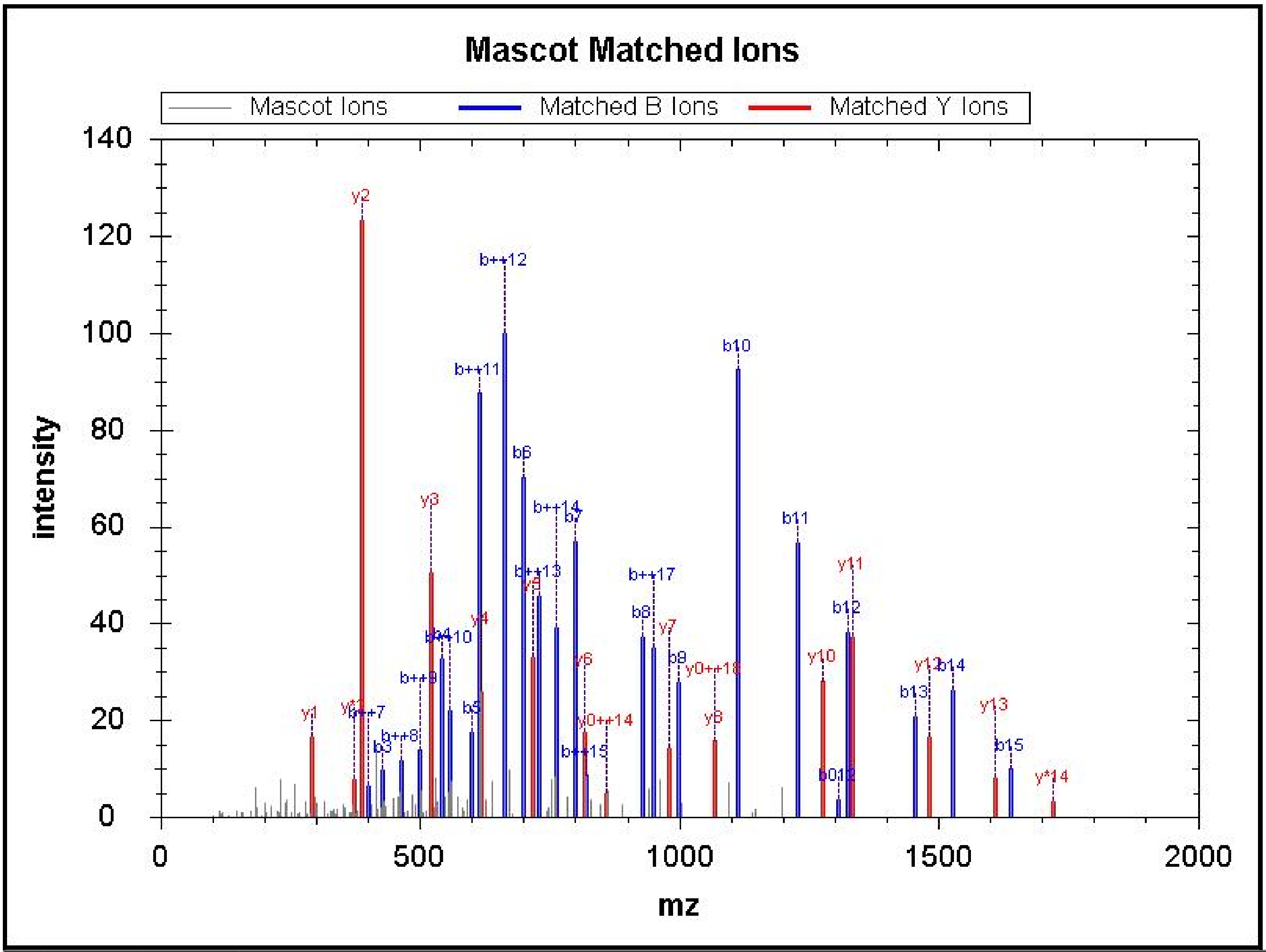
# Spectra S2: The information of single-peptide-based protein identifications in the small-scale experiment.

Query 2912 Hit 1

MS/MS Fragmentation of GLIDGVVEADLVEALQEFGPISYVVVMPK
Found in sp|P14866|HNRPL_HUMAN, Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2
Match to Query 2912: 3374.849from(1125.957,3+)
Title: 1430: Sum of 2 scans in range 3580 (rt=89.1048, f=4, i=1046) to 3581 (rt=89.1302, f=4, i=1047)
[D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 3374.849
**Variable modifications:**
**K29** :iTRAQ4plex (K)
**Ions Score:** 138.16 **Expect:** 0.000

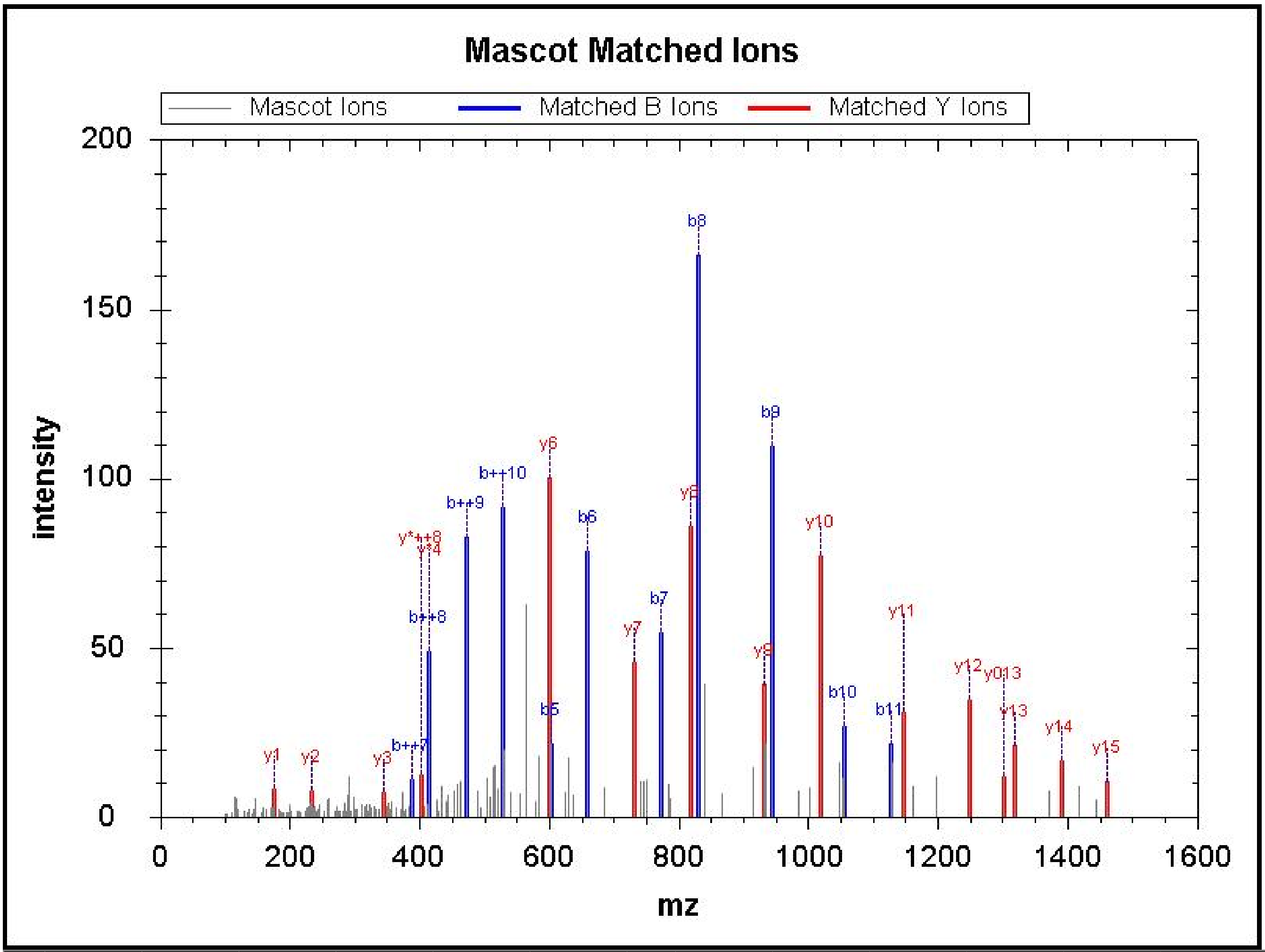


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 202.13 | 101.57 | | | | | G | | | | | | | 29 |
| 2 | 315.21 | 158.11 | | | | | L | 3,174.71 | 1,587.86 | 3,157.69 | 1,579.35 | 3,156.70 | 1,578.85 | 28 |
| 3 | 428.30 | 214.65 | | | | | I | 3,061.63 | 1,531.32 | 3,044.60 | 1,522.80 | 3,043.62 | 1,522.31 | 27 |
| 4 | 543.33 | 272.17 | | | 525.32 | 263.16 | D | 2,948.54 | 1,474.78 | 2,931.52 | 1,466.26 | 2,930.53 | 1,465.77 | 26 |
| 5 | 600.35 | 300.68 | | | 582.34 | 291.67 | G | 2,833.52 | 1,417.26 | 2,816.49 | 1,408.75 | 2,815.51 | 1,408.26 | 25 |
| 6 | 699.42 | 350.21 | | | 681.41 | 341.21 | V | 2,776.50 | 1,388.75 | 2,759.47 | 1,380.24 | 2,758.49 | 1,379.75 | 24 |
| 7 | 798.48 | 399.75 | | | 780.47 | 390.74 | V | 2,677.43 | 1,339.22 | 2,660.40 | 1,330.70 | 2,659.42 | 1,330.21 | 23 |
| 8 | 927.53 | 464.27 | | | 909.52 | 455.26 | E | 2,578.36 | 1,289.68 | 2,561.33 | 1,281.17 | 2,560.35 | 1,280.68 | 22 |
| 9 | 998.56 | 499.79 | | | 980.55 | 490.78 | A | 2,449.32 | 1,225.16 | 2,432.29 | 1,216.65 | 2,431.31 | 1,216.16 | 21 |
| 10 | 1,113.59 | 557.30 | | | 1,095.58 | 548.29 | D | 2,378.28 | 1,189.64 | 2,361.25 | 1,181.13 | 2,360.27 | 1,180.64 | 20 |
| 11 | 1,226.67 | 613.84 | | | 1,208.66 | 604.84 | L | 2,263.25 | 1,132.13 | 2,246.23 | 1,123.62 | 2,245.24 | 1,123.12 | 19 |
| 12 | 1,325.74 | 663.38 | | | 1,307.73 | 654.37 | V | 2,150.17 | 1,075.59 | 2,133.14 | 1,067.07 | 2,132.16 | 1,066.58 | 18 |
| 13 | 1,454.79 | 727.90 | | | 1,436.78 | 718.89 | E | 2,051.10 | 1,026.05 | 2,034.07 | 1,017.54 | 2,033.09 | 1,017.05 | 17 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **14** | **1,525.82** | **763.42** | | | 1,507.81 | 754.41 | **A** | 1,922.06 | 961.53 | 1,905.03 | 953.02 | 1,904.05 | 952.53 | **16** |
| **15** | **1,638.91** | **819.96** | | | 1,620.90 | 810.95 | **L** | 1,851.02 | 926.01 | 1,833.99 | 917.50 | 1,833.01 | 917.01 | **15** |
| **16** | 1,766.97 | 883.99 | 1,749.94 | 875.47 | 1,748.96 | 874.98 | **Q** | 1,737.94 | 869.47 | **1,720.91** | 860.96 | 1,719.93 | **860.47** | **14** |
| **17** | 1,896.01 | **948.51** | 1,878.98 | 939.99 | 1,878.00 | 939.50 | **E** | **1,609.88** | 805.44 | 1,592.85 | 796.93 | 1,591.87 | 796.44 | **13** |
| **18** | 2,043.08 | 1,022.04 | 2,026.05 | 1,013.53 | 2,025.07 | 1,013.04 | **F** | **1,480.84** | 740.92 | 1,463.81 | 732.41 | 1,462.82 | 731.92 | **12** |
| **19** | 2,100.10 | 1,050.55 | 2,083.07 | 1,042.04 | 2,082.09 | 1,041.55 | **G** | **1,333.77** | 667.39 | 1,316.74 | 658.87 | 1,315.76 | 658.38 | **11** |
| **20** | 2,197.15 | 1,099.08 | 2,180.12 | 1,090.57 | 2,179.14 | 1,090.07 | **P** | **1,276.75** | 638.88 | 1,259.72 | 630.36 | 1,258.73 | 629.87 | **10** |
| **21** | 2,310.23 | 1,155.62 | 2,293.21 | 1,147.11 | 2,292.22 | 1,146.62 | **I** | 1,179.69 | 590.35 | 1,162.67 | 581.84 | 1,161.68 | 581.34 | **9** |
| **22** | 2,397.27 | 1,199.14 | 2,380.24 | 1,190.62 | 2,379.26 | 1,190.13 | **S** | **1,066.61** | 533.81 | 1,049.58 | 525.29 | 1,048.60 | 524.80 | **8** |
| **23** | 2,560.33 | 1,280.67 | 2,543.30 | 1,272.16 | 2,542.32 | 1,271.66 | **Y** | **979.58** | 490.29 | 962.55 | 481.78 | | | **7** |
| **24** | 2,659.40 | 1,330.20 | 2,642.37 | 1,321.69 | 2,641.39 | 1,321.20 | **V** | **816.51** | 408.76 | 799.49 | 400.25 | | | **6** |
| **25** | 2,758.47 | 1,379.74 | 2,741.44 | 1,371.22 | 2,740.46 | 1,370.73 | **V** | **717.44** | 359.23 | 700.42 | 350.71 | | | **5** |
| **26** | 2,857.54 | 1,429.27 | 2,840.51 | 1,420.76 | 2,839.52 | 1,420.27 | **V** | **618.38** | 309.69 | 601.35 | 301.18 | | | **4** |
| **27** | 2,988.58 | 1,494.79 | 2,971.55 | 1,486.28 | 2,970.57 | 1,485.79 | **M** | **519.31** | 260.16 | 502.28 | 251.64 | | | **3** |
| **28** | 3,085.63 | 1,543.32 | 3,068.60 | 1,534.80 | 3,067.62 | 1,534.31 | **P** | **388.27** | 194.64 | **371.24** | 186.12 | | | **2** |
| **29** | | | | | | | **K** | **291.21** | 146.11 | 274.19 | 137.60 | | | **1** |

Query 2629 Hit 1

MS/MS Fragmentation of **DLSAAGIGLLAAATQSLSMPASLGR**
Found in **sp|P43243|MATR3_HUMAN**, Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2
Match to Query 2629: 2514.369from(839.1303,3+)
Title: 1158: Sum of 2 scans in range 2964 (rt=74.7768, f=4, i=814) to 2965 (rt=74.8022, f=4, i=815) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2514.369
**Variable modifications:**
**Ions Score:** 125.9 **Expect:** 0.000

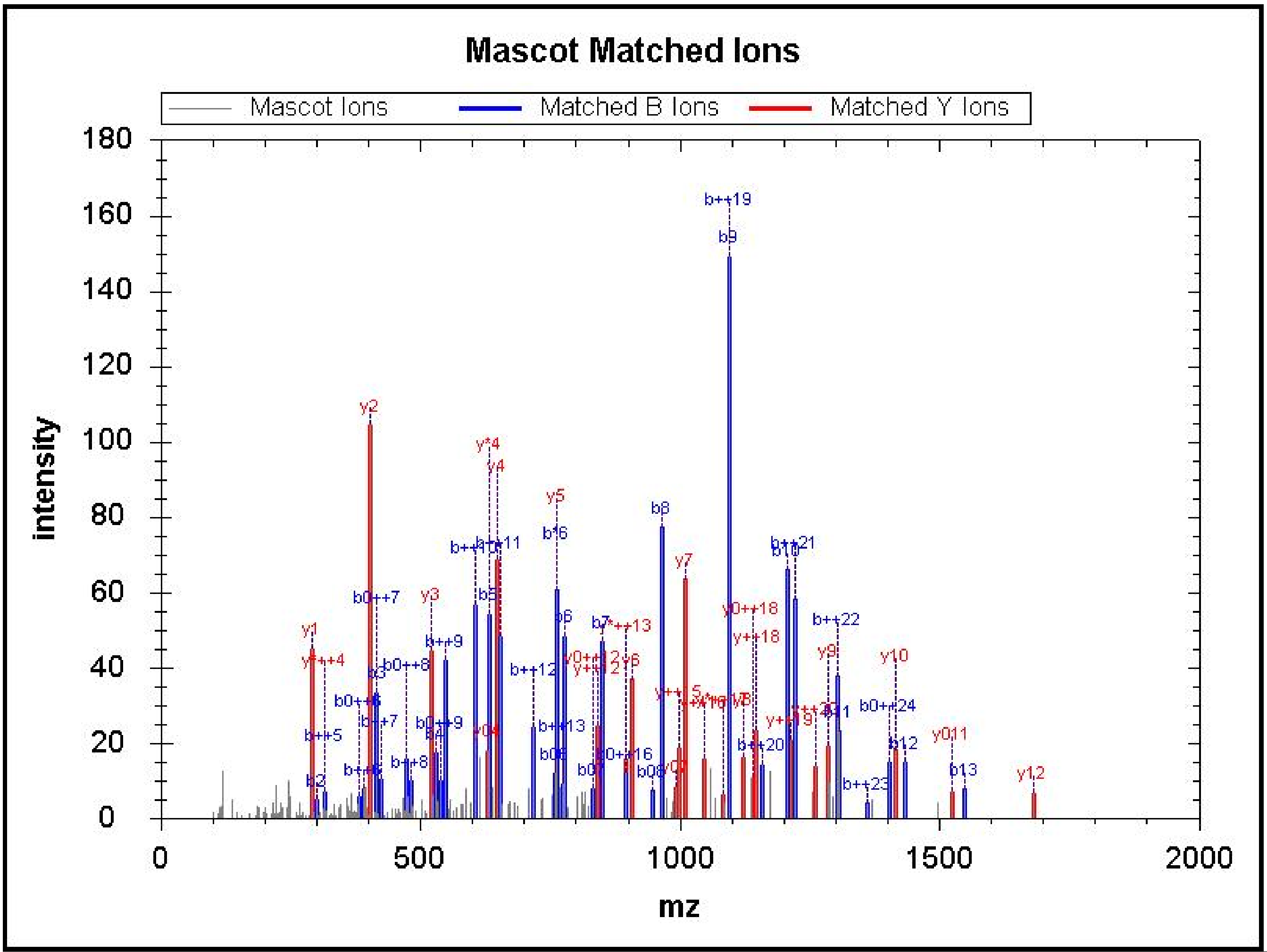


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 260.14 | 130.57 |  |  | 242.13 | 121.57 | D |  |  |  |  |  |  | 25 |
| 2 | 373.22 | 187.11 |  |  | 355.21 | 178.11 | L | 2,256.24 | 1,128.62 | 2,239.21 | 1,120.11 | 2,238.23 | 1,119.62 | 24 |
| 3 | 460.25 | 230.63 |  |  | 442.24 | 221.62 | S | 2,143.15 | 1,072.08 | 2,126.13 | 1,063.57 | 2,125.14 | 1,063.08 | 23 |
| 4 | 531.29 | 266.15 |  |  | 513.28 | 257.14 | A | 2,056.12 | 1,028.56 | 2,039.10 | 1,020.05 | 2,038.11 | 1,019.56 | 22 |
| 5 | 602.33 | 301.67 |  |  | 584.32 | 292.66 | A | 1,985.08 | 993.05 | 1,968.06 | 984.53 | 1,967.07 | 984.04 | 21 |
| 6 | 659.35 | 330.18 |  |  | 641.34 | 321.17 | G | 1,914.05 | 957.53 | 1,897.02 | 949.01 | 1,896.04 | 948.52 | 20 |
| 7 | 772.43 | 386.72 |  |  | 754.42 | 377.71 | I | 1,857.03 | 929.02 | 1,840.00 | 920.50 | 1,839.02 | 920.01 | 19 |
| 8 | 829.45 | 415.23 |  |  | 811.44 | 406.23 | G | 1,743.94 | 872.47 | 1,726.92 | 863.96 | 1,725.93 | 863.47 | 18 |
| 9 | 942.54 | 471.77 |  |  | 924.53 | 462.77 | L | 1,686.92 | 843.96 | 1,669.89 | 835.45 | 1,668.91 | 834.96 | 17 |
| 10 | 1,055.62 | 528.31 |  |  | 1,037.61 | 519.31 | L | 1,573.84 | 787.42 | 1,556.81 | 778.91 | 1,555.83 | 778.42 | 16 |
| 11 | 1,126.66 | 563.83 |  |  | 1,108.65 | 554.83 | A | 1,460.75 | 730.88 | 1,443.73 | 722.37 | 1,442.74 | 721.87 | 15 |
| 12 | 1,197.70 | 599.35 |  |  | 1,179.69 | 590.35 | A | 1,389.72 | 695.36 | 1,372.69 | 686.85 | 1,371.70 | 686.36 | 14 |
| 13 | 1,268.73 | 634.87 |  |  | 1,250.72 | 625.86 | A | 1,318.68 | 659.84 | 1,301.65 | 651.33 | 1,300.67 | 650.84 | 13 |
| 14 | 1,369.78 | 685.39 |  |  | 1,351.77 | 676.39 | T | 1,247.64 | 624.32 | 1,230.61 | 615.81 | 1,229.63 | 615.32 | 12 |
| 15 | 1,497.84 | 749.42 | 1,480.81 | 740.91 | 1,479.83 | 740.42 | Q | 1,146.59 | 573.80 | 1,129.57 | 565.29 | 1,128.58 | 564.80 | 11 |
| 16 | 1,584.87 | 792.94 | 1,567.84 | 784.43 | 1,566.86 | 783.93 | S | 1,018.53 | 509.77 | 1,001.51 | 501.26 | 1,000.52 | 500.77 | 10 |
| 17 | 1,697.96 | 849.48 | 1,680.93 | 840.97 | 1,679.94 | 840.48 | L | 931.50 | 466.26 | 914.48 | 457.74 | 913.49 | 457.25 | 9 |
| 18 | 1,784.99 | 893.00 | 1,767.96 | 884.48 | 1,766.98 | 883.99 | S | 818.42 | 409.71 | 801.39 | 401.20 | 800.41 | 400.71 | 8 |
| 19 | 1,916.03 | 958.52 | 1,899.00 | 950.00 | 1,898.02 | 949.51 | M | 731.39 | 366.20 | 714.36 | 357.68 | 713.38 | 357.19 | 7 |
| 20 | 2,013.08 | 1,007.04 | 1,996.05 | 998.53 | 1,995.07 | 998.04 | P | 600.35 | 300.68 | 583.32 | 292.16 | 582.34 | 291.67 | 6 |
| 21 | 2,084.12 | 1,042.56 | 2,067.09 | 1,034.05 | 2,066.11 | 1,033.56 | A | 503.29 | 252.15 | 486.27 | 243.64 | 485.28 | 243.15 | 5 |
| 22 | 2,171.15 | 1,086.08 | 2,154.12 | 1,077.57 | 2,153.14 | 1,077.07 | S | 432.26 | 216.63 | 415.23 | 208.12 | 414.25 | 207.63 | 4 |
| 23 | 2,284.23 | 1,142.62 | 2,267.21 | 1,134.11 | 2,266.22 | 1,133.62 | L | 345.22 | 173.12 | 328.20 | 164.60 |  |  | 3 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 24 | 2,341.26 | 1,171.13 | 2,324.23 | 1,162.62 | 2,323.24 | 1,162.13 | G | **232.14** | 116.57 | 215.11 | 108.06 | | | 2 |
| 25 | | | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 2964 Hit 1

MS/MS Fragmentation of **GVDNTFADELVELSTALEHQEYITFLEDLK**
Found in **sp|Q07021|C1QBP_HUMAN**, Complement component 1 Q subcomponent-binding protein
Match to Query 2964: 3726.892from(932.7303,4+)
Title: 1331: Scan 3428 (rt=85.2295, f=3, i=491) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 3726.892
**Variable modifications:**
**K30** :iTRAQ4plex (K)
**Ions Score:** 118.68 **Expect:** 0.000

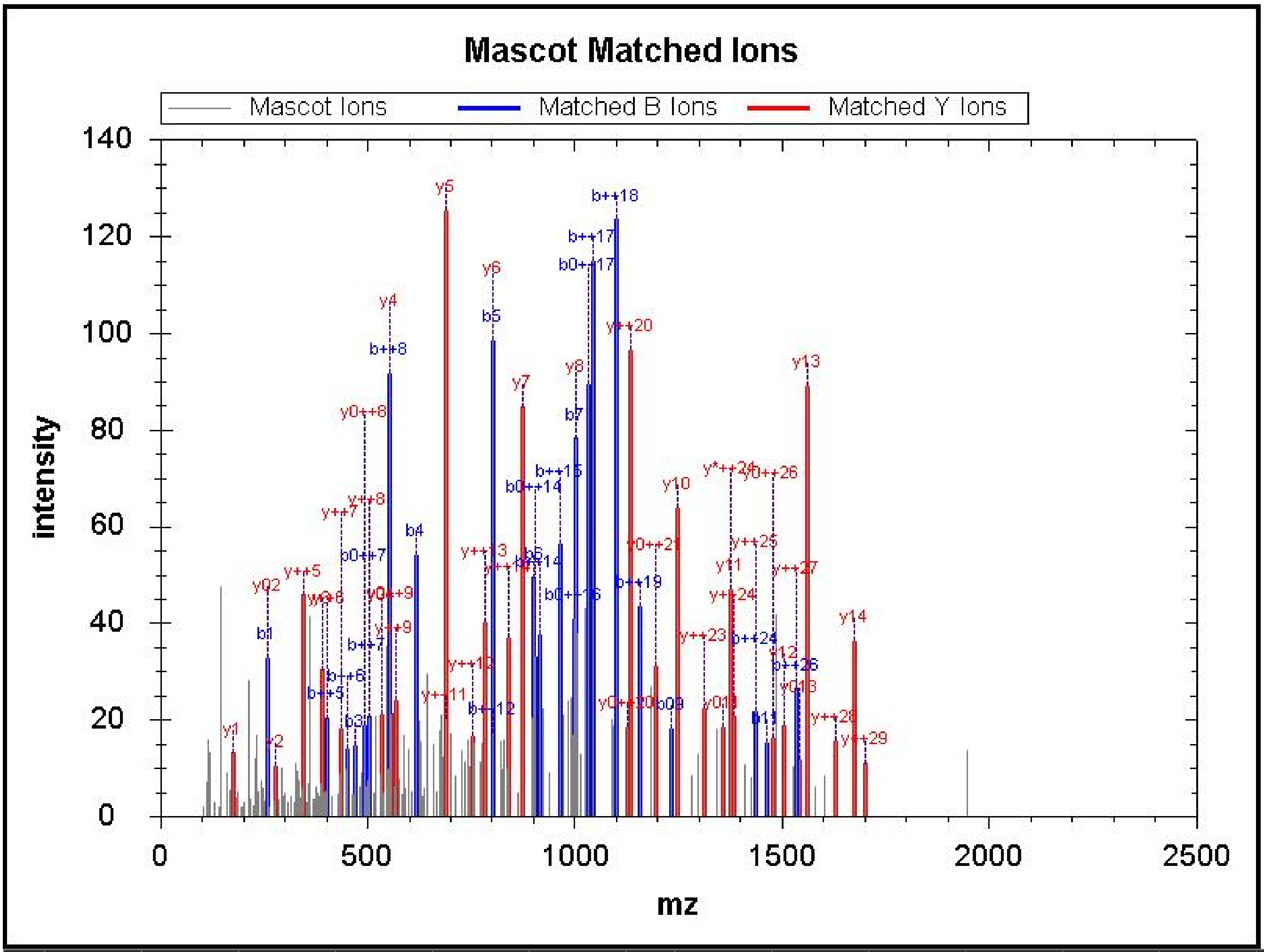


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 202.13 | 101.57 | | | | | G | | | | | | | 30 |
| 2 | **301.20** | 151.10 | | | | | V | 3,526.76 | 1,763.88 | 3,509.73 | 1,755.37 | 3,508.75 | 1,754.88 | 29 |
| 3 | **416.23** | 208.62 | | | 398.22 | 199.61 | D | 3,427.69 | 1,714.35 | 3,410.66 | 1,705.84 | 3,409.68 | 1,705.34 | 28 |
| 4 | **530.27** | 265.64 | 513.24 | 257.12 | 512.26 | 256.63 | N | 3,312.66 | 1,656.84 | 3,295.64 | 1,648.32 | 3,294.65 | 1,647.83 | 27 |
| 5 | **631.32** | **316.16** | 614.29 | 307.65 | 613.31 | 307.16 | T | 3,198.62 | 1,599.81 | 3,181.59 | 1,591.30 | 3,180.61 | 1,590.81 | 26 |
| 6 | **778.39** | **389.70** | **761.36** | 381.18 | **760.37** | **380.69** | F | 3,097.57 | 1,549.29 | 3,080.55 | 1,540.78 | 3,079.56 | 1,540.29 | 25 |
| 7 | **849.42** | **425.21** | 832.40 | 416.70 | **831.41** | **416.21** | A | 2,950.50 | 1,475.76 | 2,933.48 | 1,467.24 | 2,932.49 | 1,466.75 | 24 |
| 8 | **964.45** | **482.73** | 947.42 | 474.21 | **946.44** | **473.72** | D | 2,879.47 | 1,440.24 | 2,862.44 | 1,431.72 | 2,861.46 | 1,431.23 | 23 |
| 9 | **1,093.49** | **547.25** | 1,076.47 | 538.74 | 1,075.48 | **538.24** | E | 2,764.44 | 1,382.72 | 2,747.41 | 1,374.21 | 2,746.43 | 1,373.72 | 22 |
| 10 | **1,206.58** | **603.79** | 1,189.55 | 595.28 | 1,188.57 | 594.79 | L | 2,635.40 | 1,318.20 | 2,618.37 | 1,309.69 | 2,617.39 | 1,309.20 | 21 |
| 11 | **1,305.64** | **653.33** | 1,288.62 | 644.81 | 1,287.63 | 644.32 | V | 2,522.31 | **1,261.66** | 2,505.29 | 1,253.15 | 2,504.30 | 1,252.66 | 20 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **12** | **1,434.69** | **717.85** | 1,417.66 | 709.33 | 1,416.68 | 708.84 | **E** | 2,423.25 | **1,212.13** | 2,406.22 | 1,203.61 | 2,405.24 | 1,203.12 | **19** |
| **13** | **1,547.77** | **774.39** | 1,530.74 | 765.88 | 1,529.76 | 765.38 | **L** | 2,294.20 | **1,147.61** | 2,277.18 | 1,139.09 | 2,276.19 | **1,138.60** | **18** |
| **14** | 1,634.80 | 817.91 | 1,617.78 | 809.39 | 1,616.79 | 808.90 | **S** | 2,181.12 | 1,091.06 | 2,164.09 | **1,082.55** | 2,163.11 | 1,082.06 | **17** |
| **15** | 1,735.85 | 868.43 | 1,718.82 | 859.92 | 1,717.84 | 859.42 | **T** | 2,094.09 | **1,047.55** | 2,077.06 | 1,039.03 | 2,076.08 | 1,038.54 | **16** |
| **16** | 1,806.89 | 903.95 | 1,789.86 | 895.43 | 1,788.88 | **894.94** | **A** | 1,993.04 | **997.02** | 1,976.01 | 988.51 | 1,975.03 | 988.02 | **15** |
| **17** | 1,919.97 | 960.49 | 1,902.95 | 951.98 | 1,901.96 | 951.48 | **L** | 1,922.00 | 961.51 | 1,904.98 | 952.99 | 1,903.99 | 952.50 | **14** |
| **18** | 2,049.01 | 1,025.01 | 2,031.99 | 1,016.50 | 2,031.00 | 1,016.01 | **E** | 1,808.92 | 904.96 | 1,791.89 | **896.45** | 1,790.91 | 895.96 | **13** |
| **19** | 2,186.07 | **1,093.54** | 2,169.05 | 1,085.03 | 2,168.06 | 1,084.54 | **H** | **1,679.88** | **840.44** | 1,662.85 | 831.93 | 1,661.87 | **831.44** | **12** |
| **20** | 2,314.13 | **1,157.57** | 2,297.11 | 1,149.06 | 2,296.12 | 1,148.56 | **Q** | 1,542.82 | 771.91 | 1,525.79 | 763.40 | **1,524.81** | 762.91 | **11** |
| **21** | 2,443.17 | **1,222.09** | 2,426.15 | 1,213.58 | 2,425.16 | 1,213.09 | **E** | **1,414.76** | 707.88 | 1,397.73 | 699.37 | 1,396.75 | 698.88 | **10** |
| **22** | 2,606.24 | **1,303.62** | 2,589.21 | 1,295.11 | 2,588.23 | 1,294.62 | **Y** | **1,285.72** | 643.36 | 1,268.69 | 634.85 | 1,267.71 | 634.36 | **9** |
| **23** | 2,719.32 | **1,360.16** | 2,702.29 | 1,351.65 | 2,701.31 | 1,351.16 | **I** | **1,122.65** | 561.83 | 1,105.63 | 553.32 | 1,104.64 | 552.82 | **8** |
| **24** | 2,820.37 | 1,410.69 | 2,803.34 | 1,402.17 | 2,802.36 | **1,401.68** | **T** | **1,009.57** | 505.29 | 992.54 | 496.77 | **991.56** | 496.28 | **7** |
| **25** | 2,967.44 | 1,484.22 | 2,950.41 | 1,475.71 | 2,949.43 | 1,475.22 | **F** | **908.52** | 454.76 | 891.49 | 446.25 | 890.51 | 445.76 | **6** |
| **26** | 3,080.52 | 1,540.76 | 3,063.49 | 1,532.25 | 3,062.51 | 1,531.76 | **L** | **761.45** | 381.23 | 744.43 | 372.72 | 743.44 | 372.22 | **5** |
| **27** | 3,209.56 | 1,605.29 | 3,192.54 | 1,596.77 | 3,191.55 | 1,596.28 | **E** | **648.37** | 324.69 | **631.34** | **316.17** | **630.36** | 315.68 | **4** |
| **28** | 3,324.59 | 1,662.80 | 3,307.56 | 1,654.29 | 3,306.58 | 1,653.79 | **D** | **519.33** | 260.17 | 502.30 | 251.65 | 501.32 | 251.16 | **3** |
| **29** | 3,437.67 | 1,719.34 | 3,420.65 | 1,710.83 | 3,419.66 | 1,710.34 | **L** | **404.30** | 202.65 | 387.27 | 194.14 |  |  | **2** |
| **30** |  |  |  |  |  |  | **K** | **291.21** | 146.11 | 274.19 | 137.60 |  |  | **1** |

Query 2977 Hit 1

MS/MS Fragmentation of **IPNFWVTTFVNHPQVSALLGEEDEEALHYLTR**
Found in **sp|Q01105|SET_HUMAN**, Protein SET OS=Homo sapiens GN=SET PE=1 SV=3
Match to Query 2977: 3868.96from(968.2472,4+)
Title: 1098: Scan 2819 (rt=71.505, f=2, i=420) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 3868.96
**Variable modifications:**
**Ions Score:** 107.9 **Expect:** 0.000

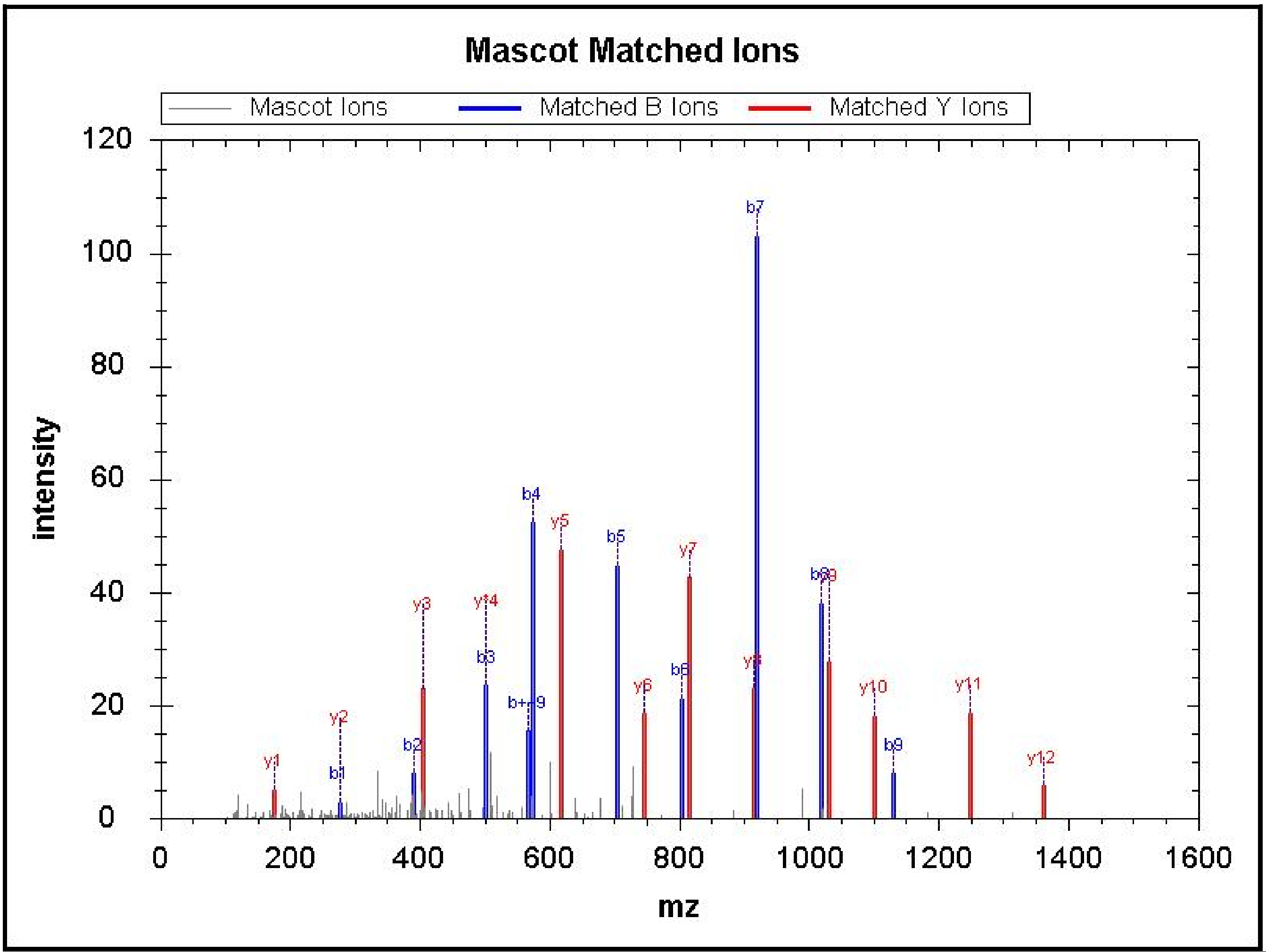


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 |  |  |  |  | I |  |  |  |  |  |  | 32 |
| 2 | 355.25 | 178.13 |  |  |  |  | P | 3,612.78 | 1,806.89 | 3,595.75 | 1,798.38 | 3,594.76 | 1,797.89 | 31 |
| 3 | 469.29 | 235.15 | 452.26 | 226.63 |  |  | N | 3,515.72 | 1,758.36 | 3,498.70 | 1,749.85 | 3,497.71 | 1,749.36 | 30 |
| 4 | 616.36 | 308.68 | 599.33 | 300.17 |  |  | F | 3,401.68 | 1,701.34 | 3,384.65 | 1,692.83 | 3,383.67 | 1,692.34 | 29 |
| 5 | 802.44 | 401.72 | 785.41 | 393.21 |  |  | W | 3,254.61 | 1,627.81 | 3,237.58 | 1,619.30 | 3,236.60 | 1,618.80 | 28 |
| 6 | 901.51 | 451.26 | 884.48 | 442.74 |  |  | V | 3,068.53 | 1,534.77 | 3,051.51 | 1,526.26 | 3,050.52 | 1,525.76 | 27 |
| 7 | 1,002.55 | 501.78 | 985.53 | 493.27 | 984.54 | 492.77 | T | 2,969.46 | 1,485.24 | 2,952.44 | 1,476.72 | 2,951.45 | 1,476.23 | 26 |
| 8 | 1,103.60 | 552.30 | 1,086.57 | 543.79 | 1,085.59 | 543.30 | T | 2,868.42 | 1,434.71 | 2,851.39 | 1,426.20 | 2,850.41 | 1,425.71 | 25 |
| 9 | 1,250.67 | 625.84 | 1,233.64 | 617.33 | 1,232.66 | 616.83 | F | 2,767.37 | 1,384.19 | 2,750.34 | 1,375.67 | 2,749.36 | 1,375.18 | 24 |
| 10 | 1,349.74 | 675.37 | 1,332.71 | 666.86 | 1,331.73 | 666.37 | V | 2,620.30 | 1,310.65 | 2,603.27 | 1,302.14 | 2,602.29 | 1,301.65 | 23 |
| 11 | 1,463.78 | 732.39 | 1,446.75 | 723.88 | 1,445.77 | 723.39 | N | 2,521.23 | 1,261.12 | 2,504.21 | 1,252.61 | 2,503.22 | 1,252.11 | 22 |
| 12 | 1,600.84 | 800.92 | 1,583.81 | 792.41 | 1,582.83 | 791.92 | H | 2,407.19 | 1,204.10 | 2,390.16 | 1,195.58 | 2,389.18 | 1,195.09 | 21 |
| 13 | 1,697.89 | 849.45 | 1,680.87 | 840.94 | 1,679.88 | 840.44 | P | 2,270.13 | 1,135.57 | 2,253.10 | 1,127.06 | 2,252.12 | 1,126.56 | 20 |
| 14 | 1,825.95 | 913.48 | 1,808.92 | 904.97 | 1,807.94 | 904.47 | Q | 2,173.08 | 1,087.04 | 2,156.05 | 1,078.53 | 2,155.07 | 1,078.04 | 19 |
| 15 | 1,925.02 | 963.01 | 1,907.99 | 954.50 | 1,907.01 | 954.01 | V | 2,045.02 | 1,023.01 | 2,027.99 | 1,014.50 | 2,027.01 | 1,014.01 | 18 |
| 16 | 2,012.05 | 1,006.53 | 1,995.02 | 998.02 | 1,994.04 | 997.52 | S | 1,945.95 | 973.48 | 1,928.92 | 964.97 | 1,927.94 | 964.47 | 17 |
| 17 | 2,083.09 | 1,042.05 | 2,066.06 | 1,033.53 | 2,065.08 | 1,033.04 | A | 1,858.92 | 929.96 | 1,841.89 | 921.45 | 1,840.91 | 920.96 | 16 |
| 18 | 2,196.17 | 1,098.59 | 2,179.15 | 1,090.08 | 2,178.16 | 1,089.58 | L | 1,787.88 | 894.44 | 1,770.85 | 885.93 | 1,769.87 | 885.44 | 15 |
| 19 | 2,309.26 | 1,155.13 | 2,292.23 | 1,146.62 | 2,291.25 | 1,146.13 | L | 1,674.80 | 837.90 | 1,657.77 | 829.39 | 1,656.79 | 828.90 | 14 |
| 20 | 2,366.28 | 1,183.64 | 2,349.25 | 1,175.13 | 2,348.27 | 1,174.64 | G | 1,561.71 | 781.36 | 1,544.69 | 772.85 | 1,543.70 | 772.35 | 13 |
| 21 | 2,495.32 | 1,248.16 | 2,478.29 | 1,239.65 | 2,477.31 | 1,239.16 | E | 1,504.69 | 752.85 | 1,487.66 | 744.34 | 1,486.68 | 743.84 | 12 |
| 22 | 2,624.36 | 1,312.69 | 2,607.34 | 1,304.17 | 2,606.35 | 1,303.68 | E | 1,375.65 | 688.33 | 1,358.62 | 679.81 | 1,357.64 | 679.32 | 11 |
| 23 | 2,739.39 | 1,370.20 | 2,722.36 | 1,361.69 | 2,721.38 | 1,361.19 | D | 1,246.61 | 623.81 | 1,229.58 | 615.29 | 1,228.60 | 614.80 | 10 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 24 | 2,868.43 | **1,434.72** | 2,851.41 | 1,426.21 | 2,850.42 | 1,425.71 | E | 1,131.58 | **566.29** | 1,114.55 | 557.78 | 1,113.57 | **557.29** | 9 |
| 25 | 2,997.47 | 1,499.24 | 2,980.45 | 1,490.73 | 2,979.46 | 1,490.24 | E | **1,002.54** | **501.77** | 985.51 | 493.26 | 984.53 | **492.77** | 8 |
| 26 | 3,068.51 | **1,534.76** | 3,051.49 | 1,526.25 | 3,050.50 | 1,525.75 | A | **873.49** | **437.25** | 856.47 | 428.74 | 855.48 | 428.25 | 7 |
| 27 | 3,181.60 | 1,591.30 | 3,164.57 | 1,582.79 | 3,163.59 | 1,582.30 | L | **802.46** | **401.73** | 785.43 | 393.22 | 784.45 | 392.73 | 6 |
| 28 | 3,318.65 | 1,659.83 | 3,301.63 | 1,651.32 | 3,300.64 | 1,650.83 | H | **689.37** | **345.19** | 672.35 | 336.68 | 671.36 | 336.18 | 5 |
| 29 | 3,481.72 | 1,741.36 | 3,464.69 | 1,732.85 | 3,463.71 | 1,732.36 | Y | **552.31** | 276.66 | 535.29 | 268.15 | **534.30** | 267.66 | 4 |
| 30 | 3,594.80 | 1,797.90 | 3,577.78 | 1,789.39 | 3,576.79 | 1,788.90 | L | **389.25** | 195.13 | 372.22 | 186.62 | 371.24 | 186.12 | 3 |
| 31 | 3,695.85 | 1,848.43 | 3,678.82 | 1,839.92 | 3,677.84 | 1,839.42 | T | **276.17** | 138.59 | 259.14 | 130.07 | **258.16** | 129.58 | 2 |
| 32 | | | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 2511 Hit 1

MS/MS Fragmentation of **MLIAMVDVIFADVAQPDQTR**
Found in **sp|P22087|FBRL_HUMAN**, rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2
Match to Query 2511: 2376.245from(793.0888,3+)
Title: 1399: Scan 3478 (rt=86.8031, f=2, i=536) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2376.245
**Variable modifications:**
**Ions Score:** 103.99 **Expect:** 0.000

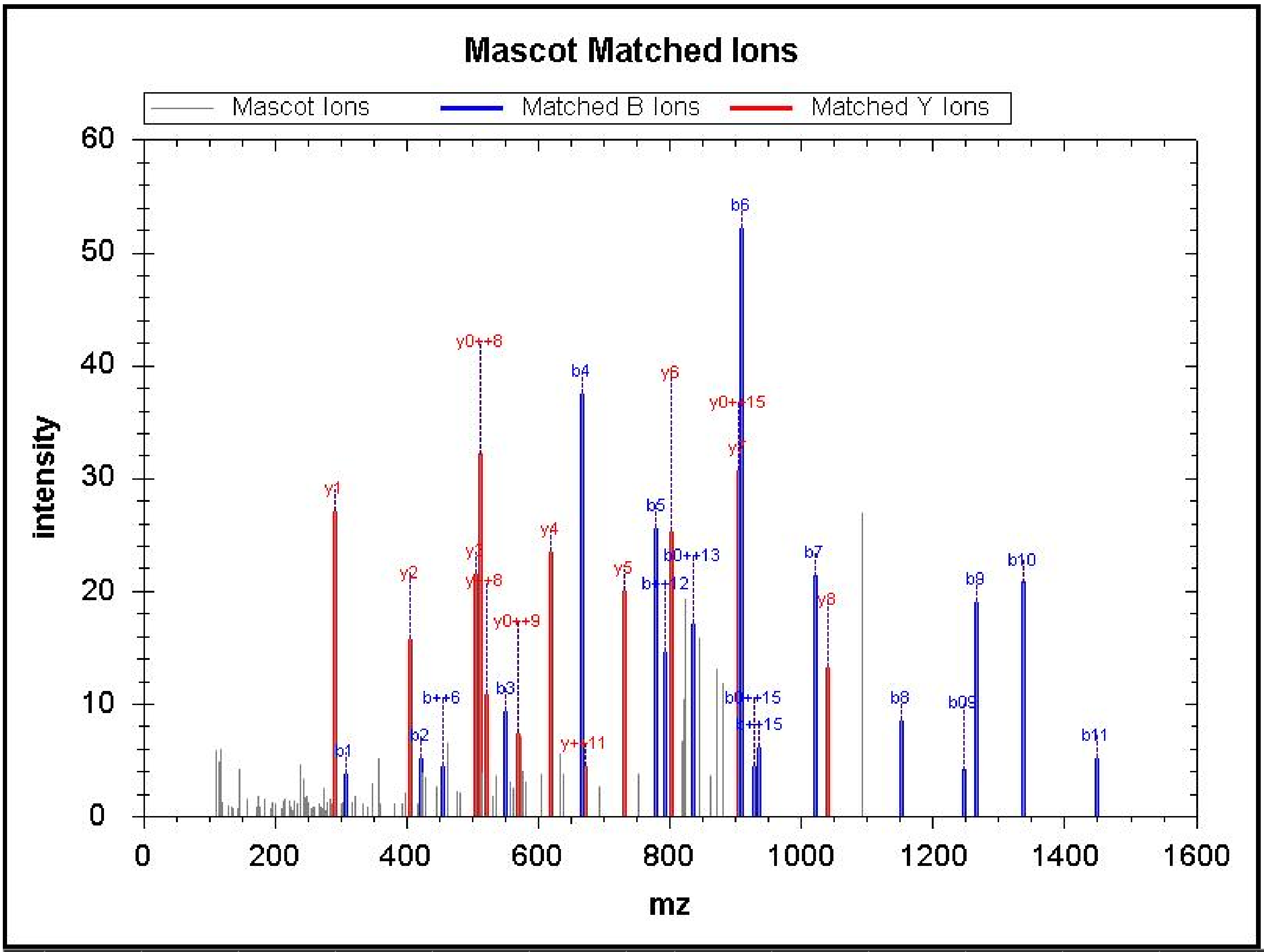


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **276.15** | 138.58 | | | | | M | | | | | | | 20 |
| 2 | **389.23** | 195.12 | | | | | L | 2,102.10 | 1,051.55 | 2,085.07 | 1,043.04 | 2,084.08 | 1,042.55 | 19 |
| 3 | **502.32** | 251.66 | | | | | I | 1,989.01 | 995.01 | 1,971.98 | 986.50 | 1,971.00 | 986.00 | 18 |
| 4 | **573.36** | 287.18 | | | | | A | 1,875.93 | 938.47 | 1,858.90 | 929.95 | 1,857.92 | 929.46 | 17 |
| 5 | **704.40** | 352.70 | | | | | M | 1,804.89 | 902.95 | 1,787.86 | 894.44 | 1,786.88 | 893.94 | 16 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **6** | **803.46** | 402.24 | | | | | **V** | 1,673.85 | 837.43 | 1,656.82 | 828.92 | 1,655.84 | 828.42 | **15** |
| **7** | **918.49** | 459.75 | | | 900.48 | 450.74 | **D** | 1,574.78 | 787.89 | 1,557.75 | 779.38 | 1,556.77 | 778.89 | **14** |
| **8** | **1,017.56** | 509.28 | | | 999.55 | 500.28 | **V** | 1,459.75 | 730.38 | 1,442.73 | 721.87 | 1,441.74 | 721.38 | **13** |
| **9** | **1,130.64** | **565.83** | | | 1,112.63 | 556.82 | **I** | **1,360.69** | 680.85 | 1,343.66 | 672.33 | 1,342.68 | 671.84 | **12** |
| **10** | 1,277.71 | 639.36 | | | 1,259.70 | 630.35 | **F** | **1,247.60** | 624.30 | 1,230.58 | 615.79 | 1,229.59 | 615.30 | **11** |
| **11** | 1,348.75 | 674.88 | | | 1,330.74 | 665.87 | **A** | **1,100.53** | 550.77 | 1,083.51 | 542.26 | 1,082.52 | 541.76 | **10** |
| **12** | 1,463.78 | 732.39 | | | 1,445.77 | 723.39 | **D** | **1,029.50** | 515.25 | 1,012.47 | 506.74 | 1,011.49 | 506.25 | **9** |
| **13** | 1,562.84 | 781.93 | | | 1,544.83 | 772.92 | **V** | **914.47** | 457.74 | 897.44 | 449.22 | 896.46 | 448.73 | **8** |
| **14** | 1,633.88 | 817.44 | | | 1,615.87 | 808.44 | **A** | **815.40** | 408.20 | 798.37 | 399.69 | 797.39 | 399.20 | **7** |
| **15** | 1,761.94 | 881.47 | 1,744.91 | 872.96 | 1,743.93 | 872.47 | **Q** | **744.36** | 372.69 | 727.34 | 364.17 | 726.35 | 363.68 | **6** |
| **16** | 1,858.99 | 930.00 | 1,841.97 | 921.49 | 1,840.98 | 920.99 | **P** | **616.30** | 308.66 | 599.28 | 300.14 | 598.29 | 299.65 | **5** |
| **17** | 1,974.02 | 987.51 | 1,956.99 | 979.00 | 1,956.01 | 978.51 | **D** | 519.25 | 260.13 | **502.23** | 251.62 | 501.24 | 251.12 | **4** |
| **18** | 2,102.08 | 1,051.54 | 2,085.05 | 1,043.03 | 2,084.07 | 1,042.54 | **Q** | **404.23** | 202.62 | 387.20 | 194.10 | 386.21 | 193.61 | **3** |
| **19** | 2,203.13 | 1,102.07 | 2,186.10 | 1,093.55 | 2,185.12 | 1,093.06 | **T** | **276.17** | 138.59 | 259.14 | 130.07 | 258.16 | 129.58 | **2** |
| **20** | | | | | | | **R** | **175.12** | 88.06 | 158.09 | 79.55 | | | **1** |

Query 2602 Hit 1

MS/MS Fragmentation of **YNEDLELEDAIHTAILTLK**
Found in **sp|P25787|PSA2_HUMAN**, Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2
Match to Query 2602: 2488.347from(830.4564,3+)
Title: 1116: Scan 2711 (rt=69.5208, f=3, i=386) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2488.347
**Variable modifications:**
**K19** :iTRAQ4plex (K)
**Ions Score:** 97.39 **Expect:** 0.000

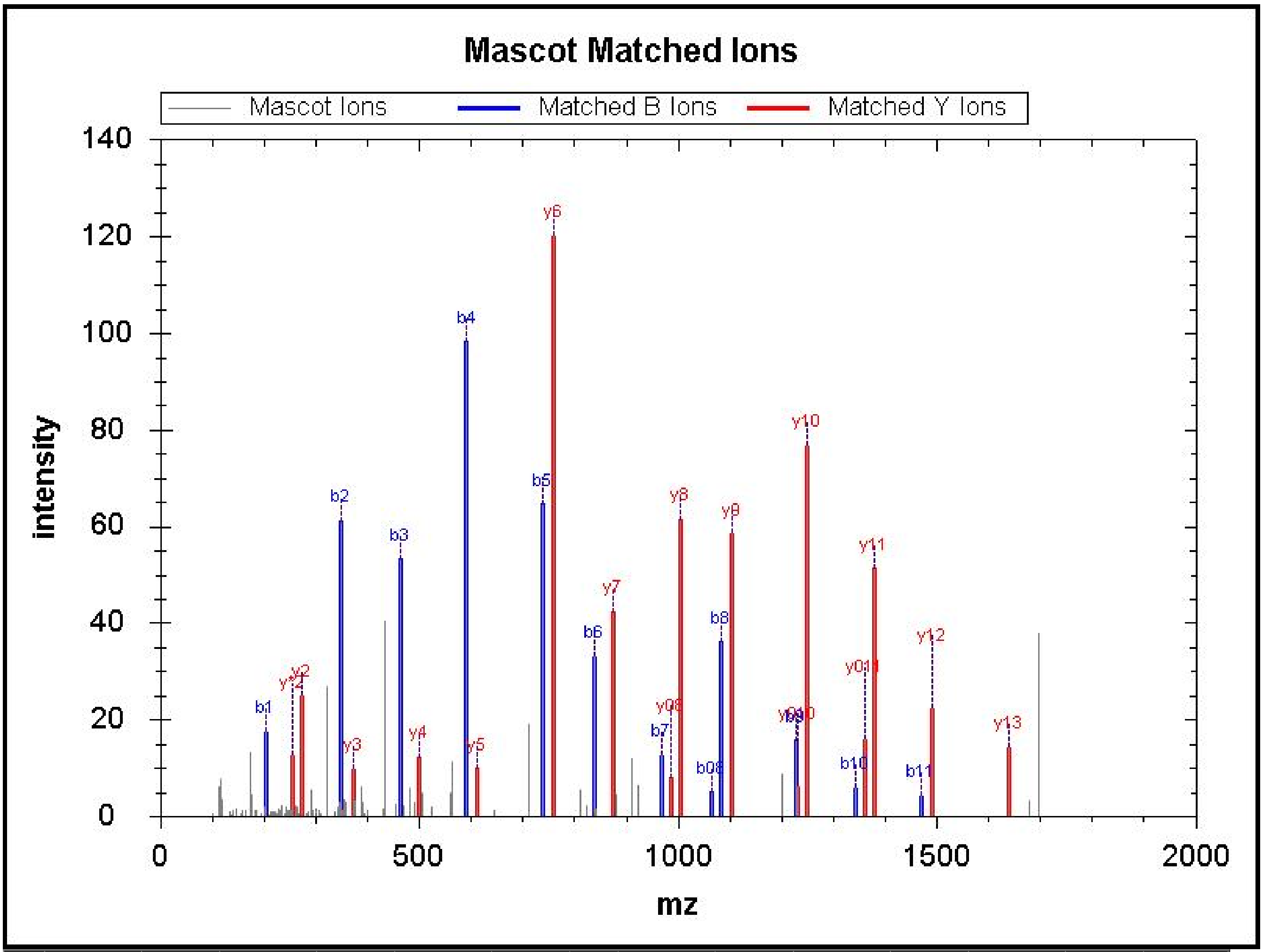


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **308.17** | 154.59 | | | | | **Y** | | | | | | | 19 |
| 2 | **422.22** | 211.61 | 405.19 | 203.10 | | | **N** | 2,182.17 | 1,091.59 | 2,165.15 | 1,083.08 | 2,164.16 | 1,082.58 | 18 |
| 3 | **551.26** | 276.13 | 534.23 | 267.62 | 533.25 | 267.13 | **E** | 2,068.13 | 1,034.57 | 2,051.10 | 1,026.06 | 2,050.12 | 1,025.56 | 17 |
| 4 | **666.29** | 333.65 | 649.26 | 325.13 | 648.27 | 324.64 | **D** | 1,939.09 | 970.05 | 1,922.06 | 961.53 | 1,921.08 | 961.04 | 16 |
| 5 | **779.37** | 390.19 | 762.34 | 381.67 | 761.36 | 381.18 | **L** | 1,824.06 | 912.53 | 1,807.03 | 904.02 | 1,806.05 | **903.53** | 15 |
| 6 | **908.41** | **454.71** | 891.39 | 446.20 | 890.40 | 445.70 | **E** | 1,710.98 | 855.99 | 1,693.95 | 847.48 | 1,692.97 | 846.99 | 14 |
| 7 | **1,021.50** | 511.25 | 1,004.47 | 502.74 | 1,003.49 | 502.25 | **L** | 1,581.93 | 791.47 | 1,564.91 | 782.96 | 1,563.92 | 782.46 | 13 |
| 8 | **1,150.54** | 575.77 | 1,133.51 | 567.26 | 1,132.53 | 566.77 | **E** | 1,468.85 | 734.93 | 1,451.82 | 726.41 | 1,450.84 | 725.92 | 12 |
| 9 | **1,265.57** | 633.29 | 1,248.54 | 624.77 | **1,247.55** | 624.28 | **D** | 1,339.81 | **670.41** | 1,322.78 | 661.89 | 1,321.80 | 661.40 | 11 |
| 10 | **1,336.60** | 668.80 | 1,319.58 | 660.29 | 1,318.59 | 659.80 | **A** | 1,224.78 | 612.89 | 1,207.75 | 604.38 | 1,206.77 | 603.89 | 10 |
| 11 | **1,449.69** | 725.35 | 1,432.66 | 716.83 | 1,431.68 | 716.34 | **I** | 1,153.74 | 577.37 | 1,136.72 | 568.86 | 1,135.73 | **568.37** | 9 |
| 12 | 1,586.75 | **793.88** | 1,569.72 | 785.36 | 1,568.73 | 784.87 | **H** | **1,040.66** | **520.83** | 1,023.63 | 512.32 | 1,022.65 | **511.83** | 8 |
| 13 | 1,687.79 | 844.40 | 1,670.77 | 835.89 | 1,669.78 | **835.40** | **T** | **903.60** | 452.30 | 886.57 | 443.79 | 885.59 | 443.30 | 7 |
| 14 | 1,758.83 | 879.92 | 1,741.80 | 871.41 | 1,740.82 | 870.91 | **A** | **802.55** | 401.78 | 785.53 | 393.27 | 784.54 | 392.77 | 6 |
| 15 | 1,871.91 | **936.46** | 1,854.89 | 927.95 | 1,853.90 | **927.46** | **I** | **731.51** | 366.26 | 714.49 | 357.75 | 713.50 | 357.26 | 5 |
| 16 | 1,985.00 | 993.00 | 1,967.97 | 984.49 | 1,966.99 | 984.00 | **L** | **618.43** | 309.72 | 601.40 | 301.21 | 600.42 | 300.71 | 4 |
| 17 | 2,086.05 | 1,043.53 | 2,069.02 | 1,035.01 | 2,068.04 | 1,034.52 | **T** | **505.35** | 253.18 | 488.32 | 244.66 | 487.34 | 244.17 | 3 |
| 18 | 2,199.13 | 1,100.07 | 2,182.10 | 1,091.56 | 2,181.12 | 1,091.06 | **L** | **404.30** | 202.65 | 387.27 | 194.14 | | | 2 |
| 19 | | | | | | | **K** | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 1896 Hit 1

MS/MS Fragmentation of **GFLEFVEDFIQVPR**
Found in **sp|P51114|FXR1_HUMAN**, Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=3

Match to Query 1896: 1838.974from(920.4941,2+)
Title: 1297: Sum of 2 scans in range 3293 (rt=82.1891, f=4, i=920) to 3294 (rt=82.2145, f=4, i=921) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1838.974
**Variable modifications:**
**Ions Score:** 97.35 **Expect:** 0.000

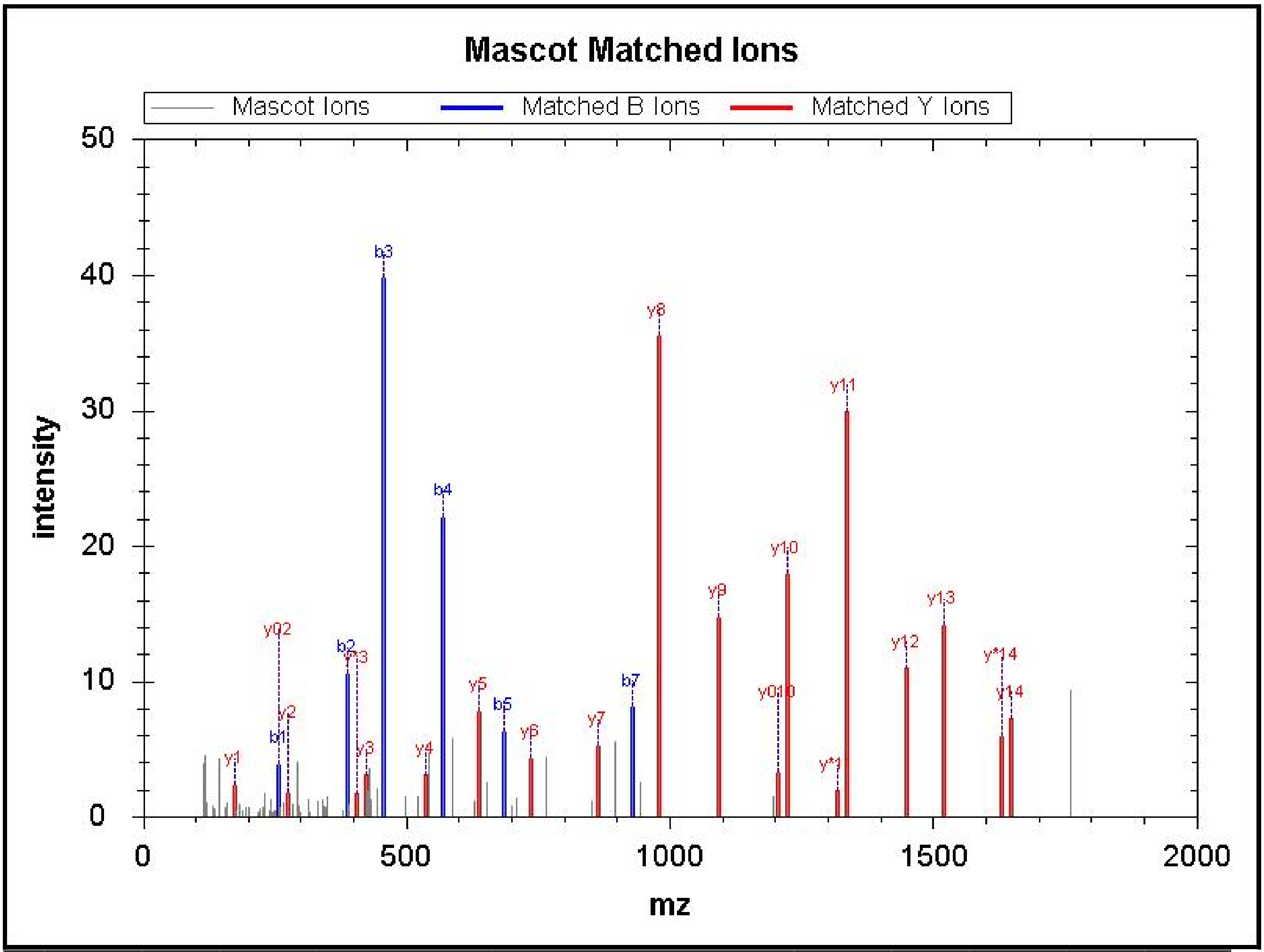


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **202.13** | 101.57 | | | | | G | | | | | | | 14 |
| 2 | **349.20** | 175.10 | | | | | F | **1,638.85** | 819.93 | 1,621.83 | 811.42 | 1,620.84 | 810.92 | 13 |
| 3 | **462.28** | 231.65 | | | | | L | **1,491.78** | 746.40 | 1,474.76 | 737.88 | 1,473.77 | 737.39 | 12 |
| 4 | **591.33** | 296.17 | | | 573.32 | 287.16 | E | **1,378.70** | 689.85 | 1,361.67 | 681.34 | **1,360.69** | 680.85 | 11 |
| 5 | **738.39** | 369.70 | | | 720.38 | 360.70 | F | **1,249.66** | 625.33 | 1,232.63 | 616.82 | **1,231.65** | 616.33 | 10 |
| 6 | **837.46** | 419.23 | | | 819.45 | 410.23 | V | **1,102.59** | 551.80 | 1,085.56 | 543.28 | 1,084.58 | 542.79 | 9 |
| 7 | **966.51** | 483.76 | | | 948.49 | 474.75 | E | **1,003.52** | 502.26 | 986.49 | 493.75 | **985.51** | 493.26 | 8 |
| 8 | **1,081.53** | 541.27 | | | **1,063.52** | 532.26 | D | **874.48** | 437.74 | 857.45 | 429.23 | 856.47 | 428.74 | 7 |
| 9 | **1,228.60** | 614.80 | | | 1,210.59 | 605.80 | F | **759.45** | 380.23 | 742.42 | 371.72 | | | 6 |
| 10 | **1,341.68** | 671.35 | | | 1,323.67 | 662.34 | I | **612.38** | 306.70 | 595.36 | 298.18 | | | 5 |
| 11 | **1,469.74** | 735.38 | 1,452.72 | 726.86 | 1,451.73 | 726.37 | Q | **499.30** | 250.15 | 482.27 | 241.64 | | | 4 |
| 12 | 1,568.81 | 784.91 | 1,551.79 | 776.40 | 1,550.80 | 775.90 | V | **371.24** | 186.12 | 354.21 | 177.61 | | | 3 |
| 13 | 1,665.86 | 833.44 | 1,648.84 | 824.92 | 1,647.85 | 824.43 | P | **272.17** | 136.59 | **255.15** | 128.08 | | | 2 |
| 14 | | | | | | | R | 175.12 | 88.06 | 158.09 | 79.55 | | | 1 |

Query 1984 Hit 1

MS/MS Fragmentation of **LQAILEDIQVTLFTR**
Found in **sp|P07814|SYEP_HUMAN**, Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5

Match to Query 1984: 1903.095from(952.5549,2+)
Title: 1312: Scan 3335 (rt=83.1339, f=3, i=476) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1903.095
**Variable modifications:**
**Ions Score:** 92.2 **Expect:** 0.000

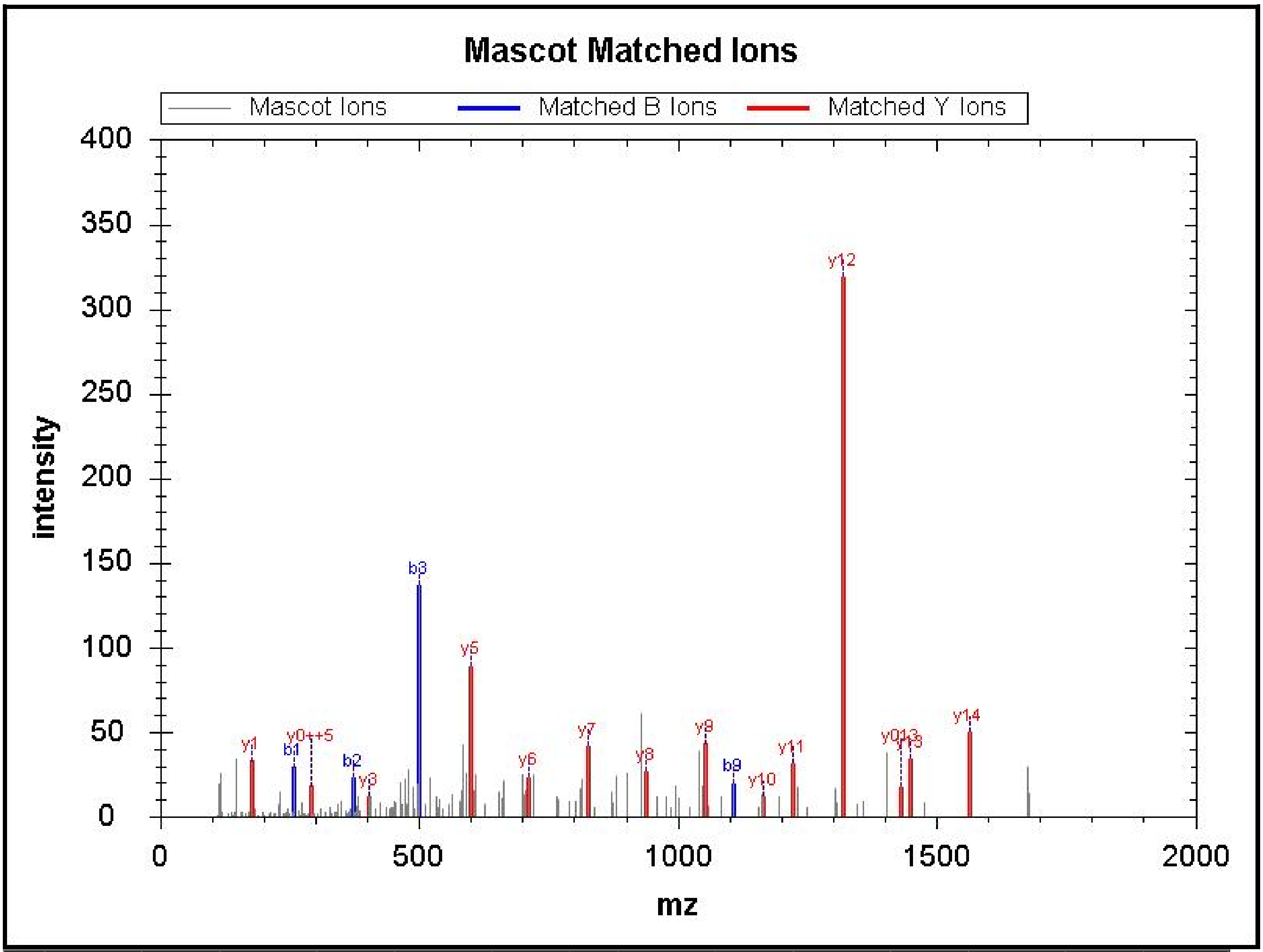


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | | | | | L | | | | | | | 15 |
| 2 | 386.25 | 193.63 | 369.23 | 185.12 | | | Q | 1,646.91 | 823.96 | 1,629.88 | 815.45 | 1,628.90 | 814.95 | 14 |
| 3 | 457.29 | 229.15 | 440.26 | 220.63 | | | A | 1,518.85 | 759.93 | 1,501.83 | 751.42 | 1,500.84 | 750.92 | 13 |
| 4 | 570.37 | 285.69 | 553.35 | 277.18 | | | I | 1,447.82 | 724.41 | 1,430.79 | 715.90 | 1,429.80 | 715.41 | 12 |
| 5 | 683.46 | 342.23 | 666.43 | 333.72 | | | L | 1,334.73 | 667.87 | 1,317.70 | 659.36 | 1,316.72 | 658.86 | 11 |
| 6 | 812.50 | 406.75 | 795.47 | 398.24 | 794.49 | 397.75 | E | 1,221.65 | 611.33 | 1,204.62 | 602.81 | 1,203.64 | 602.32 | 10 |
| 7 | 927.53 | 464.27 | 910.50 | 455.75 | 909.52 | 455.26 | D | 1,092.60 | 546.81 | 1,075.58 | 538.29 | 1,074.59 | 537.80 | 9 |
| 8 | 1,040.61 | 520.81 | 1,023.58 | 512.30 | 1,022.60 | 511.80 | I | 977.58 | 489.29 | 960.55 | 480.78 | 959.57 | 480.29 | 8 |
| 9 | 1,168.67 | 584.84 | 1,151.64 | 576.33 | 1,150.66 | 575.83 | Q | 864.49 | 432.75 | 847.47 | 424.24 | 846.48 | 423.75 | 7 |
| 10 | 1,267.74 | 634.37 | 1,250.71 | 625.86 | 1,249.73 | 625.37 | V | 736.44 | 368.72 | 719.41 | 360.21 | 718.42 | 359.72 | 6 |
| 11 | 1,368.79 | 684.90 | 1,351.76 | 676.38 | 1,350.77 | 675.89 | T | 637.37 | 319.19 | 620.34 | 310.67 | 619.36 | 310.18 | 5 |
| 12 | 1,481.87 | 741.44 | 1,464.84 | 732.93 | 1,463.86 | 732.43 | L | 536.32 | 268.66 | 519.29 | 260.15 | 518.31 | 259.66 | 4 |
| 13 | 1,628.94 | 814.97 | 1,611.91 | 806.46 | 1,610.93 | 805.97 | F | 423.24 | 212.12 | 406.21 | 203.61 | 405.22 | 203.12 | 3 |
| 14 | 1,729.99 | 865.50 | 1,712.96 | 856.98 | 1,711.98 | 856.49 | T | 276.17 | 138.59 | 259.14 | 130.07 | 258.16 | 129.58 | 2 |
| 15 | | | | | | | R | 175.12 | 88.06 | 158.09 | 79.55 | | | 1 |

Query 1877 Hit 1

MS/MS Fragmentation of **ILEPGLNILIPVLDR**

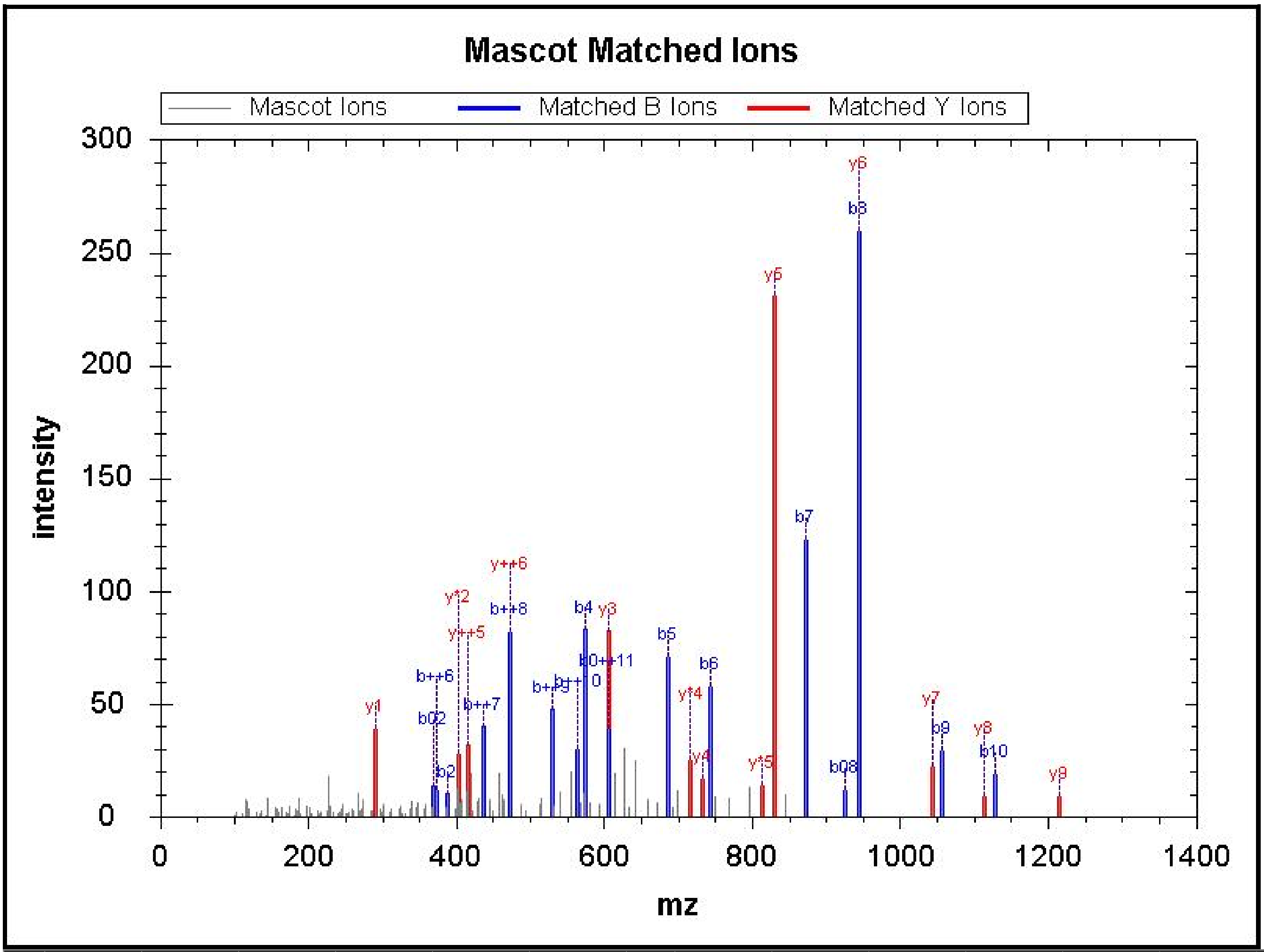
Found in **sp|Q9UJZ1|STML2_HUMAN**, Stomatin-like protein 2 OS=Homo sapiens GN=STOML2 PE=1 SV=1
Match to Query 1877: 1818.116from(910.0654,2+)
Title: 1149: Sum of 2 scans in range 2792 (rt=71.3506, f=4, i=792) to 2793 (rt=71.376, f=4, i=793)
[D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1818.116
**Variable modifications:**
**Ions Score:** 88.19 **Expect:** 0.000



| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **258.19** | 129.60 | | | | | I | | | | | | | 15 |
| 2 | **371.28** | 186.14 | | | | | L | **1,561.93** | 781.47 | 1,544.90 | 772.96 | 1,543.92 | 772.46 | 14 |
| 3 | **500.32** | 250.66 | | | 482.31 | 241.66 | E | **1,448.85** | 724.93 | 1,431.82 | 716.41 | **1,430.84** | 715.92 | 13 |
| 4 | 597.37 | 299.19 | | | 579.36 | 290.18 | P | **1,319.80** | 660.41 | 1,302.78 | 651.89 | 1,301.79 | 651.40 | 12 |
| 5 | 654.39 | 327.70 | | | 636.38 | 318.70 | G | **1,222.75** | 611.88 | 1,205.73 | 603.37 | 1,204.74 | 602.87 | 11 |
| 6 | 767.48 | 384.24 | | | 749.47 | 375.24 | L | **1,165.73** | 583.37 | 1,148.70 | 574.86 | 1,147.72 | 574.36 | 10 |
| 7 | 881.52 | 441.26 | 864.49 | 432.75 | 863.51 | 432.26 | N | **1,052.65** | 526.83 | 1,035.62 | 518.31 | 1,034.64 | 517.82 | 9 |
| 8 | 994.61 | 497.81 | 977.58 | 489.29 | 976.59 | 488.80 | I | **938.60** | 469.81 | 921.58 | 461.29 | 920.59 | 460.80 | 8 |
| 9 | **1,107.69** | 554.35 | 1,090.66 | 545.84 | 1,089.68 | 545.34 | L | **825.52** | 413.26 | 808.49 | 404.75 | 807.51 | 404.26 | 7 |
| 10 | 1,220.77 | 610.89 | 1,203.75 | 602.38 | 1,202.76 | 601.89 | I | **712.44** | 356.72 | 695.41 | 348.21 | 694.42 | 347.72 | 6 |
| 11 | 1,317.83 | 659.42 | 1,300.80 | 650.90 | 1,299.82 | 650.41 | P | **599.35** | 300.18 | 582.32 | 291.67 | 581.34 | **291.17** | 5 |
| 12 | 1,416.89 | 708.95 | 1,399.87 | 700.44 | 1,398.88 | 699.95 | V | 502.30 | 251.65 | 485.27 | 243.14 | 484.29 | 242.65 | 4 |
| 13 | 1,529.98 | 765.49 | 1,512.95 | 756.98 | 1,511.97 | 756.49 | L | **403.23** | 202.12 | 386.20 | 193.61 | 385.22 | 193.11 | 3 |
| 14 | 1,645.01 | 823.01 | 1,627.98 | 814.49 | 1,627.00 | 814.00 | D | 290.15 | 145.58 | 273.12 | 137.06 | 272.14 | 136.57 | 2 |
| 15 | | | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 2488 Hit 1

MS/MS Fragmentation of **EIADLGEALATAVIPQWQK**
Found in **sp|P49588|SYAC_HUMAN**, Alanine--tRNA ligase
Match to Query 2488: 2340.3from(781.1071,3+)
Title: 1071: Sum of 2 scans in range 2753 (rt=70.023, f=4, i=746) to 2754 (rt=70.0484, f=4, i=747) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2340.3
**Variable modifications:**
**K19** :iTRAQ4plex (K)
**Ions Score:** 87.59 **Expect:** 0.000

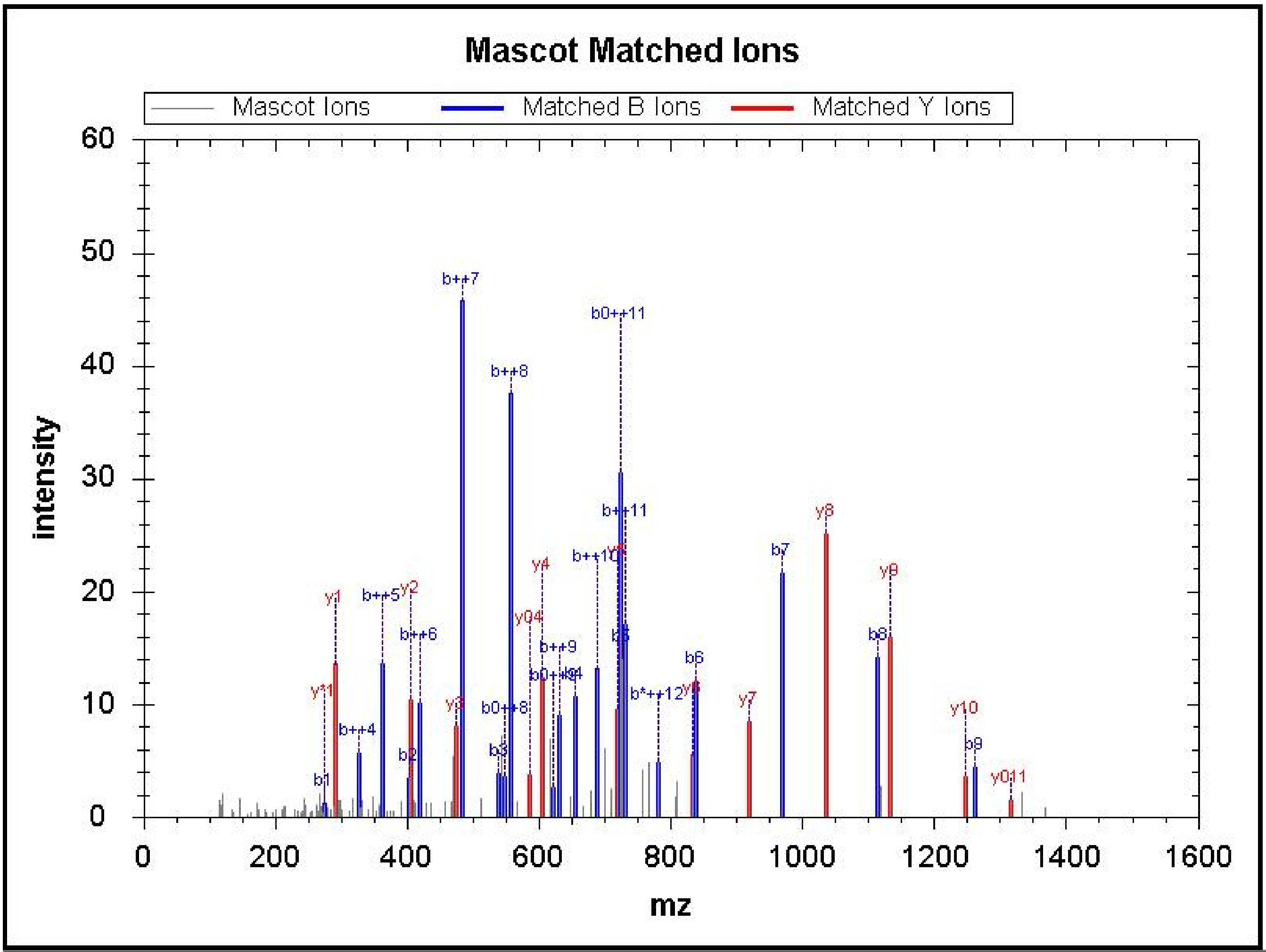


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 274.15 | 137.58 | | | 256.14 | 128.57 | E | | | | | | | 19 |
| 2 | **387.24** | 194.12 | | | **369.23** | 185.12 | I | 2,068.16 | 1,034.58 | 2,051.13 | 1,026.07 | 2,050.15 | 1,025.58 | 18 |
| 3 | 458.27 | 229.64 | | | 440.26 | 220.63 | A | 1,955.07 | 978.04 | 1,938.05 | 969.53 | 1,937.06 | 969.03 | 17 |
| 4 | **573.30** | 287.15 | | | 555.29 | 278.15 | D | 1,884.03 | 942.52 | 1,867.01 | 934.01 | 1,866.02 | 933.52 | 16 |
| 5 | **686.38** | 343.70 | | | 668.37 | 334.69 | L | 1,769.01 | 885.01 | 1,751.98 | 876.49 | 1,751.00 | 876.00 | 15 |
| 6 | **743.41** | **372.21** | | | 725.39 | 363.20 | G | 1,655.92 | 828.47 | 1,638.90 | 819.95 | 1,637.91 | 819.46 | 14 |
| 7 | **872.45** | **436.73** | | | 854.44 | 427.72 | E | 1,598.90 | 799.95 | 1,581.88 | 791.44 | 1,580.89 | 790.95 | 13 |
| 8 | **943.49** | **472.25** | | | **925.47** | 463.24 | A | 1,469.86 | 735.43 | 1,452.83 | 726.92 | 1,451.85 | 726.43 | 12 |
| 9 | **1,056.57** | **528.79** | | | 1,038.56 | 519.78 | L | 1,398.82 | 699.91 | 1,381.80 | 691.40 | 1,380.81 | 690.91 | 11 |
| 10 | **1,127.61** | **564.31** | | | 1,109.60 | 555.30 | A | 1,285.74 | 643.37 | 1,268.71 | 634.86 | 1,267.73 | 634.37 | 10 |
| 11 | 1,228.65 | 614.83 | | | 1,210.64 | **605.83** | T | **1,214.70** | 607.85 | 1,197.67 | 599.34 | 1,196.69 | 598.85 | 9 |
| 12 | 1,299.69 | 650.35 | | | 1,281.68 | 641.34 | A | **1,113.65** | 557.33 | 1,096.63 | 548.82 | | | 8 |
| 13 | 1,398.76 | 699.88 | | | 1,380.75 | 690.88 | V | **1,042.62** | 521.81 | 1,025.59 | 513.30 | | | 7 |
| 14 | 1,511.84 | 756.43 | | | 1,493.83 | 747.42 | I | **943.55** | **472.28** | 926.52 | 463.76 | | | 6 |
| 15 | 1,608.90 | 804.95 | | | 1,590.89 | 795.95 | P | **830.46** | **415.74** | **813.44** | 407.22 | | | 5 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 16 | 1,736.96 | 868.98 | 1,719.93 | 860.47 | 1,718.94 | 859.98 | Q | 733.41 | 367.21 | 716.38 | 358.70 | | | 4 |
| 17 | 1,923.03 | 962.02 | 1,906.01 | 953.51 | 1,905.02 | 953.02 | W | 605.35 | 303.18 | 588.33 | 294.67 | | | 3 |
| 18 | 2,051.09 | 1,026.05 | 2,034.07 | 1,017.54 | 2,033.08 | 1,017.04 | Q | 419.27 | 210.14 | 402.25 | 201.63 | | | 2 |
| 19 | | | | | | | K | 291.21 | 146.11 | 274.19 | 137.60 | | | 1 |

Query 2722 Hit 1

MS/MS Fragmentation of **EQHDALEFFNSLVDSLDEALK**
Found in **sp|Q93008|USP9X_HUMAN**, Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3
Match to Query 2722: 2707.373from(903.4651,3+)
Title: 1306: Scan 3323 (rt=82.8623, f=3, i=474) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2707.373
**Variable modifications:**
**K21** :iTRAQ4plex (K)
**Ions Score:** 85.86 **Expect:** 0.000

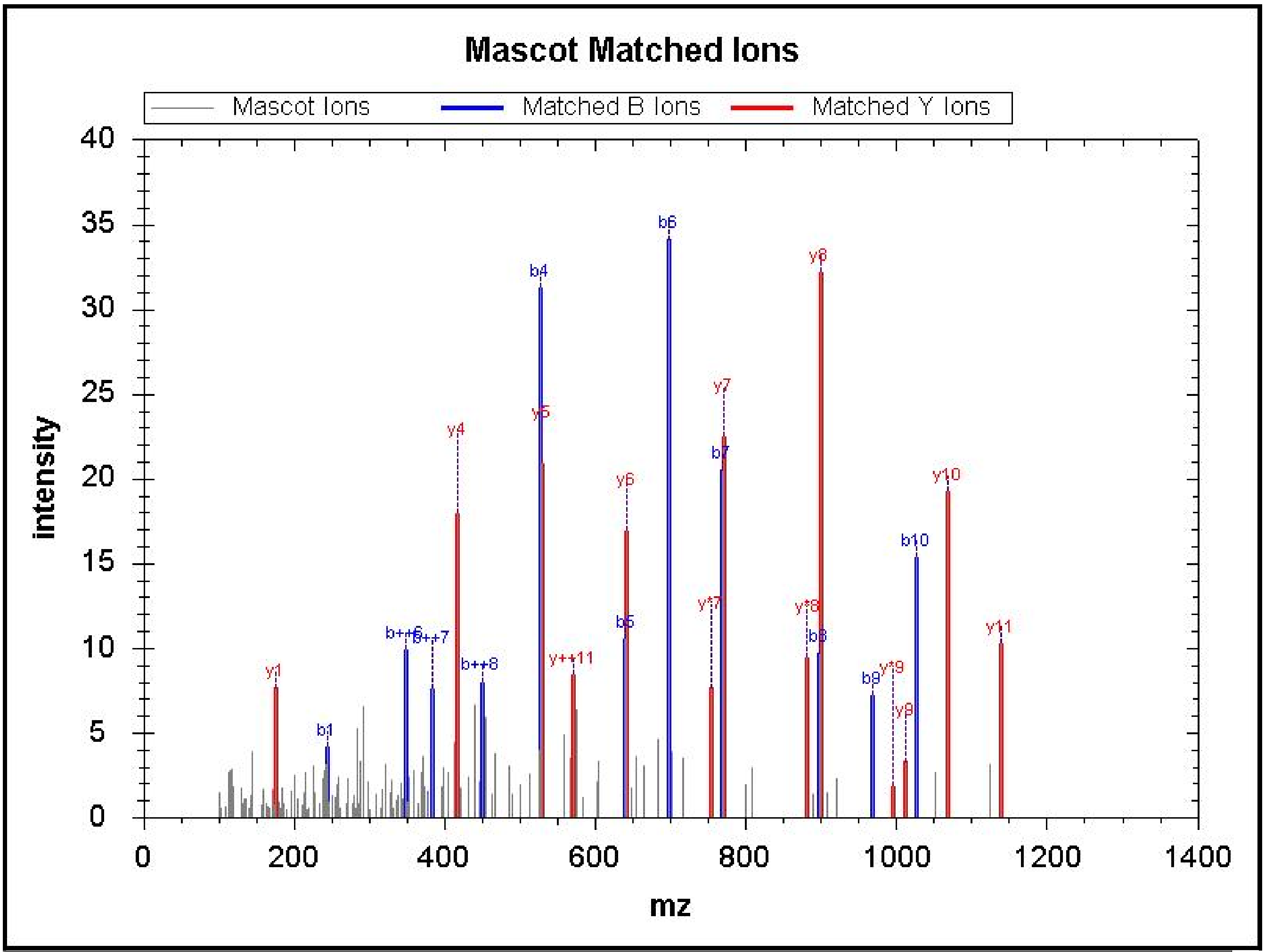


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 274.15 | 137.58 | | | 256.14 | 128.57 | E | | | | | | | 21 |
| 2 | 402.21 | 201.61 | 385.18 | 193.10 | 384.20 | 192.60 | Q | 2,435.22 | 1,218.11 | 2,418.19 | 1,209.60 | 2,417.21 | 1,209.11 | 20 |
| 3 | 539.27 | 270.14 | 522.24 | 261.63 | 521.26 | 261.13 | H | 2,307.16 | 1,154.08 | 2,290.14 | 1,145.57 | 2,289.15 | 1,145.08 | 19 |
| 4 | 654.30 | 327.65 | 637.27 | 319.14 | 636.29 | 318.65 | D | 2,170.10 | 1,085.56 | 2,153.08 | 1,077.04 | 2,152.09 | 1,076.55 | 18 |
| 5 | 725.33 | 363.17 | 708.31 | 354.66 | 707.32 | 354.17 | A | 2,055.08 | 1,028.04 | 2,038.05 | 1,019.53 | 2,037.07 | 1,019.04 | 17 |
| 6 | 838.42 | 419.71 | 821.39 | 411.20 | 820.41 | 410.71 | L | 1,984.04 | 992.52 | 1,967.01 | 984.01 | 1,966.03 | 983.52 | 16 |
| 7 | 967.46 | 484.23 | 950.43 | 475.72 | 949.45 | 475.23 | E | 1,870.96 | 935.98 | 1,853.93 | 927.47 | 1,852.94 | 926.98 | 15 |
| 8 | 1,114.53 | 557.77 | 1,097.50 | 549.25 | 1,096.52 | 548.76 | F | 1,741.91 | 871.46 | 1,724.89 | 862.95 | 1,723.90 | 862.45 | 14 |
| 9 | 1,261.60 | 631.30 | 1,244.57 | 622.79 | 1,243.59 | 622.30 | F | 1,594.84 | 797.93 | 1,577.82 | 789.41 | 1,576.83 | 788.92 | 13 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 10 | 1,375.64 | **688.32** | 1,358.61 | 679.81 | 1,357.63 | 679.32 | N | 1,447.78 | 724.39 | 1,430.75 | 715.88 | 1,429.77 | 715.39 | 12 |
| 11 | 1,462.67 | **731.84** | 1,445.65 | 723.33 | 1,444.66 | **722.83** | S | 1,333.73 | 667.37 | 1,316.71 | 658.86 | **1,315.72** | 658.36 | 11 |
| 12 | 1,575.76 | 788.38 | 1,558.73 | **779.87** | 1,557.75 | 779.38 | L | **1,246.70** | 623.85 | 1,229.67 | 615.34 | 1,228.69 | 614.85 | 10 |
| 13 | 1,674.82 | 837.92 | 1,657.80 | 829.40 | 1,656.81 | 828.91 | V | **1,133.62** | 567.31 | 1,116.59 | 558.80 | 1,115.61 | 558.31 | 9 |
| 14 | 1,789.85 | 895.43 | 1,772.82 | 886.92 | 1,771.84 | 886.42 | D | **1,034.55** | 517.78 | 1,017.52 | 509.26 | 1,016.54 | 508.77 | 8 |
| 15 | 1,876.88 | 938.95 | 1,859.86 | 930.43 | 1,858.87 | 929.94 | S | **919.52** | 460.26 | 902.50 | 451.75 | 901.51 | 451.26 | 7 |
| 16 | 1,989.97 | 995.49 | 1,972.94 | 986.97 | 1,971.96 | 986.48 | L | **832.49** | 416.75 | 815.46 | 408.24 | 814.48 | 407.74 | 6 |
| 17 | 2,104.99 | 1,053.00 | 2,087.97 | 1,044.49 | 2,086.98 | 1,044.00 | D | **719.41** | 360.21 | 702.38 | 351.69 | 701.39 | 351.20 | 5 |
| 18 | 2,234.04 | 1,117.52 | 2,217.01 | 1,109.01 | 2,216.03 | 1,108.52 | E | **604.38** | 302.69 | 587.35 | 294.18 | **586.37** | 293.69 | 4 |
| 19 | 2,305.07 | 1,153.04 | 2,288.05 | 1,144.53 | 2,287.06 | 1,144.04 | A | **475.34** | 238.17 | 458.31 | 229.66 | | | 3 |
| 20 | 2,418.16 | 1,209.58 | 2,401.13 | 1,201.07 | 2,400.15 | 1,200.58 | L | **404.30** | 202.65 | 387.27 | 194.14 | | | 2 |
| 21 | | | | | | | K | **291.21** | 146.11 | **274.19** | 137.60 | | | 1 |

Query 2148 Hit 1

MS/MS Fragmentation of **VPADLGAEAGLQQLLGALR**
Found in **sp|P35270|SPRE_HUMAN**, Sepiapterin reductase OS=Homo sapiens GN=SPR PE=1 SV=1
Match to Query 2148: 2035.164from(679.3952,3+)
Title: 1073: Scan 2758 (rt=70.1334, f=3, i=383) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2035.164
**Variable modifications:**
**Ions Score:** 83.99 **Expect:** 0.000

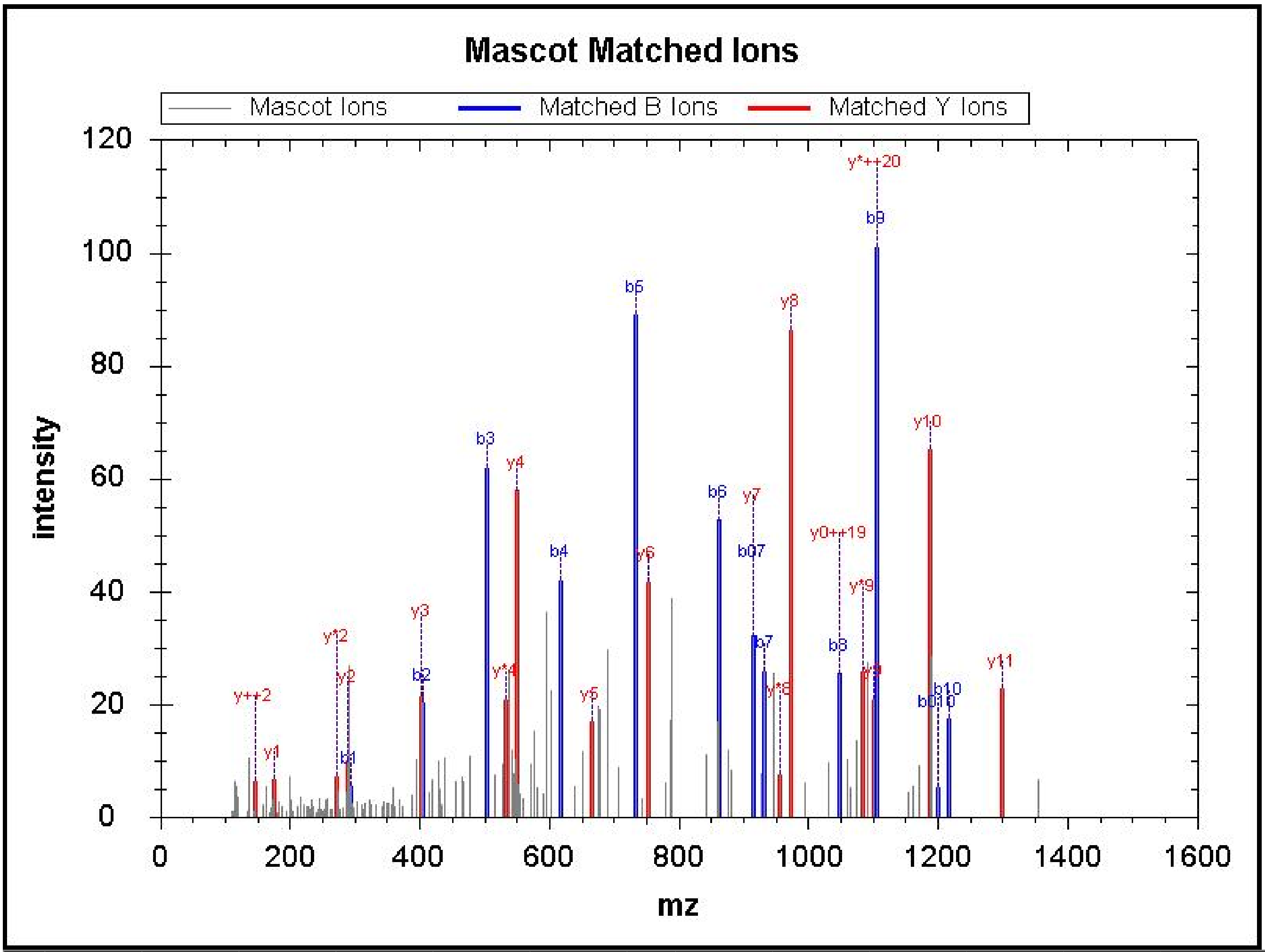


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **244.18** | 122.59 | | | | | V | | | | | | | 19 |
| 2 | 341.23 | 171.12 | | | | | P | 1,792.99 | 897.00 | 1,775.97 | 888.49 | 1,774.98 | 887.99 | 18 |
| 3 | 412.27 | 206.64 | | | | | A | 1,695.94 | 848.47 | 1,678.91 | 839.96 | 1,677.93 | 839.47 | 17 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **4** | **527.29** | 264.15 | | | 509.28 | 255.15 | **D** | 1,624.90 | 812.95 | 1,607.88 | 804.44 | 1,606.89 | 803.95 | **16** |
| **5** | **640.38** | 320.69 | | | 622.37 | 311.69 | **L** | 1,509.87 | 755.44 | 1,492.85 | 746.93 | 1,491.86 | 746.44 | **15** |
| **6** | **697.40** | **349.20** | | | 679.39 | 340.20 | **G** | 1,396.79 | 698.90 | 1,379.76 | 690.39 | 1,378.78 | 689.89 | **14** |
| **7** | **768.44** | **384.72** | | | 750.43 | 375.72 | **A** | 1,339.77 | 670.39 | 1,322.74 | 661.88 | 1,321.76 | 661.38 | **13** |
| **8** | **897.48** | **449.24** | | | 879.47 | 440.24 | **E** | 1,268.73 | 634.87 | 1,251.71 | 626.36 | 1,250.72 | 625.86 | **12** |
| **9** | **968.52** | 484.76 | | | 950.51 | 475.76 | **A** | **1,139.69** | **570.35** | 1,122.66 | 561.84 | | | **11** |
| **10** | **1,025.54** | 513.27 | | | 1,007.53 | 504.27 | **G** | **1,068.65** | 534.83 | 1,051.63 | 526.32 | | | **10** |
| **11** | 1,138.62 | 569.81 | | | 1,120.61 | 560.81 | **L** | **1,011.63** | 506.32 | **994.60** | 497.81 | | | **9** |
| **12** | 1,266.68 | 633.84 | 1,249.65 | 625.33 | 1,248.67 | 624.84 | **Q** | **898.55** | 449.78 | **881.52** | 441.26 | | | **8** |
| **13** | 1,394.74 | 697.87 | 1,377.71 | 689.36 | 1,376.73 | 688.87 | **Q** | **770.49** | 385.75 | **753.46** | 377.23 | | | **7** |
| **14** | 1,507.82 | 754.42 | 1,490.80 | 745.90 | 1,489.81 | 745.41 | **L** | **642.43** | 321.72 | 625.40 | 313.21 | | | **6** |
| **15** | 1,620.91 | 810.96 | 1,603.88 | 802.44 | 1,602.90 | 801.95 | **L** | **529.35** | 265.18 | 512.32 | 256.66 | | | **5** |
| **16** | 1,677.93 | 839.47 | 1,660.90 | 830.96 | 1,659.92 | 830.46 | **G** | **416.26** | 208.63 | 399.24 | 200.12 | | | **4** |
| **17** | 1,748.97 | 874.99 | 1,731.94 | 866.47 | 1,730.96 | 865.98 | **A** | 359.24 | 180.12 | 342.21 | 171.61 | | | **3** |
| **18** | 1,862.05 | 931.53 | 1,845.02 | 923.02 | 1,844.04 | 922.52 | **L** | 288.20 | 144.61 | 271.18 | 136.09 | | | **2** |
| **19** | | | | | | | **R** | **175.12** | 88.06 | 158.09 | 79.55 | | | **1** |

Query 2630 Hit 1

MS/MS Fragmentation of **FLVLDEADGLLSQGYSDFINR**
Found in **sp|Q92499|DDX1_HUMAN**, ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2
Match to Query 2630: 2515.292from(839.4378,3+)
Title: 1236: Sum of 2 scans in range 2997 (rt=75.9688, f=4, i=858) to 2998 (rt=75.9942, f=4, i=859) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2515.292
**Variable modifications:**
**Ions Score:** 83.31 **Expect:** 0.000

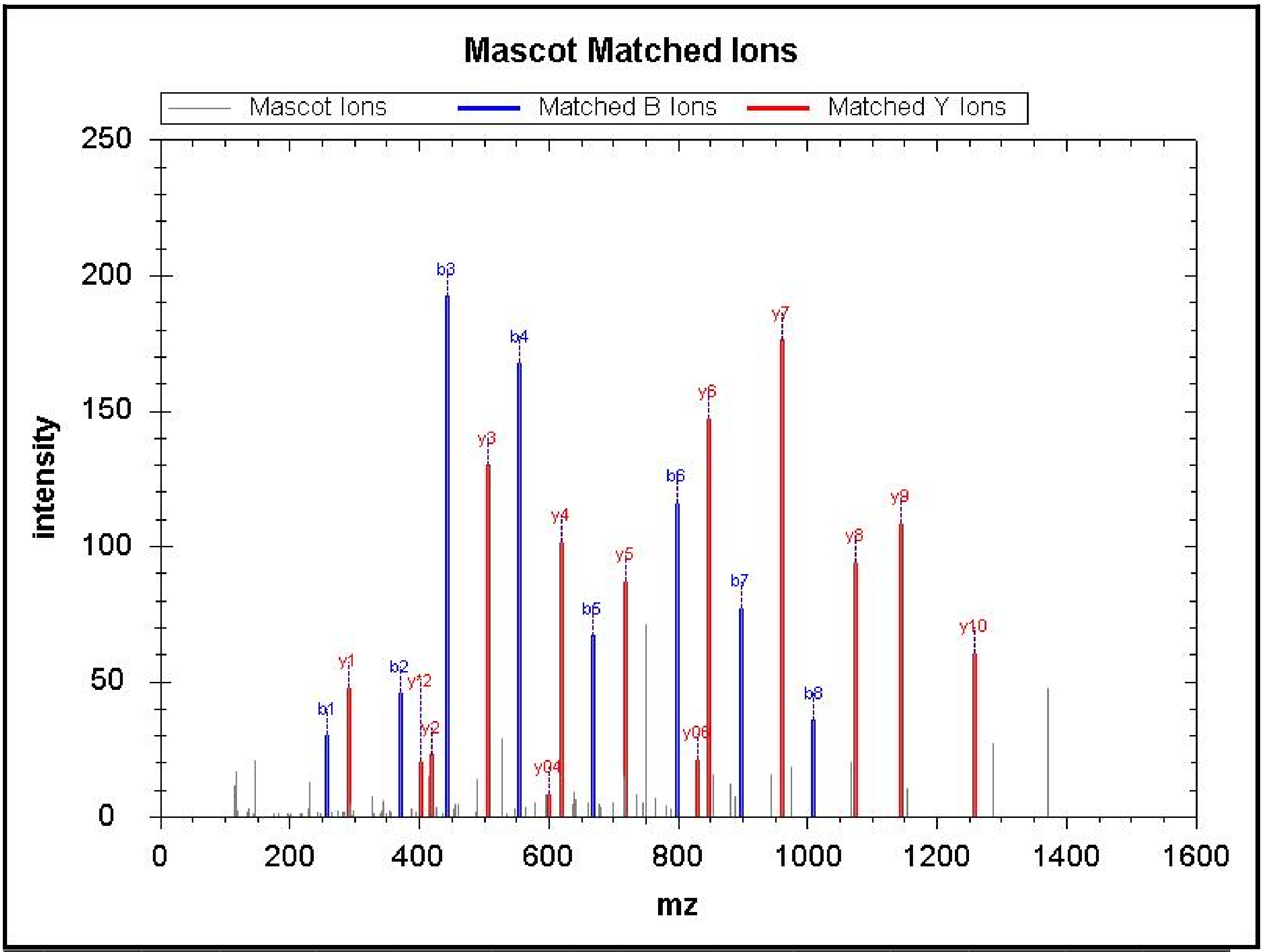


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **292.18** | 146.59 | | | | | F | | | | | | | 21 |
| 2 | **405.26** | 203.13 | | | | | L | 2,225.11 | 1,113.06 | 2,208.08 | **1,104.54** | 2,207.10 | 1,104.05 | 20 |
| 3 | **504.33** | 252.67 | | | | | V | 2,112.02 | 1,056.52 | 2,095.00 | 1,048.00 | 2,094.01 | **1,047.51** | 19 |
| 4 | **617.41** | 309.21 | | | | | L | 2,012.96 | 1,006.98 | 1,995.93 | 998.47 | 1,994.95 | 997.98 | 18 |
| 5 | **732.44** | 366.72 | | | 714.43 | 357.72 | D | 1,899.87 | 950.44 | 1,882.85 | 941.93 | 1,881.86 | 941.43 | 17 |
| 6 | **861.48** | 431.25 | | | 843.47 | 422.24 | E | 1,784.85 | 892.93 | 1,767.82 | 884.41 | 1,766.83 | 883.92 | 16 |
| 7 | **932.52** | 466.76 | | | **914.51** | 457.76 | A | 1,655.80 | 828.40 | 1,638.78 | 819.89 | 1,637.79 | 819.40 | 15 |
| 8 | **1,047.55** | 524.28 | | | 1,029.54 | 515.27 | D | 1,584.77 | 792.89 | 1,567.74 | 784.37 | 1,566.75 | 783.88 | 14 |
| 9 | **1,104.57** | 552.79 | | | 1,086.56 | 543.78 | G | 1,469.74 | 735.37 | 1,452.71 | 726.86 | 1,451.73 | 726.37 | 13 |
| 10 | **1,217.65** | 609.33 | | | **1,199.64** | 600.33 | L | 1,412.72 | 706.86 | 1,395.69 | 698.35 | 1,394.71 | 697.86 | 12 |
| 11 | 1,330.74 | 665.87 | | | 1,312.73 | 656.87 | L | **1,299.63** | 650.32 | 1,282.61 | 641.81 | 1,281.62 | 641.31 | 11 |
| 12 | 1,417.77 | 709.39 | | | 1,399.76 | 700.38 | S | **1,186.55** | 593.78 | 1,169.52 | 585.26 | 1,168.54 | 584.77 | 10 |
| 13 | 1,545.83 | 773.42 | 1,528.80 | 764.90 | 1,527.82 | 764.41 | Q | **1,099.52** | 550.26 | **1,082.49** | 541.75 | 1,081.51 | 541.26 | 9 |
| 14 | 1,602.85 | 801.93 | 1,585.82 | 793.42 | 1,584.84 | 792.92 | G | **971.46** | 486.23 | **954.43** | 477.72 | 953.45 | 477.23 | 8 |
| 15 | 1,765.91 | 883.46 | 1,748.89 | 874.95 | 1,747.90 | 874.45 | Y | **914.44** | 457.72 | 897.41 | 449.21 | 896.43 | 448.72 | 7 |
| 16 | 1,852.94 | 926.98 | 1,835.92 | 918.46 | 1,834.93 | 917.97 | S | **751.37** | 376.19 | 734.35 | 367.68 | 733.36 | 367.18 | 6 |
| 17 | 1,967.97 | 984.49 | 1,950.95 | 975.98 | 1,949.96 | 975.48 | D | **664.34** | 332.67 | 647.31 | 324.16 | 646.33 | 323.67 | 5 |
| 18 | 2,115.04 | 1,058.02 | 2,098.01 | 1,049.51 | 2,097.03 | 1,049.02 | F | **549.31** | 275.16 | **532.29** | 266.65 | | | 4 |
| 19 | 2,228.12 | 1,114.57 | 2,211.10 | 1,106.05 | 2,210.11 | 1,105.56 | I | **402.25** | 201.63 | 385.22 | 193.11 | | | 3 |
| 20 | 2,342.17 | 1,171.59 | 2,325.14 | 1,163.07 | 2,324.16 | 1,162.58 | N | **289.16** | **145.08** | **272.14** | 136.57 | | | 2 |
| 21 | | | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 1421 Hit 1

MS/MS Fragmentation of **LIALLEVLSQK**

Found in **sp|P21333|FLNA_HUMAN**, Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4
Match to Query 1421: 1513.98from(757.9973,2+)
Title: 1173: Scan 2852 (rt=72.6968, f=2, i=435) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1513.98
**Variable modifications:**
**K11** :iTRAQ4plex (K)
**Ions Score:** 77.64 **Expect:** 0.000

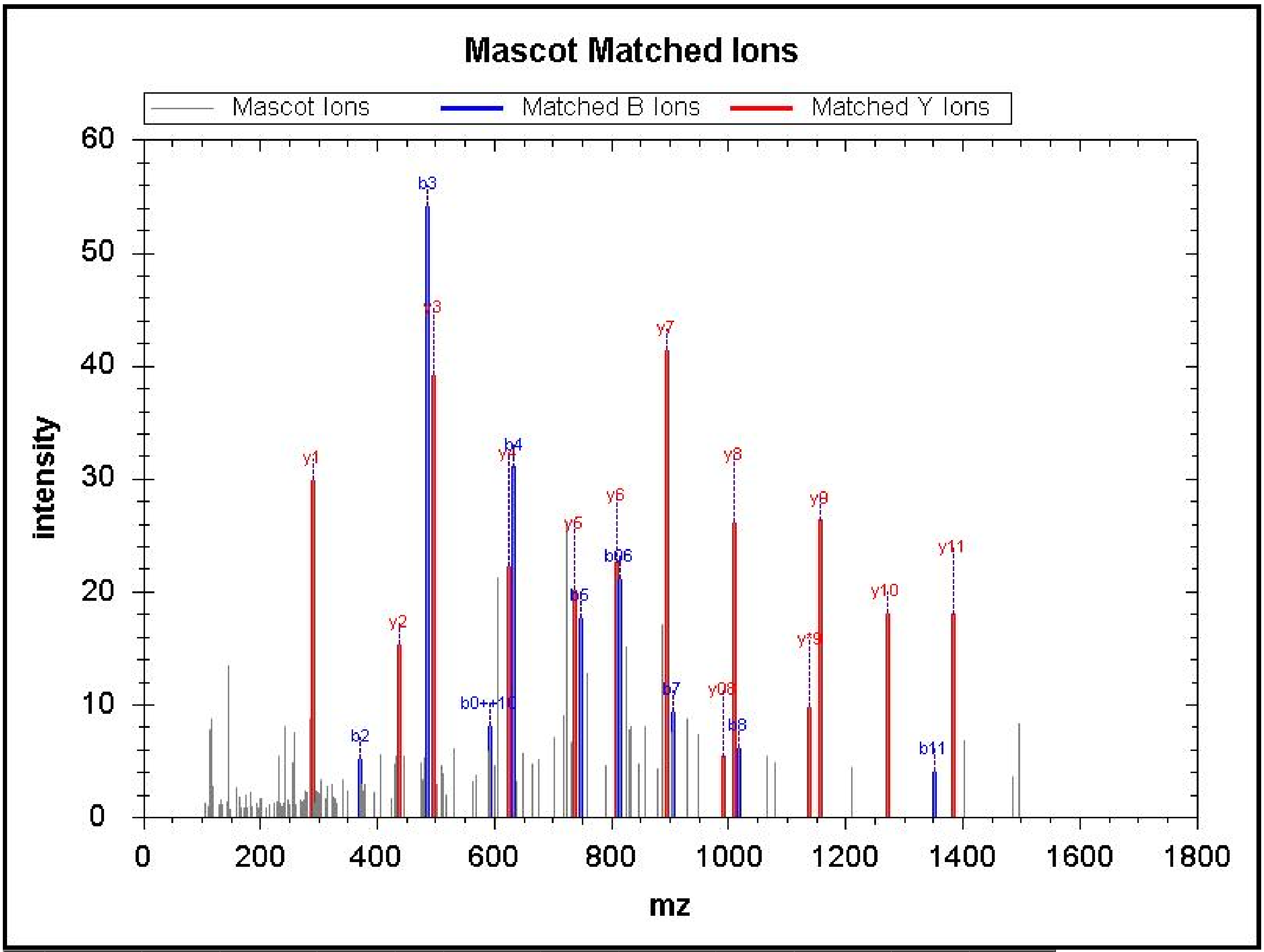


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **258.19** | 129.60 | | | | | L | | | | | | | 11 |
| 2 | **371.28** | 186.14 | | | | | I | **1,257.79** | 629.40 | 1,240.76 | 620.89 | 1,239.78 | 620.39 | 10 |
| 3 | **442.31** | 221.66 | | | | | A | **1,144.71** | 572.86 | 1,127.68 | 564.34 | 1,126.70 | 563.85 | 9 |
| 4 | **555.40** | 278.20 | | | | | L | **1,073.67** | 537.34 | 1,056.64 | 528.82 | 1,055.66 | 528.33 | 8 |
| 5 | **668.48** | 334.74 | | | | | L | **960.58** | 480.80 | 943.56 | 472.28 | 942.57 | 471.79 | 7 |
| 6 | **797.53** | 399.27 | | | 779.51 | 390.26 | E | **847.50** | 424.25 | 830.47 | 415.74 | **829.49** | 415.25 | 6 |
| 7 | **896.59** | 448.80 | | | 878.58 | 439.80 | V | **718.46** | 359.73 | 701.43 | 351.22 | 700.45 | 350.73 | 5 |
| 8 | **1,009.68** | 505.34 | | | 991.67 | 496.34 | L | **619.39** | 310.20 | 602.36 | 301.69 | **601.38** | 301.19 | 4 |
| 9 | 1,096.71 | 548.86 | | | 1,078.70 | 539.85 | S | **506.31** | 253.66 | 489.28 | 245.14 | 488.29 | 244.65 | 3 |
| 10 | 1,224.77 | 612.89 | 1,207.74 | 604.37 | 1,206.76 | 603.88 | Q | **419.27** | 210.14 | **402.25** | 201.63 | | | 2 |
| 11 | | | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 1638 Hit 1

MS/MS Fragmentation of **IIDFLSALEGFK**
Found in **sp|P52701|MSH6_HUMAN**, DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=1 SV=2
Match to Query 1638: 1639.943from(820.9789,2+)
Title: 1196: Sum of 2 scans in range 3057 (rt=76.8723, f=4, i=844) to 3058 (rt=76.8977, f=4, i=845)
[D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]

Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1639.943
**Variable modifications:**
**K12** :iTRAQ4plex (K)
**Ions Score:** 76.84 **Expect:** 0.000

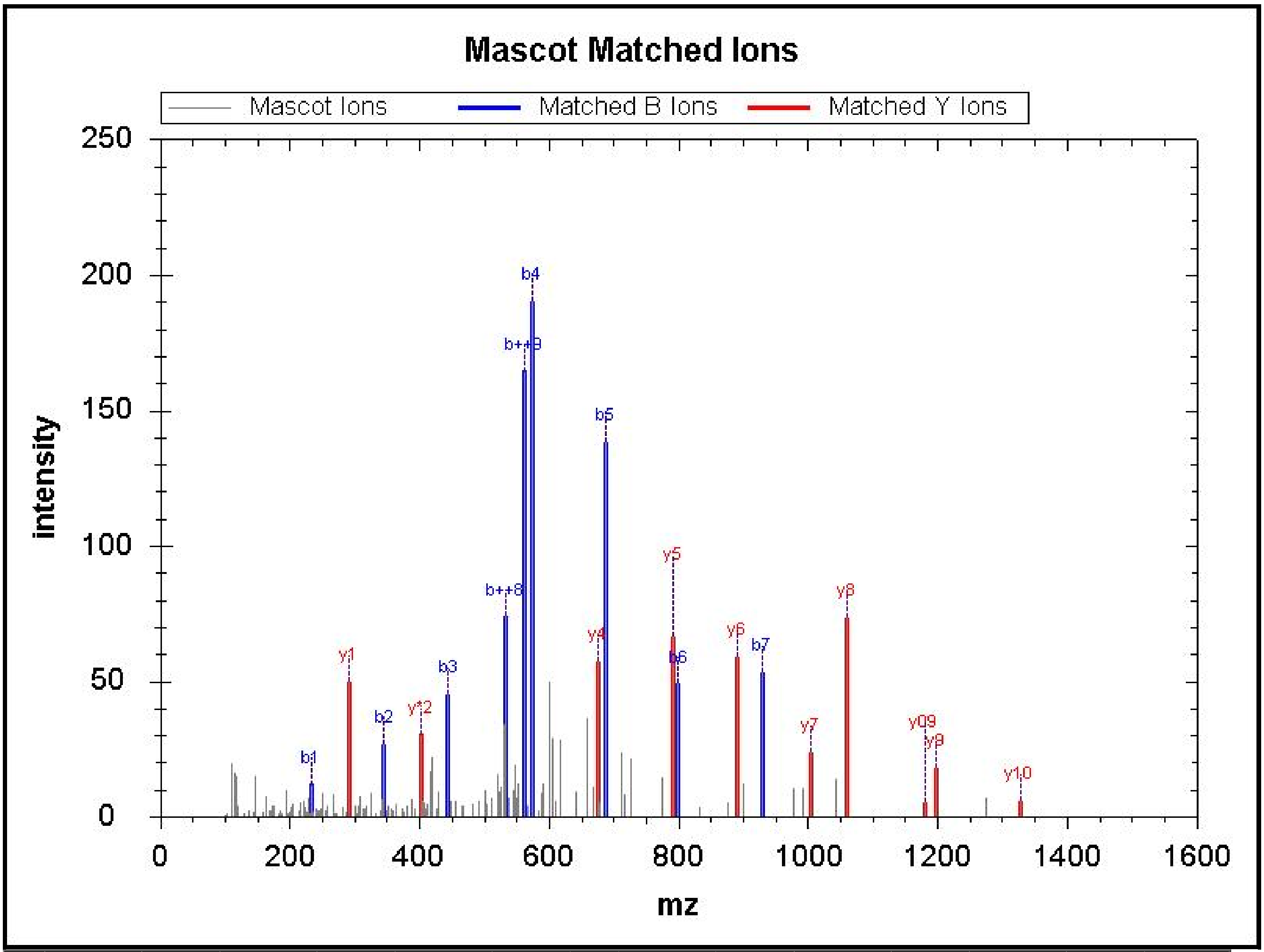


| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | | | I | | | | | | | 12 |
| 2 | **371.28** | 186.14 | | | I | **1,383.76** | 692.39 | 1,366.74 | 683.87 | 1,365.75 | 683.38 | 11 |
| 3 | **486.30** | 243.66 | 468.29 | 234.65 | D | **1,270.68** | 635.84 | 1,253.65 | 627.33 | 1,252.67 | 626.84 | 10 |
| 4 | **633.37** | 317.19 | 615.36 | 308.18 | F | **1,155.65** | 578.33 | **1,138.63** | 569.82 | 1,137.64 | 569.32 | 9 |
| 5 | **746.46** | 373.73 | 728.45 | 364.73 | L | **1,008.58** | 504.80 | 991.56 | 496.28 | **990.57** | 495.79 | 8 |
| 6 | 833.49 | 417.25 | **815.48** | 408.24 | S | **895.50** | 448.25 | 878.47 | 439.74 | 877.49 | 439.25 | 7 |
| 7 | **904.53** | 452.77 | 886.52 | 443.76 | A | **808.47** | 404.74 | 791.44 | 396.22 | 790.46 | 395.73 | 6 |
| 8 | **1,017.61** | 509.31 | 999.60 | 500.30 | L | **737.43** | 369.22 | 720.40 | 360.71 | 719.42 | 360.21 | 5 |
| 9 | 1,146.65 | 573.83 | 1,128.64 | 564.82 | E | **624.35** | 312.68 | 607.32 | 304.16 | 606.34 | 303.67 | 4 |
| 10 | 1,203.67 | 602.34 | 1,185.66 | **593.34** | G | **495.30** | 248.16 | 478.28 | 239.64 | | | 3 |
| 11 | **1,350.74** | 675.88 | 1,332.73 | 666.87 | F | **438.28** | 219.65 | 421.26 | 211.13 | | | 2 |
| 12 | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 2266 Hit 1

MS/MS Fragmentation of **SLVEIIEHGLVDEQQK**
Found in **sp|O75533|SF3B1_HUMAN**, Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3
Match to Query 2266: 2124.173 from(709.0649,3+)
Title: 872: Scan 2331 (rt=60.5096, f=3, i=314) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2124.173
**Variable modifications:**

**K16** :iTRAQ4plex (K)
**Ions Score:** 76.48 **Expect:** 0.000

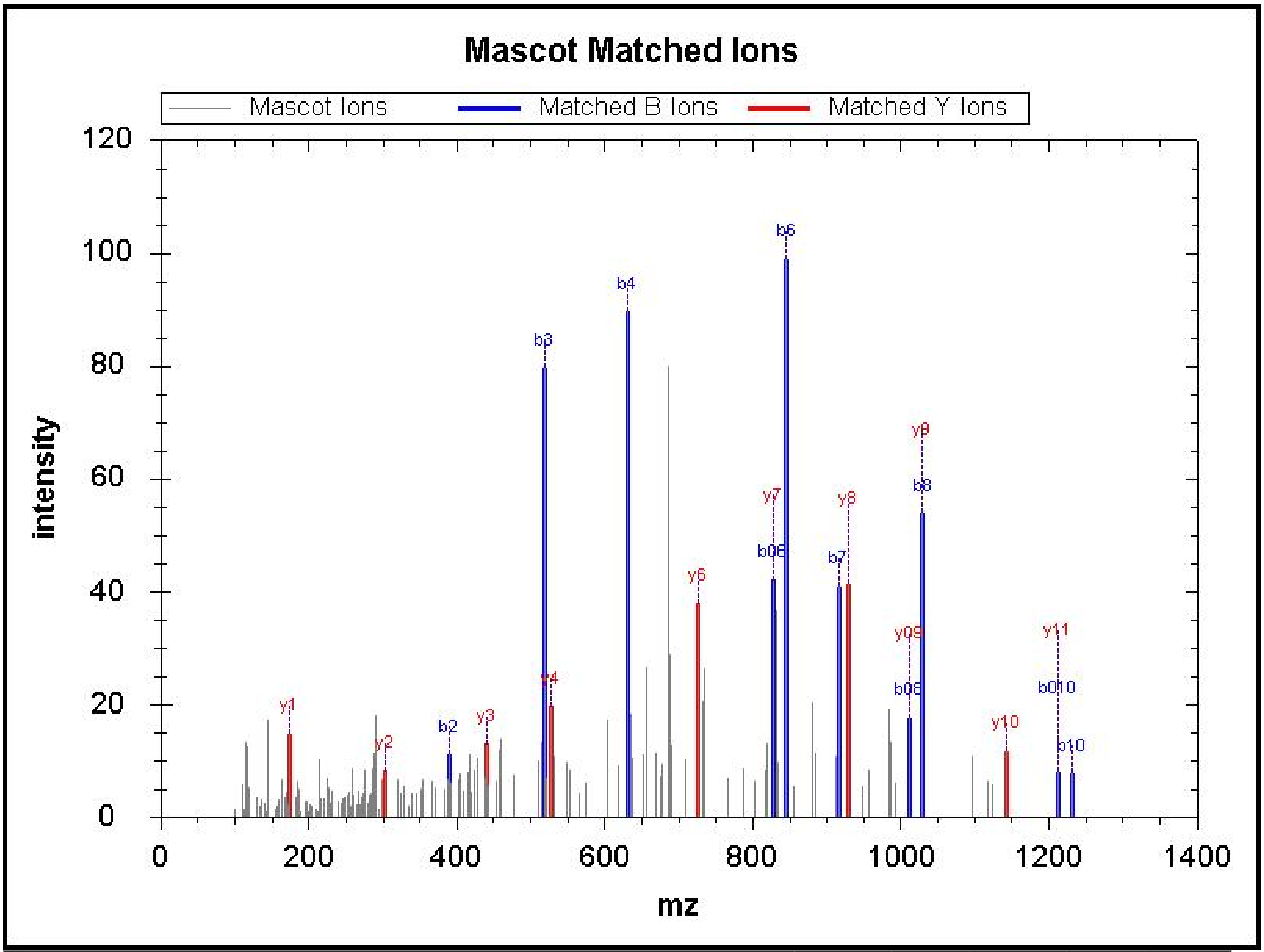


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | **232.14** | 116.57 | | | 214.13 | 107.57 | **S** | | | | | | | **16** |
| **2** | **345.23** | 173.12 | | | 327.21 | 164.11 | **L** | 1,894.04 | 947.52 | 1,877.01 | 939.01 | 1,876.03 | 938.52 | **15** |
| **3** | **444.29** | 222.65 | | | 426.28 | 213.65 | **V** | 1,780.96 | 890.98 | 1,763.93 | 882.47 | 1,762.95 | 881.98 | **14** |
| **4** | **573.34** | 287.17 | | | 555.33 | 278.17 | **E** | 1,681.89 | 841.45 | 1,664.86 | 832.93 | 1,663.88 | 832.44 | **13** |
| **5** | **686.42** | 343.71 | | | 668.41 | 334.71 | **I** | 1,552.85 | 776.93 | 1,535.82 | 768.41 | 1,534.83 | 767.92 | **12** |
| **6** | **799.50** | 400.26 | | | 781.49 | 391.25 | **I** | 1,439.76 | 720.38 | 1,422.73 | 711.87 | 1,421.75 | 711.38 | **11** |
| **7** | **928.55** | 464.78 | | | 910.54 | 455.77 | **E** | **1,326.68** | 663.84 | 1,309.65 | 655.33 | 1,308.67 | 654.84 | **10** |
| **8** | 1,065.61 | **533.31** | | | 1,047.60 | 524.30 | **H** | **1,197.63** | 599.32 | 1,180.61 | 590.81 | **1,179.62** | 590.32 | **9** |
| **9** | 1,122.63 | **561.82** | | | 1,104.62 | 552.81 | **G** | **1,060.58** | 530.79 | 1,043.55 | 522.28 | 1,042.56 | 521.79 | **8** |
| **10** | 1,235.71 | 618.36 | | | 1,217.70 | 609.35 | **L** | **1,003.55** | 502.28 | 986.53 | 493.77 | 985.54 | 493.28 | **7** |
| **11** | 1,334.78 | 667.89 | | | 1,316.77 | 658.89 | **V** | **890.47** | 445.74 | 873.44 | 437.23 | 872.46 | 436.73 | **6** |
| **12** | 1,449.81 | 725.41 | | | 1,431.80 | 716.40 | **D** | **791.40** | 396.20 | 774.38 | 387.69 | 773.39 | 387.20 | **5** |
| **13** | 1,578.85 | 789.93 | | | 1,560.84 | 780.92 | **E** | **676.37** | 338.69 | 659.35 | 330.18 | 658.36 | 329.69 | **4** |
| **14** | 1,706.91 | 853.96 | 1,689.88 | 845.44 | 1,688.90 | 844.95 | **Q** | 547.33 | 274.17 | 530.31 | 265.66 | | | **3** |
| **15** | 1,834.97 | 917.99 | 1,817.94 | 909.47 | 1,816.96 | 908.98 | **Q** | 419.27 | 210.14 | **402.25** | 201.63 | | | **2** |
| **16** | | | | | | | **K** | **291.21** | 146.11 | 274.19 | 137.60 | | | **1** |

Query 2187 Hit 1

MS/MS Fragmentation of **IMEIVDAITTTAQSHQR**
Found in **sp|P08237|K6PF_HUMAN**, 6-phosphofructokinase
Match to Query 2187: 2057.081 from(686.7009,3+)
Title: 941: Sum of 2 scans in range 2352 (rt=61.4357, f=4, i=650) to 2353 (rt=61.4611, f=4, i=651)

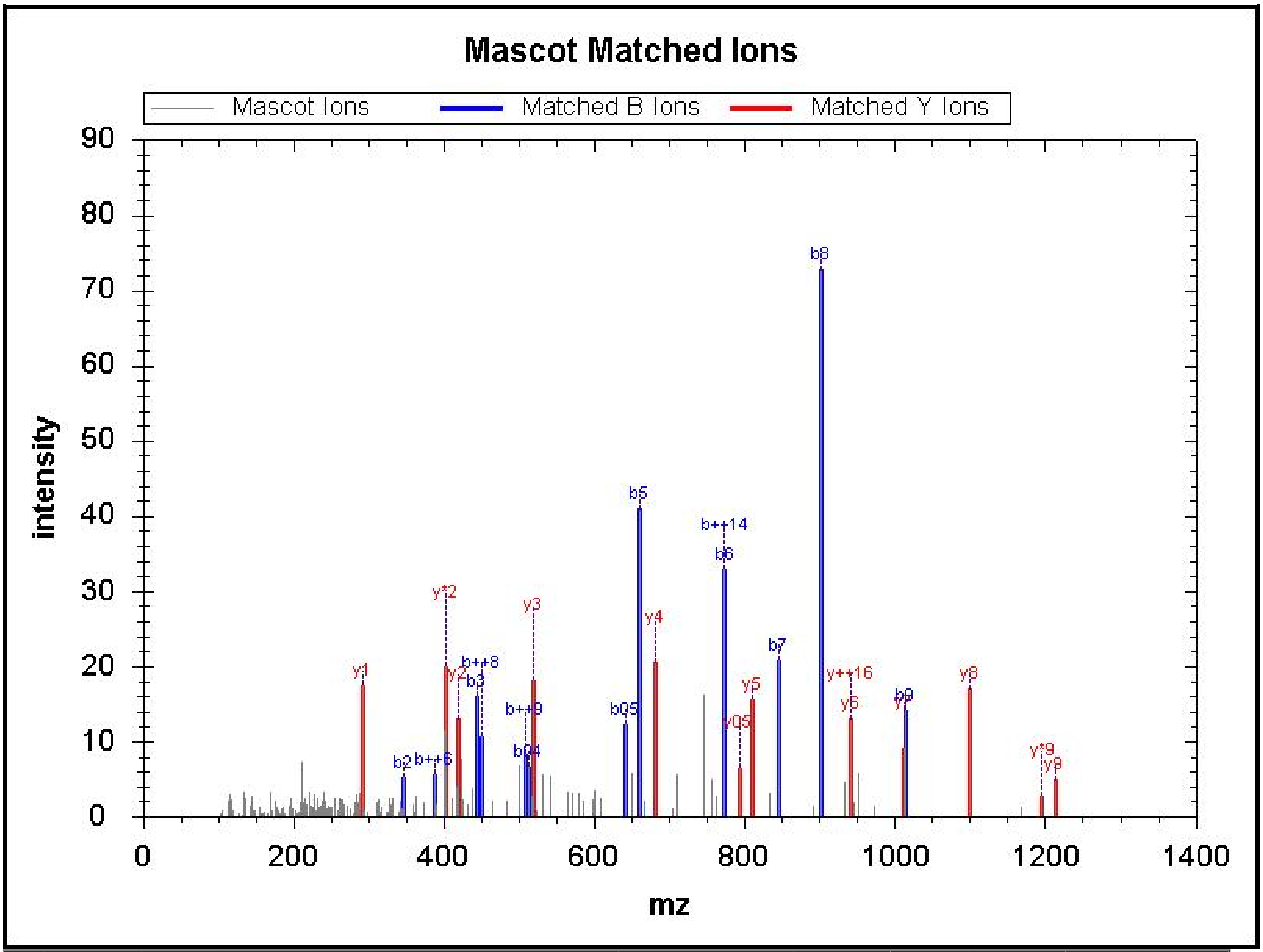
[D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2057.081
**Variable modifications:**
**Ions Score:** 75.88 **Expect:** 0.000



| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | 258.19 | 129.60 | | | | | **I** | | | | | | | **17** |
| **2** | **389.23** | 195.12 | | | | | **M** | 1,800.89 | 900.95 | 1,783.86 | 892.44 | 1,782.88 | 891.94 | **16** |
| **3** | **518.28** | 259.64 | | | 500.27 | 250.64 | **E** | 1,669.85 | 835.43 | 1,652.82 | 826.92 | 1,651.84 | 826.42 | **15** |
| **4** | **631.36** | 316.18 | | | 613.35 | 307.18 | **I** | 1,540.81 | 770.91 | 1,523.78 | 762.39 | 1,522.80 | 761.90 | **14** |
| **5** | 730.43 | 365.72 | | | 712.42 | 356.71 | **V** | 1,427.72 | 714.37 | 1,410.70 | 705.85 | 1,409.71 | 705.36 | **13** |
| **6** | **845.46** | 423.23 | | | **827.45** | 414.23 | **D** | 1,328.66 | 664.83 | 1,311.63 | 656.32 | 1,310.64 | 655.83 | **12** |
| **7** | **916.49** | 458.75 | | | 898.48 | 449.74 | **A** | **1,213.63** | 607.32 | 1,196.60 | 598.80 | 1,195.62 | 598.31 | **11** |
| **8** | **1,029.58** | 515.29 | | | **1,011.57** | 506.29 | **I** | **1,142.59** | 571.80 | 1,125.56 | 563.29 | 1,124.58 | 562.79 | **10** |
| **9** | 1,130.62 | 565.82 | | | 1,112.61 | 556.81 | **T** | **1,029.51** | 515.26 | 1,012.48 | 506.74 | **1,011.50** | 506.25 | **9** |
| **10** | **1,231.67** | 616.34 | | | **1,213.66** | 607.33 | **T** | **928.46** | 464.73 | 911.43 | 456.22 | 910.45 | 455.73 | **8** |
| **11** | 1,332.72 | 666.86 | | | 1,314.71 | 657.86 | **T** | **827.41** | 414.21 | 810.39 | 405.70 | 809.40 | 405.20 | **7** |
| **12** | 1,403.76 | 702.38 | | | 1,385.75 | 693.38 | **A** | **726.36** | 363.69 | 709.34 | 355.17 | 708.35 | 354.68 | **6** |
| **13** | 1,531.82 | 766.41 | 1,514.79 | 757.90 | 1,513.81 | 757.41 | **Q** | 655.33 | 328.17 | 638.30 | 319.65 | 637.32 | 319.16 | **5** |
| **14** | 1,618.85 | 809.93 | 1,601.82 | 801.41 | 1,600.84 | 800.92 | **S** | **527.27** | 264.14 | 510.24 | 255.62 | 509.26 | 255.13 | **4** |
| **15** | 1,755.91 | 878.46 | 1,738.88 | 869.94 | 1,737.90 | 869.45 | **H** | **440.24** | 220.62 | 423.21 | 212.11 | | | **3** |
| **16** | 1,883.97 | 942.49 | 1,866.94 | 933.97 | 1,865.95 | 933.48 | **Q** | **303.18** | 152.09 | 286.15 | 143.58 | | | **2** |
| **17** | | | | | | | **R** | **175.12** | 88.06 | 158.09 | 79.55 | | | **1** |

Query 2375 Hit 1

MS/MS Fragmentation of **SIVSELAGLLSAMEYVQK**
Found in **sp|P40763|STAT3_HUMAN**, Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2
Match to Query 2375: 2225.236from(742.7526,3+)
Title: 1390: Sum of 2 scans in range 3400 (rt=85.0496, f=4, i=988) to 3401 (rt=85.075, f=4, i=989)
[D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2225.236
**Variable modifications:**
**K18** :iTRAQ4plex (K)
**Ions Score:** 75.38 **Expect:** 0.000

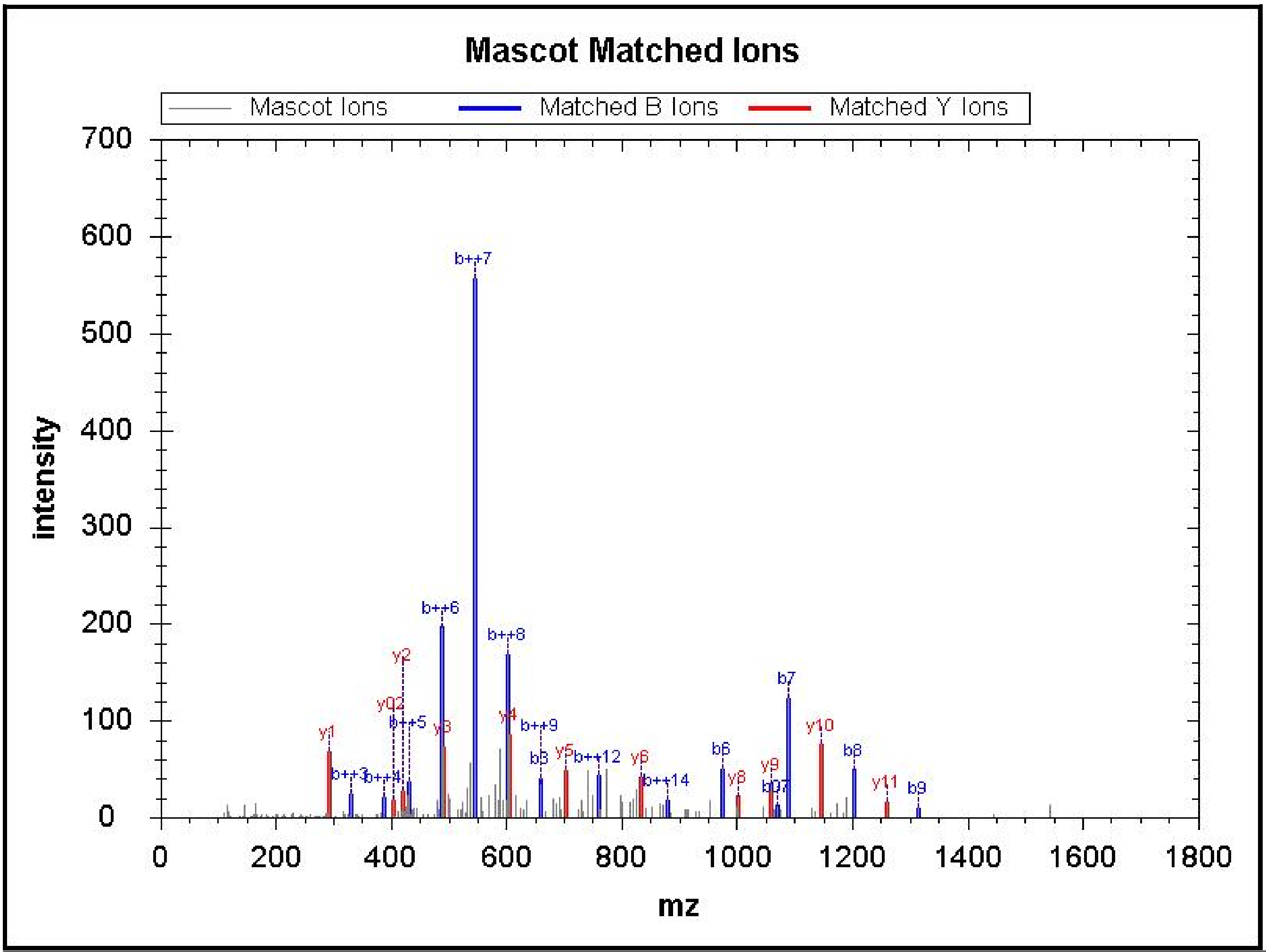


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 232.14 | 116.57 | | | 214.13 | 107.57 | S | | | | | | | 18 |
| 2 | **345.23** | 173.12 | | | 327.21 | 164.11 | I | 1,995.10 | 998.05 | 1,978.07 | 989.54 | 1,977.08 | 989.05 | 17 |
| 3 | **444.29** | 222.65 | | | 426.28 | 213.65 | V | 1,882.01 | **941.51** | 1,864.98 | 933.00 | 1,864.00 | 932.50 | 16 |
| 4 | 531.33 | 266.17 | | | **513.32** | 257.16 | S | 1,782.94 | 891.98 | 1,765.92 | 883.46 | 1,764.93 | 882.97 | 15 |
| 5 | **660.37** | 330.69 | | | **642.36** | 321.68 | E | 1,695.91 | 848.46 | 1,678.88 | 839.95 | 1,677.90 | 839.45 | 14 |
| 6 | **773.45** | **387.23** | | | 755.44 | 378.22 | L | 1,566.87 | 783.94 | 1,549.84 | 775.42 | 1,548.86 | 774.93 | 13 |
| 7 | **844.49** | 422.75 | | | 826.48 | 413.74 | A | 1,453.78 | 727.40 | 1,436.76 | 718.88 | 1,435.77 | 718.39 | 12 |
| 8 | **901.51** | **451.26** | | | 883.50 | 442.25 | G | 1,382.75 | 691.88 | 1,365.72 | 683.36 | 1,364.74 | 682.87 | 11 |
| 9 | **1,014.60** | **507.80** | | | 996.58 | 498.80 | L | 1,325.73 | 663.37 | 1,308.70 | 654.85 | 1,307.71 | 654.36 | 10 |
| 10 | 1,127.68 | 564.34 | | | 1,109.67 | 555.34 | L | **1,212.64** | 606.82 | **1,195.61** | 598.31 | 1,194.63 | 597.82 | 9 |
| 11 | 1,214.71 | 607.86 | | | 1,196.70 | 598.85 | S | **1,099.56** | 550.28 | 1,082.53 | 541.77 | 1,081.55 | 541.28 | 8 |
| 12 | 1,285.75 | 643.38 | | | 1,267.74 | 634.37 | A | **1,012.53** | 506.77 | 995.50 | 498.25 | 994.51 | 497.76 | 7 |
| 13 | 1,416.79 | 708.90 | | | 1,398.78 | 699.89 | M | **941.49** | 471.25 | 924.46 | 462.73 | 923.48 | 462.24 | 6 |
| 14 | 1,545.83 | **773.42** | | | 1,527.82 | 764.41 | E | **810.45** | 405.73 | 793.42 | 397.21 | **792.44** | 396.72 | 5 |
| 15 | 1,708.89 | 854.95 | | | 1,690.88 | 845.95 | Y | **681.41** | 341.21 | 664.38 | 332.69 | | | 4 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 16 | 1,807.96 | 904.49 | | | 1,789.95 | 895.48 | V | 518.34 | 259.67 | 501.32 | 251.16 | | | 3 |
| 17 | 1,936.02 | 968.51 | 1,919.00 | 960.00 | 1,918.01 | 959.51 | Q | 419.27 | 210.14 | 402.25 | 201.63 | | | 2 |
| 18 | | | | | | | K | 291.21 | 146.11 | 274.19 | 137.60 | | | 1 |

Query 2585 Hit 1

MS/MS Fragmentation of KLELSDNIISGGLEVLAEK
Found in sp|Q9BTT0|AN32E_HUMAN, Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E PE=1 SV=1
Match to Query 2585: 2459.429from(820.8171,3+)
Title: 879: Scan 2349 (rt=60.9169, f=3, i=317) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2459.429
**Variable modifications:**
**K1** :iTRAQ4plex (K)
**K19** :iTRAQ4plex (K)
**Ions Score:** 74.41 **Expect:** 0.000

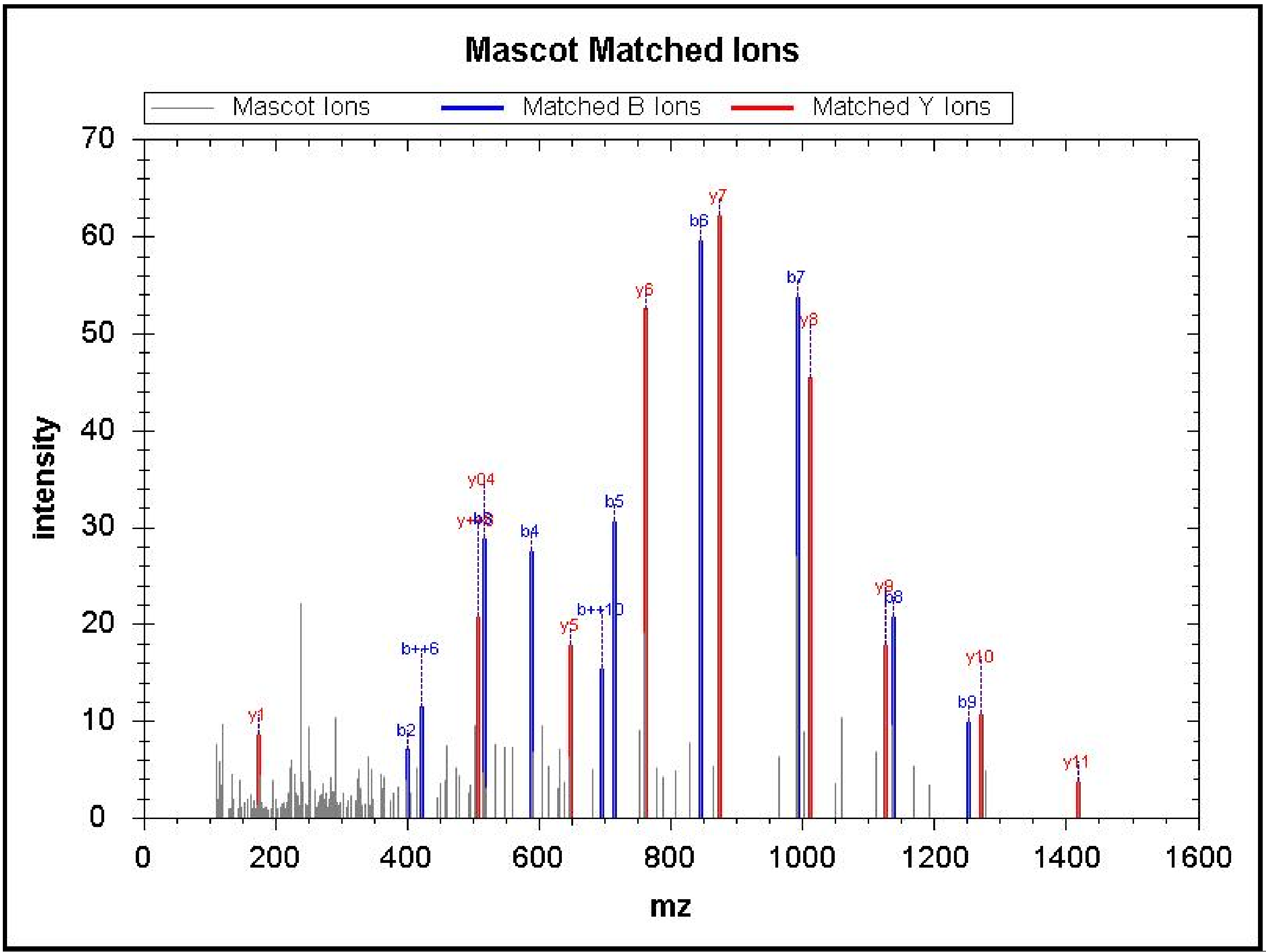


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 417.31 | 209.16 | 400.28 | 200.64 | | | K | | | | | | | 19 |
| 2 | 530.39 | 265.70 | 513.36 | 257.19 | | | L | 2,044.13 | 1,022.57 | 2,027.10 | 1,014.06 | 2,026.12 | 1,013.56 | 18 |
| 3 | 659.43 | 330.22 | 642.41 | 321.71 | 641.42 | 321.21 | E | 1,931.05 | 966.03 | 1,914.02 | 957.51 | 1,913.03 | 957.02 | 17 |
| 4 | 772.52 | 386.76 | 755.49 | 378.25 | 754.51 | 377.76 | L | 1,802.00 | 901.51 | 1,784.98 | 892.99 | 1,783.99 | 892.50 | 16 |
| 5 | 859.55 | 430.28 | 842.52 | 421.76 | 841.54 | 421.27 | S | 1,688.92 | 844.96 | 1,671.89 | 836.45 | 1,670.91 | 835.96 | 15 |
| 6 | 974.58 | 487.79 | 957.55 | 479.28 | 956.57 | 478.79 | D | 1,601.89 | 801.45 | 1,584.86 | 792.93 | 1,583.88 | 792.44 | 14 |
| 7 | 1,088.62 | 544.81 | 1,071.59 | 536.30 | 1,070.61 | 535.81 | N | 1,486.86 | 743.93 | 1,469.83 | 735.42 | 1,468.85 | 734.93 | 13 |
| 8 | 1,201.70 | 601.36 | 1,184.68 | 592.84 | 1,183.69 | 592.35 | I | 1,372.82 | 686.91 | 1,355.79 | 678.40 | 1,354.81 | 677.91 | 12 |
| 9 | 1,314.79 | 657.90 | 1,297.76 | 649.38 | 1,296.78 | 648.89 | I | 1,259.73 | 630.37 | 1,242.71 | 621.86 | 1,241.72 | 621.36 | 11 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 10 | 1,401.82 | 701.41 | 1,384.79 | 692.90 | 1,383.81 | 692.41 | S | 1,146.65 | 573.83 | 1,129.62 | 565.31 | 1,128.64 | 564.82 | 10 |
| 11 | 1,458.84 | 729.92 | 1,441.81 | 721.41 | 1,440.83 | 720.92 | G | 1,059.62 | 530.31 | 1,042.59 | 521.80 | 1,041.61 | 521.31 | 9 |
| 12 | 1,515.86 | 758.43 | 1,498.84 | 749.92 | 1,497.85 | 749.43 | G | 1,002.60 | 501.80 | 985.57 | 493.29 | 984.58 | 492.80 | 8 |
| 13 | 1,628.95 | 814.98 | 1,611.92 | 806.46 | 1,610.94 | 805.97 | L | 945.57 | 473.29 | 928.55 | 464.78 | 927.56 | 464.29 | 7 |
| 14 | 1,757.99 | 879.50 | 1,740.96 | 870.98 | 1,739.98 | 870.49 | E | 832.49 | 416.75 | 815.46 | 408.24 | 814.48 | 407.74 | 6 |
| 15 | 1,857.06 | 929.03 | 1,840.03 | 920.52 | 1,839.05 | 920.03 | V | 703.45 | 352.23 | 686.42 | 343.71 | 685.44 | 343.22 | 5 |
| 16 | 1,970.14 | 985.57 | 1,953.11 | 977.06 | 1,952.13 | 976.57 | L | 604.38 | 302.69 | 587.35 | 294.18 | 586.37 | 293.69 | 4 |
| 17 | 2,041.18 | 1,021.09 | 2,024.15 | 1,012.58 | 2,023.17 | 1,012.09 | A | 491.29 | 246.15 | 474.27 | 237.64 | 473.28 | 237.15 | 3 |
| 18 | 2,170.22 | 1,085.61 | 2,153.19 | 1,077.10 | 2,152.21 | 1,076.61 | E | 420.26 | 210.63 | 403.23 | 202.12 | 402.25 | 201.63 | 2 |
| 19 | | | | | | | K | 291.21 | 146.11 | 274.19 | 137.60 | | | 1 |

Query 2419 Hit 1

MS/MS Fragmentation of **QQDAQEFFLHLINMVER**
Found in **sp|P45974|UBP5_HUMAN**, Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2
Match to Query 2419: 2261.157from(754.7263,3+)
Title: 1193: Sum of 2 scans in range 2898 (rt=73.7373, f=4, i=826) to 2899 (rt=73.7627, f=4, i=827) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2261.157
**Variable modifications:**
**Ions Score:** 74.32 **Expect:** 0.000

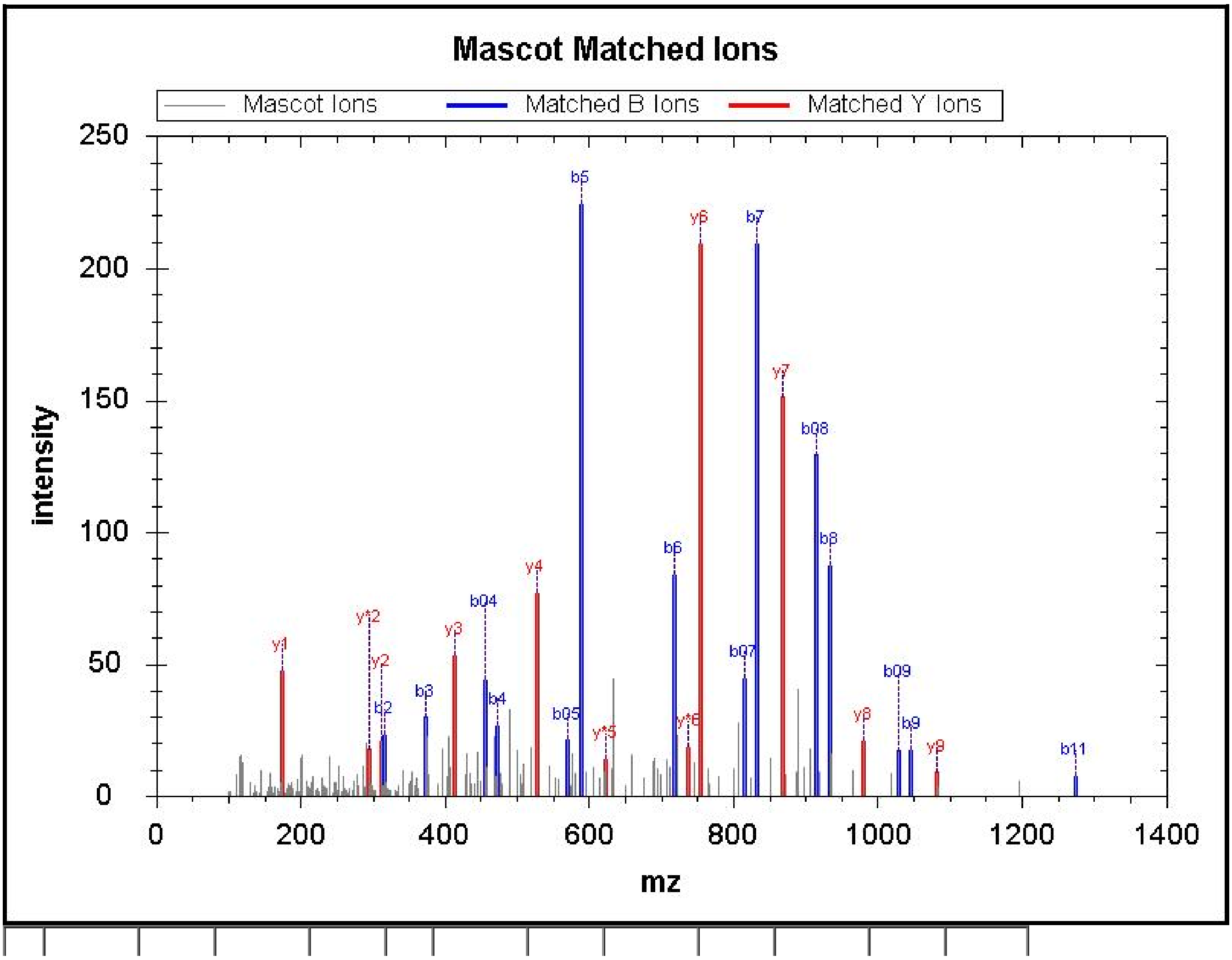


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 273.17 | 137.09 | 256.14 | 128.57 | | | Q | | | | | | | 17 |
| 2 | 401.23 | 201.12 | 384.20 | 192.60 | | | Q | 1,989.99 | 995.50 | 1,972.96 | 986.98 | 1,971.97 | 986.49 | 16 |
| 3 | 516.25 | 258.63 | 499.23 | 250.12 | 498.24 | 249.63 | D | 1,861.93 | 931.47 | 1,844.90 | 922.95 | 1,843.92 | 922.46 | 15 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 4 | **587.29** | 294.15 | 570.26 | 285.64 | 569.28 | 285.14 | A | 1,746.90 | 873.95 | 1,729.87 | 865.44 | 1,728.89 | 864.95 | 14 |
| 5 | **715.35** | 358.18 | 698.32 | 349.66 | 697.34 | 349.17 | Q | 1,675.86 | 838.43 | 1,658.84 | 829.92 | 1,657.85 | 829.43 | 13 |
| 6 | **844.39** | **422.70** | 827.37 | 414.19 | 826.38 | 413.69 | E | 1,547.80 | 774.41 | 1,530.78 | 765.89 | 1,529.79 | 765.40 | 12 |
| 7 | **991.46** | 496.23 | 974.43 | 487.72 | 973.45 | 487.23 | F | **1,418.76** | 709.88 | 1,401.73 | 701.37 | 1,400.75 | 700.88 | 11 |
| 8 | **1,138.53** | 569.77 | 1,121.50 | 561.25 | 1,120.52 | 560.76 | F | **1,271.69** | 636.35 | 1,254.67 | 627.84 | 1,253.68 | 627.34 | 10 |
| 9 | **1,251.61** | 626.31 | 1,234.59 | 617.80 | 1,233.60 | 617.30 | L | **1,124.62** | 562.82 | 1,107.60 | 554.30 | 1,106.61 | 553.81 | 9 |
| 10 | 1,388.67 | **694.84** | 1,371.65 | 686.33 | 1,370.66 | 685.83 | H | **1,011.54** | **506.27** | 994.51 | 497.76 | 993.53 | 497.27 | 8 |
| 11 | 1,501.76 | 751.38 | 1,484.73 | 742.87 | 1,483.75 | 742.38 | L | **874.48** | 437.74 | 857.45 | 429.23 | 856.47 | 428.74 | 7 |
| 12 | 1,614.84 | 807.92 | 1,597.81 | 799.41 | 1,596.83 | 798.92 | I | **761.40** | 381.20 | 744.37 | 372.69 | 743.39 | 372.20 | 6 |
| 13 | 1,728.88 | 864.95 | 1,711.86 | 856.43 | 1,710.87 | 855.94 | N | **648.31** | 324.66 | 631.29 | 316.15 | 630.30 | 315.65 | 5 |
| 14 | 1,859.92 | 930.47 | 1,842.90 | 921.95 | 1,841.91 | 921.46 | M | 534.27 | 267.64 | 517.24 | 259.13 | **516.26** | 258.63 | 4 |
| 15 | 1,958.99 | 980.00 | 1,941.97 | 971.49 | 1,940.98 | 970.99 | V | 403.23 | 202.12 | 386.20 | 193.61 | 385.22 | 193.11 | 3 |
| 16 | 2,088.03 | 1,044.52 | 2,071.01 | 1,036.01 | 2,070.02 | 1,035.52 | E | 304.16 | 152.58 | 287.13 | 144.07 | 286.15 | 143.58 | 2 |
| 17 | | | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 2000 Hit 1

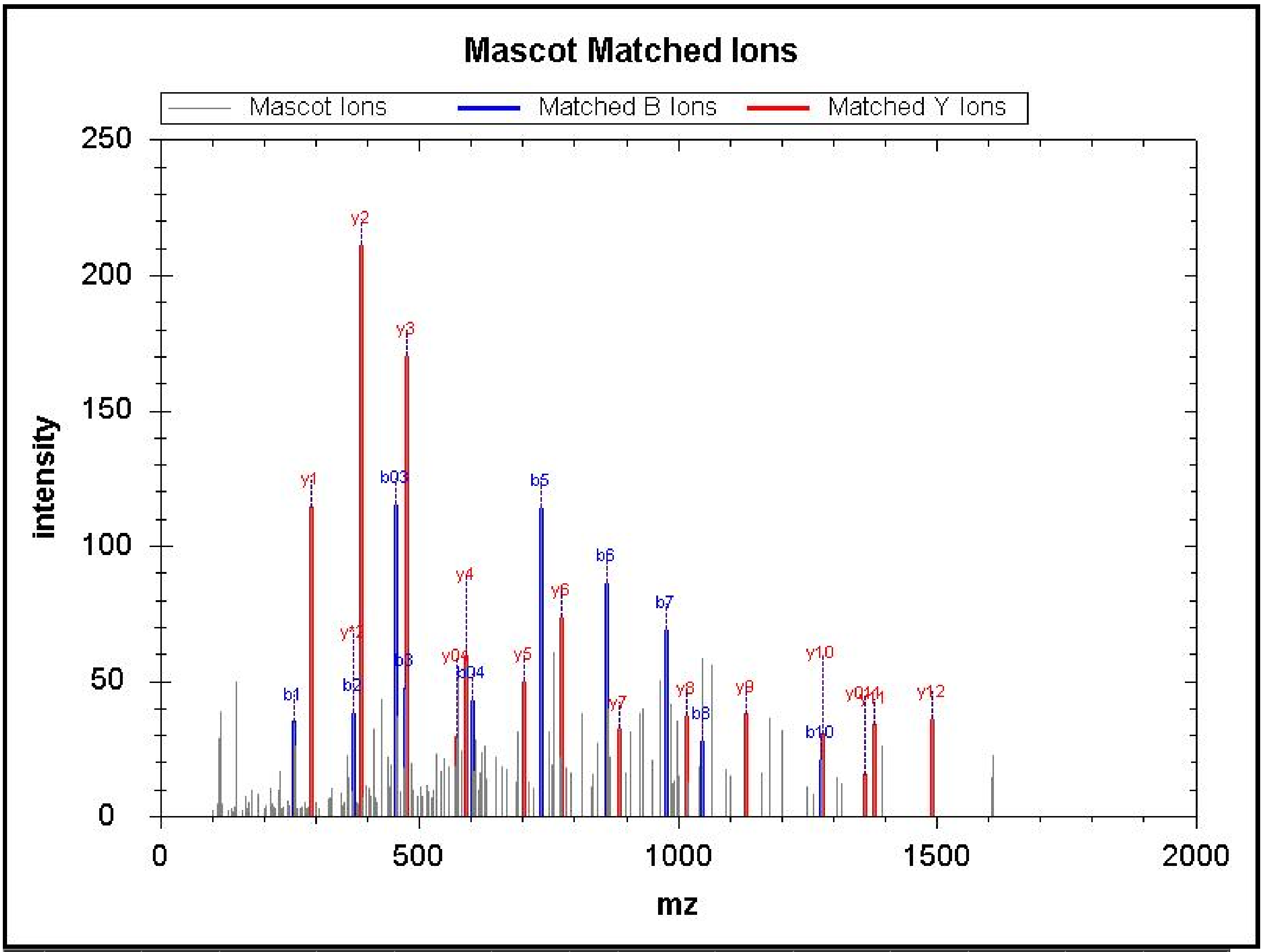
MS/MS Fragmentation of **GLGTDEDTIIDIITHR**
Found in **sp|P08133|ANXA6_HUMAN**, Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3
Match to Query 2000: 1912.012from(638.3445,3+)
Title: 922: Sum of 2 scans in range 2309 (rt=60.4656, f=4, i=636) to 2310 (rt=60.491, f=4, i=637)
[D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1912.012
**Variable modifications:**
**Ions Score:** 71.53 **Expect:** 0.000



| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | 202.13 | 101.57 | | | **G** | | | | | | | **16** |
| **2** | **315.21** | 158.11 | | | **L** | 1,711.89 | 856.45 | 1,694.86 | 847.93 | 1,693.88 | 847.44 | **15** |
| **3** | **372.24** | 186.62 | | | **G** | 1,598.80 | 799.90 | 1,581.78 | 791.39 | 1,580.79 | 790.90 | **14** |
| **4** | **473.28** | 237.15 | **455.27** | 228.14 | **T** | 1,541.78 | 771.39 | 1,524.75 | 762.88 | 1,523.77 | 762.39 | **13** |
| **5** | **588.31** | 294.66 | **570.30** | 285.65 | **D** | 1,440.73 | 720.87 | 1,423.71 | 712.36 | 1,422.72 | 711.86 | **12** |
| **6** | **717.35** | 359.18 | 699.34 | 350.18 | **E** | 1,325.71 | 663.36 | 1,308.68 | 654.84 | 1,307.70 | 654.35 | **11** |
| **7** | **832.38** | 416.69 | **814.37** | 407.69 | **D** | 1,196.66 | 598.84 | 1,179.64 | 590.32 | 1,178.65 | 589.83 | **10** |
| **8** | **933.43** | 467.22 | **915.42** | 458.21 | **T** | **1,081.64** | 541.32 | 1,064.61 | 532.81 | 1,063.63 | 532.32 | **9** |
| **9** | **1,046.51** | 523.76 | **1,028.50** | 514.75 | **I** | **980.59** | 490.80 | 963.56 | 482.28 | 962.58 | 481.79 | **8** |
| **10** | 1,159.60 | 580.30 | 1,141.59 | 571.30 | **I** | **867.50** | 434.26 | 850.48 | 425.74 | 849.49 | 425.25 | **7** |
| **11** | **1,274.62** | 637.82 | 1,256.61 | 628.81 | **D** | **754.42** | 377.71 | **737.39** | 369.20 | 736.41 | 368.71 | **6** |
| **12** | 1,387.71 | 694.36 | 1,369.70 | 685.35 | **I** | 639.39 | 320.20 | **622.37** | 311.69 | 621.38 | 311.20 | **5** |
| **13** | 1,500.79 | 750.90 | 1,482.78 | 741.89 | **I** | **526.31** | 263.66 | 509.28 | 255.15 | 508.30 | 254.65 | **4** |
| **14** | 1,601.84 | 801.42 | 1,583.83 | 792.42 | **T** | **413.23** | 207.12 | 396.20 | 198.60 | 395.21 | 198.11 | **3** |
| **15** | 1,738.90 | 869.95 | 1,720.89 | 860.95 | **H** | **312.18** | 156.59 | **295.15** | 148.08 | | | **2** |
| **16** | | | | | **R** | **175.12** | 88.06 | 158.09 | 79.55 | | | **1** |

Query 1785 Hit 1

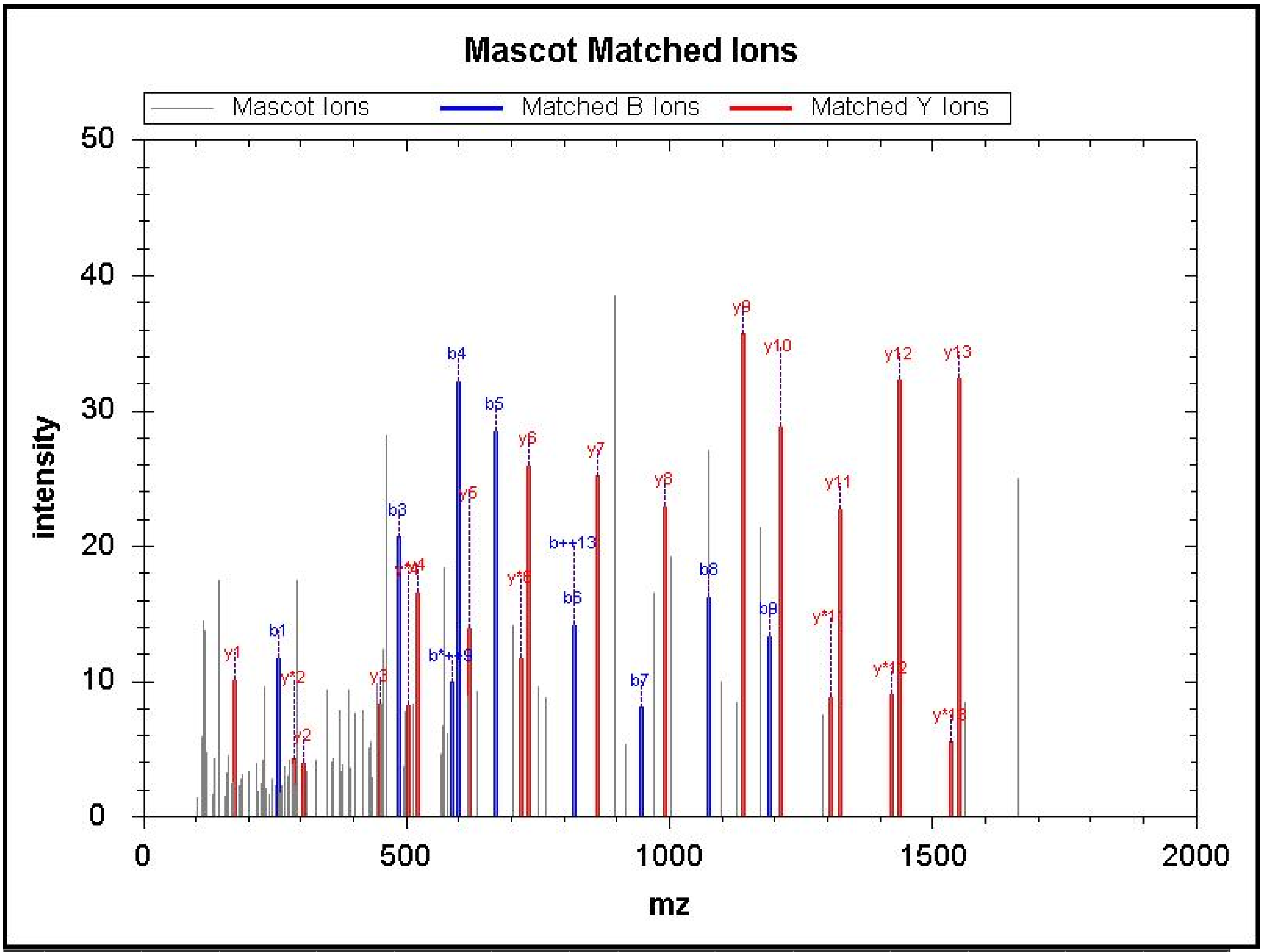
MS/MS Fragmentation of **ILTFDQLALDSPK**
Found in **sp|Q07020|RL18_HUMAN**, 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2
Match to Query 1785: 1747.995from(875.0048,2+)
Title: 775: Sum of 2 scans in range 2121 (rt=55.7811, f=4, i=542) to 2122 (rt=55.8065, f=4, i=543)
[D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1747.995
**Variable modifications:**
**K13** :iTRAQ4plex (K)
**Ions Score:** 70.96 **Expect:** 0.000



| **No** | **b** | **b++** | **b*** | **b*++** | **b0** | **b0++** | **Seq** | **y** | **y++** | **y*** | **y*++** | **y0** | **y0++** | **RevNo** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | **258.19** | 129.60 | | | | | **I** | | | | | | | **13** |
| **2** | **371.28** | 186.14 | | | | | **L** | **1,491.82** | 746.41 | 1,474.79 | 737.90 | 1,473.81 | 737.41 | **12** |
| **3** | **472.33** | 236.67 | | | **454.31** | 227.66 | **T** | **1,378.73** | 689.87 | 1,361.71 | 681.36 | **1,360.72** | 680.87 | **11** |
| **4** | 619.39 | 310.20 | | | **601.38** | 301.20 | **F** | **1,277.69** | 639.35 | 1,260.66 | 630.83 | 1,259.68 | 630.34 | **10** |
| **5** | **734.42** | 367.71 | | | 716.41 | 358.71 | **D** | **1,130.62** | 565.81 | 1,113.59 | 557.30 | 1,112.61 | 556.81 | **9** |
| **6** | **862.48** | 431.74 | 845.45 | 423.23 | 844.47 | 422.74 | **Q** | **1,015.59** | 508.30 | 998.56 | 499.79 | 997.58 | 499.29 | **8** |
| **7** | **975.56** | 488.29 | 958.54 | 479.77 | 957.55 | 479.28 | **L** | **887.53** | 444.27 | 870.51 | 435.76 | 869.52 | 435.26 | **7** |
| **8** | **1,046.60** | 523.80 | 1,029.57 | 515.29 | 1,028.59 | 514.80 | **A** | **774.45** | 387.73 | 757.42 | 379.21 | 756.44 | 378.72 | **6** |
| **9** | 1,159.68 | 580.35 | 1,142.66 | 571.83 | 1,141.67 | 571.34 | **L** | **703.41** | 352.21 | 686.38 | 343.70 | 685.40 | 343.20 | **5** |
| **10** | **1,274.71** | 637.86 | 1,257.68 | 629.35 | 1,256.70 | 628.85 | **D** | **590.33** | 295.67 | 573.30 | 287.15 | **572.32** | 286.66 | **4** |
| **11** | 1,361.74 | 681.38 | 1,344.72 | 672.86 | 1,343.73 | 672.37 | **S** | **475.30** | 238.15 | 458.27 | 229.64 | 457.29 | 229.15 | **3** |
| **12** | 1,458.80 | 729.90 | 1,441.77 | 721.39 | 1,440.79 | 720.90 | **P** | **388.27** | 194.64 | **371.24** | 186.12 | | | **2** |
| **13** | | | | | | | **K** | **291.21** | 146.11 | 274.19 | 137.60 | | | **1** |

Query 1866 Hit 1

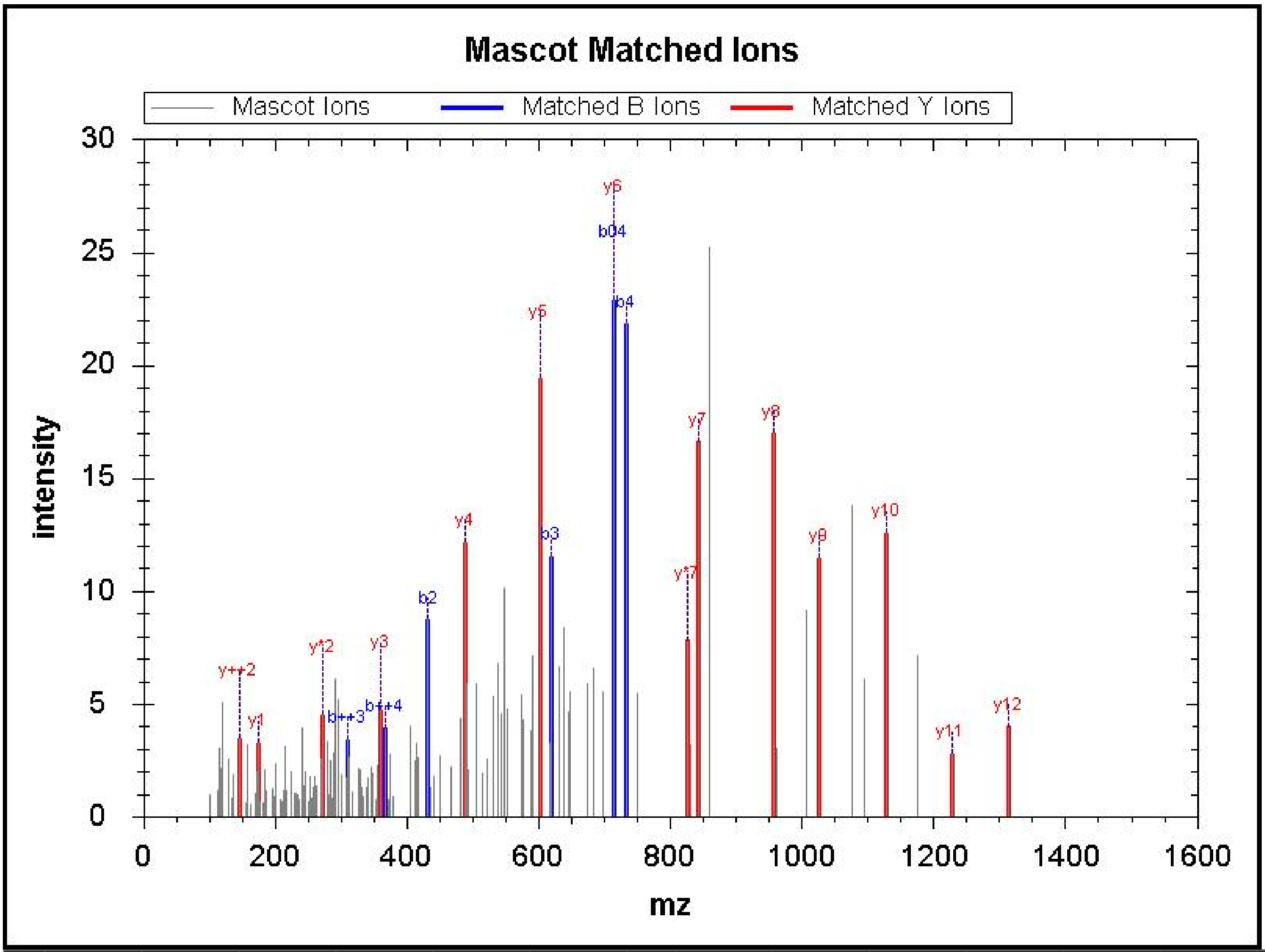
MS/MS Fragmentation of **LLNNAFEELVAFQR**
Found in **sp|P25205|MCM3_HUMAN**, DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3
Match to Query 1866: 1806.977from(904.4958,2+)
Title: 1008: Sum of 2 scans in range 2629 (rt=67.229, f=4, i=706) to 2630 (rt=67.2544, f=4, i=707) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1806.977
**Variable modifications:**
**Ions Score:** 69.62 **Expect:** 0.000



| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | **258.19** | 129.60 | | | | | **L** | | | | | | | **14** |
| **2** | 371.28 | 186.14 | | | | | **L** | **1,550.80** | 775.90 | **1,533.77** | 767.39 | 1,532.79 | 766.90 | **13** |
| **3** | **485.32** | 243.16 | 468.29 | 234.65 | | | **N** | **1,437.71** | 719.36 | **1,420.69** | 710.85 | 1,419.70 | 710.35 | **12** |
| **4** | **599.36** | 300.19 | 582.34 | 291.67 | | | **N** | **1,323.67** | 662.34 | **1,306.64** | 653.83 | 1,305.66 | 653.33 | **11** |
| **5** | **670.40** | 335.70 | 653.37 | 327.19 | | | **A** | **1,209.63** | 605.32 | 1,192.60 | 596.80 | 1,191.62 | 596.31 | **10** |
| **6** | **817.47** | 409.24 | 800.44 | 400.72 | | | **F** | **1,138.59** | 569.80 | 1,121.56 | 561.28 | 1,120.58 | 560.79 | **9** |
| **7** | **946.51** | 473.76 | 929.48 | 465.25 | 928.50 | 464.75 | **E** | **991.52** | 496.26 | 974.49 | 487.75 | 973.51 | 487.26 | **8** |
| **8** | **1,075.55** | 538.28 | 1,058.53 | 529.77 | 1,057.54 | 529.28 | **E** | **862.48** | 431.74 | 845.45 | 423.23 | 844.47 | 422.74 | **7** |
| **9** | **1,188.64** | 594.82 | 1,171.61 | **586.31** | 1,170.63 | 585.82 | **L** | **733.44** | 367.22 | **716.41** | 358.71 | | | **6** |
| **10** | 1,287.71 | 644.36 | 1,270.68 | 635.84 | 1,269.70 | 635.35 | **V** | **620.35** | 310.68 | 603.32 | 302.17 | | | **5** |
| **11** | 1,358.74 | 679.88 | 1,341.72 | 671.36 | 1,340.73 | 670.87 | **A** | **521.28** | 261.15 | **504.26** | 252.63 | | | **4** |
| **12** | 1,505.81 | 753.41 | 1,488.79 | 744.90 | 1,487.80 | 744.40 | **F** | **450.25** | 225.63 | 433.22 | 217.11 | | | **3** |
| **13** | 1,633.87 | **817.44** | 1,616.84 | 808.93 | 1,615.86 | 808.43 | **Q** | **303.18** | 152.09 | **286.15** | 143.58 | | | **2** |
| **14** | | | | | | | **R** | **175.12** | 88.06 | 158.09 | 79.55 | | | **1** |

Query 2474 Hit 1

MS/MS Fragmentation of **TWWNQFSVTALQLLQANR**
Found in **sp|Q99536|VAT1_HUMAN**, Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2
Match to Query 2474: 2320.234from(774.4186,3+)
Title: 1223: Scan 2971 (rt=75.3806, f=3, i=428) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2320.234
**Variable modifications:**
**Q5** :Deamidated (NQ)
**Ions Score:** 66.23 **Expect:** 0.000

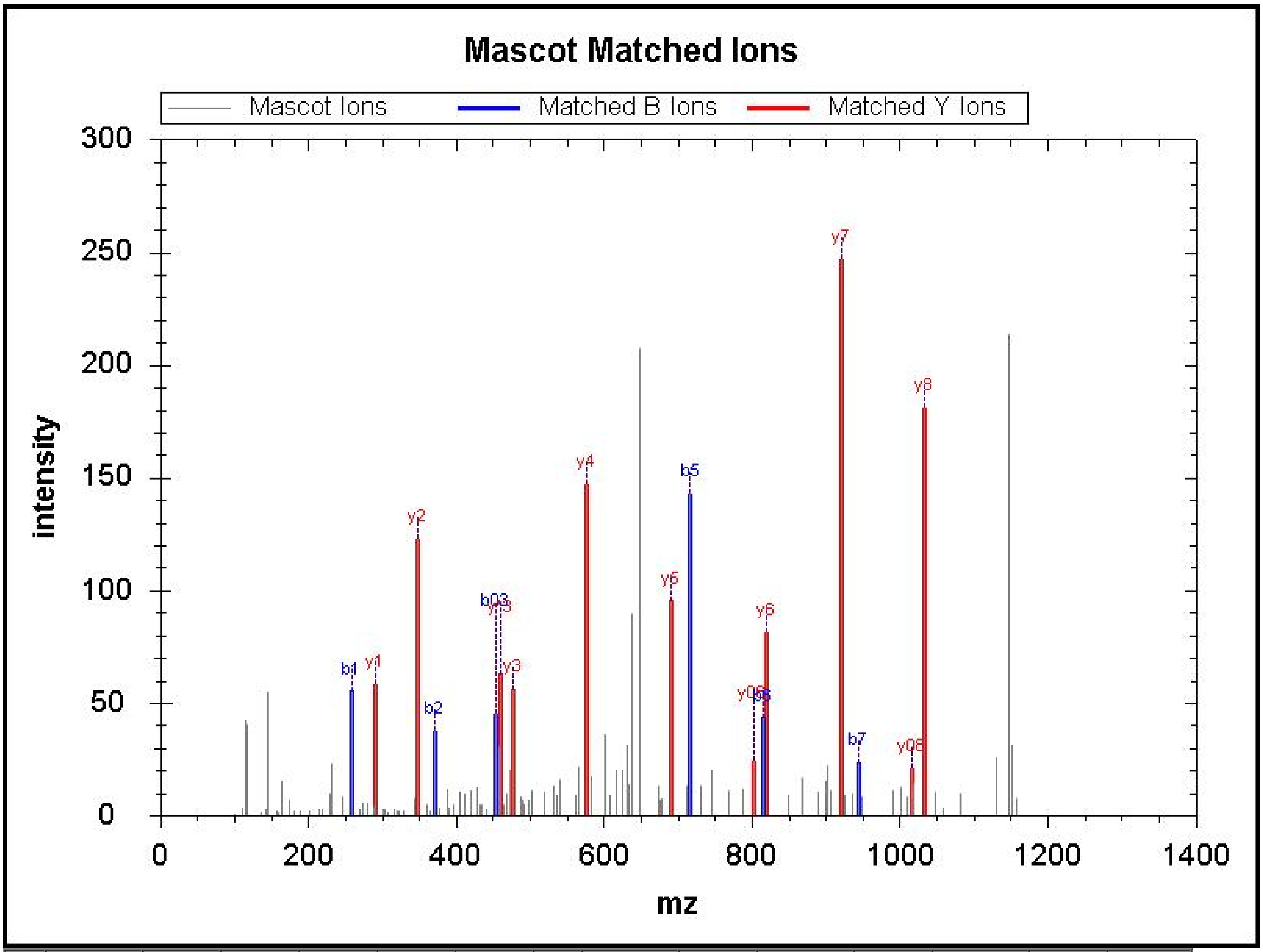


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 246.16 | 123.58 | | | 228.15 | 114.58 | T | | | | | | | 18 |
| 2 | **432.24** | 216.62 | | | 414.23 | 207.62 | W | 2,076.07 | 1,038.54 | 2,059.04 | 1,030.02 | 2,058.06 | 1,029.53 | 17 |
| 3 | **618.32** | **309.66** | | | 600.31 | 300.66 | W | 1,889.99 | 945.50 | 1,872.96 | 936.98 | 1,871.98 | 936.49 | 16 |
| 4 | **732.36** | **366.68** | 715.33 | 358.17 | **714.35** | 357.68 | N | 1,703.91 | 852.46 | 1,686.88 | 843.94 | 1,685.90 | 843.45 | 15 |
| 5 | 861.40 | 431.20 | 844.37 | 422.69 | 843.39 | 422.20 | Q | 1,589.86 | 795.44 | 1,572.84 | 786.92 | 1,571.85 | 786.43 | 14 |
| 6 | 1,008.47 | 504.74 | 991.44 | 496.23 | 990.46 | 495.73 | F | 1,460.82 | 730.91 | 1,443.80 | 722.40 | 1,442.81 | 721.91 | 13 |
| 7 | 1,095.50 | 548.25 | 1,078.48 | 539.74 | 1,077.49 | 539.25 | S | **1,313.75** | 657.38 | 1,296.73 | 648.87 | 1,295.74 | 648.38 | 12 |
| 8 | 1,194.57 | 597.79 | 1,177.54 | 589.28 | 1,176.56 | 588.78 | V | **1,226.72** | 613.86 | 1,209.69 | 605.35 | 1,208.71 | 604.86 | 11 |
| 9 | 1,295.62 | 648.31 | 1,278.59 | 639.80 | 1,277.61 | 639.31 | T | **1,127.65** | 564.33 | 1,110.63 | 555.82 | 1,109.64 | 555.32 | 10 |
| 10 | 1,366.65 | 683.83 | 1,349.63 | 675.32 | 1,348.64 | 674.83 | A | **1,026.61** | 513.81 | 1,009.58 | 505.29 | | | 9 |
| 11 | 1,479.74 | 740.37 | 1,462.71 | 731.86 | 1,461.73 | 731.37 | L | **955.57** | 478.29 | 938.54 | 469.77 | | | 8 |
| 12 | 1,607.80 | 804.40 | 1,590.77 | 795.89 | 1,589.79 | 795.40 | Q | **842.48** | 421.75 | **825.46** | 413.23 | | | 7 |
| 13 | 1,720.88 | 860.94 | 1,703.86 | 852.43 | 1,702.87 | 851.94 | L | **714.43** | 357.72 | 697.40 | 349.20 | | | 6 |
| 14 | 1,833.97 | 917.49 | 1,816.94 | 908.97 | 1,815.96 | 908.48 | L | **601.34** | 301.17 | 584.32 | 292.66 | | | 5 |
| 15 | 1,962.02 | 981.52 | 1,945.00 | 973.00 | 1,944.01 | 972.51 | Q | **488.26** | 244.63 | 471.23 | 236.12 | | | 4 |
| 16 | 2,033.06 | 1,017.03 | 2,016.03 | 1,008.52 | 2,015.05 | 1,008.03 | A | **360.20** | 180.60 | 343.17 | 172.09 | | | 3 |
| 17 | 2,147.10 | 1,074.06 | 2,130.08 | 1,065.54 | 2,129.09 | 1,065.05 | N | 289.16 | **145.08** | **272.14** | 136.57 | | | 2 |
| 18 | | | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 995 Hit 1

MS/MS Fragmentation of **LITEDVQGK**
Found in **sp|P61247|RS3A_HUMAN**, 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2
Match to Query 995: 1289.75from(645.8821,2+)

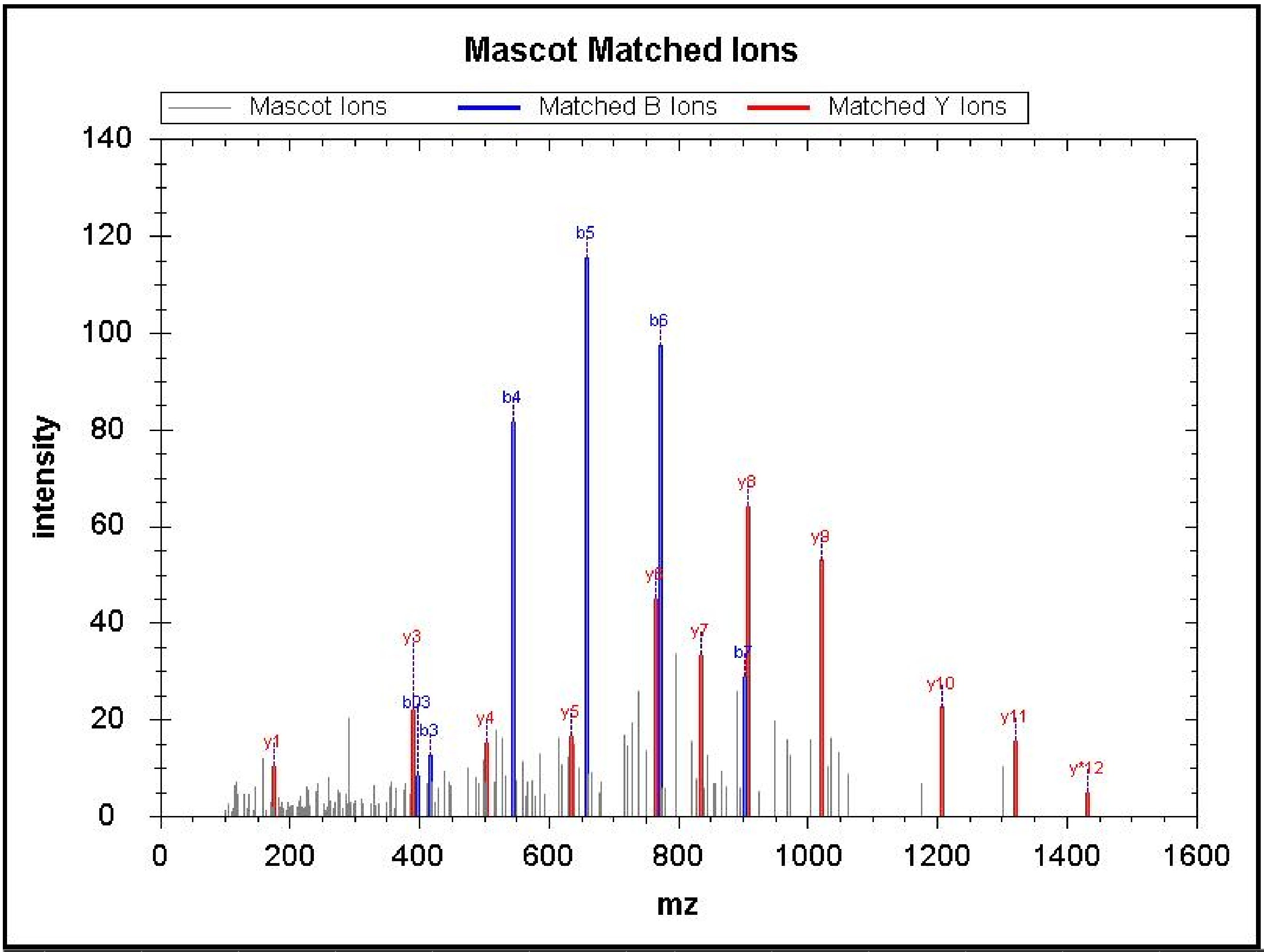
Title: 323: Sum of 2 scans in range 1147 (rt=33.8356, f=4, i=228) to 1148 (rt=33.861, f=4, i=229)
[D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1289.75
**Variable modifications:**
**K9** :iTRAQ4plex (K)
**Ions Score:** 66.2 **Expect:** 0.000



| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | **258.19** | 129.60 | | | | | **L** | | | | | | | **9** |
| **2** | **371.28** | 186.14 | | | | | **I** | **1,033.56** | 517.29 | 1,016.54 | 508.77 | **1,015.55** | 508.28 | **8** |
| **3** | 472.33 | 236.67 | | | **454.31** | 227.66 | **T** | **920.48** | 460.74 | 903.45 | 452.23 | 902.47 | 451.74 | **7** |
| **4** | 601.37 | 301.19 | | | 583.36 | 292.18 | **E** | **819.43** | 410.22 | 802.41 | 401.71 | **801.42** | 401.21 | **6** |
| **5** | **716.39** | 358.70 | | | 698.38 | 349.70 | **D** | **690.39** | 345.70 | 673.36 | 337.19 | 672.38 | 336.69 | **5** |
| **6** | **815.46** | 408.24 | | | 797.45 | 399.23 | **V** | **575.36** | 288.19 | 558.34 | 279.67 | | | **4** |
| **7** | **943.52** | 472.26 | 926.50 | 463.75 | 925.51 | 463.26 | **Q** | **476.29** | 238.65 | **459.27** | 230.14 | | | **3** |
| **8** | 1,000.54 | 500.78 | 983.52 | 492.26 | 982.53 | 491.77 | **G** | **348.24** | 174.62 | 331.21 | 166.11 | | | **2** |
| **9** | | | | | | | **K** | **291.21** | 146.11 | 274.19 | 137.60 | | | **1** |

Query 2490 Hit 1

MS/MS Fragmentation of **LASEILMQNWDAAMEDLTR**
Found in **sp|P60228|EIF3E_HUMAN**, Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1
Match to Query 2490: 2350.149from(784.3903,3+)
Title: 1190: Sum of 2 scans in range 3045 (rt=76.6007, f=4, i=840) to 3046 (rt=76.6262, f=4, i=841)
[D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2350.149
**Variable modifications:**
**Ions Score:** 66.06 **Expect:** 0.000

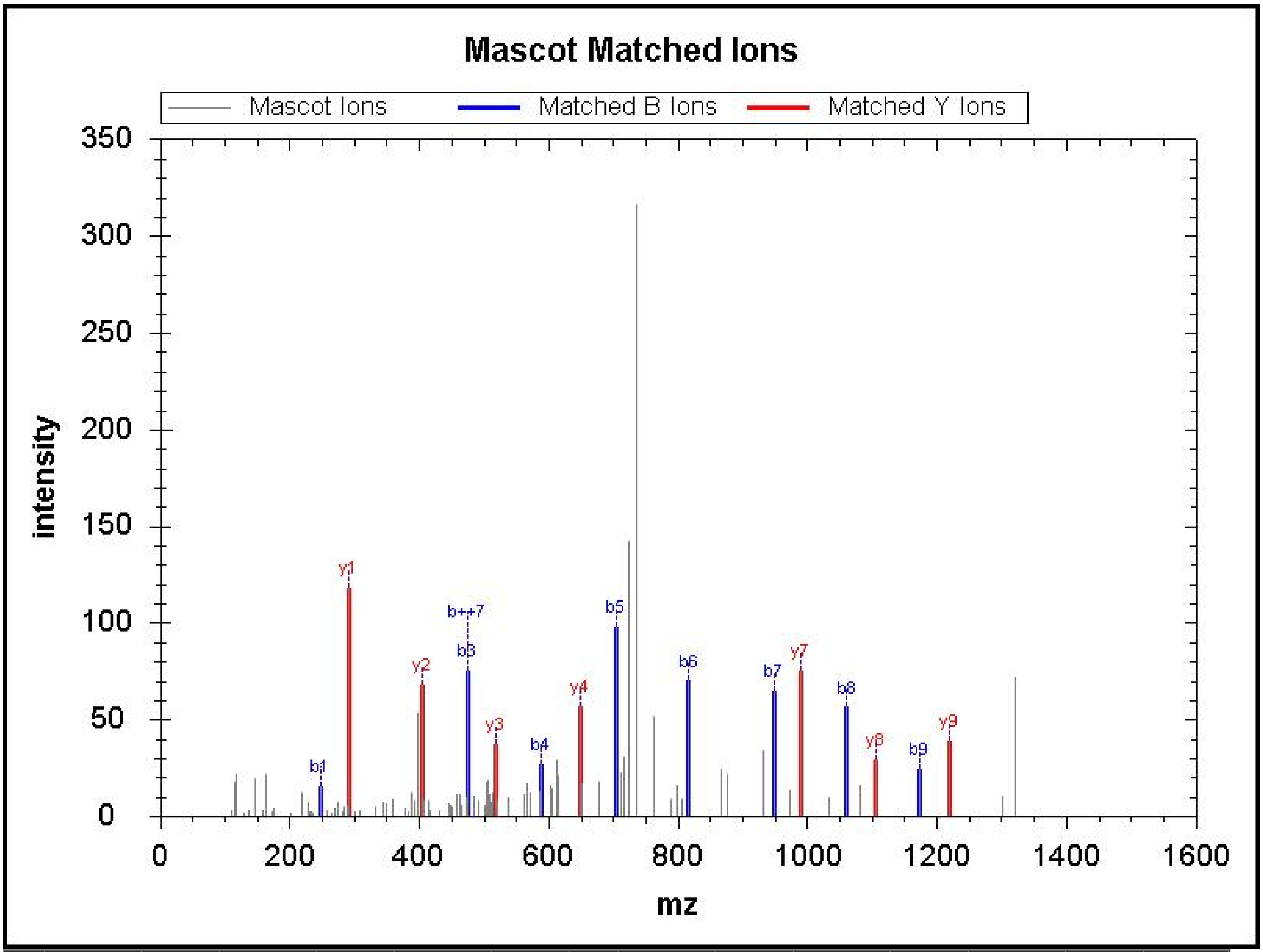


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | | | | | L | | | | | | | 19 |
| 2 | 329.23 | 165.12 | | | | | A | 2,093.96 | 1,047.49 | 2,076.94 | 1,038.97 | 2,075.95 | 1,038.48 | 18 |
| 3 | **416.26** | 208.63 | | | **398.25** | 199.63 | S | 2,022.93 | 1,011.97 | 2,005.90 | 1,003.45 | 2,004.92 | 1,002.96 | 17 |
| 4 | **545.31** | 273.16 | | | 527.29 | 264.15 | E | 1,935.89 | 968.45 | 1,918.87 | 959.94 | 1,917.88 | 959.45 | 16 |
| 5 | **658.39** | 329.70 | | | 640.38 | 320.69 | I | 1,806.85 | 903.93 | 1,789.82 | 895.42 | 1,788.84 | 894.92 | 15 |
| 6 | **771.47** | 386.24 | | | 753.46 | 377.23 | L | 1,693.77 | 847.39 | 1,676.74 | 838.87 | 1,675.76 | 838.38 | 14 |
| 7 | **902.51** | 451.76 | | | 884.50 | 442.76 | M | 1,580.68 | 790.85 | 1,563.66 | 782.33 | 1,562.67 | 781.84 | 13 |
| 8 | 1,030.57 | 515.79 | 1,013.55 | 507.28 | 1,012.56 | 506.78 | Q | 1,449.64 | 725.33 | **1,432.62** | 716.81 | 1,431.63 | 716.32 | 12 |
| 9 | 1,144.62 | 572.81 | 1,127.59 | 564.30 | 1,126.60 | 563.81 | N | **1,321.58** | 661.30 | 1,304.56 | 652.78 | 1,303.57 | 652.29 | 11 |
| 10 | 1,330.69 | 665.85 | 1,313.67 | 657.34 | 1,312.68 | 656.85 | W | **1,207.54** | 604.27 | 1,190.51 | 595.76 | 1,189.53 | 595.27 | 10 |
| 11 | 1,445.72 | 723.36 | 1,428.70 | 714.85 | 1,427.71 | 714.36 | D | **1,021.46** | 511.23 | 1,004.44 | 502.72 | 1,003.45 | 502.23 | 9 |
| 12 | 1,516.76 | 758.88 | 1,499.73 | 750.37 | 1,498.75 | 749.88 | A | **906.43** | 453.72 | 889.41 | 445.21 | 888.42 | 444.72 | 8 |
| 13 | 1,587.80 | 794.40 | 1,570.77 | 785.89 | 1,569.79 | 785.40 | A | **835.40** | 418.20 | 818.37 | 409.69 | 817.39 | 409.20 | 7 |
| 14 | 1,718.84 | 859.92 | 1,701.81 | 851.41 | 1,700.83 | 850.92 | M | **764.36** | 382.68 | 747.33 | 374.17 | 746.35 | 373.68 | 6 |
| 15 | 1,847.88 | 924.44 | 1,830.85 | 915.93 | 1,829.87 | 915.44 | E | **633.32** | 317.16 | 616.29 | 308.65 | 615.31 | 308.16 | 5 |
| 16 | 1,962.91 | 981.96 | 1,945.88 | 973.44 | 1,944.90 | 972.95 | D | **504.28** | 252.64 | 487.25 | 244.13 | 486.27 | 243.64 | 4 |
| 17 | 2,075.99 | 1,038.50 | 2,058.96 | 1,029.99 | 2,057.98 | 1,029.49 | L | **389.25** | 195.13 | 372.22 | 186.62 | 371.24 | 186.12 | 3 |
| 18 | 2,177.04 | 1,089.02 | 2,160.01 | 1,080.51 | 2,159.03 | 1,080.02 | T | 276.17 | 138.59 | 259.14 | 130.07 | 258.16 | 129.58 | 2 |
| 19 | | | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 1341 Hit 1

MS/MS Fragmentation of **TLNNDIMLIK**
Found in **sp|P07477|TRY1_HUMAN**, Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=1 SV=1

Match to Query 1341: 1462.833from(732.4239,2+)
Title: 692: Sum of 2 scans in range 1819 (rt=49.4253, f=4, i=478) to 1820 (rt=49.4507, f=4, i=479)
[D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1462.833
**Variable modifications:**
**N3** :Deamidated (NQ)
**K10** :iTRAQ4plex (K)
**Ions Score:** 64.81 **Expect:** 0.000

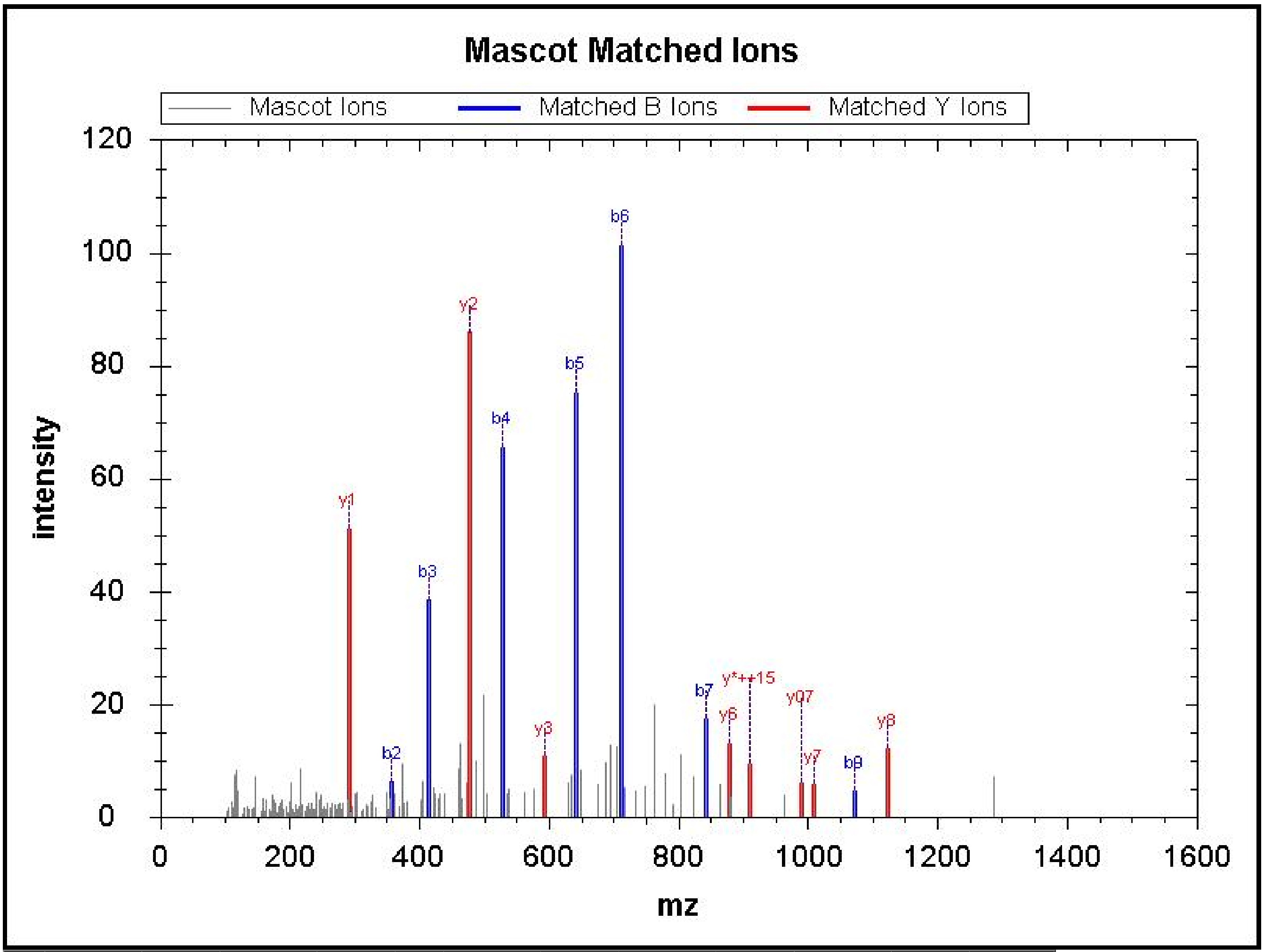


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **246.16** | 123.58 | | | 228.15 | 114.58 | T | | | | | | | 10 |
| 2 | 359.24 | 180.12 | | | 341.23 | 171.12 | L | **1,218.69** | 609.85 | 1,201.66 | 601.33 | 1,200.68 | 600.84 | 9 |
| 3 | **474.27** | 237.64 | 457.24 | 229.12 | 456.26 | 228.63 | N | **1,105.60** | 553.31 | 1,088.58 | 544.79 | 1,087.59 | 544.30 | 8 |
| 4 | **588.31** | 294.66 | 571.28 | 286.15 | 570.30 | 285.65 | N | **990.58** | 495.79 | 973.55 | 487.28 | 972.57 | 486.79 | 7 |
| 5 | **703.34** | 352.17 | 686.31 | 343.66 | 685.33 | 343.17 | D | 876.53 | 438.77 | 859.51 | 430.26 | 858.52 | 429.77 | 6 |
| 6 | **816.42** | 408.71 | 799.40 | 400.20 | 798.41 | 399.71 | I | 761.51 | 381.26 | 744.48 | 372.74 | | | 5 |
| 7 | **947.46** | **474.23** | 930.44 | 465.72 | 929.45 | 465.23 | M | **648.42** | 324.72 | 631.40 | 316.20 | | | 4 |
| 8 | **1,060.55** | 530.78 | 1,043.52 | 522.26 | 1,042.54 | 521.77 | L | **517.38** | 259.20 | 500.36 | 250.68 | | | 3 |
| 9 | **1,173.63** | 587.32 | 1,156.60 | 578.81 | 1,155.62 | 578.31 | I | **404.30** | 202.65 | 387.27 | 194.14 | | | 2 |
| 10 | | | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 2212 Hit 1

MS/MS Fragmentation of **VLGILAMIDEGETDWK**
Found in **sp|Q15181|IPYR_HUMAN**, Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2
Match to Query 2212: 2077.115from(693.3789,3+)
Title: 1121: Sum of 2 scans in range 2871 (rt=72.6813, f=4, i=784) to 2872 (rt=72.7067, f=4, i=785)
[D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]

Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2077.115
**Variable modifications:**
**K16** :iTRAQ4plex (K)
**Ions Score:** 62.8 **Expect:** 0.000

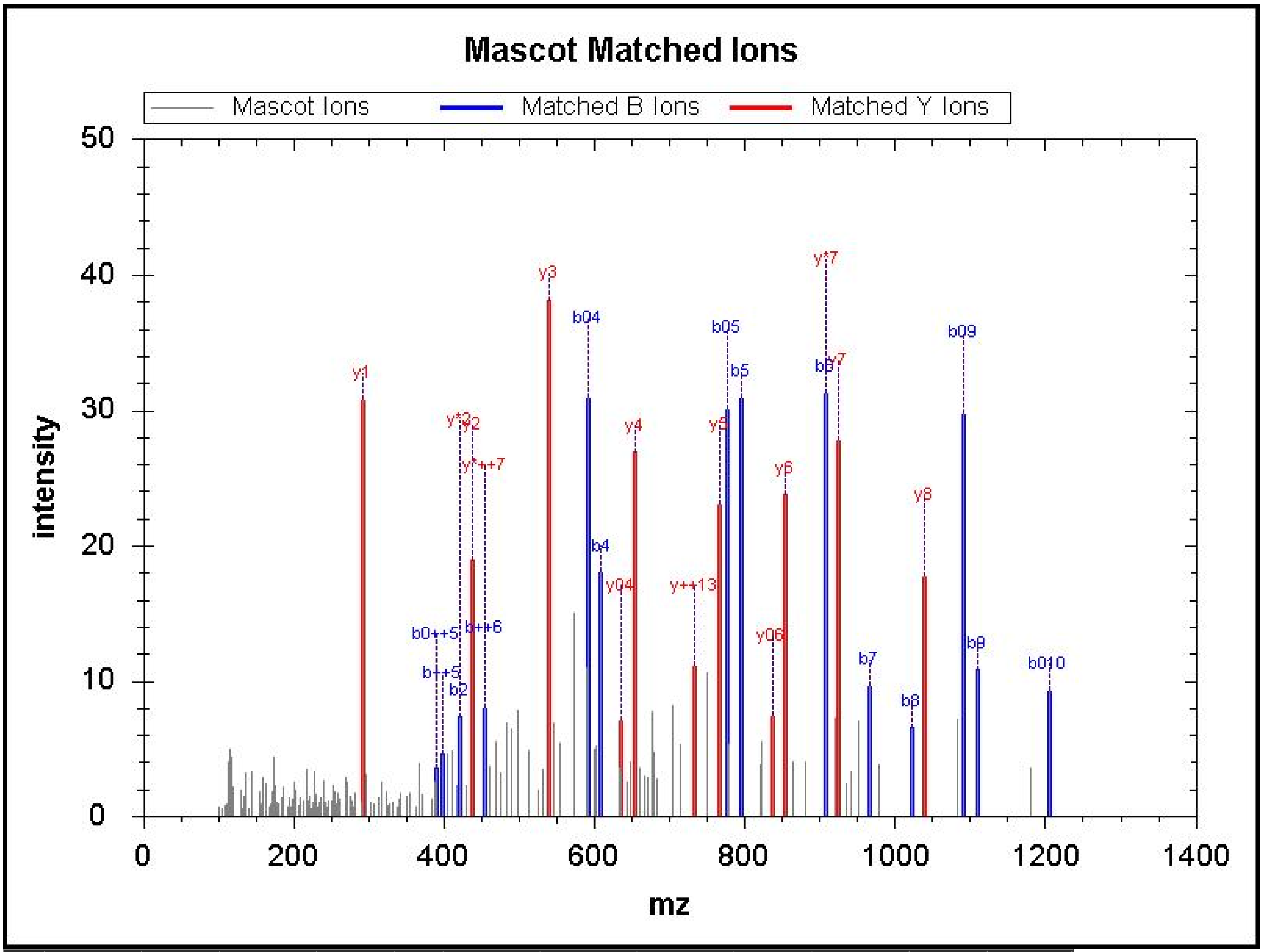


| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 244.18 | 122.59 | | | V | | | | | | | 16 |
| 2 | **357.26** | 179.13 | | | L | 1,834.94 | 917.97 | 1,817.91 | **909.46** | 1,816.93 | 908.97 | 15 |
| 3 | **414.28** | 207.65 | | | G | 1,721.85 | 861.43 | 1,704.83 | 852.92 | 1,703.84 | 852.43 | 14 |
| 4 | **527.37** | 264.19 | | | I | 1,664.83 | 832.92 | 1,647.81 | 824.41 | 1,646.82 | 823.91 | 13 |
| 5 | **640.45** | 320.73 | | | L | 1,551.75 | 776.38 | 1,534.72 | 767.86 | 1,533.74 | 767.37 | 12 |
| 6 | **711.49** | 356.25 | | | A | 1,438.66 | 719.84 | 1,421.64 | 711.32 | 1,420.65 | 710.83 | 11 |
| 7 | **842.53** | 421.77 | | | M | 1,367.63 | 684.32 | 1,350.60 | 675.80 | 1,349.62 | 675.31 | 10 |
| 8 | 955.61 | 478.31 | | | I | 1,236.59 | 618.80 | 1,219.56 | 610.28 | 1,218.58 | 609.79 | 9 |
| 9 | **1,070.64** | 535.82 | 1,052.63 | 526.82 | D | **1,123.50** | 562.25 | 1,106.48 | 553.74 | 1,105.49 | 553.25 | 8 |
| 10 | 1,199.68 | 600.34 | 1,181.67 | 591.34 | E | **1,008.48** | 504.74 | 991.45 | 496.23 | **990.46** | 495.74 | 7 |
| 11 | 1,256.70 | 628.86 | 1,238.69 | 619.85 | G | **879.43** | 440.22 | 862.41 | 431.71 | 861.42 | 431.21 | 6 |
| 12 | 1,385.75 | 693.38 | 1,367.74 | 684.37 | E | 822.41 | 411.71 | 805.38 | 403.20 | 804.40 | 402.70 | 5 |
| 13 | 1,486.79 | 743.90 | 1,468.78 | 734.90 | T | 693.37 | 347.19 | 676.34 | 338.67 | 675.36 | 338.18 | 4 |
| 14 | 1,601.82 | 801.41 | 1,583.81 | 792.41 | D | **592.32** | 296.66 | 575.29 | 288.15 | 574.31 | 287.66 | 3 |
| 15 | 1,787.90 | 894.45 | 1,769.89 | 885.45 | W | **477.29** | 239.15 | 460.27 | 230.64 | | | 2 |
| 16 | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 2416 Hit 1

MS/MS Fragmentation of **LYSTWIGGSILASLDTFK**

Found in sp|P42025|ACTY_HUMAN, Beta-centractin OS=Homo sapiens GN=ACTR1B PE=1 SV=1
Match to Query 2416: 2259.252from(754.0912,3+)
Title: 1241: Sum of 2 scans in range 3009 (rt=76.2404, f=4, i=862) to 3010 (rt=76.2658, f=4, i=863) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2259.252
**Variable modifications:**
**K18** :iTRAQ4plex (K)
**Ions Score:** 62.63 **Expect:** 0.000

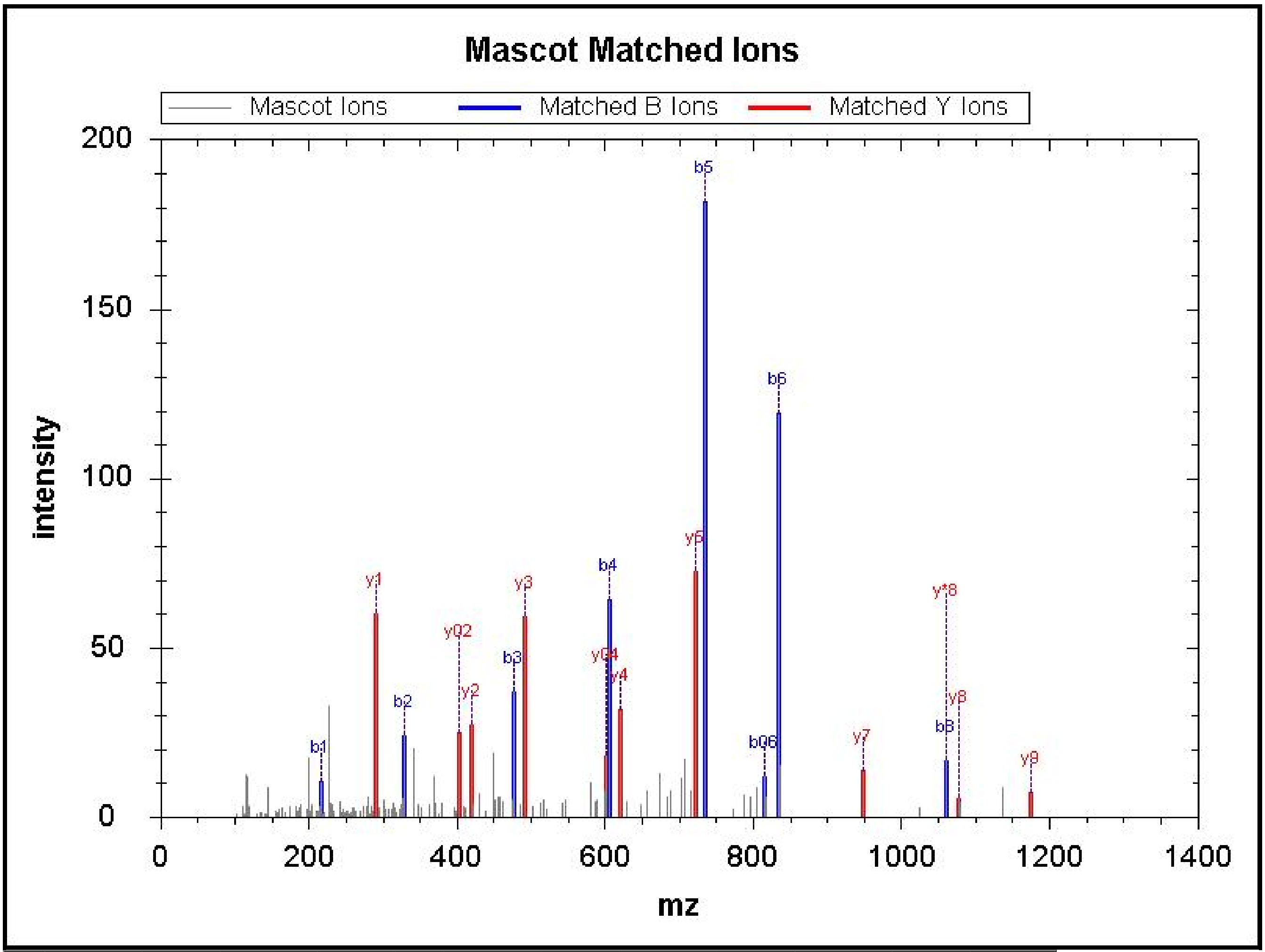


| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | | | L | | | | | | | 18 |
| 2 | 421.26 | 211.13 | | | Y | 2,003.06 | 1,002.03 | 1,986.03 | 993.52 | 1,985.05 | 993.03 | 17 |
| 3 | 508.29 | 254.65 | 490.28 | 245.64 | S | 1,840.00 | 920.50 | 1,822.97 | 911.99 | 1,821.99 | 911.50 | 16 |
| 4 | 609.34 | 305.17 | 591.33 | 296.17 | T | 1,752.97 | 876.99 | 1,735.94 | 868.47 | 1,734.95 | 867.98 | 15 |
| 5 | 795.42 | 398.21 | 777.41 | 389.21 | W | 1,651.92 | 826.46 | 1,634.89 | 817.95 | 1,633.91 | 817.46 | 14 |
| 6 | 908.50 | 454.75 | 890.49 | 445.75 | I | 1,465.84 | 733.42 | 1,448.81 | 724.91 | 1,447.83 | 724.42 | 13 |
| 7 | 965.52 | 483.26 | 947.51 | 474.26 | G | 1,352.75 | 676.88 | 1,335.73 | 668.37 | 1,334.74 | 667.88 | 12 |
| 8 | 1,022.54 | 511.77 | 1,004.53 | 502.77 | G | 1,295.73 | 648.37 | 1,278.71 | 639.86 | 1,277.72 | 639.36 | 11 |
| 9 | 1,109.57 | 555.29 | 1,091.56 | 546.29 | S | 1,238.71 | 619.86 | 1,221.68 | 611.35 | 1,220.70 | 610.85 | 10 |
| 10 | 1,222.66 | 611.83 | 1,204.65 | 602.83 | I | 1,151.68 | 576.34 | 1,134.65 | 567.83 | 1,133.67 | 567.34 | 9 |
| 11 | 1,335.74 | 668.38 | 1,317.73 | 659.37 | L | 1,038.60 | 519.80 | 1,021.57 | 511.29 | 1,020.58 | 510.80 | 8 |
| 12 | 1,406.78 | 703.89 | 1,388.77 | 694.89 | A | 925.51 | 463.26 | 908.48 | 454.75 | 907.50 | 454.25 | 7 |
| 13 | 1,493.81 | 747.41 | 1,475.80 | 738.40 | S | 854.47 | 427.74 | 837.45 | 419.23 | 836.46 | 418.74 | 6 |
| 14 | 1,606.90 | 803.95 | 1,588.89 | 794.95 | L | 767.44 | 384.22 | 750.42 | 375.71 | 749.43 | 375.22 | 5 |
| 15 | 1,721.92 | 861.47 | 1,703.91 | 852.46 | D | 654.36 | 327.68 | 637.33 | 319.17 | 636.35 | 318.68 | 4 |
| 16 | 1,822.97 | 911.99 | 1,804.96 | 902.98 | T | 539.33 | 270.17 | 522.30 | 261.66 | 521.32 | 261.16 | 3 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **17** | 1,970.04 | 985.52 | 1,952.03 | 976.52 | **F** | **438.28** | 219.65 | **421.26** | 211.13 |  |  | **2** |
| **18** |  |  |  |  | **K** | **291.21** | 146.11 | 274.19 | 137.60 |  |  | **1** |

Query 2116 Hit 1

MS/MS Fragmentation of **ALFEEVPELLTEAEK**
Found in **sp|P31939|PUR9_HUMAN**, Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3
Match to Query 2116: 2005.098from(669.3732,3+)
Title: 1028: Sum of 2 scans in range 2544 (rt=65.7625, f=4, i=712) to 2545 (rt=65.7879, f=4, i=713) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2005.098
**Variable modifications:**
**K15** :iTRAQ4plex (K)
**Ions Score:** 62.54 **Expect:** 0.000

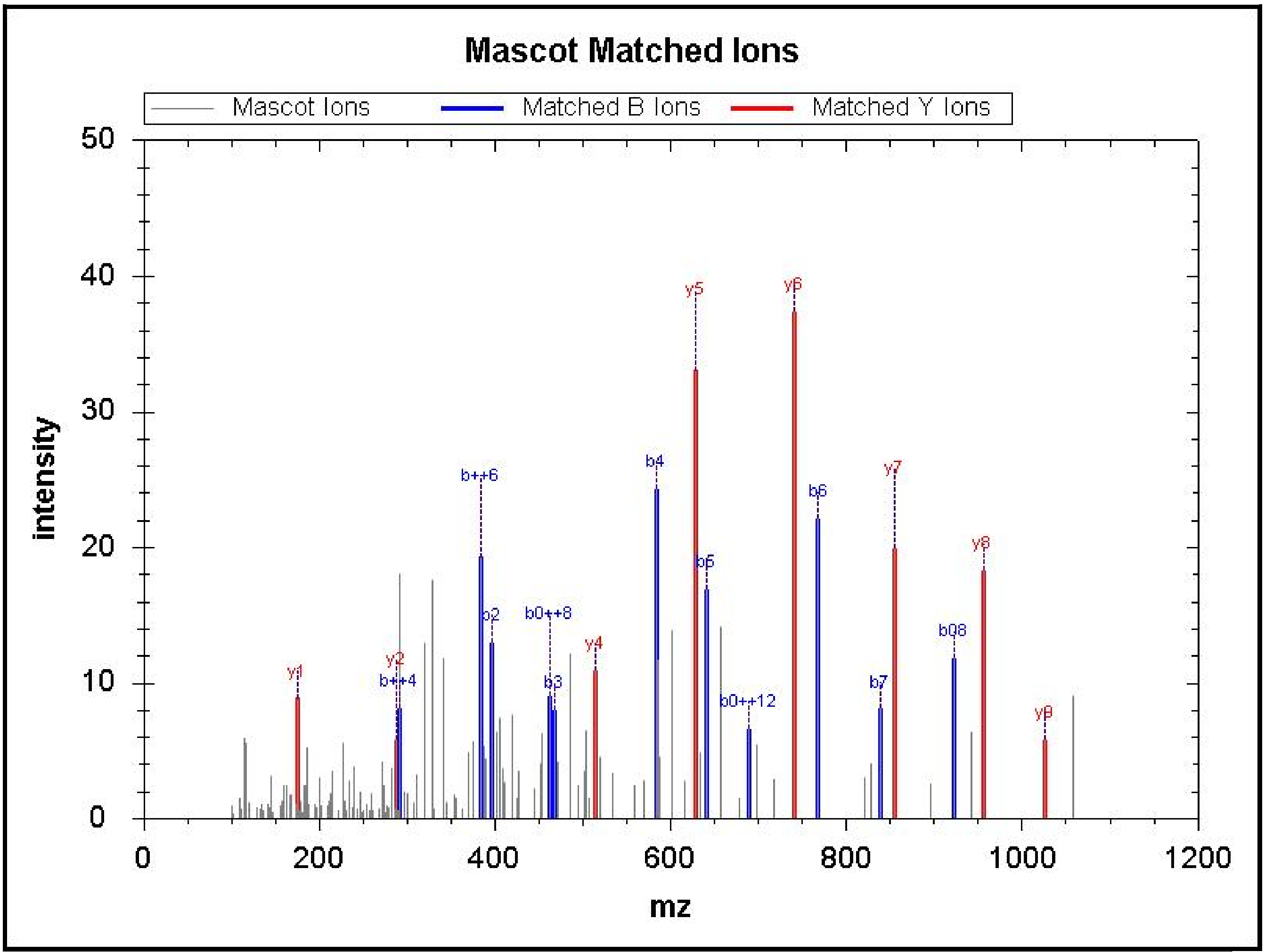


| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | **216.15** | 108.58 |  |  | **A** |  |  |  |  |  |  | **15** |
| **2** | **329.23** | 165.12 |  |  | **L** | 1,790.95 | 895.98 | 1,773.93 | 887.47 | 1,772.94 | 886.98 | **14** |
| **3** | **476.30** | 238.65 |  |  | **F** | 1,677.87 | 839.44 | 1,660.84 | 830.93 | 1,659.86 | 830.43 | **13** |
| **4** | **605.34** | 303.17 | 587.33 | 294.17 | **E** | 1,530.80 | 765.90 | 1,513.78 | 757.39 | 1,512.79 | 756.90 | **12** |
| **5** | **734.38** | 367.70 | 716.37 | 358.69 | **E** | 1,401.76 | 701.38 | 1,384.73 | 692.87 | 1,383.75 | 692.38 | **11** |
| **6** | **833.45** | 417.23 | **815.44** | 408.22 | **V** | 1,272.72 | 636.86 | 1,255.69 | 628.35 | 1,254.71 | 627.86 | **10** |
| **7** | 930.51 | 465.76 | 912.49 | 456.75 | **P** | **1,173.65** | 587.33 | 1,156.62 | 578.81 | 1,155.64 | 578.32 | **9** |
| **8** | **1,059.55** | 530.28 | 1,041.54 | 521.27 | **E** | **1,076.60** | 538.80 | **1,059.57** | 530.29 | 1,058.58 | 529.80 | **8** |
| **9** | 1,172.63 | 586.82 | 1,154.62 | 577.81 | **L** | **947.55** | 474.28 | 930.53 | 465.77 | 929.54 | 465.27 | **7** |
| **10** | 1,285.72 | 643.36 | 1,267.71 | 634.36 | **L** | 834.47 | 417.74 | 817.44 | 409.22 | 816.46 | 408.73 | **6** |
| **11** | 1,386.76 | 693.89 | 1,368.75 | 684.88 | **T** | **721.38** | 361.20 | 704.36 | 352.68 | 703.37 | 352.19 | **5** |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 12 | 1,515.81 | 758.41 | 1,497.80 | 749.40 | E | **620.34** | 310.67 | 603.31 | 302.16 | **602.33** | 301.67 | 4 |
| 13 | 1,586.84 | 793.93 | 1,568.83 | 784.92 | A | **491.29** | 246.15 | 474.27 | 237.64 | 473.28 | 237.15 | 3 |
| 14 | 1,715.89 | 858.45 | 1,697.88 | 849.44 | E | **420.26** | 210.63 | 403.23 | 202.12 | **402.25** | 201.63 | 2 |
| 15 | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 1840 Hit 1

MS/MS Fragmentation of **HDADGQATLLNLLLR**
Found in **sp|O43242|PSMD3_HUMAN**, 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2
Match to Query 1840: 1792.999from(598.6736,3+)
Title: 946: Scan 2363 (rt=61.6818, f=3, i=330) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1792.999
**Variable modifications:**
**Ions Score:** 60.84 **Expect:** 0.001

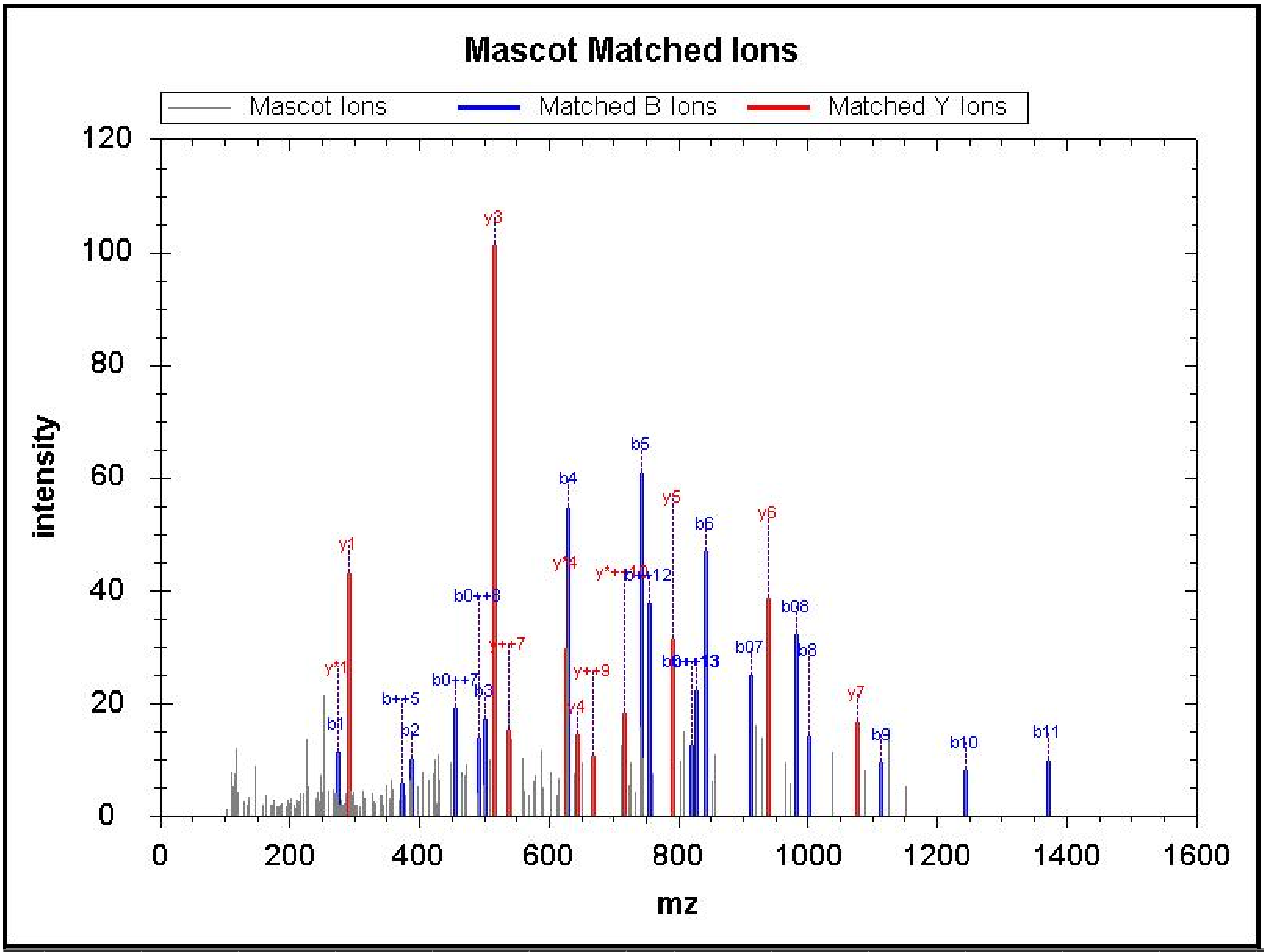


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 282.17 | 141.59 | | | | | H | | | | | | | 15 |
| 2 | **397.20** | 199.10 | | | 379.18 | 190.10 | D | 1,512.84 | 756.92 | 1,495.81 | 748.41 | 1,494.83 | 747.92 | 14 |
| 3 | **468.23** | 234.62 | | | 450.22 | 225.61 | A | 1,397.81 | 699.41 | 1,380.78 | 690.90 | 1,379.80 | 690.40 | 13 |
| 4 | **583.26** | **292.13** | | | 565.25 | 283.13 | D | 1,326.77 | 663.89 | 1,309.75 | 655.38 | 1,308.76 | 654.89 | 12 |
| 5 | **640.28** | 320.64 | | | 622.27 | 311.64 | G | 1,211.75 | 606.38 | 1,194.72 | 597.86 | 1,193.74 | 597.37 | 11 |
| 6 | **768.34** | **384.67** | 751.31 | 376.16 | 750.33 | 375.67 | Q | 1,154.73 | 577.87 | 1,137.70 | 569.35 | 1,136.71 | 568.86 | 10 |
| 7 | **839.38** | 420.19 | 822.35 | 411.68 | 821.37 | 411.19 | A | **1,026.67** | 513.84 | 1,009.64 | 505.32 | 1,008.66 | 504.83 | 9 |
| 8 | 940.42 | 470.72 | 923.40 | 462.20 | **922.41** | **461.71** | T | **955.63** | 478.32 | 938.60 | 469.81 | 937.62 | 469.31 | 8 |
| 9 | 1,053.51 | 527.26 | 1,036.48 | 518.74 | 1,035.50 | 518.25 | L | **854.58** | 427.79 | 837.56 | 419.28 | | | 7 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 10 | 1,166.59 | 583.80 | 1,149.57 | 575.29 | 1,148.58 | 574.79 | L | 741.50 | 371.25 | 724.47 | 362.74 |  |  | 6 |
| 11 | 1,280.64 | 640.82 | 1,263.61 | 632.31 | 1,262.62 | 631.82 | N | 628.41 | 314.71 | 611.39 | 306.20 |  |  | 5 |
| 12 | 1,393.72 | 697.36 | 1,376.69 | 688.85 | 1,375.71 | 688.36 | L | 514.37 | 257.69 | 497.34 | 249.18 |  |  | 4 |
| 13 | 1,506.80 | 753.91 | 1,489.78 | 745.39 | 1,488.79 | 744.90 | L | 401.29 | 201.15 | 384.26 | 192.63 |  |  | 3 |
| 14 | 1,619.89 | 810.45 | 1,602.86 | 801.93 | 1,601.88 | 801.44 | L | 288.20 | 144.61 | 271.18 | 136.09 |  |  | 2 |
| 15 |  |  |  |  |  |  | R | 175.12 | 88.06 | 158.09 | 79.55 |  |  | 1 |

Query 2576 Hit 1

MS/MS Fragmentation of ELNELVSAIEEHFFQPQK
Found in sp|Q96G03|PGM2_HUMAN, Phosphoglucomutase-2 OS=Homo sapiens GN=PGM2 PE=1 SV=4
Match to Query 2576: 2445.285from(816.1022,3+)
Title: 1152: Sum of 2 scans in range 2952 (rt=74.5052, f=4, i=810) to 2953 (rt=74.5306, f=4, i=811)
[D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2445.285
**Variable modifications:**
**K18** :iTRAQ4plex (K)
**Ions Score:** 60.54 **Expect:** 0.001

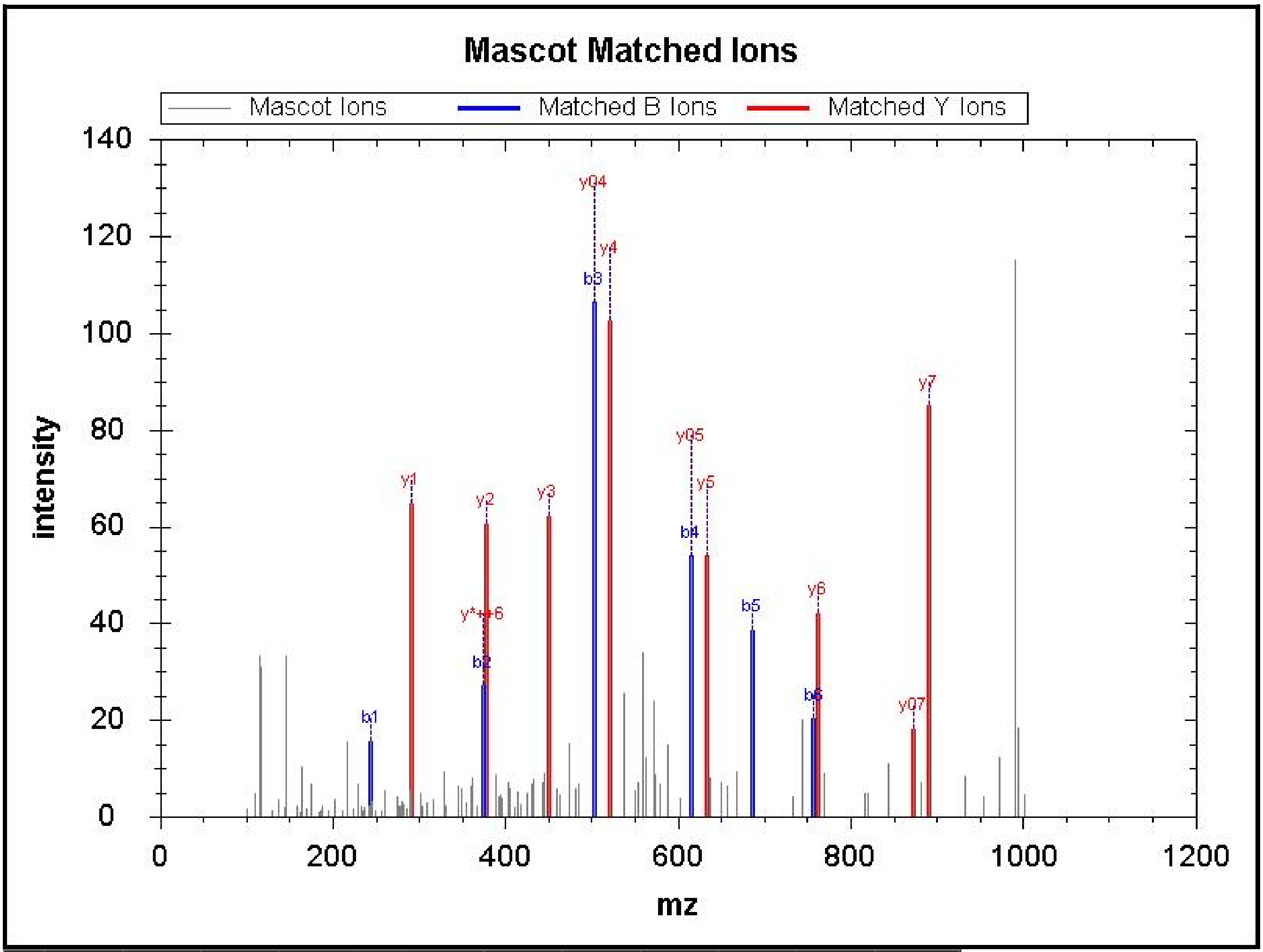


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 274.15 | 137.58 |  |  | 256.14 | 128.57 | E |  |  |  |  |  |  | 18 |
| 2 | 387.24 | 194.12 |  |  | 369.23 | 185.12 | L | 2,173.14 | 1,087.07 | 2,156.11 | 1,078.56 | 2,155.13 | 1,078.07 | 17 |
| 3 | 501.28 | 251.14 | 484.25 | 242.63 | 483.27 | 242.14 | N | 2,060.06 | 1,030.53 | 2,043.03 | 1,022.02 | 2,042.05 | 1,021.53 | 16 |
| 4 | 630.32 | 315.66 | 613.29 | 307.15 | 612.31 | 306.66 | E | 1,946.01 | 973.51 | 1,928.99 | 965.00 | 1,928.00 | 964.51 | 15 |
| 5 | 743.41 | 372.21 | 726.38 | 363.69 | 725.39 | 363.20 | L | 1,816.97 | 908.99 | 1,799.94 | 900.48 | 1,798.96 | 899.98 | 14 |
| 6 | 842.47 | 421.74 | 825.45 | 413.23 | 824.46 | 412.74 | V | 1,703.89 | 852.45 | 1,686.86 | 843.93 | 1,685.88 | 843.44 | 13 |
| 7 | 929.51 | 465.26 | 912.48 | 456.74 | 911.50 | 456.25 | S | 1,604.82 | 802.91 | 1,587.79 | 794.40 | 1,586.81 | 793.91 | 12 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 8 | **1,000.54** | 500.78 | 983.52 | 492.26 | **982.53** | **491.77** | A | 1,517.79 | 759.40 | 1,500.76 | 750.88 | 1,499.78 | 750.39 | 11 |
| 9 | **1,113.63** | 557.32 | 1,096.60 | 548.80 | 1,095.62 | 548.31 | I | 1,446.75 | 723.88 | 1,429.72 | **715.37** | 1,428.74 | 714.87 | 10 |
| 10 | **1,242.67** | 621.84 | 1,225.64 | 613.33 | 1,224.66 | 612.83 | E | 1,333.67 | **667.34** | 1,316.64 | 658.82 | 1,315.66 | 658.33 | 9 |
| 11 | **1,371.71** | 686.36 | 1,354.69 | 677.85 | 1,353.70 | 677.35 | E | 1,204.62 | 602.82 | 1,187.60 | 594.30 | 1,186.61 | 593.81 | 8 |
| 12 | 1,508.77 | **754.89** | 1,491.74 | 746.38 | 1,490.76 | 745.88 | H | **1,075.58** | **538.29** | 1,058.55 | 529.78 | | | 7 |
| 13 | 1,655.84 | **828.42** | 1,638.81 | 819.91 | 1,637.83 | **819.42** | F | **938.52** | 469.76 | 921.50 | 461.25 | | | 6 |
| 14 | 1,802.91 | 901.96 | 1,785.88 | 893.44 | 1,784.90 | 892.95 | F | **791.45** | 396.23 | 774.43 | 387.72 | | | 5 |
| 15 | 1,930.97 | 965.99 | 1,913.94 | 957.47 | 1,912.96 | 956.98 | Q | **644.38** | 322.70 | **627.36** | 314.18 | | | 4 |
| 16 | 2,028.02 | 1,014.51 | 2,010.99 | 1,006.00 | 2,010.01 | 1,005.51 | P | **516.33** | 258.67 | 499.30 | 250.15 | | | 3 |
| 17 | 2,156.08 | 1,078.54 | 2,139.05 | 1,070.03 | 2,138.07 | 1,069.54 | Q | 419.27 | 210.14 | 402.25 | 201.63 | | | 2 |
| 18 | | | | | | | K | **291.21** | 146.11 | **274.19** | 137.60 | | | 1 |

Query 551 Hit 1

MS/MS Fragmentation of **VEEIAASK**
Found in **sp|Q02543|RL18A_HUMAN**, 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2
Match to Query 551: 1133.658from(567.8362,2+)
Title: 268: Sum of 2 scans in range 901 (rt=28.7413, f=4, i=182) to 902 (rt=28.7667, f=4, i=183) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1133.658
**Variable modifications:**
**K8** :iTRAQ4plex (K)
**Ions Score:** 60.48 **Expect:** 0.001

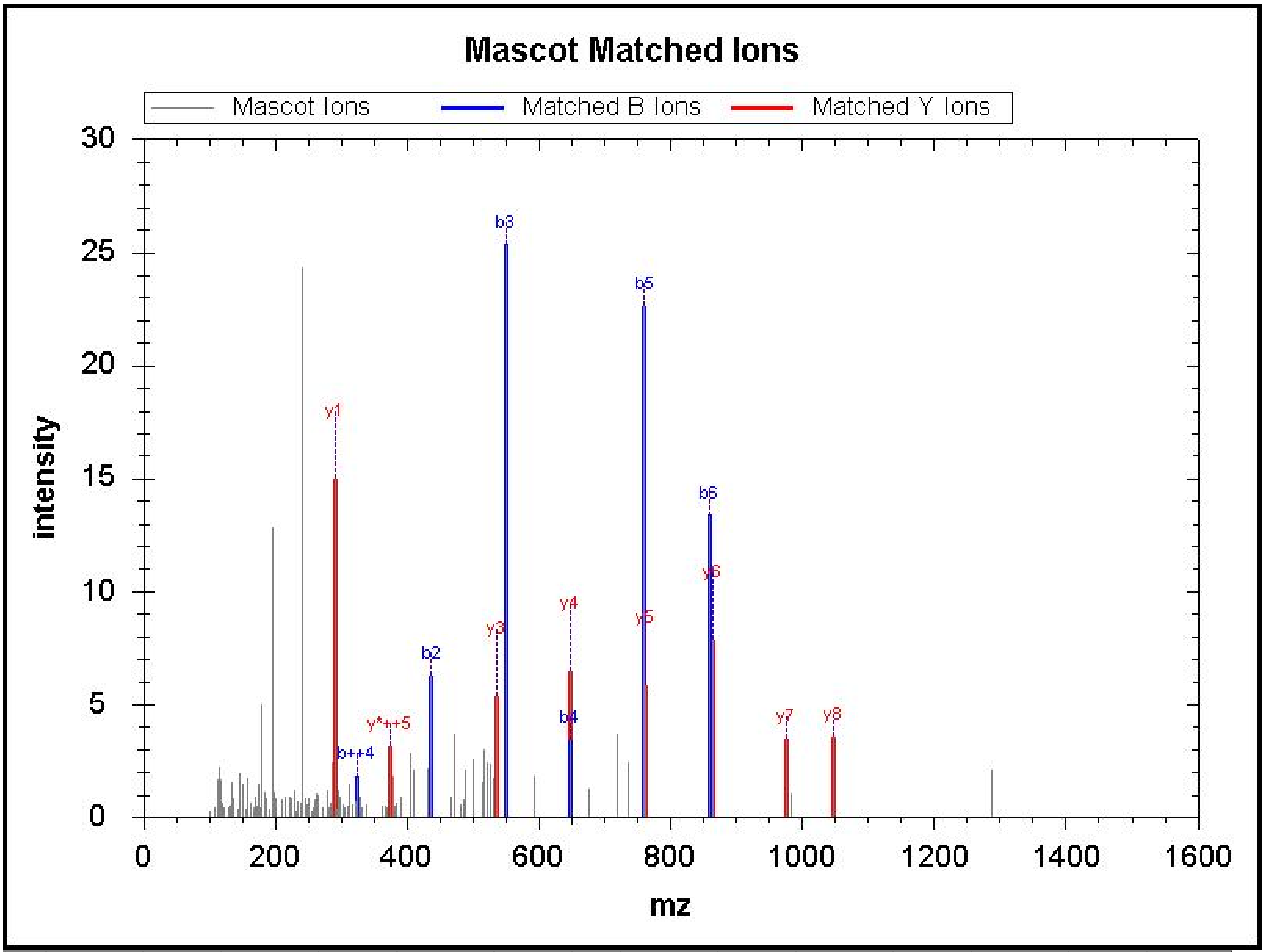


| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **244.18** | 122.59 | | | V | | | | | | | 8 |
| 2 | **373.22** | 187.11 | 355.21 | 178.11 | E | **891.49** | 446.25 | 874.46 | 437.74 | **873.48** | 437.24 | 7 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **3** | **502.26** | 251.64 | 484.25 | 242.63 | **E** | **762.45** | 381.73 | 745.42 | **373.21** | 744.44 | 372.72 | **6** |
| **4** | **615.35** | 308.18 | 597.34 | 299.17 | **I** | **633.41** | 317.21 | 616.38 | 308.69 | **615.39** | 308.20 | **5** |
| **5** | **686.38** | 343.70 | 668.37 | 334.69 | **A** | **520.32** | 260.66 | 503.29 | 252.15 | **502.31** | 251.66 | **4** |
| **6** | **757.42** | 379.21 | 739.41 | 370.21 | **A** | **449.28** | 225.15 | 432.26 | 216.63 | 431.27 | 216.14 | **3** |
| **7** | 844.45 | 422.73 | 826.44 | 413.72 | **S** | **378.25** | 189.63 | 361.22 | 181.11 | 360.24 | 180.62 | **2** |
| **8** | | | | | **K** | **291.21** | 146.11 | 274.19 | 137.60 | | | **1** |

Query 2301 Hit 1

MS/MS Fragmentation of **YELPLVIQALTNIEDK**
Found in **sp|Q96QD8|S38A2_HUMAN**, Sodium-coupled neutral amino acid transporter 2 OS=Homo sapiens GN=SLC38A2 PE=1 SV=2
Match to Query 2301: 2146.227from(716.4163,3+)
Title: 1214: Scan 2946 (rt=74.8177, f=3, i=424) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2146.227
**Variable modifications:**
**K16** :iTRAQ4plex (K)
**Ions Score:** 59.98 **Expect:** 0.000

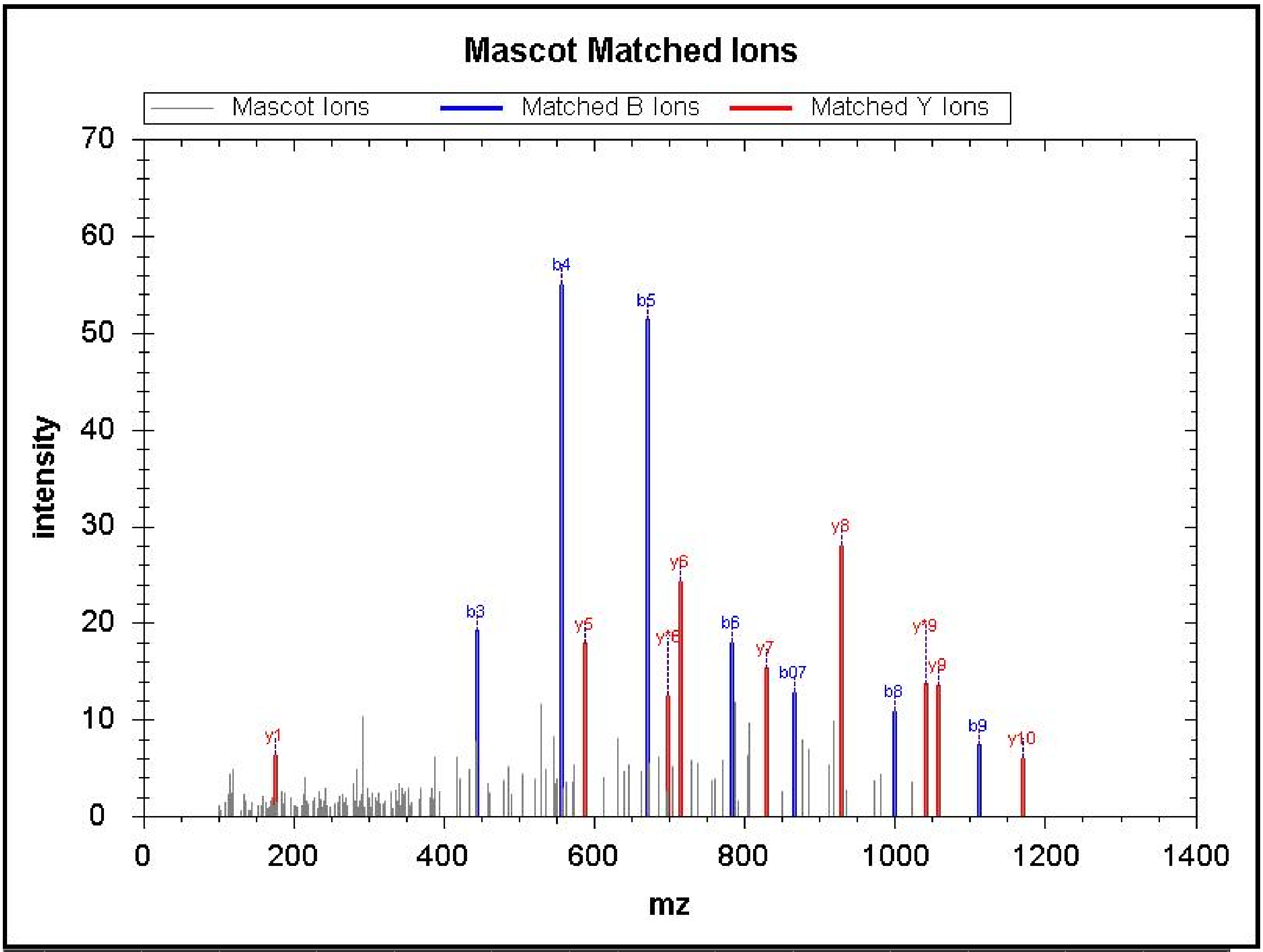


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | 308.17 | 154.59 | | | | | **Y** | | | | | | | **16** |
| **2** | **437.22** | 219.11 | | | 419.20 | 210.11 | **E** | 1,840.05 | 920.53 | 1,823.03 | 912.02 | 1,822.04 | 911.53 | **15** |
| **3** | **550.30** | 275.65 | | | 532.29 | 266.65 | **L** | 1,711.01 | 856.01 | 1,693.99 | 847.50 | 1,693.00 | 847.00 | **14** |
| **4** | **647.35** | **324.18** | | | 629.34 | 315.17 | **P** | 1,597.93 | 799.47 | 1,580.90 | 790.95 | 1,579.92 | 790.46 | **13** |
| **5** | **760.44** | 380.72 | | | 742.43 | 371.72 | **L** | 1,500.88 | 750.94 | 1,483.85 | 742.43 | 1,482.86 | 741.94 | **12** |
| **6** | **859.50** | 430.26 | | | 841.49 | 421.25 | **V** | 1,387.79 | 694.40 | 1,370.76 | 685.89 | 1,369.78 | 685.39 | **11** |
| **7** | 972.59 | 486.80 | | | 954.58 | 477.79 | **I** | 1,288.72 | 644.87 | 1,271.70 | 636.35 | 1,270.71 | 635.86 | **10** |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **8** | 1,100.65 | 550.83 | 1,083.62 | 542.31 | 1,082.64 | 541.82 | **Q** | 1,175.64 | 588.32 | 1,158.61 | 579.81 | 1,157.63 | 579.32 | **9** |
| **9** | 1,171.68 | 586.35 | 1,154.66 | 577.83 | 1,153.67 | 577.34 | **A** | **1,047.58** | 524.29 | 1,030.55 | 515.78 | 1,029.57 | 515.29 | **8** |
| **10** | 1,284.77 | 642.89 | 1,267.74 | 634.37 | 1,266.76 | 633.88 | **L** | **976.54** | 488.78 | 959.52 | 480.26 | 958.53 | 479.77 | **7** |
| **11** | 1,385.82 | 693.41 | 1,368.79 | 684.90 | 1,367.81 | 684.41 | **T** | **863.46** | 432.23 | 846.43 | 423.72 | 845.45 | 423.23 | **6** |
| **12** | 1,499.86 | 750.43 | 1,482.83 | 741.92 | 1,481.85 | 741.43 | **N** | **762.41** | 381.71 | 745.38 | **373.20** | 744.40 | 372.70 | **5** |
| **13** | 1,612.94 | 806.98 | 1,595.92 | 798.46 | 1,594.93 | 797.97 | **I** | **648.37** | 324.69 | 631.34 | 316.17 | 630.36 | 315.68 | **4** |
| **14** | 1,741.99 | 871.50 | 1,724.96 | 862.98 | 1,723.98 | 862.49 | **E** | **535.28** | 268.15 | 518.26 | 259.63 | 517.27 | 259.14 | **3** |
| **15** | 1,857.01 | 929.01 | 1,839.99 | 920.50 | 1,839.00 | 920.00 | **D** | 406.24 | 203.62 | 389.22 | 195.11 | 388.23 | 194.62 | **2** |
| **16** | | | | | | | **K** | **291.21** | 146.11 | 274.19 | 137.60 | | | **1** |

Query 2318 Hit 1

MS/MS Fragmentation of **GQNLLLTNLQTIQGILER**
Found in **sp|P12270|TPR_HUMAN**, Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3
Match to Query 2318: 2167.252from(723.4245,3+)
Title: 1209: Sum of 2 scans in range 2935 (rt=74.5716, f=4, i=838) to 2936 (rt=74.597, f=4, i=839)
[D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2167.252
**Variable modifications:**
**Ions Score:** 59.53 **Expect:** 0.000

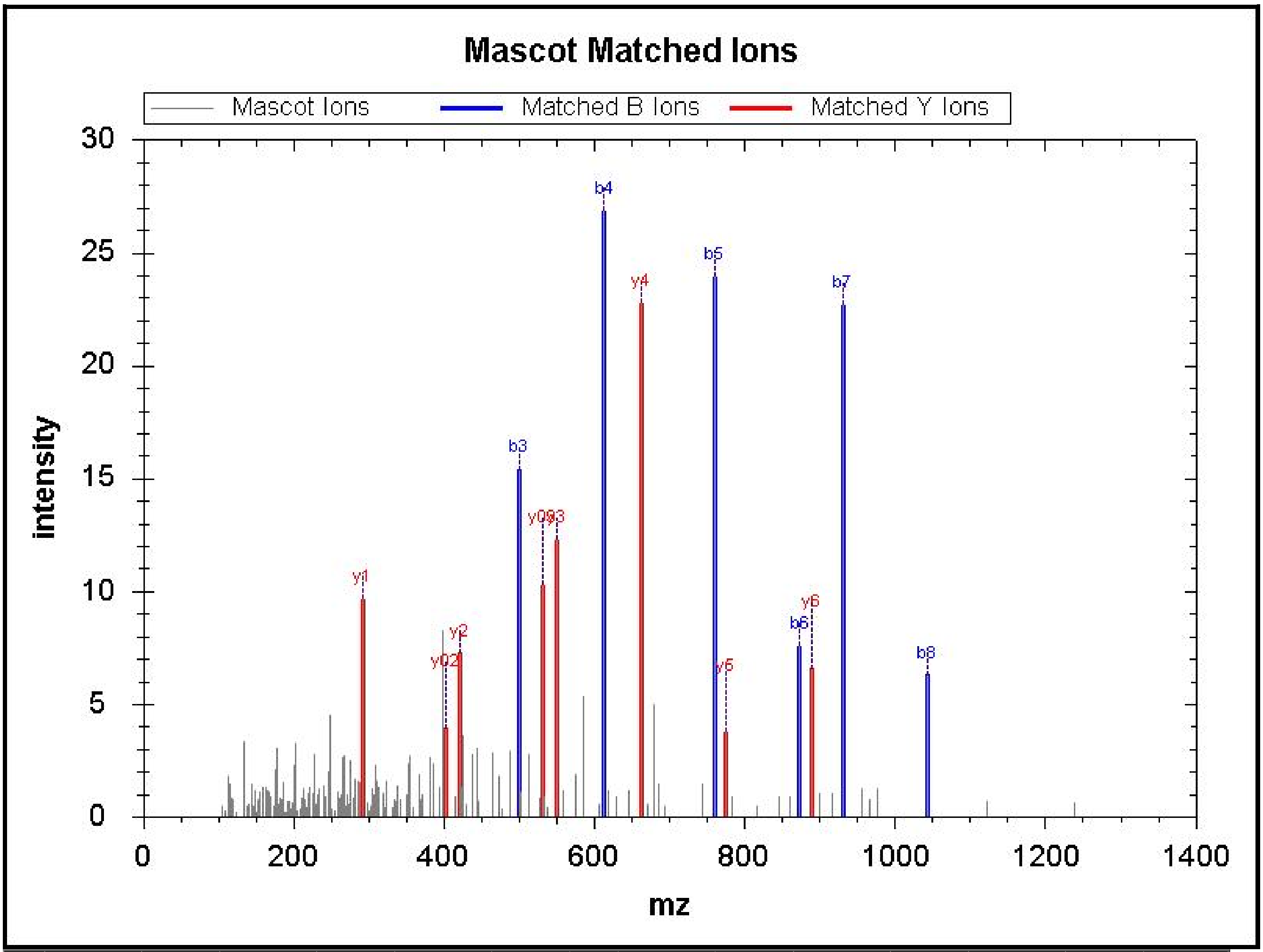


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | 202.13 | 101.57 | | | | | **G** | | | | | | | **18** |
| **2** | 330.19 | 165.60 | 313.16 | 157.09 | | | **Q** | 1,967.13 | 984.07 | 1,950.10 | 975.55 | 1,949.12 | 975.06 | **17** |
| **3** | **444.23** | 222.62 | 427.21 | 214.11 | | | **N** | 1,839.07 | 920.04 | 1,822.04 | 911.53 | 1,821.06 | 911.03 | **16** |
| **4** | **557.32** | 279.16 | 540.29 | 270.65 | | | **L** | 1,725.03 | 863.02 | 1,708.00 | 854.50 | 1,707.02 | 854.01 | **15** |
| **5** | **670.40** | 335.70 | 653.37 | 327.19 | | | **L** | 1,611.94 | 806.48 | 1,594.92 | 797.96 | 1,593.93 | 797.47 | **14** |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 6 | **783.48** | 392.25 | 766.46 | 383.73 | | | L | 1,498.86 | 749.93 | 1,481.83 | 741.42 | 1,480.85 | 740.93 | 13 |
| 7 | 884.53 | 442.77 | 867.51 | 434.26 | **866.52** | 433.76 | T | 1,385.77 | 693.39 | 1,368.75 | 684.88 | 1,367.76 | 684.39 | 12 |
| 8 | **998.58** | 499.79 | 981.55 | 491.28 | 980.56 | 490.79 | N | 1,284.73 | 642.87 | 1,267.70 | 634.35 | 1,266.72 | 633.86 | 11 |
| 9 | **1,111.66** | 556.33 | 1,094.63 | 547.82 | 1,093.65 | 547.33 | L | **1,170.68** | 585.85 | 1,153.66 | 577.33 | 1,152.67 | 576.84 | 10 |
| 10 | 1,239.72 | 620.36 | 1,222.69 | 611.85 | 1,221.71 | 611.36 | Q | **1,057.60** | 529.30 | **1,040.57** | 520.79 | 1,039.59 | 520.30 | 9 |
| 11 | 1,340.77 | 670.89 | 1,323.74 | 662.37 | 1,322.75 | 661.88 | T | **929.54** | 465.27 | 912.51 | 456.76 | 911.53 | 456.27 | 8 |
| 12 | 1,453.85 | 727.43 | 1,436.82 | 718.92 | 1,435.84 | 718.42 | I | **828.49** | 414.75 | 811.47 | 406.24 | 810.48 | 405.75 | 7 |
| 13 | 1,581.91 | 791.46 | 1,564.88 | 782.94 | 1,563.90 | 782.45 | Q | **715.41** | 358.21 | **698.38** | 349.70 | 697.40 | 349.20 | 6 |
| 14 | 1,638.93 | 819.97 | 1,621.90 | 811.46 | 1,620.92 | 810.96 | G | **587.35** | 294.18 | 570.32 | 285.67 | 569.34 | 285.17 | 5 |
| 15 | 1,752.01 | 876.51 | 1,734.99 | 868.00 | 1,734.00 | 867.51 | I | 530.33 | 265.67 | 513.30 | 257.16 | 512.32 | 256.66 | 4 |
| 16 | 1,865.10 | 933.05 | 1,848.07 | 924.54 | 1,847.09 | 924.05 | L | 417.25 | 209.13 | 400.22 | 200.61 | 399.24 | 200.12 | 3 |
| 17 | 1,994.14 | 997.57 | 1,977.11 | 989.06 | 1,976.13 | 988.57 | E | 304.16 | 152.58 | 287.13 | 144.07 | 286.15 | 143.58 | 2 |
| 18 | | | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 2140 Hit 1

MS/MS Fragmentation of **LQNIFLGLVNIIEEK**
Found in **sp|O15042|SR140_HUMAN**, U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens GN=U2SURP PE=1 SV=2
Match to Query 2140: 2030.205from(677.7423,3+)
Title: 1314: Scan 3347 (rt=83.4054, f=3, i=478) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2030.205
**Variable modifications:**
**K15** :iTRAQ4plex (K)
**Ions Score:** 59.09 **Expect:** 0.000

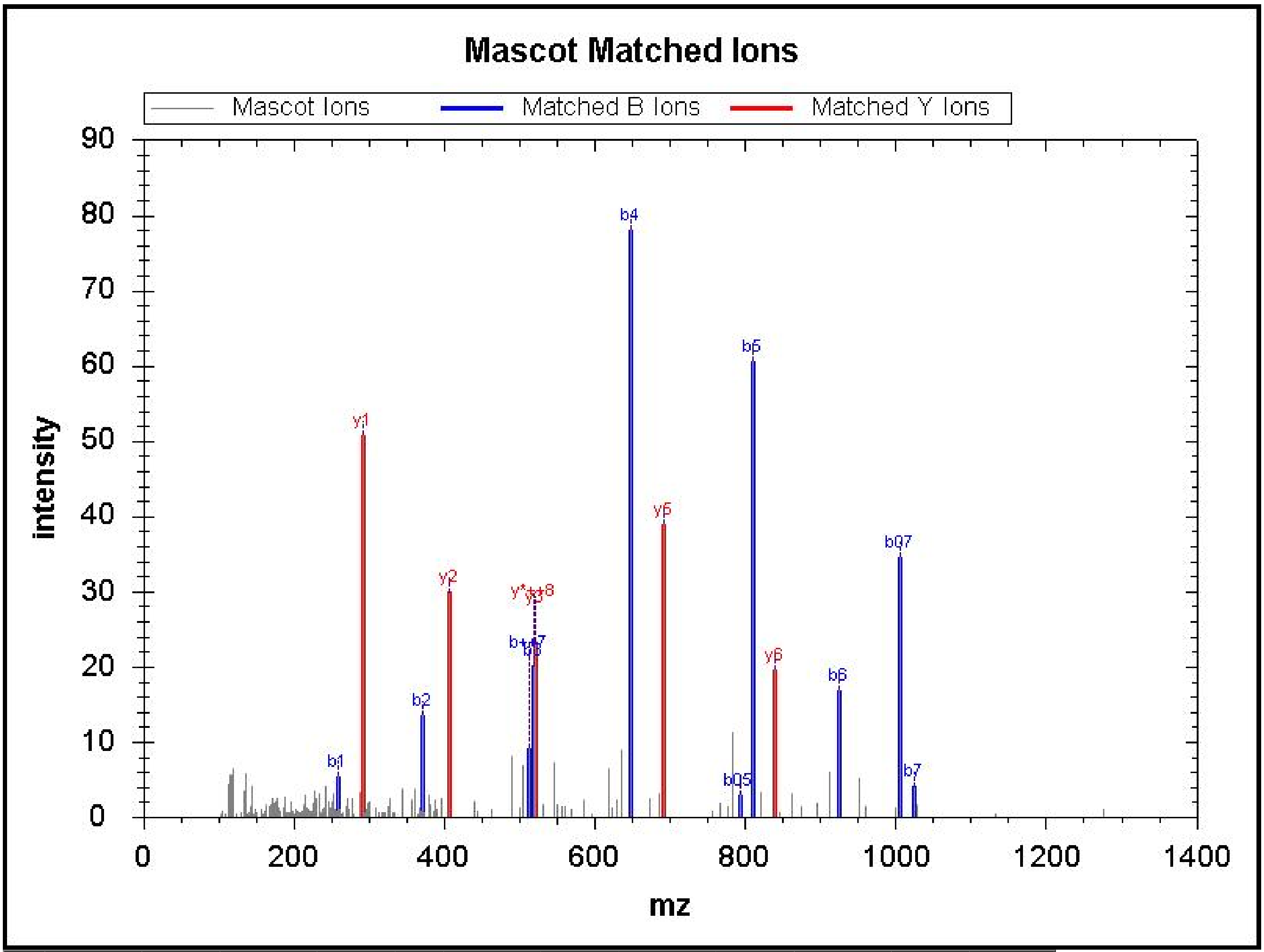


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | | | | | L | | | | | | | 15 |
| 2 | 386.25 | 193.63 | 369.23 | 185.12 | | | Q | 1,774.02 | 887.52 | 1,757.00 | 879.00 | 1,756.01 | 878.51 | 14 |
| 3 | **500.29** | 250.65 | 483.27 | 242.14 | | | N | 1,645.96 | 823.49 | 1,628.94 | 814.97 | 1,627.95 | 814.48 | 13 |
| 4 | **613.38** | 307.19 | 596.35 | 298.68 | | | I | 1,531.92 | 766.46 | 1,514.90 | 757.95 | 1,513.91 | 757.46 | 12 |
| 5 | **760.45** | 380.73 | 743.42 | 372.21 | | | F | 1,418.84 | 709.92 | 1,401.81 | 701.41 | 1,400.83 | 700.92 | 11 |
| 6 | **873.53** | 437.27 | 856.50 | 428.76 | | | L | 1,271.77 | 636.39 | 1,254.74 | 627.88 | 1,253.76 | 627.38 | 10 |
| 7 | **930.55** | 465.78 | 913.53 | 457.27 | | | G | 1,158.69 | 579.85 | 1,141.66 | 571.33 | 1,140.67 | 570.84 | 9 |
| 8 | **1,043.64** | 522.32 | 1,026.61 | 513.81 | | | L | 1,101.66 | 551.34 | 1,084.64 | 542.82 | 1,083.65 | 542.33 | 8 |
| 9 | 1,142.71 | 571.86 | 1,125.68 | 563.34 | | | V | 988.58 | 494.79 | 971.55 | 486.28 | 970.57 | 485.79 | 7 |
| 10 | 1,256.75 | 628.88 | 1,239.72 | 620.36 | | | N | **889.51** | 445.26 | 872.48 | 436.75 | 871.50 | 436.25 | 6 |
| 11 | 1,369.83 | 685.42 | 1,352.81 | 676.91 | | | I | **775.47** | 388.24 | 758.44 | 379.72 | 757.46 | 379.23 | 5 |
| 12 | 1,482.92 | 741.96 | 1,465.89 | 733.45 | | | I | **662.38** | 331.70 | 645.36 | 323.18 | 644.37 | 322.69 | 4 |
| 13 | 1,611.96 | 806.48 | 1,594.93 | 797.97 | 1,593.95 | 797.48 | E | **549.30** | 275.15 | 532.27 | 266.64 | **531.29** | 266.15 | 3 |
| 14 | 1,741.00 | 871.00 | 1,723.98 | 862.49 | 1,722.99 | 862.00 | E | **420.26** | 210.63 | 403.23 | 202.12 | **402.25** | 201.63 | 2 |
| 15 | | | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 2079 Hit 1

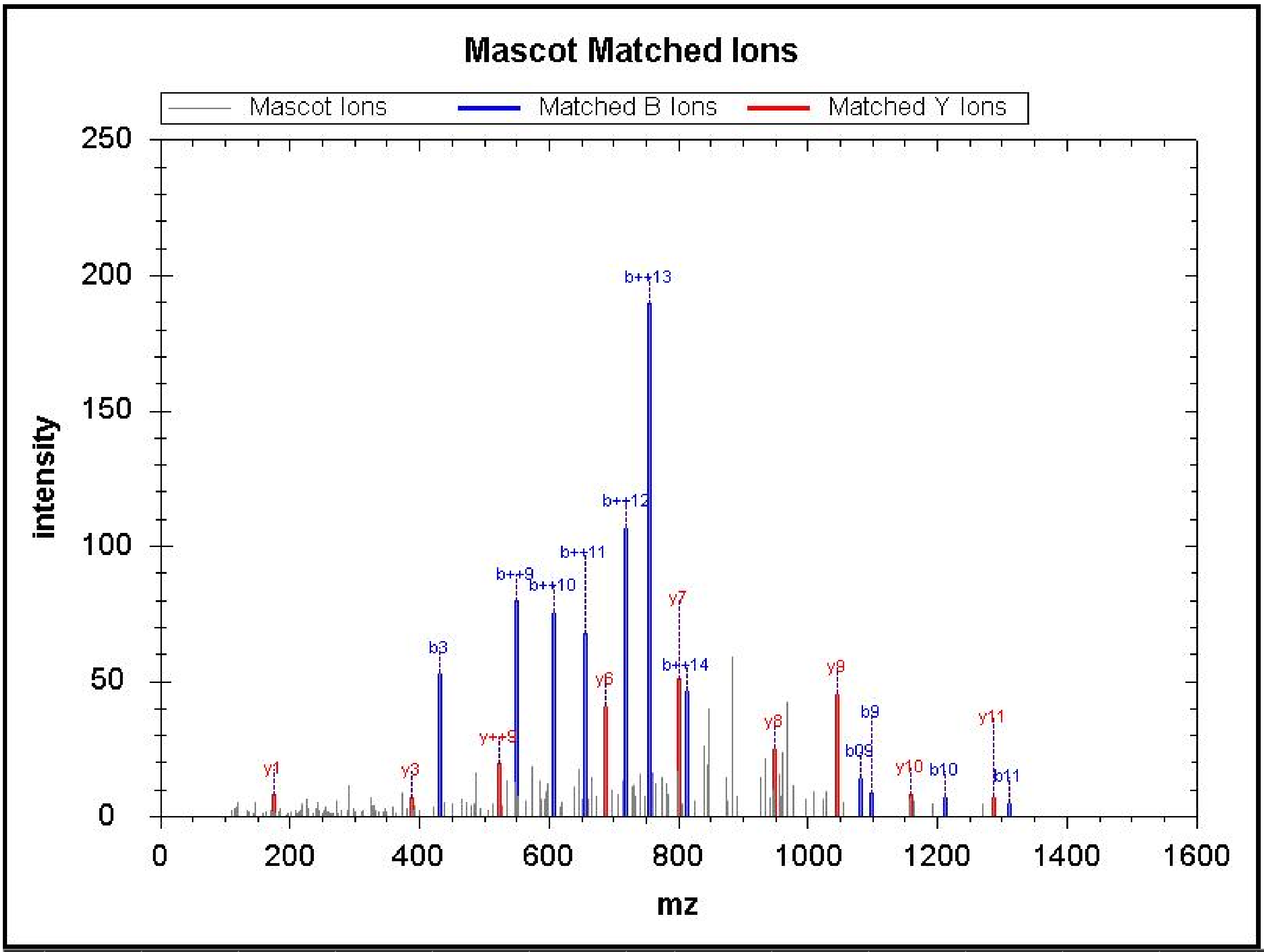
MS/MS Fragmentation of **LLFEYLTLFGIDDK**
Found in **sp|P12081|SYHC_HUMAN**, Histidine--tRNA ligase
Match to Query 2079: 1974.111from(659.0444,3+)
Title: 1260: Sum of 2 scans in range 3206 (rt=80.2292, f=4, i=892) to 3207 (rt=80.2546, f=4, i=893) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1974.111
**Variable modifications:**
**K14** :iTRAQ4plex (K)
**Ions Score:** 58.97 **Expect:** 0.001



| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | | | L | | | | | | | 14 |
| 2 | 371.28 | 186.14 | | | L | 1,717.92 | 859.46 | 1,700.89 | 850.95 | 1,699.91 | 850.46 | 13 |
| 3 | 518.35 | 259.68 | | | F | 1,604.83 | 802.92 | 1,587.81 | 794.41 | 1,586.82 | 793.91 | 12 |
| 4 | 647.39 | 324.20 | 629.38 | 315.19 | E | 1,457.76 | 729.39 | 1,440.74 | 720.87 | 1,439.75 | 720.38 | 11 |
| 5 | 810.45 | 405.73 | 792.44 | 396.72 | Y | 1,328.72 | 664.86 | 1,311.70 | 656.35 | 1,310.71 | 655.86 | 10 |
| 6 | 923.54 | 462.27 | 905.53 | 453.27 | L | 1,165.66 | 583.33 | 1,148.63 | 574.82 | 1,147.65 | 574.33 | 9 |
| 7 | 1,024.58 | 512.80 | 1,006.57 | 503.79 | T | 1,052.57 | 526.79 | 1,035.55 | 518.28 | 1,034.56 | 517.79 | 8 |
| 8 | 1,137.67 | 569.34 | 1,119.66 | 560.33 | L | 951.53 | 476.27 | 934.50 | 467.75 | 933.52 | 467.26 | 7 |
| 9 | 1,284.74 | 642.87 | 1,266.73 | 633.87 | F | 838.44 | 419.72 | 821.42 | 411.21 | 820.43 | 410.72 | 6 |
| 10 | 1,341.76 | 671.38 | 1,323.75 | 662.38 | G | 691.37 | 346.19 | 674.35 | 337.68 | 673.36 | 337.19 | 5 |
| 11 | 1,454.84 | 727.92 | 1,436.83 | 718.92 | I | 634.35 | 317.68 | 617.33 | 309.17 | 616.34 | 308.67 | 4 |
| 12 | 1,569.87 | 785.44 | 1,551.86 | 776.43 | D | 521.27 | 261.14 | 504.24 | 252.62 | 503.26 | 252.13 | 3 |
| 13 | 1,684.90 | 842.95 | 1,666.89 | 833.95 | D | 406.24 | 203.62 | 389.22 | 195.11 | 388.23 | 194.62 | 2 |
| 14 | | | | | K | 291.21 | 146.11 | 274.19 | 137.60 | | | 1 |

Query 2823 Hit 1

MS/MS Fragmentation of **LGDPAEYAHLVQAIIENPFLNGEVIR**
Found in **sp|Q99714|HCD2_HUMAN**, 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3
Match to Query 2823: 3021.615from(756.4109,4+)
Title: 1243: Sum of 2 scans in range 3169 (rt=79.3949, f=4, i=880) to 3170 (rt=79.4203, f=4, i=881) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 3021.615
**Variable modifications:**
**Ions Score:** 55.42 **Expect:** 0.002

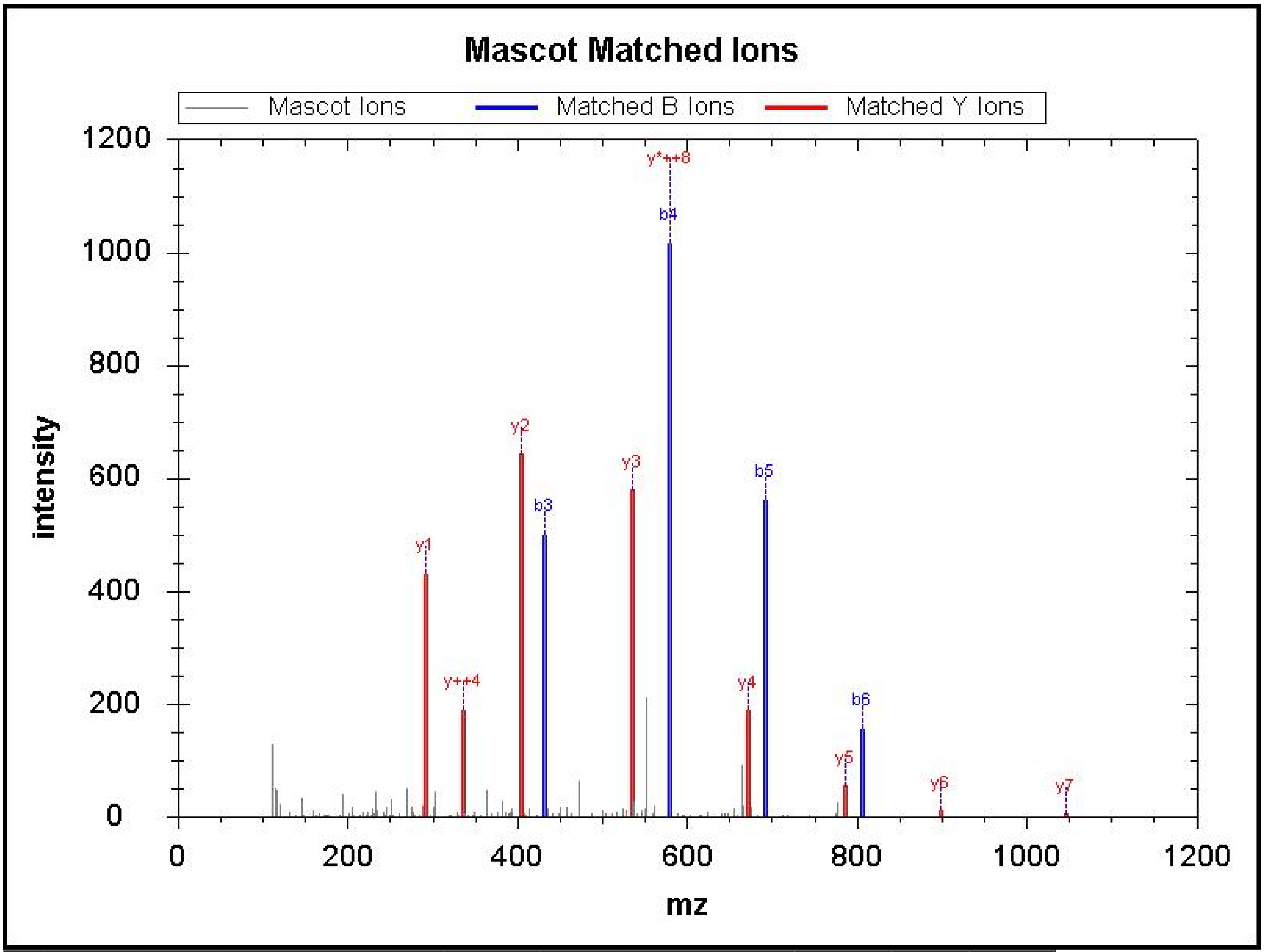


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | | | | | L | | | | | | | 26 |
| 2 | 315.21 | 158.11 | | | | | G | 2,765.43 | 1,383.22 | 2,748.40 | 1,374.70 | 2,747.42 | 1,374.21 | 25 |
| 3 | 430.24 | 215.62 | | | 412.23 | 206.62 | D | 2,708.40 | 1,354.71 | 2,691.38 | 1,346.19 | 2,690.39 | 1,345.70 | 24 |
| 4 | 527.29 | 264.15 | | | 509.28 | 255.15 | P | 2,593.38 | 1,297.19 | 2,576.35 | 1,288.68 | 2,575.37 | 1,288.19 | 23 |
| 5 | 598.33 | 299.67 | | | 580.32 | 290.66 | A | 2,496.32 | 1,248.67 | 2,479.30 | 1,240.15 | 2,478.31 | 1,239.66 | 22 |
| 6 | 727.37 | 364.19 | | | 709.36 | 355.19 | E | 2,425.29 | 1,213.15 | 2,408.26 | 1,204.63 | 2,407.28 | 1,204.14 | 21 |
| 7 | 890.44 | 445.72 | | | 872.43 | 436.72 | Y | 2,296.24 | 1,148.63 | 2,279.22 | 1,140.11 | 2,278.23 | 1,139.62 | 20 |
| 8 | 961.47 | 481.24 | | | 943.46 | 472.24 | A | 2,133.18 | 1,067.09 | 2,116.16 | 1,058.58 | 2,115.17 | 1,058.09 | 19 |
| 9 | 1,098.53 | 549.77 | | | 1,080.52 | 540.77 | H | 2,062.14 | 1,031.58 | 2,045.12 | 1,023.06 | 2,044.13 | 1,022.57 | 18 |
| 10 | 1,211.62 | 606.31 | | | 1,193.61 | 597.31 | L | 1,925.09 | 963.05 | 1,908.06 | 954.53 | 1,907.07 | 954.04 | 17 |
| 11 | 1,310.69 | 655.85 | | | 1,292.68 | 646.84 | V | 1,812.00 | 906.50 | 1,794.97 | 897.99 | 1,793.99 | 897.50 | 16 |
| 12 | 1,438.74 | 719.88 | 1,421.72 | 711.36 | 1,420.73 | 710.87 | Q | 1,712.93 | 856.97 | 1,695.91 | 848.46 | 1,694.92 | 847.96 | 15 |
| 13 | 1,509.78 | 755.39 | 1,492.76 | 746.88 | 1,491.77 | 746.39 | A | 1,584.87 | 792.94 | 1,567.85 | 784.43 | 1,566.86 | 783.94 | 14 |
| 14 | 1,622.87 | 811.94 | 1,605.84 | 803.42 | 1,604.86 | 802.93 | I | 1,513.84 | 757.42 | 1,496.81 | 748.91 | 1,495.83 | 748.42 | 13 |
| 15 | 1,735.95 | 868.48 | 1,718.92 | 859.97 | 1,717.94 | 859.47 | I | 1,400.75 | 700.88 | 1,383.73 | 692.37 | 1,382.74 | 691.88 | 12 |
| 16 | 1,864.99 | 933.00 | 1,847.97 | 924.49 | 1,846.98 | 923.99 | E | 1,287.67 | 644.34 | 1,270.64 | 635.83 | 1,269.66 | 635.33 | 11 |
| 17 | 1,979.04 | 990.02 | 1,962.01 | 981.51 | 1,961.03 | 981.02 | N | 1,158.63 | 579.82 | 1,141.60 | 571.30 | 1,140.62 | 570.81 | 10 |
| 18 | 2,076.09 | 1,038.55 | 2,059.06 | 1,030.03 | 2,058.08 | 1,029.54 | P | 1,044.58 | 522.80 | 1,027.56 | 514.28 | 1,026.57 | 513.79 | 9 |
| 19 | 2,223.16 | 1,112.08 | 2,206.13 | 1,103.57 | 2,205.15 | 1,103.08 | F | 947.53 | 474.27 | 930.50 | 465.76 | 929.52 | 465.26 | 8 |
| 20 | 2,336.24 | 1,168.62 | 2,319.21 | 1,160.11 | 2,318.23 | 1,159.62 | L | 800.46 | 400.73 | 783.44 | 392.22 | 782.45 | 391.73 | 7 |
| 21 | 2,450.28 | 1,225.65 | 2,433.26 | 1,217.13 | 2,432.27 | 1,216.64 | N | 687.38 | 344.19 | 670.35 | 335.68 | 669.37 | 335.19 | 6 |
| 22 | 2,507.31 | 1,254.16 | 2,490.28 | 1,245.64 | 2,489.29 | 1,245.15 | G | 573.34 | 287.17 | 556.31 | 278.66 | 555.32 | 278.17 | 5 |
| 23 | 2,636.35 | 1,318.68 | 2,619.32 | 1,310.16 | 2,618.34 | 1,309.67 | E | 516.31 | 258.66 | 499.29 | 250.15 | 498.30 | 249.66 | 4 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 24 | 2,735.42 | 1,368.21 | 2,718.39 | 1,359.70 | 2,717.41 | 1,359.21 | V | **387.27** | 194.14 | 370.24 | 185.63 | | | 3 |
| 25 | 2,848.50 | 1,424.75 | 2,831.47 | 1,416.24 | 2,830.49 | 1,415.75 | I | 288.20 | 144.61 | 271.18 | 136.09 | | | 2 |
| 26 | | | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 1374 Hit 1

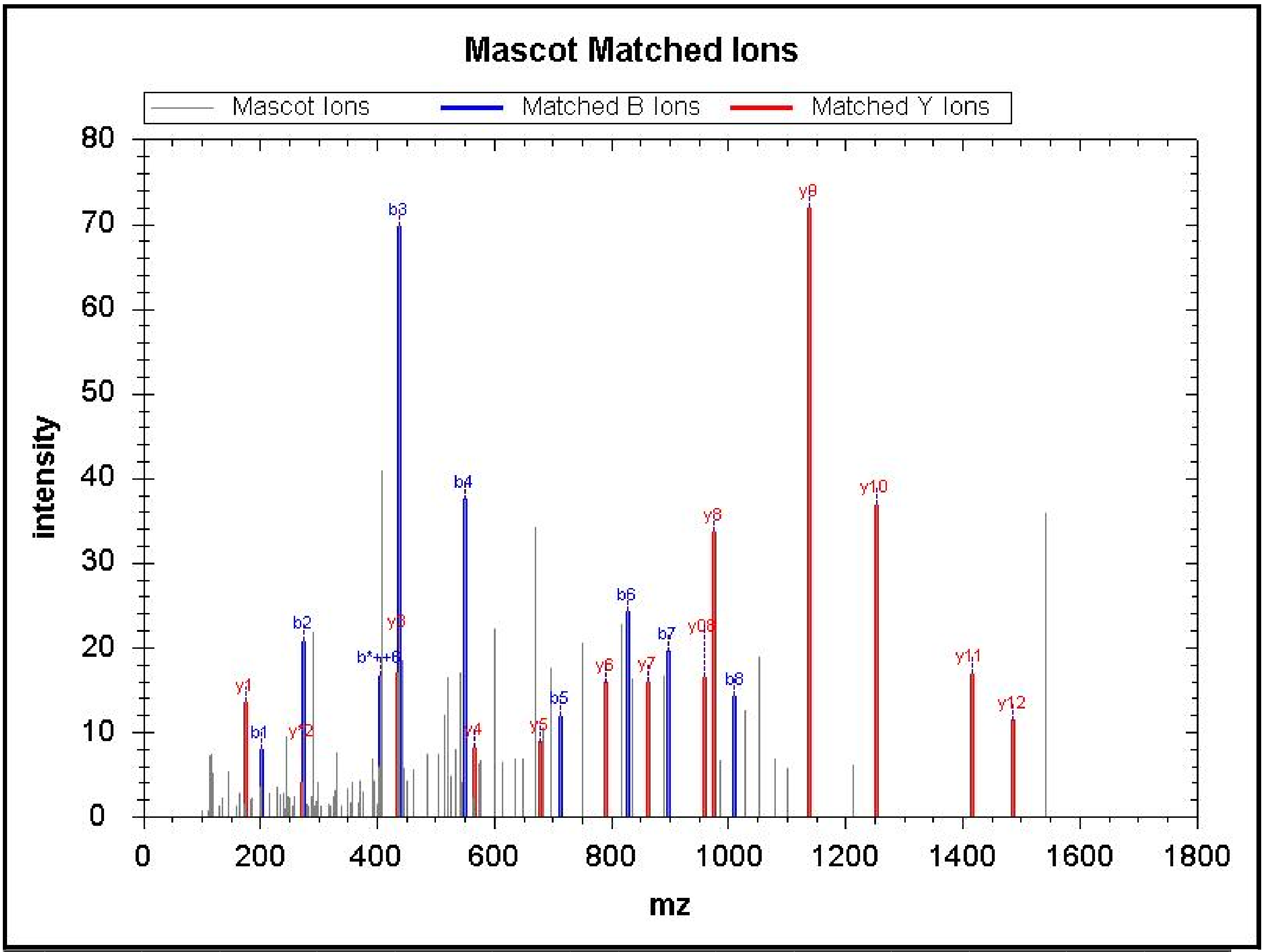
MS/MS Fragmentation of **SAEFLLHMLK**
Found in **sp|P18621|RL17_HUMAN**, 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3
Match to Query 1374: 1475.849from(492.9569,3+)
Title: 751: Sum of 2 scans in range 2071 (rt=54.6555, f=4, i=526) to 2072 (rt=54.6809, f=4, i=527)
[D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1475.849
**Variable modifications:**
**K10** :iTRAQ4plex (K)
**Ions Score:** 53.93 **Expect:** 0.003



| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 232.14 | 116.57 | 214.13 | 107.57 | S | | | | | | | 10 |
| 2 | 303.18 | 152.09 | 285.17 | 143.09 | A | 1,245.71 | 623.36 | 1,228.69 | 614.85 | 1,227.70 | 614.36 | 9 |
| 3 | **432.22** | 216.61 | 414.21 | 207.61 | E | 1,174.68 | 587.84 | 1,157.65 | **579.33** | 1,156.67 | 578.84 | 8 |
| 4 | **579.29** | 290.15 | 561.28 | 281.14 | F | **1,045.63** | 523.32 | 1,028.61 | 514.81 | | | 7 |
| 5 | **692.37** | 346.69 | 674.36 | 337.69 | L | **898.57** | 449.79 | 881.54 | 441.27 | | | 6 |
| 6 | **805.46** | 403.23 | 787.45 | 394.23 | L | **785.48** | 393.24 | 768.46 | 384.73 | | | 5 |
| 7 | 942.52 | 471.76 | 924.51 | 462.76 | H | **672.40** | **336.70** | 655.37 | 328.19 | | | 4 |
| 8 | 1,073.56 | 537.28 | 1,055.55 | 528.28 | M | **535.34** | 268.17 | 518.31 | 259.66 | | | 3 |
| 9 | 1,186.64 | 593.82 | 1,168.63 | 584.82 | L | **404.30** | 202.65 | 387.27 | 194.14 | | | 2 |
| 10 | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 1684 Hit 1

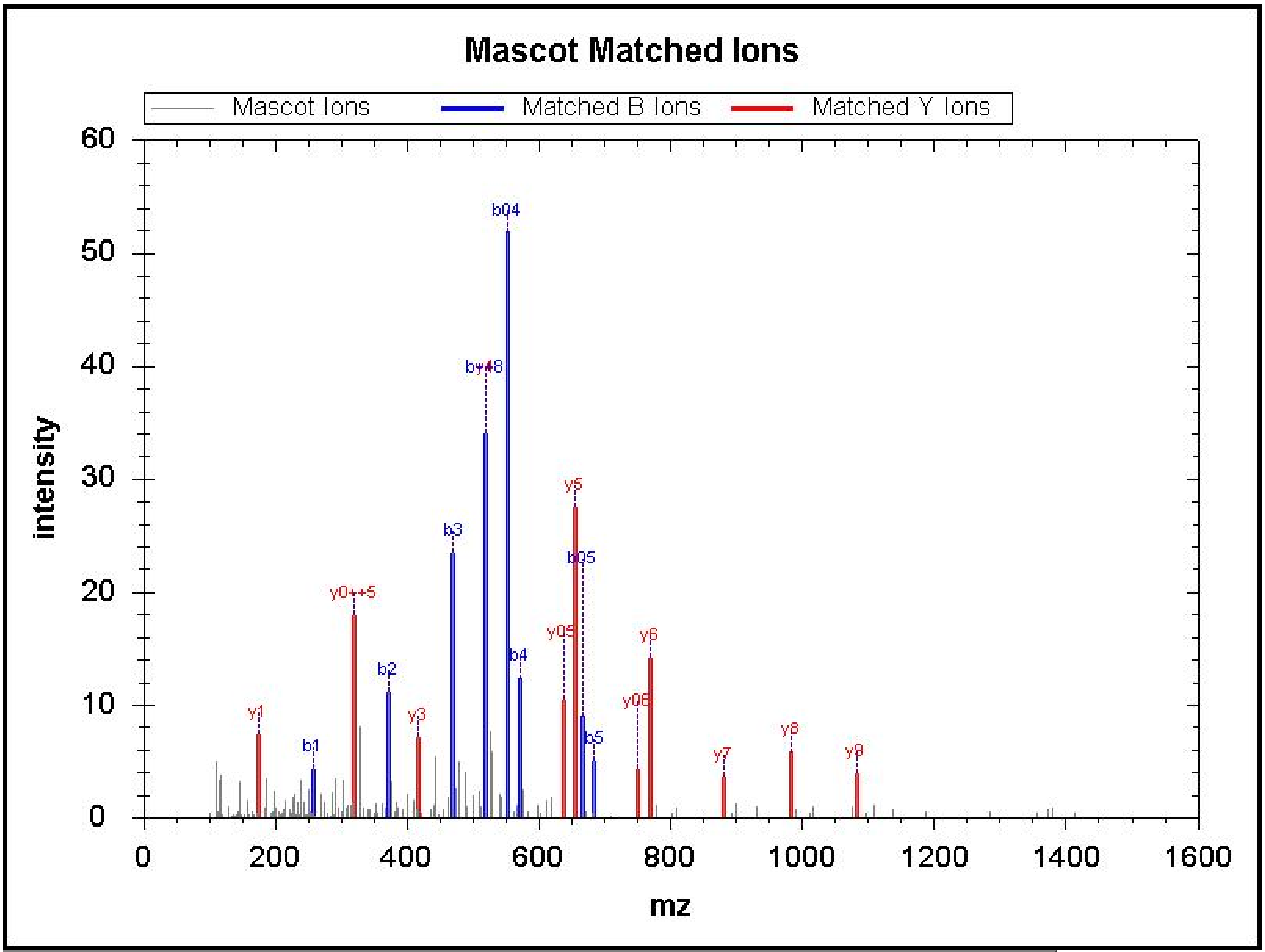
MS/MS Fragmentation of **GAYIYNALIEFIR**
Found in **sp|P26639|SYTC_HUMAN**, Threonine--tRNA ligase
Match to Query 1684: 1685.935from(843.9747,2+)
Title: 1178: Sum of 2 scans in range 2860 (rt=72.8834, f=4, i=814) to 2861 (rt=72.9088, f=4, i=815) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1685.935
**Variable modifications:**
**Ions Score:** 53.57 **Expect:** 0.003



| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **202.13** | 101.57 | | | | | G | | | | | | | 13 |
| 2 | **273.17** | 137.09 | | | | | A | **1,485.81** | 743.41 | 1,468.78 | 734.90 | 1,467.80 | 734.40 | 12 |
| 3 | **436.23** | 218.62 | | | | | Y | **1,414.77** | 707.89 | 1,397.75 | 699.38 | 1,396.76 | 698.88 | 11 |
| 4 | **549.32** | 275.16 | | | | | I | **1,251.71** | 626.36 | 1,234.68 | 617.85 | 1,233.70 | 617.35 | 10 |
| 5 | **712.38** | 356.69 | | | | | Y | **1,138.63** | 569.82 | 1,121.60 | 561.30 | 1,120.61 | 560.81 | 9 |
| 6 | **826.42** | 413.71 | 809.39 | **405.20** | | | N | **975.56** | 488.28 | 958.54 | 479.77 | **957.55** | 479.28 | 8 |
| 7 | **897.46** | 449.23 | 880.43 | 440.72 | | | A | **861.52** | 431.26 | 844.49 | 422.75 | 843.51 | 422.26 | 7 |
| 8 | **1,010.54** | 505.77 | 993.52 | 497.26 | | | L | **790.48** | 395.74 | 773.46 | 387.23 | 772.47 | 386.74 | 6 |
| 9 | 1,123.63 | 562.32 | 1,106.60 | 553.80 | | | I | **677.40** | 339.20 | 660.37 | 330.69 | 659.39 | 330.20 | 5 |
| 10 | 1,252.67 | 626.84 | 1,235.64 | 618.33 | 1,234.66 | 617.83 | E | **564.31** | 282.66 | 547.29 | 274.15 | 546.30 | 273.66 | 4 |
| 11 | 1,399.74 | 700.37 | 1,382.71 | 691.86 | 1,381.73 | 691.37 | F | **435.27** | 218.14 | 418.24 | 209.63 | | | 3 |
| 12 | 1,512.82 | 756.91 | 1,495.80 | 748.40 | 1,494.81 | 747.91 | I | 288.20 | 144.61 | **271.18** | 136.09 | | | 2 |
| 13 | | | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 1308 Hit 1

MS/MS Fragmentation of **ILVTLLHTLER**
Found in **sp|Q9BWD1|THIC_HUMAN**, Acetyl-CoA acetyltransferase
Match to Query 1308: 1450.909from(484.6436,3+)
Title: 1018: Scan 2525 (rt=65.3297, f=3, i=356) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1450.909
**Variable modifications:**
**Ions Score:** 52.76 **Expect:** 0.001

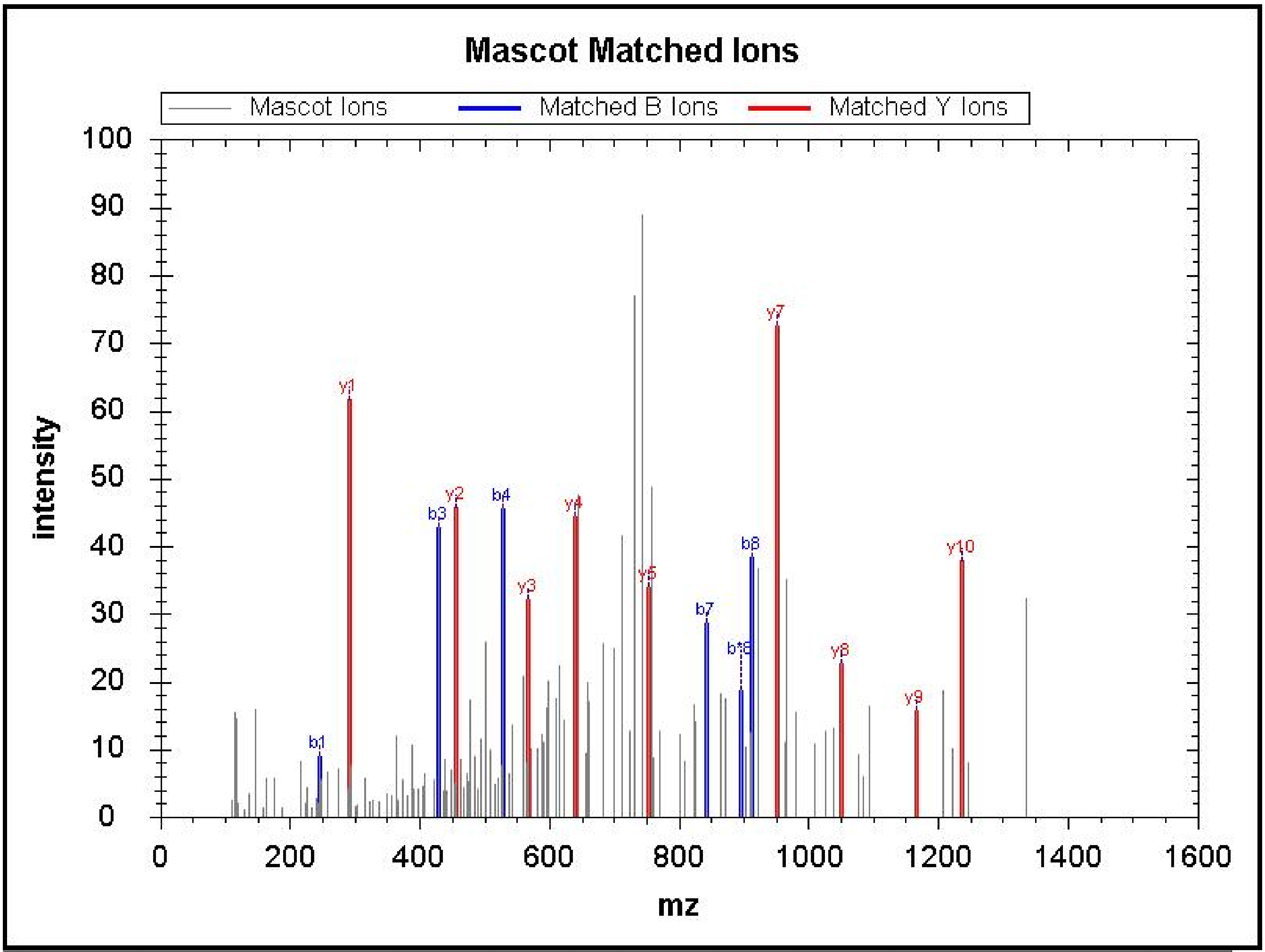


| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | | | I | | | | | | | 11 |
| 2 | 371.28 | 186.14 | | | L | 1,194.72 | 597.86 | 1,177.69 | 589.35 | 1,176.71 | 588.86 | 10 |
| 3 | 470.35 | 235.68 | | | V | 1,081.64 | 541.32 | 1,064.61 | 532.81 | 1,063.63 | 532.32 | 9 |
| 4 | 571.39 | 286.20 | 553.38 | 277.20 | T | 982.57 | 491.79 | 965.54 | 483.27 | 964.56 | 482.78 | 8 |
| 5 | 684.48 | 342.74 | 666.47 | 333.74 | L | 881.52 | 441.26 | 864.49 | 432.75 | 863.51 | 432.26 | 7 |
| 6 | 797.56 | 399.28 | 779.55 | 390.28 | L | 768.44 | 384.72 | 751.41 | 376.21 | 750.43 | 375.72 | 6 |
| 7 | 934.62 | 467.81 | 916.61 | 458.81 | H | 655.35 | 328.18 | 638.33 | 319.67 | 637.34 | 319.17 | 5 |
| 8 | 1,035.67 | 518.34 | 1,017.66 | 509.33 | T | 518.29 | 259.65 | 501.27 | 251.14 | 500.28 | 250.64 | 4 |
| 9 | 1,148.75 | 574.88 | 1,130.74 | 565.87 | L | 417.25 | 209.13 | 400.22 | 200.61 | 399.24 | 200.12 | 3 |
| 10 | 1,277.80 | 639.40 | 1,259.78 | 630.40 | E | 304.16 | 152.58 | 287.13 | 144.07 | 286.15 | 143.58 | 2 |
| 11 | | | | | R | 175.12 | 88.06 | 158.09 | 79.55 | | | 1 |

Query 1376 Hit 1

MS/MS Fragmentation of **VANVSLLALYK**
Found in **sp|P62266|RS23_HUMAN**, 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3
Match to Query 1376: 1477.917from(739.9656,2+)

Title: 769: Sum of 2 scans in range 1980 (rt=53.0536, f=4, i=530) to 1981 (rt=53.079, f=4, i=531) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1477.917
**Variable modifications:**
**K11** :iTRAQ4plex (K)
**Ions Score:** 51.68 **Expect:** 0.002

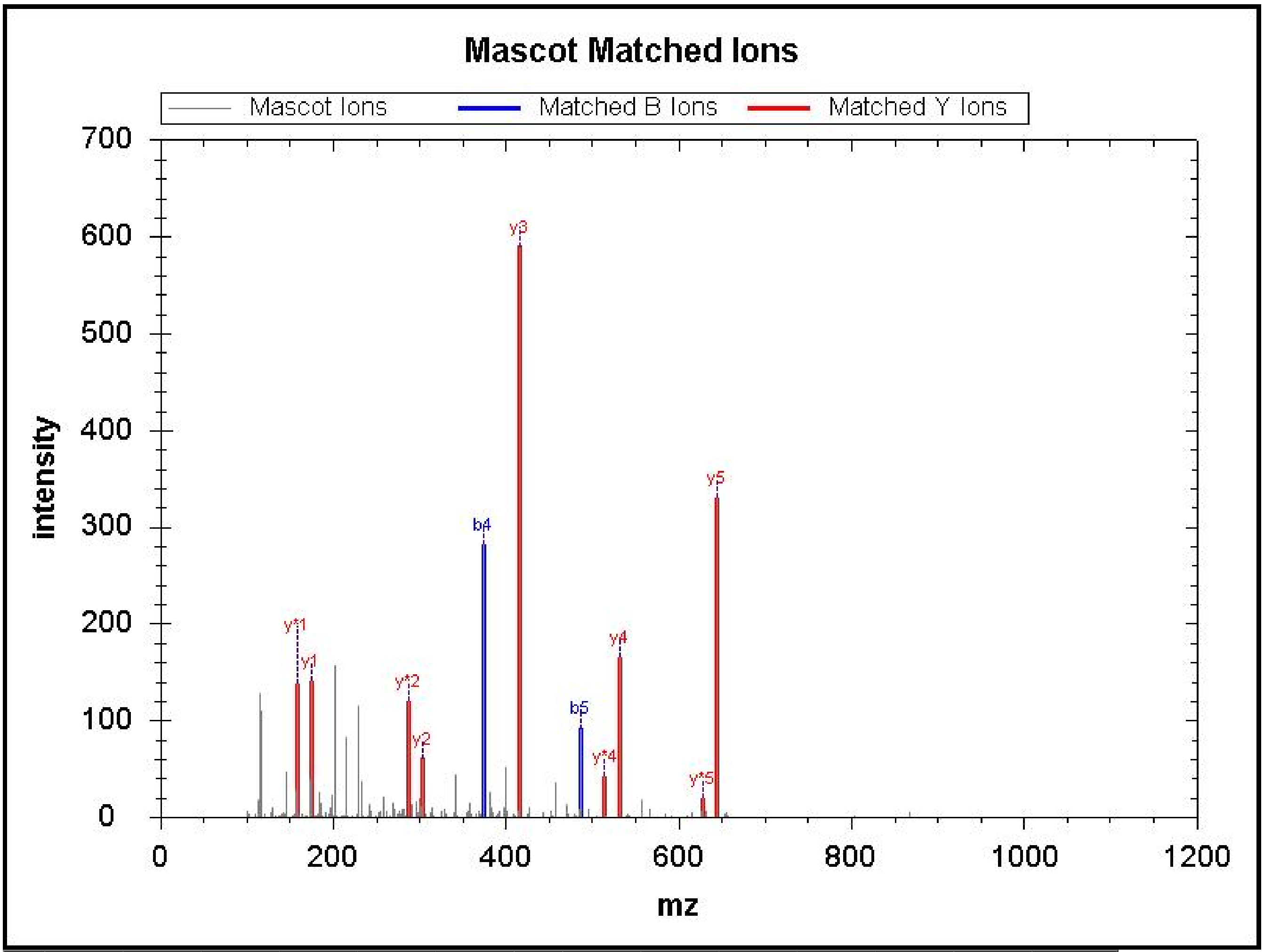


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **244.18** | 122.59 | | | | | V | | | | | | | 11 |
| 2 | 315.21 | 158.11 | | | | | A | **1,235.75** | 618.38 | 1,218.72 | 609.86 | 1,217.74 | 609.37 | 10 |
| 3 | **429.26** | 215.13 | 412.23 | 206.62 | | | N | **1,164.71** | 582.86 | 1,147.68 | 574.35 | 1,146.70 | 573.85 | 9 |
| 4 | **528.33** | 264.67 | 511.30 | 256.15 | | | V | **1,050.67** | 525.84 | 1,033.64 | 517.32 | 1,032.66 | 516.83 | 8 |
| 5 | 615.36 | 308.18 | 598.33 | 299.67 | 597.35 | 299.18 | S | **951.60** | 476.30 | 934.57 | 467.79 | 933.59 | 467.30 | 7 |
| 6 | 728.44 | 364.72 | 711.42 | 356.21 | 710.43 | 355.72 | L | 864.57 | 432.79 | 847.54 | 424.27 | | | 6 |
| 7 | **841.53** | 421.27 | 824.50 | 412.75 | 823.52 | 412.26 | L | **751.48** | 376.25 | 734.46 | 367.73 | | | 5 |
| 8 | **912.56** | 456.79 | **895.54** | 448.27 | 894.55 | 447.78 | A | **638.40** | 319.70 | 621.37 | 311.19 | | | 4 |
| 9 | 1,025.65 | 513.33 | 1,008.62 | 504.81 | 1,007.64 | 504.32 | L | **567.36** | 284.18 | 550.34 | 275.67 | | | 3 |
| 10 | 1,188.71 | 594.86 | 1,171.68 | 586.35 | 1,170.70 | 585.85 | Y | **454.28** | 227.64 | 437.25 | 219.13 | | | 2 |
| 11 | | | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 37 Hit 1

MS/MS Fragmentation of **GSINLKR**
Found in **sp|Q7Z5Q5|DPOLN_HUMAN**, DNA polymerase nu OS=Homo sapiens GN=POLN PE=1 SV=2
Match to Query 37: 787.4729from(394.7437,2+)
Title: 323: Scan 1017 (rt=31.3488, f=2, i=139) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 787.4729

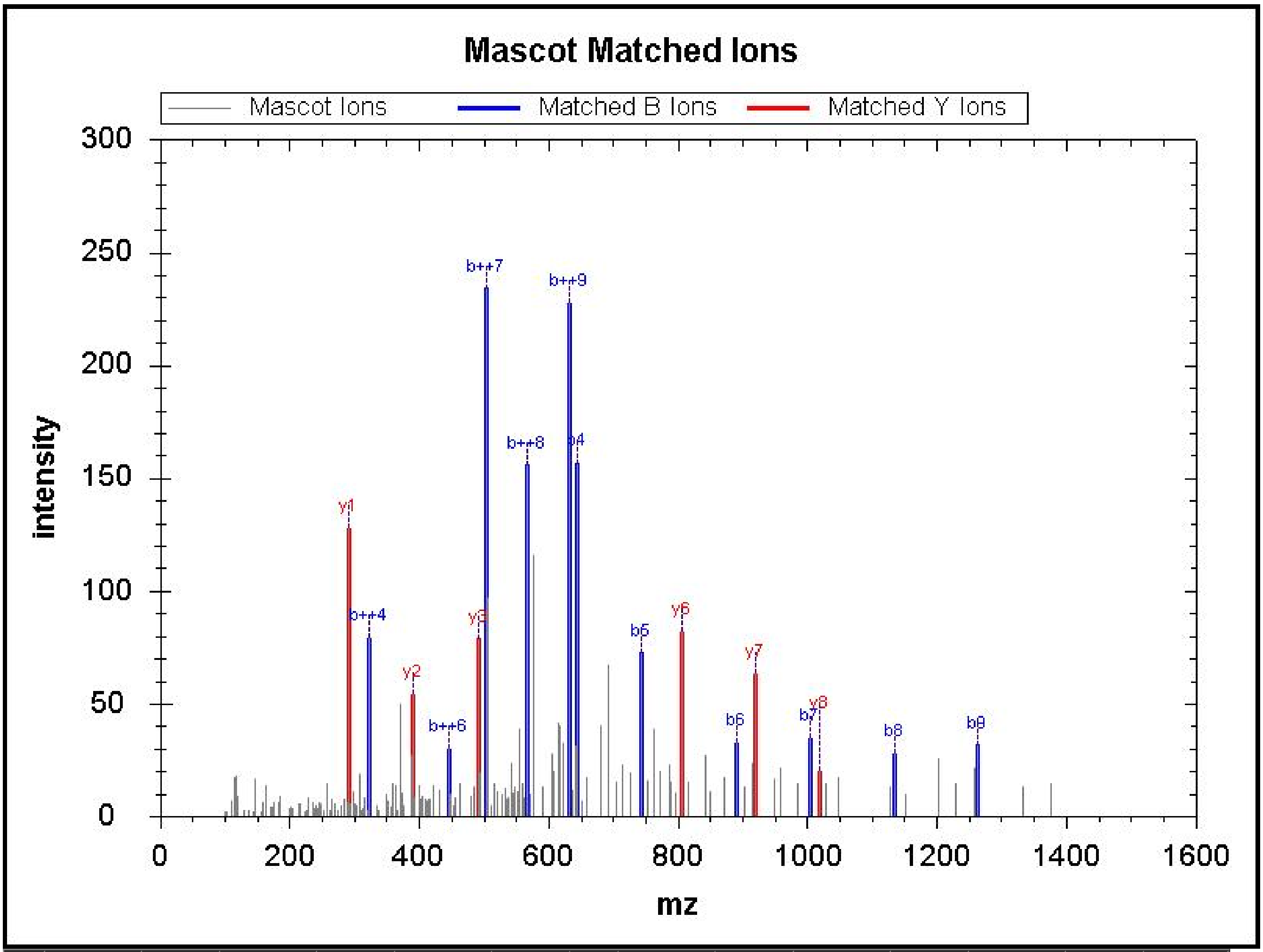
**Variable modifications:**
**N4** :Deamidated (NQ)
**Ions Score:** 49.69 **Expect:** 0.007



| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.03 | 29.52 | | | | | G | | | | | | | 7 |
| 2 | 145.06 | 73.03 | | | 127.05 | 64.03 | S | 731.44 | 366.22 | 714.41 | 357.71 | 713.43 | 357.22 | 6 |
| 3 | 258.14 | 129.58 | | | 240.13 | 120.57 | I | **644.41** | 322.71 | **627.38** | 314.19 | | | 5 |
| 4 | **373.17** | 187.09 | 356.15 | 178.58 | 355.16 | 178.08 | N | **531.32** | 266.17 | **514.30** | 257.65 | | | 4 |
| 5 | **486.26** | 243.63 | 469.23 | 235.12 | 468.25 | 234.63 | L | **416.30** | 208.65 | 399.27 | 200.14 | | | 3 |
| 6 | 614.35 | 307.68 | 597.32 | 299.17 | 596.34 | 298.67 | K | **303.21** | 152.11 | **286.19** | 143.60 | | | 2 |
| 7 | | | | | | | R | **175.12** | 88.06 | **158.09** | 79.55 | | | 1 |

Query 2432 Hit 1

MS/MS Fragmentation of **FVDHVFDEQVIDSLTVK**
Found in **sp|P04843|RPN1_HUMAN**, Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1
Match to Query 2432: 2278.222from(760.4145,3+)
Title: 845: Sum of 2 scans in range 2141 (rt=56.6819, f=4, i=582) to 2142 (rt=56.7074, f=4, i=583) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2278.222
**Variable modifications:**
**K17** :iTRAQ4plex (K)
**Ions Score:** 49.17 **Expect:** 0.010

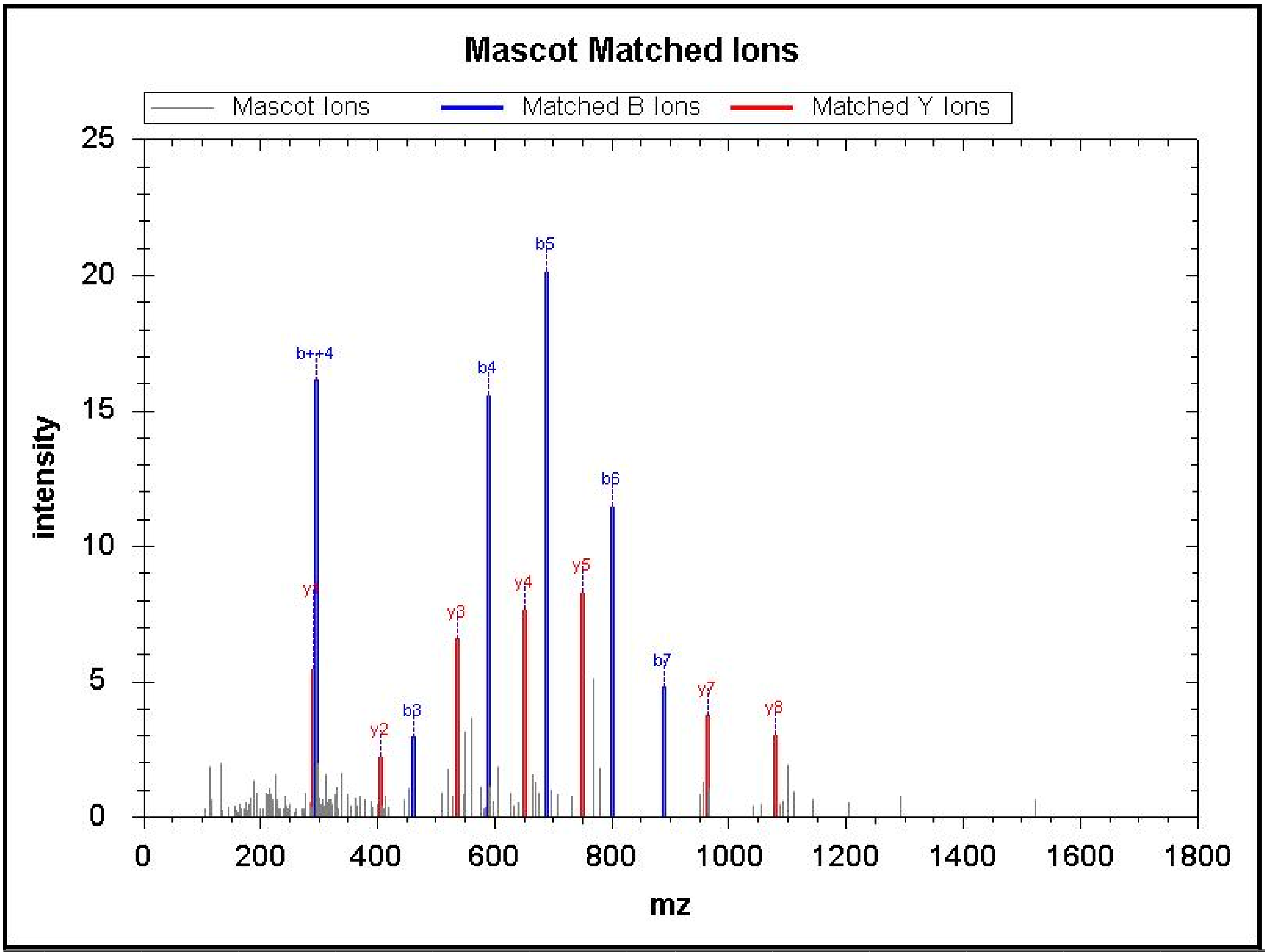


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 292.18 | 146.59 | | | | | F | | | | | | | 17 |
| 2 | 391.25 | 196.13 | | | | | V | 1,988.05 | 994.53 | 1,971.02 | 986.01 | 1,970.04 | 985.52 | 16 |
| 3 | 506.27 | 253.64 | | | 488.26 | 244.63 | D | 1,888.98 | 944.99 | 1,871.95 | 936.48 | 1,870.97 | 935.99 | 15 |
| 4 | 643.33 | 322.17 | | | 625.32 | 313.16 | H | 1,773.95 | 887.48 | 1,756.92 | 878.97 | 1,755.94 | 878.47 | 14 |
| 5 | 742.40 | 371.70 | | | 724.39 | 362.70 | V | 1,636.89 | 818.95 | 1,619.86 | 810.44 | 1,618.88 | 809.94 | 13 |
| 6 | 889.47 | 445.24 | | | 871.46 | 436.23 | F | 1,537.82 | 769.42 | 1,520.80 | 760.90 | 1,519.81 | 760.41 | 12 |
| 7 | 1,004.50 | 502.75 | | | 986.49 | 493.75 | D | 1,390.75 | 695.88 | 1,373.73 | 687.37 | 1,372.74 | 686.88 | 11 |
| 8 | 1,133.54 | 567.27 | | | 1,115.53 | 558.27 | E | 1,275.73 | 638.37 | 1,258.70 | 629.85 | 1,257.72 | 629.36 | 10 |
| 9 | 1,261.60 | 631.30 | 1,244.57 | 622.79 | 1,243.59 | 622.30 | Q | 1,146.68 | 573.85 | 1,129.66 | 565.33 | 1,128.67 | 564.84 | 9 |
| 10 | 1,360.67 | 680.84 | 1,343.64 | 672.32 | 1,342.65 | 671.83 | V | 1,018.63 | 509.82 | 1,001.60 | 501.30 | 1,000.62 | 500.81 | 8 |
| 11 | 1,473.75 | 737.38 | 1,456.72 | 728.87 | 1,455.74 | 728.37 | I | 919.56 | 460.28 | 902.53 | 451.77 | 901.55 | 451.28 | 7 |
| 12 | 1,588.78 | 794.89 | 1,571.75 | 786.38 | 1,570.77 | 785.89 | D | 806.47 | 403.74 | 789.45 | 395.23 | 788.46 | 394.74 | 6 |
| 13 | 1,675.81 | 838.41 | 1,658.78 | 829.89 | 1,657.80 | 829.40 | S | 691.45 | 346.23 | 674.42 | 337.71 | 673.44 | 337.22 | 5 |
| 14 | 1,788.89 | 894.95 | 1,771.87 | 886.44 | 1,770.88 | 885.94 | L | 604.41 | 302.71 | 587.39 | 294.20 | 586.40 | 293.71 | 4 |
| 15 | 1,889.94 | 945.47 | 1,872.91 | 936.96 | 1,871.93 | 936.47 | T | 491.33 | 246.17 | 474.30 | 237.66 | 473.32 | 237.16 | 3 |
| 16 | 1,989.01 | 995.01 | 1,971.98 | 986.49 | 1,971.00 | 986.00 | V | 390.28 | 195.65 | 373.26 | 187.13 | | | 2 |
| 17 | | | | | | | K | 291.21 | 146.11 | 274.19 | 137.60 | | | 1 |

Query 2459 Hit 1

MS/MS Fragmentation of **DAEEVISQTIDTIVDMIK**
Found in **sp|Q04857|CO6A1_MOUSE**, Collagen alpha-1(VI) chain OS=Mus musculus GN=Col6a1 PE=2 SV=1
Match to Query 2459: 2308.229from(770.4171,3+)
Title: 1398: Scan 3904 (rt=94.9306, f=2, i=603) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2308.229

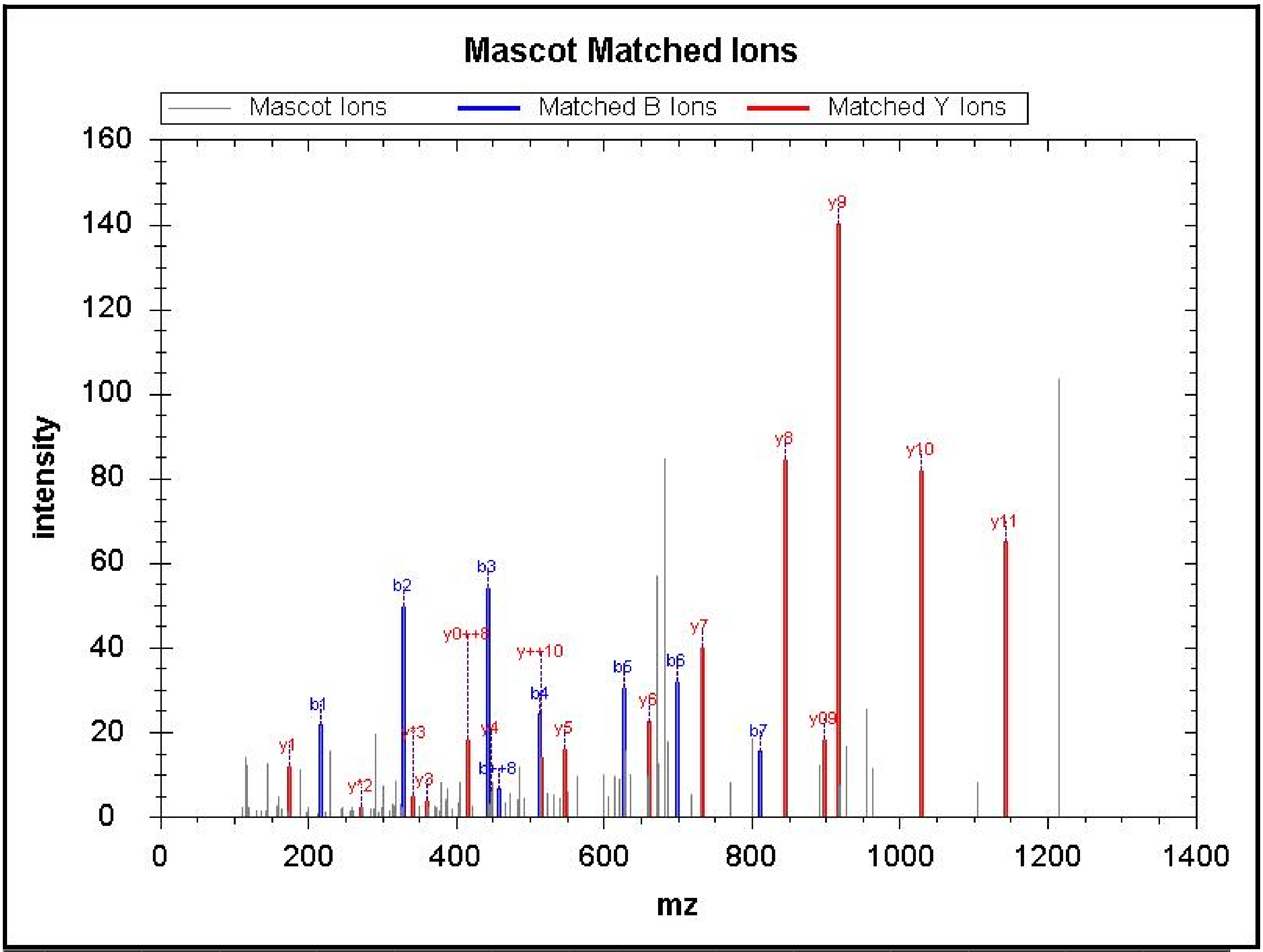
**Variable modifications:**
**Q8** :Deamidated (NQ)
**K18** :iTRAQ4plex (K)
**Ions Score:** 48.66 **Expect:** 0.011



| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 260.14 | 130.57 | | | 242.13 | 121.57 | D | | | | | | | 18 |
| 2 | 331.17 | 166.09 | | | 313.16 | 157.09 | A | 2,050.07 | 1,025.54 | 2,033.05 | 1,017.03 | 2,032.06 | 1,016.54 | 17 |
| 3 | **460.22** | 230.61 | | | 442.21 | 221.61 | E | 1,979.04 | 990.02 | 1,962.01 | 981.51 | 1,961.03 | 981.02 | 16 |
| 4 | **589.26** | **295.13** | | | 571.25 | 286.13 | E | 1,849.99 | 925.50 | 1,832.97 | 916.99 | 1,831.98 | 916.50 | 15 |
| 5 | **688.33** | 344.67 | | | 670.32 | 335.66 | V | 1,720.95 | 860.98 | 1,703.93 | 852.47 | 1,702.94 | 851.97 | 14 |
| 6 | **801.41** | 401.21 | | | 783.40 | 392.20 | I | 1,621.88 | 811.45 | 1,604.86 | 802.93 | 1,603.87 | 802.44 | 13 |
| 7 | **888.44** | 444.73 | | | 870.43 | 435.72 | S | 1,508.80 | 754.90 | 1,491.77 | 746.39 | 1,490.79 | 745.90 | 12 |
| 8 | 1,017.49 | 509.25 | 1,000.46 | 500.73 | 999.48 | 500.24 | Q | 1,421.77 | 711.39 | 1,404.74 | 702.87 | 1,403.76 | 702.38 | 11 |
| 9 | 1,118.53 | 559.77 | 1,101.51 | 551.26 | 1,100.52 | 550.77 | T | 1,292.73 | 646.87 | 1,275.70 | 638.35 | 1,274.71 | 637.86 | 10 |
| 10 | 1,231.62 | 616.31 | 1,214.59 | 607.80 | 1,213.61 | 607.31 | I | 1,191.68 | 596.34 | 1,174.65 | 587.83 | 1,173.67 | 587.34 | 9 |
| 11 | 1,346.64 | 673.83 | 1,329.62 | 665.31 | 1,328.63 | 664.82 | D | **1,078.59** | 539.80 | 1,061.57 | 531.29 | 1,060.58 | 530.80 | 8 |
| 12 | 1,447.69 | 724.35 | 1,430.67 | 715.84 | 1,429.68 | 715.34 | T | **963.57** | 482.29 | 946.54 | 473.77 | 945.56 | 473.28 | 7 |
| 13 | 1,560.78 | 780.89 | 1,543.75 | 772.38 | 1,542.77 | 771.89 | I | 862.52 | 431.76 | 845.49 | 423.25 | 844.51 | 422.76 | 6 |
| 14 | 1,659.84 | 830.43 | 1,642.82 | 821.91 | 1,641.83 | 821.42 | V | **749.43** | 375.22 | 732.41 | 366.71 | 731.42 | 366.22 | 5 |
| 15 | 1,774.87 | 887.94 | 1,757.85 | 879.43 | 1,756.86 | 878.93 | D | **650.37** | 325.69 | 633.34 | 317.17 | 632.36 | 316.68 | 4 |
| 16 | 1,905.91 | 953.46 | 1,888.89 | 944.95 | 1,887.90 | 944.45 | M | **535.34** | 268.17 | 518.31 | 259.66 | | | 3 |
| 17 | 2,019.00 | 1,010.00 | 2,001.97 | 1,001.49 | 2,000.99 | 1,001.00 | I | **404.30** | 202.65 | 387.27 | 194.14 | | | 2 |
| 18 | | | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 1123 Hit 1

MS/MS Fragmentation of **ALLANALTSALR**
Found in **sp|P57088|TMM33_HUMAN**, Transmembrane protein 33 OS=Homo sapiens GN=TMEM33 PE=1 SV=2
Match to Query 1123: 1356.825from(679.4199,2+)
Title: 840: Scan 2133 (rt=56.4953, f=2, i=319) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1356.825
**Variable modifications:**
**Ions Score:** 47.7 **Expect:** 0.007

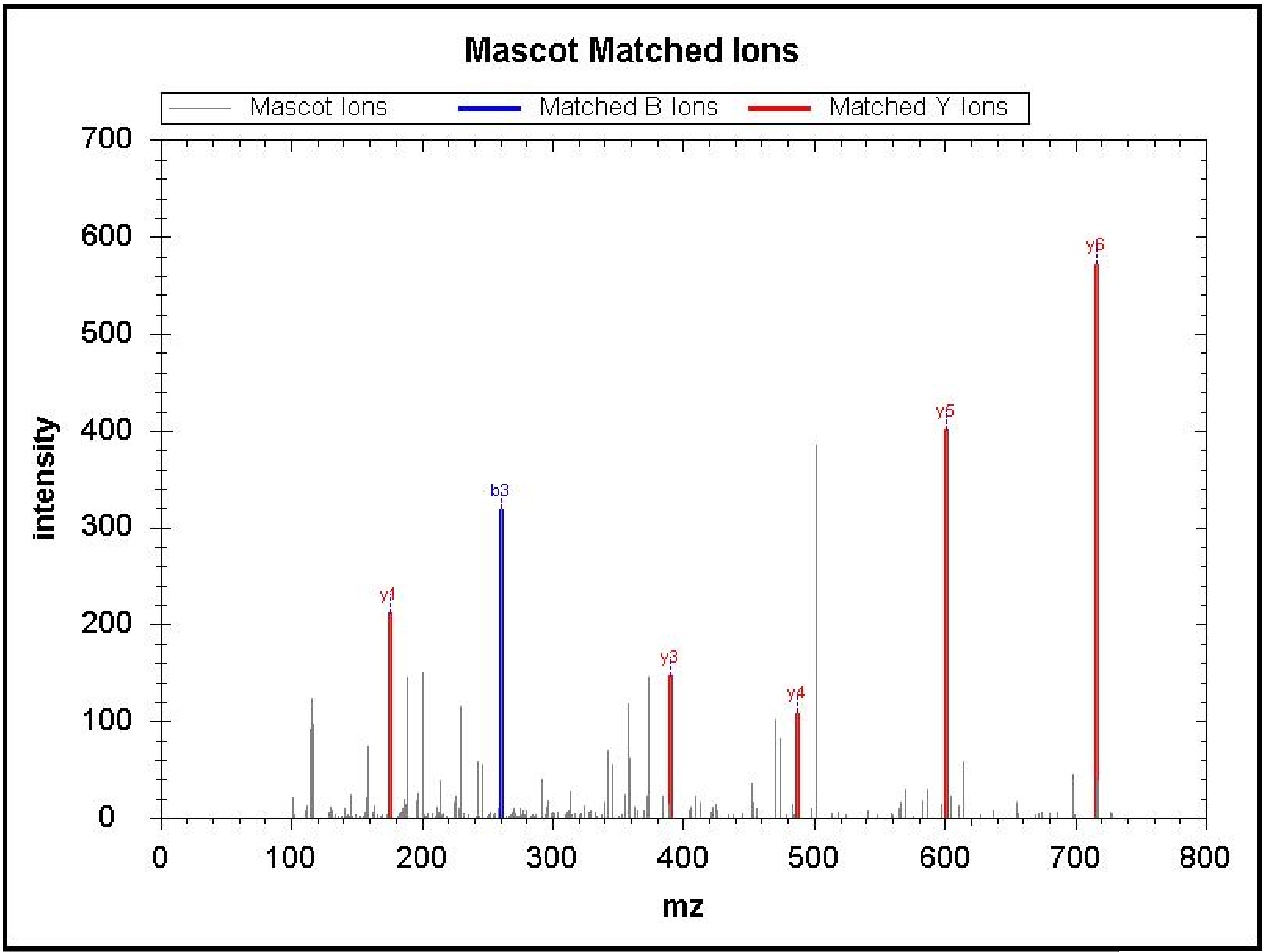


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 216.15 | 108.58 | | | | | A | | | | | | | 12 |
| 2 | 329.23 | 165.12 | | | | | L | 1,142.69 | 571.85 | 1,125.66 | 563.33 | 1,124.68 | 562.84 | 11 |
| 3 | 442.31 | 221.66 | | | | | L | 1,029.61 | 515.31 | 1,012.58 | 506.79 | 1,011.59 | 506.30 | 10 |
| 4 | 513.35 | 257.18 | | | | | A | 916.52 | 458.76 | 899.49 | 450.25 | 898.51 | 449.76 | 9 |
| 5 | 627.39 | 314.20 | 610.37 | 305.69 | | | N | 845.48 | 423.25 | 828.46 | 414.73 | 827.47 | 414.24 | 8 |
| 6 | 698.43 | 349.72 | 681.41 | 341.21 | | | A | 731.44 | 366.22 | 714.41 | 357.71 | 713.43 | 357.22 | 7 |
| 7 | 811.52 | 406.26 | 794.49 | 397.75 | | | L | 660.40 | 330.71 | 643.38 | 322.19 | 642.39 | 321.70 | 6 |
| 8 | 912.56 | 456.79 | 895.54 | 448.27 | 894.55 | 447.78 | T | 547.32 | 274.16 | 530.29 | 265.65 | 529.31 | 265.16 | 5 |
| 9 | 999.60 | 500.30 | 982.57 | 491.79 | 981.58 | 491.30 | S | 446.27 | 223.64 | 429.25 | 215.13 | 428.26 | 214.63 | 4 |
| 10 | 1,070.63 | 535.82 | 1,053.61 | 527.31 | 1,052.62 | 526.81 | A | 359.24 | 180.12 | 342.21 | 171.61 | | | 3 |
| 11 | 1,183.72 | 592.36 | 1,166.69 | 583.85 | 1,165.71 | 583.36 | L | 288.20 | 144.61 | 271.18 | 136.09 | | | 2 |
| 12 | | | | | | | R | 175.12 | 88.06 | 158.09 | 79.55 | | | 1 |

Query 88 Hit 1

MS/MS Fragmentation of **SGNLPSKR**
Found in **sp|P46013|KI67_HUMAN**, Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2
Match to Query 88: 858.5085from(430.2615,2+)
Title: 201: Scan 892 (rt=28.0862, f=3, i=82) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]

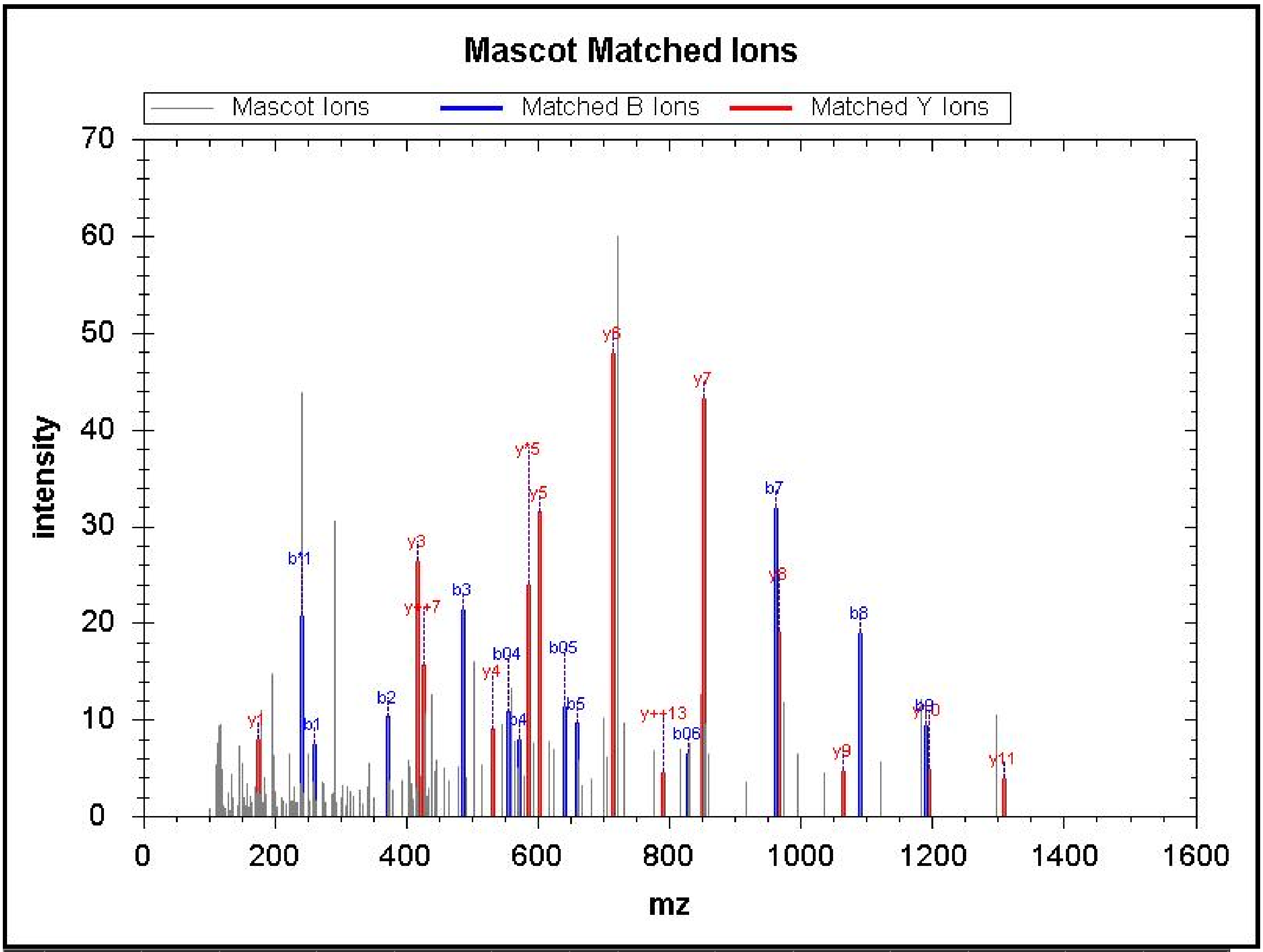
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 858.5085
**Variable modifications:**
**N3** :Deamidated (NQ)
**Ions Score:** 47.12 **Expect:** 0.012



| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.04 | 44.52 | | | 70.03 | 35.52 | S | | | | | | | 8 |
| 2 | 145.06 | 73.03 | | | 127.05 | 64.03 | G | 772.43 | 386.72 | 755.40 | 378.21 | 754.42 | 377.71 | 7 |
| 3 | **260.09** | 130.55 | 243.06 | 122.03 | 242.08 | 121.54 | N | **715.41** | 358.21 | 698.38 | 349.70 | 697.40 | 349.20 | 6 |
| 4 | 373.17 | 187.09 | 356.15 | 178.58 | 355.16 | 178.08 | L | **600.38** | 300.70 | 583.36 | 292.18 | 582.37 | 291.69 | 5 |
| 5 | 470.22 | 235.62 | 453.20 | 227.10 | 452.21 | 226.61 | P | **487.30** | 244.15 | 470.27 | 235.64 | 469.29 | 235.15 | 4 |
| 6 | 557.26 | 279.13 | 540.23 | 270.62 | 539.25 | 270.13 | S | **390.25** | 195.63 | 373.22 | 187.11 | 372.24 | 186.62 | 3 |
| 7 | 685.35 | 343.18 | 668.32 | 334.67 | 667.34 | 334.17 | K | 303.21 | 152.11 | 286.19 | 143.60 | | | 2 |
| 8 | | | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 2302 Hit 1

MS/MS Fragmentation of **NLLSSWDEVIHIADQLR**
Found in **sp|Q15813|TBCE_HUMAN**, Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE PE=1 SV=1
Match to Query 2302: 2152.149from(718.3903,3+)
Title: 1133: Sum of 2 scans in range 2902 (rt=73.3798, f=4, i=794) to 2903 (rt=73.4052, f=4, i=795) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2152.149
**Variable modifications:**
**Ions Score:** 46.84 **Expect:** 0.018

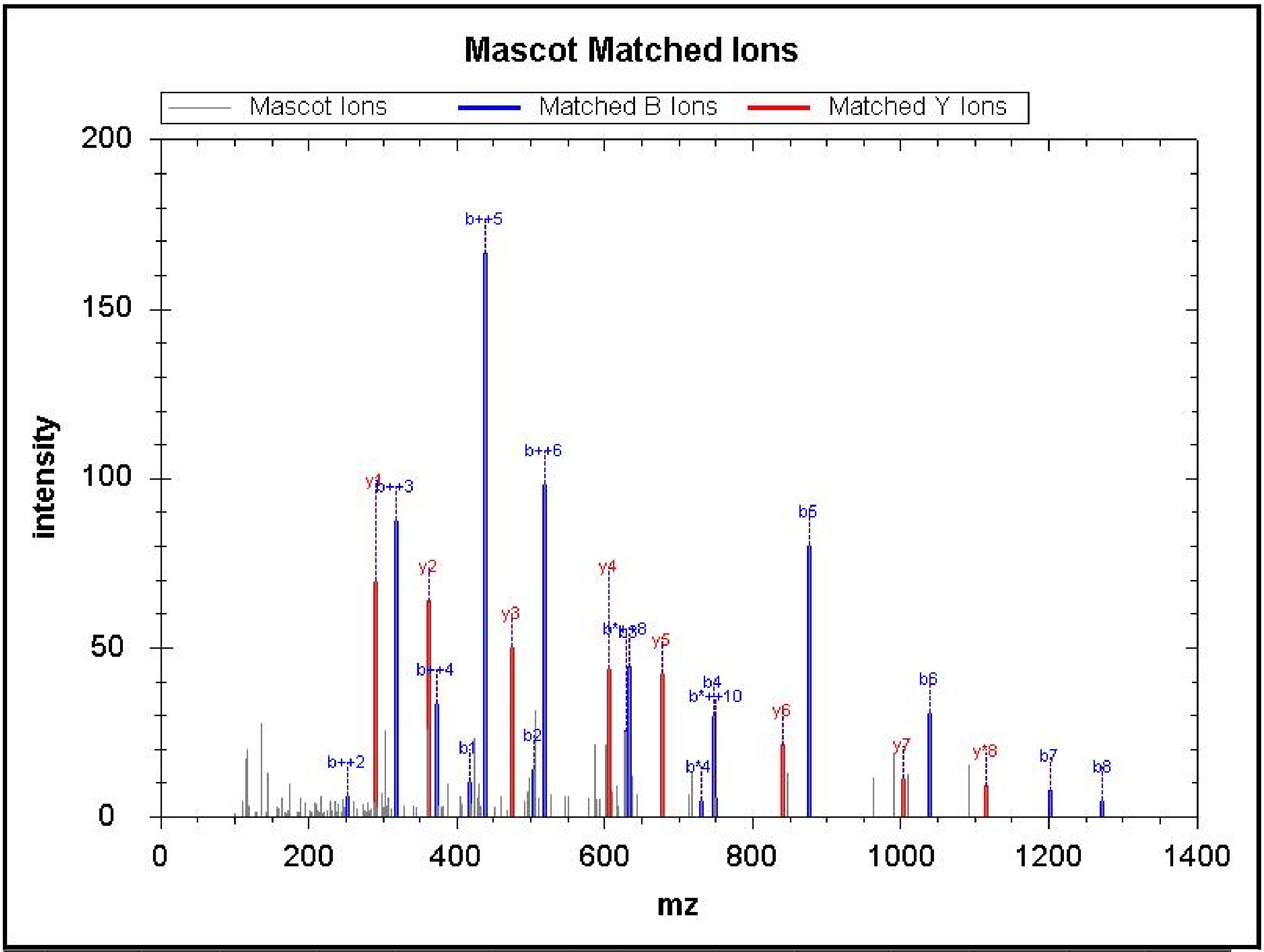


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **259.15** | 130.08 | **242.13** | 121.57 | | | N | | | | | | | 17 |
| 2 | **372.24** | 186.62 | 355.21 | 178.11 | | | L | 1,895.00 | 948.00 | 1,877.98 | 939.49 | 1,876.99 | 939.00 | 16 |
| 3 | **485.32** | 243.16 | 468.29 | 234.65 | | | L | 1,781.92 | 891.46 | 1,764.89 | 882.95 | 1,763.91 | 882.46 | 15 |
| 4 | **572.35** | 286.68 | 555.33 | 278.17 | **554.34** | 277.67 | S | 1,668.83 | 834.92 | 1,651.81 | 826.41 | 1,650.82 | 825.92 | 14 |
| 5 | **659.38** | 330.20 | 642.36 | 321.68 | **641.37** | 321.19 | S | 1,581.80 | **791.40** | 1,564.78 | 782.89 | 1,563.79 | 782.40 | 13 |
| 6 | 845.46 | 423.24 | 828.44 | 414.72 | **827.45** | 414.23 | W | 1,494.77 | 747.89 | 1,477.74 | 739.38 | 1,476.76 | 738.88 | 12 |
| 7 | **960.49** | 480.75 | 943.46 | 472.24 | 942.48 | 471.74 | D | **1,308.69** | 654.85 | 1,291.66 | 646.34 | 1,290.68 | 645.84 | 11 |
| 8 | **1,089.53** | 545.27 | 1,072.51 | 536.76 | 1,071.52 | 536.27 | E | **1,193.66** | 597.34 | 1,176.64 | 588.82 | 1,175.65 | 588.33 | 10 |
| 9 | **1,188.60** | 594.80 | 1,171.58 | 586.29 | 1,170.59 | 585.80 | V | **1,064.62** | 532.81 | 1,047.59 | 524.30 | 1,046.61 | 523.81 | 9 |
| 10 | 1,301.69 | 651.35 | 1,284.66 | 642.83 | 1,283.68 | 642.34 | I | **965.55** | 483.28 | 948.53 | 474.77 | 947.54 | 474.27 | 8 |
| 11 | 1,438.74 | 719.88 | 1,421.72 | 711.36 | 1,420.73 | 710.87 | H | **852.47** | **426.74** | 835.44 | 418.22 | 834.46 | 417.73 | 7 |
| 12 | 1,551.83 | 776.42 | 1,534.80 | 767.90 | 1,533.82 | 767.41 | I | **715.41** | 358.21 | 698.38 | 349.70 | 697.40 | 349.20 | 6 |
| 13 | 1,622.87 | 811.94 | 1,605.84 | 803.42 | 1,604.86 | 802.93 | A | **602.33** | 301.67 | **585.30** | 293.15 | 584.32 | 292.66 | 5 |
| 14 | 1,737.89 | 869.45 | 1,720.87 | 860.94 | 1,719.88 | 860.44 | D | **531.29** | 266.15 | 514.26 | 257.63 | 513.28 | 257.14 | 4 |
| 15 | 1,865.95 | 933.48 | 1,848.93 | 924.97 | 1,847.94 | 924.47 | Q | **416.26** | 208.63 | 399.24 | 200.12 | | | 3 |
| 16 | 1,979.04 | 990.02 | 1,962.01 | 981.51 | 1,961.03 | 981.02 | L | 288.20 | 144.61 | 271.18 | 136.09 | | | 2 |
| 17 | | | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 1948 Hit 1

MS/MS Fragmentation of **KSEIEYYAMLAK**
Found in **sp|P62888|RL30_HUMAN**, 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2
Match to Query 1948: 1877.041 from(626.6876,3+)
Title: 535: Scan 1617 (rt=44.418, f=2, i=226) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1877.041

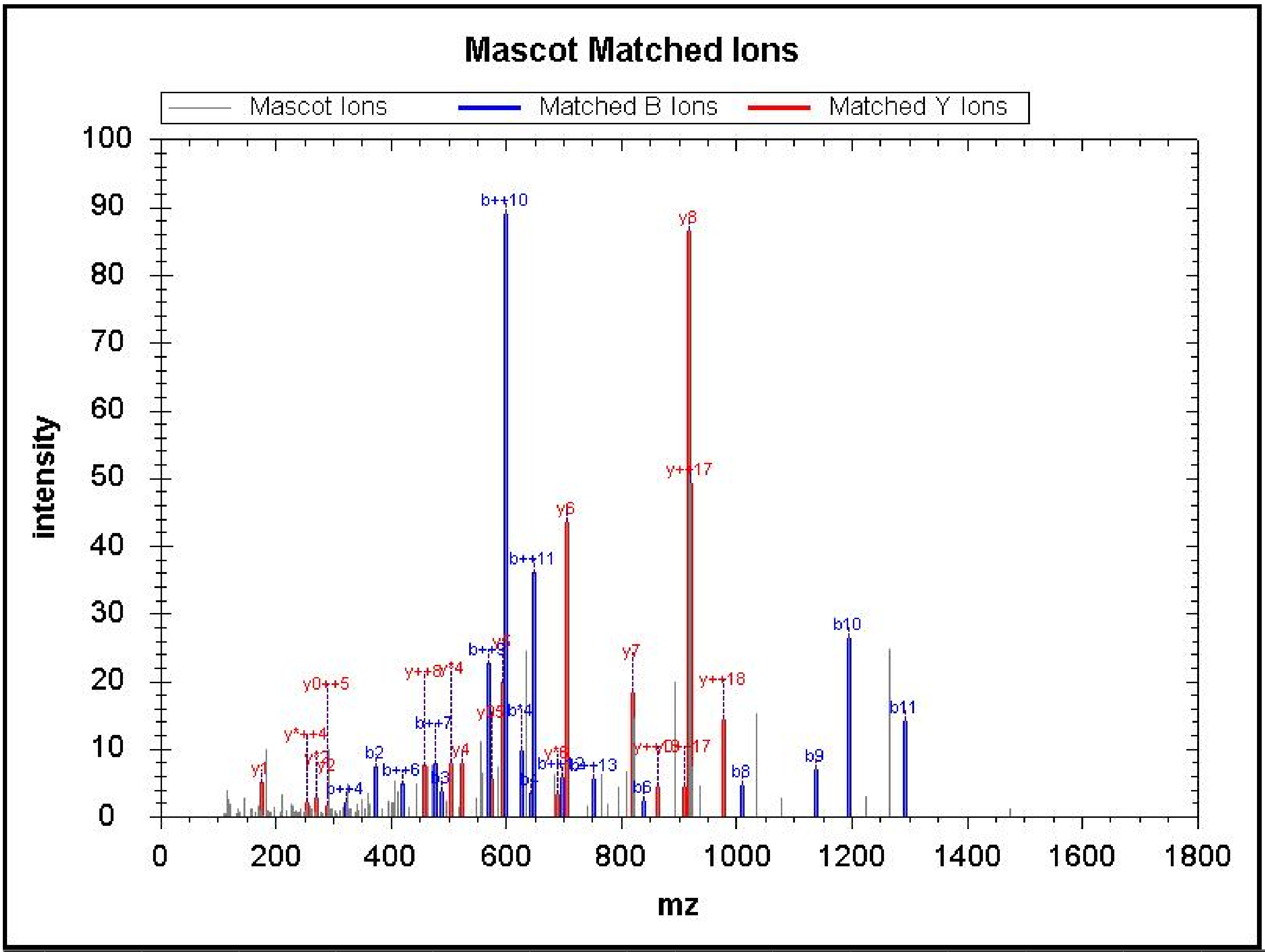
**Variable modifications:**
**K1** :iTRAQ4plex (K)
**K12** :iTRAQ4plex (K)
**Ions Score:** 46.59 **Expect:** 0.017



| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 417.31 | 209.16 | 400.28 | 200.64 | | | K | | | | | | | 12 |
| 2 | 504.34 | 252.67 | 487.31 | 244.16 | 486.33 | 243.67 | S | 1,461.74 | 731.37 | 1,444.72 | 722.86 | 1,443.73 | 722.37 | 11 |
| 3 | 633.38 | 317.19 | 616.35 | 308.68 | 615.37 | 308.19 | E | 1,374.71 | 687.86 | 1,357.68 | 679.35 | 1,356.70 | 678.85 | 10 |
| 4 | 746.47 | 373.74 | 729.44 | 365.22 | 728.45 | 364.73 | I | 1,245.67 | 623.34 | 1,228.64 | 614.82 | 1,227.66 | 614.33 | 9 |
| 5 | 875.51 | 438.26 | 858.48 | 429.74 | 857.50 | 429.25 | E | 1,132.58 | 566.80 | 1,115.56 | 558.28 | 1,114.57 | 557.79 | 8 |
| 6 | 1,038.57 | 519.79 | 1,021.54 | 511.28 | 1,020.56 | 510.78 | Y | 1,003.54 | 502.27 | 986.51 | 493.76 | | | 7 |
| 7 | 1,201.63 | 601.32 | 1,184.61 | 592.81 | 1,183.62 | 592.32 | Y | 840.48 | 420.74 | 823.45 | 412.23 | | | 6 |
| 8 | 1,272.67 | 636.84 | 1,255.65 | 628.33 | 1,254.66 | 627.83 | A | 677.41 | 339.21 | 660.39 | 330.70 | | | 5 |
| 9 | 1,403.71 | 702.36 | 1,386.69 | 693.85 | 1,385.70 | 693.35 | M | 606.38 | 303.69 | 589.35 | 295.18 | | | 4 |
| 10 | 1,516.80 | 758.90 | 1,499.77 | 750.39 | 1,498.79 | 749.90 | L | 475.34 | 238.17 | 458.31 | 229.66 | | | 3 |
| 11 | 1,587.83 | 794.42 | 1,570.81 | 785.91 | 1,569.82 | 785.41 | A | 362.25 | 181.63 | 345.23 | 173.12 | | | 2 |
| 12 | | | | | | | K | 291.21 | 146.11 | 274.19 | 137.60 | | | 1 |

Query 2362 Hit 1

MS/MS Fragmentation of IDLRPVLGEGVPILASFLR
Found in sp|Q86VP6|CAND1_HUMAN, Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2
Match to Query 2362: 2208.309from(737.1104,3+)
Title: 1159: Scan 2969 (rt=74.8872, f=3, i=417) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2208.309
**Variable modifications:**
**Ions Score:** 46.27 **Expect:** 0.006

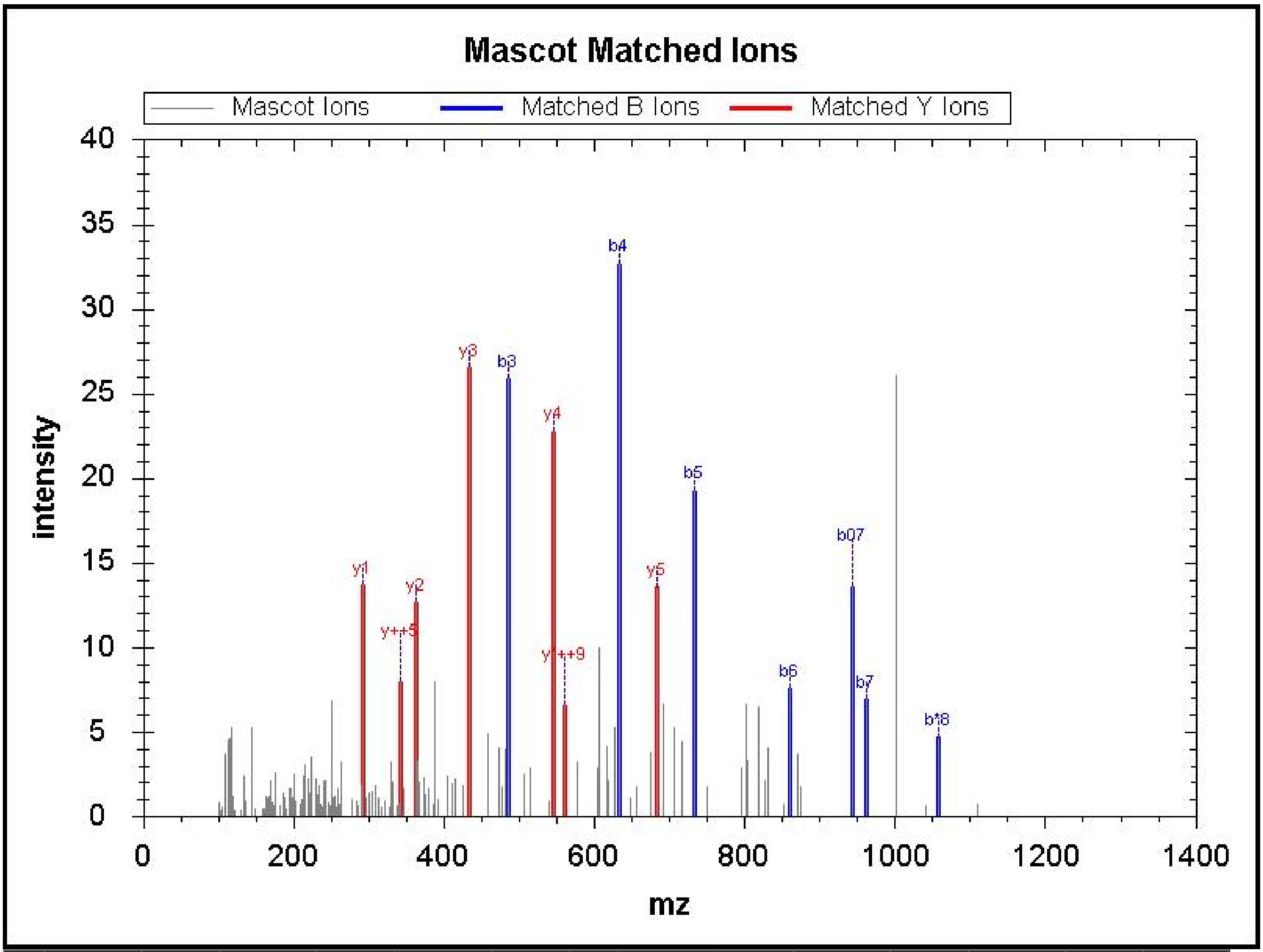


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | | | | | I | | | | | | | 19 |
| 2 | **373.22** | 187.11 | | | 355.21 | 178.11 | D | 1,952.13 | **976.57** | 1,935.11 | 968.06 | 1,934.12 | 967.56 | 18 |
| 3 | **486.30** | 243.66 | | | 468.29 | 234.65 | L | 1,837.11 | **919.06** | 1,820.08 | 910.54 | 1,819.10 | **910.05** | 17 |
| 4 | **642.41** | **321.71** | **625.38** | 313.19 | 624.39 | 312.70 | R | 1,724.02 | **862.51** | 1,707.00 | 854.00 | 1,706.01 | 853.51 | 16 |
| 5 | 739.46 | 370.23 | 722.43 | 361.72 | 721.45 | 361.23 | P | 1,567.92 | 784.46 | 1,550.89 | 775.95 | 1,549.91 | 775.46 | 15 |
| 6 | **838.53** | **419.77** | 821.50 | 411.25 | 820.52 | 410.76 | V | 1,470.87 | 735.94 | 1,453.84 | 727.42 | 1,452.86 | 726.93 | 14 |
| 7 | 951.61 | **476.31** | 934.58 | 467.80 | 933.60 | 467.30 | L | 1,371.80 | 686.40 | 1,354.77 | 677.89 | 1,353.79 | 677.40 | 13 |
| 8 | **1,008.63** | 504.82 | 991.61 | 496.31 | 990.62 | 495.81 | G | 1,258.72 | 629.86 | 1,241.69 | 621.35 | 1,240.70 | 620.86 | 12 |
| 9 | **1,137.67** | **569.34** | 1,120.65 | 560.83 | 1,119.66 | 560.34 | E | 1,201.69 | 601.35 | 1,184.67 | 592.84 | 1,183.68 | 592.35 | 11 |
| 10 | **1,194.70** | **597.85** | 1,177.67 | 589.34 | 1,176.69 | 588.85 | G | 1,072.65 | 536.83 | 1,055.62 | 528.32 | 1,054.64 | 527.82 | 10 |
| 11 | **1,293.76** | **647.39** | 1,276.74 | 638.87 | 1,275.75 | 638.38 | V | 1,015.63 | 508.32 | 998.60 | 499.81 | 997.62 | 499.31 | 9 |
| 12 | 1,390.82 | **695.91** | 1,373.79 | 687.40 | 1,372.81 | 686.91 | P | **916.56** | **458.78** | 899.53 | 450.27 | 898.55 | 449.78 | 8 |
| 13 | 1,503.90 | **752.45** | 1,486.88 | 743.94 | 1,485.89 | 743.45 | I | **819.51** | 410.26 | 802.48 | 401.74 | 801.50 | 401.25 | 7 |
| 14 | 1,616.99 | 809.00 | 1,599.96 | 800.48 | 1,598.97 | 799.99 | L | **706.42** | 353.72 | **689.40** | 345.20 | 688.41 | 344.71 | 6 |
| 15 | 1,688.02 | 844.52 | 1,671.00 | 836.00 | 1,670.01 | 835.51 | A | **593.34** | 297.17 | 576.31 | 288.66 | **575.33** | **288.17** | 5 |
| 16 | 1,775.05 | 888.03 | 1,758.03 | 879.52 | 1,757.04 | 879.03 | S | **522.30** | 261.66 | **505.28** | **253.14** | 504.29 | 252.65 | 4 |
| 17 | 1,922.12 | 961.57 | 1,905.10 | 953.05 | 1,904.11 | 952.56 | F | 435.27 | 218.14 | 418.24 | 209.63 | | | 3 |
| 18 | 2,035.21 | 1,018.11 | 2,018.18 | 1,009.59 | 2,017.20 | 1,009.10 | L | **288.20** | 144.61 | **271.18** | 136.09 | | | 2 |
| 19 | | | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 1940 Hit 1

MS/MS Fragmentation of **IEVFVQTLLHLAAK**
Found in **sp|Q09161|NCBP1_HUMAN**, Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1
Match to Query 1940: 1869.144from(624.0551,3+)

Title: 1255: Sum of 2 scans in range 3040 (rt=76.939, f=4, i=872) to 3041 (rt=76.9644, f=4, i=873) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1869.144
**Variable modifications:**
**K14** :iTRAQ4plex (K)
**Ions Score:** 45.88 **Expect:** 0.005

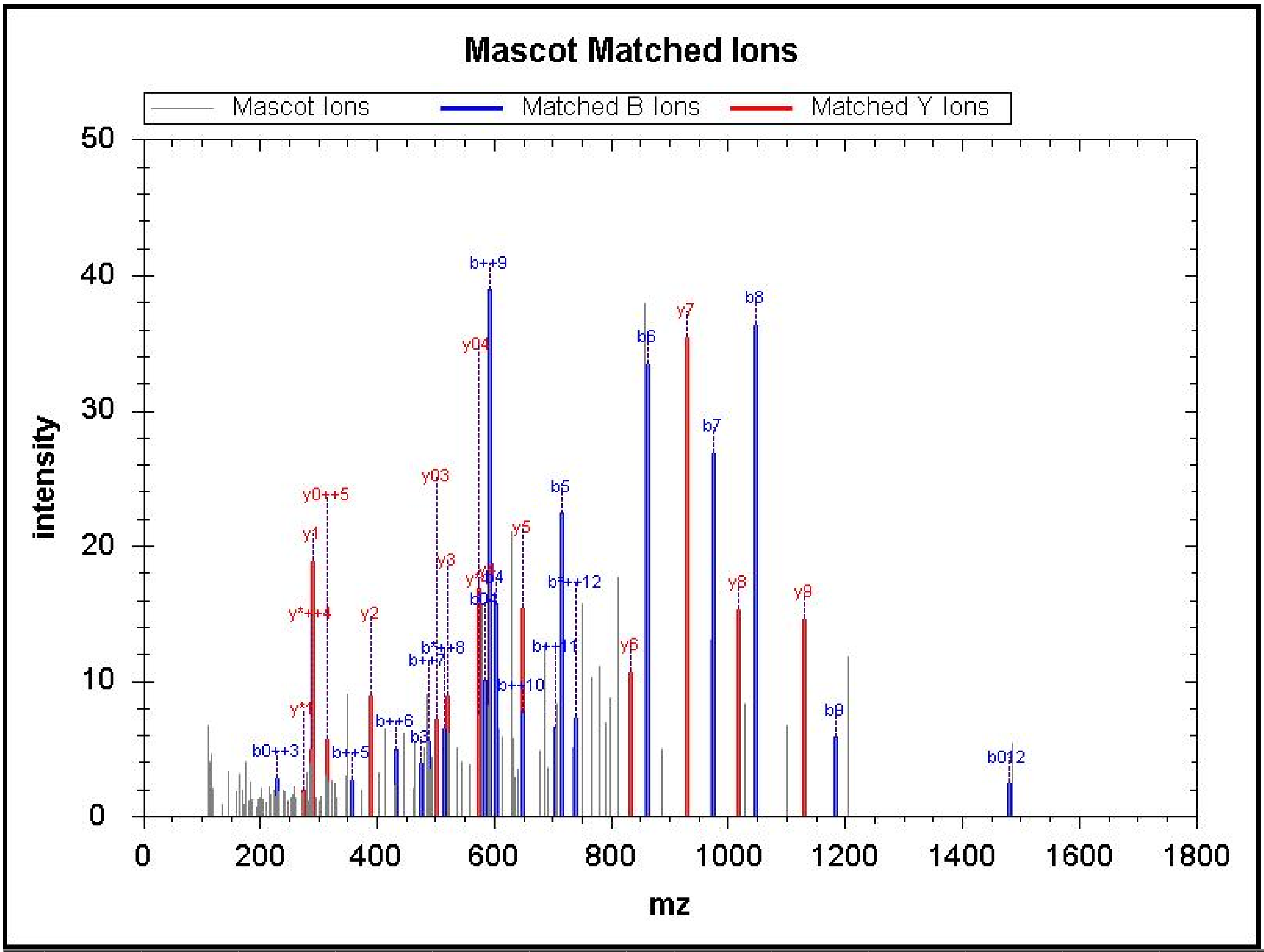


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | | | | | I | | | | | | | 14 |
| 2 | 387.24 | 194.12 | | | 369.23 | 185.12 | E | 1,612.95 | 806.98 | 1,595.93 | 798.47 | 1,594.94 | 797.98 | 13 |
| 3 | **486.30** | 243.66 | | | 468.29 | 234.65 | V | 1,483.91 | 742.46 | 1,466.88 | 733.95 | 1,465.90 | 733.45 | 12 |
| 4 | **633.37** | 317.19 | | | 615.36 | 308.18 | F | 1,384.84 | 692.93 | 1,367.82 | 684.41 | 1,366.83 | 683.92 | 11 |
| 5 | **732.44** | 366.72 | | | 714.43 | 357.72 | V | 1,237.77 | 619.39 | 1,220.75 | 610.88 | 1,219.76 | 610.39 | 10 |
| 6 | **860.50** | 430.75 | 843.47 | 422.24 | 842.49 | 421.75 | Q | 1,138.71 | 569.86 | 1,121.68 | **561.34** | 1,120.70 | 560.85 | 9 |
| 7 | **961.55** | 481.28 | 944.52 | 472.76 | **943.54** | 472.27 | T | 1,010.65 | 505.83 | 993.62 | 497.31 | 992.64 | 496.82 | 8 |
| 8 | 1,074.63 | 537.82 | **1,057.61** | 529.31 | 1,056.62 | 528.81 | L | 909.60 | 455.30 | 892.57 | 446.79 | | | 7 |
| 9 | 1,187.72 | 594.36 | 1,170.69 | 585.85 | 1,169.71 | 585.36 | L | 796.52 | 398.76 | 779.49 | 390.25 | | | 6 |
| 10 | 1,324.77 | 662.89 | 1,307.75 | 654.38 | 1,306.76 | 653.89 | H | **683.43** | **342.22** | 666.41 | 333.71 | | | 5 |
| 11 | 1,437.86 | 719.43 | 1,420.83 | 710.92 | 1,419.85 | 710.43 | L | **546.37** | 273.69 | 529.35 | 265.18 | | | 4 |
| 12 | 1,508.90 | 754.95 | 1,491.87 | 746.44 | 1,490.89 | 745.95 | A | **433.29** | 217.15 | 416.26 | 208.63 | | | 3 |
| 13 | 1,579.93 | 790.47 | 1,562.91 | 781.96 | 1,561.92 | 781.46 | A | **362.25** | 181.63 | 345.23 | 173.12 | | | 2 |
| 14 | | | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 2567 Hit 1

MS/MS Fragmentation of **SLQELFLAHILSPWGAEVK**
Found in **sp|P09874|PARP1_HUMAN**, Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4

Match to Query 2567: 2425.354from(809.4587,3+)
Title: 1099: Scan 2820 (rt=71.5304, f=3, i=393) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2425.354
**Variable modifications:**
**K19** :iTRAQ4plex (K)
**Ions Score:** 45.25 **Expect:** 0.015

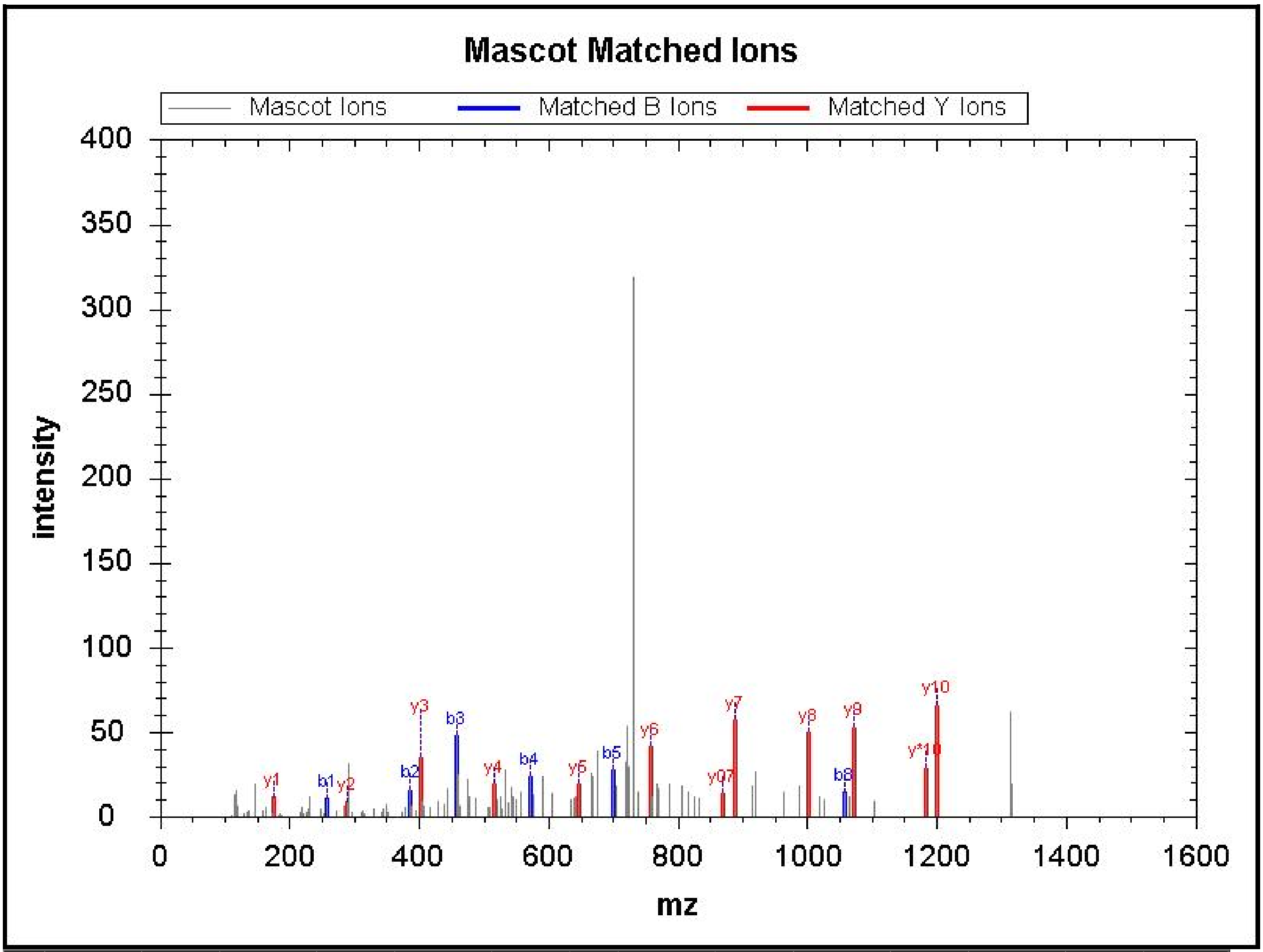


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 232.14 | 116.57 | | | 214.13 | 107.57 | S | | | | | | | 19 |
| 2 | 345.23 | 173.12 | | | 327.21 | 164.11 | L | 2,195.23 | 1,098.12 | 2,178.21 | 1,089.61 | 2,177.22 | 1,089.12 | 18 |
| 3 | **473.28** | 237.15 | 456.26 | 228.63 | 455.27 | **228.14** | Q | 2,082.15 | 1,041.58 | 2,065.12 | 1,033.07 | 2,064.14 | 1,032.57 | 17 |
| 4 | **602.33** | 301.67 | 585.30 | 293.15 | **584.32** | 292.66 | E | 1,954.09 | 977.55 | 1,937.07 | 969.04 | 1,936.08 | 968.54 | 16 |
| 5 | **715.41** | **358.21** | 698.38 | 349.70 | 697.40 | 349.20 | L | 1,825.05 | 913.03 | 1,808.02 | 904.52 | 1,807.04 | 904.02 | 15 |
| 6 | **862.48** | **431.74** | 845.45 | 423.23 | 844.47 | 422.74 | F | 1,711.97 | 856.49 | 1,694.94 | 847.97 | 1,693.95 | 847.48 | 14 |
| 7 | **975.56** | **488.29** | 958.54 | 479.77 | 957.55 | 479.28 | L | 1,564.90 | 782.95 | 1,547.87 | 774.44 | 1,546.89 | 773.95 | 13 |
| 8 | **1,046.60** | 523.80 | 1,029.57 | **515.29** | 1,028.59 | 514.80 | A | 1,451.81 | 726.41 | 1,434.79 | 717.90 | 1,433.80 | 717.40 | 12 |
| 9 | **1,183.66** | **592.33** | 1,166.63 | 583.82 | 1,165.65 | 583.33 | H | 1,380.78 | 690.89 | 1,363.75 | 682.38 | 1,362.77 | 681.89 | 11 |
| 10 | 1,296.74 | **648.88** | 1,279.72 | 640.36 | 1,278.73 | 639.87 | I | 1,243.72 | 622.36 | 1,226.69 | 613.85 | 1,225.71 | 613.36 | 10 |
| 11 | 1,409.83 | **705.42** | 1,392.80 | 696.90 | 1,391.82 | 696.41 | L | **1,130.63** | 565.82 | 1,113.61 | 557.31 | 1,112.62 | 556.81 | 9 |
| 12 | 1,496.86 | 748.93 | 1,479.83 | **740.42** | **1,478.85** | 739.93 | S | **1,017.55** | 509.28 | 1,000.52 | 500.76 | 999.54 | 500.27 | 8 |
| 13 | 1,593.91 | 797.46 | 1,576.89 | 788.95 | 1,575.90 | 788.45 | P | **930.52** | 465.76 | 913.49 | 457.25 | 912.51 | 456.76 | 7 |
| 14 | 1,779.99 | 890.50 | 1,762.97 | 881.99 | 1,761.98 | 881.49 | W | **833.46** | 417.24 | 816.44 | 408.72 | 815.45 | 408.23 | 6 |
| 15 | 1,837.01 | 919.01 | 1,819.99 | 910.50 | 1,819.00 | 910.00 | G | **647.38** | 324.20 | 630.36 | 315.68 | 629.37 | **315.19** | 5 |
| 16 | 1,908.05 | 954.53 | 1,891.02 | 946.02 | 1,890.04 | 945.52 | A | **590.36** | 295.69 | **573.34** | **287.17** | **572.35** | 286.68 | 4 |
| 17 | 2,037.09 | 1,019.05 | 2,020.07 | 1,010.54 | 2,019.08 | 1,010.04 | E | **519.33** | 260.17 | 502.30 | 251.65 | **501.32** | 251.16 | 3 |
| 18 | 2,136.16 | 1,068.58 | 2,119.13 | 1,060.07 | 2,118.15 | 1,059.58 | V | **390.28** | 195.65 | 373.26 | 187.13 | | | 2 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 19 | | | | | | | K | **291.21** | 146.11 | **274.19** | 137.60 | | | 1 |

Query 1322 Hit 1

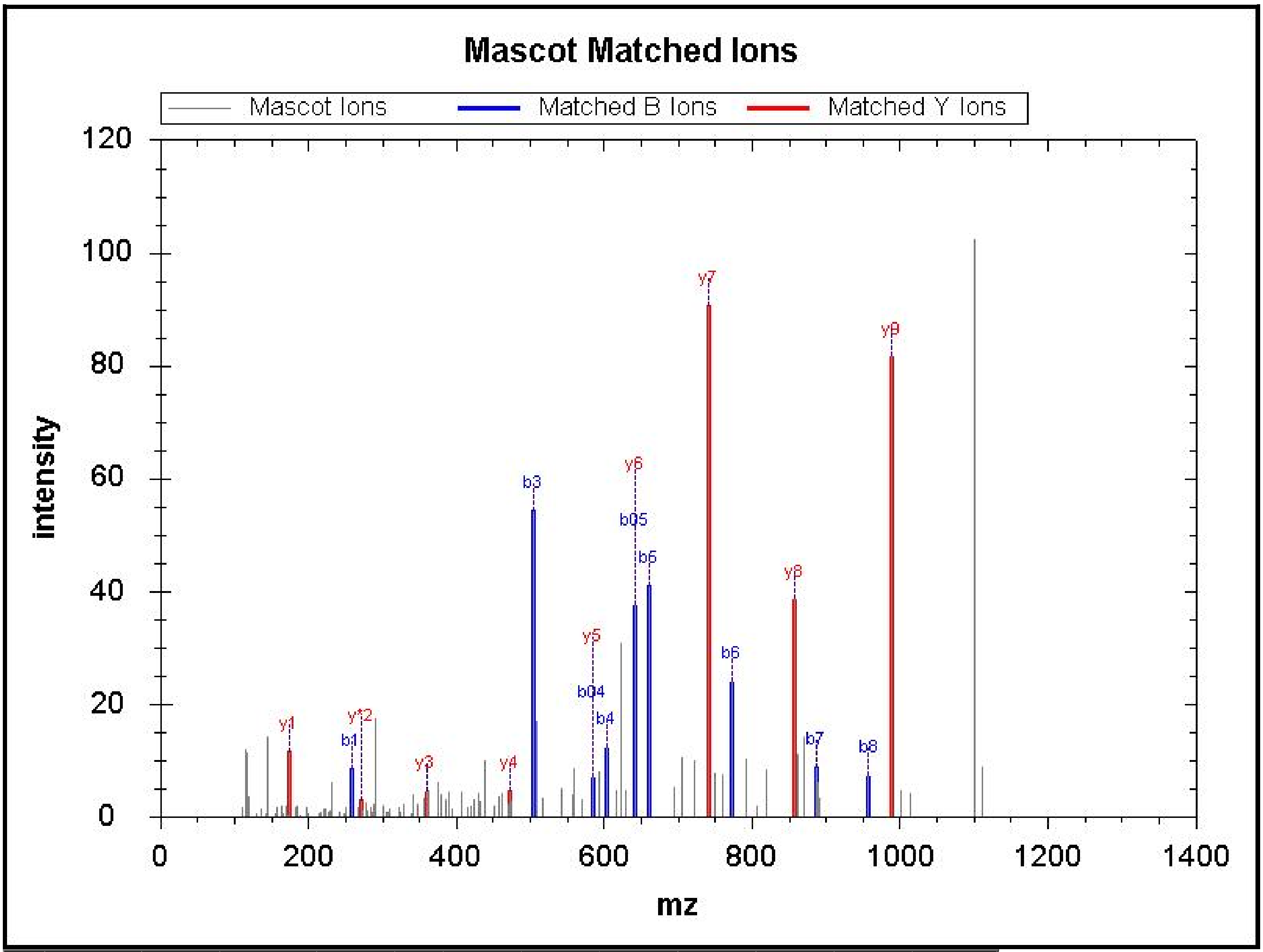
MS/MS Fragmentation of **IQAIELEDLLR**
Found in **sp|P21810|PGS1_HUMAN**, Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2
Match to Query 1322: 1455.845from(728.9296,2+)
Title: 883: Sum of 2 scans in range 2356 (rt=61.0782, f=4, i=618) to 2357 (rt=61.1036, f=4, i=619) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1455.845
**Variable modifications:**
**Ions Score:** 45.11 **Expect:** 0.018



| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **258.19** | 129.60 | | | | | I | | | | | | | 11 |
| 2 | **386.25** | 193.63 | 369.23 | 185.12 | | | Q | **1,199.66** | 600.34 | **1,182.64** | 591.82 | 1,181.65 | 591.33 | 10 |
| 3 | **457.29** | 229.15 | 440.26 | 220.63 | | | A | **1,071.60** | 536.31 | 1,054.58 | 527.79 | 1,053.59 | 527.30 | 9 |
| 4 | **570.37** | 285.69 | 553.35 | 277.18 | | | I | **1,000.57** | 500.79 | 983.54 | 492.27 | 982.56 | 491.78 | 8 |
| 5 | **699.42** | 350.21 | 682.39 | 341.70 | 681.41 | 341.21 | E | **887.48** | 444.25 | 870.46 | 435.73 | **869.47** | 435.24 | 7 |
| 6 | 812.50 | 406.75 | 795.47 | 398.24 | 794.49 | 397.75 | L | **758.44** | 379.72 | 741.41 | 371.21 | 740.43 | 370.72 | 6 |
| 7 | 941.54 | 471.27 | 924.52 | 462.76 | 923.53 | 462.27 | E | **645.36** | 323.18 | 628.33 | 314.67 | 627.35 | 314.18 | 5 |
| 8 | **1,056.57** | 528.79 | 1,039.54 | 520.28 | 1,038.56 | 519.78 | D | **516.31** | 258.66 | 499.29 | 250.15 | 498.30 | 249.66 | 4 |
| 9 | 1,169.65 | 585.33 | 1,152.63 | 576.82 | 1,151.64 | 576.33 | L | **401.29** | 201.15 | 384.26 | 192.63 | | | 3 |
| 10 | 1,282.74 | 641.87 | 1,265.71 | 633.36 | 1,264.73 | 632.87 | L | **288.20** | 144.61 | 271.18 | 136.09 | | | 2 |
| 11 | | | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 856 Hit 1

MS/MS Fragmentation of **LMDVGLIAIR**
Found in **sp|P31948|STIP1_HUMAN**, Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1
Match to Query 856: 1243.751from(622.8829,2+)
Title: 853: Scan 2159 (rt=57.0835, f=3, i=297) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1243.751
**Variable modifications:**
**Ions Score:** 44.76 **Expect:** 0.019

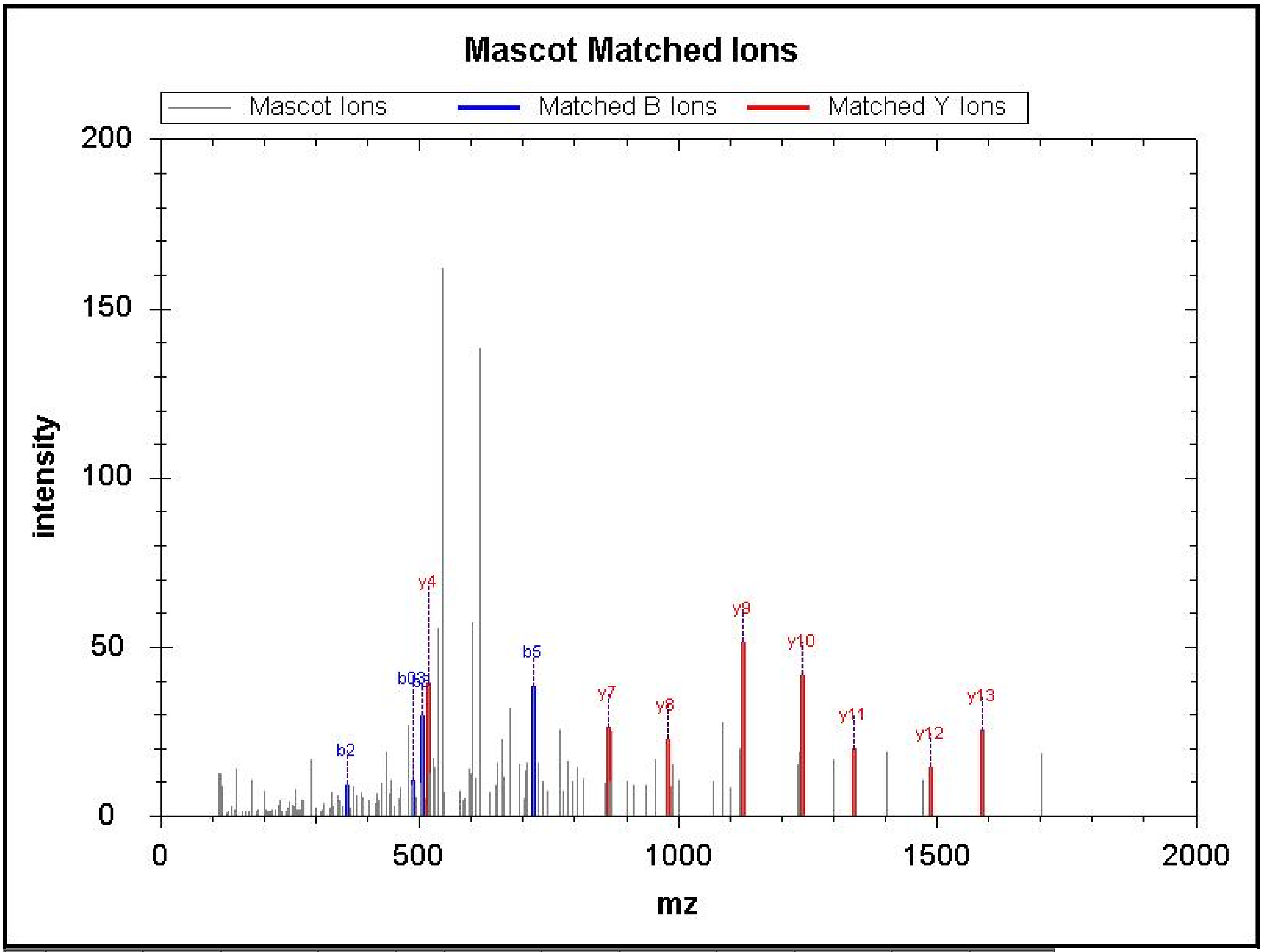


| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **258.19** | 129.60 | | | L | | | | | | | 10 |
| 2 | 389.23 | 195.12 | | | M | **987.57** | 494.29 | 970.54 | 485.77 | 969.55 | 485.28 | 9 |
| 3 | **504.26** | 252.63 | 486.25 | 243.63 | D | **856.53** | 428.77 | 839.50 | 420.25 | 838.51 | 419.76 | 8 |
| 4 | **603.33** | 302.17 | **585.32** | 293.16 | V | **741.50** | 371.25 | 724.47 | 362.74 | | | 7 |
| 5 | **660.35** | 330.68 | **642.34** | 321.67 | G | **642.43** | 321.72 | 625.40 | 313.21 | | | 6 |
| 6 | **773.43** | 387.22 | 755.42 | 378.22 | L | **585.41** | 293.21 | 568.38 | 284.69 | | | 5 |
| 7 | **886.52** | 443.76 | 868.51 | 434.76 | I | **472.32** | 236.67 | 455.30 | 228.15 | | | 4 |
| 8 | **957.56** | 479.28 | 939.55 | 470.28 | A | **359.24** | 180.12 | 342.21 | 171.61 | | | 3 |
| 9 | 1,070.64 | 535.82 | 1,052.63 | 526.82 | I | 288.20 | 144.61 | **271.18** | 136.09 | | | 2 |
| 10 | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 1906 Hit 1

MS/MS Fragmentation of **ITFVDFIAYDVLER**
Found in **sp|P28161|GSTM2_HUMAN**, Glutathione S-transferase Mu 2 OS=Homo sapiens GN=GSTM2 PE=1 SV=2
Match to Query 1906: 1843.994from(923.0045,2+)
Title: 1184: Sum of 2 scans in range 3026 (rt=76.1738, f=4, i=834) to 3027 (rt=76.1992, f=4, i=835)
[D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]

Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1843.994
**Variable modifications:**
**Ions Score:** 44.08 **Expect:** 0.032

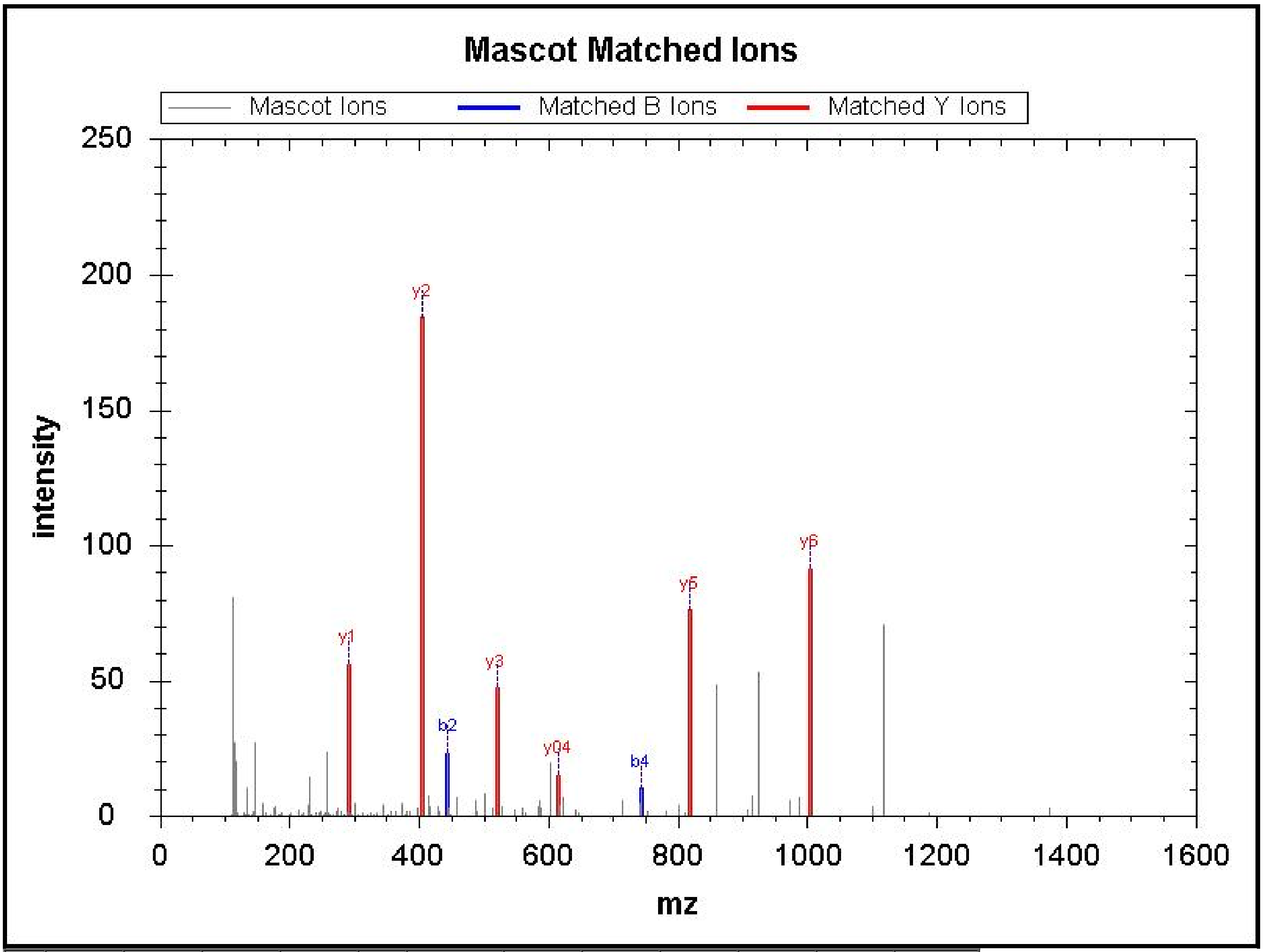


| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | 258.19 | 129.60 | | | **I** | | | | | | | **14** |
| **2** | **359.24** | 180.12 | 341.23 | 171.12 | **T** | **1,587.81** | 794.41 | 1,570.78 | 785.89 | 1,569.79 | 785.40 | **13** |
| **3** | **506.31** | 253.66 | **488.30** | 244.65 | **F** | **1,486.76** | 743.88 | 1,469.73 | 735.37 | 1,468.75 | 734.88 | **12** |
| **4** | 605.38 | 303.19 | 587.37 | 294.19 | **V** | **1,339.69** | 670.35 | 1,322.66 | 661.83 | 1,321.68 | 661.34 | **11** |
| **5** | **720.40** | 360.71 | 702.39 | 351.70 | **D** | **1,240.62** | 620.81 | 1,223.59 | 612.30 | 1,222.61 | 611.81 | **10** |
| **6** | 867.47 | 434.24 | 849.46 | 425.23 | **F** | **1,125.59** | 563.30 | 1,108.57 | 554.79 | 1,107.58 | 554.30 | **9** |
| **7** | 980.56 | 490.78 | 962.55 | 481.78 | **I** | **978.53** | 489.77 | 961.50 | 481.25 | 960.51 | 480.76 | **8** |
| **8** | 1,051.59 | 526.30 | 1,033.58 | 517.30 | **A** | **865.44** | 433.22 | 848.41 | 424.71 | 847.43 | 424.22 | **7** |
| **9** | 1,214.66 | 607.83 | 1,196.65 | 598.83 | **Y** | 794.40 | 397.71 | 777.38 | 389.19 | 776.39 | 388.70 | **6** |
| **10** | 1,329.68 | 665.35 | 1,311.67 | 656.34 | **D** | 631.34 | 316.17 | 614.31 | 307.66 | 613.33 | 307.17 | **5** |
| **11** | 1,428.75 | 714.88 | 1,410.74 | 705.87 | **V** | **516.31** | 258.66 | 499.29 | 250.15 | 498.30 | 249.66 | **4** |
| **12** | 1,541.84 | 771.42 | 1,523.83 | 762.42 | **L** | 417.25 | 209.13 | 400.22 | 200.61 | 399.24 | 200.12 | **3** |
| **13** | 1,670.88 | 835.94 | 1,652.87 | 826.94 | **E** | 304.16 | 152.58 | 287.13 | 144.07 | 286.15 | 143.58 | **2** |
| **14** | | | | | **R** | 175.12 | 88.06 | 158.09 | 79.55 | | | **1** |

Query 906 Hit 1

MS/MS Fragmentation of **LWWLDLK**
Found in **sp|P02790|HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2
Match to Query 906: 1260.756from(631.3855,2+)
Title: 943: Scan 2492 (rt=64.138, f=3, i=340) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:

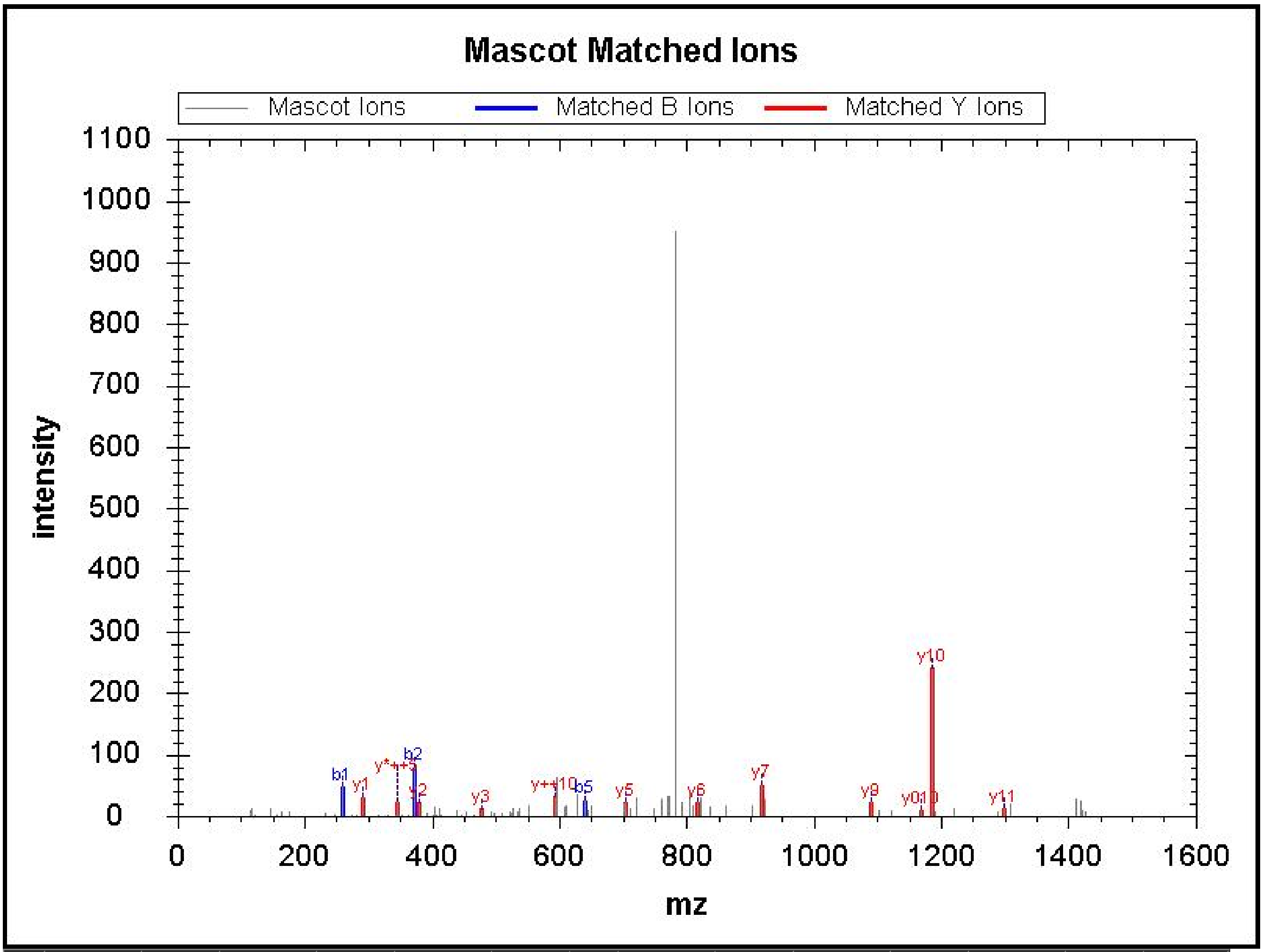
**Monoisotopic mass of neutral peptide Mr(calc):** 1260.756
**Variable modifications:**
**K7** :iTRAQ4plex (K)
**Ions Score:** 43.71 **Expect:** 0.027



| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | | | L | | | | | | | 7 |
| 2 | 444.27 | 222.64 | | | W | 1,004.57 | 502.79 | 987.54 | 494.27 | 986.56 | 493.78 | 6 |
| 3 | 630.35 | 315.68 | | | W | 818.49 | 409.75 | 801.46 | 401.23 | 800.48 | 400.74 | 5 |
| 4 | 743.44 | 372.22 | | | L | 632.41 | 316.71 | 615.38 | 308.20 | 614.40 | 307.70 | 4 |
| 5 | 858.46 | 429.74 | 840.45 | 420.73 | D | 519.33 | 260.17 | 502.30 | 251.65 | 501.32 | 251.16 | 3 |
| 6 | 971.55 | 486.28 | 953.54 | 477.27 | L | 404.30 | 202.65 | 387.27 | 194.14 | | | 2 |
| 7 | | | | | K | 291.21 | 146.11 | 274.19 | 137.60 | | | 1 |

Query 1489 Hit 1

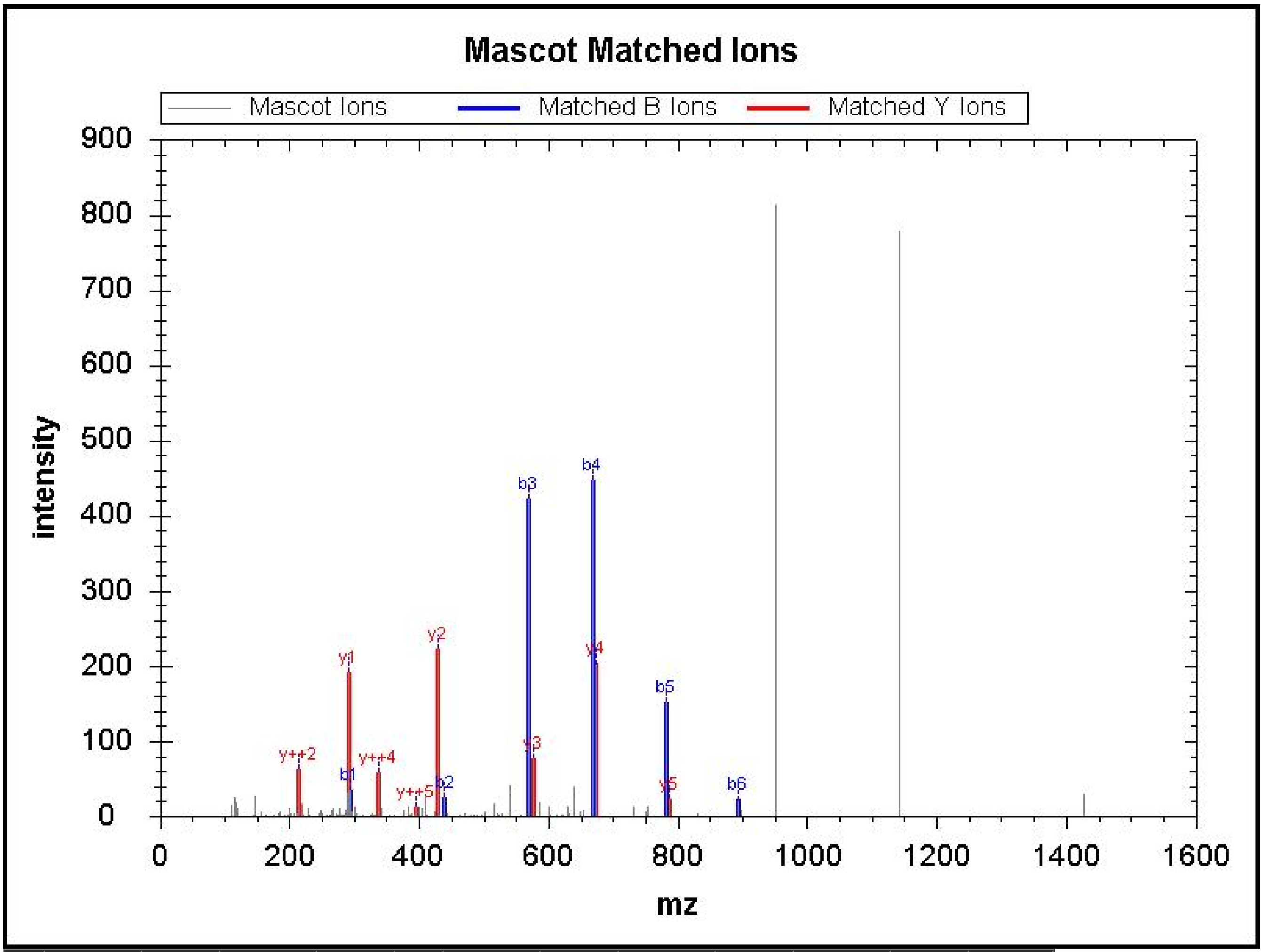
MS/MS Fragmentation of NIPGITLLNVSK
Found in sp|P36578|RL4_HUMAN, 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5
Match to Query 1489: 1555.964from(778.9894,2+)
Title: 751: Sum of 2 scans in range 1943 (rt=52.2193, f=4, i=518) to 1944 (rt=52.2447, f=4, i=519)
[D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1555.964
**Variable modifications:**
**K12** :iTRAQ4plex (K)
**Ions Score:** 42.92 **Expect:** 0.014



| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **259.15** | 130.08 | 242.13 | 121.57 | | | N | | | | | | | 12 |
| 2 | **372.24** | 186.62 | 355.21 | 178.11 | | | I | **1,298.82** | 649.91 | 1,281.79 | 641.40 | 1,280.81 | 640.91 | 11 |
| 3 | 469.29 | 235.15 | 452.26 | 226.63 | | | P | **1,185.73** | **593.37** | 1,168.71 | 584.86 | **1,167.72** | 584.36 | 10 |
| 4 | 526.31 | 263.66 | 509.28 | 255.15 | | | G | **1,088.68** | 544.84 | 1,071.65 | 536.33 | 1,070.67 | 535.84 | 9 |
| 5 | **639.39** | 320.20 | 622.37 | 311.69 | | | I | 1,031.66 | 516.33 | 1,014.63 | 507.82 | 1,013.65 | 507.33 | 8 |
| 6 | 740.44 | 370.72 | 723.42 | 362.21 | 722.43 | 361.72 | T | **918.57** | 459.79 | 901.55 | 451.28 | 900.56 | 450.79 | 7 |
| 7 | 853.53 | 427.27 | 836.50 | 418.75 | 835.52 | 418.26 | L | **817.53** | 409.27 | 800.50 | 400.75 | 799.52 | 400.26 | 6 |
| 8 | 966.61 | 483.81 | 949.58 | 475.30 | 948.60 | 474.80 | L | **704.44** | 352.72 | 687.42 | **344.21** | 686.43 | 343.72 | 5 |
| 9 | 1,080.65 | 540.83 | 1,063.63 | 532.32 | 1,062.64 | 531.83 | N | 591.36 | 296.18 | 574.33 | 287.67 | 573.35 | 287.18 | 4 |
| 10 | 1,179.72 | 590.36 | 1,162.70 | 581.85 | 1,161.71 | 581.36 | V | **477.32** | 239.16 | 460.29 | 230.65 | 459.30 | 230.16 | 3 |
| 11 | 1,266.75 | 633.88 | 1,249.73 | 625.37 | 1,248.74 | 624.88 | S | **378.25** | 189.63 | 361.22 | 181.11 | 360.24 | 180.62 | 2 |
| 12 | | | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 1838 Hit 1

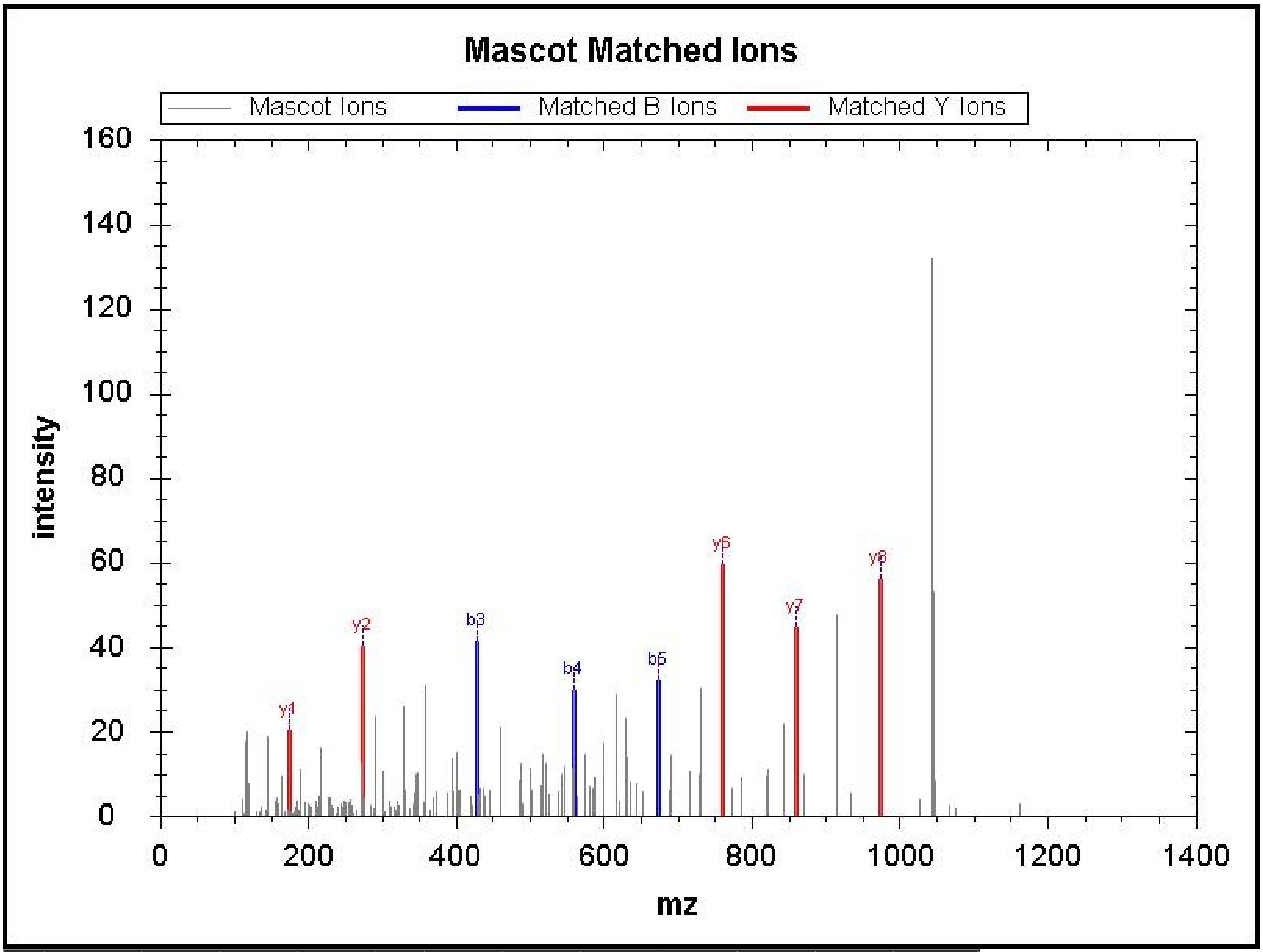
MS/MS Fragmentation of **FFEVILIDPFHK**
Found in **sp|P61313|RL15_HUMAN**, 60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2
Match to Query 1838: 1792.025from(598.3489,3+)
Title: 1000: Scan 2615 (rt=66.9066, f=2, i=387) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1792.025
**Variable modifications:**
**K12** :iTRAQ4plex (K)
**Ions Score:** 42.89 **Expect:** 0.032



| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 292.18 | 146.59 | | | F | | | | | | | 12 |
| 2 | 439.25 | 220.13 | | | F | 1,501.85 | 751.43 | 1,484.83 | 742.92 | 1,483.84 | 742.42 | 11 |
| 3 | 568.29 | 284.65 | 550.28 | 275.64 | E | 1,354.78 | 677.90 | 1,337.76 | 669.38 | 1,336.77 | 668.89 | 10 |
| 4 | 667.36 | 334.18 | 649.35 | 325.18 | V | 1,225.74 | 613.37 | 1,208.72 | 604.86 | 1,207.73 | 604.37 | 9 |
| 5 | 780.44 | 390.72 | 762.43 | 381.72 | I | 1,126.67 | 563.84 | 1,109.65 | 555.33 | 1,108.66 | 554.84 | 8 |
| 6 | 893.53 | 447.27 | 875.51 | 438.26 | L | 1,013.59 | 507.30 | 996.56 | 498.79 | 995.58 | 498.29 | 7 |
| 7 | 1,006.61 | 503.81 | 988.60 | 494.80 | I | 900.51 | 450.76 | 883.48 | 442.24 | 882.50 | 441.75 | 6 |
| 8 | 1,121.64 | 561.32 | 1,103.63 | 552.32 | D | 787.42 | 394.21 | 770.40 | 385.70 | 769.41 | 385.21 | 5 |
| 9 | 1,218.69 | 609.85 | 1,200.68 | 600.84 | P | 672.39 | 336.70 | 655.37 | 328.19 | | | 4 |
| 10 | 1,365.76 | 683.38 | 1,347.75 | 674.38 | F | 575.34 | 288.17 | 558.32 | 279.66 | | | 3 |
| 11 | 1,502.82 | 751.91 | 1,484.81 | 742.91 | H | 428.27 | 214.64 | 411.25 | 206.13 | | | 2 |
| 12 | | | | | K | 291.21 | 146.11 | 274.19 | 137.60 | | | 1 |

Query 687 Hit 1

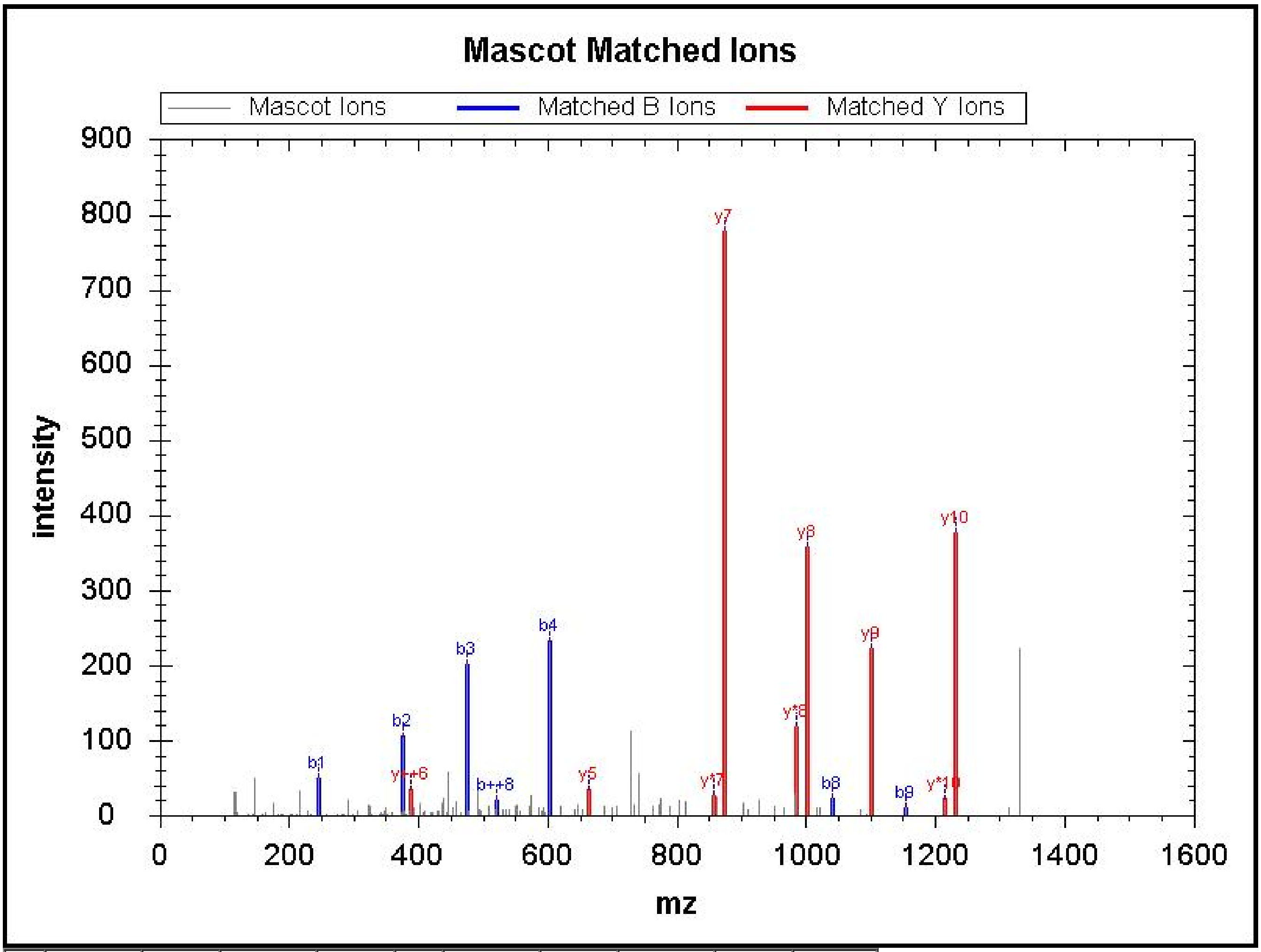
MS/MS Fragmentation of ALVMLLEVR
Found in sp|Q92973|TNPO1_HUMAN, Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2
Match to Query 687: 1186.727from(594.3709,2+)
Title: 916: Sum of 2 scans in range 2296 (rt=60.1744, f=4, i=632) to 2297 (rt=60.1999, f=4, i=633) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1186.727
**Variable modifications:**
**Ions Score:** 42.82 **Expect:** 0.027



| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 216.15 | 108.58 | | | A | | | | | | | 9 |
| 2 | 329.23 | 165.12 | | | L | 972.59 | 486.80 | 955.56 | 478.29 | 954.58 | 477.79 | 8 |
| 3 | 428.30 | 214.65 | | | V | 859.51 | 430.26 | 842.48 | 421.74 | 841.50 | 421.25 | 7 |
| 4 | 559.34 | 280.17 | | | M | 760.44 | 380.72 | 743.41 | 372.21 | 742.43 | 371.72 | 6 |
| 5 | 672.42 | 336.72 | | | L | 629.40 | 315.20 | 612.37 | 306.69 | 611.39 | 306.20 | 5 |
| 6 | 785.51 | 393.26 | | | L | 516.31 | 258.66 | 499.29 | 250.15 | 498.30 | 249.66 | 4 |
| 7 | 914.55 | 457.78 | 896.54 | 448.77 | E | 403.23 | 202.12 | 386.20 | 193.61 | 385.22 | 193.11 | 3 |
| 8 | 1,013.62 | 507.31 | 995.61 | 498.31 | V | 274.19 | 137.60 | 257.16 | 129.08 | | | 2 |
| 9 | | | | | R | 175.12 | 88.06 | 158.09 | 79.55 | | | 1 |

Query 1365 Hit 1

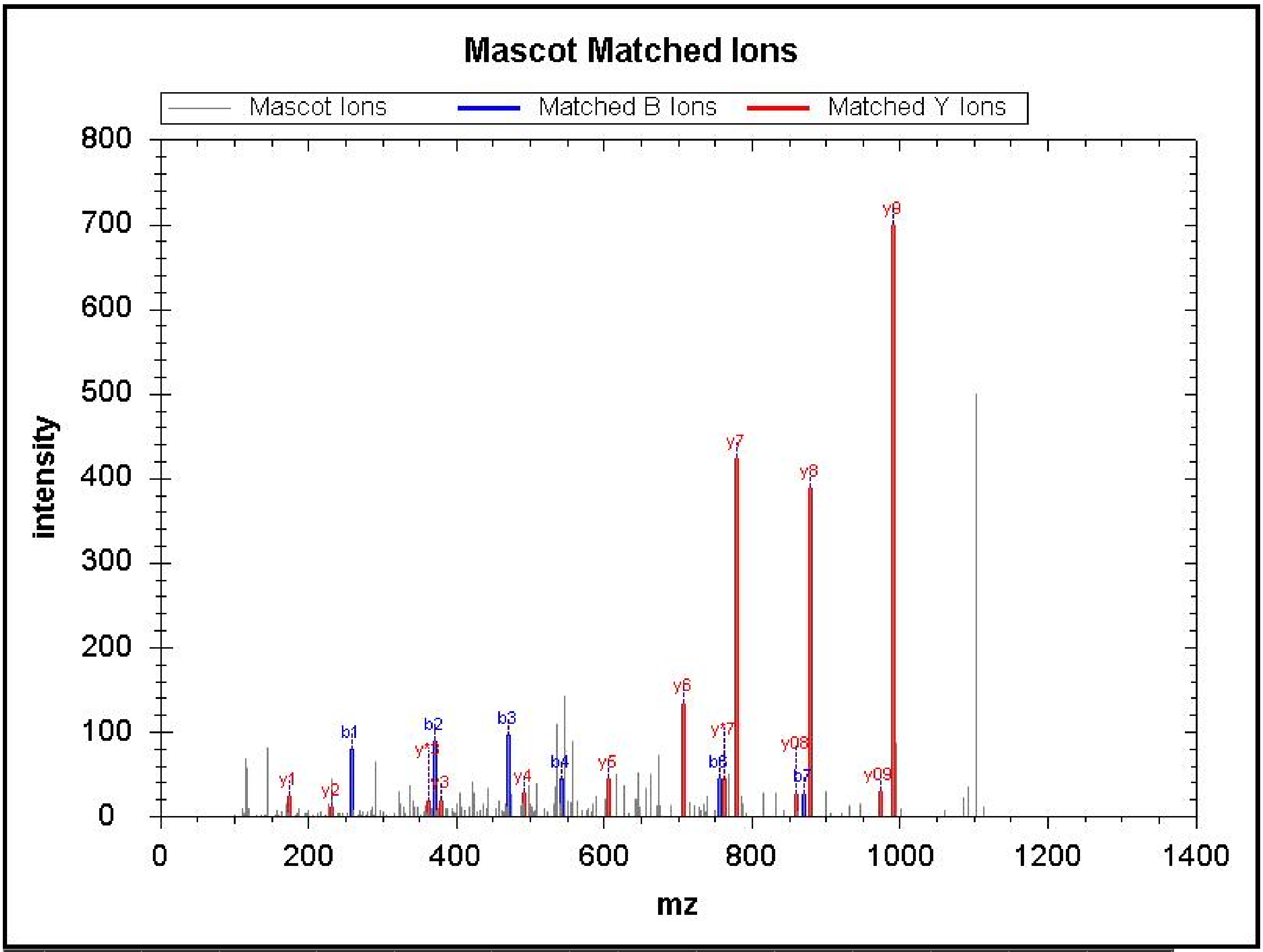
MS/MS Fragmentation of VMVQPINLIFR
Found in sp|P62304|RUXE_HUMAN, Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1
Match to Query 1365: 1472.871from(737.4426,2+)
Title: 903: Scan 2399 (rt=62.0425, f=3, i=325) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1472.871
**Variable modifications:**
**Ions Score:** 42.71 **Expect:** 0.031



| No | b | b++ | b* | b*++ | Seq | y | y++ | y* | y*++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **244.18** | 122.59 | | | V | | | | | 11 |
| 2 | **375.22** | 188.11 | | | M | **1,230.70** | 615.85 | **1,213.68** | 607.34 | 10 |
| 3 | **474.29** | 237.65 | | | V | **1,099.66** | 550.33 | 1,082.64 | 541.82 | 9 |
| 4 | **602.35** | 301.68 | 585.32 | 293.16 | Q | **1,000.59** | 500.80 | **983.57** | 492.29 | 8 |
| 5 | 699.40 | 350.20 | 682.37 | 341.69 | P | **872.54** | 436.77 | **855.51** | 428.26 | 7 |
| 6 | 812.48 | 406.74 | 795.46 | 398.23 | I | 775.48 | **388.24** | 758.46 | 379.73 | 6 |
| 7 | 926.52 | 463.77 | 909.50 | 455.25 | N | **662.40** | 331.70 | 645.37 | 323.19 | 5 |
| 8 | **1,039.61** | **520.31** | 1,022.58 | 511.79 | L | 548.36 | 274.68 | 531.33 | 266.17 | 4 |
| 9 | **1,152.69** | 576.85 | 1,135.67 | 568.34 | I | 435.27 | 218.14 | 418.24 | 209.63 | 3 |
| 10 | 1,299.76 | 650.38 | 1,282.74 | 641.87 | F | 322.19 | 161.60 | 305.16 | 153.08 | 2 |
| 11 | | | | | R | 175.12 | 88.06 | 158.09 | 79.55 | 1 |

Query 867 Hit 1

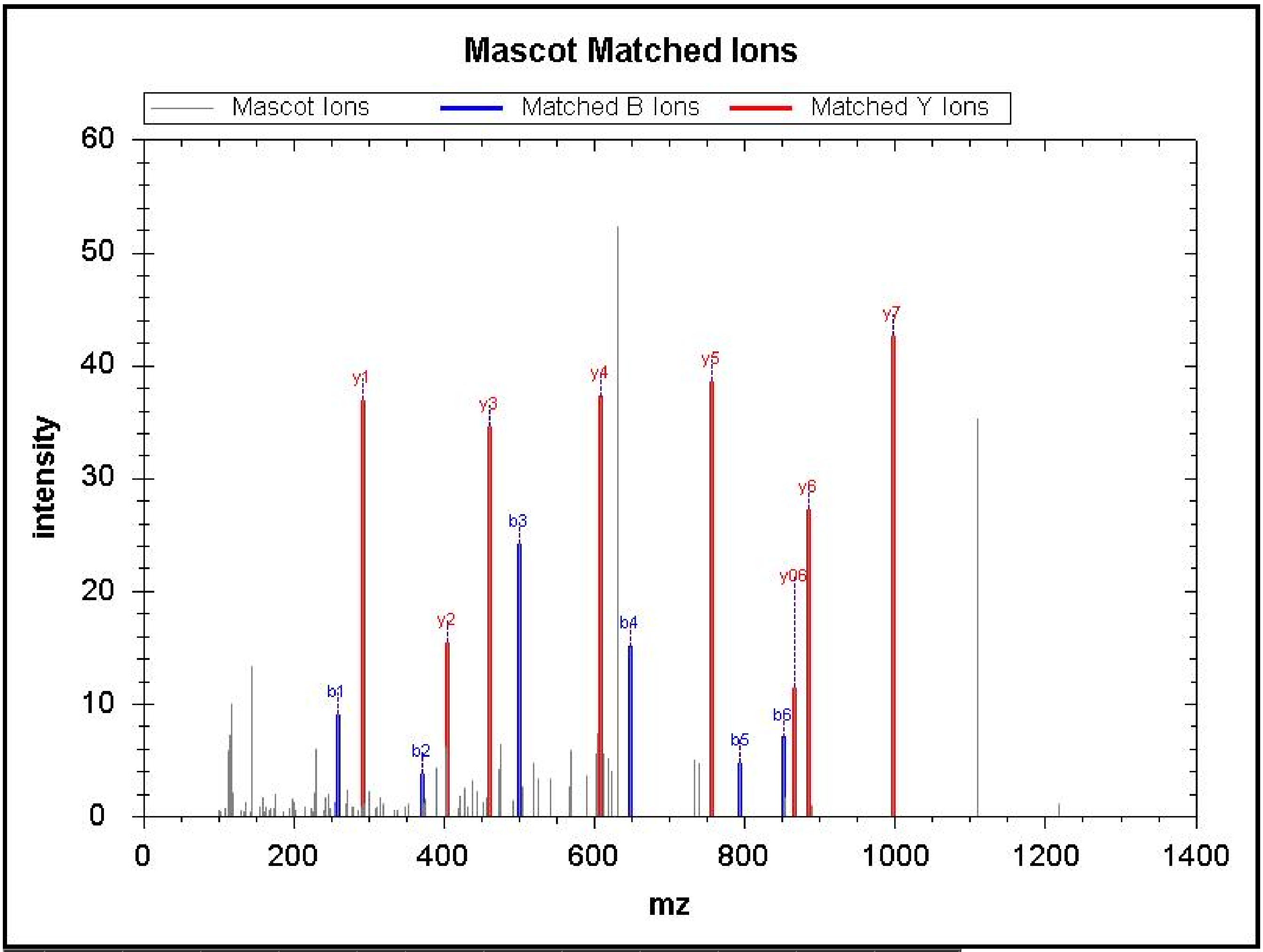
MS/MS Fragmentation of **ILVATNLFGR**
Found in **sp|O00148|DX39A_HUMAN**, ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2
Match to Query 867: 1246.755from(624.3847,2+)
Title: 798: Sum of 2 scans in range 2042 (rt=54.4506, f=4, i=550) to 2043 (rt=54.476, f=4, i=551) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1246.755
**Variable modifications:**
**Ions Score:** 42.29 **Expect:** 0.037



| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | | | | | I | | | | | | | 10 |
| 2 | 371.28 | 186.14 | | | | | L | 990.57 | 495.79 | 973.55 | 487.28 | 972.56 | 486.78 | 9 |
| 3 | 470.35 | 235.68 | | | | | V | 877.49 | 439.25 | 860.46 | 430.73 | 859.48 | 430.24 | 8 |
| 4 | 541.38 | 271.20 | | | | | A | 778.42 | 389.71 | 761.39 | 381.20 | 760.41 | 380.71 | 7 |
| 5 | 642.43 | 321.72 | | | 624.42 | 312.71 | T | 707.38 | 354.20 | 690.36 | 345.68 | 689.37 | 345.19 | 6 |
| 6 | 756.47 | 378.74 | 739.45 | 370.23 | 738.46 | 369.74 | N | 606.34 | 303.67 | 589.31 | 295.16 | | | 5 |
| 7 | 869.56 | 435.28 | 852.53 | 426.77 | 851.55 | 426.28 | L | 492.29 | 246.65 | 475.27 | 238.14 | | | 4 |
| 8 | 1,016.63 | 508.82 | 999.60 | 500.30 | 998.62 | 499.81 | F | 379.21 | 190.11 | 362.18 | 181.59 | | | 3 |
| 9 | 1,073.65 | 537.33 | 1,056.62 | 528.81 | 1,055.64 | 528.32 | G | 232.14 | 116.57 | 215.11 | 108.06 | | | 2 |
| 10 | | | | | | | R | 175.12 | 88.06 | 158.09 | 79.55 | | | 1 |

Query 884 Hit 1

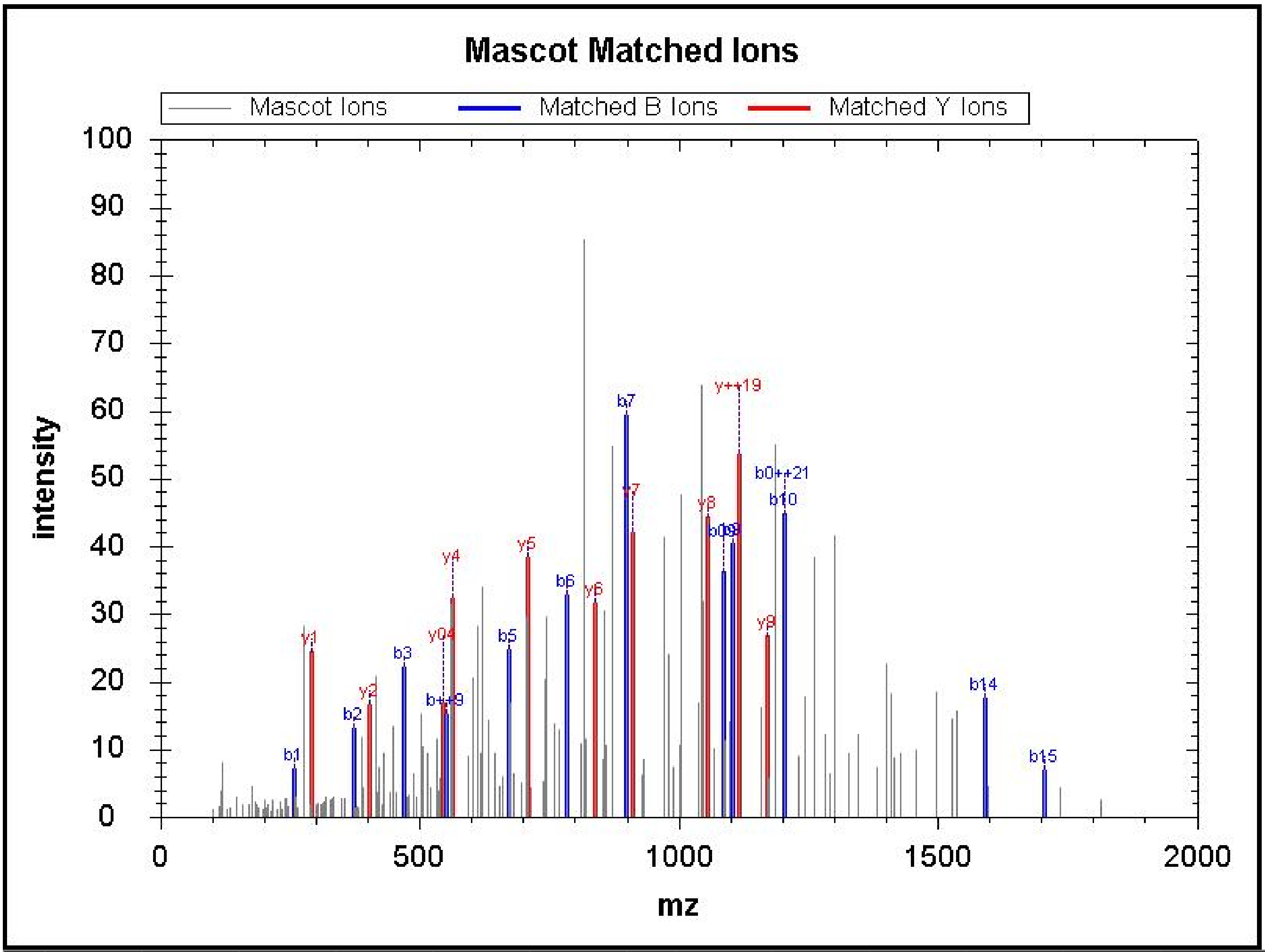
MS/MS Fragmentation of ILEFFGLK
Found in sp|P07237|PDIA1_HUMAN, Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3
Match to Query 884: 1253.772from(627.8932,2+)
Title: 1010: Scan 2506 (rt=64.9028, f=3, i=353) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1253.772
**Variable modifications:**
**K8** :iTRAQ4plex (K)
**Ions Score:** 42.11 **Expect:** 0.022



| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **258.19** | 129.60 | | | I | | | | | | | 8 |
| 2 | **371.28** | 186.14 | | | L | **997.58** | 499.30 | 980.56 | 490.78 | 979.57 | 490.29 | 7 |
| 3 | **500.32** | 250.66 | 482.31 | 241.66 | E | **884.50** | 442.75 | 867.47 | 434.24 | **866.49** | 433.75 | 6 |
| 4 | **647.39** | 324.20 | 629.38 | 315.19 | F | **755.46** | 378.23 | 738.43 | 369.72 | | | 5 |
| 5 | **794.46** | 397.73 | 776.45 | 388.73 | F | **608.39** | 304.70 | 591.36 | 296.18 | | | 4 |
| 6 | **851.48** | 426.24 | 833.47 | 417.24 | G | **461.32** | 231.16 | 444.29 | 222.65 | | | 3 |
| 7 | 964.56 | 482.78 | 946.55 | 473.78 | L | **404.30** | 202.65 | 387.27 | 194.14 | | | 2 |
| 8 | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 2844 Hit 1

MS/MS Fragmentation of **LLVSNLDFGVSDADIQELFAEFGTLK**
Found in **sp|Q86V81|THOC4_HUMAN**, THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=1 SV=3
Match to Query 2844: 3129.667from(1044.23,3+)
Title: 1307: Sum of 2 scans in range 3324 (rt=82.8877, f=4, i=930) to 3325 (rt=82.9131, f=4, i=931) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 3129.667
**Variable modifications:**
**Q16** :Deamidated (NQ)
**K26** :iTRAQ4plex (K)
**Ions Score:** 41.48 **Expect:** 0.042

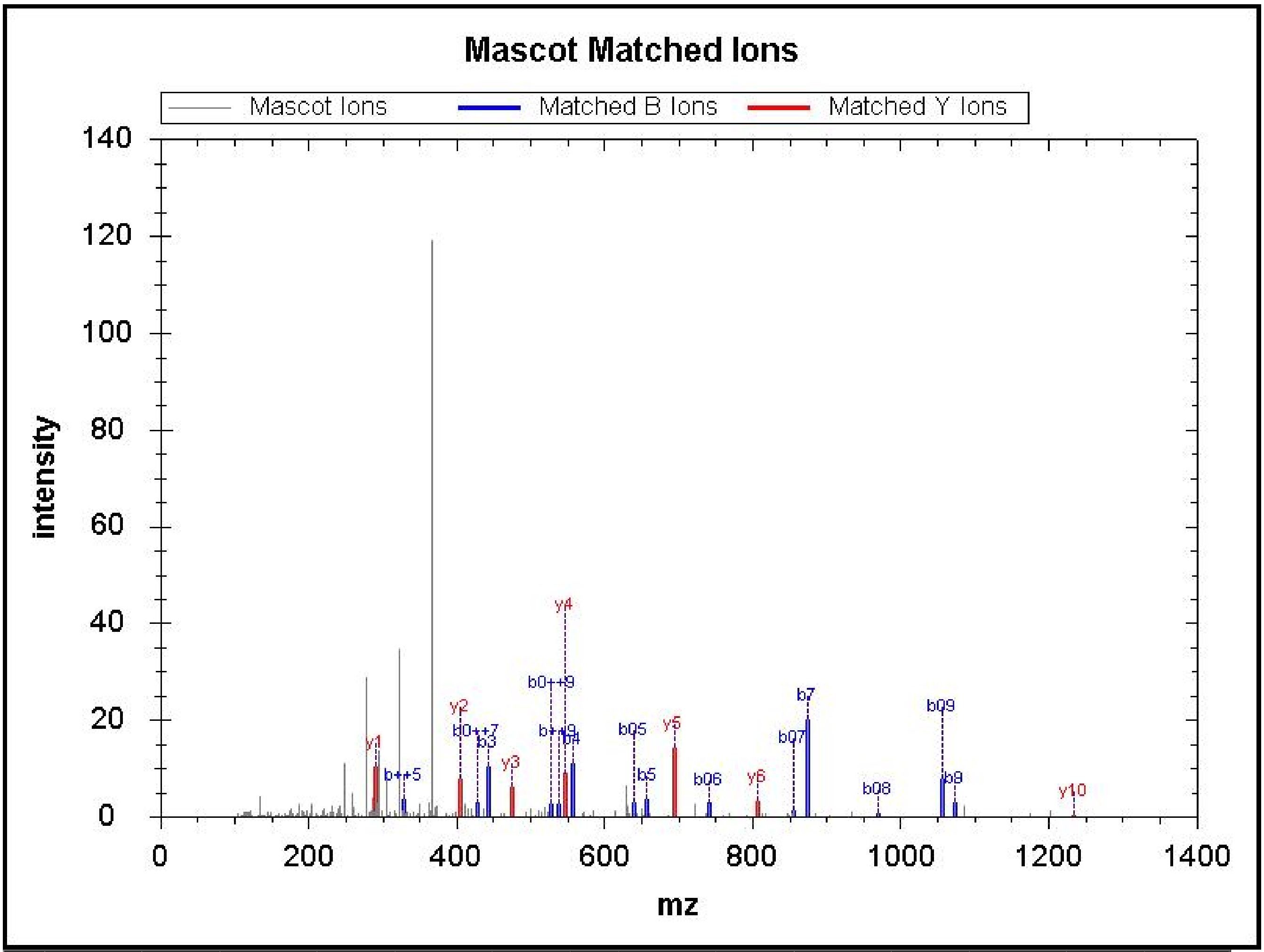


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **258.19** | 129.60 | | | | | L | | | | | | | 26 |
| 2 | **371.28** | 186.14 | | | | | L | 2,873.46 | 1,437.23 | 2,856.43 | 1,428.72 | 2,855.45 | 1,428.23 | 25 |
| 3 | **470.35** | 235.68 | | | | | V | 2,760.37 | 1,380.69 | 2,743.35 | 1,372.18 | 2,742.36 | 1,371.69 | 24 |
| 4 | 557.38 | 279.19 | | | 539.37 | 270.19 | S | 2,661.30 | 1,331.16 | 2,644.28 | 1,322.64 | 2,643.29 | 1,322.15 | 23 |
| 5 | **671.42** | 336.21 | 654.39 | 327.70 | 653.41 | 327.21 | N | 2,574.27 | 1,287.64 | 2,557.25 | 1,279.13 | 2,556.26 | 1,278.63 | 22 |
| 6 | **784.50** | 392.76 | 767.48 | 384.24 | 766.49 | 383.75 | L | 2,460.23 | 1,230.62 | 2,443.20 | 1,222.11 | 2,442.22 | 1,221.61 | 21 |
| 7 | **899.53** | 450.27 | 882.51 | 441.76 | 881.52 | 441.26 | D | 2,347.15 | 1,174.08 | 2,330.12 | 1,165.56 | 2,329.14 | 1,165.07 | 20 |
| 8 | 1,046.60 | 523.80 | 1,029.57 | 515.29 | 1,028.59 | 514.80 | F | 2,232.12 | **1,116.56** | 2,215.09 | 1,108.05 | 2,214.11 | 1,107.56 | 19 |
| 9 | **1,103.62** | **552.31** | 1,086.60 | 543.80 | **1,085.61** | 543.31 | G | 2,085.05 | 1,043.03 | 2,068.02 | 1,034.52 | 2,067.04 | 1,034.02 | 18 |
| 10 | **1,202.69** | 601.85 | 1,185.66 | 593.34 | 1,184.68 | 592.84 | V | 2,028.03 | 1,014.52 | 2,011.00 | 1,006.01 | 2,010.02 | 1,005.51 | 17 |
| 11 | 1,289.72 | 645.36 | 1,272.70 | 636.85 | 1,271.71 | 636.36 | S | 1,928.96 | 964.98 | 1,911.93 | 956.47 | 1,910.95 | 955.98 | 16 |
| 12 | 1,404.75 | 702.88 | 1,387.72 | 694.36 | 1,386.74 | 693.87 | D | 1,841.93 | 921.47 | 1,824.90 | 912.95 | 1,823.92 | 912.46 | 15 |
| 13 | 1,475.79 | 738.40 | 1,458.76 | 729.88 | 1,457.78 | 729.39 | A | 1,726.90 | 863.95 | 1,709.88 | 855.44 | 1,708.89 | 854.95 | 14 |
| 14 | **1,590.81** | 795.91 | 1,573.79 | 787.40 | 1,572.80 | 786.90 | D | 1,655.86 | 828.44 | 1,638.84 | 819.92 | 1,637.85 | 819.43 | 13 |
| 15 | **1,703.90** | 852.45 | 1,686.87 | 843.94 | 1,685.89 | 843.45 | I | 1,540.84 | 770.92 | 1,523.81 | 762.41 | 1,522.83 | 761.92 | 12 |
| 16 | 1,832.94 | 916.97 | 1,815.91 | 908.46 | 1,814.93 | 907.97 | Q | 1,427.75 | 714.38 | 1,410.73 | 705.87 | 1,409.74 | 705.38 | 11 |
| 17 | 1,961.98 | 981.49 | 1,944.96 | 972.98 | 1,943.97 | 972.49 | E | 1,298.71 | 649.86 | 1,281.68 | 641.35 | 1,280.70 | 640.85 | 10 |
| 18 | 2,075.07 | 1,038.04 | 2,058.04 | 1,029.52 | 2,057.06 | 1,029.03 | L | **1,169.67** | 585.34 | 1,152.64 | 576.82 | 1,151.66 | 576.33 | 9 |
| 19 | 2,222.14 | 1,111.57 | 2,205.11 | 1,103.06 | 2,204.12 | 1,102.57 | F | **1,056.58** | 528.80 | 1,039.56 | 520.28 | 1,038.57 | 519.79 | 8 |
| 20 | 2,293.17 | 1,147.09 | 2,276.15 | 1,138.58 | 2,275.16 | 1,138.08 | A | **909.52** | 455.26 | 892.49 | 446.75 | 891.51 | 446.26 | 7 |
| 21 | 2,422.21 | 1,211.61 | 2,405.19 | 1,203.10 | 2,404.20 | **1,202.61** | E | **838.48** | 419.74 | 821.45 | 411.23 | 820.47 | 410.74 | 6 |
| 22 | 2,569.28 | 1,285.15 | 2,552.26 | 1,276.63 | 2,551.27 | 1,276.14 | F | **709.44** | 355.22 | 692.41 | 346.71 | 691.43 | 346.22 | 5 |
| 23 | 2,626.30 | 1,313.66 | 2,609.28 | 1,305.14 | 2,608.29 | 1,304.65 | G | **562.37** | 281.69 | 545.34 | 273.17 | **544.36** | 272.68 | 4 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 24 | 2,727.35 | 1,364.18 | 2,710.33 | 1,355.67 | 2,709.34 | 1,355.17 | T | 505.35 | 253.18 | 488.32 | 244.66 | 487.34 | 244.17 | 3 |
| 25 | 2,840.44 | 1,420.72 | 2,823.41 | 1,412.21 | 2,822.43 | 1,411.72 | L | **404.30** | 202.65 | 387.27 | 194.14 | | | 2 |
| 26 | | | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 2100 Hit 1

MS/MS Fragmentation of **VQALTTDISLIFAALK**
Found in **sp|Q6PKG0|LARP1_HUMAN**, La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2
Match to Query 2100: 1991.206from(664.7427,3+)
Title: 1354: Scan 3275 (rt=82.2301, f=3, i=477) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1991.206
**Variable modifications:**
**K16** :iTRAQ4plex (K)
**Ions Score:** 41.14 **Expect:** 0.017

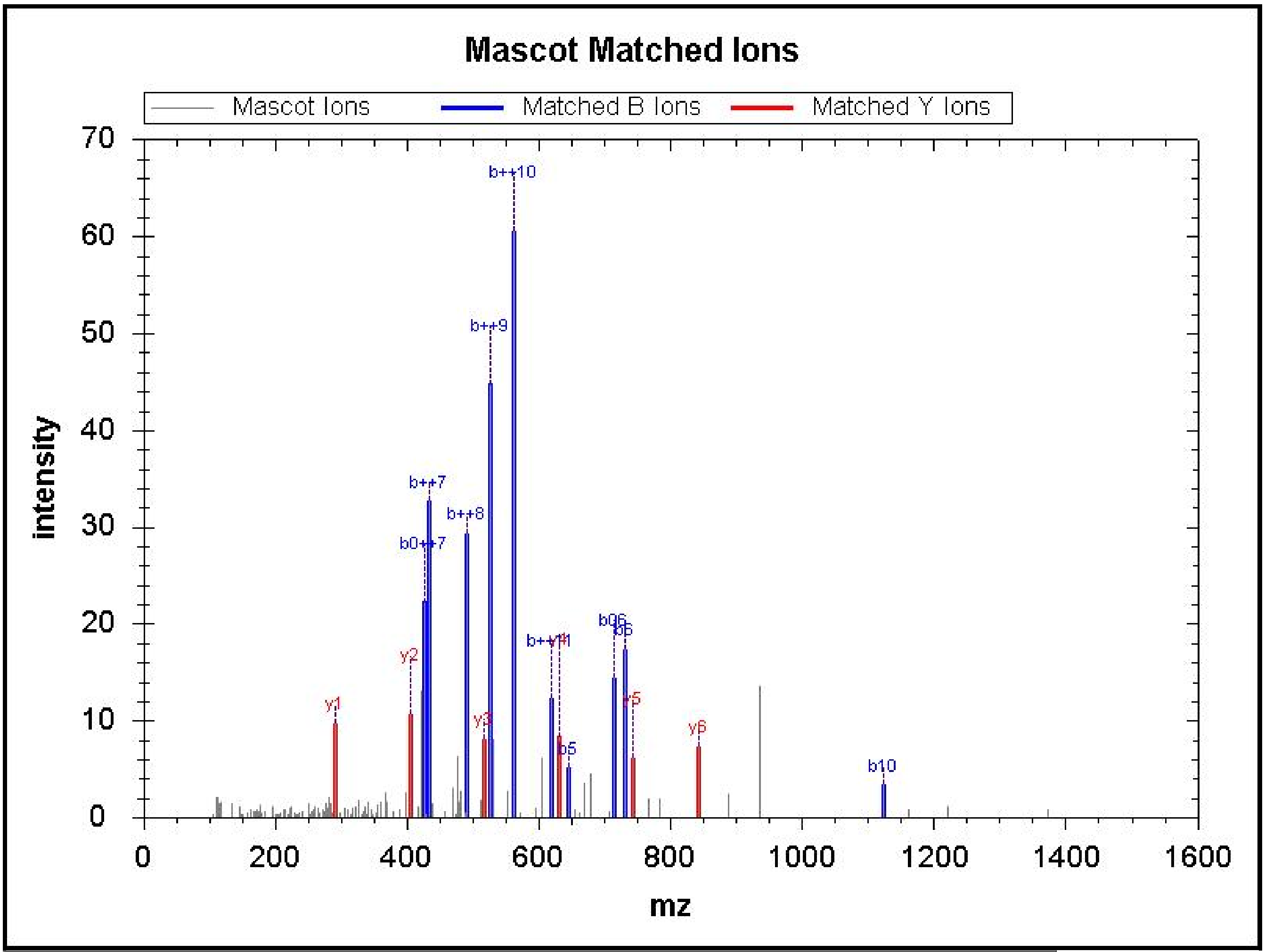


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 244.18 | 122.59 | | | | | V | | | | | | | 16 |
| 2 | 372.24 | 186.62 | 355.21 | 178.11 | | | Q | 1,749.03 | 875.02 | 1,732.00 | 866.50 | 1,731.02 | 866.01 | 15 |
| 3 | **443.27** | 222.14 | 426.25 | 213.63 | | | A | 1,620.97 | 810.99 | 1,603.94 | 802.48 | 1,602.96 | 801.98 | 14 |
| 4 | **556.36** | 278.68 | 539.33 | 270.17 | | | L | 1,549.93 | 775.47 | 1,532.91 | 766.96 | 1,531.92 | 766.46 | 13 |
| 5 | **657.41** | **329.21** | 640.38 | 320.69 | **639.39** | 320.20 | T | 1,436.85 | 718.93 | 1,419.82 | 710.41 | 1,418.84 | 709.92 | 12 |
| 6 | 758.45 | 379.73 | 741.43 | 371.22 | **740.44** | 370.72 | T | 1,335.80 | 668.40 | 1,318.77 | 659.89 | 1,317.79 | 659.40 | 11 |
| 7 | **873.48** | 437.24 | 856.45 | 428.73 | **855.47** | **428.24** | D | **1,234.75** | 617.88 | 1,217.73 | 609.37 | 1,216.74 | 608.87 | 10 |
| 8 | 986.56 | 493.79 | 969.54 | 485.27 | **968.55** | 484.78 | I | 1,119.73 | 560.37 | 1,102.70 | 551.85 | 1,101.72 | 551.36 | 9 |
| 9 | **1,073.60** | **537.30** | 1,056.57 | 528.79 | **1,055.59** | **528.30** | S | 1,006.64 | 503.82 | 989.62 | 495.31 | 988.63 | 494.82 | 8 |
| 10 | 1,186.68 | 593.84 | 1,169.65 | 585.33 | 1,168.67 | 584.84 | L | 919.61 | 460.31 | 902.58 | 451.80 | | | 7 |
| 11 | 1,299.76 | 650.39 | 1,282.74 | 641.87 | 1,281.75 | 641.38 | I | **806.53** | 403.77 | 789.50 | 395.25 | | | 6 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 12 | 1,446.83 | 723.92 | 1,429.81 | 715.41 | 1,428.82 | 714.91 | F | 693.44 | 347.22 | 676.41 | 338.71 | | | 5 |
| 13 | 1,517.87 | 759.44 | 1,500.84 | 750.93 | 1,499.86 | 750.43 | A | 546.37 | 273.69 | 529.35 | 265.18 | | | 4 |
| 14 | 1,588.91 | 794.96 | 1,571.88 | 786.44 | 1,570.90 | 785.95 | A | 475.34 | 238.17 | 458.31 | 229.66 | | | 3 |
| 15 | 1,701.99 | 851.50 | 1,684.96 | 842.99 | 1,683.98 | 842.49 | L | 404.30 | 202.65 | 387.27 | 194.14 | | | 2 |
| 16 | | | | | | | K | 291.21 | 146.11 | 274.19 | 137.60 | | | 1 |

Query 2214 Hit 1

MS/MS Fragmentation of **LTGDLSHLAAIVILLLK**
Found in **sp|P33947|ERD22_HUMAN**, ER lumen protein retaining receptor 2 OS=Homo sapiens GN=KDELR2 PE=1 SV=1
Match to Query 2214: 2077.323from(693.4484,3+)
Title: 1421: Scan 3553 (rt=88.4912, f=2, i=548) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 2077.323
**Variable modifications:**
**K17** :iTRAQ4plex (K)
**Ions Score:** 40.95 **Expect:** 0.004

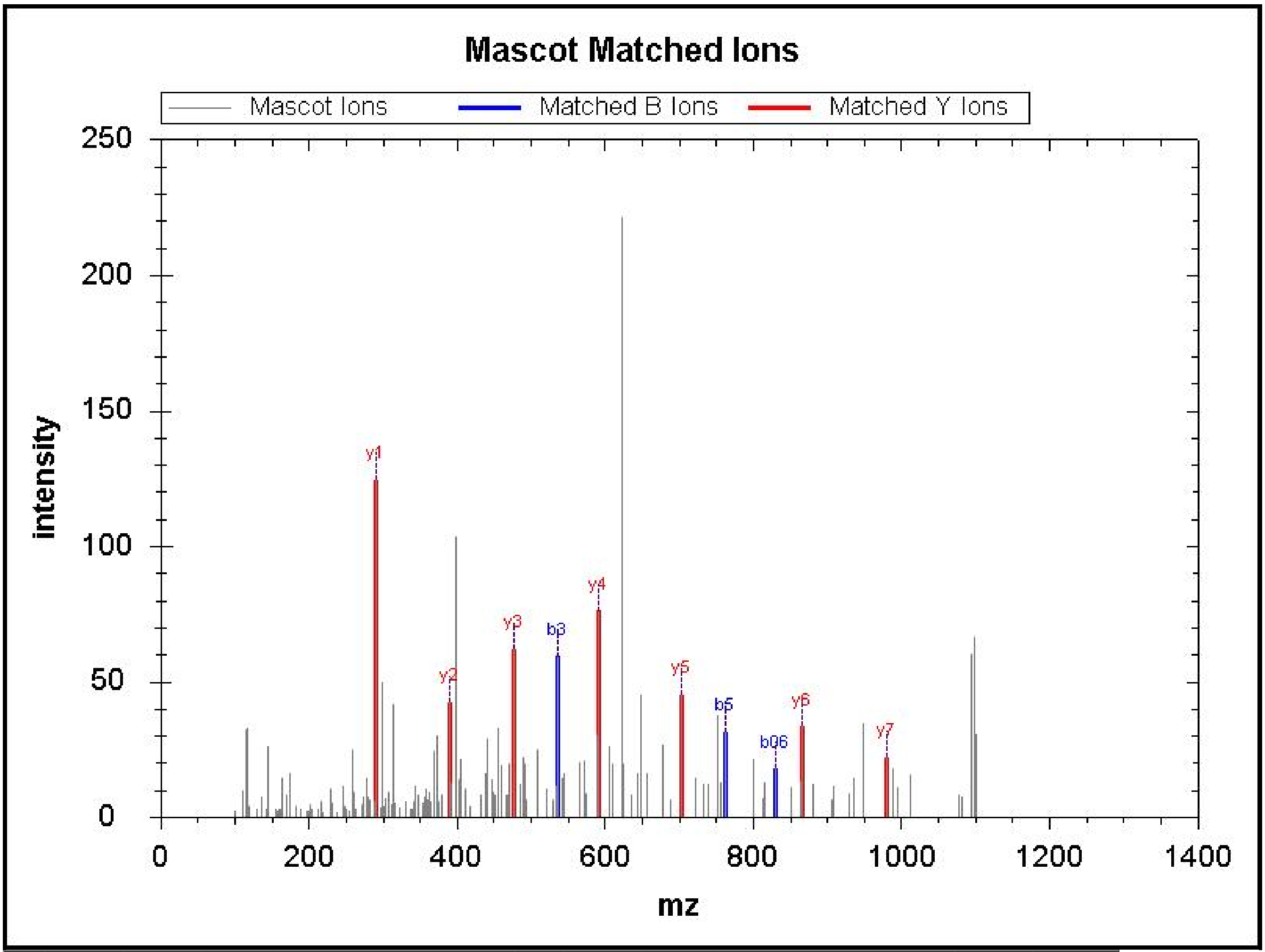


| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | | | L | | | | | | | 17 |
| 2 | 359.24 | 180.12 | 341.23 | 171.12 | T | 1,821.13 | 911.07 | 1,804.11 | 902.56 | 1,803.12 | 902.06 | 16 |
| 3 | 416.26 | 208.63 | 398.25 | 199.63 | G | 1,720.09 | 860.55 | 1,703.06 | 852.03 | 1,702.07 | 851.54 | 15 |
| 4 | 531.29 | 266.15 | 513.28 | 257.14 | D | 1,663.06 | 832.04 | 1,646.04 | 823.52 | 1,645.05 | 823.03 | 14 |
| 5 | 644.37 | 322.69 | 626.36 | 313.69 | L | 1,548.04 | 774.52 | 1,531.01 | 766.01 | 1,530.03 | 765.52 | 13 |
| 6 | 731.41 | 366.21 | 713.39 | 357.20 | S | 1,434.95 | 717.98 | 1,417.93 | 709.47 | 1,416.94 | 708.97 | 12 |
| 7 | 868.46 | 434.74 | 850.45 | 425.73 | H | 1,347.92 | 674.46 | 1,330.89 | 665.95 | | | 11 |
| 8 | 981.55 | 491.28 | 963.54 | 482.27 | L | 1,210.86 | 605.93 | 1,193.84 | 597.42 | | | 10 |
| 9 | 1,052.59 | 526.80 | 1,034.58 | 517.79 | A | 1,097.78 | 549.39 | 1,080.75 | 540.88 | | | 9 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 10 | **1,123.62** | **562.32** | 1,105.61 | 553.31 | A | 1,026.74 | 513.87 | 1,009.71 | 505.36 | | | 8 |
| 11 | 1,236.71 | **618.86** | 1,218.70 | 609.85 | I | 955.70 | 478.36 | 938.68 | 469.84 | | | 7 |
| 12 | 1,335.78 | 668.39 | 1,317.76 | 659.39 | V | **842.62** | 421.81 | 825.59 | 413.30 | | | 6 |
| 13 | 1,448.86 | 724.93 | 1,430.85 | 715.93 | I | **743.55** | 372.28 | 726.52 | 363.77 | | | 5 |
| 14 | 1,561.94 | 781.48 | 1,543.93 | 772.47 | L | **630.47** | 315.74 | 613.44 | 307.22 | | | 4 |
| 15 | 1,675.03 | 838.02 | 1,657.02 | 829.01 | L | **517.38** | 259.20 | 500.36 | 250.68 | | | 3 |
| 16 | 1,788.11 | 894.56 | 1,770.10 | 885.55 | L | **404.30** | 202.65 | 387.27 | 194.14 | | | 2 |
| 17 | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 841 Hit 1

MS/MS Fragmentation of **NLYIISVK**
Found in **sp|P62829|RL23_HUMAN**, 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1
Match to Query 841: 1236.768from(619.3913,2+)
Title: 612: Sum of 2 scans in range 1651 (rt=45.6413, f=4, i=424) to 1652 (rt=45.6667, f=4, i=425)
[D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1236.768
**Variable modifications:**
**K8** :iTRAQ4plex (K)
**Ions Score:** 40.33 **Expect:** 0.038

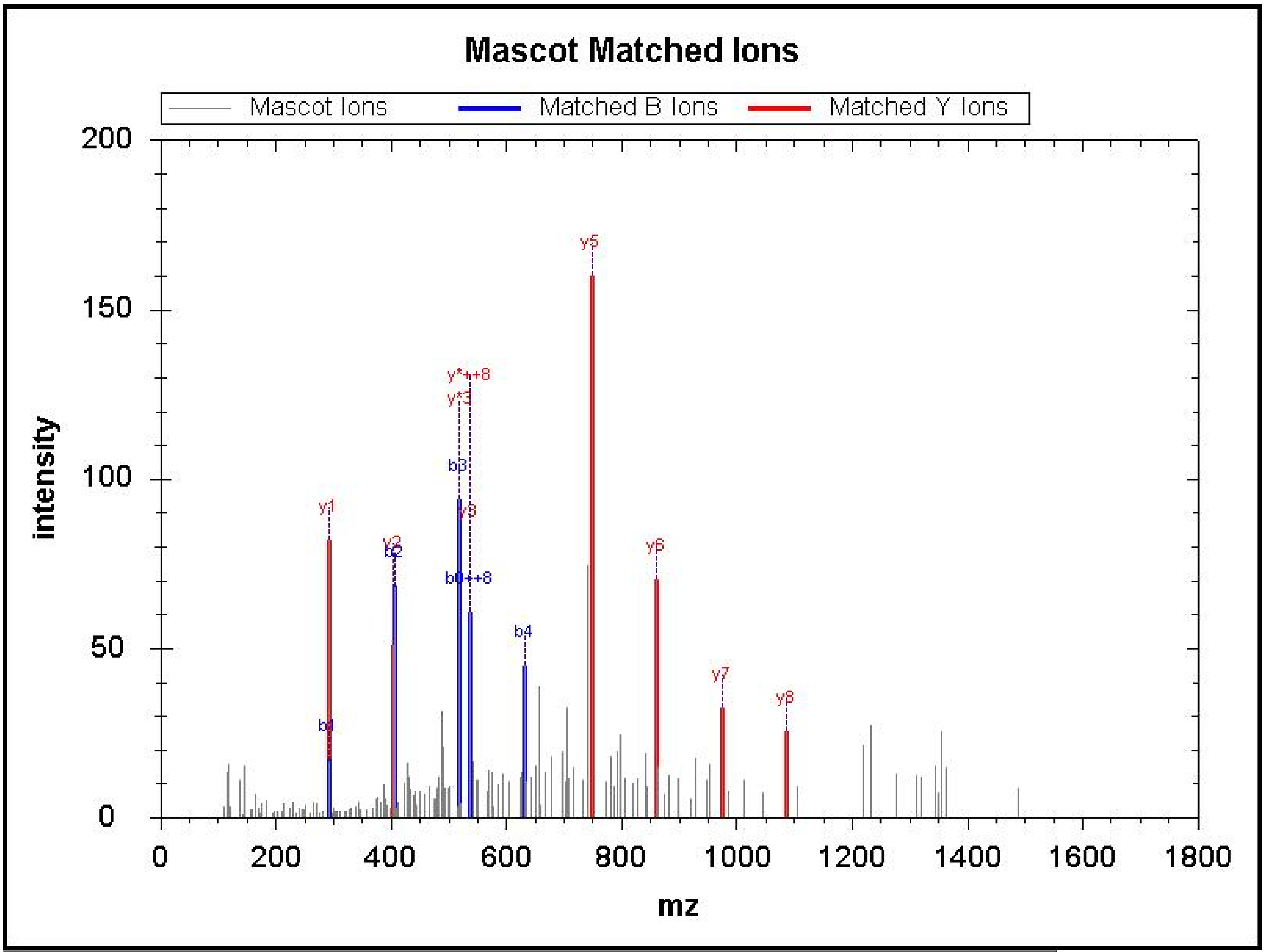


| No | b | b++ | b* | b*++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 259.15 | 130.08 | 242.13 | 121.57 | | | N | | | | | | | 8 |
| 2 | 372.24 | 186.62 | 355.21 | 178.11 | | | L | **979.63** | 490.32 | 962.60 | 481.81 | 961.62 | 481.31 | 7 |
| 3 | **535.30** | 268.15 | 518.27 | 259.64 | | | Y | **866.55** | 433.78 | 849.52 | 425.26 | 848.54 | 424.77 | 6 |
| 4 | 648.38 | 324.70 | 631.36 | 316.18 | | | I | **703.48** | 352.25 | 686.46 | 343.73 | 685.47 | 343.24 | 5 |
| 5 | **761.47** | 381.24 | 744.44 | 372.72 | | | I | **590.40** | 295.70 | 573.37 | 287.19 | 572.39 | 286.70 | 4 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 6 | 848.50 | 424.75 | 831.47 | 416.24 | **830.49** | 415.75 | S | **477.32** | 239.16 | 460.29 | 230.65 | 459.30 | 230.16 | 3 |
| 7 | 947.57 | 474.29 | 930.54 | 465.77 | 929.56 | 465.28 | V | **390.28** | 195.65 | 373.26 | 187.13 | | | 2 |
| 8 | | | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 1167 Hit 1

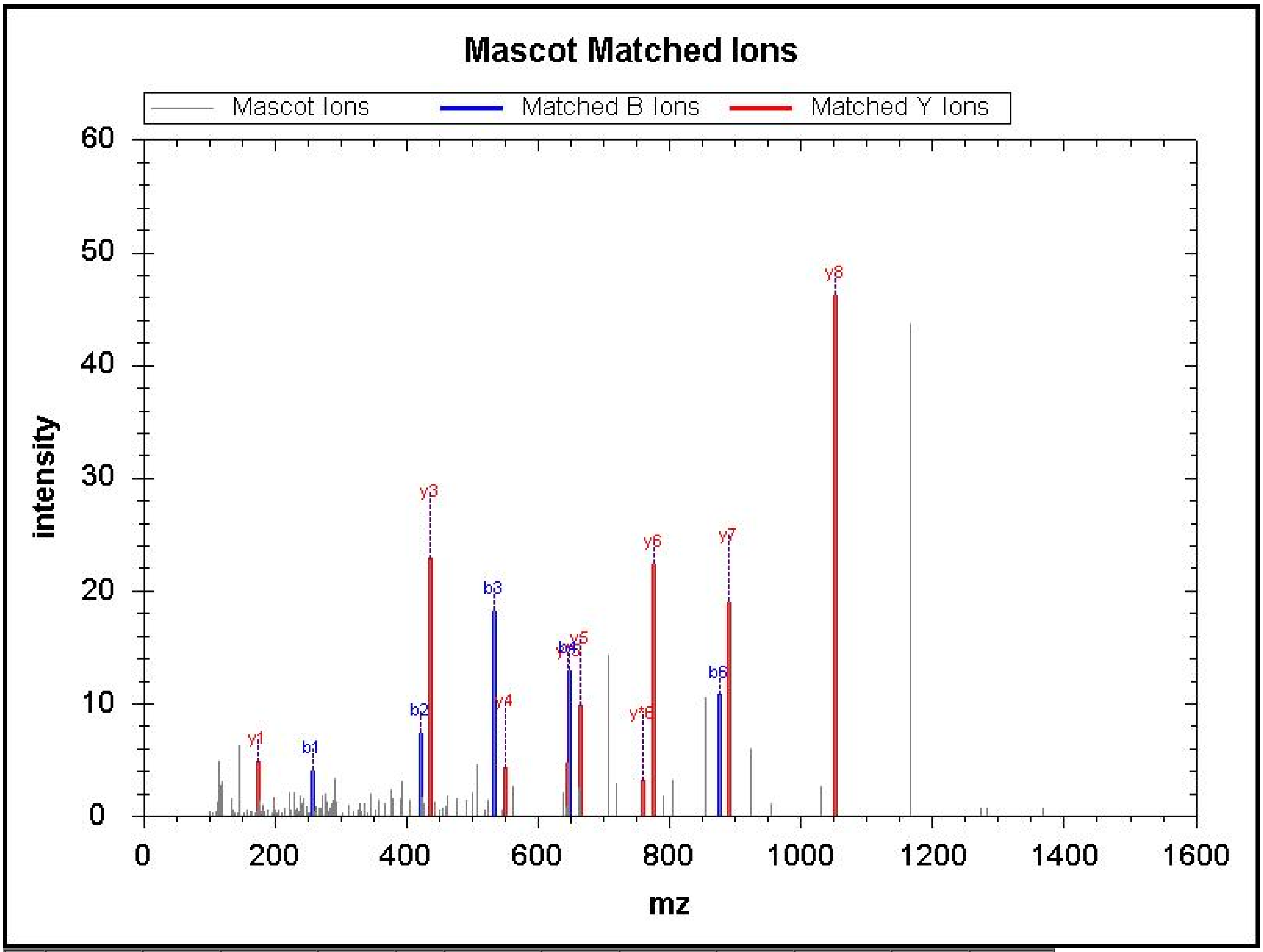
MS/MS Fragmentation of **FLILPDMLK**
Found in **sp|P62318|SMD3_HUMAN**, Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1
Match to Query 1167: 1376.843from(689.4288,2+)
Title: 980: Sum of 2 scans in range 2439 (rt=63.3954, f=4, i=678) to 2440 (rt=63.4208, f=4, i=679) [D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1376.843
**Variable modifications:**
**K9** :iTRAQ4plex (K)
**Ions Score:** 39.56 **Expect:** 0.054



| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **292.18** | 146.59 | | | F | | | | | | | 9 |
| 2 | **405.26** | 203.13 | | | L | **1,086.67** | 543.84 | 1,069.64 | **535.33** | 1,068.66 | 534.83 | 8 |
| 3 | **518.35** | 259.68 | | | I | **973.59** | 487.30 | 956.56 | 478.78 | 955.58 | 478.29 | 7 |
| 4 | **631.43** | 316.22 | | | L | **860.50** | 430.76 | 843.48 | 422.24 | 842.49 | 421.75 | 6 |
| 5 | 728.48 | 364.74 | | | P | **747.42** | 374.21 | 730.39 | 365.70 | 729.41 | 365.21 | 5 |
| 6 | 843.51 | 422.26 | 825.50 | 413.25 | D | 650.37 | 325.69 | 633.34 | 317.17 | 632.36 | 316.68 | 4 |
| 7 | 974.55 | 487.78 | 956.54 | 478.77 | M | **535.34** | 268.17 | **518.31** | 259.66 | | | 3 |
| 8 | 1,087.63 | 544.32 | 1,069.62 | **535.32** | L | **404.30** | 202.65 | 387.27 | 194.14 | | | 2 |
| 9 | | | | | K | **291.21** | 146.11 | 274.19 | 137.60 | | | 1 |

Query 1029 Hit 1

MS/MS Fragmentation of **LYLILDFLR**
Found in **sp|Q15418|KS6A1_HUMAN**, Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 PE=1 SV=2
Match to Query 1029: 1308.797from(655.4058,2+)
Title: 1208: Scan 3087 (rt=77.5454, f=3, i=436) [D:\lab212\membrane\Grace\20120305-iTRAQ-1.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1308.797
**Variable modifications:**
**Ions Score:** 39.55 **Expect:** 0.049

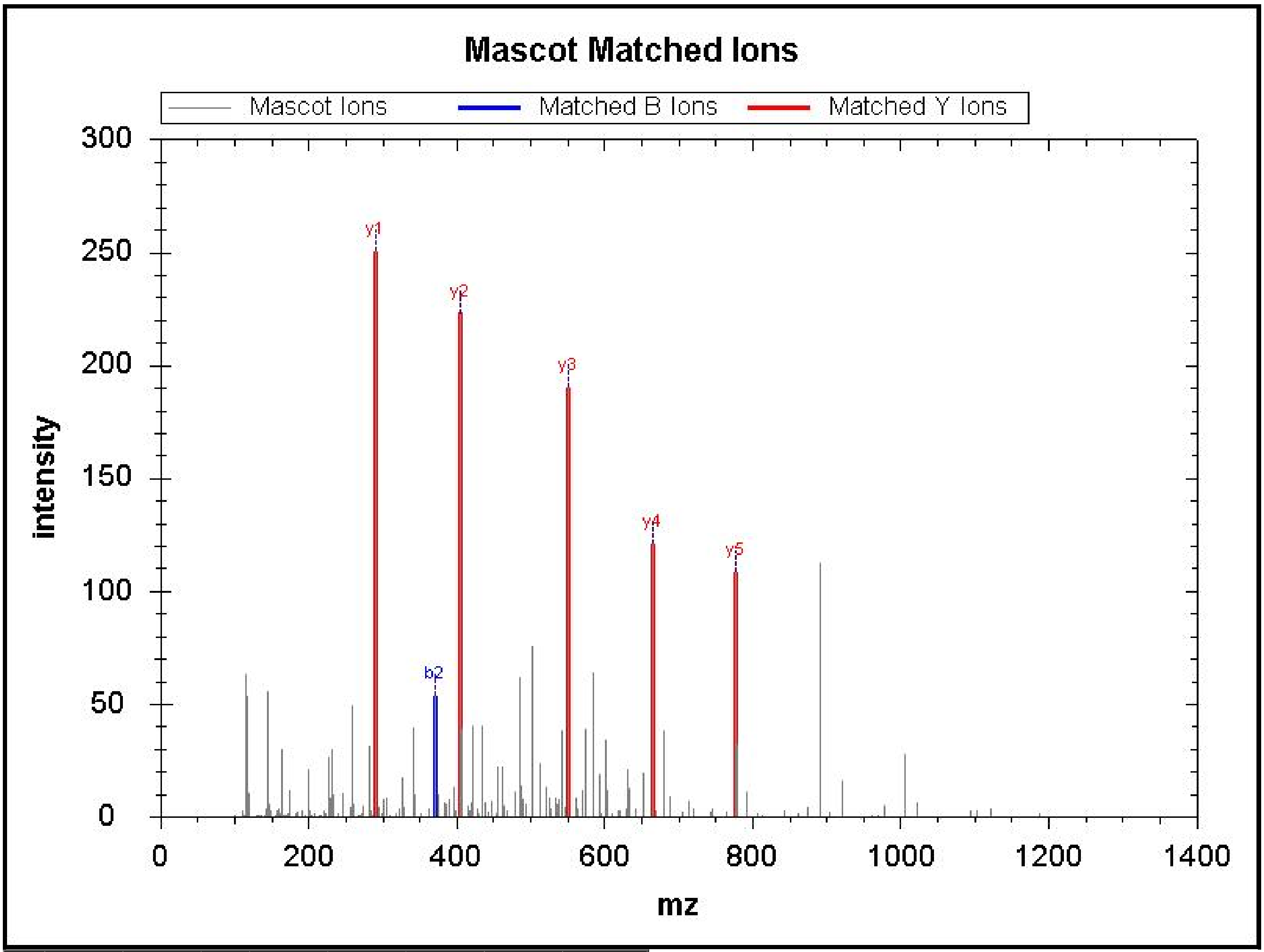


| No | b | b++ | b0 | b0++ | Seq | y | y++ | y* | y*++ | y0 | y0++ | RevNo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **258.19** | 129.60 | | | L | | | | | | | 9 |
| 2 | **421.26** | 211.13 | | | Y | **1,052.61** | 526.81 | 1,035.59 | 518.30 | 1,034.60 | 517.81 | 8 |
| 3 | **534.34** | 267.67 | | | L | **889.55** | 445.28 | 872.52 | 436.77 | 871.54 | 436.27 | 7 |
| 4 | **647.42** | 324.22 | | | I | **776.47** | 388.74 | **759.44** | 380.22 | 758.46 | 379.73 | 6 |
| 5 | 760.51 | 380.76 | | | L | **663.38** | 332.19 | **646.36** | 323.68 | 645.37 | 323.19 | 5 |
| 6 | **875.54** | 438.27 | 857.53 | 429.27 | D | **550.30** | 275.65 | 533.27 | 267.14 | 532.29 | 266.65 | 4 |
| 7 | 1,022.60 | 511.81 | 1,004.59 | 502.80 | F | **435.27** | 218.14 | 418.24 | 209.63 | | | 3 |
| 8 | 1,135.69 | 568.35 | 1,117.68 | 559.34 | L | 288.20 | 144.61 | 271.18 | 136.09 | | | 2 |
| 9 | | | | | R | **175.12** | 88.06 | 158.09 | 79.55 | | | 1 |

Query 329 Hit 1

MS/MS Fragmentation of **LLLFLK**
Found in **sp|Q7L1Q6|BZW1_HUMAN**, Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1
Match to Query 329: 1033.72from(517.8672,2+)
Title: 904: Sum of 2 scans in range 2271 (rt=59.6117, f=4, i=624) to 2272 (rt=59.6371, f=4, i=625)

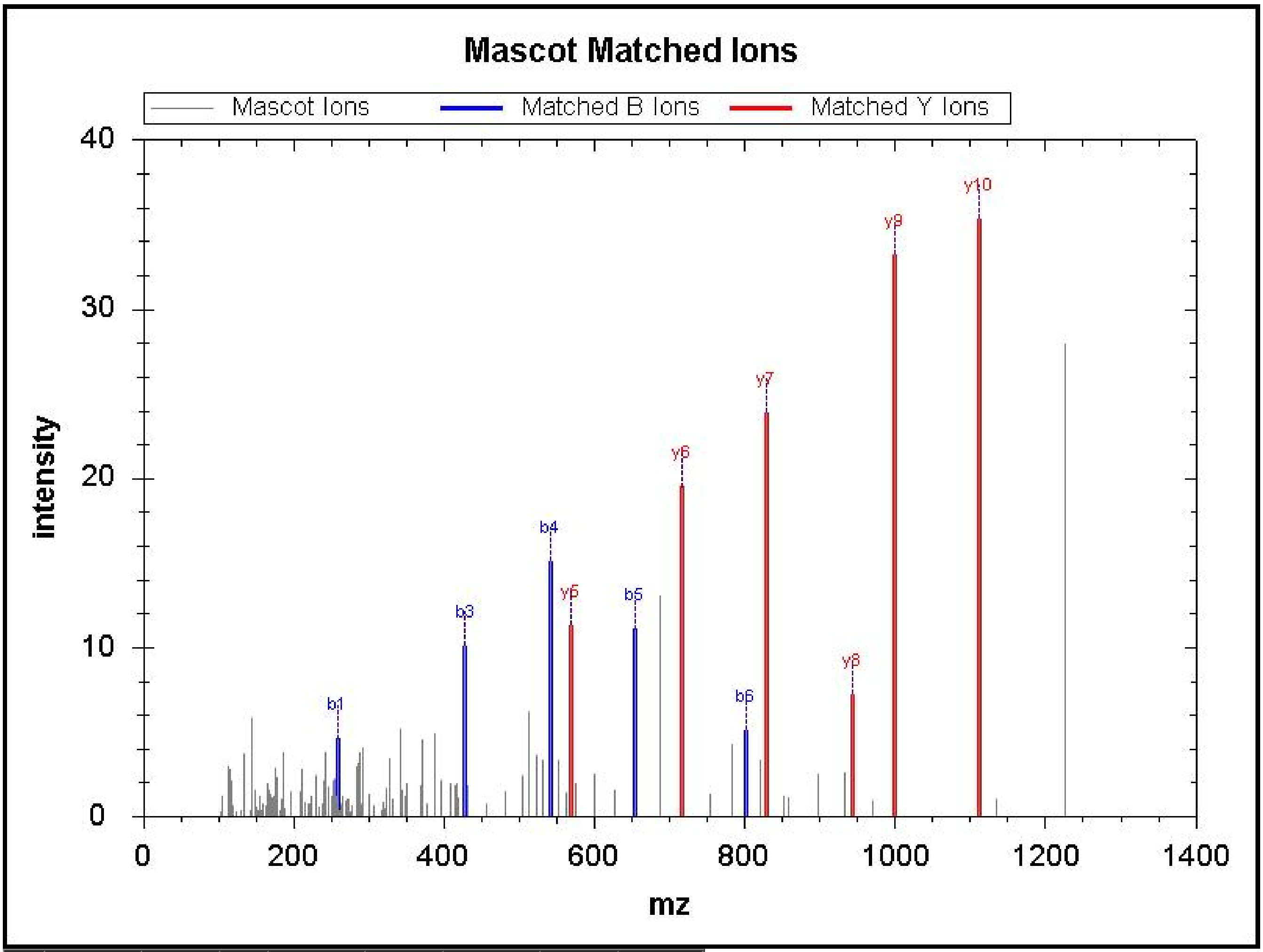
[D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1033.72
**Variable modifications:**
**K6** :iTRAQ4plex (K)
**Ions Score:** 37.61 **Expect:** 0.034



| No | b | b++ | Seq | y | y++ | y* | y*++ | RevNo |
|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | L |  |  |  |  | 6 |
| 2 | 371.28 | 186.14 | L | 777.54 | 389.27 | 760.51 | 380.76 | 5 |
| 3 | 484.36 | 242.68 | L | 664.45 | 332.73 | 647.42 | 324.22 | 4 |
| 4 | 631.43 | 316.22 | F | 551.37 | 276.19 | 534.34 | 267.67 | 3 |
| 5 | 744.51 | 372.76 | L | 404.30 | 202.65 | 387.27 | 194.14 | 2 |
| 6 |  |  | K | 291.21 | 146.11 | 274.19 | 137.60 | 1 |

Query 1143 Hit 1

MS/MS Fragmentation of **LLGLLFPLLAR**
Found in **sp|Q8TEX9|IPO4_HUMAN**, Importin-4 OS=Homo sapiens GN=IPO4 PE=1 SV=2
Match to Query 1143: 1368.897from(685.4559,2+)
Title: 1371: Sum of 2 scans in range 3332 (rt=83.5168, f=4, i=966) to 3333 (rt=83.5422, f=4, i=967)
[D:\lab212\membrane\Grace\20120305-iTRAQ-2.raw]
Data File:
**Monoisotopic mass of neutral peptide Mr(calc):** 1368.897
**Variable modifications:**
**Ions Score:** 36.01 **Expect:** 0.035



| No | b | b++ | Seq | y | y++ | y* | y*++ | RevNo |
|---|---|---|---|---|---|---|---|---|
| 1 | 258.19 | 129.60 | L | | | | | 11 |
| 2 | 371.28 | 186.14 | L | 1,112.72 | 556.86 | 1,095.69 | 548.35 | 10 |
| 3 | 428.30 | 214.65 | G | 999.63 | 500.32 | 982.61 | 491.81 | 9 |
| 4 | 541.38 | 271.20 | L | 942.61 | 471.81 | 925.59 | 463.30 | 8 |
| 5 | 654.47 | 327.74 | L | 829.53 | 415.27 | 812.50 | 406.76 | 7 |
| 6 | 801.54 | 401.27 | F | 716.45 | 358.73 | 699.42 | 350.21 | 6 |
| 7 | 898.59 | 449.80 | P | 569.38 | 285.19 | 552.35 | 276.68 | 5 |
| 8 | 1,011.67 | 506.34 | L | 472.32 | 236.67 | 455.30 | 228.15 | 4 |
| 9 | 1,124.76 | 562.88 | L | 359.24 | 180.12 | 342.21 | 171.61 | 3 |
| 10 | 1,195.79 | 598.40 | A | 246.16 | 123.58 | 229.13 | 115.07 | 2 |
| 11 | | | R | 175.12 | 88.06 | 158.09 | 79.55 | 1 |