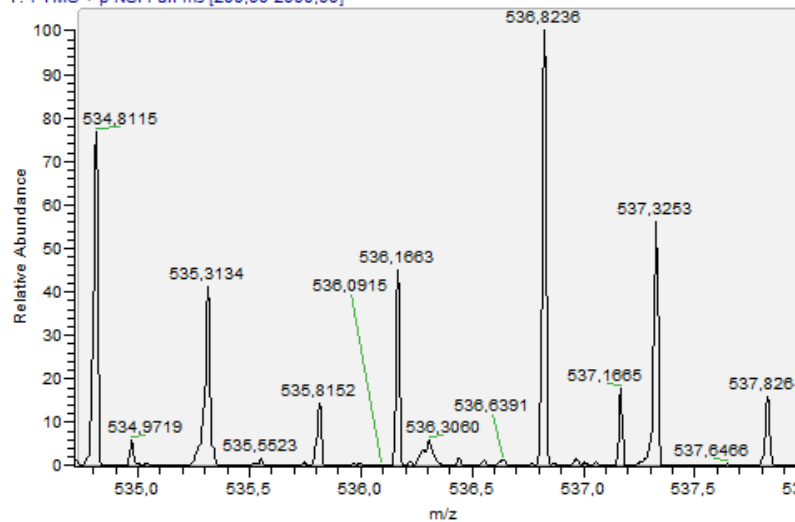
cortex_01 #3140-3344 RT: 23,37-24,41 AV: 10 NL: 2,26E5

T: FTMS + p NSI Full ms [200,00-2000,00]



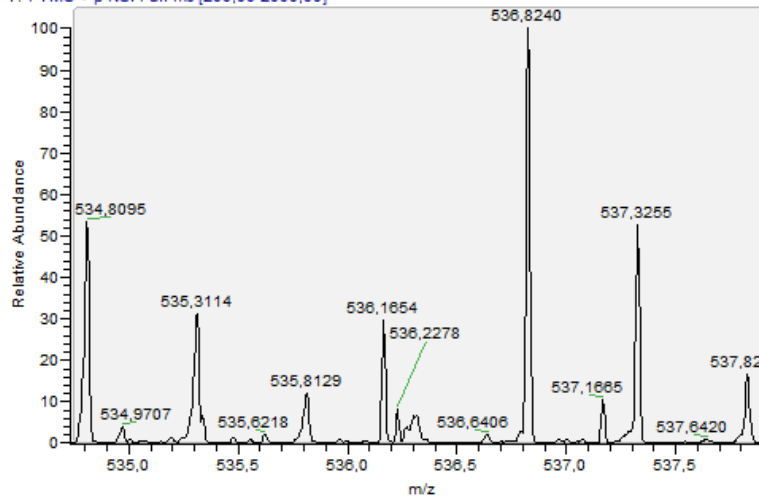
cortex_03 #4103-4370 RT: 30,38-31,48 AV: 58 NL: 2,14E4

T: FTMS + p NSI Full ms [200,00-2000,00]



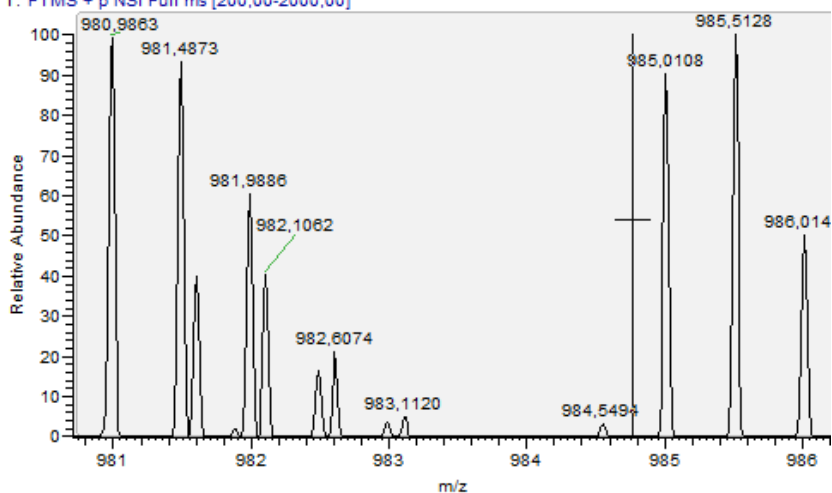
cortex_04 #3935-4285 RT: 28,89-30,37 AV: 97 NL: 3,68E4

T: FTMS + p NSI Full ms [200,00-2000,00]

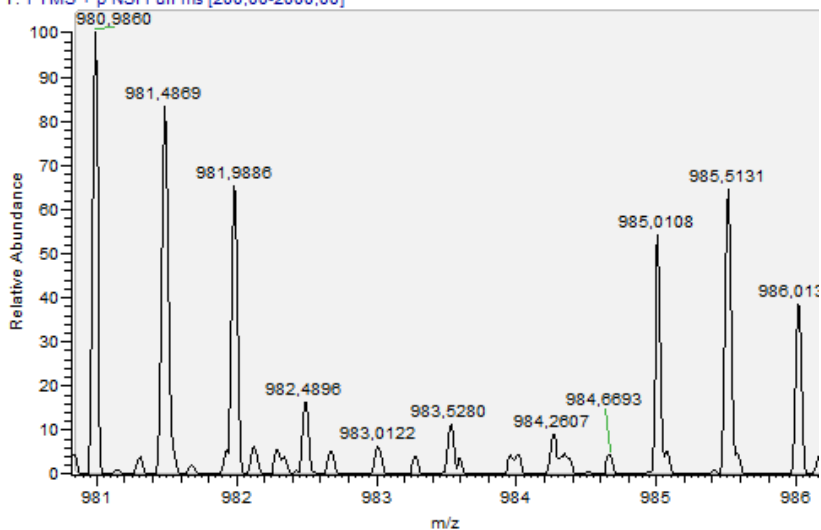


KGP GPGGPGGAGGARGGAGGGPSGD 2+

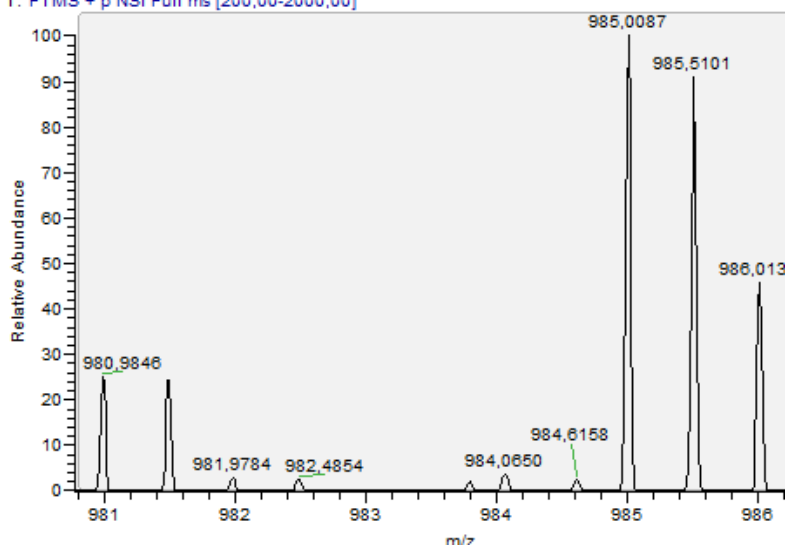
cortex_01 #2174-2416 RT: 17.83-19.24 AV: 12 NL: 7,27E3
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #2453-2681 RT: 22.97-24.08 AV: 77 NL: 1,85E2
T: FTMS + p NSI Full ms [200,00-2000,00]



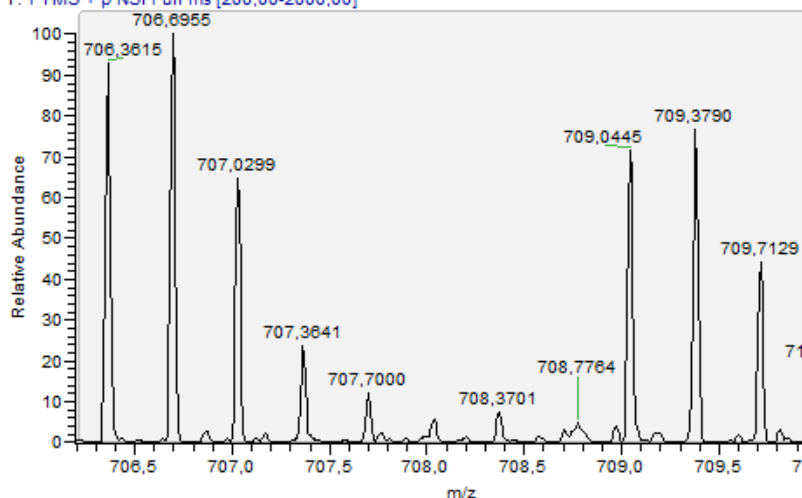
cortex_04 #2337-2510 RT: 22.22-22.96 AV: 42 NL: 9,71E2
T: FTMS + p NSI Full ms [200,00-2000,00]



RKGP GPGPGGAGGARGGAGGGPSGD 3+

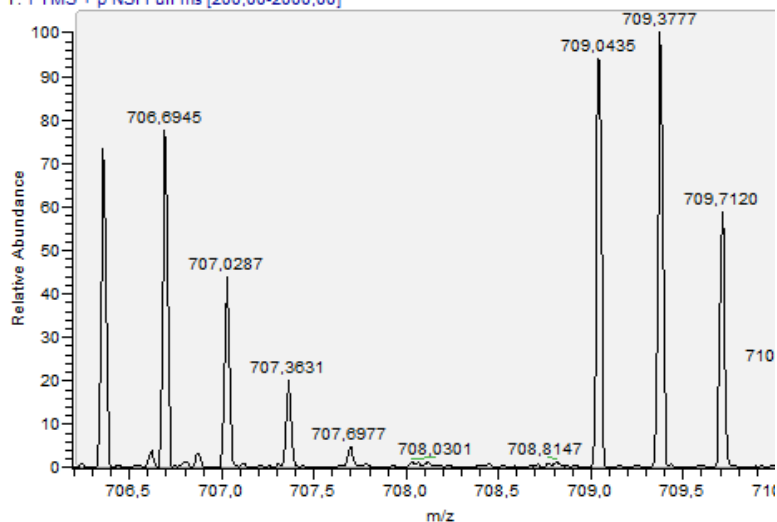
cortex_01 #1881-2174 RT: 15,92-17,70 AV: 16 NL: 1,51E4

T: FTMS + p NSI Full ms [200,00-2000,00]



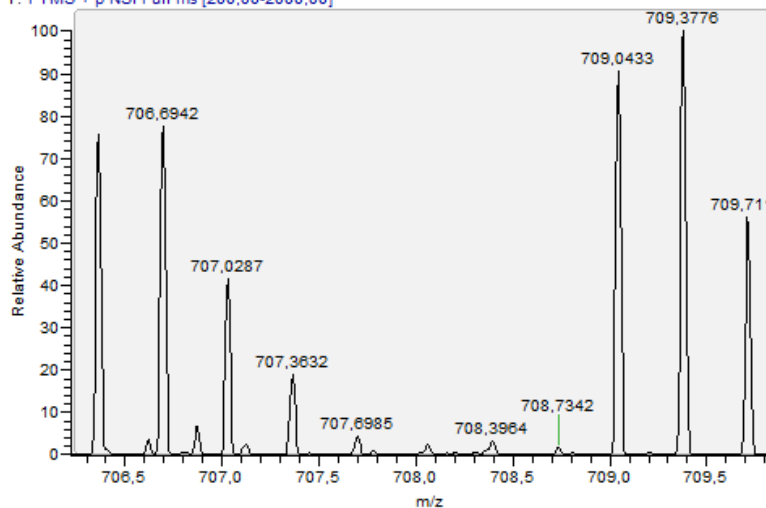
cortex_03 #2312-2599 RT: 22,23-23,70 AV: 111 NL: 2,48E3

T: FTMS + p NSI Full ms [200,00-2000,00]



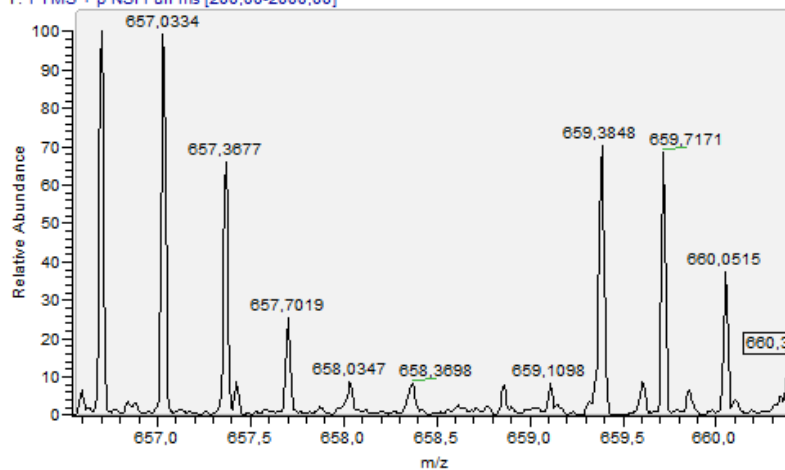
cortex_04 #2005-2250 RT: 20,75-21,85 AV: 70 NL: 2,38E3

T: FTMS + p NSI Full ms [200,00-2000,00]

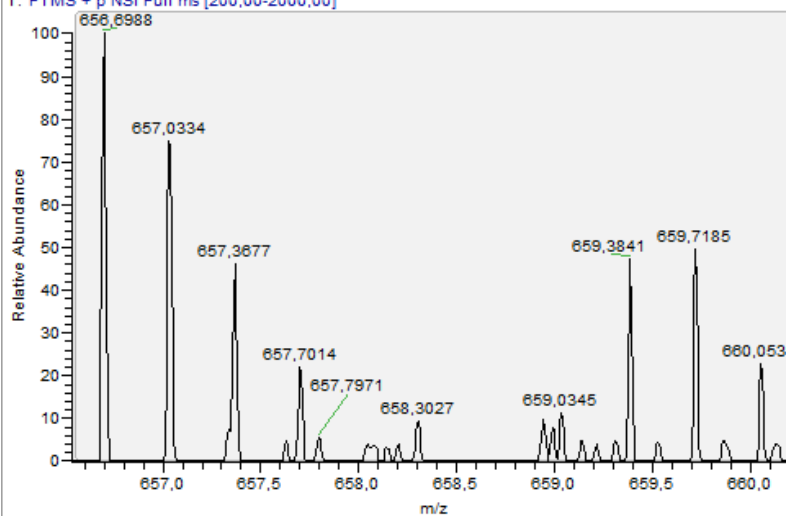


KQATVGDVNTDRPGLLDL 3+

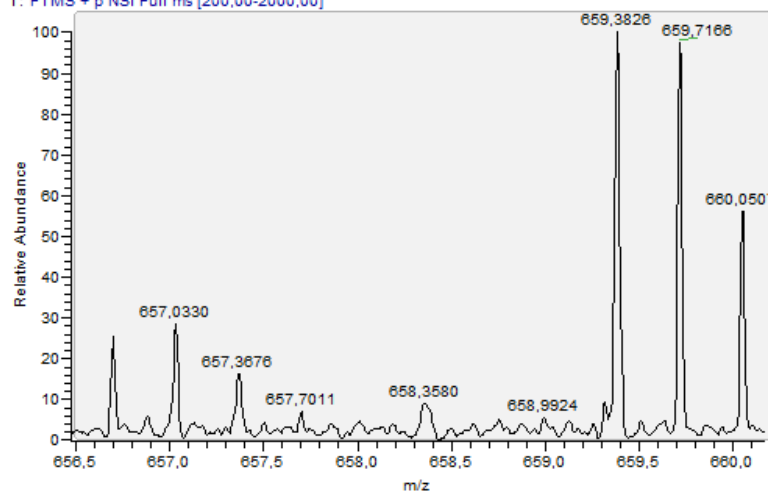
cortex_01 #7716-8022 RT: 49,26-51,05 AV: 26 NL: 6,71E4
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #10648 RT: 56,97 AV: 1 NL: 5,26E4
T: FTMS + p NSI Full ms [200,00-2000,00]

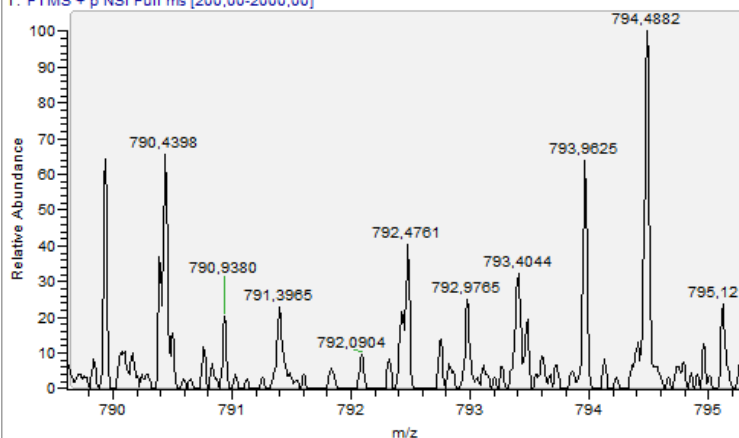


cortex_04 #9943-10203 RT: 54,82-55,93 AV: 59 NL: 2,21E4
T: FTMS + p NSI Full ms [200,00-2000,00]

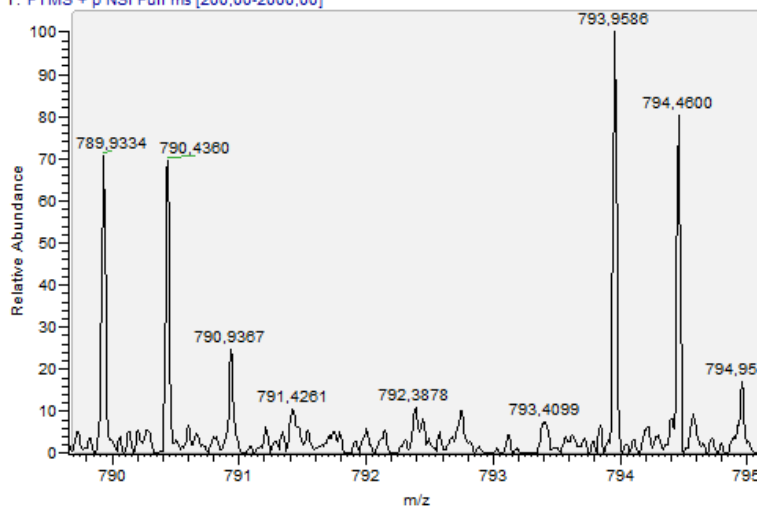


AANSKVAFSVRSTN 2+

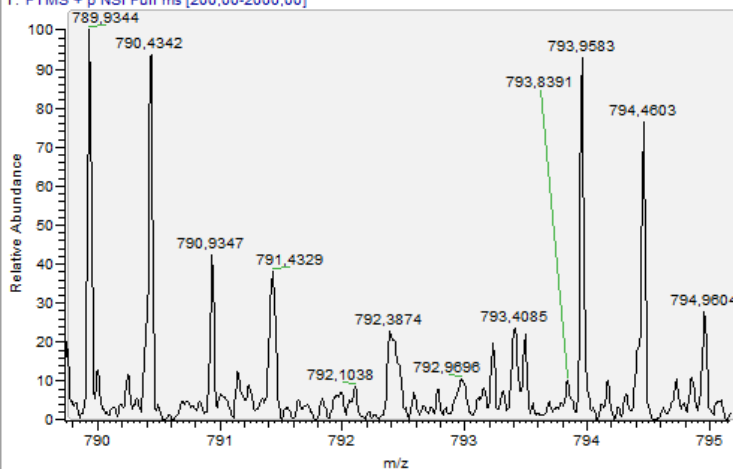
cortex_01 #3478-3830 RT: 25,21-26,96 AV: 17 NL: 1,34E4
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #4715-4986 RT: 32,98-34,08 AV: 57 NL: 2,45E3
T: FTMS + p NSI Full ms [200,00-2000,00]



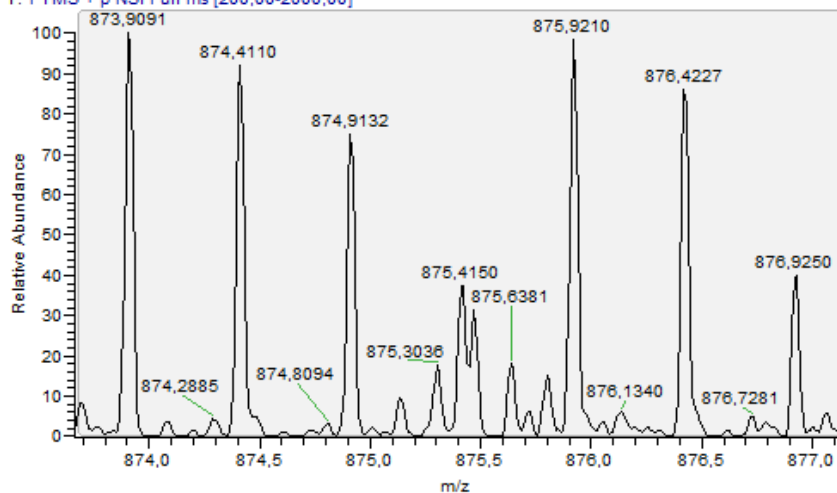
cortex_04 #4368-4982 RT: 30,74-33,32 AV: 160 NL: 2,43E3
T: FTMS + p NSI Full ms [200,00-2000,00]



HNPHVNPLPTGYEDE 2+

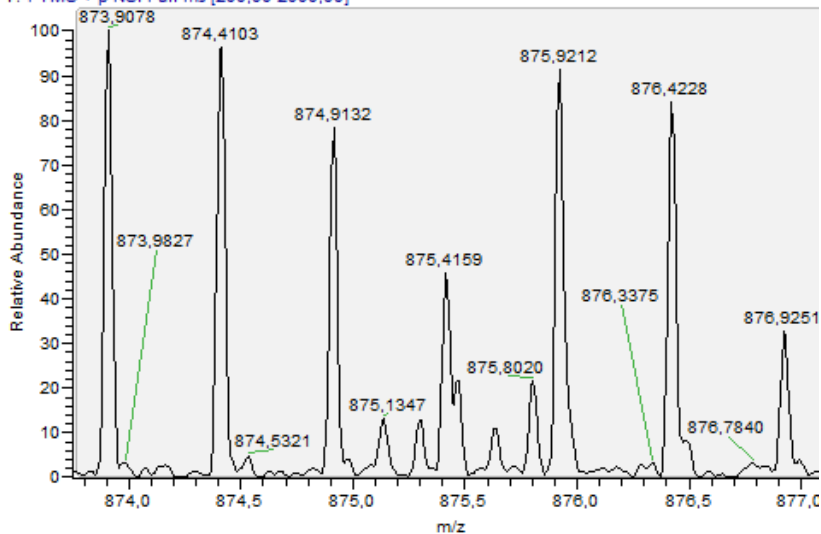
cortex_01 #4724-5052 RT: 31,85-33,59 AV: 19 NL: 3,98E4

T: FTMS + p NSI Full ms [200,00-2000,00]



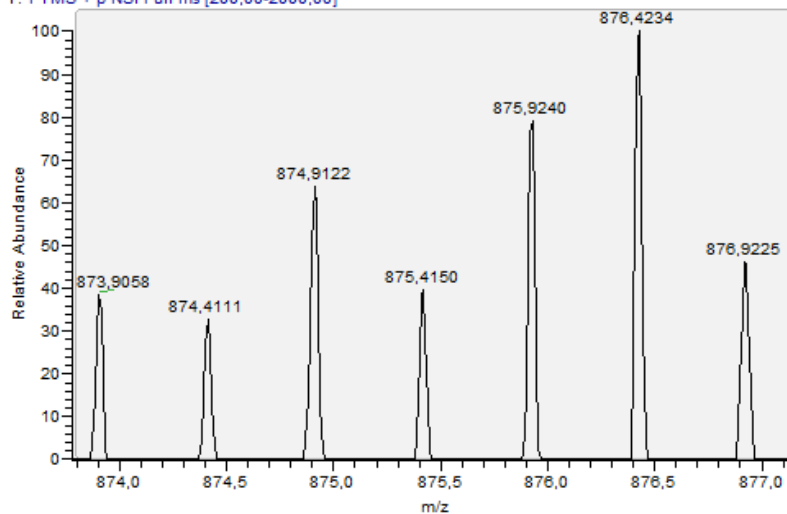
cortex_03 #5965-6232 RT: 38,15-39,25 AV: 57 NL: 5,47E3

T: FTMS + p NSI Full ms [200,00-2000,00]



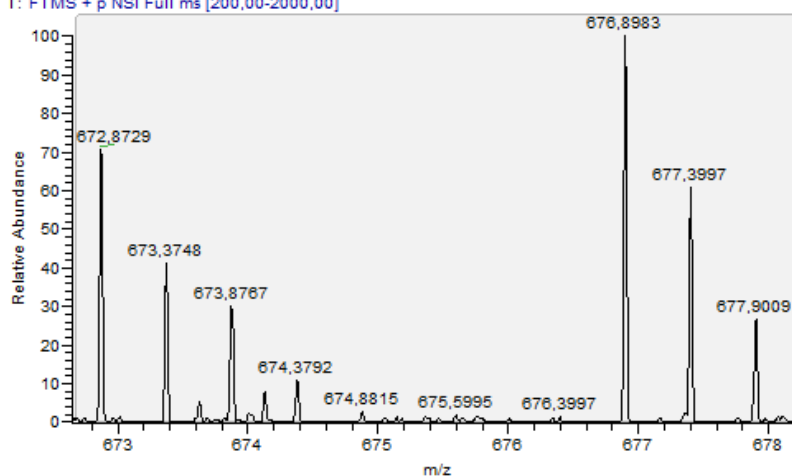
cortex_04 #6044 RT: 37,94 AV: 1 NL: 2,24E4

T: FTMS + p NSI Full ms [200,00-2000,00]

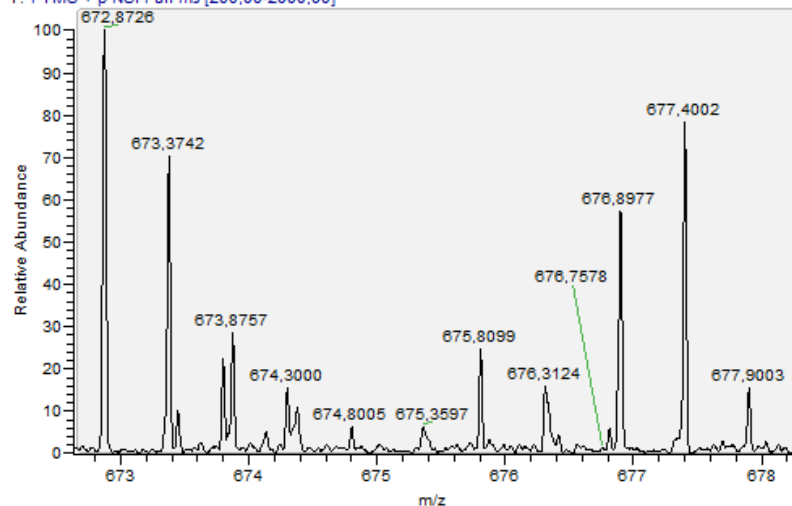


ADEVASLAKQGL

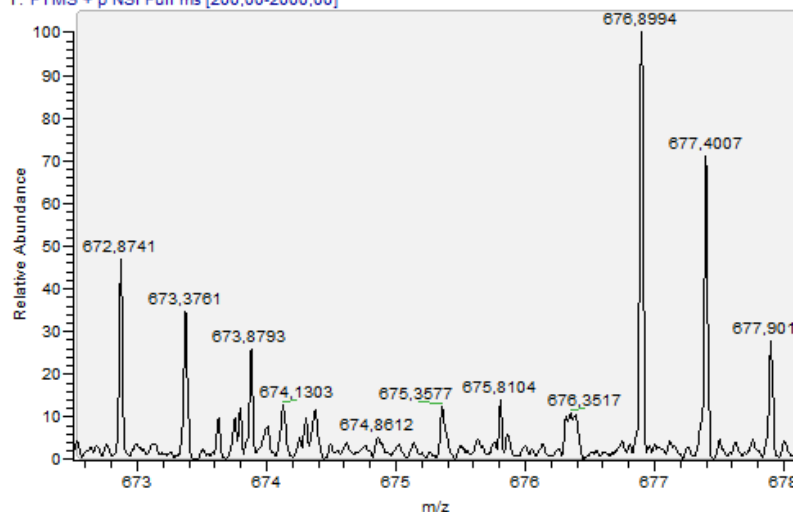
cortex_01 #6303 RT: 40.82 AV: 1 NL: 6.33E5
T: FTMS + p NSI Full ms [200.00-2000.00]



cortex_03 #8076-8432 RT: 46.68-48.13 AV: 76 NL: 2.76E4
T: FTMS + p NSI Full ms [200.00-2000.00]

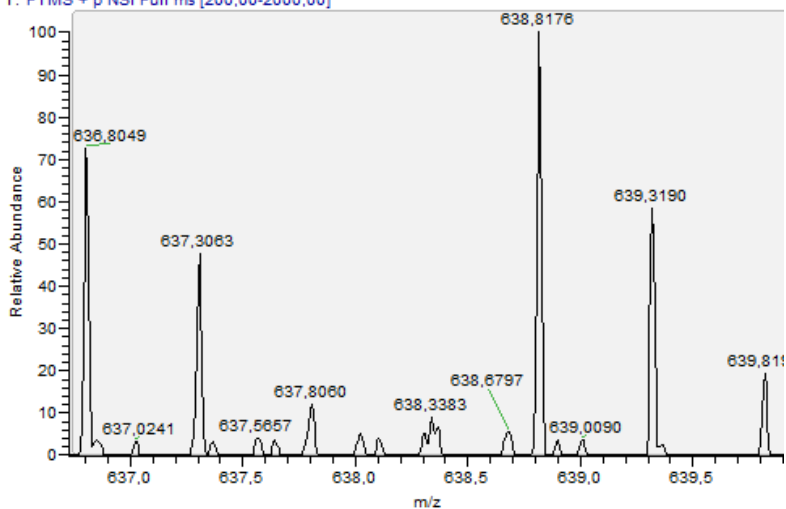


cortex_04 #7883-8213 RT: 45.94-47.40 AV: 79 NL: 1.67E4
T: FTMS + p NSI Full ms [200.00-2000.00]

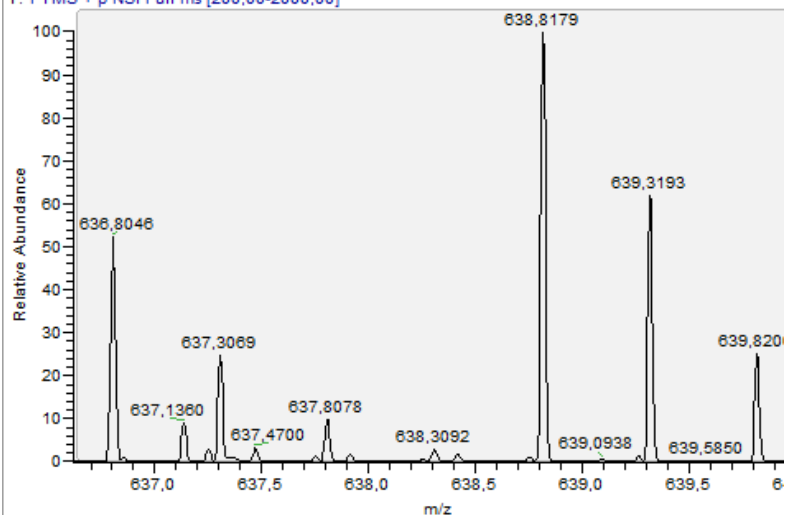


SANSNPAMAPRE 2+

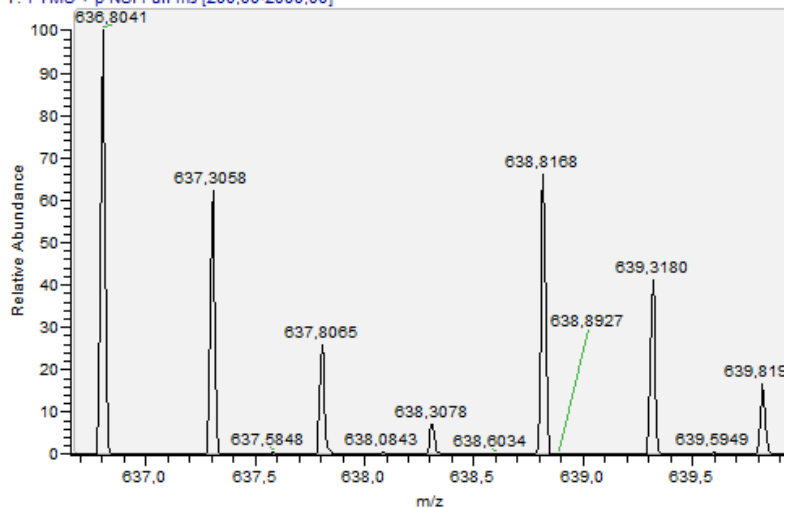
cortex_01 #2610 RT: 20,40 AV: 1 NL: 1,39E5
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #3085-3415 RT: 25,92-27,40 AV: 92 NL: 3,27E4
T: FTMS + p NSI Full ms [200,00-2000,00]

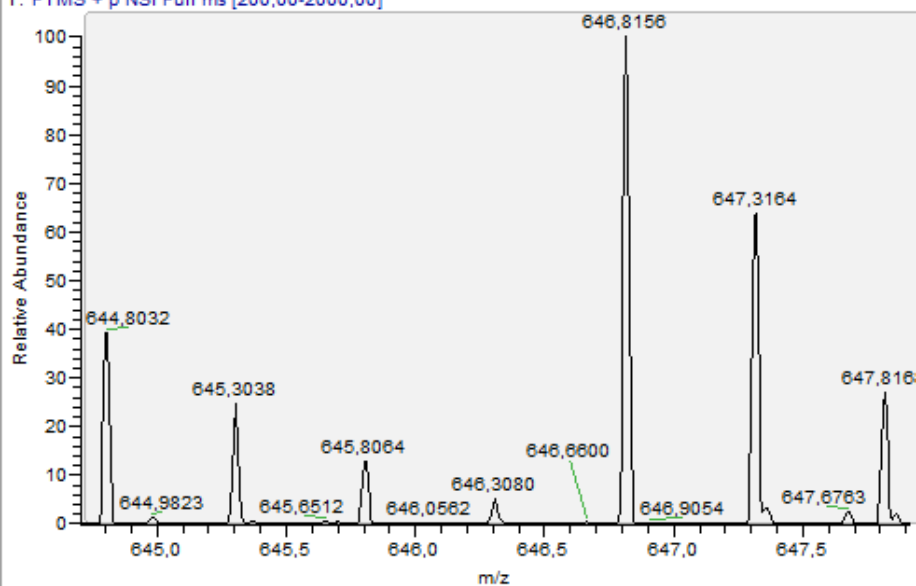


cortex_04 #3231-3329 RT: 25,94-26,28 AV: 13 NL: 2,22E5
T: FTMS + p NSI Full ms [200,00-2000,00]

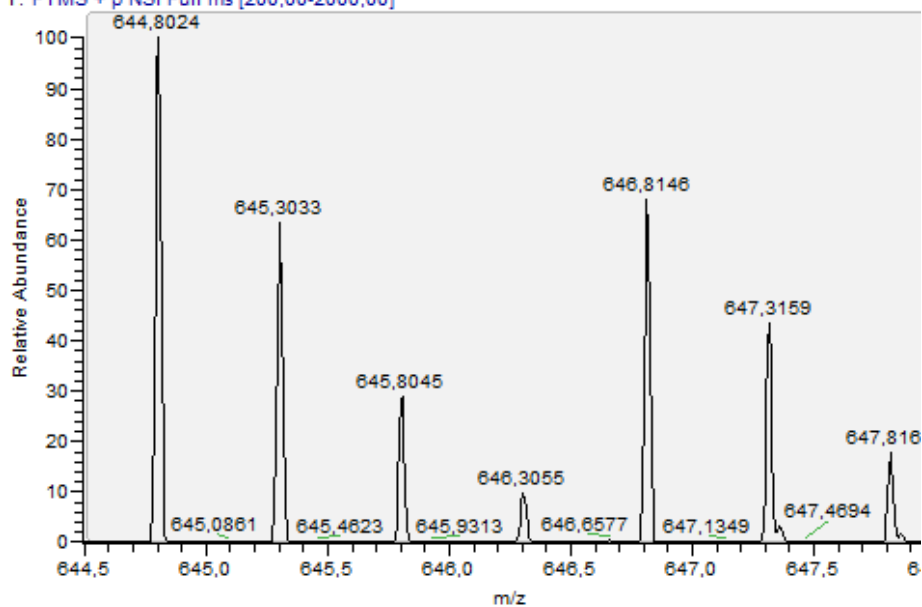


SANSNPAMAPRE 2+ (methionine oxidation)

cortex_03 #2453-3085 RT: 22,97-25,92 AV: 190 NL: 2,43E4
T: FTMS + p NSI Full ms [200,00-2000,00]



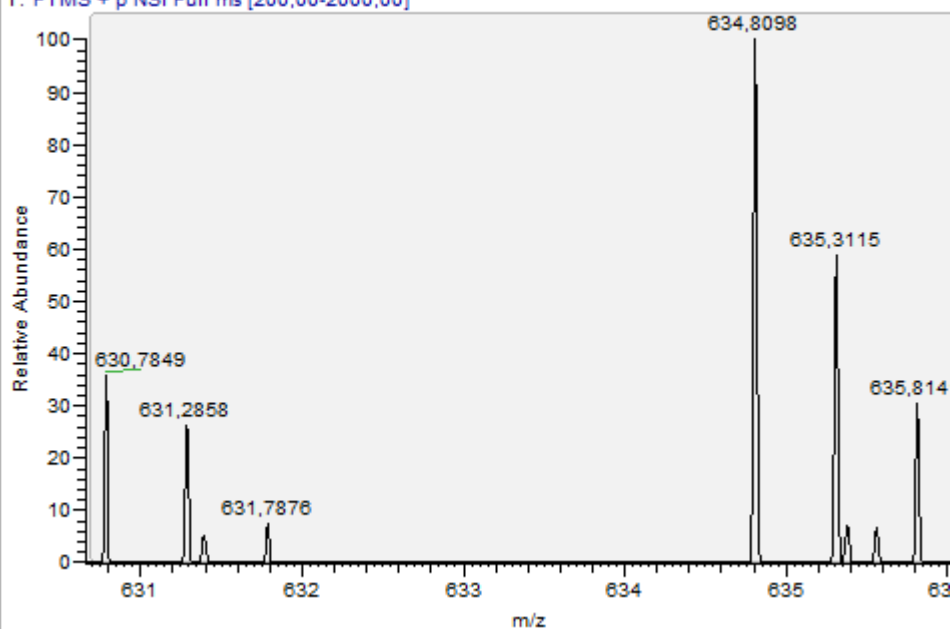
cortex_04 #2354-2826 RT: 22,30-24,24 AV: 103 NL: 8,07E4
T: FTMS + p NSI Full ms [200,00-2000,00]



DDEESEAQGPK 2+

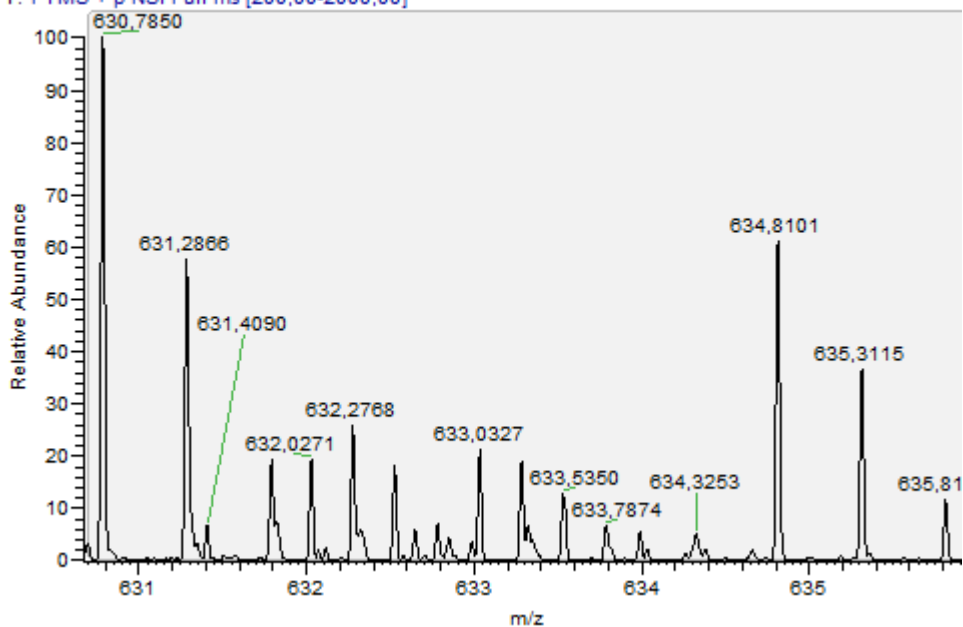
cortex_03 #2283 RT: 22,06 AV: 1 NL: 8,14E3

T: FTMS + p NSI Full ms [200,00-2000,00]



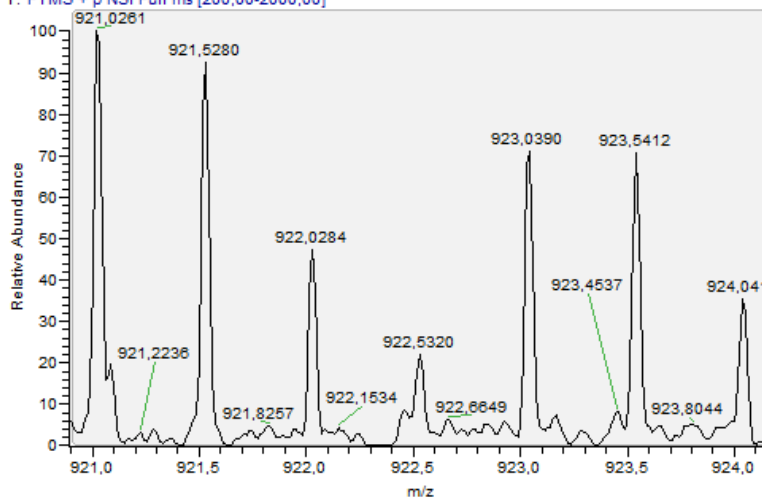
cortex_04 #2082-2419 RT: 21,12-22,59 AV: 88 NL: 2,41E3

T: FTMS + p NSI Full ms [200,00-2000,00]

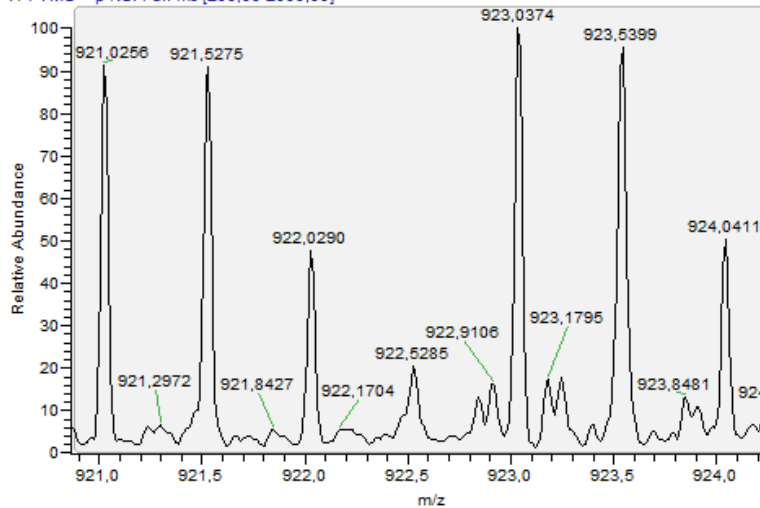


SLSAASAPLVETSTPLRL 2+

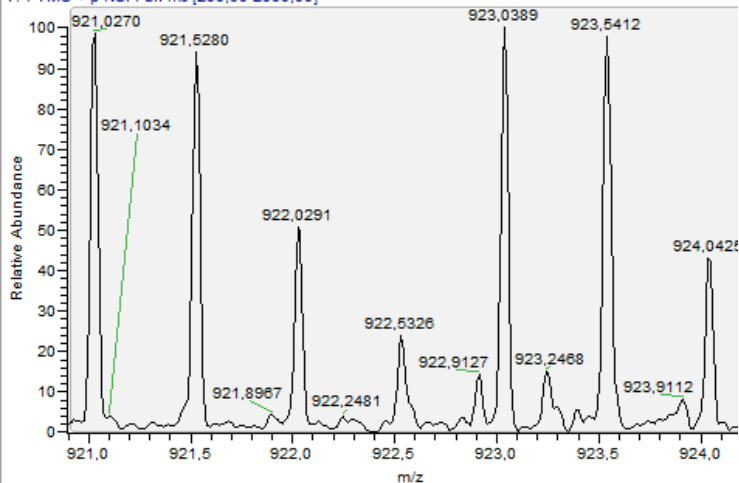
cortex_01 #10219-10600 RT: 64,16-66,19 AV: 18 NL: 1,47E4
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #12979-13245 RT: 66,31-67,41 AV: 46 NL: 1,13E4
T: FTMS + p NSI Full ms [200,00-2000,00]

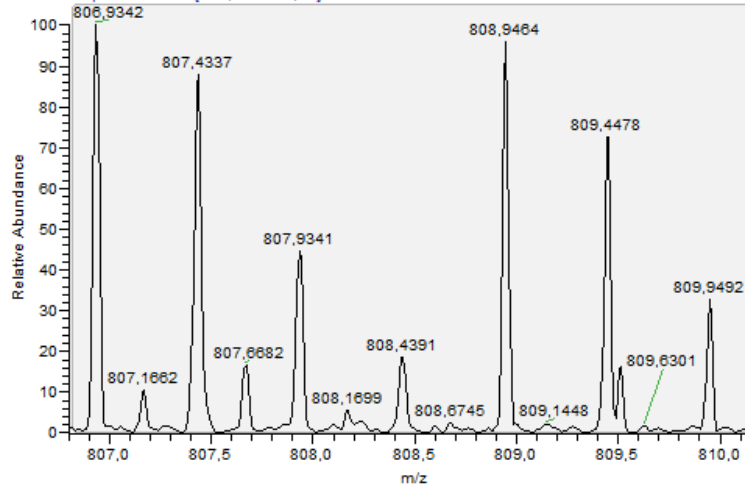


cortex_04 #12509-12758 RT: 65,93-67,01 AV: 50 NL: 1,24E4
T: FTMS + p NSI Full ms [200,00-2000,00]

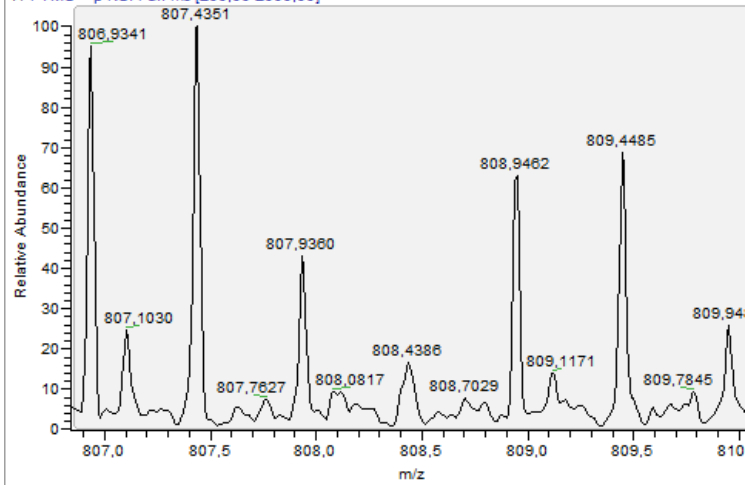


TVGDVNTDRPGLLDL 2+

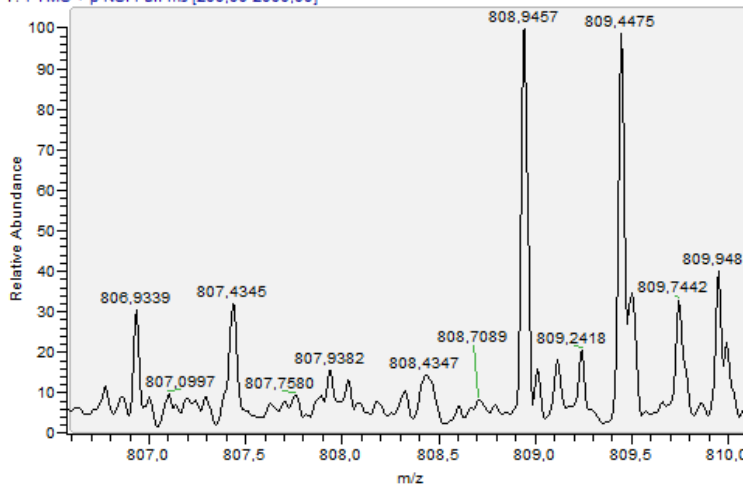
cortex_01 #9337-9526 RT: 58,89-59,94 AV: 12 NL: 6,60E4
T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_03 #12160-12521 RT: 62,99-64,43 AV: 56 NL: 1,62E4
T: FTMS + p NSI Full ms [200,00-2000,00]



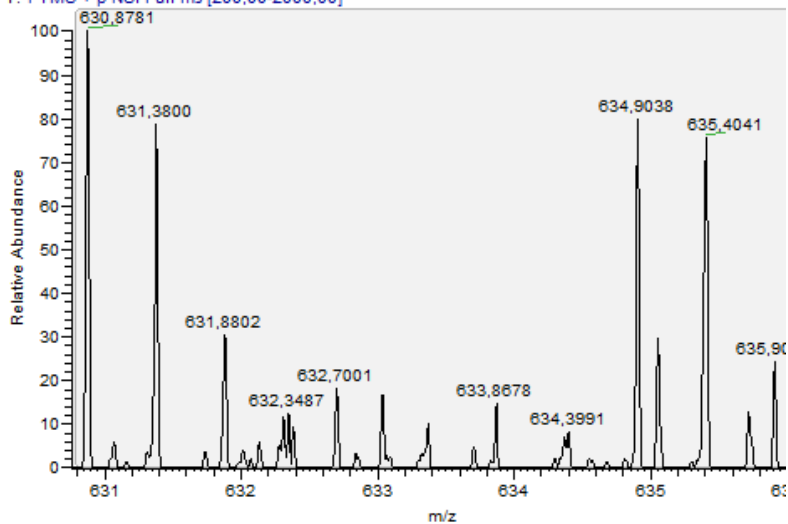
cortex_04 #11632-11979 RT: 62,22-63,70 AV: 73 NL: 1,30E4
T: FTMS + p NSI Full ms [200,00-2000,00]



VFDVELLKLE 2+

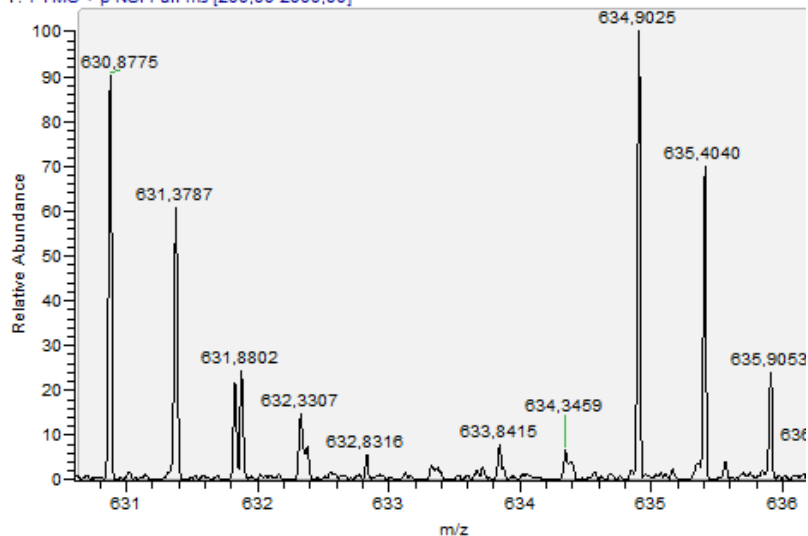
cortex_01 #11352-11414 RT: 70.79-71.04 AV: 3 NL: 2.87E4

T: FTMS + p NSI Full ms [200.00-2000.00]



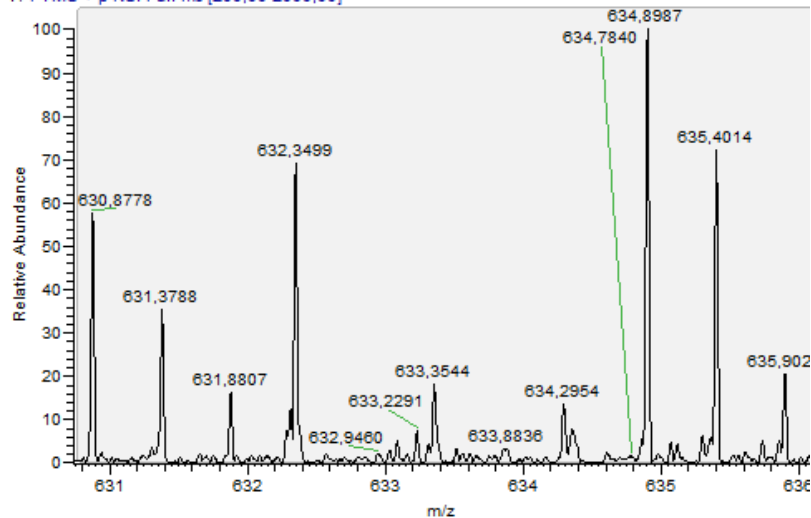
cortex_03 #14420-14787 RT: 72.24-73.68 AV: 56 NL: 2.43E4

T: FTMS + p NSI Full ms [200.00-2000.00]



cortex_04 #14109-14287 RT: 72.61-73.32 AV: 31 NL: 1.26E4

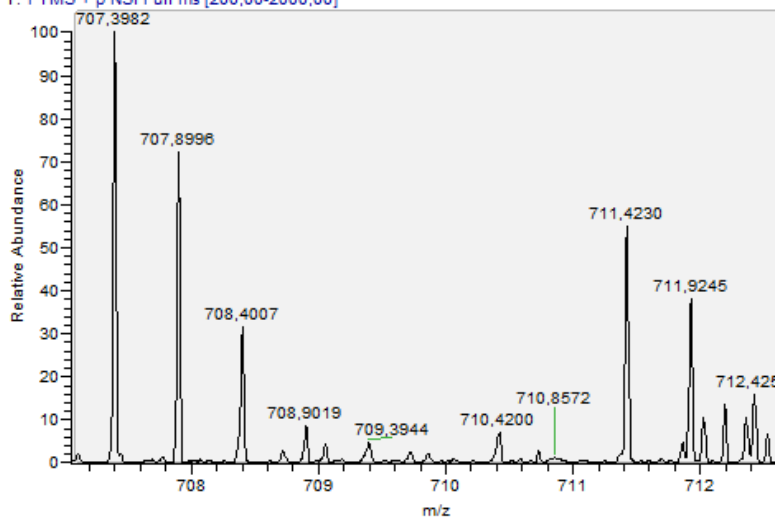
T: FTMS + p NSI Full ms [200.00-2000.00]



GISTPEELGLDKV 2+

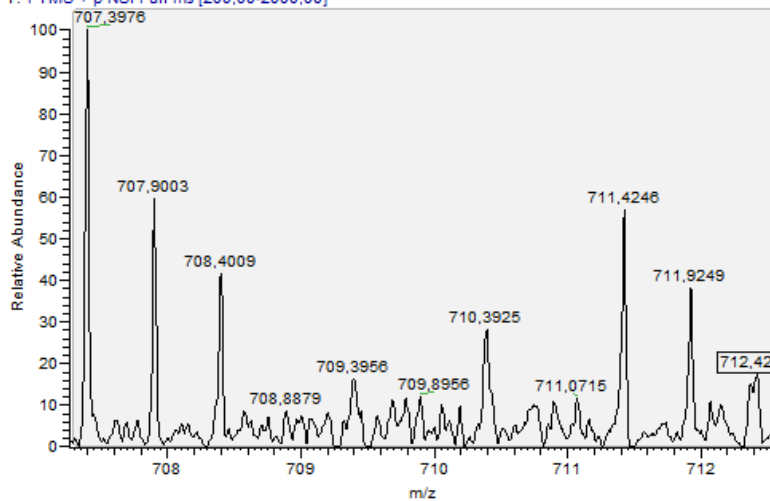
cortex_01 #8458-8713 RT: 53,76-55,12 AV: 19 NL: 1,52E5

T: FTMS + p NSI Full ms [200,00-2000,00]



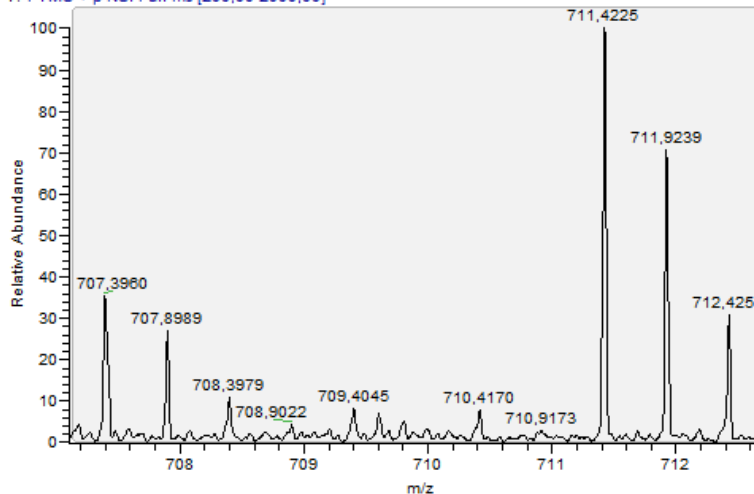
cortex_03 #13079-13322 RT: 66,78-67,74 AV: 39 NL: 6,86E3

T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_04 #10539-10798 RT: 57,40-58,50 AV: 57 NL: 5,27E4

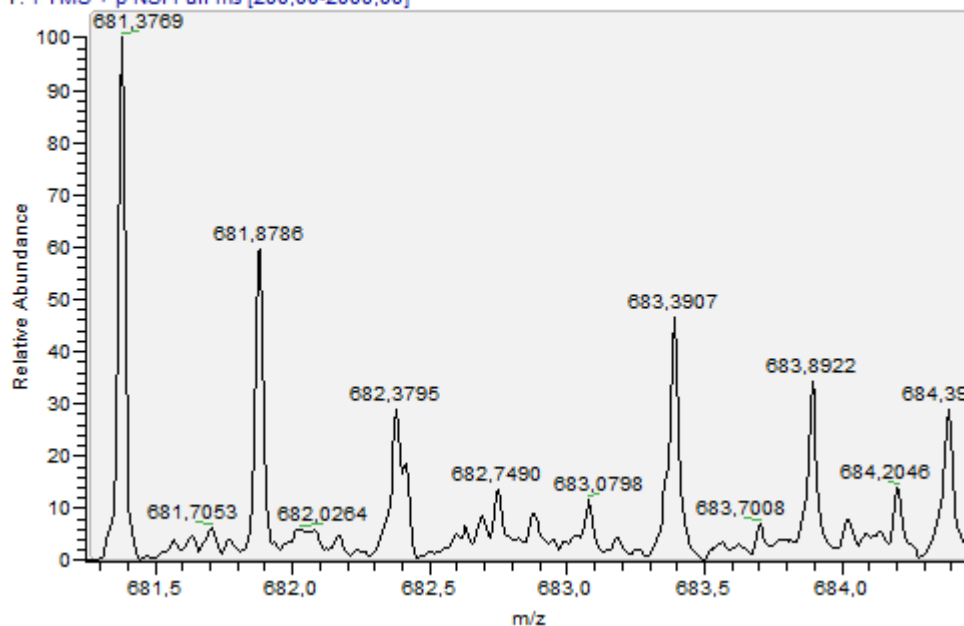
T: FTMS + p NSI Full ms [200,00-2000,00]



NDFASAVRILEV 2+

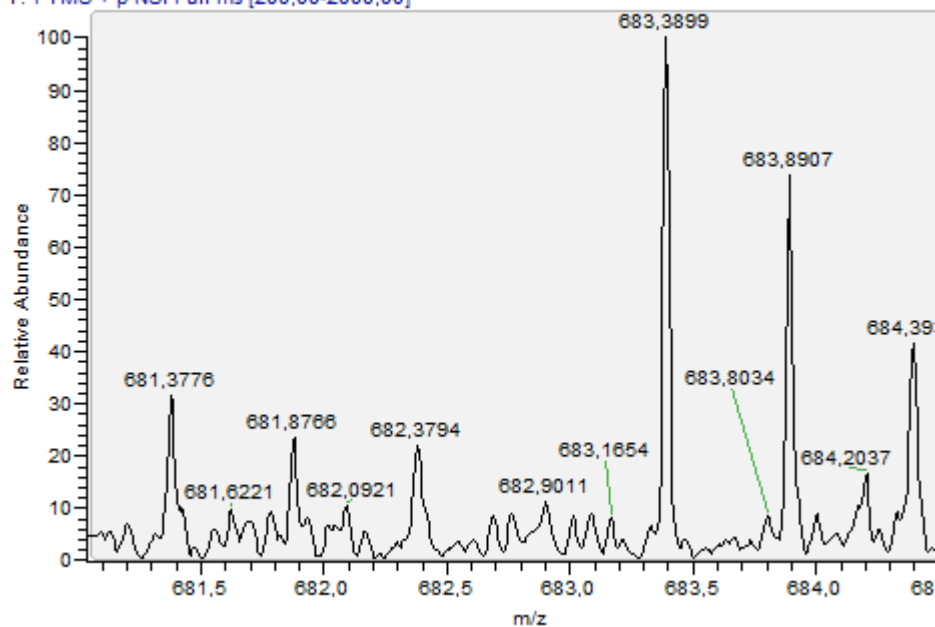
cortex_03 #14972-15398 RT: 74,47-76,30 AV: 93 NL: 4,34E3

T: FTMS + p NSI Full ms [200,00-2000,00]



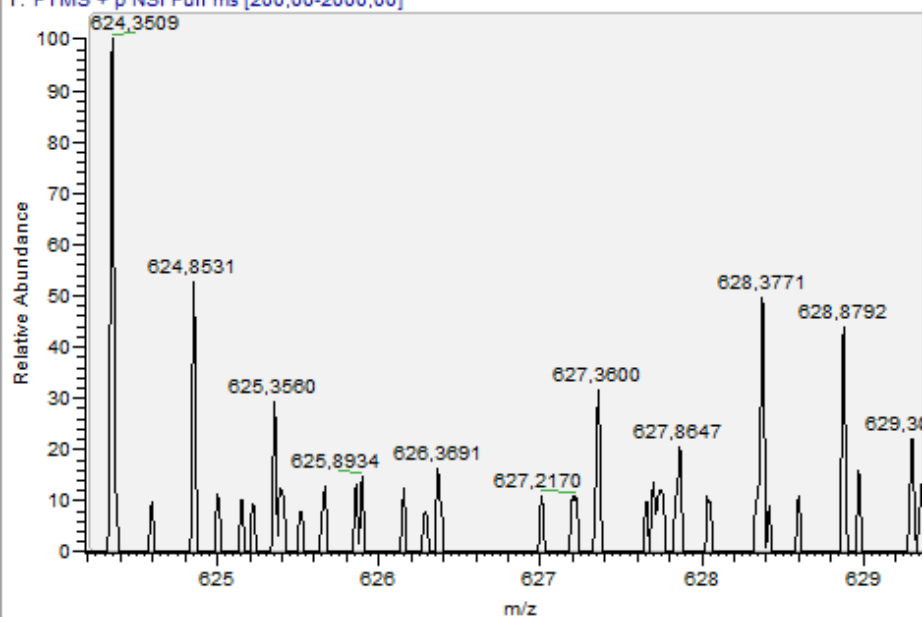
cortex_04 #13930-14287 RT: 71,87-73,32 AV: 58 NL: 5,38E3

T: FTMS + p NSI Full ms [200,00-2000,00]

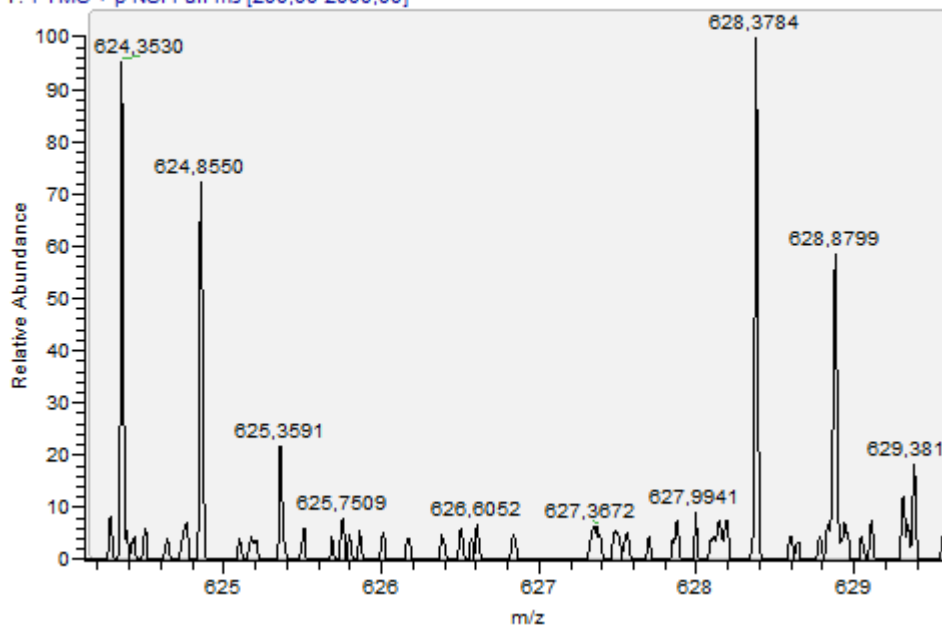


DGLDPGKLYTL 2+

cortex_01 #9516 RT: 59.94 AV: 1 NL: 2.80E4
T: FTMS + p NSI Full ms [200.00-2000.00]



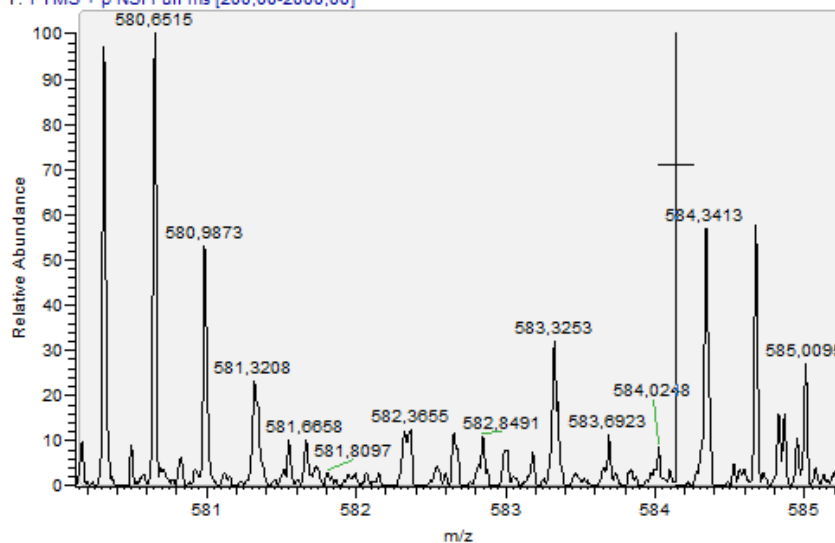
cortex_03 #12030 RT: 62.46 AV: 1 NL: 3.02E4
T: FTMS + p NSI Full ms [200.00-2000.00]



DDYVPKLYEQLSGK 2+

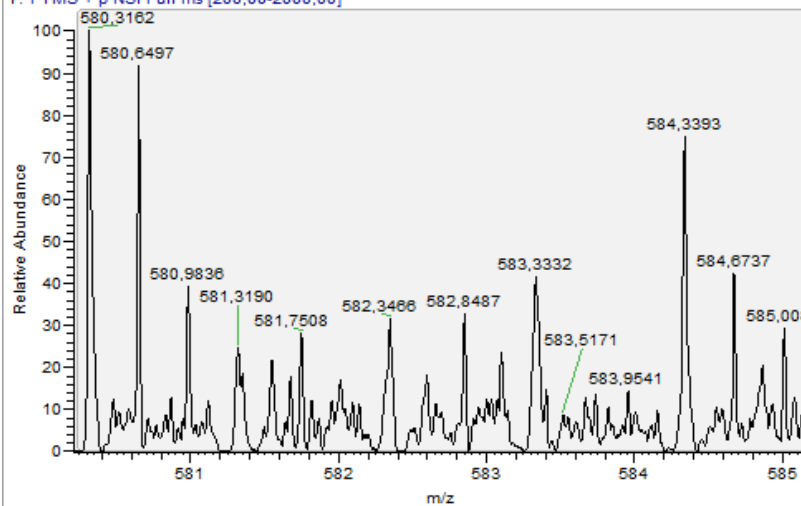
cortex_01 #8898-9086 RT: 56,30-57,32 AV: 14 NL: 2,36E4

T: FTMS + p NSI Full ms [200,00-2000,00]



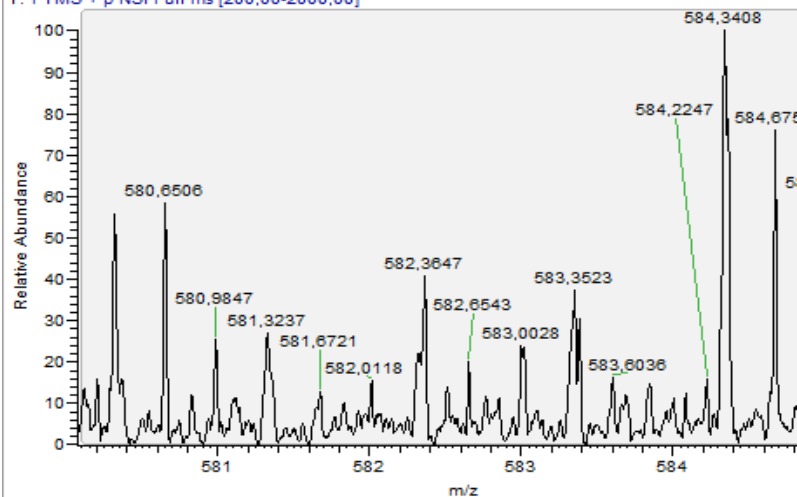
cortex_03 #11416-11693 RT: 60,01-61,11 AV: 46 NL: 9,17E3

T: FTMS + p NSI Full ms [200,00-2000,00]



cortex_04 #11051-11292 RT: 59,63-60,74 AV: 63 NL: 4,72E3

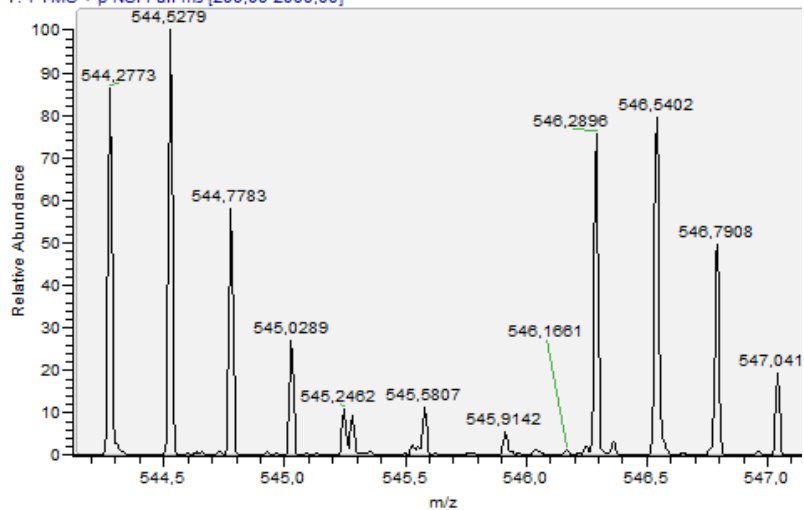
T: FTMS + p NSI Full ms [200,00-2000,00]



GRKGPGPGGGAGGARGGAGGGPSGD 4+

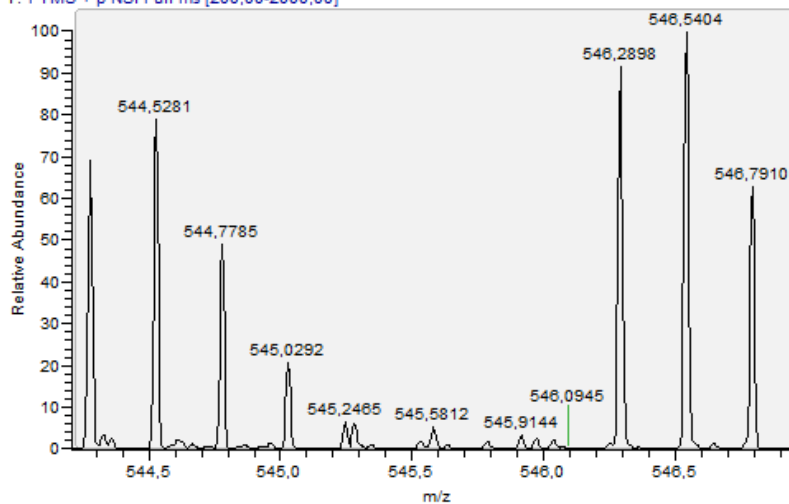
estriado_01 #2140-2258 RT: 17,49-18,10 AV: 7 NL: 7,03E4

T: FTMS + p NSI Full ms [200,00-2000,00]



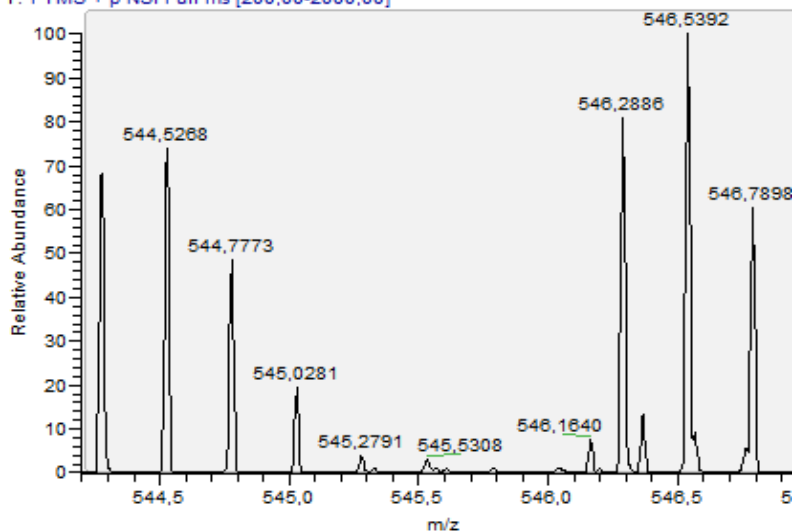
estriado_02 #2083-2319 RT: 17,04-18,46 AV: 18 NL: 5,14E4

T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_04 #3148 RT: 22,10 AV: 1 NL: 7,81E4

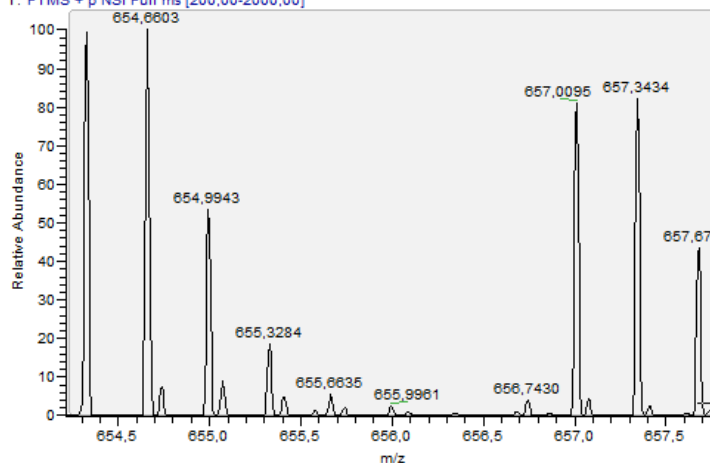
T: FTMS + p NSI Full ms [200,00-2000,00]



KGPGPGGPGGAGGARGGAGGGPSGD 3+

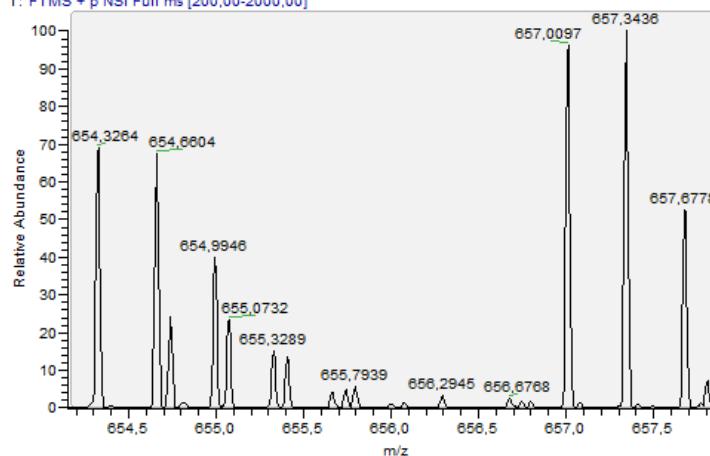
estriado_01 #2444 RT: 19,31 AV: 1 NL: 1,70E5

T: FTMS + p NSI Full ms [200,00-2000,00]



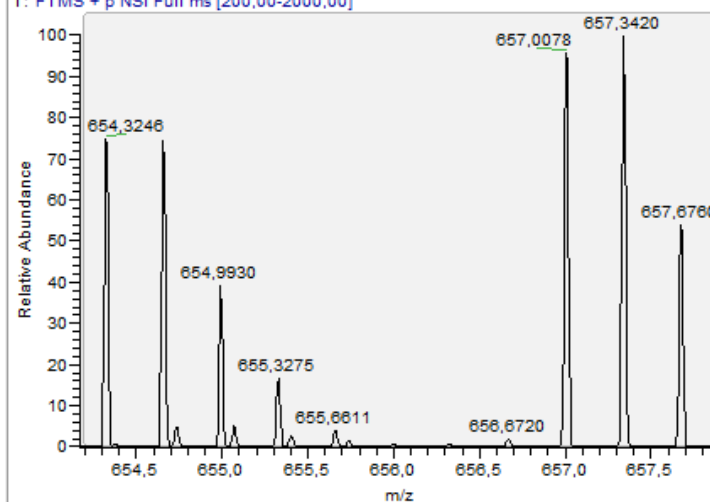
estriado_02 #2258-2438 RT: 18,24-19,21 AV: 10 NL: 7,63E4

T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_04 #3477 RT: 23,33 AV: 1 NL: 1,86E5

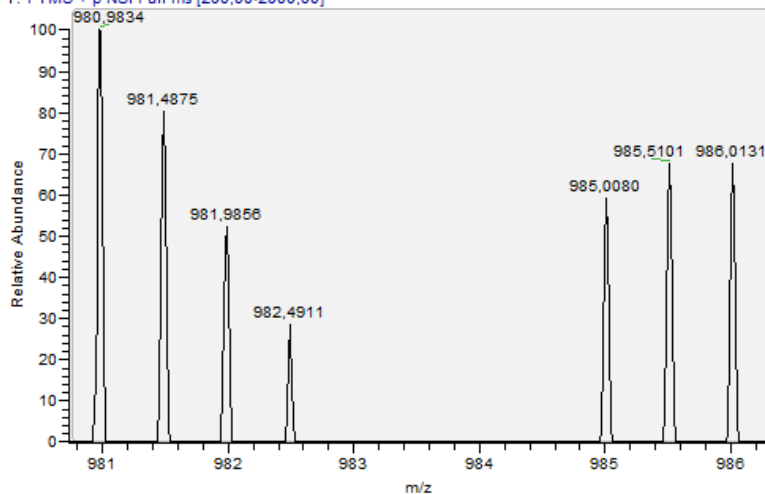
T: FTMS + p NSI Full ms [200,00-2000,00]



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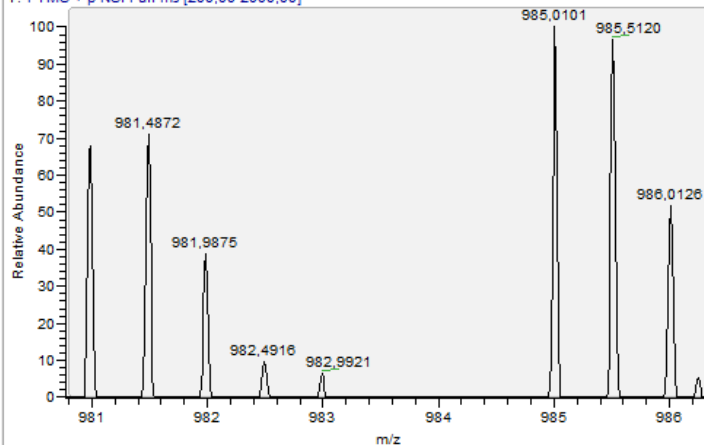
estriado_01 #2444 RT: 19,31 AV: 1 NL: 5,38E3

T: FTMS + p NSI Full ms [200,00-2000,00]



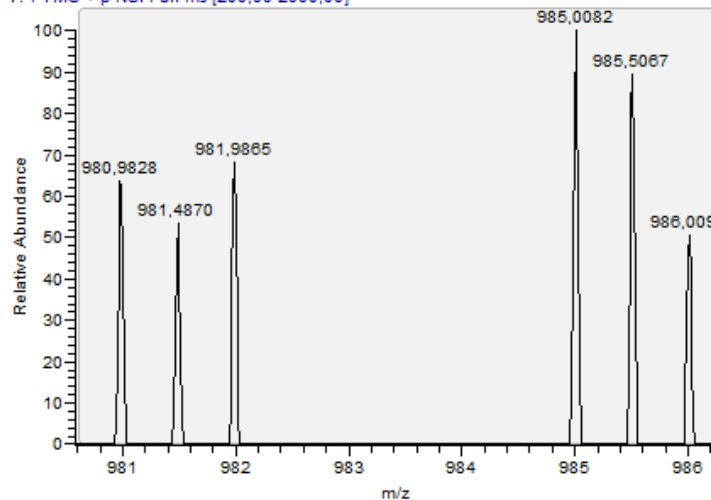
estriado_02 #2258-2379 RT: 18,24-18,83 AV: 6 NL: 3,13E3

T: FTMS + p NSI Full ms [200,00-2000,00]



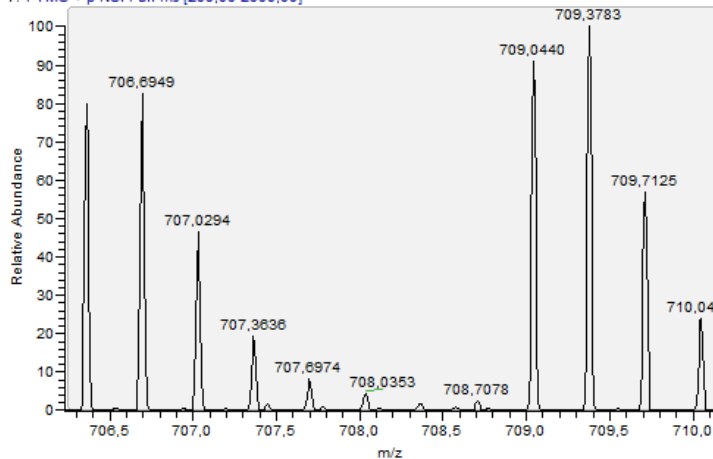
estriado_04 #3477 RT: 23,33 AV: 1 NL: 5,57E3

T: FTMS + p NSI Full ms [200,00-2000,00]

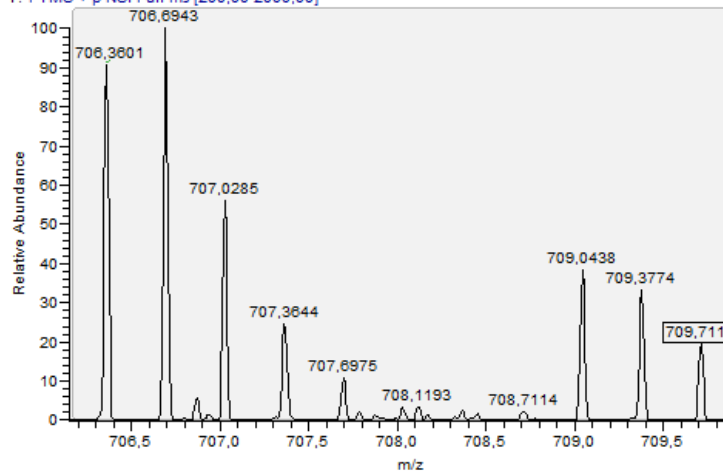


RKGP GPGGGAGGARGGAGGGPSGD 3+

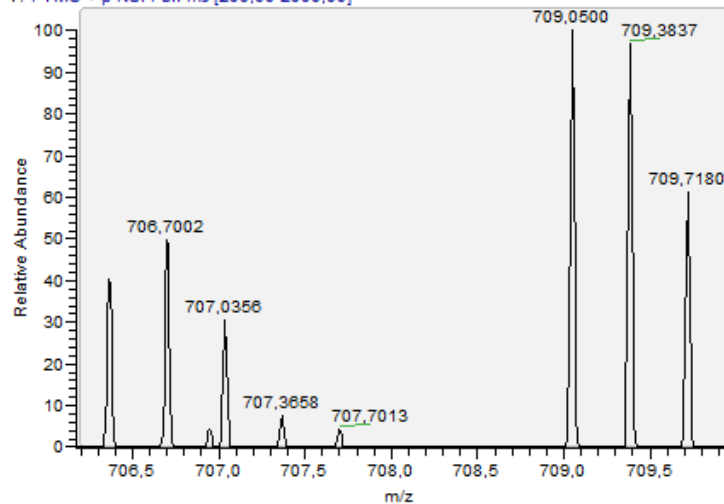
estriado_01 #2083-2200 RT: 17,07-17,71 AV: 8 NL: 2,14E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #1805-2083 RT: 15,19-17,04 AV: 67 NL: 2,94E3
T: FTMS + p NSI Full ms [200,00-2000,00]

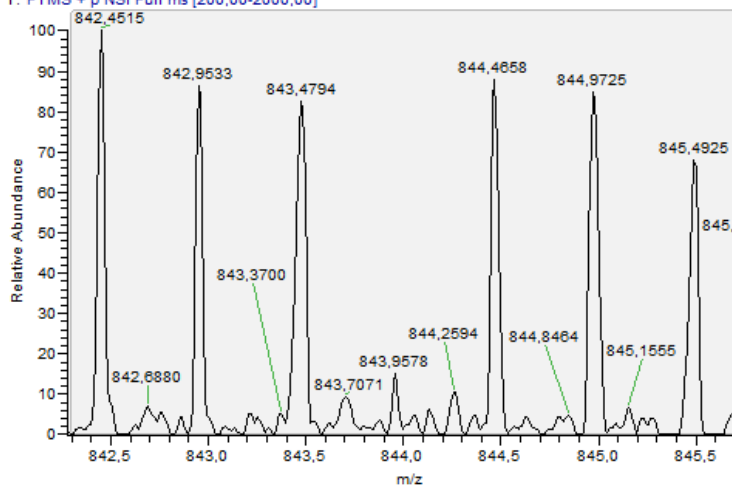


estriado_04 #3077 RT: 21,84 AV: 1 NL: 2,73E3
T: FTMS + p NSI Full ms [200,00-2000,00]

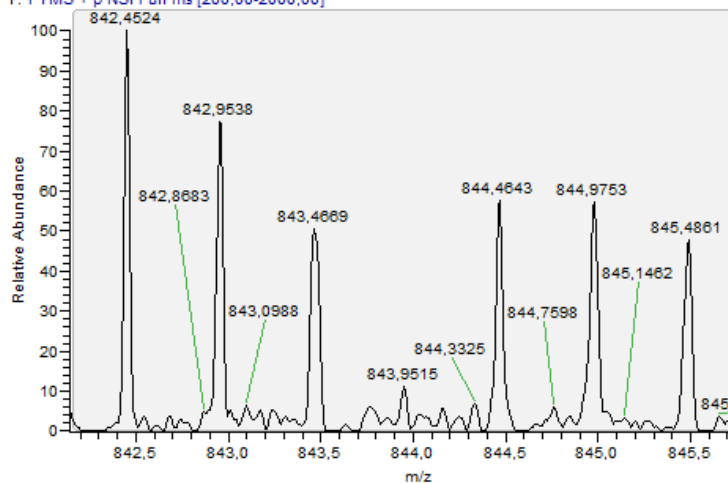


ATVGDVNTDRPGLLDL 2+

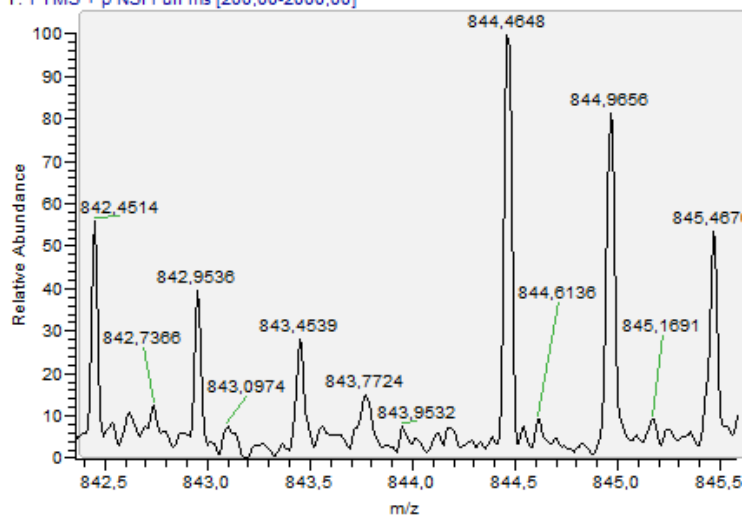
estriado_01 #9578-9762 RT: 60,85-61,77 AV: 10 NL: 1,61E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #9574-9756 RT: 60,76-61,77 AV: 12 NL: 1,74E4
T: FTMS + p NSI Full ms [200,00-2000,00]

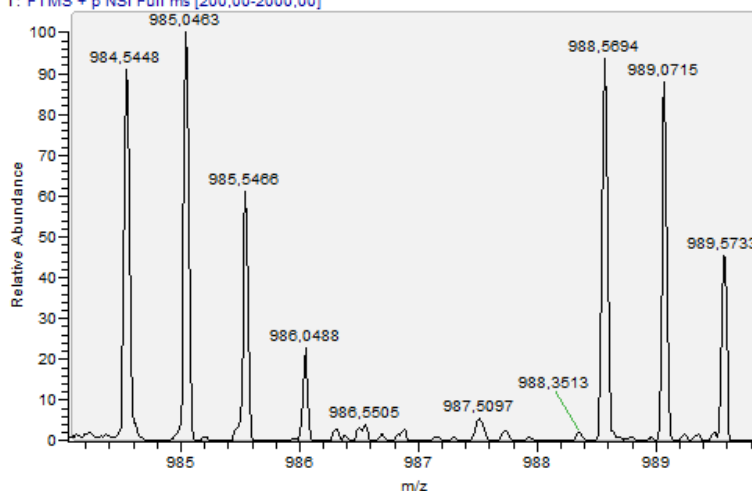


estriado_04 #14445-14505 RT: 64,72-64,93 AV: 10 NL: 1,09E4
T: FTMS + p NSI Full ms [200,00-2000,00]

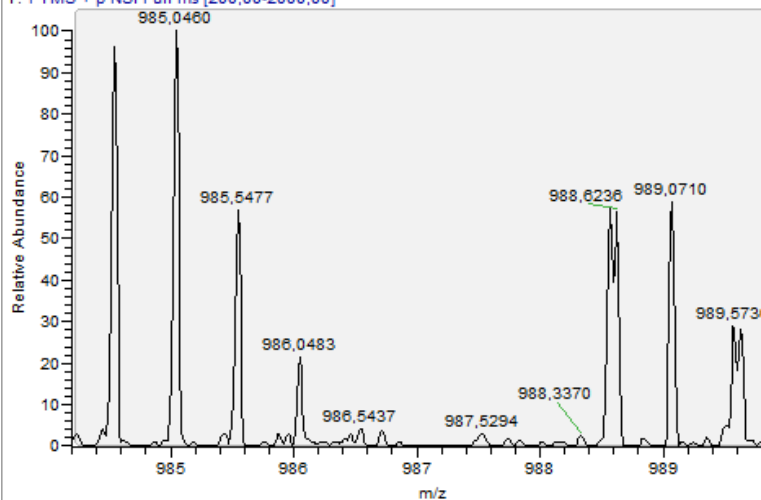


KQATVGDVNTDRPGLLDL 2+

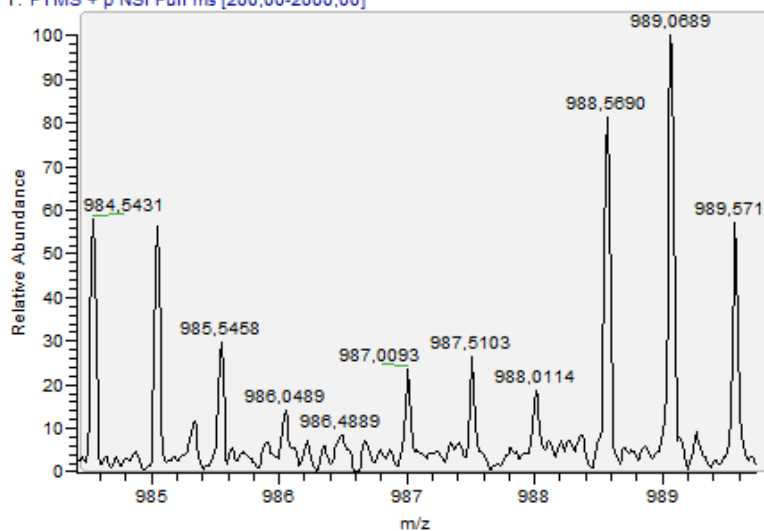
estriado_01 #8025-8149 RT: 51.52-52.16 AV: 9 NL: 5.90E4
T: FTMS + p NSI Full ms [200.00-2000.00]



estriado_02 #8224-8348 RT: 52.66-53.29 AV: 13 NL: 3.42E4
T: FTMS + p NSI Full ms [200.00-2000.00]

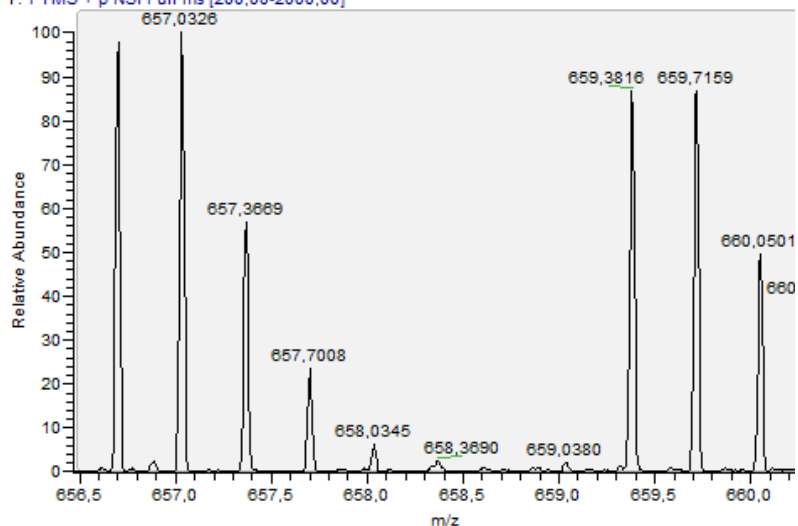


estriado_04 #12661-12788 RT: 57.50-57.99 AV: 19 NL: 2.82E4
T: FTMS + p NSI Full ms [200.00-2000.00]

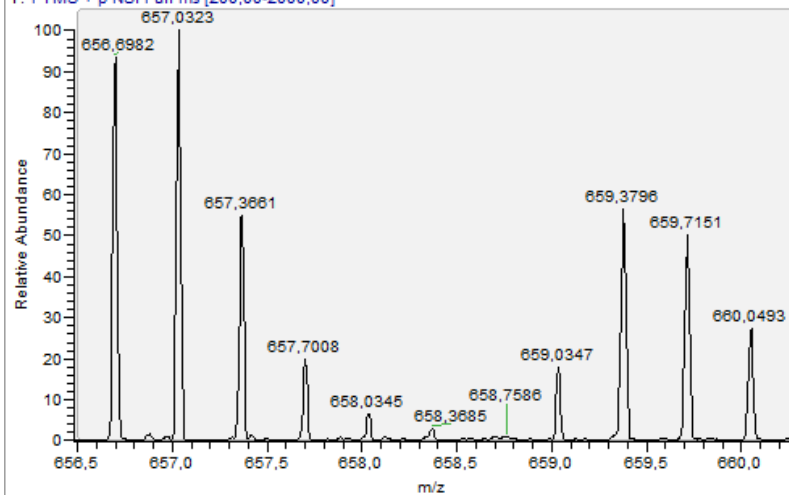


KQATVGDVNTDRPGLLDL 3+

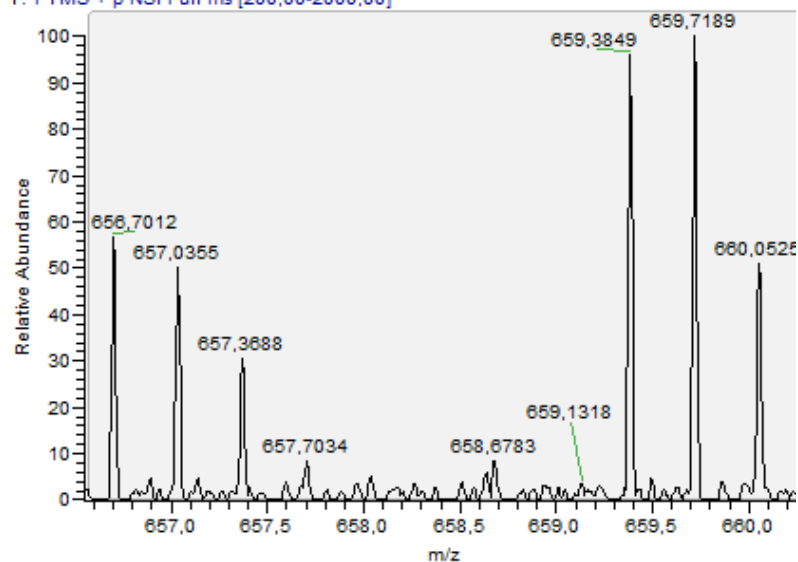
estriado_01 #8025-8211 RT: 51,52-52,54 AV: 13 NL: 2,55E5
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #8224-8348 RT: 52,66-53,29 AV: 13 NL: 1,62E5
T: FTMS + p NSI Full ms [200,00-2000,00]



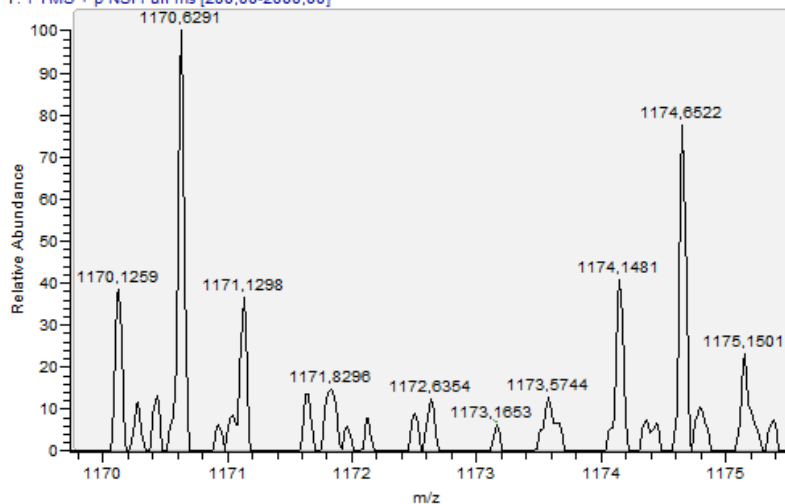
estriado_04 #12704 RT: 57,66 AV: 1 NL: 1,11E5
T: FTMS + p NSI Full ms [200,00-2000,00]



SHFKQATVGDVNTDRPGLLDL 2+

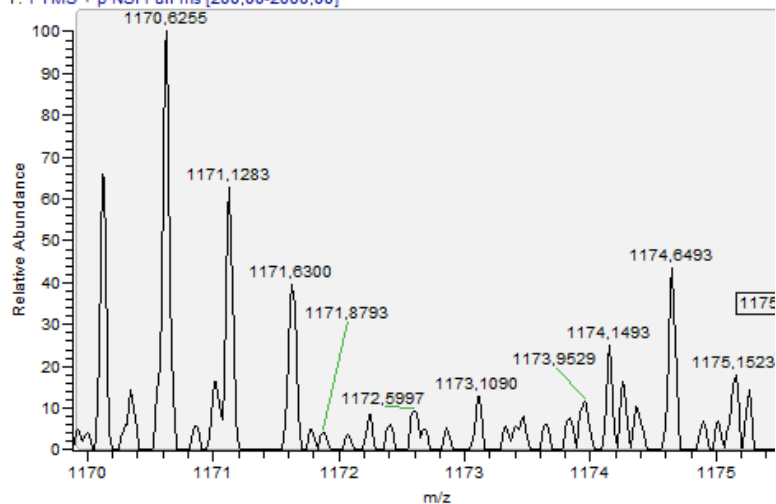
estriado_01 #7900-8086 RT: 50,77-51,77 AV: 14 NL: 5,39E3

T: FTMS + p NSI Full ms [200,00-2000,00]



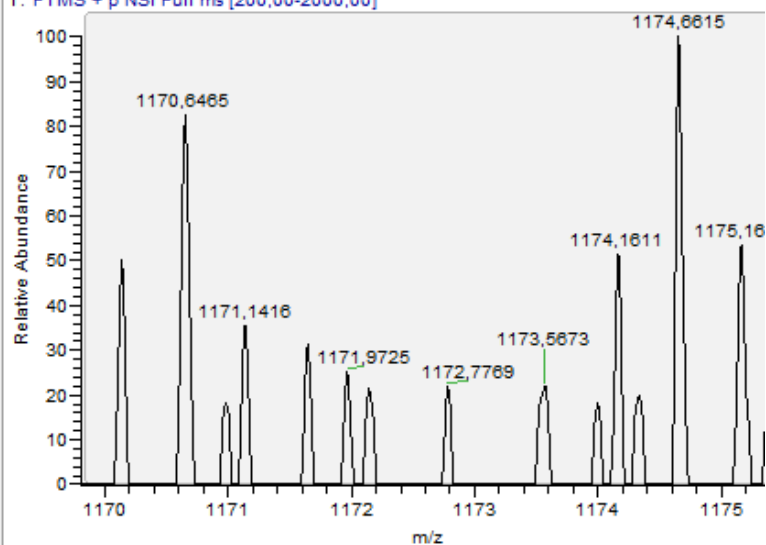
estriado_02 #7849-8224 RT: 50,38-52,54 AV: 32 NL: 2,76E3

T: FTMS + p NSI Full ms [200,00-2000,00]



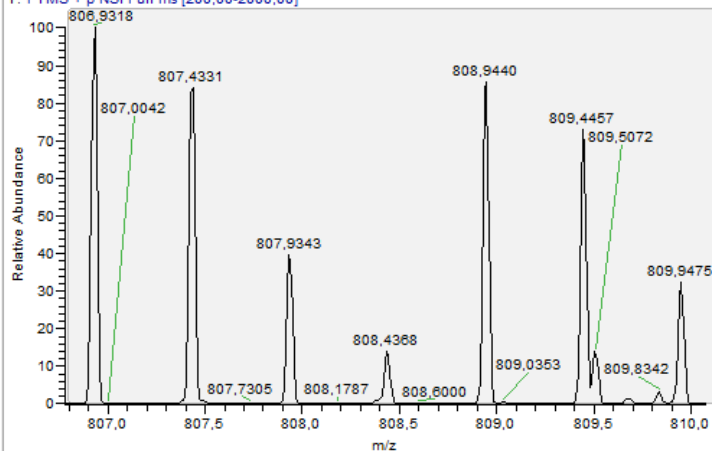
estriado_04 #12449 RT: 56,65 AV: 1 NL: 6,21E2

T: FTMS + p NSI Full ms [200,00-2000,00]

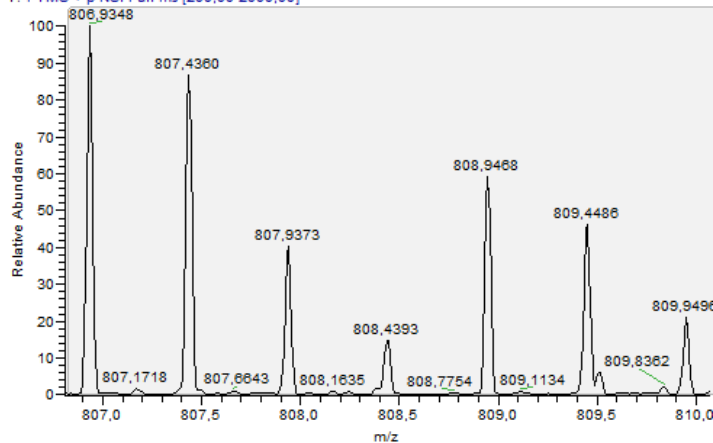


TVGDVNTDRPGLLDL 2+

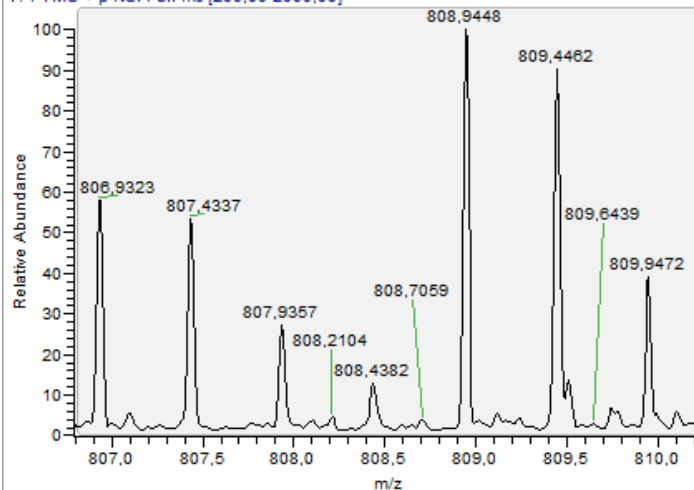
estriado_01 #9394-9517 RT: 59,66-60,34 AV: 14 NL: 1,39E5
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #9326-9695 RT: 59,26-61,35 AV: 25 NL: 9,87E4
T: FTMS + p NSI Full ms [200,00-2000,00]

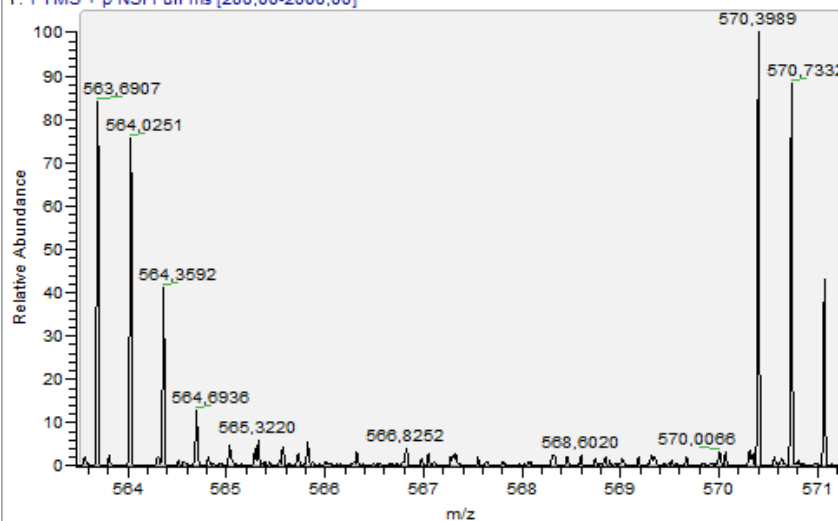


estriado_04 #14214-14653 RT: 63,78-65,50 AV: 64 NL: 3,55E4
T: FTMS + p NSI Full ms [200,00-2000,00]

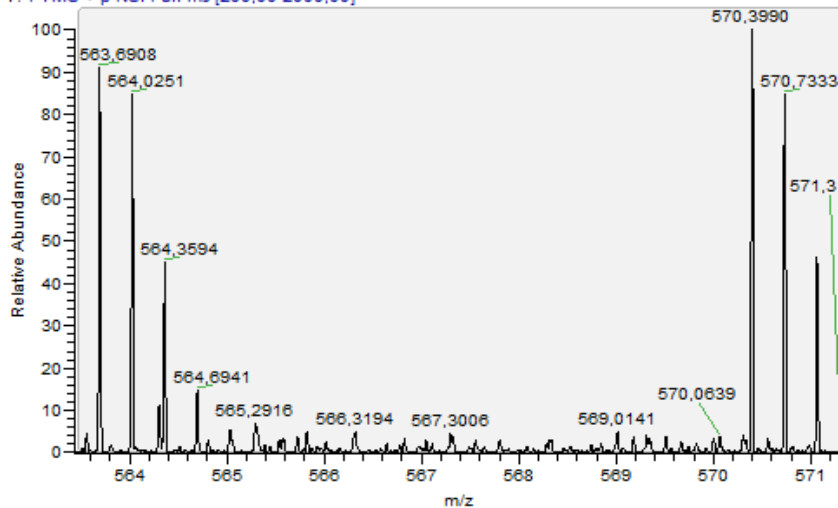


VEKVDLKKKYGI 3+

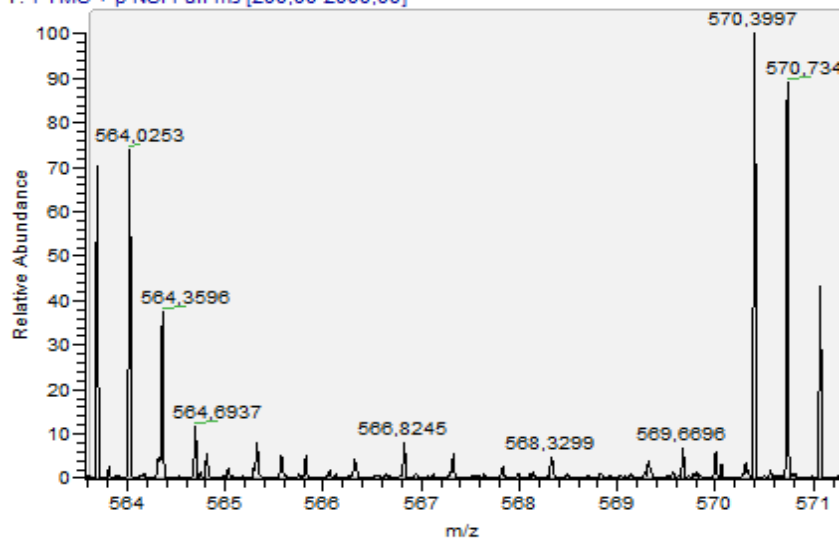
estriado_01 #5439-5568 RT: 36,33-37,04 AV: 8 NL: 3,62E5
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #5449-5581 RT: 36,36-36,98 AV: 7 NL: 2,85E5
T: FTMS + p NSI Full ms [200,00-2000,00]



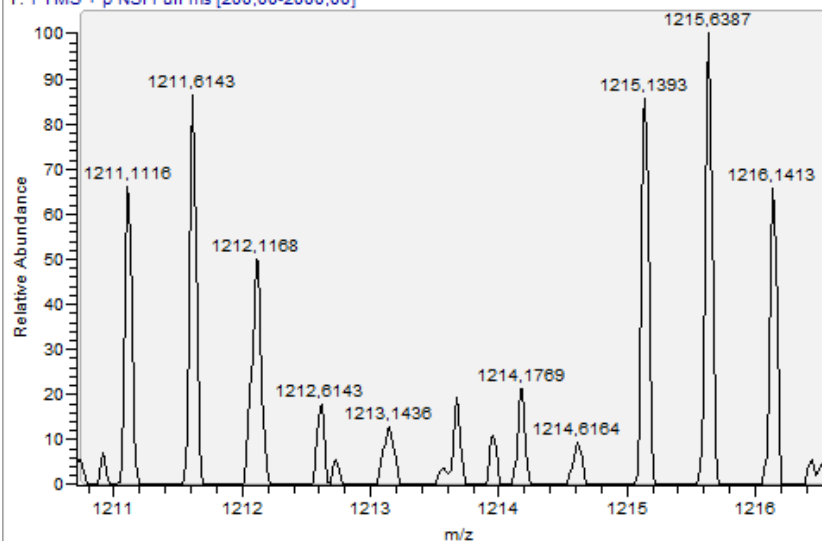
estriado_04 #8392-8502 RT: 41,26-41,62 AV: 13 NL: 8,13E4
T: FTMS + p NSI Full ms [200,00-2000,00]



KGNDISSGTVLSDYVGSGPPSGTGL 2+

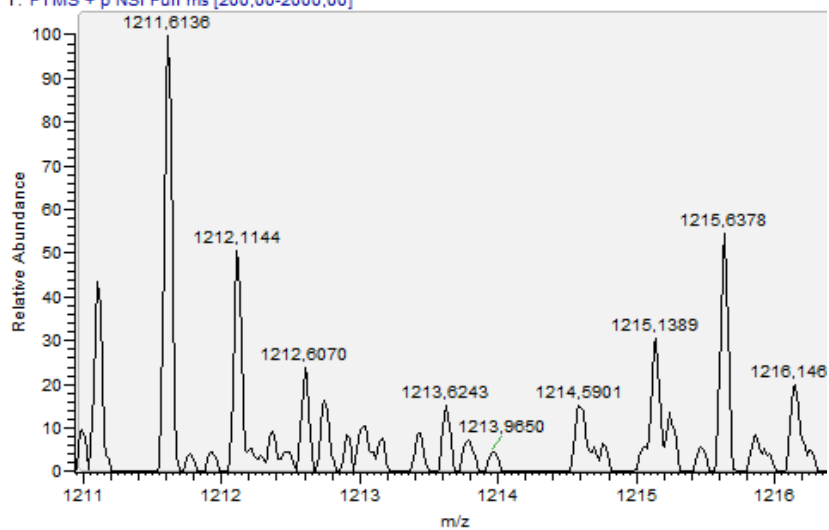
estriado_01 #9639-9762 RT: 61,14-61,77 AV: 7 NL: 9,00E3

T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #9512-9756 RT: 60,37-61,77 AV: 17 NL: 3,67E3

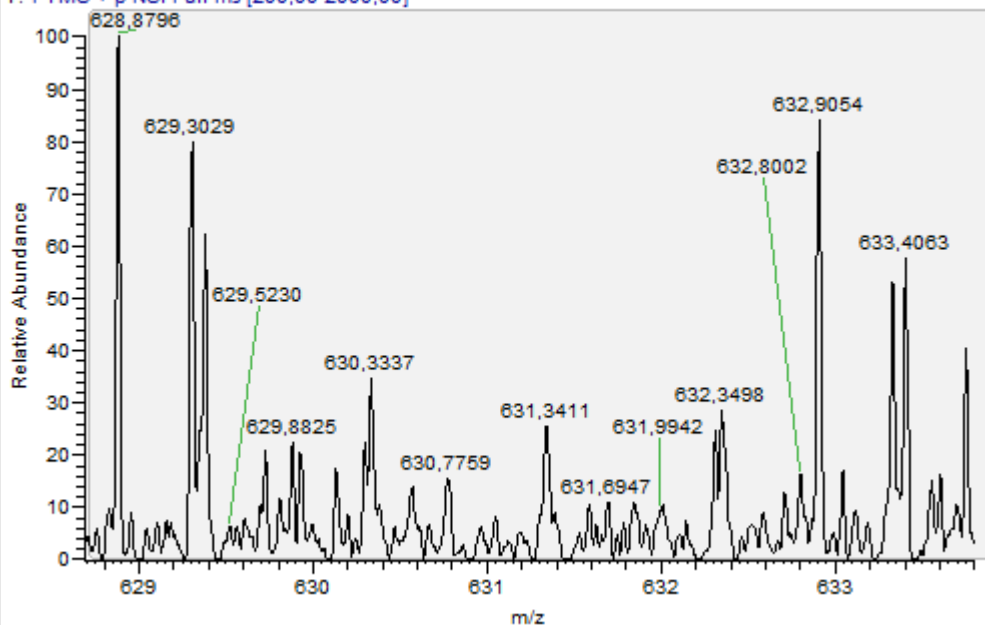
T: FTMS + p NSI Full ms [200,00-2000,00]



AGVTVDDELGKVL 2+

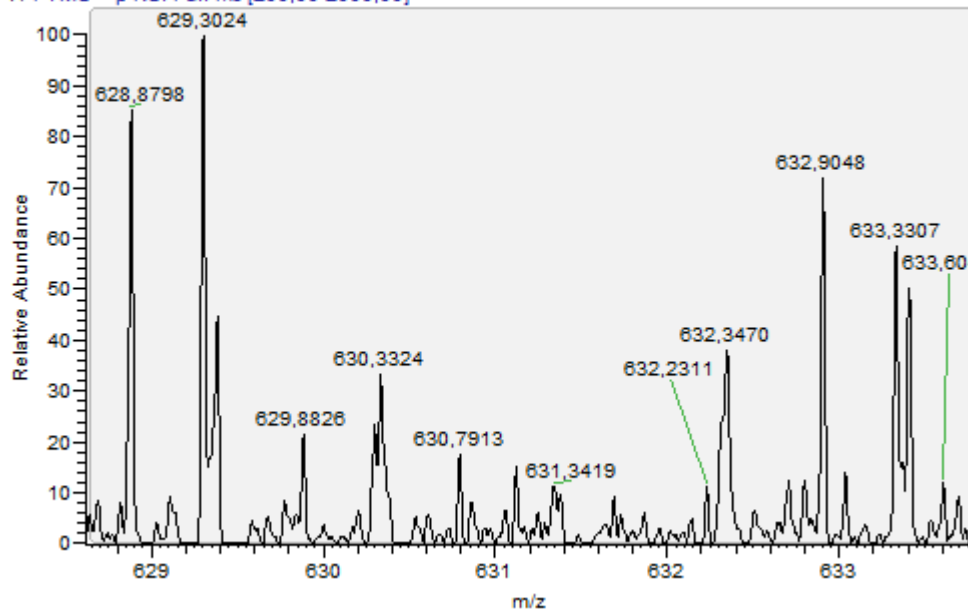
estriado_01 #9517-9762 RT: 60.41-61.77 AV: 14 NL: 1,21E4

T: FTMS + p NSI Full ms [200,00-2000,00]



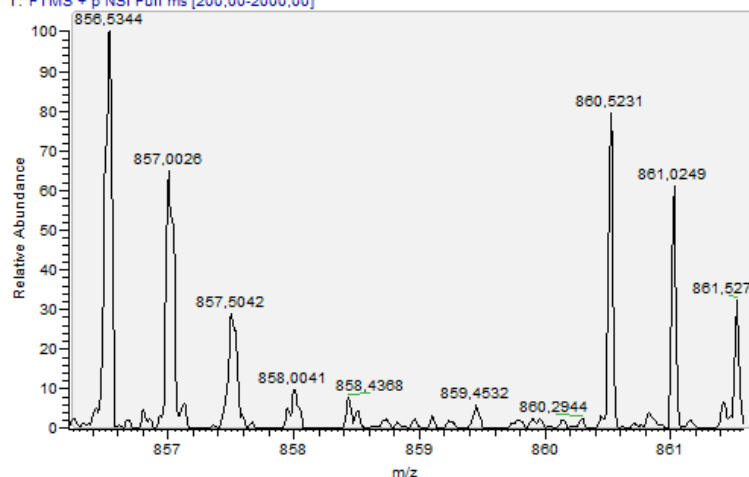
estriado_02 #9574-9756 RT: 60.76-61.77 AV: 12 NL: 1,35E4

T: FTMS + p NSI Full ms [200,00-2000,00]

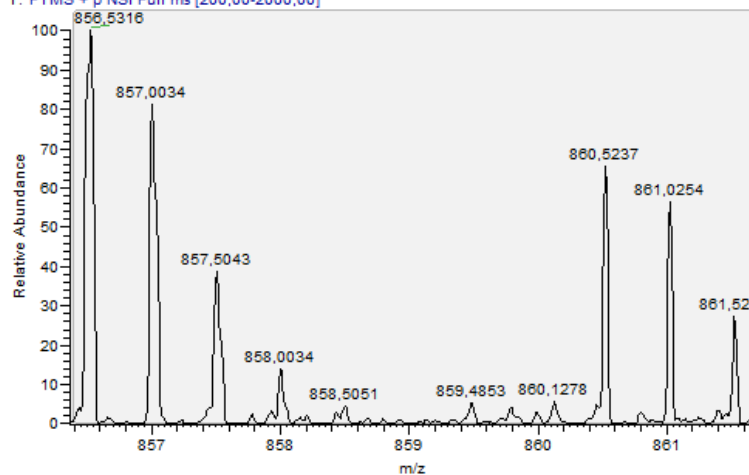


GVTVDELGKVLTPQV 2+

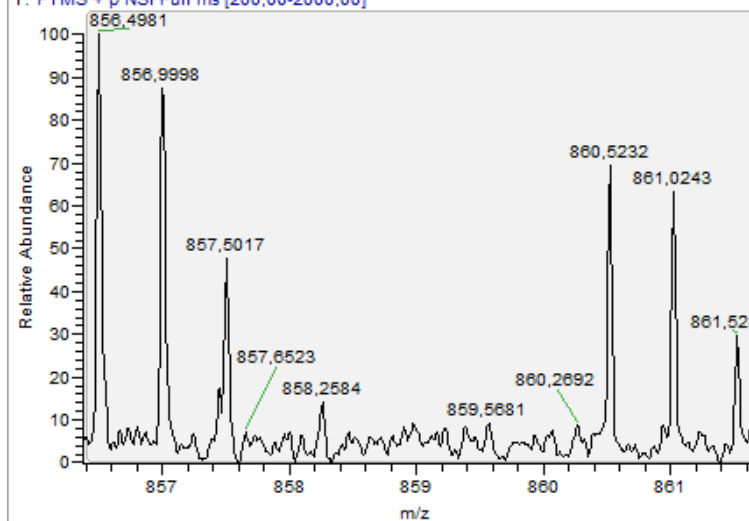
estriado_01 #10132-10307 RT: 64,16-65,15 AV: 14 NL: 2,26E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #10182-10424 RT: 64,49-65,89 AV: 19 NL: 2,77E4
T: FTMS + p NSI Full ms [200,00-2000,00]

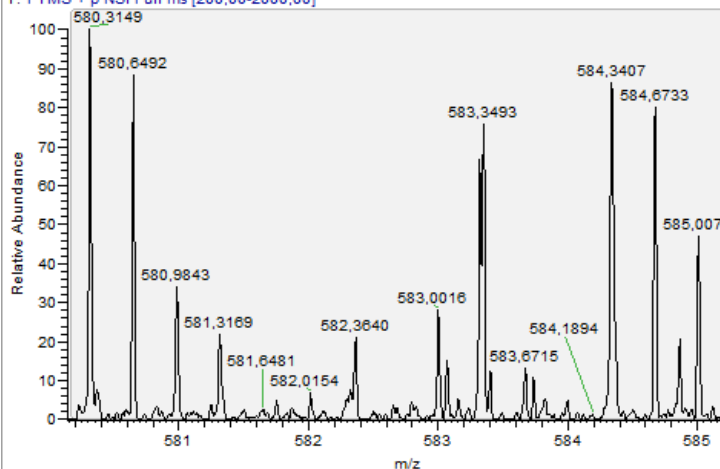


estriado_04 #14862-14947 RT: 66,44-66,70 AV: 11 NL: 1,60E4
T: FTMS + p NSI Full ms [200,00-2000,00]

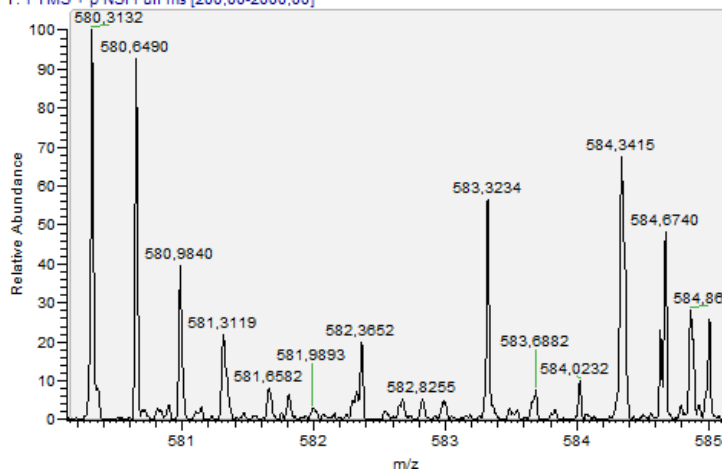


DDYVPKLYEQLSGK 2+

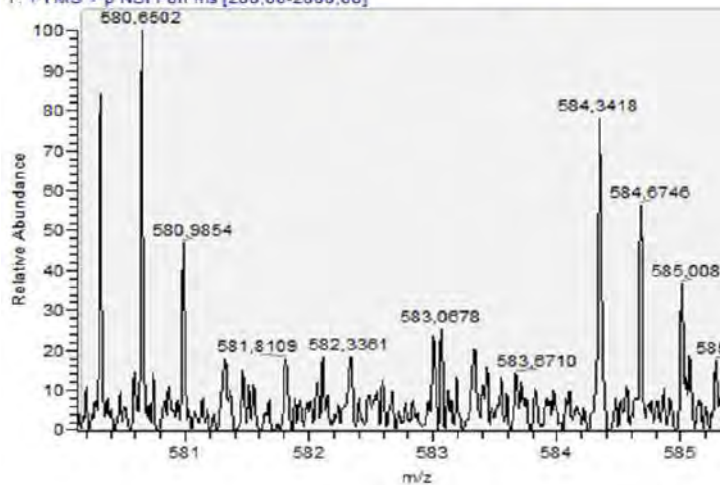
estriado_01 #8896-9083 RT: 56,69-57,78 AV: 20 NL: 2,24E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #8901-9081 RT: 56,70-57,73 AV: 26 NL: 2,24E4
T: FTMS + p NSI Full ms [200,00-2000,00]

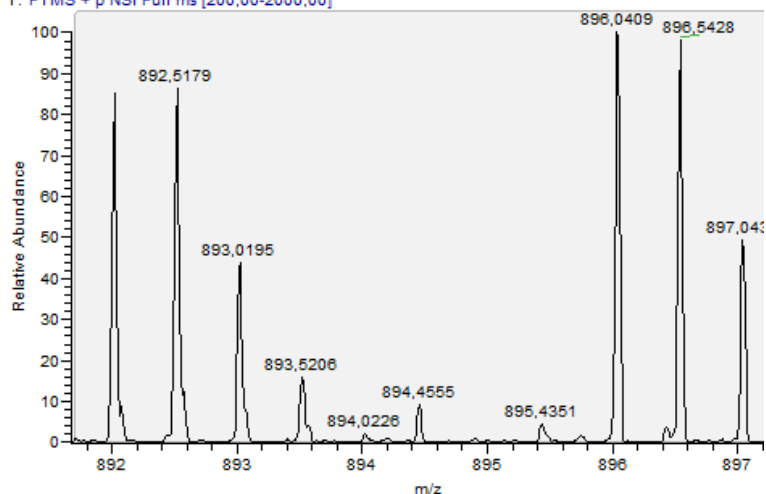


estriado_04 #13457-13566 RT: 60,71-61,09 AV: 14 NL: 8,18E3
T: FTMS + p NSI Full ms [200,00-2000,00]

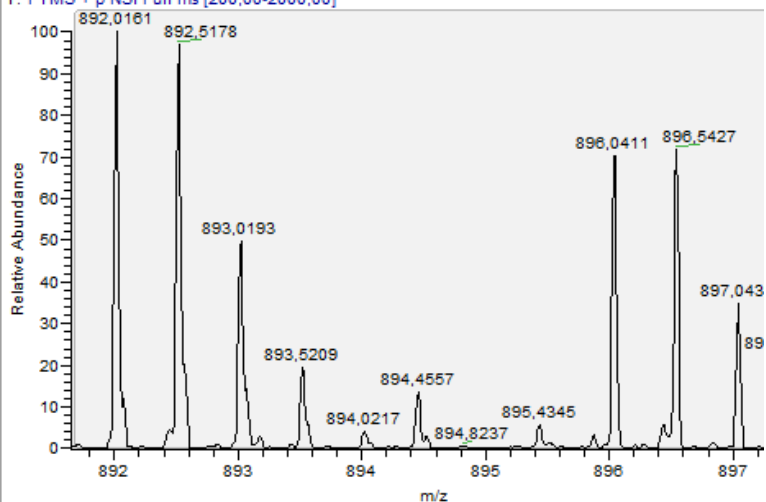


AGVTVDELGKVLTPQV 2+

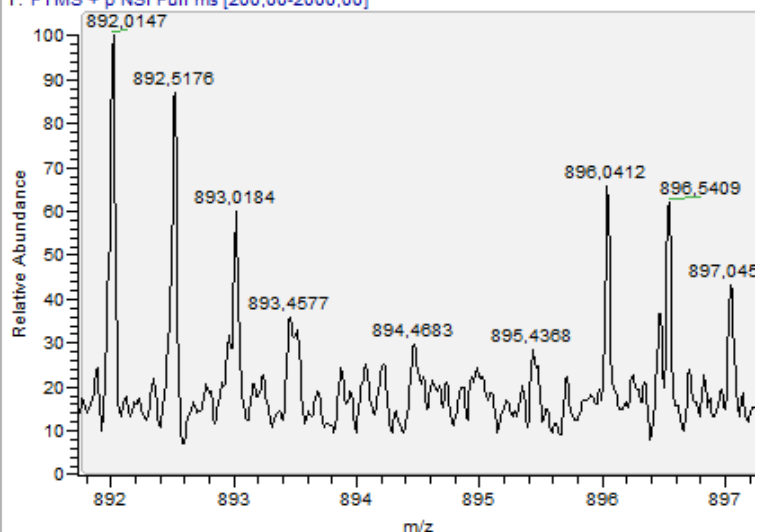
estriado_01 #10373-10493 RT: 65,62-66,19 AV: 10 NL: 5,25E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #10364-10545 RT: 65,59-66,64 AV: 15 NL: 4,52E4
T: FTMS + p NSI Full ms [200,00-2000,00]

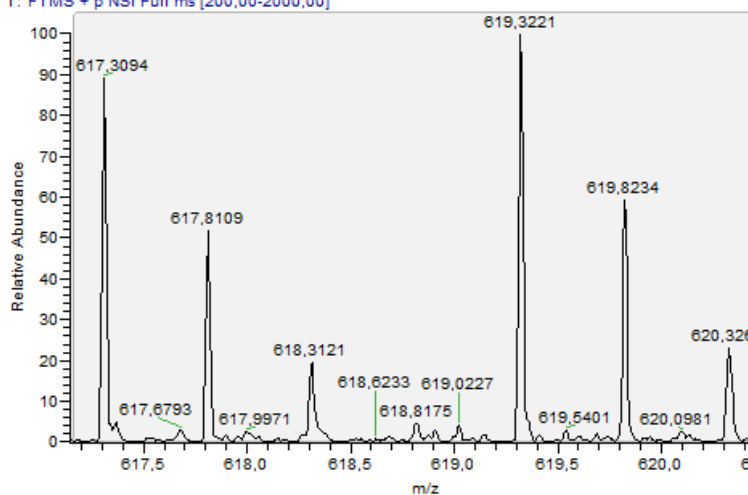


estriado_04 #14978-15417 RT: 66,86-68,60 AV: 59 NL: 5,31E3
T: FTMS + p NSI Full ms [200,00-2000,00]

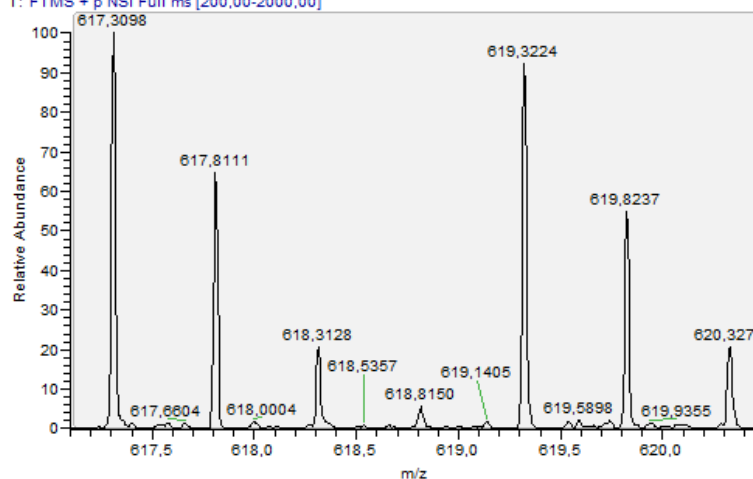


ADDEPLGRVSF 2+

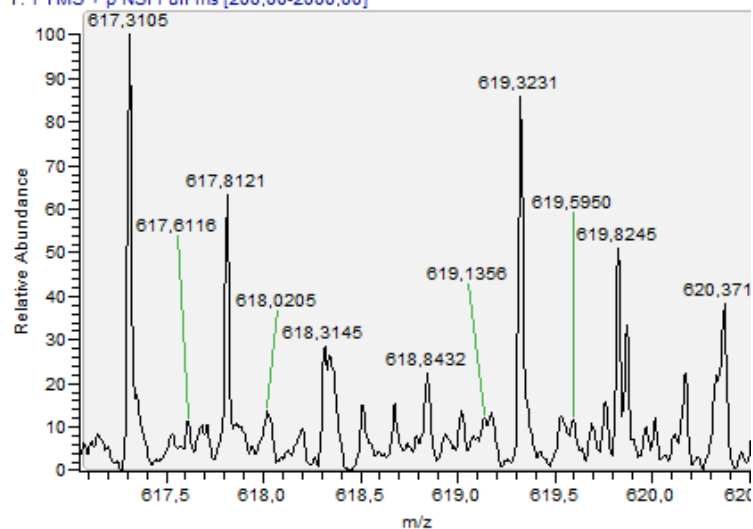
estriado_01 #7588-7837 RT: 48,95-50,35 AV: 27 NL: 7,75E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #7666-7849 RT: 49,31-50,25 AV: 20 NL: 9,27E4
T: FTMS + p NSI Full ms [200,00-2000,00]

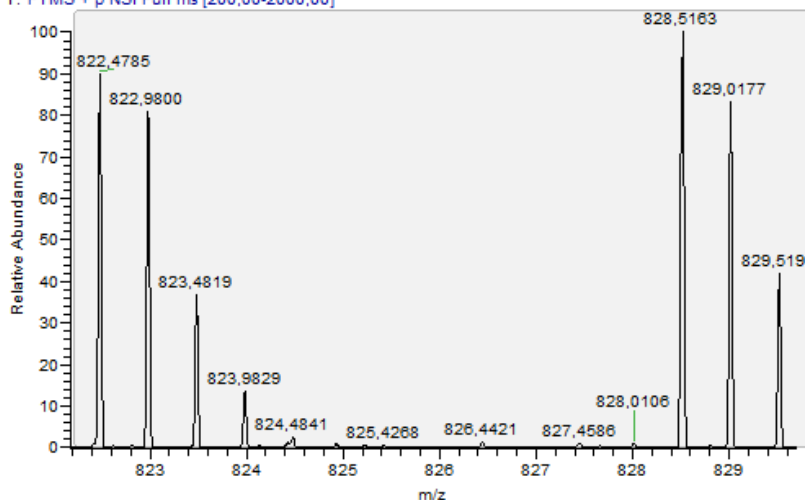


estriado_04 #12033-12469 RT: 55,00-56,73 AV: 61 NL: 8,21E3
T: FTMS + p NSI Full ms [200,00-2000,00]

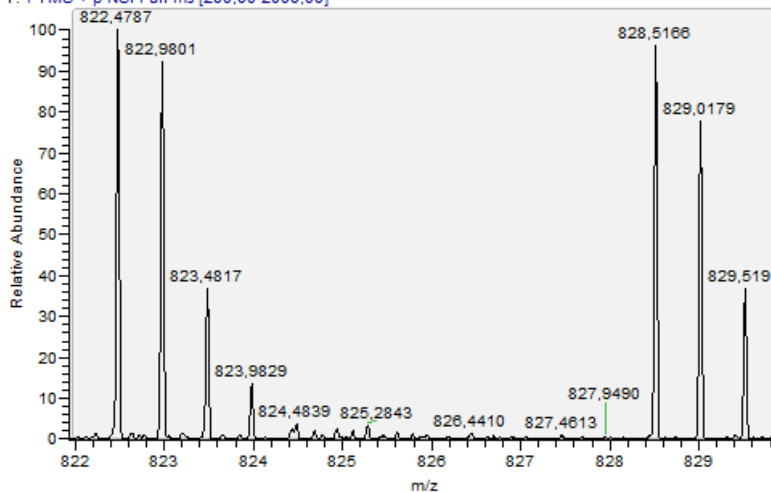


ADKVPKTAENFRAL 2+

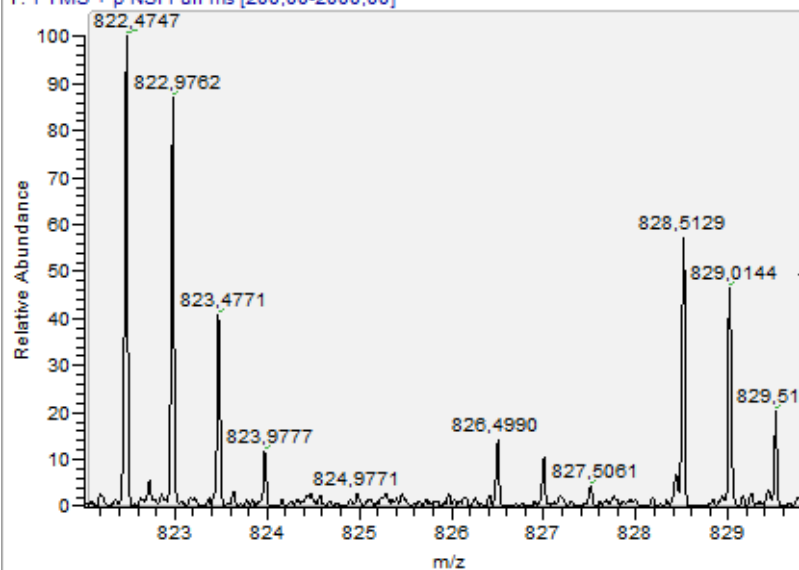
estriado_01 #4913-5113 RT: 33,37-34,38 AV: 14 NL: 1,50E5
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #4852-5122 RT: 33,07-34,42 AV: 16 NL: 1,17E5
T: FTMS + p NSI Full ms [200,00-2000,00]

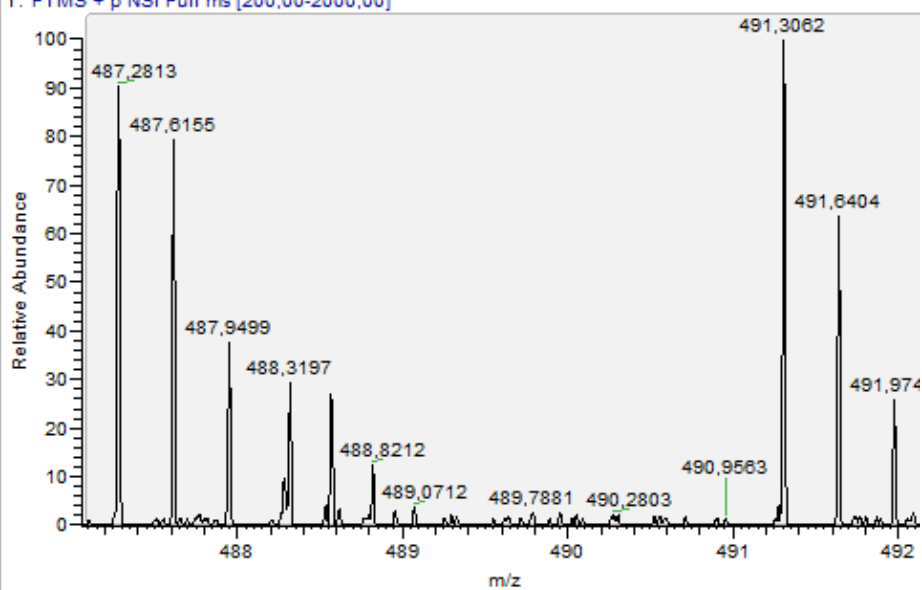


estriado_04 #7486-7943 RT: 37,85-39,57 AV: 67 NL: 1,48E4
T: FTMS + p NSI Full ms [200,00-2000,00]

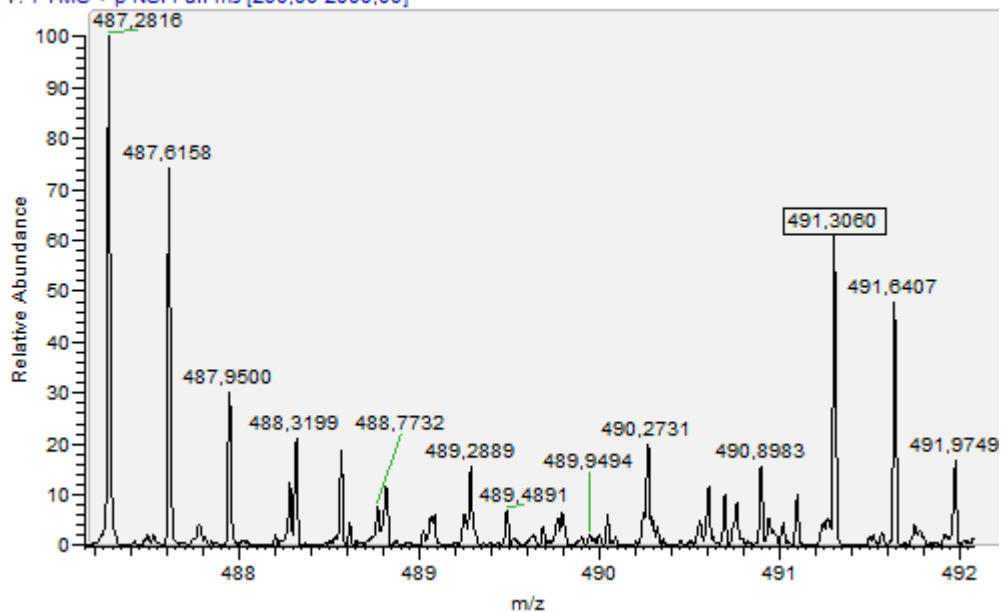


ADKVPKTAENFR 3+

estriado_01 #3239 RT: 24,05 AV: 1 NL: 2,32E5
T: FTMS + p NSI Full ms [200,00-2000,00]



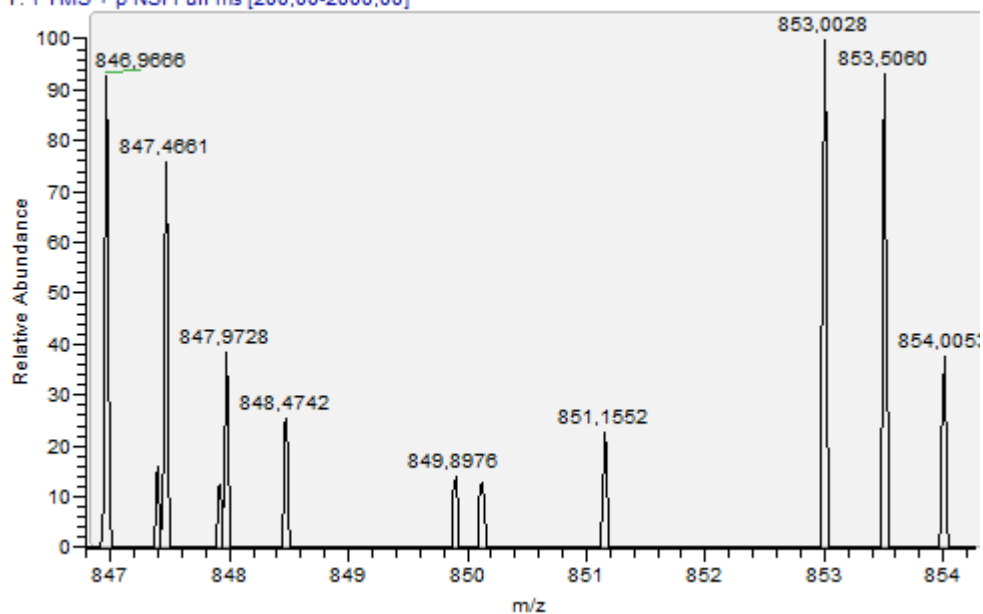
estriado_02 #3058-3318 RT: 23,04-24,36 AV: 12 NL: 6,68E4
T: FTMS + p NSI Full ms [200,00-2000,00]



ELFADKVPKTAENF 2+

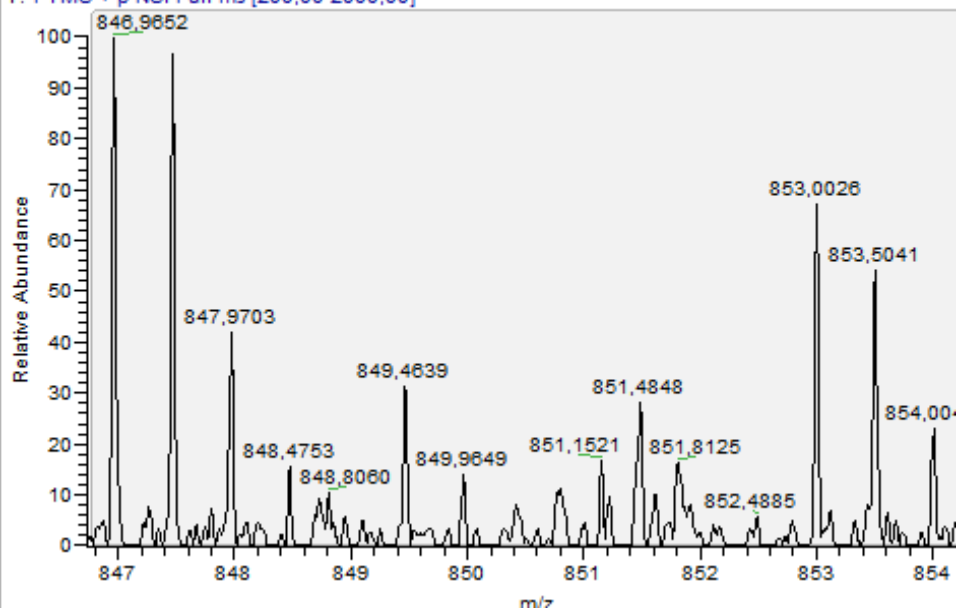
estriado_01 #7511 RT: 48.43 AV: 1 NL: 3,04E4

T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #7478-7603 RT: 48.17-48.89 AV: 10 NL: 3,16E4

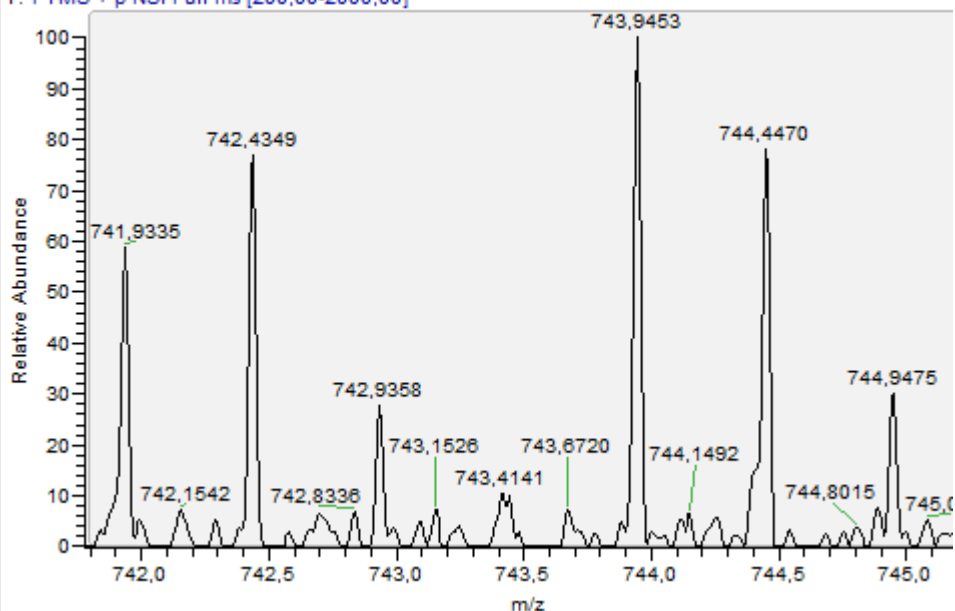
T: FTMS + p NSI Full ms [200,00-2000,00]



ASAPLVETSTPLRL 2+

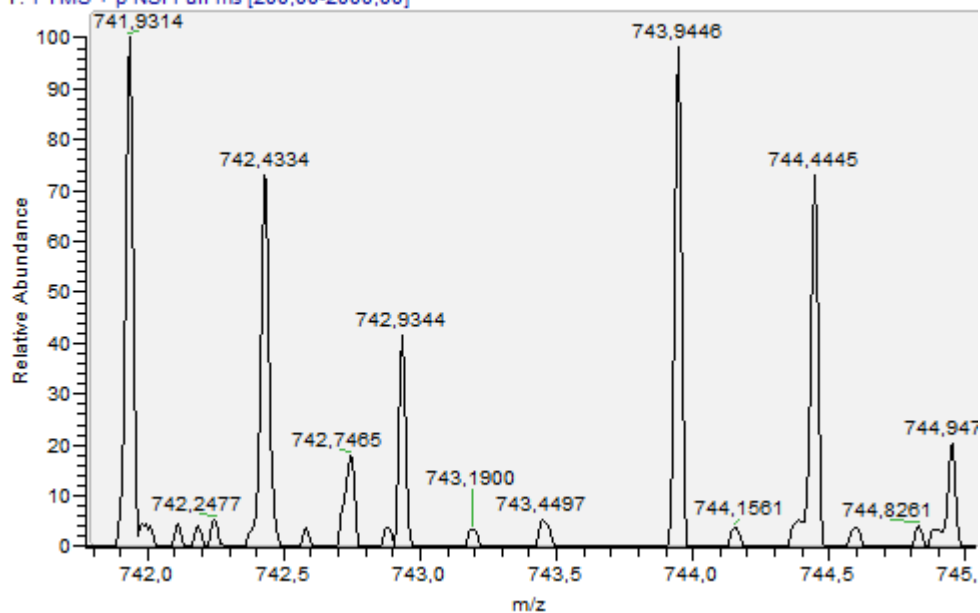
estriado_01 #9083-9145 RT: 57,78-58,11 AV: 5 NL: 2,75E4

T: FTMS + p NSI Full ms [200,00-2000,00]



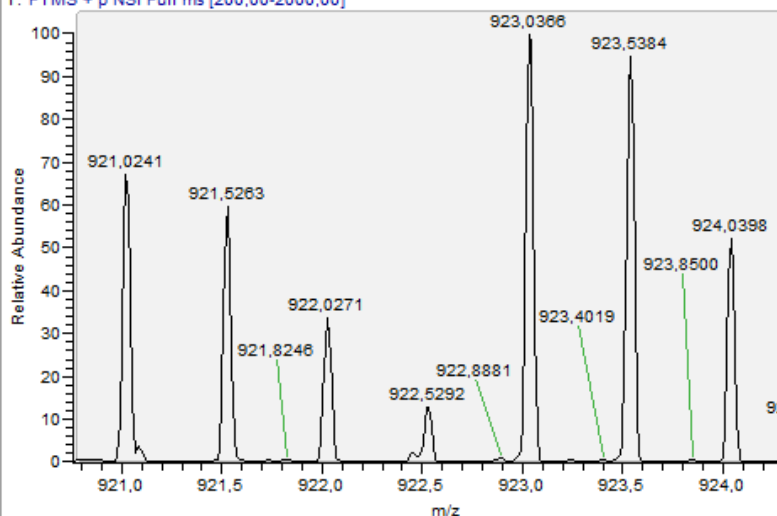
estriado_02 #9176-9204 RT: 58,36-58,46 AV: 3 NL: 2,09E4

T: FTMS + p NSI Full ms [200,00-2000,00]

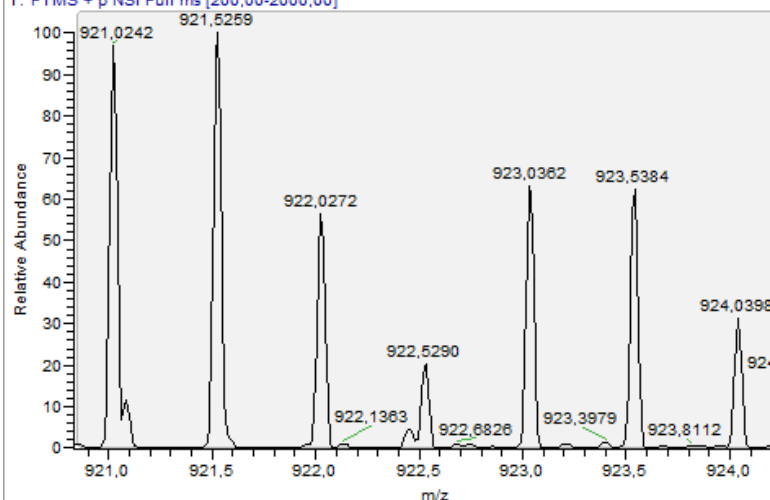


SLSAASAPLVETSTPLRL 2+

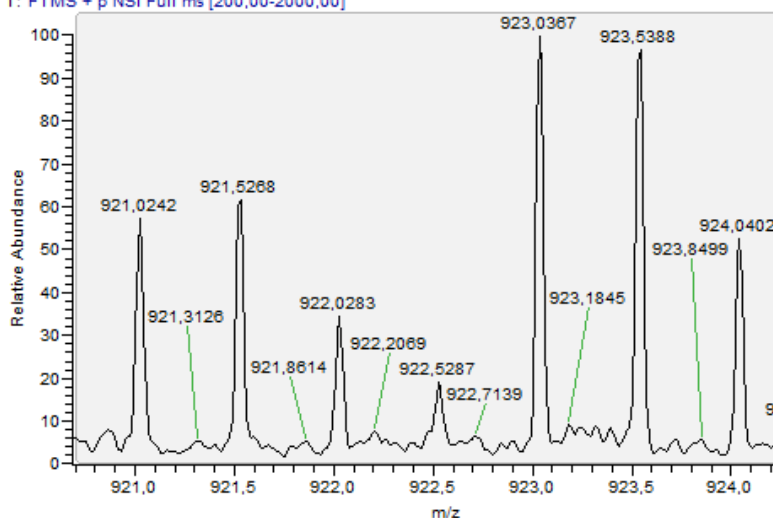
estriado_01 #10373-10493 RT: 65,62-66,19 AV: 10 NL: 6,51E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #10364-10605 RT: 65,59-67,04 AV: 19 NL: 3,74E4
T: FTMS + p NSI Full ms [200,00-2000,00]

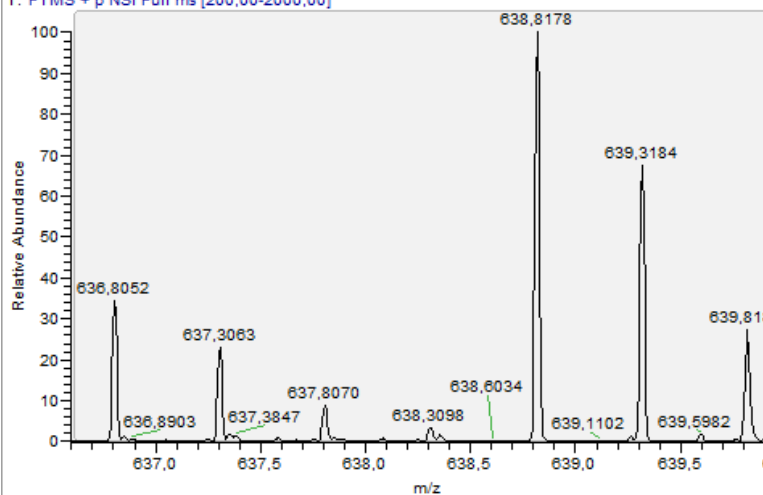


estriado_04 #15024-15300 RT: 67,04-68,13 AV: 38 NL: 1,60E4
T: FTMS + p NSI Full ms [200,00-2000,00]

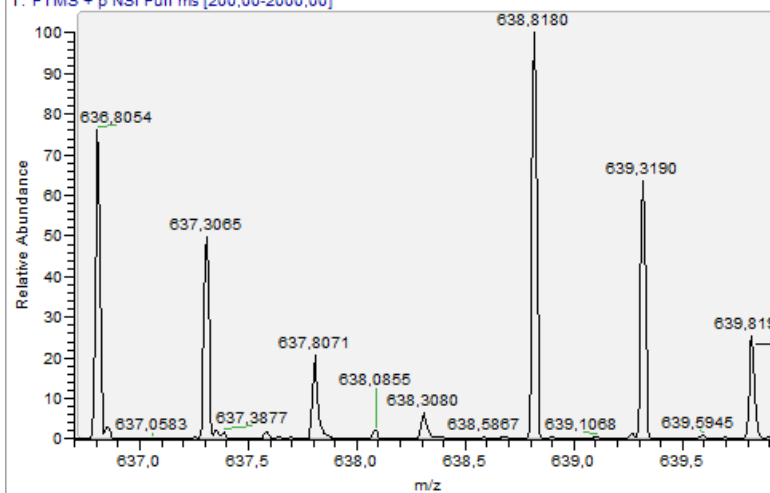


SANSNPAMAPRE 2+

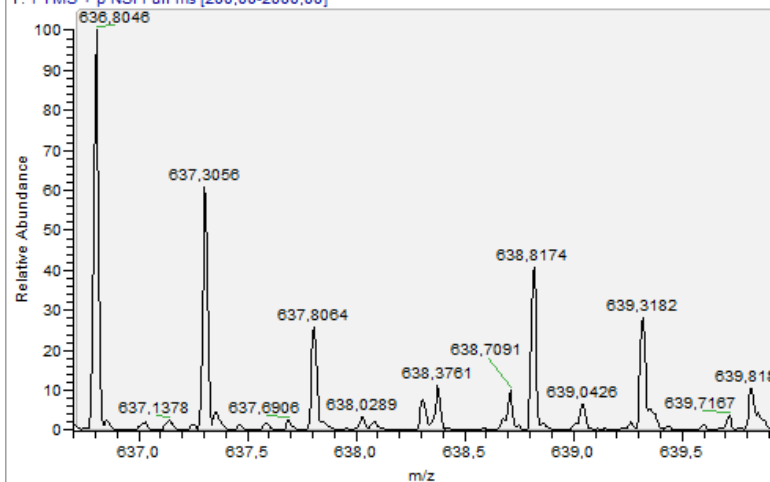
estriado_01 #2799-3052 RT: 21,66-22,87 AV: 12 NL: 1,61E5
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #2803-2994 RT: 21,48-22,55 AV: 10 NL: 1,24E5
T: FTMS + p NSI Full ms [200,00-2000,00]

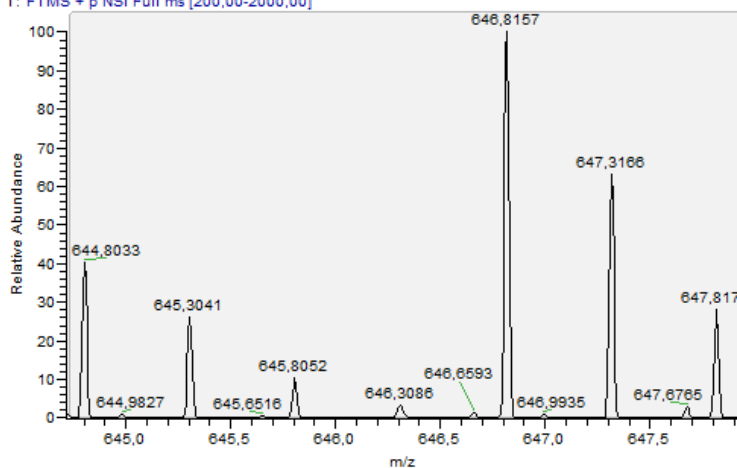


estriado_04 #4066-4578 RT: 25,56-27,40 AV: 49 NL: 2,56E4
T: FTMS + p NSI Full ms [200,00-2000,00]

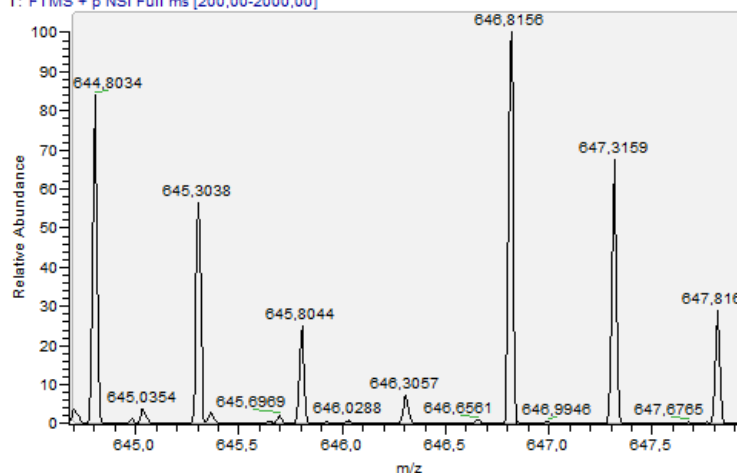


SANSNPAMAPRE 2+ (methionine oxidation)

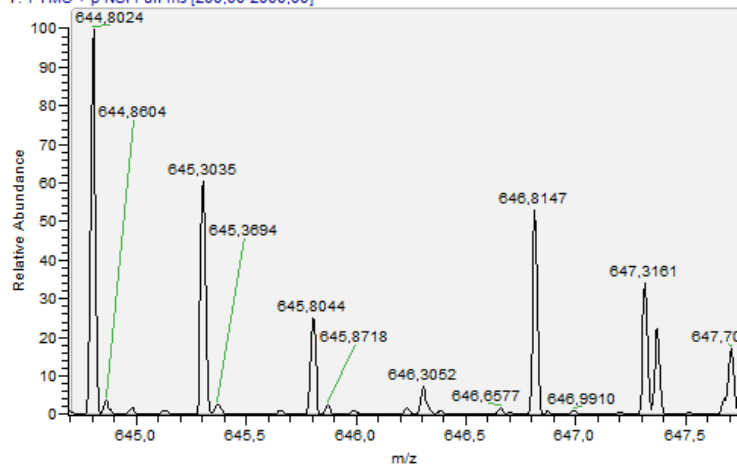
estriado_01 #2258-2436 RT: 18,18-19,18 AV: 11 NL: 2,18E5
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #2258-2438 RT: 18,24-19,21 AV: 10 NL: 1,85E5
T: FTMS + p NSI Full ms [200,00-2000,00]

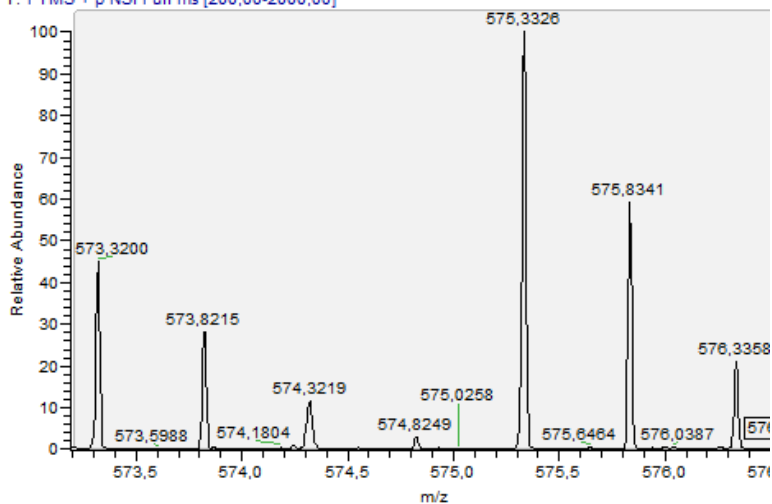


estriado_04 #3340-3426 RT: 22,81-23,11 AV: 13 NL: 4,17E4
T: FTMS + p NSI Full ms [200,00-2000,00]

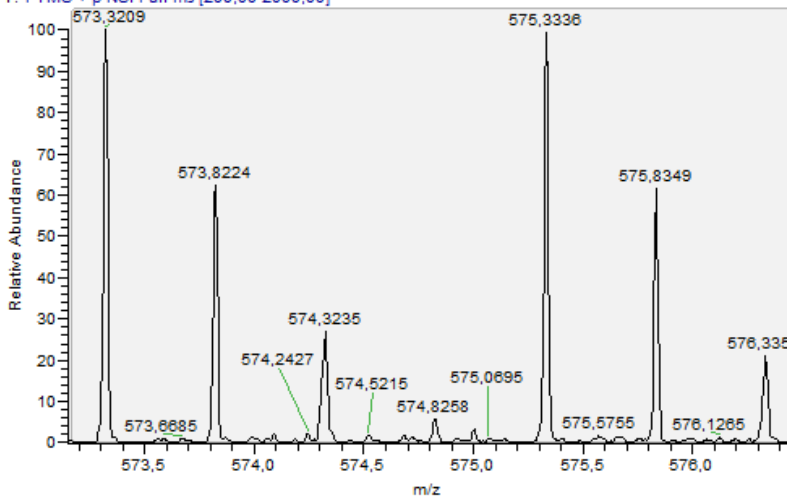


SFARAPQLDL 2+

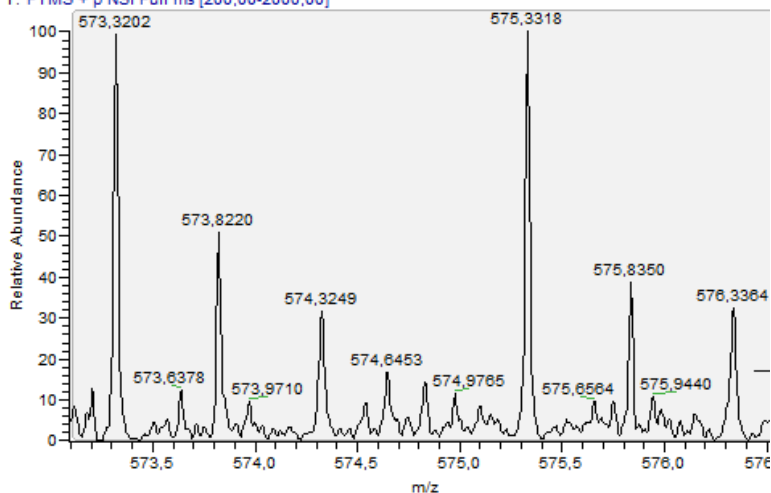
estriado_01 #8025-8211 RT: 51,52-52,54 AV: 13 NL: 2,65E5
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #7974-8224 RT: 51,13-52,54 AV: 15 NL: 1,15E5
T: FTMS + p NSI Full ms [200,00-2000,00]

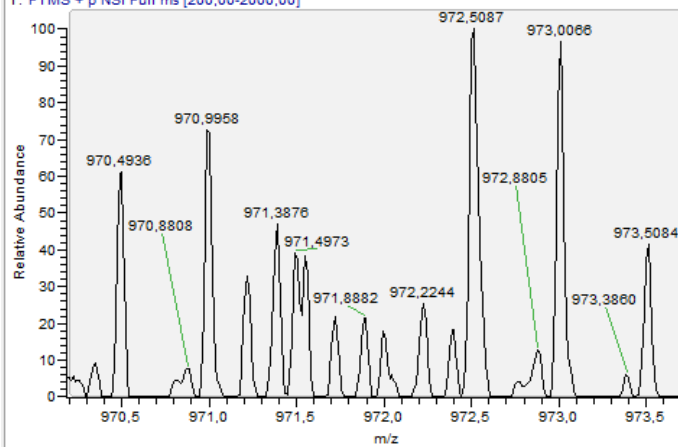


estriado_04 #12451-12822 RT: 56,67-58,12 AV: 52 NL: 1,07E4
T: FTMS + p NSI Full ms [200,00-2000,00]

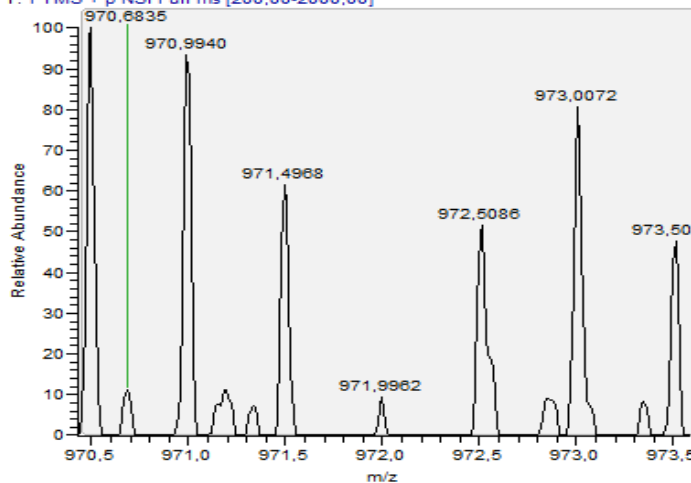


LLDEGHYPVRESPIDTA 2+

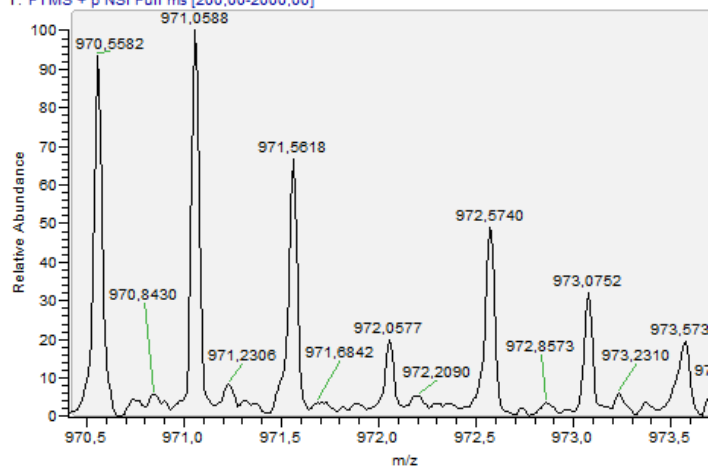
estriado_01 #6279-6405 RT: 41,14-41,82 AV: 7 NL: 2,21E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #6355-6385 RT: 41,47-41,59 AV: 2 NL: 3,88E4
T: FTMS + p NSI Full ms [200,00-2000,00]

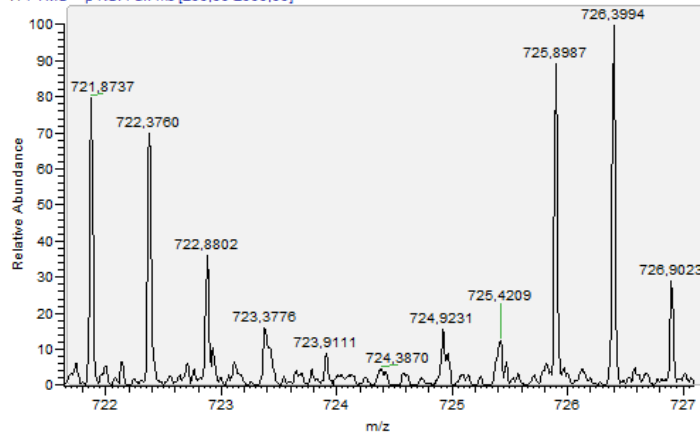


estriado_04 #2722-4578 RT: 20,38-27,40 AV: 219 NL: 2,07E3
T: FTMS + p NSI Full ms [200,00-2000,00]

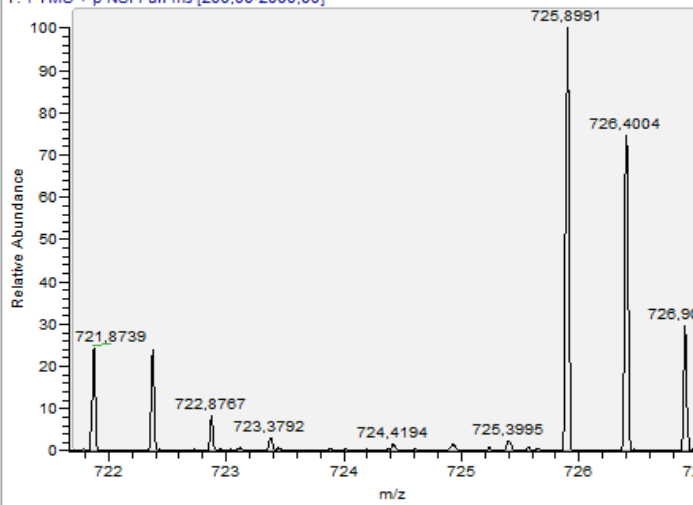


SPQLEDEAKELQ 2 +

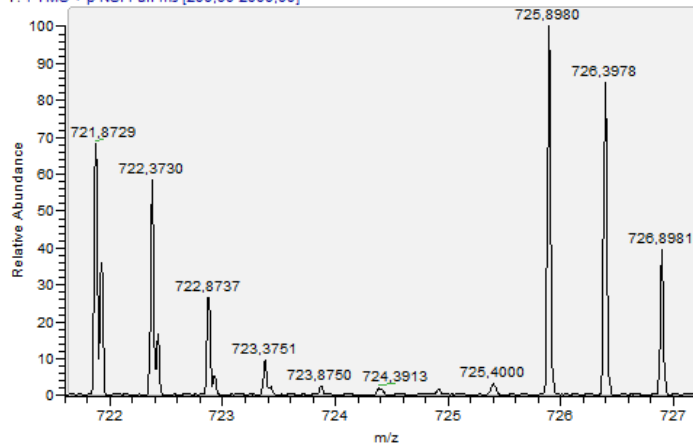
estriado_01 #5831-6088 RT: 38,53-39,97 AV: 18 NL: 4,19E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #5827-5870 RT: 38,48-38,66 AV: 3 NL: 5,76E5
T: FTMS + p NSI Full ms [200,00-2000,00]



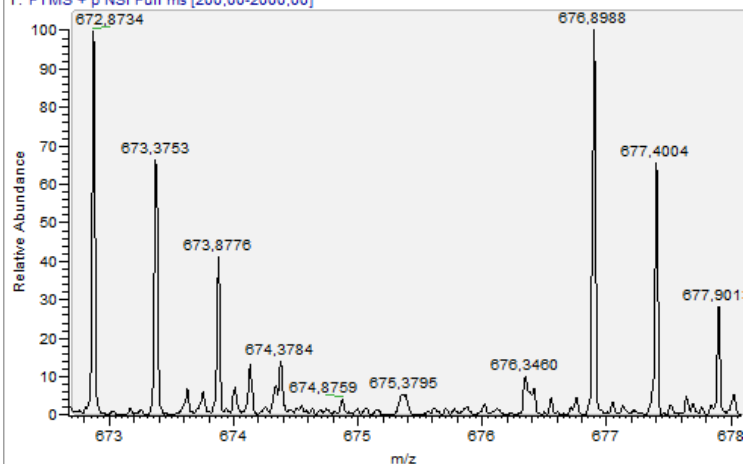
estriado_04 #8966-10436 RT: 43,35-48,84 AV: 178 NL: 8,62E4
T: FTMS + p NSI Full ms [200,00-2000,00]



ADEVSLAKQGL 2+

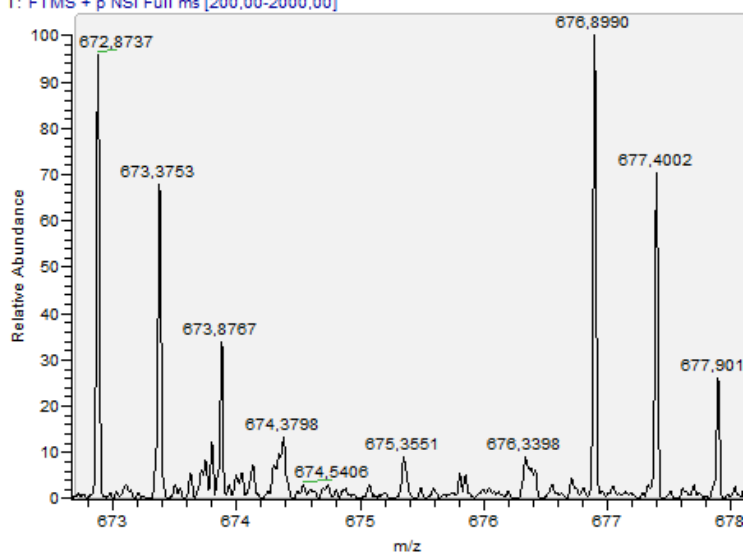
estriado_01 #6469-6717 RT: 42,25-43,65 AV: 30 NL: 6,82E4

T: FTMS + p NSI Full ms [200,00-2000,00]



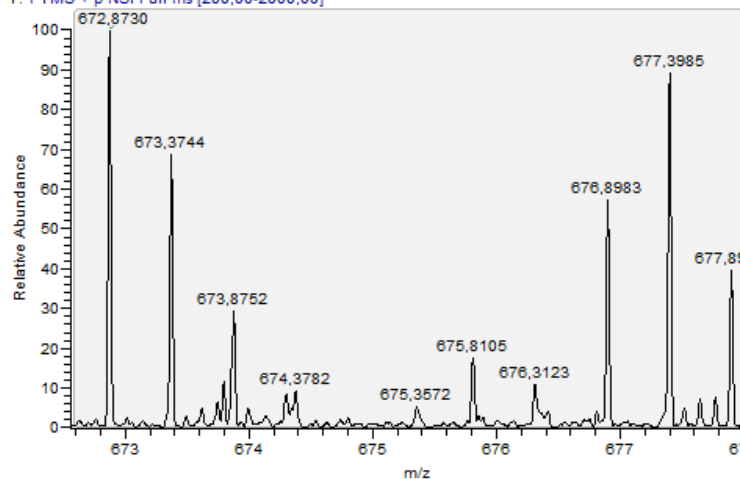
estriado_02 #6386-6729 RT: 41,71-43,64 AV: 27 NL: 6,28E4

T: FTMS + p NSI Full ms [200,00-2000,00]



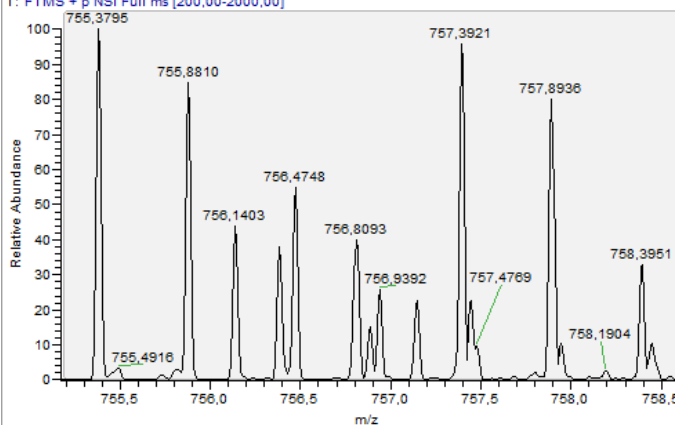
estriado_04 #9947-10330 RT: 47,05-48,51 AV: 51 NL: 3,14E4

T: FTMS + p NSI Full ms [200,00-2000,00]

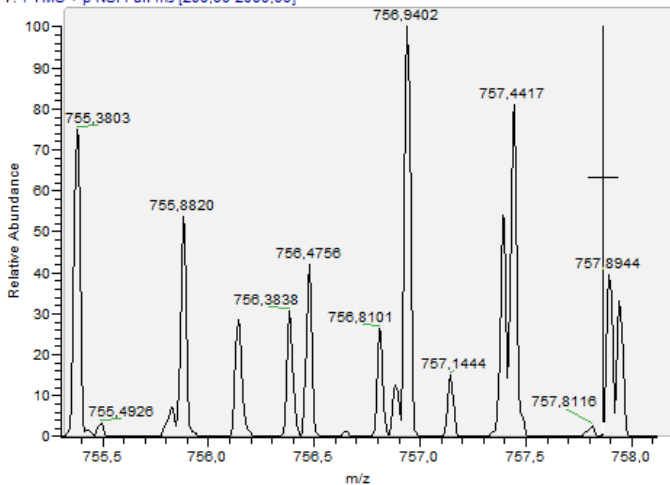


SGPFGQIFRPDNF 2+

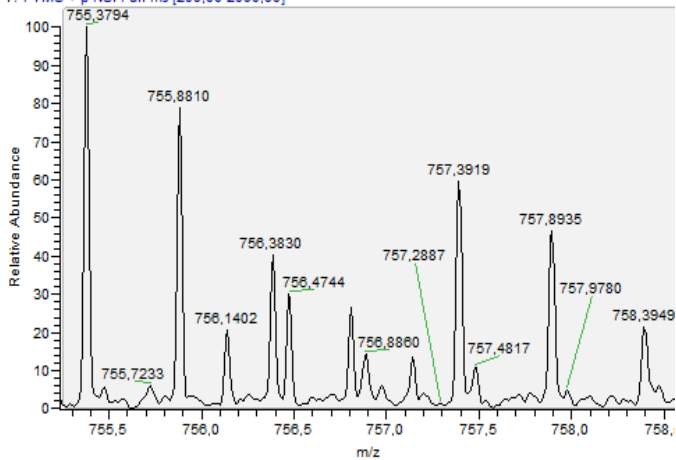
estriado_01 #10554-10736 RT: 66,70-67,76 AV: 10 NL: 4,21E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #10623-10651 RT: 67,16-67,27 AV: 2 NL: 6,72E4
T: FTMS + p NSI Full ms [200,00-2000,00]

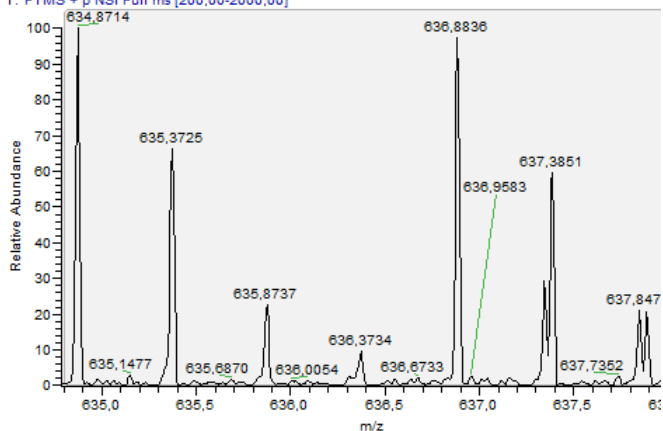


estriado_04 #15674-15860 RT: 69,64-70,36 AV: 23 NL: 2,91E4
T: FTMS + p NSI Full ms [200,00-2000,00]

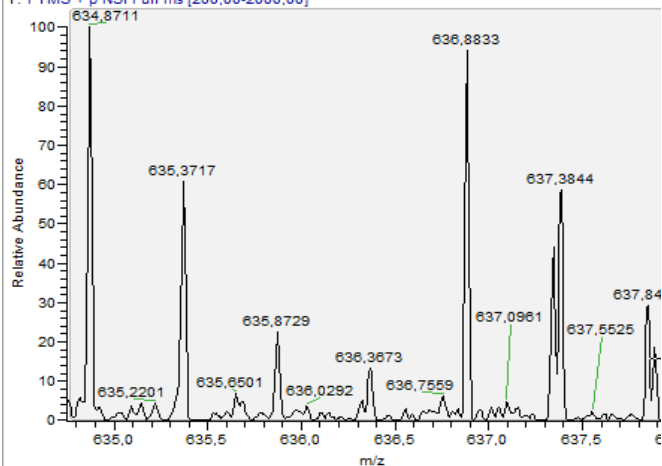


SGQAAARPLVATV 2+

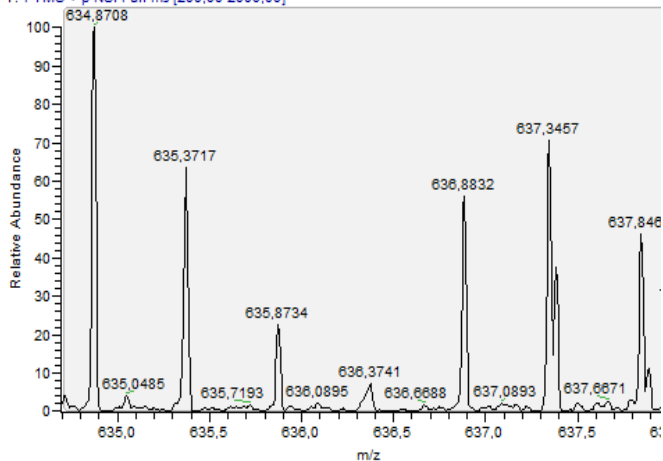
estriado_01 #5245-5503 RT: 35,19-36,60 AV: 19 NL: 1,14E5
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #5319-5538 RT: 35,60-36,74 AV: 12 NL: 9,55E4
T: FTMS + p NSI Full ms [200,00-2000,00]

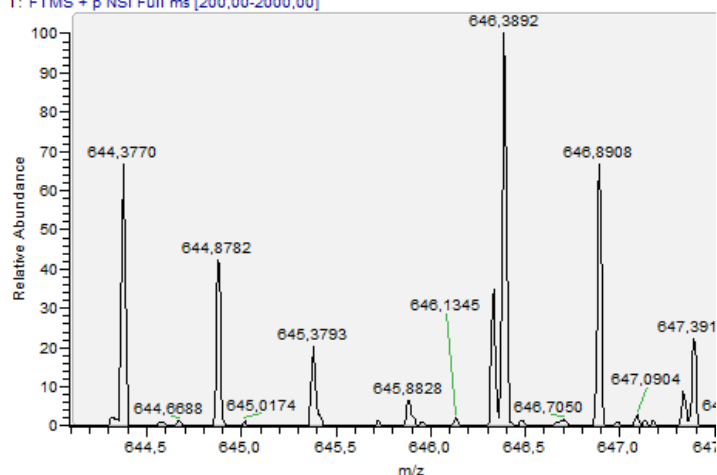


estriado_04 #8057-8462 RT: 40,00-41,43 AV: 38 NL: 4,50E4
T: FTMS + p NSI Full ms [200,00-2000,00]

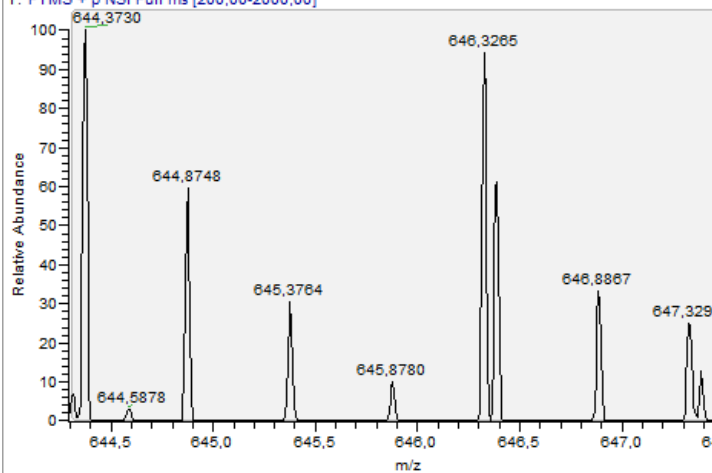


TVGLNVPASVRF 2+

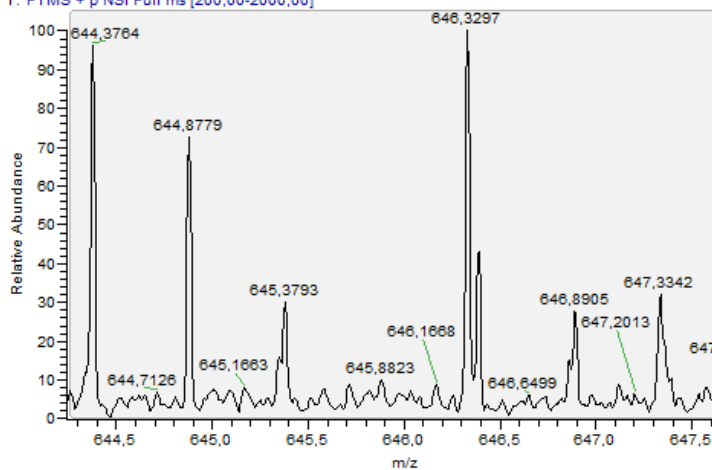
estriado_01 #9257 RT: 58,83 AV: 1 NL: 2,71E5
T: FTMS + p NSI Full ms [200,00-2000,00]



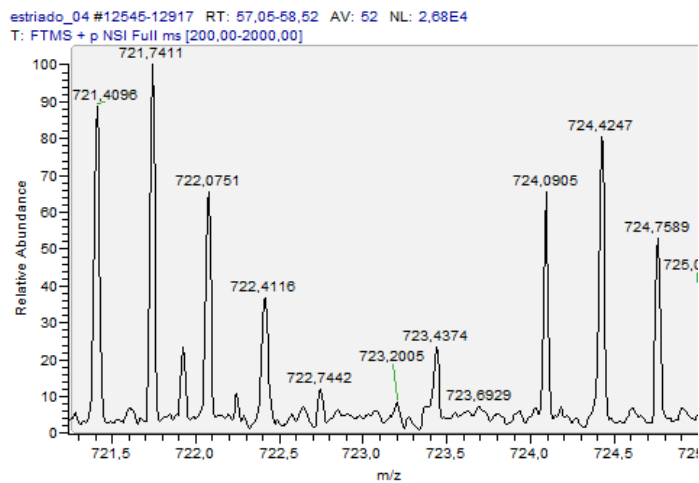
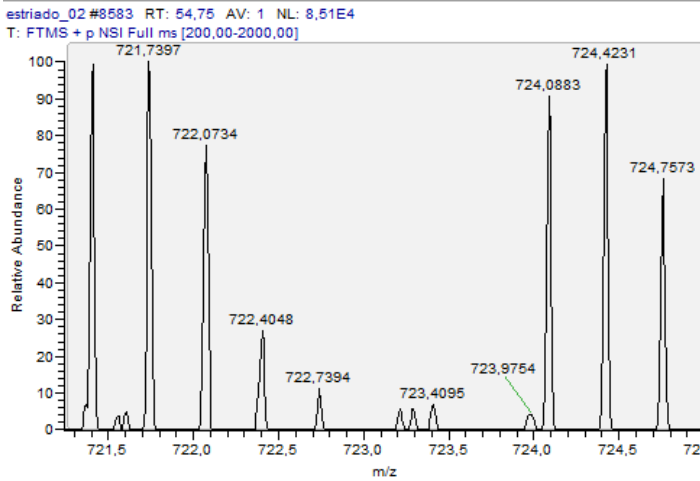
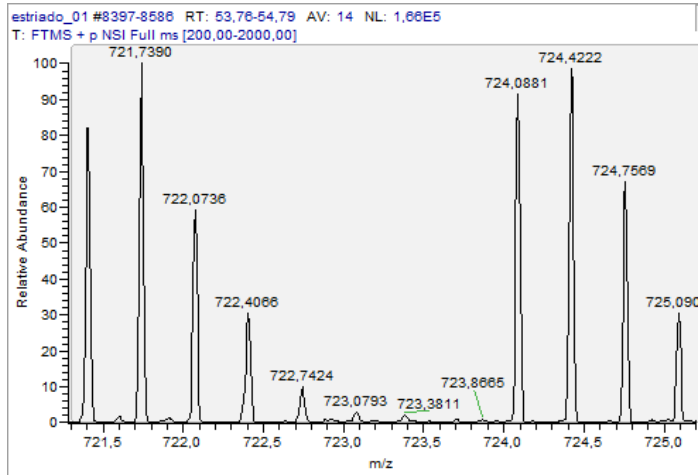
estriado_02 #9326 RT: 59,26 AV: 1 NL: 2,68E5
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_04 #13462-13831 RT: 60,76-62,19 AV: 53 NL: 1,19E4
T: FTMS + p NSI Full ms [200,00-2000,00]

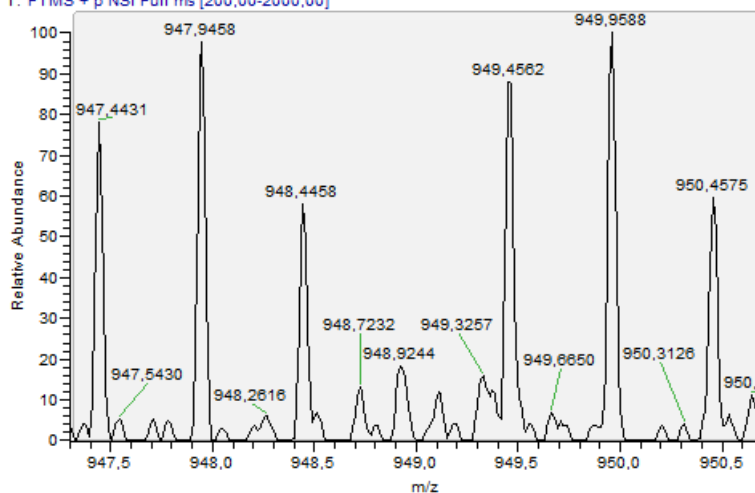


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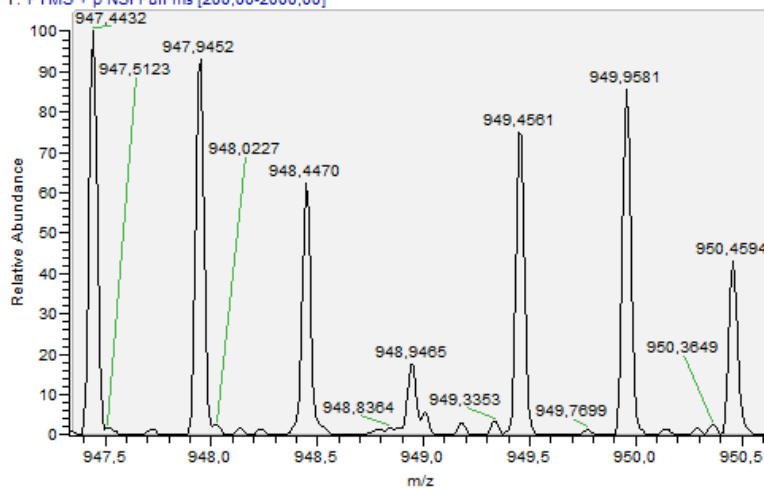


FHNPHVNPLPTGYEDE 2+

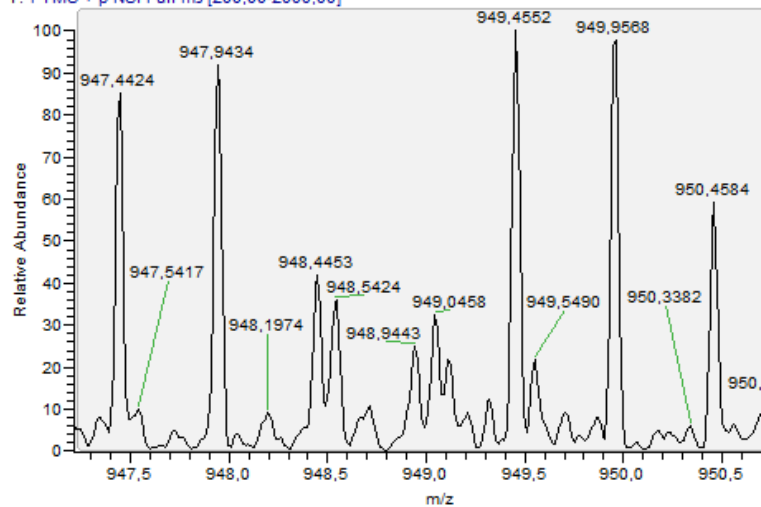
estriado_01 #5958-6151 RT: 39,35-40,37 AV: 11 NL: 1,66E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #5909-6102 RT: 38,99-39,95 AV: 14 NL: 4,01E4
T: FTMS + p NSI Full ms [200,00-2000,00]

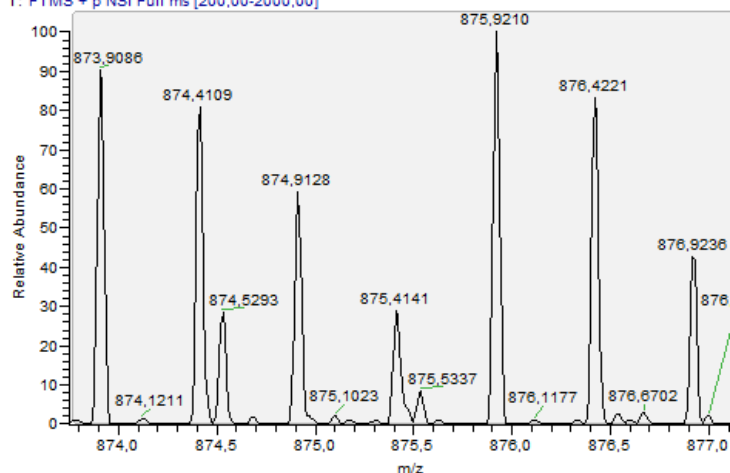


estriado_04 #8966-9349 RT: 43,35-44,81 AV: 54 NL: 4,38E3
T: FTMS + p NSI Full ms [200,00-2000,00]

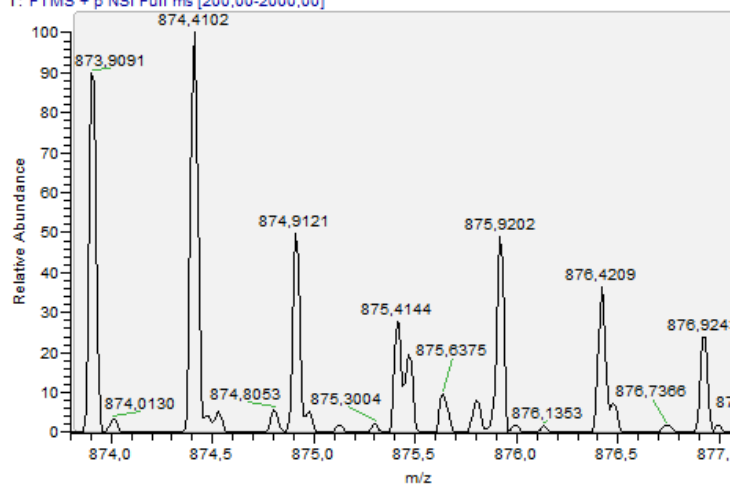


HNPHVNPLPTGYEDE 2+

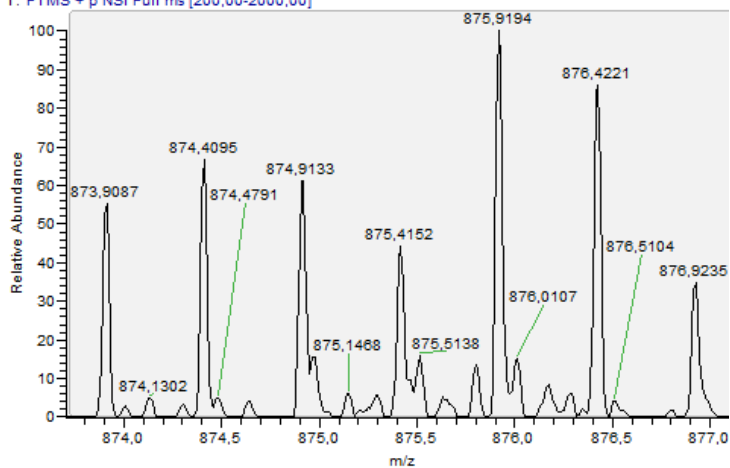
estriado_01 #4913-5177 RT: 33,37-34,76 AV: 18 NL: 3,53E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #5057-5251 RT: 34,08-35,10 AV: 11 NL: 2,99E4
T: FTMS + p NSI Full ms [200,00-2000,00]



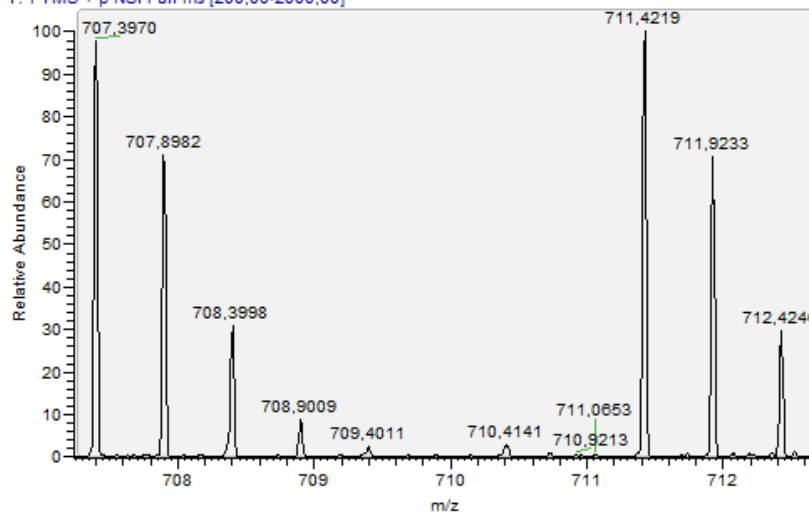
estriado_04 #7570-7706 RT: 38,16-38,65 AV: 15 NL: 1,29E4
T: FTMS + p NSI Full ms [200,00-2000,00]



GISTPEELGLDKV 2+

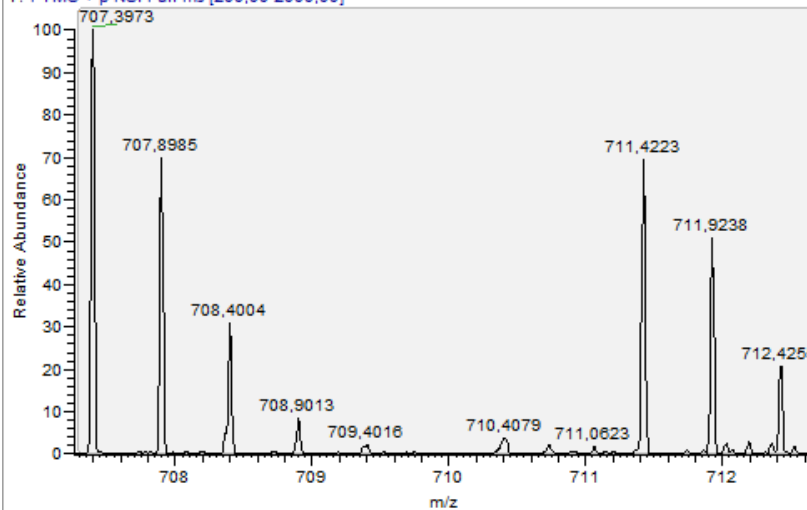
estriado_01 #8461-8649 RT: 54,12-55,13 AV: 15 NL: 3,09E5

T: FTMS + p NSI Full ms [200,00-2000,00]



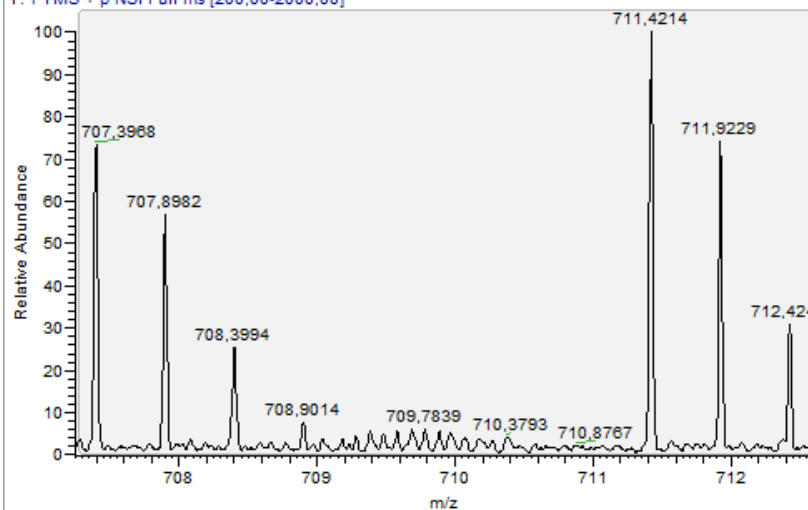
estriado_02 #8533-8716 RT: 54,46-55,54 AV: 16 NL: 2,46E5

T: FTMS + p NSI Full ms [200,00-2000,00]



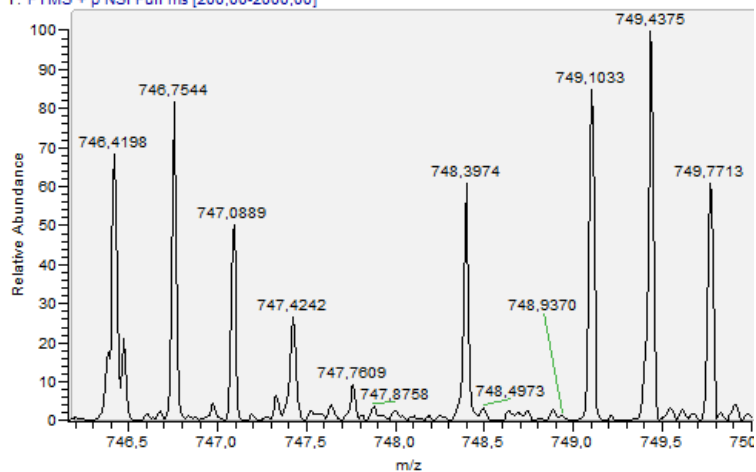
estriado_04 #12733-13097 RT: 57,79-59,26 AV: 58 NL: 7,02E4

T: FTMS + p NSI Full ms [200,00-2000,00]

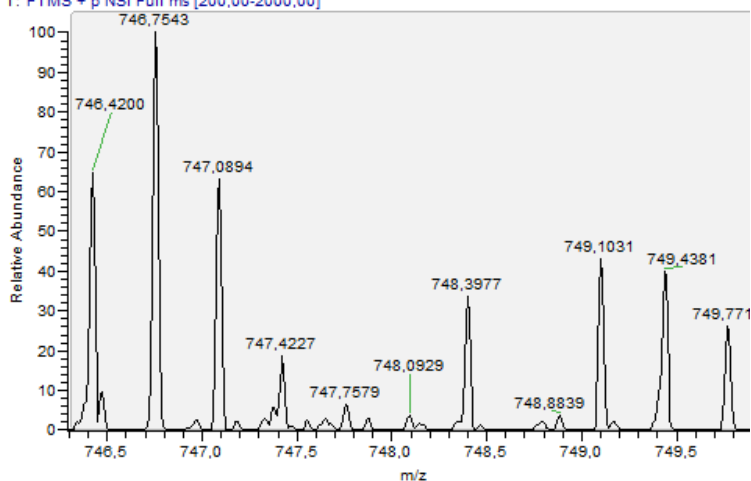


RPTLNELGISTPEELGLDKV 3+

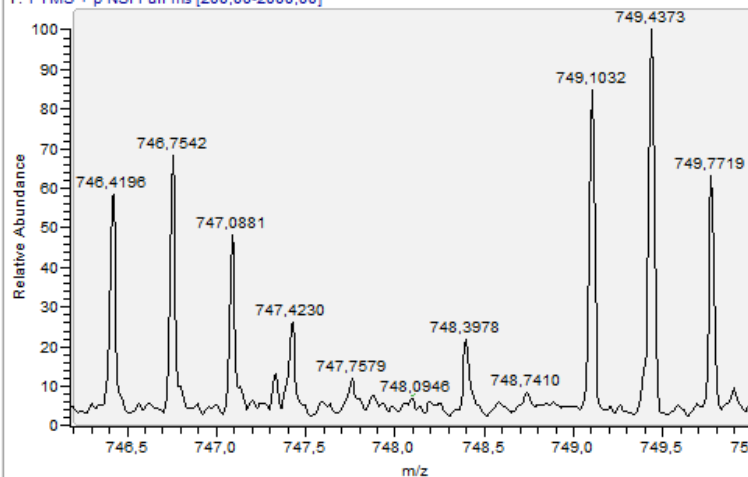
estriado_01 #10190-10373 RT: 64,46-65,51 AV: 12 NL: 2,90E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #10292-10348 RT: 65,20-65,43 AV: 3 NL: 6,34E4
T: FTMS + p NSI Full ms [200,00-2000,00]

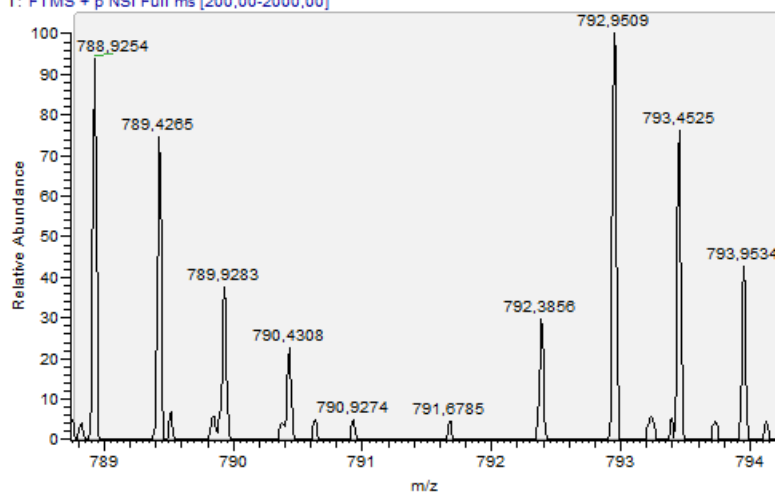


estriado_04 #14657-15487 RT: 65,57-68,84 AV: 118 NL: 1,27E4
T: FTMS + p NSI Full ms [200,00-2000,00]

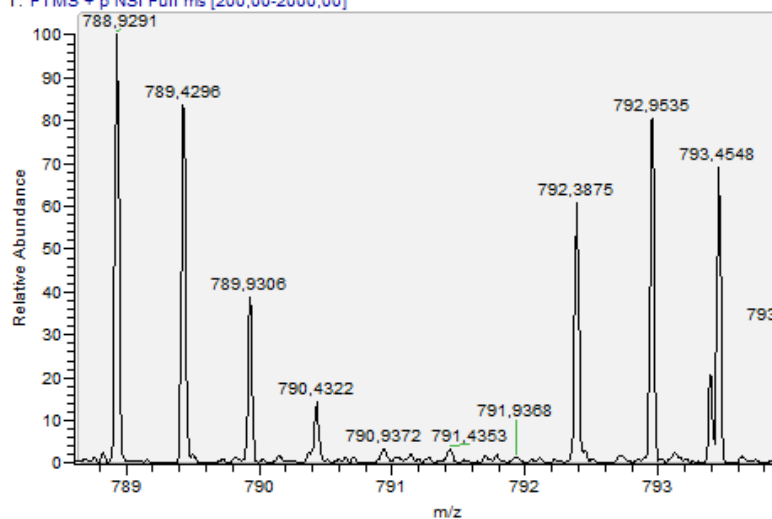


ASKGLGSDLDSSLASL 2+

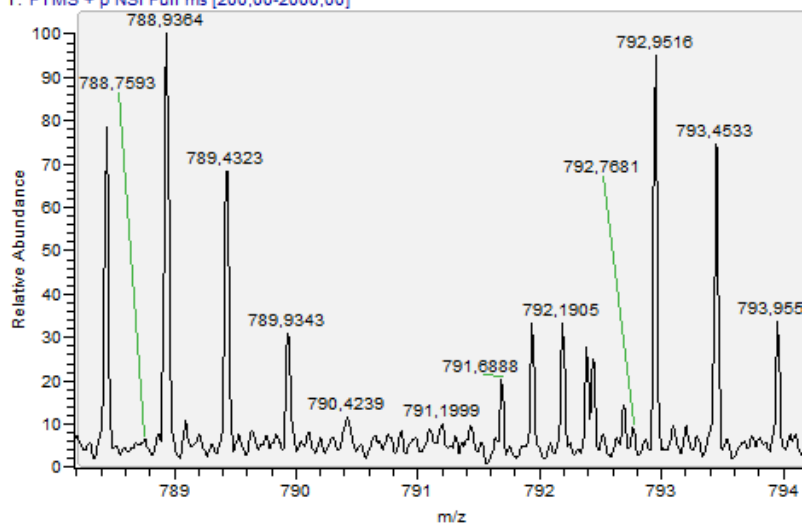
estriado_01 #9645 RT: 61,14 AV: 1 NL: 5,41E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #9574-9756 RT: 60,76-61,77 AV: 12 NL: 6,65E4
T: FTMS + p NSI Full ms [200,00-2000,00]

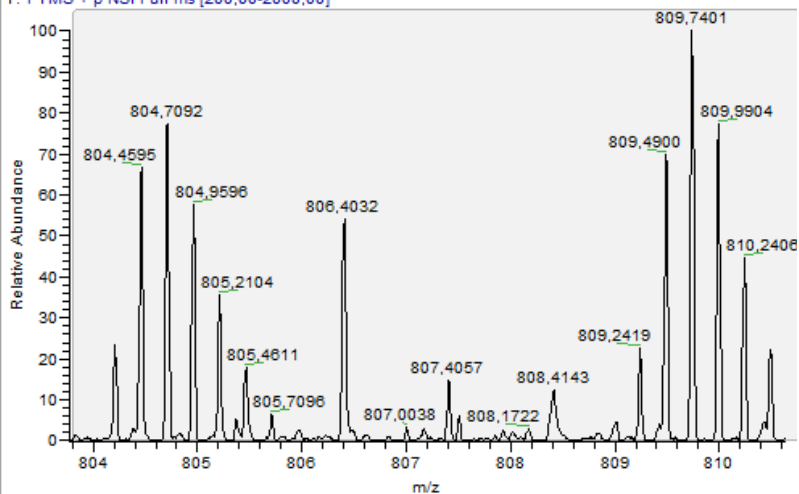


estriado_04 #14195-14472 RT: 63,74-64,81 AV: 41 NL: 1,91E4
T: FTMS + p NSI Full ms [200,00-2000,00]

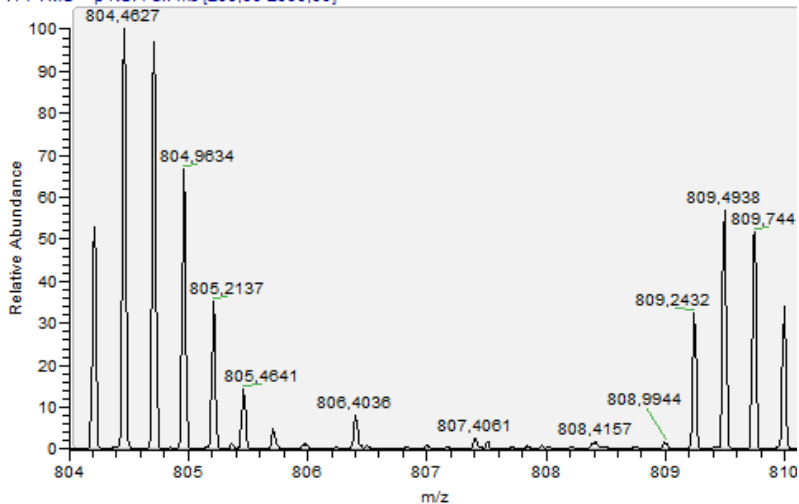


SPSPTPATQSPKKPPAKDPLADLNIKDFL 4+

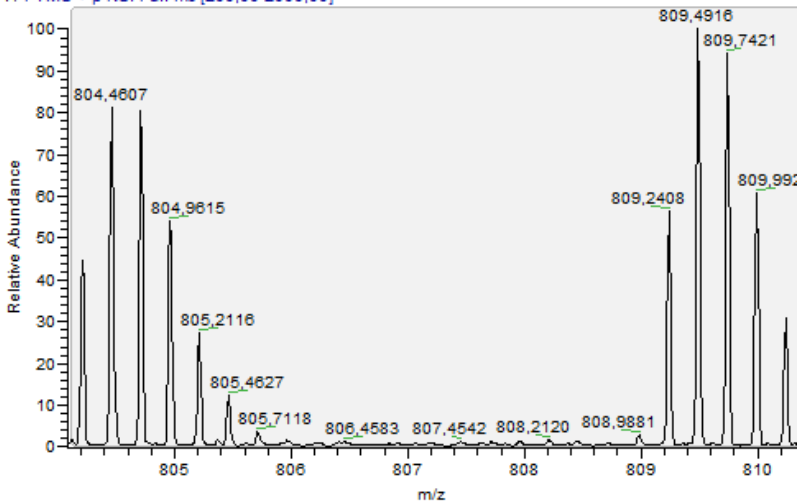
estriado_01 #10736-10916 RT: 67,88-68,83 AV: 13 NL: 4,12E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #10665-10842 RT: 67,45-68,51 AV: 14 NL: 1,87E5
T: FTMS + p NSI Full ms [200,00-2000,00]

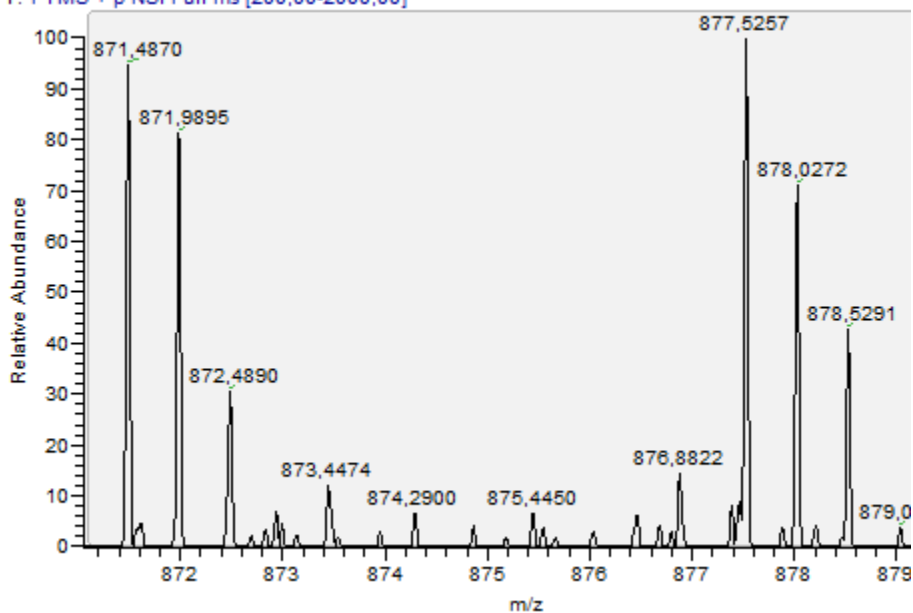


estriado_04 #15211-15674 RT: 67,80-68,60 AV: 61 NL: 1,26E5
T: FTMS + p NSI Full ms [200,00-2000,00]

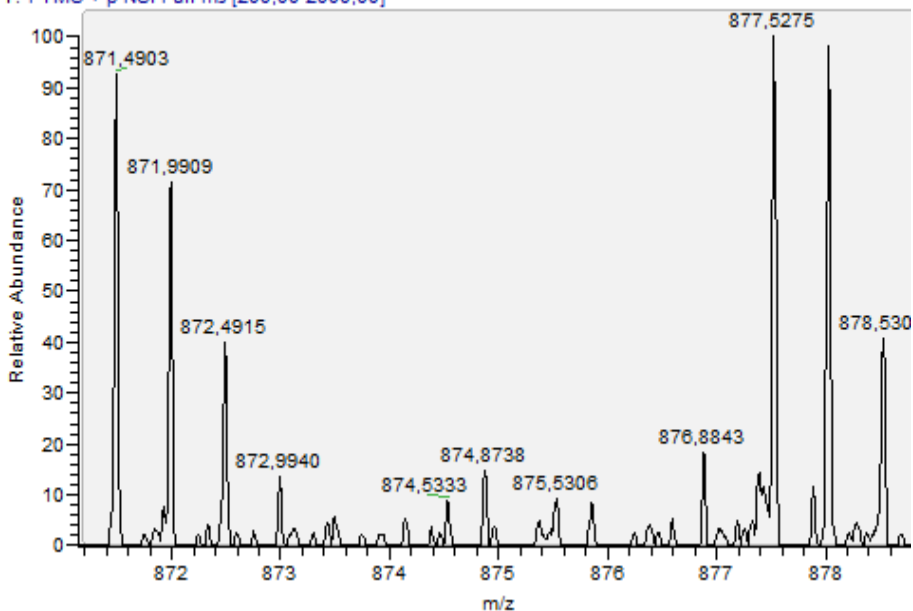


AVGSGGKGKSGEIEPVSV

estriado_01 #4580-4848 RT: 31,52-32,86 AV: 13 NL: 1,93E4
T: FTMS + p NSI Full ms [200,00-2000,00]

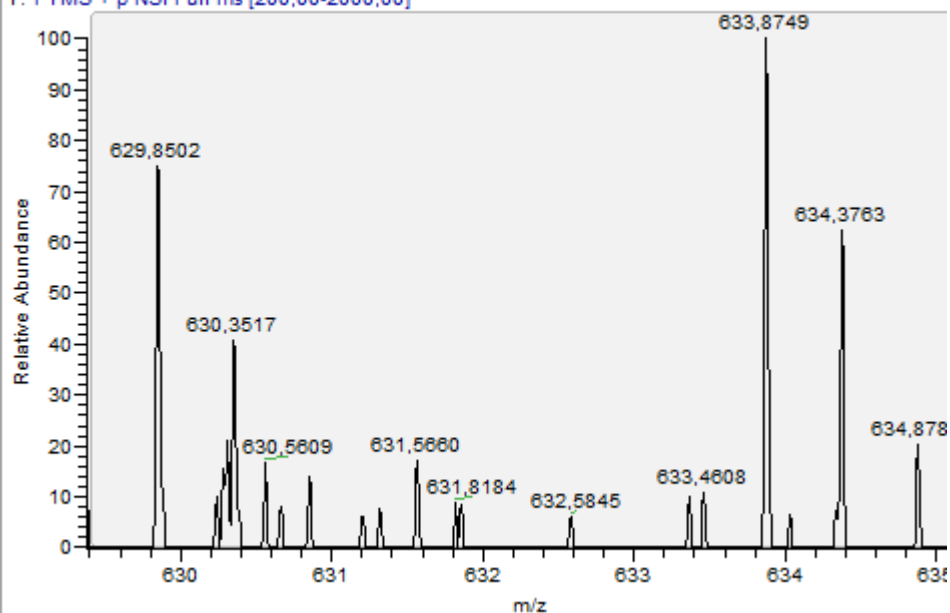


estriado_02 #4519-4852 RT: 31,15-32,95 AV: 19 NL: 1,19E4
T: FTMS + p NSI Full ms [200,00-2000,00]

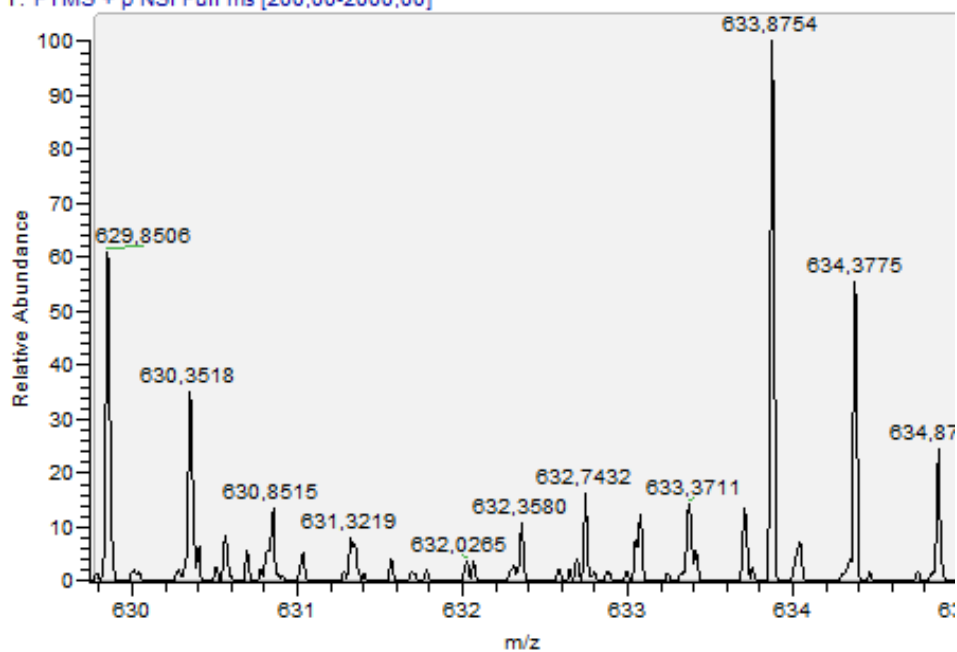


AGGPPHPQLNKS

estriado_01 #2951 RT: 22,39 AV: 1 NL: 4,11E4
T: FTMS + p NSI Full ms [200,00-2000,00]

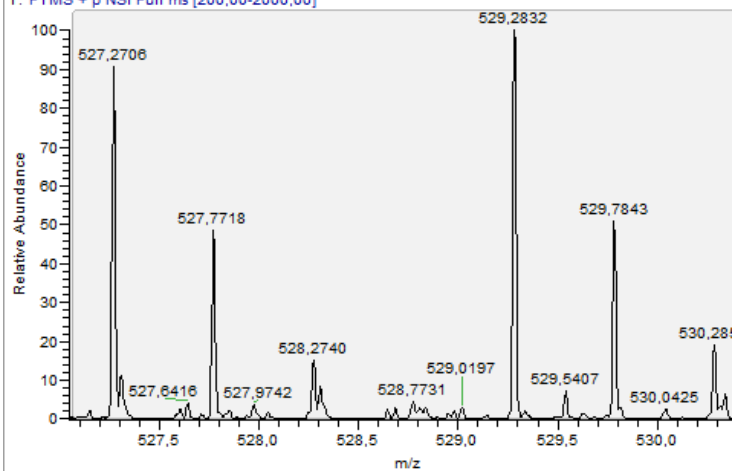


estriado_02 #2855-2943 RT: 21,83-22,19 AV: 4 NL: 4,03E4
T: FTMS + p NSI Full ms [200,00-2000,00]

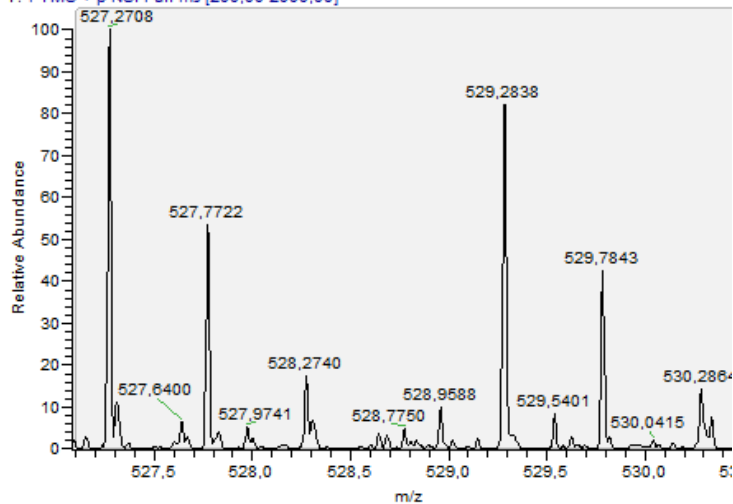


GQGAGALVHSE 2+

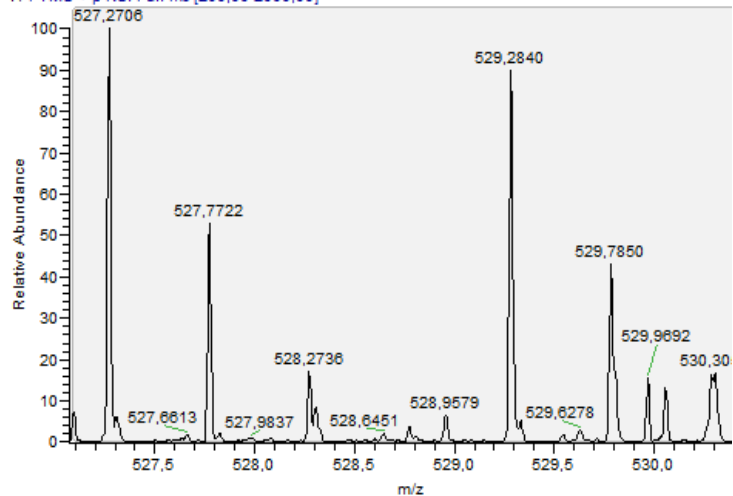
estriado_01 #3177-3375 RT: 23,82-24,80 AV: 10 NL: 9,51E4
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #3072-3357 RT: 23,16-24,60 AV: 13 NL: 7,21E4
T: FTMS + p NSI Full ms [200,00-2000,00]

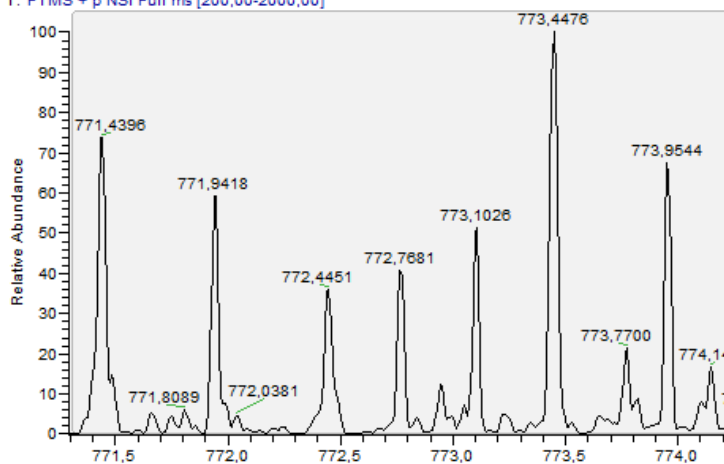


estriado_04 #4787-5208 RT: 28,20-29,60 AV: 32 NL: 2,09E4
T: FTMS + p NSI Full ms [200,00-2000,00]

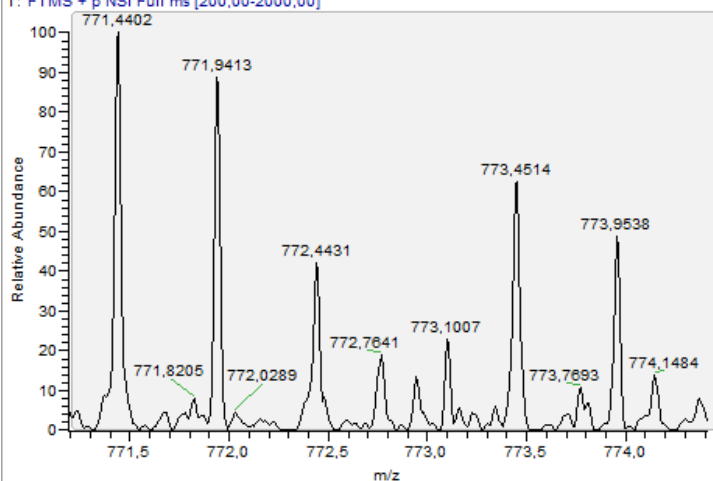


AFRVPTPNVSVVDL 2+

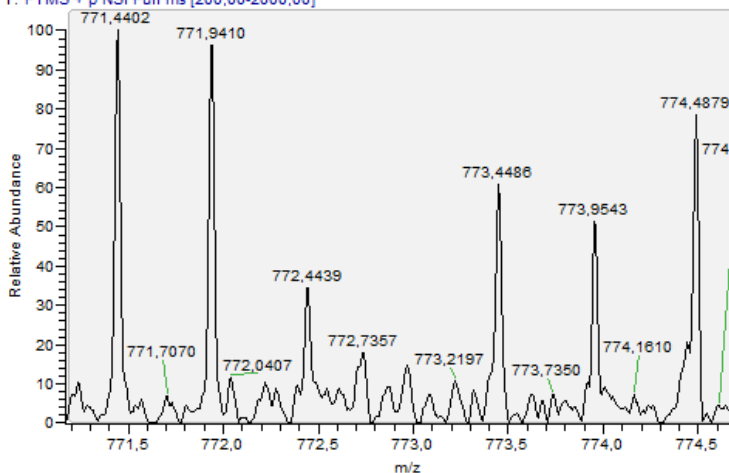
estriado_01 #10797-11154 RT: 68,21-70,34 AV: 26 NL: 8,93E3
T: FTMS + p NSI Full ms [200,00-2000,00]



estriado_02 #10747-10941 RT: 67,97-69,12 AV: 13 NL: 9,41E3
T: FTMS + p NSI Full ms [200,00-2000,00]

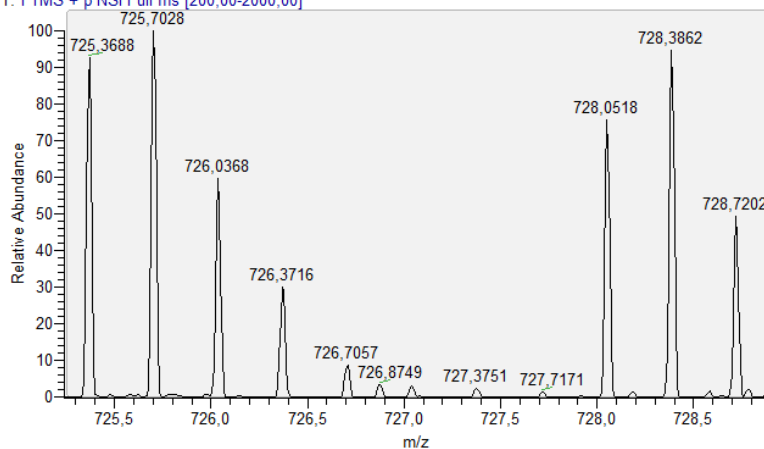


estriado_04 #15627-15691 RT: 69,47-69,70 AV: 8 NL: 8,21E3
T: FTMS + p NSI Full ms [200,00-2000,00]

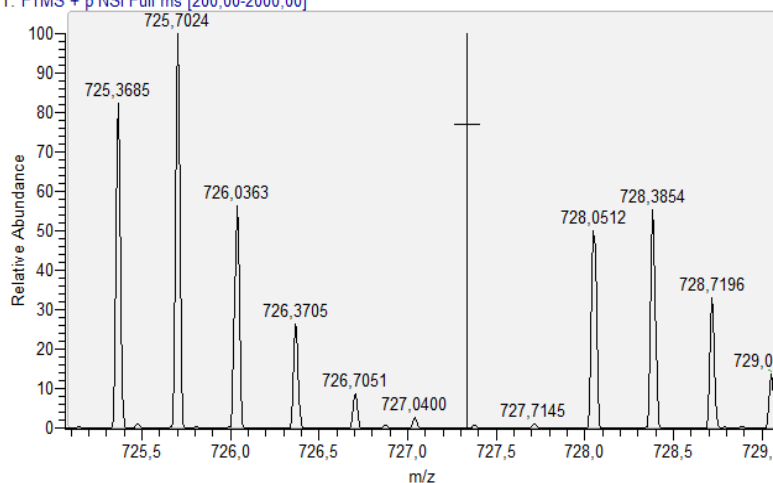


GRKGP GPGGGAGGARGGAGGGPSGD 3+

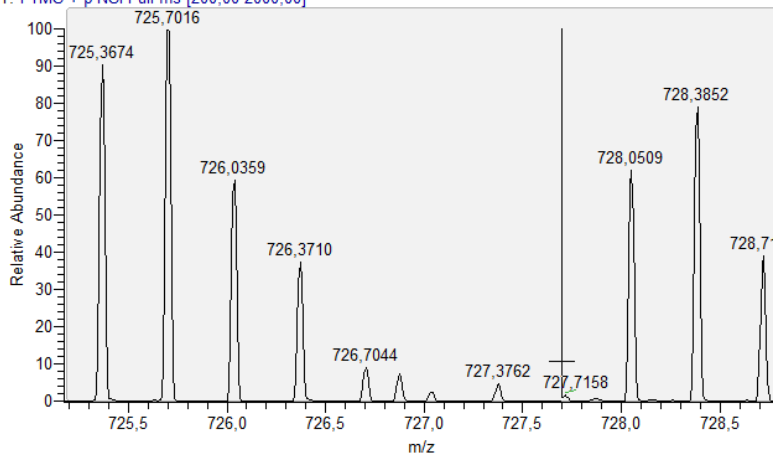
hipocampo_01 #2076-2214 RT: 17,01-17,79 AV: 7 NL: 7,53E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #1973 RT: 16,40 AV: 1 NL: 3,60E5
T: FTMS + p NSI Full ms [200,00-2000,00]

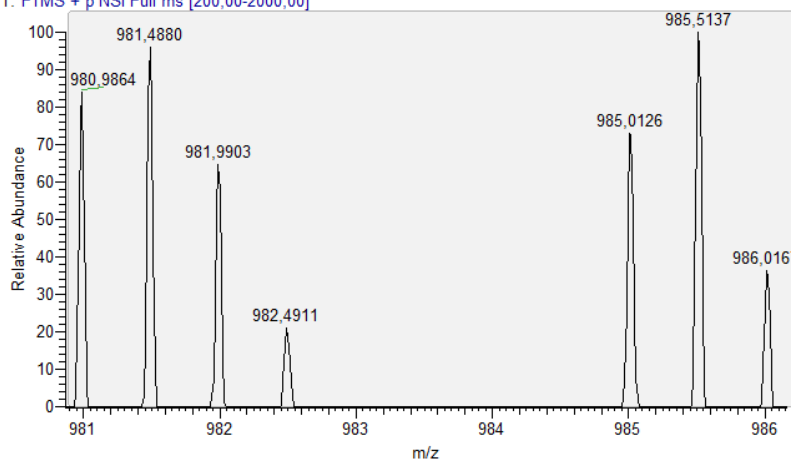


hipocampo_04 #2386-2623 RT: 21,27-22,38 AV: 71 NL: 1,34E4
T: FTMS + p NSI Full ms [200,00-2000,00]

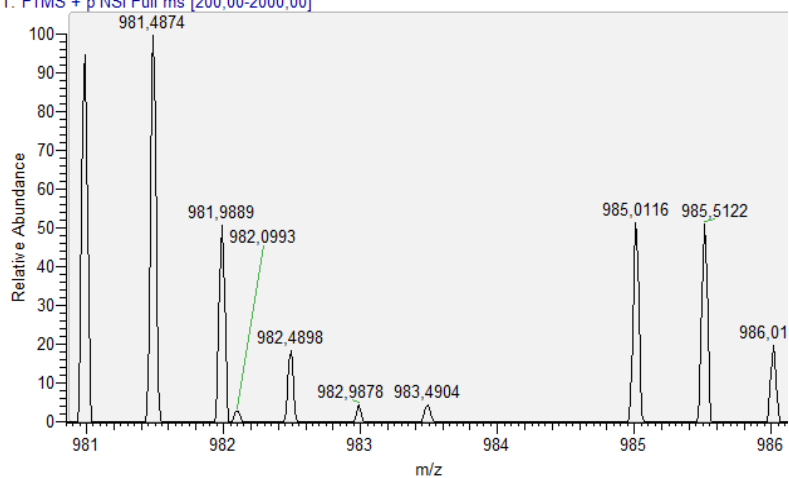


KGPGPGGGPGGAGGARGGAGGGPSGD 2+

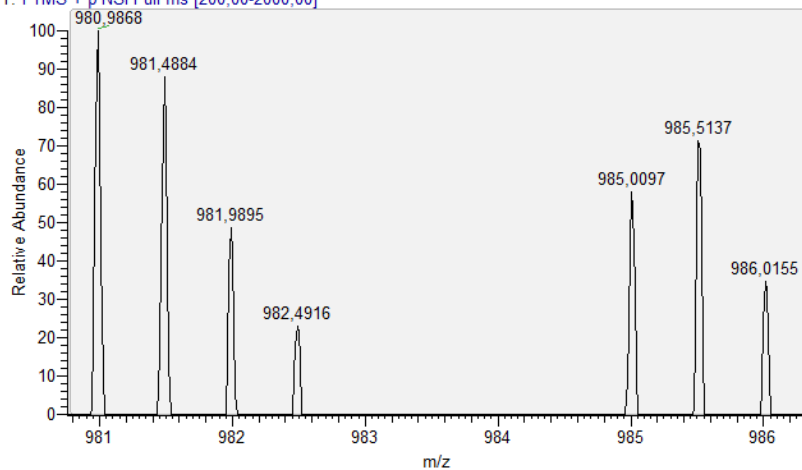
hipocampo_01 #2349 RT: 18,68 AV: 1 NL: 2,61E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #2159-2250 RT: 17,62-18,13 AV: 5 NL: 8,73E3
T: FTMS + p NSI Full ms [200,00-2000,00]

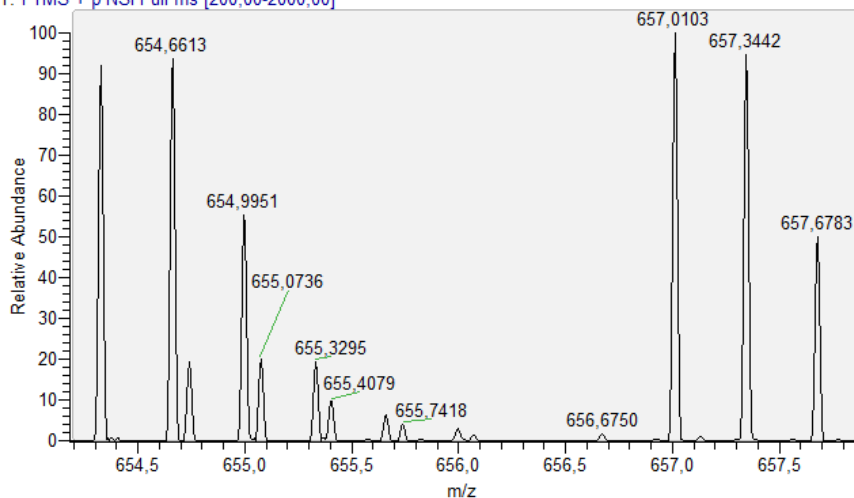


hipocampo_04 #2722 RT: 22,83 AV: 1 NL: 2,90E3
T: FTMS + p NSI Full ms [200,00-2000,00]

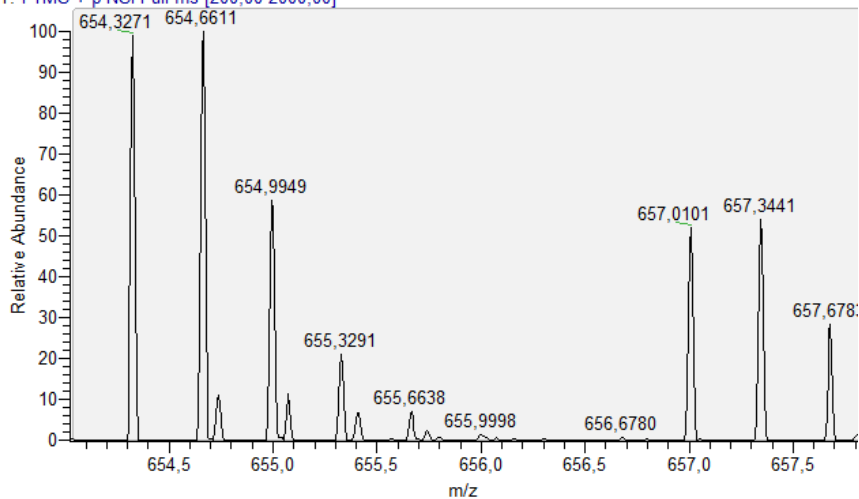


KGPGPGGGAGGARGGAGGGPSGD 3+

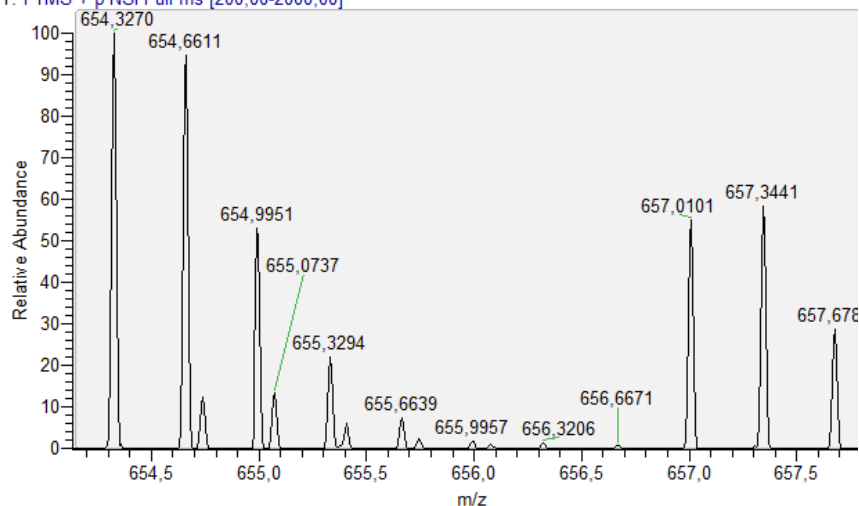
hipocampo_01 #2349 RT: 18,68 AV: 1 NL: 5,06E5
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #2228 RT: 18,00 AV: 1 NL: 3,57E5
T: FTMS + p NSI Full ms [200,00-2000,00]



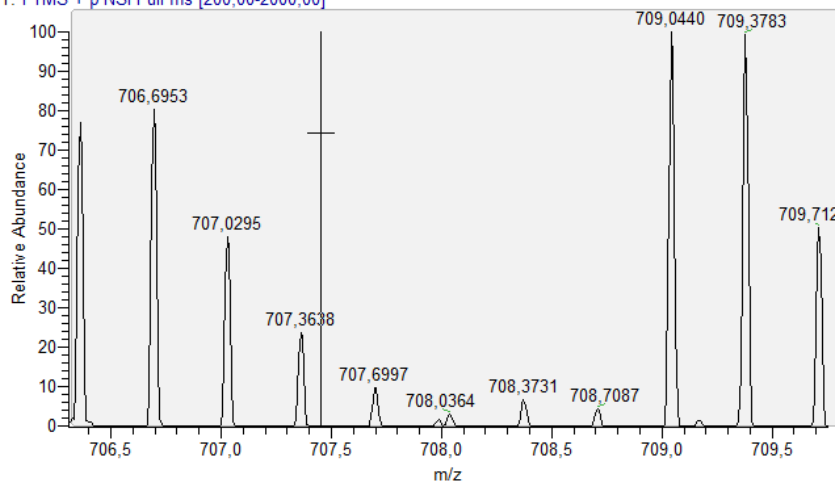
hipocampo_04 #2727 RT: 22,85 AV: 1 NL: 1,14E5
T: FTMS + p NSI Full ms [200,00-2000,00]



RKGP GPGGPGGAGGARGGAGGGPSGD 3+

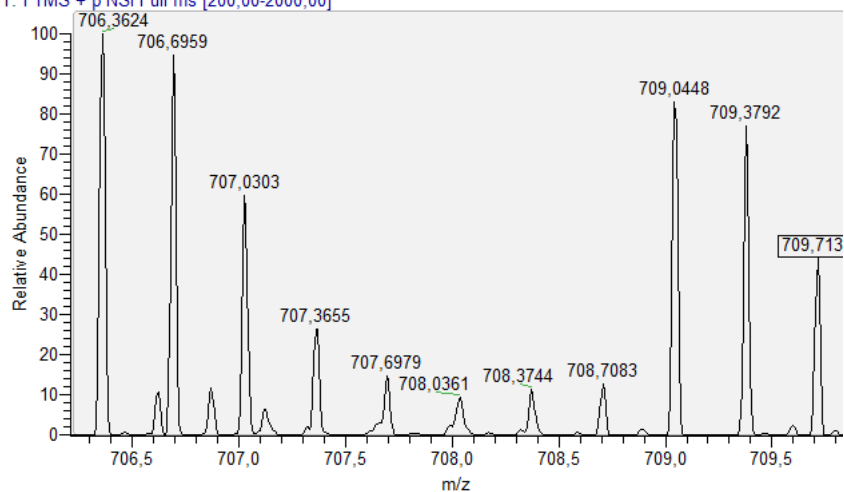
hipocampo_01 #2076 RT: 17.01 AV: 1 NL: 9,28E4

T: FTMS + p NSI Full ms [200,00-2000,00]



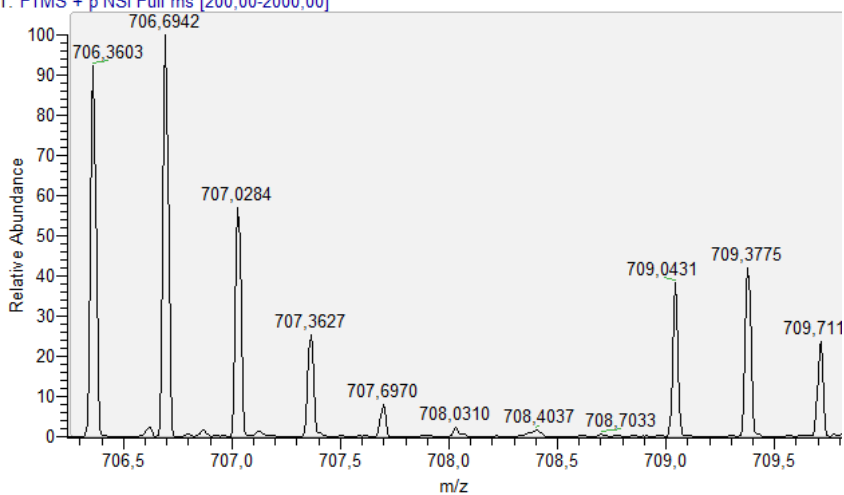
hipocampo_02 #1892-2114 RT: 15,89-17,29 AV: 12 NL: 1,34E4

T: FTMS + p NSI Full ms [200,00-2000,00]



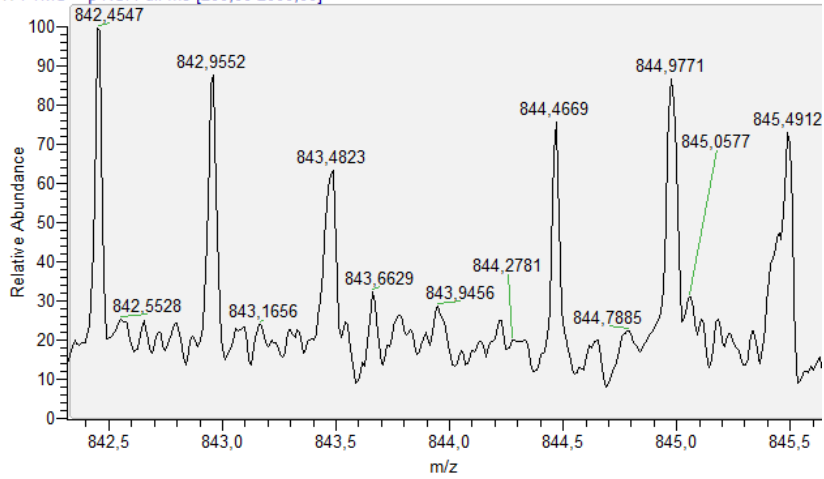
hipocampo_04 #2339-2946 RT: 20,98-23,78 AV: 173 NL: 6,22E3

T: FTMS + p NSI Full ms [200,00-2000,00]

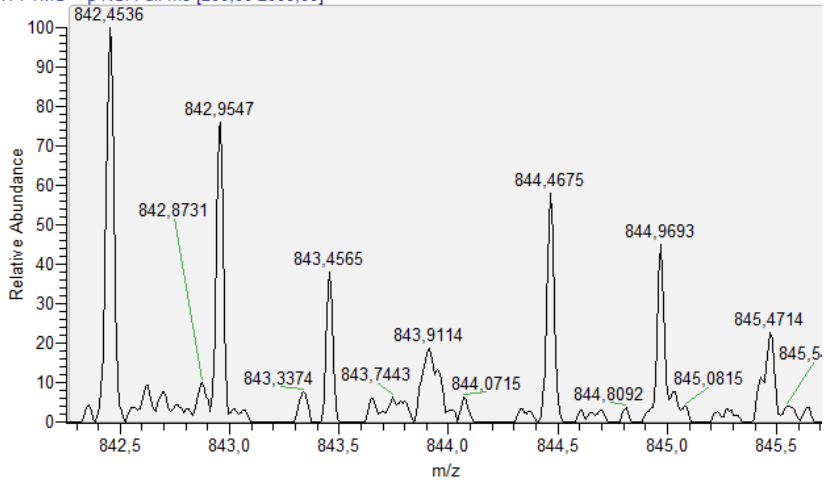


ATVGDVNTDRPGLLDL 2+

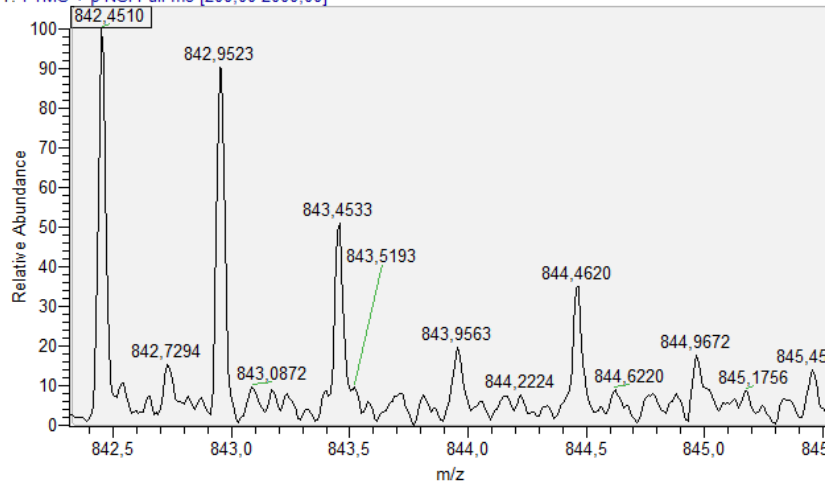
hipocampo_01 #9668-9947 RT: 60,40-62,06 AV: 31 NL: 8,51E3
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #9060-9107 RT: 57,59-57,82 AV: 5 NL: 2,80E4
T: FTMS + p NSI Full ms [200,00-2000,00]

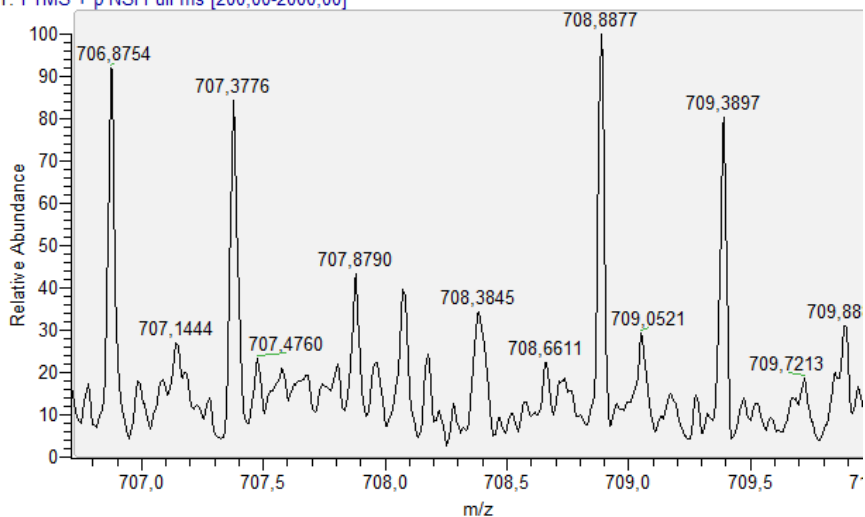


hipocampo_04 #12922-13068 RT: 64,08-64,63 AV: 20 NL: 1,31E4
T: FTMS + p NSI Full ms [200,00-2000,00]

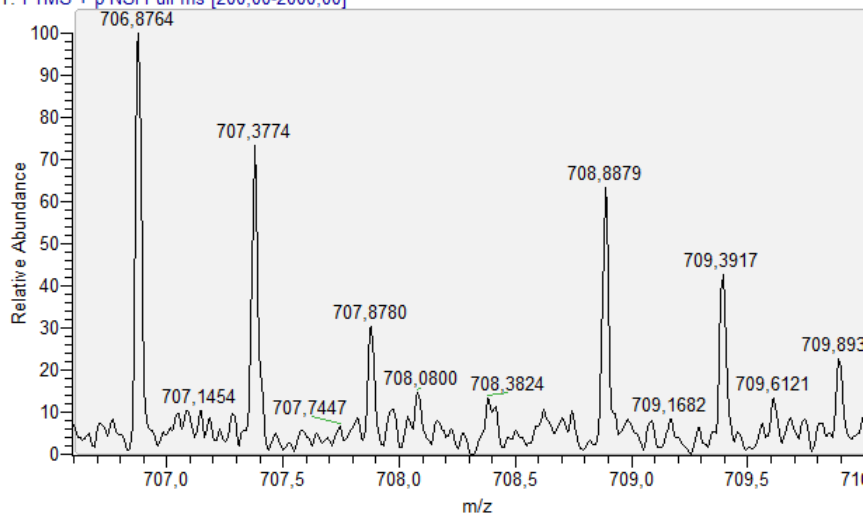


GDVNTDRPGLLDL 2+

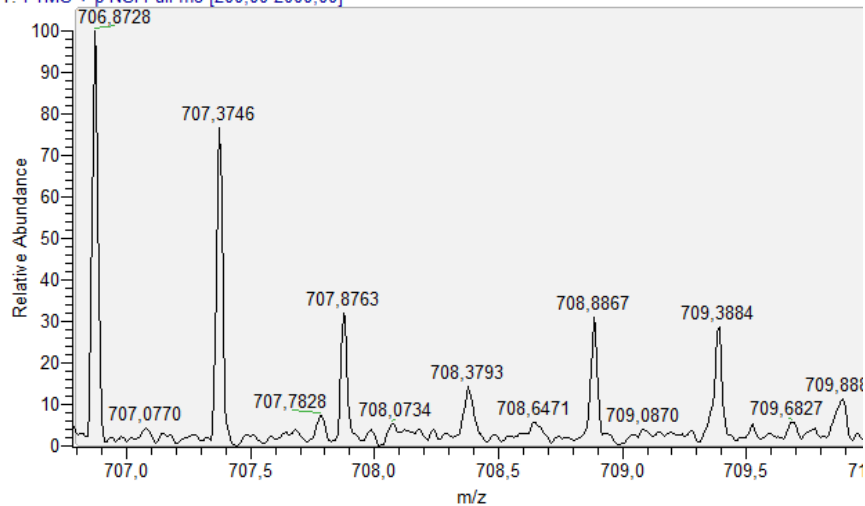
hipocampo_01 #8431-8720 RT: 53.03-54.70 AV: 32 NL: 1,98E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #8057-8152 RT: 51.67-52,15 AV: 9 NL: 4,98E4
T: FTMS + p NSI Full ms [200,00-2000,00]

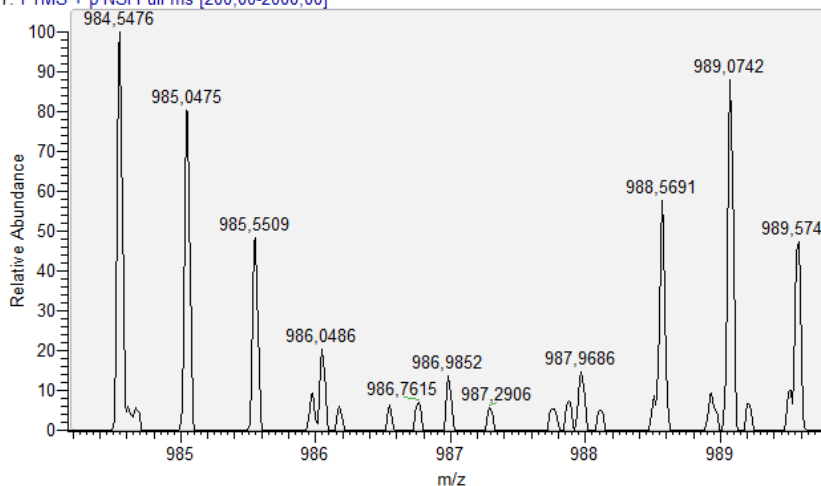


hipocampo_04 #12128-12339 RT: 60,98-61,80 AV: 37 NL: 2,40E4
T: FTMS + p NSI Full ms [200,00-2000,00]

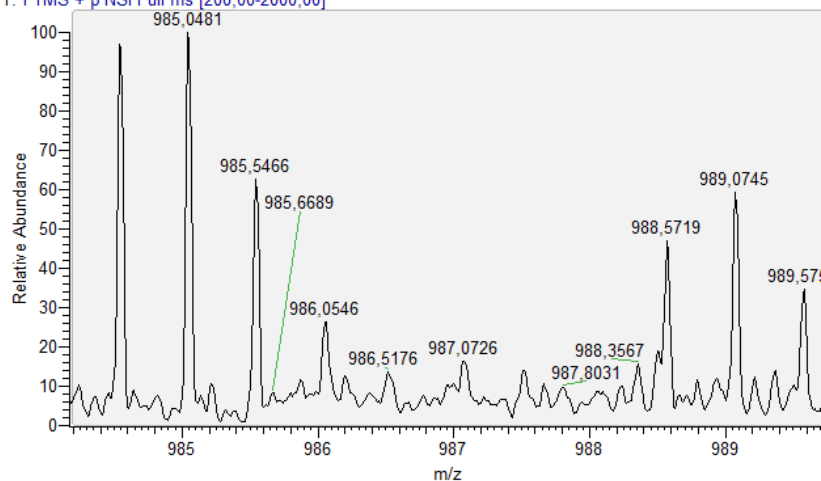


KQATVGDVNTDRPGLLDL 2+

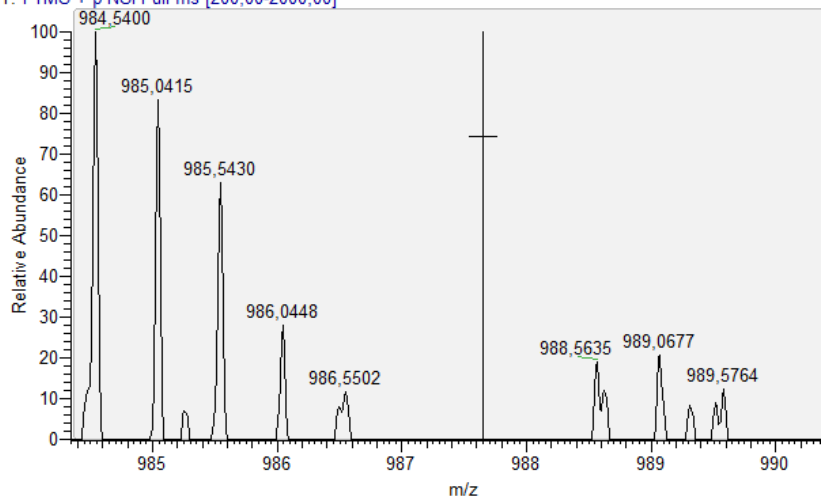
hipocampo_01 #7749 RT: 49.03 AV: 1 NL: 8.01E4
T: FTMS + p NSI Full ms [200.00-2000.00]



hipocampo_02 #7292-7674 RT: 47.09-49.33 AV: 34 NL: 2.47E4
T: FTMS + p NSI Full ms [200.00-2000.00]

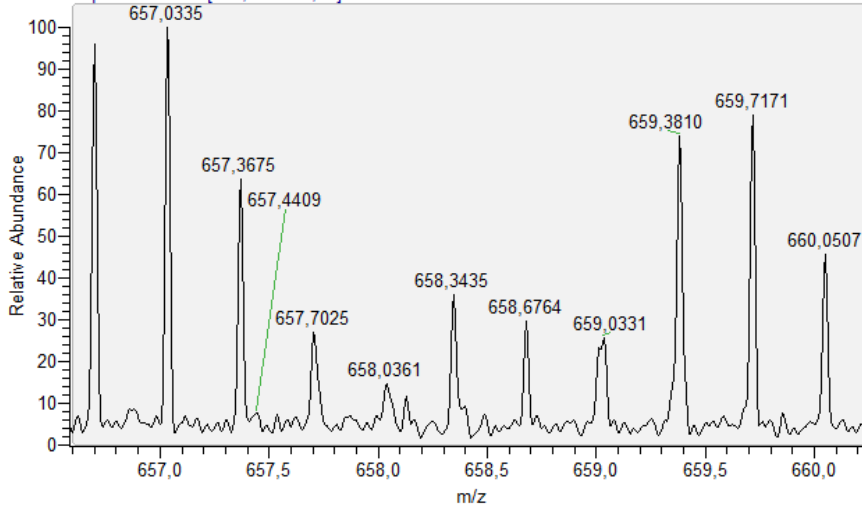


hipocampo_04 #11141 RT: 57.10 AV: 1 NL: 5.75E4
T: FTMS + p NSI Full ms [200.00-2000.00]

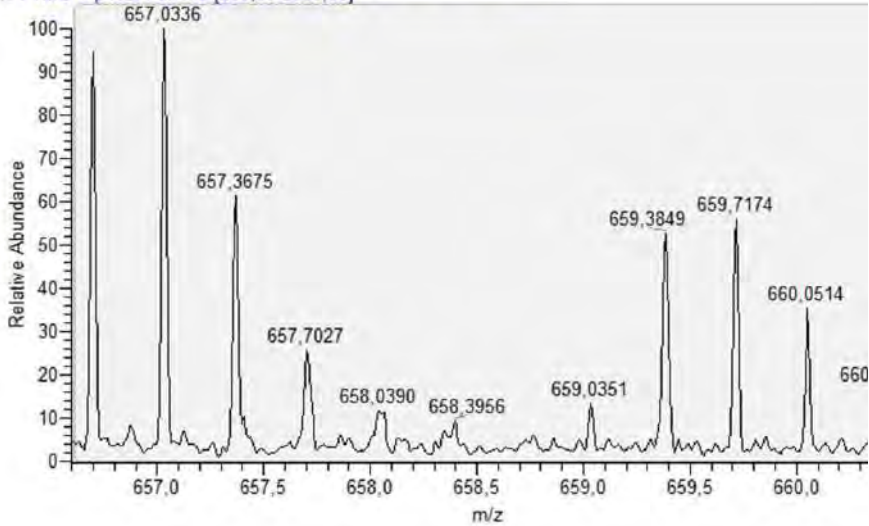


KQATVGDVNTDRPGLLDL 3+

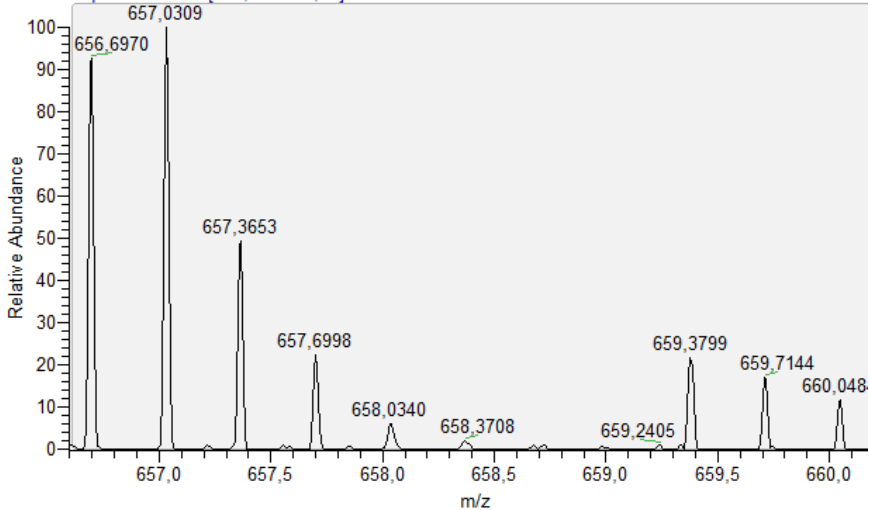
hipocampo_01 #7704-8136 RT: 48,78-51,31 AV: 38 NL: 6,98E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #7292-7674 RT: 47,09-49,33 AV: 34 NL: 9,42E4
T: FTMS + p NSI Full ms [200,00-2000,00]

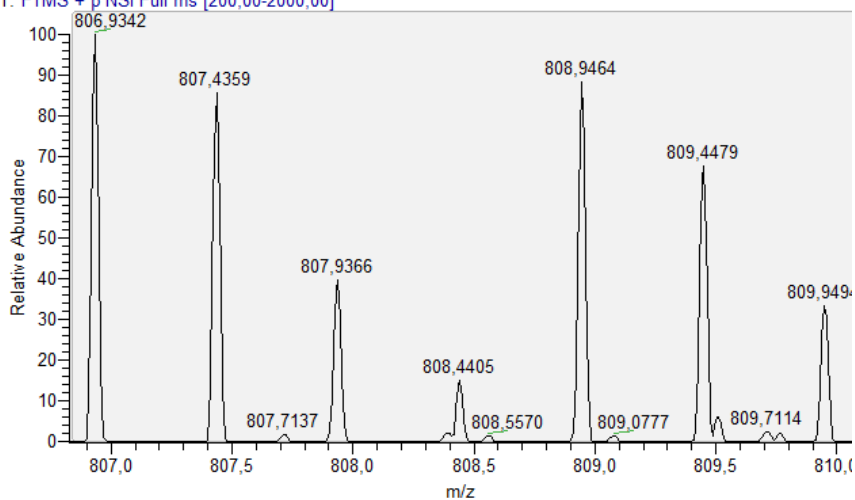


hipocampo_04 #11141 RT: 57,10 AV: 1 NL: 5,11E5
T: FTMS + p NSI Full ms [200,00-2000,00]

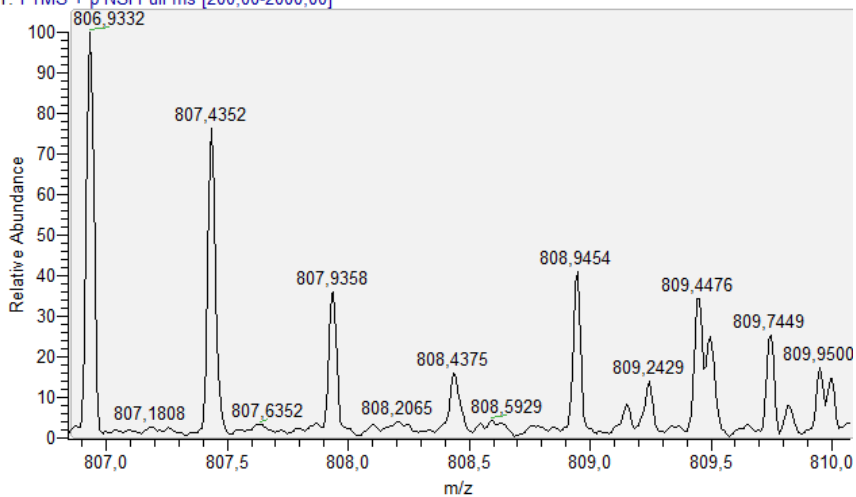


TVGDVNTDRPGLLDL 2+

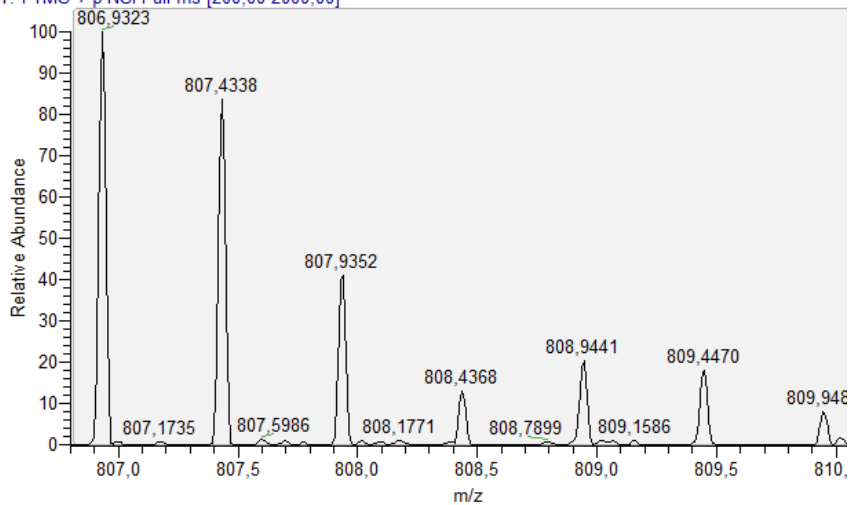
hipocampo_01 #9388 RT: 58,71 AV: 1 NL: 1,94E5
T: FTMS + p NSI Full ms [200,00-2000,00]



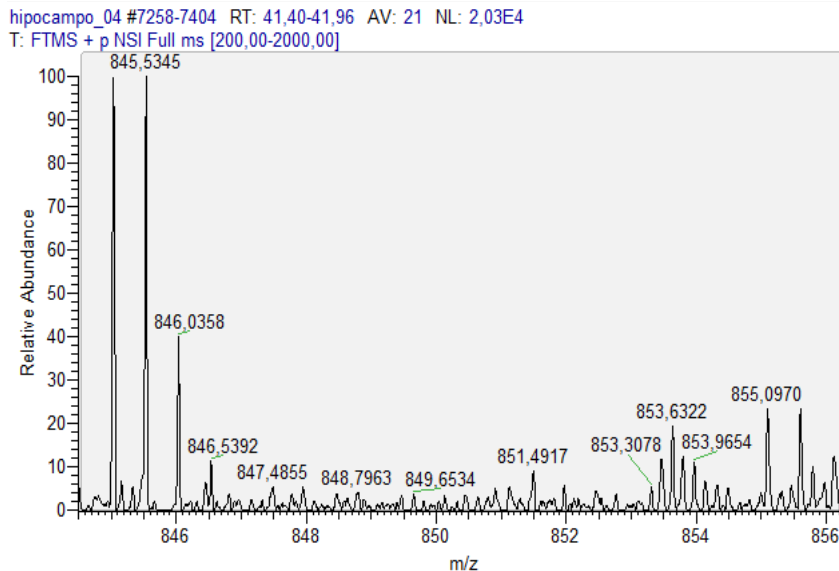
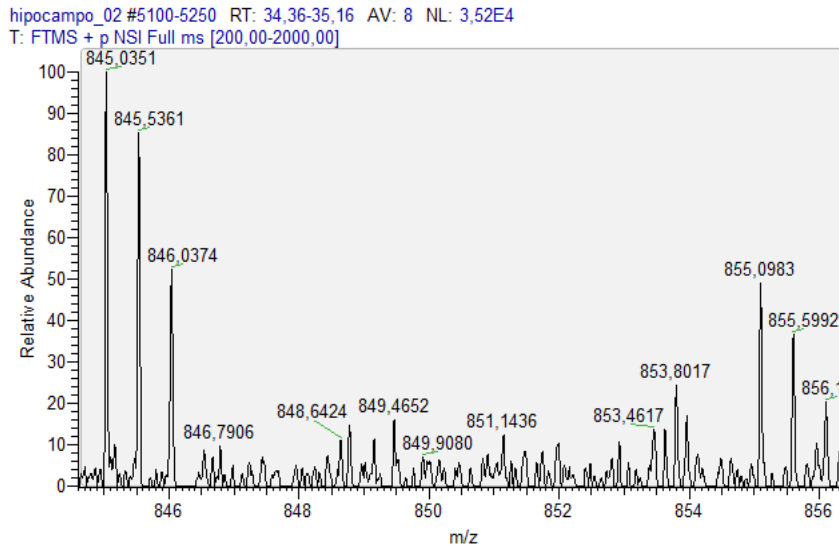
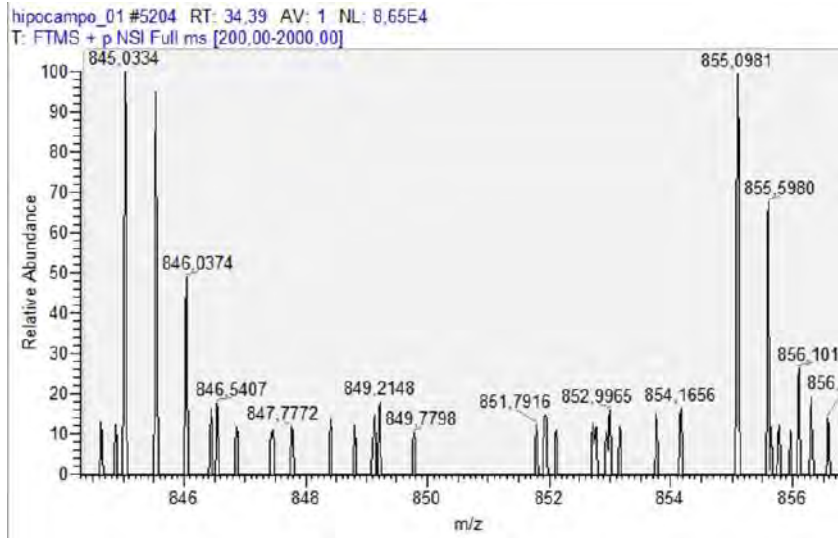
hipocampo_02 #8822-8965 RT: 56,19-56,95 AV: 16 NL: 8,24E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_04 #12847 RT: 63,79 AV: 1 NL: 2,89E5
T: FTMS + p NSI Full ms [200,00-2000,00]

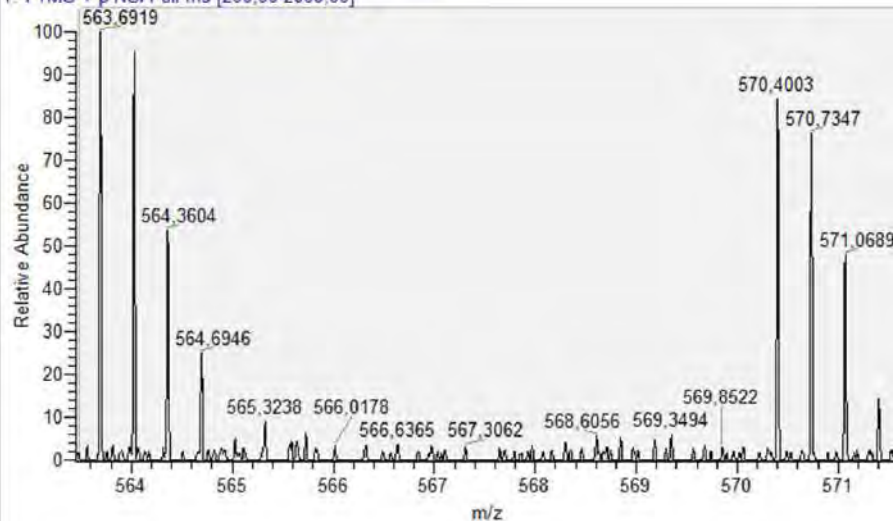


VEKVDELKKKYGI 2+

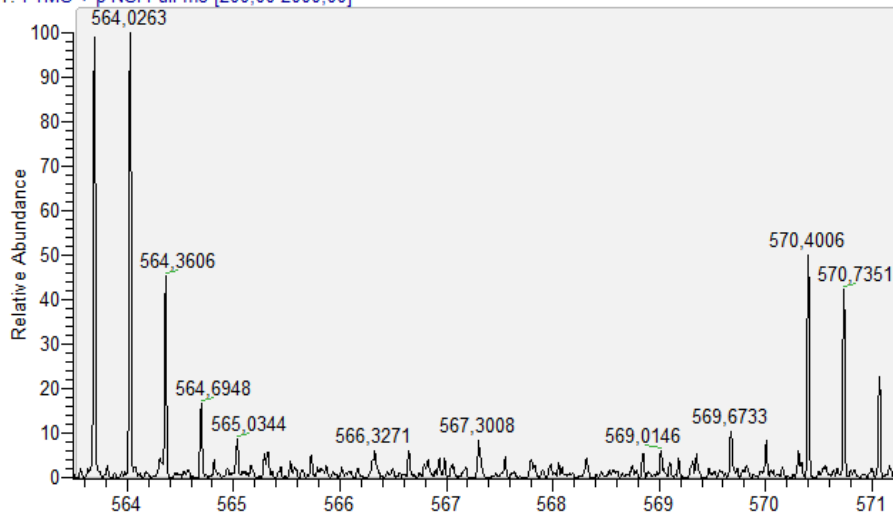


VEKVDLKKKYGI 3+

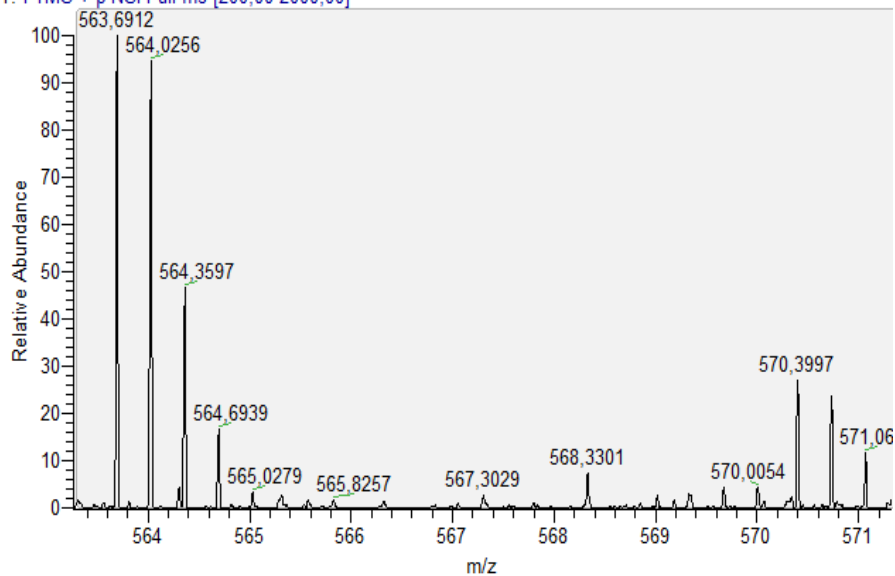
hipocampo_01 #5204 RT: 34.39 AV: 1 NL: 4,64E5
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #5100-5250 RT: 34.36-35.16 AV: 8 NL: 1,70E5
T: FTMS + p NSI Full ms [200,00-2000,00]

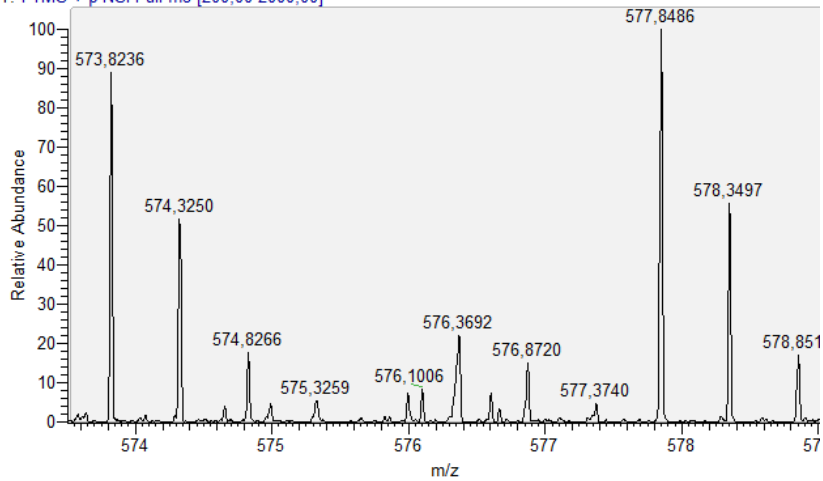


hipocampo_04 #7258-7404 RT: 41.40-41.96 AV: 21 NL: 1,55E5
T: FTMS + p NSI Full ms [200,00-2000,00]

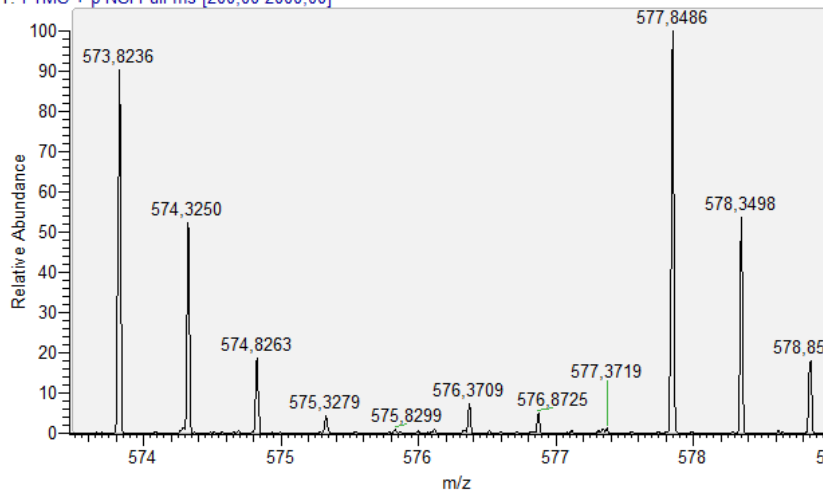


KGNDISSGTVL 2+

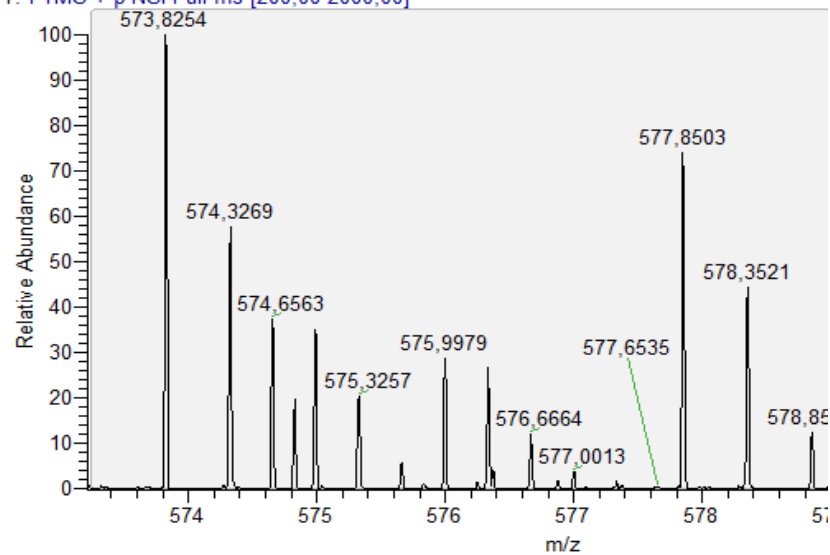
hipocampo_01 #4615-4718 RT: 31,23-31,76 AV: 6 NL: 5,96E5
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #4571-4632 RT: 31,49-31,61 AV: 2 NL: 1,66E6
T: FTMS + p NSI Full ms [200,00-2000,00]

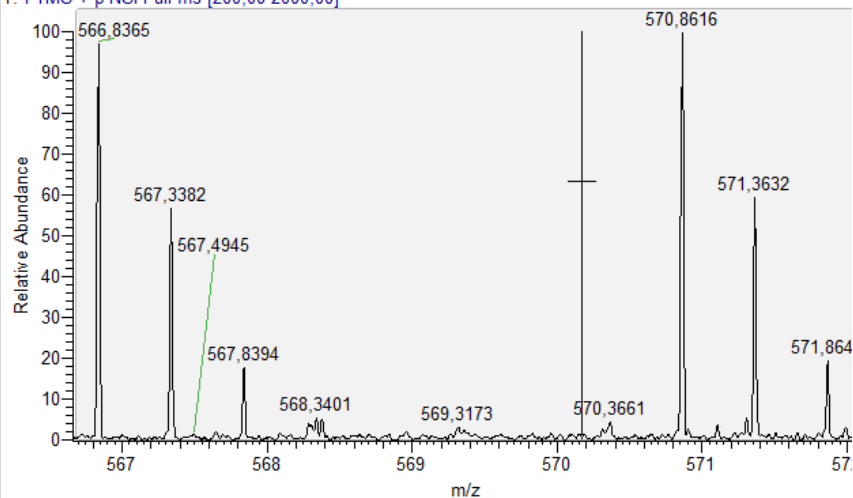


hipocampo_04 #6353 RT: 37,46 AV: 1 NL: 2,64E5
T: FTMS + p NSI Full ms [200,00-2000,00]

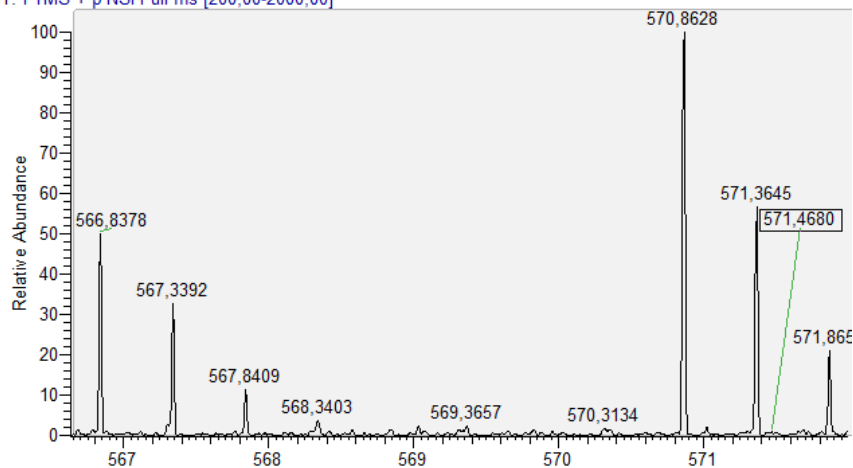


GLDPGKLYTL 2+

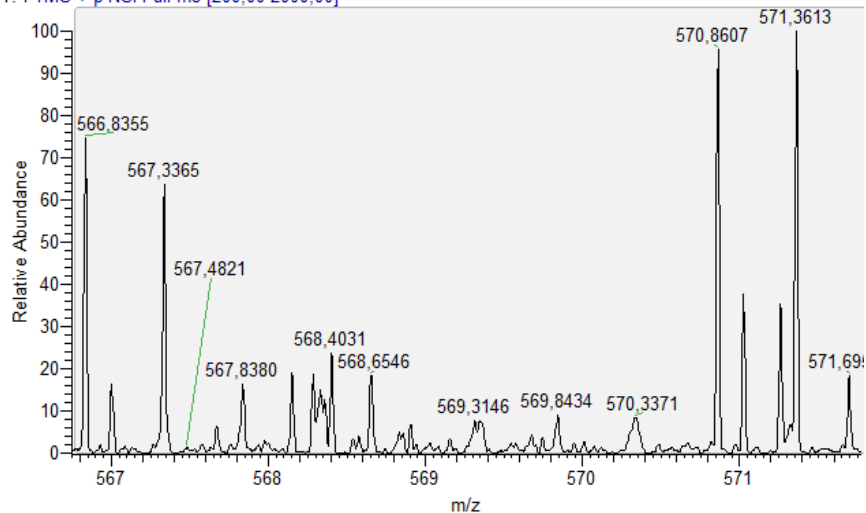
hipocampo_01 #8481-8720 RT: 53.33-54.70 AV: 27 NL: 1,23E5
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #8057-8246 RT: 51.67-52.73 AV: 17 NL: 1,60E5
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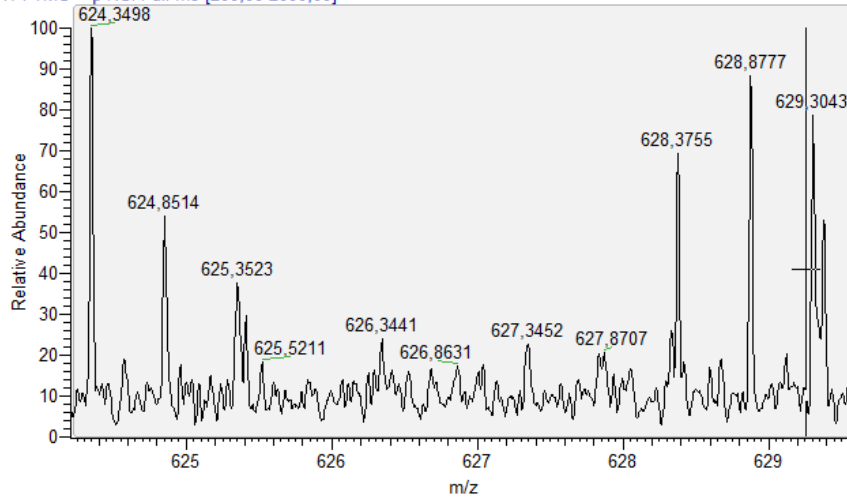


hipocampo_04 #11982-12339 RT: 60.41-61.80 AV: 58 NL: 1,87E4
T: FTMS + p NSI Full ms [200,00-2000,00]

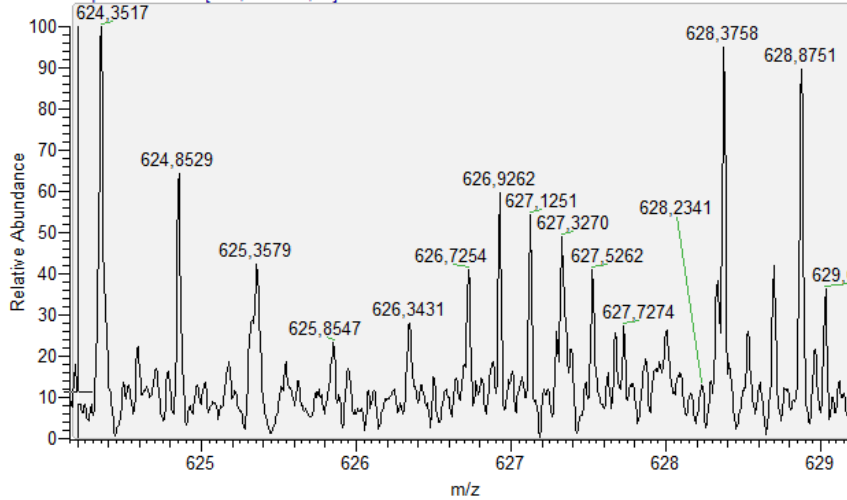


DGLDPGKLYTL 2+

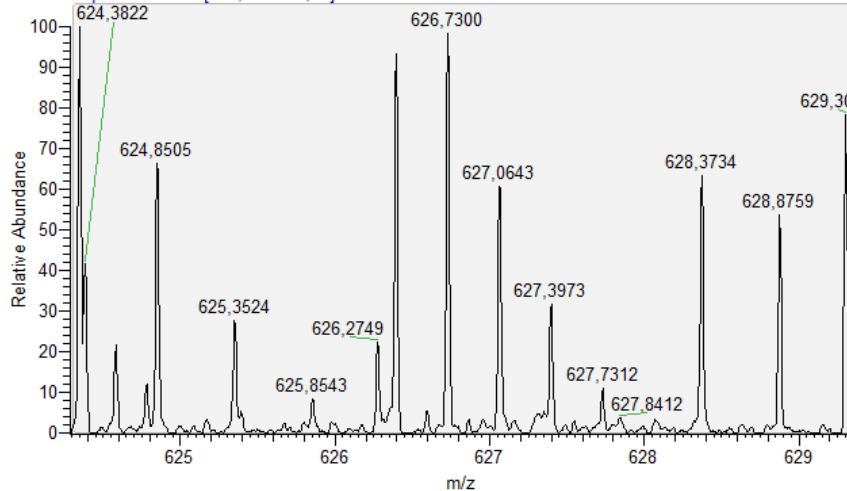
hipocampo_01 #9480-9854 RT: 59,28-61,50 AV: 45 NL: 1,04E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #9012-9294 RT: 57,31-58,95 AV: 31 NL: 1,05E4
T: FTMS + p NSI Full ms [200,00-2000,00]

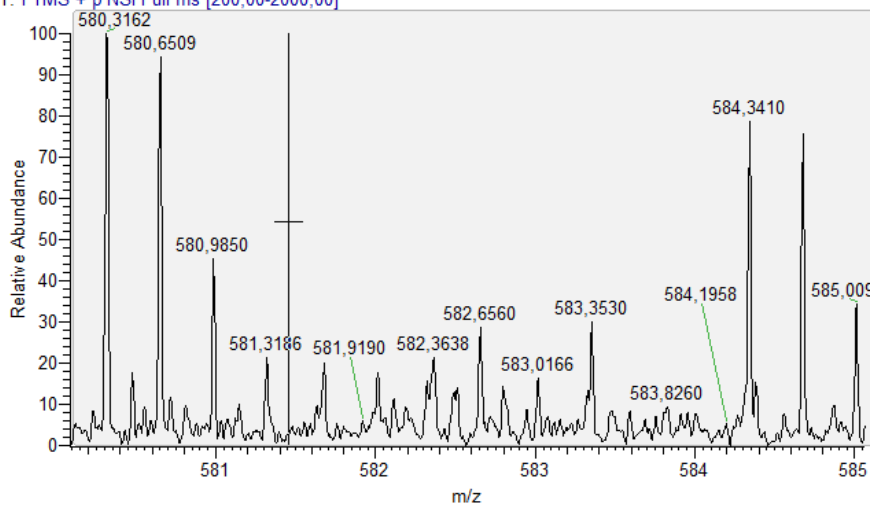


hipocampo_04 #12732-12883 RT: 63,37-63,92 AV: 22 NL: 2,41E4
T: FTMS + p NSI Full ms [200,00-2000,00]

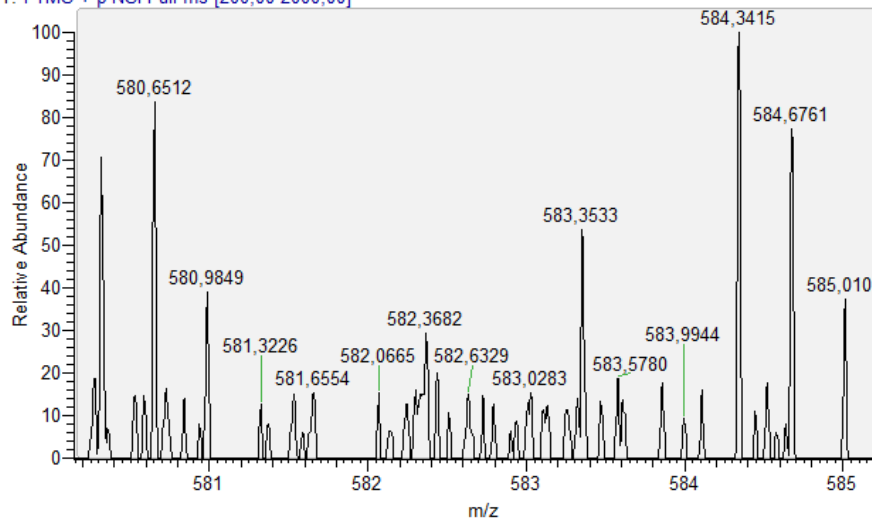


DDYVPKLYEQLSGK 3+

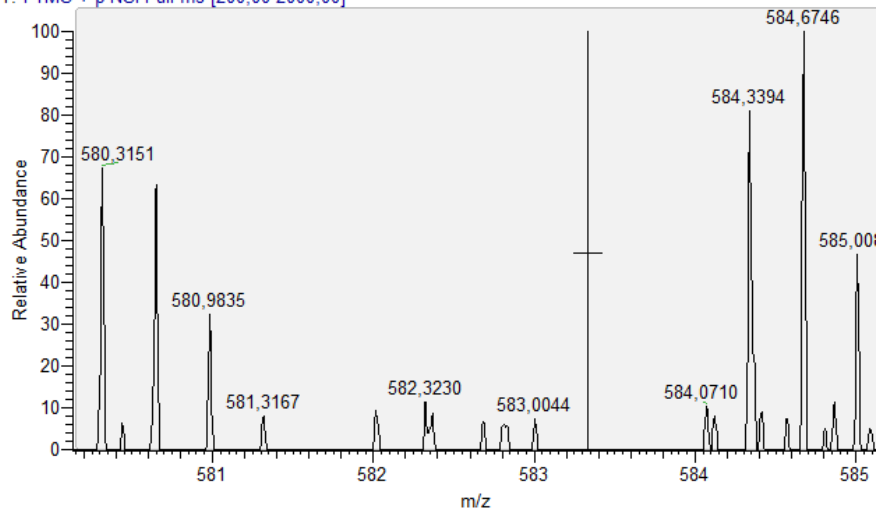
hipocampo_01 #8816-9006 RT: 55,32-56,42 AV: 23 NL: 2,81E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #8386 RT: 53,57 AV: 1 NL: 4,42E4
T: FTMS + p NSI Full ms [200,00-2000,00]

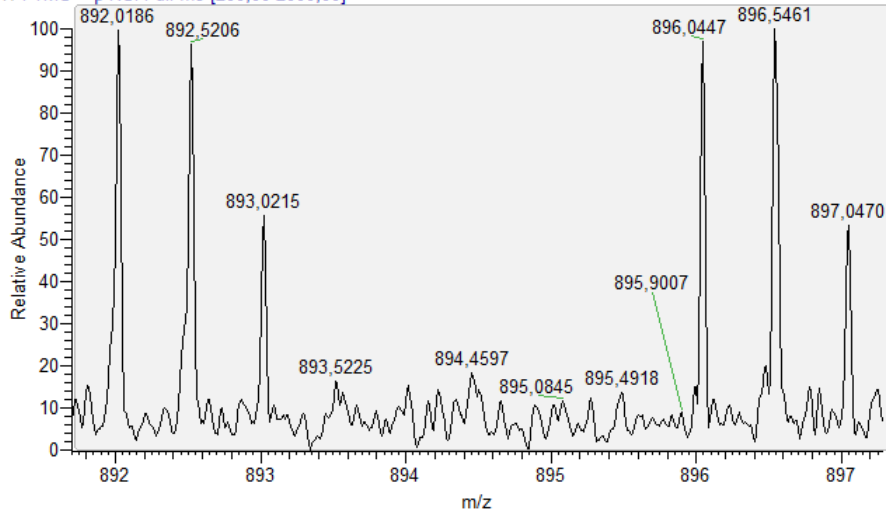


hipocampo_04 #11993 RT: 60,44 AV: 1 NL: 3,95E4
T: FTMS + p NSI Full ms [200,00-2000,00]

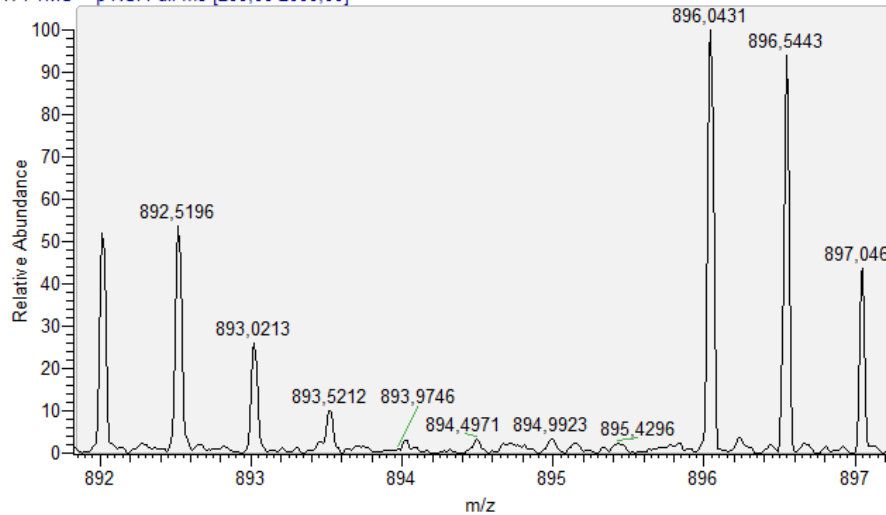


AGVTVDDELGKVLTPQTQV 2+

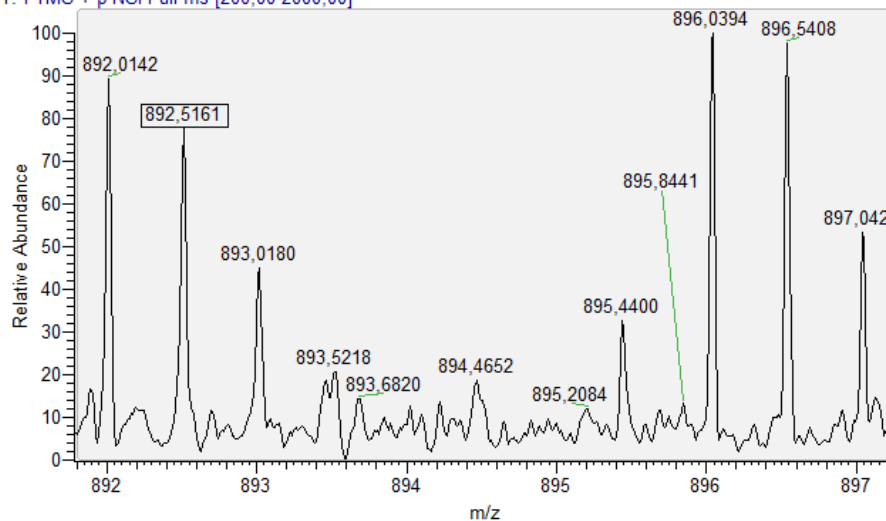
hipocampo_01 #10411-10600 RT: 65,02-65,94 AV: 10 NL: 2,47E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #10046-10139 RT: 63,60-64,07 AV: 7 NL: 1,14E5
T: FTMS + p NSI Full ms [200,00-2000,00]

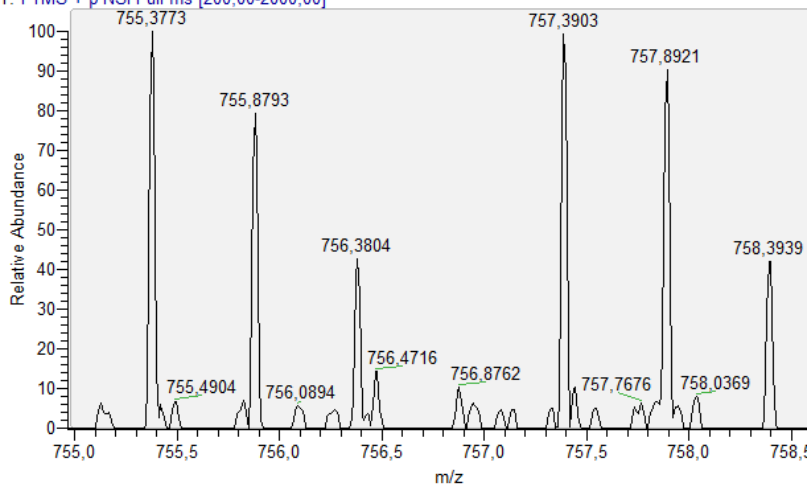


hipocampo_04 #13577-13940 RT: 66,64-68,04 AV: 52 NL: 7,85E3
T: FTMS + p NSI Full ms [200,00-2000,00]

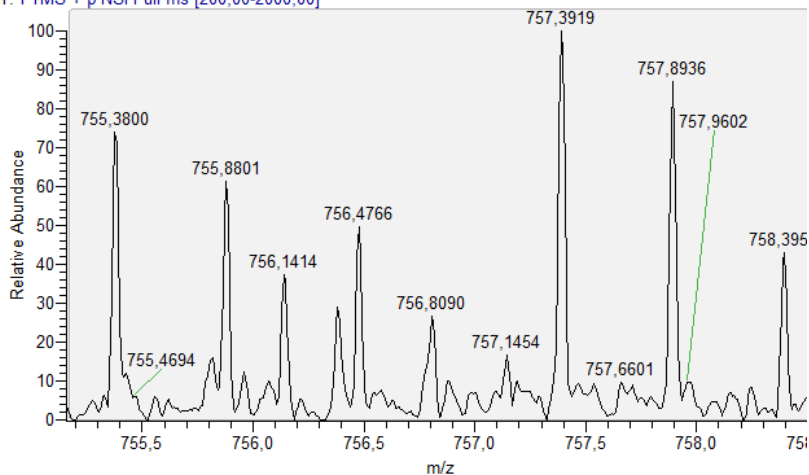


SGPFGQIFRPDNF 2+

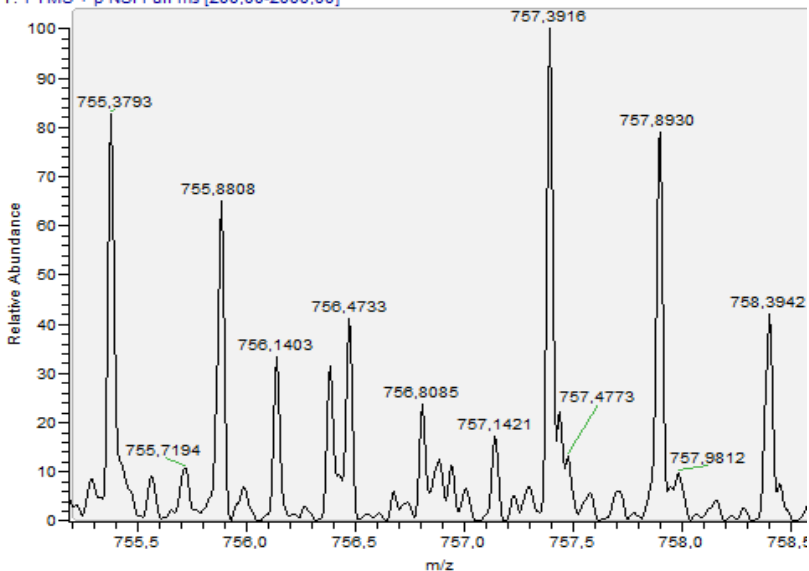
hipocampo_01 #10622 RT: 66.20 AV: 1 NL: 7,91E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #10371-10511 RT: 65.62-66,31 AV: 8 NL: 1,45E4
T: FTMS + p NSI Full ms [200,00-2000,00]

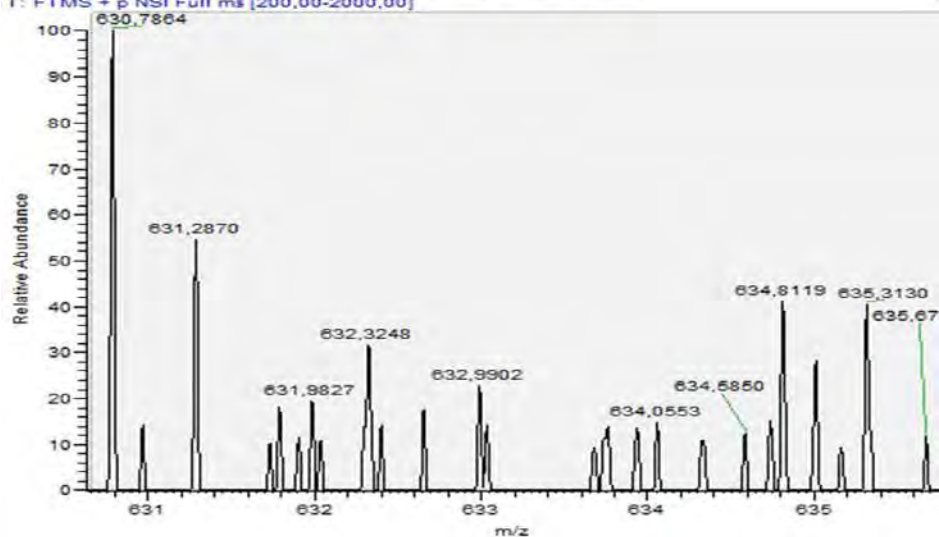


hipocampo_04 #14339-14535 RT: 69,63-70,37 AV: 20 NL: 1,74E4
T: FTMS + p NSI Full ms [200,00-2000,00]

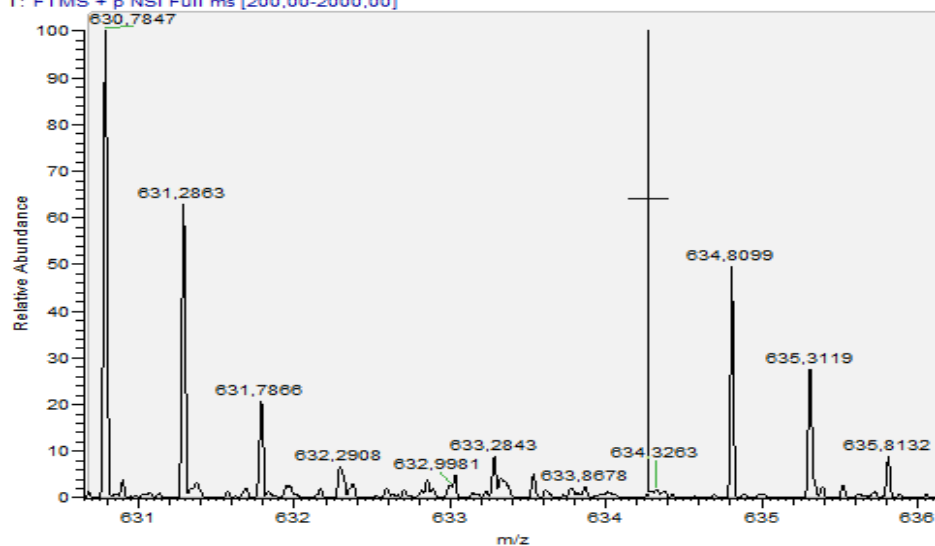


DDEESEAQGPK 2+

hipocampo_01 #2110-2150 RT: 17.26-17.40 AV: 2 NL: 6,50E3
T: FTMS + p NSI Full ms [200,00-2000,00]

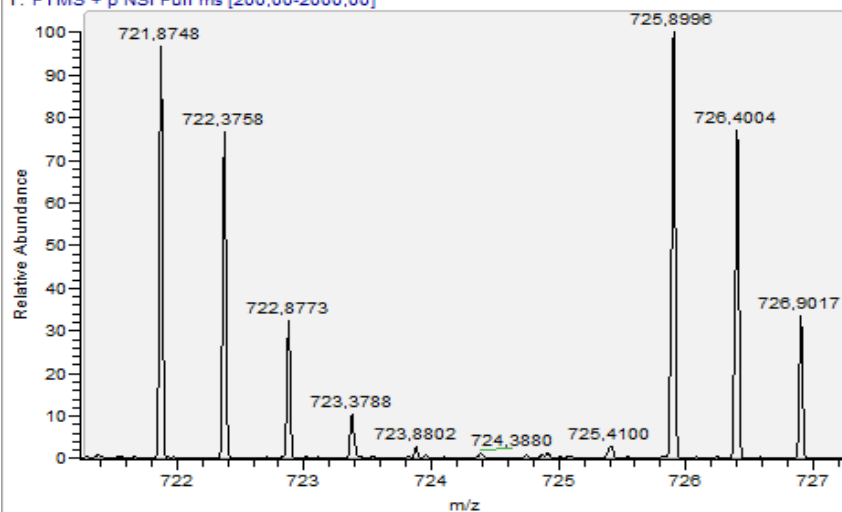


hipocampo_04 #2362-2501 RT: 21.11-21.85 AV: 56 NL: 4,05E3
T: FTMS + p NSI Full ms [200,00-2000,00]

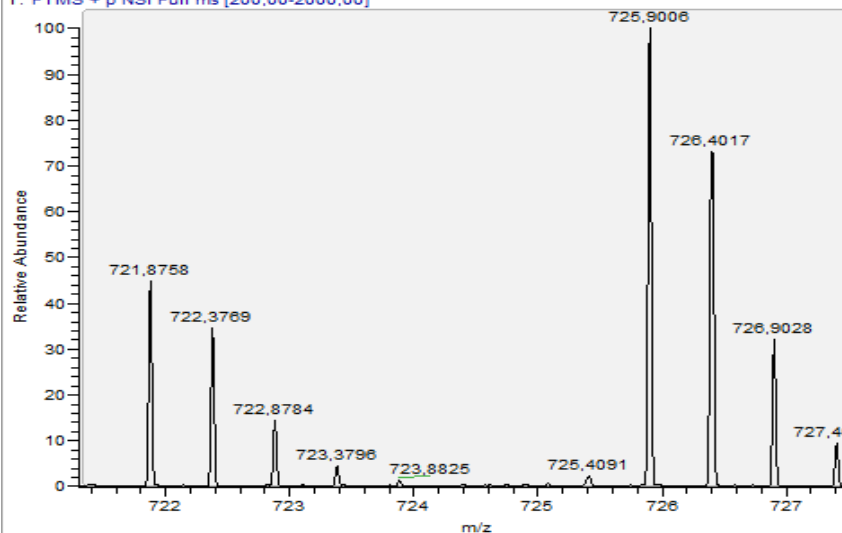


SPQLEDEAKELQ 2+

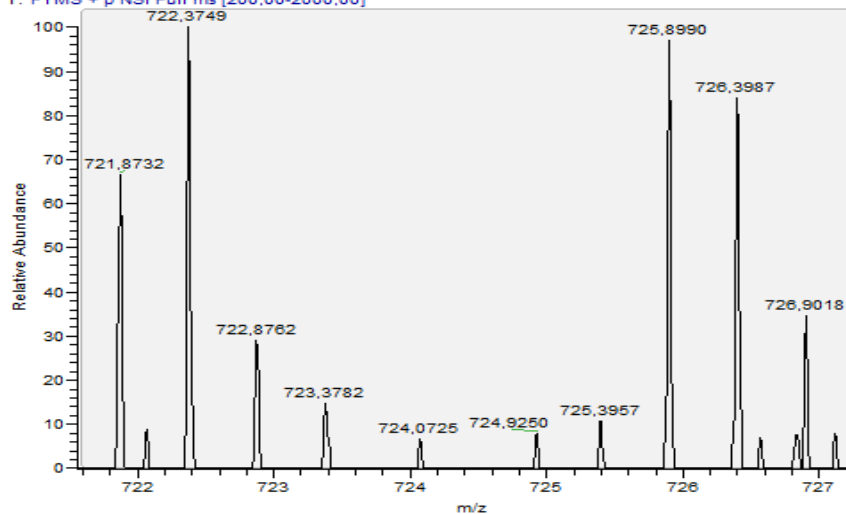
hipocampo_01 #5670-6023 RT: 36,97-38,77 AV: 20 NL: 8,28E5
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #5523-5790 RT: 36,67-38,10 AV: 14 NL: 1,26E6
T: FTMS + p NSI Full ms [200,00-2000,00]



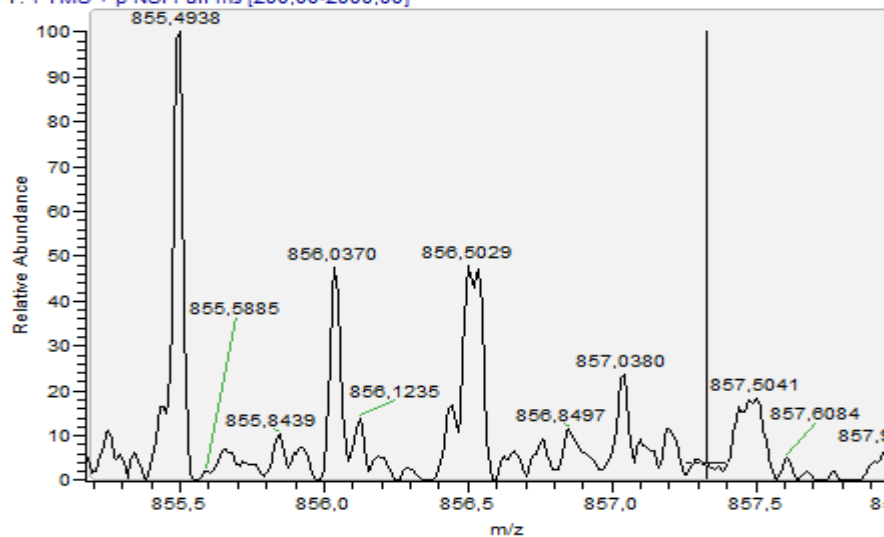
hipocampo_04 #7922 RT: 44,10 AV: 1 NL: 4,67E4
T: FTMS + p NSI Full ms [200,00-2000,00]



FDITADDEPLGRVSF 2+

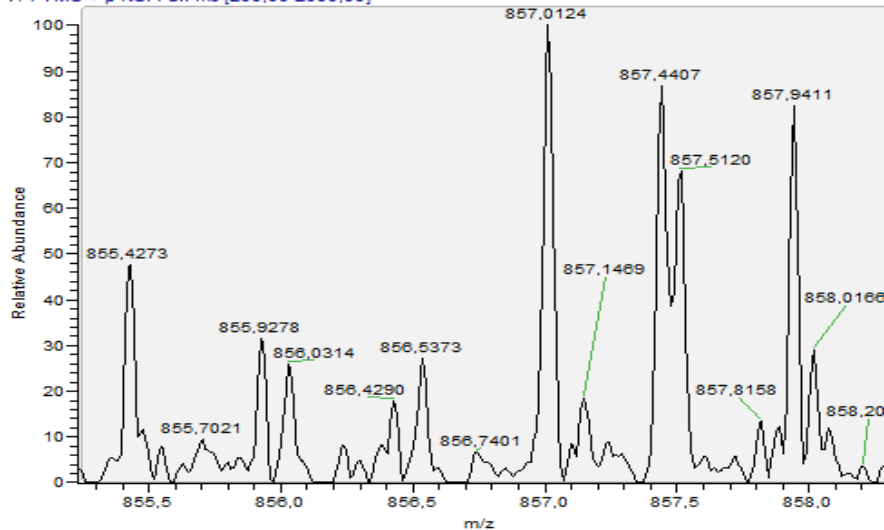
hipocampo_01 #10779-10907 RT: 67,18-67,93 AV: 8 NL: 1,26E4

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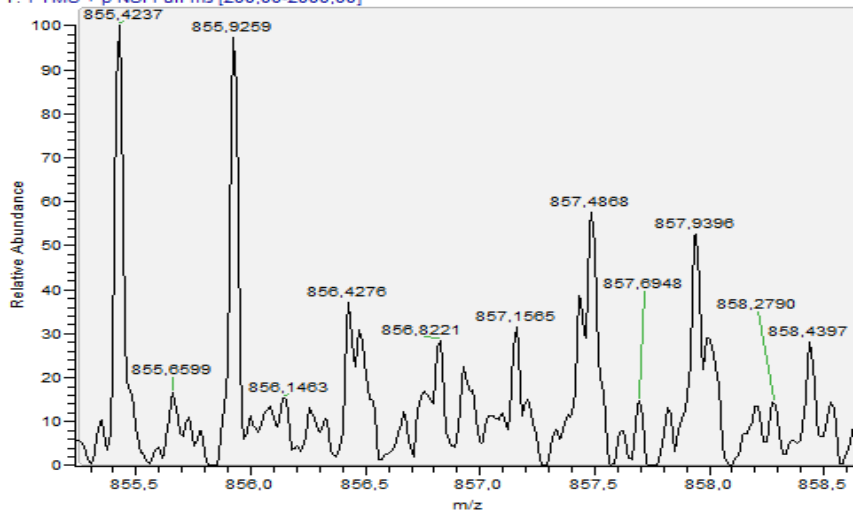
hipocampo_02 #10685-10754 RT: 67,49-67,77 AV: 4 NL: 1,56E4

T: FTMS + p NSI Full ms [200,00-2000,00]



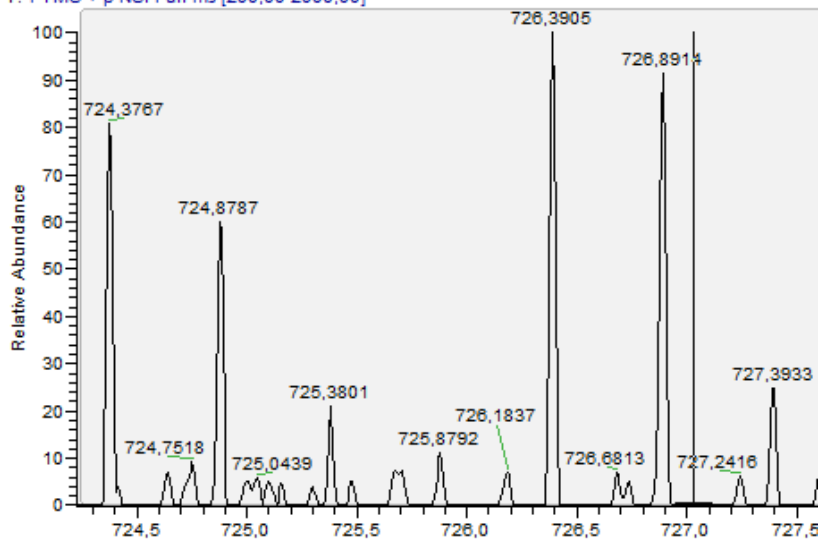
hipocampo_04 #14627-14824 RT: 70,77-71,47 AV: 19 NL: 5,41E3

T: FTMS + p NSI Full ms [200,00-2000,00]

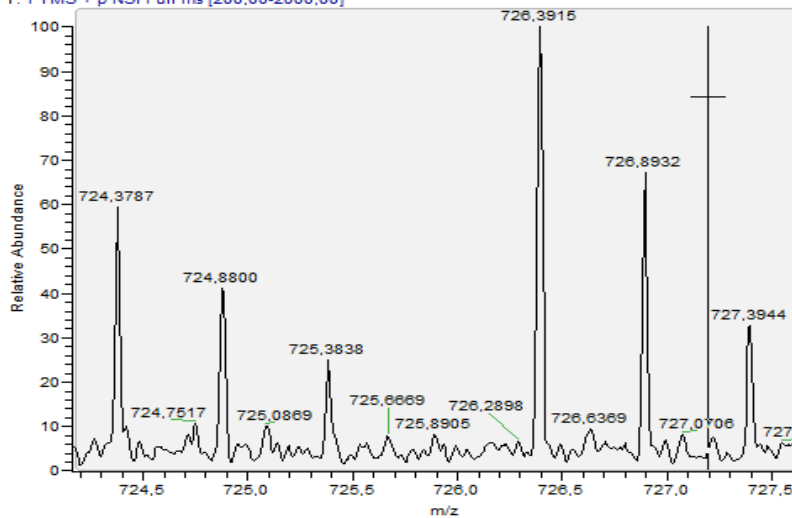


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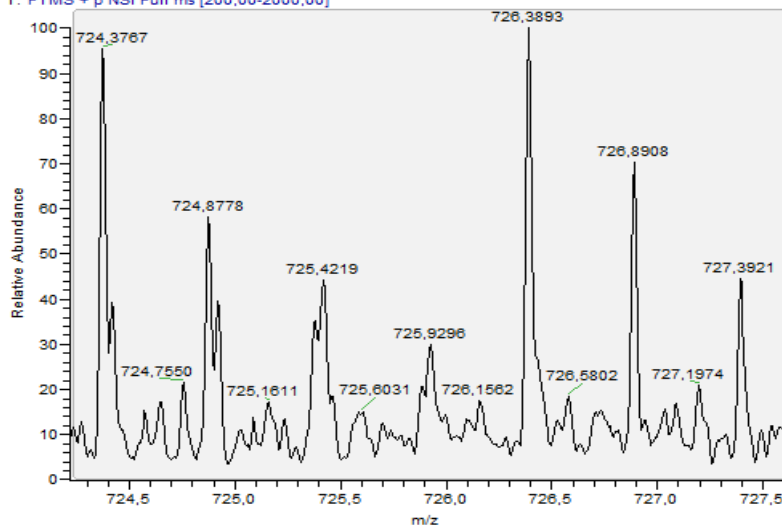
hipocampo_01 #8553 RT: 53,74 AV: 1 NL: 1,48E5
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #8098-8285 RT: 51,89-52,94 AV: 16 NL: 6,28E4
T: FTMS + p NSI Full ms [200,00-2000,00]

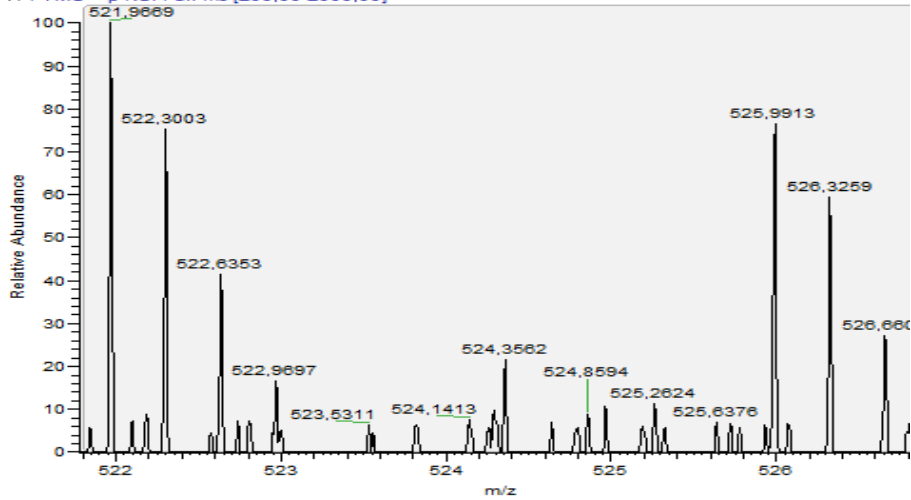


hipocampo_04 #11688-12070 RT: 59,27-60,74 AV: 59 NL: 8,09E3
T: FTMS + p NSI Full ms [200,00-2000,00]

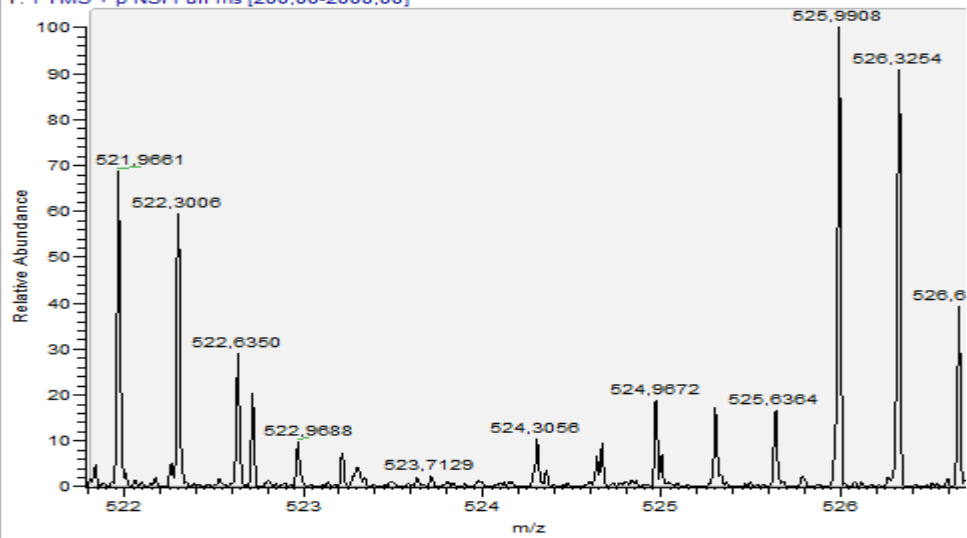


LFADKVPKTAENF 3+

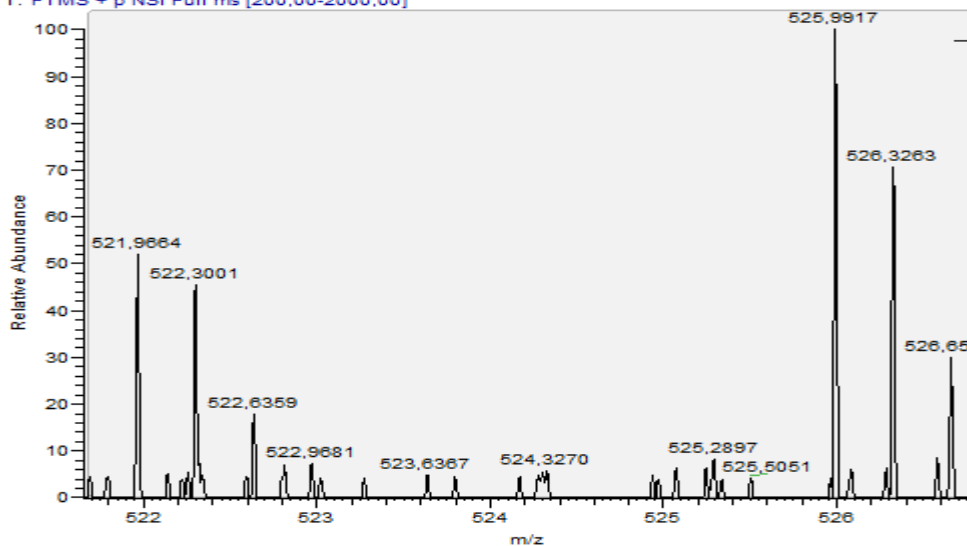
hipocampo_01 #6300 RT: 40.44 AV: 1 NL: 1,08E5
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #5925-6115 RT: 38.90-39.97 AV: 13 NL: 8,47E4
T: FTMS + p NSI Full ms [200,00-2000,00]

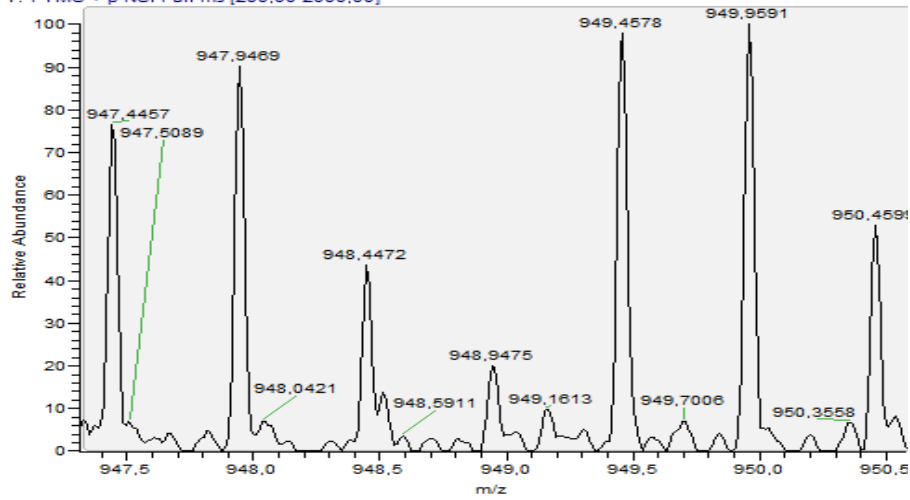


hipocampo_04 #8644 RT: 47.01 AV: 1 NL: 4,73E4
T: FTMS + p NSI Full ms [200,00-2000,00]

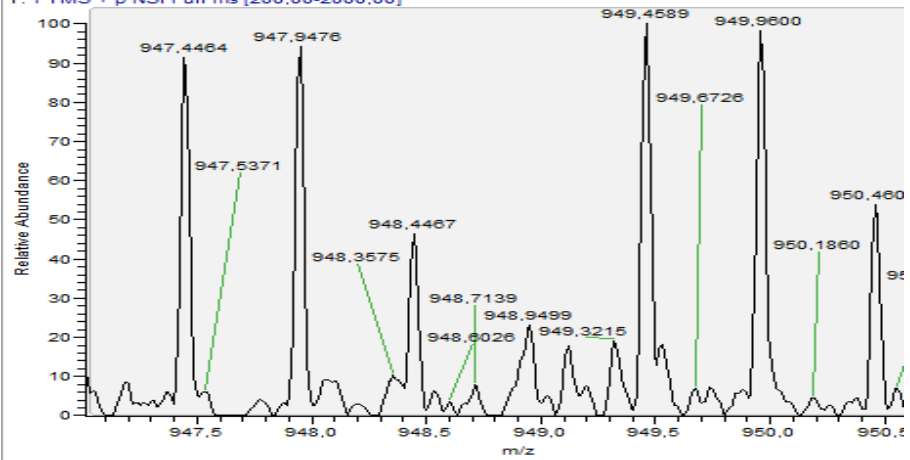


FHNPHVNPLPTGYEDE 2+

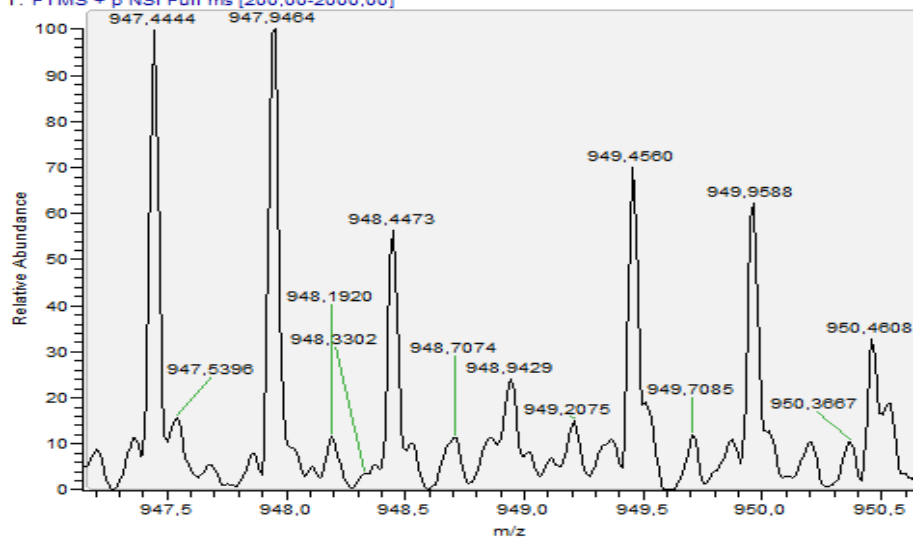
hipocampo_01 #5599-5811 RT: 36,57-37,64 AV: 15 NL: 2,44E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #5523-5722 RT: 36,67-37,76 AV: 11 NL: 2,96E4
T: FTMS + p NSI Full ms [200,00-2000,00]

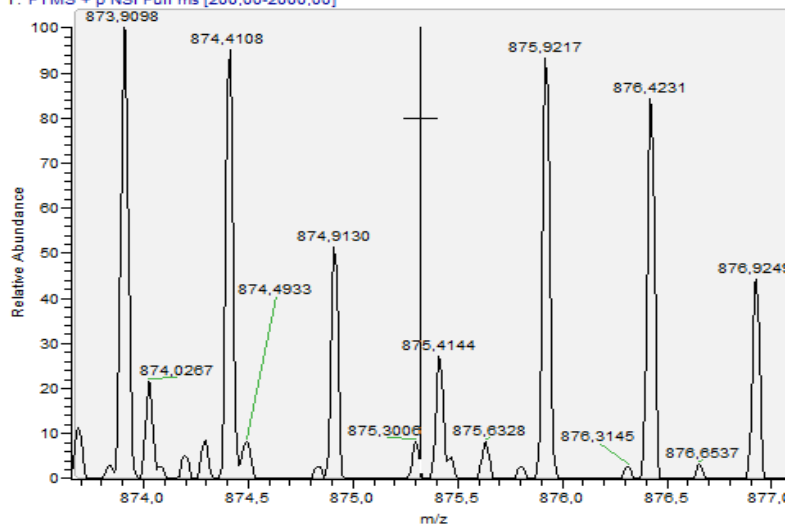


hipocampo_04 #7915-8378 RT: 44,08-45,93 AV: 77 NL: 7,95E3
T: FTMS + p NSI Full ms [200,00-2000,00]

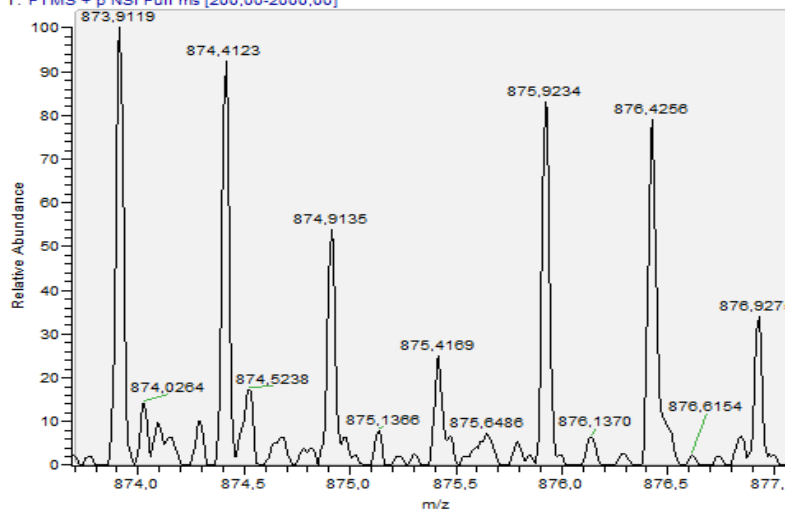


HNP HVNPLPTGYEDE 2+

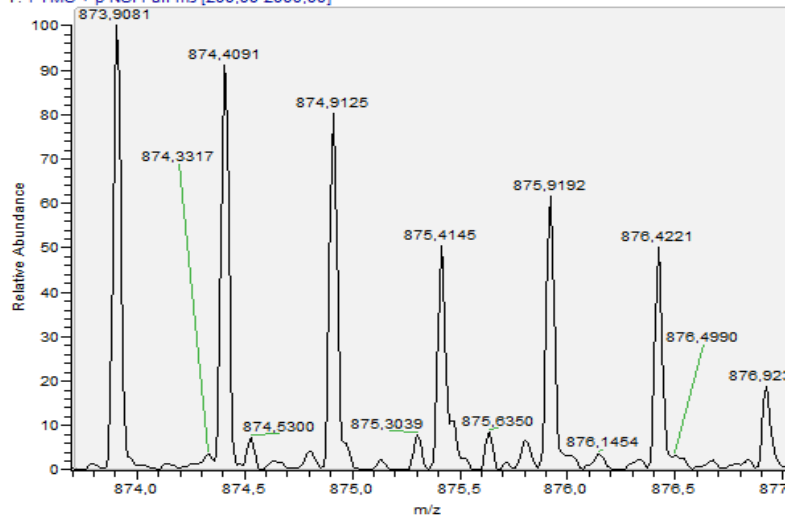
hipocampo_01 #4872-4941 RT: 32,65-32,95 AV: 4 NL: 8,12E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #4657-4859 RT: 31,94-32,95 AV: 13 NL: 2,73E4
T: FTMS + p NSI Full ms [200,00-2000,00]

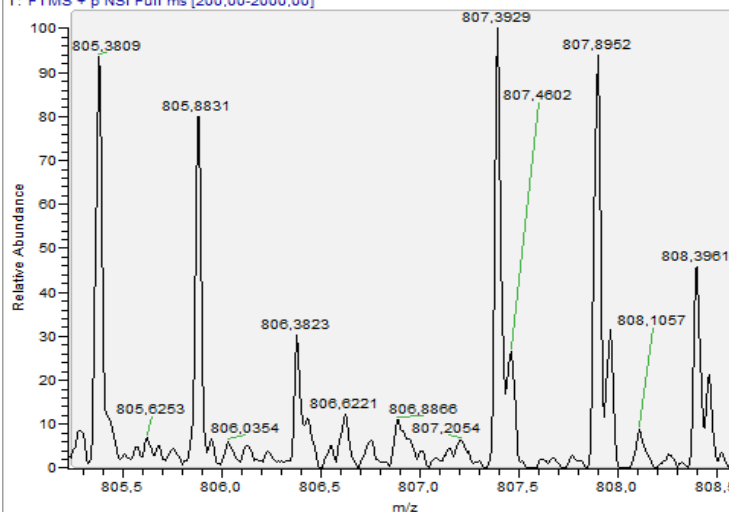


hipocampo_04 #6343-6679 RT: 37,41-38,89 AV: 97 NL: 1,09E4
T: FTMS + p NSI Full ms [200,00-2000,00]

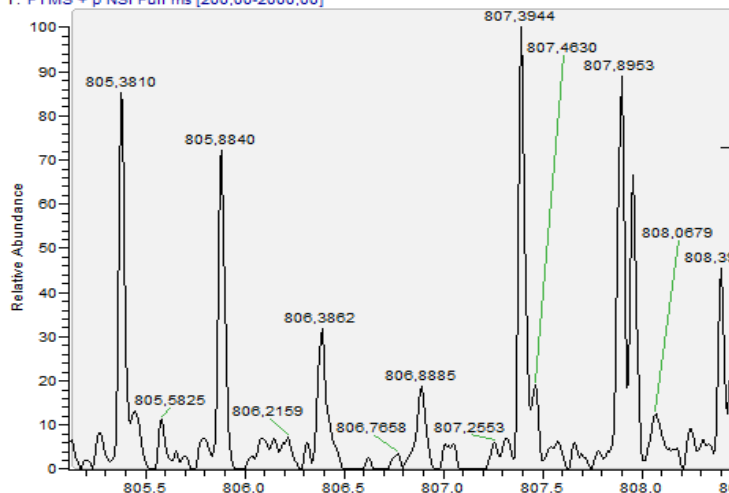


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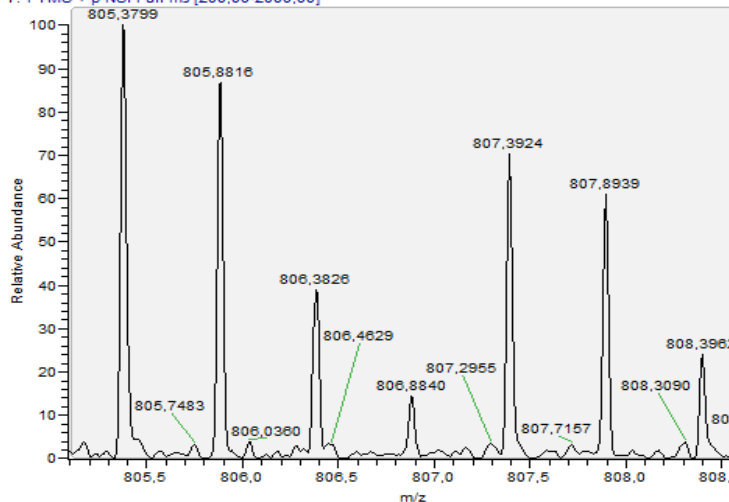
hipocampo_01 #5692-5892 RT: 37,08-38,14 AV: 12 NL: 4,36E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #5523-5656 RT: 36,67-37,40 AV: 8 NL: 4,13E4
T: FTMS + p NSI Full ms [200,00-2000,00]

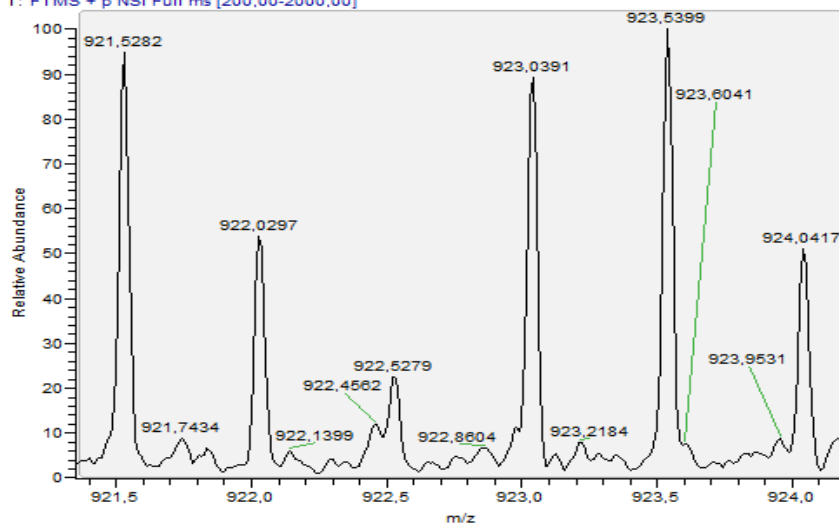


hipocampo_04 #7734-7915 RT: 43,33-44,06 AV: 37 NL: 2,46E4
T: FTMS + p NSI Full ms [200,00-2000,00]

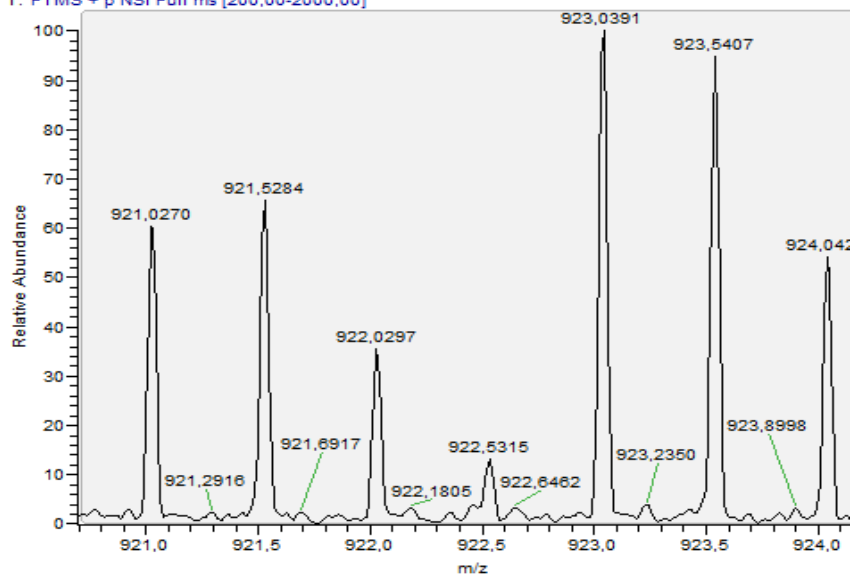


SLSAASAPLVETSTPLRL 2+

hipocampo_01 #10391-10577 RT: 64,90-65,85 AV: 10 NL: 3,32E4
T: FTMS + p NSI Full ms [200,00-2000,00]

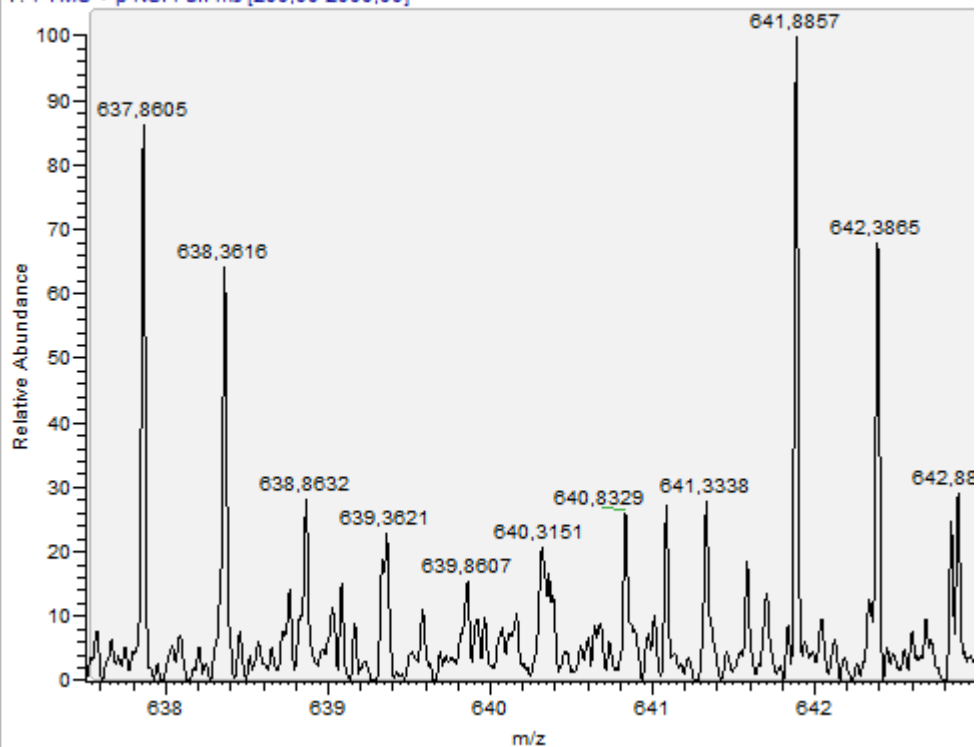


hipocampo_02 #9831-10076 RT: 62,30-63,60 AV: 15 NL: 7,18E4
T: FTMS + p NSI Full ms [200,00-2000,00]

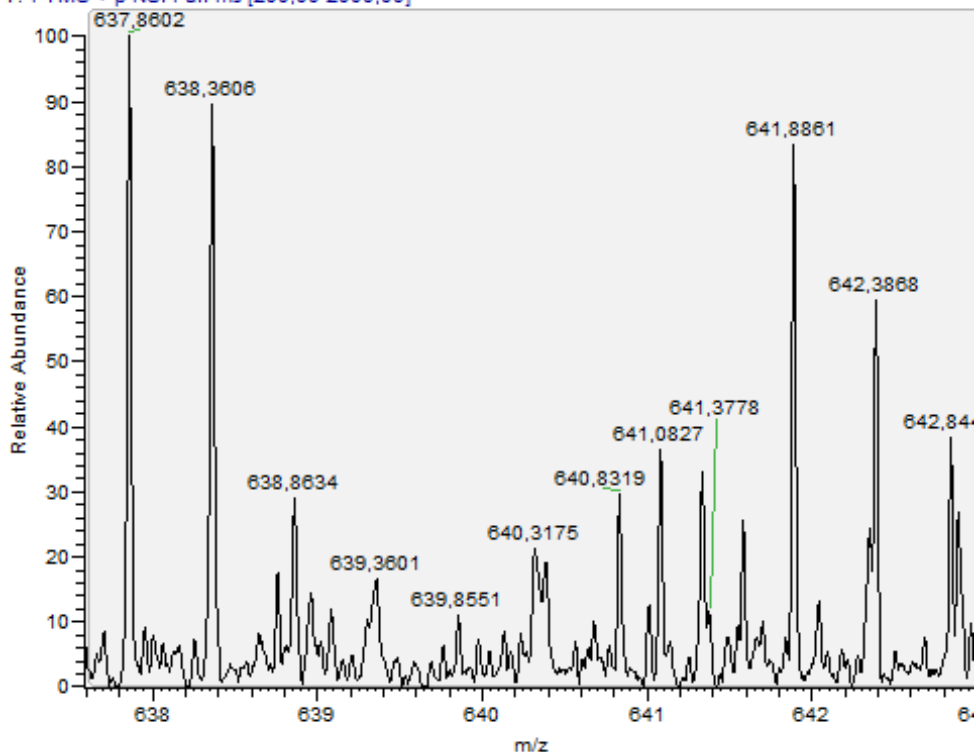


AQATGKPAQYIA 2+

hipocampo_01 #3700-4053 RT: 26,36-28,10 AV: 18 NL: 3,88E4
T: FTMS + p NSI Full ms [200,00-2000,00]

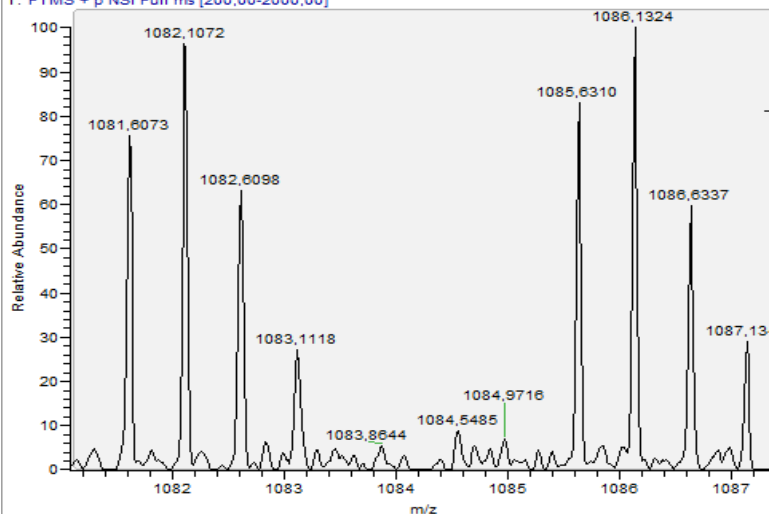


hipocampo_02 #3656-3992 RT: 26,39-28,04 AV: 16 NL: 2,86E4
T: FTMS + p NSI Full ms [200,00-2000,00]

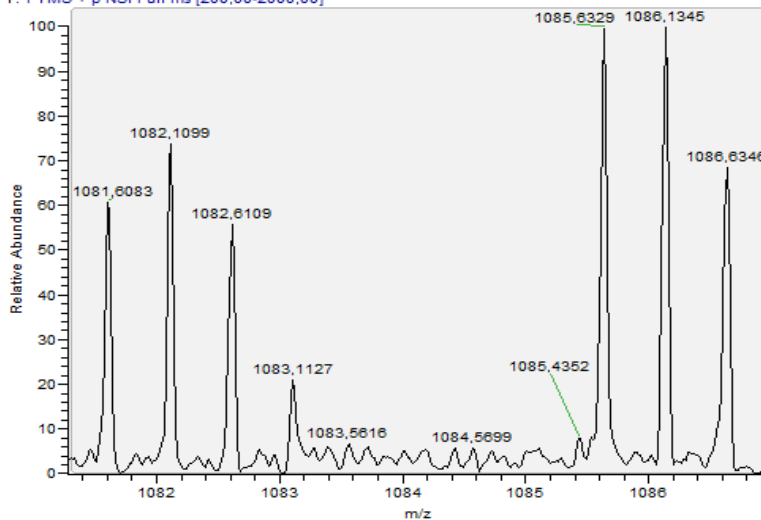


AQATGKPAQYIAVHVVPDQL 2+

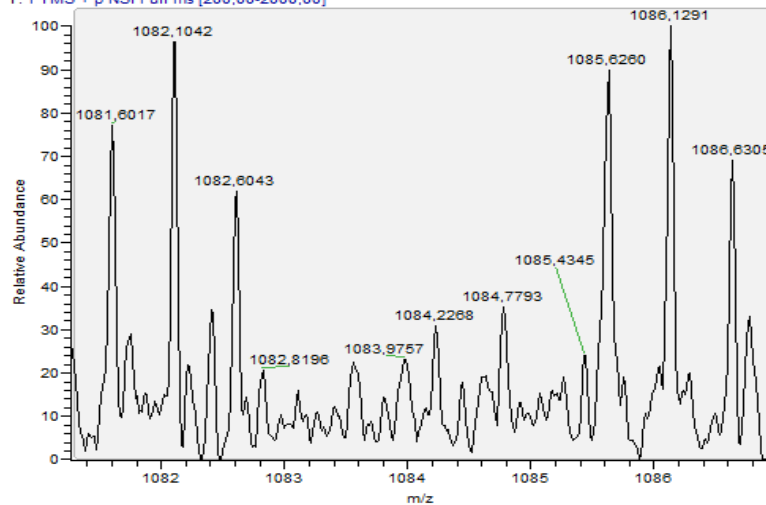
hipocampo_01 #8037-8227 RT: 50,75-51,78 AV: 14 NL: 3,64E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #7660-7912 RT: 49,26-50,69 AV: 26 NL: 3,10E4
T: FTMS + p NSI Full ms [200,00-2000,00]

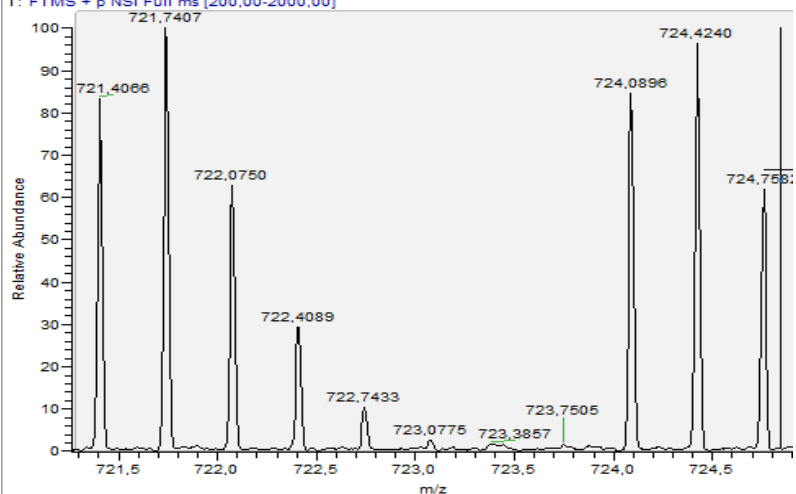


hipocampo_04 #11031-11309 RT: 56,68-57,77 AV: 47 NL: 4,25E3
T: FTMS + p NSI Full ms [200,00-2000,00]

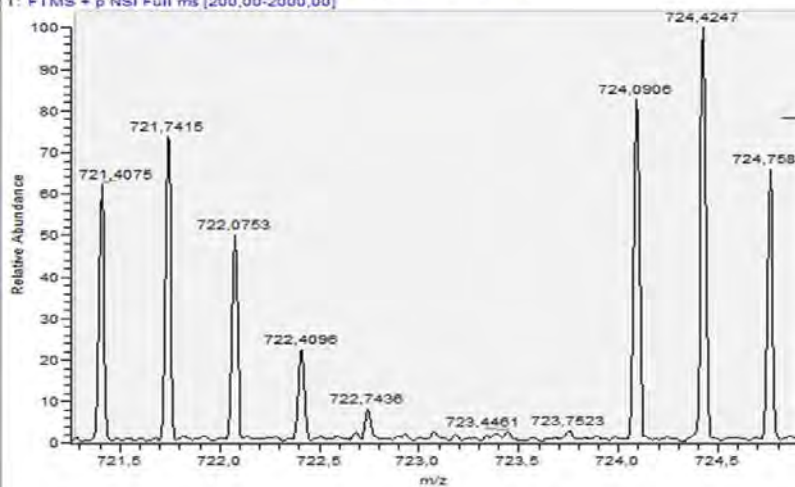


AQATGKPAQYIAVHVVPDQL 3+

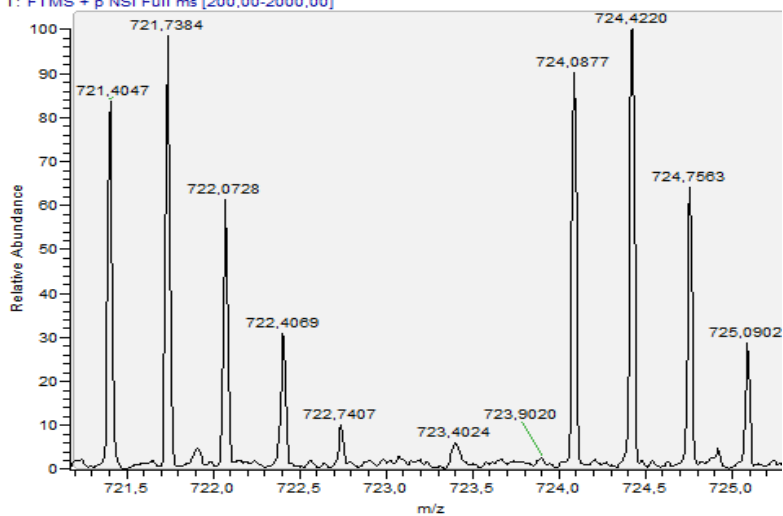
hipocampo_01 #8037-8227 RT: 50,75-51,78 AV: 14 NL: 3,86E5
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #7660-7912 RT: 49,26-50,69 AV: 26 NL: 2,90E5
T: FTMS + p NSI Full ms [200,00-2000,00]

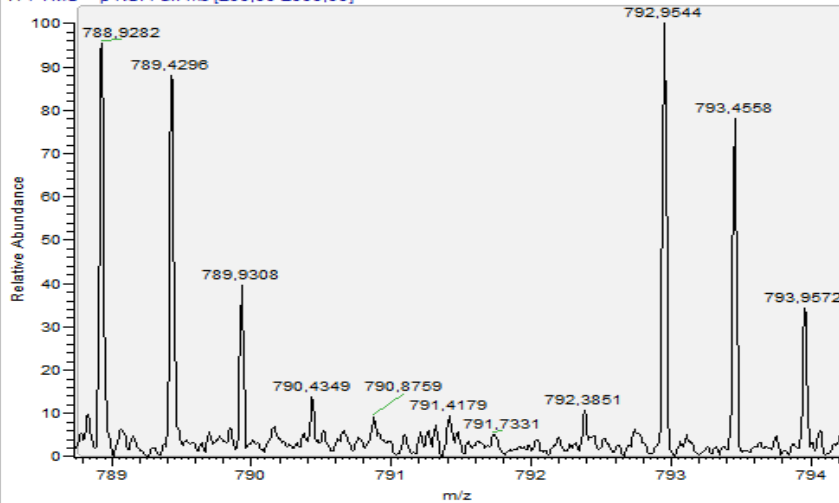


hipocampo_04 #11124-11407 RT: 57,04-58,12 AV: 45 NL: 6,19E4
T: FTMS + p NSI Full ms [200,00-2000,00]

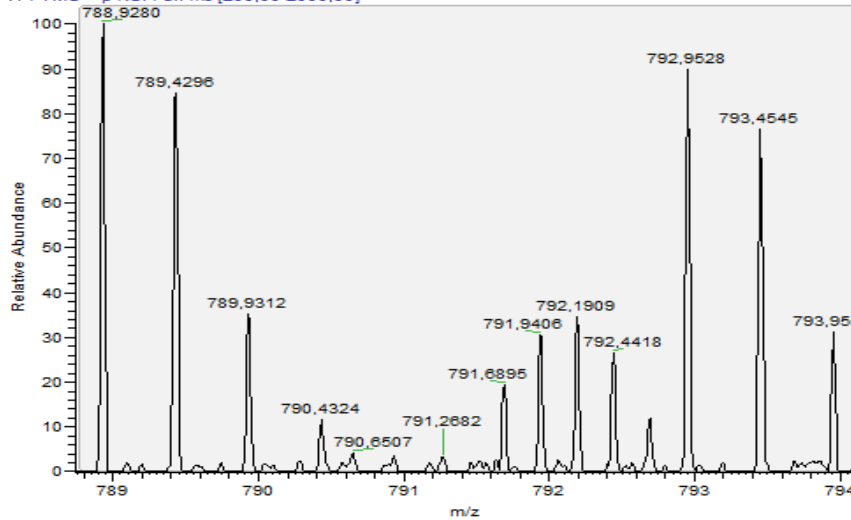


ASKGLGSDLSSLASL 2+

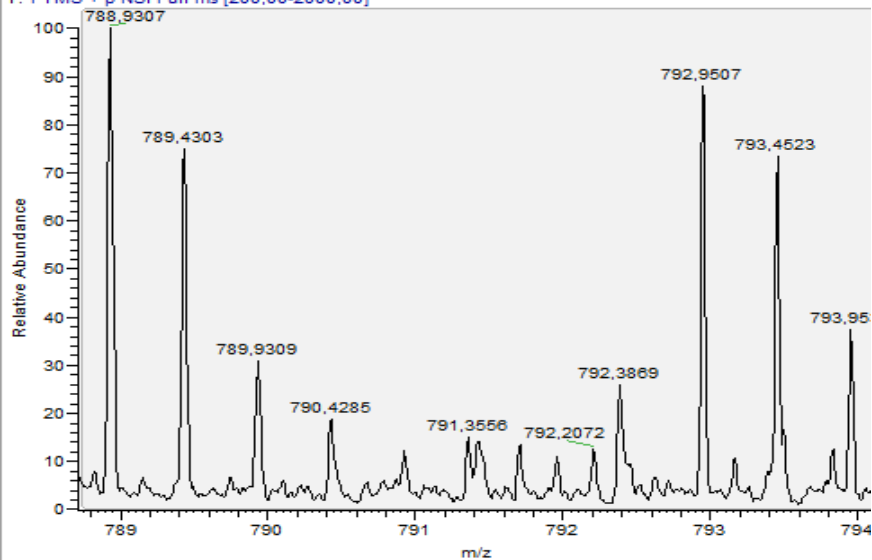
hipocampo_01 #9725-9785 RT: 60.74-61.10 AV: 7 NL: 6.99E4
T: FTMS + p NSI Full ms [200.00-2000.00]



hipocampo_02 #9145 RT: 58.08 AV: 1 NL: 5.28E5
T: FTMS + p NSI Full ms [200.00-2000.00]

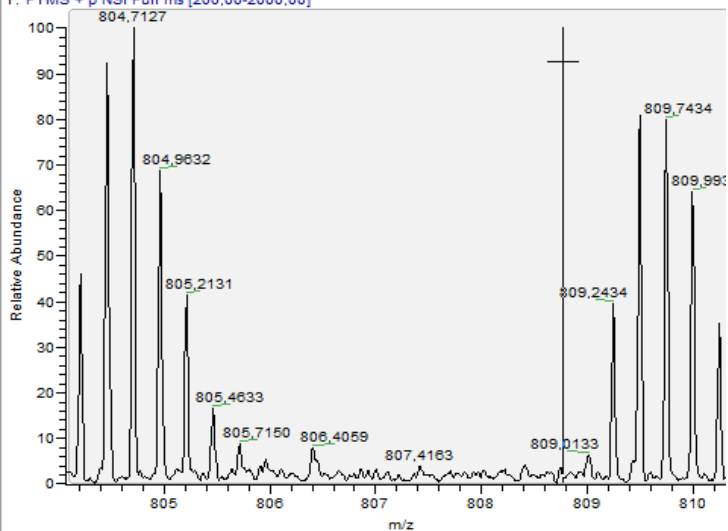


hipocampo_04 #12826-13301 RT: 63.71-65.54 AV: 67 NL: 1.87E4
T: FTMS + p NSI Full ms [200.00-2000.00]

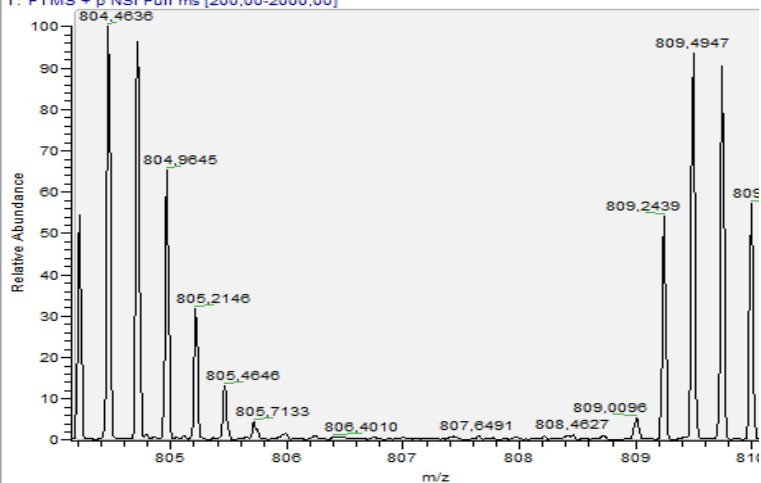


SPSPTPATQSPKKPPAKDPLADLNKDFL 2+

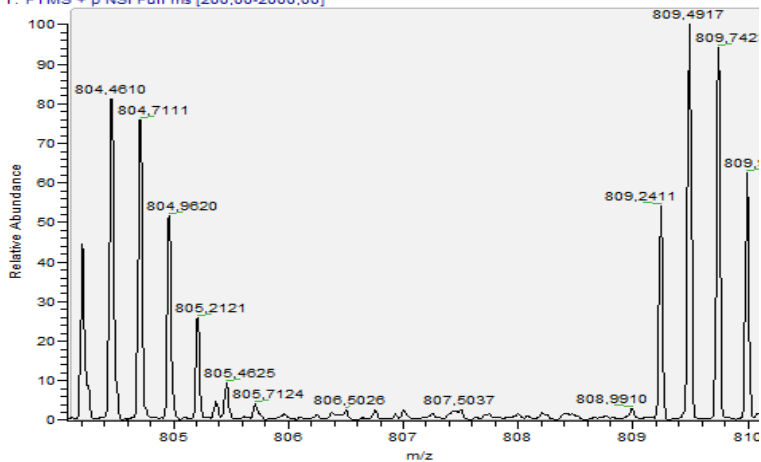
hipocampo_01 #10577-10883 RT: 65.94-67.73 AV: 16 NL: 5.28E4
T: FTMS + p NSI Full ms [200.00-2000.00]



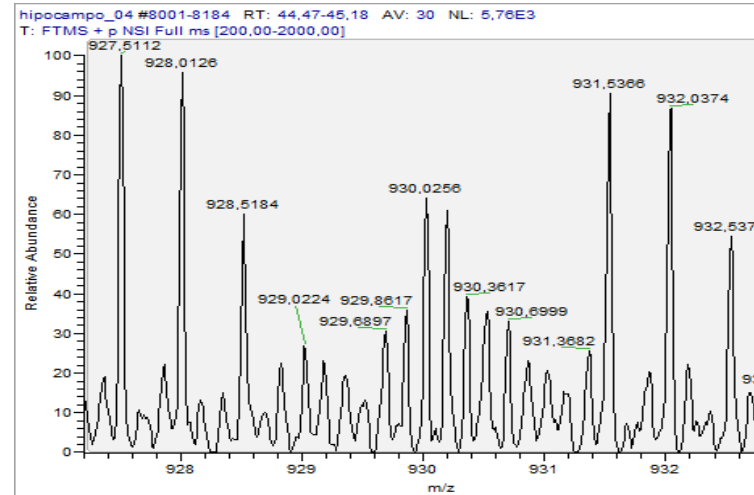
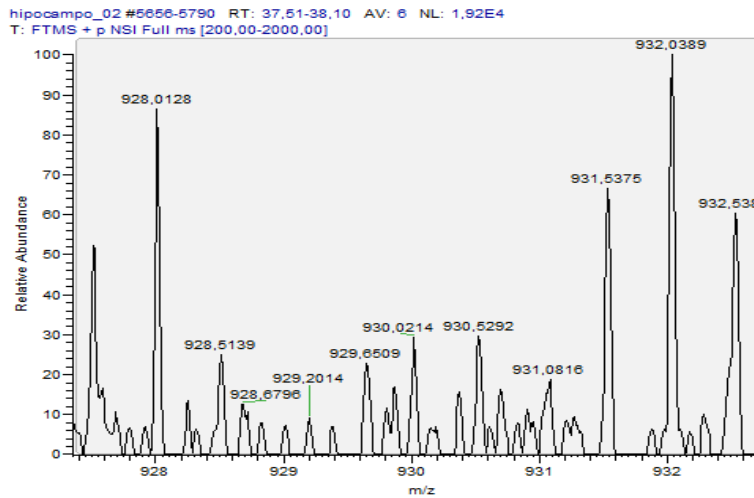
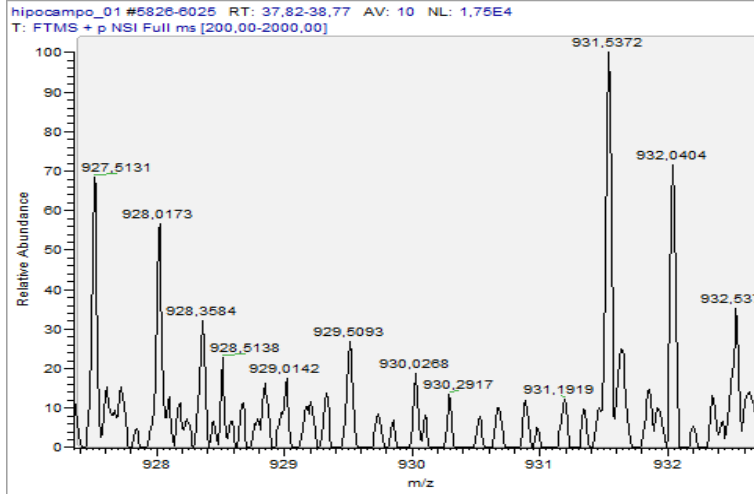
hipocampo_02 #9831-10260 RT: 62.30-64.77 AV: 28 NL: 2.70E5
T: FTMS + p NSI Full ms [200.00-2000.00]



hipocampo_04 #13872-14433 RT: 67.78-69.93 AV: 77 NL: 8.08E4
T: FTMS + p NSI Full ms [200.00-2000.00]

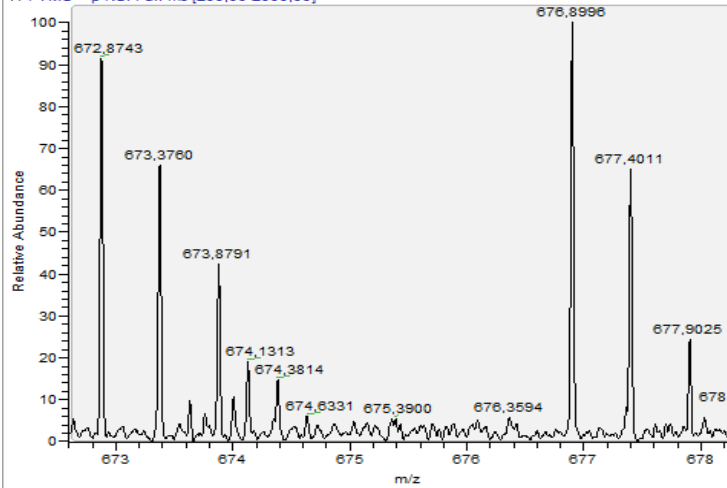


TQVVSDAAYKGVQPHVV 2+

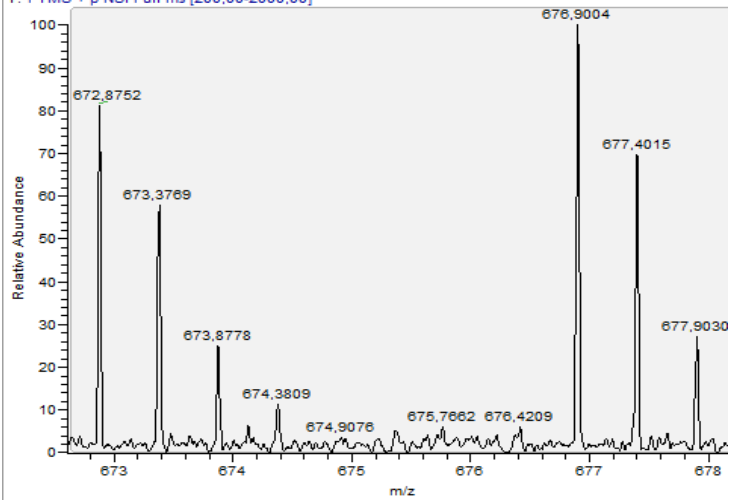


ADEVSASLAKQGL 2+

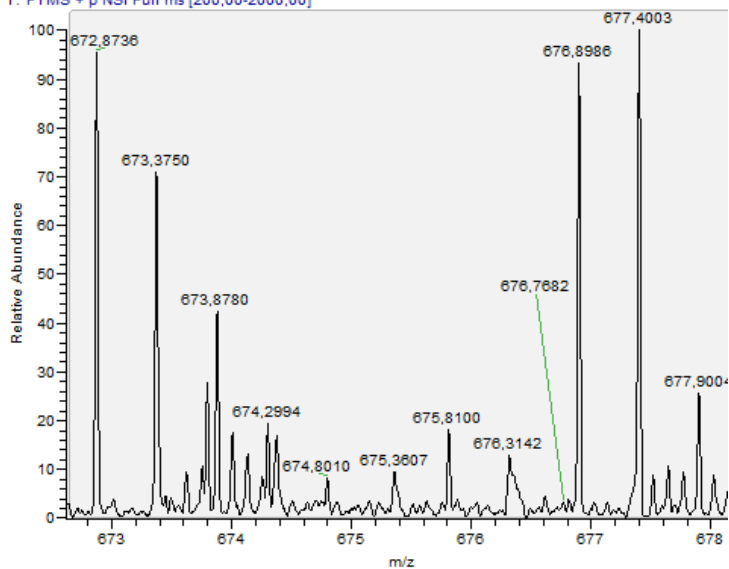
hipocampo_01 #6351-6603 RT: 40.76-42.19 AV: 15 NL: 9,50E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #6175-6427 RT: 40.47-41.77 AV: 15 NL: 1,02E5
T: FTMS + p NSI Full ms [200,00-2000,00]

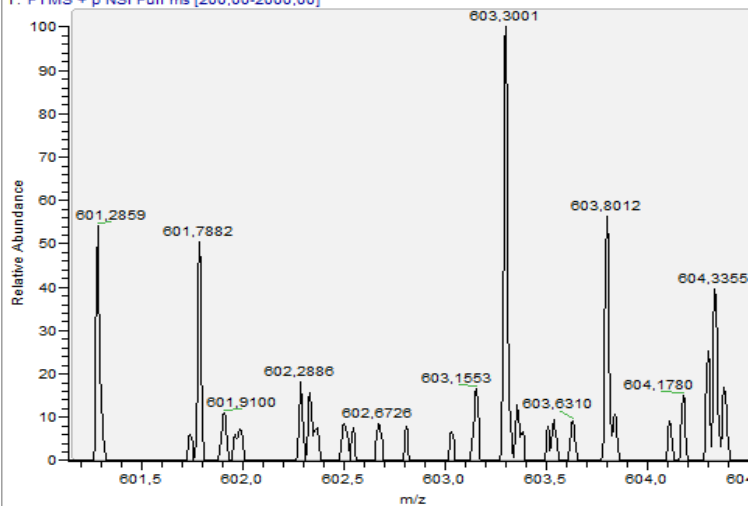


hipocampo_04 #8651-9119 RT: 47.05-48.89 AV: 64 NL: 1,90E4
T: FTMS + p NSI Full ms [200,00-2000,00]

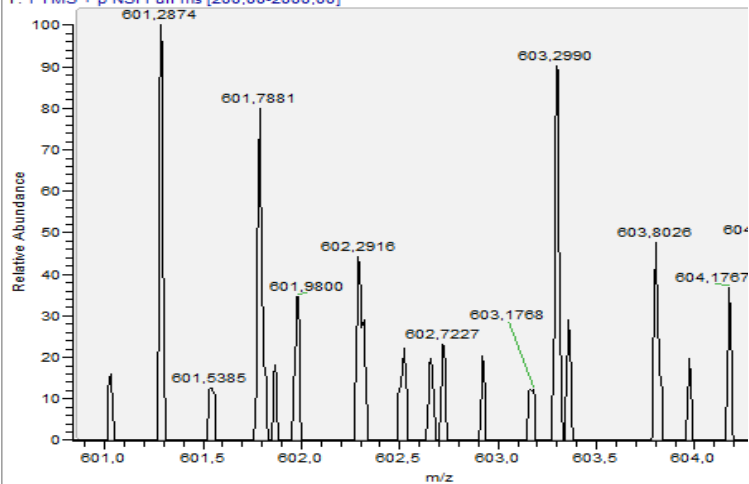


ANSNPAMAPRE 2 (METHIONINE OXIDATION)

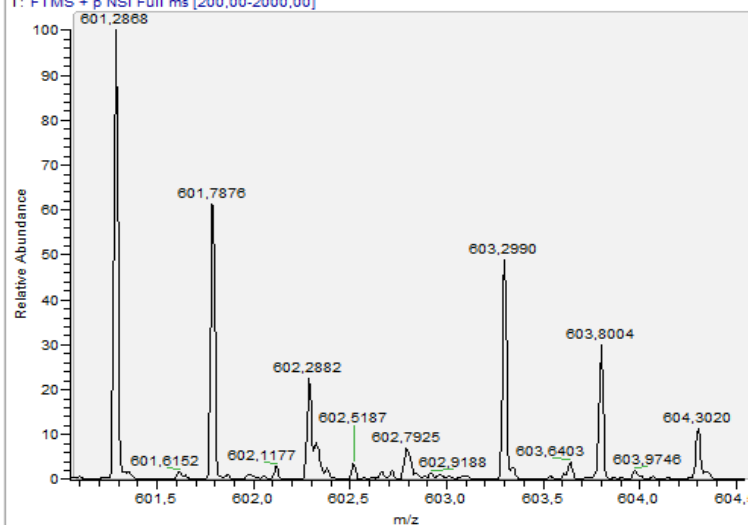
hipocampo_01 #2265 RT: 18,17 AV: 1 NL: 2,64E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #2133 RT: 17,42 AV: 1 NL: 7,51E3
T: FTMS + p NSI Full ms [200,00-2000,00]

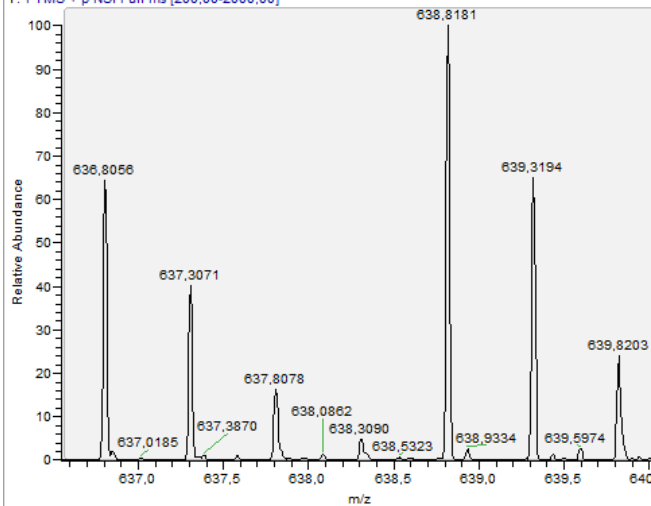


hipocampo_04 #2501-2751 RT: 21,87-22,96 AV: 60 NL: 5,16E3
T: FTMS + p NSI Full ms [200,00-2000,00]

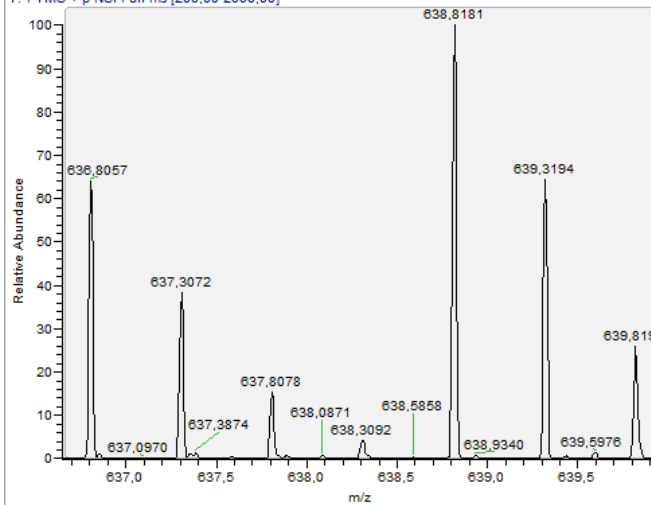


SANSNPAMAPRE 2+

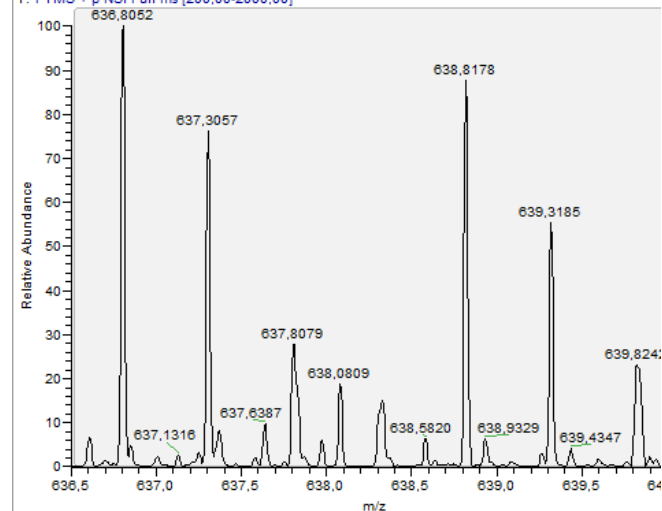
hipocampo_01 #2763-2896 RT: 21,14-21,84 AV: 7 NL: 3,45E5
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #2675-2807 RT: 20,82-21,41 AV: 6 NL: 6,45E5
T: FTMS + p NSI Full ms [200,00-2000,00]

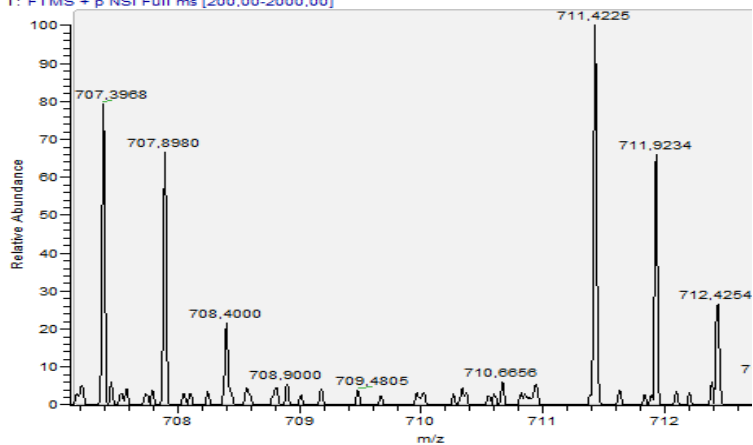


hipocampo_04 #3088-3856 RT: 24,45-27,39 AV: 106 NL: 2,21E4
T: FTMS + p NSI Full ms [200,00-2000,00]

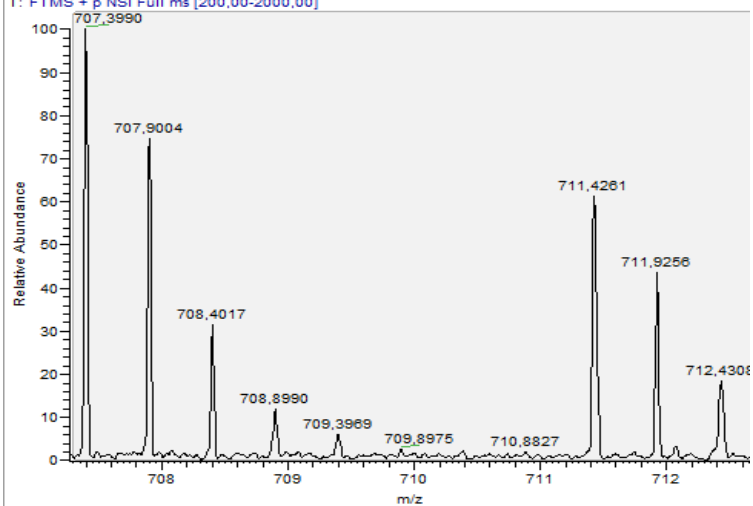


GISTPEELGLDKV 2+

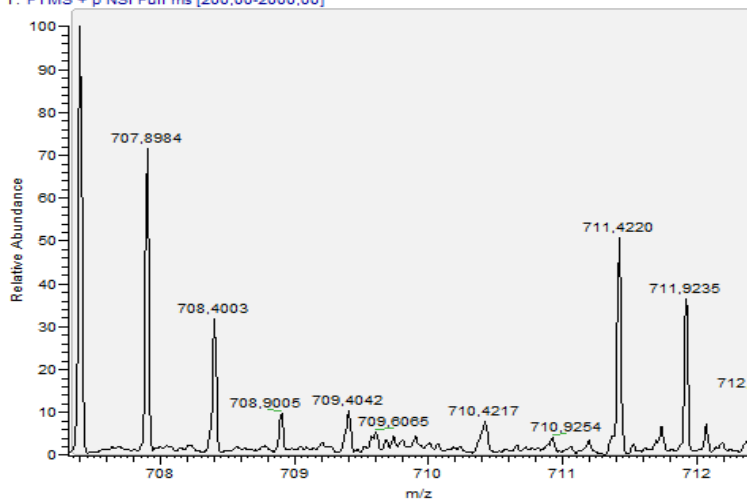
hipocampo_01 #8235 RT: 51.90 AV: 1 NL: 3,34E5
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #7849-8160 RT: 50.37-52.15 AV: 30 NL: 2,33E5
T: FTMS + p NSI Full ms [200,00-2000,00]



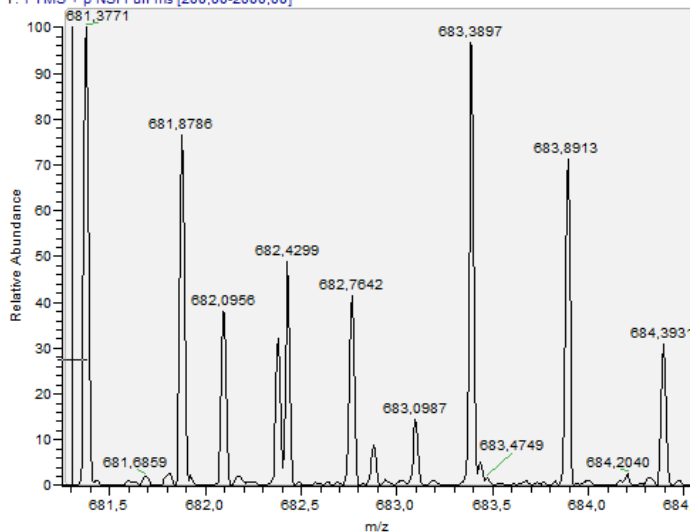
hipocampo_04 #11217-11879 RT: 57.42-59.98 AV: 100 NL: 5,25E4
T: FTMS + p NSI Full ms [200,00-2000,00]



NDFASAVRILEV 2+

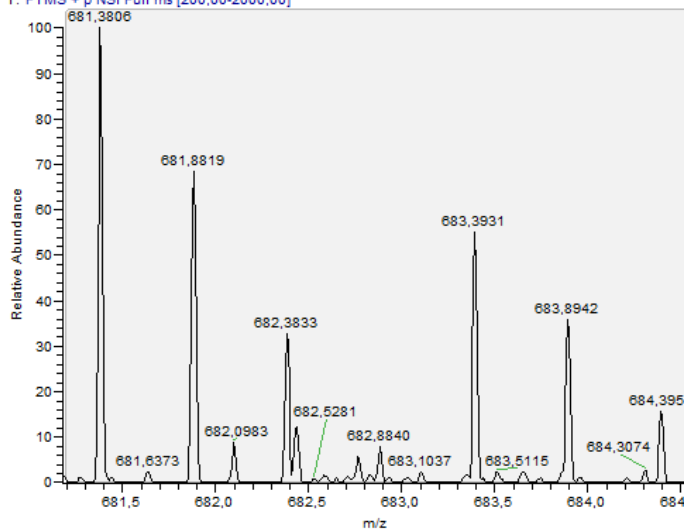
hipocampo_01 #11123-11243 RT: 69,36-69,93 AV: 6 NL: 6,30E4

T: FTMS + p NSI Full ms [200,00-2000,00]



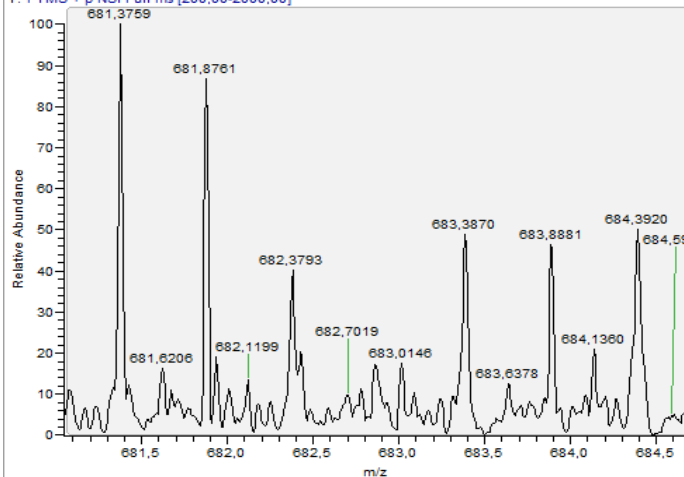
hipocampo_02 #10808 RT: 68,17 AV: 1 NL: 1,40E5

T: FTMS + p NSI Full ms [200,00-2000,00]



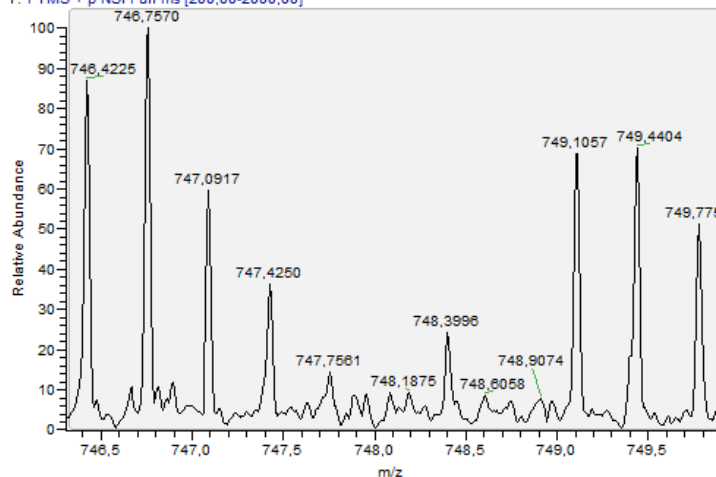
hipocampo_04 #14919-15477 RT: 71,86-74,06 AV: 92 NL: 4,56E3

T: FTMS + p NSI Full ms [200,00-2000,00]

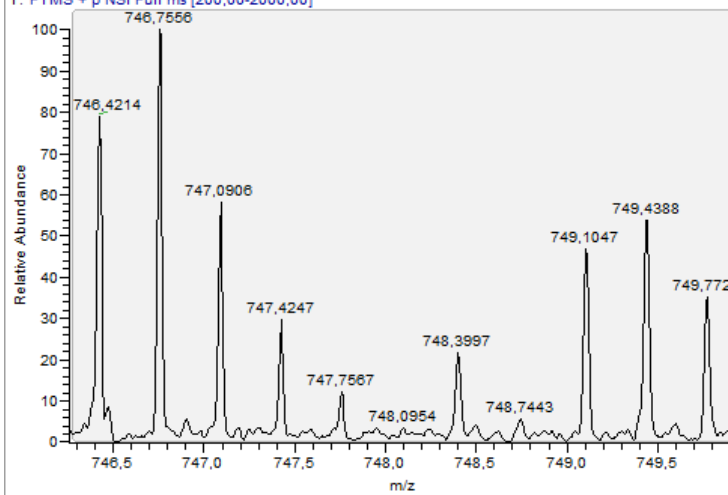


RPTLNELGISTPEELGLDKV 3+

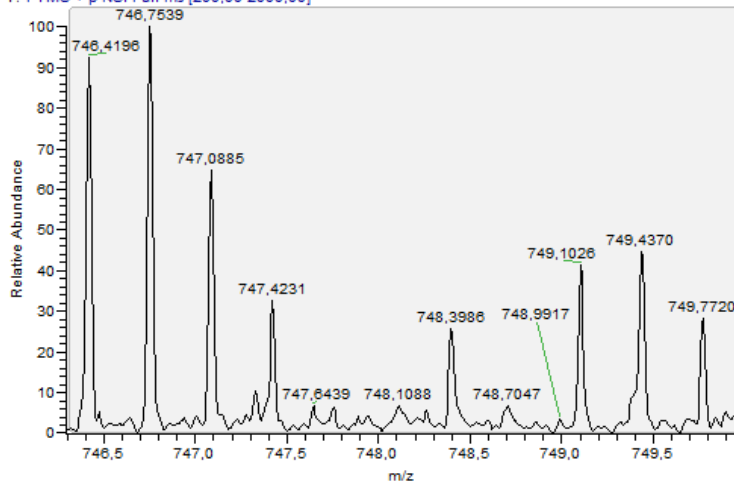
hipocampo_01 #10330-10577 RT: 64,56-65,85 AV: 13 NL: 3,32E4
T: FTMS + p NSI Full ms [200,00-2000,00]



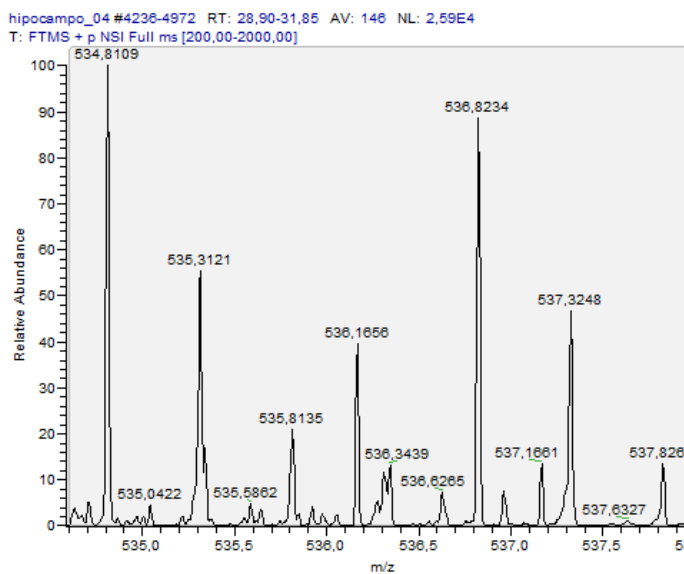
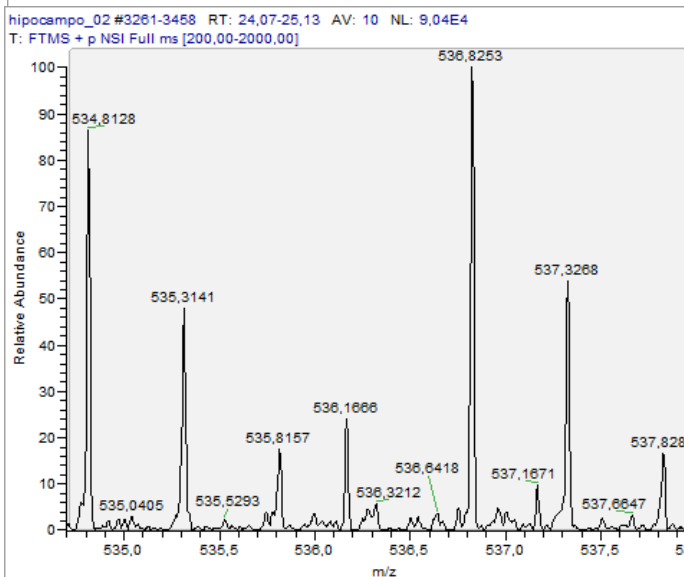
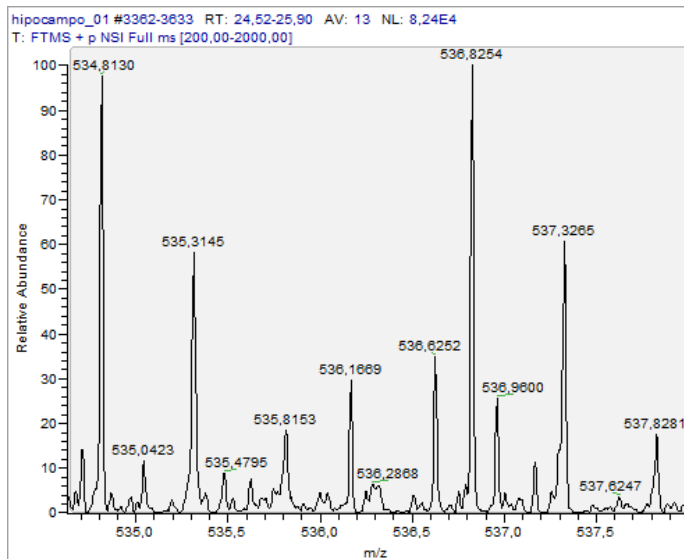
hipocampo_02 #9831-10076 RT: 62,30-63,60 AV: 15 NL: 5,17E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_04 #13395-13686 RT: 65,93-66,99 AV: 36 NL: 2,35E4
T: FTMS + p NSI Full ms [200,00-2000,00]



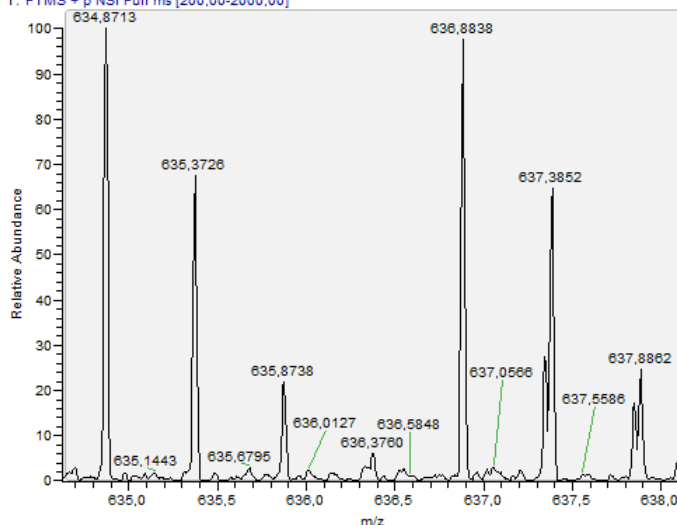
SGQAAARPLVA 2+



SGQAAARPLVATV 2+

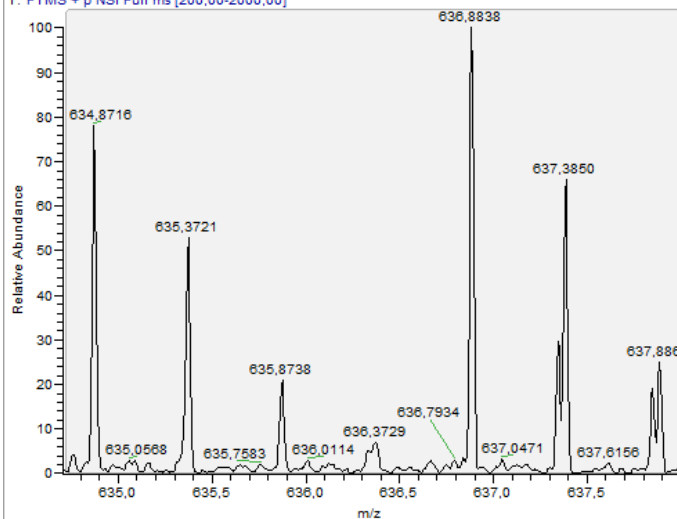
hipocampo_01 #5075-5214 RT: 33,73-34,39 AV: 7 NL: 3,30E5

T: FTMS + p NSI Full ms [200,00-2000,00]



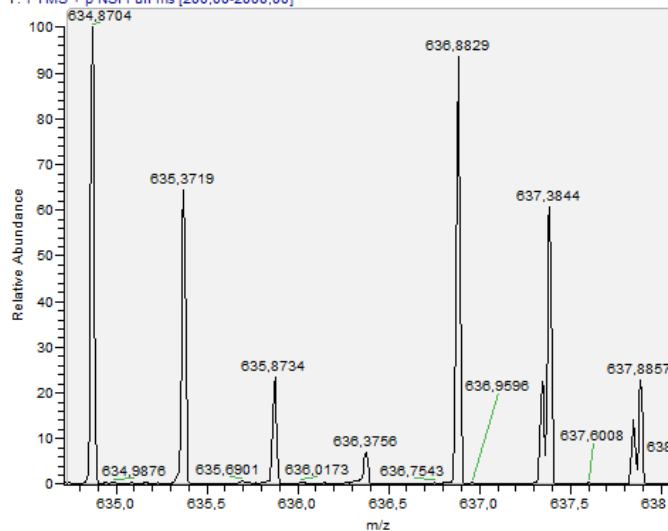
hipocampo_02 #4859-5255 RT: 33,05-35,16 AV: 20 NL: 1,46E5

T: FTMS + p NSI Full ms [200,00-2000,00]



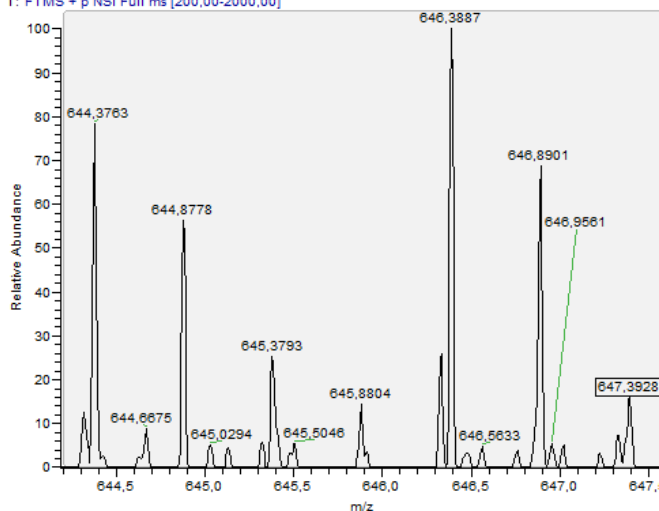
hipocampo_04 #8837-7096 RT: 39,63-40,73 AV: 63 NL: 7,14E4

T: FTMS + p NSI Full ms [200,00-2000,00]

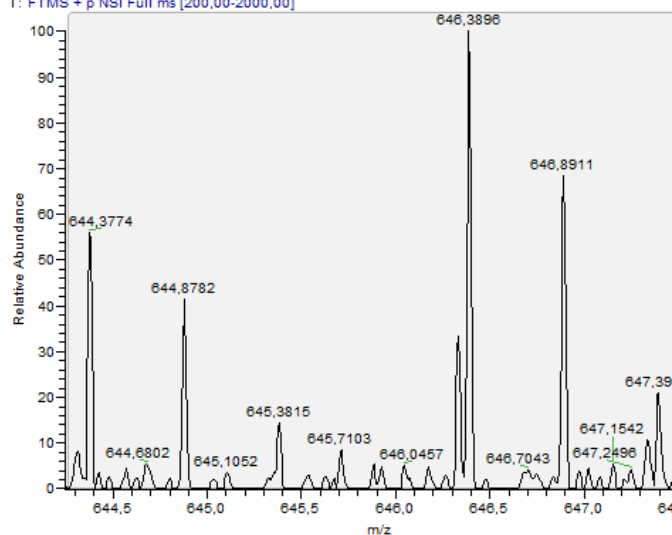


TVGLNVPASVRF 2+

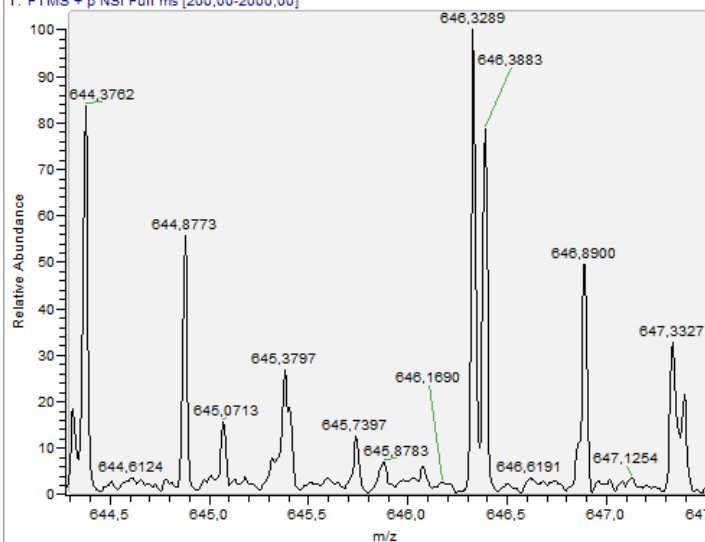
hipocampo_01 #9173 RT: 57.42 AV: 1 NL: 1,57E5
T: FTMS + p NSI Full ms [200,00-2000,00]



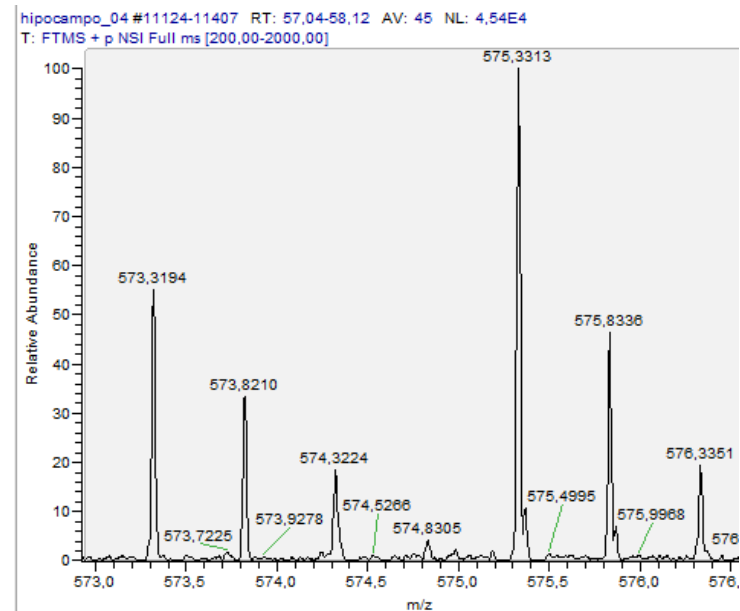
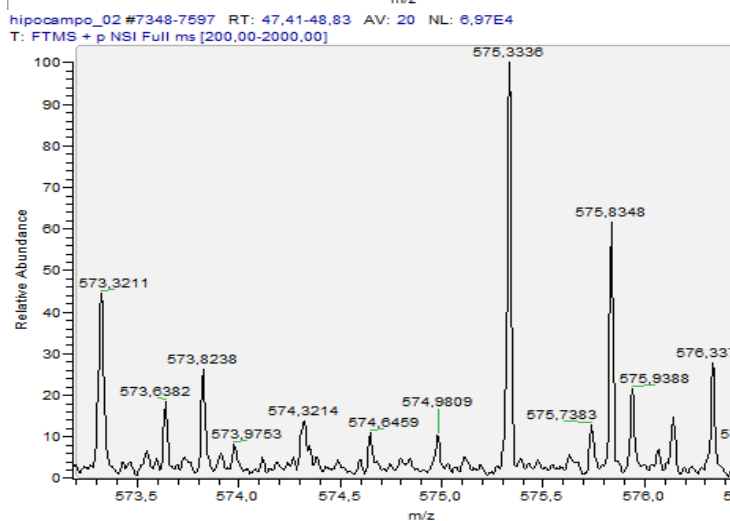
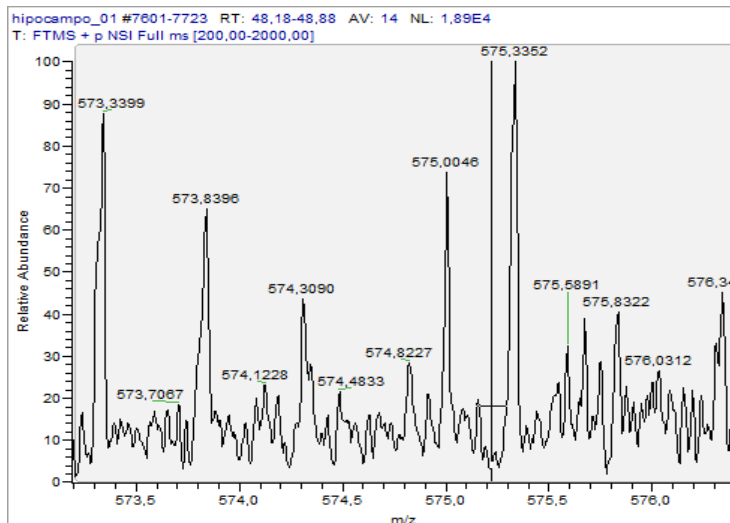
hipocampo_02 #8587 RT: 54.77 AV: 1 NL: 3,14E5
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_04 #12070-12730 RT: 60.76-63.30 AV: 99 NL: 2,10E4
T: FTMS + p NSI Full ms [200,00-2000,00]

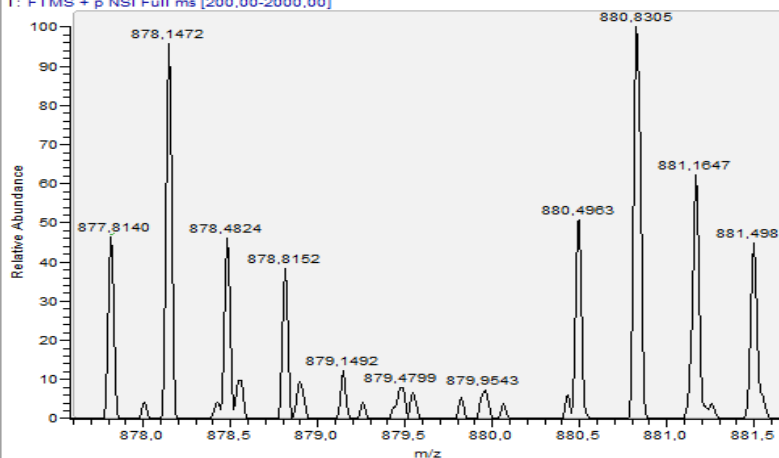


SFARAPQLDL 2+

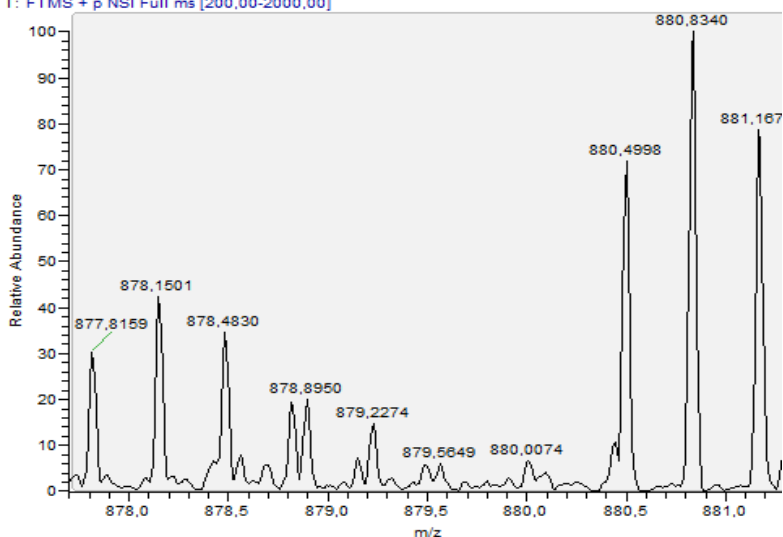


AGNSDLILPVPAFNVINGGSHAGNKL 3+

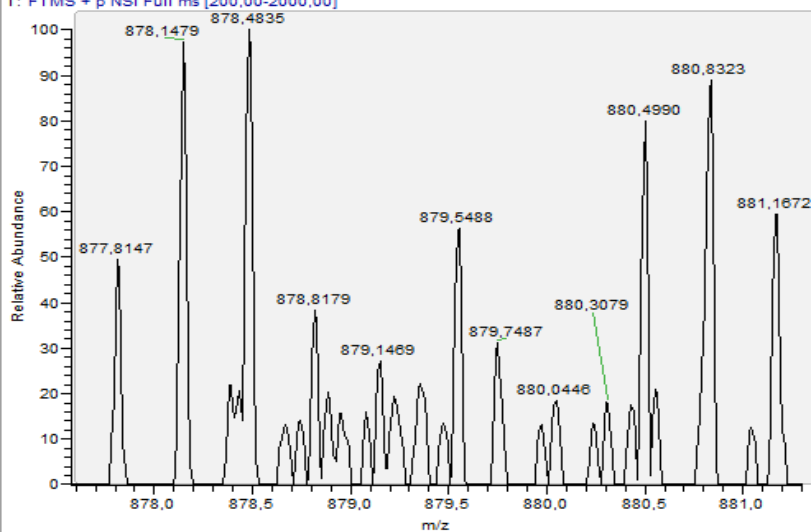
hipocampo_01 #11518 RT: 71.73 AV: 1 NL: 8,61E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #10983-11162 RT: 69.31-70.37 AV: 10 NL: 6,10E4
T: FTMS + p NSI Full ms [200,00-2000,00]

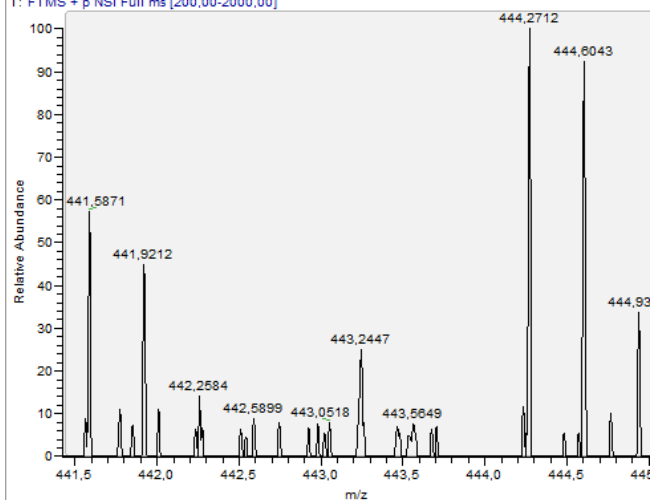


hipocampo_04 #15174 RT: 72.84 AV: 1 NL: 1,26E4
T: FTMS + p NSI Full ms [200,00-2000,00]

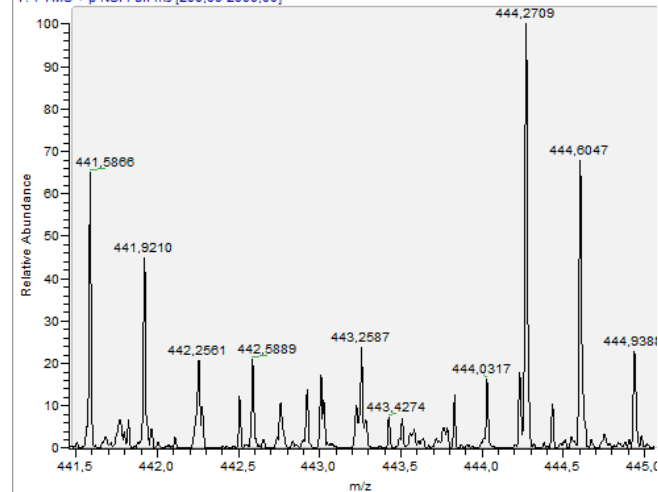


SKVAFS AVRSTN 2+

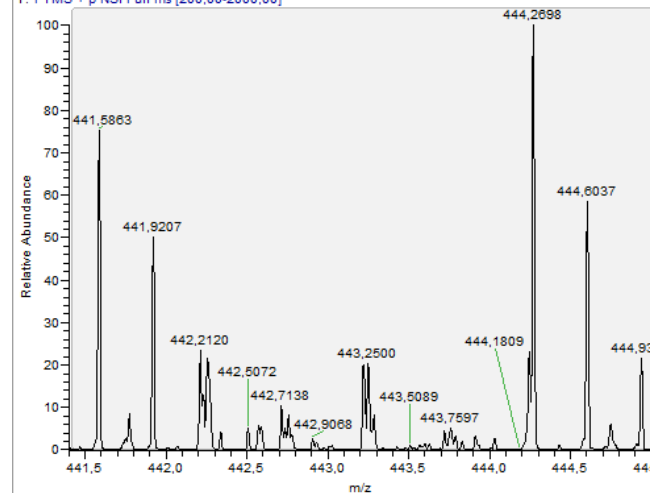
hipocampo_01 #3459 RT: 24.97 AV: 1 NL: 9,64E4
T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #3261-3458 RT: 24,07-25,13 AV: 10 NL: 7,35E4
T: FTMS + p NSI Full ms [200,00-2000,00]



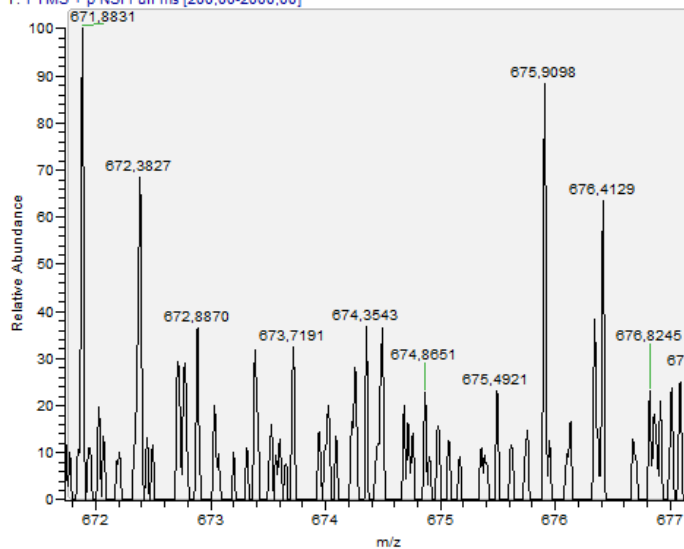
hipocampo_04 #4425-4691 RT: 29,63-30,73 AV: 62 NL: 2,66E4
T: FTMS + p NSI Full ms [200,00-2000,00]



AEDVTAALAKQGL 2+

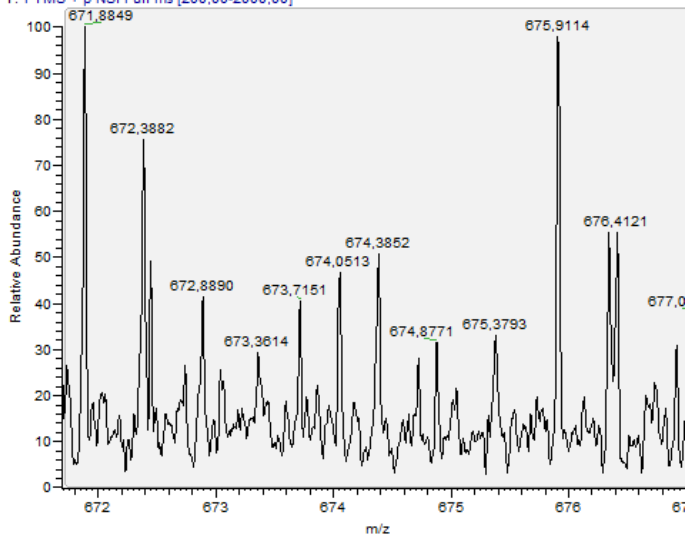
hipocampo_01 #7589 RT: 48,07 AV: 1 NL: 4,94E4

T: FTMS + p NSI Full ms [200,00-2000,00]



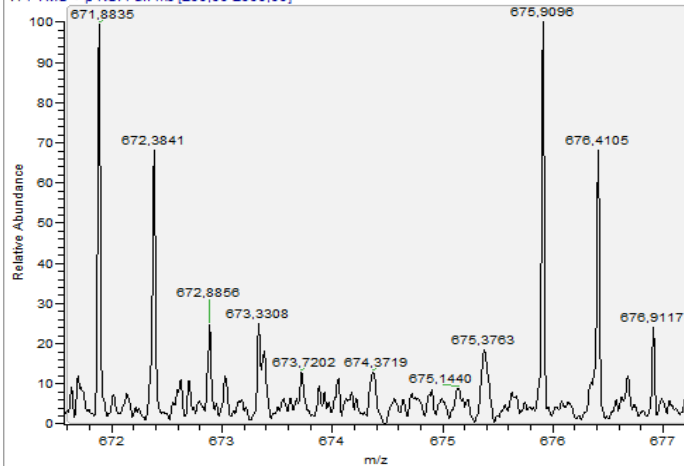
hipocampo_02 #7286-7536 RT: 47,05-48,50 AV: 23 NL: 2,31E4

T: FTMS + p NSI Full ms [200,00-2000,00]



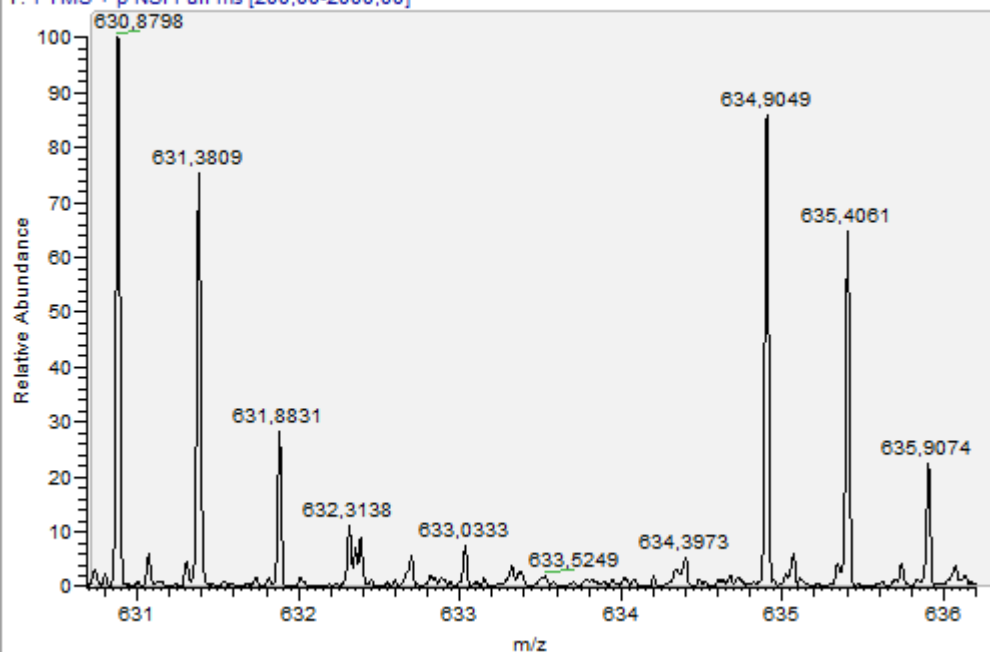
hipocampo_04 #10478-10757 RT: 54,44-55,55 AV: 46 NL: 1,18E4

T: FTMS + p NSI Full ms [200,00-2000,00]

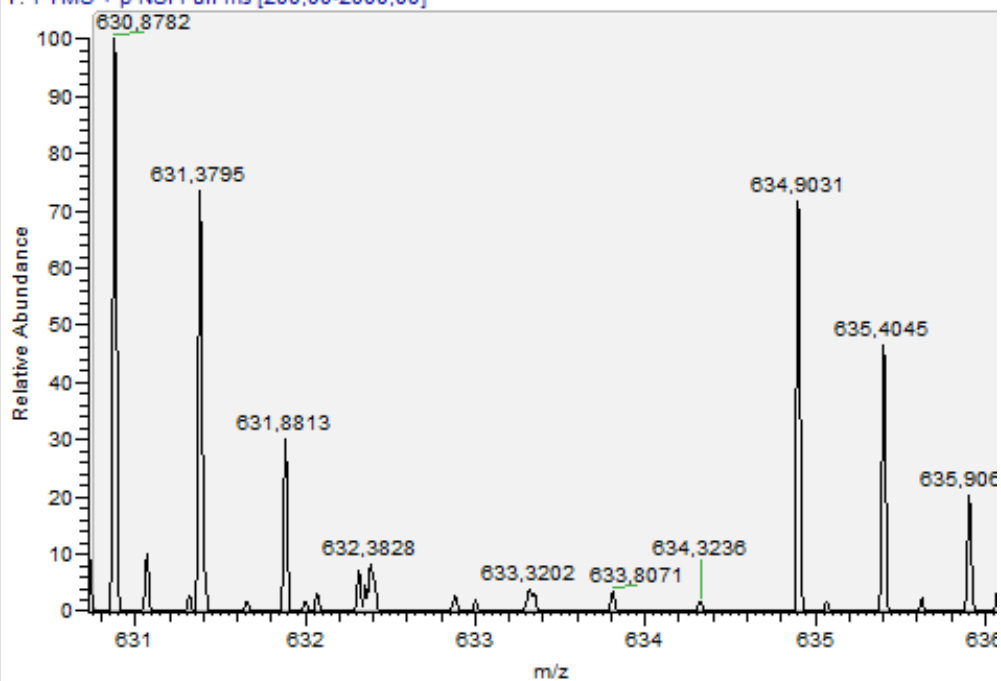


VFDVELLKLE 2+

hipocampo_01 #11301-11596 RT: 70,42-72,22 AV: 17 NL: 2,57E4
T: FTMS + p NSI Full ms [200,00-2000,00]



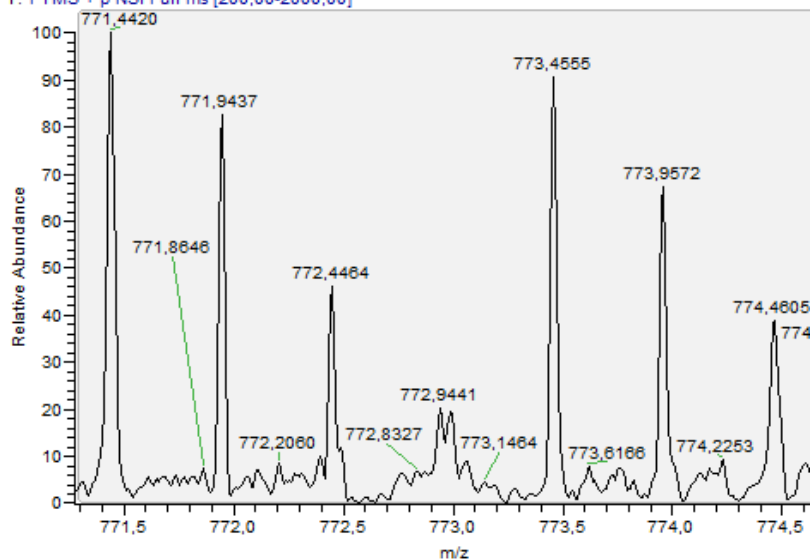
hipocampo_02 #10904 RT: 68,76 AV: 1 NL: 9,97E4
T: FTMS + p NSI Full ms [200,00-2000,00]



AFRVPTPNVSVVDL 2+

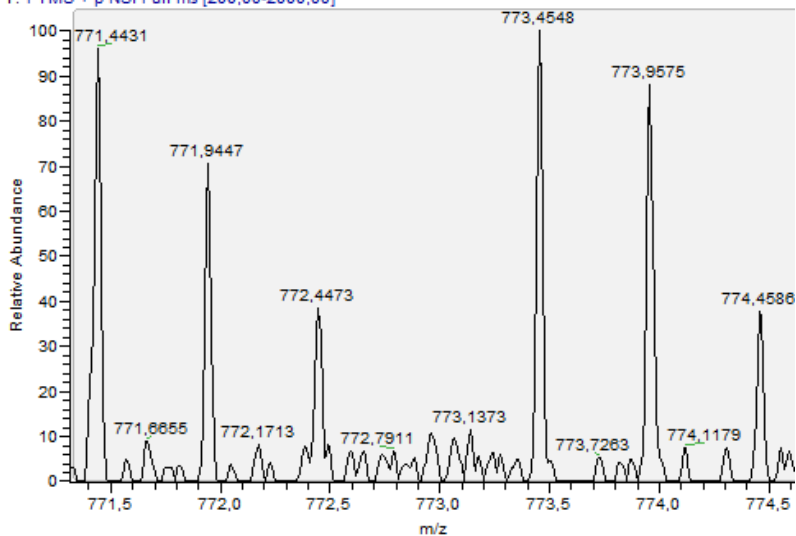
hipocampo_01 #10639-10822 RT: 66,32-67,37 AV: 10 NL: 2,18E4

T: FTMS + p NSI Full ms [200,00-2000,00]



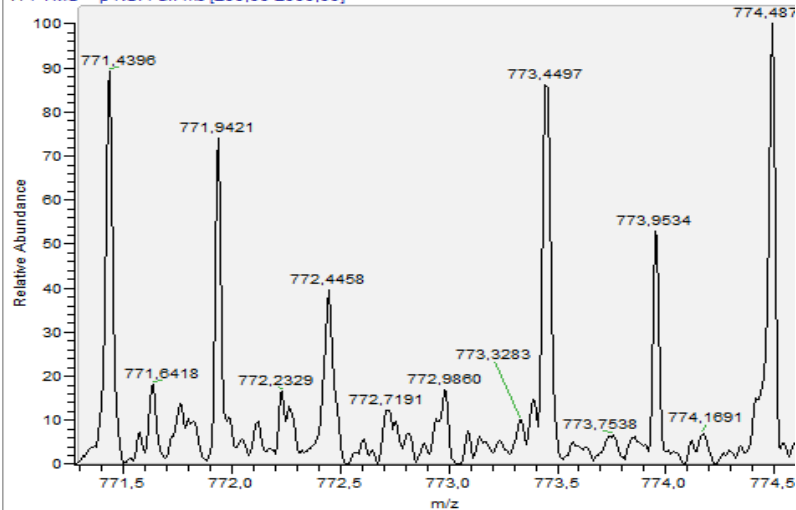
hipocampo_02 #10463 RT: 66,06 AV: 1 NL: 4,89E4

T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_04 #14155-14339 RT: 68,90-69,61 AV: 27 NL: 5,94E3

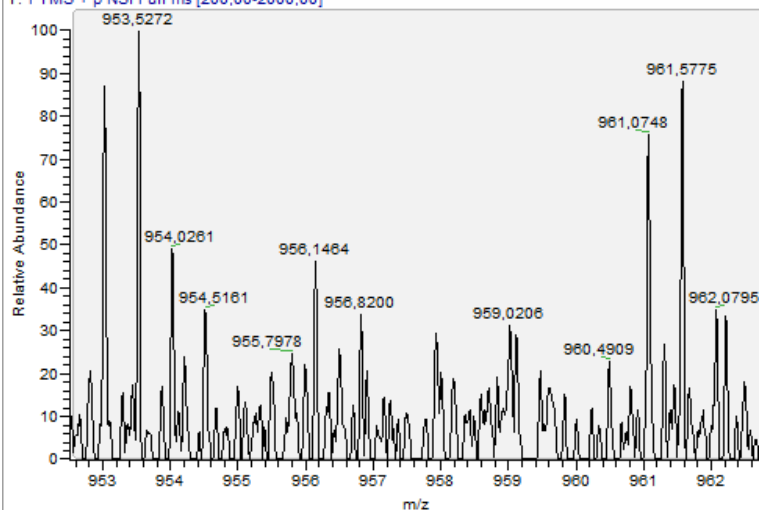
T: FTMS + p NSI Full ms [200,00-2000,00]



KFDDPKFEVIDKPQS 2+

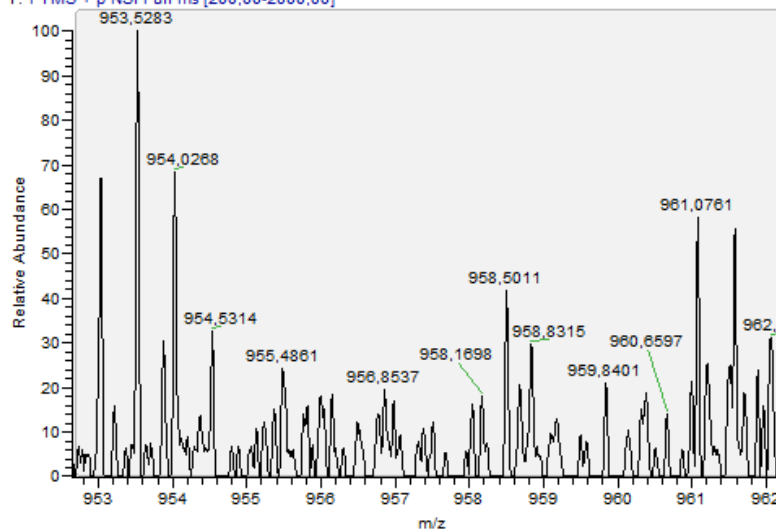
hipocampo_01 #5826-6026 RT: 37.82-38.77 AV: 10 NL: 1,33E4

T: FTMS + p NSI Full ms [200.00-2000.00]



hipocampo_02 #5856-5860 RT: 37.51-38.44 AV: 9 NL: 1,46E4

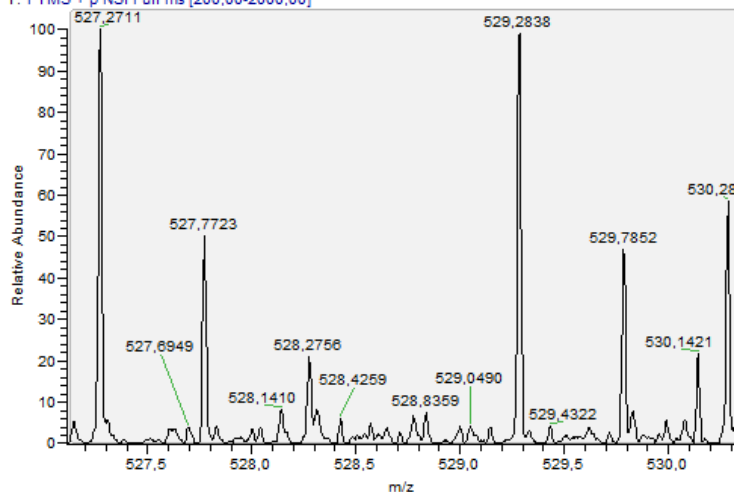
T: FTMS + p NSI Full ms [200.00-2000.00]



QQGAGALVHSE 2+

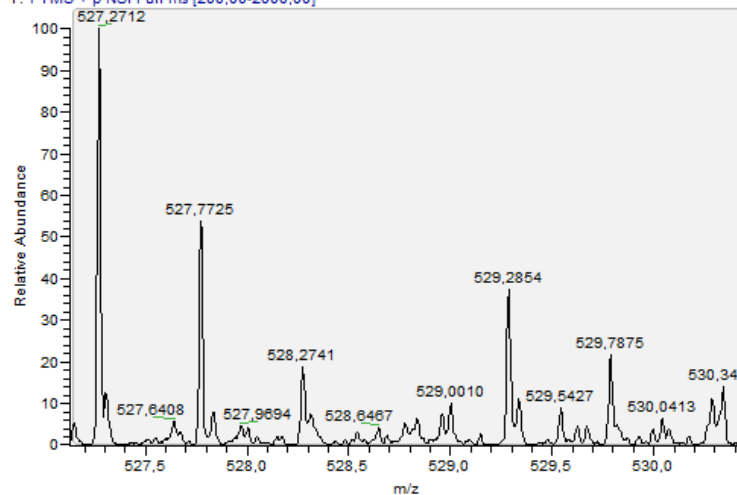
hipocampo_01 #3093-3297 RT: 22,99-24,01 AV: 10 NL: 9,49E4

T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_02 #2740-3261 RT: 21,18-24,07 AV: 26 NL: 6,89E4

T: FTMS + p NSI Full ms [200,00-2000,00]



hipocampo_04 #3950-4236 RT: 27,80-28,86 AV: 43 NL: 1,78E4

T: FTMS + p NSI Full ms [200,00-2000,00]

