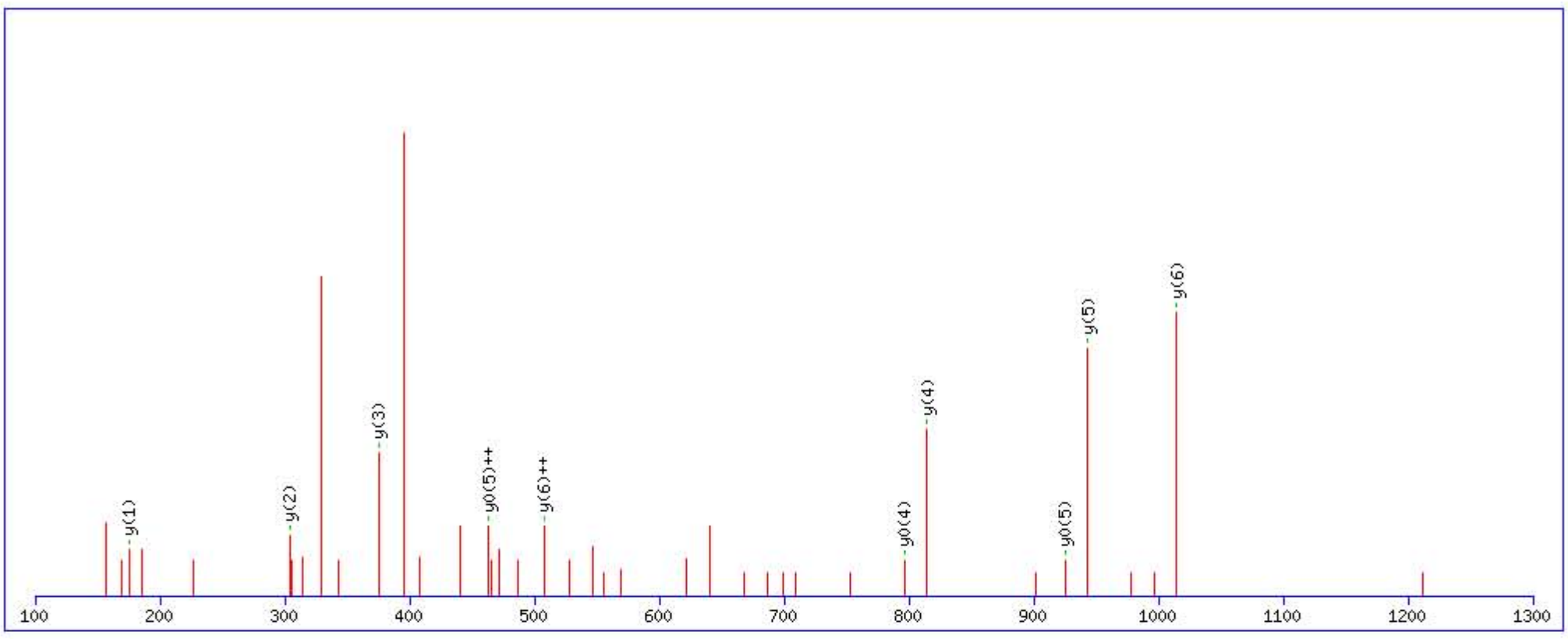
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LAEQAER**
Found in **1433B_HUMAN**, 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3

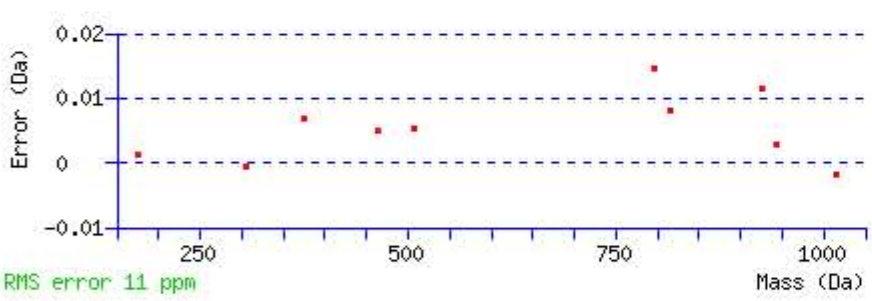
Match to Query 17501: 1126.586508 from(564.300530,2+) rtinseconds(1412) index(46413)
Title: Locus:1.1.1.1729.22 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

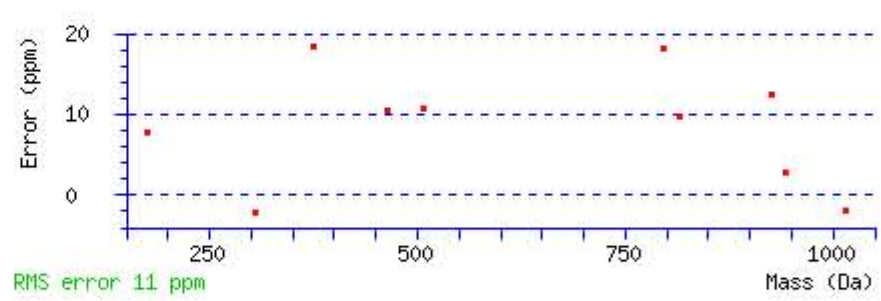
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1126.580444
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 35 **Expect:** 0.0057
**Matches :** 10/60 fragment ions using 18 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 7 |
| 2 | 185.128454 | 93.067865 | | | | | A | *1014.503692* | 507.755484 | 997.477143 | 499.242210 | 996.493127 | 498.750202 | 6 |
| 3 | 314.171047 | 157.589161 | | | 296.160482 | 148.583879 | E | *943.466578* | 472.236927 | 926.440029 | 463.723653 | 925.456013 | 463.231645 | 5 |
| 4 | 753.396373 | 377.201825 | 736.369824 | 368.688550 | 735.385808 | 368.196542 | Q | *814.423985* | 407.715631 | 797.397436 | 399.202356 | 796.413420 | 398.710348 | 4 |
| 5 | 824.433487 | 412.720382 | 807.406938 | 404.207107 | 806.422922 | 403.715099 | A | *375.198659* | 188.102968 | 358.172110 | 179.589693 | 357.188094 | 179.097685 | 3 |
| 6 | 953.476080 | 477.241678 | 936.449531 | 468.728404 | 935.465515 | 468.236396 | E | *304.161545* | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 7 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 35.3 | 1126.580444 | 0.006064 | LAEQAER |
| 14.3 | 1126.598221 | -0.011713 | LISDPAGELGR |
| 11.8 | 1126.580444 | 0.006064 | LAQAEER |
| 8.6 | 1126.573074 | 0.013434 | SPERPTGDLR |
| 4.0 | 1126.580444 | 0.006064 | LEAEQAR |
| 2.7 | 1126.580444 | 0.006064 | AIQAEER |
| 2.5 | 1126.588318 | -0.001810 | SPFHEIKNR |
| 2.2 | 1126.599075 | -0.012567 | MAMFKKSLR |

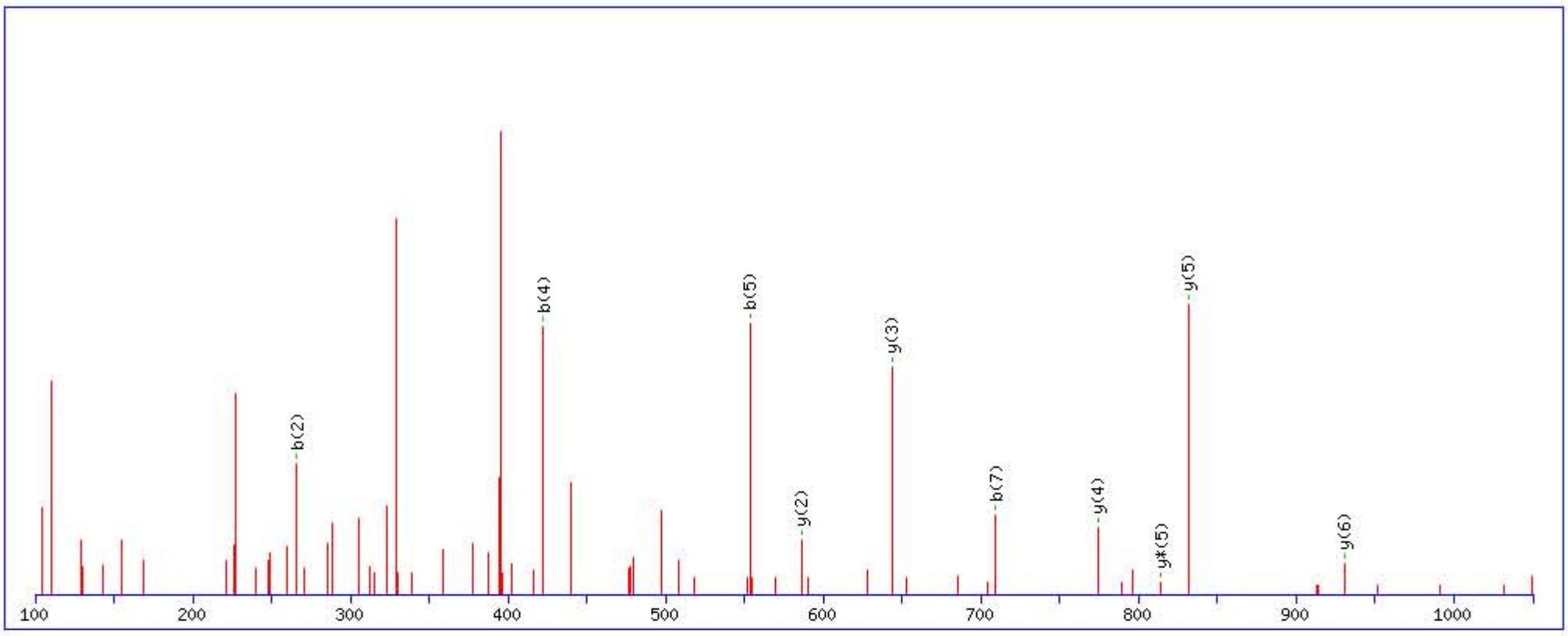
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HQGVMVGMGQK**
Found in **ACTA_HUMAN**, Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1

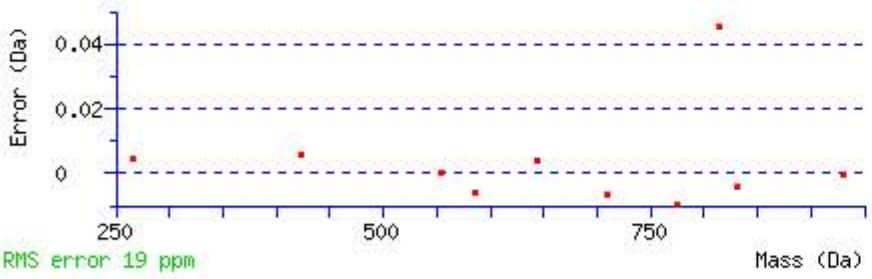
Match to Query 30638: 1481.731242 from(494.917690,3+) rtinseconds(1604) index(17650)
Title: Locus:1.1.1.2941.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

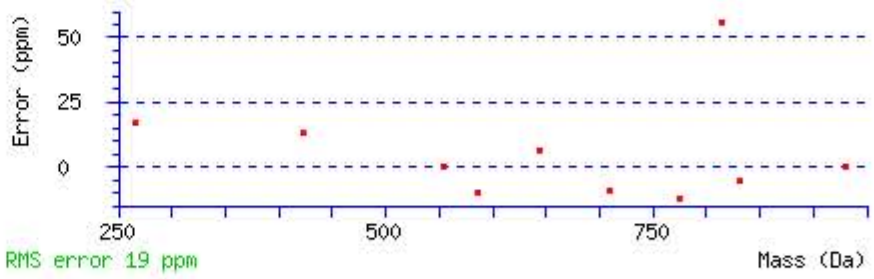
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1481.730545
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 27 **Expect:** 0.039
**Matches :** 10/78 fragment ions using 20 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | H | | | | | 11 |
| 2 | *266.124766* | 133.566021 | 249.098217 | 125.052746 | Q | 1345.678898 | 673.343087 | 1328.652349 | 664.829813 | 10 |
| 3 | 323.146230 | 162.076753 | 306.119681 | 153.563478 | G | 1217.620320 | 609.313798 | 1200.593771 | 600.800524 | 9 |
| 4 | *422.214644* | 211.610960 | 405.188095 | 203.097685 | V | 1160.598856 | 580.803066 | 1143.572307 | 572.289792 | 8 |
| 5 | *553.255129* | 277.131203 | 536.228580 | 268.617928 | M | 1061.530442 | 531.268859 | 1044.503893 | 522.755585 | 7 |
| 6 | 652.323543 | 326.665410 | 635.296994 | 318.152135 | V | *930.489957* | 465.748617 | 913.463408 | 457.235342 | 6 |
| 7 | *709.345007* | 355.176142 | 692.318458 | 346.662867 | G | *831.421543* | 416.214410 | 814.394994 | 407.701135 | 5 |
| 8 | 840.385492 | 420.696384 | 823.358943 | 412.183110 | M | *774.400079* | 387.703678 | 757.373530 | 379.190403 | 4 |
| 9 | 897.406956 | 449.207116 | 880.380407 | 440.693842 | G | *643.359594* | 322.183435 | 626.333045 | 313.670161 | 3 |
| 10 | 1336.632282 | 668.819779 | 1319.605733 | 660.306505 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | 2 |
| 11 | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 26.6 | 1481.730545 | 0.000697 | HQGVMVGMGQK |

**Mascot:** http://www.matrixscience.com/

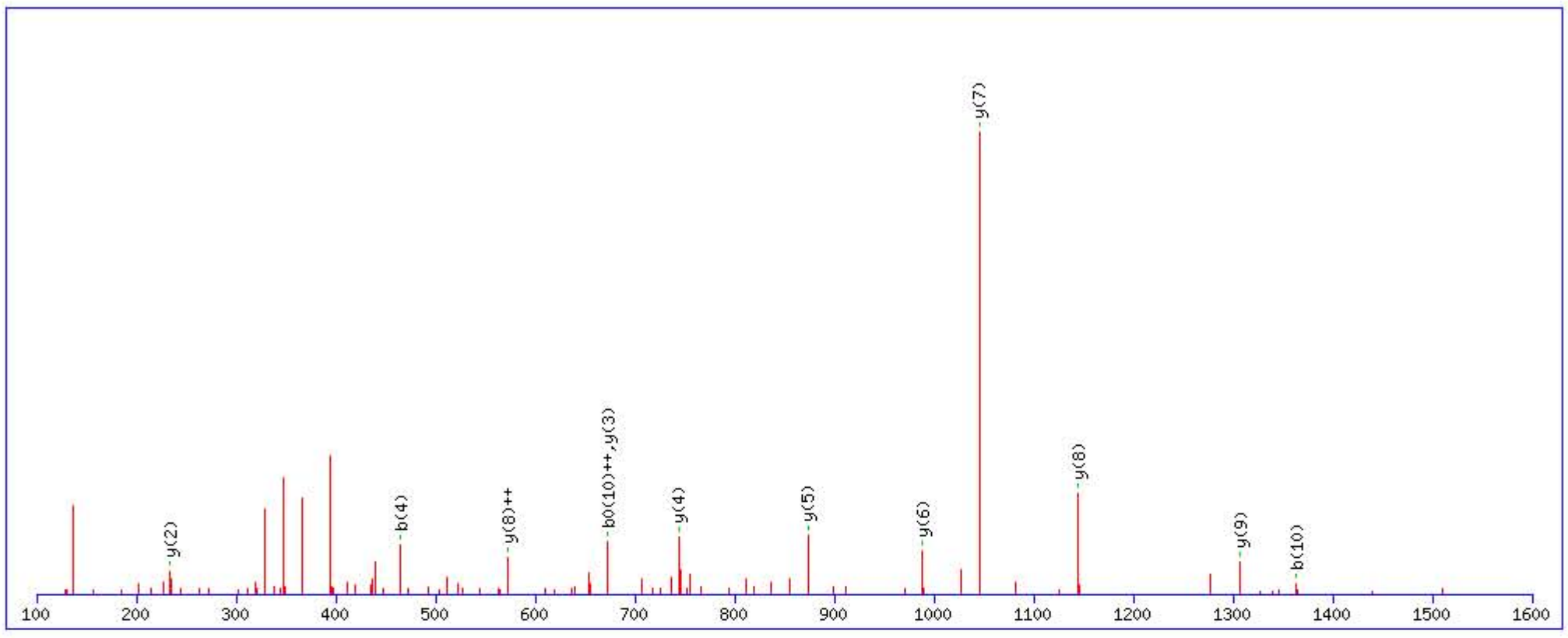
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DSYVGDEAQSK**
Found in **ACTA_HUMAN**, Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1

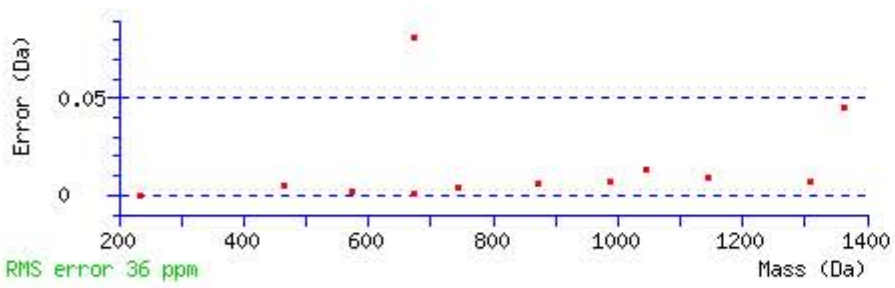
Match to Query 31437: 1508.692888 from(755.353720,2+) rtinseconds(1599) index(47625)
Title: Locus:1.1.1.1794.22 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

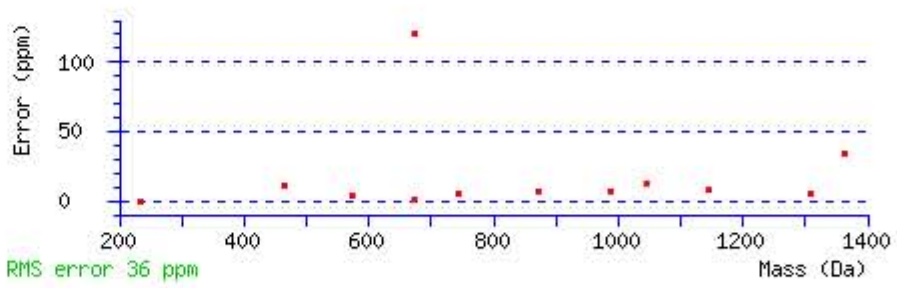
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1508.681702
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 69 **Expect:** 1.5e-006
**Matches :** 12/102 fragment ions using 14 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 11 |
| 2 | 203.066247 | 102.036761 | | | 185.055682 | 93.031479 | S | 1394.662043 | 697.834660 | 1377.635494 | 689.321385 | 1376.651478 | 688.829377 | 10 |
| 3 | 366.129576 | 183.568426 | | | 348.119011 | 174.563144 | Y | *1307.630015* | 654.318646 | 1290.603466 | 645.805371 | 1289.619450 | 645.313363 | 9 |
| 4 | **465.197990** | 233.102633 | | | 447.187425 | 224.097351 | V | *1144.566686* | 572.786981 | 1127.540137 | 564.273707 | 1126.556121 | 563.781699 | 8 |
| 5 | 522.219454 | 261.613365 | | | 504.208889 | 252.608083 | G | *1045.498272* | 523.252774 | 1028.471723 | 514.739500 | 1027.487707 | 514.247492 | 7 |
| 6 | 637.246397 | 319.126837 | | | 619.235832 | 310.121554 | D | *988.476808* | 494.742042 | 971.450259 | 486.228768 | 970.466243 | 485.736760 | 6 |
| 7 | 766.288990 | 383.648133 | | | 748.278425 | 374.642851 | E | *873.449865* | 437.228571 | 856.423316 | 428.715296 | 855.439300 | 428.223288 | 5 |
| 8 | 837.326104 | 419.166690 | | | 819.315539 | 410.161408 | A | *744.407272* | 372.707274 | 727.380723 | 364.194000 | 726.396707 | 363.701992 | 4 |
| 9 | 1276.551430 | 638.779353 | 1259.524881 | 630.266079 | 1258.540865 | 629.774070 | Q | *673.370158* | 337.188717 | 656.343609 | 328.675443 | 655.359593 | 328.183435 | 3 |
| 10 | **1363.583458** | 682.295367 | 1346.556909 | 673.782093 | 1345.572893 | 673.290085 | S | *234.144832* | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 11 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 69.0 | 1508.681702 | 0.011186 | DSYVGDEAQSK |
| 8.4 | 1508.690277 | 0.002611 | GGRGGMGGSDRGGFNK |
| 0.8 | 1508.714066 | -0.021178 | EGTQLSSQQSVMSK |

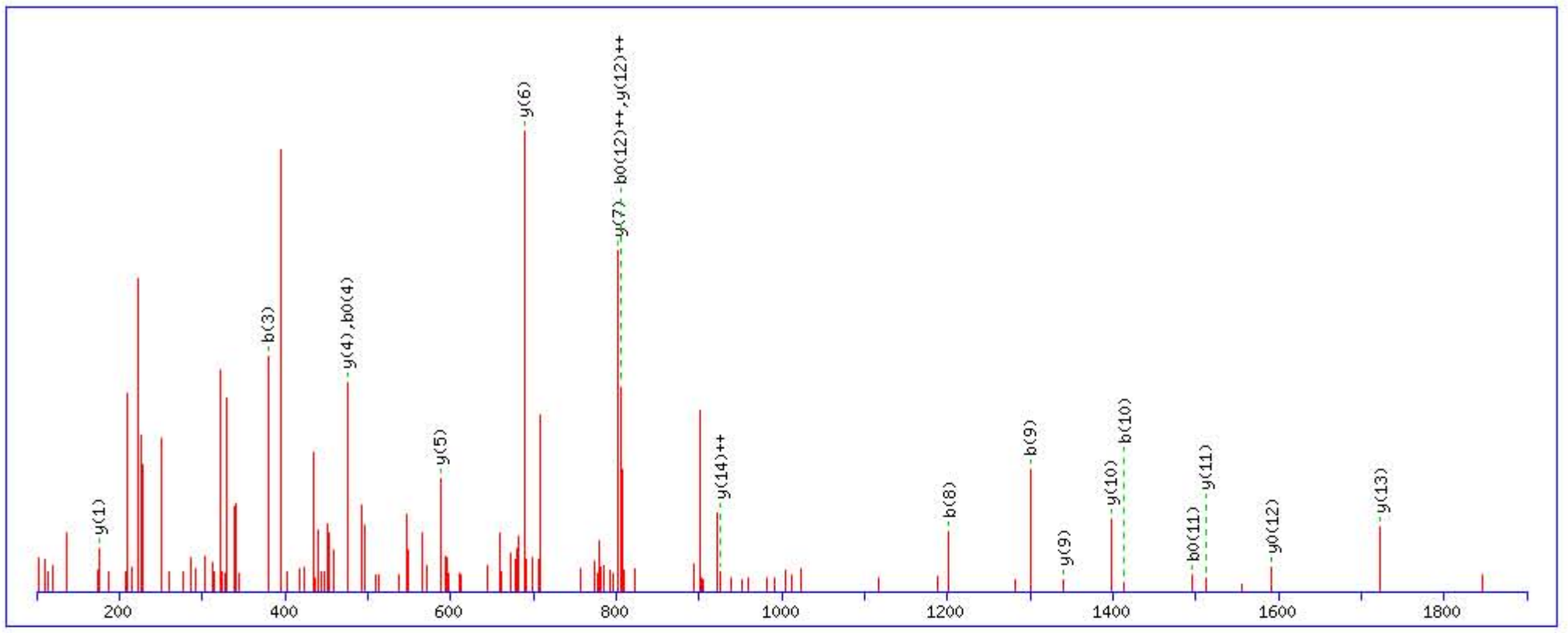
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SYELPDGQVITIGNER**
Found in **ACTA_HUMAN**, Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1

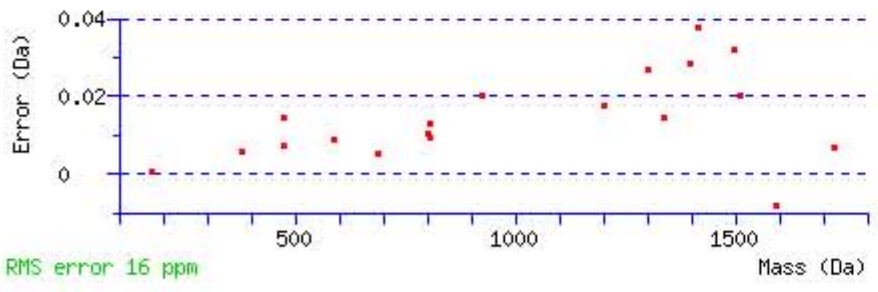
Match to Query 46615: 2101.061412 from(701.361080,3+) rtinseconds(2629) index(54170)
Title: Locus:1.1.1.2152.4 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

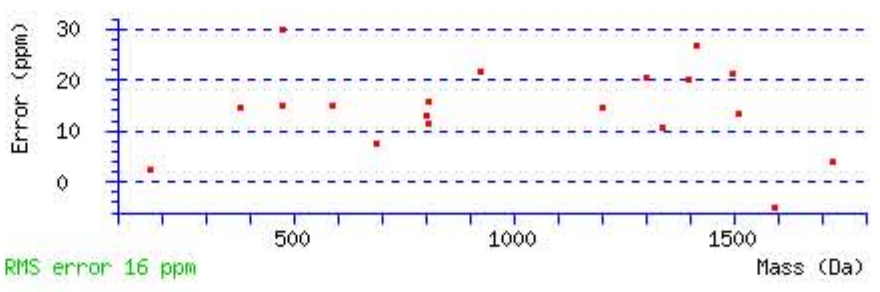
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2101.051376
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 0.00052
**Matches :** 19/164 fragment ions using 32 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 16 |
| 2 | 251.102633 | 126.054954 | | | 233.092068 | 117.049672 | Y | 2015.026640 | 1008.016958 | 1998.000091 | 999.503683 | 1997.016075 | 999.011675 | 15 |
| 3 | **380.145226** | 190.576251 | | | 362.134661 | 181.570969 | E | 1851.963311 | 926.485294 | 1834.936762 | 917.972019 | 1833.952746 | 917.480011 | 14 |
| 4 | 493.229290 | 247.118283 | | | 475.218725 | 238.113001 | L | *1722.920718* | 861.963997 | 1705.894169 | 853.450722 | 1704.910153 | 852.958714 | 13 |
| 5 | 590.282054 | 295.644665 | | | 572.271489 | 286.639383 | P | 1609.836654 | 805.421965 | 1592.810105 | 796.908691 | 1591.826089 | 796.416682 | 12 |
| 6 | 705.308997 | 353.158137 | | | 687.298432 | 344.152854 | D | *1512.783890* | 756.895583 | 1495.757341 | 748.382309 | 1494.773325 | 747.890300 | 11 |
| 7 | 762.330461 | 381.668869 | | | 744.319896 | 372.663586 | G | *1397.756947* | 699.382111 | 1380.730398 | 690.868837 | 1379.746382 | 690.376829 | 10 |
| 8 | **1201.555787** | 601.281532 | 1184.529238 | 592.768257 | 1183.545222 | 592.276249 | Q | *1340.735483* | 670.871379 | 1323.708934 | 662.358105 | 1322.724918 | 661.866097 | 9 |
| 9 | **1300.624201** | 650.815739 | 1283.597652 | 642.302464 | 1282.613636 | 641.810456 | V | 901.510157 | 451.258716 | 884.483608 | 442.745442 | 883.499592 | 442.253434 | 8 |
| 10 | **1413.708265** | 707.357771 | 1396.681716 | 698.844496 | 1395.697700 | 698.352488 | I | *802.441743* | 401.724509 | 785.415194 | 393.211235 | 784.431178 | 392.719227 | 7 |
| 11 | 1514.755944 | 757.881610 | 1497.729395 | 749.368336 | 1496.745379 | 748.876328 | T | *689.357679* | 345.182478 | 672.331130 | 336.669203 | 671.347114 | 336.177195 | 6 |
| 12 | 1627.840008 | 814.423642 | 1610.813459 | 805.910368 | 1609.829443 | 805.418359 | I | *588.310000* | 294.658638 | 571.283451 | 286.145363 | 570.299435 | 285.653355 | 5 |
| 13 | 1684.861472 | 842.934374 | 1667.834923 | 834.421099 | 1666.850907 | 833.929091 | G | *475.225936* | 238.116606 | 458.199387 | 229.603331 | 457.215371 | 229.111323 | 4 |
| 14 | 1798.904399 | 899.955837 | 1781.877850 | 891.442563 | 1780.893834 | 890.950555 | N | 418.204472 | 209.605874 | 401.177923 | 201.092600 | 400.193907 | 200.600592 | 3 |
| 15 | 1927.946992 | 964.477134 | 1910.920443 | 955.963860 | 1909.936427 | 955.471851 | E | 304.161545 | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 16 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 47.6 | 2101.051376 | 0.010036 | SYELPDGQVITIGNER |

**Mascot:** http://www.matrixscience.com/

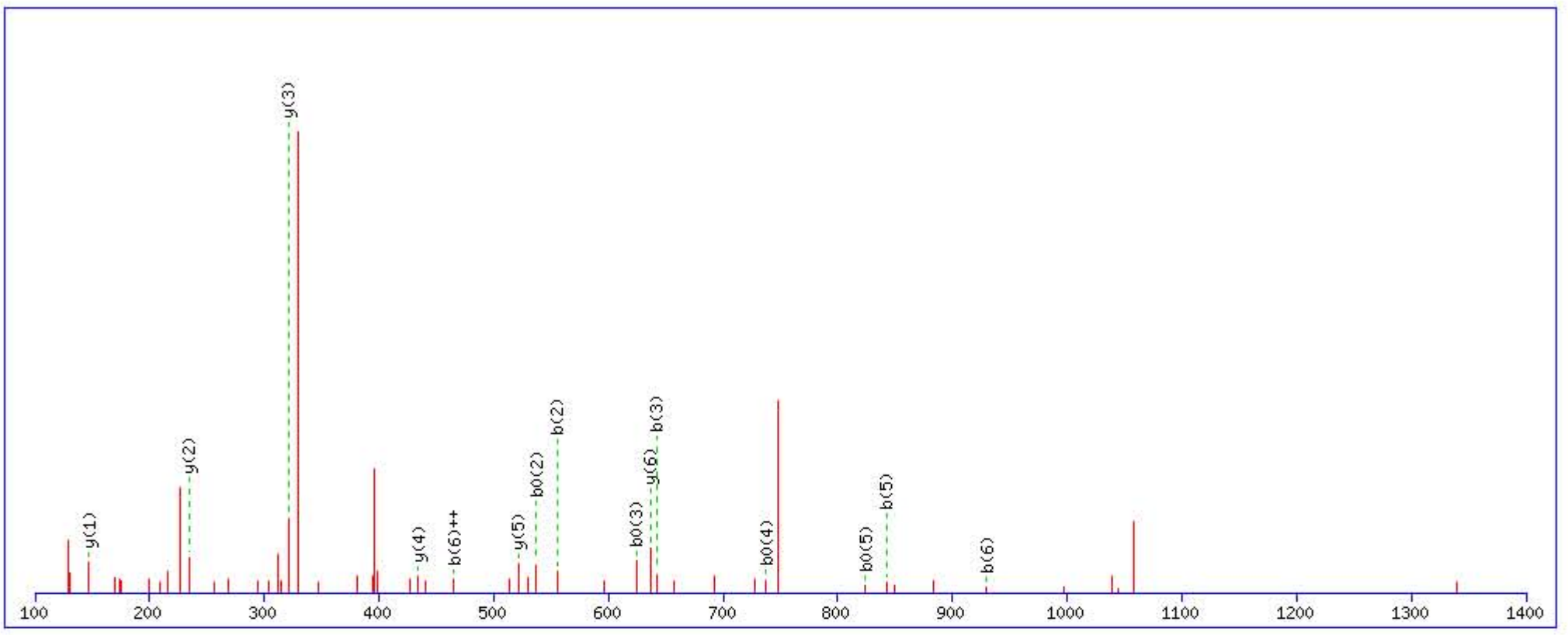
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QDSISSK**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

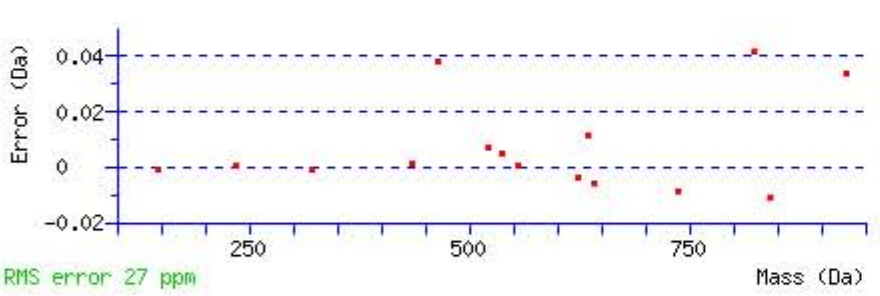
Match to Query 15754: 1074.538248 from(538.276400,2+) rtinseconds(1372) index(1759)
Title: Locus:1.1.1.1754.21 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

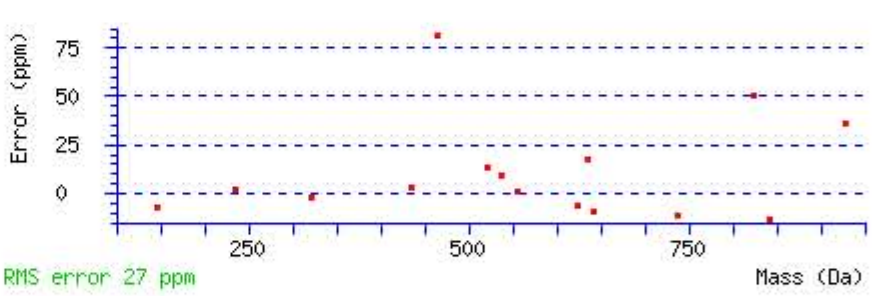
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1074.537933
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.0068
**Matches** : 15/68 fragment ions using 30 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 7 |
| 2 | **555.259545** | 278.133411 | 538.232996 | 269.620136 | 537.248980 | 269.128128 | D | ***636.319895*** | 318.663586 | 619.293346 | 310.150311 | 618.309330 | 309.658303 | 6 |
| 3 | **642.291573** | 321.649425 | 625.265024 | 313.136150 | 624.281008 | 312.644142 | S | ***521.292952*** | 261.150114 | 504.266403 | 252.636840 | 503.282387 | 252.144832 | 5 |
| 4 | 755.375637 | 378.191457 | 738.349088 | 369.678182 | 737.365072 | 369.186174 | I | ***434.260924*** | 217.634100 | 417.234375 | 209.120826 | 416.250359 | 208.628818 | 4 |
| 5 | **842.407665** | 421.707471 | 825.381116 | 413.194196 | 824.397100 | 412.702188 | S | ***321.176860*** | 161.092068 | 304.150311 | 152.578794 | 303.166295 | 152.086786 | 3 |
| 6 | **929.439693** | 465.223484 | 912.413144 | 456.710210 | 911.429128 | 456.218202 | S | ***234.144832*** | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 7 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546766 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.7 | 1074.537933 | 0.000315 | QDSISSK |
| 8.1 | 1074.530548 | 0.007700 | QVTEPTSSAR |
| 7.6 | 1074.537933 | 0.000315 | QDSSKSI |
| 3.7 | 1074.549164 | -0.010916 | NIRPVDMSK |
| 3.6 | 1074.553192 | -0.014944 | QPSFSAK |
| 3.4 | 1074.553207 | -0.014959 | QDGGLFK |
| 2.8 | 1074.531418 | 0.006830 | LLACPSVCR |
| 2.0 | 1074.541763 | -0.003515 | KSNSVQEQR |
| 1.1 | 1074.537933 | 0.000315 | SQEVSSK |
| 1.0 | 1074.530518 | 0.007730 | VDNAASEKNK |

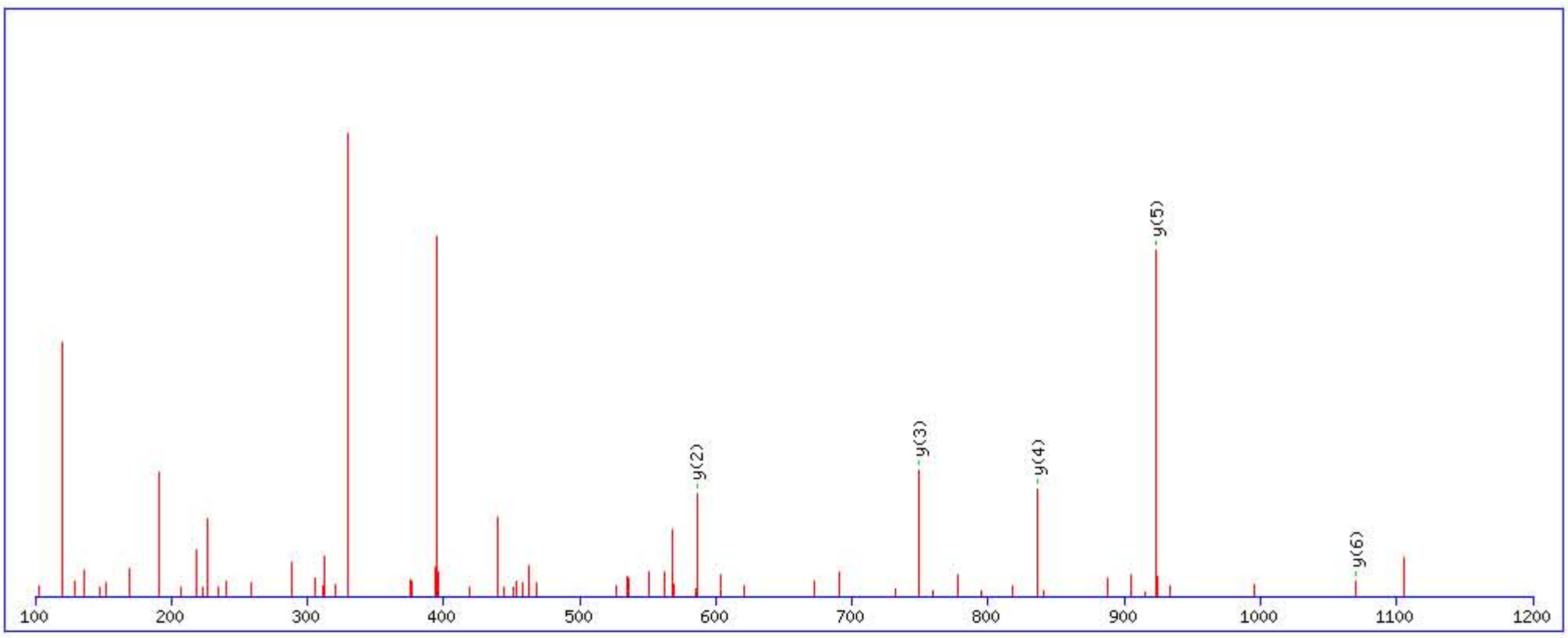
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AFSSYQK**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

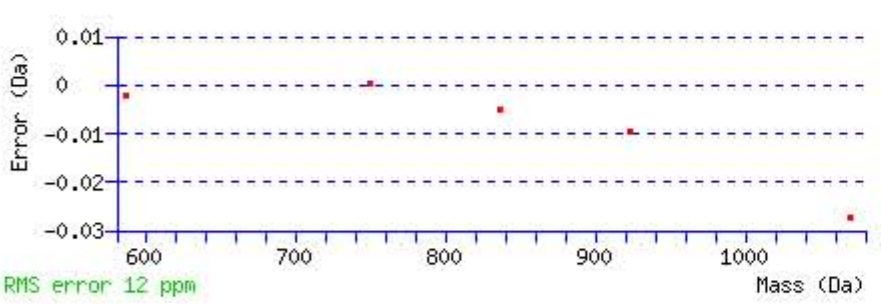
Match to Query 18676: 1140.564408 from(571.289480,2+) rtinseconds(1601) index(17624)
Title: Locus:1.1.1.2940.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

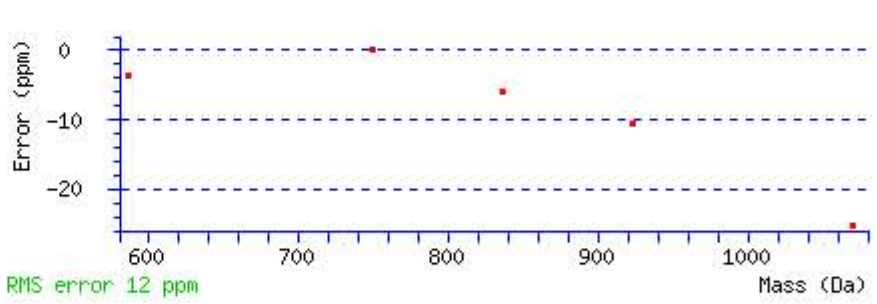
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1140.563751
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 26 **Expect:** 0.011
**Matches :** 5/52 fragment ions using 11 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 7 |
| 2 | 219.112804 | 110.060040 | | | | | F | *1070.533929* | 535.770603 | 1053.507380 | 527.257328 | 1052.523364 | 526.765320 | 6 |
| 3 | 306.144832 | 153.576054 | | | 288.134267 | 144.570772 | S | *923.465515* | 462.236396 | 906.438966 | 453.723121 | 905.454950 | 453.231113 | 5 |
| 4 | 393.176860 | 197.092068 | | | 375.166295 | 188.086785 | S | *836.433487* | 418.720382 | 819.406938 | 410.207107 | 818.422922 | 409.715099 | 4 |
| 5 | 556.240189 | 278.623733 | | | 538.229624 | 269.618450 | Y | *749.401459* | 375.204368 | 732.374910 | 366.691093 | | | 3 |
| 6 | 995.465515 | 498.236396 | 978.438966 | 489.723121 | 977.454950 | 489.231113 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 7 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.9 | 1140.563751 | 0.000657 | AFSSYQK |
| 4.8 | 1140.559723 | 0.004685 | AFSRSSDLMK |
| 1.4 | 1140.581497 | -0.017089 | AFEAVDKAYK |
| 0.9 | 1140.548477 | 0.015931 | MATAAYEQLK |
| 0.0 | 1140.552322 | 0.012086 | AHDEAVRSEK |

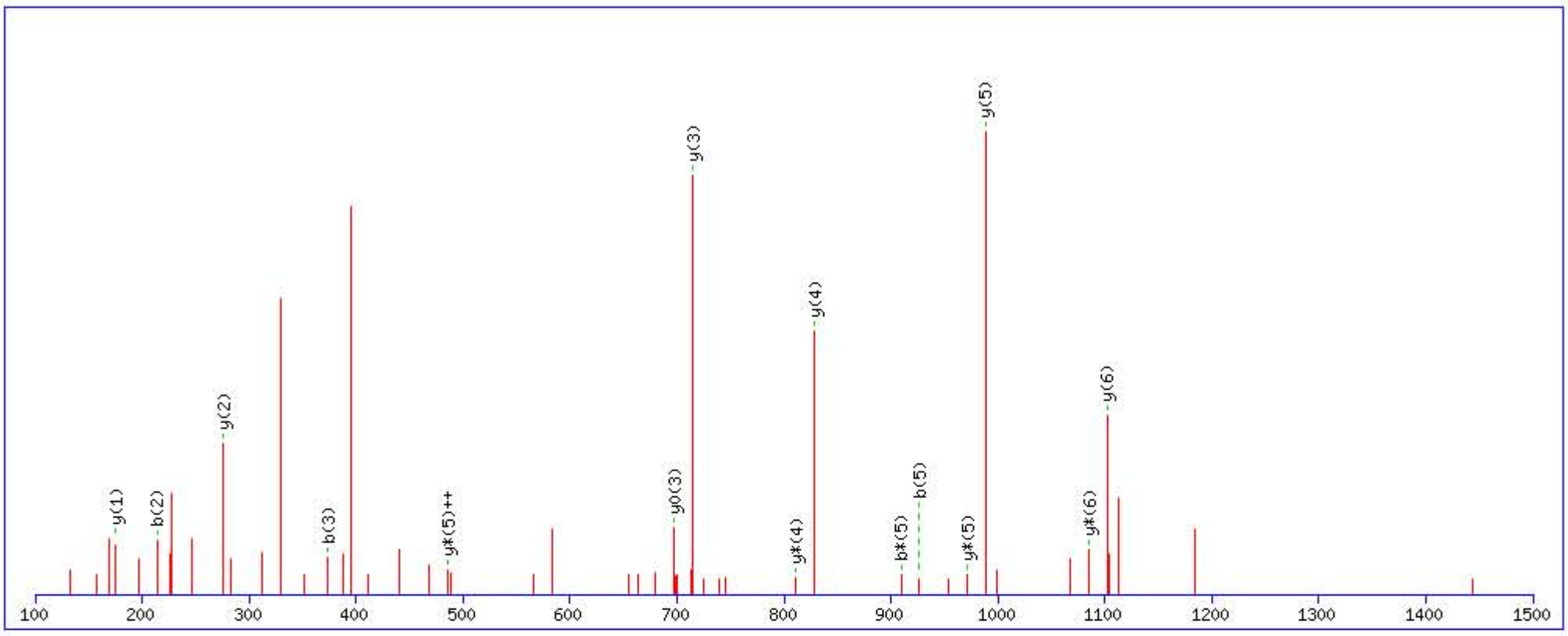
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VNCLQTR**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

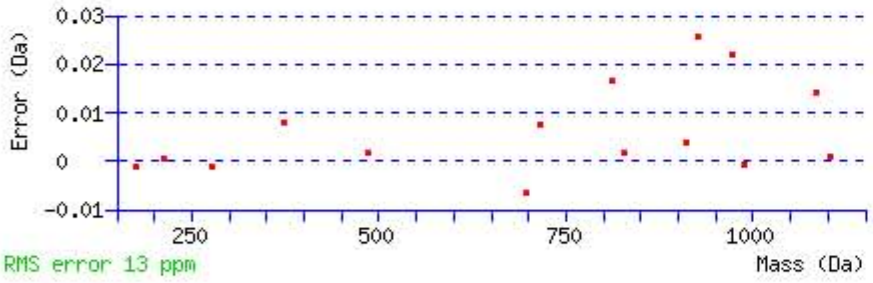
Match to Query 20555: 1200.607868 from(601.311210,2+) rtinseconds(1572) index(3135)
Title: Locus:1.1.1.1824.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

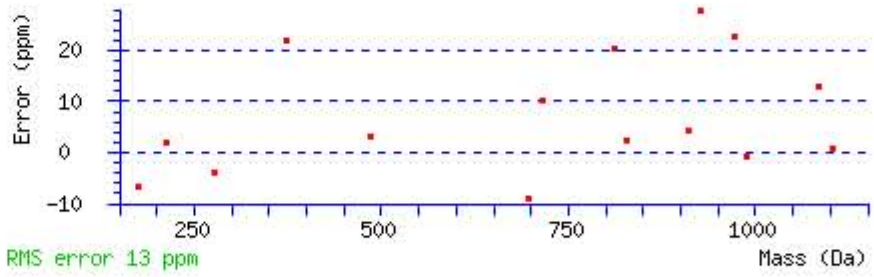
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1200.610733
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 29 **Expect:** 0.0026
**Matches :** 15/58 fragment ions using 38 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 7 |
| 2 | **214.118617** | 107.562947 | 197.092068 | 99.049672 | | | N | *1102.549597* | 551.778437 | 1085.523048 | 543.265162 | 1084.539032 | 542.773154 | 6 |
| 3 | **374.149266** | 187.578271 | 357.122717 | 179.064997 | | | C | *988.506670* | 494.756973 | 971.480121 | 486.243698 | 970.496105 | 485.751691 | 5 |
| 4 | 487.233330 | 244.120303 | 470.206781 | 235.607029 | | | L | *828.476021* | 414.741649 | 811.449472 | 406.228374 | 810.465456 | 405.736366 | 4 |
| 5 | **926.458656** | 463.732966 | 909.432107 | 455.219692 | | | Q | *715.391957* | 358.199617 | 698.365408 | 349.686342 | 697.381392 | 349.194334 | 3 |
| 6 | 1027.506335 | 514.256806 | 1010.479786 | 505.743531 | 1009.495770 | 505.251523 | T | *276.166631* | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 7 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 28.9 | 1200.610733 | -0.002865 | VNCLQTR |
| 1.3 | 1200.617233 | -0.009365 | VMEETPNILR |
| 1.2 | 1200.603333 | 0.004535 | VMSKSGHSNVR |

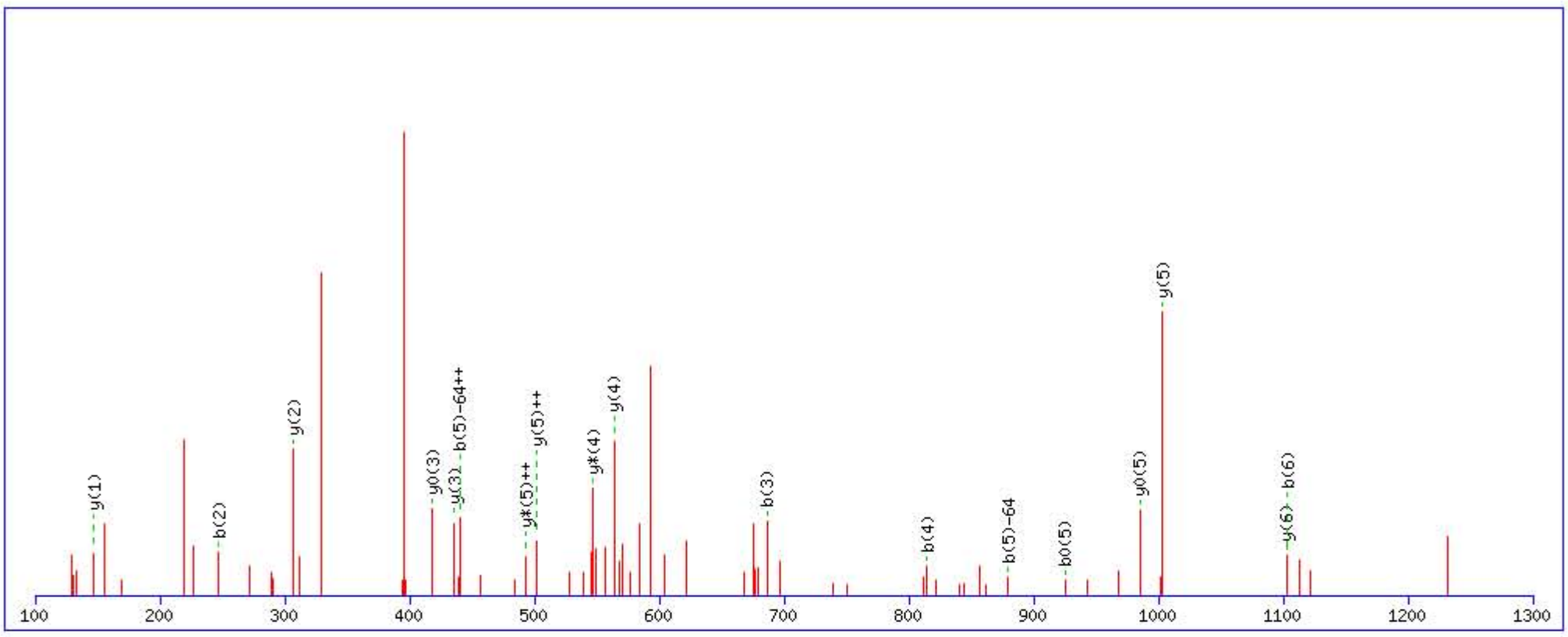
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MVQQECK**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

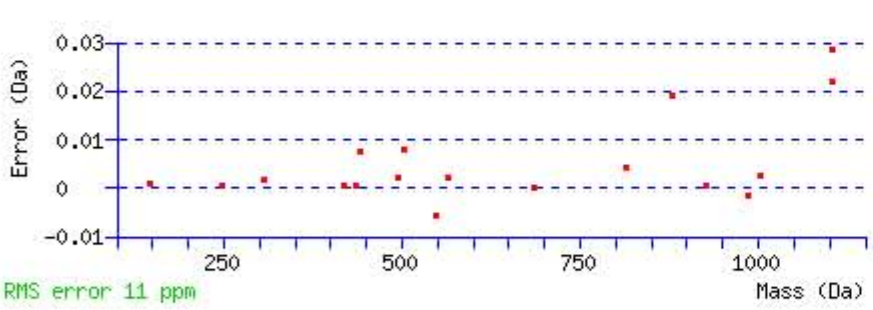
Match to Query 21830: 1248.566888 from(625.290720,2+) rtinseconds(1165) index(789)
Title: Locus:1.1.1.1682.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

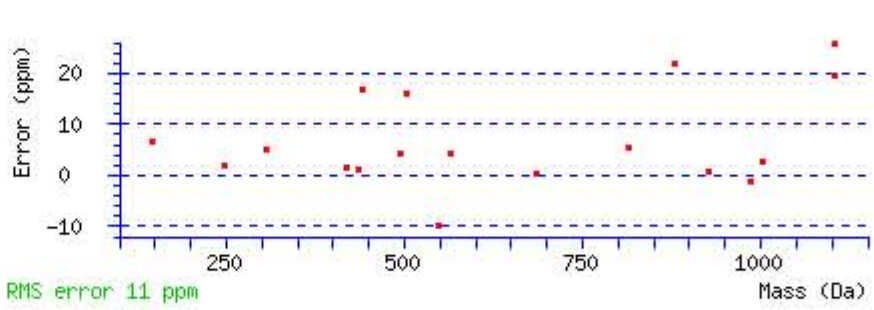
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1248.566483
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**M1** : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
**Q3** : Biotin:Thermo-21345 (Q)
**Ions Score:** 26 **Expect:** 0.025
**Matches** : 18/80 fragment ions using 41 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.042676 | 74.524976 | | | | | M | | | | | | | 7 |
| 2 | **247.111090** | 124.059183 | | | | | V | ***1102.538364*** | 551.772820 | 1085.511815 | 543.259546 | 1084.527799 | 542.767538 | 6 |
| 3 | **686.336416** | 343.671846 | 669.309867 | 335.158572 | | | Q | ***1003.469950*** | 502.238613 | 986.443401 | 493.725339 | 985.459385 | 493.233331 | 5 |
| 4 | **814.394994** | 407.701135 | 797.368445 | 399.187861 | | | Q | ***564.244624*** | 282.625950 | 547.218075 | 274.112676 | 546.234059 | 273.620668 | 4 |
| 5 | 943.437587 | 472.222432 | 926.411038 | 463.709157 | 925.427022 | 463.217149 | E | ***436.186046*** | 218.596661 | 419.159497 | 210.083387 | 418.175481 | 209.591379 | 3 |
| 6 | **1103.468236** | 552.237756 | 1086.441687 | 543.724482 | 1085.457671 | 543.232474 | C | ***307.143453*** | 154.075365 | 290.116904 | 145.562090 | | | 2 |
| 7 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.6 | 1248.566483 | 0.000405 | MVQQECK |
| 15.7 | 1248.566483 | 0.000405 | MVQQECK |

**Mascot:** http://www.matrixscience.com/

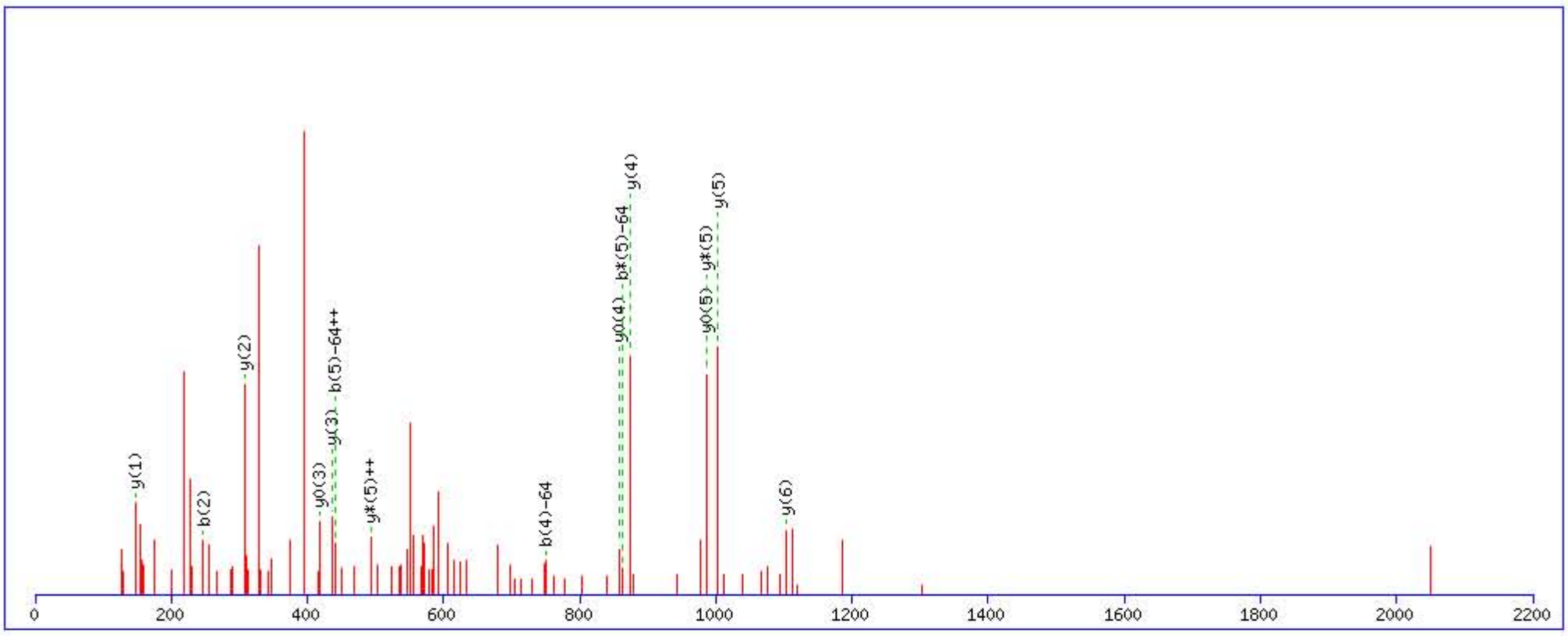
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MVQQECK**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

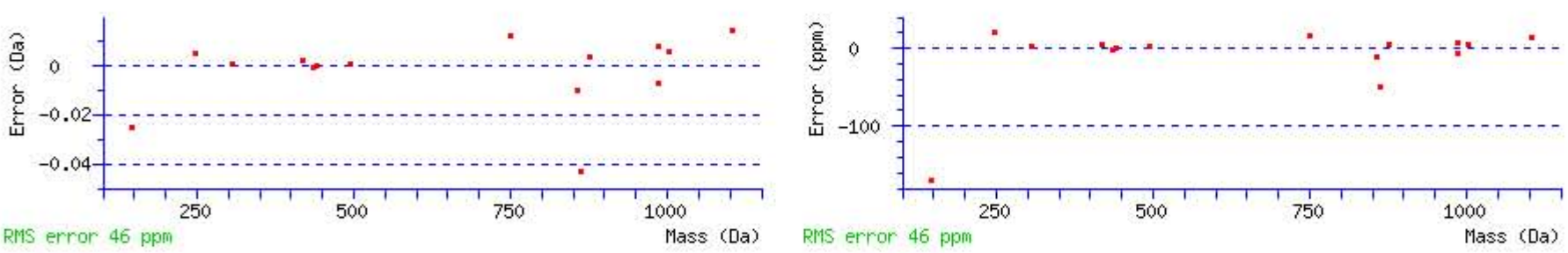
Match to Query 21834: 1248.570908 from(625.292730,2+) rtinseconds(1232) index(980)
Title: Locus:1.1.1.1705.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1248.566483
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**M1** : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
**Q4** : Biotin:Thermo-21345 (Q)
**Ions Score:** 27 **Expect:** 0.0076
**Matches :** 15/80 fragment ions using 31 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 84.044391 | 42.525833 | | | | | M | | | | | | | 7 |
| 2 | 183.112805 | 92.060040 | | | | | V | *1102.538364* | 551.772820 | 1085.511815 | 543.259546 | 1084.527799 | 542.767538 | 6 |
| 3 | 311.171383 | 156.089329 | 294.144834 | 147.576055 | | | Q | *1003.469950* | 502.238613 | 986.443401 | 493.725338 | 985.459385 | 493.233330 | 5 |
| 4 | 750.396709 | 375.701993 | 733.370160 | 367.188718 | | | Q | *875.411372* | 438.209324 | 858.384823 | 429.696050 | 857.400807 | 429.204042 | 4 |
| 5 | 879.439302 | 440.223289 | 862.412753 | 431.710015 | 861.428737 | 431.218007 | E | *436.186046* | 218.596661 | 419.159497 | 210.083386 | 418.175481 | 209.591378 | 3 |
| 6 | 1039.469951 | 520.238614 | 1022.443402 | 511.725339 | 1021.459386 | 511.233331 | C | *307.143453* | 154.075364 | 290.116904 | 145.562090 | | | 2 |
| 7 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 26.8 | 1248.566483 | 0.004425 | MVQQECK |
| 16.0 | 1248.566483 | 0.004425 | MVQQECK |
| 4.0 | 1248.576813 | -0.005905 | KCESLEQEAR |
| 3.5 | 1248.588089 | -0.017181 | MVDVGGQRSER |
| 2.8 | 1248.584244 | -0.013336 | MHSMISSVDVK |
| 1.5 | 1248.580872 | -0.009964 | AQMTTYYTVR |

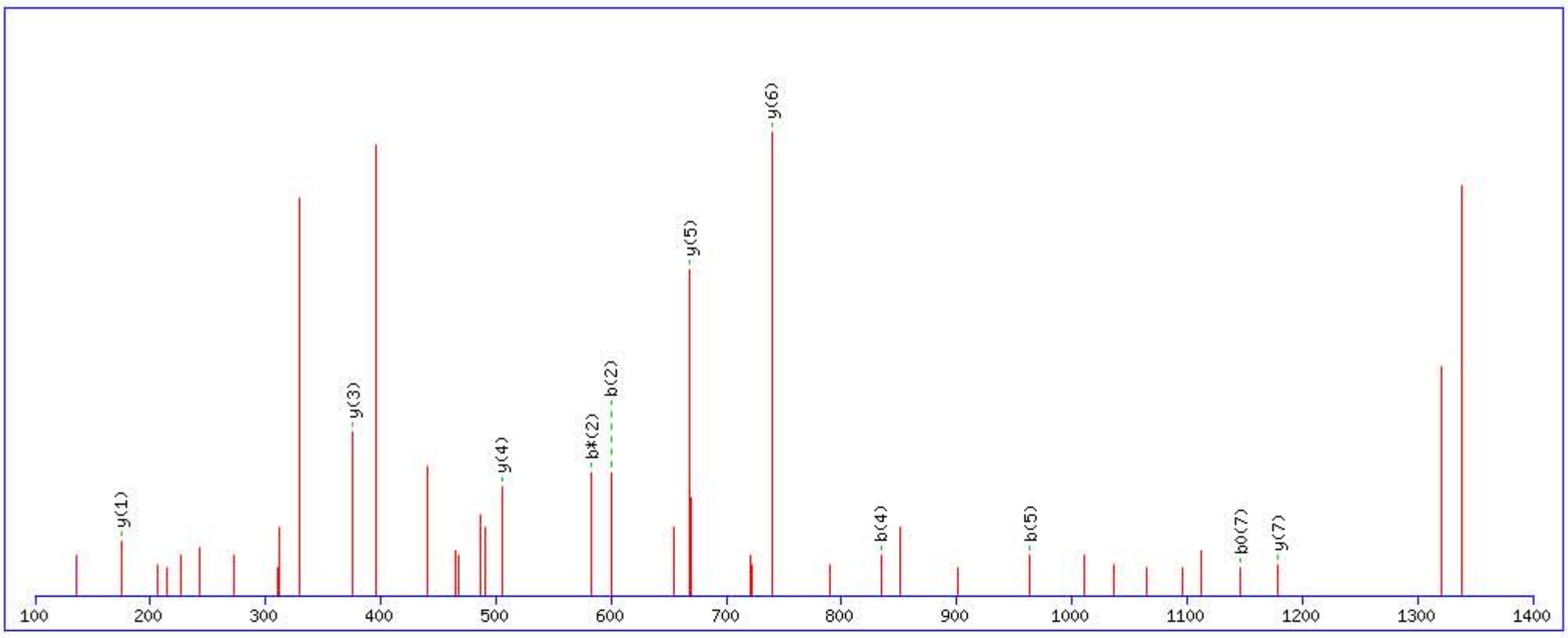
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **CQAYESNR**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

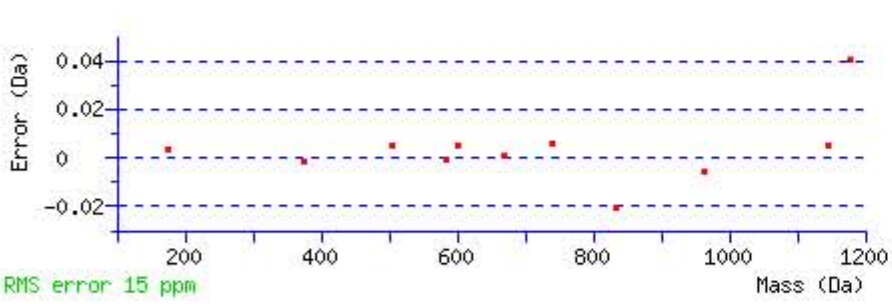
Match to Query 24052: 1337.588488 from(669.801520,2+) rtinseconds(1369) index(1736)
Title: Locus:1.1.1.1753.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

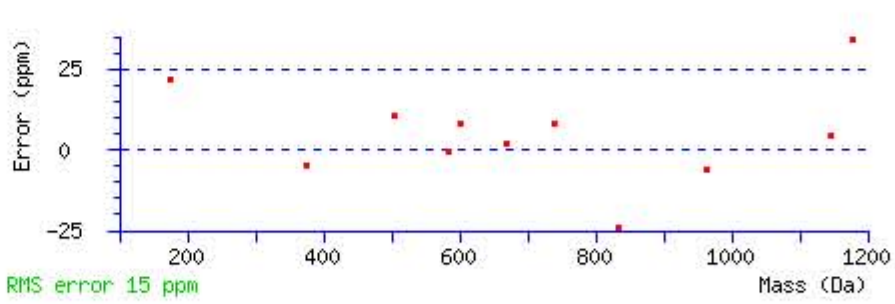
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1337.585617
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.0032
**Matches :** 11/70 fragment ions using 23 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 161.037925 | 81.022600 | | | | | C | | | | | | | 8 |
| 2 | **600.263251** | 300.635264 | 583.236702 | 292.121989 | | | Q | *1178.562269* | 589.784773 | 1161.535720 | 581.271498 | 1160.551704 | 580.779490 | 7 |
| 3 | 671.300365 | 336.153821 | 654.273816 | 327.640546 | | | A | *739.336943* | 370.172110 | 722.310394 | 361.658835 | 721.326378 | 361.166827 | 6 |
| 4 | **834.363694** | 417.685485 | 817.337145 | 409.172211 | | | Y | *668.299829* | 334.653553 | 651.273280 | 326.140278 | 650.289264 | 325.648270 | 5 |
| 5 | **963.406287** | 482.206782 | 946.379738 | 473.693507 | 945.395722 | 473.201499 | E | *505.236500* | 253.121888 | 488.209951 | 244.608613 | 487.225935 | 244.116605 | 4 |
| 6 | 1050.438315 | 525.722796 | 1033.411766 | 517.209521 | 1032.427750 | 516.717513 | S | *376.193907* | 188.600591 | 359.167358 | 180.087317 | 358.183342 | 179.595309 | 3 |
| 7 | 1164.481242 | 582.744259 | 1147.454693 | 574.230985 | 1146.470677 | 573.738977 | N | 289.161879 | 145.084577 | 272.135330 | 136.571303 | | | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 32.2 | 1337.585617 | 0.002871 | CQAYESNR |
| 15.5 | 1337.596848 | -0.008360 | CYEMASHLRR |

**Mascot:** http://www.matrixscience.com/

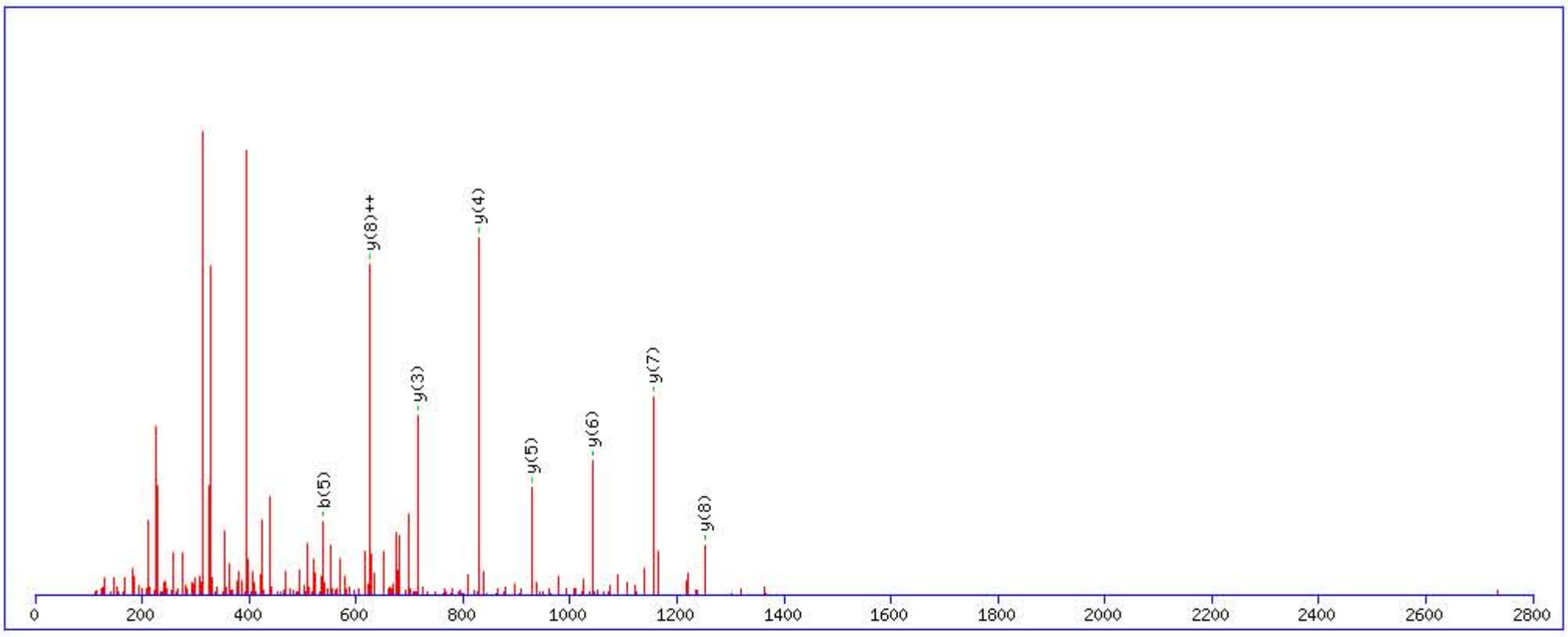
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LPNNVLQEK**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

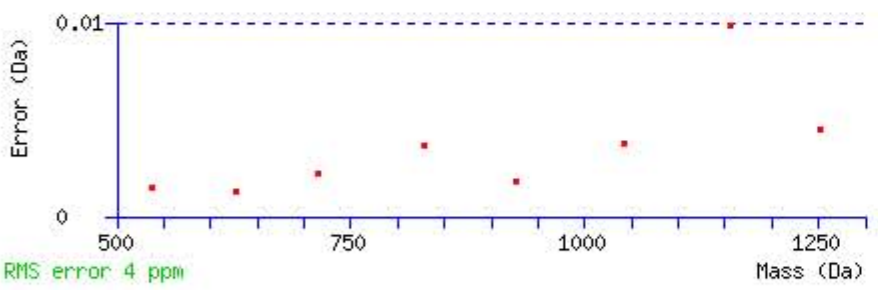
Match to Query 26083: 1364.759868 from(683.387210,2+) rtinseconds(1849) index(4571)
Title: Locus:1.1.1.1921.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

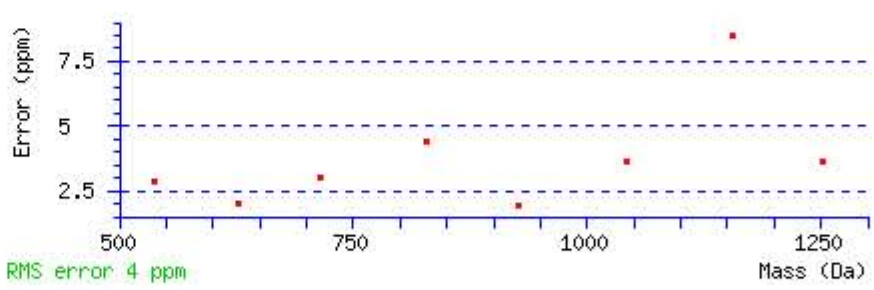
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1364.748581
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.0014
**Matches :** 8/76 fragment ions using 13 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 9 |
| 2 | 211.144104 | 106.075690 | | | | | P | *1252.671819* | 626.839548 | 1235.645270 | 618.326273 | 1234.661254 | 617.834265 | 8 |
| 3 | 325.187031 | 163.097153 | 308.160482 | 154.583879 | | | N | *1155.619055* | 578.313166 | 1138.592506 | 569.799891 | 1137.608490 | 569.307883 | 7 |
| 4 | 439.229958 | 220.118617 | 422.203409 | 211.605343 | | | N | *1041.576128* | 521.291702 | 1024.549579 | 512.778428 | 1023.565563 | 512.286420 | 6 |
| 5 | 538.298372 | 269.652824 | 521.271823 | 261.139550 | | | V | *927.533201* | 464.270239 | 910.506652 | 455.756964 | 909.522636 | 455.264956 | 5 |
| 6 | 651.382436 | 326.194856 | 634.355887 | 317.681582 | | | L | *828.464787* | 414.736032 | 811.438238 | 406.222757 | 810.454222 | 405.730749 | 4 |
| 7 | 1090.607762 | 545.807519 | 1073.581213 | 537.294245 | | | Q | *715.380723* | 358.194000 | 698.354174 | 349.680725 | 697.370158 | 349.188717 | 3 |
| 8 | 1219.650355 | 610.328816 | 1202.623806 | 601.815541 | 1201.639790 | 601.323533 | E | 276.155397 | 138.581336 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 9 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 37.9 | 1364.748581 | 0.011287 | LPNNVLQEK |
| 7.0 | 1364.759827 | 0.000041 | QTSSLIIHR |
| 5.9 | 1364.745239 | 0.014629 | KVVSWIDVYTR |
| 2.4 | 1364.752609 | 0.007259 | ILPIMFPSLYR |
| 1.7 | 1364.752609 | 0.007259 | KQFLDYLK |
| 1.0 | 1364.777573 | -0.017705 | LNSSPRAPVSPLK |

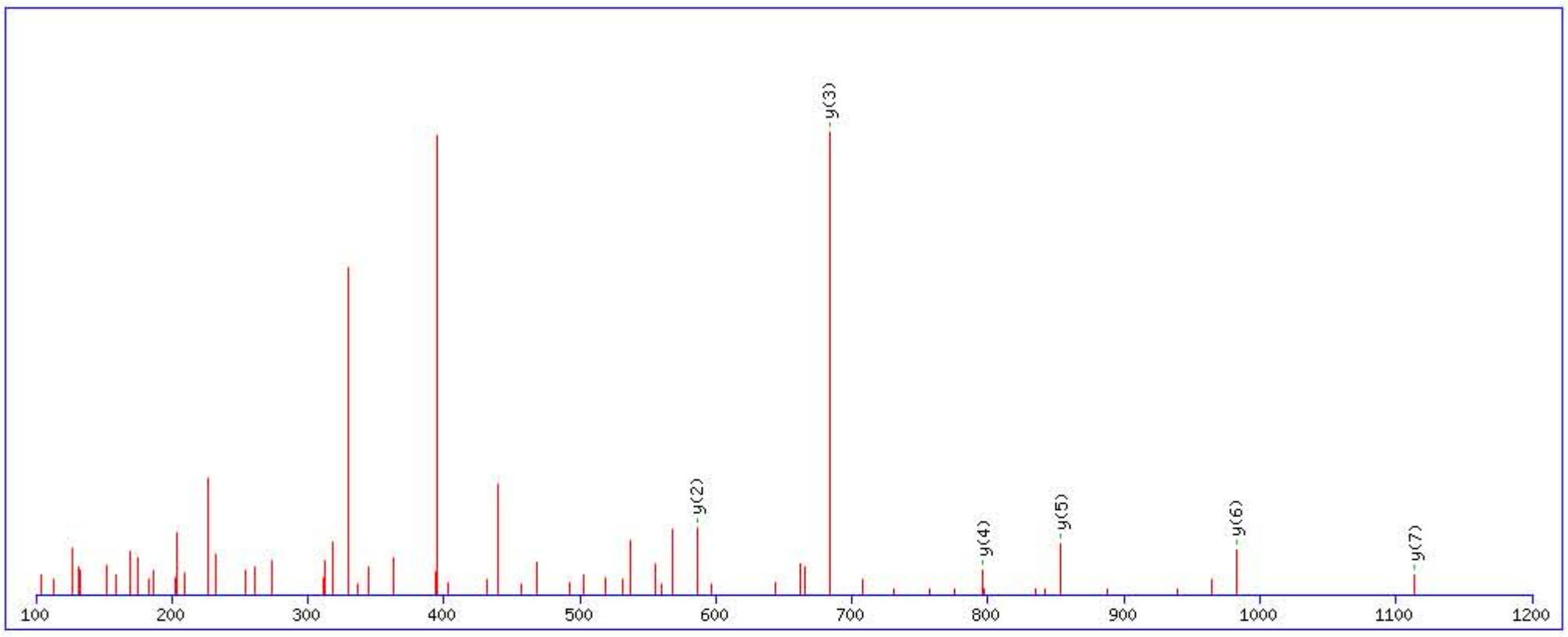
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ICAMEGLPQK**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

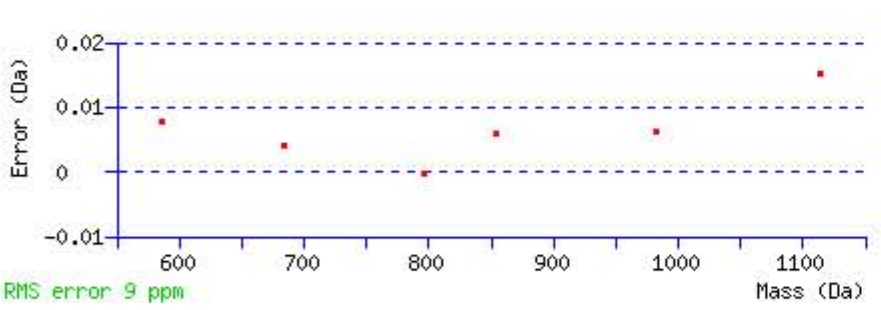
Match to Query 29841: 1456.722612 from(486.581480,3+) rtinseconds(1950) index(5381)
Title: Locus:1.1.1.1956.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

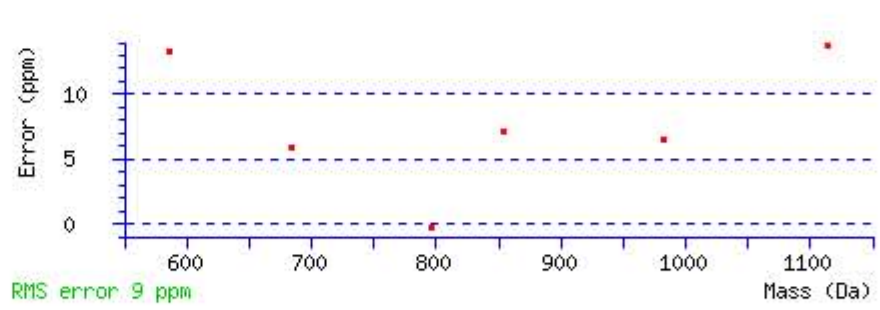
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1456.724030
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.00093
**Matches :** 6/74 fragment ions using 10 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 10 |
| 2 | 274.121989 | 137.564632 | | | | | C | 1344.647263 | 672.827270 | 1327.620714 | 664.313995 | 1326.636698 | 663.821987 | 9 |
| 3 | 345.159103 | 173.083190 | | | | | A | 1184.616614 | 592.811945 | 1167.590065 | 584.298671 | 1166.606049 | 583.806663 | 8 |
| 4 | 476.199588 | 238.603432 | | | | | M | *1113.579500* | 557.293388 | 1096.552951 | 548.780114 | 1095.568935 | 548.288106 | 7 |
| 5 | 605.242181 | 303.124729 | | | 587.231616 | 294.119446 | E | *982.539015* | 491.773146 | 965.512466 | 483.259871 | 964.528450 | 482.767863 | 6 |
| 6 | 662.263645 | 331.635461 | | | 644.253080 | 322.630178 | G | *853.496422* | 427.251849 | 836.469873 | 418.738575 | | | 5 |
| 7 | 775.347709 | 388.177493 | | | 757.337144 | 379.172210 | L | *796.474958* | 398.741117 | 779.448409 | 390.227843 | | | 4 |
| 8 | 872.400473 | 436.703875 | | | 854.389908 | 427.698592 | P | *683.390894* | 342.199085 | 666.364345 | 333.685811 | | | 3 |
| 9 | 1311.625799 | 656.316538 | 1294.599250 | 647.803263 | 1293.615234 | 647.311255 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 10 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.0 | 1456.724030 | -0.001418 | ICAMEGLPQK |
| 5.3 | 1456.734390 | -0.011778 | QDQISASELR |
| 3.2 | 1456.740921 | -0.018309 | ATVPAGEGVSLEEAK |
| 0.5 | 1456.723145 | -0.000533 | QQTLEAEEAK |

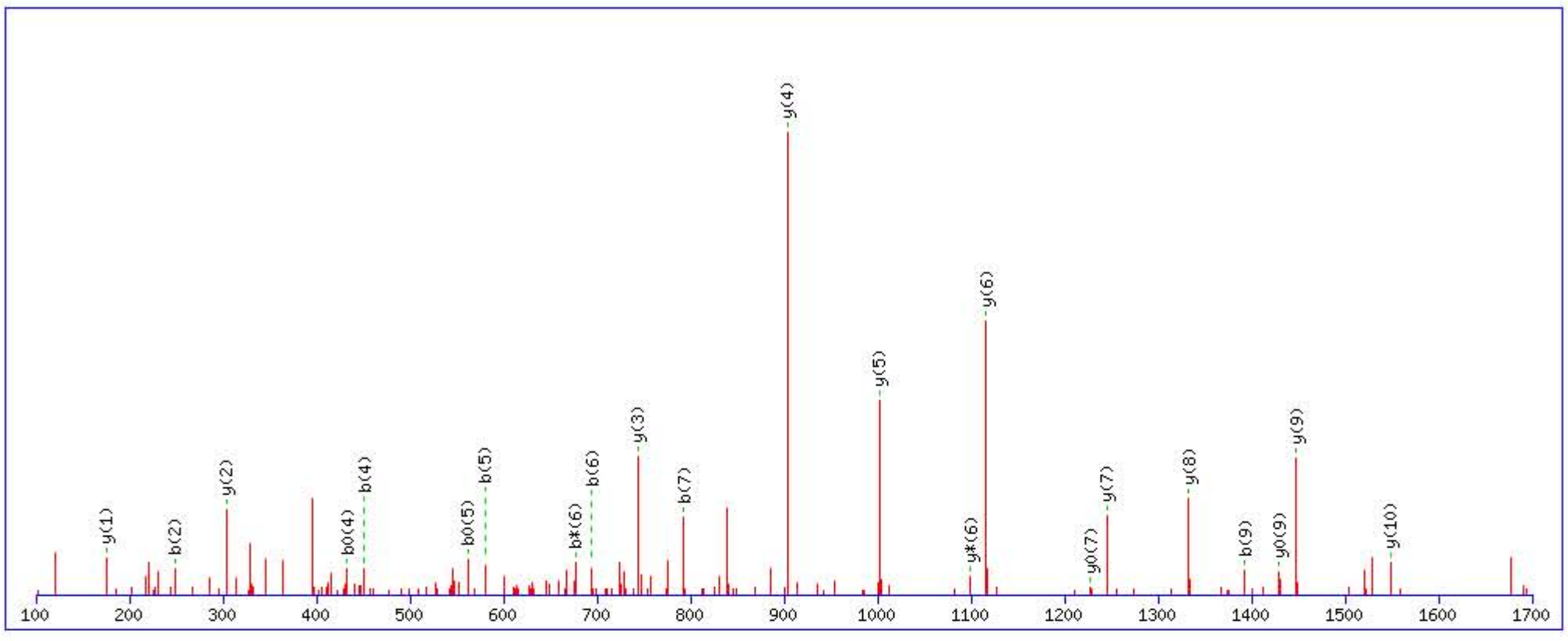
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FTDSENVCQER**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

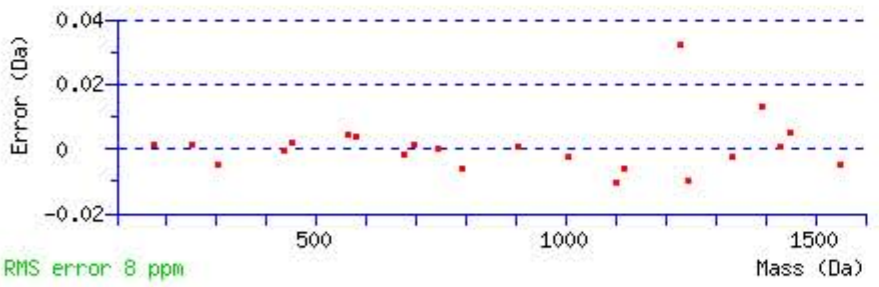
Match to Query 37825: 1694.745788 from(848.380170,2+) rtinseconds(1553) index(2986)
Title: Locus:1.1.1.1817.21 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

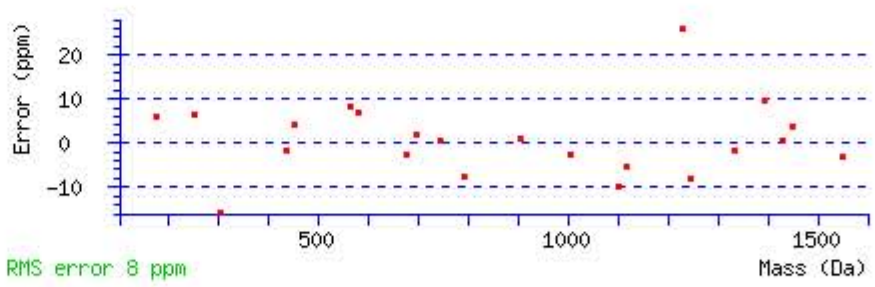
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1694.739243
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 83 **Expect:** 2.6e-008
**Matches :** 22/106 fragment ions using 32 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 11 |
| 2 | **249.123369** | 125.065322 | | | 231.112804 | 116.060040 | T | *1548.678104* | 774.842690 | 1531.651555 | 766.329416 | 1530.667539 | 765.837408 | 10 |
| 3 | 364.150312 | 182.578794 | | | 346.139747 | 173.573512 | D | *1447.630425* | 724.318851 | 1430.603876 | 715.805576 | 1429.619860 | 715.313568 | 9 |
| 4 | **451.182340** | 226.094808 | | | 433.171775 | 217.089526 | S | *1332.603482* | 666.805379 | 1315.576933 | 658.292105 | 1314.592917 | 657.800097 | 8 |
| 5 | **580.224933** | 290.616105 | | | 562.214368 | 281.610822 | E | *1245.571454* | 623.289365 | 1228.544905 | 614.776091 | 1227.560889 | 614.284083 | 7 |
| 6 | **694.267860** | 347.637568 | 677.241311 | 339.124294 | 676.257295 | 338.632286 | N | *1116.528861* | 558.768069 | 1099.502312 | 550.254794 | 1098.518296 | 549.762786 | 6 |
| 7 | **793.336274** | 397.171775 | 776.309725 | 388.658501 | 775.325709 | 388.166493 | V | *1002.485934* | 501.746605 | 985.459385 | 493.233331 | 984.475369 | 492.741323 | 5 |
| 8 | 953.366923 | 477.187100 | 936.340374 | 468.673825 | 935.356358 | 468.181817 | C | *903.417520* | 452.212398 | 886.390971 | 443.699124 | 885.406955 | 443.207116 | 4 |
| 9 | **1392.592249** | 696.799763 | 1375.565700 | 688.286488 | 1374.581684 | 687.794480 | Q | *743.386871* | 372.197074 | 726.360322 | 363.683799 | 725.376306 | 363.191791 | 3 |
| 10 | 1521.634842 | 761.321059 | 1504.608293 | 752.807785 | 1503.624277 | 752.315777 | E | *304.161545* | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 83.1 | 1694.739243 | 0.006545 | FTDSENVCQER |
| 9.5 | 1694.768219 | -0.022431 | EQSVDCRAGLEFER |

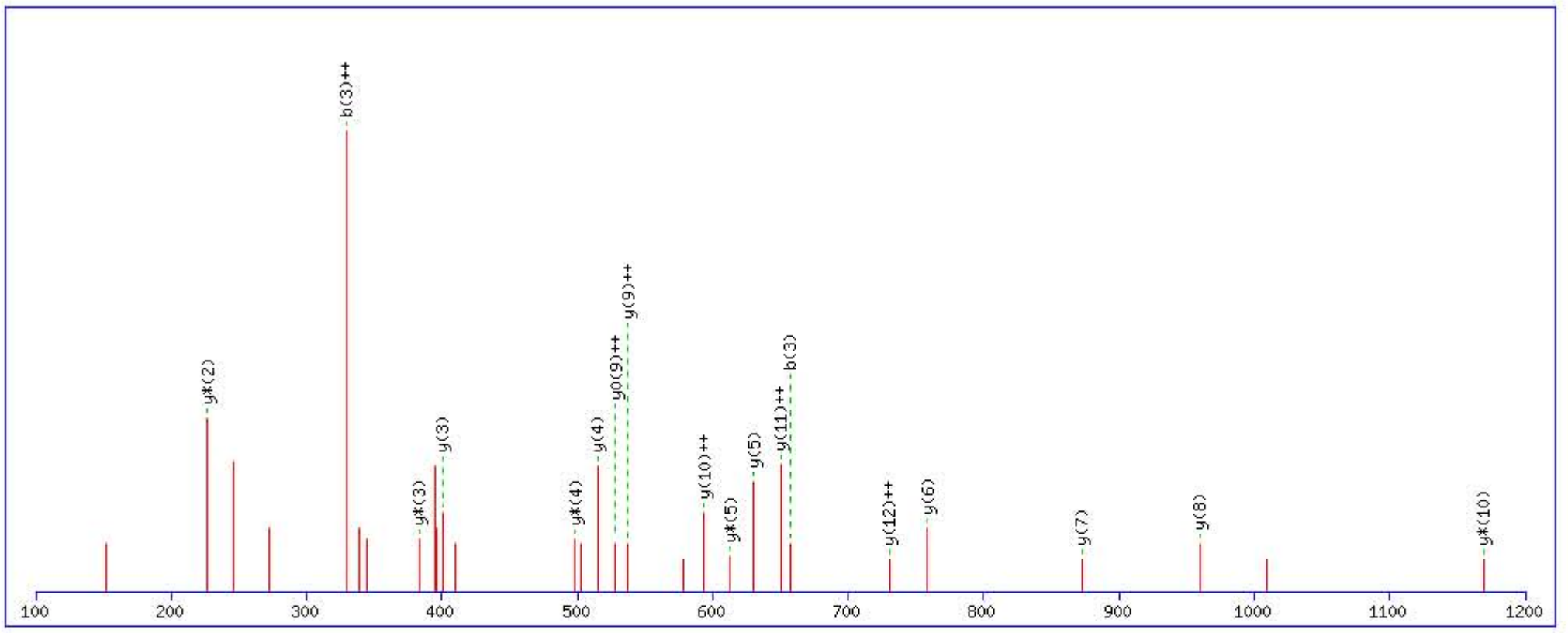
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GQCIINSNKDDRPK**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

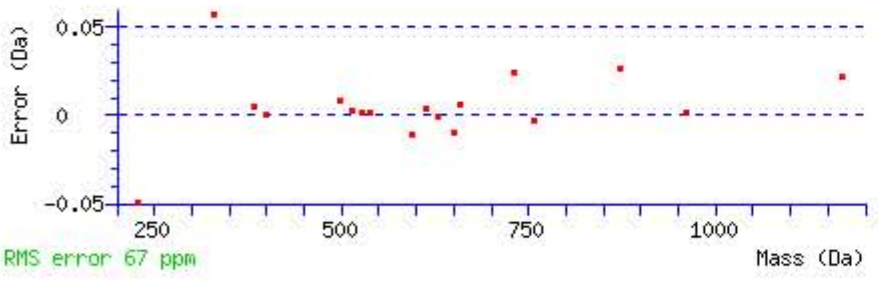
Match to Query 43201: 1954.970056 from(489.749790,4+) rtinseconds(1389) index(1888)
Title: Locus:1.1.1.1760.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

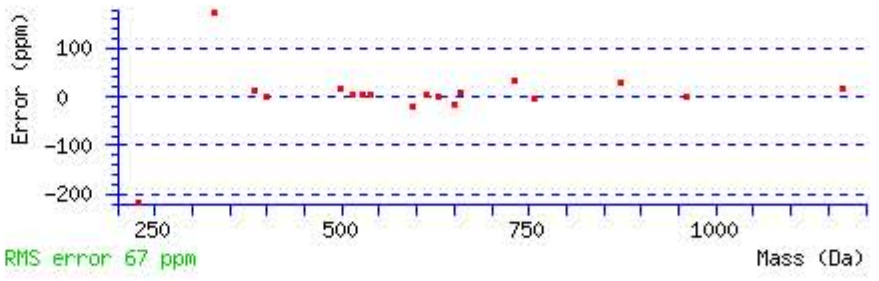
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1954.971680
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.00035
**Matches :** 18/136 fragment ions using 29 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 14 |
| 2 | 497.254066 | 249.130671 | 480.227517 | 240.617397 | | | Q | 1898.957513 | 949.982395 | 1881.930964 | 941.469120 | 1880.946948 | 940.977112 | 13 |
| 3 | 657.284715 | 329.145996 | 640.258166 | 320.632721 | | | C | 1459.732187 | 730.369732 | 1442.705638 | 721.856457 | 1441.721622 | 721.364449 | 12 |
| 4 | 770.368779 | 385.688028 | 753.342230 | 377.174753 | | | I | 1299.701538 | 650.354407 | 1282.674989 | 641.841133 | 1281.690973 | 641.349125 | 11 |
| 5 | 883.452843 | 442.230060 | 866.426294 | 433.716785 | | | I | 1186.617474 | 593.812375 | 1169.590925 | 585.299101 | 1168.606909 | 584.807093 | 10 |
| 6 | 997.495770 | 499.251523 | 980.469221 | 490.738249 | | | N | 1073.533410 | 537.270343 | 1056.506861 | 528.757069 | 1055.522845 | 528.265061 | 9 |
| 7 | 1084.527798 | 542.767537 | 1067.501249 | 534.254263 | 1066.517233 | 533.762255 | S | *959.490483* | 480.248880 | 942.463934 | 471.735605 | 941.479918 | 471.243597 | 8 |
| 8 | 1198.570725 | 599.789001 | 1181.544176 | 591.275726 | 1180.560160 | 590.783718 | N | *872.458455* | 436.732866 | 855.431906 | 428.219591 | 854.447890 | 427.727583 | 7 |
| 9 | 1326.665688 | 663.836482 | 1309.639139 | 655.323208 | 1308.655123 | 654.831200 | K | *758.415528* | 379.711402 | 741.388979 | 371.198128 | 740.404963 | 370.706120 | 6 |
| 10 | 1441.692631 | 721.349954 | 1424.666082 | 712.836679 | 1423.682066 | 712.344671 | D | *630.320565* | 315.663921 | 613.294016 | 307.150646 | 612.310000 | 306.658638 | 5 |
| 11 | 1556.719574 | 778.863425 | 1539.693025 | 770.350151 | 1538.709009 | 769.858143 | D | *515.293622* | 258.150449 | 498.267073 | 249.637175 | 497.283057 | 249.145167 | 4 |
| 12 | 1712.820685 | 856.913981 | 1695.794136 | 848.400706 | 1694.810120 | 847.908698 | R | *400.266679* | 200.636977 | 383.240130 | 192.123703 | | | 3 |
| 13 | 1809.873449 | 905.440363 | 1792.846900 | 896.927088 | 1791.862884 | 896.435080 | P | 244.165568 | 122.586422 | 227.139019 | 114.073148 | | | 2 |
| 14 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.0 | 1954.971680 | -0.001624 | GQCIINSNKDDRPK |
| 1.2 | 1954.964981 | 0.005075 | STAIRQTFFPGGDQFQR |
| 1.0 | 1954.975708 | -0.005652 | IVLLMAYSGKGYHGMQR |

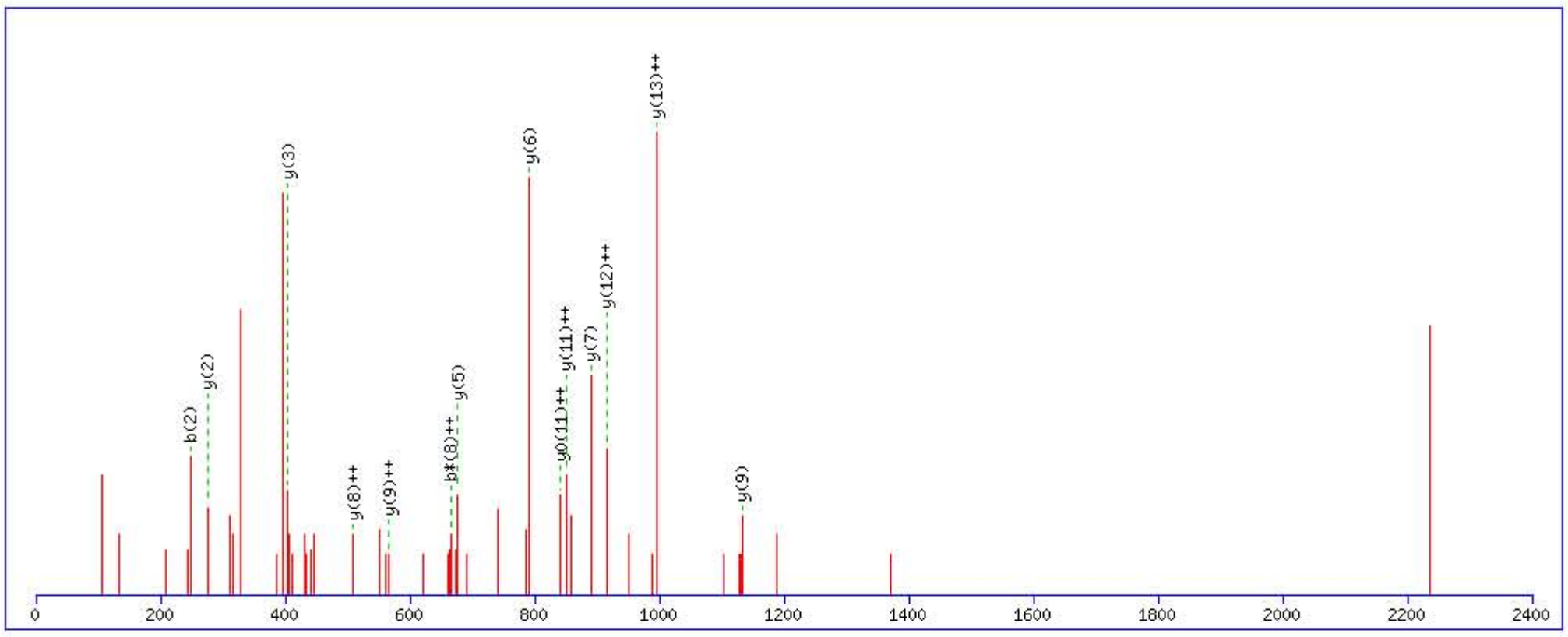
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SCCEEQNKVNCLQTR**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

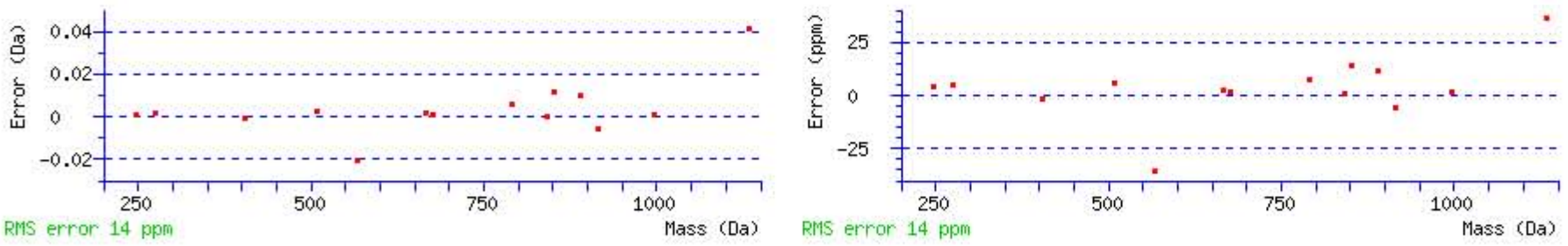
Match to Query 49225: 2235.984432 from(746.335420,3+) rtinseconds(1438) index(2243)
Title: Locus:1.1.1.1777.24 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2235.985703
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q6** : Biotin:Thermo-21345 (Q)
**Ions Score:** 26 **Expect:** 0.013
**Matches** : 14/156 fragment ions using 32 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 15 |
| 2 | 248.069953 | 124.538614 | | | 230.059388 | 115.533332 | C | 2149.960963 | 1075.484119 | 2132.934414 | 1066.970845 | 2131.950398 | 1066.478837 | 14 |
| 3 | 408.100602 | 204.553939 | | | 390.090037 | 195.548657 | C | 1989.930314 | 995.468795 | 1972.903765 | 986.955521 | 1971.919749 | 986.463512 | 13 |
| 4 | 537.143195 | 269.075236 | | | 519.132630 | 260.069953 | E | 1829.899665 | 915.453470 | 1812.873116 | 906.940196 | 1811.889100 | 906.448188 | 12 |
| 5 | 666.185788 | 333.596532 | | | 648.175223 | 324.591250 | E | 1700.857072 | 850.932174 | 1683.830523 | 842.418899 | 1682.846507 | 841.926891 | 11 |
| 6 | 1105.411114 | 553.209195 | 1088.384565 | 544.695921 | 1087.400549 | 544.203913 | Q | 1571.814479 | 786.410877 | 1554.787930 | 777.897603 | 1553.803914 | 777.405595 | 10 |
| 7 | 1219.454041 | 610.230659 | 1202.427492 | 601.717384 | 1201.443476 | 601.225376 | N | *1132.589153* | 566.798214 | 1115.562604 | 558.284940 | 1114.578588 | 557.792932 | 9 |
| 8 | 1347.549004 | 674.278140 | 1330.522455 | 665.764866 | 1329.538439 | 665.272858 | K | 1018.546226 | 509.776751 | 1001.519677 | 501.263476 | 1000.535661 | 500.771468 | 8 |
| 9 | 1446.617418 | 723.812347 | 1429.590869 | 715.299073 | 1428.606853 | 714.807065 | V | *890.451263* | 445.729269 | 873.424714 | 437.215995 | 872.440698 | 436.723987 | 7 |
| 10 | 1560.660345 | 780.833811 | 1543.633796 | 772.320536 | 1542.649780 | 771.828528 | N | *791.382849* | 396.195062 | 774.356300 | 387.681788 | 773.372284 | 387.189780 | 6 |
| 11 | 1720.690994 | 860.849135 | 1703.664445 | 852.335861 | 1702.680429 | 851.843853 | C | *677.339922* | 339.173599 | 660.313373 | 330.660324 | 659.329357 | 330.168316 | 5 |
| 12 | 1833.775058 | 917.391167 | 1816.748509 | 908.877893 | 1815.764493 | 908.385885 | L | 517.309273 | 259.158274 | 500.282724 | 250.645000 | 499.298708 | 250.152992 | 4 |
| 13 | 1961.833636 | 981.420456 | 1944.807087 | 972.907182 | 1943.823071 | 972.415174 | Q | *404.225209* | 202.616242 | 387.198660 | 194.102968 | 386.214644 | 193.610960 | 3 |
| 14 | 2062.881315 | 1031.944295 | 2045.854766 | 1023.431021 | 2044.870750 | 1022.939013 | T | *276.166631* | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 15 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 26.1 | 2235.985703 | -0.001271 | SCCEEQNKVNCLQTR |
| 0.1 | 2235.985703 | -0.001271 | SCCEEQNKVNCLQTR |

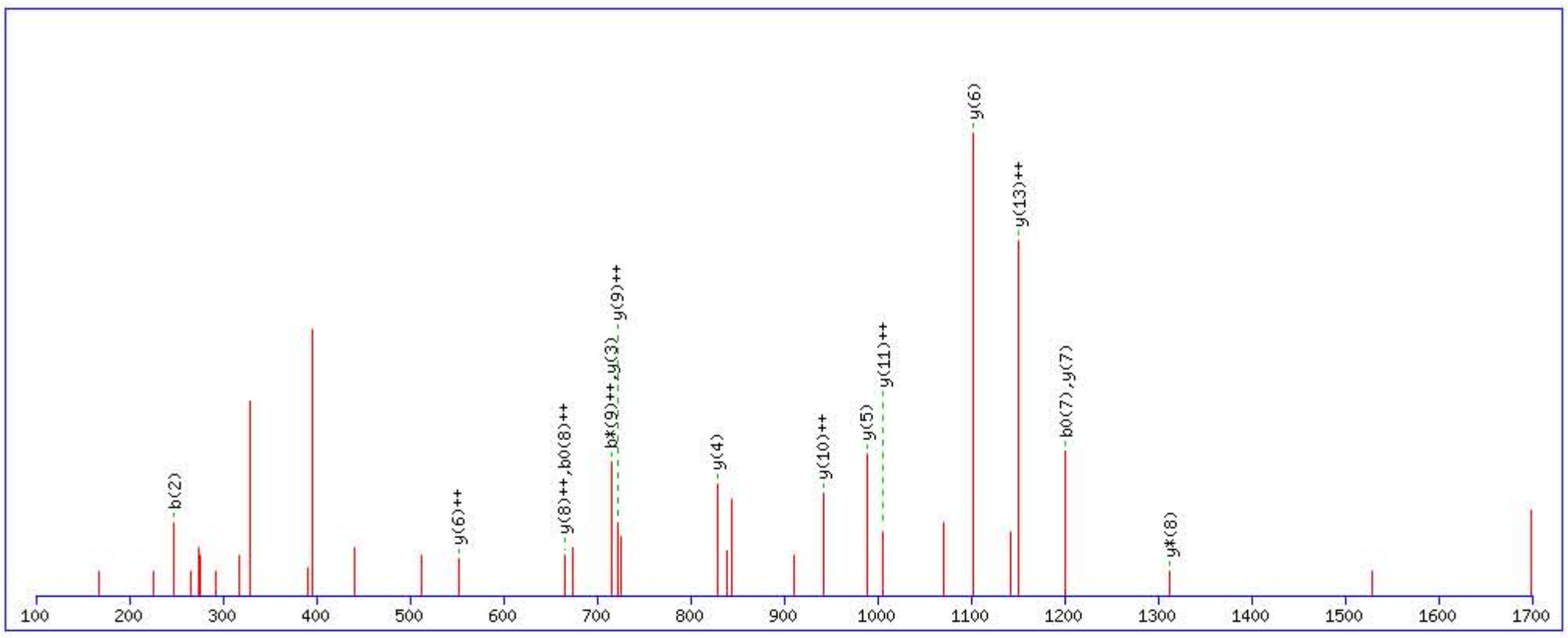
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SCCEEQNKVNCLQTR**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

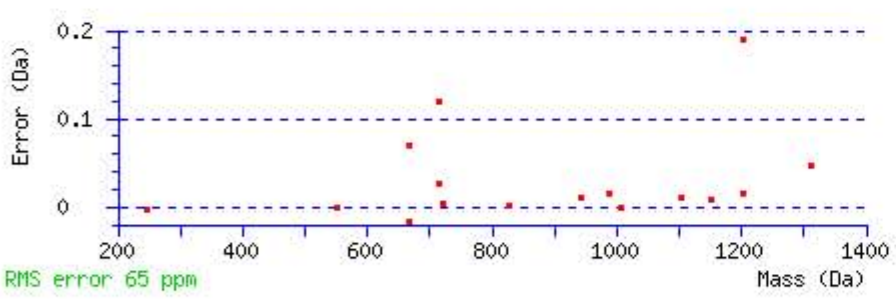
Match to Query 54981: 2547.172122 from(850.064650,3+) rtinseconds(1764) index(4184)
Title: Locus:1.1.1.1891.22 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

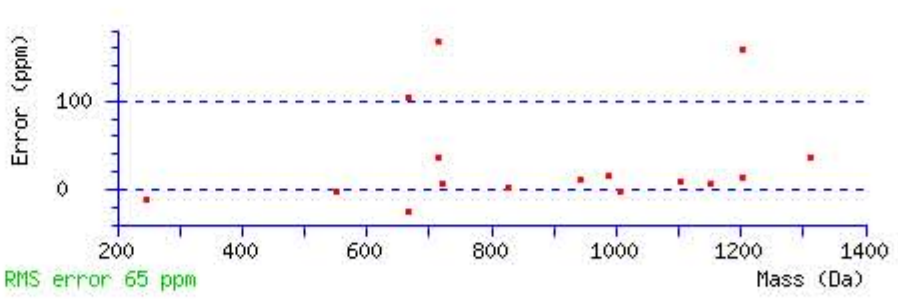
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2547.152451
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 36 **Expect:** 0.00084
**Matches :** 16/156 fragment ions using 23 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 15 |
| 2 | 248.069953 | 124.538614 | | | 230.059388 | 115.533332 | C | 2461.127711 | 1231.067493 | 2444.101162 | 1222.554219 | 2443.117146 | 1222.062211 | 14 |
| 3 | 408.100602 | 204.553939 | | | 390.090037 | 195.548657 | C | 2301.097062 | 1151.052169 | 2284.070513 | 1142.538894 | 2283.086497 | 1142.046886 | 13 |
| 4 | 537.143195 | 269.075236 | | | 519.132630 | 260.069953 | E | 2141.066413 | 1071.036844 | 2124.039864 | 1062.523570 | 2123.055848 | 1062.031562 | 12 |
| 5 | 666.185788 | 333.596532 | | | 648.175223 | 324.591250 | E | 2012.023820 | 1006.515548 | 1994.997271 | 998.002274 | 1994.013255 | 997.510265 | 11 |
| 6 | 1105.411114 | 553.209195 | 1088.384565 | 544.695921 | 1087.400549 | 544.203913 | Q | 1882.981227 | 941.994252 | 1865.954678 | 933.480977 | 1864.970662 | 932.988969 | 10 |
| 7 | 1219.454041 | 610.230659 | 1202.427492 | 601.717384 | 1201.443476 | 601.225376 | N | 1443.755901 | 722.381588 | 1426.729352 | 713.868314 | 1425.745336 | 713.376306 | 9 |
| 8 | 1347.549004 | 674.278140 | 1330.522455 | 665.764866 | 1329.538439 | 665.272858 | K | 1329.712974 | 665.360125 | 1312.686425 | 656.846850 | 1311.702409 | 656.354842 | 8 |
| 9 | 1446.617418 | 723.812347 | 1429.590869 | 715.299073 | 1428.606853 | 714.807065 | V | *1201.618011* | 601.312643 | 1184.591462 | 592.799369 | 1183.607446 | 592.307361 | 7 |
| 10 | 1560.660345 | 780.833811 | 1543.633796 | 772.320536 | 1542.649780 | 771.828528 | N | *1102.549597* | 551.778436 | 1085.523048 | 543.265162 | 1084.539032 | 542.773154 | 6 |
| 11 | 1720.690994 | 860.849135 | 1703.664445 | 852.335861 | 1702.680429 | 851.843853 | C | *988.506670* | 494.756973 | 971.480121 | 486.243698 | 970.496105 | 485.751690 | 5 |
| 12 | 1833.775058 | 917.391167 | 1816.748509 | 908.877893 | 1815.764493 | 908.385885 | L | *828.476021* | 414.741648 | 811.449472 | 406.228374 | 810.465456 | 405.736366 | 4 |
| 13 | 2273.000384 | 1137.003830 | 2255.973835 | 1128.490555 | 2254.989819 | 1127.998547 | Q | *715.391957* | 358.199616 | 698.365408 | 349.686342 | 697.381392 | 349.194334 | 3 |
| 14 | 2374.048063 | 1187.527669 | 2357.021514 | 1179.014395 | 2356.037498 | 1178.522387 | T | 276.166631 | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 15 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 36.4 | 2547.152451 | 0.019671 | SCCEEQNKVNCLQTR |
| 3.5 | 2547.197632 | -0.025510 | LNQLESSLWEEASDEGTLGGSPTK |
| 2.0 | 2547.201859 | -0.029737 | ASKYSGSQMEILANQLTGLMDMK |
| 2.0 | 2547.201859 | -0.029737 | ASKYSGSQMEILANQLTGLMDMK |

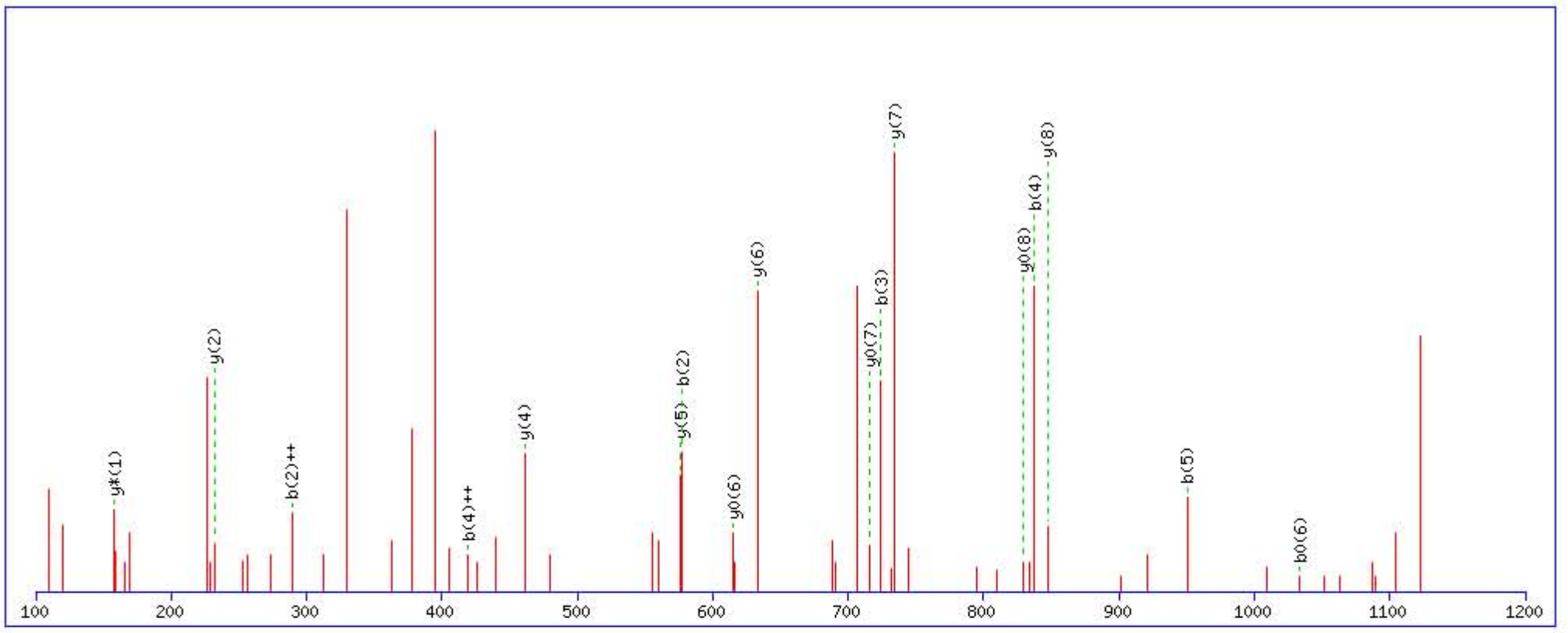
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HQFLLTGDTQGR**
Found in **A1BG_HUMAN**, Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4

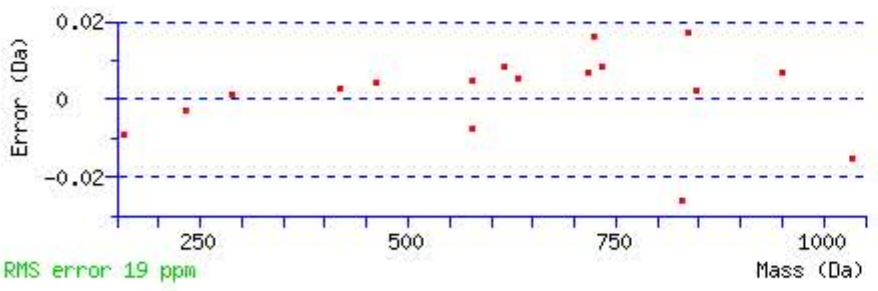
Match to Query 37601: 1682.860002 from(561.960610,3+) rtinseconds(1936) index(5255)
Title: Locus:1.1.1.1951.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

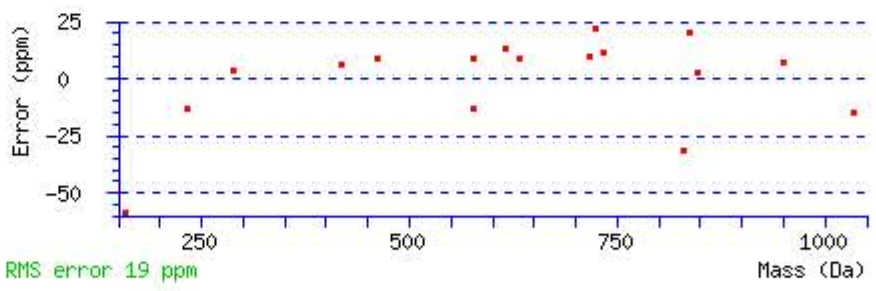
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1682.856277
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 30 **Expect:** 0.0018
**Matches :** 17/114 fragment ions using 31 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 12 |
| 2 | *577.291514* | **289.149395** | 560.264965 | 280.636121 | | | Q | 1546.804627 | 773.905951 | 1529.778078 | 765.392677 | 1528.794062 | 764.900669 | 11 |
| 3 | *724.359928* | 362.683602 | 707.333379 | 354.170327 | | | F | 1107.579301 | 554.293288 | 1090.552752 | 545.780014 | 1089.568736 | 545.288006 | 10 |
| 4 | *837.443992* | **419.225634** | 820.417443 | 410.712359 | | | L | 960.510887 | 480.759081 | 943.484338 | 472.245807 | 942.500322 | 471.753799 | 9 |
| 5 | *950.528056* | 475.767666 | 933.501507 | 467.254392 | | | L | *847.426823* | 424.217049 | 830.400274 | 415.703775 | 829.416258 | 415.211767 | 8 |
| 6 | 1051.575735 | 526.291505 | 1034.549186 | 517.778231 | 1033.565170 | 517.286223 | T | *734.342759* | 367.675017 | 717.316210 | 359.161743 | 716.332194 | 358.669735 | 7 |
| 7 | 1108.597199 | 554.802237 | 1091.570650 | 546.288963 | 1090.586634 | 545.796955 | G | *633.295080* | 317.151178 | 616.268531 | 308.637903 | 615.284515 | 308.145895 | 6 |
| 8 | 1223.624142 | 612.315709 | 1206.597593 | 603.802435 | 1205.613577 | 603.310426 | D | *576.273616* | 288.640446 | 559.247067 | 280.127171 | 558.263051 | 279.635163 | 5 |
| 9 | 1324.671821 | 662.839548 | 1307.645272 | 654.326274 | 1306.661256 | 653.834266 | T | *461.246673* | 231.126974 | 444.220124 | 222.613700 | 443.236108 | 222.121692 | 4 |
| 10 | 1452.730399 | 726.868837 | 1435.703850 | 718.355563 | 1434.719834 | 717.863555 | Q | 360.198994 | 180.603135 | 343.172445 | 172.089860 | | | 3 |
| 11 | 1509.751863 | 755.379569 | 1492.725314 | 746.866295 | 1491.741298 | 746.374287 | G | *232.140416* | 116.573846 | 215.113867 | 108.060571 | | | 2 |
| 12 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 29.9 | 1682.856277 | 0.003725 | HQFLLTGDTQGR |
| 0.6 | 1682.845032 | 0.014970 | QFHLTDDDLLR |

**Mascot:** http://www.matrixscience.com/

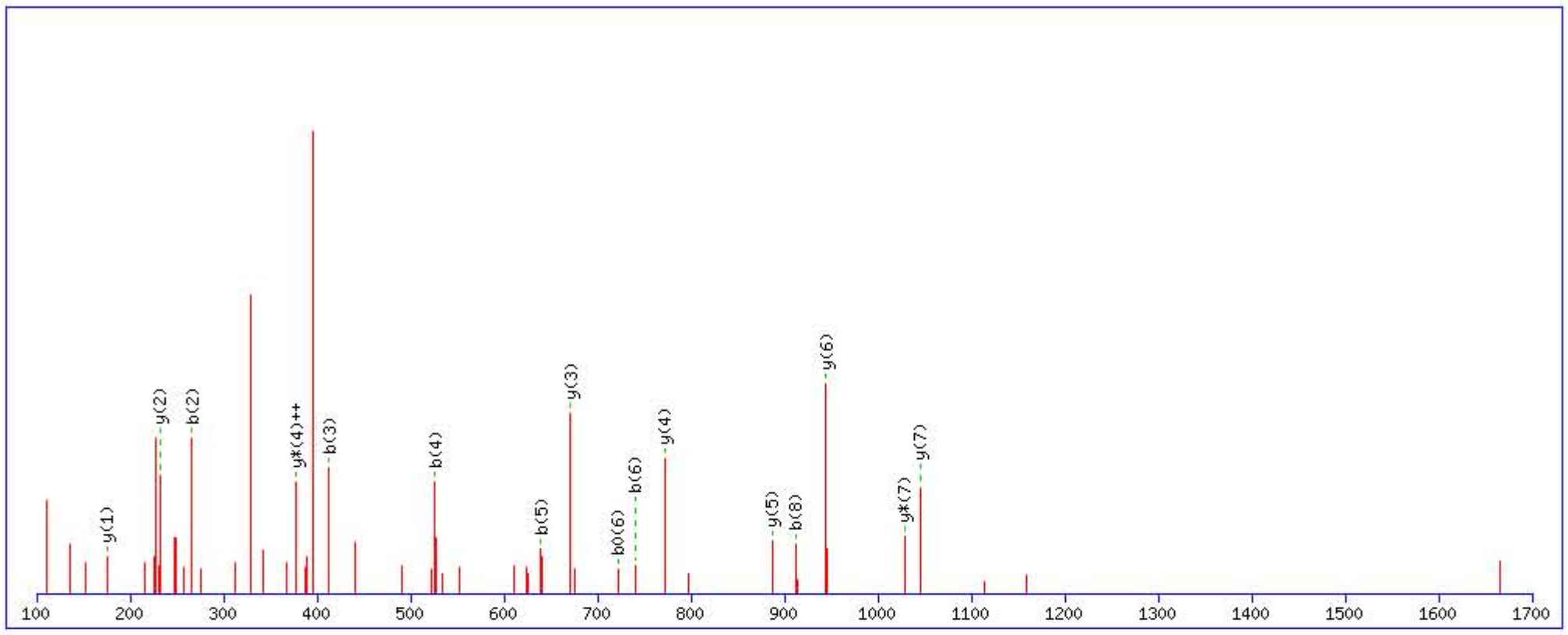
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HQFLLTGDTQGR**
Found in **A1BG_HUMAN**, Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4

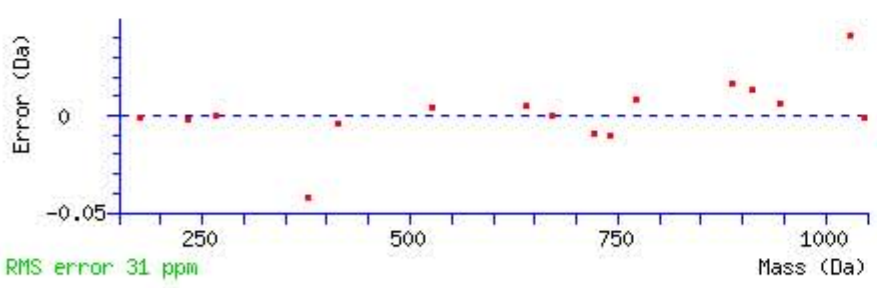
Match to Query 37605: 1682.863902 from(561.961910,3+) rtinseconds(1873) index(4722)
Title: Locus:1.1.1.1929.21 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

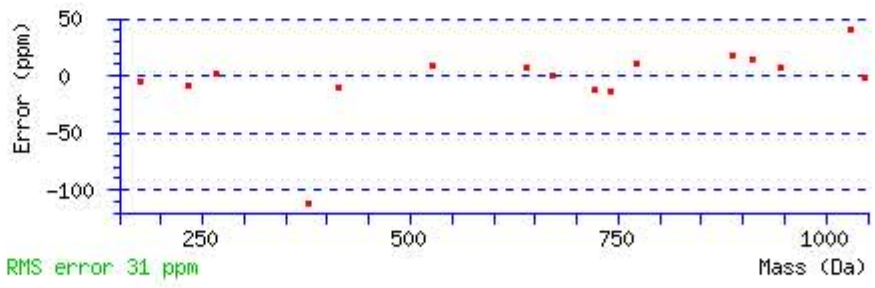
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1682.856277
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.00027
**Matches :** 16/114 fragment ions using 31 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 12 |
| 2 | *266.124766* | 133.566021 | 249.098217 | 125.052746 | | | Q | 1546.804627 | 773.905952 | 1529.778078 | 765.392677 | 1528.794062 | 764.900669 | 11 |
| 3 | *413.193180* | 207.100228 | 396.166631 | 198.586953 | | | F | 1418.746049 | 709.876663 | 1401.719500 | 701.363388 | 1400.735484 | 700.871380 | 10 |
| 4 | *526.277244* | 263.642260 | 509.250695 | 255.128986 | | | L | 1271.677635 | 636.342456 | 1254.651086 | 627.829181 | 1253.667070 | 627.337173 | 9 |
| 5 | *639.361308* | 320.184292 | 622.334759 | 311.671018 | | | L | 1158.593571 | 579.800424 | 1141.567022 | 571.287149 | 1140.583006 | 570.795141 | 8 |
| 6 | *740.408987* | 370.708132 | 723.382438 | 362.194857 | 722.398422 | 361.702849 | T | *1045.509507* | 523.258392 | 1028.482958 | 514.745117 | 1027.498942 | 514.253109 | 7 |
| 7 | 797.430451 | 399.218864 | 780.403902 | 390.705589 | 779.419886 | 390.213581 | G | *944.461828* | 472.734552 | 927.435279 | 464.221278 | 926.451263 | 463.729270 | 6 |
| 8 | *912.457394* | 456.732335 | 895.430845 | 448.219061 | 894.446829 | 447.727053 | D | *887.440364* | 444.223820 | 870.413815 | 435.710546 | 869.429799 | 435.218538 | 5 |
| 9 | 1013.505073 | 507.256175 | 996.478524 | 498.742900 | 995.494508 | 498.250892 | T | *772.413421* | 386.710349 | 755.386872 | 378.197074 | 754.402856 | 377.705066 | 4 |
| 10 | 1452.730399 | 726.868838 | 1435.703850 | 718.355563 | 1434.719834 | 717.863555 | Q | *671.365742* | 336.186509 | 654.339193 | 327.673235 | | | 3 |
| 11 | 1509.751863 | 755.379570 | 1492.725314 | 746.866295 | 1491.741298 | 746.374287 | G | *232.140416* | 116.573846 | 215.113867 | 108.060571 | | | 2 |
| 12 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.0 | 1682.856277 | 0.007625 | HQFLLTGDTQGR |
| 7.0 | 1682.856232 | 0.007670 | RWPLMIDPQSQANK |

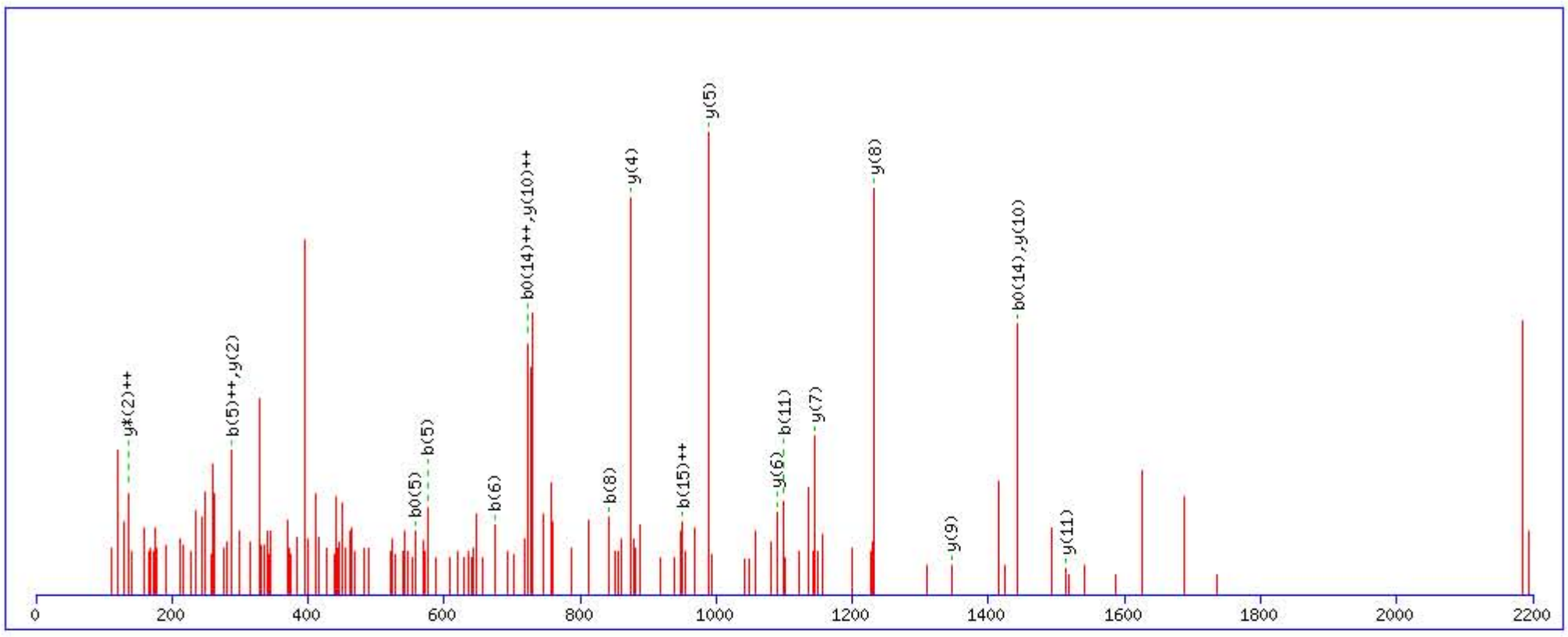
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VTLTCVAPLSGVDFQLR**
Found in **A1BG_HUMAN**, Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4

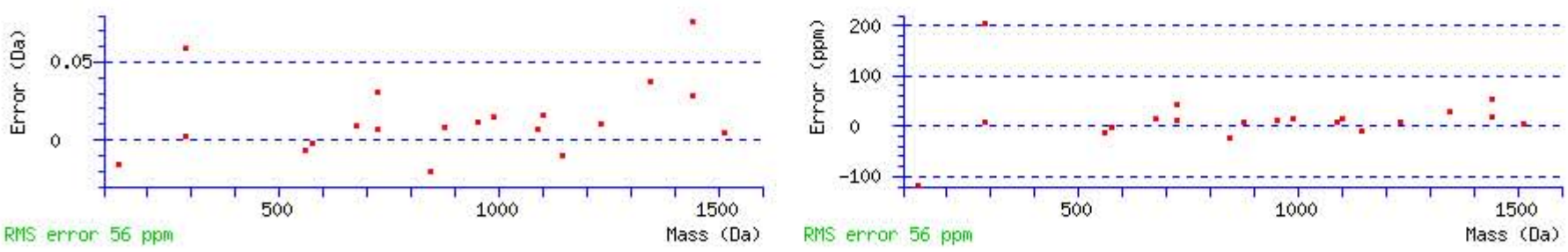
Match to Query 48242: 2186.172402 from(729.731410,3+) rtinseconds(2726) index(9492)
Title: Locus:1.1.1.2226.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2186.159195
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q15 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 8e-005
**Matches :** 20/154 fragment ions using 33 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 17 |
| 2 | 201.123369 | 101.065322 | | | 183.112804 | 92.060040 | T | 2088.098032 | 1044.552654 | 2071.071483 | 1036.039379 | 2070.087467 | 1035.547371 | 16 |
| 3 | 314.207433 | 157.607354 | | | 296.196868 | 148.602072 | L | 1987.050353 | 994.028815 | 1970.023804 | 985.515540 | 1969.039788 | 985.023532 | 15 |
| 4 | 415.255112 | 208.131194 | | | 397.244547 | 199.125912 | T | 1873.966289 | 937.486783 | 1856.939740 | 928.973508 | 1855.955724 | 928.481500 | 14 |
| 5 | **575.285761** | **288.146519** | | | 557.275196 | 279.141236 | C | 1772.918610 | 886.962943 | 1755.892061 | 878.449669 | 1754.908045 | 877.957661 | 13 |
| 6 | **674.354175** | 337.680726 | | | 656.343610 | 328.675443 | V | 1612.887961 | 806.947619 | 1595.861412 | 798.434344 | 1594.877396 | 797.942336 | 12 |
| 7 | 745.391289 | 373.199283 | | | 727.380724 | 364.194000 | A | *1513.819547* | 757.413412 | 1496.792998 | 748.900137 | 1495.808982 | 748.408129 | 11 |
| 8 | **842.444053** | 421.725665 | | | 824.433488 | 412.720382 | P | *1442.782433* | 721.894855 | 1425.755884 | 713.381580 | 1424.771868 | 712.889572 | 10 |
| 9 | 955.528117 | 478.267697 | | | 937.517552 | 469.262414 | L | *1345.729669* | 673.368473 | 1328.703120 | 664.855198 | 1327.719104 | 664.363190 | 9 |
| 10 | 1042.560145 | 521.783711 | | | 1024.549580 | 512.778428 | S | *1232.645605* | 616.826441 | 1215.619056 | 608.313166 | 1214.635040 | 607.821158 | 8 |
| 11 | **1099.581609** | 550.294443 | | | 1081.571044 | 541.289160 | G | *1145.613577* | 573.310427 | 1128.587028 | 564.797152 | 1127.603012 | 564.305144 | 7 |
| 12 | 1198.650023 | 599.828650 | | | 1180.639458 | 590.823367 | V | *1088.592113* | 544.799695 | 1071.565564 | 536.286420 | 1070.581548 | 535.794412 | 6 |
| 13 | 1313.676966 | 657.342121 | | | 1295.666401 | 648.336839 | D | *989.523699* | 495.265488 | 972.497150 | 486.752213 | 971.513134 | 486.260205 | 5 |
| 14 | 1460.745380 | 730.876328 | | | 1442.734815 | 721.871046 | F | *874.496756* | 437.752016 | 857.470207 | 429.238742 | | | 4 |
| 15 | 1899.970706 | **950.488991** | 1882.944157 | 941.975717 | 1881.960141 | 941.483709 | Q | 727.428342 | 364.217809 | 710.401793 | 355.704535 | | | 3 |
| 16 | 2013.054770 | 1007.031023 | 1996.028221 | 998.517749 | 1995.044205 | 998.025741 | L | *288.203016* | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 17 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.2 | 2186.159195 | 0.013207 | VTLTCVAPLSGVDFQLR |
| 1.5 | 2186.188126 | -0.015724 | KLTSHQMLSSTEILKWLR |

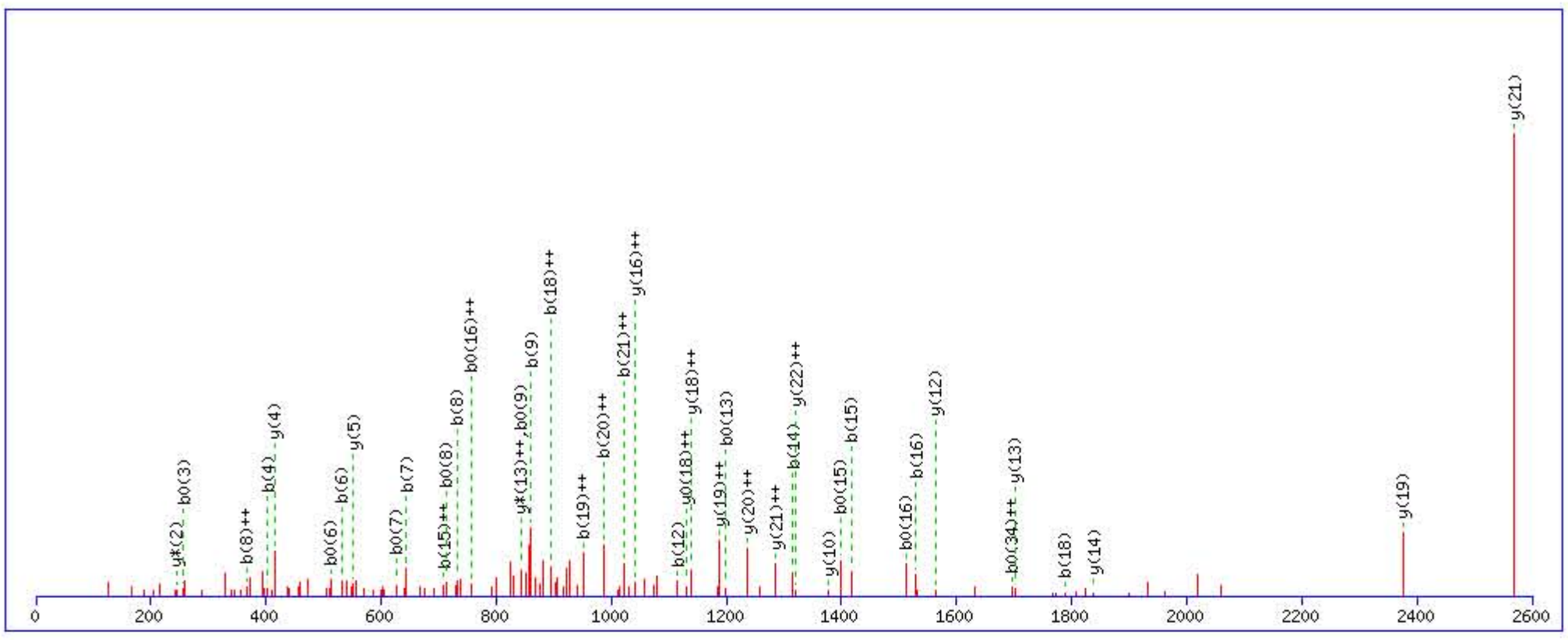
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TDGEGALSEPSATVTIEELAAPPPPVLMHHGESSQVLHPGNK**
Found in **A1BG_HUMAN**, Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4

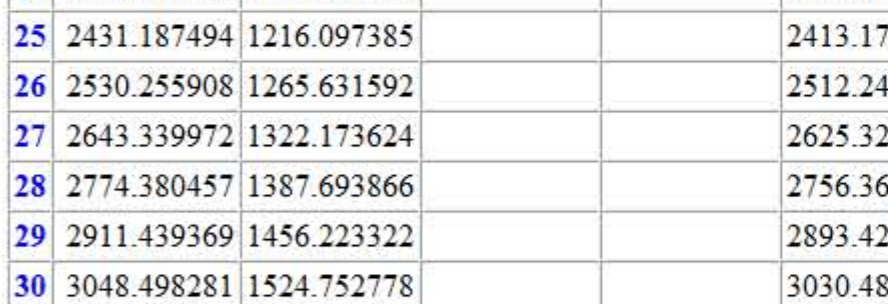
Match to Query 72695: 4610.335820 from(923.074440,5+) rtinseconds(2393) index(7810)
Title: Locus:1.1.1.2110.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 4610.278503
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q35 : Biotin:Thermo-21345 (Q)
**Ions Score:** 35 **Expect:** 0.006
**Matches :** 43/408 fragment ions using 103 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 42 |
| 2 | 217.081898 | 109.044587 | | | 199.071333 | 100.039304 | D | 4510.238114 | 2255.622695 | 4493.211565 | 2247.109421 | 4492.227549 | 2246.617413 | 41 |
| 3 | 274.103362 | 137.555319 | | | 256.092797 | 128.550037 | G | 4395.211171 | 2198.109224 | 4378.184622 | 2189.595949 | 4377.200606 | 2189.103941 | 40 |
| 4 | *403.145955* | 202.076616 | | | 385.135390 | 193.071333 | E | 4338.189707 | 2169.598492 | 4321.163158 | 2161.085217 | 4320.179142 | 2160.593209 | 39 |
| 5 | 460.167419 | 230.587347 | | | 442.156854 | 221.582065 | G | 4209.147114 | 2105.077195 | 4192.120565 | 2096.563921 | 4191.136549 | 2096.071913 | 38 |
| 6 | *531.204533* | 266.105905 | | | 513.193968 | 257.100622 | A | 4152.125650 | 2076.566463 | 4135.099101 | 2068.053189 | 4134.115085 | 2067.561181 | 37 |
| 7 | *644.288597* | 322.647937 | | | 626.278032 | 313.642654 | L | 4081.088536 | 2041.047906 | 4064.061987 | 2032.534632 | 4063.077971 | 2032.042624 | 36 |
| 8 | *731.320625* | **366.163951** | | | 713.310060 | 357.158668 | S | 3968.004472 | 1984.505874 | 3950.977923 | 1975.992600 | 3949.993907 | 1975.500592 | 35 |
| 9 | *860.363218* | 430.685247 | | | 842.352653 | 421.679965 | E | 3880.972444 | 1940.989860 | 3863.945895 | 1932.476586 | 3862.961879 | 1931.984578 | 34 |
| 10 | 957.415982 | 479.211629 | | | 939.405417 | 470.206347 | P | 3751.929851 | 1876.468564 | 3734.903302 | 1867.955289 | 3733.919286 | 1867.463281 | 33 |
| 11 | 1044.448010 | 522.727643 | | | 1026.437445 | 513.722361 | S | 3654.877087 | 1827.942182 | 3637.850538 | 1819.428907 | 3636.866522 | 1818.936899 | 32 |
| 12 | *1115.485124* | 558.246200 | | | 1097.474559 | 549.240918 | A | 3567.845059 | 1784.426168 | 3550.818510 | 1775.912893 | 3549.834494 | 1775.420885 | 31 |
| 13 | 1216.532803 | 608.770040 | | | 1198.522238 | 599.764757 | T | 3496.807945 | 1748.907611 | 3479.781396 | 1740.394336 | 3478.797380 | 1739.902328 | 30 |
| 14 | *1315.601217* | 658.304247 | | | 1297.590652 | 649.298964 | V | 3395.760266 | 1698.383771 | 3378.733717 | 1689.870497 | 3377.749701 | 1689.378489 | 29 |
| 15 | *1416.648896* | **708.828086** | | | 1398.638331 | 699.822804 | T | 3296.691852 | 1648.849564 | 3279.665303 | 1640.336290 | 3278.681287 | 1639.844282 | 28 |
| 16 | *1529.732960* | 765.370118 | | | 1511.722395 | 756.364836 | I | 3195.644173 | 1598.325725 | 3178.617624 | 1589.812450 | 3177.633608 | 1589.320442 | 27 |
| 17 | 1658.775553 | 829.891415 | | | 1640.764988 | 820.886132 | E | 3082.560109 | 1541.783693 | 3065.533560 | 1533.270418 | 3064.549544 | 1532.778410 | 26 |
| 18 | *1787.818146* | **894.412711** | | | 1769.807581 | 885.407429 | E | 2953.517516 | 1477.262396 | 2936.490967 | 1468.749122 | 2935.506951 | 1468.257114 | 25 |
| 19 | 1900.902210 | **950.954743** | | | 1882.891645 | 941.949461 | L | 2824.474923 | 1412.741100 | 2807.448374 | 1404.227825 | 2806.464358 | 1403.735817 | 24 |
| 20 | 1971.939324 | **986.473300** | | | 1953.928759 | 977.468018 | A | 2711.390859 | 1356.199068 | 2694.364310 | 1347.685793 | 2693.380294 | 1347.193785 | 23 |
| 21 | 2042.976438 | **1021.991857** | | | 2024.965873 | 1012.986575 | A | 2640.353745 | 1320.680511 | 2623.327196 | 1312.167236 | 2622.343180 | 1311.675228 | 22 |
| 22 | 2140.029202 | 1070.518239 | | | 2122.018637 | 1061.512956 | P | *2569.316631* | 1285.161954 | 2552.290082 | 1276.648679 | 2551.306066 | 1276.156671 | 21 |
| 23 | 2237.081966 | 1119.044621 | | | 2219.071401 | 1110.039338 | P | 2472.263867 | 1236.635572 | 2455.237318 | 1228.122297 | 2454.253302 | 1227.630289 | 20 |
| 24 | 2334.134730 | 1167.571003 | | | 2316.124165 | 1158.565720 | P | *2375.211103* | 1188.109190 | 2358.184554 | 1179.595915 | 2357.200538 | 1179.103907 | 19 |
| 25 | 2431.187494 | 1216.097385 | | | 2413.176929 | 1207.092102 | P | 2278.158339 | 1139.582808 | 2261.131790 | 1131.069533 | 2260.147774 | 1130.577525 | 18 |
| 26 | 2530.255908 | 1265.631592 | | | 2512.245343 | 1256.626309 | V | 2181.105575 | 1091.056426 | 2164.079026 | 1082.543151 | 2163.095010 | 1082.051143 | 17 |
| 27 | 2643.339972 | 1322.173624 | | | 2625.329407 | 1313.168341 | L | 2082.037161 | 1041.522219 | 2065.010612 | 1033.008944 | 2064.026596 | 1032.516936 | 16 |
| 28 | 2774.380457 | 1387.693866 | | | 2756.369892 | 1378.688584 | M | 1968.953097 | 984.980187 | 1951.926548 | 976.466912 | 1950.942532 | 975.974904 | 15 |
| 29 | 2911.439369 | 1456.223322 | | | 2893.428804 | 1447.218040 | H | *1837.912612* | 919.459944 | 1820.886063 | 910.946670 | 1819.902047 | 910.454662 | 14 |
| 30 | 3048.498281 | 1524.752778 | | | 3030.487716 | 1515.747496 | H | *1700.853700* | 850.930488 | 1683.827151 | 842.417214 | 1682.843135 | 841.925206 | 13 |
| 31 | 3105.519745 | 1553.263510 | | | 3087.509180 | 1544.258228 | G | *1563.794788* | 782.401032 | 1546.768239 | 773.887758 | 1545.784223 | 773.395750 | 12 |
| 32 | 3234.562338 | 1617.784807 | | | 3216.551773 | 1608.779524 | E | 1506.773324 | 753.890300 | 1489.746775 | 745.377026 | 1488.762759 | 744.885018 | 11 |
| 33 | 3321.594366 | 1661.300821 | | | 3303.583801 | 1652.295538 | S | *1377.730731* | 689.369004 | 1360.704182 | 680.855729 | 1359.720166 | 680.363721 | 10 |
| 34 | 3408.626394 | 1704.816835 | | | 3390.615829 | 1695.811552 | S | 1290.698703 | 645.852990 | 1273.672154 | 637.339715 | 1272.688138 | 636.847707 | 9 |
| 35 | 3847.851720 | 1924.429498 | 3830.825171 | 1915.916223 | 3829.841155 | 1915.424215 | Q | 1203.666675 | 602.336976 | 1186.640126 | 593.823701 | | | 8 |
| 36 | 3946.920134 | 1973.963705 | 3929.893585 | 1965.450430 | 3928.909569 | 1964.958422 | V | 764.441349 | 382.724313 | 747.414800 | 374.211038 | | | 7 |
| 37 | 4060.004198 | 2030.505737 | 4042.977649 | 2021.992462 | 4041.993633 | 2021.500454 | L | 665.372935 | 333.190106 | 648.346386 | 324.676831 | | | 6 |
| 38 | 4197.063110 | 2099.035193 | 4180.036561 | 2090.521919 | 4179.052545 | 2090.029911 | H | *552.288871* | 276.648074 | 535.262322 | 268.134799 | | | 5 |
| 39 | 4294.115874 | 2147.561575 | 4277.089325 | 2139.048301 | 4276.105309 | 2138.556293 | P | *415.229959* | 208.118618 | 398.203410 | 199.605343 | | | 4 |
| 40 | 4351.137338 | 2176.072307 | 4334.110789 | 2167.559033 | 4333.126773 | 2167.067025 | G | 318.177195 | 159.592236 | 301.150646 | 151.078961 | | | 3 |
| 41 | 4465.180265 | 2233.093771 | 4448.153716 | 2224.580496 | 4447.169700 | 2224.088488 | N | 261.155731 | 131.081504 | 244.129182 | 122.568229 | | | 2 |
| 42 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546766 | | | 1 |



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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 35.4 | 4610.278503 | 0.057317 | TDGEGALSEPSATVTIEELAAPPPPVLMHHGESSQVLHPGNK |

**Mascot:** http://www.matrixscience.com/

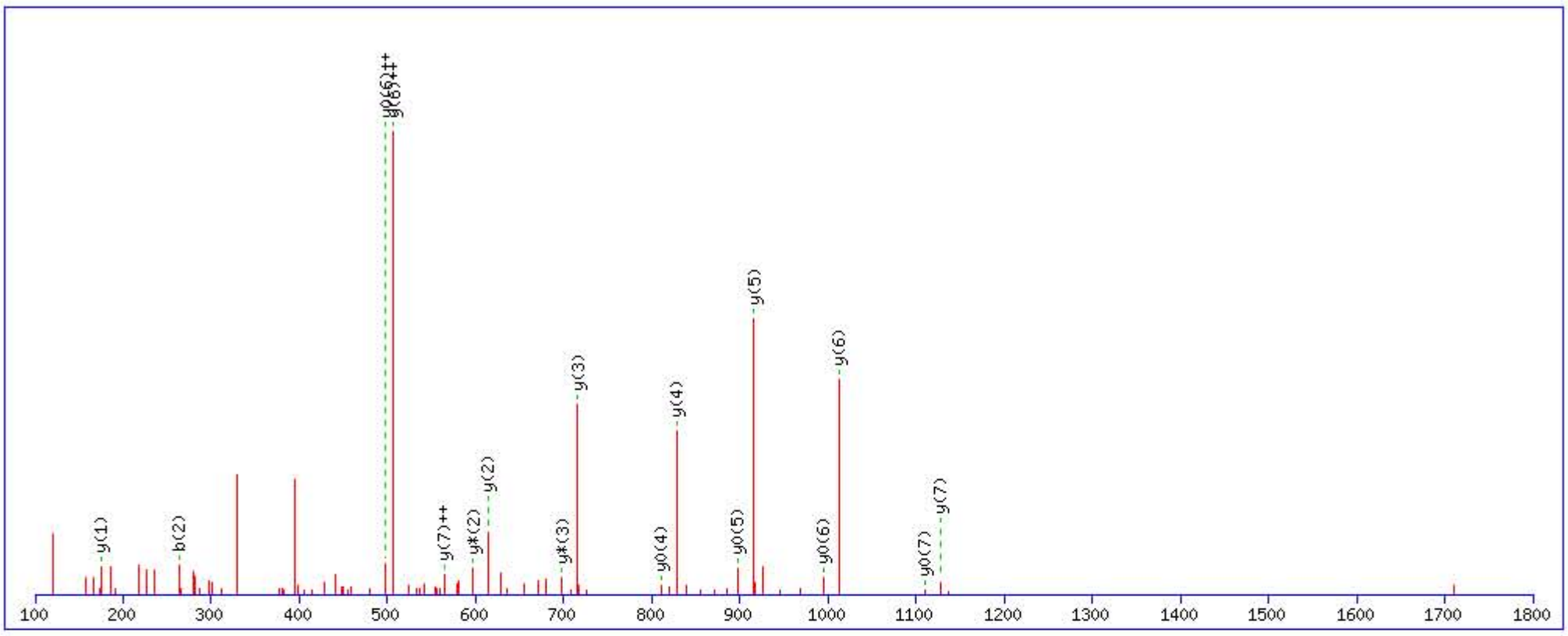
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FDPSLTQR**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

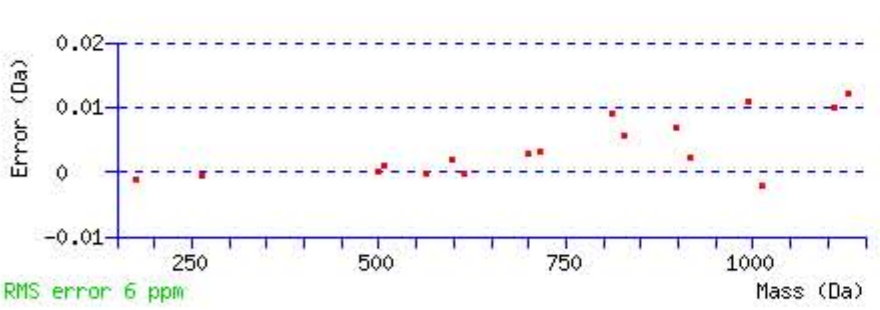
Match to Query 22558: 1273.654328 from(637.834440,2+) rtinseconds(1882) index(4796)
Title: Locus:1.1.1.1932.21 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

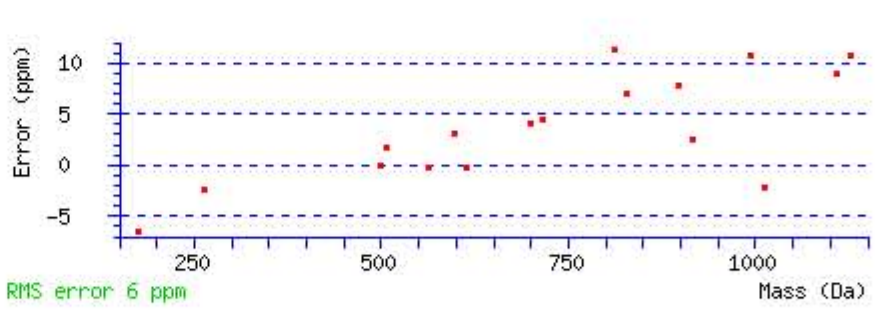
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1273.648895
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.00078
**Matches :** 17/66 fragment ions using 29 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 8 |
| 2 | 263.102633 | 132.054954 | | | 245.092068 | 123.049672 | D | *1127.587756* | 564.297516 | 1110.561207 | 555.784242 | 1109.577191 | 555.292233 | 7 |
| 3 | 360.155397 | 180.581336 | | | 342.144832 | 171.576054 | P | *1012.560813* | 506.784045 | 995.534264 | 498.270770 | 994.550248 | 497.778762 | 6 |
| 4 | 447.187425 | 224.097350 | | | 429.176860 | 215.092068 | S | *915.508049* | 458.257663 | 898.481500 | 449.744388 | 897.497484 | 449.252380 | 5 |
| 5 | 560.271489 | 280.639383 | | | 542.260924 | 271.634100 | L | *828.476021* | 414.741649 | 811.449472 | 406.228374 | 810.465456 | 405.736366 | 4 |
| 6 | 661.319168 | 331.163222 | | | 643.308603 | 322.157940 | T | *715.391957* | 358.199617 | 698.365408 | 349.686342 | 697.381392 | 349.194334 | 3 |
| 7 | 1100.544494 | 550.775885 | 1083.517945 | 542.262611 | 1082.533929 | 541.770603 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.2 | 1273.648895 | 0.005433 | FDPSLTQR |
| 20.7 | 1273.670654 | -0.016326 | FDIAIIYYTR |
| 6.6 | 1273.670029 | -0.015701 | TDPSILGGMIVR |

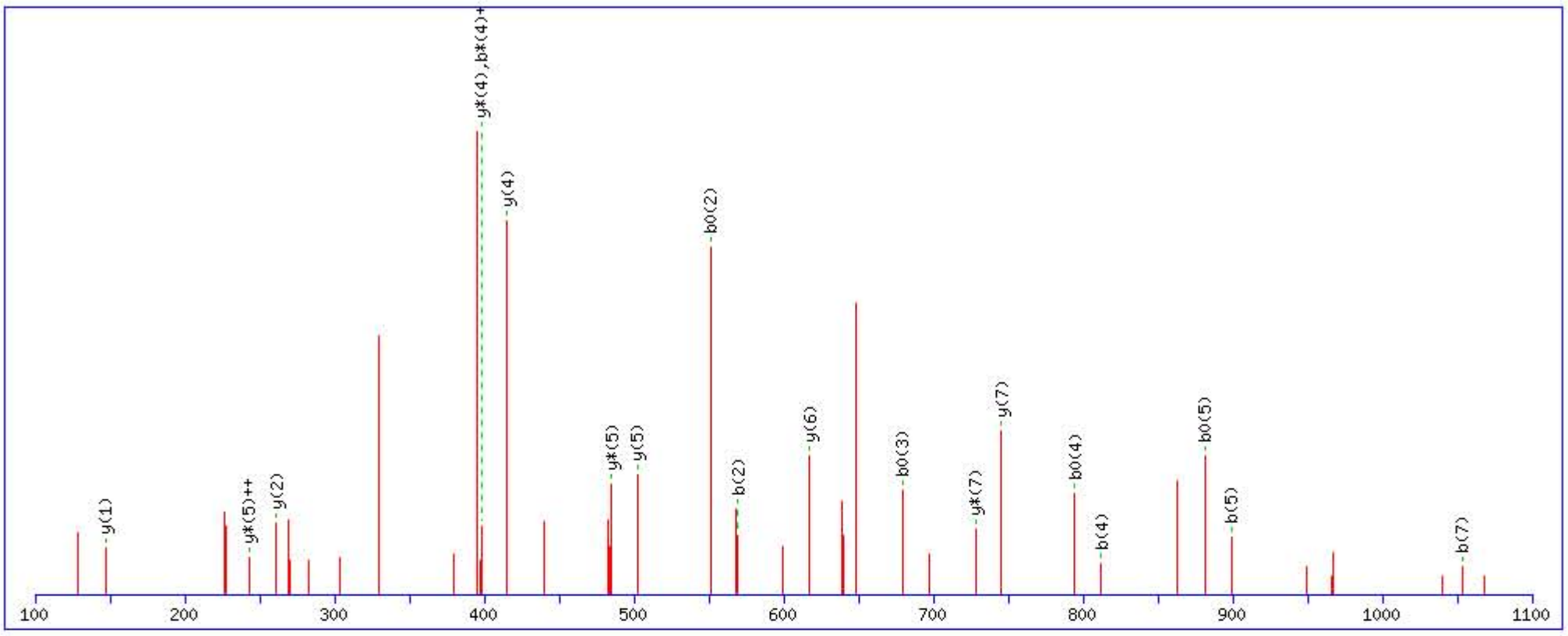
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EQQDSPGNK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

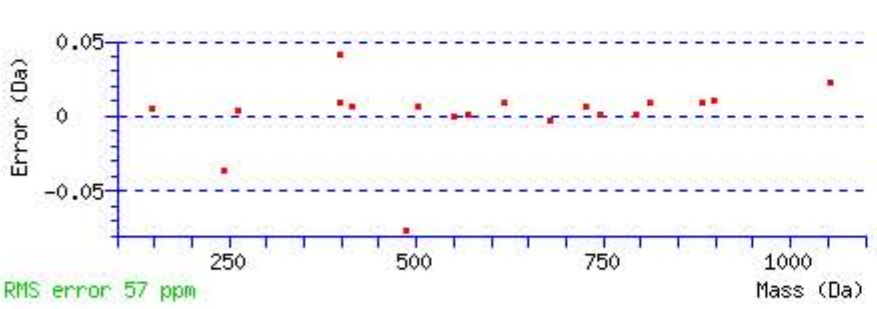
Match to Query 23538: 1312.611288 from(657.312920,2+) rtinseconds(1153) index(61445)
Title: Locus:1.1.1.1676.8 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

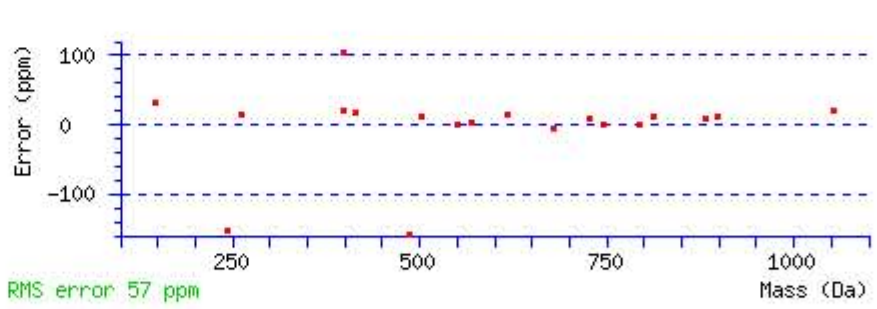
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1312.608139
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.0029
**Matches :** 19/86 fragment ions using 36 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 9 |
| 2 | **569.275195** | 285.141236 | 552.248646 | 276.627961 | 551.264630 | 276.135953 | Q | 1184.572834 | 592.790055 | 1167.546285 | 584.276780 | 1166.562269 | 583.784772 | 8 |
| 3 | 697.333773 | 349.170525 | 680.307224 | 340.657250 | 679.323208 | 340.165242 | Q | *745.347508* | 373.177392 | 728.320959 | 364.664117 | 727.336943 | 364.172109 | 7 |
| 4 | **812.360716** | 406.683996 | 795.334167 | 398.170722 | 794.350151 | 397.678714 | D | *617.288930* | 309.148103 | 600.262381 | 300.634828 | 599.278365 | 300.142820 | 6 |
| 5 | **899.392744** | 450.200010 | 882.366195 | 441.686736 | 881.382179 | 441.194728 | S | *502.261987* | 251.634631 | 485.235438 | 243.121357 | 484.251422 | 242.629349 | 5 |
| 6 | 996.445508 | 498.726392 | 979.418959 | 490.213118 | 978.434943 | 489.721110 | P | *415.229959* | 208.118617 | 398.203410 | 199.605343 | | | 4 |
| 7 | **1053.466972** | 527.237124 | 1036.440423 | 518.723850 | 1035.456407 | 518.231841 | G | 318.177195 | 159.592235 | 301.150646 | 151.078961 | | | 3 |
| 8 | 1167.509899 | 584.258587 | 1150.483350 | 575.745313 | 1149.499334 | 575.253305 | N | *261.155731* | 131.081503 | 244.129182 | 122.568229 | | | 2 |
| 9 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.7 | 1312.608139 | 0.003149 | EQQDSPGNK |
| 18.4 | 1312.608139 | 0.003149 | EQQDSPGNK |
| 4.3 | 1312.596878 | 0.014410 | KYMEENDQLK |
| 0.7 | 1312.601624 | 0.009664 | CGECGKAFTRK |

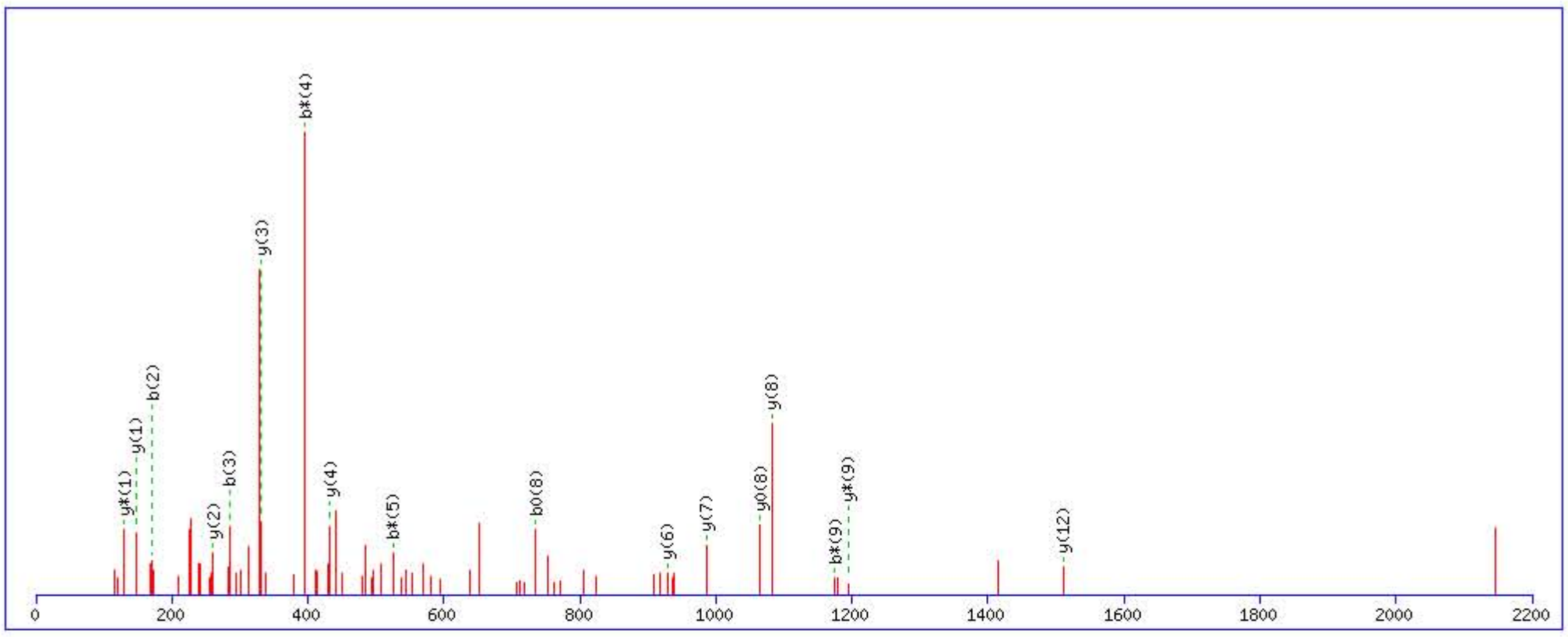
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LGNQEPGGQTALK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

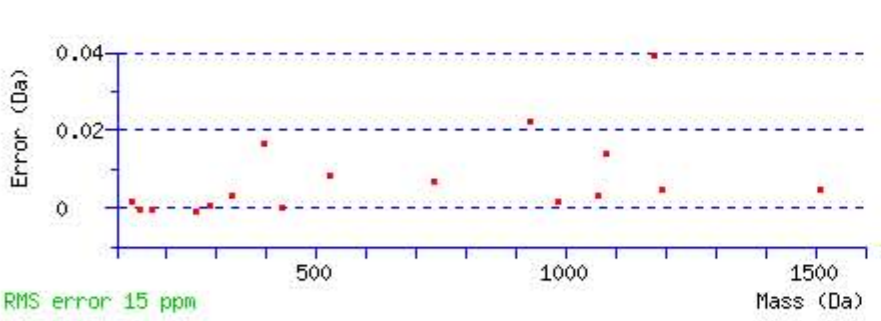
Match to Query 35657: 1622.844852 from(541.955560,3+) rtinseconds(1624) index(3396)
Title: Locus:1.1.1.1842.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

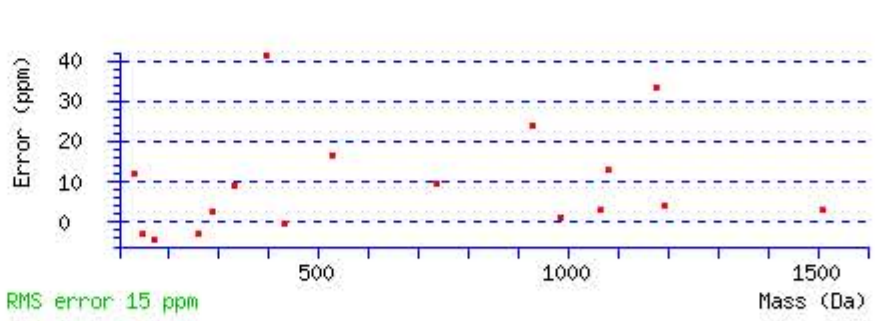
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1622.845016
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 27 **Expect:** 0.0035
**Matches :** 17/126 fragment ions using 50 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 13 |
| 2 | 171.112804 | 86.060040 | | | | | G | 1510.768241 | 755.887759 | 1493.741692 | 747.374484 | 1492.757676 | 746.882476 | 12 |
| 3 | 285.155731 | 143.081504 | 268.129182 | 134.568229 | | | N | 1453.746777 | 727.377027 | 1436.720228 | 718.863752 | 1435.736212 | 718.371744 | 11 |
| 4 | 413.214309 | 207.110793 | 396.187760 | 198.597518 | | | Q | 1339.703850 | 670.355563 | 1322.677301 | 661.842289 | 1321.693285 | 661.350281 | 10 |
| 5 | 542.256902 | 271.632089 | 525.230353 | 263.118815 | 524.246337 | 262.626807 | E | 1211.645272 | 606.326274 | 1194.618723 | 597.813000 | 1193.634707 | 597.320991 | 9 |
| 6 | 639.309666 | 320.158471 | 622.283117 | 311.645197 | 621.299101 | 311.153189 | P | 1082.602679 | 541.804978 | 1065.576130 | 533.291703 | 1064.592114 | 532.799695 | 8 |
| 7 | 696.331130 | 348.669203 | 679.304581 | 340.155929 | 678.320565 | 339.663921 | G | 985.549915 | 493.278596 | 968.523366 | 484.765321 | 967.539350 | 484.273313 | 7 |
| 8 | 753.352594 | 377.179935 | 736.326045 | 368.666661 | 735.342029 | 368.174653 | G | 928.528451 | 464.767864 | 911.501902 | 456.254589 | 910.517886 | 455.762581 | 6 |
| 9 | 1192.577920 | 596.792598 | 1175.551371 | 588.279324 | 1174.567355 | 587.787316 | Q | 871.506987 | 436.257132 | 854.480438 | 427.743857 | 853.496422 | 427.251849 | 5 |
| 10 | 1293.625599 | 647.316438 | 1276.599050 | 638.803163 | 1275.615034 | 638.311155 | T | 432.281661 | 216.644468 | 415.255112 | 208.131194 | 414.271096 | 207.639186 | 4 |
| 11 | 1364.662713 | 682.834995 | 1347.636164 | 674.321720 | 1346.652148 | 673.829712 | A | 331.233982 | 166.120629 | 314.207433 | 157.607354 | | | 3 |
| 12 | 1477.746777 | 739.377027 | 1460.720228 | 730.863752 | 1459.736212 | 730.371744 | L | 260.196868 | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 13 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 26.8 | 1622.845016 | -0.000164 | LGNQEPGGQTALK |
| 7.8 | 1622.845016 | -0.000164 | LGNQEPGGQTALK |
| 0.5 | 1622.849045 | -0.004193 | IPMPDFDLHLKGPK |
| 0.2 | 1622.820511 | 0.024341 | FPPEASGYLHIGHAK |

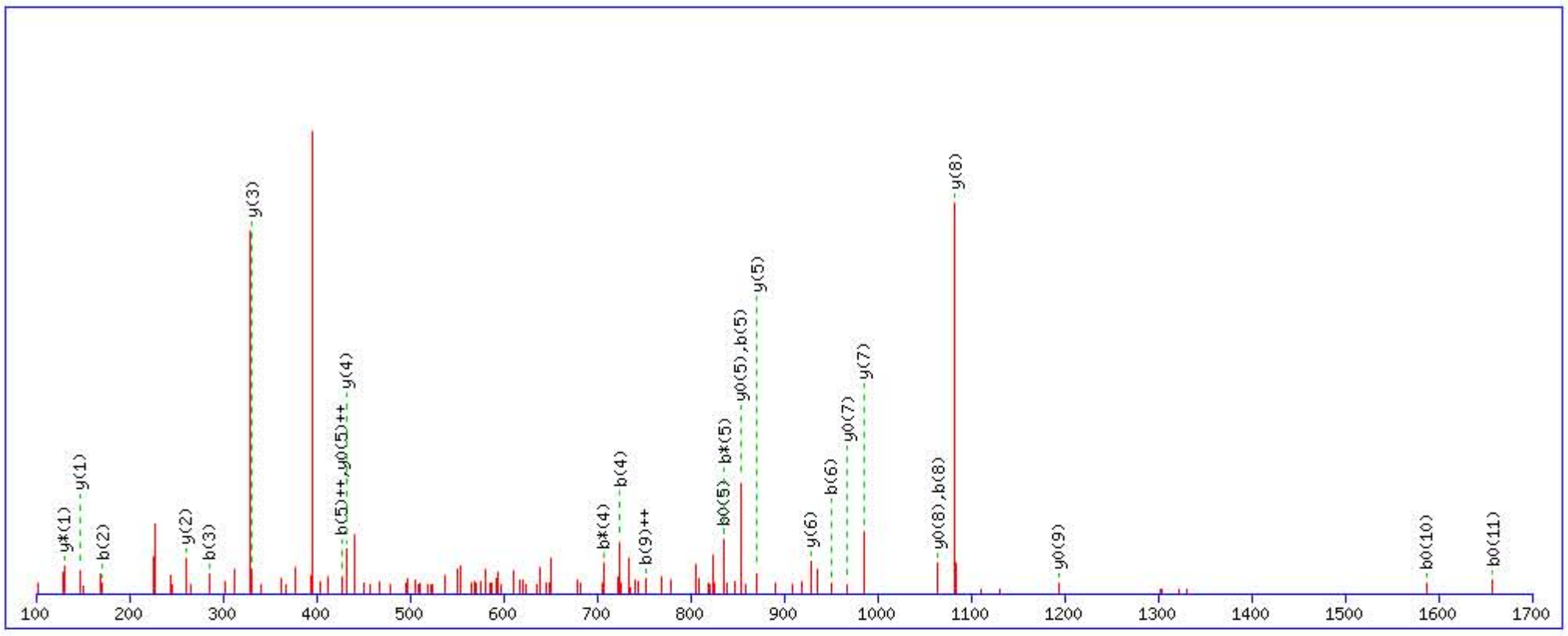
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LGNQEPGGQTALK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

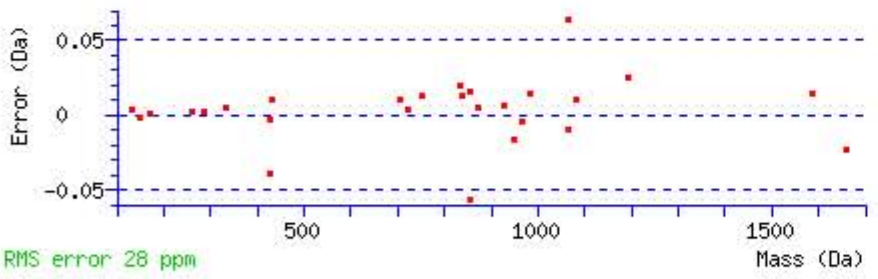
Match to Query 42834: 1934.019912 from(645.680580,3+) rtinseconds(1959) index(66203)
Title: Locus:1.1.1.1957.13 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

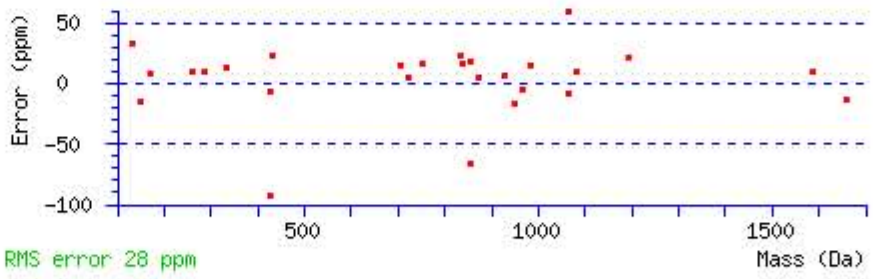
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1934.011765
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 28 **Expect:** 0.011
**Matches** : 27/126 fragment ions using 66 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 13 |
| 2 | *171.112804* | 86.060040 | | | | | G | 1821.934989 | 911.471133 | 1804.908440 | 902.957858 | 1803.924424 | 902.465850 | 12 |
| 3 | *285.155731* | 143.081504 | 268.129182 | 134.568229 | | | N | 1764.913525 | 882.960400 | 1747.886976 | 874.447126 | 1746.902960 | 873.955118 | 11 |
| 4 | *724.381057* | 362.694167 | 707.354508 | 354.180892 | | | Q | 1650.870598 | 825.938937 | 1633.844049 | 817.425663 | 1632.860033 | 816.933654 | 10 |
| 5 | *853.423650* | *427.215463* | 836.397101 | 418.702189 | 835.413085 | 418.210181 | E | 1211.645272 | 606.326274 | 1194.618723 | 597.813000 | 1193.634707 | 597.320991 | 9 |
| 6 | *950.476414* | 475.741845 | 933.449865 | 467.228571 | 932.465849 | 466.736563 | P | *1082.602679* | 541.804977 | 1065.576130 | 533.291703 | 1064.592114 | 532.799695 | 8 |
| 7 | 1007.497878 | 504.252577 | 990.471329 | 495.739303 | 989.487313 | 495.247295 | G | *985.549915* | 493.278595 | 968.523366 | 484.765321 | 967.539350 | 484.273313 | 7 |
| 8 | *1064.519342* | 532.763309 | 1047.492793 | 524.250035 | 1046.508777 | 523.758027 | G | *928.528451* | 464.767863 | 911.501902 | 456.254589 | 910.517886 | 455.762581 | 6 |
| 9 | 1503.744668 | *752.375972* | 1486.718119 | 743.862698 | 1485.734103 | 743.370690 | Q | *871.506987* | 436.257132 | 854.480438 | 427.743857 | 853.496422 | 427.251849 | 5 |
| 10 | 1604.792347 | 802.899812 | 1587.765798 | 794.386537 | 1586.781782 | 793.894529 | T | *432.281661* | 216.644468 | 415.255112 | 208.131194 | 414.271096 | 207.639186 | 4 |
| 11 | 1675.829461 | 838.418369 | 1658.802912 | 829.905094 | 1657.818896 | 829.413086 | A | *331.233982* | 166.120629 | 314.207433 | 157.607354 | | | 3 |
| 12 | 1788.913525 | 894.960400 | 1771.886976 | 886.447126 | 1770.902960 | 885.955118 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 13 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 27.7 | 1934.011765 | 0.008147 | LGNQEPGGQTALK |
| 6.8 | 1934.032867 | -0.012955 | KSRPLTGLMDLAKEMTK |
| 0.0 | 1934.032867 | -0.012955 | KSRPLTGLMDLAKEMTK |

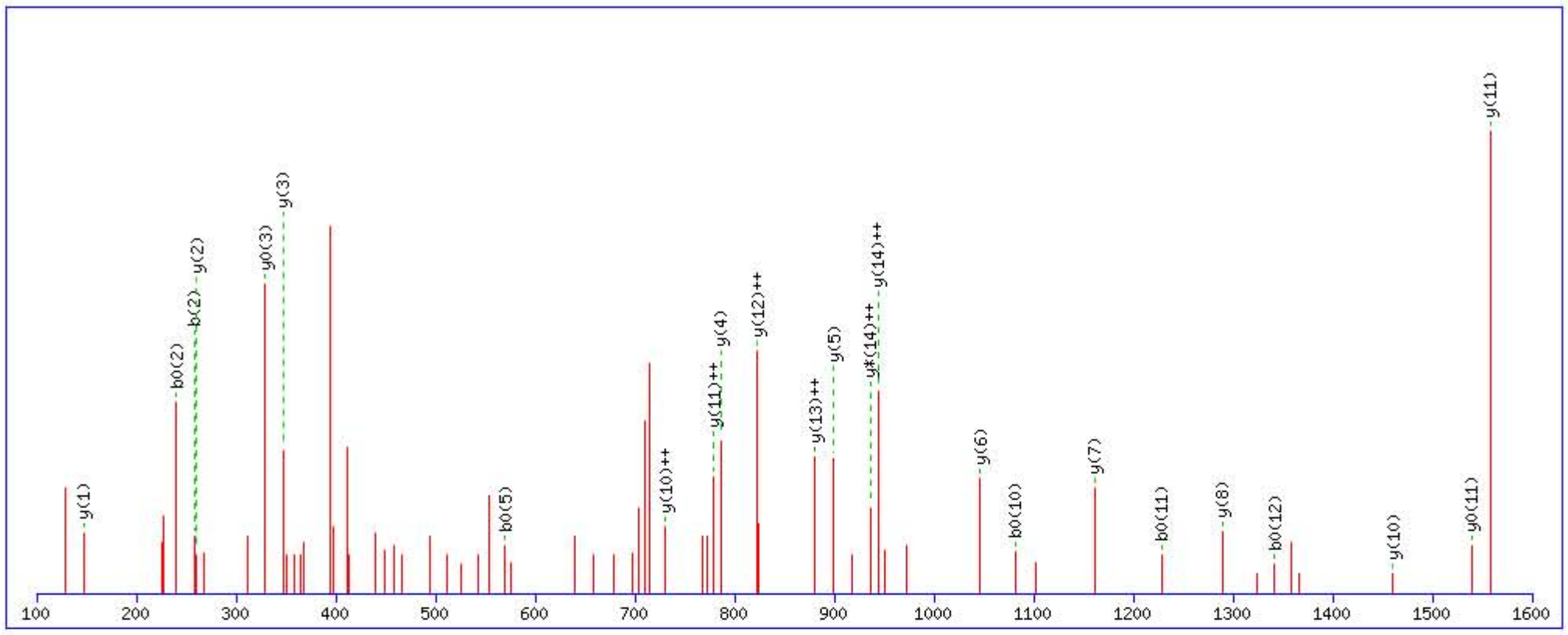
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EQQDSPGNKDFLQSLK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

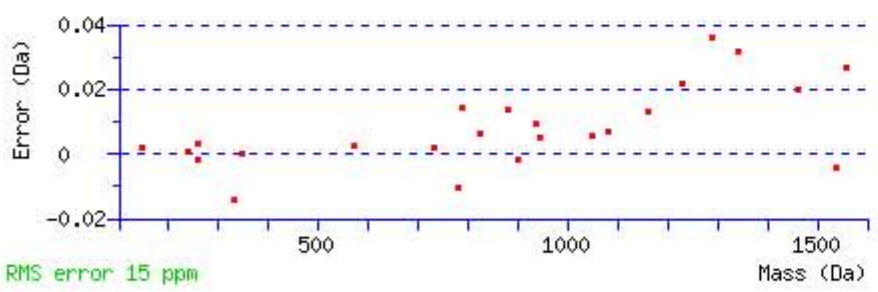
Match to Query 47309: 2144.076252 from(715.699360,3+) rtinseconds(2019) index(5714)
Title: Locus:1.1.1.1980.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

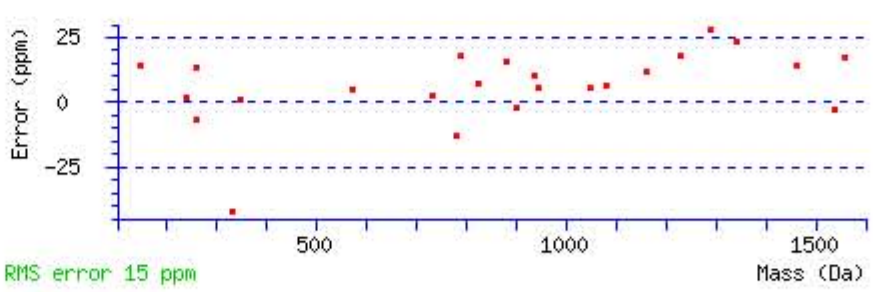
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2144.057190
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q13** : Biotin:Thermo-21345 (Q)
**Ions Score:** 35 **Expect:** 0.0081
**Matches :** 24/174 fragment ions using 55 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 16 |
| 2 | 258.108447 | 129.557862 | 241.081898 | 121.044587 | 240.097882 | 120.552579 | Q | 2016.021888 | 1008.514582 | 1998.995339 | 1000.001308 | 1998.011323 | 999.509300 | 15 |
| 3 | 386.167025 | 193.587151 | 369.140476 | 185.073876 | 368.156460 | 184.581868 | Q | 1887.963310 | 944.485293 | 1870.936761 | 935.972019 | 1869.952745 | 935.480011 | 14 |
| 4 | 501.193968 | 251.100622 | 484.167419 | 242.587348 | 483.183403 | 242.095340 | D | 1759.904732 | 880.456004 | 1742.878183 | 871.942730 | 1741.894167 | 871.450722 | 13 |
| 5 | 588.225996 | 294.616636 | 571.199447 | 286.103362 | 570.215431 | 285.611354 | S | 1644.877789 | 822.942533 | 1627.851240 | 814.429258 | 1626.867224 | 813.937250 | 12 |
| 6 | 685.278760 | 343.143018 | 668.252211 | 334.629744 | 667.268195 | 334.137736 | P | *1557.845761* | 779.426519 | 1540.819212 | 770.913244 | 1539.835196 | 770.421236 | 11 |
| 7 | 742.300224 | 371.653750 | 725.273675 | 363.140476 | 724.289659 | 362.648468 | G | *1460.792997* | 730.900137 | 1443.766448 | 722.386862 | 1442.782432 | 721.894854 | 10 |
| 8 | 856.343151 | 428.675214 | 839.316602 | 420.161939 | 838.332586 | 419.669931 | N | 1403.771533 | 702.389405 | 1386.744984 | 693.876130 | 1385.760968 | 693.384122 | 9 |
| 9 | 984.438114 | 492.722695 | 967.411565 | 484.209421 | 966.427549 | 483.717413 | K | *1289.728606* | 645.367941 | 1272.702057 | 636.854667 | 1271.718041 | 636.362659 | 8 |
| 10 | 1099.465057 | 550.236167 | 1082.438508 | 541.722892 | 1081.454492 | 541.230884 | D | *1161.633643* | 581.320460 | 1144.607094 | 572.807185 | 1143.623078 | 572.315177 | 7 |
| 11 | 1246.533471 | 623.770374 | 1229.506922 | 615.257099 | 1228.522906 | 614.765091 | F | *1046.606700* | 523.806988 | 1029.580151 | 515.293714 | 1028.596135 | 514.801706 | 6 |
| 12 | 1359.617535 | 680.312406 | 1342.590986 | 671.799131 | 1341.606970 | 671.307123 | L | *899.538286* | 450.272781 | 882.511737 | 441.759507 | 881.527721 | 441.267499 | 5 |
| 13 | 1798.842861 | 899.925069 | 1781.816312 | 891.411794 | 1780.832296 | 890.919786 | Q | *786.454222* | 393.730749 | 769.427673 | 385.217475 | 768.443657 | 384.725467 | 4 |
| 14 | 1885.874889 | 943.441083 | 1868.848340 | 934.927808 | 1867.864324 | 934.435800 | S | *347.228896* | 174.118086 | 330.202347 | 165.604812 | 329.218331 | 165.112804 | 3 |
| 15 | 1998.958953 | 999.983115 | 1981.932404 | 991.469840 | 1980.948388 | 990.977832 | L | *260.196868* | 130.602072 | 243.170319 | 122.088798 | | | 2 |
| 16 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546766 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 35.3 | 2144.057190 | 0.019062 | EQQDSPGNKDFLQSLK |

**Mascot:** http://www.matrixscience.com/

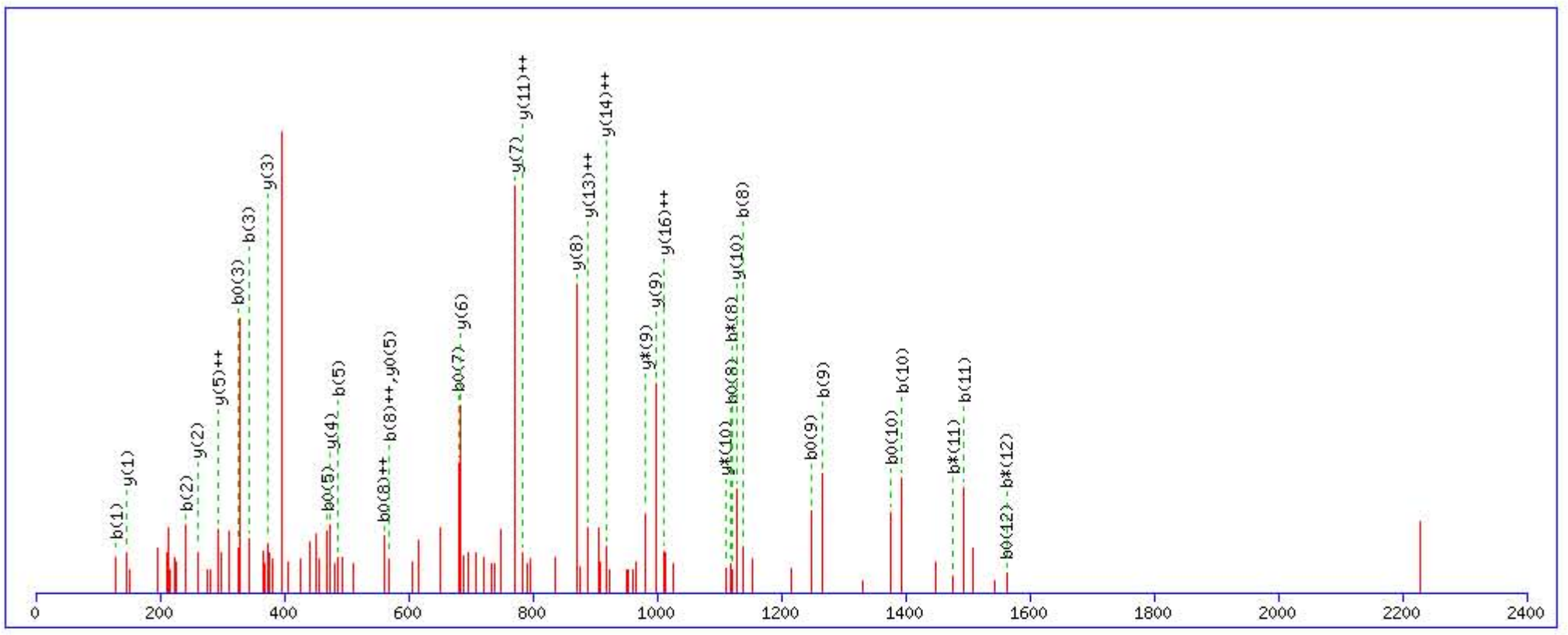
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QLTSGPNQEQVSPLTLLK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

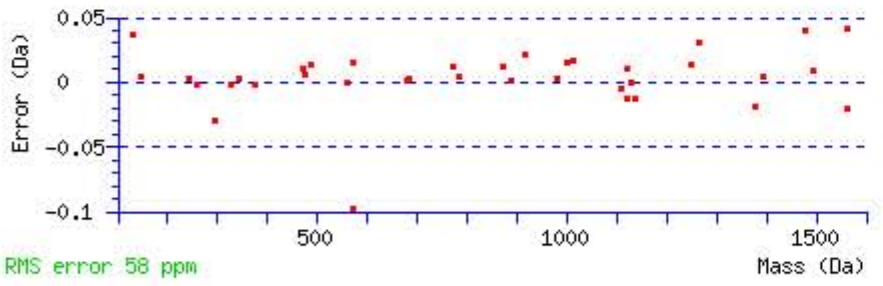
Match to Query 49791: 2263.244832 from(755.422220,3+) rtinseconds(2535) index(8513)
Title: Locus:1.1.1.2160.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

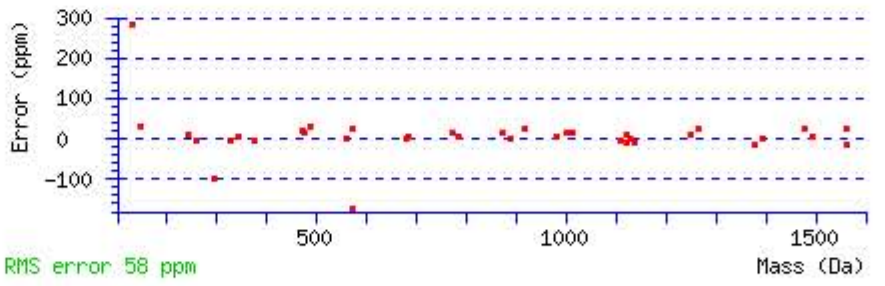
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2263.224594
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 7.5e-005
**Matches :** 37/194 fragment ions using 65 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *129.065854* | 65.036565 | 112.039305 | 56.523291 | | | Q | | | | | | | 18 |
| 2 | *242.149918* | 121.578597 | 225.123369 | 113.065323 | | | L | 2136.173304 | 1068.590290 | 2119.146755 | 1060.077015 | 2118.162739 | 1059.585007 | 17 |
| 3 | *343.197597* | 172.102437 | 326.171048 | 163.589162 | 325.187032 | 163.097154 | T | 2023.089240 | 1012.048258 | 2006.062691 | 1003.534984 | 2005.078675 | 1003.042976 | 16 |
| 4 | 430.229625 | 215.618450 | 413.203076 | 207.105176 | 412.219060 | 206.613168 | S | 1922.041561 | 961.524419 | 1905.015012 | 953.011144 | 1904.030996 | 952.519136 | 15 |
| 5 | *487.251089* | 244.129182 | 470.224540 | 235.615908 | 469.240524 | 235.123900 | G | 1835.009533 | 918.008405 | 1817.982984 | 909.495130 | 1816.998968 | 909.003122 | 14 |
| 6 | 584.303853 | 292.655565 | 567.277304 | 284.142290 | 566.293288 | 283.650282 | P | 1777.988069 | 889.497673 | 1760.961520 | 880.984398 | 1759.977504 | 880.492390 | 13 |
| 7 | 698.346780 | 349.677028 | 681.320231 | 341.163753 | 680.336215 | 340.671745 | N | 1680.935305 | 840.971291 | 1663.908756 | 832.458016 | 1662.924740 | 831.966008 | 12 |
| 8 | *1137.572106* | 569.289691 | 1120.545557 | 560.776416 | 1119.561541 | 560.284408 | Q | 1566.892378 | 783.949827 | 1549.865829 | 775.436553 | 1548.881813 | 774.944545 | 11 |
| 9 | *1266.614699* | 633.810988 | 1249.588150 | 625.297713 | 1248.604134 | 624.805705 | E | *1127.667052* | 564.337164 | 1110.640503 | 555.823890 | 1109.656487 | 555.331882 | 10 |
| 10 | *1394.673277* | 697.840277 | 1377.646728 | 689.327002 | 1376.662712 | 688.834994 | Q | *998.624459* | 499.815868 | 981.597910 | 491.302593 | 980.613894 | 490.810585 | 9 |
| 11 | *1493.741691* | 747.374484 | 1476.715142 | 738.861209 | 1475.731126 | 738.369201 | V | *870.565881* | 435.786579 | 853.539332 | 427.273304 | 852.555316 | 426.781296 | 8 |
| 12 | 1580.773719 | 790.890498 | 1563.747170 | 782.377223 | 1562.763154 | 781.885215 | S | *771.497467* | 386.252372 | 754.470918 | 377.739097 | 753.486902 | 377.247089 | 7 |
| 13 | 1677.826483 | 839.416880 | 1660.799934 | 830.903605 | 1659.815918 | 830.411597 | P | *684.465439* | 342.736358 | 667.438890 | 334.223083 | 666.454874 | 333.731075 | 6 |
| 14 | 1790.910547 | 895.958912 | 1773.883998 | 887.445637 | 1772.899982 | 886.953629 | L | 587.412675 | 294.209976 | 570.386126 | 285.696701 | 569.402110 | 285.204693 | 5 |
| 15 | 1891.958226 | 946.482751 | 1874.931677 | 937.969477 | 1873.947661 | 937.477469 | T | *474.328611* | 237.667944 | 457.302062 | 229.154669 | 456.318046 | 228.662661 | 4 |
| 16 | 2005.042290 | 1003.024783 | 1988.015741 | 994.511509 | 1987.031725 | 994.019501 | L | *373.280932* | 187.144104 | 356.254383 | 178.630830 | | | 3 |
| 17 | 2118.126354 | 1059.566815 | 2101.099805 | 1051.053540 | 2100.115789 | 1050.561532 | L | *260.196868* | 130.602072 | 243.170319 | 122.088798 | | | 2 |
| 18 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.9 | 2263.224594 | 0.020238 | QLTSGPNQEQVSPLTLLK |
| 39.4 | 2263.224594 | 0.020238 | QLTSGPNQEQVSPLTLLK |
| 30.0 | 2263.224594 | 0.020238 | QLTSGPNQEQVSPLTLLK |
| 12.4 | 2263.224594 | 0.020238 | GLALSSNKVKSVVMVVFDNEK |

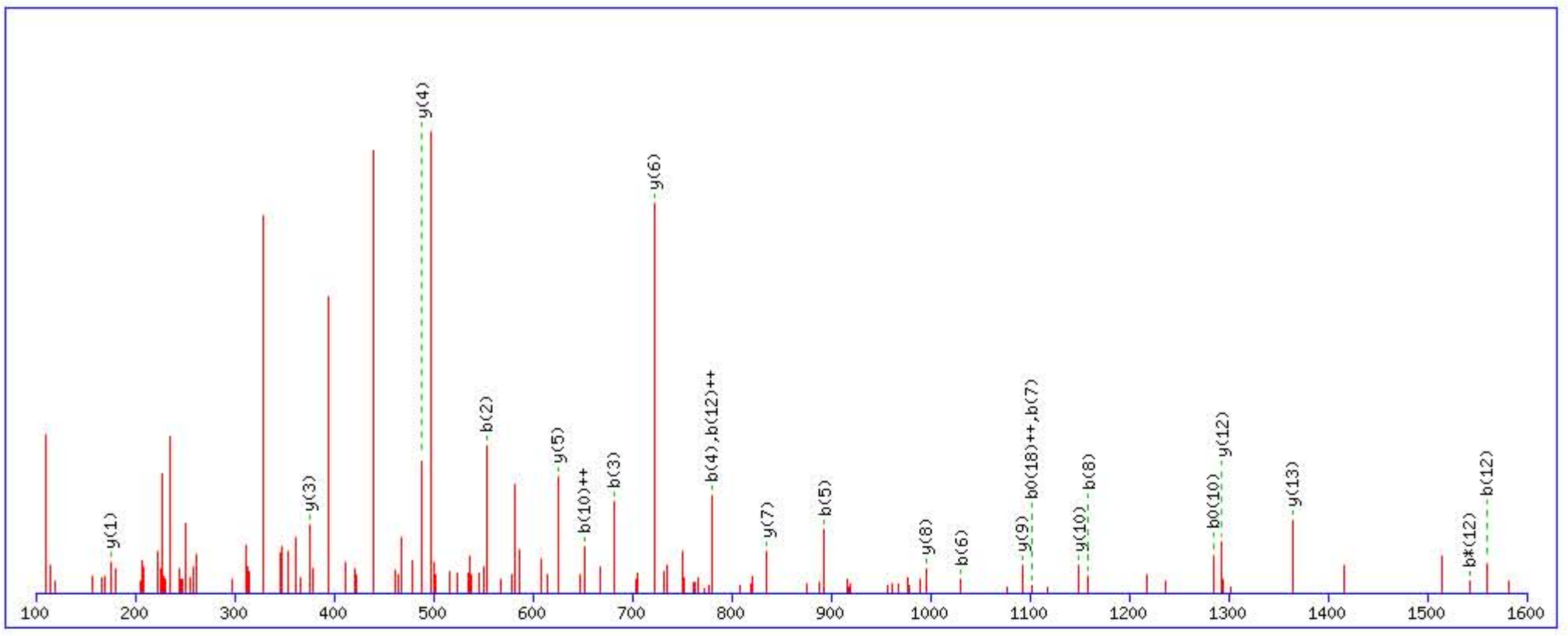
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LQQVLHAGSGPCLPHLLSR**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

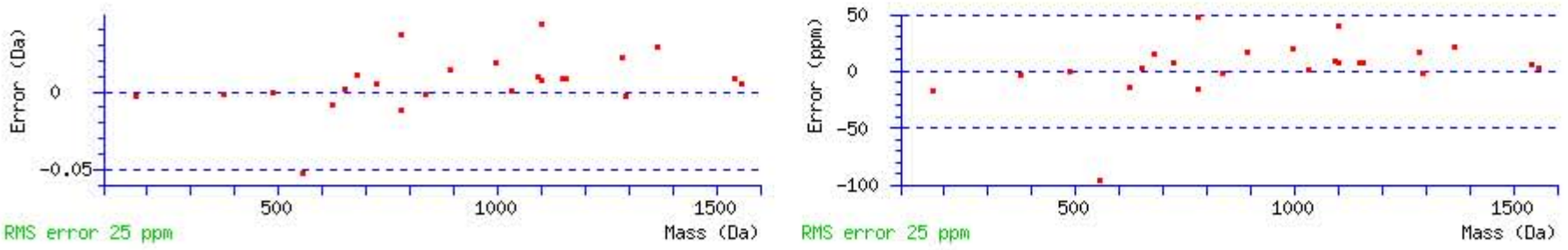
Match to Query 51831: 2393.294416 from(599.330880,4+) rtinseconds(2122) index(6301)
Title: Locus:1.1.1.2016.4 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2393.282410
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 68 **Expect:** 3.4e-006
**Matches** : 24/196 fragment ions using 41 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 19 |
| 2 | *553.316666* | 277.161971 | 536.290117 | 268.648697 | | | Q | 2281.205625 | 1141.106450 | 2264.179076 | 1132.593176 | 2263.195060 | 1132.101168 | 18 |
| 3 | *681.375244* | 341.191260 | 664.348695 | 332.677986 | | | Q | 1841.980299 | 921.493788 | 1824.953750 | 912.980513 | 1823.969734 | 912.488505 | 17 |
| 4 | *780.443658* | 390.725467 | 763.417109 | 382.212193 | | | V | 1713.921721 | 857.464498 | 1696.895172 | 848.951224 | 1695.911156 | 848.459216 | 16 |
| 5 | *893.527722* | 447.267499 | 876.501173 | 438.754225 | | | L | 1614.853307 | 807.930292 | 1597.826758 | 799.417017 | 1596.842742 | 798.925009 | 15 |
| 6 | *1030.586634* | 515.796955 | 1013.560085 | 507.283681 | | | H | 1501.769243 | 751.388260 | 1484.742694 | 742.874985 | 1483.758678 | 742.382977 | 14 |
| 7 | *1101.623748* | 551.315512 | 1084.597199 | 542.802238 | | | A | *1364.710331* | 682.858804 | 1347.683782 | 674.345529 | 1346.699766 | 673.853521 | 13 |
| 8 | *1158.645212* | 579.826244 | 1141.618663 | 571.312970 | | | G | *1293.673217* | 647.340247 | 1276.646668 | 638.826972 | 1275.662652 | 638.334964 | 12 |
| 9 | 1245.677240 | 623.342258 | 1228.650691 | 614.828984 | 1227.666675 | 614.336975 | S | 1236.651753 | 618.829515 | 1219.625204 | 610.316240 | 1218.641188 | 609.824232 | 11 |
| 10 | 1302.698704 | **651.852990** | 1285.672155 | 643.339716 | 1284.688139 | 642.847707 | G | *1149.619725* | 575.313501 | 1132.593176 | 566.800226 | 1131.609160 | 566.308218 | 10 |
| 11 | 1399.751468 | 700.379372 | 1382.724919 | 691.866098 | 1381.740903 | 691.374089 | P | *1092.598261* | 546.802769 | 1075.571712 | 538.289494 | 1074.587696 | 537.797486 | 9 |
| 12 | *1559.782117* | **780.394697** | 1542.755568 | 771.881422 | 1541.771552 | 771.389414 | C | *995.545497* | 498.276387 | 978.518948 | 489.763112 | 977.534932 | 489.271104 | 8 |
| 13 | 1672.866181 | 836.936728 | 1655.839632 | 828.423454 | 1654.855616 | 827.931446 | L | *835.514848* | 418.261062 | 818.488299 | 409.747788 | 817.504283 | 409.255780 | 7 |
| 14 | 1769.918945 | 885.463110 | 1752.892396 | 876.949836 | 1751.908380 | 876.457828 | P | *722.430784* | 361.719030 | 705.404235 | 353.205756 | 704.420219 | 352.713748 | 6 |
| 15 | 1906.977857 | 953.992566 | 1889.951308 | 945.479292 | 1888.967292 | 944.987284 | H | *625.378020* | 313.192648 | 608.351471 | 304.679374 | 607.367455 | 304.187366 | 5 |
| 16 | 2020.061921 | 1010.534598 | 2003.035372 | 1002.021324 | 2002.051356 | 1001.529316 | L | *488.319108* | 244.663192 | 471.292559 | 236.149918 | 470.308543 | 235.657910 | 4 |
| 17 | 2133.145985 | 1067.076630 | 2116.119436 | 1058.563356 | 2115.135420 | 1058.071348 | L | *375.235044* | 188.121160 | 358.208495 | 179.607886 | 357.224479 | 179.115878 | 3 |
| 18 | 2220.178013 | 1110.592644 | 2203.151464 | 1102.079370 | 2202.167448 | 1101.587362 | S | 262.150980 | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 19 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 67.8 | 2393.282410 | 0.012006 | LQQVLHAGSGPCLPHLLSR |
| 62.1 | 2393.282410 | 0.012006 | LQQVLHAGSGPCLPHLLSR |

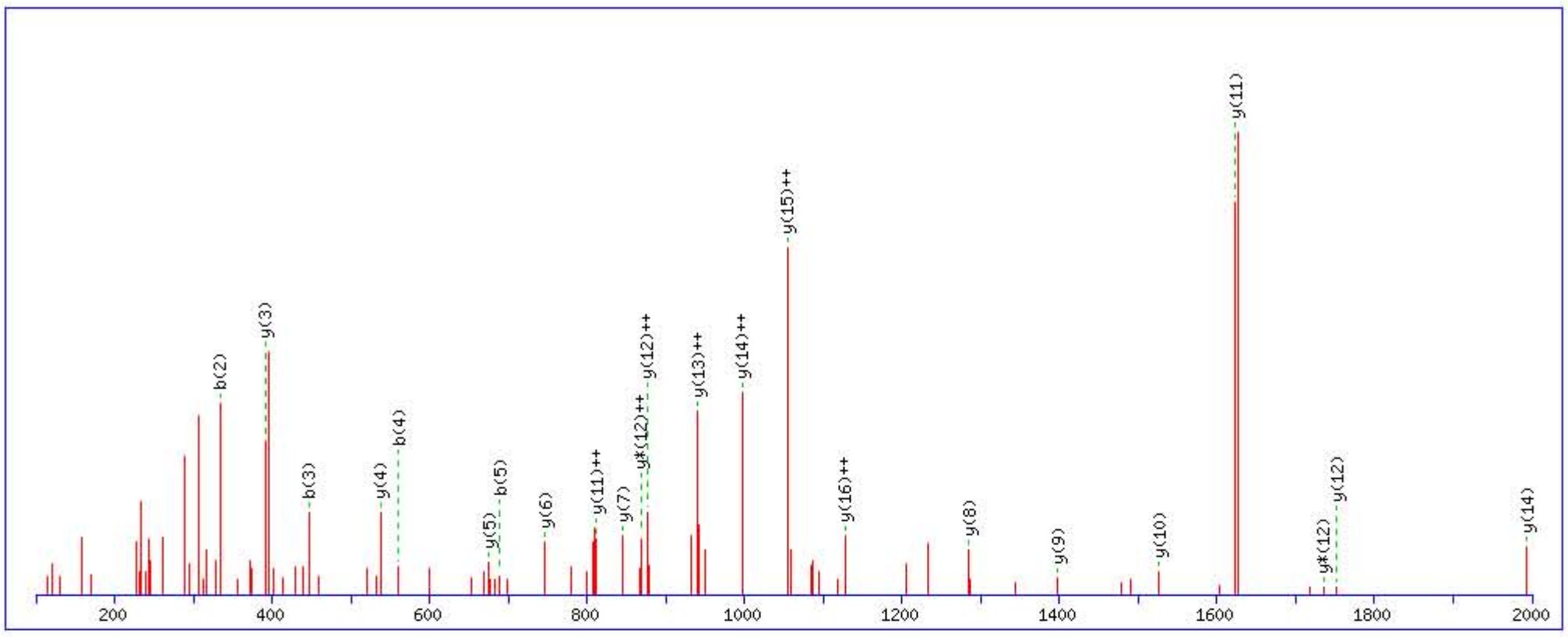
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **WFLLEQPEIQVAHFPFK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

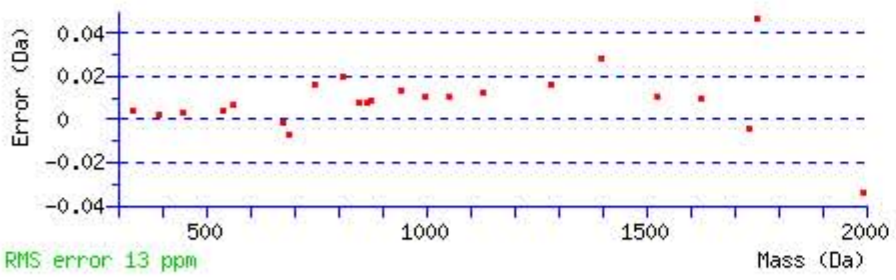
Match to Query 52799: 2439.305622 from(814.109150,3+) rtinseconds(2930) index(10727)
Title: Locus:1.1.1.2296.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

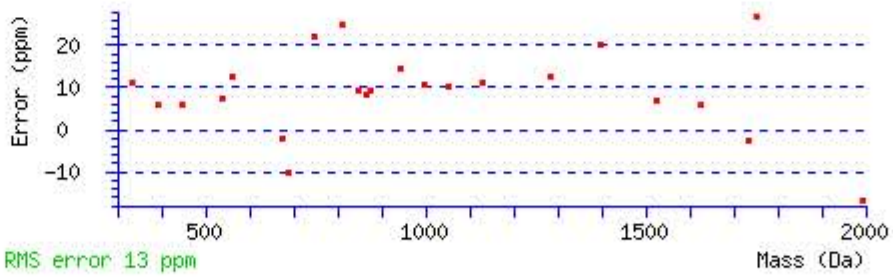
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2439.281326
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 54 **Expect:** 8.8e-005
**Matches :** 23/156 fragment ions using 48 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 187.086589 | 94.046932 | | | | | W | | | | | | | 17 |
| 2 | **334.155003** | 167.581140 | | | | | F | 2254.209296 | 1127.608286 | 2237.182747 | 1119.095011 | 2236.198731 | 1118.603003 | 16 |
| 3 | **447.239067** | 224.123172 | | | | | L | 2107.140882 | 1054.074079 | 2090.114333 | 1045.560804 | 2089.130317 | 1045.068796 | 15 |
| 4 | **560.323131** | 280.665204 | | | | | L | *1994.056818* | 997.532047 | 1977.030269 | 989.018772 | 1976.046253 | 988.526764 | 14 |
| 5 | **689.365724** | 345.186500 | | | 671.355159 | 336.181218 | E | 1880.972754 | 940.990015 | 1863.946205 | 932.476741 | 1862.962189 | 931.984732 | 13 |
| 6 | 817.424302 | 409.215789 | 800.397753 | 400.702515 | 799.413737 | 400.210507 | Q | *1751.930161* | 876.468719 | 1734.903612 | 867.955444 | 1733.919596 | 867.463436 | 12 |
| 7 | 914.477066 | 457.742171 | 897.450517 | 449.228897 | 896.466501 | 448.736889 | P | *1623.871583* | 812.439429 | 1606.845034 | 803.926155 | 1605.861018 | 803.434147 | 11 |
| 8 | 1043.519659 | 522.263468 | 1026.493110 | 513.750193 | 1025.509094 | 513.258185 | E | *1526.818819* | 763.913047 | 1509.792270 | 755.399773 | 1508.808254 | 754.907765 | 10 |
| 9 | 1156.603723 | 578.805500 | 1139.577174 | 570.292225 | 1138.593158 | 569.800217 | I | *1397.776226* | 699.391751 | 1380.749677 | 690.878476 | | | 9 |
| 10 | 1595.829049 | 798.418163 | 1578.802500 | 789.904888 | 1577.818484 | 789.412880 | Q | *1284.692162* | 642.849719 | 1267.665613 | 634.336444 | | | 8 |
| 11 | 1694.897463 | 847.952370 | 1677.870914 | 839.439095 | 1676.886898 | 838.947087 | V | *845.466836* | 423.237056 | 828.440287 | 414.723781 | | | 7 |
| 12 | 1765.934577 | 883.470927 | 1748.908028 | 874.957652 | 1747.924012 | 874.465644 | A | *746.398422* | 373.702849 | 729.371873 | 365.189574 | | | 6 |
| 13 | 1902.993489 | 952.000383 | 1885.966940 | 943.487108 | 1884.982924 | 942.995100 | H | *675.361308* | 338.184292 | 658.334759 | 329.671017 | | | 5 |
| 14 | 2050.061903 | 1025.534589 | 2033.035354 | 1017.021315 | 2032.051338 | 1016.529307 | F | *538.302396* | 269.654836 | 521.275847 | 261.141561 | | | 4 |
| 15 | 2147.114667 | 1074.060971 | 2130.088118 | 1065.547697 | 2129.104102 | 1065.055689 | P | *391.233982* | 196.120629 | 374.207433 | 187.607354 | | | 3 |
| 16 | 2294.183081 | 1147.595178 | 2277.156532 | 1139.081904 | 2276.172516 | 1138.589896 | F | 294.181218 | 147.594247 | 277.154669 | 139.080972 | | | 2 |
| 17 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 53.9 | 2439.281326 | 0.024296 | WFLLEQPEIQVAHFPFK |
| 25.4 | 2439.281326 | 0.024296 | WFLLEQPEIQVAHFPFK |

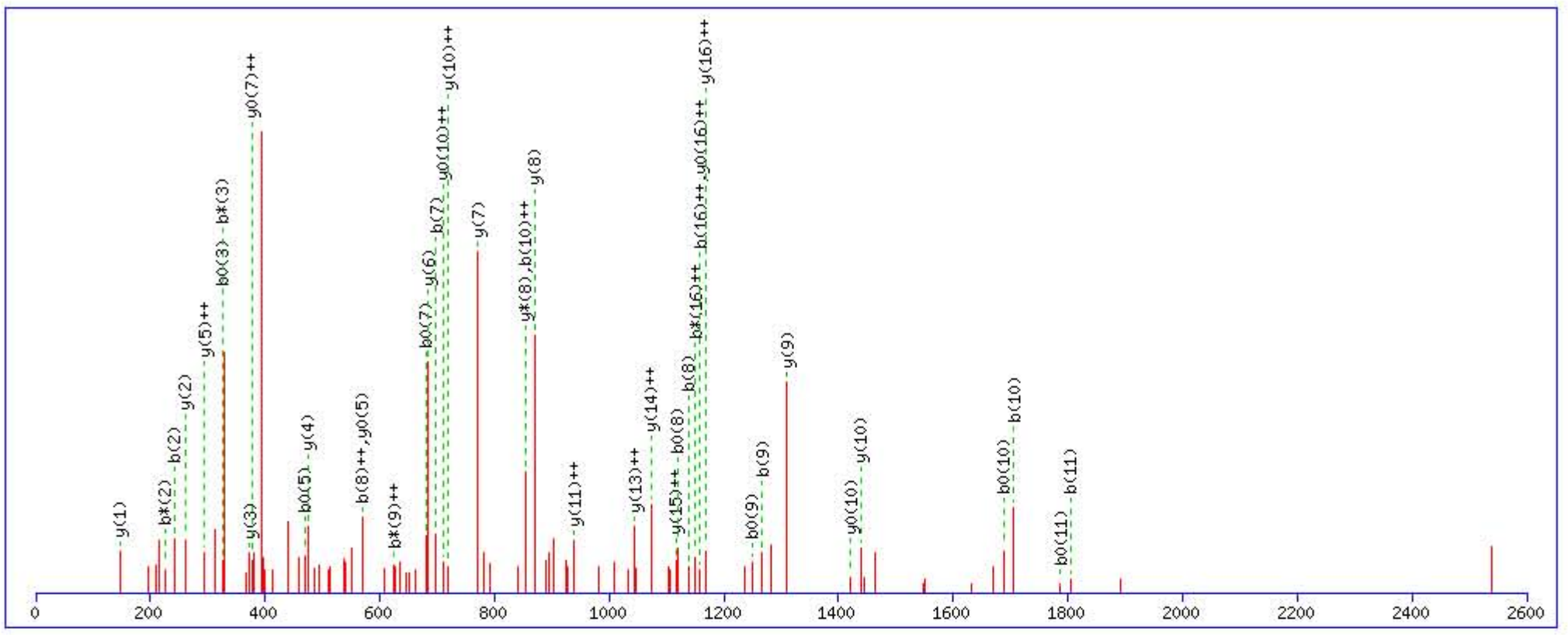
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QLTSGPNQEQVSPLTLLK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

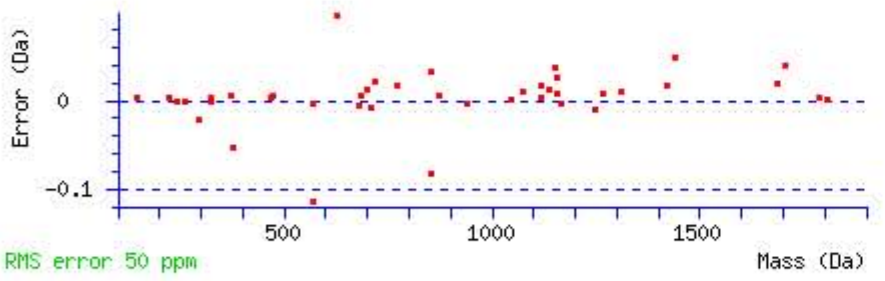
Match to Query 55235: 2574.414792 from(859.145540,3+) rtinseconds(2709) index(9405)
Title: Locus:1.1.1.2220.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

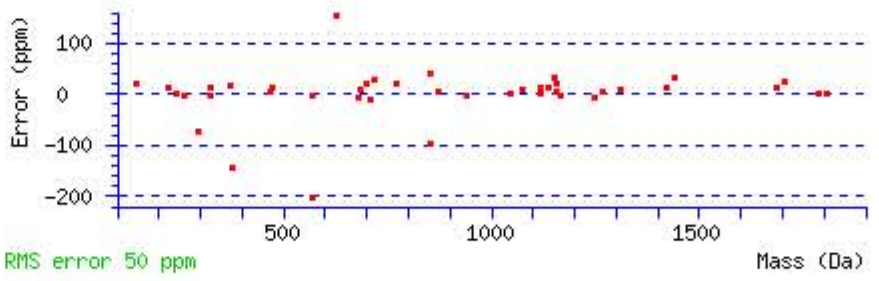
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2574.391342
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.00041
**Matches :** 42/194 fragment ions using 82 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.065854 | 65.036565 | 112.039305 | 56.523291 | | | Q | | | | | | | 18 |
| 2 | **242.149918** | 121.578597 | 225.123369 | 113.065323 | | | L | 2447.340052 | 1224.173664 | 2430.313503 | 1215.660389 | 2429.329487 | 1215.168381 | 17 |
| 3 | 343.197597 | 172.102437 | 326.171048 | 163.589162 | 325.187032 | 163.097154 | T | 2334.255988 | 1167.631632 | 2317.229439 | 1159.118357 | 2316.245423 | 1158.626349 | 16 |
| 4 | 430.229625 | 215.618450 | 413.203076 | 207.105176 | 412.219060 | 206.613168 | S | 2233.208309 | 1117.107792 | 2216.181760 | 1108.594518 | 2215.197744 | 1108.102510 | 15 |
| 5 | 487.251089 | 244.129182 | 470.224540 | 235.615908 | 469.240524 | 235.123900 | G | 2146.176281 | 1073.591778 | 2129.149732 | 1065.078504 | 2128.165716 | 1064.586496 | 14 |
| 6 | 584.303853 | 292.655565 | 567.277304 | 284.142290 | 566.293288 | 283.650282 | P | 2089.154817 | 1045.081046 | 2072.128268 | 1036.567772 | 2071.144252 | 1036.075764 | 13 |
| 7 | **698.346780** | 349.677028 | 681.320231 | 341.163753 | 680.336215 | 340.671745 | N | 1992.102053 | 996.554665 | 1975.075504 | 988.041390 | 1974.091488 | 987.549382 | 12 |
| 8 | **1137.572106** | **569.289691** | 1120.545557 | 560.776416 | 1119.561541 | 560.284408 | Q | 1878.059126 | 939.533201 | 1861.032577 | 931.019927 | 1860.048561 | 930.527919 | 11 |
| 9 | **1266.614699** | 633.810988 | 1249.588150 | 625.297713 | 1248.604134 | 624.805705 | E | *1438.833800* | 719.920538 | 1421.807251 | 711.407264 | 1420.823235 | 710.915256 | 10 |
| 10 | **1705.840025** | **853.423651** | 1688.813476 | 844.910376 | 1687.829460 | 844.418368 | Q | *1309.791207* | 655.399242 | 1292.764658 | 646.885967 | 1291.780642 | 646.393959 | 9 |
| 11 | **1804.908439** | 902.957858 | 1787.881890 | 894.444583 | 1786.897874 | 893.952575 | V | *870.565881* | 435.786579 | 853.539332 | 427.273304 | 852.555316 | 426.781296 | 8 |
| 12 | 1891.940467 | 946.473872 | 1874.913918 | 937.960597 | 1873.929902 | 937.468589 | S | *771.497467* | 386.252372 | 754.470918 | 377.739097 | 753.486902 | 377.247089 | 7 |
| 13 | 1988.993231 | 995.000254 | 1971.966682 | 986.486979 | 1970.982666 | 985.994971 | P | *684.465439* | 342.736358 | 667.438890 | 334.223083 | 666.454874 | 333.731075 | 6 |
| 14 | 2102.077295 | 1051.542285 | 2085.050746 | 1043.029011 | 2084.066730 | 1042.537003 | L | 587.412675 | 294.209976 | 570.386126 | 285.696701 | 569.402110 | 285.204693 | 5 |
| 15 | 2203.124974 | 1102.066125 | 2186.098425 | 1093.552850 | 2185.114409 | 1093.060842 | T | *474.328611* | 237.667944 | 457.302062 | 229.154669 | 456.318046 | 228.662661 | 4 |
| 16 | 2316.209038 | **1158.608157** | 2299.182489 | 1150.094882 | 2298.198473 | 1149.602874 | L | *373.280932* | 187.144104 | 356.254383 | 178.630830 | | | 3 |
| 17 | 2429.293102 | 1215.150189 | 2412.266553 | 1206.636914 | 2411.282537 | 1206.144906 | L | *260.196868* | 130.602072 | 243.170319 | 122.088798 | | | 2 |
| 18 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.0 | 2574.391342 | 0.023450 | QLTSGPNQEQVSPLTLLK |
| 27.9 | 2574.391342 | 0.023450 | QLTSGPNQEQVSPLTLLK |
| 11.8 | 2574.391342 | 0.023450 | QLTSGPNQEQVSPLTLLK |

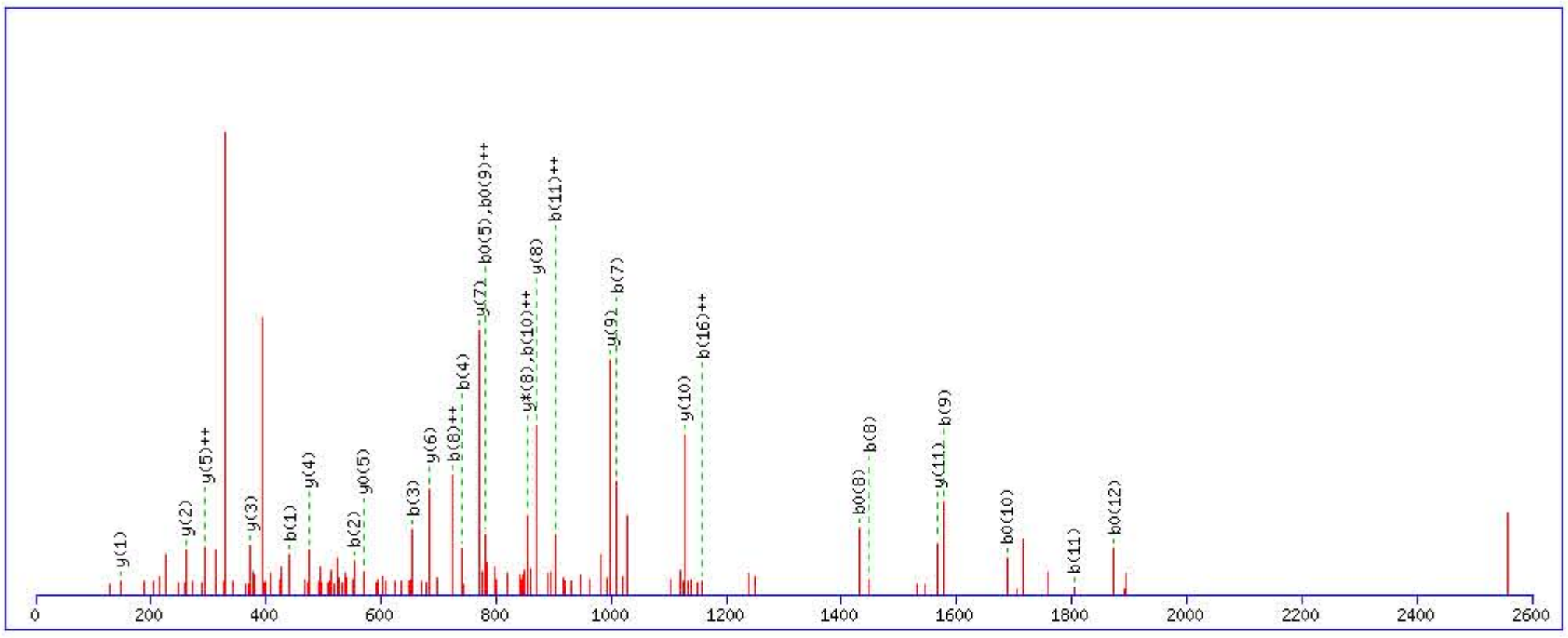
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QLTSGPNQEQVSPLTLLK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

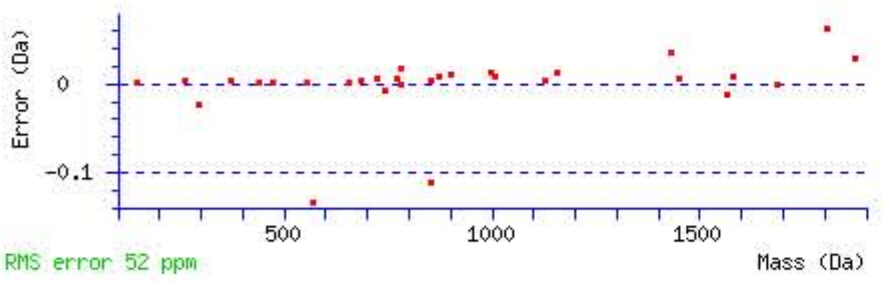
Match to Query 55236: 2574.427812 from(859.149880,3+) rtinseconds(2659) index(9030)
Title: Locus:1.1.1.2203.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

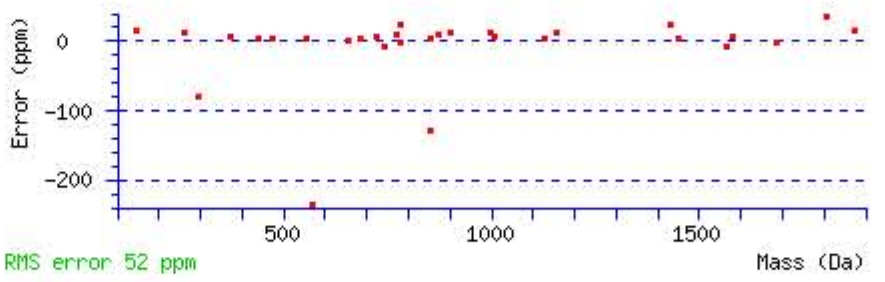
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2574.391342
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q1 : Biotin:Thermo-21345 (Q)
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 3.5e-006
**Matches :** 30/194 fragment ions using 50 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *440.232602* | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 18 |
| 2 | *553.316666* | 277.161971 | 536.290117 | 268.648697 | | | L | 2136.173304 | 1068.590290 | 2119.146755 | 1060.077015 | 2118.162739 | 1059.585007 | 17 |
| 3 | *654.364345* | 327.685811 | 637.337796 | 319.172536 | 636.353780 | 318.680528 | T | 2023.089240 | 1012.048258 | 2006.062691 | 1003.534984 | 2005.078675 | 1003.042976 | 16 |
| 4 | *741.396373* | 371.201825 | 724.369824 | 362.688550 | 723.385808 | 362.196542 | S | 1922.041561 | 961.524419 | 1905.015012 | 953.011144 | 1904.030996 | 952.519136 | 15 |
| 5 | 798.417837 | 399.712557 | 781.391288 | 391.199282 | 780.407272 | 390.707274 | G | 1835.009533 | 918.008405 | 1817.982984 | 909.495130 | 1816.998968 | 909.003122 | 14 |
| 6 | 895.470601 | 448.238939 | 878.444052 | 439.725664 | 877.460036 | 439.233656 | P | 1777.988069 | 889.497673 | 1760.961520 | 880.984398 | 1759.977504 | 880.492390 | 13 |
| 7 | *1009.513528* | 505.260402 | 992.486979 | 496.747128 | 991.502963 | 496.255120 | N | 1680.935305 | 840.971291 | 1663.908756 | 832.458016 | 1662.924740 | 831.966008 | 12 |
| 8 | *1448.738854* | **724.873065** | 1431.712305 | 716.359791 | 1430.728289 | 715.867782 | Q | *1566.892378* | 783.949827 | 1549.865829 | 775.436553 | 1548.881813 | 774.944545 | 11 |
| 9 | *1577.781447* | 789.394362 | 1560.754898 | 780.881087 | 1559.770882 | 780.389079 | E | *1127.667052* | 564.337164 | 1110.640503 | 555.823890 | 1109.656487 | 555.331882 | 10 |
| 10 | 1705.840025 | **853.423651** | 1688.813476 | 844.910376 | 1687.829460 | 844.418368 | Q | *998.624459* | 499.815868 | 981.597910 | 491.302593 | 980.613894 | 490.810585 | 9 |
| 11 | *1804.908439* | **902.957858** | 1787.881890 | 894.444583 | 1786.897874 | 893.952575 | V | *870.565881* | 435.786579 | 853.539332 | 427.273304 | 852.555316 | 426.781296 | 8 |
| 12 | 1891.940467 | 946.473872 | 1874.913918 | 937.960597 | 1873.929902 | 937.468589 | S | *771.497467* | 386.252372 | 754.470918 | 377.739097 | 753.486902 | 377.247089 | 7 |
| 13 | 1988.993231 | 995.000254 | 1971.966682 | 986.486979 | 1970.982666 | 985.994971 | P | *684.465439* | 342.736358 | 667.438890 | 334.223083 | 666.454874 | 333.731075 | 6 |
| 14 | 2102.077295 | 1051.542285 | 2085.050746 | 1043.029011 | 2084.066730 | 1042.537003 | L | 587.412675 | 294.209976 | 570.386126 | 285.696701 | 569.402110 | 285.204693 | 5 |
| 15 | 2203.124974 | 1102.066125 | 2186.098425 | 1093.552850 | 2185.114409 | 1093.060842 | T | *474.328611* | 237.667944 | 457.302062 | 229.154669 | 456.318046 | 228.662661 | 4 |
| 16 | 2316.209038 | **1158.608157** | 2299.182489 | 1150.094882 | 2298.198473 | 1149.602874 | L | *373.280932* | 187.144104 | 356.254383 | 178.630830 | | | 3 |
| 17 | 2429.293102 | 1215.150189 | 2412.266553 | 1206.636914 | 2411.282537 | 1206.144906 | L | *260.196868* | 130.602072 | 243.170319 | 122.088798 | | | 2 |
| 18 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.7 | 2574.391342 | 0.036470 | QLTSGPNQEQVSPLTLLK |
| 42.0 | 2574.391342 | 0.036470 | QLTSGPNQEQVSPLTLLK |
| 14.9 | 2574.391342 | 0.036470 | QLTSGPNQEQVSPLTLLK |
| 0.5 | 2574.402542 | 0.025270 | NTLAVANMKVSRPVMEKVPYALK |

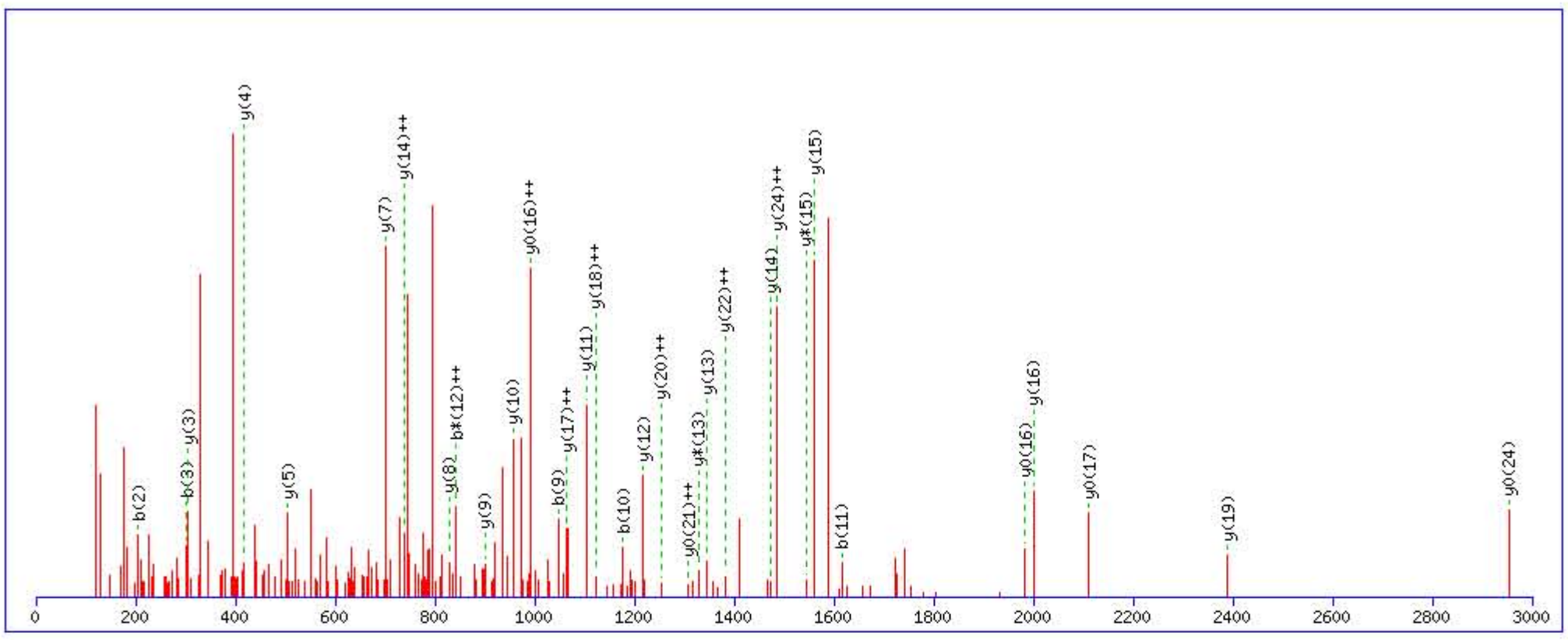
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GFPIKEDFLEQSEQLFGAKPVSLTGK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

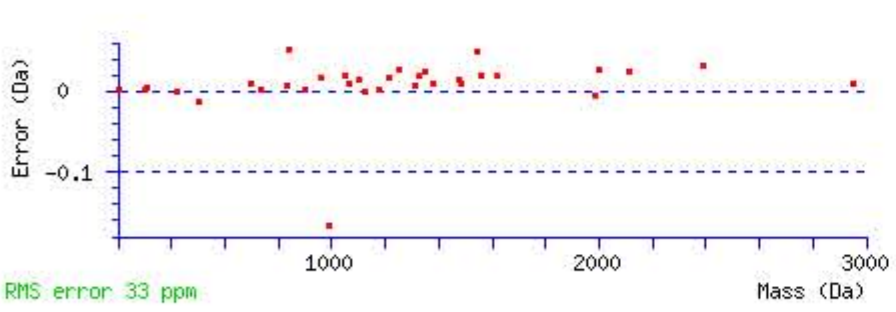
Match to Query 61514: 3175.694896 from(794.931000,4+) rtinseconds(2767) index(9728)
Title: Locus:1.1.1.2240.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

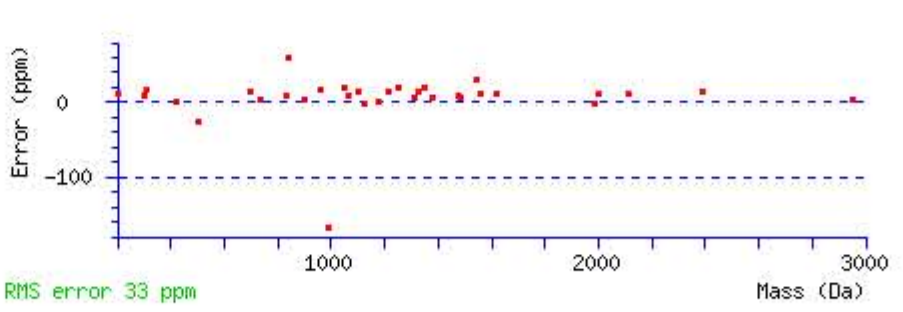
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3175.662750
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 63 **Expect:** 8.1e-006
**Matches :** 33/278 fragment ions using 72 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 26 |
| 2 | **205.097154** | 103.052215 | | | | | F | 3119.648573 | 1560.327924 | 3102.622024 | 1551.814650 | 3101.638008 | 1551.322642 | 25 |
| 3 | **302.149918** | 151.578597 | | | | | P | 2972.580159 | 1486.793717 | 2955.553610 | 1478.280443 | 2954.569594 | 1477.788435 | 24 |
| 4 | 415.233982 | 208.120629 | | | | | I | 2875.527395 | 1438.267335 | 2858.500846 | 1429.754061 | 2857.516830 | 1429.262053 | 23 |
| 5 | 543.328945 | 272.168111 | 526.302396 | 263.654836 | | | K | 2762.443331 | 1381.725303 | 2745.416782 | 1373.212029 | 2744.432766 | 1372.720021 | 22 |
| 6 | 672.371538 | 336.689407 | 655.344989 | 328.176133 | 654.360973 | 327.684125 | E | 2634.348368 | 1317.677822 | 2617.321819 | 1309.164547 | 2616.337803 | 1308.672539 | 21 |
| 7 | 787.398481 | 394.202879 | 770.371932 | 385.689604 | 769.387916 | 385.197596 | D | 2505.305775 | 1253.156525 | 2488.279226 | 1244.643251 | 2487.295210 | 1244.151243 | 20 |
| 8 | 934.466895 | 467.737086 | 917.440346 | 459.223811 | 916.456330 | 458.731803 | F | *2390.278832* | 1195.643054 | 2373.252283 | 1187.129779 | 2372.268267 | 1186.637771 | 19 |
| 9 | **1047.550959** | 524.279117 | 1030.524410 | 515.765843 | 1029.540394 | 515.273835 | L | 2243.210418 | 1122.108847 | 2226.183869 | 1113.595572 | 2225.199853 | 1113.103564 | 18 |
| 10 | **1176.593552** | 588.800414 | 1159.567003 | 580.287140 | 1158.582987 | 579.795132 | E | 2130.126354 | 1065.566815 | 2113.099805 | 1057.053540 | 2112.115789 | 1056.561532 | 17 |
| 11 | **1615.818878** | 808.413077 | 1598.792329 | 799.899803 | 1597.808313 | 799.407795 | Q | *2001.083761* | 1001.045519 | 1984.057212 | 992.532244 | 1983.073196 | 992.040236 | 16 |
| 12 | 1702.850906 | 851.929091 | 1685.824357 | 843.415817 | 1684.840341 | 842.923809 | S | *1561.858435* | 781.432856 | 1544.831886 | 772.919581 | 1543.847870 | 772.427573 | 15 |
| 13 | 1831.893499 | 916.450388 | 1814.866950 | 907.937113 | 1813.882934 | 907.445105 | E | *1474.826407* | 737.916842 | 1457.799858 | 729.403567 | 1456.815842 | 728.911559 | 14 |
| 14 | 1959.952077 | 980.479677 | 1942.925528 | 971.966402 | 1941.941512 | 971.474394 | Q | *1345.783814* | 673.395545 | 1328.757265 | 664.882271 | 1327.773249 | 664.390263 | 13 |
| 15 | 2073.036141 | 1037.021709 | 2056.009592 | 1028.508434 | 2055.025576 | 1028.016426 | L | *1217.725236* | 609.366256 | 1200.698687 | 600.852982 | 1199.714671 | 600.360974 | 12 |
| 16 | 2220.104555 | 1110.555916 | 2203.078006 | 1102.042641 | 2202.093990 | 1101.550633 | F | *1104.641172* | 552.824224 | 1087.614623 | 544.310949 | 1086.630607 | 543.818941 | 11 |
| 17 | 2277.126019 | 1139.066648 | 2260.099470 | 1130.553373 | 2259.115454 | 1130.061365 | G | *957.572758* | 479.290017 | 940.546209 | 470.776743 | 939.562193 | 470.284735 | 10 |
| 18 | 2348.163133 | 1174.585205 | 2331.136584 | 1166.071930 | 2330.152568 | 1165.579922 | A | *900.551294* | 450.779285 | 883.524745 | 442.266011 | 882.540729 | 441.774003 | 9 |
| 19 | 2476.258096 | 1238.632686 | 2459.231547 | 1230.119412 | 2458.247531 | 1229.627404 | K | *829.514180* | 415.260728 | 812.487631 | 406.747453 | 811.503615 | 406.255445 | 8 |
| 20 | 2573.310860 | 1287.159068 | 2556.284311 | 1278.645794 | 2555.300295 | 1278.153786 | P | *701.419217* | 351.213246 | 684.392668 | 342.699972 | 683.408652 | 342.207964 | 7 |
| 21 | 2672.379274 | 1336.693275 | 2655.352725 | 1328.180001 | 2654.368709 | 1327.687993 | V | 604.366453 | 302.686864 | 587.339904 | 294.173590 | 586.355888 | 293.681582 | 6 |
| 22 | 2759.411302 | 1380.209289 | 2742.384753 | 1371.696015 | 2741.400737 | 1371.204007 | S | *505.298039* | 253.152657 | 488.271490 | 244.639383 | 487.287474 | 244.147375 | 5 |
| 23 | 2872.495366 | 1436.751321 | 2855.468817 | 1428.238047 | 2854.484801 | 1427.746039 | L | *418.266011* | 209.636643 | 401.239462 | 201.123369 | 400.255446 | 200.631361 | 4 |
| 24 | 2973.543045 | 1487.275161 | 2956.516496 | 1478.761886 | 2955.532480 | 1478.269878 | T | *305.181947* | 153.094611 | 288.155398 | 144.581337 | 287.171382 | 144.089329 | 3 |
| 25 | 3030.564509 | 1515.785893 | 3013.537960 | 1507.272618 | 3012.553944 | 1506.780610 | G | 204.134268 | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 26 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 63.5 | 3175.662750 | 0.032146 | GFPIKEDFLEQSEQLFGAKPVSLTGK |
| 34.8 | 3175.662750 | 0.032146 | GFPIKEDFLEQSEQLFGAKPVSLTGK |

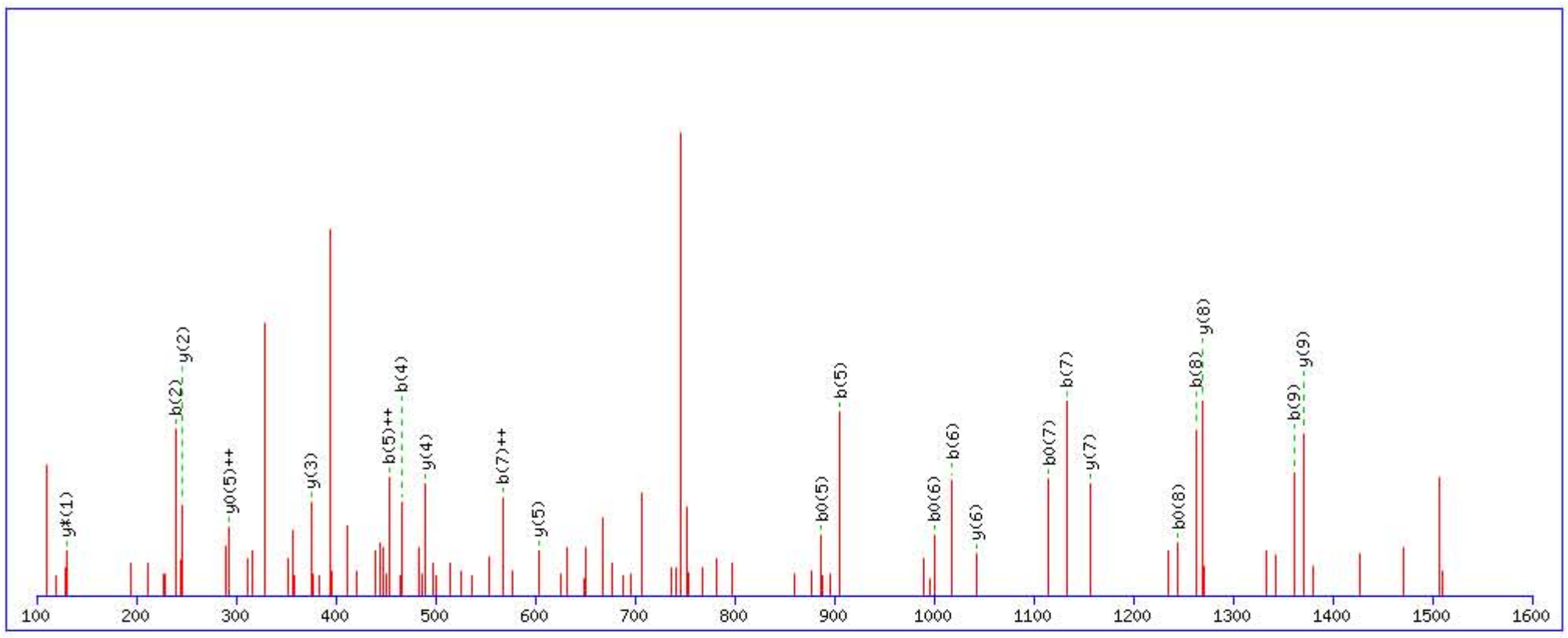
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HTLNQIDEVK**
Found in **FETUA_HUMAN**, Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1

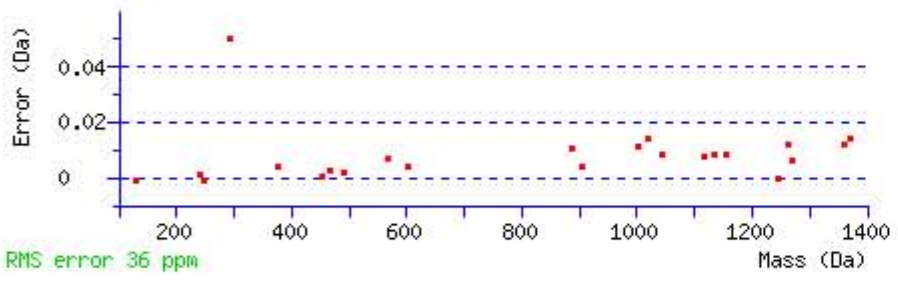
Match to Query 31351: 1506.791328 from(754.402940,2+) rtinseconds(1636) index(47897)
Title: Locus:1.1.1.1807.22 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

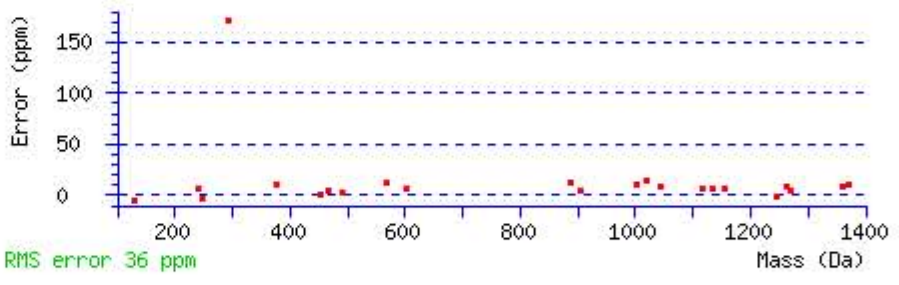
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1506.786438
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 52 **Expect:** 0.00013
**Matches :** 23/96 fragment ions using 40 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 10 |
| 2 | *239.113867* | 120.060571 | | | 221.103302 | 111.055289 | T | *1370.734814* | 685.871045 | 1353.708265 | 677.357771 | 1352.724249 | 676.865763 | 9 |
| 3 | 352.197931 | 176.602603 | | | 334.187366 | 167.597321 | L | *1269.687135* | 635.347206 | 1252.660586 | 626.833931 | 1251.676570 | 626.341923 | 8 |
| 4 | *466.240858* | 233.624067 | 449.214309 | 225.110793 | 448.230293 | 224.618785 | N | *1156.603071* | 578.805174 | 1139.576522 | 570.291899 | 1138.592506 | 569.799891 | 7 |
| 5 | *905.466184* | **453.236730** | 888.439635 | 444.723456 | 887.455619 | 444.231448 | Q | *1042.560144* | 521.783710 | 1025.533595 | 513.270436 | 1024.549579 | 512.778428 | 6 |
| 6 | *1018.550248* | 509.778762 | 1001.523699 | 501.265488 | 1000.539683 | 500.773480 | I | *603.334818* | 302.171047 | 586.308269 | 293.657773 | 585.324253 | 293.165765 | 5 |
| 7 | *1133.577191* | **567.292234** | 1116.550642 | 558.778959 | 1115.566626 | 558.286951 | D | *490.250754* | 245.629015 | 473.224205 | 237.115741 | 472.240189 | 236.623733 | 4 |
| 8 | *1262.619784* | 631.813530 | 1245.593235 | 623.300256 | 1244.609219 | 622.808248 | E | *375.223811* | 188.115544 | 358.197262 | 179.602269 | 357.213246 | 179.110261 | 3 |
| 9 | *1361.688198* | 681.347737 | 1344.661649 | 672.834463 | 1343.677633 | 672.342455 | V | *246.181218* | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 10 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.0 | 1506.786438 | 0.004890 | HTLNQIDEVK |
| 9.8 | 1506.779037 | 0.012291 | EHQALQDLVDLAR |
| 4.5 | 1506.790253 | 0.001075 | SSRFLKEGNNLSR |
| 3.9 | 1506.771149 | 0.020179 | GEKSSMERLLTEK |
| 3.9 | 1506.792969 | -0.001641 | IGDFGLTKAIETDK |
| 3.6 | 1506.769150 | 0.022178 | VFSRSSQLQYHR |
| 3.3 | 1506.794983 | -0.003655 | HRATQSGQRR |
| 2.4 | 1506.792953 | -0.001625 | EDFEKTLSQAIVK |
| 1.9 | 1506.808899 | -0.017571 | HDVIMKSQLRHK |

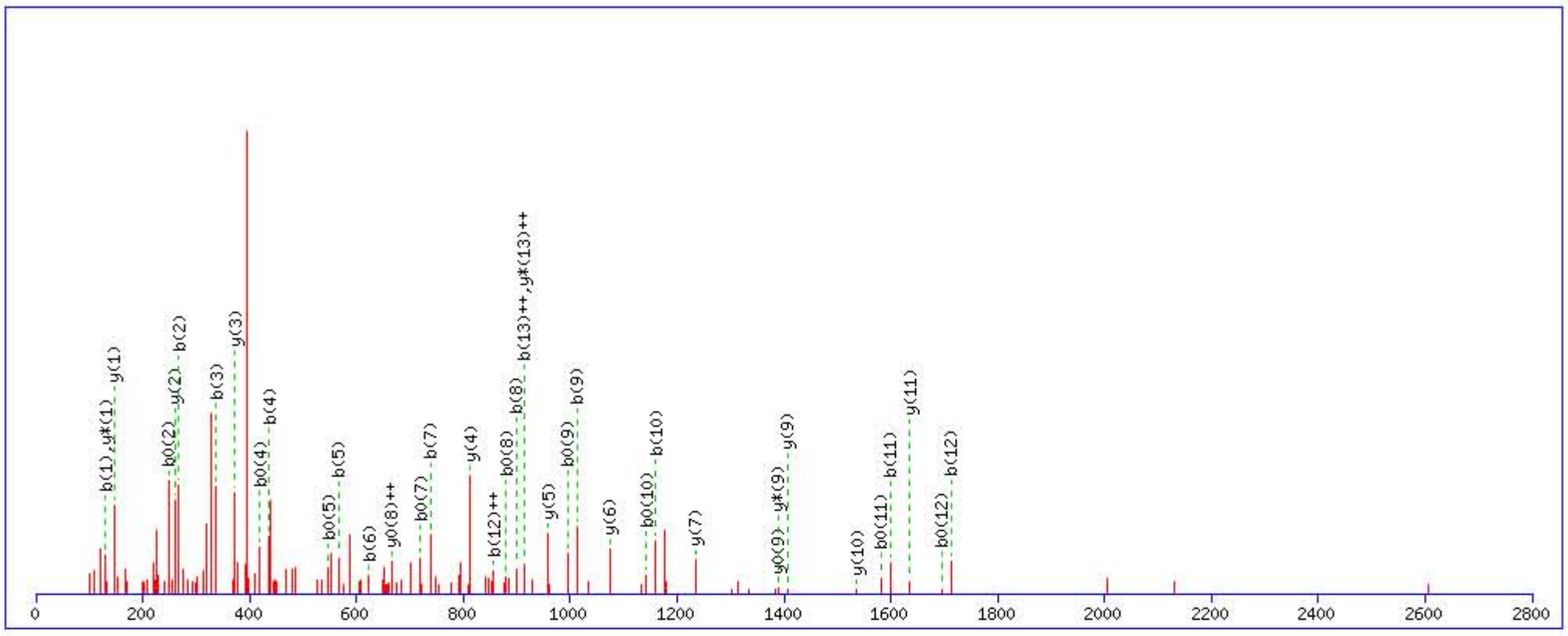
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EHAVEGDCDFQLLK**
Found in **FETUA_HUMAN**, Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1

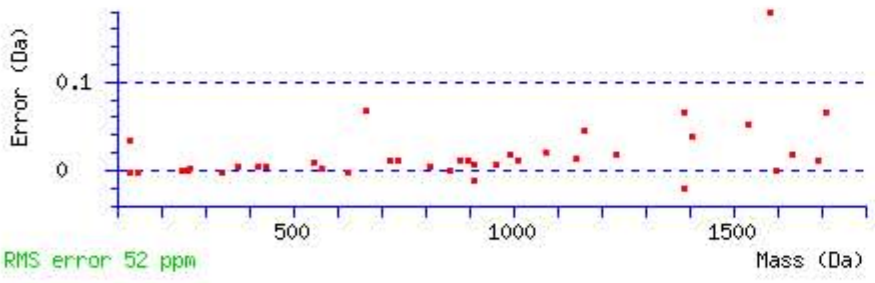
Match to Query 43596: 1970.934972 from(657.985600,3+) rtinseconds(2080) index(6097)
Title: Locus:1.1.1.2001.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

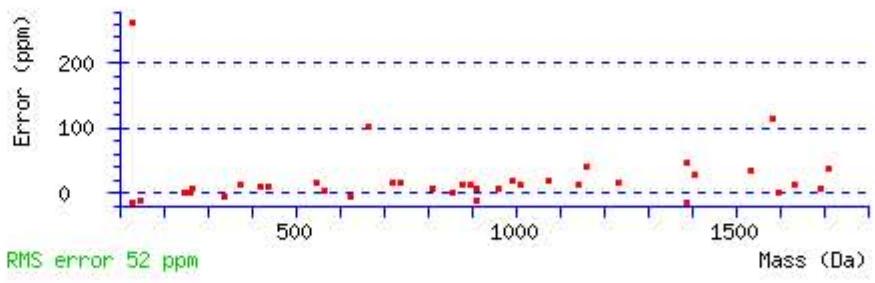
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1970.923019
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 81 **Expect:** 1e-007
**Matches** : 38/126 fragment ions using 56 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *130.049869* | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 14 |
| 2 | *267.108781* | 134.058028 | | | 249.098216 | 125.052746 | H | 1842.887704 | 921.947490 | 1825.861155 | 913.434216 | 1824.877139 | 912.942207 | 13 |
| 3 | *338.145895* | 169.576585 | | | 320.135330 | 160.571303 | A | 1705.828792 | 853.418034 | 1688.802243 | 844.904760 | 1687.818227 | 844.412752 | 12 |
| 4 | *437.214309* | 219.110792 | | | 419.203744 | 210.105510 | V | **1634.791678** | 817.899477 | 1617.765129 | 809.386203 | 1616.781113 | 808.894195 | 11 |
| 5 | *566.256902* | 283.632089 | | | 548.246337 | 274.626807 | E | **1535.723264** | 768.365270 | 1518.696715 | 759.851996 | 1517.712699 | 759.359988 | 10 |
| 6 | *623.278366* | 312.142821 | | | 605.267801 | 303.137539 | G | **1406.680671** | 703.843974 | 1389.654122 | 695.330699 | 1388.670106 | 694.838691 | 9 |
| 7 | *738.305309* | 369.656293 | | | 720.294744 | 360.651010 | D | 1349.659207 | 675.333241 | 1332.632658 | 666.819967 | 1331.648642 | 666.327959 | 8 |
| 8 | *898.335958* | 449.671617 | | | 880.325393 | 440.666335 | C | **1234.632264** | 617.819770 | 1217.605715 | 609.306496 | 1216.621699 | 608.814488 | 7 |
| 9 | *1013.362901* | 507.185089 | | | 995.352336 | 498.179806 | D | **1074.601615** | 537.804446 | 1057.575066 | 529.291171 | 1056.591050 | 528.799163 | 6 |
| 10 | *1160.431315* | 580.719296 | | | 1142.420750 | 571.714013 | F | **959.574672** | 480.290974 | 942.548123 | 471.777700 | | | 5 |
| 11 | *1599.656641* | 800.331959 | 1582.630092 | 791.818684 | 1581.646076 | 791.326676 | Q | **812.506258** | 406.756767 | 795.479709 | 398.243493 | | | 4 |
| 12 | *1712.740705* | **856.873991** | 1695.714156 | 848.360716 | 1694.730140 | 847.868708 | L | **373.280932** | 187.144104 | 356.254383 | 178.630829 | | | 3 |
| 13 | 1825.824769 | **913.416023** | 1808.798220 | 904.902748 | 1807.814204 | 904.410740 | L | **260.196868** | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 14 | | | | | | | K | **147.112804** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 80.9 | 1970.923019 | 0.011953 | EHAVEGDCDFQLLK |
| 6.2 | 1970.959396 | -0.024424 | DVQSAMDRYTAFLK |
| 3.2 | 1970.959381 | -0.024409 | NEEKPVQMMFKQSTFK |

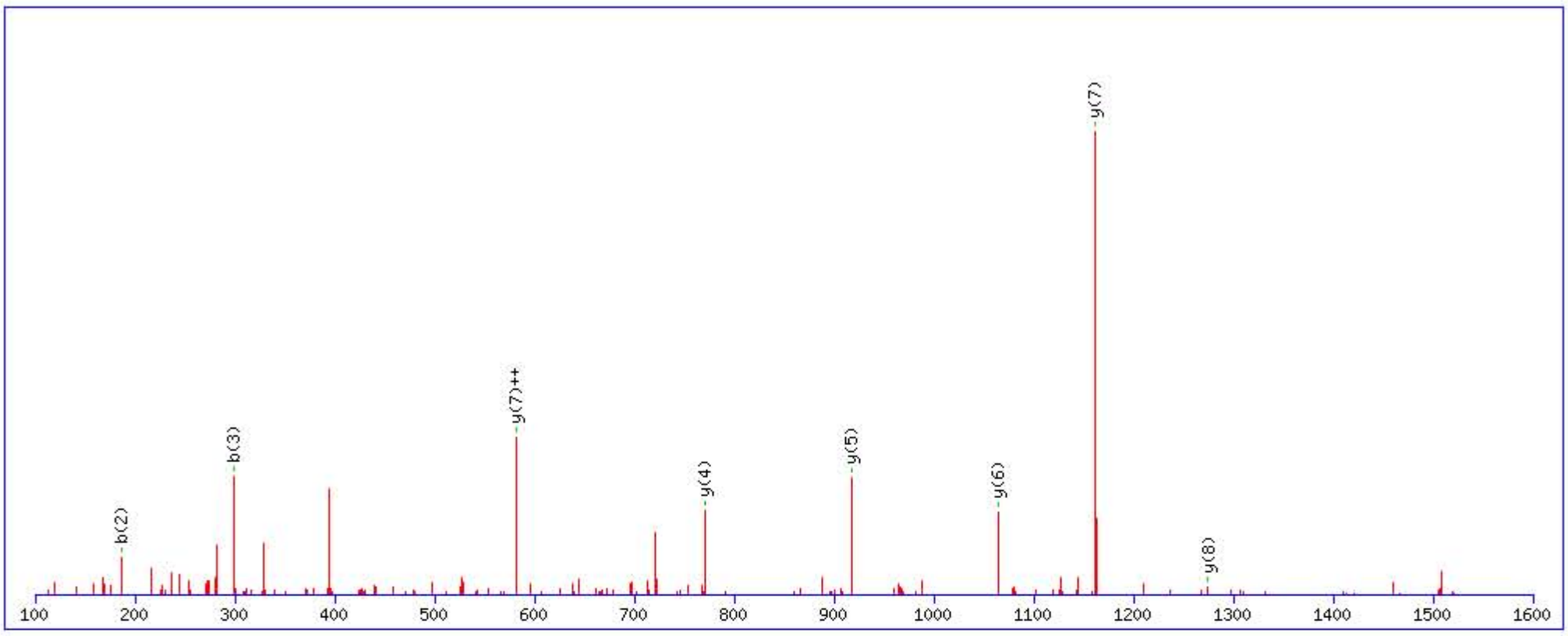
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QGIPFFGQVR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

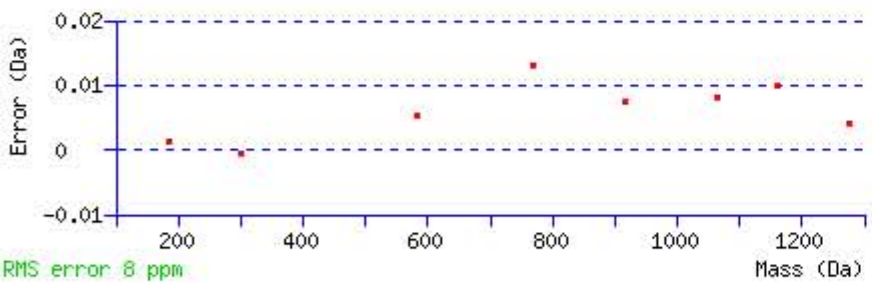
Match to Query 29910: 1458.798768 from(730.406660,2+) rtinseconds(2539) index(23443)
Title: Locus:1.1.1.3266.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

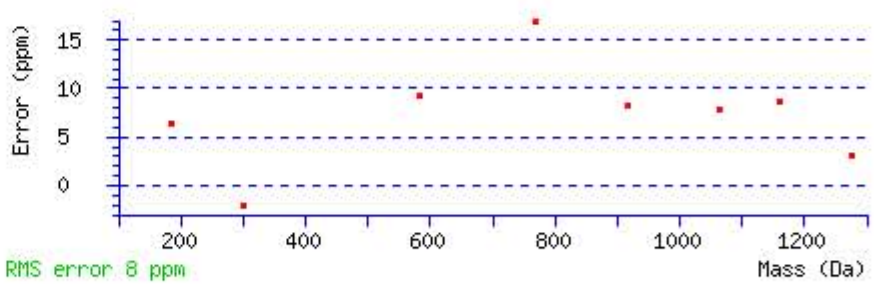
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1458.780594
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 29 **Expect:** 0.0025
**Matches :** 8/72 fragment ions using 14 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.065854 | 65.036565 | 112.039305 | 56.523291 | Q | | | | | 10 |
| 2 | 186.087318 | 93.547297 | 169.060769 | 85.034023 | G | 1331.729276 | 666.368276 | 1314.702727 | 657.855002 | 9 |
| 3 | 299.171382 | 150.089329 | 282.144833 | 141.576055 | I | *1274.707812* | 637.857544 | 1257.681263 | 629.344270 | 8 |
| 4 | 396.224146 | 198.615711 | 379.197597 | 190.102436 | P | *1161.623748* | 581.315512 | 1144.597199 | 572.802238 | 7 |
| 5 | 543.292560 | 272.149918 | 526.266011 | 263.636643 | F | *1064.570984* | 532.789130 | 1047.544435 | 524.275856 | 6 |
| 6 | 690.360974 | 345.684125 | 673.334425 | 337.170850 | F | *917.502570* | 459.254923 | 900.476021 | 450.741649 | 5 |
| 7 | 747.382438 | 374.194857 | 730.355889 | 365.681582 | G | *770.434156* | 385.720716 | 753.407607 | 377.207442 | 4 |
| 8 | 1186.607764 | 593.807520 | 1169.581215 | 585.294246 | Q | 713.412692 | 357.209984 | 696.386143 | 348.696710 | 3 |
| 9 | 1285.676178 | 643.341727 | 1268.649629 | 634.828453 | V | 274.187366 | 137.597321 | 257.160817 | 129.084047 | 2 |
| 10 | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 28.5 | 1458.780594 | 0.018174 | QGIPFFGQVR |
| 0.9 | 1458.805054 | -0.006286 | AVQPLLKVSMSMR |

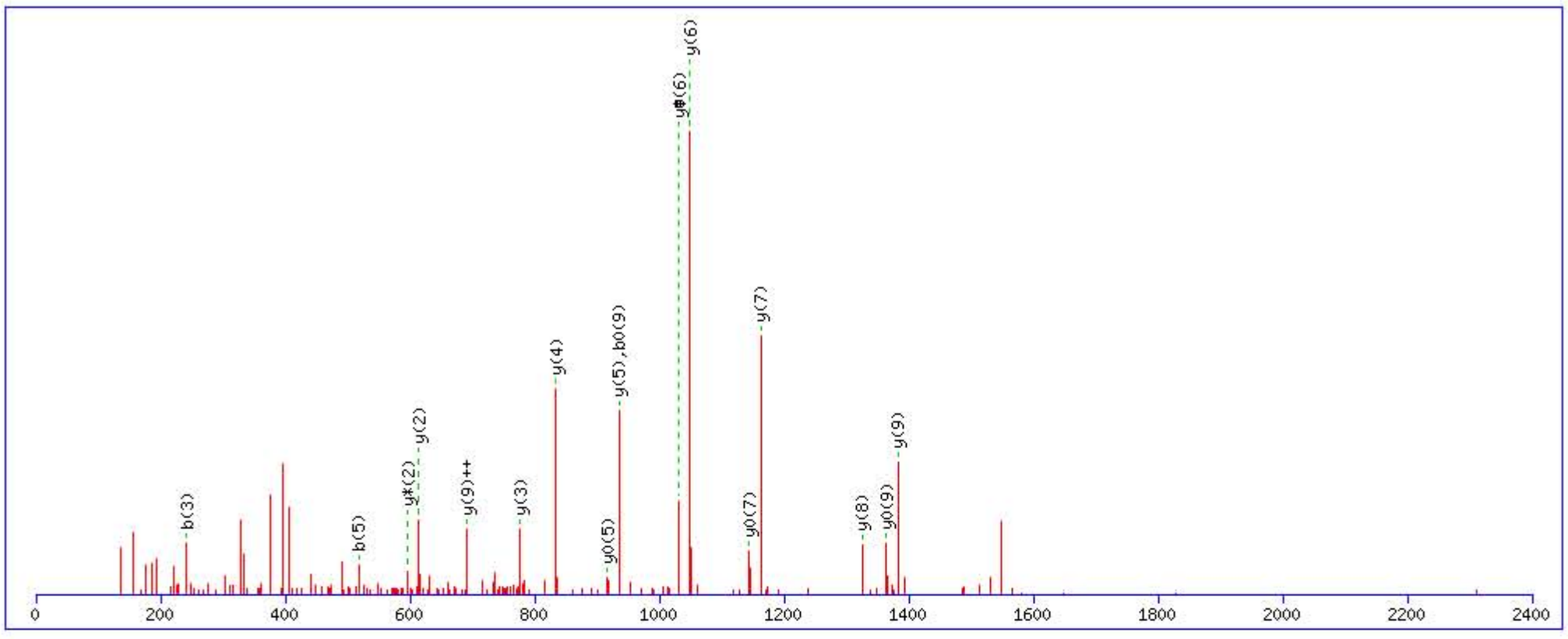
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AIGYLNTGYQR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

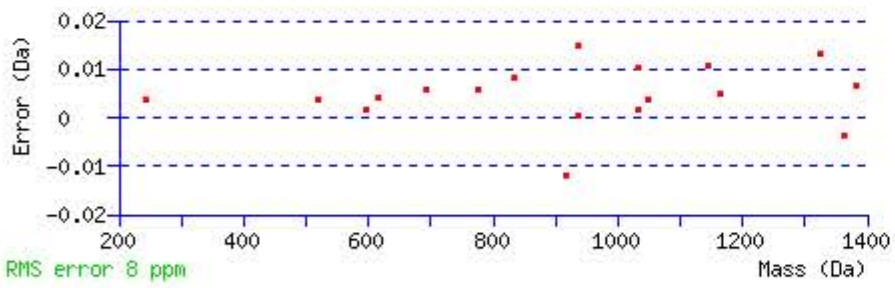
Match to Query 33116: 1565.812628 from(783.913590,2+) rtinseconds(1987) index(20164)
Title: Locus:1.1.1.3074.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

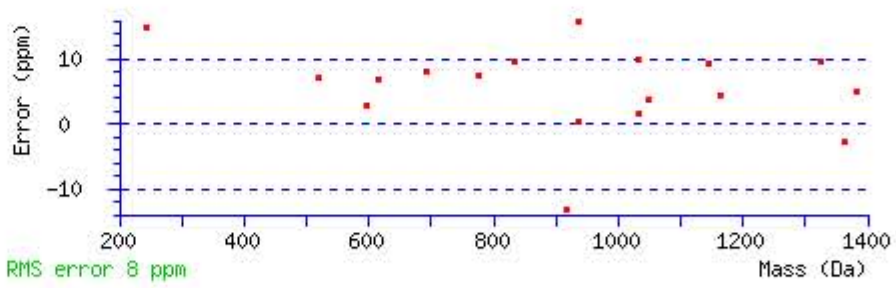
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1565.802414
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 52 **Expect:** 0.00014
**Matches :** 18/90 fragment ions using 29 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 11 |
| 2 | 185.128454 | 93.067865 | | | | | I | 1495.772598 | 748.389937 | 1478.746049 | 739.876663 | 1477.762033 | 739.384655 | 10 |
| 3 | **242.149918** | 121.578597 | | | | | G | *1382.688534* | 691.847905 | 1365.661985 | 683.334631 | 1364.677969 | 682.842623 | 9 |
| 4 | 405.213247 | 203.110261 | | | | | Y | *1325.667070* | 663.337173 | 1308.640521 | 654.823899 | 1307.656505 | 654.331890 | 8 |
| 5 | **518.297311** | 259.652294 | | | | | L | *1162.603741* | 581.805509 | 1145.577192 | 573.292234 | 1144.593176 | 572.800226 | 7 |
| 6 | 632.340238 | 316.673757 | 615.313689 | 308.160483 | | | N | *1049.519677* | 525.263477 | 1032.493128 | 516.750202 | 1031.509112 | 516.258194 | 6 |
| 7 | 733.387917 | 367.197597 | 716.361368 | 358.684322 | 715.377352 | 358.192314 | T | *935.476750* | 468.242013 | 918.450201 | 459.728739 | 917.466185 | 459.236731 | 5 |
| 8 | 790.409381 | 395.708329 | 773.382832 | 387.195054 | 772.398816 | 386.703046 | G | *834.429071* | 417.718174 | 817.402522 | 409.204899 | | | 4 |
| 9 | 953.472710 | 477.239993 | 936.446161 | 468.726719 | 935.462145 | 468.234711 | Y | *777.407607* | 389.207442 | 760.381058 | 380.694167 | | | 3 |
| 10 | 1392.698036 | 696.852656 | 1375.671487 | 688.339382 | 1374.687471 | 687.847374 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 11 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.3 | 1565.802414 | 0.010214 | AIGYLNTGYQR |
| 11.5 | 1565.827393 | -0.014765 | VHPALNVSTRTSER |
| 4.8 | 1565.802399 | 0.010229 | FQELPFRKNEMK |

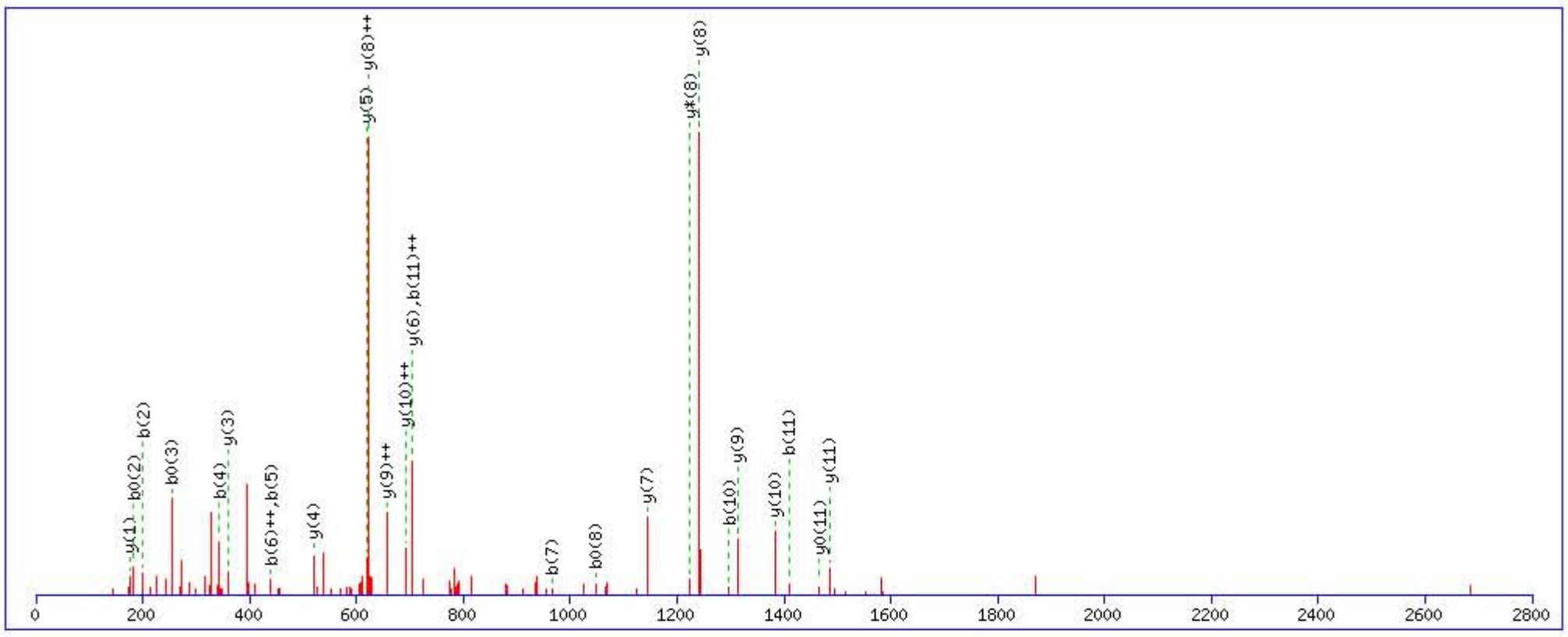
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VTAAPQSVCALR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

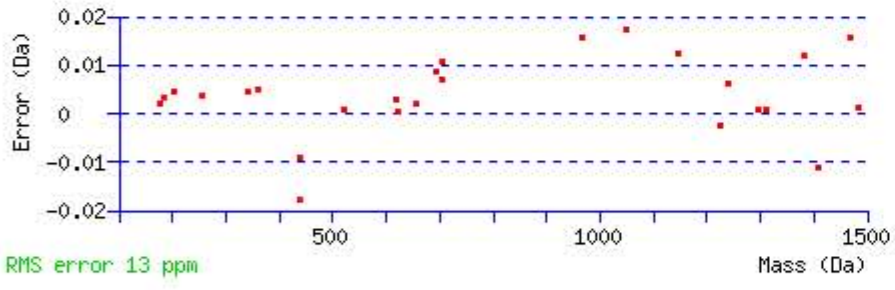
Match to Query 33799: 1582.841868 from(792.428210,2+) rtinseconds(1837) index(19093)
Title: Locus:1.1.1.3022.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

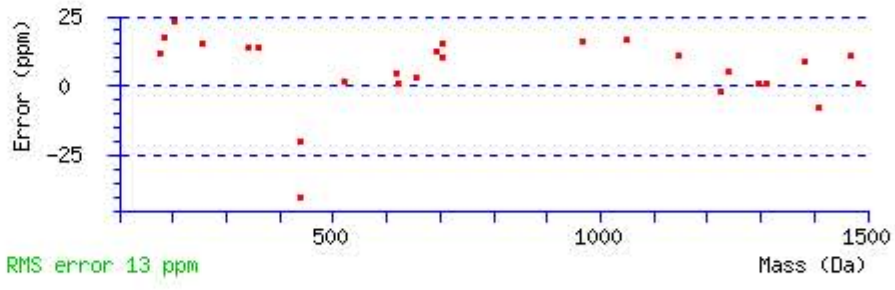
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1582.832352
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 68 **Expect:** 1.5e-006
**Matches :** 26/110 fragment ions using 42 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 12 |
| 2 | **201.123369** | 101.065322 | | | 183.112804 | 92.060040 | T | *1484.771218* | 742.889247 | 1467.744669 | 734.375972 | 1466.760653 | 733.883964 | 11 |
| 3 | 272.160483 | 136.583879 | | | 254.149918 | 127.578597 | A | *1383.723539* | 692.365407 | 1366.696990 | 683.852133 | 1365.712974 | 683.360125 | 10 |
| 4 | **343.197597** | 172.102437 | | | 325.187032 | 163.097154 | A | *1312.686425* | 656.846850 | 1295.659876 | 648.333576 | 1294.675860 | 647.841568 | 9 |
| 5 | **440.250361** | 220.628819 | | | 422.239796 | 211.623536 | P | *1241.649311* | 621.328293 | 1224.622762 | 612.815019 | 1223.638746 | 612.323011 | 8 |
| 6 | 879.475687 | **440.241482** | 862.449138 | 431.728207 | 861.465122 | 431.236199 | Q | *1144.596547* | 572.801911 | 1127.569998 | 564.288637 | 1126.585982 | 563.796629 | 7 |
| 7 | **966.507715** | 483.757496 | 949.481166 | 475.244221 | 948.497150 | 474.752213 | S | *705.371221* | 353.189248 | 688.344672 | 344.675974 | 687.360656 | 344.183966 | 6 |
| 8 | 1065.576129 | 533.291703 | 1048.549580 | 524.778428 | 1047.565564 | 524.286420 | V | *618.339193* | 309.673234 | 601.312644 | 301.159960 | | | 5 |
| 9 | 1225.606778 | 613.307027 | 1208.580229 | 604.793753 | 1207.596213 | 604.301745 | C | *519.270779* | 260.139028 | 502.244230 | 251.625753 | | | 4 |
| 10 | **1296.643892** | 648.825584 | 1279.617343 | 640.312310 | 1278.633327 | 639.820302 | A | *359.240130* | 180.123703 | 342.213581 | 171.610428 | | | 3 |
| 11 | **1409.727956** | **705.367616** | 1392.701407 | 696.854342 | 1391.717391 | 696.362333 | L | 288.203016 | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 12 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 67.9 | 1582.832352 | 0.009516 | VTAAPQSVCALR |
| 5.4 | 1582.865356 | -0.023488 | QPAPGPVEKPPR |
| 2.3 | 1582.850067 | -0.008199 | AEQEASLQKLR |
| 1.9 | 1582.853943 | -0.012075 | LSSGSQSSHILVRGR |
| 1.5 | 1582.821564 | 0.020304 | LSKAVATWHANTER |
| 1.0 | 1582.861328 | -0.019460 | RDKGETIQGLR |
| 0.9 | 1582.853912 | -0.012044 | RKPASGGLAASSSAPAR |
| 0.6 | 1582.857956 | -0.016088 | LEDVKSQWVRPAR |
| 0.6 | 1582.831451 | 0.010417 | SAKELVEQDIQPAR |
| 0.5 | 1582.846756 | -0.004888 | VTEVWTLPQVAGQR |

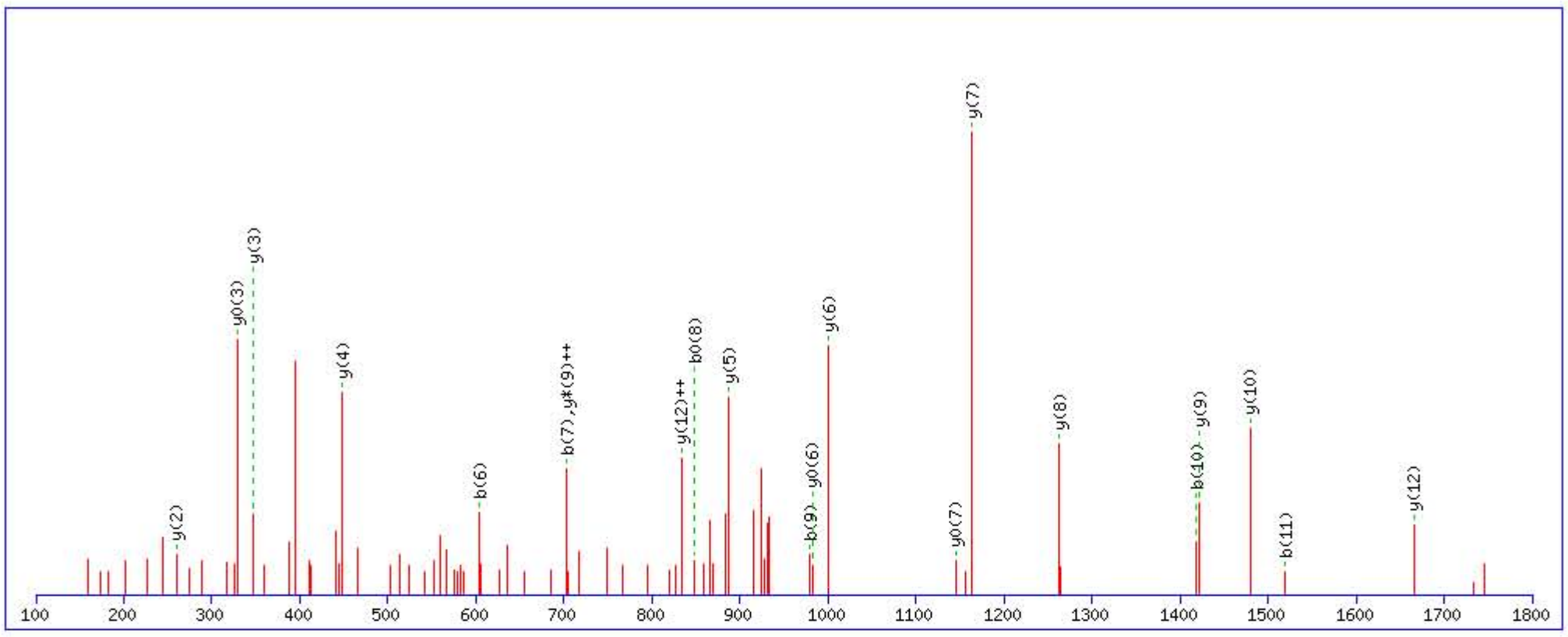
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VTGEGCVYLQTSLK**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

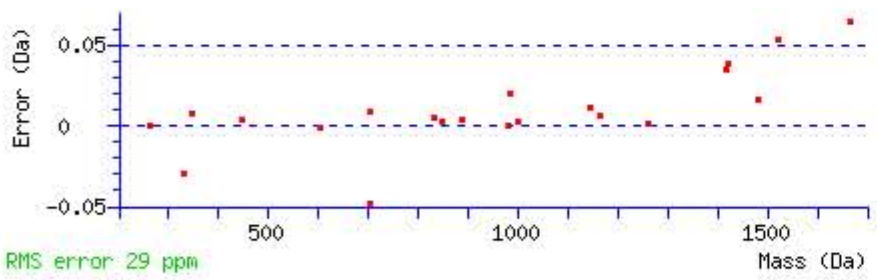
Match to Query 41616: 1864.965428 from(933.489990,2+) rtinseconds(2106) index(20876)
Title: Locus:1.1.1.3115.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

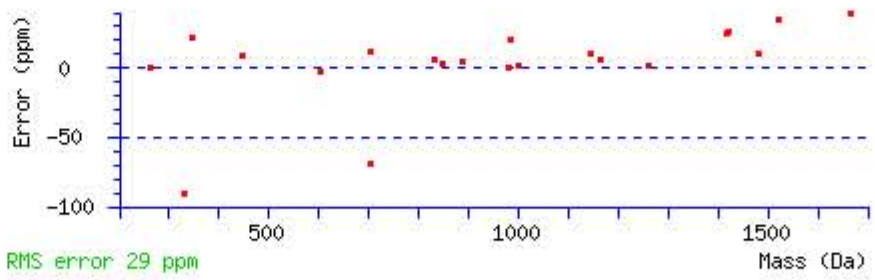
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1864.942703
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 9.6e-005
**Matches :** 21/132 fragment ions using 40 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 14 |
| 2 | 201.123369 | 101.065322 | | | 183.112804 | 92.060040 | T | 1766.881557 | 883.944417 | 1749.855008 | 875.431142 | 1748.870992 | 874.939134 | 13 |
| 3 | 258.144833 | 129.576055 | | | 240.134268 | 120.570772 | G | *1665.833878* | 833.420577 | 1648.807329 | 824.907303 | 1647.823313 | 824.415295 | 12 |
| 4 | 387.187426 | 194.097351 | | | 369.176861 | 185.092069 | E | 1608.812414 | 804.909845 | 1591.785865 | 796.396571 | 1590.801849 | 795.904563 | 11 |
| 5 | 444.208890 | 222.608083 | | | 426.198325 | 213.602801 | G | *1479.769821* | 740.388549 | 1462.743272 | 731.875274 | 1461.759256 | 731.383266 | 10 |
| 6 | **604.239539** | 302.623408 | | | 586.228974 | 293.618125 | C | *1422.748357* | 711.877817 | 1405.721808 | 703.364542 | 1404.737792 | 702.872534 | 9 |
| 7 | **703.307953** | 352.157615 | | | 685.297388 | 343.152332 | V | *1262.717708* | 631.862492 | 1245.691159 | 623.349218 | 1244.707143 | 622.857210 | 8 |
| 8 | 866.371282 | 433.689279 | | | 848.360717 | 424.683997 | Y | *1163.649294* | 582.328285 | 1146.622745 | 573.815011 | 1145.638729 | 573.323003 | 7 |
| 9 | **979.455346** | 490.231311 | | | 961.444781 | 481.226029 | L | *1000.585965* | 500.796621 | 983.559416 | 492.283346 | 982.575400 | 491.791338 | 6 |
| 10 | **1418.680672** | 709.843974 | 1401.654123 | 701.330700 | 1400.670107 | 700.838692 | Q | *887.501901* | 444.254589 | 870.475352 | 435.741314 | 869.491336 | 435.249306 | 5 |
| 11 | **1519.728351** | 760.367814 | 1502.701802 | 751.854539 | 1501.717786 | 751.362531 | T | *448.276575* | 224.641925 | 431.250026 | 216.128651 | 430.266010 | 215.636643 | 4 |
| 12 | 1606.760379 | 803.883828 | 1589.733830 | 795.370553 | 1588.749814 | 794.878545 | S | *347.228896* | 174.118086 | 330.202347 | 165.604811 | 329.218331 | 165.112803 | 3 |
| 13 | 1719.844443 | 860.425860 | 1702.817894 | 851.912585 | 1701.833878 | 851.420577 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 14 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 59.1 | 1864.942703 | 0.022725 | VTGEGCVYLQTSLK |

**Mascot:** http://www.matrixscience.com/

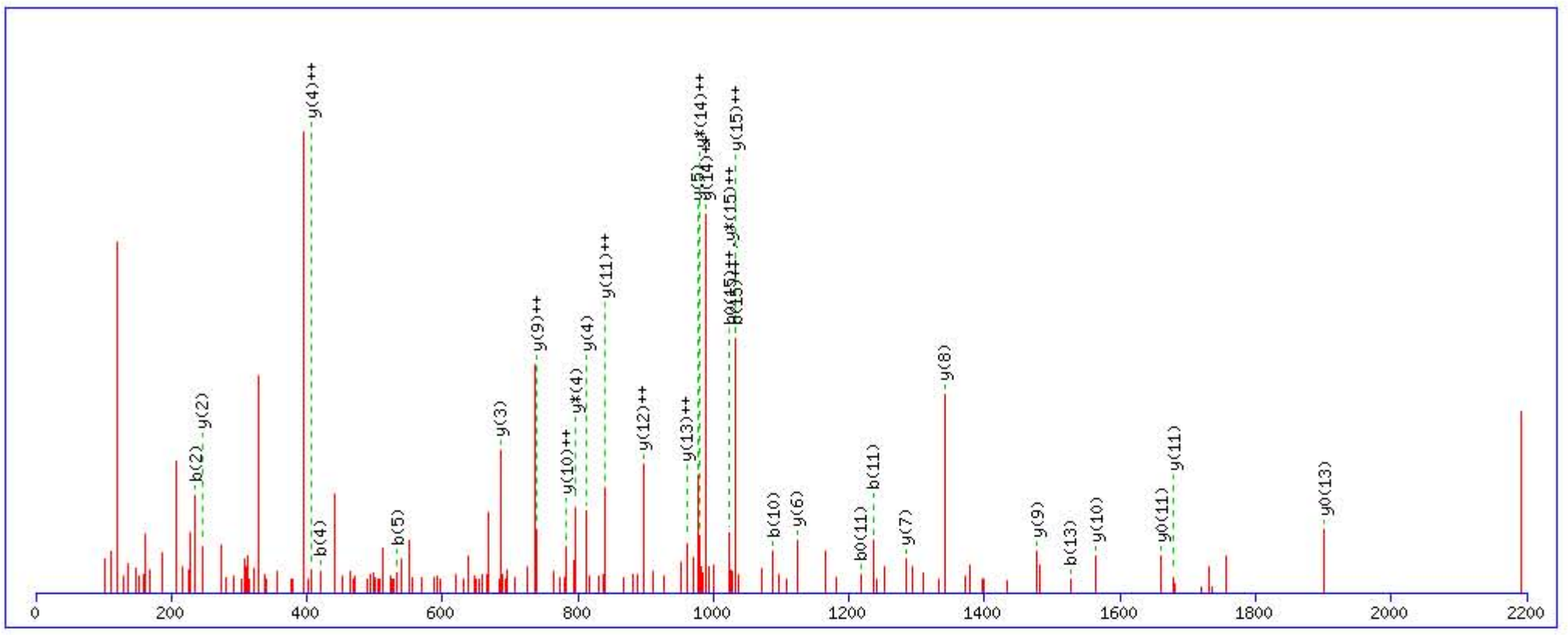
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FSGQLNSHGCFYQQVK**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

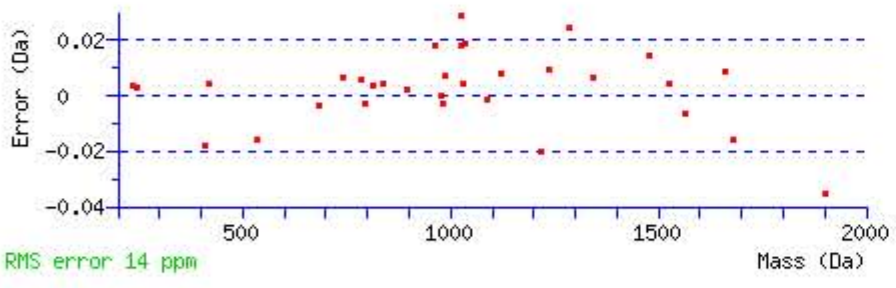
Match to Query 48617: 2210.053722 from(737.691850,3+) rtinseconds(1852) index(19199)
Title: Locus:1.1.1.3027.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

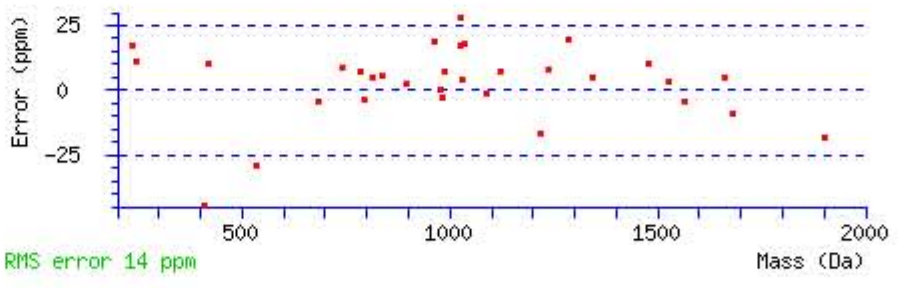
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2210.040131
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q14 : Biotin:Thermo-21345 (Q)
**Ions Score:** 41 **Expect:** 0.0003
**Matches :** 32/154 fragment ions using 80 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 16 |
| 2 | **235.107718** | 118.057497 | | | 217.097153 | 109.052214 | S | 2063.978979 | 1032.493127 | 2046.952430 | 1023.979853 | 2045.968414 | 1023.487845 | 15 |
| 3 | 292.129182 | 146.568229 | | | 274.118617 | 137.562946 | G | 1976.946951 | 988.977114 | 1959.920402 | 980.463839 | 1958.936386 | 979.971831 | 14 |
| 4 | **420.187760** | 210.597518 | 403.161211 | 202.084243 | 402.177195 | 201.592235 | Q | 1919.925487 | 960.466382 | 1902.898938 | 951.953107 | 1901.914922 | 951.461099 | 13 |
| 5 | **533.271824** | 267.139550 | 516.245275 | 258.626276 | 515.261259 | 258.134268 | L | 1791.866909 | 896.437093 | 1774.840360 | 887.923818 | 1773.856344 | 887.431810 | 12 |
| 6 | 647.314751 | 324.161014 | 630.288202 | 315.647739 | 629.304186 | 315.155731 | N | *1678.782845* | 839.895061 | 1661.756296 | 831.381786 | 1660.772280 | 830.889778 | 11 |
| 7 | 734.346779 | 367.677028 | 717.320230 | 359.163753 | 716.336214 | 358.671745 | S | *1564.739918* | 782.873597 | 1547.713369 | 774.360323 | 1546.729353 | 773.868315 | 10 |
| 8 | 871.405691 | 436.206483 | 854.379142 | 427.693209 | 853.395126 | 427.201201 | H | *1477.707890* | 739.357583 | 1460.681341 | 730.844309 | | | 9 |
| 9 | 928.427155 | 464.717216 | 911.400606 | 456.203941 | 910.416590 | 455.711933 | G | *1340.648978* | 670.828127 | 1323.622429 | 662.314853 | | | 8 |
| 10 | **1088.457804** | 544.732540 | 1071.431255 | 536.219266 | 1070.447239 | 535.727257 | C | *1283.627514* | 642.317395 | 1266.600965 | 633.804121 | | | 7 |
| 11 | **1235.526218** | 618.266747 | 1218.499669 | 609.753473 | 1217.515653 | 609.261464 | F | *1123.596865* | 562.302071 | 1106.570316 | 553.788796 | | | 6 |
| 12 | 1398.589547 | 699.798412 | 1381.562998 | 691.285137 | 1380.578982 | 690.793129 | Y | *976.528451* | 488.767864 | 959.501902 | 480.254589 | | | 5 |
| 13 | **1526.648125** | 763.827700 | 1509.621576 | 755.314426 | 1508.637560 | 754.822418 | Q | *813.465122* | 407.236199 | 796.438573 | 398.722925 | | | 4 |
| 14 | 1965.873451 | 983.440364 | 1948.846902 | 974.927089 | 1947.862886 | 974.435081 | Q | *685.406544* | 343.206910 | 668.379995 | 334.693636 | | | 3 |
| 15 | 2064.941865 | 1032.974570 | 2047.915316 | 1024.461296 | 2046.931300 | 1023.969288 | V | *246.181218* | 123.594247 | 229.154669 | 115.080972 | | | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 40.6 | 2210.040131 | 0.013591 | FSGQLNSHGCFYQQVK |
| 33.1 | 2210.040131 | 0.013591 | FSGQLNSHGCFYQQVK |
| 3.0 | 2210.058075 | -0.004353 | FSHLSRNMTMQRTMK |
| 3.0 | 2210.058075 | -0.004353 | FSHLSRNMTMQRTMK |
| 1.1 | 2210.045486 | 0.008236 | MSMKEVDEQMLAIQSK |

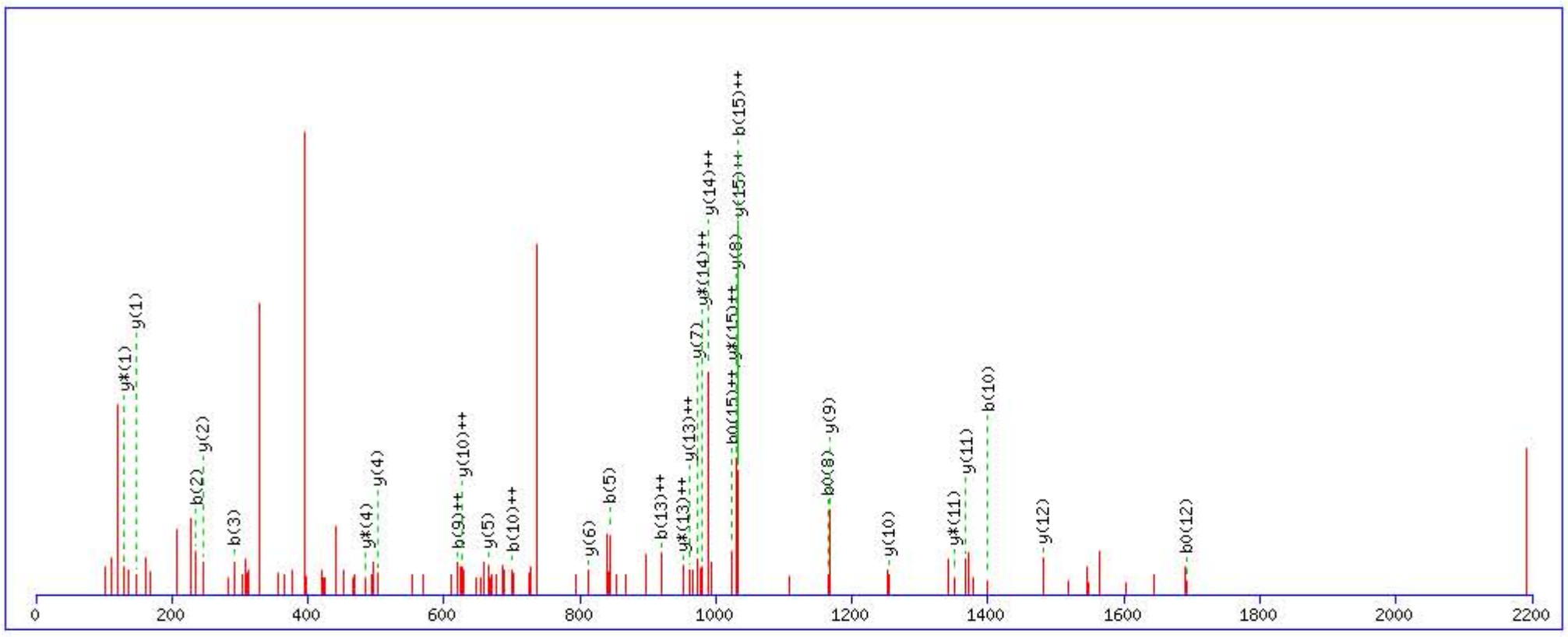
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FSGQLNSHGCFYQQVK**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

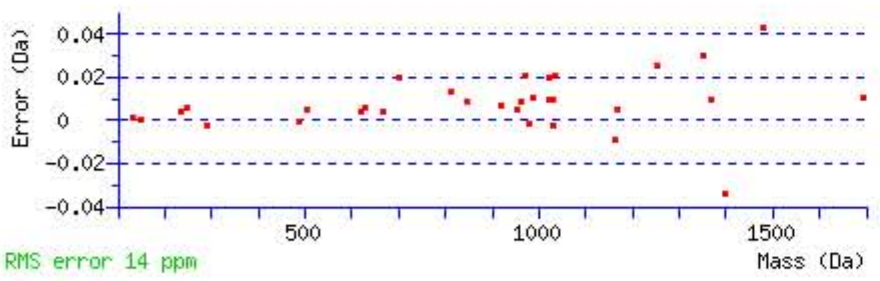
Match to Query 48620: 2210.055432 from(737.692420,3+) rtinseconds(1834) index(19079)
Title: Locus:1.1.1.3021.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

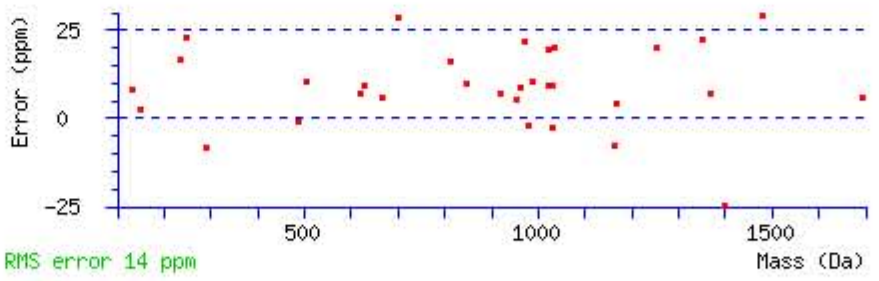
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2210.040131
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 30 **Expect:** 0.02
**Matches :** 32/154 fragment ions using 100 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 16 |
| 2 | **235.107718** | 118.057497 | | | 217.097153 | 109.052214 | S | 2063.978979 | 1032.493127 | 2046.952430 | 1023.979853 | 2045.968414 | 1023.487845 | 15 |
| 3 | **292.129182** | 146.568229 | | | 274.118617 | 137.562946 | G | 1976.946951 | 988.977114 | 1959.920402 | 980.463839 | 1958.936386 | 979.971831 | 14 |
| 4 | 731.354508 | 366.180892 | 714.327959 | 357.667618 | 713.343943 | 357.175610 | Q | 1919.925487 | 960.466382 | 1902.898938 | 951.953107 | 1901.914922 | 951.461099 | 13 |
| 5 | **844.438572** | 422.722924 | 827.412023 | 414.209650 | 826.428007 | 413.717642 | L | *1480.700161* | 740.853719 | 1463.673612 | 732.340444 | 1462.689596 | 731.848436 | 12 |
| 6 | 958.481499 | 479.744388 | 941.454950 | 471.231113 | 940.470934 | 470.739105 | N | *1367.616097* | 684.311687 | 1350.589548 | 675.798412 | 1349.605532 | 675.306404 | 11 |
| 7 | 1045.513527 | 523.260402 | 1028.486978 | 514.747127 | 1027.502962 | 514.255119 | S | *1253.573170* | 627.290223 | 1236.546621 | 618.776949 | 1235.562605 | 618.284941 | 10 |
| 8 | 1182.572439 | 591.789858 | 1165.545890 | 583.276583 | 1164.561874 | 582.784575 | H | *1166.541142* | 583.774209 | 1149.514593 | 575.260935 | | | 9 |
| 9 | 1239.593903 | **620.300590** | 1222.567354 | 611.787315 | 1221.583338 | 611.295307 | G | *1029.482230* | 515.244753 | 1012.455681 | 506.731479 | | | 8 |
| 10 | **1399.624552** | **700.315914** | 1382.598003 | 691.802640 | 1381.613987 | 691.310632 | C | *972.460766* | 486.734021 | 955.434217 | 478.220747 | | | 7 |
| 11 | 1546.692966 | 773.850121 | 1529.666417 | 765.336847 | 1528.682401 | 764.844839 | F | *812.430117* | 406.718697 | 795.403568 | 398.205422 | | | 6 |
| 12 | 1709.756295 | 855.381786 | 1692.729746 | 846.868511 | 1691.745730 | 846.376503 | Y | *665.361703* | 333.184490 | 648.335154 | 324.671215 | | | 5 |
| 13 | 1837.814873 | **919.411075** | 1820.788324 | 910.897800 | 1819.804308 | 910.405792 | Q | *502.298374* | 251.652825 | 485.271825 | 243.139550 | | | 4 |
| 14 | 1965.873451 | 983.440364 | 1948.846902 | 974.927089 | 1947.862886 | 974.435081 | Q | 374.239796 | 187.623536 | 357.213247 | 179.110261 | | | 3 |
| 15 | 2064.941865 | **1032.974570** | 2047.915316 | 1024.461296 | 2046.931300 | 1023.969288 | V | *246.181218* | 123.594247 | 229.154669 | 115.080972 | | | 2 |
| 16 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 29.7 | 2210.040131 | 0.015301 | FSGQLNSHGCFYQQVK |
| 2.0 | 2210.040131 | 0.015301 | FSGQLNSHGCFYQQVK |

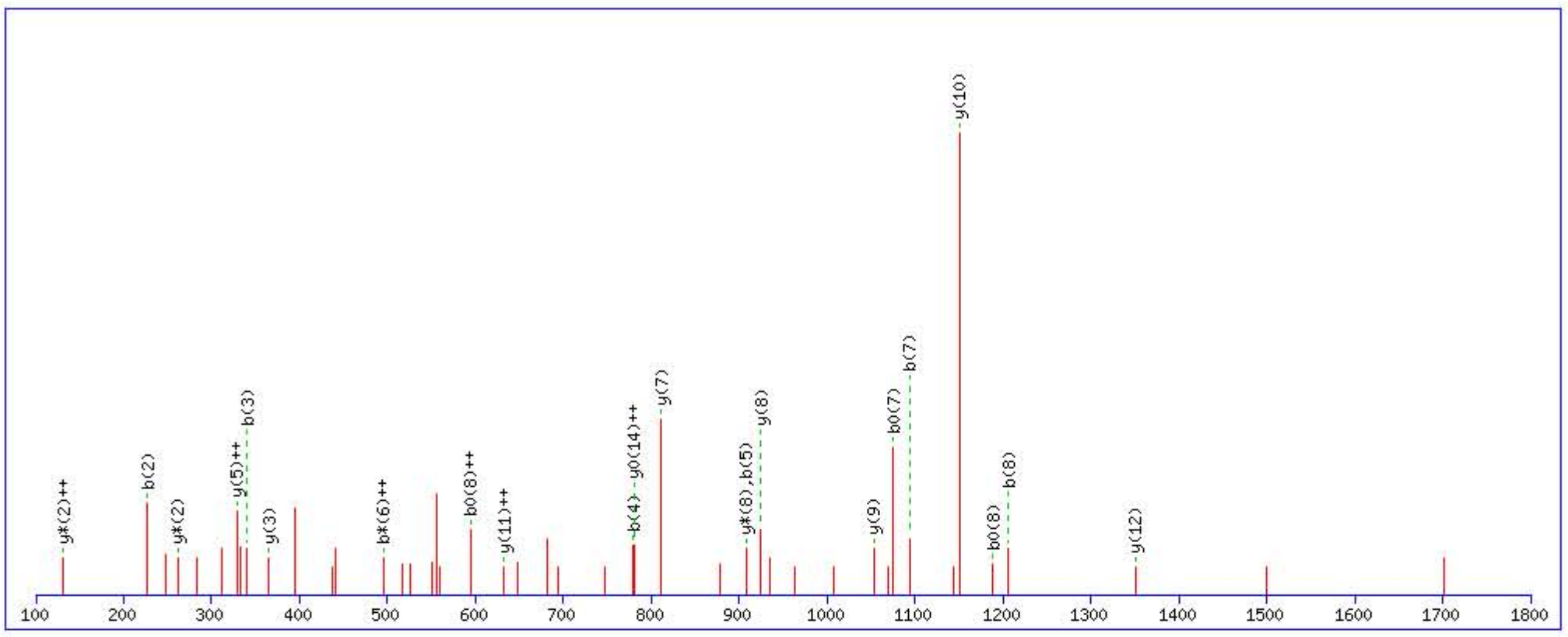
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LLLQQVSLPELPGEYSMK**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

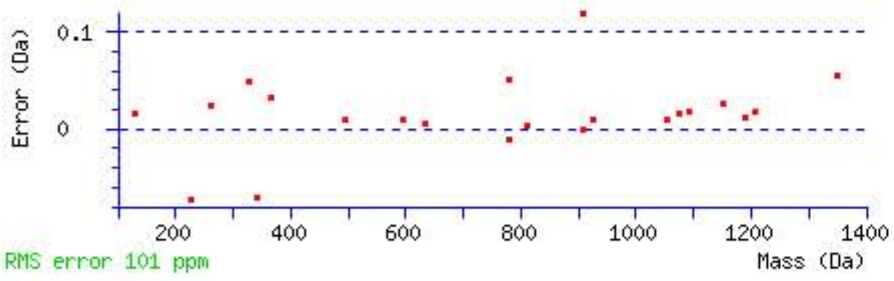
Match to Query 51399: 2355.289092 from(786.103640,3+) rtinseconds(2874) index(25414)
Title: Locus:1.1.1.3381.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

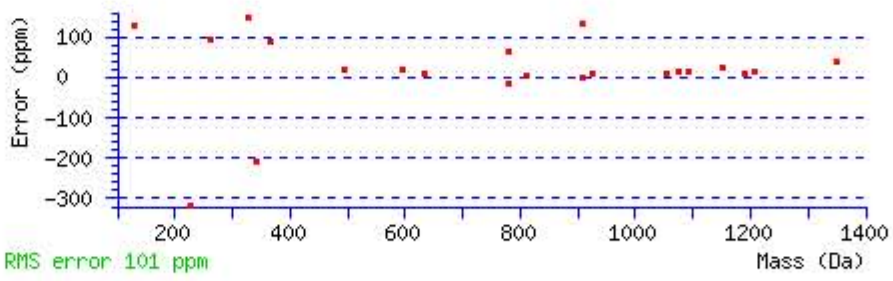
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2355.258179
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 35 **Expect:** 0.0006
**Matches :** 22/182 fragment ions using 43 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 18 |
| 2 | *227.175404* | 114.091340 | | | | | L | 2243.181426 | 1122.094351 | 2226.154877 | 1113.581076 | 2225.170861 | 1113.089068 | 17 |
| 3 | *340.259468* | 170.633372 | | | | | L | 2130.097362 | 1065.552319 | 2113.070813 | 1057.039044 | 2112.086797 | 1056.547036 | 16 |
| 4 | *779.484794* | 390.246035 | 762.458245 | 381.732760 | | | Q | 2017.013298 | 1009.010287 | 1999.986749 | 1000.497013 | 1999.002733 | 1000.005005 | 15 |
| 5 | *907.543372* | 454.275324 | 890.516823 | 445.762049 | | | Q | 1577.787972 | 789.397624 | 1560.761423 | 780.884350 | 1559.777407 | 780.392342 | 14 |
| 6 | 1006.611786 | 503.809531 | 989.585237 | 495.296256 | | | V | 1449.729394 | 725.368335 | 1432.702845 | 716.855061 | 1431.718829 | 716.363053 | 13 |
| 7 | *1093.643814* | 547.325545 | 1076.617265 | 538.812271 | 1075.633249 | 538.320263 | S | *1350.660980* | 675.834128 | 1333.634431 | 667.320854 | 1332.650415 | 666.828846 | 12 |
| 8 | *1206.727878* | 603.867577 | 1189.701329 | 595.354303 | 1188.717313 | 594.862294 | L | 1263.628952 | 632.318114 | 1246.602403 | 623.804840 | 1245.618387 | 623.312832 | 11 |
| 9 | 1303.780642 | 652.393959 | 1286.754093 | 643.880685 | 1285.770077 | 643.388676 | P | *1150.544888* | 575.776082 | 1133.518339 | 567.262808 | 1132.534323 | 566.770800 | 10 |
| 10 | 1432.823235 | 716.915256 | 1415.796686 | 708.401981 | 1414.812670 | 707.909973 | E | *1053.492124* | 527.249700 | 1036.465575 | 518.736426 | 1035.481559 | 518.244418 | 9 |
| 11 | 1545.907299 | 773.457288 | 1528.880750 | 764.944013 | 1527.896734 | 764.452005 | L | *924.449531* | 462.728404 | 907.422982 | 454.215129 | 906.438966 | 453.723121 | 8 |
| 12 | 1642.960063 | 821.983670 | 1625.933514 | 813.470395 | 1624.949498 | 812.978387 | P | *811.365467* | 406.186372 | 794.338918 | 397.673097 | 793.354902 | 397.181089 | 7 |
| 13 | 1699.981527 | 850.494401 | 1682.954978 | 841.981127 | 1681.970962 | 841.489119 | G | 714.312703 | 357.659990 | 697.286154 | 349.146715 | 696.302138 | 348.654707 | 6 |
| 14 | 1829.024120 | 915.015698 | 1811.997571 | 906.502423 | 1811.013555 | 906.010415 | E | 657.291239 | 329.149258 | 640.264690 | 320.635983 | 639.280674 | 320.143975 | 5 |
| 15 | 1992.087449 | 996.547362 | 1975.060900 | 988.034088 | 1974.076884 | 987.542080 | Y | 528.248646 | 264.627961 | 511.222097 | 256.114687 | 510.238081 | 255.622679 | 4 |
| 16 | 2079.119477 | 1040.063376 | 2062.092928 | 1031.550102 | 2061.108912 | 1031.058094 | S | *365.185317* | 183.096297 | 348.158768 | 174.583022 | 347.174752 | 174.091014 | 3 |
| 17 | 2210.159962 | 1105.583619 | 2193.133413 | 1097.070344 | 2192.149397 | 1096.578336 | M | 278.153289 | 139.580282 | 261.126740 | 131.067008 | | | 2 |
| 18 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 34.5 | 2355.258179 | 0.030913 | LLLQQVSLPELPGEYSMK |
| 27.0 | 2355.258179 | 0.030913 | LLLQQVSLPELPGEYSMK |
| 0.1 | 2355.259354 | 0.029738 | SQPRASGPPRSIQPQVSPR |

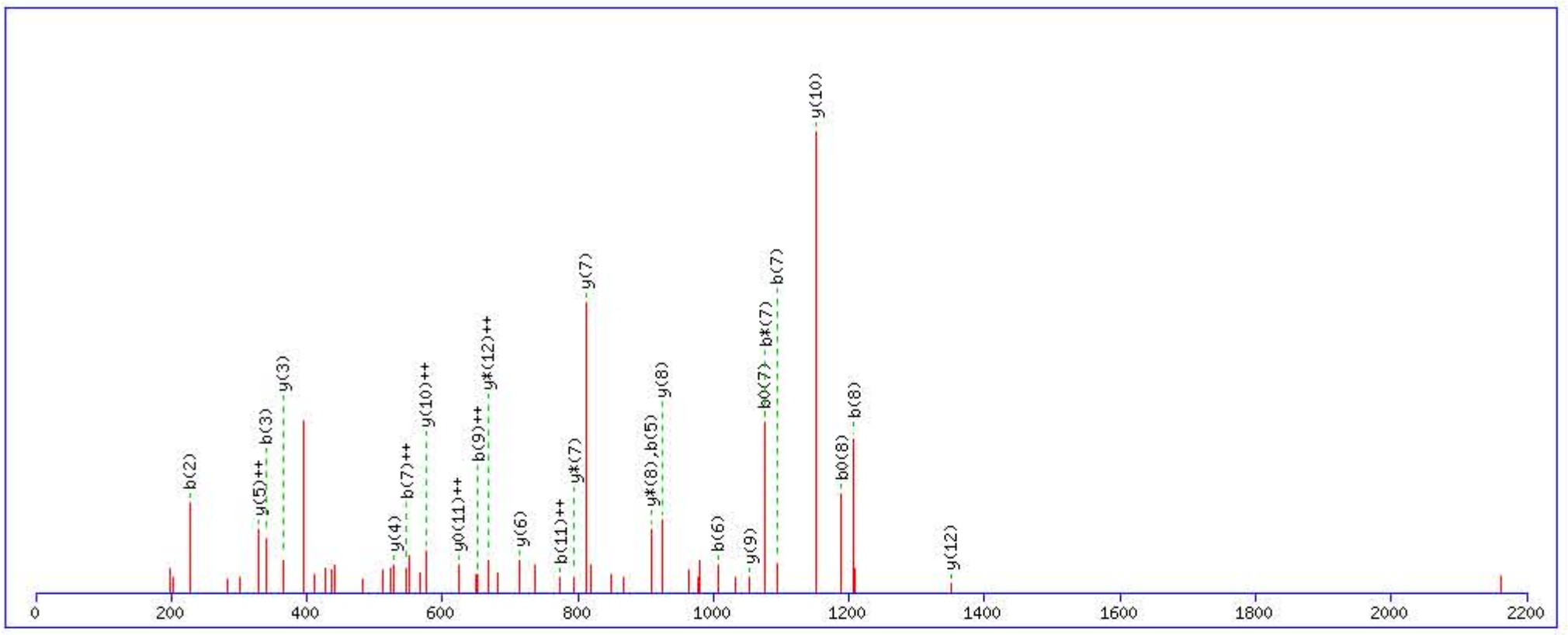
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LLLQQVSLPELPGEYSMK**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

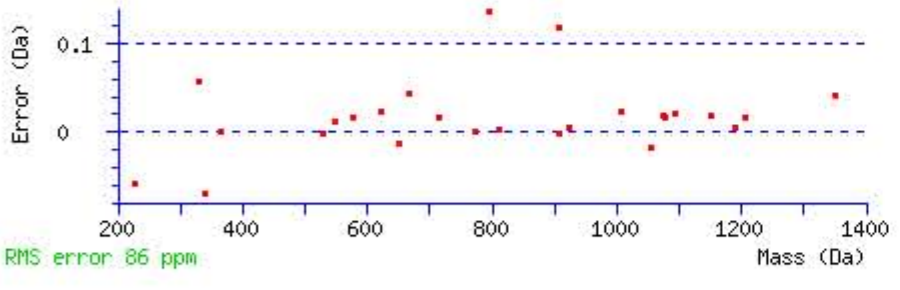
Match to Query 51402: 2355.289422 from(786.103750,3+) rtinseconds(2841) index(25147)
Title: Locus:1.1.1.3370.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

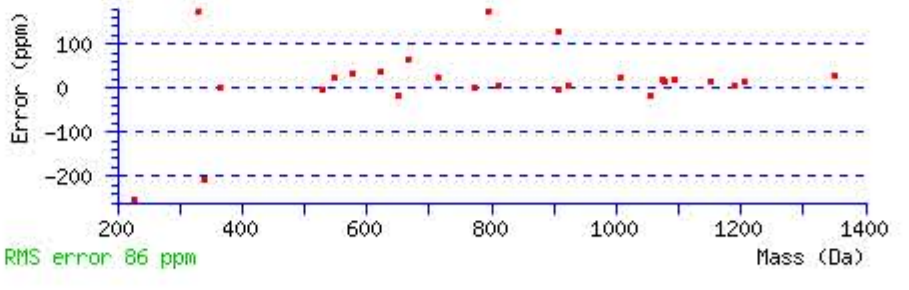
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2355.258179
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 42 **Expect:** 0.00048
**Matches :** 26/182 fragment ions using 50 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 18 |
| 2 | *227.175404* | 114.091340 | | | | | L | 2243.181426 | 1122.094351 | 2226.154877 | 1113.581076 | 2225.170861 | 1113.089068 | 17 |
| 3 | *340.259468* | 170.633372 | | | | | L | 2130.097362 | 1065.552319 | 2113.070813 | 1057.039044 | 2112.086797 | 1056.547036 | 16 |
| 4 | 468.318046 | 234.662661 | 451.291497 | 226.149386 | | | Q | 2017.013298 | 1009.010287 | 1999.986749 | 1000.497013 | 1999.002733 | 1000.005005 | 15 |
| 5 | *907.543372* | 454.275324 | 890.516823 | 445.762049 | | | Q | 1888.954720 | 944.980998 | 1871.928171 | 936.467724 | 1870.944155 | 935.975715 | 14 |
| 6 | *1006.611786* | 503.809531 | 989.585237 | 495.296256 | | | V | 1449.729394 | 725.368335 | 1432.702845 | 716.855061 | 1431.718829 | 716.363053 | 13 |
| 7 | *1093.643814* | **547.325545** | 1076.617265 | 538.812271 | 1075.633249 | 538.320263 | S | *1350.660980* | 675.834128 | 1333.634431 | 667.320854 | 1332.650415 | 666.828846 | 12 |
| 8 | *1206.727878* | 603.867577 | 1189.701329 | 595.354303 | 1188.717313 | 594.862294 | L | 1263.628952 | 632.318114 | 1246.602403 | 623.804840 | 1245.618387 | 623.312832 | 11 |
| 9 | 1303.780642 | **652.393959** | 1286.754093 | 643.880685 | 1285.770077 | 643.388676 | P | *1150.544888* | 575.776082 | 1133.518339 | 567.262808 | 1132.534323 | 566.770800 | 10 |
| 10 | 1432.823235 | 716.915256 | 1415.796686 | 708.401981 | 1414.812670 | 707.909973 | E | *1053.492124* | 527.249700 | 1036.465575 | 518.736426 | 1035.481559 | 518.244418 | 9 |
| 11 | 1545.907299 | **773.457288** | 1528.880750 | 764.944013 | 1527.896734 | 764.452005 | L | *924.449531* | 462.728404 | 907.422982 | 454.215129 | 906.438966 | 453.723121 | 8 |
| 12 | 1642.960063 | 821.983670 | 1625.933514 | 813.470395 | 1624.949498 | 812.978387 | P | *811.365467* | 406.186372 | 794.338918 | 397.673097 | 793.354902 | 397.181089 | 7 |
| 13 | 1699.981527 | 850.494401 | 1682.954978 | 841.981127 | 1681.970962 | 841.489119 | G | *714.312703* | 357.659990 | 697.286154 | 349.146715 | 696.302138 | 348.654707 | 6 |
| 14 | 1829.024120 | 915.015698 | 1811.997571 | 906.502423 | 1811.013555 | 906.010415 | E | 657.291239 | 329.149258 | 640.264690 | 320.635983 | 639.280674 | 320.143975 | 5 |
| 15 | 1992.087449 | 996.547362 | 1975.060900 | 988.034088 | 1974.076884 | 987.542080 | Y | *528.248646* | 264.627961 | 511.222097 | 256.114687 | 510.238081 | 255.622679 | 4 |
| 16 | 2079.119477 | 1040.063376 | 2062.092928 | 1031.550102 | 2061.108912 | 1031.058094 | S | *365.185317* | 183.096297 | 348.158768 | 174.583022 | 347.174752 | 174.091014 | 3 |
| 17 | 2210.159962 | 1105.583619 | 2193.133413 | 1097.070344 | 2192.149397 | 1096.578336 | M | 278.153289 | 139.580282 | 261.126740 | 131.067008 | | | 2 |
| 18 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 41.7 | 2355.258179 | 0.031243 | LLLQQVSLPELPGEYSMK |
| 41.7 | 2355.258179 | 0.031243 | LLLQQVSLPELPGEYSMK |
| 6.0 | 2355.288498 | 0.000924 | LIQQERALLNFTEWKR |
| 6.0 | 2355.288498 | 0.000924 | LIQQERALLNFTEWKR |
| 0.9 | 2355.259354 | 0.030068 | SQPRASGPPRSIQPQVSPR |
| 0.3 | 2355.273270 | 0.016152 | NQLGSQEVHLSQLIITHK |

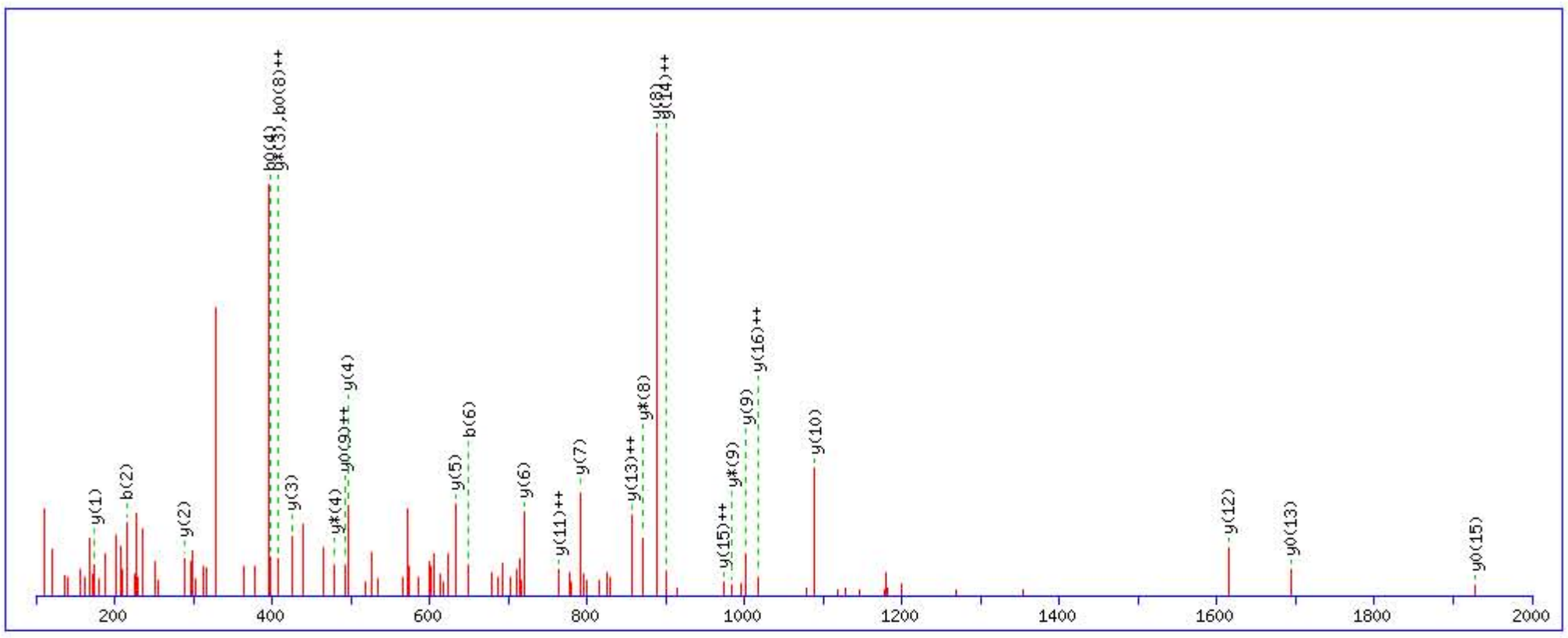
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VDLSFSPSQSLPASHAHLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

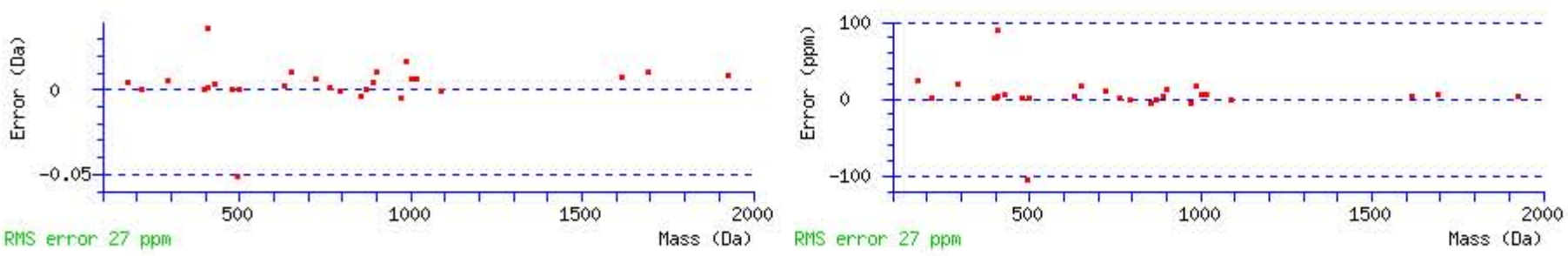
Match to Query 51448: 2359.218976 from(590.812020,4+) rtinseconds(1997) index(20220)
Title: Locus:1.1.1.3078.3 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2359.210678
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 43 **Expect:** 0.0016
**Matches :** 27/188 fragment ions using 76 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 19 |
| 2 | **215.102633** | 108.054954 | | | 197.092068 | 99.049672 | D | 2261.149547 | 1131.078411 | 2244.122998 | 1122.565137 | 2243.138982 | 1122.073129 | 18 |
| 3 | 328.186697 | 164.596986 | | | 310.176132 | 155.591704 | L | 2146.122604 | 1073.564940 | 2129.096055 | 1065.051665 | 2128.112039 | 1064.559657 | 17 |
| 4 | 415.218725 | 208.113001 | | | 397.208160 | 199.107718 | S | 2033.038540 | 1017.022908 | 2016.011991 | 1008.509634 | 2015.027975 | 1008.017626 | 16 |
| 5 | 562.287139 | 281.647208 | | | 544.276574 | 272.641925 | F | 1946.006512 | 973.506894 | 1928.979963 | 964.993620 | 1927.995947 | 964.501612 | 15 |
| 6 | **649.319167** | 325.163222 | | | 631.308602 | 316.157939 | S | 1798.938098 | 899.972687 | 1781.911549 | 891.459413 | 1780.927533 | 890.967405 | 14 |
| 7 | 746.371931 | 373.689604 | | | 728.361366 | 364.684321 | P | 1711.906070 | 856.456673 | 1694.879521 | 847.943399 | 1693.895505 | 847.451391 | 13 |
| 8 | 833.403959 | 417.205618 | | | 815.393394 | 408.200335 | S | *1614.853306* | 807.930291 | 1597.826757 | 799.417017 | 1596.842741 | 798.925009 | 12 |
| 9 | 1272.629285 | 636.818281 | 1255.602736 | 628.305006 | 1254.618720 | 627.812998 | Q | 1527.821278 | 764.414277 | 1510.794729 | 755.901003 | 1509.810713 | 755.408995 | 11 |
| 10 | 1359.661313 | 680.334295 | 1342.634764 | 671.821020 | 1341.650748 | 671.329012 | S | *1088.595952* | 544.801614 | 1071.569403 | 536.288340 | 1070.585387 | 535.796332 | 10 |
| 11 | 1472.745377 | 736.876327 | 1455.718828 | 728.363052 | 1454.734812 | 727.871044 | L | *1001.563924* | 501.285600 | 984.537375 | 492.772326 | 983.553359 | 492.280318 | 9 |
| 12 | 1569.798141 | 785.402709 | 1552.771592 | 776.889434 | 1551.787576 | 776.397426 | P | *888.479860* | 444.743568 | 871.453311 | 436.230294 | 870.469295 | 435.738286 | 8 |
| 13 | 1640.835255 | 820.921266 | 1623.808706 | 812.407991 | 1622.824690 | 811.915983 | A | *791.427096* | 396.217186 | 774.400547 | 387.703912 | 773.416531 | 387.211904 | 7 |
| 14 | 1727.867283 | 864.437280 | 1710.840734 | 855.924005 | 1709.856718 | 855.431997 | S | *720.389982* | 360.698629 | 703.363433 | 352.185355 | 702.379417 | 351.693347 | 6 |
| 15 | 1864.926195 | 932.966736 | 1847.899646 | 924.453461 | 1846.915630 | 923.961453 | H | *633.357954* | 317.182615 | 616.331405 | 308.669341 | | | 5 |
| 16 | 1935.963309 | 968.485293 | 1918.936760 | 959.972018 | 1917.952744 | 959.480010 | A | *496.299042* | 248.653159 | 479.272493 | 240.139884 | | | 4 |
| 17 | 2073.022221 | 1037.014748 | 2055.995672 | 1028.501474 | 2055.011656 | 1028.009466 | H | *425.261928* | 213.134602 | 408.235379 | 204.621328 | | | 3 |
| 18 | 2186.106285 | 1093.556780 | 2169.079736 | 1085.043506 | 2168.095720 | 1084.551498 | L | *288.203016* | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 19 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 42.9 | 2359.210678 | 0.008298 | VDLSFSPSQSLPASHAHLR |

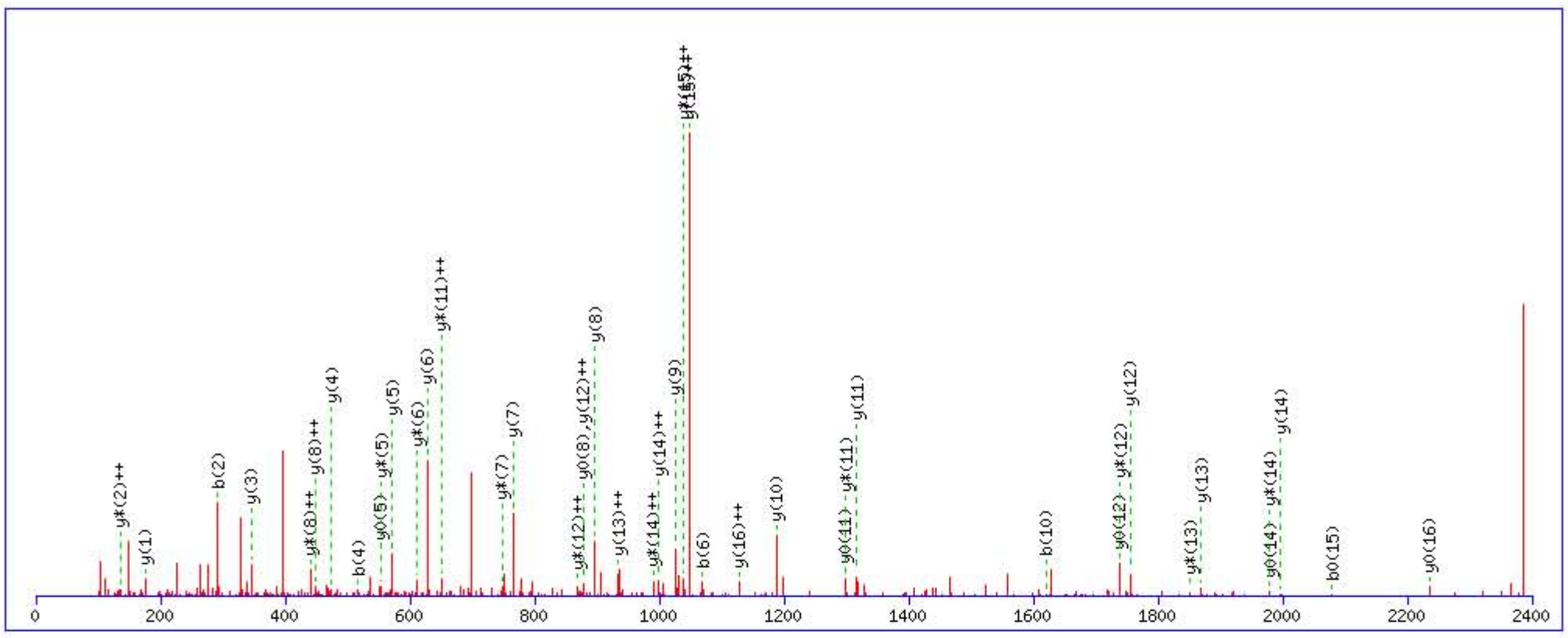
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

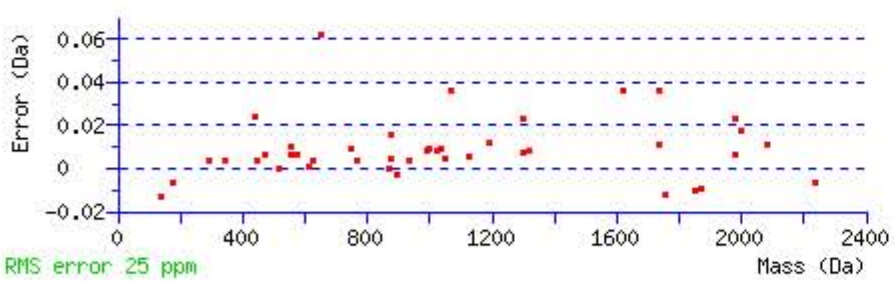
Match to Query 51697: 2384.106222 from(795.709350,3+) rtinseconds(2045) index(20491)
Title: Locus:1.1.1.3094.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

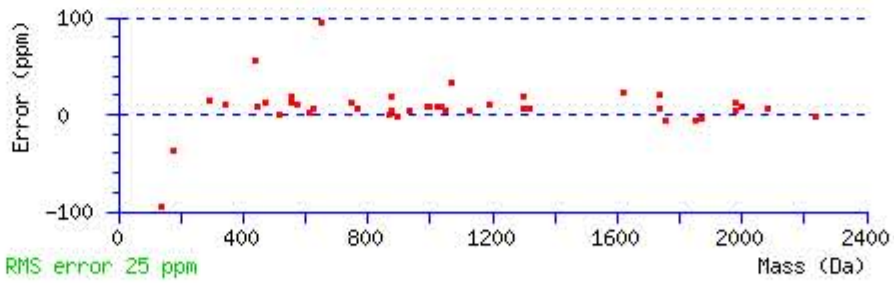
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2384.089767
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 37 **Expect:** 0.0031
**Matches :** 43/164 fragment ions using 137 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.047761 | 66.527518 | | | | | M | | | | | | | 17 |
| 2 | **292.078410** | 146.542843 | | | | | C | 2254.056579 | 1127.531927 | 2237.030030 | 1119.018653 | 2236.046014 | 1118.526645 | 16 |
| 3 | 389.131174 | 195.069225 | | | | | P | 2094.025930 | 1047.516603 | 2076.999381 | 1039.003328 | 2076.015365 | 1038.511320 | 15 |
| 4 | **517.189752** | 259.098514 | 500.163203 | 250.585240 | | | Q | *1996.973166* | 998.990221 | 1979.946617 | 990.476947 | 1978.962601 | 989.984939 | 14 |
| 5 | 630.273816 | 315.640546 | 613.247267 | 307.127272 | | | L | *1868.914588* | 934.960932 | 1851.888039 | 926.447658 | 1850.904023 | 925.955650 | 13 |
| 6 | **1069.499142** | 535.253209 | 1052.472593 | 526.739935 | | | Q | *1755.830524* | 878.418900 | 1738.803975 | 869.905626 | 1737.819959 | 869.413618 | 12 |
| 7 | 1197.557720 | 599.282498 | 1180.531171 | 590.769224 | | | Q | *1316.605198* | 658.806237 | 1299.578649 | 650.292963 | 1298.594633 | 649.800955 | 11 |
| 8 | 1360.621049 | 680.814163 | 1343.594500 | 672.300888 | | | Y | *1188.546620* | 594.776948 | 1171.520071 | 586.263674 | 1170.536055 | 585.771666 | 10 |
| 9 | 1489.663642 | 745.335459 | 1472.637093 | 736.822185 | 1471.653077 | 736.330177 | E | *1025.483291* | 513.245284 | 1008.456742 | 504.732009 | 1007.472726 | 504.240001 | 9 |
| 10 | **1620.704127** | 810.855702 | 1603.677578 | 802.342427 | 1602.693562 | 801.850419 | M | *896.440698* | 448.723987 | 879.414149 | 440.210713 | 878.430133 | 439.718705 | 8 |
| 11 | 1757.763039 | 879.385158 | 1740.736490 | 870.871883 | 1739.752474 | 870.379875 | H | *765.400213* | 383.203745 | 748.373664 | 374.690470 | 747.389648 | 374.198462 | 7 |
| 12 | 1814.784503 | 907.895890 | 1797.757954 | 899.382615 | 1796.773938 | 898.890607 | G | *628.341301* | 314.674289 | 611.314752 | 306.161014 | 610.330736 | 305.669006 | 6 |
| 13 | 1911.837267 | 956.422272 | 1894.810718 | 947.908997 | 1893.826702 | 947.416989 | P | *571.319837* | 286.163557 | 554.293288 | 277.650282 | 553.309272 | 277.158274 | 5 |
| 14 | 2040.879860 | 1020.943568 | 2023.853311 | 1012.430294 | 2022.869295 | 1011.938286 | E | *474.267073* | 237.637175 | 457.240524 | 229.123900 | 456.256508 | 228.631892 | 4 |
| 15 | 2097.901324 | 1049.454300 | 2080.874775 | 1040.941025 | 2079.890759 | 1040.449017 | G | *345.224480* | 173.115878 | 328.197931 | 164.602603 | | | 3 |
| 16 | 2210.985388 | 1105.996332 | 2193.958839 | 1097.483057 | 2192.974823 | 1096.991049 | L | 288.203016 | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 17 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 36.8 | 2384.089767 | 0.016455 | MCPQLQQYEMHGPEGLR |
| 35.2 | 2384.089767 | 0.016455 | MCPQLQQYEMHGPEGLR |
| 34.4 | 2384.089767 | 0.016455 | MCPQLQQYEMHGPEGLR |

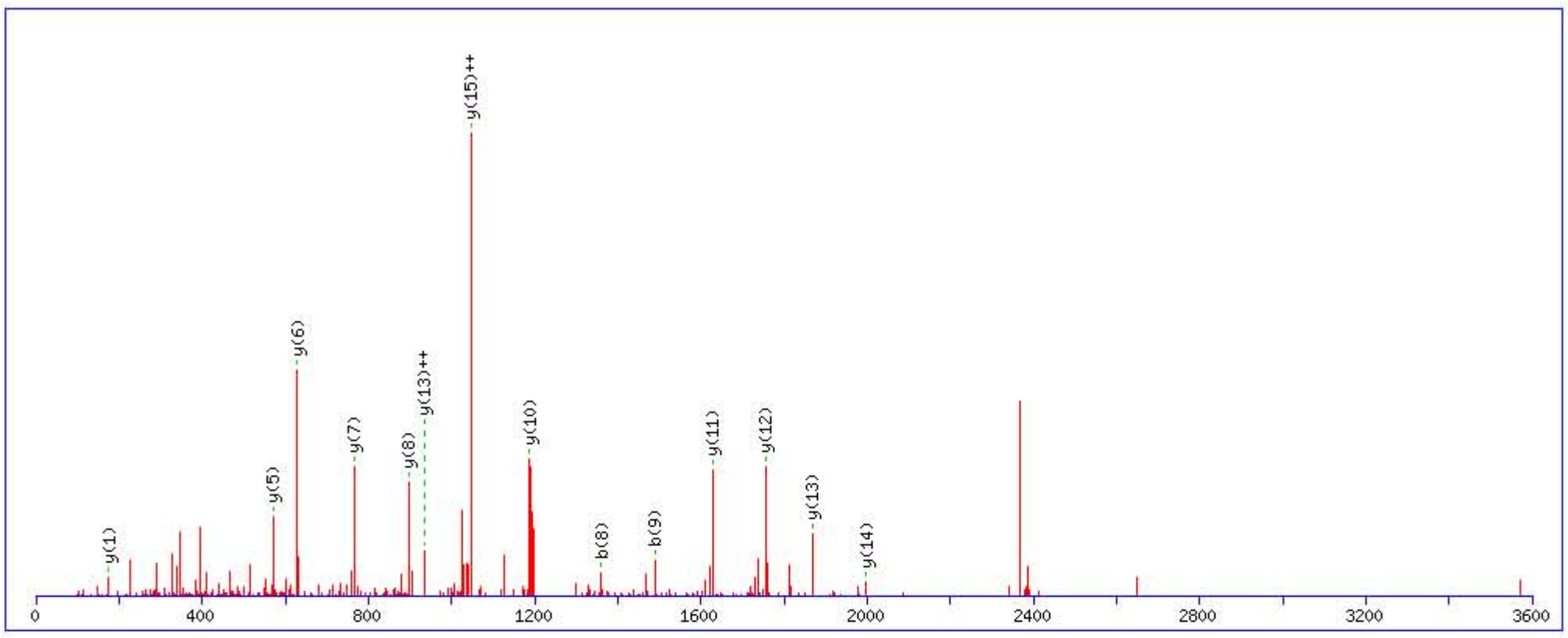
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

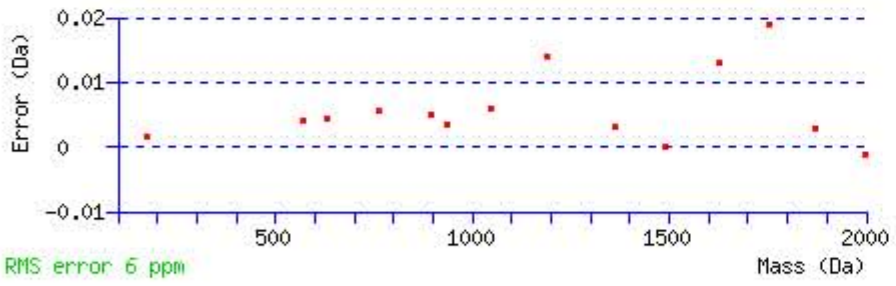
Match to Query 51710: 2384.114768 from(1193.064660,2+) rtinseconds(2017) index(20341)
Title: Locus:1.1.1.3084.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

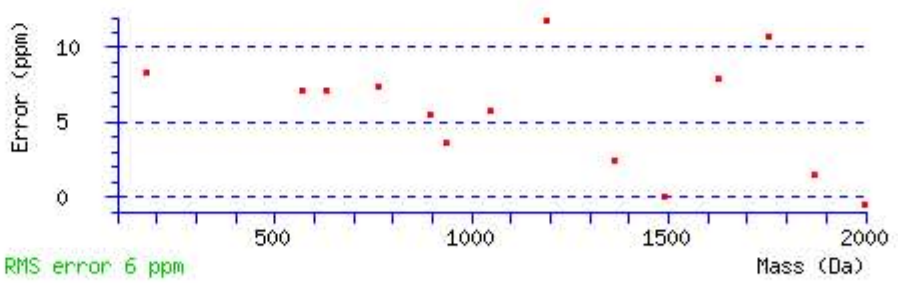
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2384.089767
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 73 **Expect:** 1.7e-007
**Matches :** 14/164 fragment ions using 21 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.047761 | 66.527518 | | | | | M | | | | | | | 17 |
| 2 | 292.078410 | 146.542843 | | | | | C | 2254.056579 | 1127.531927 | 2237.030030 | 1119.018653 | 2236.046014 | 1118.526645 | 16 |
| 3 | 389.131174 | 195.069225 | | | | | P | 2094.025930 | 1047.516603 | 2076.999381 | 1039.003328 | 2076.015365 | 1038.511320 | 15 |
| 4 | 517.189752 | 259.098514 | 500.163203 | 250.585240 | | | Q | *1996.973166* | 998.990221 | 1979.946617 | 990.476947 | 1978.962601 | 989.984939 | 14 |
| 5 | 630.273816 | 315.640546 | 613.247267 | 307.127272 | | | L | *1868.914588* | 934.960932 | 1851.888039 | 926.447658 | 1850.904023 | 925.955650 | 13 |
| 6 | 758.332394 | 379.669835 | 741.305845 | 371.156561 | | | Q | *1755.830524* | 878.418900 | 1738.803975 | 869.905626 | 1737.819959 | 869.413618 | 12 |
| 7 | 1197.557720 | 599.282498 | 1180.531171 | 590.769224 | | | Q | *1627.771946* | 814.389611 | 1610.745397 | 805.876337 | 1609.761381 | 805.384329 | 11 |
| 8 | **1360.621049** | 680.814163 | 1343.594500 | 672.300888 | | | Y | *1188.546620* | 594.776948 | 1171.520071 | 586.263674 | 1170.536055 | 585.771666 | 10 |
| 9 | **1489.663642** | 745.335459 | 1472.637093 | 736.822185 | 1471.653077 | 736.330177 | E | 1025.483291 | 513.245284 | 1008.456742 | 504.732009 | 1007.472726 | 504.240001 | 9 |
| 10 | 1620.704127 | 810.855702 | 1603.677578 | 802.342427 | 1602.693562 | 801.850419 | M | *896.440698* | 448.723987 | 879.414149 | 440.210713 | 878.430133 | 439.718705 | 8 |
| 11 | 1757.763039 | 879.385158 | 1740.736490 | 870.871883 | 1739.752474 | 870.379875 | H | *765.400213* | 383.203745 | 748.373664 | 374.690470 | 747.389648 | 374.198462 | 7 |
| 12 | 1814.784503 | 907.895890 | 1797.757954 | 899.382615 | 1796.773938 | 898.890607 | G | *628.341301* | 314.674289 | 611.314752 | 306.161014 | 610.330736 | 305.669006 | 6 |
| 13 | 1911.837267 | 956.422272 | 1894.810718 | 947.908997 | 1893.826702 | 947.416989 | P | *571.319837* | 286.163557 | 554.293288 | 277.650282 | 553.309272 | 277.158274 | 5 |
| 14 | 2040.879860 | 1020.943568 | 2023.853311 | 1012.430294 | 2022.869295 | 1011.938286 | E | 474.267073 | 237.637175 | 457.240524 | 229.123900 | 456.256508 | 228.631892 | 4 |
| 15 | 2097.901324 | 1049.454300 | 2080.874775 | 1040.941025 | 2079.890759 | 1040.449017 | G | 345.224480 | 173.115878 | 328.197931 | 164.602603 | | | 3 |
| 16 | 2210.985388 | 1105.996332 | 2193.958839 | 1097.483057 | 2192.974823 | 1096.991049 | L | 288.203016 | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 17 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 73.1 | 2384.089767 | 0.025001 | MCPQLQQYEMHGPEGLR |
| 62.3 | 2384.089767 | 0.025001 | MCPQLQQYEMHGPEGLR |
| 33.4 | 2384.089767 | 0.025001 | MCPQLQQYEMHGPEGLR |
| 0.9 | 2384.094772 | 0.019996 | TASEQINCTQTSMEVSDLRSK |

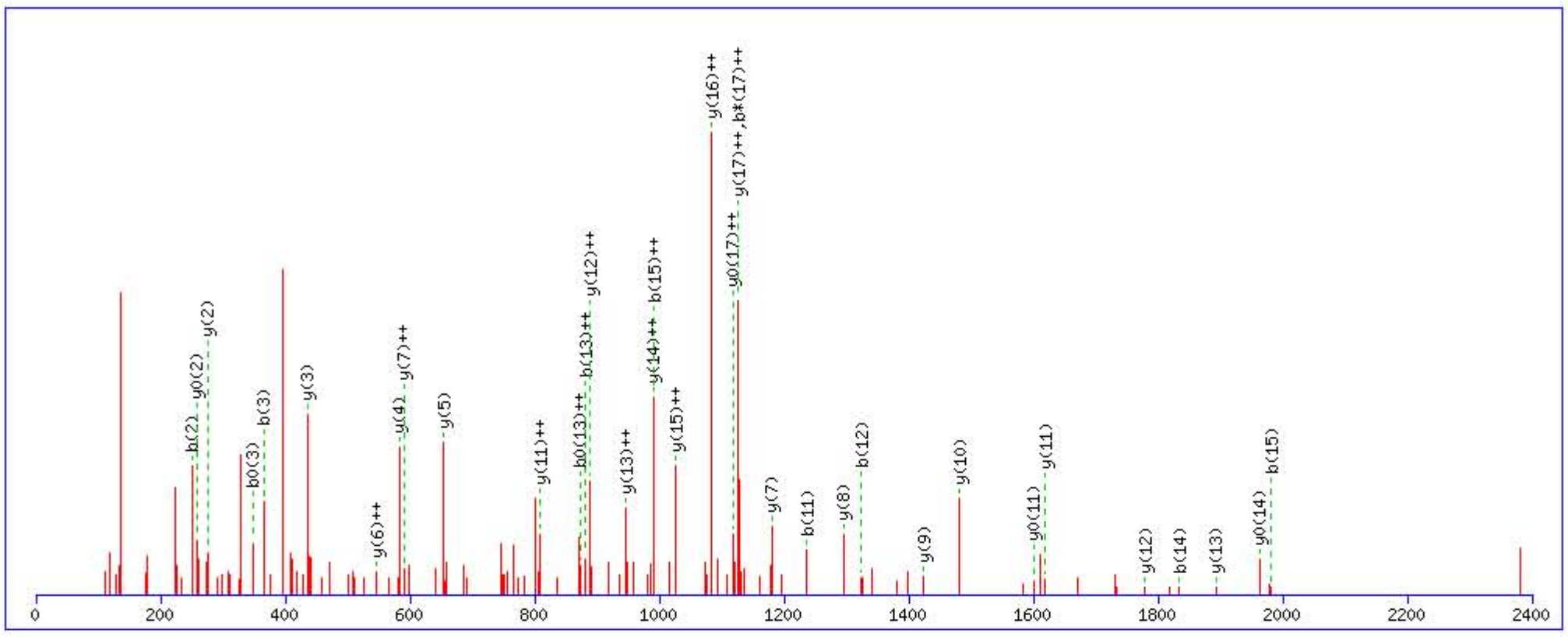
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YSDASDCHGEDSQAFCEK**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

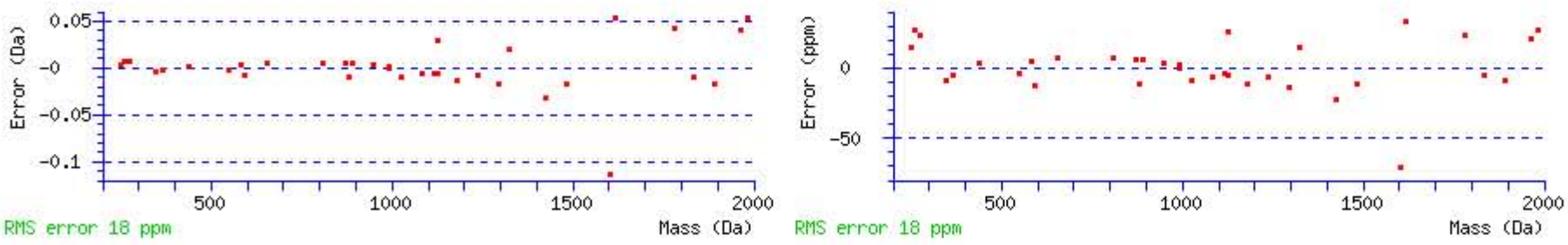
Match to Query 52346: 2415.942252 from(806.321360,3+) rtinseconds(1544) index(17225)
Title: Locus:1.1.1.2920.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2415.940598
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 65 **Expect:** 3.1e-007
**Matches :** 35/176 fragment ions using 68 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 18 |
| 2 | **251.102633** | 126.054954 | | | 233.092068 | 117.049672 | S | 2253.884545 | 1127.445910 | 2236.857996 | 1118.932636 | 2235.873980 | 1118.440628 | 17 |
| 3 | **366.129576** | 183.568426 | | | 348.119011 | 174.563144 | D | 2166.852517 | 1083.929896 | 2149.825968 | 1075.416622 | 2148.841952 | 1074.924614 | 16 |
| 4 | 437.166690 | 219.086983 | | | 419.156125 | 210.081700 | A | 2051.825574 | 1026.416425 | 2034.799025 | 1017.903150 | 2033.815009 | 1017.411142 | 15 |
| 5 | 524.198718 | 262.602997 | | | 506.188153 | 253.597715 | S | 1980.788460 | 990.897868 | 1963.761911 | 982.384594 | 1962.777895 | 981.892586 | 14 |
| 6 | 639.225661 | 320.116469 | | | 621.215096 | 311.111186 | D | *1893.756432* | 947.381854 | 1876.729883 | 938.868580 | 1875.745867 | 938.376572 | 13 |
| 7 | 799.256310 | 400.131793 | | | 781.245745 | 391.126510 | C | *1778.729489* | 889.868383 | 1761.702940 | 881.355108 | 1760.718924 | 880.863100 | 12 |
| 8 | 936.315222 | 468.661249 | | | 918.304657 | 459.655966 | H | *1618.698840* | 809.853058 | 1601.672291 | 801.339784 | 1600.688275 | 800.847776 | 11 |
| 9 | 993.336686 | 497.171981 | | | 975.326121 | 488.166699 | G | *1481.639928* | 741.323602 | 1464.613379 | 732.810328 | 1463.629363 | 732.318320 | 10 |
| 10 | 1122.379279 | 561.693278 | | | 1104.368714 | 552.687995 | E | *1424.618464* | 712.812870 | 1407.591915 | 704.299596 | 1406.607899 | 703.807588 | 9 |
| 11 | **1237.406222** | 619.206749 | | | 1219.395657 | 610.201467 | D | *1295.575871* | 648.291574 | 1278.549322 | 639.778299 | 1277.565306 | 639.286291 | 8 |
| 12 | **1324.438250** | 662.722763 | | | 1306.427685 | 653.717481 | S | *1180.548928* | 590.778102 | 1163.522379 | 582.264828 | 1162.538363 | 581.772820 | 7 |
| 13 | 1763.663576 | **882.335426** | 1746.637027 | 873.822152 | 1745.653011 | 873.330144 | Q | 1093.516900 | 547.262088 | 1076.490351 | 538.748814 | 1075.506335 | 538.256806 | 6 |
| 14 | **1834.700690** | 917.853983 | 1817.674141 | 909.340709 | 1816.690125 | 908.848701 | A | *654.291574* | 327.649425 | 637.265025 | 319.136151 | 636.281009 | 318.644143 | 5 |
| 15 | **1981.769104** | **991.388190** | 1964.742555 | 982.874916 | 1963.758539 | 982.382908 | F | *583.254460* | 292.130868 | 566.227911 | 283.617594 | 565.243895 | 283.125586 | 4 |
| 16 | 2141.799753 | 1071.403514 | 2124.773204 | 1062.890240 | 2123.789188 | 1062.398232 | C | *436.186046* | 218.596661 | 419.159497 | 210.083386 | 418.175481 | 209.591378 | 3 |
| 17 | 2270.842346 | 1135.924811 | 2253.815797 | 1127.411536 | 2252.831781 | 1126.919528 | E | *276.155397* | 138.581337 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 18 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 65.1 | 2415.940598 | 0.001654 | YSDASDCHGEDSQAFCEK |

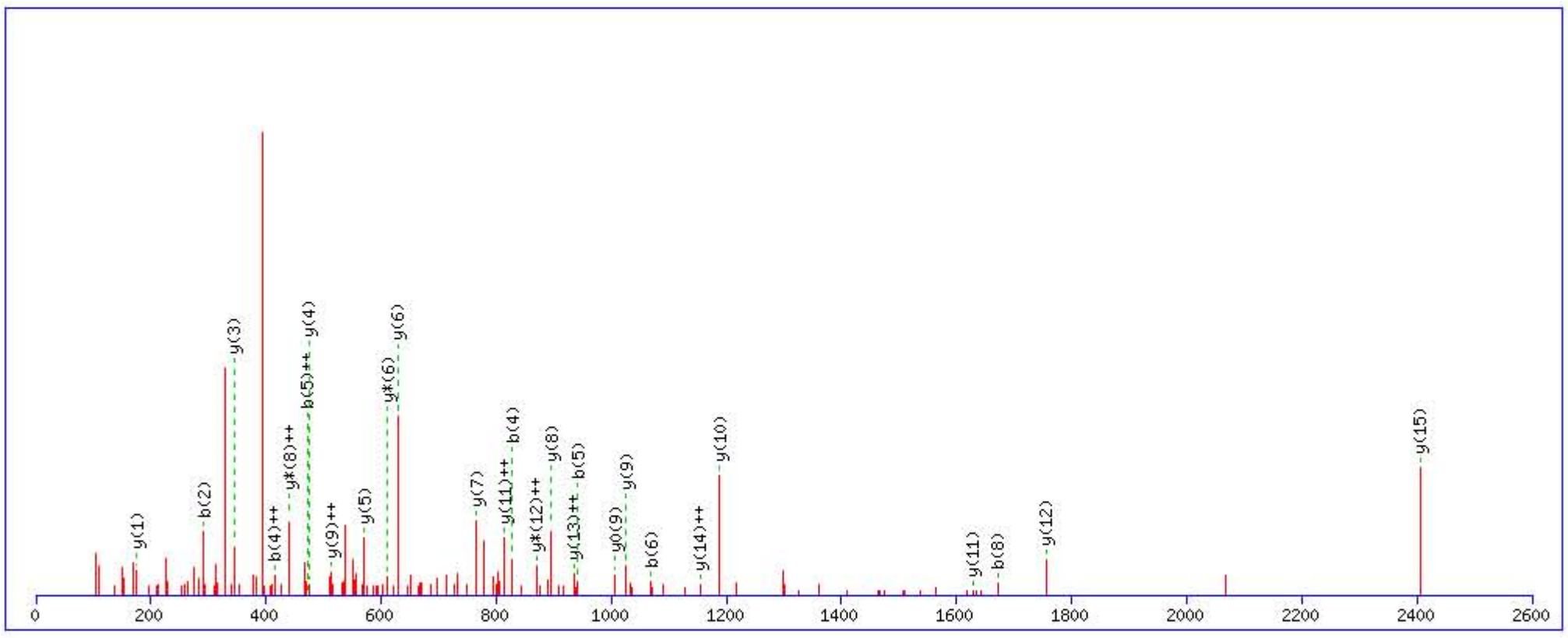
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

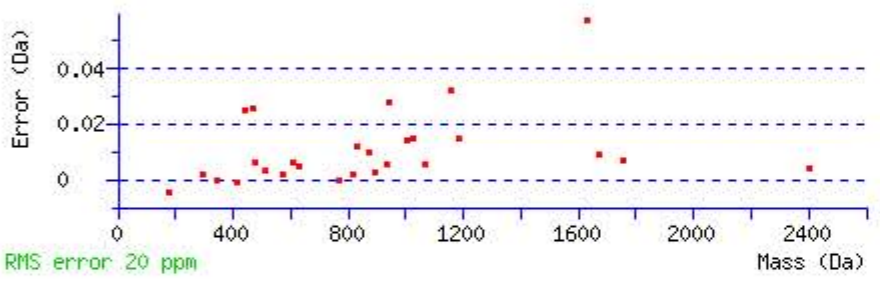
Match to Query 56287: 2695.275096 from(674.826050,4+) rtinseconds(2199) index(21488)
Title: Locus:1.1.1.3148.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

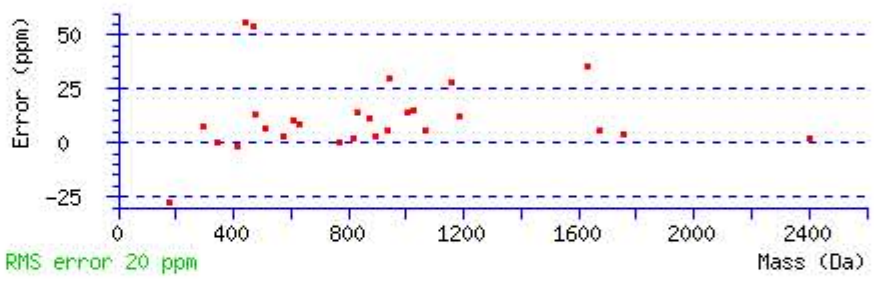
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2695.256516
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 41 **Expect:** 0.0015
**Matches :** 27/164 fragment ions using 74 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.047761 | 66.527518 | | | | | M | | | | | | | 17 |
| 2 | **292.078410** | 146.542843 | | | | | C | 2565.223327 | 1283.115301 | 2548.196778 | 1274.602027 | 2547.212762 | 1274.110019 | 16 |
| 3 | 389.131174 | 195.069225 | | | | | P | *2405.192678* | 1203.099977 | 2388.166129 | 1194.586702 | 2387.182113 | 1194.094694 | 15 |
| 4 | **828.356500** | **414.681888** | 811.329951 | 406.168614 | | | Q | 2308.139914 | 1154.573595 | 2291.113365 | 1146.060320 | 2290.129349 | 1145.568312 | 14 |
| 5 | **941.440564** | **471.223920** | 924.414015 | 462.710646 | | | L | 1868.914588 | 934.960932 | 1851.888039 | 926.447658 | 1850.904023 | 925.955650 | 13 |
| 6 | **1069.499142** | 535.253209 | 1052.472593 | 526.739935 | | | Q | *1755.830524* | 878.418900 | 1738.803975 | 869.905626 | 1737.819959 | 869.413618 | 12 |
| 7 | 1508.724468 | 754.865872 | 1491.697919 | 746.352598 | | | Q | *1627.771946* | 814.389611 | 1610.745397 | 805.876337 | 1609.761381 | 805.384329 | 11 |
| 8 | **1671.787797** | 836.397537 | 1654.761248 | 827.884262 | | | Y | *1188.546620* | 594.776948 | 1171.520071 | 586.263674 | 1170.536055 | 585.771666 | 10 |
| 9 | 1800.830390 | 900.918833 | 1783.803841 | 892.405559 | 1782.819825 | 891.913551 | E | *1025.483291* | 513.245284 | 1008.456742 | 504.732009 | 1007.472726 | 504.240001 | 9 |
| 10 | 1931.870875 | 966.439076 | 1914.844326 | 957.925801 | 1913.860310 | 957.433793 | M | *896.440698* | 448.723987 | 879.414149 | 440.210713 | 878.430133 | 439.718705 | 8 |
| 11 | 2068.929787 | 1034.968531 | 2051.903238 | 1026.455257 | 2050.919222 | 1025.963249 | H | *765.400213* | 383.203745 | 748.373664 | 374.690470 | 747.389648 | 374.198462 | 7 |
| 12 | 2125.951251 | 1063.479263 | 2108.924702 | 1054.965989 | 2107.940686 | 1054.473981 | G | *628.341301* | 314.674289 | 611.314752 | 306.161014 | 610.330736 | 305.669006 | 6 |
| 13 | 2223.004015 | 1112.005645 | 2205.977466 | 1103.492371 | 2204.993450 | 1103.000363 | P | *571.319837* | 286.163557 | 554.293288 | 277.650282 | 553.309272 | 277.158274 | 5 |
| 14 | 2352.046608 | 1176.526942 | 2335.020059 | 1168.013667 | 2334.036043 | 1167.521659 | E | *474.267073* | 237.637175 | 457.240524 | 229.123900 | 456.256508 | 228.631892 | 4 |
| 15 | 2409.068072 | 1205.037674 | 2392.041523 | 1196.524399 | 2391.057507 | 1196.032391 | G | *345.224480* | 173.115878 | 328.197931 | 164.602603 | | | 3 |
| 16 | 2522.152136 | 1261.579706 | 2505.125587 | 1253.066431 | 2504.141571 | 1252.574424 | L | 288.203016 | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 17 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 41.0 | 2695.256516 | 0.018580 | MCPQLQQYEMHGPEGLR |
| 34.9 | 2695.256516 | 0.018580 | MCPQLQQYEMHGPEGLR |
| 33.7 | 2695.256516 | 0.018580 | MCPQLQQYEMHGPEGLR |

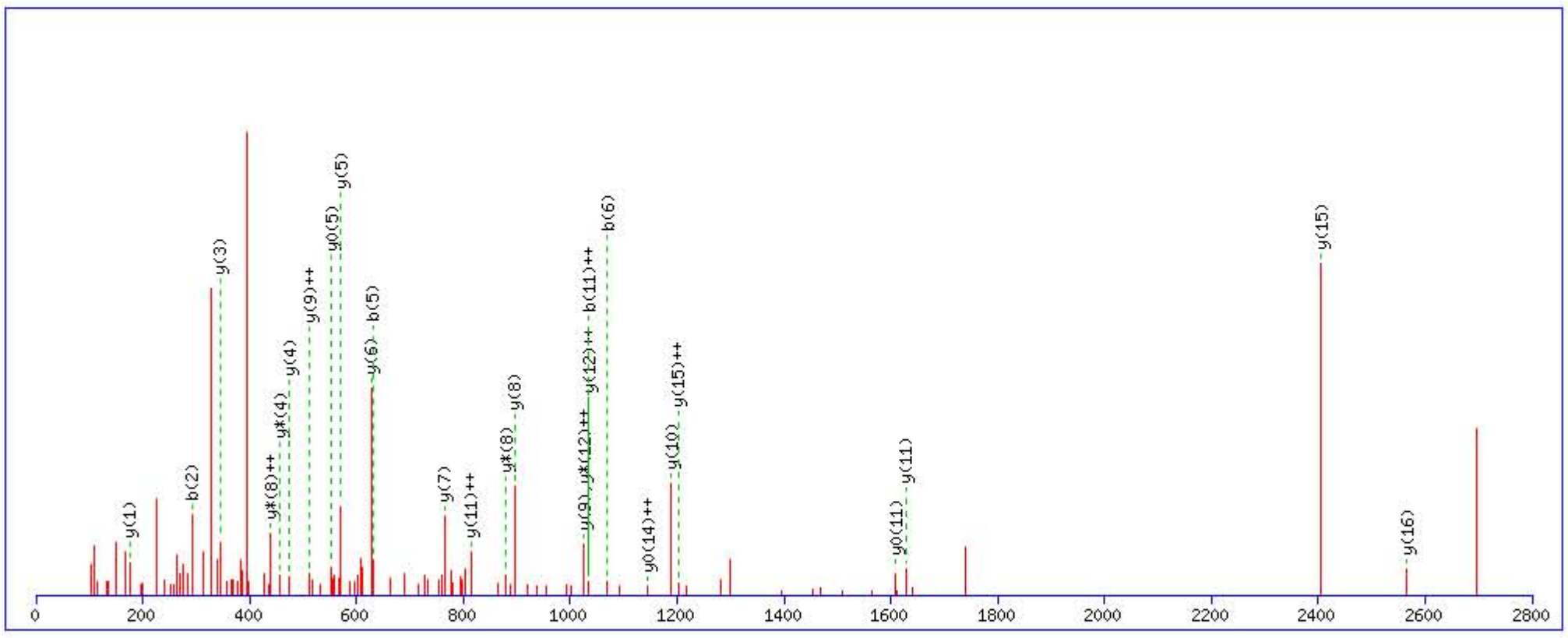
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

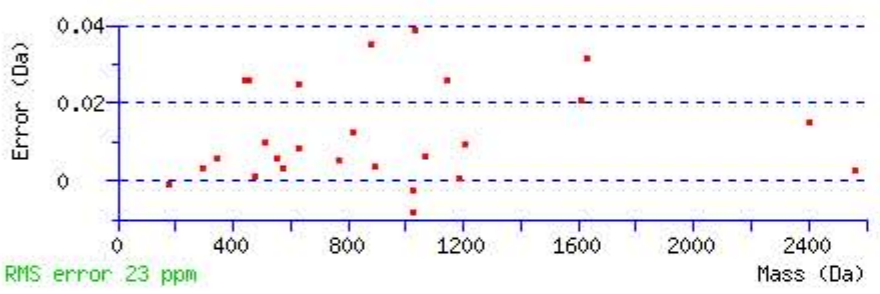
Match to Query 56289: 2695.276376 from(674.826370,4+) rtinseconds(2182) index(6671)
Title: Locus:1.1.1.2037.4 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

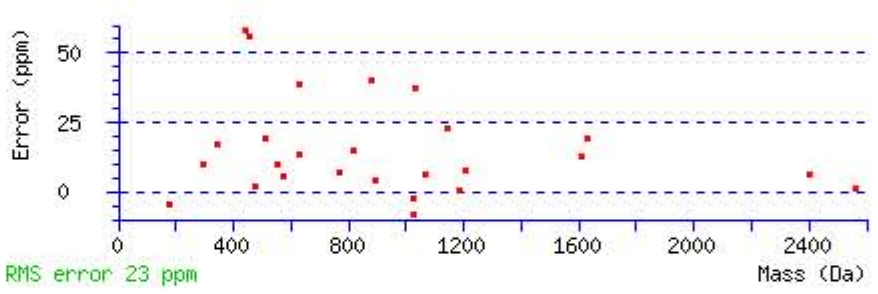
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2695.256516
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 0.00027
**Matches :** 27/164 fragment ions using 61 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.047761 | 66.527518 | | | | | M | | | | | | | 17 |
| 2 | **292.078410** | 146.542843 | | | | | C | *2565.223327* | 1283.115301 | 2548.196778 | 1274.602027 | 2547.212762 | 1274.110019 | 16 |
| 3 | 389.131174 | 195.069225 | | | | | P | *2405.192678* | 1203.099977 | 2388.166129 | 1194.586702 | 2387.182113 | 1194.094694 | 15 |
| 4 | 517.189752 | 259.098514 | 500.163203 | 250.585240 | | | Q | 2308.139914 | 1154.573595 | 2291.113365 | 1146.060320 | 2290.129349 | 1145.568312 | 14 |
| 5 | **630.273816** | 315.640546 | 613.247267 | 307.127272 | | | L | 2180.081336 | 1090.544306 | 2163.054787 | 1082.031031 | 2162.070771 | 1081.539023 | 13 |
| 6 | **1069.499142** | 535.253209 | 1052.472593 | 526.739935 | | | Q | 2066.997272 | 1034.002274 | 2049.970723 | 1025.488999 | 2048.986707 | 1024.996991 | 12 |
| 7 | 1508.724468 | 754.865872 | 1491.697919 | 746.352598 | | | Q | *1627.771946* | 814.389611 | 1610.745397 | 805.876337 | 1609.761381 | 805.384329 | 11 |
| 8 | 1671.787797 | 836.397537 | 1654.761248 | 827.884262 | | | Y | *1188.546620* | 594.776948 | 1171.520071 | 586.263674 | 1170.536055 | 585.771666 | 10 |
| 9 | 1800.830390 | 900.918833 | 1783.803841 | 892.405559 | 1782.819825 | 891.913551 | E | *1025.483291* | 513.245284 | 1008.456742 | 504.732009 | 1007.472726 | 504.240001 | 9 |
| 10 | 1931.870875 | 966.439076 | 1914.844326 | 957.925801 | 1913.860310 | 957.433793 | M | *896.440698* | 448.723987 | 879.414149 | 440.210713 | 878.430133 | 439.718705 | 8 |
| 11 | 2068.929787 | 1034.968531 | 2051.903238 | 1026.455257 | 2050.919222 | 1025.963249 | H | *765.400213* | 383.203745 | 748.373664 | 374.690470 | 747.389648 | 374.198462 | 7 |
| 12 | 2125.951251 | 1063.479263 | 2108.924702 | 1054.965989 | 2107.940686 | 1054.473981 | G | *628.341301* | 314.674289 | 611.314752 | 306.161014 | 610.330736 | 305.669006 | 6 |
| 13 | 2223.004015 | 1112.005645 | 2205.977466 | 1103.492371 | 2204.993450 | 1103.000363 | P | *571.319837* | 286.163557 | 554.293288 | 277.650282 | 553.309272 | 277.158274 | 5 |
| 14 | 2352.046608 | 1176.526942 | 2335.020059 | 1168.013667 | 2334.036043 | 1167.521659 | E | *474.267073* | 237.637175 | 457.240524 | 229.123900 | 456.256508 | 228.631892 | 4 |
| 15 | 2409.068072 | 1205.037674 | 2392.041523 | 1196.524399 | 2391.057507 | 1196.032391 | G | *345.224480* | 173.115878 | 328.197931 | 164.602603 | | | 3 |
| 16 | 2522.152136 | 1261.579706 | 2505.125587 | 1253.066431 | 2504.141571 | 1252.574424 | L | 288.203016 | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 17 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.5 | 2695.256516 | 0.019860 | MCPQLQQYEMHGPEGLR |
| 47.1 | 2695.256516 | 0.019860 | MCPQLQQYEMHGPEGLR |
| 42.7 | 2695.256516 | 0.019860 | MCPQLQQYEMHGPEGLR |

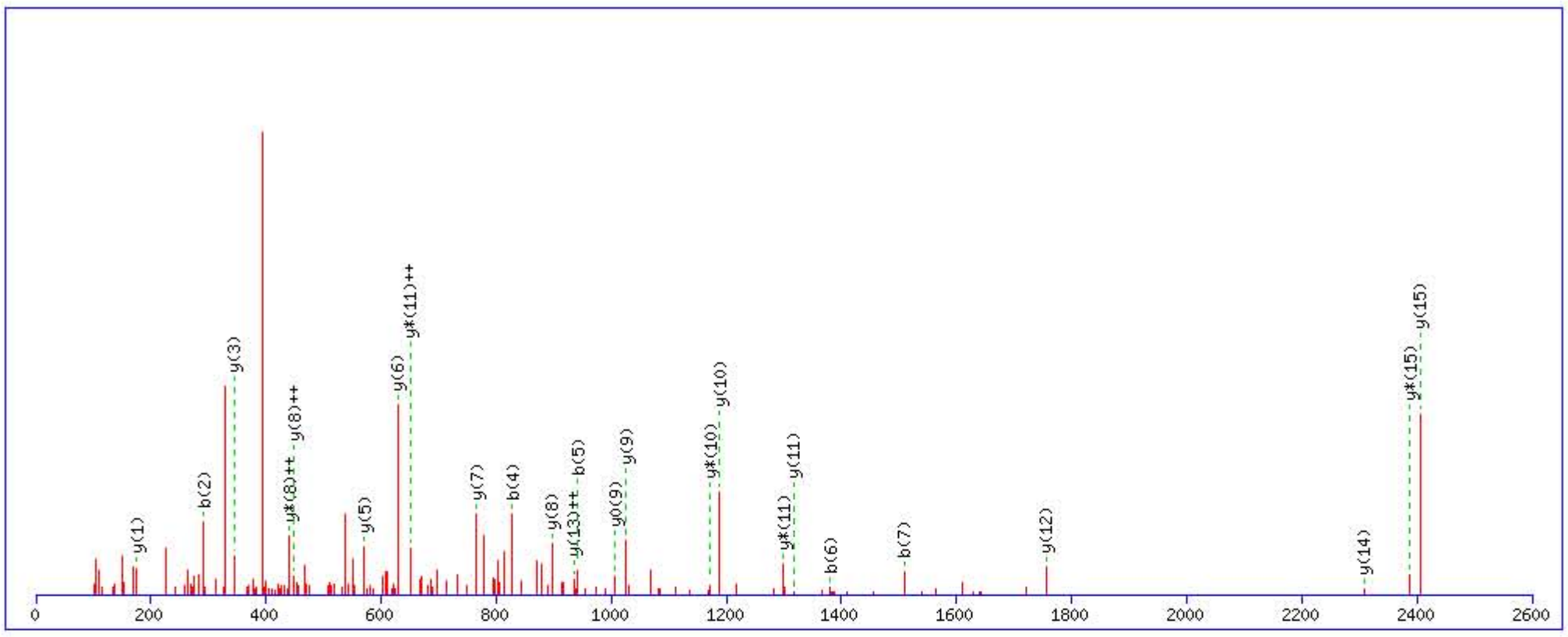
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

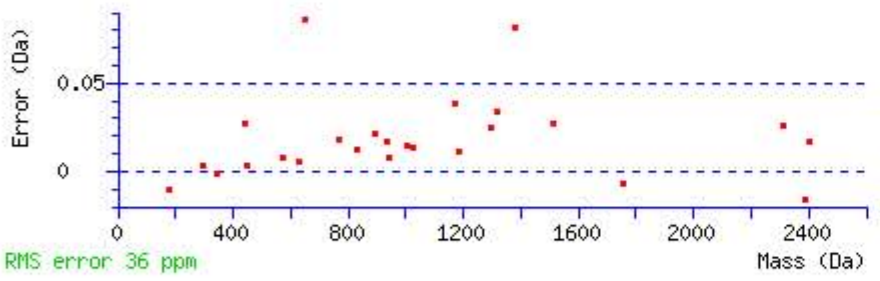
Match to Query 56297: 2695.286376 from(674.828870,4+) rtinseconds(2224) index(35600)
Title: Locus:1.1.1.883.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

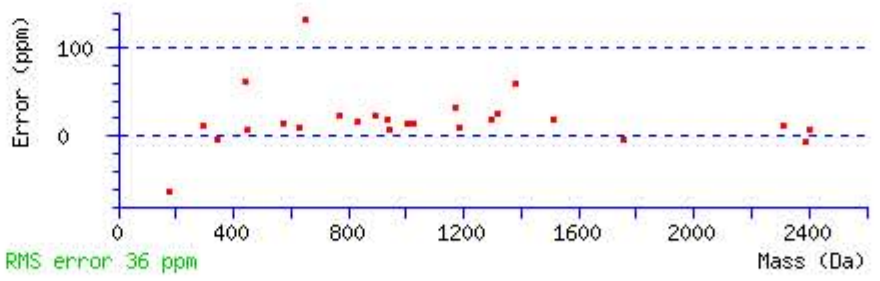
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2695.256516
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 43 **Expect:** 0.00011
**Matches :** 25/164 fragment ions using 68 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.047761 | 66.527518 | | | | | M | | | | | | | 17 |
| 2 | **292.078410** | 146.542843 | | | | | C | 2565.223327 | 1283.115301 | 2548.196778 | 1274.602027 | 2547.212762 | 1274.110019 | 16 |
| 3 | 389.131174 | 195.069225 | | | | | P | *2405.192678* | 1203.099977 | 2388.166129 | 1194.586702 | 2387.182113 | 1194.094694 | 15 |
| 4 | **828.356500** | 414.681888 | 811.329951 | 406.168614 | | | Q | *2308.139914* | 1154.573595 | 2291.113365 | 1146.060320 | 2290.129349 | 1145.568312 | 14 |
| 5 | **941.440564** | 471.223920 | 924.414015 | 462.710646 | | | L | 1868.914588 | 934.960932 | 1851.888039 | 926.447658 | 1850.904023 | 925.955650 | 13 |
| 6 | **1380.665890** | 690.836583 | 1363.639341 | 682.323309 | | | Q | *1755.830524* | 878.418900 | 1738.803975 | 869.905626 | 1737.819959 | 869.413618 | 12 |
| 7 | **1508.724468** | 754.865872 | 1491.697919 | 746.352598 | | | Q | *1316.605198* | 658.806237 | 1299.578649 | 650.292963 | 1298.594633 | 649.800955 | 11 |
| 8 | 1671.787797 | 836.397537 | 1654.761248 | 827.884262 | | | Y | *1188.546620* | 594.776948 | 1171.520071 | 586.263674 | 1170.536055 | 585.771666 | 10 |
| 9 | 1800.830390 | 900.918833 | 1783.803841 | 892.405559 | 1782.819825 | 891.913551 | E | *1025.483291* | 513.245284 | 1008.456742 | 504.732009 | 1007.472726 | 504.240001 | 9 |
| 10 | 1931.870875 | 966.439076 | 1914.844326 | 957.925801 | 1913.860310 | 957.433793 | M | *896.440698* | 448.723987 | 879.414149 | 440.210713 | 878.430133 | 439.718705 | 8 |
| 11 | 2068.929787 | 1034.968531 | 2051.903238 | 1026.455257 | 2050.919222 | 1025.963249 | H | *765.400213* | 383.203745 | 748.373664 | 374.690470 | 747.389648 | 374.198462 | 7 |
| 12 | 2125.951251 | 1063.479263 | 2108.924702 | 1054.965989 | 2107.940686 | 1054.473981 | G | *628.341301* | 314.674289 | 611.314752 | 306.161014 | 610.330736 | 305.669006 | 6 |
| 13 | 2223.004015 | 1112.005645 | 2205.977466 | 1103.492371 | 2204.993450 | 1103.000363 | P | *571.319837* | 286.163557 | 554.293288 | 277.650282 | 553.309272 | 277.158274 | 5 |
| 14 | 2352.046608 | 1176.526942 | 2335.020059 | 1168.013667 | 2334.036043 | 1167.521659 | E | 474.267073 | 237.637175 | 457.240524 | 229.123900 | 456.256508 | 228.631892 | 4 |
| 15 | 2409.068072 | 1205.037674 | 2392.041523 | 1196.524399 | 2391.057507 | 1196.032391 | G | *345.224480* | 173.115878 | 328.197931 | 164.602603 | | | 3 |
| 16 | 2522.152136 | 1261.579706 | 2505.125587 | 1253.066431 | 2504.141571 | 1252.574424 | L | 288.203016 | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 17 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 42.7 | 2695.256516 | 0.029860 | MCPQLQQYEMHGPEGLR |
| 38.2 | 2695.256516 | 0.029860 | MCPQLQQYEMHGPEGLR |
| 26.1 | 2695.256516 | 0.029860 | MCPQLQQYEMHGPEGLR |
| 0.4 | 2695.299408 | -0.013032 | MSGMEKLQNASWIYQQK |

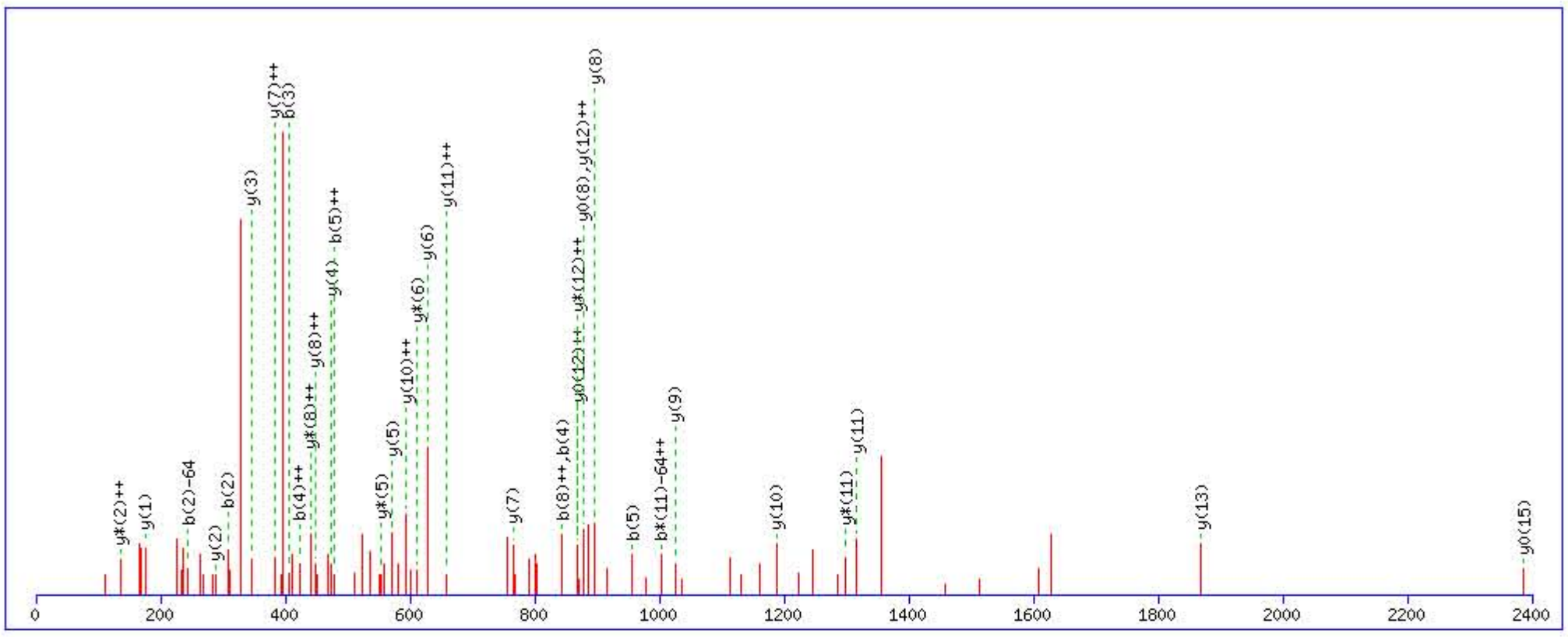
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

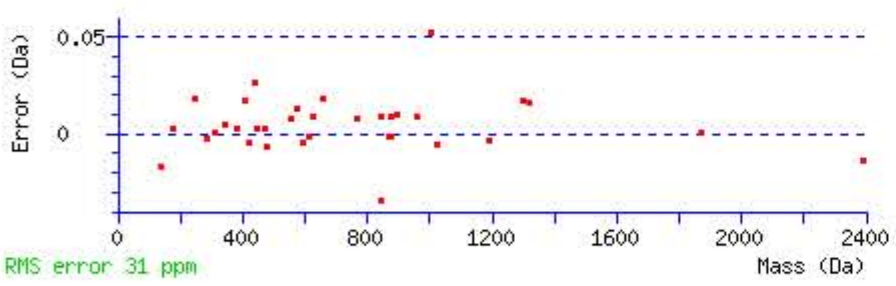
Match to Query 56478: 2711.268896 from(678.824500,4+) rtinseconds(2155) index(6483)
Title: Locus:1.1.1.2027.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

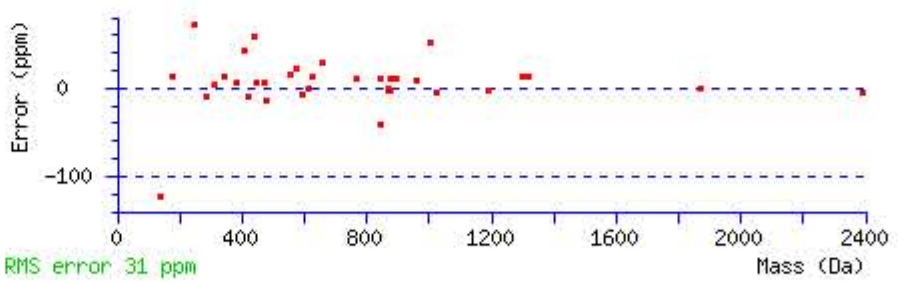
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2711.251434
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
M1 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q4 : Biotin:Thermo-21345 (Q)
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 43 **Expect:** 0.00078
**Matches :** 35/238 fragment ions using 81 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.042676 | 74.524976 | | | | | M | | | | | | | 17 |
| 2 | 308.073325 | 154.540301 | | | | | C | 2565.223327 | 1283.115302 | 2548.196778 | 1274.602027 | 2547.212762 | 1274.110019 | 16 |
| 3 | 405.126089 | 203.066683 | | | | | P | 2405.192678 | 1203.099977 | 2388.166129 | 1194.586702 | 2387.182113 | 1194.094694 | 15 |
| 4 | 844.351415 | 422.679346 | 827.324866 | 414.166071 | | | Q | 2308.139914 | 1154.573595 | 2291.113365 | 1146.060320 | 2290.129349 | 1145.568312 | 14 |
| 5 | 957.435479 | 479.221378 | 940.408930 | 470.708103 | | | L | 1868.914588 | 934.960932 | 1851.888039 | 926.447658 | 1850.904023 | 925.955650 | 13 |
| 6 | 1396.660805 | 698.834041 | 1379.634256 | 690.320766 | | | Q | 1755.830524 | 878.418900 | 1738.803975 | 869.905626 | 1737.819959 | 869.413618 | 12 |
| 7 | 1524.719383 | 762.863330 | 1507.692834 | 754.350055 | | | Q | 1316.605198 | 658.806237 | 1299.578649 | 650.292963 | 1298.594633 | 649.800955 | 11 |
| 8 | 1687.782712 | 844.394994 | 1670.756163 | 835.881720 | | | Y | 1188.546620 | 594.776948 | 1171.520071 | 586.263674 | 1170.536055 | 585.771666 | 10 |
| 9 | 1816.825305 | 908.916291 | 1799.798756 | 900.403016 | 1798.814740 | 899.911008 | E | 1025.483291 | 513.245284 | 1008.456742 | 504.732009 | 1007.472726 | 504.240001 | 9 |
| 10 | 1947.865790 | 974.436533 | 1930.839241 | 965.923259 | 1929.855225 | 965.431251 | M | 896.440698 | 448.723987 | 879.414149 | 440.210713 | 878.430133 | 439.718705 | 8 |
| 11 | 2084.924702 | 1042.965989 | 2067.898153 | 1034.452715 | 2066.914137 | 1033.960707 | H | 765.400213 | 383.203745 | 748.373664 | 374.690470 | 747.389648 | 374.198462 | 7 |
| 12 | 2141.946166 | 1071.476721 | 2124.919617 | 1062.963446 | 2123.935601 | 1062.471439 | G | 628.341301 | 314.674289 | 611.314752 | 306.161014 | 610.330736 | 305.669006 | 6 |
| 13 | 2238.998930 | 1120.003103 | 2221.972381 | 1111.489828 | 2220.988365 | 1110.997821 | P | 571.319837 | 286.163557 | 554.293288 | 277.650282 | 553.309272 | 277.158274 | 5 |
| 14 | 2368.041523 | 1184.524400 | 2351.014974 | 1176.011125 | 2350.030958 | 1175.519117 | E | 474.267073 | 237.637175 | 457.240524 | 229.123900 | 456.256508 | 228.631892 | 4 |
| 15 | 2425.062987 | 1213.035132 | 2408.036438 | 1204.521857 | 2407.052422 | 1204.029849 | G | 345.224480 | 173.115878 | 328.197931 | 164.602603 | | | 3 |
| 16 | 2538.147051 | 1269.577164 | 2521.120502 | 1261.063889 | 2520.136486 | 1260.571881 | L | 288.203016 | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 17 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 43.4 | 2711.251434 | 0.017462 | MCPQLQQYEMHGPEGLR |
| 43.4 | 2711.251434 | 0.017462 | MCPQLQQYEMHGPEGLR |
| 30.2 | 2711.251434 | 0.017462 | MCPQLQQYEMHGPEGLR |
| 0.1 | 2711.251434 | 0.017462 | MCPQLQQYEMHGPEGLR |
| 0.1 | 2711.251434 | 0.017462 | MCPQLQQYEMHGPEGLR |

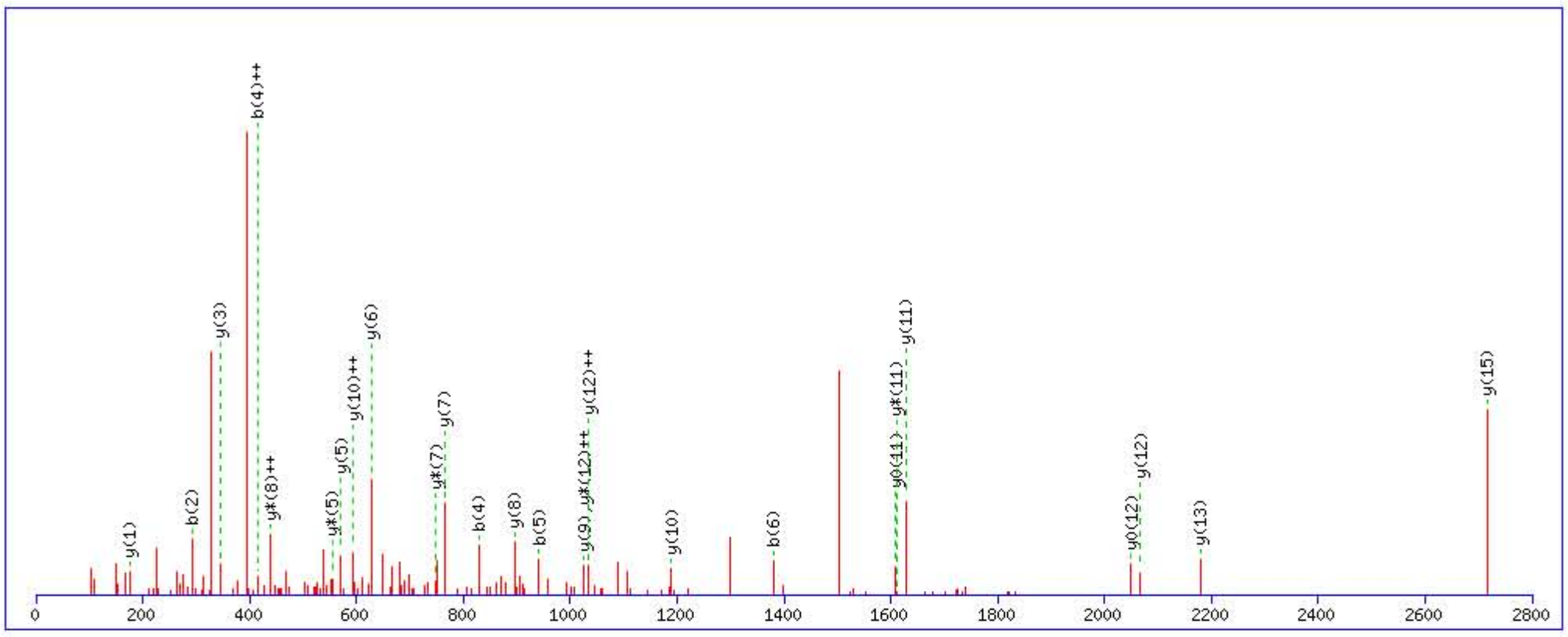
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

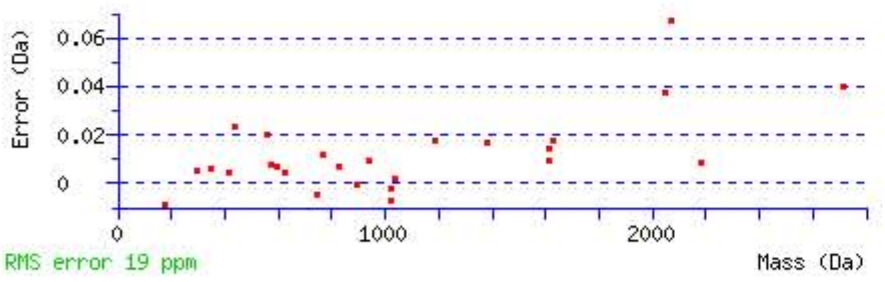
Match to Query 60183: 3006.455096 from(752.621050,4+) rtinseconds(2338) index(22240)
Title: Locus:1.1.1.3196.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

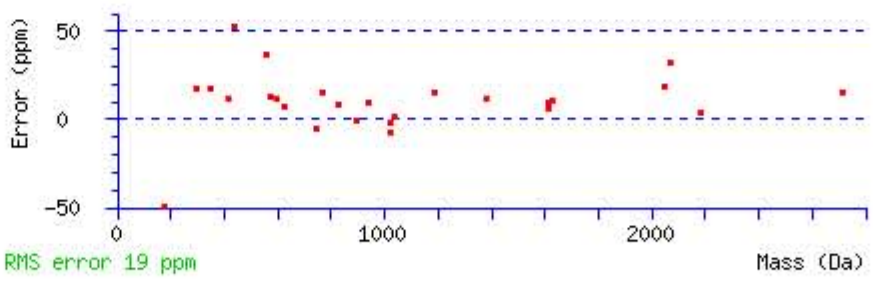
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3006.423264
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
Q6 : Biotin:Thermo-21345 (Q)
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 40 **Expect:** 0.0025
**Matches :** 26/164 fragment ions using 68 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.047761 | 66.527518 | | | | | M | | | | | | | 17 |
| 2 | **292.078410** | 146.542843 | | | | | C | 2876.390075 | 1438.698675 | 2859.363526 | 1430.185401 | 2858.379510 | 1429.693393 | 16 |
| 3 | 389.131174 | 195.069225 | | | | | P | *2716.359426* | 1358.683351 | 2699.332877 | 1350.170076 | 2698.348861 | 1349.678068 | 15 |
| 4 | **828.356500** | 414.681888 | 811.329951 | 406.168614 | | | Q | 2619.306662 | 1310.156969 | 2602.280113 | 1301.643694 | 2601.296097 | 1301.151686 | 14 |
| 5 | **941.440564** | 471.223920 | 924.414015 | 462.710646 | | | L | *2180.081336* | 1090.544306 | 2163.054787 | 1082.031031 | 2162.070771 | 1081.539023 | 13 |
| 6 | **1380.665890** | 690.836583 | 1363.639341 | 682.323309 | | | Q | *2066.997272* | 1034.002274 | 2049.970723 | 1025.488999 | 2048.986707 | 1024.996991 | 12 |
| 7 | 1819.891216 | 910.449246 | 1802.864667 | 901.935972 | | | Q | *1627.771946* | 814.389611 | 1610.745397 | 805.876337 | 1609.761381 | 805.384329 | 11 |
| 8 | 1982.954545 | 991.980911 | 1965.927996 | 983.467636 | | | Y | *1188.546620* | 594.776948 | 1171.520071 | 586.263674 | 1170.536055 | 585.771666 | 10 |
| 9 | 2111.997138 | 1056.502207 | 2094.970589 | 1047.988932 | 2093.986573 | 1047.496925 | E | *1025.483291* | 513.245284 | 1008.456742 | 504.732009 | 1007.472726 | 504.240001 | 9 |
| 10 | 2243.037623 | 1122.022450 | 2226.011074 | 1113.509175 | 2225.027058 | 1113.017167 | M | *896.440698* | 448.723987 | 879.414149 | 440.210713 | 878.430133 | 439.718705 | 8 |
| 11 | 2380.096535 | 1190.551906 | 2363.069986 | 1182.038631 | 2362.085970 | 1181.546623 | H | *765.400213* | 383.203745 | 748.373664 | 374.690470 | 747.389648 | 374.198462 | 7 |
| 12 | 2437.117999 | 1219.062637 | 2420.091450 | 1210.549363 | 2419.107434 | 1210.057355 | G | *628.341301* | 314.674289 | 611.314752 | 306.161014 | 610.330736 | 305.669006 | 6 |
| 13 | 2534.170763 | 1267.589019 | 2517.144214 | 1259.075745 | 2516.160198 | 1258.583737 | P | *571.319837* | 286.163557 | 554.293288 | 277.650282 | 553.309272 | 277.158274 | 5 |
| 14 | 2663.213356 | 1332.110316 | 2646.186807 | 1323.597041 | 2645.202791 | 1323.105034 | E | 474.267073 | 237.637175 | 457.240524 | 229.123900 | 456.256508 | 228.631892 | 4 |
| 15 | 2720.234820 | 1360.621048 | 2703.208271 | 1352.107773 | 2702.224255 | 1351.615766 | G | *345.224480* | 173.115878 | 328.197931 | 164.602603 | | | 3 |
| 16 | 2833.318884 | 1417.163080 | 2816.292335 | 1408.649806 | 2815.308319 | 1408.157798 | L | 288.203016 | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 17 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 40.4 | 3006.423264 | 0.031832 | MCPQLQQYEMHGPEGLR |

**Mascot:** http://www.matrixscience.com/

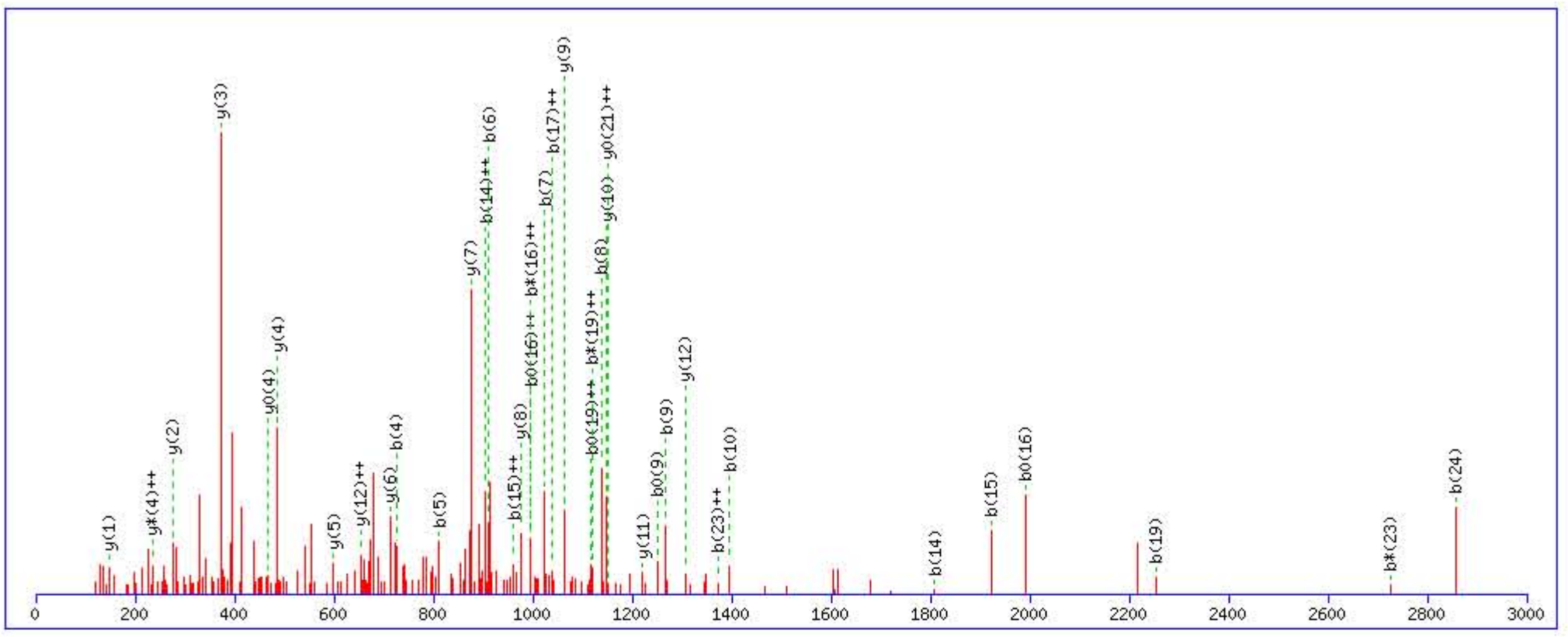
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AVDQSVLLMKPDAELSASSVYNLLPEK**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

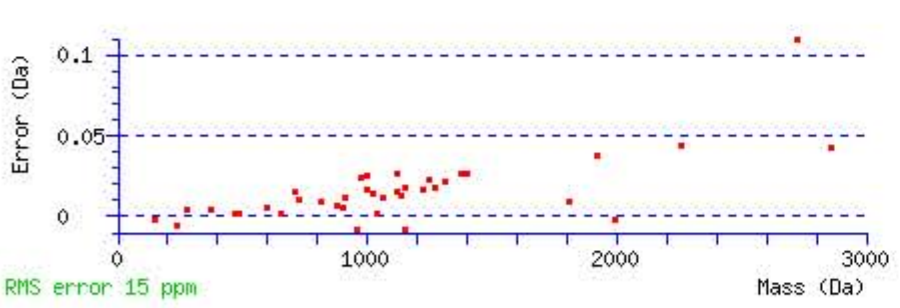
Match to Query 62709: 3227.726536 from(807.938910,4+) rtinseconds(2766) index(24867)
Title: Locus:1.1.1.3344.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

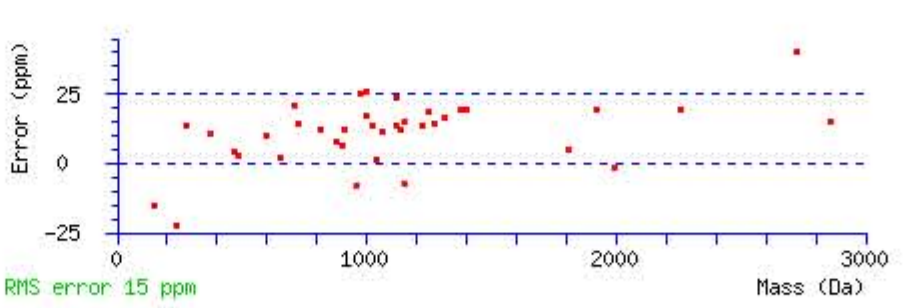
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3227.682129
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 71 **Expect:** 2.6e-007
**Matches :** 38/300 fragment ions using 79 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 27 |
| 2 | 171.112804 | 86.060040 | | | | | V | 3157.652336 | 1579.329806 | 3140.625787 | 1570.816531 | 3139.641771 | 1570.324523 | 26 |
| 3 | 286.139747 | 143.573512 | | | 268.129182 | 134.568229 | D | 3058.583922 | 1529.795599 | 3041.557373 | 1521.282324 | 3040.573357 | 1520.790316 | 25 |
| 4 | *725.365073* | 363.186175 | 708.338524 | 354.672900 | 707.354508 | 354.180892 | Q | 2943.556979 | 1472.282127 | 2926.530430 | 1463.768853 | 2925.546414 | 1463.276845 | 24 |
| 5 | *812.397101* | 406.702189 | 795.370552 | 398.188914 | 794.386536 | 397.696906 | S | 2504.331653 | 1252.669464 | 2487.305104 | 1244.156190 | 2486.321088 | 1243.664182 | 23 |
| 6 | *911.465515* | 456.236396 | 894.438966 | 447.723121 | 893.454950 | 447.231113 | V | 2417.299625 | 1209.153451 | 2400.273076 | 1200.640176 | 2399.289060 | 1200.148168 | 22 |
| 7 | *1024.549579* | 512.778427 | 1007.523030 | 504.265153 | 1006.539014 | 503.773145 | L | 2318.231211 | 1159.619243 | 2301.204662 | 1151.105969 | 2300.220646 | 1150.613961 | 21 |
| 8 | *1137.633643* | 569.320459 | 1120.607094 | 560.807185 | 1119.623078 | 560.315177 | L | 2205.147147 | 1103.077212 | 2188.120598 | 1094.563937 | 2187.136582 | 1094.071929 | 20 |
| 9 | *1268.674128* | 634.840702 | 1251.647579 | 626.327428 | 1250.663563 | 625.835419 | M | 2092.063083 | 1046.535179 | 2075.036534 | 1038.021905 | 2074.052518 | 1037.529897 | 19 |
| 10 | *1396.769091* | 698.888183 | 1379.742542 | 690.374909 | 1378.758526 | 689.882901 | K | 1961.022598 | 981.014937 | 1943.996049 | 972.501663 | 1943.012033 | 972.009655 | 18 |
| 11 | 1493.821855 | 747.414565 | 1476.795306 | 738.901291 | 1475.811290 | 738.409283 | P | 1832.927635 | 916.967456 | 1815.901086 | 908.454181 | 1814.917070 | 907.962173 | 17 |
| 12 | 1608.848798 | 804.928037 | 1591.822249 | 796.414763 | 1590.838233 | 795.922755 | D | 1735.874871 | 868.441074 | 1718.848322 | 859.927799 | 1717.864306 | 859.435791 | 16 |
| 13 | 1679.885912 | 840.446594 | 1662.859363 | 831.933320 | 1661.875347 | 831.441311 | A | 1620.847928 | 810.927602 | 1603.821379 | 802.414328 | 1602.837363 | 801.922320 | 15 |
| 14 | *1808.928505* | **904.967891** | 1791.901956 | 896.454616 | 1790.917940 | 895.962608 | E | 1549.810814 | 775.409045 | 1532.784265 | 766.895771 | 1531.800249 | 766.403763 | 14 |
| 15 | *1922.012569* | **961.509923** | 1904.986020 | 952.996648 | 1904.002004 | 952.504640 | L | 1420.768221 | 710.887749 | 1403.741672 | 702.374474 | 1402.757656 | 701.882466 | 13 |
| 16 | 2009.044597 | 1005.025937 | 1992.018048 | 996.512662 | 1991.034032 | 996.020654 | S | *1307.684157* | 654.345717 | 1290.657608 | 645.832442 | 1289.673592 | 645.340434 | 12 |
| 17 | 2080.081711 | **1040.544493** | 2063.055162 | 1032.031219 | 2062.071146 | 1031.539211 | A | *1220.652129* | 610.829703 | 1203.625580 | 602.316428 | 1202.641564 | 601.824420 | 11 |
| 18 | 2167.113739 | 1084.060507 | 2150.087190 | 1075.547233 | 2149.103174 | 1075.055225 | S | *1149.615015* | 575.311146 | 1132.588466 | 566.797871 | 1131.604450 | 566.305863 | 10 |
| 19 | *2254.145767* | 1127.576521 | 2237.119218 | 1119.063247 | 2236.135202 | 1118.571239 | S | *1062.582987* | 531.795132 | 1045.556438 | 523.281857 | 1044.572422 | 522.789849 | 9 |
| 20 | 2353.214181 | 1177.110728 | 2336.187632 | 1168.597454 | 2335.203616 | 1168.105446 | V | *975.550959* | 488.279118 | 958.524410 | 479.765843 | 957.540394 | 479.273835 | 8 |
| 21 | 2516.277510 | 1258.642393 | 2499.250961 | 1250.129118 | 2498.266945 | 1249.637110 | Y | *876.482545* | 438.744911 | 859.455996 | 430.231636 | 858.471980 | 429.739628 | 7 |
| 22 | 2630.320437 | 1315.663856 | 2613.293888 | 1307.150582 | 2612.309872 | 1306.658574 | N | *713.419216* | 357.213246 | 696.392667 | 348.699972 | 695.408651 | 348.207964 | 6 |
| 23 | 2743.404501 | **1372.205888** | 2726.377952 | 1363.692614 | 2725.393936 | 1363.200606 | L | *599.376289* | 300.191783 | 582.349740 | 291.678508 | 581.365724 | 291.186500 | 5 |
| 24 | *2856.488565* | 1428.747921 | 2839.462016 | 1420.234646 | 2838.478000 | 1419.742638 | L | *486.292225* | 243.649751 | 469.265676 | 235.136476 | 468.281660 | 234.644468 | 4 |
| 25 | 2953.541329 | 1477.274303 | 2936.514780 | 1468.761028 | 2935.530764 | 1468.269020 | P | *373.208161* | 187.107719 | 356.181612 | 178.594444 | 355.197596 | 178.102436 | 3 |
| 26 | 3082.583922 | 1541.795599 | 3065.557373 | 1533.282325 | 3064.573357 | 1532.790317 | E | *276.155397* | 138.581337 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 27 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 70.7 | 3227.682129 | 0.044407 | AVDQSVLLMKPDAELSASSVYNLLPEK |
| 0.5 | 3227.749542 | -0.023006 | LVAGLLLWASLLTGAWPSFPTQDHLPATPR |

**Mascot:** http://www.matrixscience.com/

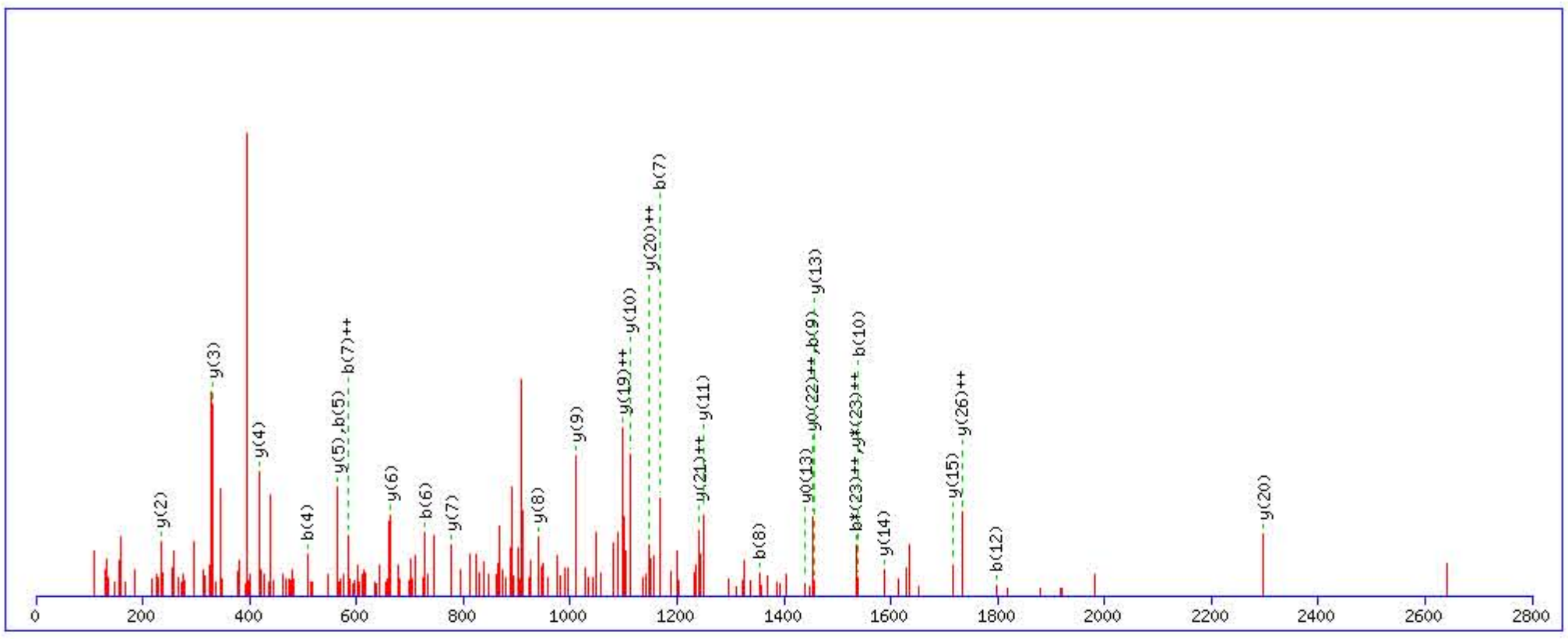
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SPCYGYQWVSEEHEEAHHTAYLVFSPSK**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

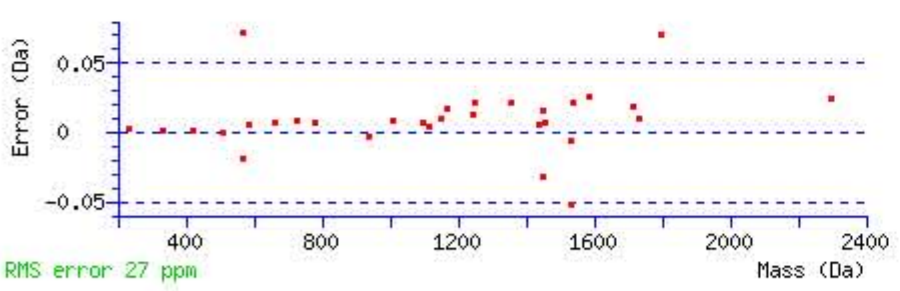
Match to Query 66934: 3648.683376 from(913.178120,4+) rtinseconds(2155) index(21228)
Title: Locus:1.1.1.3132.23 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

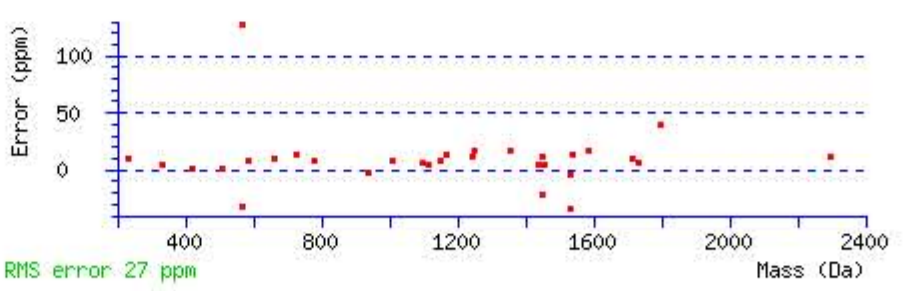
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3648.644211
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 69 **Expect:** 1.8e-006
**Matches :** 31/310 fragment ions using 58 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 28 |
| 2 | 185.092068 | 93.049672 | | | 167.081503 | 84.044389 | P | 3562.619476 | 1781.813376 | 3545.592927 | 1773.300101 | 3544.608911 | 1772.808093 | 27 |
| 3 | 345.122717 | 173.064997 | | | 327.112152 | 164.059714 | C | 3465.566712 | 1733.286994 | 3448.540163 | 1724.773719 | 3447.556147 | 1724.281711 | 26 |
| 4 | *508.186046* | 254.596661 | | | 490.175481 | 245.591379 | Y | 3305.536063 | 1653.271669 | 3288.509514 | 1644.758395 | 3287.525498 | 1644.266387 | 25 |
| 5 | *565.207510* | 283.107393 | | | 547.196945 | 274.102111 | G | 3142.472734 | 1571.740005 | 3125.446185 | 1563.226730 | 3124.462169 | 1562.734722 | 24 |
| 6 | *728.270839* | 364.639058 | | | 710.260274 | 355.633775 | Y | 3085.451270 | 1543.229273 | 3068.424721 | 1534.715998 | 3067.440705 | 1534.223990 | 23 |
| 7 | *1167.496165* | 584.251721 | 1150.469616 | 575.738446 | 1149.485600 | 575.246438 | Q | 2922.387941 | 1461.697608 | 2905.361392 | 1453.184334 | 2904.377376 | 1452.692326 | 22 |
| 8 | *1353.575478* | 677.291377 | 1336.548929 | 668.778103 | 1335.564913 | 668.286094 | W | 2483.162615 | 1242.084945 | 2466.136066 | 1233.571671 | 2465.152050 | 1233.079663 | 21 |
| 9 | *1452.643892* | 726.825584 | 1435.617343 | 718.312310 | 1434.633327 | 717.820302 | V | *2297.083302* | 1149.045289 | 2280.056753 | 1140.532014 | 2279.072737 | 1140.040006 | 20 |
| 10 | *1539.675920* | 770.341598 | 1522.649371 | 761.828324 | 1521.665355 | 761.336316 | S | 2198.014888 | 1099.511082 | 2180.988339 | 1090.997807 | 2180.004323 | 1090.505800 | 19 |
| 11 | 1668.718513 | 834.862895 | 1651.691964 | 826.349620 | 1650.707948 | 825.857612 | E | 2110.982860 | 1055.995068 | 2093.956311 | 1047.481793 | 2092.972295 | 1046.989785 | 18 |
| 12 | *1797.761106* | 899.384191 | 1780.734557 | 890.870917 | 1779.750541 | 890.378909 | E | 1981.940267 | 991.473772 | 1964.913718 | 982.960497 | 1963.929702 | 982.468489 | 17 |
| 13 | 1934.820018 | 967.913647 | 1917.793469 | 959.400373 | 1916.809453 | 958.908365 | H | 1852.897674 | 926.952475 | 1835.871125 | 918.439201 | 1834.887109 | 917.947193 | 16 |
| 14 | 2063.862611 | 1032.434943 | 2046.836062 | 1023.921669 | 2045.852046 | 1023.429661 | E | *1715.838762* | 858.423019 | 1698.812213 | 849.909745 | 1697.828197 | 849.417737 | 15 |
| 15 | 2192.905204 | 1096.956240 | 2175.878655 | 1088.442965 | 2174.894639 | 1087.950958 | E | *1586.796169* | 793.901723 | 1569.769620 | 785.388448 | 1568.785604 | 784.896440 | 14 |
| 16 | 2263.942318 | 1132.474797 | 2246.915769 | 1123.961523 | 2245.931753 | 1123.469515 | A | *1457.753576* | 729.380426 | 1440.727027 | 720.867152 | 1439.743011 | 720.375144 | 13 |
| 17 | 2401.001230 | 1201.004253 | 2383.974681 | 1192.490979 | 2382.990665 | 1191.998971 | H | 1386.716462 | 693.861869 | 1369.689913 | 685.348595 | 1368.705897 | 684.856587 | 12 |
| 18 | 2538.060142 | 1269.533709 | 2521.033593 | 1261.020435 | 2520.049577 | 1260.528427 | H | *1249.657550* | 625.332413 | 1232.631001 | 616.819139 | 1231.646985 | 616.327131 | 11 |
| 19 | 2639.107821 | 1320.057548 | 2622.081272 | 1311.544274 | 2621.097256 | 1311.052266 | T | *1112.598638* | 556.802957 | 1095.572089 | 548.289683 | 1094.588073 | 547.797675 | 10 |
| 20 | 2710.144935 | 1355.576106 | 2693.118386 | 1347.062831 | 2692.134370 | 1346.570823 | A | *1011.550959* | 506.279118 | 994.524410 | 497.765843 | 993.540394 | 497.273835 | 9 |
| 21 | 2873.208264 | 1437.107770 | 2856.181715 | 1428.594496 | 2855.197699 | 1428.102488 | Y | *940.513845* | 470.760561 | 923.487296 | 462.247286 | 922.503280 | 461.755278 | 8 |
| 22 | 2986.292328 | 1493.649802 | 2969.265779 | 1485.136528 | 2968.281763 | 1484.644520 | L | *777.450516* | 389.228896 | 760.423967 | 380.715622 | 759.439951 | 380.223614 | 7 |
| 23 | 3085.360742 | 1543.184009 | 3068.334193 | 1534.670735 | 3067.350177 | 1534.178727 | V | *664.366452* | 332.686864 | 647.339903 | 324.173589 | 646.355887 | 323.681581 | 6 |
| 24 | 3232.429156 | 1616.718216 | 3215.402607 | 1608.204941 | 3214.418591 | 1607.712934 | F | *565.298038* | 283.152657 | 548.271489 | 274.639383 | 547.287473 | 274.147375 | 5 |
| 25 | 3319.461184 | 1660.234230 | 3302.434635 | 1651.720955 | 3301.450619 | 1651.228948 | S | *418.229624* | 209.618450 | 401.203075 | 201.105176 | 400.219059 | 200.613168 | 4 |
| 26 | 3416.513948 | 1708.760612 | 3399.487399 | 1700.247338 | 3398.503383 | 1699.755330 | P | *331.197596* | 166.102436 | 314.171047 | 157.589162 | 313.187031 | 157.097154 | 3 |
| 27 | 3503.545976 | 1752.276626 | 3486.519427 | 1743.763352 | 3485.535411 | 1743.271344 | S | *234.144832* | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 28 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 68.9 | 3648.644211 | 0.039165 | SPCYGYQWVSEEHEEAHHTAYLVFSPSK |

**Mascot:** http://www.matrixscience.com/

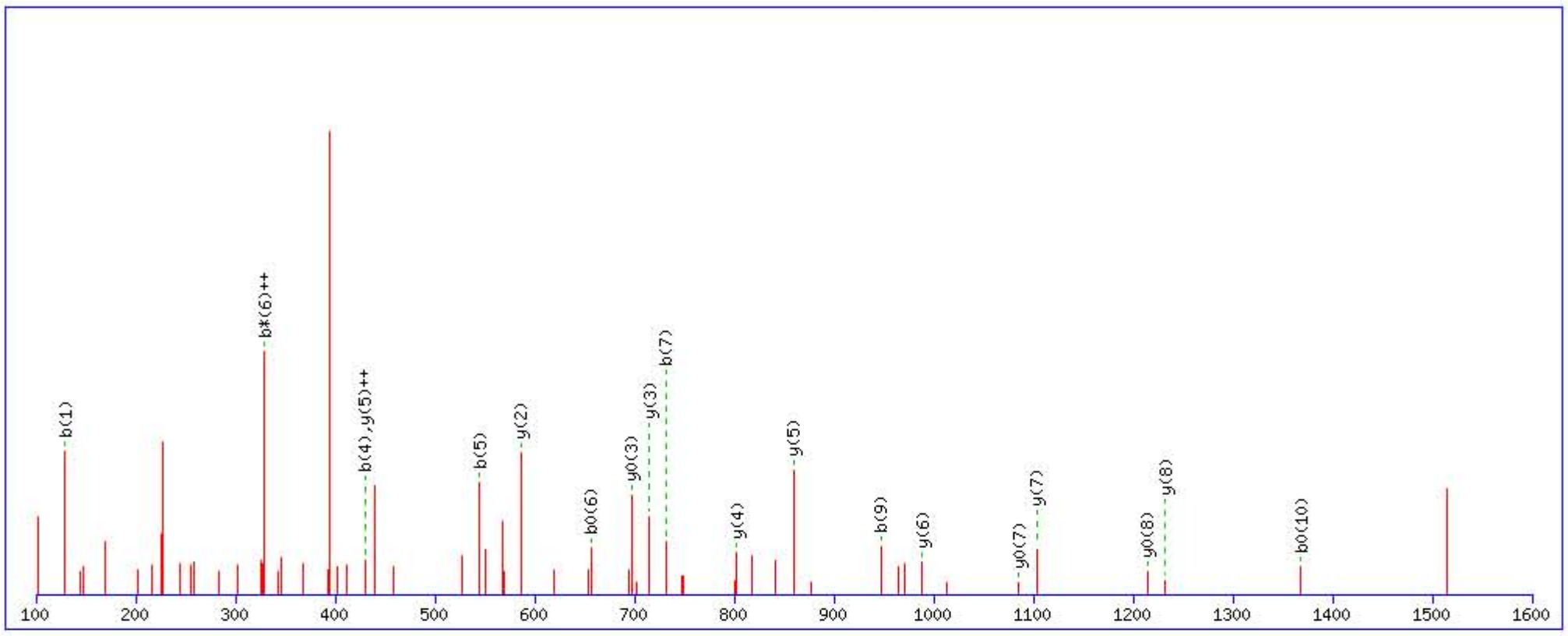
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KATEDEGSEQK**
Found in **ANT3_HUMAN**, Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

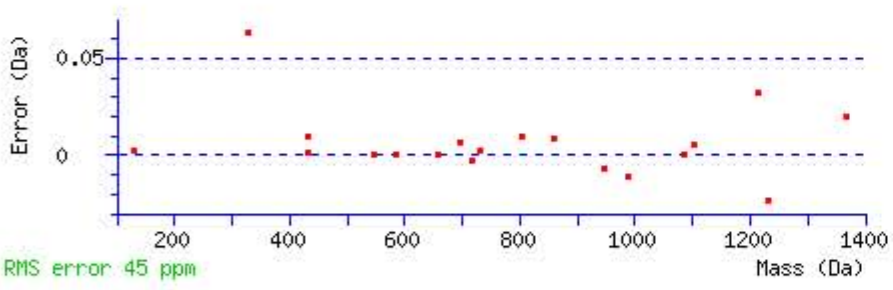
Match to Query 32082: 1531.718982 from(511.580270,3+) rtinseconds(1029) index(14604)
Title: Locus:1.1.1.2740.4 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

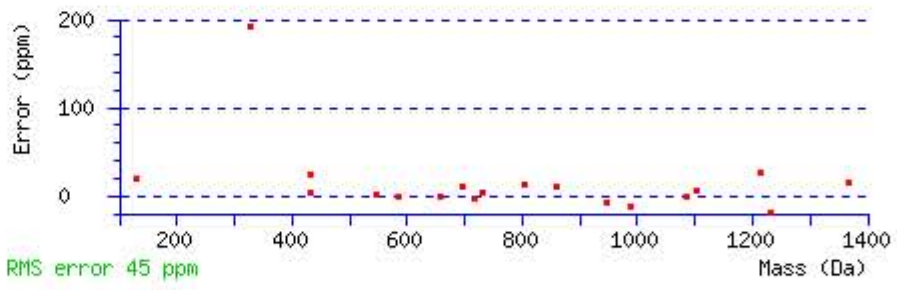
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1531.718796
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 51 **Expect:** 0.00013
**Matches :** 19/112 fragment ions using 25 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.102239 | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 11 |
| 2 | 200.139353 | 100.573315 | 183.112804 | 92.060040 | | | A | 1404.631137 | 702.819207 | 1387.604588 | 694.305932 | 1386.620572 | 693.813924 | 10 |
| 3 | 301.187032 | 151.097154 | 284.160483 | 142.583879 | 283.176467 | 142.091872 | T | 1333.594023 | 667.300650 | 1316.567474 | 658.787375 | 1315.583458 | 658.295367 | 9 |
| 4 | 430.229625 | 215.618450 | 413.203076 | 207.105176 | 412.219060 | 206.613168 | E | *1232.546344* | 616.776810 | 1215.519795 | 608.263536 | 1214.535779 | 607.771528 | 8 |
| 5 | 545.256568 | 273.131922 | 528.230019 | 264.618648 | 527.246003 | 264.126640 | D | *1103.503751* | 552.255514 | 1086.477202 | 543.742239 | 1085.493186 | 543.250231 | 7 |
| 6 | 674.299161 | 337.653219 | 657.272612 | 329.139944 | 656.288596 | 328.647936 | E | *988.476808* | 494.742042 | 971.450259 | 486.228768 | 970.466243 | 485.736760 | 6 |
| 7 | 731.320625 | 366.163951 | 714.294076 | 357.650676 | 713.310060 | 357.158668 | G | *859.434215* | 430.220746 | 842.407666 | 421.707471 | 841.423650 | 421.215463 | 5 |
| 8 | 818.352653 | 409.679965 | 801.326104 | 401.166690 | 800.342088 | 400.674682 | S | *802.412751* | 401.710014 | 785.386202 | 393.196739 | 784.402186 | 392.704731 | 4 |
| 9 | 947.395246 | 474.201261 | 930.368697 | 465.687987 | 929.384681 | 465.195979 | E | *715.380723* | 358.194000 | 698.354174 | 349.680725 | 697.370158 | 349.188717 | 3 |
| 10 | 1386.620572 | 693.813924 | 1369.594023 | 685.300650 | 1368.610007 | 684.808642 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 11 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 51.0 | 1531.718796 | 0.000186 | KATEDEGSEQK |
| 9.9 | 1531.715454 | 0.003528 | EWNGVVSESDSPVK |
| 9.9 | 1531.716309 | 0.002673 | QVDSMWAEQK |
| 1.4 | 1531.734055 | -0.015073 | VNPQEESYQK |
| 0.6 | 1531.711380 | 0.007602 | KDSEEEAASPEGKR |

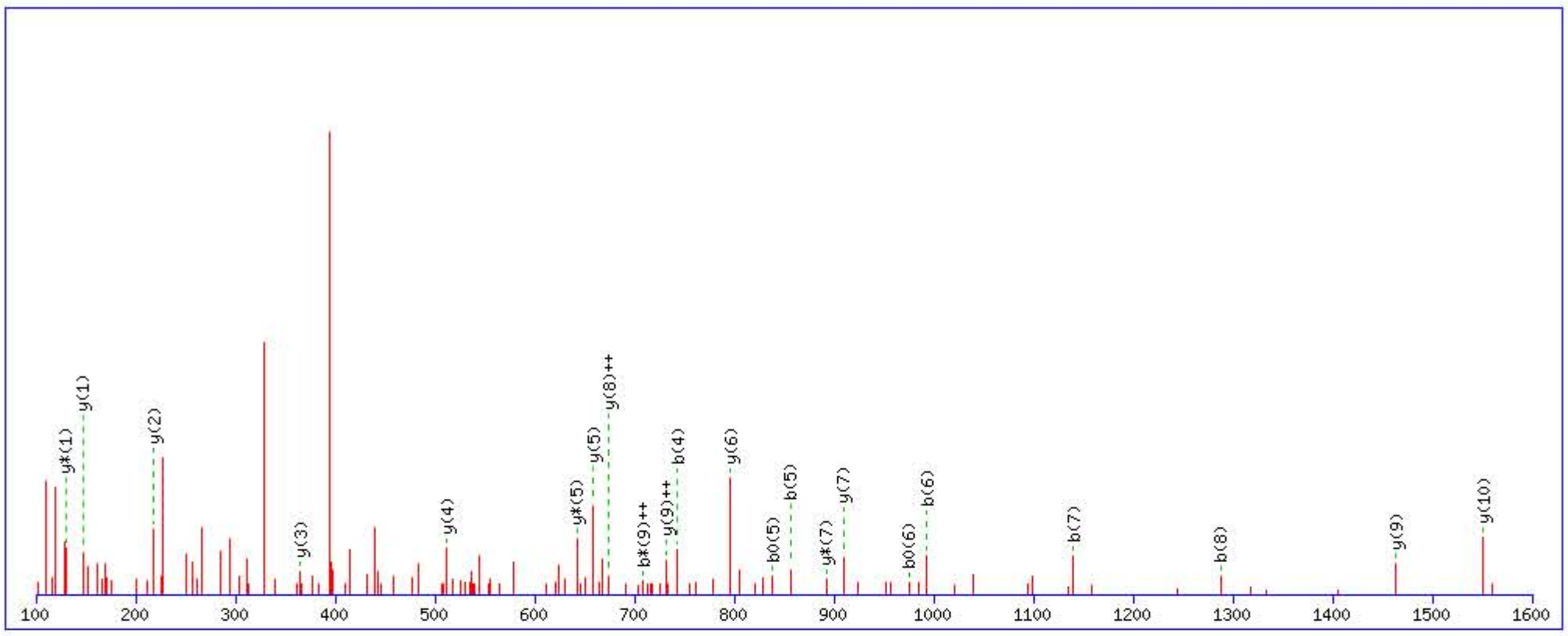
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TSDQIHFFFAK**
Found in **ANT3_HUMAN**, Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

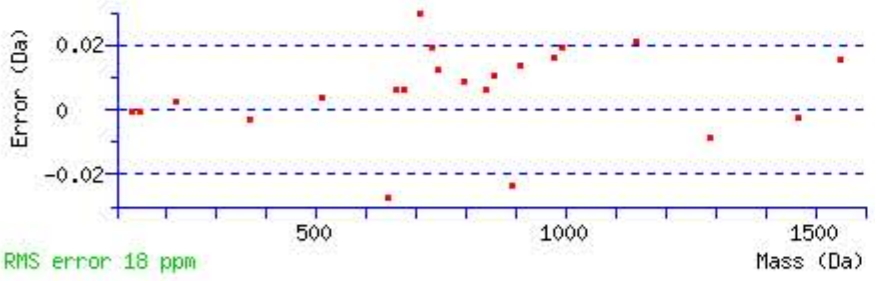
Match to Query 36903: 1650.834012 from(551.285280,3+) rtinseconds(2339) index(22251)
Title: Locus:1.1.1.3197.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

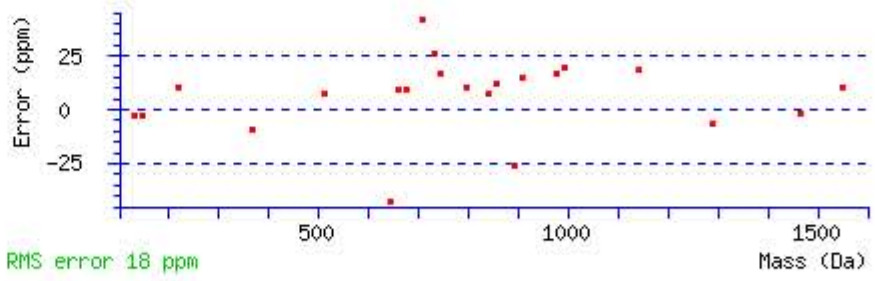
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1650.822845
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 28 **Expect:** 0.038
**Matches :** 22/98 fragment ions using 70 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 11 |
| 2 | 189.086983 | 95.047129 | | | 171.076418 | 86.041847 | S | *1550.782433* | 775.894855 | 1533.755884 | 767.381580 | 1532.771868 | 766.889572 | 10 |
| 3 | 304.113926 | 152.560601 | | | 286.103361 | 143.555319 | D | *1463.750405* | 732.378841 | 1446.723856 | 723.865566 | 1445.739840 | 723.373558 | 9 |
| 4 | **743.339252** | 372.173264 | 726.312703 | 363.659989 | 725.328687 | 363.167982 | Q | 1348.723462 | 674.865369 | 1331.696913 | 666.352095 | | | 8 |
| 5 | **856.423316** | 428.715296 | 839.396767 | 420.202022 | 838.412751 | 419.710014 | I | *909.498136* | 455.252706 | 892.471587 | 446.739432 | | | 7 |
| 6 | **993.482228** | 497.244752 | 976.455679 | 488.731477 | 975.471663 | 488.239469 | H | *796.414072* | 398.710674 | 779.387523 | 390.197400 | | | 6 |
| 7 | **1140.550642** | 570.778959 | 1123.524093 | 562.265685 | 1122.540077 | 561.773676 | F | *659.355160* | 330.181218 | 642.328611 | 321.667944 | | | 5 |
| 8 | **1287.619056** | 644.313166 | 1270.592507 | 635.799892 | 1269.608491 | 635.307884 | F | *512.286746* | 256.647011 | 495.260197 | 248.133737 | | | 4 |
| 9 | 1434.687470 | 717.847373 | 1417.660921 | 709.334099 | 1416.676905 | 708.842091 | F | *365.218332* | 183.112804 | 348.191783 | 174.599530 | | | 3 |
| 10 | 1505.724584 | 753.365930 | 1488.698035 | 744.852656 | 1487.714019 | 744.360648 | A | *218.149918* | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 11 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 27.9 | 1650.822845 | 0.011167 | TSDQIHFFFAK |

**Mascot:** http://www.matrixscience.com/

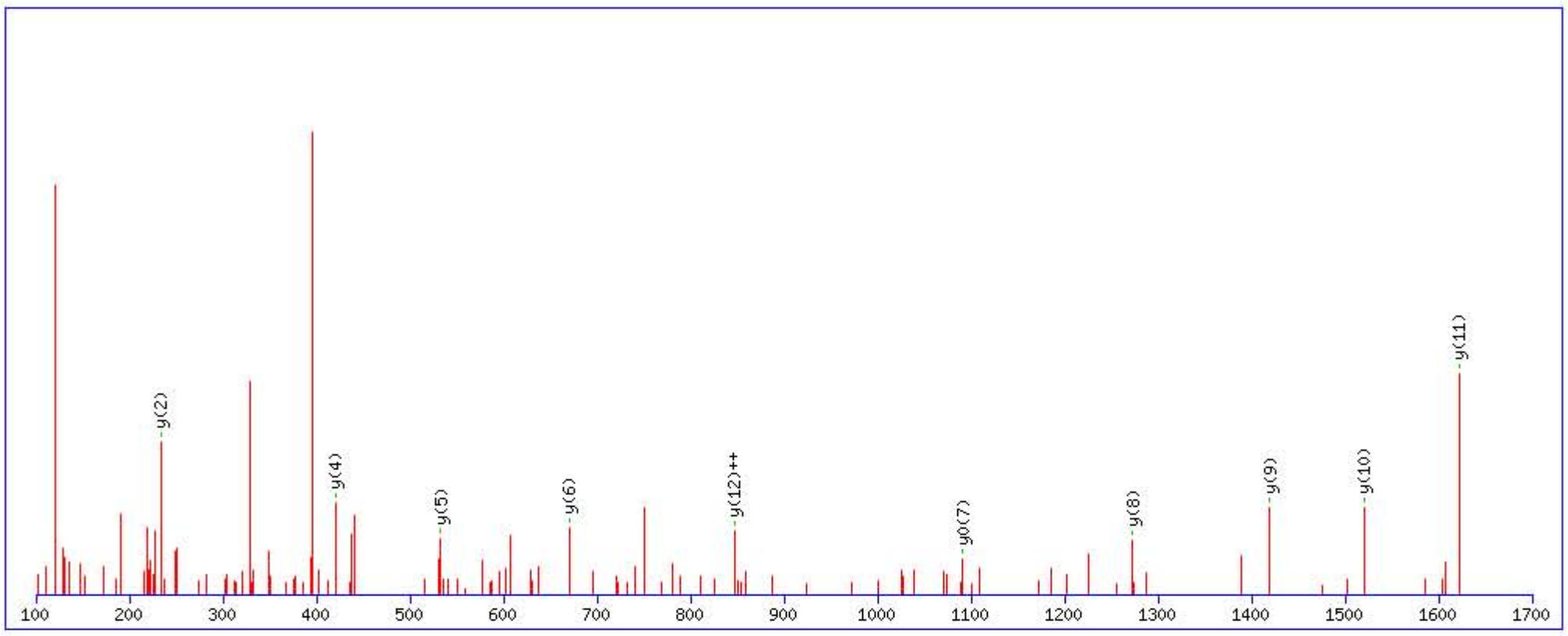
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FATTFYQHLADSK**
Found in **ANT3_HUMAN**, Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

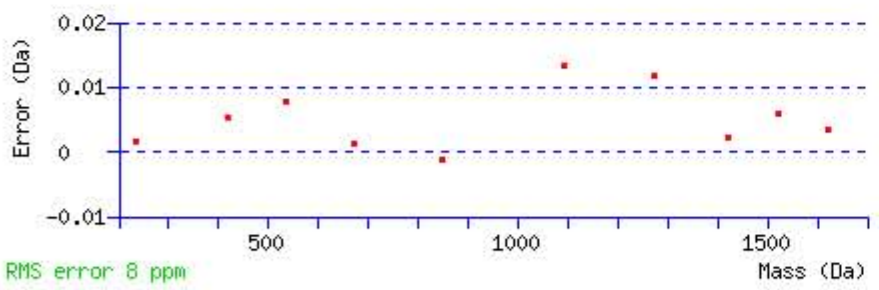
Match to Query 41030: 1838.912652 from(613.978160,3+) rtinseconds(2056) index(20571)
Title: Locus:1.1.1.3098.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

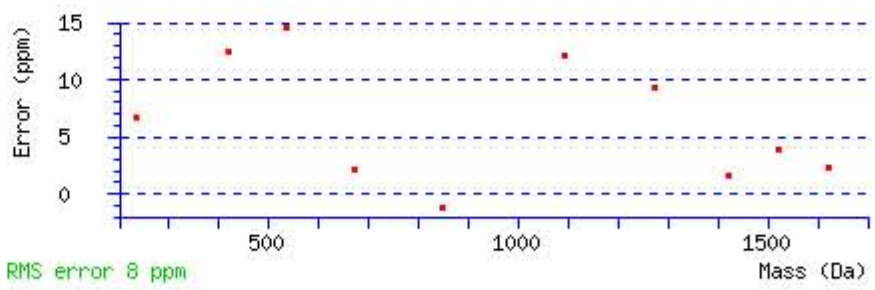
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1838.902542
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 49 **Expect:** 0.0003
**Matches :** 10/126 fragment ions using 16 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 13 |
| 2 | 219.112804 | 110.060040 | | | | | A | 1692.841406 | 846.924341 | 1675.814857 | 838.411067 | 1674.830841 | 837.919059 | 12 |
| 3 | 320.160483 | 160.583879 | | | 302.149918 | 151.578597 | T | *1621.804292* | 811.405784 | 1604.777743 | 802.892510 | 1603.793727 | 802.400502 | 11 |
| 4 | 421.208162 | 211.107719 | | | 403.197597 | 202.102437 | T | *1520.756613* | 760.881945 | 1503.730064 | 752.368670 | 1502.746048 | 751.876662 | 10 |
| 5 | 568.276576 | 284.641926 | | | 550.266011 | 275.636644 | F | *1419.708934* | 710.358105 | 1402.682385 | 701.844831 | 1401.698369 | 701.352823 | 9 |
| 6 | 731.339905 | 366.173591 | | | 713.329340 | 357.168308 | Y | *1272.640520* | 636.823898 | 1255.613971 | 628.310624 | 1254.629955 | 627.818616 | 8 |
| 7 | 1170.565231 | 585.786254 | 1153.538682 | 577.272979 | 1152.554666 | 576.780971 | Q | 1109.577191 | 555.292234 | 1092.550642 | 546.778959 | 1091.566626 | 546.286951 | 7 |
| 8 | 1307.624143 | 654.315710 | 1290.597594 | 645.802435 | 1289.613578 | 645.310427 | H | *670.351865* | 335.679571 | 653.325316 | 327.166296 | 652.341300 | 326.674288 | 6 |
| 9 | 1420.708207 | 710.857741 | 1403.681658 | 702.344467 | 1402.697642 | 701.852459 | L | *533.292953* | 267.150115 | 516.266404 | 258.636840 | 515.282388 | 258.144832 | 5 |
| 10 | 1491.745321 | 746.376298 | 1474.718772 | 737.863024 | 1473.734756 | 737.371016 | A | *420.208889* | 210.608083 | 403.182340 | 202.094808 | 402.198324 | 201.602800 | 4 |
| 11 | 1606.772264 | 803.889770 | 1589.745715 | 795.376496 | 1588.761699 | 794.884487 | D | 349.171775 | 175.089526 | 332.145226 | 166.576251 | 331.161210 | 166.084243 | 3 |
| 12 | 1693.804292 | 847.405784 | 1676.777743 | 838.892510 | 1675.793727 | 838.400502 | S | *234.144832* | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 13 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.9 | 1838.902542 | 0.010110 | FATTFYQHLADSK |

**Mascot:** http://www.matrixscience.com/

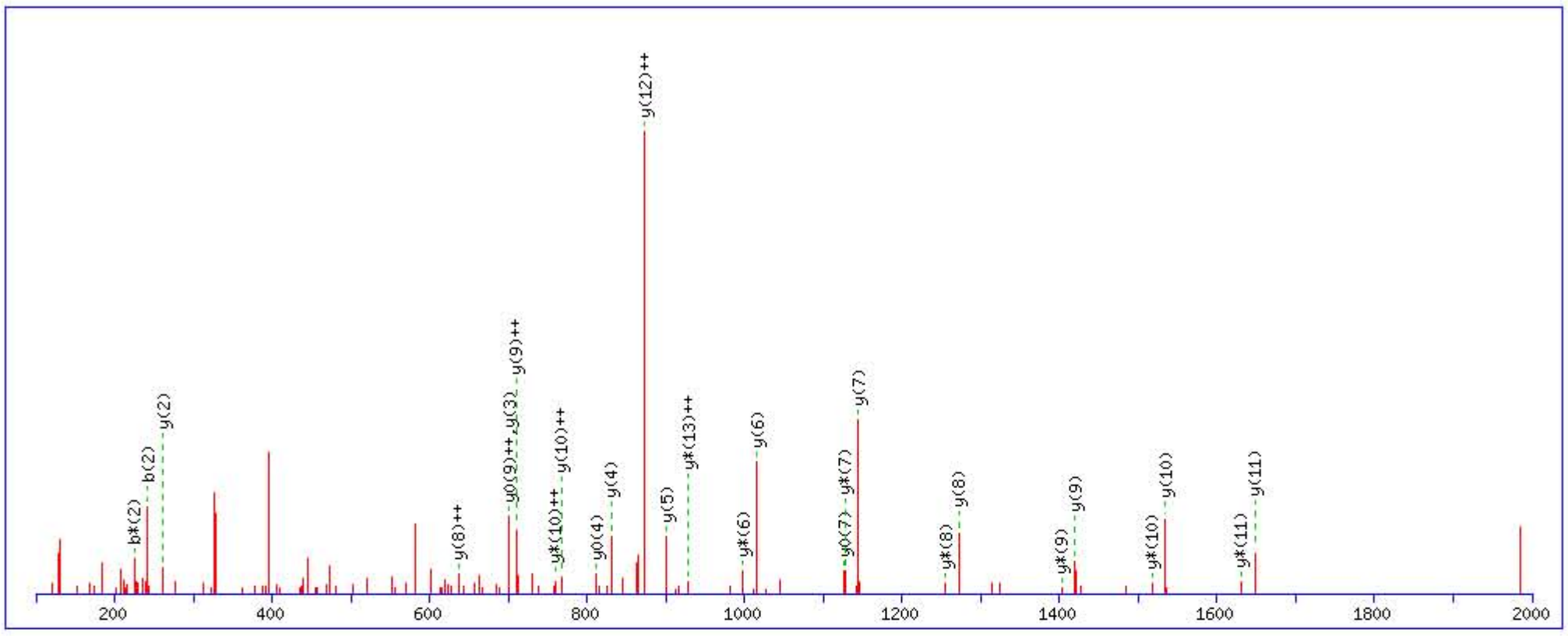
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LQPLDFKENAEQSR**
Found in **ANT3_HUMAN**, Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

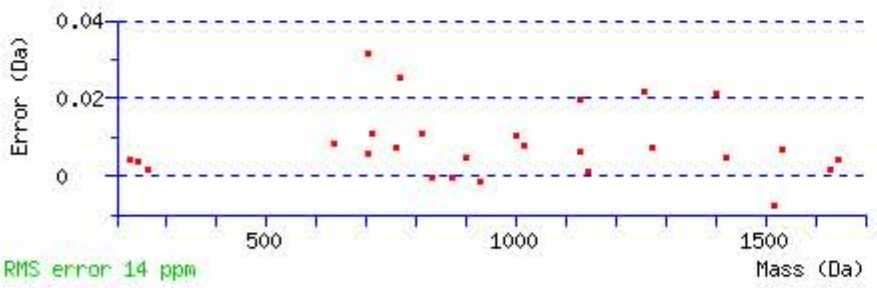
Match to Query 43836: 1985.014122 from(662.678650,3+) rtinseconds(1898) index(19583)
Title: Locus:1.1.1.3043.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

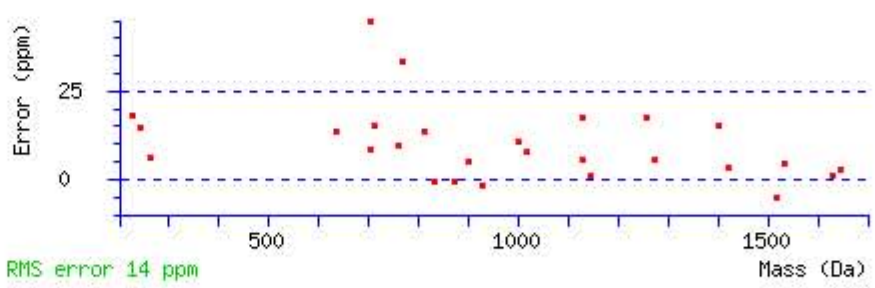
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1985.004013
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.00012
**Matches :** 27/144 fragment ions using 58 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 14 |
| 2 | 242.149918 | 121.578597 | 225.123369 | 113.065323 | | | Q | 1872.927259 | 936.967268 | 1855.900710 | 928.453993 | 1854.916694 | 927.961985 | 13 |
| 3 | 339.202682 | 170.104979 | 322.176133 | 161.591705 | | | P | 1744.868681 | 872.937979 | 1727.842132 | 864.424704 | 1726.858116 | 863.932696 | 12 |
| 4 | 452.286746 | 226.647011 | 435.260197 | 218.133737 | | | L | *1647.815917* | 824.411597 | 1630.789368 | 815.898322 | 1629.805352 | 815.406314 | 11 |
| 5 | 567.313689 | 284.160483 | 550.287140 | 275.647208 | 549.303124 | 275.155200 | D | *1534.731853* | 767.869565 | 1517.705304 | 759.356290 | 1516.721288 | 758.864282 | 10 |
| 6 | 714.382103 | 357.694690 | 697.355554 | 349.181415 | 696.371538 | 348.689407 | F | *1419.704910* | 710.356093 | 1402.678361 | 701.842819 | 1401.694345 | 701.350811 | 9 |
| 7 | 842.477066 | 421.742171 | 825.450517 | 413.228897 | 824.466501 | 412.736889 | K | *1272.636496* | 636.821886 | 1255.609947 | 628.308612 | 1254.625931 | 627.816604 | 8 |
| 8 | 971.519659 | 486.263468 | 954.493110 | 477.750193 | 953.509094 | 477.258185 | E | *1144.541533* | 572.774405 | 1127.514984 | 564.261130 | 1126.530968 | 563.769122 | 7 |
| 9 | 1085.562586 | 543.284931 | 1068.536037 | 534.771657 | 1067.552021 | 534.279649 | N | *1015.498940* | 508.253108 | 998.472391 | 499.739834 | 997.488375 | 499.247826 | 6 |
| 10 | 1156.599700 | 578.803488 | 1139.573151 | 570.290214 | 1138.589135 | 569.798205 | A | *901.456013* | 451.231645 | 884.429464 | 442.718370 | 883.445448 | 442.226362 | 5 |
| 11 | 1285.642293 | 643.324785 | 1268.615744 | 634.811510 | 1267.631728 | 634.319502 | E | *830.418899* | 415.713088 | 813.392350 | 407.199813 | 812.408334 | 406.707805 | 4 |
| 12 | 1724.867619 | 862.937448 | 1707.841070 | 854.424173 | 1706.857054 | 853.932165 | Q | *701.376306* | 351.191791 | 684.349757 | 342.678517 | 683.365741 | 342.186509 | 3 |
| 13 | 1811.899647 | 906.453462 | 1794.873098 | 897.940187 | 1793.889082 | 897.448179 | S | *262.150980* | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 14 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 43.6 | 1985.004013 | 0.010109 | LQPLDFKENAEQSR |
| 1.9 | 1985.043762 | -0.029640 | QLIEKMNLSAIQDR |

**Mascot:** http://www.matrixscience.com/

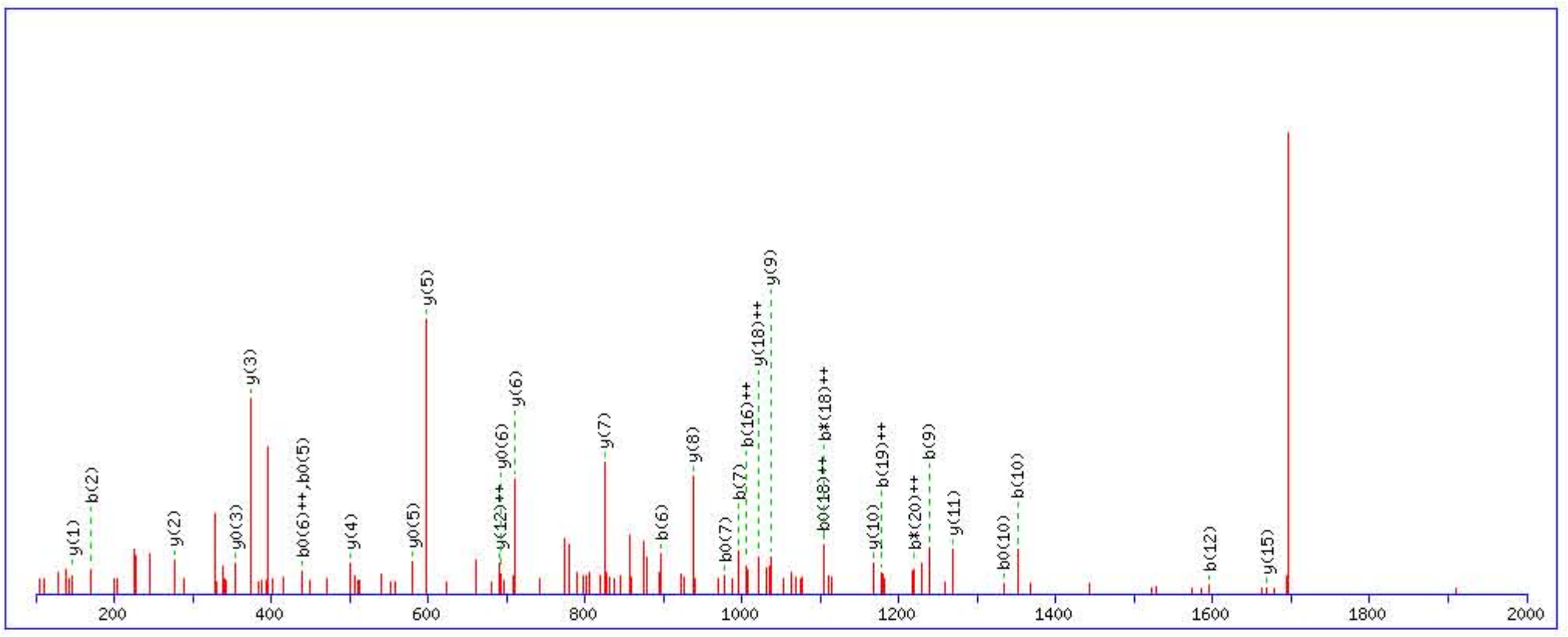
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VAEGTQVLELPFKGDDITMVLILPKPEK**
Found in **ANT3_HUMAN**, Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

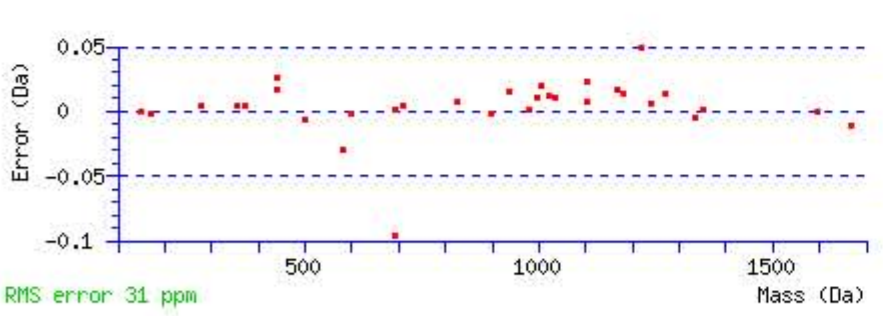
Match to Query 64892: 3390.904536 from(848.733410,4+) rtinseconds(2889) index(25543)
Title: Locus:1.1.1.3386.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

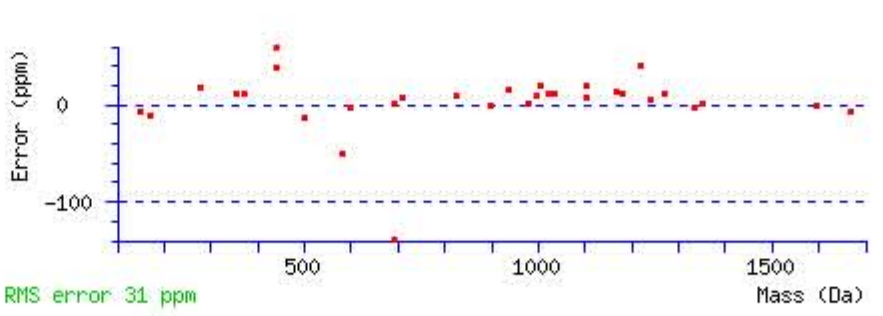
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3390.854645
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 60 **Expect:** 3.6e-006
**Matches :** 32/308 fragment ions using 62 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 28 |
| 2 | *171.112804* | 86.060040 | | | | | A | 3292.793524 | 1646.900400 | 3275.766975 | 1638.387125 | 3274.782959 | 1637.895117 | 27 |
| 3 | 300.155397 | 150.581336 | | | 282.144832 | 141.576054 | E | 3221.756410 | 1611.381843 | 3204.729861 | 1602.868568 | 3203.745845 | 1602.376560 | 26 |
| 4 | 357.176861 | 179.092068 | | | 339.166296 | 170.086786 | G | 3092.713817 | 1546.860546 | 3075.687268 | 1538.347272 | 3074.703252 | 1537.855264 | 25 |
| 5 | 458.224540 | 229.615908 | | | 440.213975 | 220.610626 | T | 3035.692353 | 1518.349814 | 3018.665804 | 1509.836540 | 3017.681788 | 1509.344532 | 24 |
| 6 | *897.449866* | 449.228571 | 880.423317 | 440.715297 | 879.439301 | 440.223289 | Q | 2934.644674 | 1467.825975 | 2917.618125 | 1459.312700 | 2916.634109 | 1458.820692 | 23 |
| 7 | *996.518280* | 498.762778 | 979.491731 | 490.249504 | 978.507715 | 489.757496 | V | 2495.419348 | 1248.213312 | 2478.392799 | 1239.700037 | 2477.408783 | 1239.208029 | 22 |
| 8 | 1109.602344 | 555.304810 | 1092.575795 | 546.791536 | 1091.591779 | 546.299527 | L | 2396.350934 | 1198.679105 | 2379.324385 | 1190.165830 | 2378.340369 | 1189.673822 | 21 |
| 9 | *1238.644937* | 619.826106 | 1221.618388 | 611.312832 | 1220.634372 | 610.820824 | E | 2283.266870 | 1142.137073 | 2266.240321 | 1133.623798 | 2265.256305 | 1133.131790 | 20 |
| 10 | *1351.729001* | 676.368138 | 1334.702452 | 667.854864 | 1333.718436 | 667.362856 | L | 2154.224277 | 1077.615776 | 2137.197728 | 1069.102502 | 2136.213712 | 1068.610494 | 19 |
| 11 | 1448.781765 | 724.894520 | 1431.755216 | 716.381246 | 1430.771200 | 715.889238 | P | 2041.140213 | 1021.073745 | 2024.113664 | 1012.560470 | 2023.129648 | 1012.068462 | 18 |
| 12 | *1595.850179* | 798.428727 | 1578.823630 | 789.915453 | 1577.839614 | 789.423445 | F | 1944.087449 | 972.547363 | 1927.060900 | 964.034088 | 1926.076884 | 963.542080 | 17 |
| 13 | 1723.945142 | 862.476209 | 1706.918593 | 853.962934 | 1705.934577 | 853.470926 | K | 1797.019035 | 899.013156 | 1779.992486 | 890.499881 | 1779.008470 | 890.007873 | 16 |
| 14 | 1780.966606 | 890.986941 | 1763.940057 | 882.473666 | 1762.956041 | 881.981658 | G | *1668.924072* | 834.965674 | 1651.897523 | 826.452400 | 1650.913507 | 825.960392 | 15 |
| 15 | 1895.993549 | 948.500412 | 1878.967000 | 939.987138 | 1877.982984 | 939.495130 | D | 1611.902608 | 806.454942 | 1594.876059 | 797.941668 | 1593.892043 | 797.449660 | 14 |
| 16 | 2011.020492 | **1006.013884** | 1993.993943 | 997.500610 | 1993.009927 | 997.008601 | D | 1496.875665 | 748.941471 | 1479.849116 | 740.428196 | 1478.865100 | 739.936188 | 13 |
| 17 | 2124.104556 | 1062.555916 | 2107.078007 | 1054.042641 | 2106.093991 | 1053.550633 | I | 1381.848722 | 691.427999 | 1364.822173 | 682.914725 | 1363.838157 | 682.422717 | 12 |
| 18 | 2225.152235 | 1113.079755 | 2208.125686 | 1104.566481 | 2207.141670 | 1104.074473 | T | *1268.764658* | 634.885967 | 1251.738109 | 626.372693 | 1250.754093 | 625.880685 | 11 |
| 19 | 2356.192720 | **1178.599998** | 2339.166171 | 1170.086723 | 2338.182155 | 1169.594715 | M | *1167.716979* | 584.362128 | 1150.690430 | 575.848853 | 1149.706414 | 575.356845 | 10 |
| 20 | 2455.261134 | 1228.134205 | 2438.234585 | 1219.620930 | 2437.250569 | 1219.128922 | V | *1036.676494* | 518.841885 | 1019.649945 | 510.328611 | 1018.665929 | 509.836603 | 9 |
| 21 | 2568.345198 | 1284.676237 | 2551.318649 | 1276.162962 | 2550.334633 | 1275.670954 | L | *937.608080* | 469.307678 | 920.581531 | 460.794404 | 919.597515 | 460.302396 | 8 |
| 22 | 2681.429262 | 1341.218269 | 2664.402713 | 1332.704994 | 2663.418697 | 1332.212986 | I | *824.524016* | 412.765646 | 807.497467 | 404.252372 | 806.513451 | 403.760364 | 7 |
| 23 | 2794.513326 | 1397.760301 | 2777.486777 | 1389.247026 | 2776.502761 | 1388.755018 | L | *711.439952* | 356.223614 | 694.413403 | 347.710340 | 693.429387 | 347.218332 | 6 |
| 24 | 2891.566090 | 1446.286683 | 2874.539541 | 1437.773408 | 2873.555525 | 1437.281400 | P | *598.355888* | 299.681582 | 581.329339 | 291.168308 | 580.345323 | 290.676300 | 5 |
| 25 | 3019.661053 | 1510.334164 | 3002.634504 | 1501.820890 | 3001.650488 | 1501.328882 | K | *501.303124* | 251.155200 | 484.276575 | 242.641926 | 483.292559 | 242.149918 | 4 |
| 26 | 3116.713817 | 1558.860546 | 3099.687268 | 1550.347272 | 3098.703252 | 1549.855264 | P | *373.208161* | 187.107719 | 356.181612 | 178.594444 | 355.197596 | 178.102436 | 3 |
| 27 | 3245.756410 | 1623.381843 | 3228.729861 | 1614.868568 | 3227.745845 | 1614.376560 | E | *276.155397* | 138.581337 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 28 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 60.3 | 3390.854645 | 0.049891 | VAEGTQVLELPFKGDDITMVLILPKPEK |
| 5.6 | 3390.924728 | -0.020192 | TRASGVLLVNLSLGHLLLAALDMPFTLLGVMR |

**Mascot:** http://www.matrixscience.com/

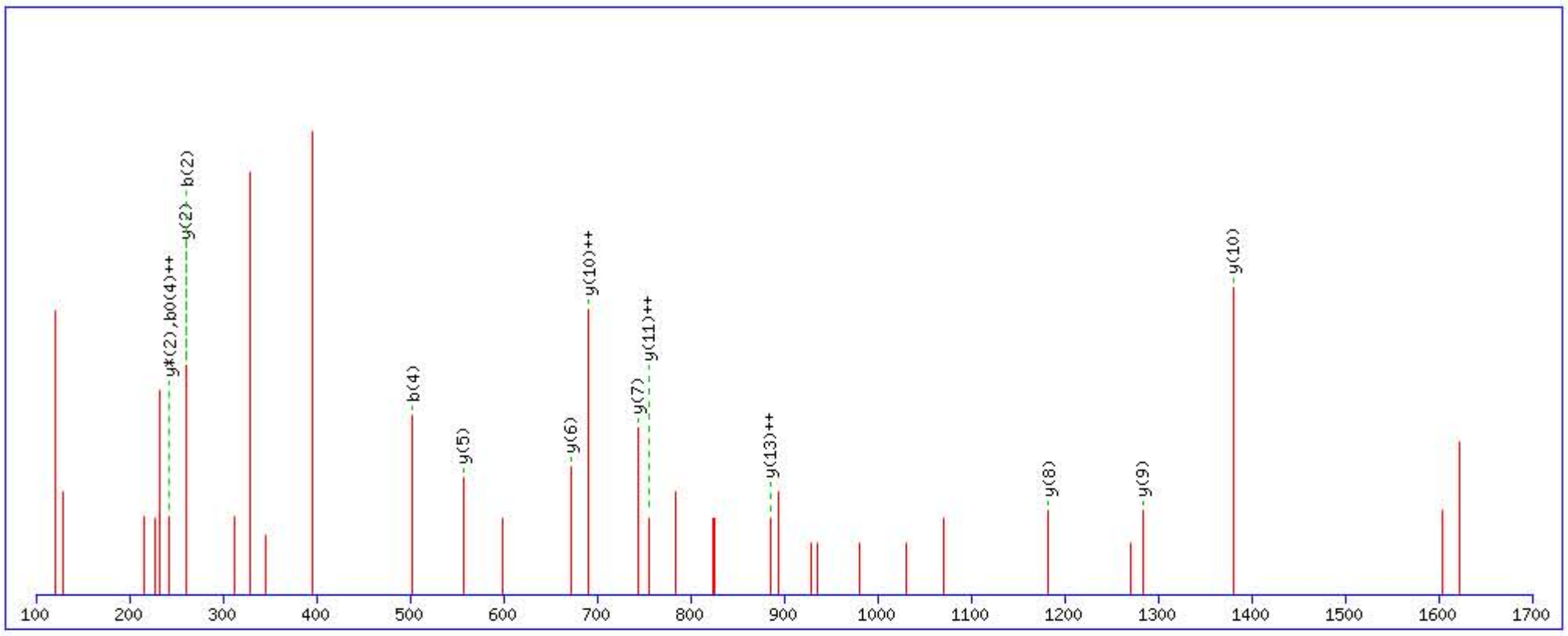
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LFLEPTQADIALLK**
Found in **APOA_HUMAN**, Apolipoprotein(a) OS=Homo sapiens GN=LPA PE=1 SV=1

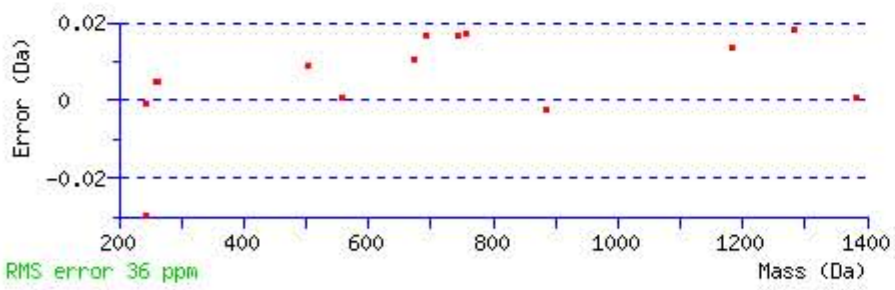
Match to Query 41880: 1882.086942 from(628.369590,3+) rtinseconds(2778) index(38989)
Title: Locus:1.1.1.1075.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

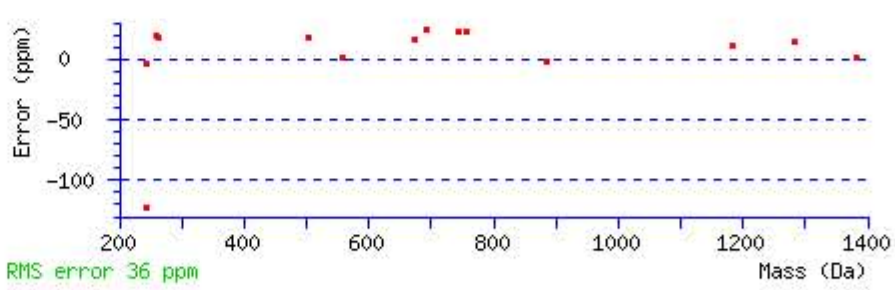
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1882.063766
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 27 **Expect:** 0.014
**Matches :** 14/128 fragment ions using 33 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 14 |
| 2 | **261.159754** | 131.083515 | | | | | F | 1769.987007 | 885.497142 | 1752.960458 | 876.983867 | 1751.976442 | 876.491859 | 13 |
| 3 | 374.243818 | 187.625547 | | | | | L | 1622.918593 | 811.962934 | 1605.892044 | 803.449660 | 1604.908028 | 802.957652 | 12 |
| 4 | **503.286411** | 252.146843 | | | 485.275846 | 243.141561 | E | 1509.834529 | 755.420903 | 1492.807980 | 746.907628 | 1491.823964 | 746.415620 | 11 |
| 5 | 600.339175 | 300.673226 | | | 582.328610 | 291.667943 | P | *1380.791936* | 690.899606 | 1363.765387 | 682.386331 | 1362.781371 | 681.894323 | 10 |
| 6 | 701.386854 | 351.197065 | | | 683.376289 | 342.191783 | T | *1283.739172* | 642.373224 | 1266.712623 | 633.859949 | 1265.728607 | 633.367941 | 9 |
| 7 | 1140.612180 | 570.809728 | 1123.585631 | 562.296454 | 1122.601615 | 561.804446 | Q | *1182.691493* | 591.849384 | 1165.664944 | 583.336110 | 1164.680928 | 582.844102 | 8 |
| 8 | 1211.649294 | 606.328285 | 1194.622745 | 597.815011 | 1193.638729 | 597.323003 | A | *743.466167* | 372.236721 | 726.439618 | 363.723447 | 725.455602 | 363.231439 | 7 |
| 9 | 1326.676237 | 663.841757 | 1309.649688 | 655.328482 | 1308.665672 | 654.836474 | D | *672.429053* | 336.718164 | 655.402504 | 328.204890 | 654.418488 | 327.712882 | 6 |
| 10 | 1439.760301 | 720.383789 | 1422.733752 | 711.870514 | 1421.749736 | 711.378506 | I | *557.402110* | 279.204693 | 540.375561 | 270.691418 | | | 5 |
| 11 | 1510.797415 | 755.902346 | 1493.770866 | 747.389071 | 1492.786850 | 746.897063 | A | 444.318046 | 222.662661 | 427.291497 | 214.149386 | | | 4 |
| 12 | 1623.881479 | 812.444377 | 1606.854930 | 803.931103 | 1605.870914 | 803.439095 | L | 373.280932 | 187.144104 | 356.254383 | 178.630829 | | | 3 |
| 13 | 1736.965543 | 868.986409 | 1719.938994 | 860.473135 | 1718.954978 | 859.981127 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 14 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 27.0 | 1882.063766 | 0.023176 | LFLEPTQADIALLK |

**Mascot:** http://www.matrixscience.com/

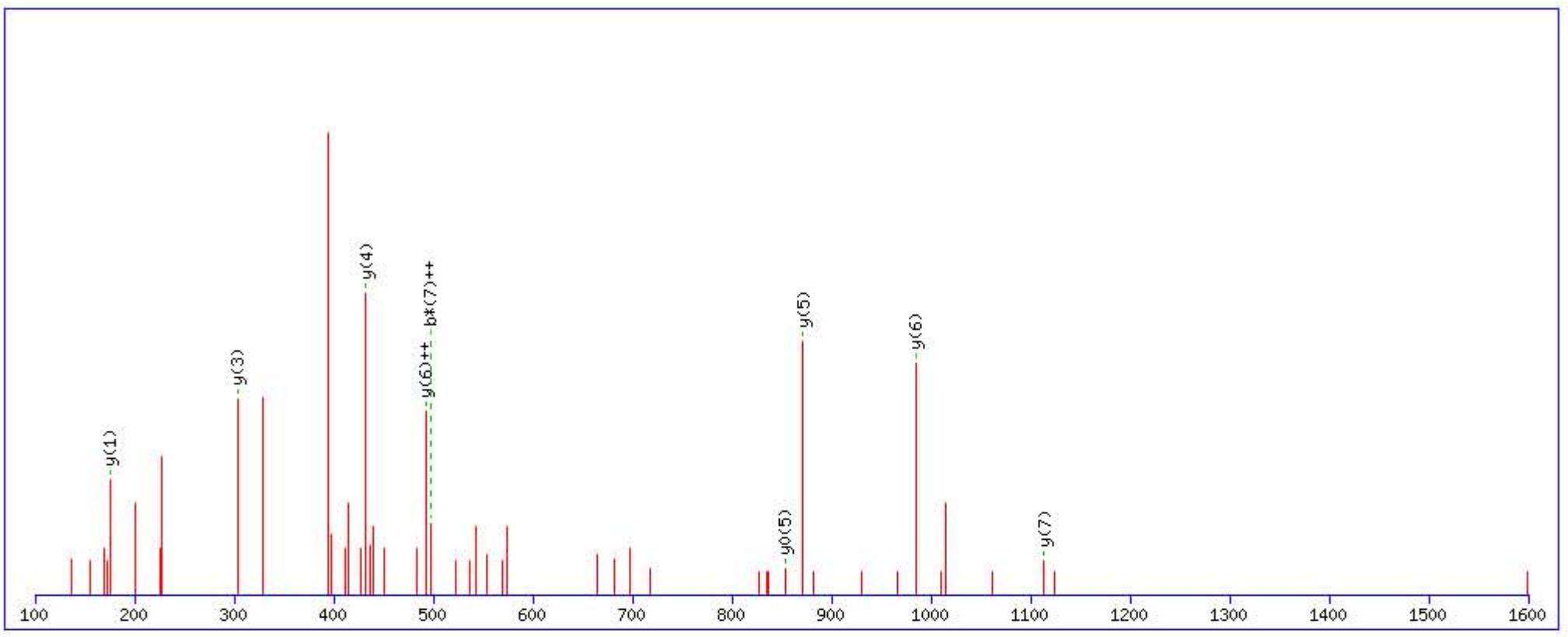
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AELQEGAR**
Found in **APOA1_HUMAN**, Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1

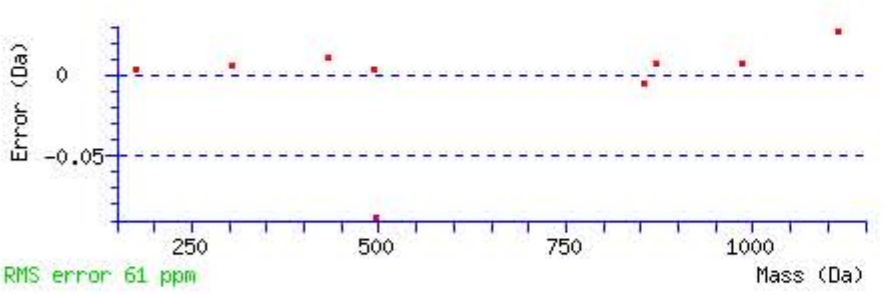
Match to Query 20117: 1183.601408 from(592.807980,2+) rtinseconds(1455) index(63221)
Title: Locus:1.1.1.1781.23 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

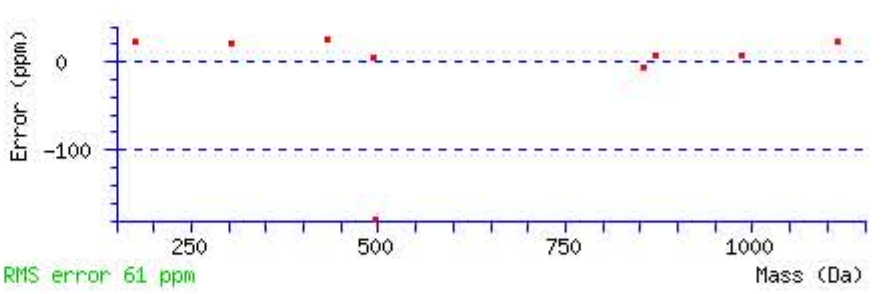
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1183.601913
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 28 **Expect:** 0.02
**Matches :** 9/70 fragment ions using 20 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 8 |
| 2 | 201.086983 | 101.047130 | | | 183.076418 | 92.041847 | E | *1113.572106* | 557.289691 | 1096.545557 | 548.776417 | 1095.561541 | 548.284409 | 7 |
| 3 | 314.171047 | 157.589161 | | | 296.160482 | 148.583879 | L | *984.529513* | 492.768395 | 967.502964 | 484.255120 | 966.518948 | 483.763112 | 6 |
| 4 | 753.396373 | 377.201825 | 736.369824 | 368.688550 | 735.385808 | 368.196542 | Q | *871.445449* | 436.226363 | 854.418900 | 427.713088 | 853.434884 | 427.221080 | 5 |
| 5 | 882.438966 | 441.723121 | 865.412417 | 433.209847 | 864.428401 | 432.717839 | E | *432.220123* | 216.613699 | 415.193574 | 208.100425 | 414.209558 | 207.608417 | 4 |
| 6 | 939.460430 | 470.233853 | 922.433881 | 461.720579 | 921.449865 | 461.228571 | G | *303.177530* | 152.092403 | 286.150981 | 143.579128 | | | 3 |
| 7 | 1010.497544 | 505.752410 | 993.470995 | 497.239136 | 992.486979 | 496.747128 | A | 246.156066 | 123.581671 | 229.129517 | 115.068396 | | | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 28.0 | 1183.601913 | -0.000505 | AELQEGAR |
| 9.4 | 1183.601913 | -0.000505 | EALEQQR |
| 4.2 | 1183.601913 | -0.000505 | EALEQQR |
| 3.9 | 1183.587357 | 0.014051 | SSVDFQAFGVK |
| 2.9 | 1183.601913 | -0.000505 | ELQAEAGR |
| 1.8 | 1183.601913 | -0.000505 | LQEAQER |

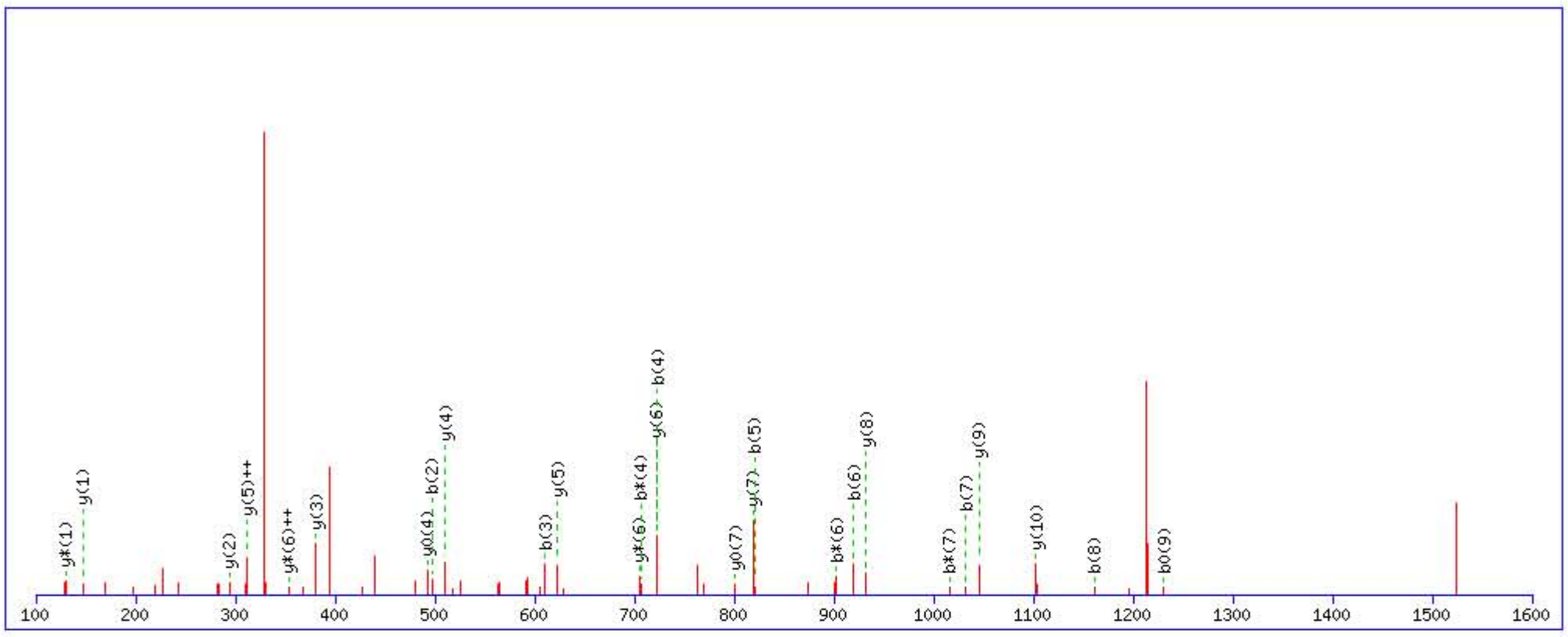
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QGLLPVLESFK**
Found in **APOA1_HUMAN**, Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1

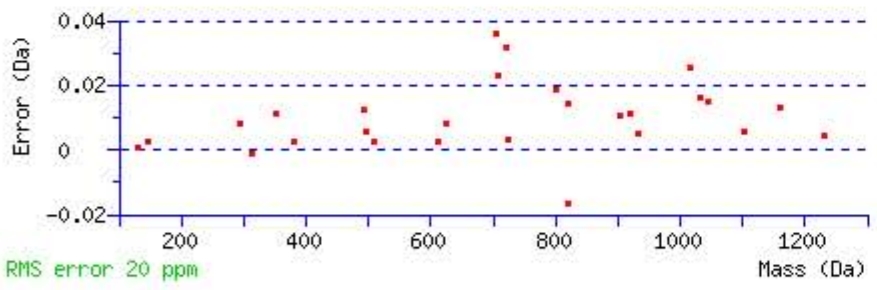
Match to Query 32304: 1540.882488 from(771.448520,2+) rtinseconds(2830) index(10091)
Title: Locus:1.1.1.2262.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

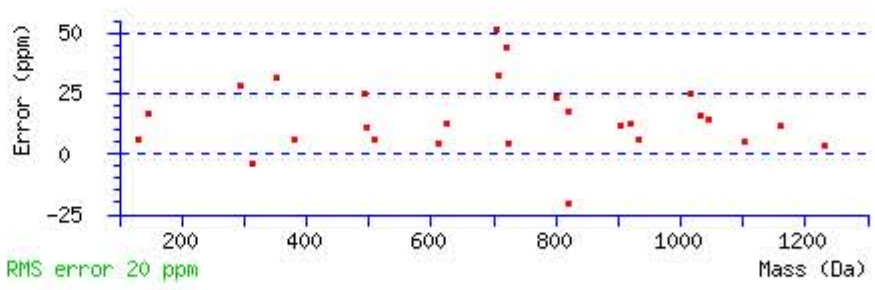
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1540.868713
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 62 **Expect:** 6.4e-006
**Matches** : 27/102 fragment ions using 50 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 11 |
| 2 | **497.254066** | 249.130671 | 480.227517 | 240.617396 | | | G | *1102.650673* | 551.828975 | 1085.624124 | 543.315700 | 1084.640108 | 542.823692 | 10 |
| 3 | **610.338130** | 305.672703 | 593.311581 | 297.159428 | | | L | *1045.629209* | 523.318243 | 1028.602660 | 514.804968 | 1027.618644 | 514.312960 | 9 |
| 4 | **723.422194** | 362.214735 | 706.395645 | 353.701461 | | | L | *932.545145* | 466.776211 | 915.518596 | 458.262936 | 914.534580 | 457.770928 | 8 |
| 5 | **820.474958** | 410.741117 | 803.448409 | 402.227843 | | | P | *819.461081* | 410.234179 | 802.434532 | 401.720904 | 801.450516 | 401.228896 | 7 |
| 6 | **919.543372** | 460.275324 | 902.516823 | 451.762049 | | | V | *722.408317* | 361.707797 | 705.381768 | 353.194522 | 704.397752 | 352.702514 | 6 |
| 7 | **1032.627436** | 516.817356 | 1015.600887 | 508.304082 | | | L | *623.339903* | 312.173590 | 606.313354 | 303.660315 | 605.329338 | 303.168307 | 5 |
| 8 | **1161.670029** | 581.338653 | 1144.643480 | 572.825378 | 1143.659464 | 572.333370 | E | *510.255839* | 255.631558 | 493.229290 | 247.118283 | 492.245274 | 246.626275 | 4 |
| 9 | 1248.702057 | 624.854667 | 1231.675508 | 616.341392 | 1230.691492 | 615.849384 | S | *381.213246* | 191.110261 | 364.186697 | 182.596987 | 363.202681 | 182.104979 | 3 |
| 10 | 1395.770471 | 698.388874 | 1378.743922 | 689.875599 | 1377.759906 | 689.383591 | F | *294.181218* | 147.594247 | 277.154669 | 139.080973 | | | 2 |
| 11 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 62.4 | 1540.868713 | 0.013775 | QGLLPVLESFK |
| 11.6 | 1540.894531 | -0.012043 | QAVLSMVRKAK |
| 2.6 | 1540.872559 | 0.009929 | ELSRVLHTNVVFK |

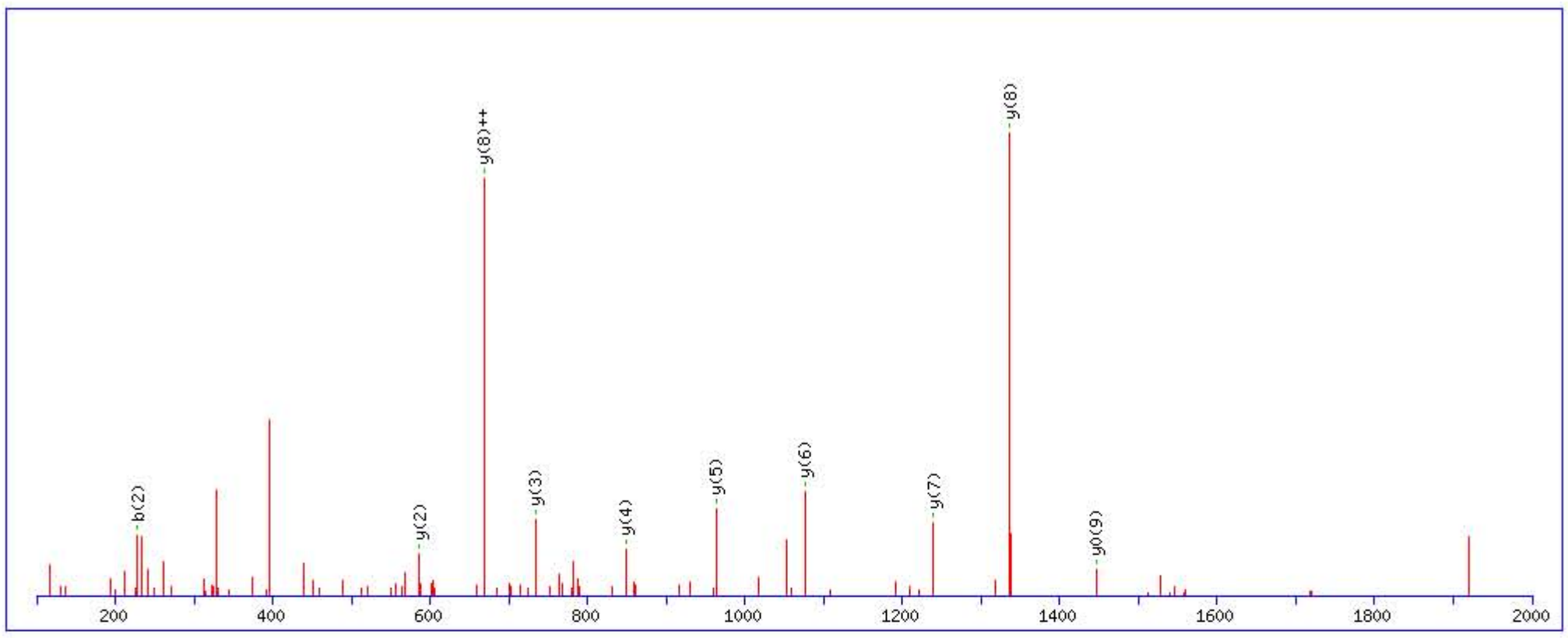
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VQPYLDDFQK**
Found in **APOA1_HUMAN**, Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1

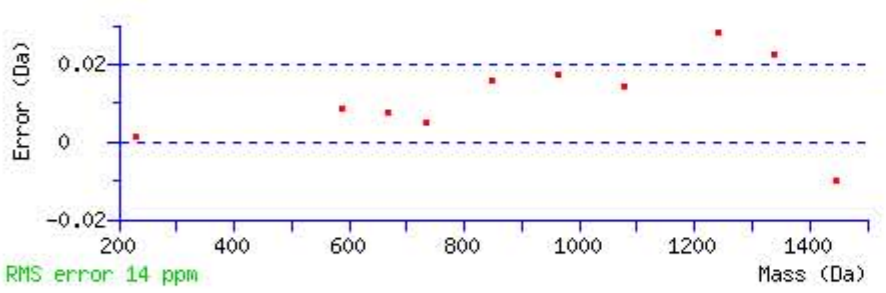
Match to Query 32945: 1562.800068 from(782.407310,2+) rtinseconds(2198) index(35455)
Title: Locus:1.1.1.874.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

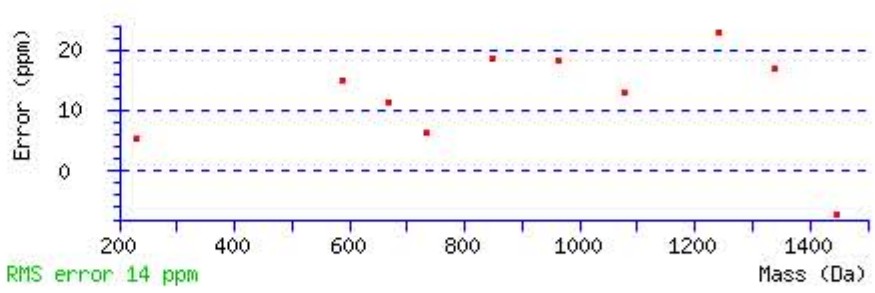
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1562.780304
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.00032
**Matches :** 10/90 fragment ions using 15 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 10 |
| 2 | 228.134268 | 114.570772 | 211.107719 | 106.057498 | | | Q | 1464.719165 | 732.863221 | 1447.692616 | 724.349946 | 1446.708600 | 723.857938 | 9 |
| 3 | 325.187032 | 163.097154 | 308.160483 | 154.583879 | | | P | *1336.660587* | 668.833932 | 1319.634038 | 660.320657 | 1318.650022 | 659.828649 | 8 |
| 4 | 488.250361 | 244.628818 | 471.223812 | 236.115544 | | | Y | *1239.607823* | 620.307550 | 1222.581274 | 611.794275 | 1221.597258 | 611.302267 | 7 |
| 5 | 601.334425 | 301.170851 | 584.307876 | 292.657576 | | | L | *1076.544494* | 538.775885 | 1059.517945 | 530.262611 | 1058.533929 | 529.770603 | 6 |
| 6 | 716.361368 | 358.684322 | 699.334819 | 350.171047 | 698.350803 | 349.679039 | D | *963.460430* | 482.233853 | 946.433881 | 473.720579 | 945.449865 | 473.228571 | 5 |
| 7 | 831.388311 | 416.197793 | 814.361762 | 407.684519 | 813.377746 | 407.192511 | D | *848.433487* | 424.720382 | 831.406938 | 416.207107 | 830.422922 | 415.715099 | 4 |
| 8 | 978.456725 | 489.732000 | 961.430176 | 481.218726 | 960.446160 | 480.726718 | F | *733.406544* | 367.206910 | 716.379995 | 358.693636 | | | 3 |
| 9 | 1417.682051 | 709.344664 | 1400.655502 | 700.831389 | 1399.671486 | 700.339381 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 10 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 44.3 | 1562.780304 | 0.019764 | VQPYLDDFQK |
| 6.5 | 1562.804764 | -0.004696 | QVEELLMAMEKVK |
| 6.2 | 1562.808624 | -0.008556 | LNSPTTTSQIMARK |
| 1.1 | 1562.787521 | 0.012547 | VQLVDNVYCIGQR |
| 0.9 | 1562.804764 | -0.004696 | QVEELLMAMEKVK |
| 0.3 | 1562.779633 | 0.020435 | QQTGKLSMSEK |
| 0.2 | 1562.795364 | 0.004704 | KVKFTQQNYHDR |

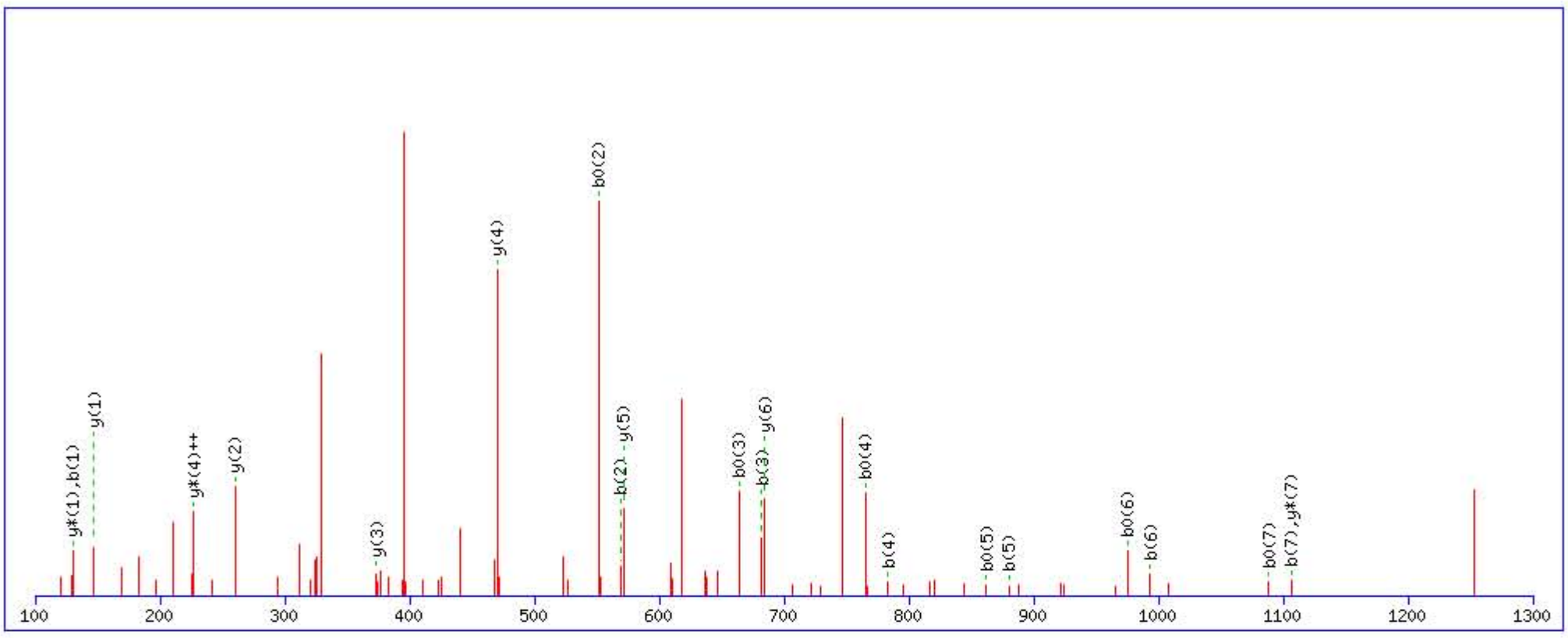
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EQLTPLIK**
Found in **APOA2_HUMAN**, Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1

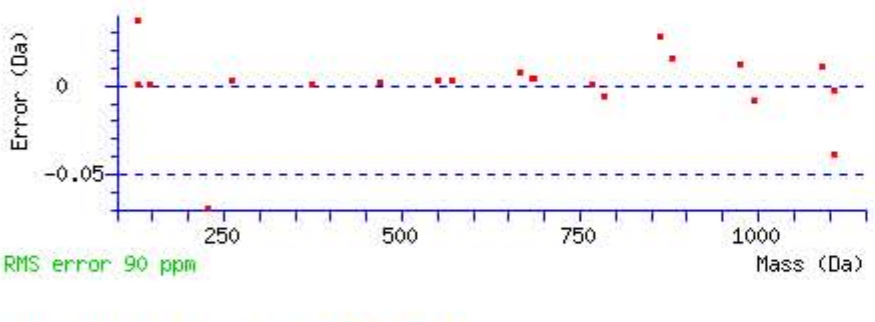
Match to Query 21987: 1251.732468 from(626.873510,2+) rtinseconds(2110) index(20900)
Title: Locus:1.1.1.3117.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

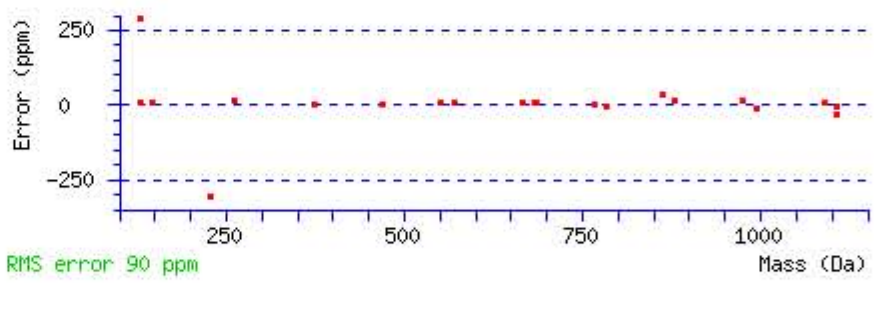
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1251.726059
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 28 **Expect:** 0.013
**Matches :** 22/74 fragment ions using 55 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *130.049869* | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 8 |
| 2 | *569.275195* | 285.141236 | 552.248646 | 276.627961 | 551.264630 | 276.135953 | Q | 1123.690765 | 562.349021 | 1106.664216 | 553.835746 | 1105.680200 | 553.343738 | 7 |
| 3 | *682.359259* | 341.683268 | 665.332710 | 333.169993 | 664.348694 | 332.677985 | L | **684.465439** | 342.736358 | 667.438890 | 334.223083 | 666.454874 | 333.731075 | 6 |
| 4 | *783.406938* | 392.207107 | 766.380389 | 383.693833 | 765.396373 | 383.201825 | T | **571.381375** | 286.194326 | 554.354826 | 277.681051 | 553.370810 | 277.189043 | 5 |
| 5 | *880.459702* | 440.733489 | 863.433153 | 432.220215 | 862.449137 | 431.728207 | P | **470.333696** | 235.670486 | 453.307147 | 227.157212 | | | 4 |
| 6 | *993.543766* | 497.275521 | 976.517217 | 488.762247 | 975.533201 | 488.270239 | L | **373.280932** | 187.144104 | 356.254383 | 178.630830 | | | 3 |
| 7 | *1106.627830* | 553.817553 | 1089.601281 | 545.304279 | 1088.617265 | 544.812271 | I | **260.196868** | 130.602072 | 243.170319 | 122.088798 | | | 2 |
| 8 | | | | | | | K | **147.112804** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 28.4 | 1251.726059 | 0.006409 | EQLTPLIK |
| 13.5 | 1251.722672 | 0.009796 | NYIPYLTKLK |
| 12.1 | 1251.744690 | -0.012222 | QMLPIVLK |
| 11.1 | 1251.729874 | 0.002594 | RHKLESELIK |
| 8.2 | 1251.722702 | 0.009766 | FFKTLQDLLK |
| 7.2 | 1251.718689 | 0.013779 | ASGVGLPGGSLPIK |
| 3.8 | 1251.733917 | -0.001449 | IRGYVFKELK |
| 3.2 | 1251.748520 | -0.016052 | AILTAVHMIRK |
| 1.8 | 1251.733932 | -0.001464 | LPVIQLWDLR |
| 0.9 | 1251.729874 | 0.002594 | LEKSLEHLRK |

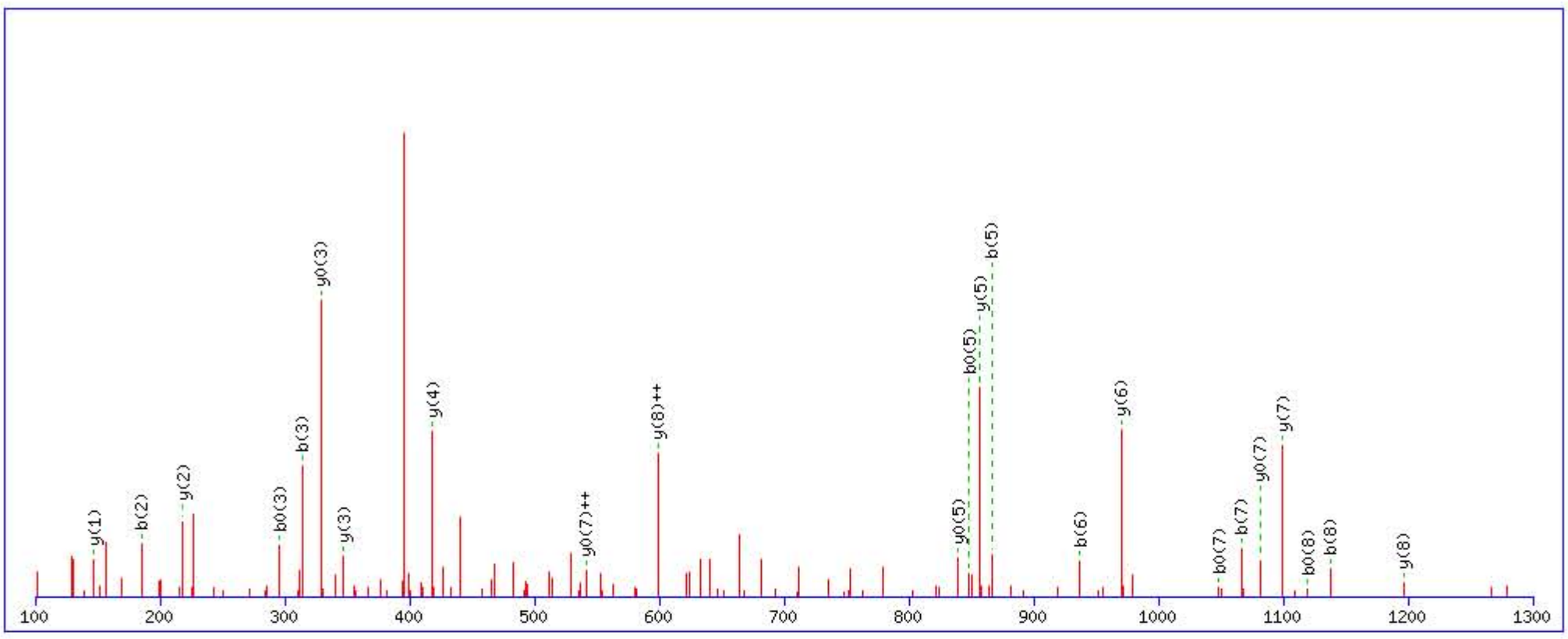
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SPELQAEAK**
Found in **APOA2_HUMAN**, Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1

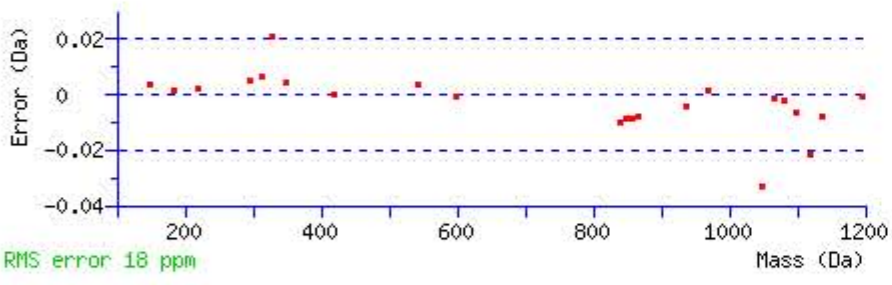
Match to Query 22917: 1282.659168 from(642.336860,2+) rtinseconds(1558) index(17338)
Title: Locus:1.1.1.2925.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

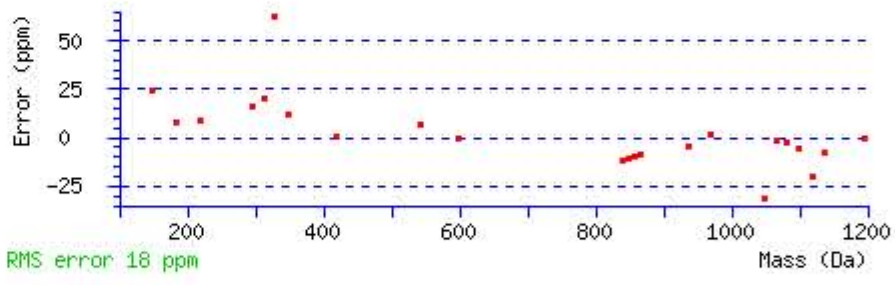
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1282.659088
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 46 **Expect:** 0.00057
**Matches :** 23/84 fragment ions using 46 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 9 |
| 2 | 185.092068 | 93.049672 | | | 167.081503 | 84.044389 | P | *1196.634372* | 598.820824 | 1179.607823 | 590.307550 | 1178.623807 | 589.815541 | 8 |
| 3 | 314.134661 | 157.570968 | | | 296.124096 | 148.565686 | E | *1099.581608* | 550.294442 | 1082.555059 | 541.781168 | 1081.571043 | 541.289160 | 7 |
| 4 | 427.218725 | 214.113001 | | | 409.208160 | 205.107718 | L | *970.539015* | 485.773146 | 953.512466 | 477.259871 | 952.528450 | 476.767863 | 6 |
| 5 | 866.444051 | 433.725664 | 849.417502 | 425.212389 | 848.433486 | 424.720381 | Q | *857.454951* | 429.231114 | 840.428402 | 420.717839 | 839.444386 | 420.225831 | 5 |
| 6 | 937.481165 | 469.244221 | 920.454616 | 460.730946 | 919.470600 | 460.238938 | A | *418.229625* | 209.618450 | 401.203076 | 201.105176 | 400.219060 | 200.613168 | 4 |
| 7 | 1066.523758 | 533.765517 | 1049.497209 | 525.252243 | 1048.513193 | 524.760235 | E | *347.192511* | 174.099893 | 330.165962 | 165.586619 | 329.181946 | 165.094611 | 3 |
| 8 | 1137.560872 | 569.284074 | 1120.534323 | 560.770800 | 1119.550307 | 560.278792 | A | *218.149918* | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 9 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.7 | 1282.659088 | 0.000080 | SPELQAEAK |
| 14.7 | 1282.676865 | -0.017697 | ITANEDPPVISK |
| 2.8 | 1282.641815 | 0.017353 | SEAFFRKADGR |
| 2.3 | 1282.641830 | 0.017338 | SYPGHVQPATAR |
| 1.8 | 1282.655716 | 0.003452 | ALEAEKYGFQK |
| 1.7 | 1282.662949 | -0.003781 | KLGQSESQGPPR |
| 1.6 | 1282.670334 | -0.011166 | EPIQASTAR |
| 1.5 | 1282.662949 | -0.003781 | DLSDTQRHLAK |
| 0.4 | 1282.670334 | -0.011166 | QLEAVQER |
| 0.1 | 1282.670334 | -0.011166 | ELPSPRISCPK |

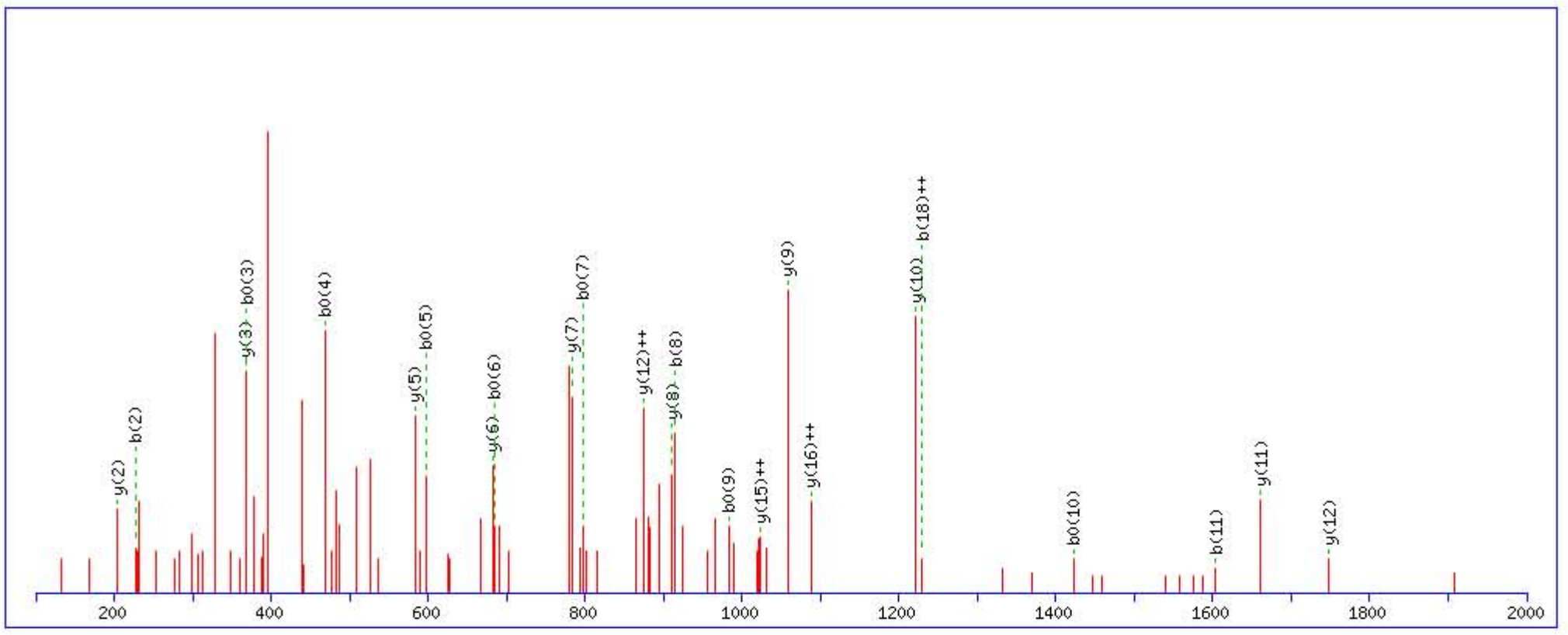
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EPCVESLVSQYFQTVTDYGK**
Found in **APOA2_HUMAN**, Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1

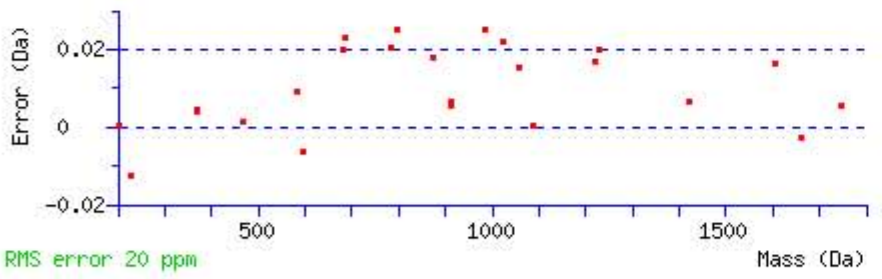
Match to Query 55982: 2660.276892 from(887.766240,3+) rtinseconds(3159) index(12010)
Title: Locus:1.1.1.2375.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

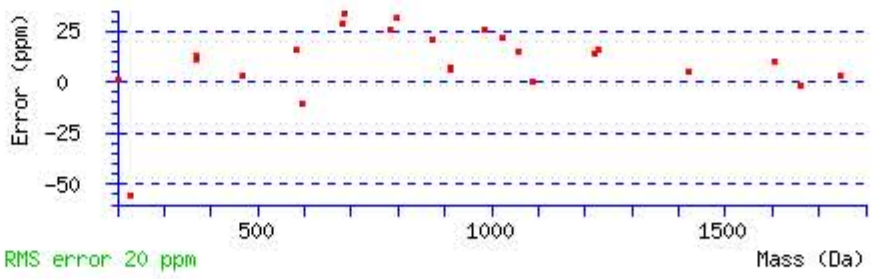
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2660.250244
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 49 **Expect:** 0.00028
**Matches :** 24/204 fragment ions using 43 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 20 |
| 2 | **227.102633** | 114.054954 | | | 209.092068 | 105.049672 | P | 2532.214913 | 1266.611094 | 2515.188364 | 1258.097820 | 2514.204348 | 1257.605812 | 19 |
| 3 | 387.133282 | 194.070279 | | | 369.122717 | 185.064997 | C | 2435.162149 | 1218.084712 | 2418.135600 | 1209.571438 | 2417.151584 | 1209.079430 | 18 |
| 4 | 486.201696 | 243.604486 | | | 468.191131 | 234.599204 | V | 2275.131500 | 1138.069388 | 2258.104951 | 1129.556113 | 2257.120935 | 1129.064105 | 17 |
| 5 | 615.244289 | 308.125783 | | | 597.233724 | 299.120500 | E | 2176.063086 | 1088.535181 | 2159.036537 | 1080.021906 | 2158.052521 | 1079.529898 | 16 |
| 6 | 702.276317 | 351.641797 | | | 684.265752 | 342.636514 | S | 2047.020493 | 1024.013884 | 2029.993944 | 1015.500610 | 2029.009928 | 1015.008602 | 15 |
| 7 | 815.360381 | 408.183829 | | | 797.349816 | 399.178546 | L | 1959.988465 | 980.497870 | 1942.961916 | 971.984596 | 1941.977900 | 971.492588 | 14 |
| 8 | **914.428795** | 457.718036 | | | 896.418230 | 448.712753 | V | 1846.904401 | 923.955838 | 1829.877852 | 915.442564 | 1828.893836 | 914.950556 | 13 |
| 9 | 1001.460823 | 501.234050 | | | 983.450258 | 492.228767 | S | *1747.835987* | 874.421631 | 1730.809438 | 865.908357 | 1729.825422 | 865.416349 | 12 |
| 10 | 1440.686149 | 720.846712 | 1423.659600 | 712.333438 | 1422.675584 | 711.841430 | Q | *1660.803959* | 830.905617 | 1643.777410 | 822.392343 | 1642.793394 | 821.900335 | 11 |
| 11 | **1603.749478** | 802.378377 | 1586.722929 | 793.865103 | 1585.738913 | 793.373094 | Y | *1221.578633* | 611.292954 | 1204.552084 | 602.779680 | 1203.568068 | 602.287672 | 10 |
| 12 | 1750.817892 | 875.912584 | 1733.791343 | 867.399310 | 1732.807327 | 866.907302 | F | *1058.515304* | 529.761290 | 1041.488755 | 521.248015 | 1040.504739 | 520.756007 | 9 |
| 13 | 1878.876470 | 939.941873 | 1861.849921 | 931.428599 | 1860.865905 | 930.936590 | Q | *911.446890* | 456.227083 | 894.420341 | 447.713808 | 893.436325 | 447.221800 | 8 |
| 14 | 1979.924149 | 990.465713 | 1962.897600 | 981.952438 | 1961.913584 | 981.460430 | T | *783.388312* | 392.197794 | 766.361763 | 383.684519 | 765.377747 | 383.192511 | 7 |
| 15 | 2078.992563 | 1039.999919 | 2061.966014 | 1031.486645 | 2060.981998 | 1030.994637 | V | *682.340633* | 341.673954 | 665.314084 | 333.160680 | 664.330068 | 332.668672 | 6 |
| 16 | 2180.040242 | 1090.523759 | 2163.013693 | 1082.010484 | 2162.029677 | 1081.518476 | T | *583.272219* | 292.139747 | 566.245670 | 283.626473 | 565.261654 | 283.134465 | 5 |
| 17 | 2295.067185 | 1148.037230 | 2278.040636 | 1139.523956 | 2277.056620 | 1139.031948 | D | 482.224540 | 241.615908 | 465.197991 | 233.102633 | 464.213975 | 232.610625 | 4 |
| 18 | 2458.130514 | 1229.568895 | 2441.103965 | 1221.055620 | 2440.119949 | 1220.563612 | Y | *367.197597* | 184.102436 | 350.171048 | 175.589162 | | | 3 |
| 19 | 2515.151978 | 1258.079627 | 2498.125429 | 1249.566352 | 2497.141413 | 1249.074344 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 20 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 49.2 | 2660.250244 | 0.026648 | EPCVESLVSQYFQTVTDYGK |
| 28.7 | 2660.250244 | 0.026648 | EPCVESLVSQYFQTVTDYGK |

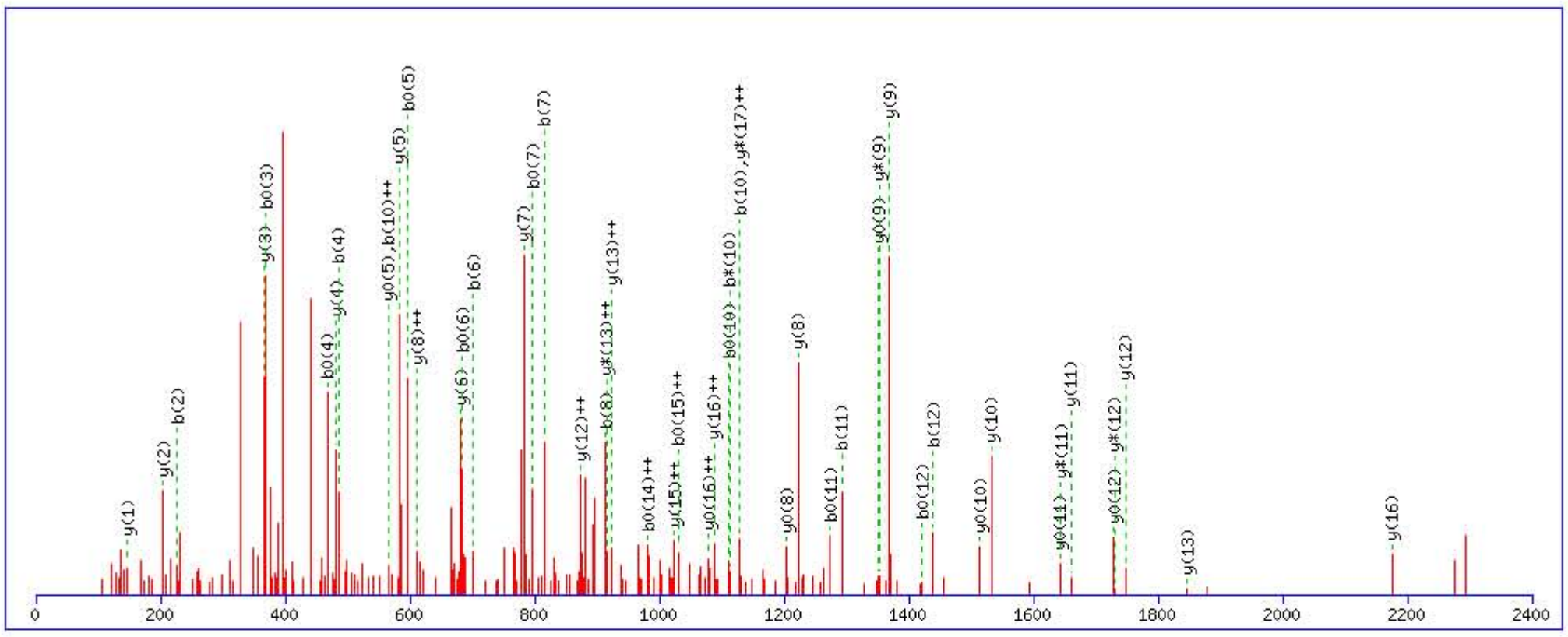
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EPCVESLVSQYFQTVTDYGK**
Found in **APOA2_HUMAN**, Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1

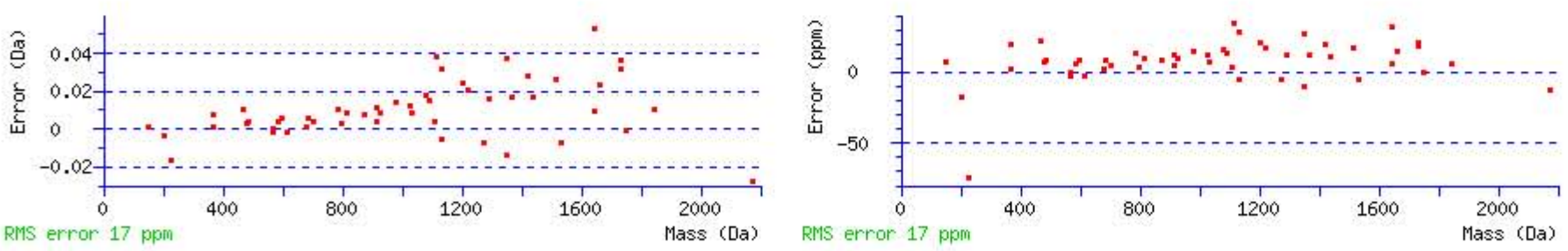
Match to Query 55984: 2660.278002 from(887.766610,3+) rtinseconds(3131) index(11828)
Title: Locus:1.1.1.2365.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2660.250244
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 77 **Expect:** 4.7e-007
**Matches :** 51/204 fragment ions using 85 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 20 |
| 2 | **227.102633** | 114.054954 | | | 209.092068 | 105.049672 | P | 2532.214913 | 1266.611094 | 2515.188364 | 1258.097820 | 2514.204348 | 1257.605812 | 19 |
| 3 | 387.133282 | 194.070279 | | | 369.122717 | 185.064997 | C | 2435.162149 | 1218.084712 | 2418.135600 | 1209.571438 | 2417.151584 | 1209.079430 | 18 |
| 4 | **486.201696** | 243.604486 | | | 468.191131 | 234.599204 | V | 2275.131500 | 1138.069388 | 2258.104951 | 1129.556113 | 2257.120935 | 1129.064105 | 17 |
| 5 | 615.244289 | 308.125783 | | | 597.233724 | 299.120500 | E | *2176.063086* | 1088.535181 | 2159.036537 | 1080.021906 | 2158.052521 | 1079.529898 | 16 |
| 6 | **702.276317** | 351.641797 | | | 684.265752 | 342.636514 | S | 2047.020493 | 1024.013885 | 2029.993944 | 1015.500610 | 2029.009928 | 1015.008602 | 15 |
| 7 | **815.360381** | 408.183829 | | | 797.349816 | 399.178546 | L | 1959.988465 | 980.497871 | 1942.961916 | 971.984596 | 1941.977900 | 971.492588 | 14 |
| 8 | **914.428795** | 457.718036 | | | 896.418230 | 448.712753 | V | *1846.904401* | 923.955839 | 1829.877852 | 915.442564 | 1828.893836 | 914.950556 | 13 |
| 9 | 1001.460823 | 501.234050 | | | 983.450258 | 492.228767 | S | *1747.835987* | 874.421632 | 1730.809438 | 865.908357 | 1729.825422 | 865.416349 | 12 |
| 10 | **1129.519401** | 565.263339 | 1112.492852 | 556.750064 | 1111.508836 | 556.258056 | Q | *1660.803959* | 830.905618 | 1643.777410 | 822.392343 | 1642.793394 | 821.900335 | 11 |
| 11 | **1292.582730** | 646.795003 | 1275.556181 | 638.281729 | 1274.572165 | 637.789721 | Y | *1532.745381* | 766.876329 | 1515.718832 | 758.363054 | 1514.734816 | 757.871046 | 10 |
| 12 | **1439.651144** | 720.329210 | 1422.624595 | 711.815936 | 1421.640579 | 711.323928 | F | *1369.682052* | 685.344664 | 1352.655503 | 676.831390 | 1351.671487 | 676.339382 | 9 |
| 13 | 1878.876470 | 939.941873 | 1861.849921 | 931.428599 | 1860.865905 | 930.936591 | Q | *1222.613638* | 611.810457 | 1205.587089 | 603.297183 | 1204.603073 | 602.805175 | 8 |
| 14 | 1979.924149 | 990.465713 | 1962.897600 | 981.952438 | 1961.913584 | 981.460430 | T | *783.388312* | 392.197794 | 766.361763 | 383.684519 | 765.377747 | 383.192511 | 7 |
| 15 | 2078.992563 | 1039.999920 | 2061.966014 | 1031.486645 | 2060.981998 | 1030.994637 | V | *682.340633* | 341.673954 | 665.314084 | 333.160680 | 664.330068 | 332.668672 | 6 |
| 16 | 2180.040242 | 1090.523759 | 2163.013693 | 1082.010484 | 2162.029677 | 1081.518476 | T | *583.272219* | 292.139747 | 566.245670 | 283.626473 | 565.261654 | 283.134465 | 5 |
| 17 | 2295.067185 | 1148.037230 | 2278.040636 | 1139.523956 | 2277.056620 | 1139.031948 | D | *482.224540* | 241.615908 | 465.197991 | 233.102633 | 464.213975 | 232.610625 | 4 |
| 18 | 2458.130514 | 1229.568895 | 2441.103965 | 1221.055620 | 2440.119949 | 1220.563612 | Y | *367.197597* | 184.102436 | 350.171048 | 175.589162 | | | 3 |
| 19 | 2515.151978 | 1258.079627 | 2498.125429 | 1249.566352 | 2497.141413 | 1249.074344 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 20 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 77.0 | 2660.250244 | 0.027758 | EPCVESLVSQYFQTVTDYGK |
| 37.7 | 2660.250244 | 0.027758 | EPCVESLVSQYFQTVTDYGK |

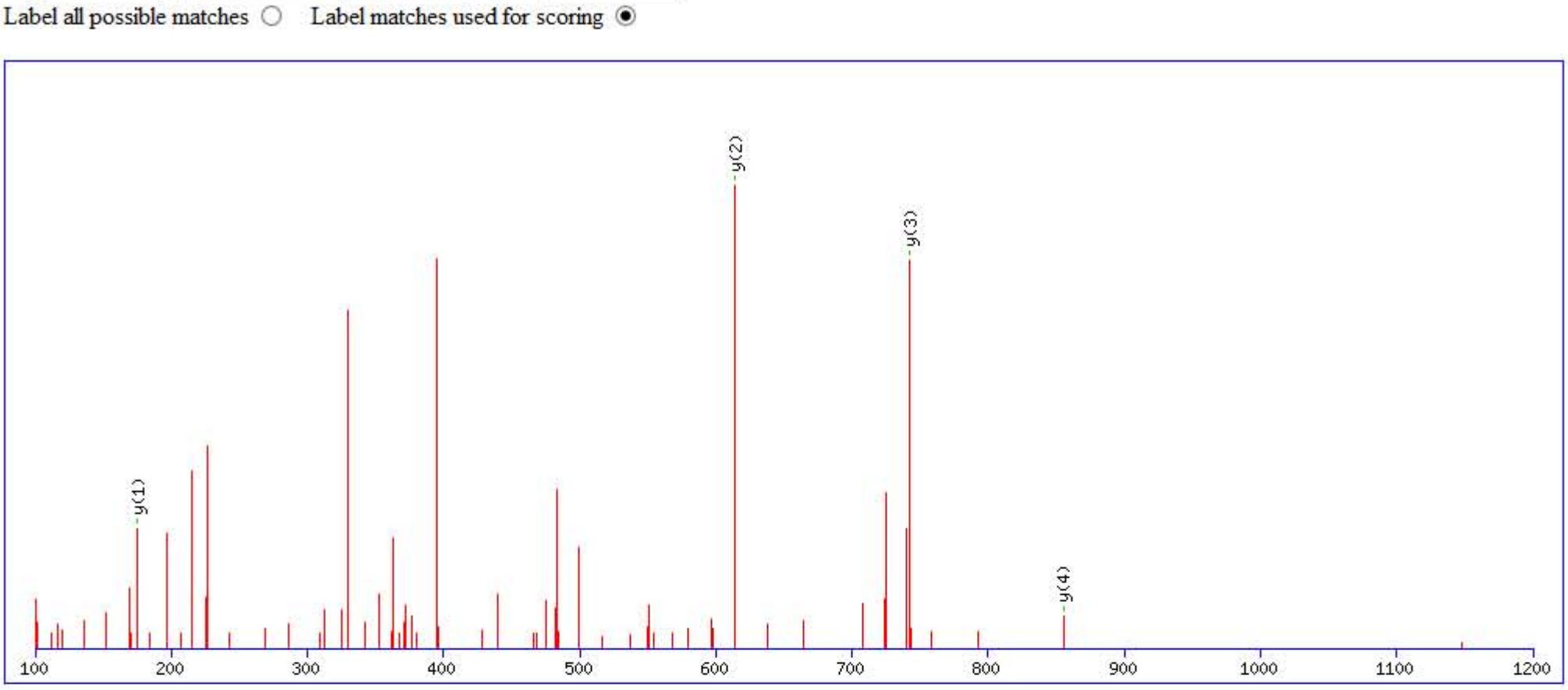
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EIQQR**
Found in **T161A_HUMAN**, Transmembrane protein 161A OS=Homo sapiens GN=TMEM161A PE=2 SV=1

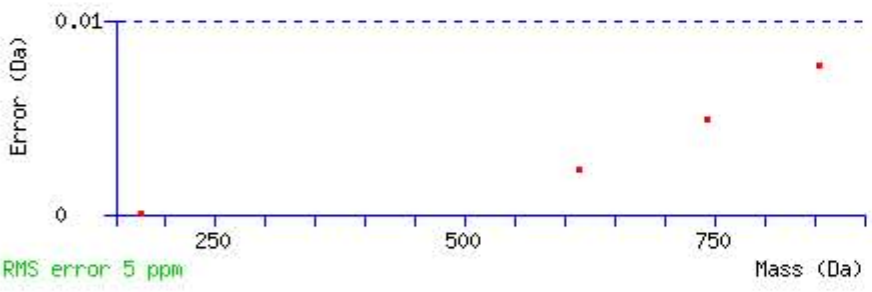
Match to Query 13167: 983.519408 from(492.766980,2+) rtinseconds(1380) index(1827)
Title: Locus:1.1.1.1757.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

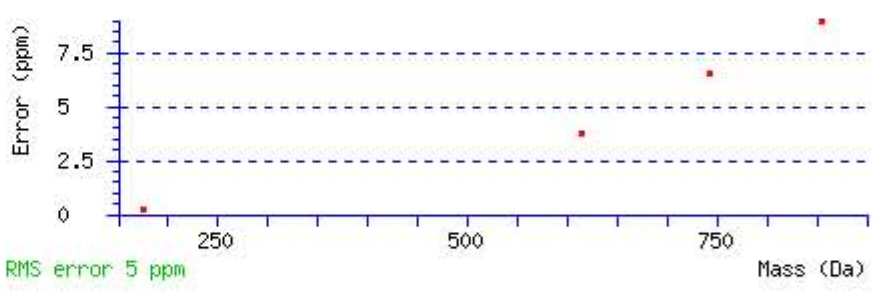
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 983.522217
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 25 **Expect:** 0.06
**Matches :** 4/36 fragment ions using 8 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | 5 |
| 2 | 243.133933 | 122.070605 | | | 225.123368 | 113.065322 | I | *855.486920* | 428.247098 | 838.460371 | 419.733824 | 4 |
| 3 | 371.192511 | 186.099894 | 354.165962 | 177.586619 | 353.181946 | 177.094611 | Q | *742.402856* | 371.705066 | 725.376307 | 363.191792 | 3 |
| 4 | 810.417837 | 405.712557 | 793.391288 | 397.199282 | 792.407272 | 396.707274 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | 2 |
| 5 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.3 | 983.522217 | -0.002809 | EIQQR |
| 25.3 | 983.522217 | -0.002809 | ELQQR |
| 13.2 | 983.522217 | -0.002809 | IEQQR |
| 13.2 | 983.507599 | 0.011809 | LEKEFYR |
| 13.2 | 983.522217 | -0.002809 | LEQQR |
| 11.6 | 983.522217 | -0.002809 | EAAVQR |
| 11.6 | 983.522217 | -0.002809 | EGLAQR |
| 11.6 | 983.514816 | 0.004592 | EKISHNTR |
| 11.6 | 983.522217 | -0.002809 | EQIQR |
| 11.6 | 983.522217 | -0.002809 | EQLQR |

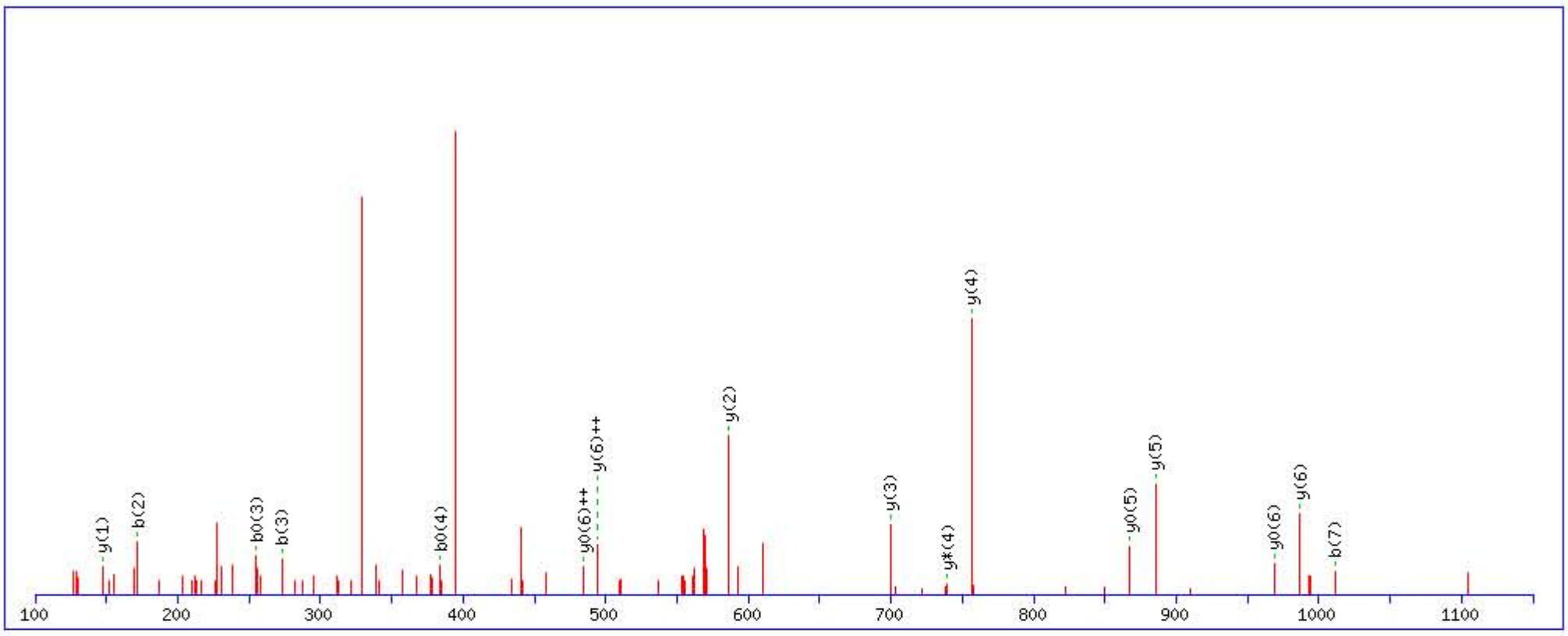
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GNTEGLQK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

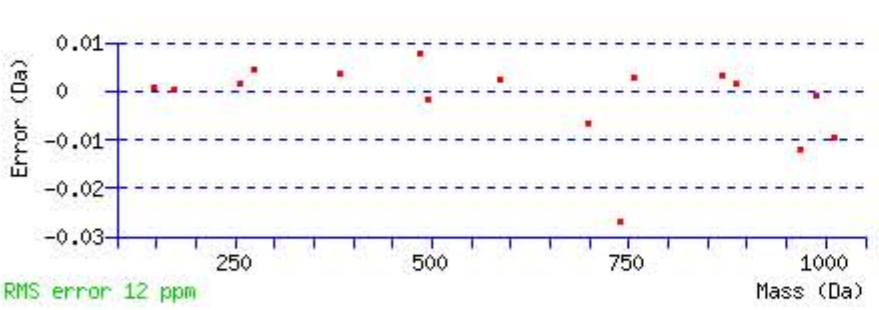
Match to Query 19120: 1156.591248 from(579.302900,2+) rtinseconds(1394) index(62745)
Title: Locus:1.1.1.1760.21 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

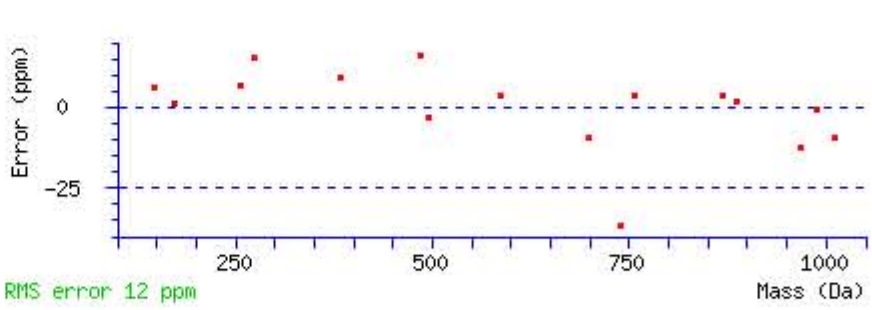
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1156.591034
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 34 **Expect:** 0.00099
**Matches :** 16/70 fragment ions using 28 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 8 |
| 2 | 172.071667 | 86.539471 | 155.045118 | 78.026197 | | | N | 1100.576857 | 550.792067 | 1083.550308 | 542.278792 | 1082.566292 | 541.786784 | 7 |
| 3 | 273.119346 | 137.063311 | 256.092797 | 128.550037 | 255.108781 | 128.058029 | T | *986.533930* | 493.770603 | 969.507381 | 485.257329 | 968.523365 | 484.765321 | 6 |
| 4 | 402.161939 | 201.584608 | 385.135390 | 193.071333 | 384.151374 | 192.579325 | E | *885.486251* | 443.246764 | 868.459702 | 434.733489 | 867.475686 | 434.241481 | 5 |
| 5 | 459.183403 | 230.095339 | 442.156854 | 221.582065 | 441.172838 | 221.090057 | G | *756.443658* | 378.725467 | 739.417109 | 370.212193 | | | 4 |
| 6 | 572.267467 | 286.637372 | 555.240918 | 278.124097 | 554.256902 | 277.632089 | L | *699.422194* | 350.214735 | 682.395645 | 341.701461 | | | 3 |
| 7 | 1011.492793 | 506.250035 | 994.466244 | 497.736760 | 993.482228 | 497.244752 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 8 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546766 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 34.1 | 1156.591034 | 0.000214 | GNTEGLQK |
| 2.0 | 1156.591003 | 0.000245 | KEEANQK |
| 0.1 | 1156.577118 | 0.014130 | QLSTRCHQK |

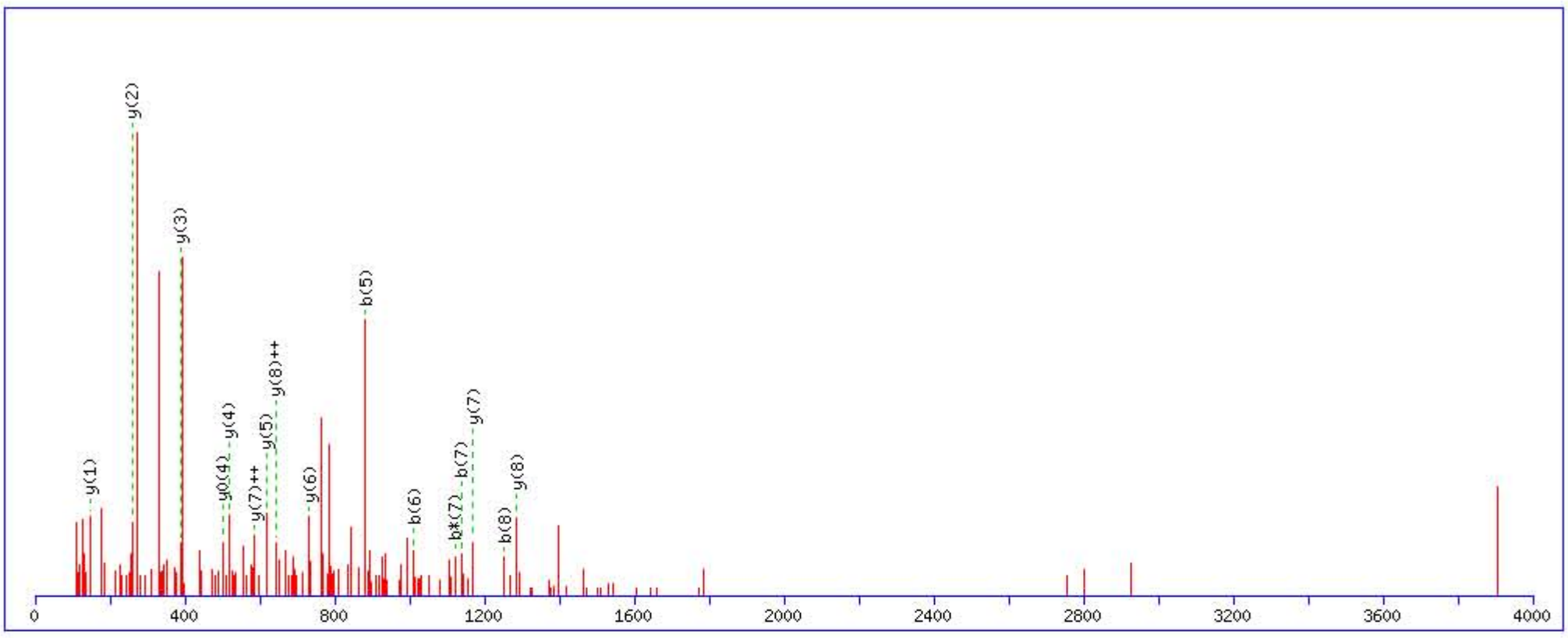
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IDQNVEELK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

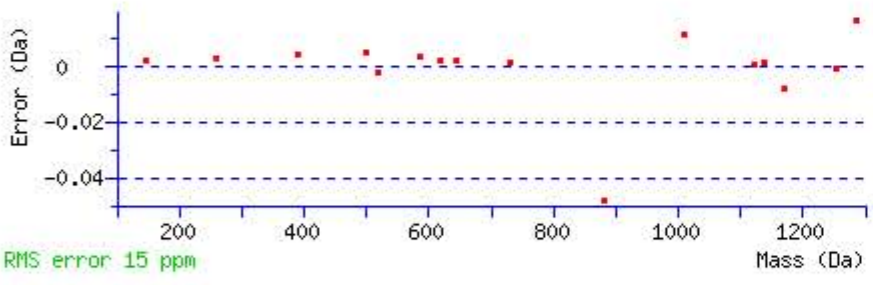
Match to Query 27247: 1397.724948 from(699.869750,2+) rtinseconds(1824) index(4449)
Title: Locus:1.1.1.1912.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

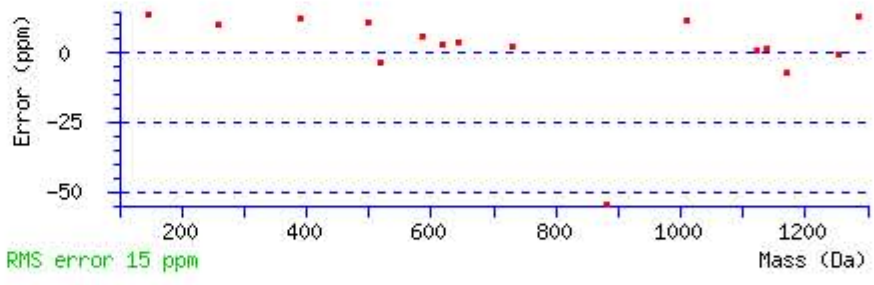
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1397.722427
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 36 **Expect:** 0.0069
**Matches :** 16/86 fragment ions using 39 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 9 |
| 2 | 229.118283 | 115.062779 | | | 211.107718 | 106.057497 | D | *1285.645664* | 643.326470 | 1268.619115 | 634.813196 | 1267.635099 | 634.321187 | 8 |
| 3 | 668.343609 | 334.675443 | 651.317060 | 326.162168 | 650.333044 | 325.670160 | Q | *1170.618721* | 585.812998 | 1153.592172 | 577.299724 | 1152.608156 | 576.807716 | 7 |
| 4 | 782.386536 | 391.696906 | 765.359987 | 383.183631 | 764.375971 | 382.691623 | N | *731.393395* | 366.200335 | 714.366846 | 357.687061 | 713.382830 | 357.195053 | 6 |
| 5 | **881.454950** | 441.231113 | 864.428401 | 432.717838 | 863.444385 | 432.225830 | V | *617.350468* | 309.178872 | 600.323919 | 300.665597 | 599.339903 | 300.173589 | 5 |
| 6 | **1010.497543** | 505.752410 | 993.470994 | 497.239135 | 992.486978 | 496.747127 | E | *518.282054* | 259.644665 | 501.255505 | 251.131390 | 500.271489 | 250.639382 | 4 |
| 7 | **1139.540136** | 570.273706 | 1122.513587 | 561.760431 | 1121.529571 | 561.268423 | E | *389.239461* | 195.123368 | 372.212912 | 186.610094 | 371.228896 | 186.118086 | 3 |
| 8 | **1252.624200** | 626.815738 | 1235.597651 | 618.302463 | 1234.613635 | 617.810455 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 9 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

### All matches to this query

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 35.9 | 1397.722427 | 0.002521 | IDQNVEELK |
| 14.0 | 1397.744873 | -0.019925 | QRREEELK |
| 12.9 | 1397.730301 | -0.005353 | ELAFGDHELVIR |
| 7.3 | 1397.733658 | -0.008710 | AQVRDLEEK |
| 6.8 | 1397.722412 | 0.002536 | QLEAQLEEK |
| 6.1 | 1397.744873 | -0.019925 | MLEKARHQELK |
| 4.5 | 1397.708496 | 0.016452 | QMEIQKHKDNK |
| 4.2 | 1397.744904 | -0.019956 | SSGPQRAGSLK |
| 3.8 | 1397.737701 | -0.012753 | VIQFYETMLVR |
| 3.6 | 1397.722427 | 0.002521 | SSPEEQLGIK |

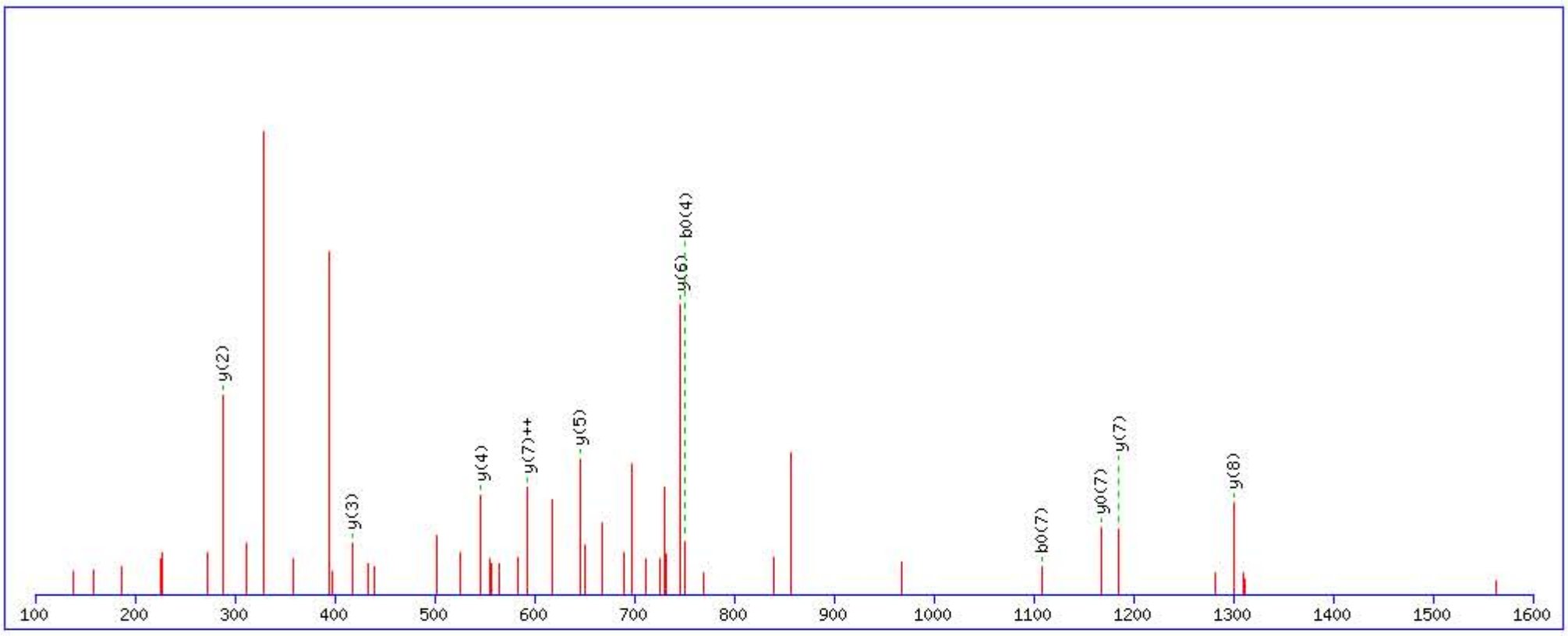
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IDQTVEELR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

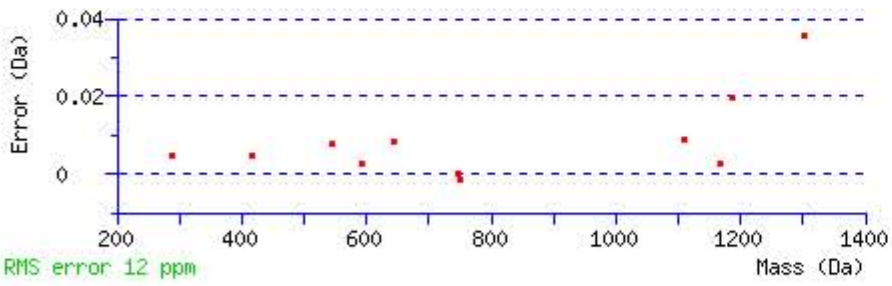
Match to Query 28181: 1412.739168 from(707.376860,2+) rtinseconds(1914) index(49688)
Title: Locus:1.1.1.1904.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

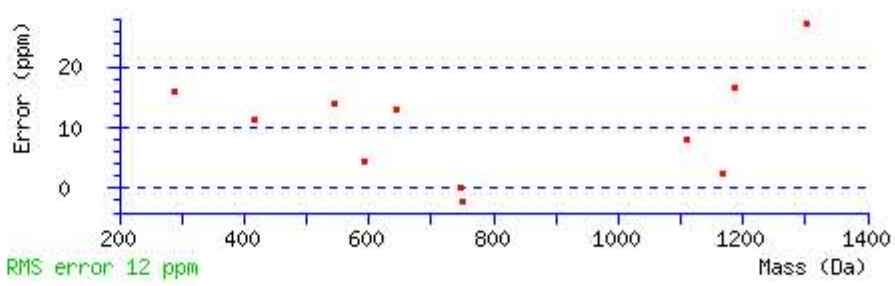
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1412.733337
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 36 **Expect:** 0.0073
**Matches :** 11/86 fragment ions using 22 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 9 |
| 2 | 229.118283 | 115.062779 | | | 211.107718 | 106.057497 | D | *1300.656564* | 650.831920 | 1283.630015 | 642.318646 | 1282.645999 | 641.826638 | 8 |
| 3 | 668.343609 | 334.675443 | 651.317060 | 326.162168 | 650.333044 | 325.670160 | Q | *1185.629621* | 593.318449 | 1168.603072 | 584.805174 | 1167.619056 | 584.313166 | 7 |
| 4 | 769.391288 | 385.199282 | 752.364739 | 376.686008 | 751.380723 | 376.194000 | T | *746.404295* | 373.705786 | 729.377746 | 365.192511 | 728.393730 | 364.700503 | 6 |
| 5 | 868.459702 | 434.733489 | 851.433153 | 426.220215 | 850.449137 | 425.728207 | V | *645.356616* | 323.181946 | 628.330067 | 314.668672 | 627.346051 | 314.176664 | 5 |
| 6 | 997.502295 | 499.254786 | 980.475746 | 490.741511 | 979.491730 | 490.249503 | E | *546.288202* | 273.647739 | 529.261653 | 265.134465 | 528.277637 | 264.642457 | 4 |
| 7 | 1126.544888 | 563.776082 | 1109.518339 | 555.262808 | 1108.534323 | 554.770800 | E | *417.245609* | 209.126442 | 400.219060 | 200.613168 | 399.235044 | 200.121160 | 3 |
| 8 | 1239.628952 | 620.318114 | 1222.602403 | 611.804840 | 1221.618387 | 611.312832 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 9 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 35.7 | 1412.733337 | 0.005831 | IDQTVEELR |

**Mascot:** http://www.matrixscience.com/

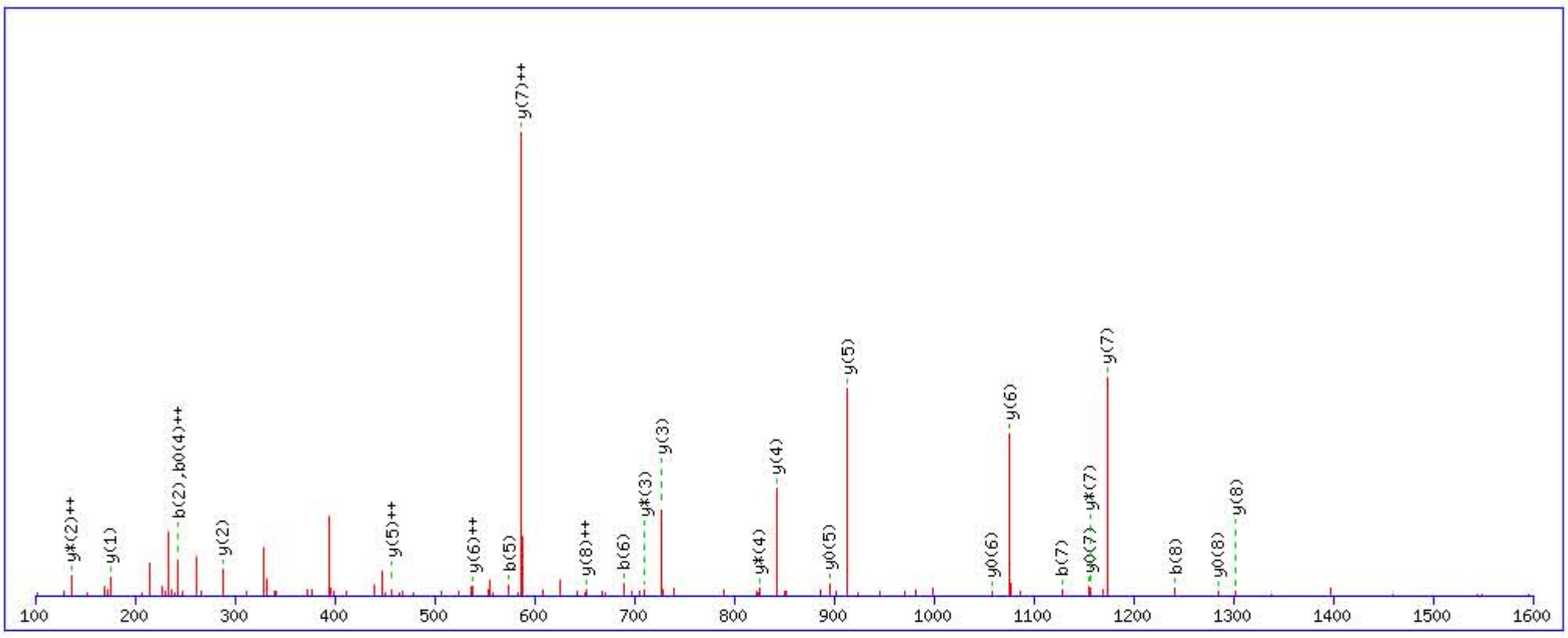
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LEPYADQLR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

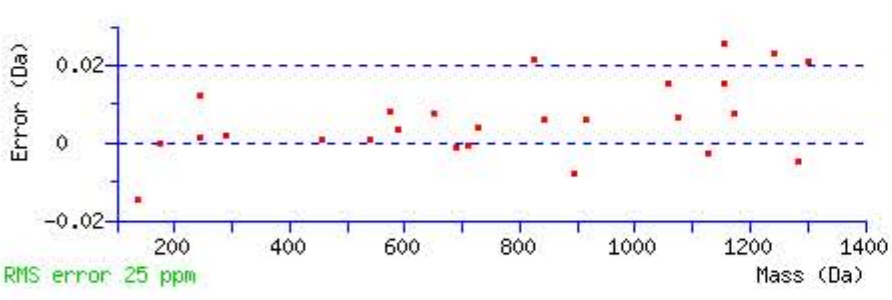
Match to Query 28215: 1414.734948 from(708.374750,2+) rtinseconds(1960) index(66208)
Title: Locus:1.1.1.1957.18 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

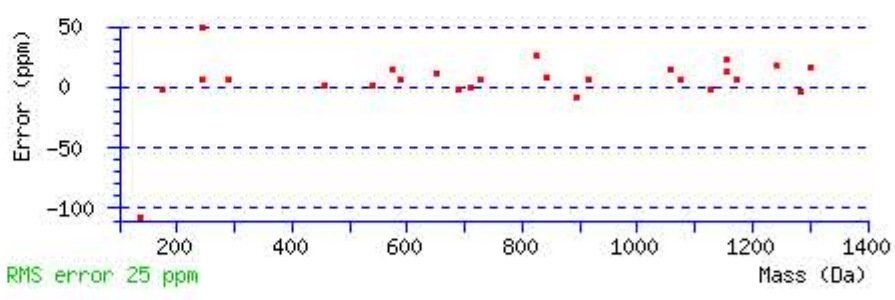
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1414.727844
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0012
**Matches :** 26/76 fragment ions using 59 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 9 |
| 2 | **243.133933** | 122.070605 | | | 225.123368 | 113.065322 | E | *1302.651085* | 651.829181 | 1285.624536 | 643.315906 | 1284.640520 | 642.823898 | 8 |
| 3 | 340.186697 | 170.596987 | | | 322.176132 | 161.591704 | P | *1173.608492* | 587.307884 | 1156.581943 | 578.794610 | 1155.597927 | 578.302602 | 7 |
| 4 | 503.250026 | 252.128651 | | | 485.239461 | 243.123369 | Y | *1076.555728* | 538.781502 | 1059.529179 | 530.268228 | 1058.545163 | 529.776220 | 6 |
| 5 | **574.287140** | 287.647208 | | | 556.276575 | 278.641926 | A | *913.492399* | 457.249838 | 896.465850 | 448.736563 | 895.481834 | 448.244555 | 5 |
| 6 | **689.314083** | 345.160680 | | | 671.303518 | 336.155397 | D | *842.455285* | 421.731281 | 825.428736 | 413.218006 | 824.444720 | 412.725998 | 4 |
| 7 | **1128.539409** | 564.773343 | 1111.512860 | 556.260068 | 1110.528844 | 555.768060 | Q | *727.428342* | 364.217809 | 710.401793 | 355.704535 | | | 3 |
| 8 | **1241.623473** | 621.315375 | 1224.596924 | 612.802100 | 1223.612908 | 612.310092 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 9 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.6 | 1414.727844 | 0.007104 | LEPYADQLR |
| 6.9 | 1414.735931 | -0.000983 | LMRGLLHCMIR |
| 6.2 | 1414.752777 | -0.017829 | KNIESARAELER |
| 4.7 | 1414.731216 | 0.003732 | LMELQEAVR |
| 4.4 | 1414.741577 | -0.006629 | ELDVEVSRLEAR |
| 3.9 | 1414.735062 | -0.000114 | IQLMQEVDRQR |
| 1.3 | 1414.731689 | 0.003259 | NKAEFHQSVISR |
| 0.7 | 1414.735077 | -0.000129 | SSMSGLHLVKQGR |
| 0.7 | 1414.716400 | 0.018548 | LEEDARLEERR |
| 0.2 | 1414.748978 | -0.014030 | NKDIPNMLDVLK |

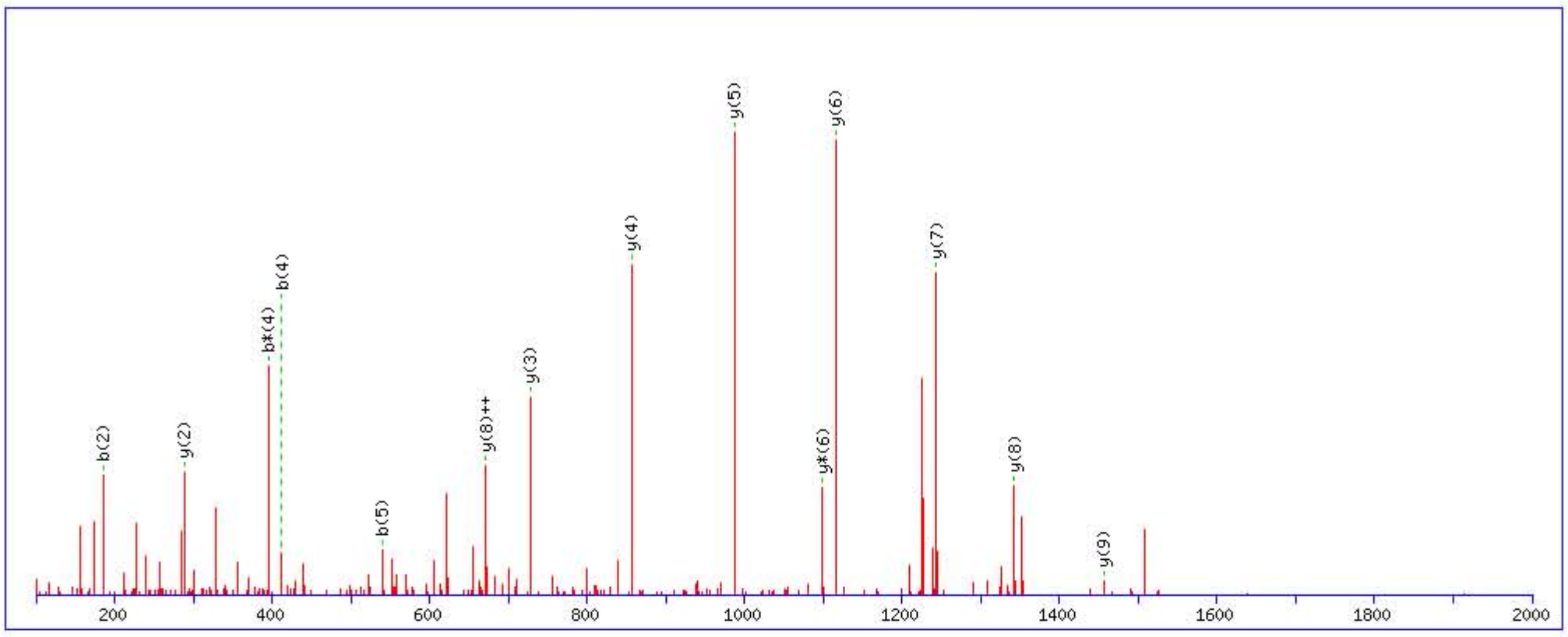
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ALVQQMEQLR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

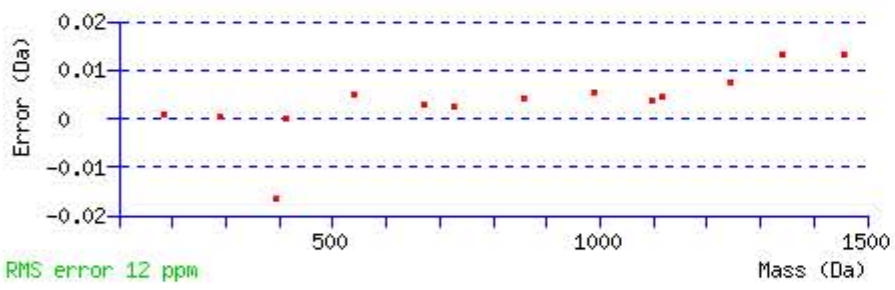
Match to Query 31955: 1525.823128 from(763.918840,2+) rtinseconds(2106) index(6223)
Title: Locus:1.1.1.2010.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

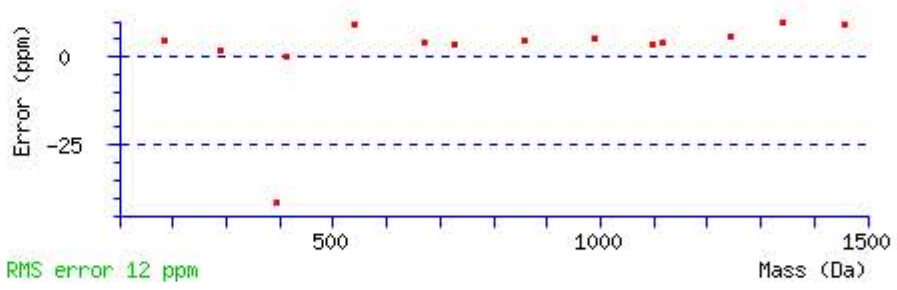
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1525.810867
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 79 **Expect:** 2.6e-007
**Matches :** 14/84 fragment ions using 15 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 10 |
| 2 | 185.128454 | 93.067865 | | | | | L | *1455.781054* | 728.394165 | 1438.754505 | 719.880890 | 1437.770489 | 719.388882 | 9 |
| 3 | 284.196868 | 142.602072 | | | | | V | *1342.696990* | 671.852133 | 1325.670441 | 663.338858 | 1324.686425 | 662.846850 | 8 |
| 4 | 412.255446 | 206.631361 | 395.228897 | 198.118087 | | | Q | *1243.628576* | 622.317926 | 1226.602027 | 613.804651 | 1225.618011 | 613.312643 | 7 |
| 5 | 540.314024 | 270.660650 | 523.287475 | 262.147376 | | | Q | *1115.569998* | 558.288637 | 1098.543449 | 549.775362 | 1097.559433 | 549.283354 | 6 |
| 6 | 671.354509 | 336.180893 | 654.327960 | 327.667618 | | | M | *987.511420* | 494.259348 | 970.484871 | 485.746073 | 969.500855 | 485.254065 | 5 |
| 7 | 800.397102 | 400.702189 | 783.370553 | 392.188915 | 782.386537 | 391.696907 | E | *856.470935* | 428.739105 | 839.444386 | 420.225831 | 838.460370 | 419.733823 | 4 |
| 8 | 1239.622428 | 620.314852 | 1222.595879 | 611.801578 | 1221.611863 | 611.309569 | Q | *727.428342* | 364.217809 | 710.401793 | 355.704534 | | | 3 |
| 9 | 1352.706492 | 676.856884 | 1335.679943 | 668.343609 | 1334.695927 | 667.851601 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 10 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 78.7 | 1525.810867 | 0.012261 | ALVQQMEQLR |
| 30.5 | 1525.810867 | 0.012261 | ALVQQMEQLR |
| 14.7 | 1525.810867 | 0.012261 | ALVQQMEQLR |
| 8.0 | 1525.803467 | 0.019661 | SPPSPRSSMAAVALR |
| 6.2 | 1525.843689 | -0.020561 | QAQADRVSLRNLR |
| 5.1 | 1525.803482 | 0.019646 | VNTPAGSSQKAR |
| 4.9 | 1525.814697 | 0.008431 | ERQRTEQLR |
| 4.7 | 1525.814682 | 0.008446 | LARASEQERR |
| 4.3 | 1525.843887 | -0.020759 | QFSLLSQHKK |
| 4.0 | 1525.807495 | 0.015633 | WPPQQLMLSAALR |

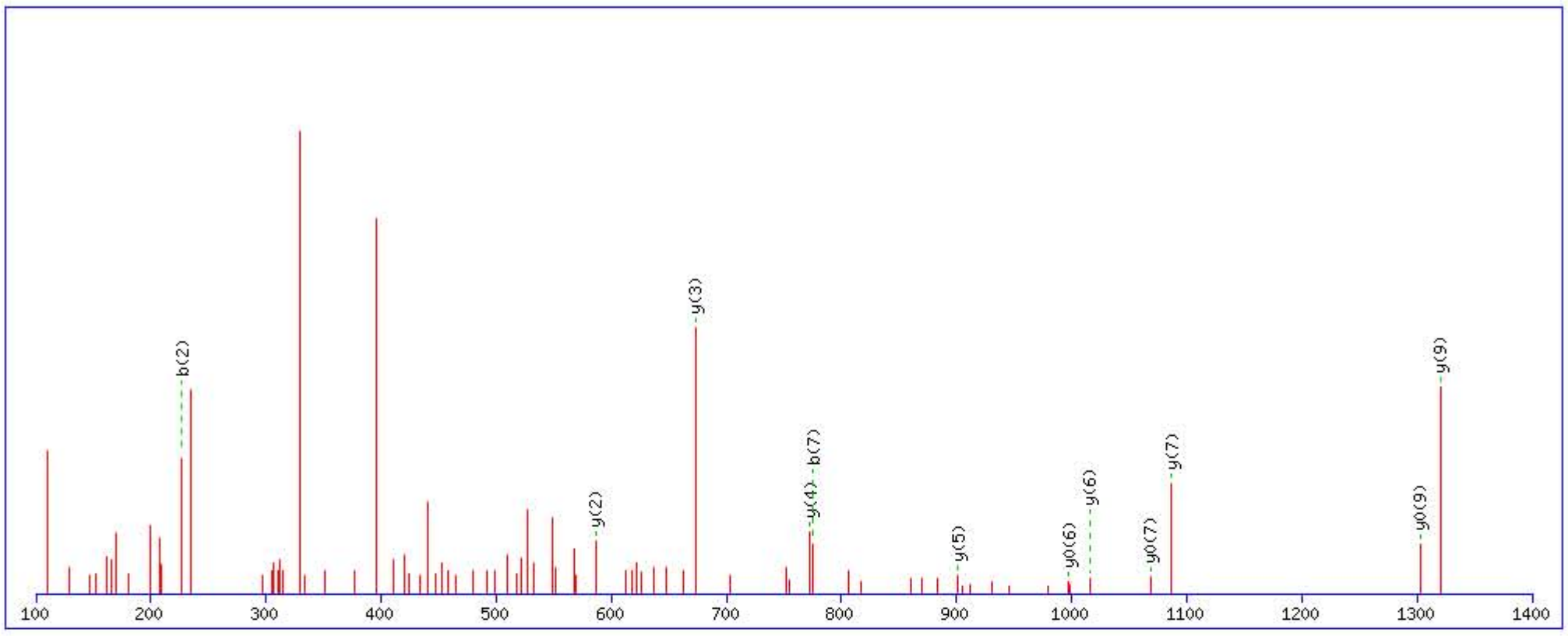
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LLPHANEVSQK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

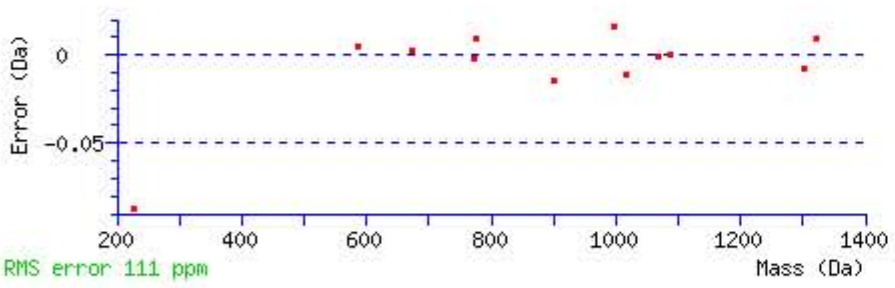
Match to Query 32419: 1545.825162 from(516.282330,3+) rtinseconds(1524) index(17081)
Title: Locus:1.1.1.2913.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

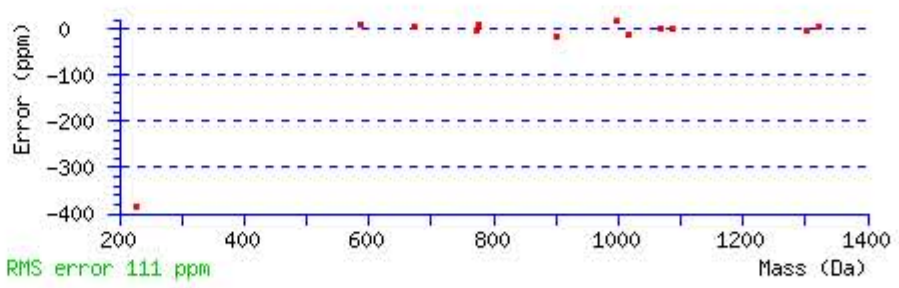
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1545.833710
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 27 **Expect:** 0.042
**Matches :** 12/94 fragment ions using 32 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 11 |
| 2 | **227.175404** | 114.091340 | | | | | L | 1433.756946 | 717.382111 | 1416.730397 | 708.868837 | 1415.746381 | 708.376828 | 10 |
| 3 | 324.228168 | 162.617722 | | | | | P | *1320.672882* | 660.840079 | 1303.646333 | 652.326804 | 1302.662317 | 651.834796 | 9 |
| 4 | 461.287080 | 231.147178 | | | | | H | 1223.620118 | 612.313697 | 1206.593569 | 603.800422 | 1205.609553 | 603.308414 | 8 |
| 5 | 532.324194 | 266.665735 | | | | | A | *1086.561206* | 543.784241 | 1069.534657 | 535.270966 | 1068.550641 | 534.778958 | 7 |
| 6 | 646.367121 | 323.687199 | 629.340572 | 315.173924 | | | N | *1015.524092* | 508.265684 | 998.497543 | 499.752409 | 997.513527 | 499.260401 | 6 |
| 7 | **775.409714** | 388.208495 | 758.383165 | 379.695221 | 757.399149 | 379.203213 | E | *901.481165* | 451.244220 | 884.454616 | 442.730946 | 883.470600 | 442.238938 | 5 |
| 8 | 874.478128 | 437.742702 | 857.451579 | 429.229427 | 856.467563 | 428.737419 | V | *772.438572* | 386.722924 | 755.412023 | 378.209649 | 754.428007 | 377.717641 | 4 |
| 9 | 961.510156 | 481.258716 | 944.483607 | 472.745441 | 943.499591 | 472.253433 | S | *673.370158* | 337.188717 | 656.343609 | 328.675442 | 655.359593 | 328.183434 | 3 |
| 10 | 1400.735482 | 700.871379 | 1383.708933 | 692.358104 | 1382.724917 | 691.866096 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159428 | | | 2 |
| 11 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 27.2 | 1545.833710 | -0.008548 | LLPHANEVSQK |

**Mascot:** http://www.matrixscience.com/

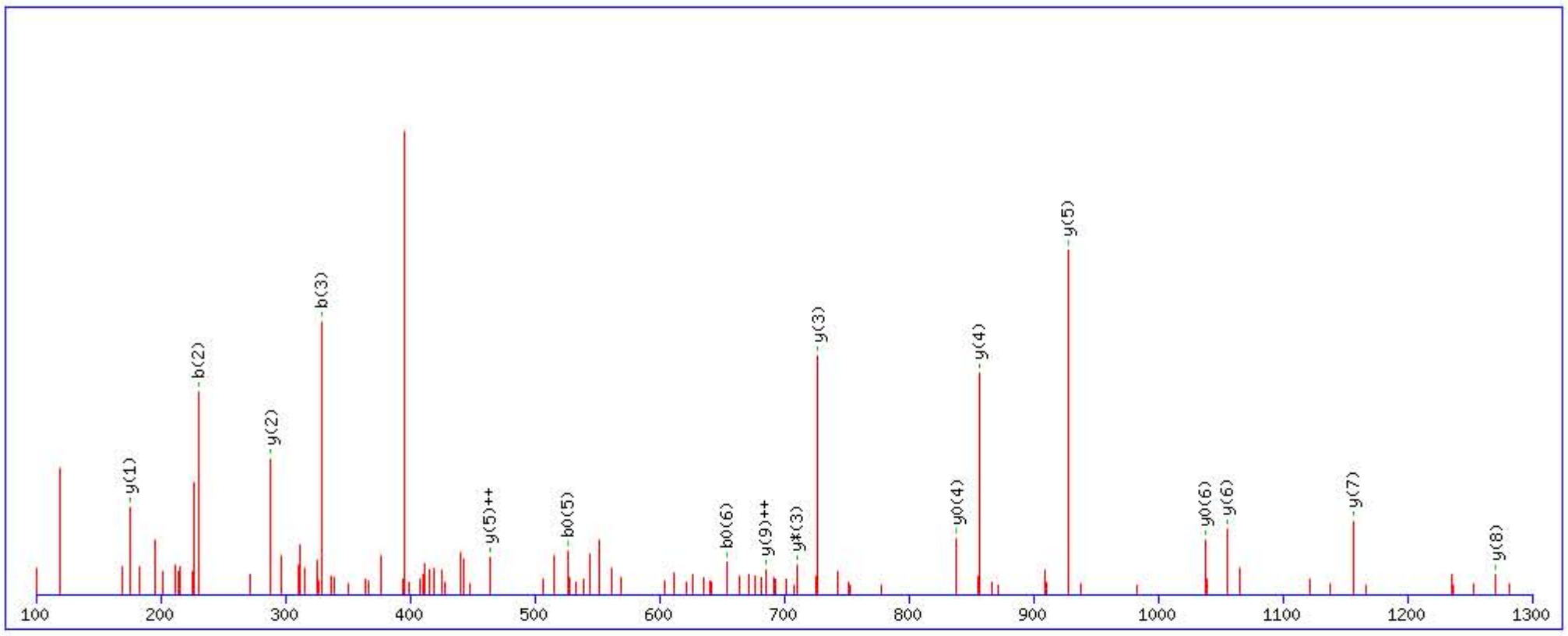
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TQVNTQAEQLR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

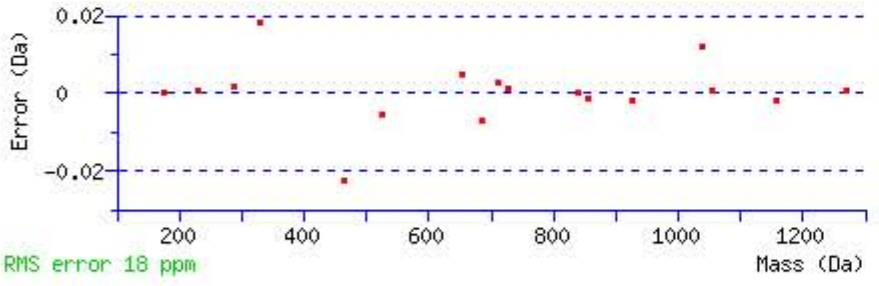
Match to Query 34636: 1597.825962 from(533.615930,3+) rtinseconds(1566) index(3084)
Title: Locus:1.1.1.1822.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

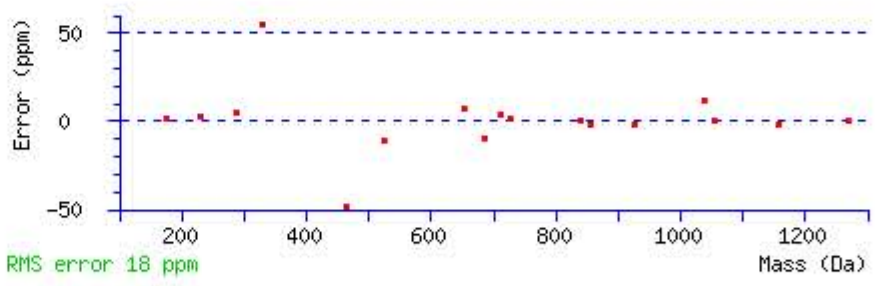
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1597.824615
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 1.9e-005
**Matches :** 17/112 fragment ions using 24 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 11 |
| 2 | **230.113533** | 115.560405 | 213.086984 | 107.047130 | 212.102968 | 106.555122 | Q | 1497.784225 | 749.395751 | 1480.757676 | 740.882476 | 1479.773660 | 740.390468 | 10 |
| 3 | **329.181947** | 165.094612 | 312.155398 | 156.581337 | 311.171382 | 156.089329 | V | 1369.725647 | 685.366462 | 1352.699098 | 676.853187 | 1351.715082 | 676.361179 | 9 |
| 4 | 443.224874 | 222.116075 | 426.198325 | 213.602801 | 425.214309 | 213.110793 | N | *1270.657233* | 635.832255 | 1253.630684 | 627.318980 | 1252.646668 | 626.826972 | 8 |
| 5 | 544.272553 | 272.639915 | 527.246004 | 264.126640 | 526.261988 | 263.634632 | T | *1156.614306* | 578.810791 | 1139.587757 | 570.297517 | 1138.603741 | 569.805509 | 7 |
| 6 | 672.331131 | 336.669204 | 655.304582 | 328.155929 | 654.320566 | 327.663921 | Q | *1055.566627* | 528.286951 | 1038.540078 | 519.773677 | 1037.556062 | 519.281669 | 6 |
| 7 | 743.368245 | 372.187761 | 726.341696 | 363.674486 | 725.357680 | 363.182478 | A | *927.508049* | 464.257663 | 910.481500 | 455.744388 | 909.497484 | 455.252380 | 5 |
| 8 | 872.410838 | 436.709057 | 855.384289 | 428.195783 | 854.400273 | 427.703775 | E | *856.470935* | 428.739106 | 839.444386 | 420.225831 | 838.460370 | 419.733823 | 4 |
| 9 | 1311.636164 | 656.321720 | 1294.609615 | 647.808446 | 1293.625599 | 647.316438 | Q | *727.428342* | 364.217809 | 710.401793 | 355.704535 | | | 3 |
| 10 | 1424.720228 | 712.863752 | 1407.693679 | 704.350478 | 1406.709663 | 703.858470 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.5 | 1597.824615 | 0.001347 | TQVNTQAEQLR |
| 14.5 | 1597.824615 | 0.001347 | TQVNTQAEQLR |
| 7.7 | 1597.835846 | -0.009884 | TKAAATAGGQGGAAR |
| 1.3 | 1597.828629 | -0.002667 | AWDILSGEQLR |
| 0.8 | 1597.846375 | -0.020413 | EQLPIFKAQNPDAK |

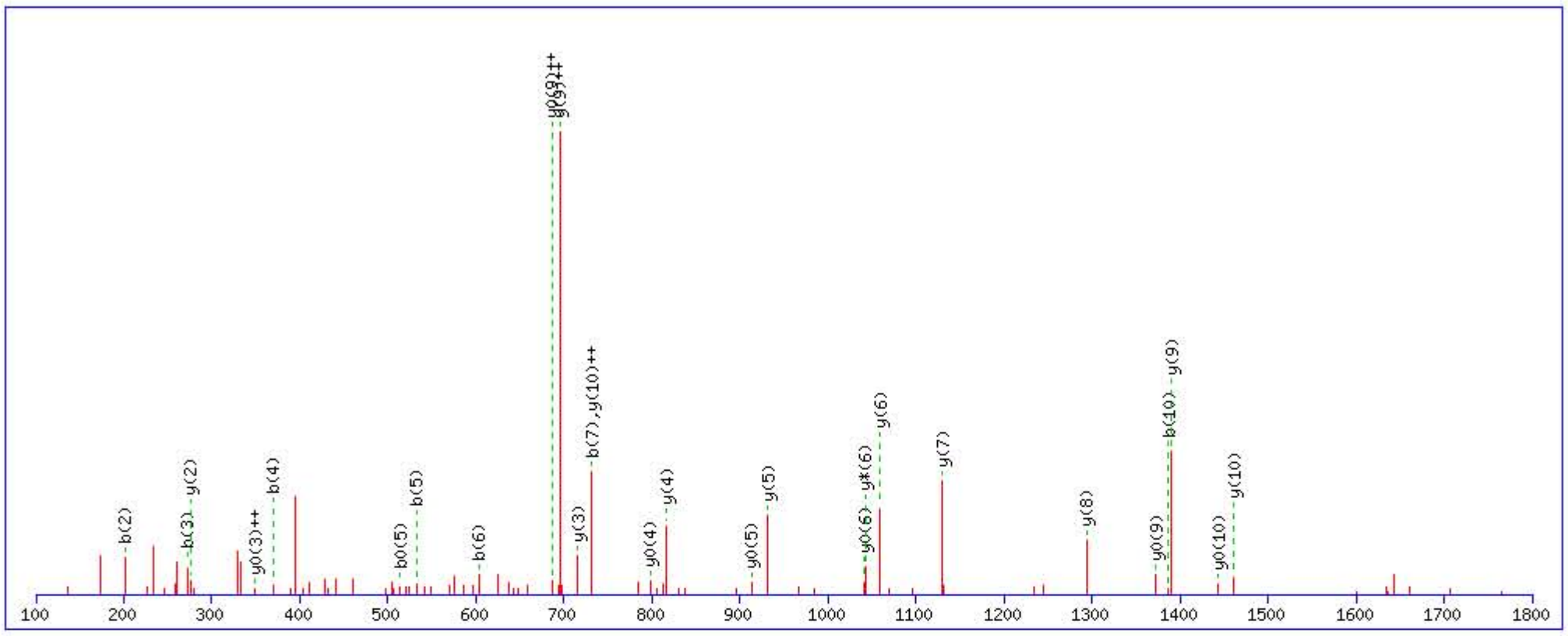
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SLAPYAQDTQEK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

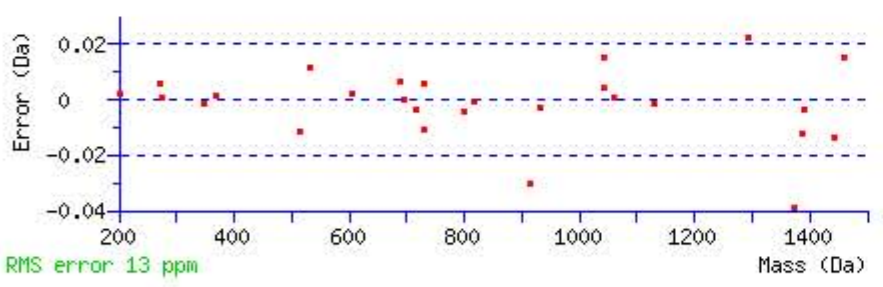
Match to Query 37128: 1660.821748 from(831.418150,2+) rtinseconds(1705) index(18273)
Title: Locus:1.1.1.2976.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

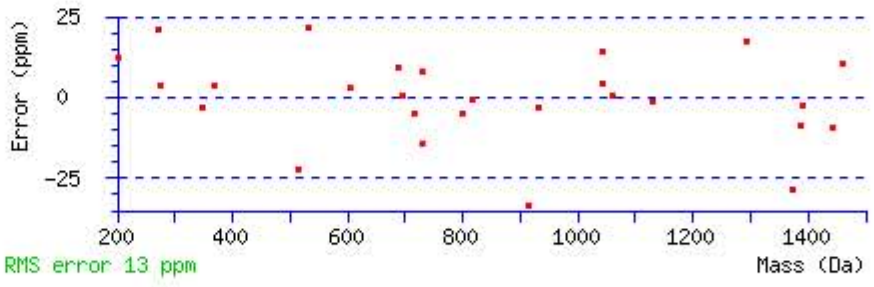
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1660.813034
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 46 **Expect:** 0.0002
**Matches :** 27/118 fragment ions using 58 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 12 |
| 2 | **201.123368** | 101.065322 | | | 183.112803 | 92.060039 | L | 1574.788308 | 787.897792 | 1557.761759 | 779.384518 | 1556.777743 | 778.892510 | 11 |
| 3 | **272.160482** | 136.583879 | | | 254.149917 | 127.578596 | A | *1461.704244* | 731.355760 | 1444.677695 | 722.842486 | 1443.693679 | 722.350478 | 10 |
| 4 | **369.213246** | 185.110261 | | | 351.202681 | 176.104978 | P | *1390.667130* | 695.837203 | 1373.640581 | 687.323929 | 1372.656565 | 686.831921 | 9 |
| 5 | **532.276575** | 266.641926 | | | 514.266010 | 257.636643 | Y | *1293.614366* | 647.310821 | 1276.587817 | 638.797547 | 1275.603801 | 638.305539 | 8 |
| 6 | **603.313689** | 302.160483 | | | 585.303124 | 293.155200 | A | *1130.551037* | 565.779157 | 1113.524488 | 557.265882 | 1112.540472 | 556.773874 | 7 |
| 7 | **731.372267** | 366.189772 | 714.345718 | 357.676497 | 713.361702 | 357.184489 | Q | *1059.513923* | 530.260600 | 1042.487374 | 521.747325 | 1041.503358 | 521.255317 | 6 |
| 8 | 846.399210 | 423.703243 | 829.372661 | 415.189969 | 828.388645 | 414.697961 | D | *931.455345* | 466.231311 | 914.428796 | 457.718036 | 913.444780 | 457.226028 | 5 |
| 9 | 947.446889 | 474.227083 | 930.420340 | 465.713808 | 929.436324 | 465.221800 | T | *816.428402* | 408.717839 | 799.401853 | 400.204565 | 798.417837 | 399.712557 | 4 |
| 10 | **1386.672215** | 693.839746 | 1369.645666 | 685.326471 | 1368.661650 | 684.834463 | Q | *715.380723* | 358.194000 | 698.354174 | 349.680725 | 697.370158 | 349.188717 | 3 |
| 11 | 1515.714808 | 758.361042 | 1498.688259 | 749.847768 | 1497.704243 | 749.355760 | E | *276.155397* | 138.581337 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 12 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.7 | 1660.813034 | 0.008714 | SLAPYAQDTQEK |
| 25.1 | 1660.813034 | 0.008714 | SLAPYAQDTQEK |
| 5.9 | 1660.820908 | 0.000840 | SLARAGFYYTGVNDK |
| 2.6 | 1660.842911 | -0.021163 | QGQEVEPPR |
| 0.5 | 1660.826782 | -0.005034 | EAATQAQQTLGSTIDK |

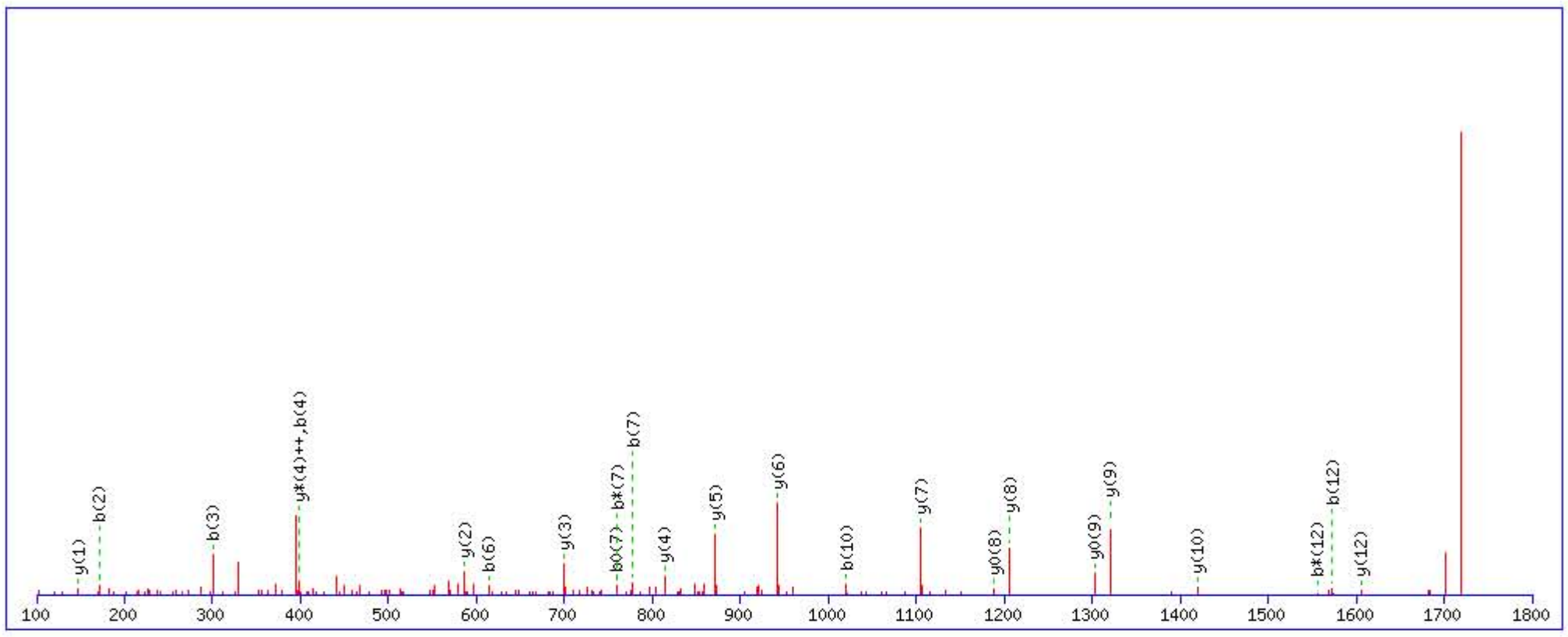
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LGEVNTYAGDLQK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

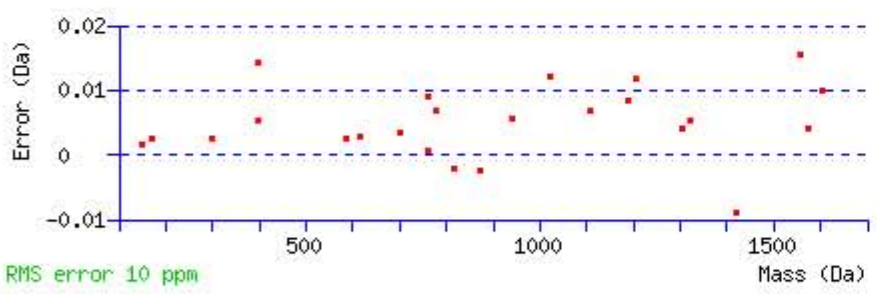
Match to Query 38354: 1717.885128 from(859.949840,2+) rtinseconds(1982) index(20135)
Title: Locus:1.1.1.3072.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

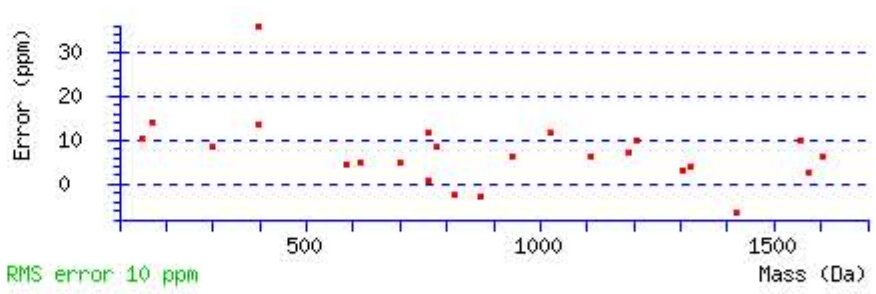
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1717.870895
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 73 **Expect:** 1.2e-006
**Matches :** 24/126 fragment ions using 44 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 13 |
| 2 | 171.112804 | 86.060040 | | | | | G | 1605.794121 | 803.400699 | 1588.767572 | 794.887424 | 1587.783556 | 794.395416 | 12 |
| 3 | 300.155397 | 150.581336 | | | 282.144832 | 141.576054 | E | 1548.772657 | 774.889967 | 1531.746108 | 766.376692 | 1530.762092 | 765.884684 | 11 |
| 4 | 399.223811 | 200.115544 | | | 381.213246 | 191.110261 | V | 1419.730064 | 710.368670 | 1402.703515 | 701.855396 | 1401.719499 | 701.363388 | 10 |
| 5 | 513.266738 | 257.137007 | 496.240189 | 248.623733 | 495.256173 | 248.131725 | N | 1320.661650 | 660.834463 | 1303.635101 | 652.321189 | 1302.651085 | 651.829181 | 9 |
| 6 | 614.314417 | 307.660847 | 597.287868 | 299.147572 | 596.303852 | 298.655564 | T | 1206.618723 | 603.813000 | 1189.592174 | 595.299725 | 1188.608158 | 594.807717 | 8 |
| 7 | 777.377746 | 389.192511 | 760.351197 | 380.679237 | 759.367181 | 380.187229 | Y | 1105.571044 | 553.289160 | 1088.544495 | 544.775886 | 1087.560479 | 544.283878 | 7 |
| 8 | 848.414860 | 424.711068 | 831.388311 | 416.197794 | 830.404295 | 415.705786 | A | 942.507715 | 471.757496 | 925.481166 | 463.244221 | 924.497150 | 462.752213 | 6 |
| 9 | 905.436324 | 453.221800 | 888.409775 | 444.708526 | 887.425759 | 444.216518 | G | 871.470601 | 436.238939 | 854.444052 | 427.725664 | 853.460036 | 427.233656 | 5 |
| 10 | 1020.463267 | 510.735272 | 1003.436718 | 502.221997 | 1002.452702 | 501.729989 | D | 814.449137 | 407.728207 | 797.422588 | 399.214932 | 796.438572 | 398.722924 | 4 |
| 11 | 1133.547331 | 567.277304 | 1116.520782 | 558.764029 | 1115.536766 | 558.272021 | L | 699.422194 | 350.214735 | 682.395645 | 341.701461 | | | 3 |
| 12 | 1572.772657 | 786.889967 | 1555.746108 | 778.376692 | 1554.762092 | 777.884684 | Q | 586.338130 | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 13 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 73.0 | 1717.870895 | 0.014233 | LGEVNTYAGDLQK |
| 9.2 | 1717.866867 | 0.018261 | IDAVNAETIREVCTK |
| 5.4 | 1717.878067 | 0.007061 | RATEKEINNMGNTLK |
| 0.8 | 1717.892014 | -0.006886 | LSTAVNIGKMDSPIEK |
| 0.2 | 1717.859634 | 0.025494 | QELLEEYEQVK |
| 0.2 | 1717.871567 | 0.013561 | EAKACSRIVQCLQR |
| 0.0 | 1717.903229 | -0.018101 | ELRSIIETMKDQQK |

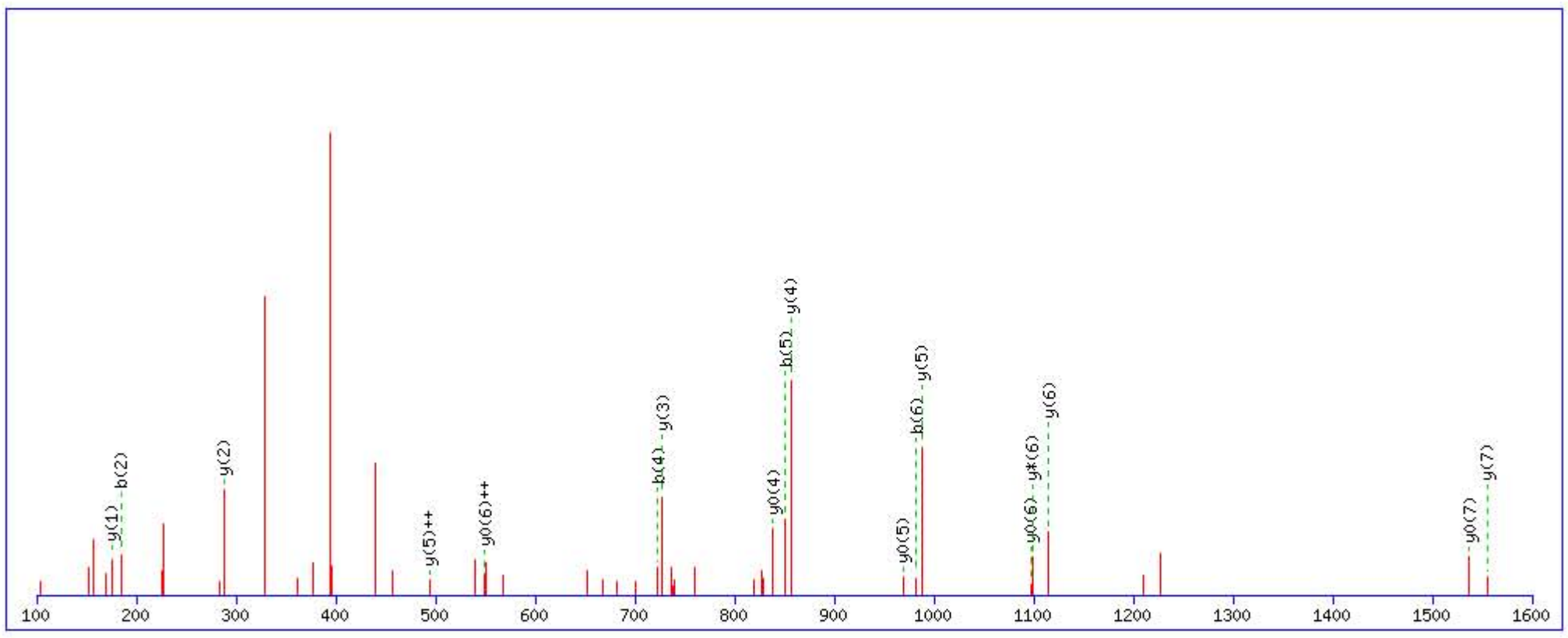
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ALVQQMEQLR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

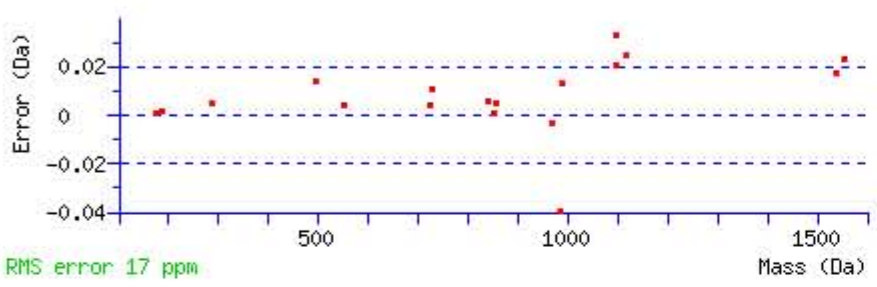
Match to Query 41005: 1836.989442 from(613.337090,3+) rtinseconds(2329) index(68313)
Title: Locus:1.1.1.2086.9 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

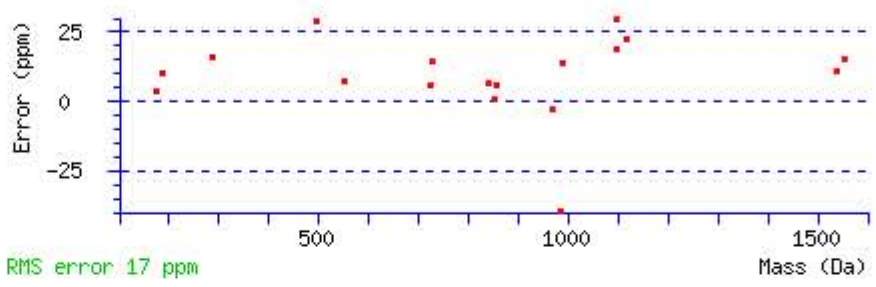
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1836.977615
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.017
**Matches** : 18/84 fragment ions using 34 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 10 |
| 2 | 185.128454 | 93.067865 | | | | | L | 1766.947802 | 883.977539 | 1749.921253 | 875.464265 | 1748.937237 | 874.972256 | 9 |
| 3 | 284.196868 | 142.602072 | | | | | V | 1653.863738 | 827.435507 | 1636.837189 | 818.922232 | 1635.853173 | 818.430224 | 8 |
| 4 | 723.422194 | 362.214735 | 706.395645 | 353.701461 | | | Q | *1554.795324* | 777.901300 | 1537.768775 | 769.388026 | 1536.784759 | 768.896017 | 7 |
| 5 | 851.480772 | 426.244024 | 834.454223 | 417.730750 | | | Q | *1115.569998* | 558.288637 | 1098.543449 | 549.775363 | 1097.559433 | 549.283354 | 6 |
| 6 | 982.521257 | 491.764267 | 965.494708 | 483.250992 | | | M | *987.511420* | 494.259348 | 970.484871 | 485.746073 | 969.500855 | 485.254065 | 5 |
| 7 | 1111.563850 | 556.285563 | 1094.537301 | 547.772289 | 1093.553285 | 547.280281 | E | *856.470935* | 428.739105 | 839.444386 | 420.225831 | 838.460370 | 419.733823 | 4 |
| 8 | 1550.789176 | 775.898226 | 1533.762627 | 767.384952 | 1532.778611 | 766.892944 | Q | *727.428342* | 364.217809 | 710.401793 | 355.704534 | | | 3 |
| 9 | 1663.873240 | 832.440258 | 1646.846691 | 823.926984 | 1645.862675 | 823.434975 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 10 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.5 | 1836.977615 | 0.011827 | ALVQQMEQLR |
| 20.4 | 1836.977615 | 0.011827 | ALVQQMEQLR |
| 17.2 | 1836.999207 | -0.009765 | QQSLQRQLEQLR |
| 4.2 | 1837.004578 | -0.015136 | RHSWRQQIFLR |
| 2.7 | 1836.995377 | -0.005935 | QVLMEHKATTIQK |
| 2.6 | 1836.977615 | 0.011827 | ALVQQMEQLR |
| 2.3 | 1837.005722 | -0.016280 | AIVTEPKTEKPERPSR |
| 0.3 | 1836.981445 | 0.007997 | ERQRTEQLR |

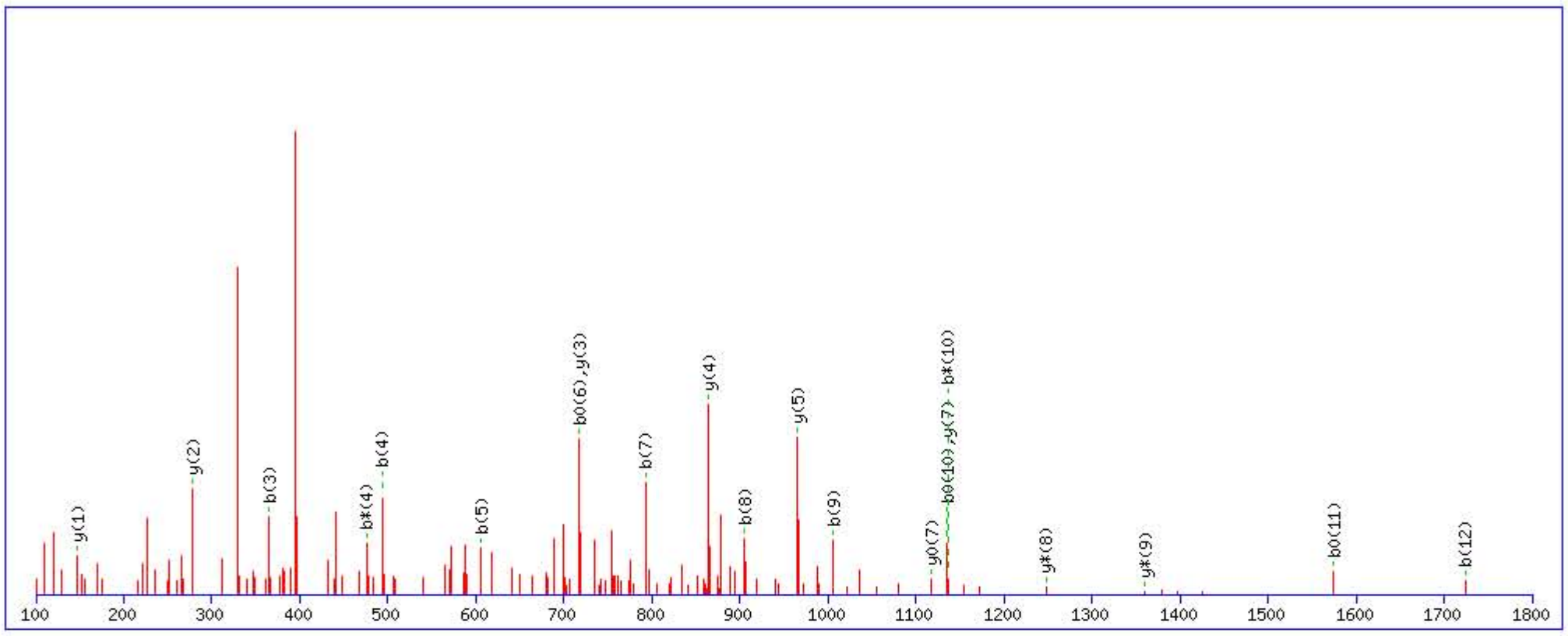
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LNHQLEGLTFQMK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

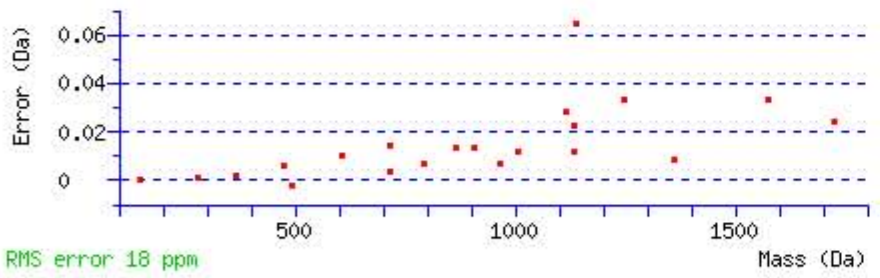
Match to Query 41661: 1868.976042 from(623.999290,3+) rtinseconds(2148) index(6434)
Title: Locus:1.1.1.2025.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

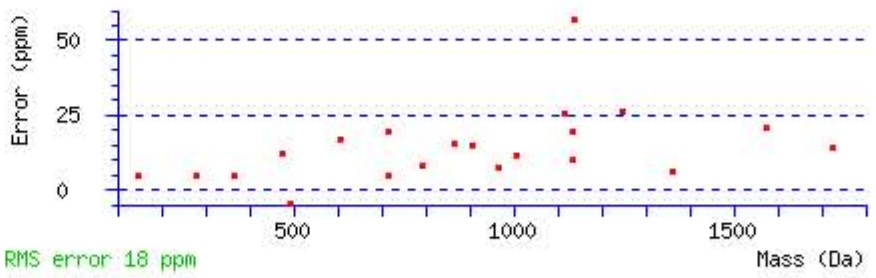
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1868.964081
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q11 : Biotin:Thermo-21345 (Q)
**Ions Score:** 35 **Expect:** 0.0092
**Matches :** 21/124 fragment ions using 40 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 13 |
| 2 | 228.134267 | 114.570771 | 211.107718 | 106.057497 | | | N | 1756.887310 | 878.947293 | 1739.860761 | 870.434019 | 1738.876745 | 869.942011 | 12 |
| 3 | *365.193179* | 183.100227 | 348.166630 | 174.586953 | | | H | 1642.844383 | 821.925830 | 1625.817834 | 813.412555 | 1624.833818 | 812.920547 | 11 |
| 4 | *493.251757* | 247.129516 | 476.225208 | 238.616242 | | | Q | 1505.785471 | 753.396374 | 1488.758922 | 744.883099 | 1487.774906 | 744.391091 | 10 |
| 5 | *606.335821* | 303.671549 | 589.309272 | 295.158274 | | | L | 1377.726893 | 689.367085 | 1360.700344 | 680.853810 | 1359.716328 | 680.361802 | 9 |
| 6 | 735.378414 | 368.192845 | 718.351865 | 359.679571 | 717.367849 | 359.187563 | E | 1264.642829 | 632.825053 | 1247.616280 | 624.311778 | 1246.632264 | 623.819770 | 8 |
| 7 | *792.399878* | 396.703577 | 775.373329 | 388.190303 | 774.389313 | 387.698295 | G | *1135.600236* | 568.303756 | 1118.573687 | 559.790482 | 1117.589671 | 559.298474 | 7 |
| 8 | *905.483942* | 453.245609 | 888.457393 | 444.732335 | 887.473377 | 444.240327 | L | 1078.578772 | 539.793024 | 1061.552223 | 531.279750 | 1060.568207 | 530.787742 | 6 |
| 9 | *1006.531621* | 503.769449 | 989.505072 | 495.256174 | 988.521056 | 494.764166 | T | *965.494708* | 483.250992 | 948.468159 | 474.737718 | 947.484143 | 474.245710 | 5 |
| 10 | 1153.600035 | 577.303656 | 1136.573486 | 568.790381 | 1135.589470 | 568.298373 | F | *864.447029* | 432.727153 | 847.420480 | 424.213878 | | | 4 |
| 11 | 1592.825361 | 796.916319 | 1575.798812 | 788.403044 | 1574.814796 | 787.911036 | Q | *717.378615* | 359.192946 | 700.352066 | 350.679671 | | | 3 |
| 12 | *1723.865846* | 862.436561 | 1706.839297 | 853.923287 | 1705.855281 | 853.431279 | M | *278.153289* | 139.580282 | 261.126740 | 131.067008 | | | 2 |
| 13 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 34.9 | 1868.964081 | 0.011961 | LNHQLEGLTFQMK |

**Mascot:** http://www.matrixscience.com/

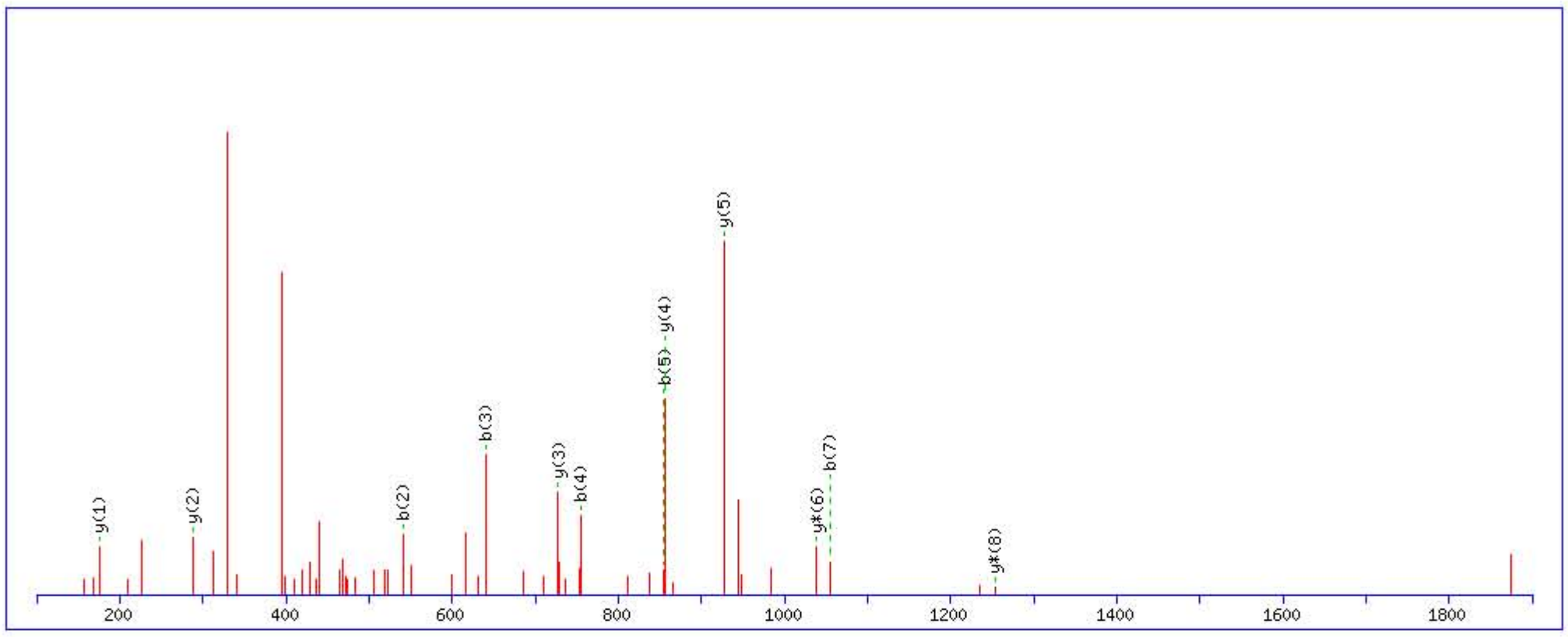
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TQVNTQAEQLR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

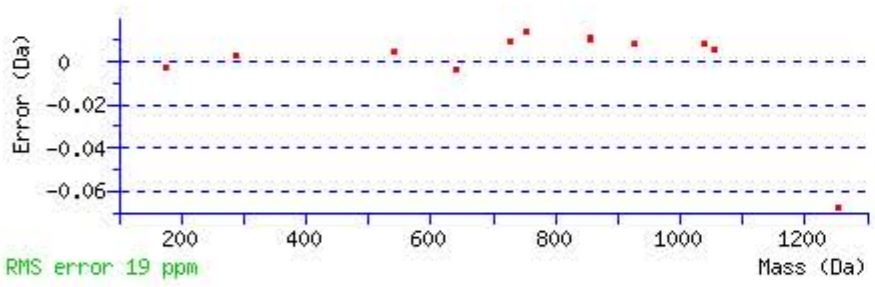
Match to Query 42299: 1908.996252 from(637.339360,3+) rtinseconds(1916) index(5094)
Title: Locus:1.1.1.1944.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

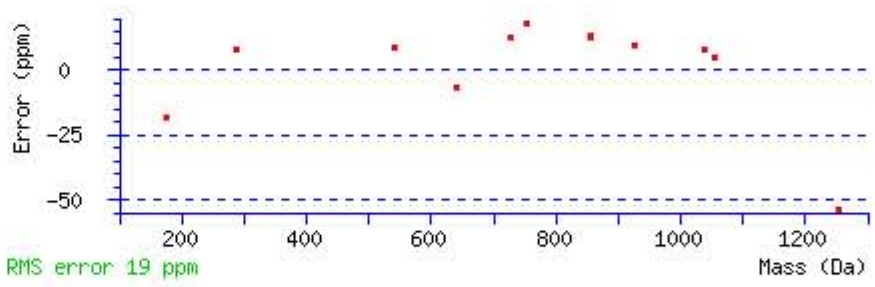
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1908.991364
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.0022
**Matches** : 12/112 fragment ions using 21 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 11 |
| 2 | *541.280281* | 271.143779 | 524.253732 | 262.630504 | 523.269716 | 262.138496 | Q | 1808.950973 | 904.979125 | 1791.924424 | 896.465850 | 1790.940408 | 895.973842 | 10 |
| 3 | *640.348695* | 320.677986 | 623.322146 | 312.164711 | 622.338130 | 311.672703 | V | 1369.725647 | 685.366462 | 1352.699098 | 676.853187 | 1351.715082 | 676.361179 | 9 |
| 4 | *754.391622* | 377.699449 | 737.365073 | 369.186174 | 736.381057 | 368.694166 | N | 1270.657233 | 635.832255 | 1253.630684 | 627.318980 | 1252.646668 | 626.826972 | 8 |
| 5 | *855.439301* | 428.223289 | 838.412752 | 419.710014 | 837.428736 | 419.218006 | T | 1156.614306 | 578.810791 | 1139.587757 | 570.297517 | 1138.603741 | 569.805509 | 7 |
| 6 | 983.497879 | 492.252578 | 966.471330 | 483.739303 | 965.487314 | 483.247295 | Q | 1055.566627 | 528.286952 | 1038.540078 | 519.773677 | 1037.556062 | 519.281669 | 6 |
| 7 | *1054.534993* | 527.771135 | 1037.508444 | 519.257860 | 1036.524428 | 518.765852 | A | *927.508049* | 464.257663 | 910.481500 | 455.744388 | 909.497484 | 455.252380 | 5 |
| 8 | 1183.577586 | 592.292431 | 1166.551037 | 583.779157 | 1165.567021 | 583.287149 | E | *856.470935* | 428.739106 | 839.444386 | 420.225831 | 838.460370 | 419.733823 | 4 |
| 9 | 1622.802912 | 811.905094 | 1605.776363 | 803.391820 | 1604.792347 | 802.899812 | Q | *727.428342* | 364.217809 | 710.401793 | 355.704535 | | | 3 |
| 10 | 1735.886976 | 868.447126 | 1718.860427 | 859.933852 | 1717.876411 | 859.441844 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 37.9 | 1908.991364 | 0.004888 | TQVNTQAEQLR |
| 16.9 | 1908.991364 | 0.004888 | TQVNTQAEQLR |
| 9.1 | 1908.991364 | 0.004888 | TQVNTQAEQLR |
| 9.0 | 1908.974045 | 0.022207 | SAQWAINRVAMEIQHR |
| 5.4 | 1909.015610 | -0.019358 | SSIALTAPDAAADPKEKPK |
| 1.8 | 1908.980591 | 0.015661 | QAHHTDKFSSQELILR |
| 1.2 | 1909.013123 | -0.016871 | EQLPIFKAQNPDAK |
| 0.4 | 1909.015610 | -0.019358 | AEQEIAALVEQLTPIER |
| 0.3 | 1908.995148 | 0.001104 | RALQEEERAAAQAR |
| 0.3 | 1908.983932 | 0.012320 | AEEQAQRQEQLLR |

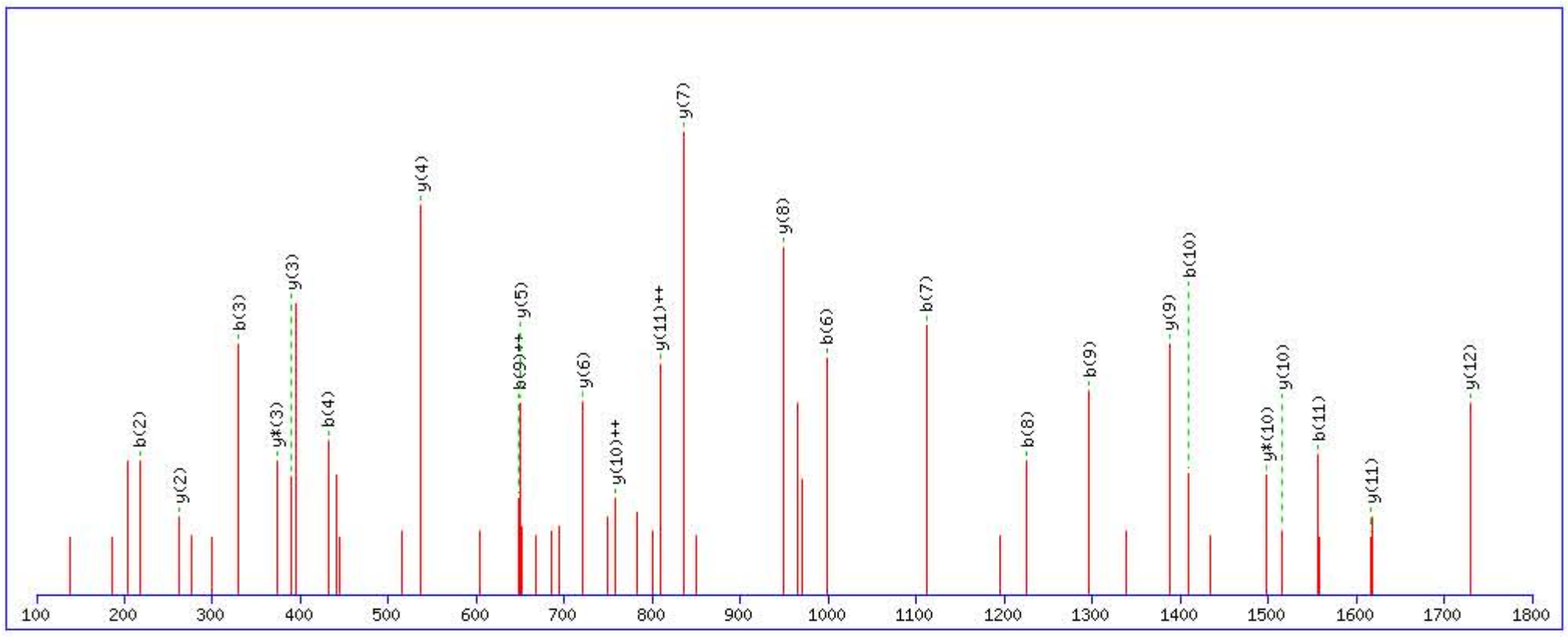
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SELTQQLNALFQDK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

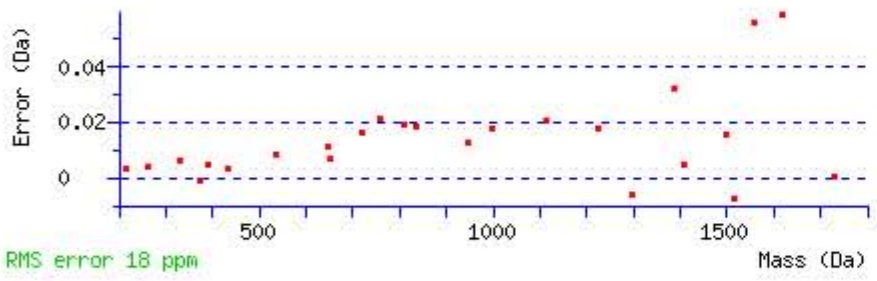
Match to Query 43006: 1945.025468 from(973.520010,2+) rtinseconds(2886) index(72055)
Title: Locus:1.1.1.2278.20 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

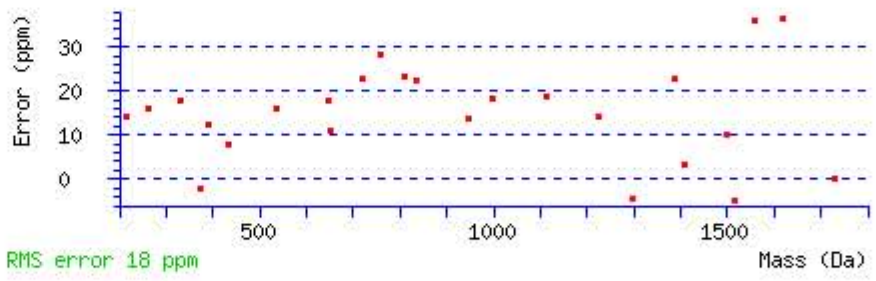
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1944.997879
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 71 **Expect:** 5.6e-007
**Matches** : 25/146 fragment ions using 45 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 14 |
| 2 | 217.081897 | 109.044586 | | | 199.071332 | 100.039304 | E | 1858.973148 | 929.990212 | 1841.946599 | 921.476938 | 1840.962583 | 920.984930 | 13 |
| 3 | 330.165961 | 165.586618 | | | 312.155396 | 156.581336 | L | *1729.930555* | 865.468916 | 1712.904006 | 856.955641 | 1711.919990 | 856.463633 | 12 |
| 4 | 431.213640 | 216.110458 | | | 413.203075 | 207.105176 | T | *1616.846491* | 808.926884 | 1599.819942 | 800.413609 | 1598.835926 | 799.921601 | 11 |
| 5 | 559.272218 | 280.139747 | 542.245669 | 271.626473 | 541.261653 | 271.134465 | Q | *1515.798812* | 758.403044 | 1498.772263 | 749.889770 | 1497.788247 | 749.397762 | 10 |
| 6 | 998.497544 | 499.752410 | 981.470995 | 491.239136 | 980.486979 | 490.747128 | Q | *1387.740234* | 694.373755 | 1370.713685 | 685.860481 | 1369.729669 | 685.368473 | 9 |
| 7 | 1111.581608 | 556.294442 | 1094.555059 | 547.781168 | 1093.571043 | 547.289159 | L | *948.514908* | 474.761092 | 931.488359 | 466.247818 | 930.504343 | 465.755810 | 8 |
| 8 | 1225.624535 | 613.315905 | 1208.597986 | 604.802631 | 1207.613970 | 604.310623 | N | *835.430844* | 418.219060 | 818.404295 | 409.705786 | 817.420279 | 409.213778 | 7 |
| 9 | 1296.661649 | 648.834462 | 1279.635100 | 640.321188 | 1278.651084 | 639.829180 | A | *721.387917* | 361.197597 | 704.361368 | 352.684322 | 703.377352 | 352.192314 | 6 |
| 10 | 1409.745713 | 705.376494 | 1392.719164 | 696.863220 | 1391.735148 | 696.371212 | L | *650.350803* | 325.679040 | 633.324254 | 317.165765 | 632.340238 | 316.673757 | 5 |
| 11 | 1556.814127 | 778.910701 | 1539.787578 | 770.397427 | 1538.803562 | 769.905419 | F | *537.266739* | 269.137008 | 520.240190 | 260.623733 | 519.256174 | 260.131725 | 4 |
| 12 | 1684.872705 | 842.939991 | 1667.846156 | 834.426716 | 1666.862140 | 833.934708 | Q | *390.198325* | 195.602801 | 373.171776 | 187.089526 | 372.187760 | 186.597518 | 3 |
| 13 | 1799.899648 | 900.453462 | 1782.873099 | 891.940188 | 1781.889083 | 891.448180 | D | *262.139747* | 131.573512 | 245.113198 | 123.060237 | 244.129182 | 122.568229 | 2 |
| 14 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 70.6 | 1944.997879 | 0.027589 | SELTQQLNALFQDK |
| 59.6 | 1944.997879 | 0.027589 | SELTQQLNALFQDK |
| 9.1 | 1944.997879 | 0.027589 | SELTQQLNALFQDK |
| 3.6 | 1945.027740 | -0.002272 | GGFGSMLRALGAQIEK |
| 1.0 | 1945.009109 | 0.016359 | ESQTALVANQRSLFA |
| 0.8 | 1945.024384 | 0.001084 | QASLWVQGDIFRSK |
| 0.5 | 1945.020325 | 0.005143 | SIQHLALGKNFNNMKSK |

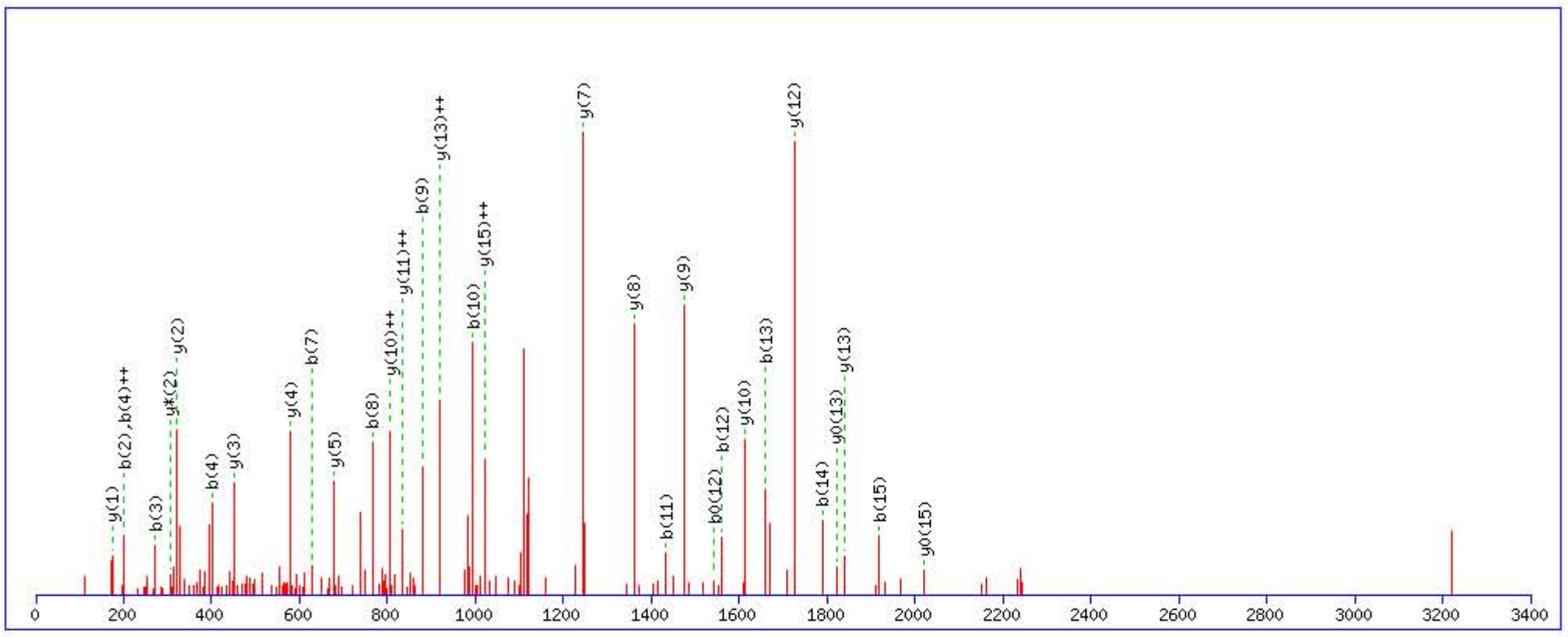
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SLAELGGHLDQQVEEFR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

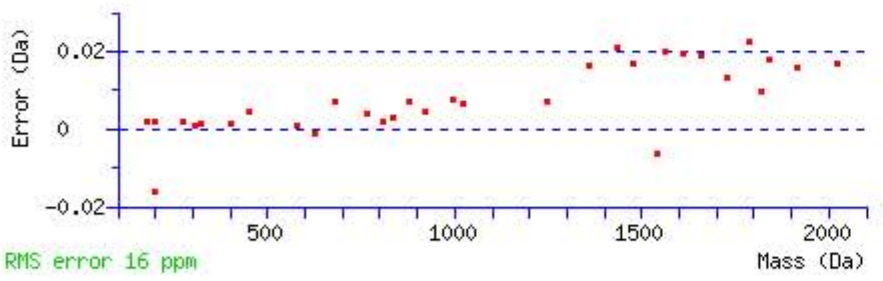
Match to Query 49262: 2238.132408 from(1120.073480,2+) rtinseconds(2236) index(6994)
Title: Locus:1.1.1.2055.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

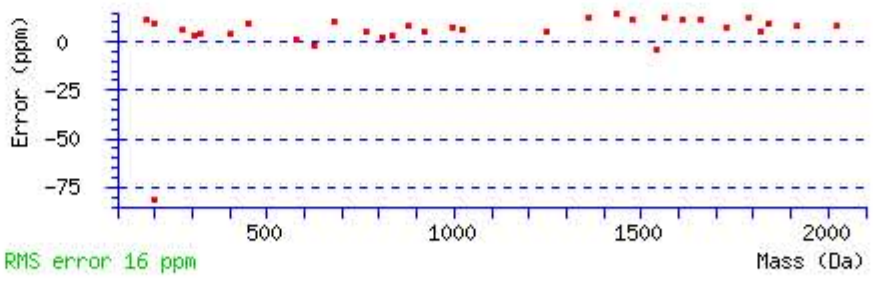
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2238.110291
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 98 **Expect:** 8e-009
**Matches :** 32/168 fragment ions using 42 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 17 |
| 2 | *201.123368* | 101.065322 | | | 183.112803 | 92.060039 | L | 2152.085552 | 1076.546414 | 2135.059003 | 1068.033139 | 2134.074987 | 1067.541131 | 16 |
| 3 | *272.160482* | 136.583879 | | | 254.149917 | 127.578596 | A | 2039.001488 | 1020.004382 | 2021.974939 | 1011.491108 | 2020.990923 | 1010.999100 | 15 |
| 4 | *401.203075* | 201.105175 | | | 383.192510 | 192.099893 | E | 1967.964374 | 984.485825 | 1950.937825 | 975.972551 | 1949.953809 | 975.480543 | 14 |
| 5 | 514.287139 | 257.647208 | | | 496.276574 | 248.641925 | L | *1838.921781* | 919.964529 | 1821.895232 | 911.451254 | 1820.911216 | 910.959246 | 13 |
| 6 | 571.308603 | 286.157940 | | | 553.298038 | 277.152657 | G | *1725.837717* | 863.422497 | 1708.811168 | 854.909222 | 1707.827152 | 854.417214 | 12 |
| 7 | *628.330067* | 314.668672 | | | 610.319502 | 305.663389 | G | 1668.816253 | 834.911765 | 1651.789704 | 826.398490 | 1650.805688 | 825.906482 | 11 |
| 8 | *765.388979* | 383.198128 | | | 747.378414 | 374.192845 | H | *1611.794789* | 806.401033 | 1594.768240 | 797.887758 | 1593.784224 | 797.395750 | 10 |
| 9 | *878.473043* | 439.740160 | | | 860.462478 | 430.734877 | L | *1474.735877* | 737.871577 | 1457.709328 | 729.358302 | 1456.725312 | 728.866294 | 9 |
| 10 | *993.499986* | 497.253631 | | | 975.489421 | 488.248349 | D | *1361.651813* | 681.329545 | 1344.625264 | 672.816270 | 1343.641248 | 672.324262 | 8 |
| 11 | *1432.725312* | 716.866294 | 1415.698763 | 708.353020 | 1414.714747 | 707.861012 | Q | *1246.624870* | 623.816073 | 1229.598321 | 615.302799 | 1228.614305 | 614.810791 | 7 |
| 12 | *1560.783890* | 780.895583 | 1543.757341 | 772.382309 | 1542.773325 | 771.890301 | Q | 807.399544 | 404.203410 | 790.372995 | 395.690136 | 789.388979 | 395.198128 | 6 |
| 13 | *1659.852304* | 830.429790 | 1642.825755 | 821.916516 | 1641.841739 | 821.424508 | V | *679.340966* | 340.174121 | 662.314417 | 331.660846 | 661.330401 | 331.168838 | 5 |
| 14 | *1788.894897* | 894.951087 | 1771.868348 | 886.437812 | 1770.884332 | 885.945804 | E | *580.272552* | 290.639914 | 563.246003 | 282.126639 | 562.261987 | 281.634631 | 4 |
| 15 | *1917.937490* | 959.472383 | 1900.910941 | 950.959109 | 1899.926925 | 950.467101 | E | *451.229959* | 226.118617 | 434.203410 | 217.605343 | 433.219394 | 217.113335 | 3 |
| 16 | 2065.005904 | 1033.006590 | 2047.979355 | 1024.493316 | 2046.995339 | 1024.001307 | F | *322.187366* | 161.597321 | 305.160817 | 153.084046 | | | 2 |
| 17 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 98.3 | 2238.110291 | 0.022117 | SLAELGGHLDQQVEEFR |
| 89.6 | 2238.110291 | 0.022117 | SLAELGGHLDQQVEEFR |

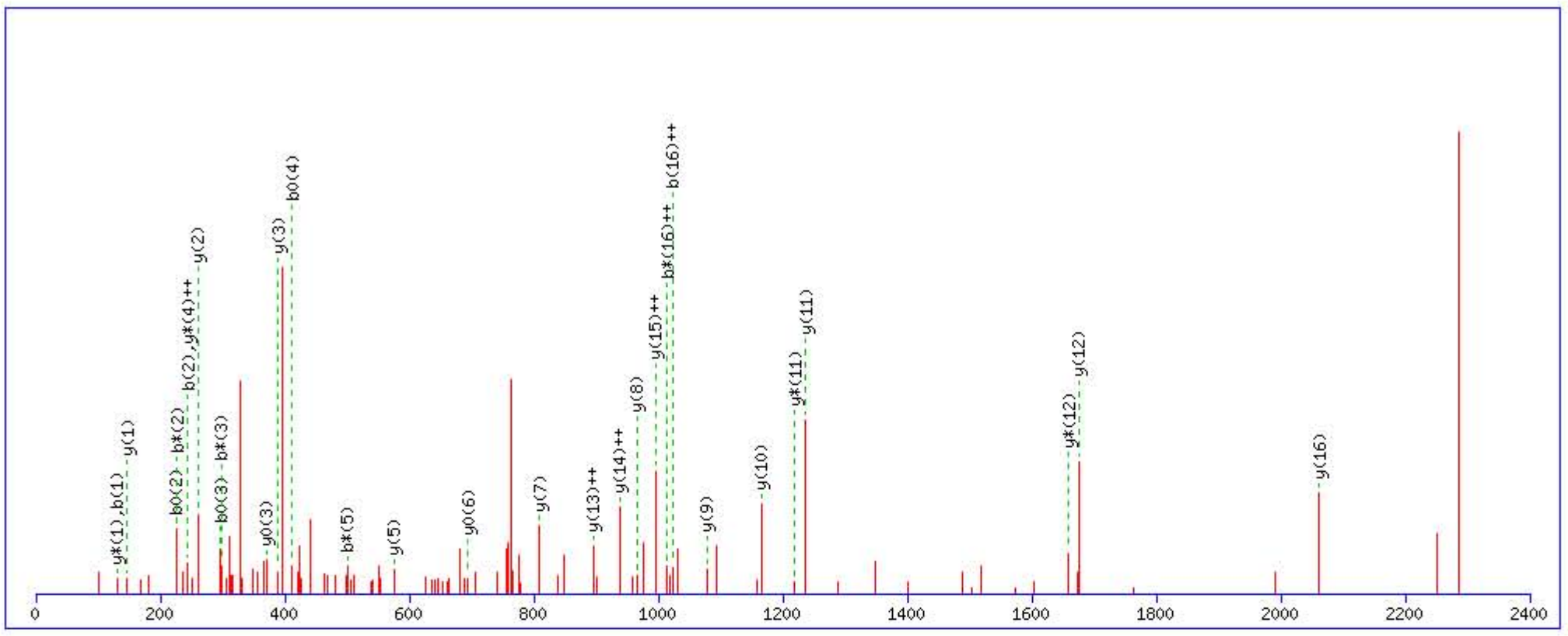
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ENADSLQASLRPHADELK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

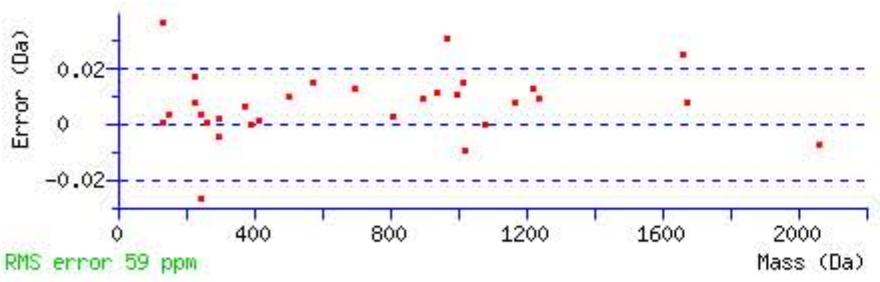
Match to Query 50604: 2304.169152 from(769.063660,3+) rtinseconds(1885) index(65570)
Title: Locus:1.1.1.1931.25 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

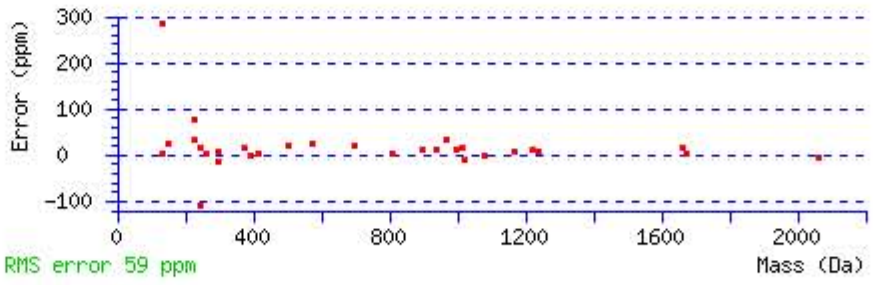
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2304.153183
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.0045
**Matches :** 30/198 fragment ions using 90 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 18 |
| 2 | 244.092796 | 122.550036 | 227.066247 | 114.036762 | 226.082231 | 113.544754 | N | 2176.117913 | 1088.562594 | 2159.091364 | 1080.049320 | 2158.107348 | 1079.557312 | 17 |
| 3 | 315.129910 | 158.068593 | 298.103361 | 149.555319 | 297.119345 | 149.063311 | A | *2062.074986* | 1031.541131 | 2045.048437 | 1023.027856 | 2044.064421 | 1022.535848 | 16 |
| 4 | 430.156853 | 215.582065 | 413.130304 | 207.068790 | 412.146288 | 206.576782 | D | 1991.037872 | 996.022574 | 1974.011323 | 987.509300 | 1973.027307 | 987.017292 | 15 |
| 5 | 517.188881 | 259.098079 | 500.162332 | 250.584804 | 499.178316 | 250.092796 | S | 1876.010929 | 938.509103 | 1858.984380 | 929.995828 | 1858.000364 | 929.503820 | 14 |
| 6 | 630.272945 | 315.640111 | 613.246396 | 307.126836 | 612.262380 | 306.634828 | L | 1788.978901 | 894.993089 | 1771.952352 | 886.479814 | 1770.968336 | 885.987806 | 13 |
| 7 | 1069.498271 | 535.252774 | 1052.471722 | 526.739499 | 1051.487706 | 526.247491 | Q | *1675.894837* | 838.451057 | 1658.868288 | 829.937782 | 1657.884272 | 829.445774 | 12 |
| 8 | 1140.535385 | 570.771331 | 1123.508836 | 562.258056 | 1122.524820 | 561.766048 | A | *1236.669511* | 618.838394 | 1219.642962 | 610.325119 | 1218.658946 | 609.833111 | 11 |
| 9 | 1227.567413 | 614.287345 | 1210.540864 | 605.774070 | 1209.556848 | 605.282062 | S | *1165.632397* | 583.319837 | 1148.605848 | 574.806562 | 1147.621832 | 574.314554 | 10 |
| 10 | 1340.651477 | 670.829377 | 1323.624928 | 662.316102 | 1322.640912 | 661.824094 | L | *1078.600369* | 539.803823 | 1061.573820 | 531.290548 | 1060.589804 | 530.798540 | 9 |
| 11 | 1496.752588 | 748.879932 | 1479.726039 | 740.366658 | 1478.742023 | 739.874650 | R | *965.516305* | 483.261791 | 948.489756 | 474.748516 | 947.505740 | 474.256508 | 8 |
| 12 | 1593.805352 | 797.406314 | 1576.778803 | 788.893040 | 1575.794787 | 788.401032 | P | *809.415194* | 405.211235 | 792.388645 | 396.697961 | 791.404629 | 396.205953 | 7 |
| 13 | 1730.864264 | 865.935770 | 1713.837715 | 857.422496 | 1712.853699 | 856.930488 | H | 712.362430 | 356.684853 | 695.335881 | 348.171579 | 694.351865 | 347.679571 | 6 |
| 14 | 1801.901378 | 901.454327 | 1784.874829 | 892.941053 | 1783.890813 | 892.449045 | A | *575.303518* | 288.155397 | 558.276969 | 279.642123 | 557.292953 | 279.150115 | 5 |
| 15 | 1916.928321 | 958.967799 | 1899.901772 | 950.454524 | 1898.917756 | 949.962516 | D | 504.266404 | 252.636840 | 487.239855 | 244.123566 | 486.255839 | 243.631558 | 4 |
| 16 | 2045.970914 | 1023.489095 | 2028.944365 | 1014.975821 | 2027.960349 | 1014.483813 | E | *389.239461* | 195.123369 | 372.212912 | 186.610094 | 371.228896 | 186.118086 | 3 |
| 17 | 2159.054978 | 1080.031127 | 2142.028429 | 1071.517852 | 2141.044413 | 1071.025844 | L | *260.196868* | 130.602072 | 243.170319 | 122.088798 | | | 2 |
| 18 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.6 | 2304.153183 | 0.015969 | ENADSLQASLRPHADELK |
| 6.5 | 2304.149384 | 0.019768 | LNCMETFEVKVDSPVKPAPK |

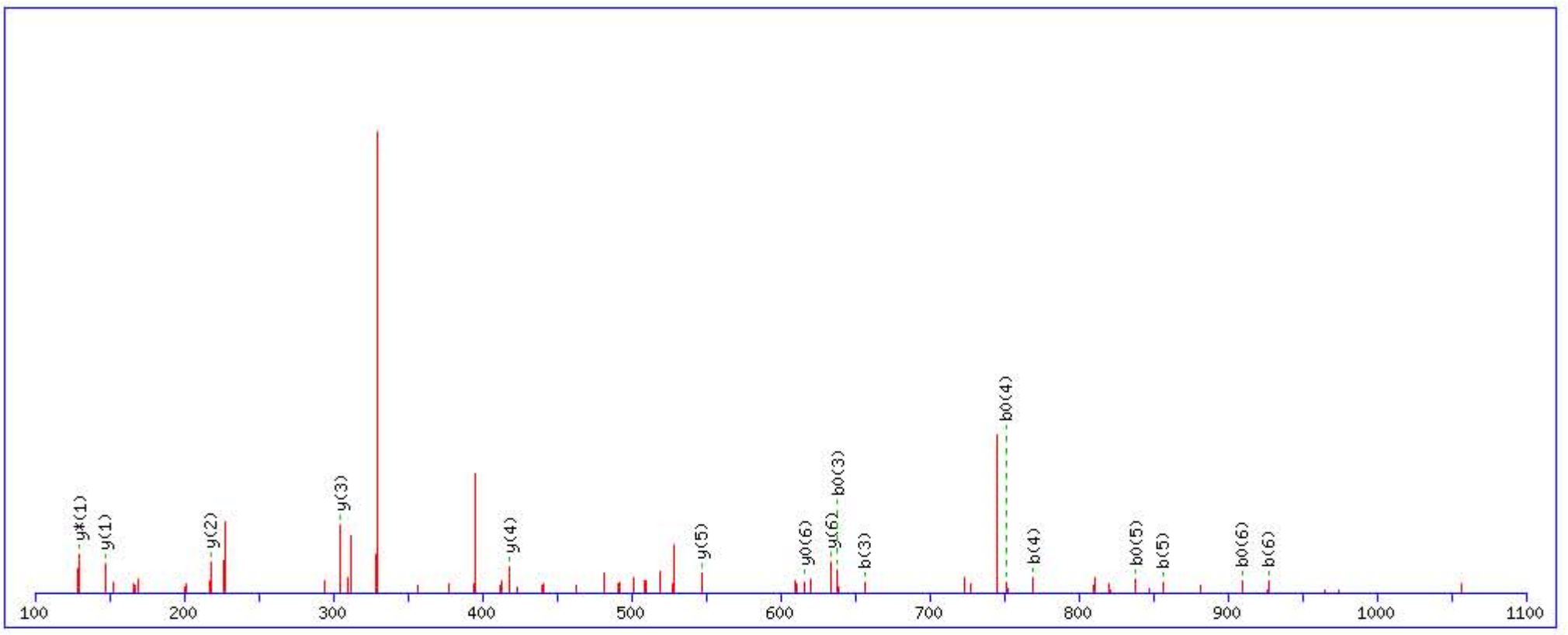
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QSELSAK**
Found in **APOC1_HUMAN**, Apolipoprotein C-I OS=Homo sapiens GN=APOC1 PE=1 SV=1

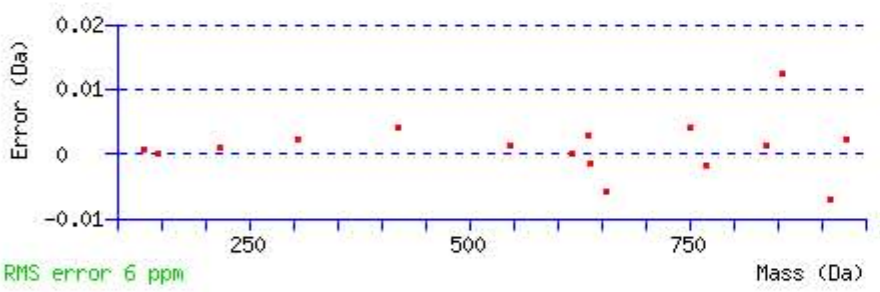
Match to Query 15710: 1072.556508 from(537.285530,2+) rtinseconds(1422) index(62970)
Title: Locus:1.1.1.1770.13 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

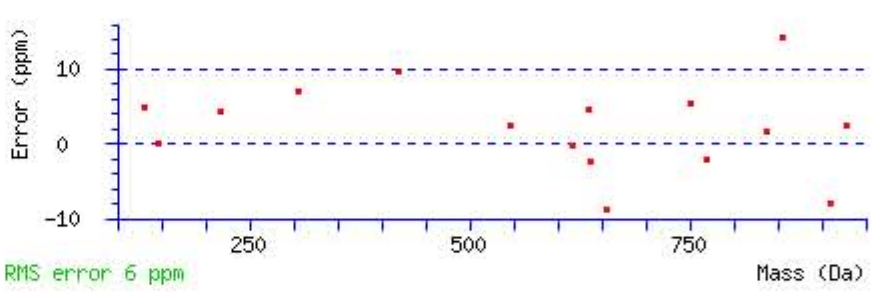
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1072.558655
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 26 **Expect:** 0.061
**Matches** : 16/66 fragment ions using 43 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 7 |
| 2 | 527.264630 | 264.135953 | 510.238081 | 255.622679 | 509.254065 | 255.130671 | S | *634.340631* | 317.673954 | 617.314082 | 309.160679 | 616.330066 | 308.668671 | 6 |
| 3 | **656.307223** | 328.657250 | 639.280674 | 320.143975 | 638.296658 | 319.651967 | E | *547.308603* | 274.157940 | 530.282054 | 265.644665 | 529.298038 | 265.152657 | 5 |
| 4 | **769.391287** | 385.199282 | 752.364738 | 376.686007 | 751.380722 | 376.193999 | L | *418.266010* | 209.636643 | 401.239461 | 201.123368 | 400.255445 | 200.631360 | 4 |
| 5 | **856.423315** | 428.715296 | 839.396766 | 420.202021 | 838.412750 | 419.710013 | S | *305.181946* | 153.094611 | 288.155397 | 144.581336 | 287.171381 | 144.089328 | 3 |
| 6 | **927.460429** | 464.233853 | 910.433880 | 455.720578 | 909.449864 | 455.228570 | A | *218.149918* | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 7 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.8 | 1072.558655 | -0.002147 | QSELSAK |
| 15.3 | 1072.544739 | 0.011769 | RPGQAAGMSAK |
| 10.6 | 1072.551239 | 0.005269 | EAERELQAK |
| 9.6 | 1072.562500 | -0.005992 | HSSTSSRIAK |
| 9.2 | 1072.551239 | 0.005269 | ERQEALEAK |
| 7.8 | 1072.558670 | -0.002162 | VTQESAK |
| 7.7 | 1072.551254 | 0.005254 | KEAPRDETK |
| 5.8 | 1072.558670 | -0.002162 | QSEGLTK |
| 5.5 | 1072.558655 | -0.002147 | QSLSAEK |
| 4.4 | 1072.562500 | -0.005992 | KQQQQQSAK |

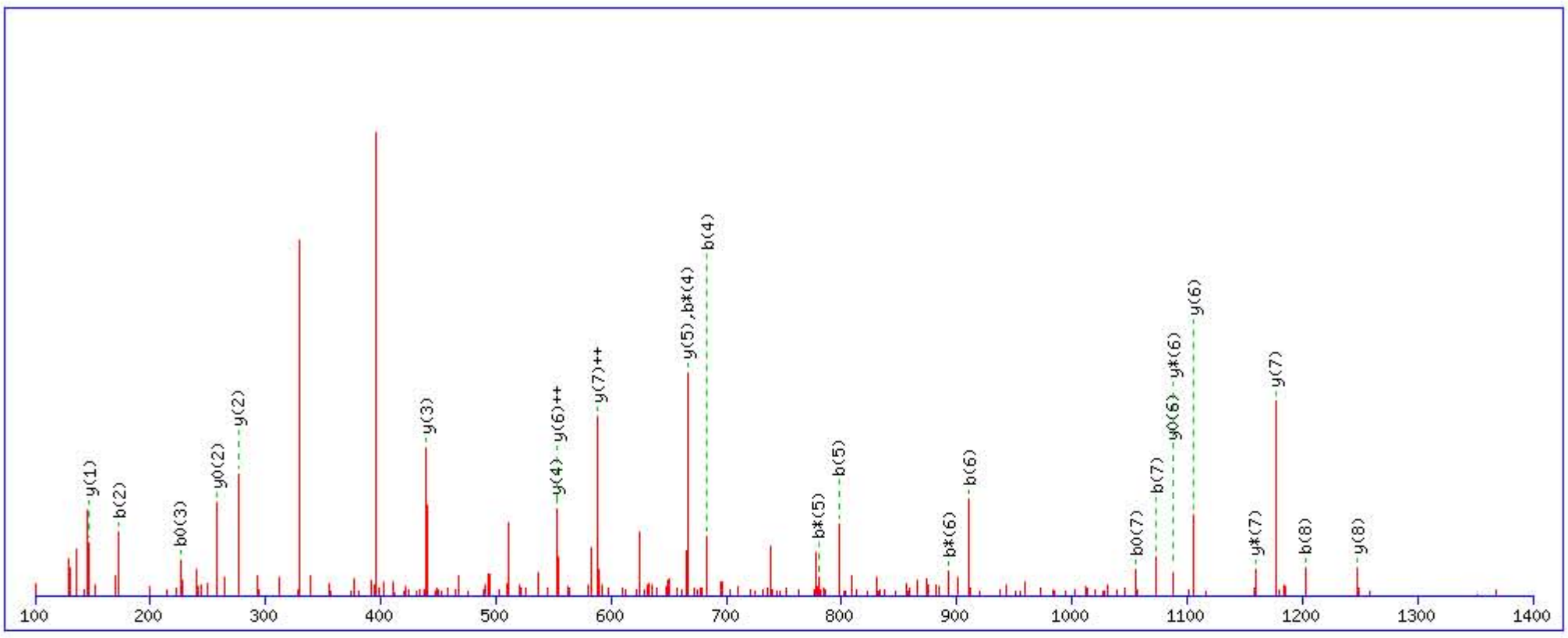
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TAAQNLYEK**
Found in **APOC2_HUMAN**, Apolipoprotein C-II OS=Homo sapiens GN=APOC2 PE=1 SV=1

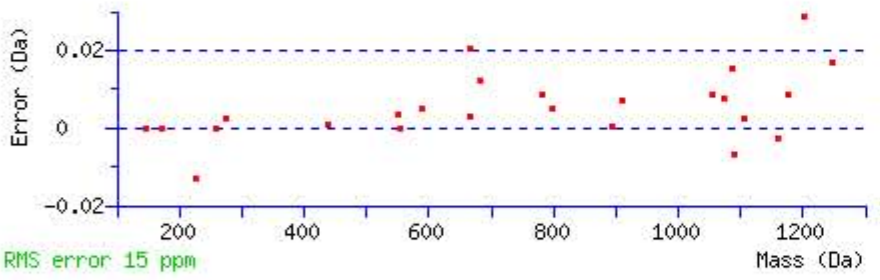
Match to Query 24302: 1347.691988 from(674.853270,2+) rtinseconds(1636) index(47893)
Title: Locus:1.1.1.1807.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

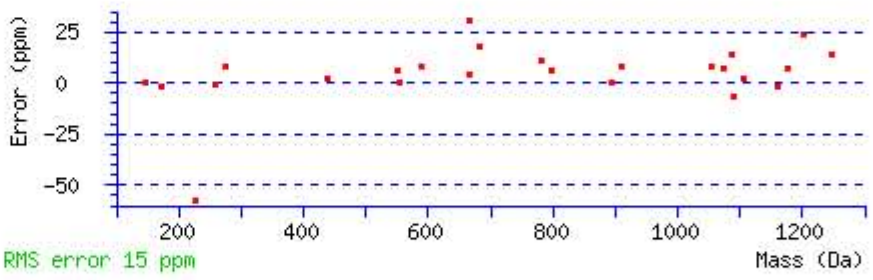
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1347.685638
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 43 **Expect:** 0.0008
**Matches :** 25/88 fragment ions using 48 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 9 |
| 2 | 173.092069 | 87.049672 | | | 155.081504 | 78.044390 | A | 1247.645271 | 624.326273 | 1230.618722 | 615.812999 | 1229.634706 | 615.320991 | 8 |
| 3 | 244.129183 | 122.568229 | | | 226.118618 | 113.562947 | A | 1176.608157 | 588.807716 | 1159.581608 | 580.294442 | 1158.597592 | 579.802434 | 7 |
| 4 | 683.354509 | 342.180893 | 666.327960 | 333.667618 | 665.343944 | 333.175610 | Q | 1105.571043 | 553.289159 | 1088.544494 | 544.775885 | 1087.560478 | 544.283877 | 6 |
| 5 | 797.397436 | 399.202356 | 780.370887 | 390.689081 | 779.386871 | 390.197073 | N | 666.345717 | 333.676496 | 649.319168 | 325.163222 | 648.335152 | 324.671214 | 5 |
| 6 | 910.481500 | 455.744388 | 893.454951 | 447.231113 | 892.470935 | 446.739105 | L | 552.302790 | 276.655033 | 535.276241 | 268.141758 | 534.292225 | 267.649750 | 4 |
| 7 | 1073.544829 | 537.276052 | 1056.518280 | 528.762778 | 1055.534264 | 528.270770 | Y | 439.218726 | 220.113001 | 422.192177 | 211.599726 | 421.208161 | 211.107718 | 3 |
| 8 | 1202.587422 | 601.797349 | 1185.560873 | 593.284074 | 1184.576857 | 592.792066 | E | 276.155397 | 138.581336 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 9 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 42.7 | 1347.685638 | 0.006350 | TAAQNLYEK |
| 9.1 | 1347.682297 | 0.009691 | TAYFSLDTRFK |
| 6.0 | 1347.682480 | 0.009508 | QSRMKMEK |
| 5.6 | 1347.681610 | 0.010378 | RSQISMEQLEK |
| 2.8 | 1347.688156 | 0.003832 | TTSEAALSVVNEK |
| 1.9 | 1347.689011 | 0.002977 | DKCMLPKSLEK |
| 1.5 | 1347.688156 | 0.003832 | LLSQDSVAASTEK |
| 0.7 | 1347.681625 | 0.010363 | GLERNLAVMSDK |
| 0.3 | 1347.681625 | 0.010363 | QMGDQLIKASNK |

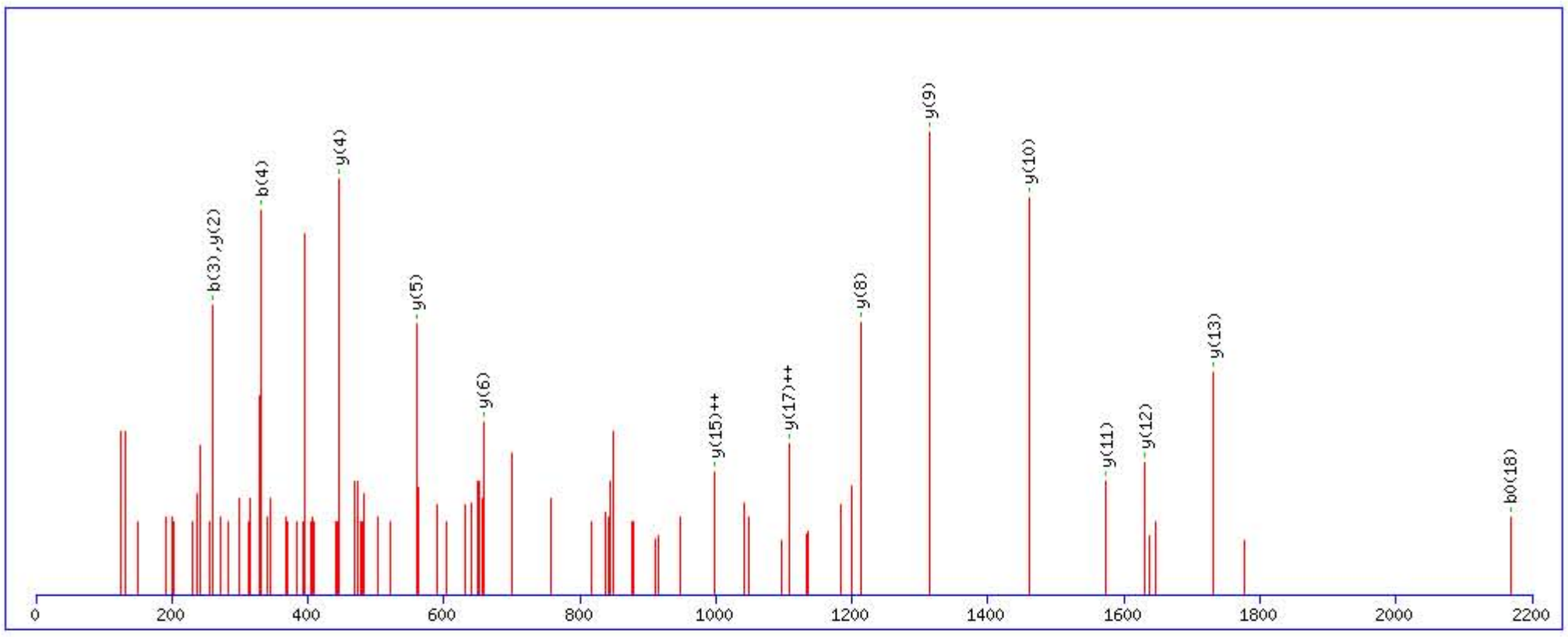
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **STAAMSTYTGIFTDQVLSVLK**
Found in **APOC2_HUMAN**, Apolipoprotein C-II OS=Homo sapiens GN=APOC2 PE=1 SV=1

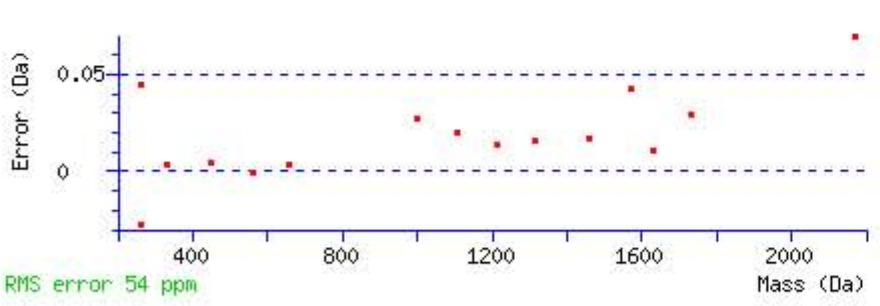
Match to Query 54920: 2543.332572 from(848.784800,3+) rtinseconds(3234) index(73923)
Title: Locus:1.1.1.2396.17 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

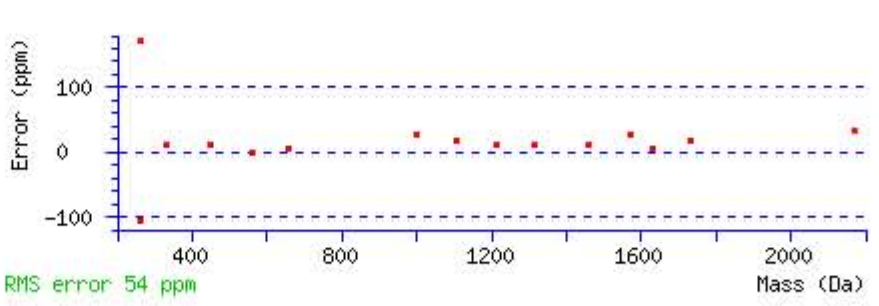
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2543.301544
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q15 : Biotin:Thermo-21345 (Q)
**Ions Score:** 81 **Expect:** 2.1e-007
**Matches :** 15/206 fragment ions using 17 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 21 |
| 2 | 189.086983 | 95.047129 | | | 171.076418 | 86.041847 | T | 2457.276785 | 1229.142030 | 2440.250236 | 1220.628756 | 2439.266220 | 1220.136748 | 20 |
| 3 | 260.124097 | 130.565686 | | | 242.113532 | 121.560404 | A | 2356.229106 | 1178.618191 | 2339.202557 | 1170.104916 | 2338.218541 | 1169.612908 | 19 |
| 4 | 331.161211 | 166.084243 | | | 313.150646 | 157.078961 | A | 2285.191992 | 1143.099634 | 2268.165443 | 1134.586359 | 2267.181427 | 1134.094351 | 18 |
| 5 | 462.201696 | 231.604486 | | | 444.191131 | 222.599203 | M | 2214.154878 | 1107.581077 | 2197.128329 | 1099.067802 | 2196.144313 | 1098.575794 | 17 |
| 6 | 549.233724 | 275.120500 | | | 531.223159 | 266.115217 | S | 2083.114393 | 1042.060834 | 2066.087844 | 1033.547560 | 2065.103828 | 1033.055552 | 16 |
| 7 | 650.281403 | 325.644340 | | | 632.270838 | 316.639057 | T | 1996.082365 | 998.544821 | 1979.055816 | 990.031546 | 1978.071800 | 989.539538 | 15 |
| 8 | 813.344732 | 407.176004 | | | 795.334167 | 398.170722 | Y | 1895.034686 | 948.020981 | 1878.008137 | 939.507707 | 1877.024121 | 939.015699 | 14 |
| 9 | 914.392411 | 457.699844 | | | 896.381846 | 448.694561 | T | *1731.971357* | 866.489317 | 1714.944808 | 857.976042 | 1713.960792 | 857.484034 | 13 |
| 10 | 971.413875 | 486.210576 | | | 953.403310 | 477.205293 | G | *1630.923678* | 815.965477 | 1613.897129 | 807.452203 | 1612.913113 | 806.960195 | 12 |
| 11 | 1084.497939 | 542.752608 | | | 1066.487374 | 533.747325 | I | *1573.902214* | 787.454745 | 1556.875665 | 778.941471 | 1555.891649 | 778.449463 | 11 |
| 12 | 1231.566353 | 616.286815 | | | 1213.555788 | 607.281532 | F | *1460.818150* | 730.912713 | 1443.791601 | 722.399439 | 1442.807585 | 721.907431 | 10 |
| 13 | 1332.614032 | 666.810654 | | | 1314.603467 | 657.805372 | T | *1313.749736* | 657.378506 | 1296.723187 | 648.865232 | 1295.739171 | 648.373224 | 9 |
| 14 | 1447.640975 | 724.324126 | | | 1429.630410 | 715.318843 | D | *1212.702057* | 606.854667 | 1195.675508 | 598.341392 | 1194.691492 | 597.849384 | 8 |
| 15 | 1886.866301 | 943.936789 | 1869.839752 | 935.423514 | 1868.855736 | 934.931506 | Q | 1097.675114 | 549.341195 | 1080.648565 | 540.827921 | 1079.664549 | 540.335913 | 7 |
| 16 | 1985.934715 | 993.470996 | 1968.908166 | 984.957721 | 1967.924150 | 984.465713 | V | *658.449788* | 329.728532 | 641.423239 | 321.215258 | 640.439223 | 320.723250 | 6 |
| 17 | 2099.018779 | 1050.013027 | 2081.992230 | 1041.499753 | 2081.008214 | 1041.007745 | L | *559.381374* | 280.194325 | 542.354825 | 271.681051 | 541.370809 | 271.189043 | 5 |
| 18 | 2186.050807 | 1093.529041 | 2169.024258 | 1085.015767 | 2168.040242 | 1084.523759 | S | *446.297310* | 223.652293 | 429.270761 | 215.139019 | 428.286745 | 214.647011 | 4 |
| 19 | 2285.119221 | 1143.063248 | 2268.092672 | 1134.549974 | 2267.108656 | 1134.057966 | V | 359.265282 | 180.136279 | 342.238733 | 171.623004 | | | 3 |
| 20 | 2398.203285 | 1199.605280 | 2381.176736 | 1191.092006 | 2380.192720 | 1190.599998 | L | *260.196868* | 130.602072 | 243.170319 | 122.088798 | | | 2 |
| 21 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 80.9 | 2543.301544 | 0.031028 | STAAMSTYTGIFTDQVLSVLK |

**Mascot:** http://www.matrixscience.com/

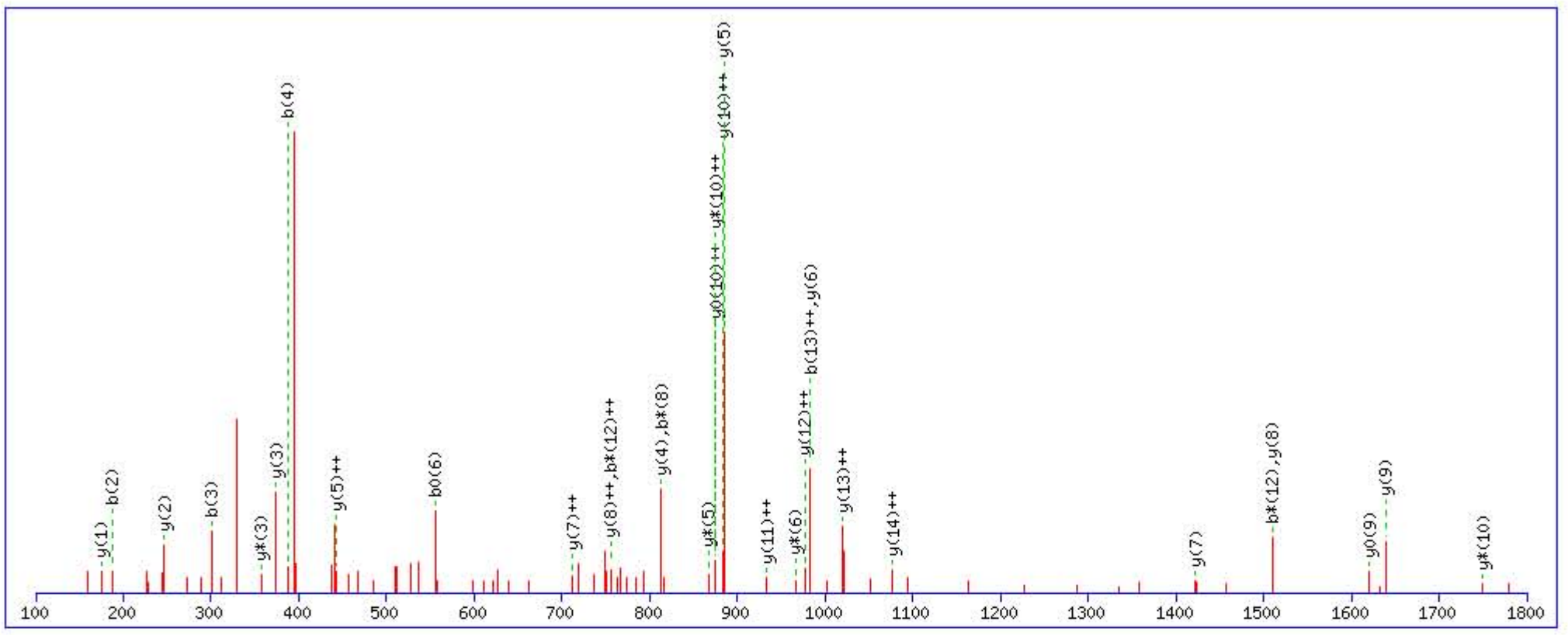
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DALSSVQESQVAQQAR**
Found in **APOC3_HUMAN**, Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1

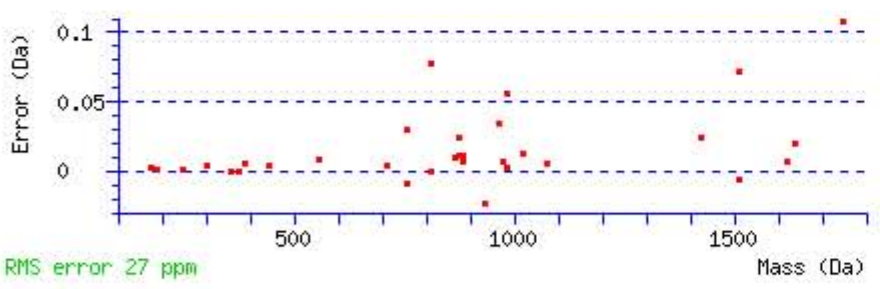
Match to Query 32682: 2338.202772 from(780.408200,3+) rtinseconds(2199) index(51685)
Title: Locus:1.1.1.2003.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

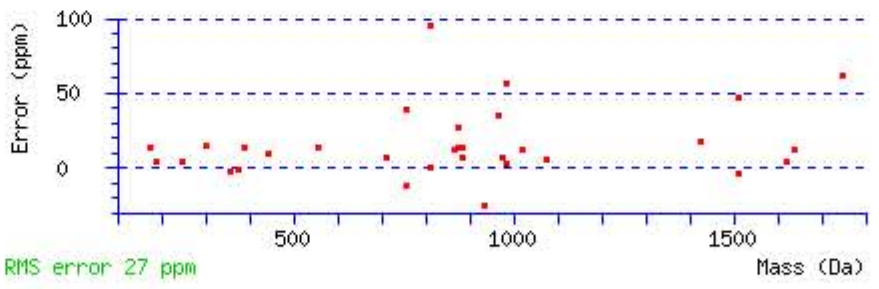
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2338.177322
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0011
**Matches :** 32/154 fragment ions using 79 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 16 |
| 2 | 187.071333 | 94.039304 | | | 169.060768 | 85.034022 | A | 2224.157671 | 1112.582473 | 2207.131122 | 1104.069199 | 2206.147106 | 1103.577191 | 15 |
| 3 | 300.155397 | 150.581336 | | | 282.144832 | 141.576054 | L | 2153.120557 | 1077.063916 | 2136.094008 | 1068.550642 | 2135.109992 | 1068.058634 | 14 |
| 4 | 387.187425 | 194.097351 | | | 369.176860 | 185.092068 | S | 2040.036493 | 1020.521885 | 2023.009944 | 1012.008610 | 2022.025928 | 1011.516602 | 13 |
| 5 | 474.219453 | 237.613364 | | | 456.208888 | 228.608082 | S | 1953.004465 | 977.005871 | 1935.977916 | 968.492596 | 1934.993900 | 968.000588 | 12 |
| 6 | 573.287867 | 287.147572 | | | 555.277302 | 278.142289 | V | 1865.972437 | 933.489857 | 1848.945888 | 924.976582 | 1847.961872 | 924.484574 | 11 |
| 7 | 701.346445 | 351.176861 | 684.319896 | 342.663586 | 683.335880 | 342.171578 | Q | 1766.904023 | 883.955650 | 1749.877474 | 875.442375 | 1748.893458 | 874.950367 | 10 |
| 8 | 830.389038 | 415.698157 | 813.362489 | 407.184883 | 812.378473 | 406.692875 | E | *1638.845445* | 819.926361 | 1621.818896 | 811.413086 | 1620.834880 | 810.921078 | 9 |
| 9 | 917.421066 | 459.214171 | 900.394517 | 450.700897 | 899.410501 | 450.208889 | S | *1509.802852* | 755.405064 | 1492.776303 | 746.891790 | 1491.792287 | 746.399782 | 8 |
| 10 | 1356.646392 | 678.826834 | 1339.619843 | 670.313560 | 1338.635827 | 669.821551 | Q | *1422.770824* | 711.889050 | 1405.744275 | 703.375776 | | | 7 |
| 11 | 1455.714806 | 728.361041 | 1438.688257 | 719.847767 | 1437.704241 | 719.355758 | V | *983.545498* | 492.276387 | 966.518949 | 483.763113 | | | 6 |
| 12 | 1526.751920 | 763.879598 | 1509.725371 | 755.366324 | 1508.741355 | 754.874315 | A | *884.477084* | 442.742180 | 867.450535 | 434.228906 | | | 5 |
| 13 | 1965.977246 | 983.492261 | 1948.950697 | 974.978987 | 1947.966681 | 974.486979 | Q | *813.439970* | 407.223623 | 796.413421 | 398.710349 | | | 4 |
| 14 | 2094.035824 | 1047.521550 | 2077.009275 | 1039.008275 | 2076.025259 | 1038.516267 | Q | *374.214644* | 187.610960 | 357.188095 | 179.097686 | | | 3 |
| 15 | 2165.072938 | 1083.040107 | 2148.046389 | 1074.526833 | 2147.062373 | 1074.034825 | A | *246.156066* | 123.581671 | 229.129517 | 115.068397 | | | 2 |
| 16 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 32.6 | 2338.177322 | 0.025450 | DALSSVQESQVAQQAR |
| 32.0 | 2338.177322 | 0.025450 | DALSSVQESQVAQQAR |
| 15.4 | 2338.177322 | 0.025450 | DALSSVQESQVAQQAR |
| 12.8 | 2338.177322 | 0.025450 | DALSSVQESQVAQQAR |
| 12.4 | 2338.177322 | 0.025450 | DALSSVQESQVAQQAR |

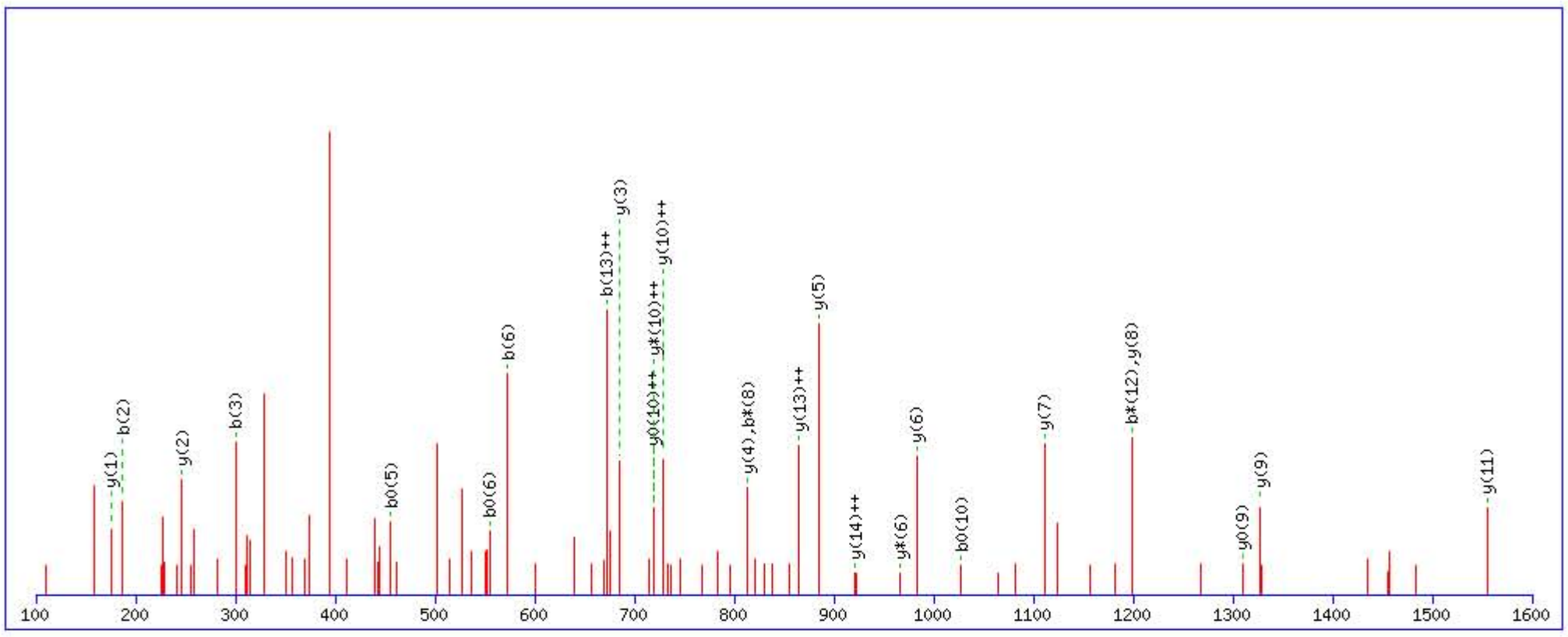
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DALSSVQESQVAQQAR**
Found in **APOC3_HUMAN**, Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1

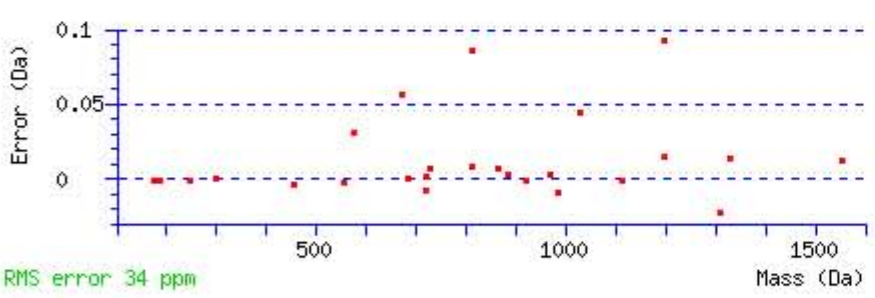
Match to Query 45162: 2027.016852 from(676.679560,3+) rtinseconds(1936) index(5263)
Title: Locus:1.1.1.1951.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

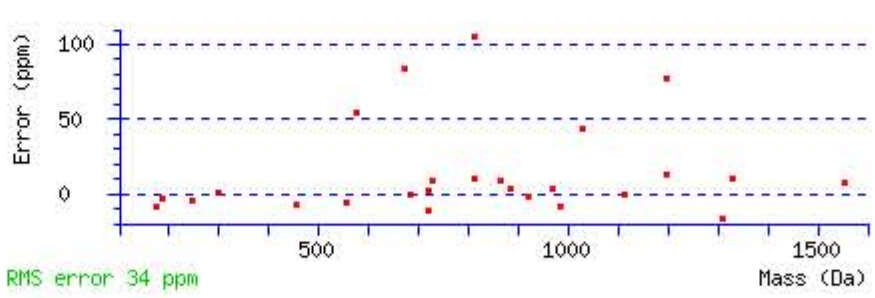
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2027.010574
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q14** : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 4.4e-005
**Matches** : 26/154 fragment ions using 41 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 16 |
| 2 | 187.071333 | 94.039304 | | | 169.060768 | 85.034022 | A | 1912.990923 | 956.999100 | 1895.964374 | 948.485825 | 1894.980358 | 947.993817 | 15 |
| 3 | 300.155397 | 150.581336 | | | 282.144832 | 141.576054 | L | 1841.953809 | 921.480543 | 1824.927260 | 912.967268 | 1823.943244 | 912.475260 | 14 |
| 4 | 387.187425 | 194.097351 | | | 369.176860 | 185.092068 | S | 1728.869745 | 864.938511 | 1711.843196 | 856.425236 | 1710.859180 | 855.933228 | 13 |
| 5 | 474.219453 | 237.613364 | | | 456.208888 | 228.608082 | S | 1641.837717 | 821.422497 | 1624.811168 | 812.909222 | 1623.827152 | 812.417214 | 12 |
| 6 | 573.287867 | 287.147572 | | | 555.277302 | 278.142289 | V | *1554.805689* | 777.906483 | 1537.779140 | 769.393208 | 1536.795124 | 768.901200 | 11 |
| 7 | 701.346445 | 351.176861 | 684.319896 | 342.663586 | 683.335880 | 342.171578 | Q | 1455.737275 | 728.372276 | 1438.710726 | 719.859001 | 1437.726710 | 719.366993 | 10 |
| 8 | 830.389038 | 415.698157 | 813.362489 | 407.184883 | 812.378473 | 406.692875 | E | *1327.678697* | 664.342987 | 1310.652148 | 655.829712 | 1309.668132 | 655.337704 | 9 |
| 9 | 917.421066 | 459.214171 | 900.394517 | 450.700897 | 899.410501 | 450.208889 | S | *1198.636104* | 599.821690 | 1181.609555 | 591.308416 | 1180.625539 | 590.816408 | 8 |
| 10 | 1045.479644 | 523.243460 | 1028.453095 | 514.730186 | 1027.469079 | 514.238178 | Q | *1111.604076* | 556.305676 | 1094.577527 | 547.792402 | | | 7 |
| 11 | 1144.548058 | 572.777667 | 1127.521509 | 564.264393 | 1126.537493 | 563.772385 | V | *983.545498* | 492.276387 | 966.518949 | 483.763113 | | | 6 |
| 12 | 1215.585172 | 608.296224 | 1198.558623 | 599.782950 | 1197.574607 | 599.290942 | A | *884.477084* | 442.742180 | 867.450535 | 434.228906 | | | 5 |
| 13 | 1343.643750 | 672.325513 | 1326.617201 | 663.812239 | 1325.633185 | 663.320230 | Q | *813.439970* | 407.223623 | 796.413421 | 398.710349 | | | 4 |
| 14 | 1782.869076 | 891.938176 | 1765.842527 | 883.424902 | 1764.858511 | 882.932894 | Q | *685.381392* | 343.194334 | 668.354843 | 334.681060 | | | 3 |
| 15 | 1853.906190 | 927.456733 | 1836.879641 | 918.943459 | 1835.895625 | 918.451451 | A | *246.156066* | 123.581671 | 229.129517 | 115.068396 | | | 2 |
| 16 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 57.5 | 2027.010574 | 0.006278 | DALSSVQESQVAQQAR |
| 57.0 | 2027.010574 | 0.006278 | DALSSVQESQVAQQAR |
| 53.8 | 2027.010574 | 0.006278 | DALSSVQESQVAQQAR |
| 25.9 | 2027.010574 | 0.006278 | DALSSVQESQVAQQAR |

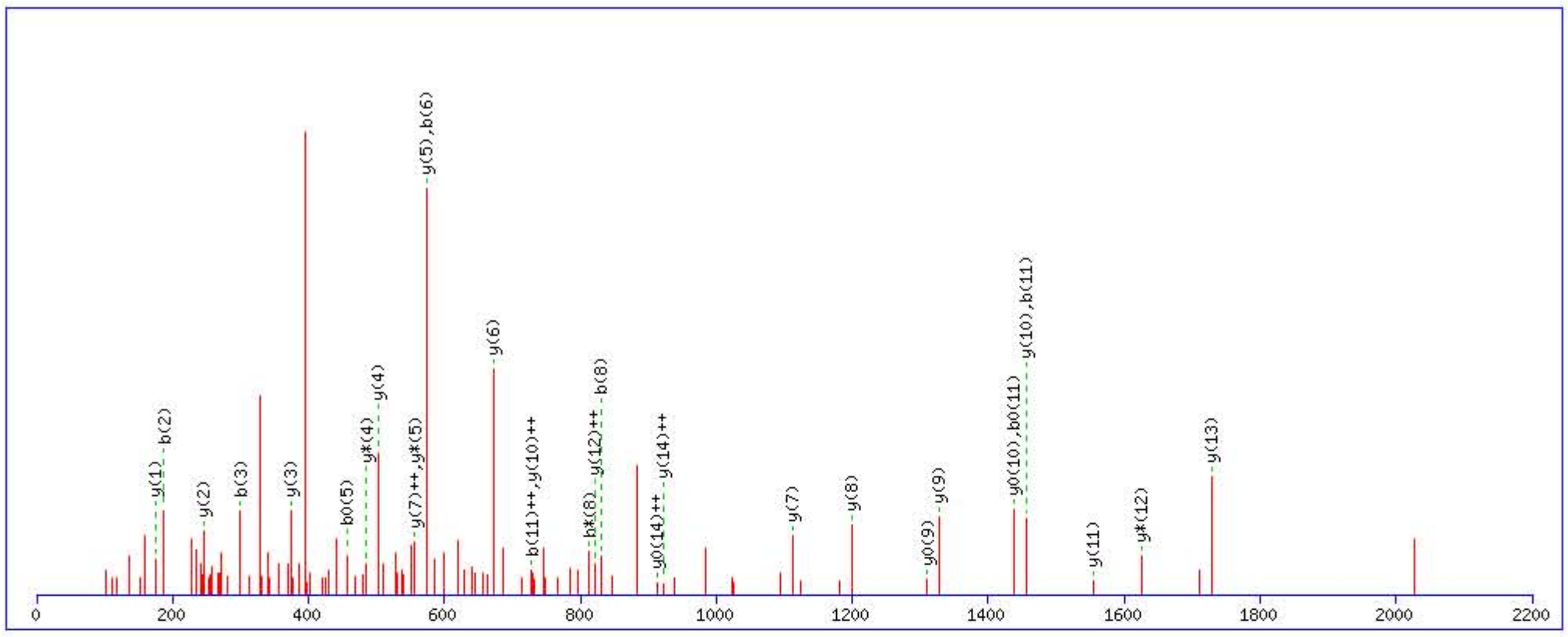
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DALSSVQESQVAQQAR**
Found in **APOC3_HUMAN**, Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1

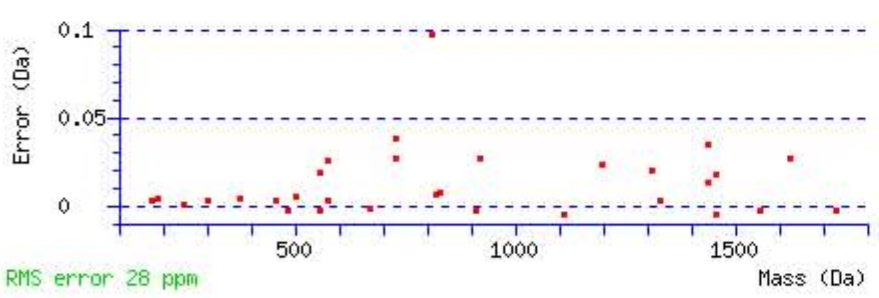
Match to Query 45168: 2027.023092 from(676.681640,3+) rtinseconds(1932) index(19866)
Title: Locus:1.1.1.3055.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

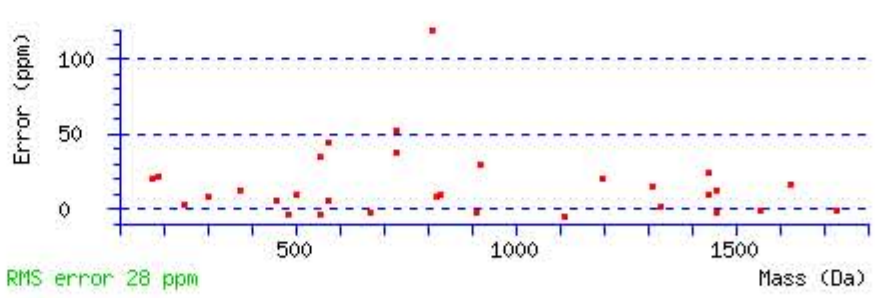
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2027.010574
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 67 **Expect:** 5.4e-006
**Matches :** 31/154 fragment ions using 53 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 16 |
| 2 | **187.071333** | 94.039304 | | | 169.060768 | 85.034022 | A | 1912.990923 | 956.999100 | 1895.964374 | 948.485825 | 1894.980358 | 947.993817 | 15 |
| 3 | **300.155397** | 150.581336 | | | 282.144832 | 141.576054 | L | 1841.953809 | 921.480543 | 1824.927260 | 912.967268 | 1823.943244 | 912.475260 | 14 |
| 4 | 387.187425 | 194.097351 | | | 369.176860 | 185.092068 | S | *1728.869745* | 864.938511 | 1711.843196 | 856.425236 | 1710.859180 | 855.933228 | 13 |
| 5 | 474.219453 | 237.613364 | | | 456.208888 | 228.608082 | S | 1641.837717 | 821.422497 | 1624.811168 | 812.909222 | 1623.827152 | 812.417214 | 12 |
| 6 | **573.287867** | 287.147572 | | | 555.277302 | 278.142289 | V | *1554.805689* | 777.906483 | 1537.779140 | 769.393208 | 1536.795124 | 768.901200 | 11 |
| 7 | 701.346445 | 351.176861 | 684.319896 | 342.663586 | 683.335880 | 342.171578 | Q | *1455.737275* | 728.372276 | 1438.710726 | 719.859001 | 1437.726710 | 719.366993 | 10 |
| 8 | **830.389038** | 415.698157 | 813.362489 | 407.184883 | 812.378473 | 406.692875 | E | *1327.678697* | 664.342987 | 1310.652148 | 655.829712 | 1309.668132 | 655.337704 | 9 |
| 9 | 917.421066 | 459.214171 | 900.394517 | 450.700897 | 899.410501 | 450.208889 | S | *1198.636104* | 599.821690 | 1181.609555 | 591.308416 | 1180.625539 | 590.816408 | 8 |
| 10 | 1356.646392 | 678.826834 | 1339.619843 | 670.313560 | 1338.635827 | 669.821551 | Q | *1111.604076* | 556.305676 | 1094.577527 | 547.792402 | | | 7 |
| 11 | **1455.714806** | 728.361041 | 1438.688257 | 719.847767 | 1437.704241 | 719.355758 | V | *672.378750* | 336.693013 | 655.352201 | 328.179739 | | | 6 |
| 12 | 1526.751920 | 763.879598 | 1509.725371 | 755.366324 | 1508.741355 | 754.874315 | A | *573.310336* | 287.158806 | 556.283787 | 278.645532 | | | 5 |
| 13 | 1654.810498 | 827.908887 | 1637.783949 | 819.395613 | 1636.799933 | 818.903605 | Q | *502.273222* | 251.640249 | 485.246673 | 243.126975 | | | 4 |
| 14 | 1782.869076 | 891.938176 | 1765.842527 | 883.424902 | 1764.858511 | 882.932894 | Q | *374.214644* | 187.610960 | 357.188095 | 179.097686 | | | 3 |
| 15 | 1853.906190 | 927.456733 | 1836.879641 | 918.943459 | 1835.895625 | 918.451451 | A | *246.156066* | 123.581671 | 229.129517 | 115.068396 | | | 2 |
| 16 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 66.9 | 2027.010574 | 0.012518 | DALSSVQESQVAQQAR |
| 65.2 | 2027.010574 | 0.012518 | DALSSVQESQVAQQAR |
| 64.8 | 2027.010574 | 0.012518 | DALSSVQESQVAQQAR |
| 33.5 | 2027.010574 | 0.012518 | DALSSVQESQVAQQAR |

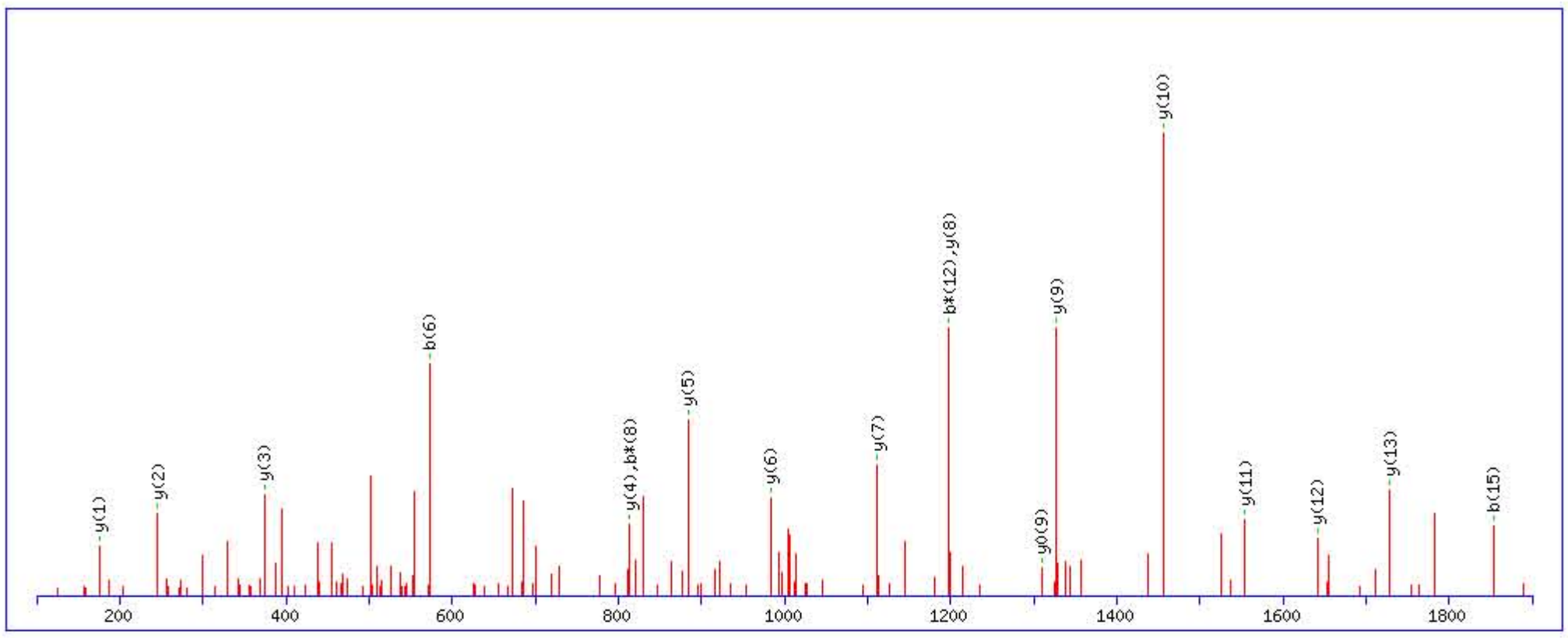
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DALSSVQESQVAQQAR**
Found in **APOC3_HUMAN**, Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1

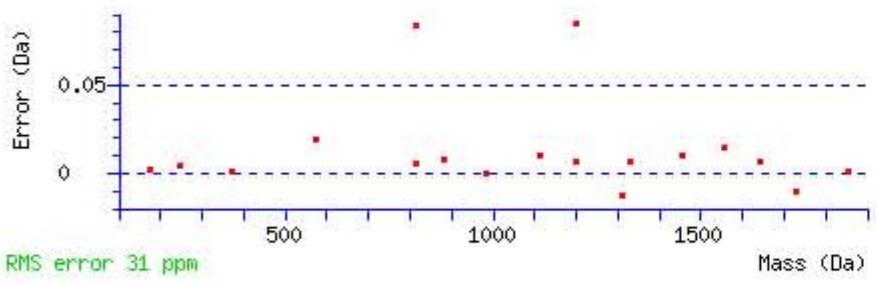
Match to Query 45169: 2027.024948 from(1014.519750,2+) rtinseconds(1928) index(19831)
Title: Locus:1.1.1.3053.21 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

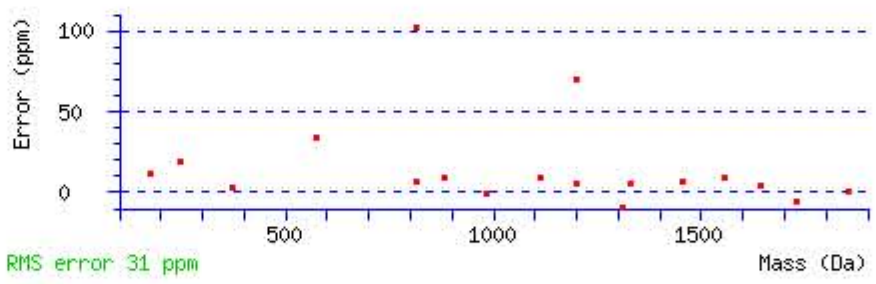
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2027.010574
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 131 **Expect:** 6.5e-012
**Matches :** 18/154 fragment ions using 18 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 16 |
| 2 | 187.071333 | 94.039304 | | | 169.060768 | 85.034022 | A | 1912.990923 | 956.999100 | 1895.964374 | 948.485825 | 1894.980358 | 947.993817 | 15 |
| 3 | 300.155397 | 150.581336 | | | 282.144832 | 141.576054 | L | 1841.953809 | 921.480543 | 1824.927260 | 912.967268 | 1823.943244 | 912.475260 | 14 |
| 4 | 387.187425 | 194.097351 | | | 369.176860 | 185.092068 | S | *1728.869745* | 864.938511 | 1711.843196 | 856.425236 | 1710.859180 | 855.933228 | 13 |
| 5 | 474.219453 | 237.613364 | | | 456.208888 | 228.608082 | S | *1641.837717* | 821.422497 | 1624.811168 | 812.909222 | 1623.827152 | 812.417214 | 12 |
| 6 | 573.287867 | 287.147572 | | | 555.277302 | 278.142289 | V | *1554.805689* | 777.906483 | 1537.779140 | 769.393208 | 1536.795124 | 768.901200 | 11 |
| 7 | 701.346445 | 351.176861 | 684.319896 | 342.663586 | 683.335880 | 342.171578 | Q | *1455.737275* | 728.372276 | 1438.710726 | 719.859001 | 1437.726710 | 719.366993 | 10 |
| 8 | 830.389038 | 415.698157 | 813.362489 | 407.184883 | 812.378473 | 406.692875 | E | *1327.678697* | 664.342987 | 1310.652148 | 655.829712 | 1309.668132 | 655.337704 | 9 |
| 9 | 917.421066 | 459.214171 | 900.394517 | 450.700897 | 899.410501 | 450.208889 | S | *1198.636104* | 599.821690 | 1181.609555 | 591.308416 | 1180.625539 | 590.816408 | 8 |
| 10 | 1045.479644 | 523.243460 | 1028.453095 | 514.730186 | 1027.469079 | 514.238178 | Q | *1111.604076* | 556.305676 | 1094.577527 | 547.792402 | | | 7 |
| 11 | 1144.548058 | 572.777667 | 1127.521509 | 564.264393 | 1126.537493 | 563.772385 | V | *983.545498* | 492.276387 | 966.518949 | 483.763113 | | | 6 |
| 12 | 1215.585172 | 608.296224 | 1198.558623 | 599.782950 | 1197.574607 | 599.290942 | A | *884.477084* | 442.742180 | 867.450535 | 434.228906 | | | 5 |
| 13 | 1654.810498 | 827.908887 | 1637.783949 | 819.395613 | 1636.799933 | 818.903605 | Q | *813.439970* | 407.223623 | 796.413421 | 398.710349 | | | 4 |
| 14 | 1782.869076 | 891.938176 | 1765.842527 | 883.424902 | 1764.858511 | 882.932894 | Q | *374.214644* | 187.610960 | 357.188095 | 179.097686 | | | 3 |
| 15 | 1853.906190 | 927.456733 | 1836.879641 | 918.943459 | 1835.895625 | 918.451451 | A | *246.156066* | 123.581671 | 229.129517 | 115.068396 | | | 2 |
| 16 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 130.9 | 2027.010574 | 0.014374 | DALSSVQESQVAQQAR |
| 130.8 | 2027.010574 | 0.014374 | DALSSVQESQVAQQAR |
| 112.2 | 2027.010574 | 0.014374 | DALSSVQESQVAQQAR |
| 70.1 | 2027.010574 | 0.014374 | DALSSVQESQVAQQAR |
| 11.1 | 2027.021805 | 0.003143 | VASVESQGQEISGNRR |
| 7.7 | 2027.017960 | 0.006988 | MFELTLRGMSEALVDKR |
| 7.6 | 2027.029633 | -0.004685 | QEESEHSHKHLIELRR |
| 3.5 | 2027.021820 | 0.003128 | DTDNKAAIRDCGGVPALVR |
| 3.2 | 2027.046936 | -0.021988 | AVESLQASLDAETRAR |
| 3.1 | 2027.039520 | -0.014572 | GLERALEEAANSGGLNLSAR |

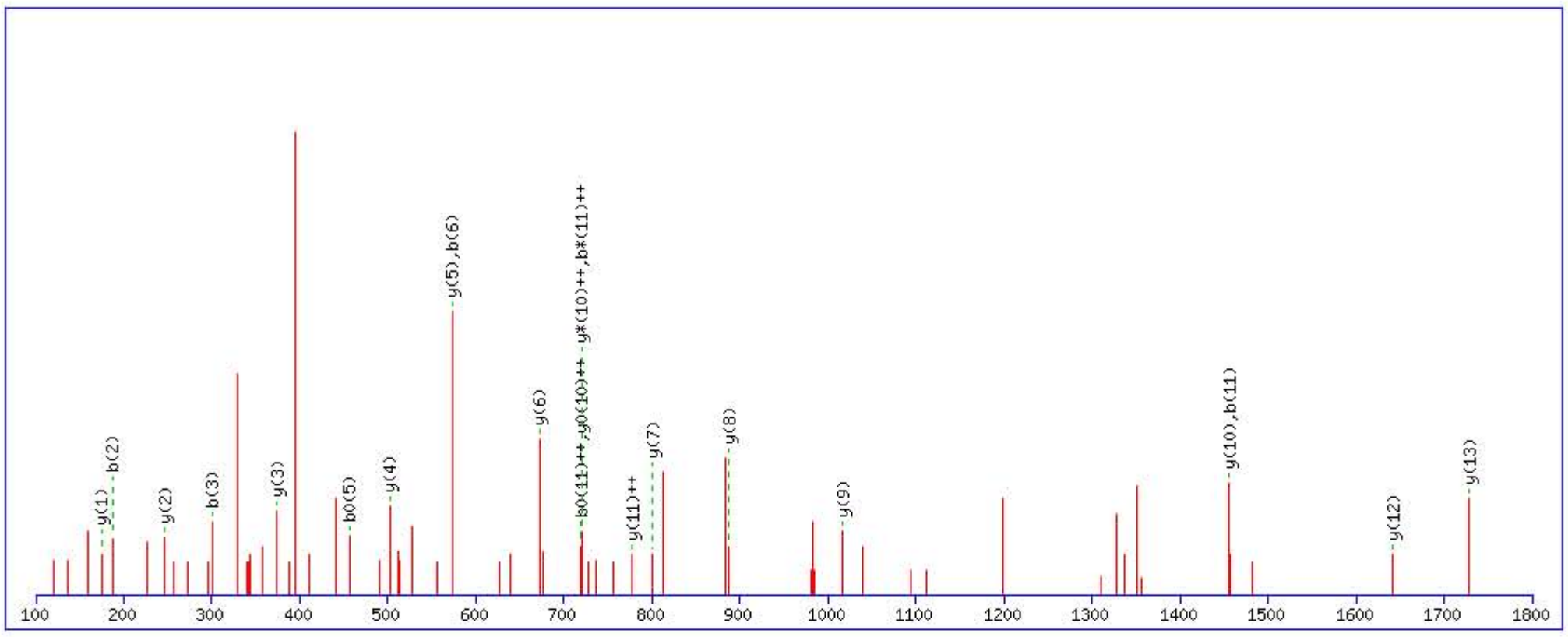
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DALSSVQESQVAQQAR**
Found in **APOC3_HUMAN**, Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1

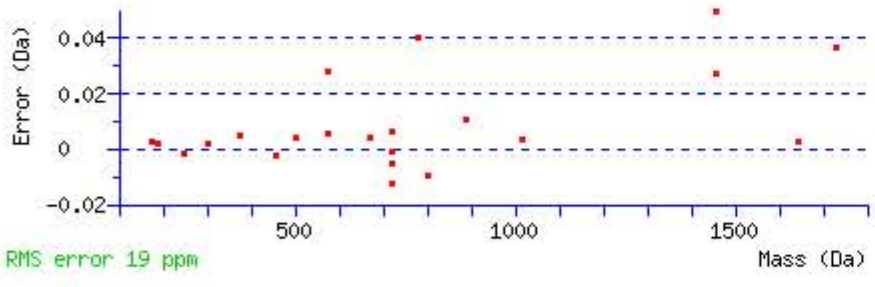
Match to Query 45171: 2027.028192 from(676.683340,3+) rtinseconds(1980) index(34142)
Title: Locus:1.1.1.798.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

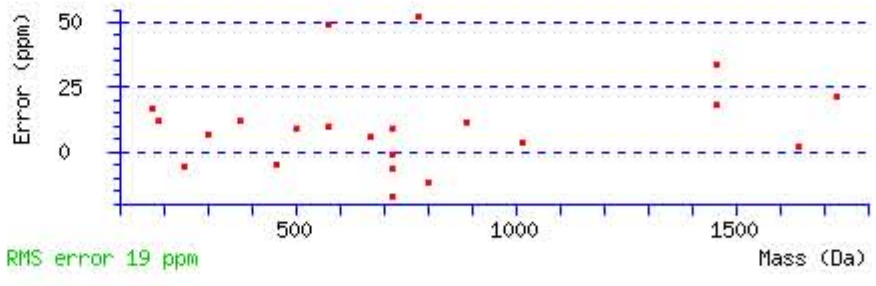
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2027.010574
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q7** : Biotin:Thermo-21345 (Q)
**Ions Score:** 65 **Expect:** 9.3e-007
**Matches :** 22/154 fragment ions using 40 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 16 |
| 2 | **187.071333** | 94.039304 | | | 169.060768 | 85.034022 | A | 1912.990923 | 956.999100 | 1895.964374 | 948.485825 | 1894.980358 | 947.993817 | 15 |
| 3 | **300.155397** | 150.581336 | | | 282.144832 | 141.576054 | L | 1841.953809 | 921.480543 | 1824.927260 | 912.967268 | 1823.943244 | 912.475260 | 14 |
| 4 | 387.187425 | 194.097351 | | | 369.176860 | 185.092068 | S | *1728.869745* | 864.938511 | 1711.843196 | 856.425236 | 1710.859180 | 855.933228 | 13 |
| 5 | 474.219453 | 237.613364 | | | 456.208888 | 228.608082 | S | *1641.837717* | 821.422497 | 1624.811168 | 812.909222 | 1623.827152 | 812.417214 | 12 |
| 6 | **573.287867** | 287.147572 | | | 555.277302 | 278.142289 | V | 1554.805689 | 777.906483 | 1537.779140 | 769.393208 | 1536.795124 | 768.901200 | 11 |
| 7 | 1012.513193 | 506.760235 | 995.486644 | 498.246960 | 994.502628 | 497.754952 | Q | *1455.737275* | 728.372276 | 1438.710726 | 719.859001 | 1437.726710 | 719.366993 | 10 |
| 8 | 1141.555786 | 571.281531 | 1124.529237 | 562.768257 | 1123.545221 | 562.276249 | E | *1016.511949* | 508.759613 | 999.485400 | 500.246338 | 998.501384 | 499.754330 | 9 |
| 9 | 1228.587814 | 614.797545 | 1211.561265 | 606.284271 | 1210.577249 | 605.792263 | S | *887.469356* | 444.238316 | 870.442807 | 435.725042 | 869.458791 | 435.233034 | 8 |
| 10 | 1356.646392 | 678.826834 | 1339.619843 | 670.313560 | 1338.635827 | 669.821552 | Q | *800.437328* | 400.722302 | 783.410779 | 392.209028 | | | 7 |
| 11 | **1455.714806** | 728.361041 | 1438.688257 | 719.847767 | 1437.704241 | 719.355759 | V | *672.378750* | 336.693013 | 655.352201 | 328.179739 | | | 6 |
| 12 | 1526.751920 | 763.879598 | 1509.725371 | 755.366324 | 1508.741355 | 754.874316 | A | *573.310336* | 287.158806 | 556.283787 | 278.645532 | | | 5 |
| 13 | 1654.810498 | 827.908887 | 1637.783949 | 819.395613 | 1636.799933 | 818.903605 | Q | *502.273222* | 251.640249 | 485.246673 | 243.126975 | | | 4 |
| 14 | 1782.869076 | 891.938176 | 1765.842527 | 883.424902 | 1764.858511 | 882.932894 | Q | *374.214644* | 187.610960 | 357.188095 | 179.097686 | | | 3 |
| 15 | 1853.906190 | 927.456733 | 1836.879641 | 918.943459 | 1835.895625 | 918.451451 | A | *246.156066* | 123.581671 | 229.129517 | 115.068396 | | | 2 |
| 16 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 65.3 | 2027.010574 | 0.017618 | DALSSVQESQVAQQAR |
| 60.4 | 2027.010574 | 0.017618 | DALSSVQESQVAQQAR |
| 60.3 | 2027.010574 | 0.017618 | DALSSVQESQVAQQAR |
| 49.5 | 2027.010574 | 0.017618 | DALSSVQESQVAQQAR |
| 1.0 | 2027.027161 | 0.001031 | IHSGKKPYQCGKAFNHR |

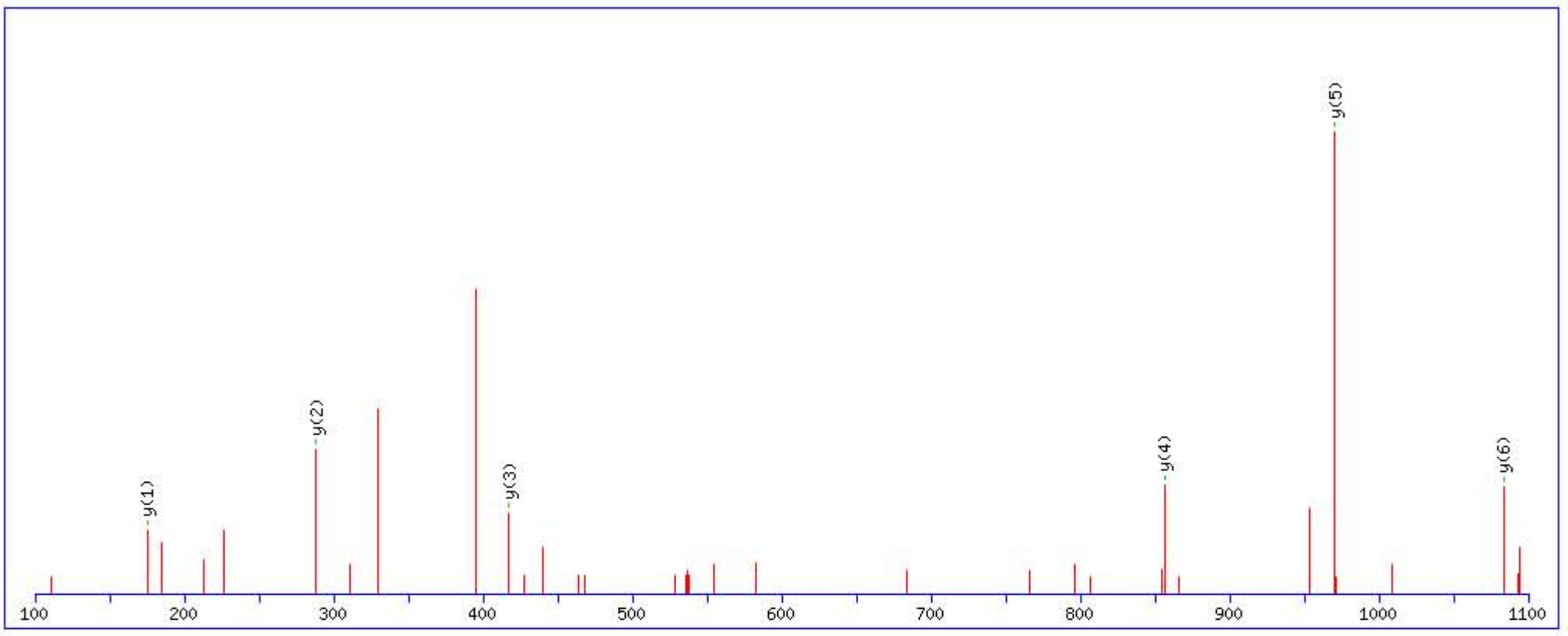
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VLNQELR**
Found in **APOD_HUMAN**, Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1

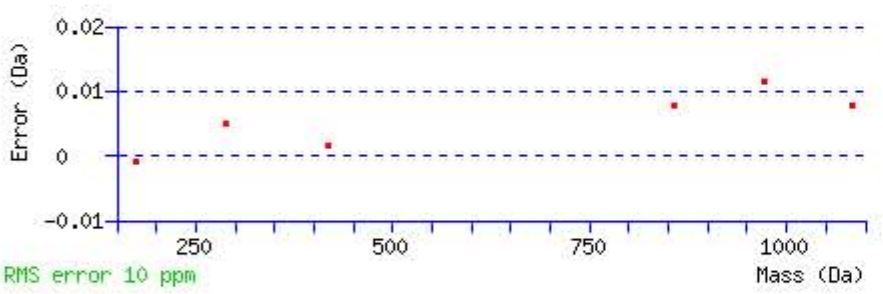
Match to Query 20098: 1181.668288 from(591.841420,2+) rtinseconds(1765) index(32694)
Title: Locus:1.1.1.723.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

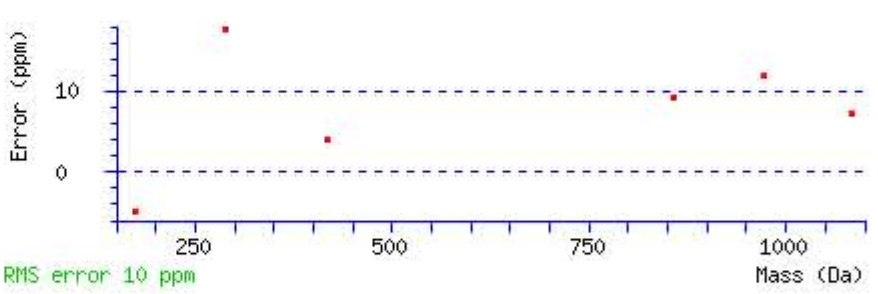
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1181.659042
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 0.00028
**Matches :** 6/56 fragment ions using 10 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 7 |
| 2 | 213.159754 | 107.083515 | | | | | L | *1083.597926* | 542.302601 | 1066.571377 | 533.789327 | 1065.587361 | 533.297318 | 6 |
| 3 | 327.202681 | 164.104978 | 310.176132 | 155.591704 | | | N | *970.513862* | 485.760569 | 953.487313 | 477.247295 | 952.503297 | 476.755287 | 5 |
| 4 | 766.428007 | 383.717642 | 749.401458 | 375.204367 | | | Q | *856.470935* | 428.739106 | 839.444386 | 420.225831 | 838.460370 | 419.733823 | 4 |
| 5 | 895.470600 | 448.238938 | 878.444051 | 439.725664 | 877.460035 | 439.233656 | E | *417.245609* | 209.126442 | 400.219060 | 200.613168 | 399.235044 | 200.121160 | 3 |
| 6 | 1008.554664 | 504.780970 | 991.528115 | 496.267696 | 990.544099 | 495.775688 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 7 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.0 | 1181.659042 | 0.009246 | VLNQELR |
| 23.3 | 1181.676788 | -0.008500 | VIPGAAEKIER |
| 10.0 | 1181.670273 | -0.001985 | VLEQARR |
| 10.0 | 1181.659058 | 0.009230 | VLLGDAQR |
| 10.0 | 1181.670273 | -0.001985 | VLQARER |
| 9.7 | 1181.676804 | -0.008516 | VLALASGPELGR |
| 9.7 | 1181.662918 | 0.005370 | VVQSVRHTTR |
| 7.2 | 1181.670273 | -0.001985 | ARVEQLR |
| 7.2 | 1181.659058 | 0.009230 | VGLQADIR |
| 7.2 | 1181.670273 | -0.001985 | VREQALR |

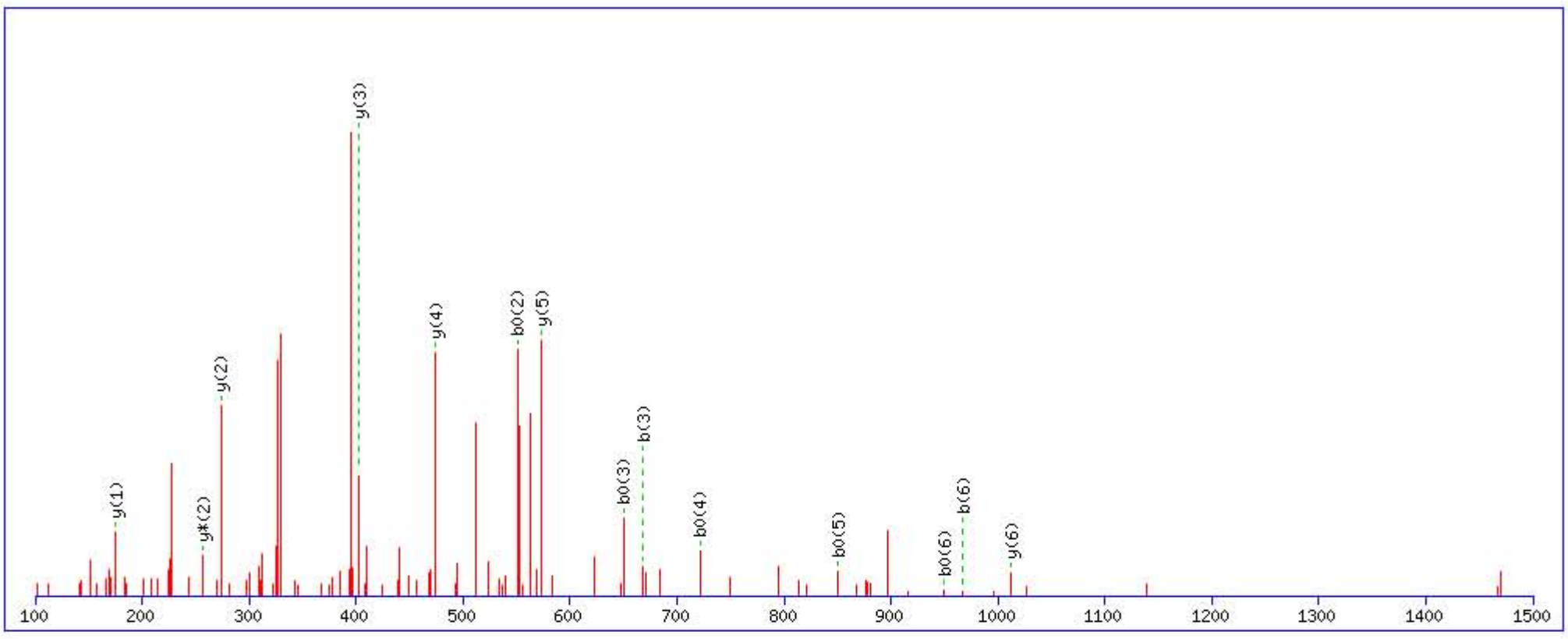
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EQVAEVR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

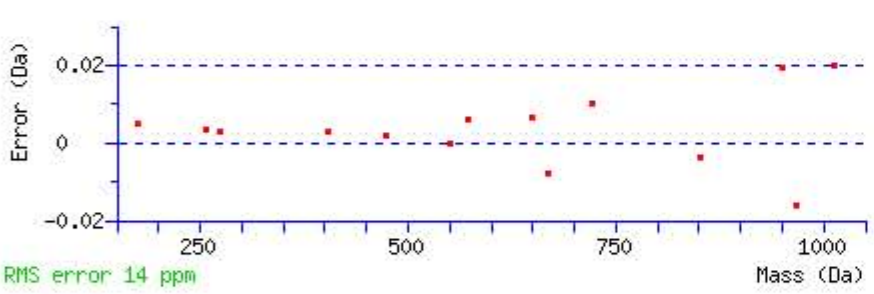
Match to Query 18683: 1140.598748 from(571.306650,2+) rtinseconds(1509) index(16964)
Title: Locus:1.1.1.2908.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

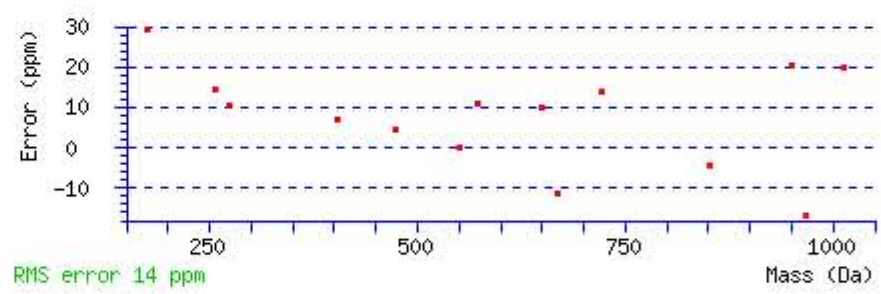
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1140.596115
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 30 **Expect:** 0.023
**Matches :** 14/66 fragment ions using 30 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 7 |
| 2 | 569.275195 | 285.141236 | 552.248646 | 276.627961 | 551.264630 | 276.135953 | Q | *1012.560813* | 506.784044 | 995.534264 | 498.270770 | 994.550248 | 497.778762 | 6 |
| 3 | **668.343609** | 334.675443 | 651.317060 | 326.162168 | 650.333044 | 325.670160 | V | *573.335487* | 287.171382 | 556.308938 | 278.658107 | 555.324922 | 278.166099 | 5 |
| 4 | 739.380723 | 370.194000 | 722.354174 | 361.680725 | 721.370158 | 361.188717 | A | *474.267073* | 237.637174 | 457.240524 | 229.123900 | 456.256508 | 228.631892 | 4 |
| 5 | 868.423316 | 434.715296 | 851.396767 | 426.202022 | 850.412751 | 425.710014 | E | *403.229959* | 202.118617 | 386.203410 | 193.605343 | 385.219394 | 193.113335 | 3 |
| 6 | **967.491730** | 484.249503 | 950.465181 | 475.736228 | 949.481165 | 475.244220 | V | *274.187366* | 137.597321 | 257.160817 | 129.084046 | | | 2 |
| 7 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 30.5 | 1140.596115 | 0.002633 | EQVAEVR |
| 12.2 | 1140.596115 | 0.002633 | EQALDVR |
| 10.2 | 1140.596115 | 0.002633 | QEVADLR |
| 3.9 | 1140.607361 | -0.008613 | QAQQTVR |
| 3.4 | 1140.599945 | -0.001197 | ERVALSHSSR |
| 3.3 | 1140.611176 | -0.012428 | GLRNRASDPR |
| 2.5 | 1140.592789 | 0.005959 | IGTGSFGTVFR |
| 1.8 | 1140.596115 | 0.002633 | EQSTLPR |
| 1.6 | 1140.613876 | -0.015128 | LLQAPDTDLR |
| 1.3 | 1140.599945 | -0.001197 | SSSKLAQHQR |

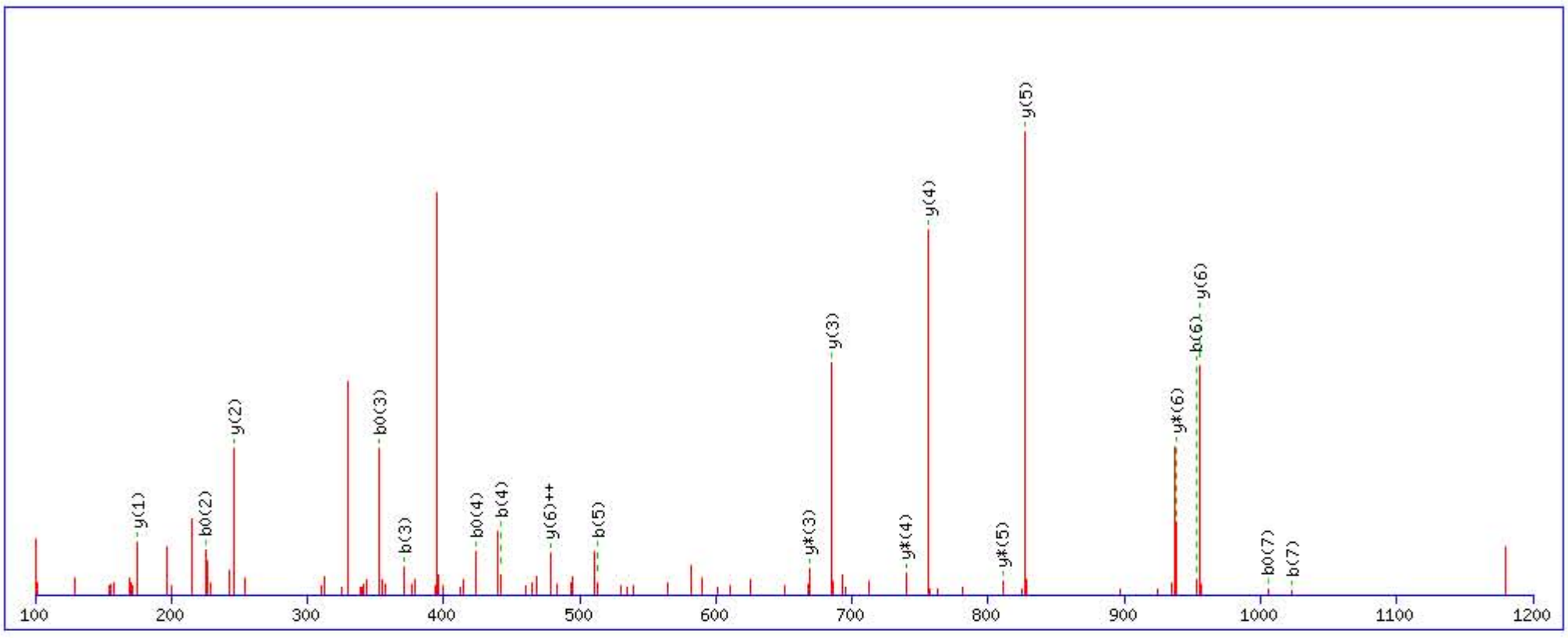
# MATRIX SCIENCE Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ELQAAQAR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

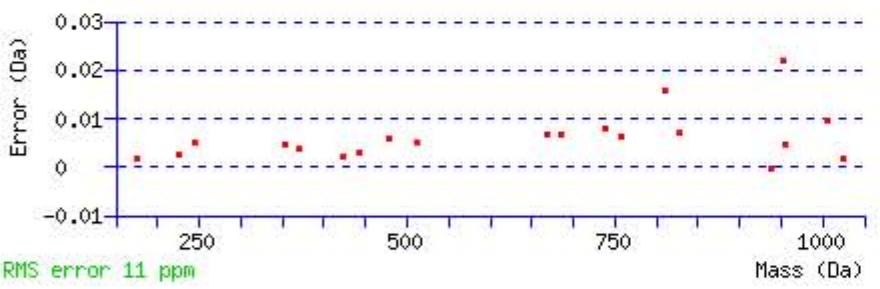
Match to Query 20476: 1196.634968 from(599.324760,2+) rtinseconds(1488) index(30988)
Title: Locus:1.1.1.626.21 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

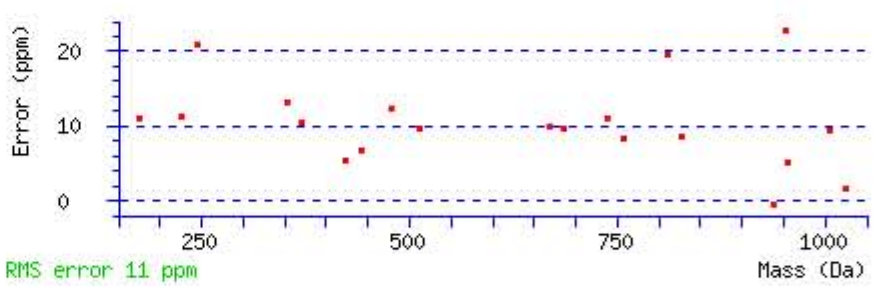
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1196.633545
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.007
**Matches :** 20/66 fragment ions using 39 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | 8 |
| 2 | 243.133933 | 122.070605 | | | 225.123368 | 113.065322 | L | 1068.598262 | 534.802769 | 1051.571713 | 526.289495 | 7 |
| 3 | 371.192511 | 186.099894 | 354.165962 | 177.586619 | 353.181946 | 177.094611 | Q | *955.514198* | 478.260737 | 938.487649 | 469.747463 | 6 |
| 4 | 442.229625 | 221.618450 | 425.203076 | 213.105176 | 424.219060 | 212.613168 | A | *827.455620* | 414.231448 | 810.429071 | 405.718174 | 5 |
| 5 | 513.266739 | 257.137008 | 496.240190 | 248.623733 | 495.256174 | 248.131725 | A | *756.418506* | 378.712891 | 739.391957 | 370.199617 | 4 |
| 6 | 952.492065 | 476.749671 | 935.465516 | 468.236396 | 934.481500 | 467.744388 | Q | *685.381392* | 343.194334 | 668.354843 | 334.681060 | 3 |
| 7 | 1023.529179 | 512.268227 | 1006.502630 | 503.754953 | 1005.518614 | 503.262945 | A | *246.156066* | 123.581671 | 229.129517 | 115.068397 | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.4 | 1196.633545 | 0.001423 | ELQAAQAR |
| 8.1 | 1196.633575 | 0.001393 | QASTQVPR |
| 5.8 | 1196.630890 | 0.004078 | TNHCRRVVR |
| 5.4 | 1196.627029 | 0.007939 | AGMPRQAR |
| 3.4 | 1196.637390 | -0.002422 | TLRQAGAPNNR |
| 3.1 | 1196.641434 | -0.006466 | STRPQAWVPR |
| 2.3 | 1196.641418 | -0.006450 | EAKKAGPGFHR |
| 0.8 | 1196.633575 | 0.001393 | QASTQVPR |

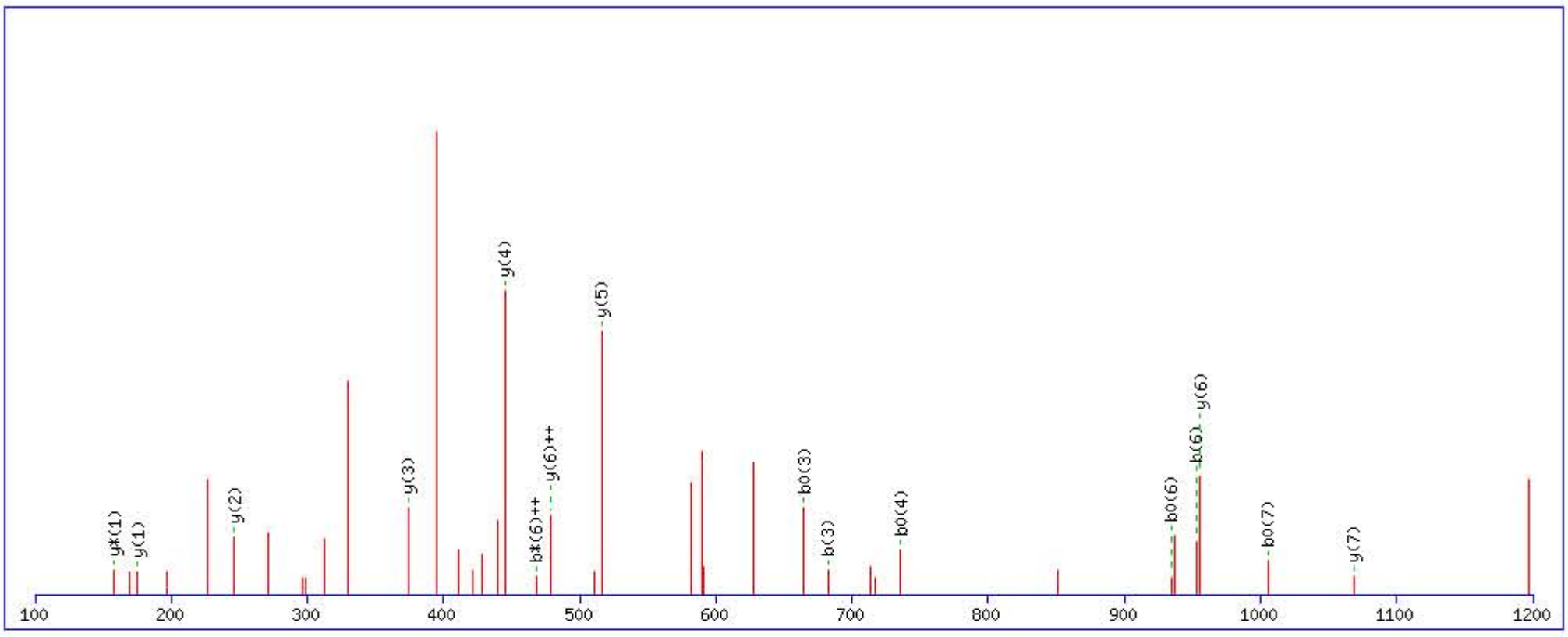
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ELQAAQAR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

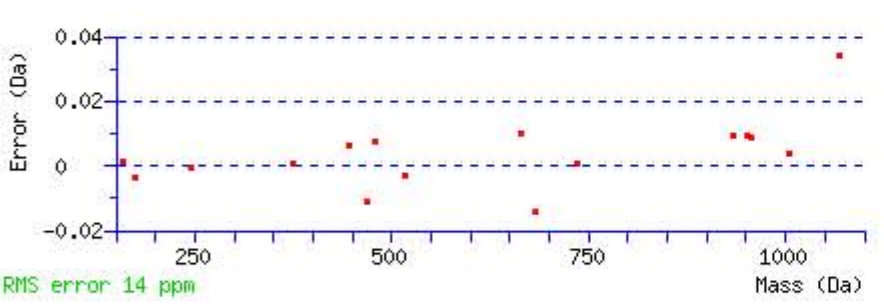
Match to Query 20479: 1196.643408 from(599.328980,2+) rtinseconds(1468) index(30840)
Title: Locus:1.1.1.619.22 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

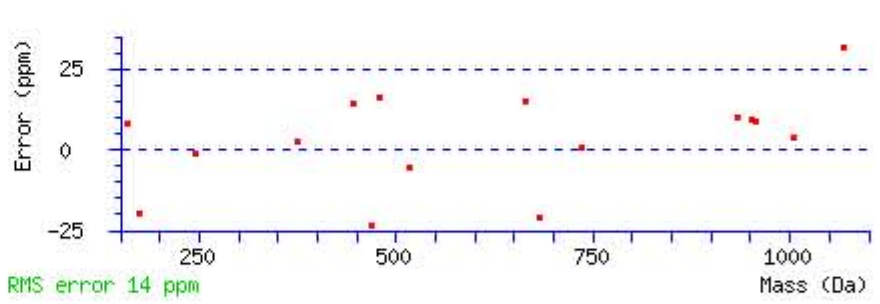
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1196.633545
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0022
**Matches :** 16/66 fragment ions using 36 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | 8 |
| 2 | 243.133933 | 122.070605 | | | 225.123368 | 113.065322 | L | *1068.598262* | 534.802769 | 1051.571713 | 526.289495 | 7 |
| 3 | **682.359259** | 341.683268 | 665.332710 | 333.169993 | 664.348694 | 332.677985 | Q | *955.514198* | 478.260737 | 938.487649 | 469.747463 | 6 |
| 4 | 753.396373 | 377.201825 | 736.369824 | 368.688550 | 735.385808 | 368.196542 | A | *516.288872* | 258.648074 | 499.262323 | 250.134800 | 5 |
| 5 | 824.433487 | 412.720382 | 807.406938 | 404.207107 | 806.422922 | 403.715099 | A | *445.251758* | 223.129517 | 428.225209 | 214.616243 | 4 |
| 6 | **952.492065** | 476.749671 | 935.465516 | 468.236396 | 934.481500 | 467.744388 | Q | *374.214644* | 187.610960 | 357.188095 | 179.097686 | 3 |
| 7 | 1023.529179 | 512.268227 | 1006.502630 | 503.754953 | 1005.518614 | 503.262945 | A | *246.156066* | 123.581671 | 229.129517 | 115.068397 | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 39.3 | 1196.633545 | 0.009863 | ELQAAQAR |
| 13.0 | 1196.641418 | 0.001990 | EAKKAGPGFHR |
| 6.9 | 1196.627701 | 0.015707 | WLWMLGVHR |
| 6.7 | 1196.644775 | -0.001367 | LEQANRR |
| 3.5 | 1196.633545 | 0.009863 | ELQAAQAR |
| 1.7 | 1196.640076 | 0.003332 | ELASPVSPELR |
| 0.2 | 1196.655304 | -0.011896 | EYLKALAAYR |

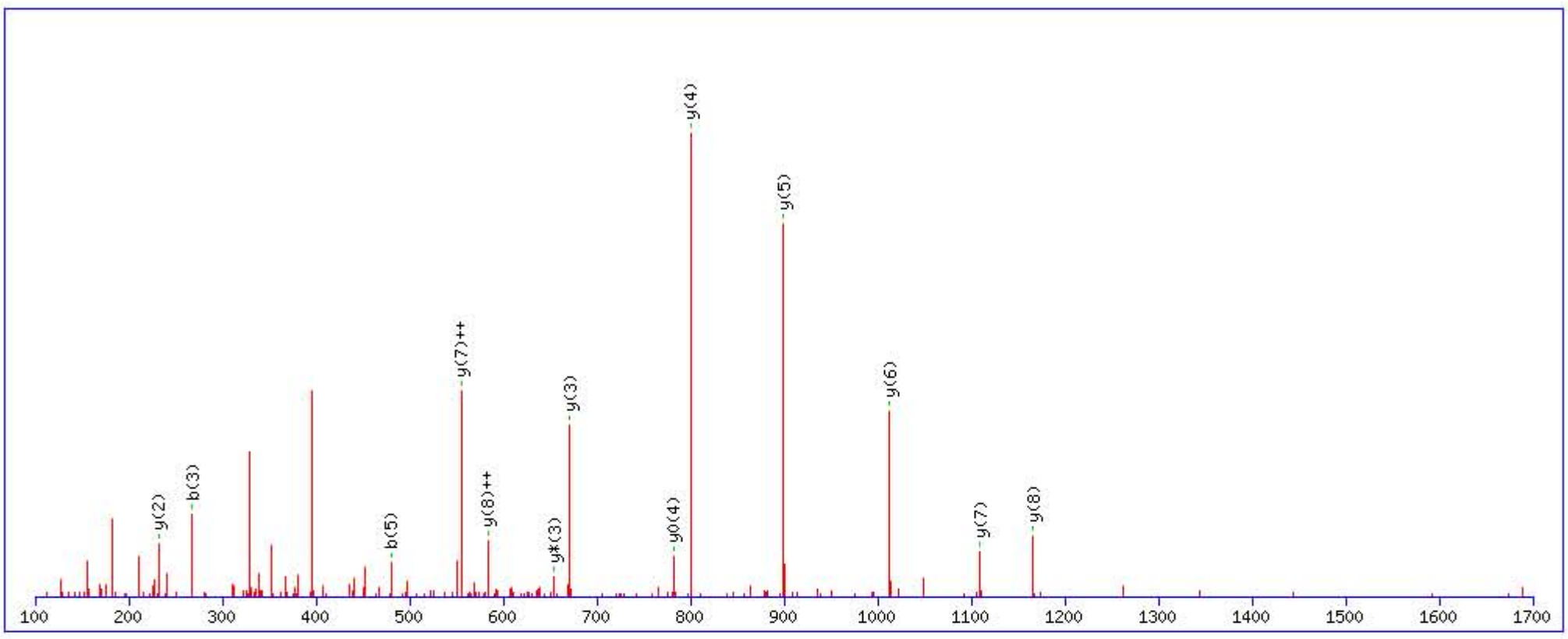
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LGPLVEQGR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

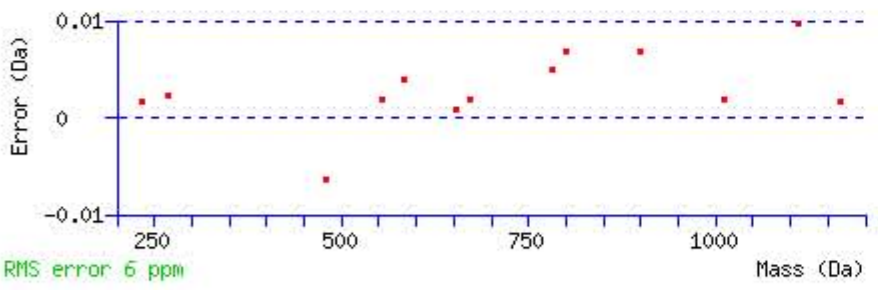
Match to Query 22690: 1278.716728 from(640.365640,2+) rtinseconds(1940) index(19913)
Title: Locus:1.1.1.3058.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

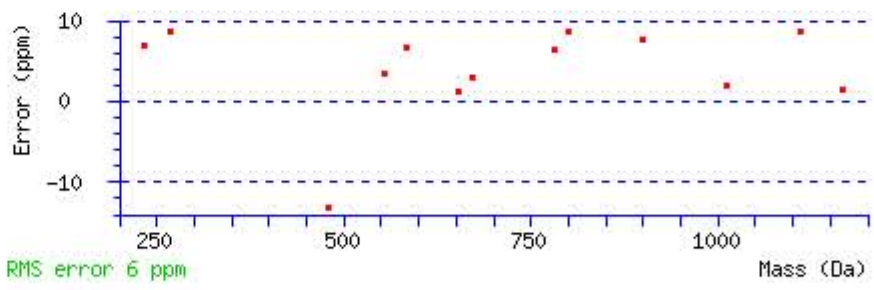
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1278.711823
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q7** : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 3.2e-005
**Matches** : 13/68 fragment ions using 23 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 9 |
| 2 | 171.112804 | 86.060040 | | | | | G | *1166.635041* | 583.821159 | 1149.608492 | 575.307884 | 1148.624476 | 574.815876 | 8 |
| 3 | **268.165568** | 134.586422 | | | | | P | *1109.613577* | 555.310426 | 1092.587028 | 546.797152 | 1091.603012 | 546.305144 | 7 |
| 4 | 381.249632 | 191.128454 | | | | | L | *1012.560813* | 506.784044 | 995.534264 | 498.270770 | 994.550248 | 497.778762 | 6 |
| 5 | **480.318046** | 240.662661 | | | | | V | *899.476749* | 450.242012 | 882.450200 | 441.728738 | 881.466184 | 441.236730 | 5 |
| 6 | 609.360639 | 305.183958 | | | 591.350074 | 296.178675 | E | *800.408335* | 400.707805 | 783.381786 | 392.194531 | 782.397770 | 391.702523 | 4 |
| 7 | 1048.585965 | 524.796621 | 1031.559416 | 516.283346 | 1030.575400 | 515.791338 | Q | *671.365742* | 336.186509 | 654.339193 | 327.673234 | | | 3 |
| 8 | 1105.607429 | 553.307352 | 1088.580880 | 544.794078 | 1087.596864 | 544.302070 | G | *232.140416* | 116.573846 | 215.113867 | 108.060571 | | | 2 |
| 9 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.3 | 1278.711823 | 0.004905 | LGPLVEQGR |
| 0.3 | 1278.697891 | 0.018837 | LGSVCRRIYR |

**Mascot:** http://www.matrixscience.com/

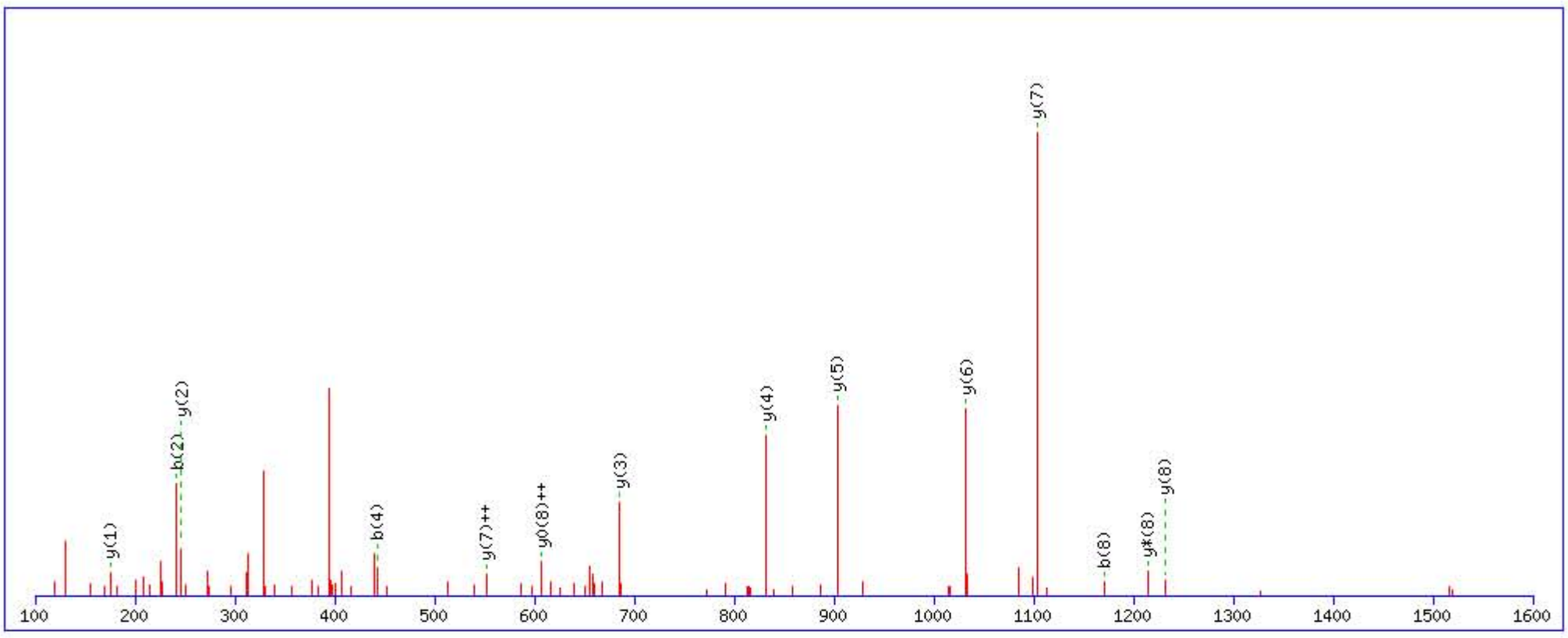
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LQAEAFQAR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

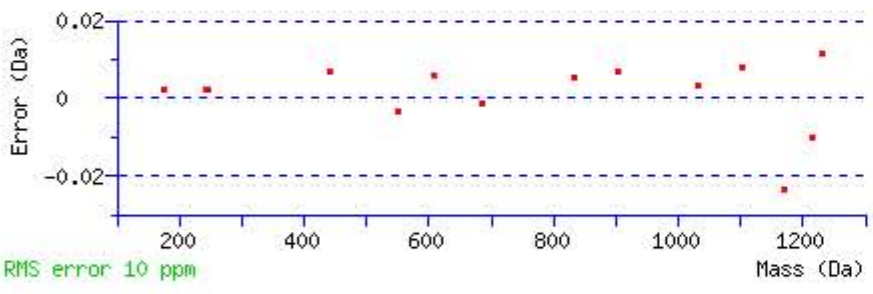
Match to Query 24204: 1343.697568 from(672.856060,2+) rtinseconds(1782) index(18758)
Title: Locus:1.1.1.3003.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

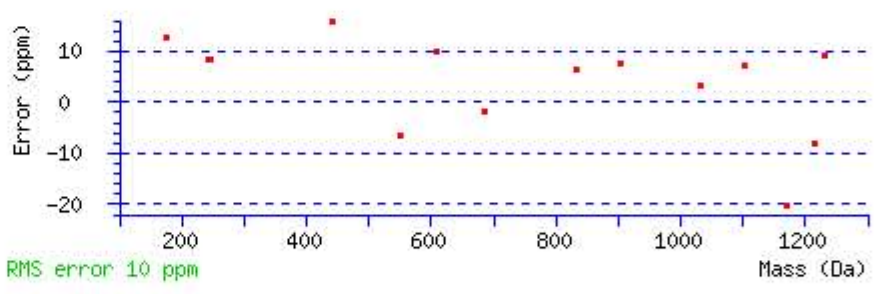
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1343.701965
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 4.6e-005
**Matches :** 14/78 fragment ions using 24 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 9 |
| 2 | **242.149918** | 121.578597 | 225.123369 | 113.065323 | | | Q | *1231.625205* | 616.316241 | 1214.598656 | 607.802966 | 1213.614640 | 607.310958 | 8 |
| 3 | 313.187032 | 157.097154 | 296.160483 | 148.583879 | | | A | *1103.566627* | 552.286951 | 1086.540078 | 543.773677 | 1085.556062 | 543.281669 | 7 |
| 4 | **442.229625** | 221.618450 | 425.203076 | 213.105176 | 424.219060 | 212.613168 | E | *1032.529513* | 516.768395 | 1015.502964 | 508.255120 | 1014.518948 | 507.763112 | 6 |
| 5 | 513.266739 | 257.137008 | 496.240190 | 248.623733 | 495.256174 | 248.131725 | A | *903.486920* | 452.247098 | 886.460371 | 443.733823 | | | 5 |
| 6 | 660.335153 | 330.671215 | 643.308604 | 322.157940 | 642.324588 | 321.665932 | F | *832.449806* | 416.728541 | 815.423257 | 408.215266 | | | 4 |
| 7 | 1099.560479 | 550.283878 | 1082.533930 | 541.770603 | 1081.549914 | 541.278595 | Q | *685.381392* | 343.194334 | 668.354843 | 334.681060 | | | 3 |
| 8 | **1170.597593** | 585.802435 | 1153.571044 | 577.289160 | 1152.587028 | 576.797152 | A | *246.156066* | 123.581671 | 229.129517 | 115.068396 | | | 2 |
| 9 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 57.6 | 1343.701965 | -0.004397 | LQAEAFQAR |
| 11.5 | 1343.694107 | 0.003461 | IQAMSEVQK |
| 11.5 | 1343.704453 | -0.006885 | IQEKKDEDIAR |
| 9.8 | 1343.715683 | -0.018115 | LKDSEAELQRR |
| 9.6 | 1343.683350 | 0.014218 | GSPAAPEGALGYVR |
| 8.3 | 1343.683350 | 0.014218 | LSKSVSSGYNFR |
| 7.1 | 1343.704453 | -0.006885 | IKGEELSEANVR |
| 7.1 | 1343.704453 | -0.006885 | LQAANAEDIKSGK |
| 5.3 | 1343.716583 | -0.019015 | LQQVMSRR |
| 5.0 | 1343.693237 | 0.004331 | LQDLELDLETR |

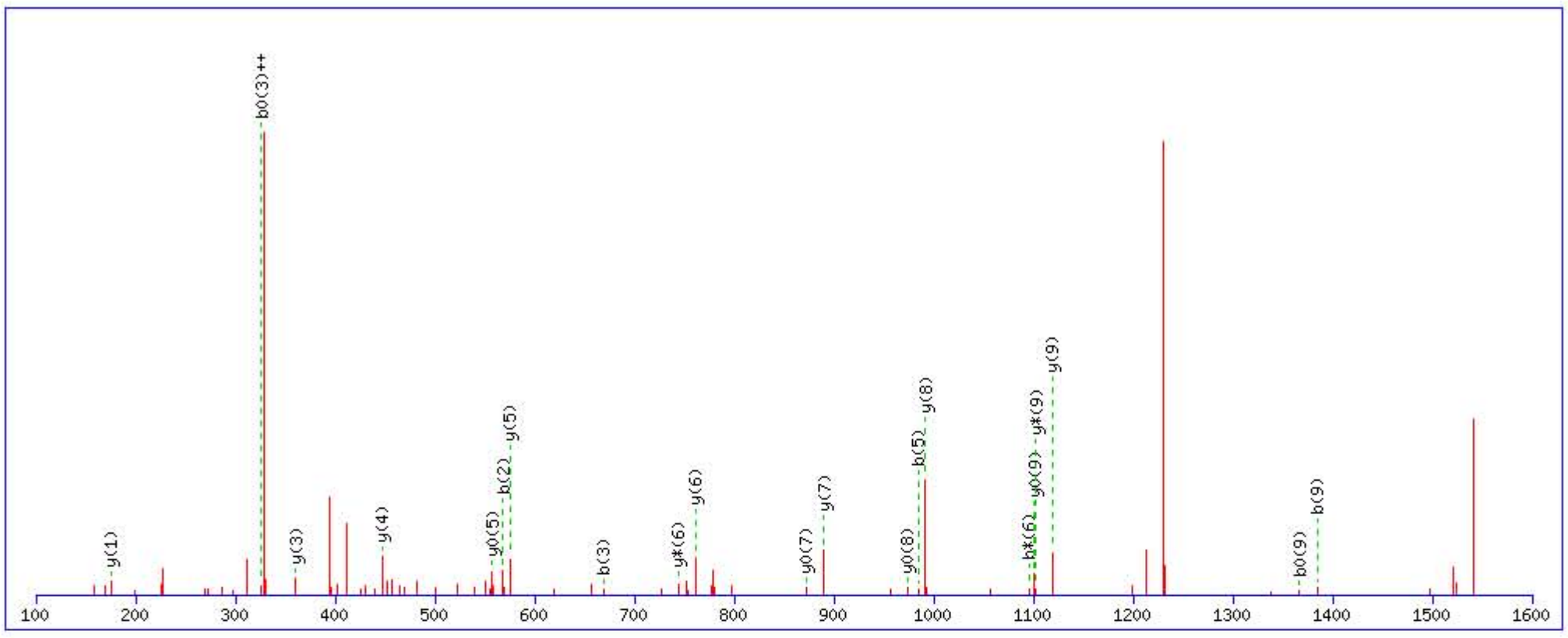
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QQTEWQSGQR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

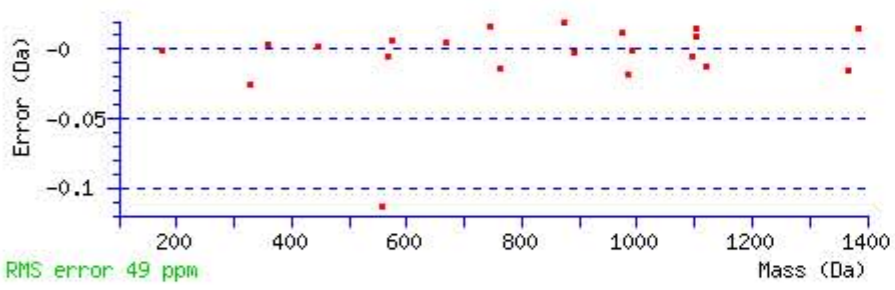
Match to Query 32655: 1557.737208 from(779.875880,2+) rtinseconds(1556) index(3011)
Title: Locus:1.1.1.1818.22 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

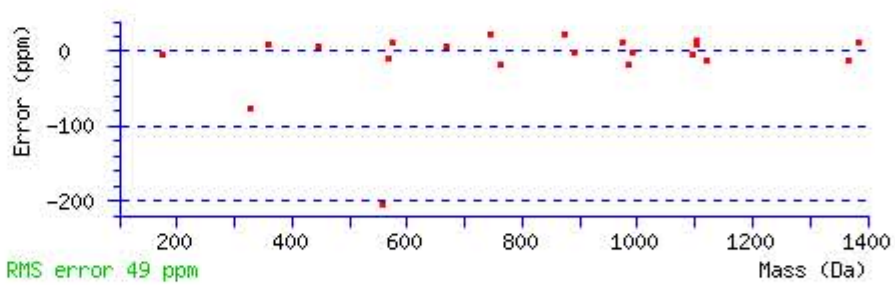
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1557.735809
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0063
**Matches** : 21/98 fragment ions using 51 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 10 |
| 2 | **568.291180** | 284.649228 | 551.264631 | 276.135954 | | | Q | *1119.517763* | 560.262520 | 1102.491214 | 551.749245 | 1101.507198 | 551.257237 | 9 |
| 3 | **669.338859** | 335.173068 | 652.312310 | 326.659793 | 651.328294 | 326.167785 | T | *991.459185* | 496.233231 | 974.432636 | 487.719956 | 973.448620 | 487.227948 | 8 |
| 4 | 798.381452 | 399.694364 | 781.354903 | 391.181090 | 780.370887 | 390.689082 | E | *890.411506* | 445.709391 | 873.384957 | 437.196117 | 872.400941 | 436.704109 | 7 |
| 5 | **984.460765** | 492.734021 | 967.434216 | 484.220746 | 966.450200 | 483.728738 | W | *761.368913* | 381.188095 | 744.342364 | 372.674820 | 743.358348 | 372.182812 | 6 |
| 6 | 1112.519343 | 556.763310 | 1095.492794 | 548.250035 | 1094.508778 | 547.758027 | Q | *575.289600* | 288.148438 | 558.263051 | 279.635164 | 557.279035 | 279.143156 | 5 |
| 7 | 1199.551371 | 600.279324 | 1182.524822 | 591.766049 | 1181.540806 | 591.274041 | S | *447.231022* | 224.119149 | 430.204473 | 215.605875 | 429.220457 | 215.113867 | 4 |
| 8 | 1256.572835 | 628.790056 | 1239.546286 | 620.276781 | 1238.562270 | 619.784773 | G | *360.198994* | 180.603135 | 343.172445 | 172.089860 | | | 3 |
| 9 | **1384.631413** | 692.819345 | 1367.604864 | 684.306070 | 1366.620848 | 683.814062 | Q | 303.177530 | 152.092403 | 286.150981 | 143.579129 | | | 2 |
| 10 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.3 | 1557.735809 | 0.001399 | QQTEWQSGQR |
| 22.3 | 1557.735809 | 0.001399 | QQTEWQSGQR |
| 9.9 | 1557.747040 | -0.009832 | AFSHCSSLTKHQR |
| 4.2 | 1557.720566 | 0.016642 | QEAATGVDTICTHR |
| 2.7 | 1557.720551 | 0.016657 | LSQVSPEDDRPCR |
| 2.4 | 1557.742340 | -0.005132 | TQSFEIPQPDSGPR |
| 2.2 | 1557.756897 | -0.019689 | MAASAAAAELQASGGPR |
| 1.8 | 1557.749496 | -0.012288 | QAEATRQAAAQEER |
| 1.1 | 1557.753571 | -0.016363 | DYSSVVRPVEDHR |
| 0.9 | 1557.728638 | 0.008570 | TFLFCTPFTPDGR |

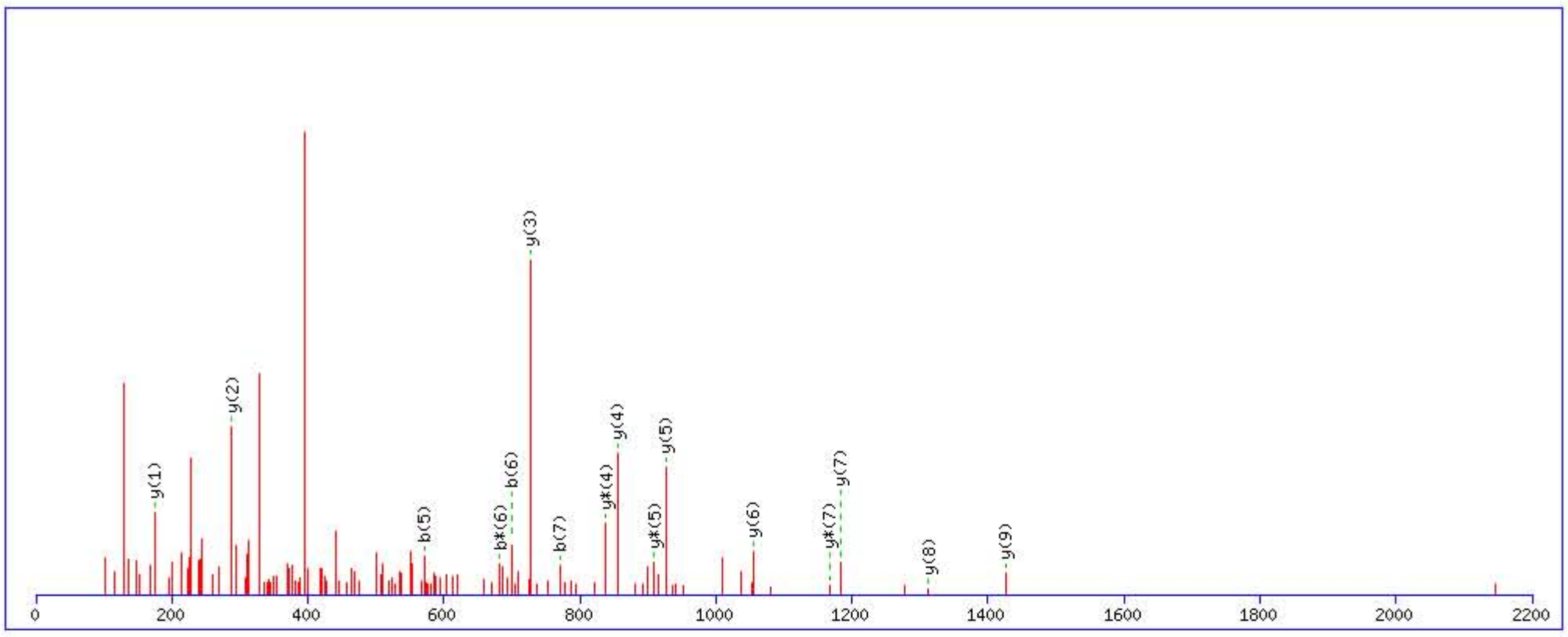
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AKLEEQAQQIR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

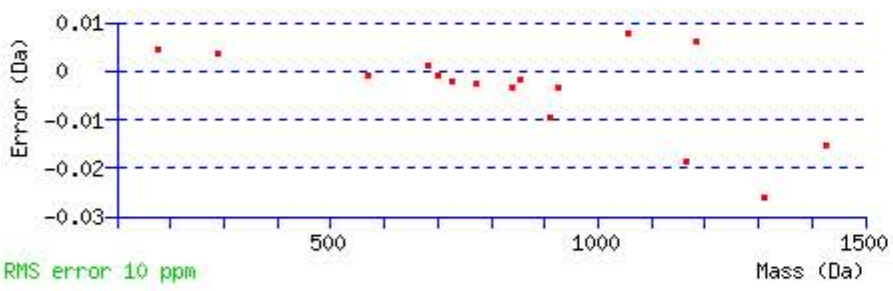
Match to Query 35710: 1623.876222 from(542.299350,3+) rtinseconds(1475) index(16732)
Title: Locus:1.1.1.2896.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

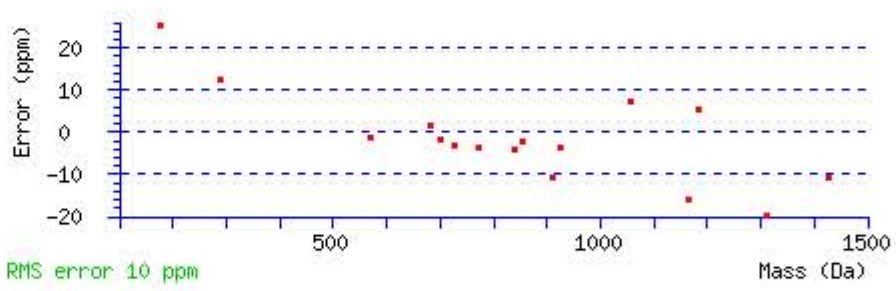
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1623.876617
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 63 **Expect:** 1.1e-005
**Matches :** 16/100 fragment ions using 25 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 11 |
| 2 | 200.139353 | 100.573315 | 183.112804 | 92.060040 | | | K | 1553.846825 | 777.427050 | 1536.820276 | 768.913776 | 1535.836260 | 768.421768 | 10 |
| 3 | 313.223417 | 157.115346 | 296.196868 | 148.602072 | | | L | *1425.751862* | 713.379569 | 1408.725313 | 704.866294 | 1407.741297 | 704.374286 | 9 |
| 4 | 442.266010 | 221.636643 | 425.239461 | 213.123369 | 424.255445 | 212.631361 | E | *1312.667798* | 656.837537 | 1295.641249 | 648.324262 | 1294.657233 | 647.832254 | 8 |
| 5 | **571.308603** | 286.157940 | 554.282054 | 277.644665 | 553.298038 | 277.152657 | E | *1183.625205* | 592.316240 | 1166.598656 | 583.802966 | 1165.614640 | 583.310958 | 7 |
| 6 | **699.367181** | 350.187229 | 682.340632 | 341.673954 | 681.356616 | 341.181946 | Q | *1054.582612* | 527.794944 | 1037.556063 | 519.281670 | | | 6 |
| 7 | **770.404295** | 385.705786 | 753.377746 | 377.192511 | 752.393730 | 376.700503 | A | *926.524034* | 463.765655 | 909.497485 | 455.252380 | | | 5 |
| 8 | 898.462873 | 449.735075 | 881.436324 | 441.221800 | 880.452308 | 440.729792 | Q | *855.486920* | 428.247098 | 838.460371 | 419.733823 | | | 4 |
| 9 | 1337.688199 | 669.347737 | 1320.661650 | 660.834463 | 1319.677634 | 660.342455 | Q | *727.428342* | 364.217809 | 710.401793 | 355.704534 | | | 3 |
| 10 | 1450.772263 | 725.889769 | 1433.745714 | 717.376495 | 1432.761698 | 716.884487 | I | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 63.2 | 1623.876617 | -0.000395 | AKLEEQAQQIR |
| 48.7 | 1623.876617 | -0.000395 | AKLEEQAQQIR |
| 27.7 | 1623.877502 | -0.001280 | QMKAQQLR |
| 18.6 | 1623.877502 | -0.001280 | QMKAQQLR |
| 13.1 | 1623.876617 | -0.000395 | AKLEEQAQQIR |
| 6.8 | 1623.877502 | -0.001280 | AQKMQQLR |
| 6.5 | 1623.866745 | 0.009477 | QAQAQPHLPPAR |
| 6.5 | 1623.876617 | -0.000395 | QAEEAVAKLQAR |
| 4.1 | 1623.877502 | -0.001280 | QMKAQQLR |
| 3.5 | 1623.876633 | -0.000411 | QKALVDNEQLR |

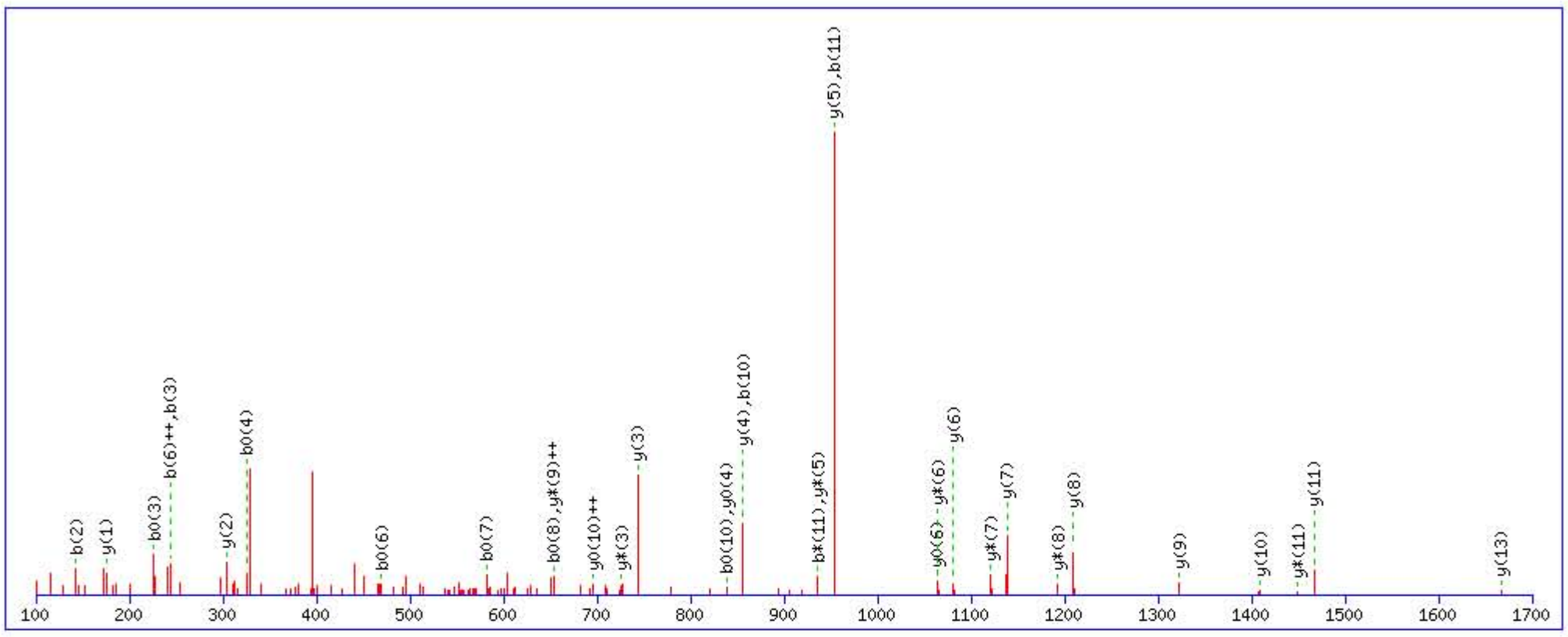
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AATVGSLAGQPLQER**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

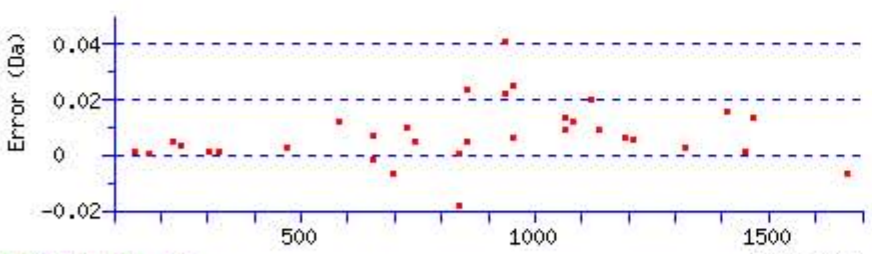
Match to Query 40406: 1807.971612 from(603.664480,3+) rtinseconds(1932) index(19864)
Title: Locus:1.1.1.3055.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

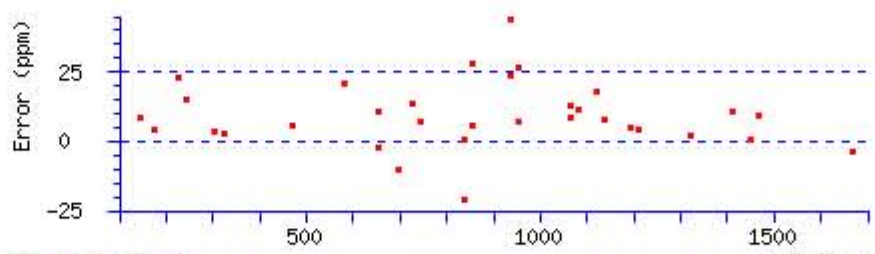
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1807.961441
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q13** : Biotin:Thermo-21345 (Q)
**Ions Score:** 77 **Expect:** 5e-007
**Matches :** 34/144 fragment ions using 52 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 15 |
| 2 | **143.081504** | 72.044390 | | | | | A | 1737.931618 | 869.469447 | 1720.905069 | 860.956173 | 1719.921053 | 860.464165 | 14 |
| 3 | **244.129183** | 122.568230 | | | 226.118618 | 113.562947 | T | ***1666.894504*** | 833.950890 | 1649.867955 | 825.437616 | 1648.883939 | 824.945608 | 13 |
| 4 | 343.197597 | 172.102437 | | | 325.187032 | 163.097154 | V | 1565.846825 | 783.427051 | 1548.820276 | 774.913776 | 1547.836260 | 774.421768 | 12 |
| 5 | 400.219061 | 200.613169 | | | 382.208496 | 191.607886 | G | ***1466.778411*** | 733.892844 | 1449.751862 | 725.379569 | 1448.767846 | 724.887561 | 11 |
| 6 | 487.251089 | 244.129183 | | | 469.240524 | 235.123900 | S | ***1409.756947*** | 705.382112 | 1392.730398 | 696.868837 | 1391.746382 | 696.376829 | 10 |
| 7 | 600.335153 | 300.671215 | | | 582.324588 | 291.665932 | L | ***1322.724919*** | 661.866098 | 1305.698370 | 653.352823 | 1304.714354 | 652.860815 | 9 |
| 8 | 671.372267 | 336.189772 | | | 653.361702 | 327.184489 | A | ***1209.640855*** | 605.324066 | 1192.614306 | 596.810791 | 1191.630290 | 596.318783 | 8 |
| 9 | 728.393731 | 364.700504 | | | 710.383166 | 355.695221 | G | ***1138.603741*** | 569.805509 | 1121.577192 | 561.292234 | 1120.593176 | 560.800226 | 7 |
| 10 | **856.452309** | 428.729793 | 839.425760 | 420.216518 | 838.441744 | 419.724510 | Q | ***1081.582277*** | 541.294777 | 1064.555728 | 532.781502 | 1063.571712 | 532.289494 | 6 |
| 11 | **953.505073** | 477.256175 | 936.478524 | 468.742900 | 935.494508 | 468.250892 | P | ***953.523699*** | 477.265488 | 936.497150 | 468.752213 | 935.513134 | 468.260205 | 5 |
| 12 | 1066.589137 | 533.798207 | 1049.562588 | 525.284932 | 1048.578572 | 524.792924 | L | ***856.470935*** | 428.739106 | 839.444386 | 420.225831 | 838.460370 | 419.733823 | 4 |
| 13 | 1505.814463 | 753.410870 | 1488.787914 | 744.897595 | 1487.803898 | 744.405587 | Q | ***743.386871*** | 372.197074 | 726.360322 | 363.683799 | 725.376306 | 363.191791 | 3 |
| 14 | 1634.857056 | 817.932166 | 1617.830507 | 809.418892 | 1616.846491 | 808.926884 | E | ***304.161545*** | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 15 | | | | | | | R | ***175.118952*** | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 76.6 | 1807.961441 | 0.010171 | AATVGSLAGQPLQER |
| 35.5 | 1807.961441 | 0.010171 | AATVGSLAGQPLQER |
| 15.3 | 1807.947510 | 0.024102 | VGLAQIAAMDISRGNHR |

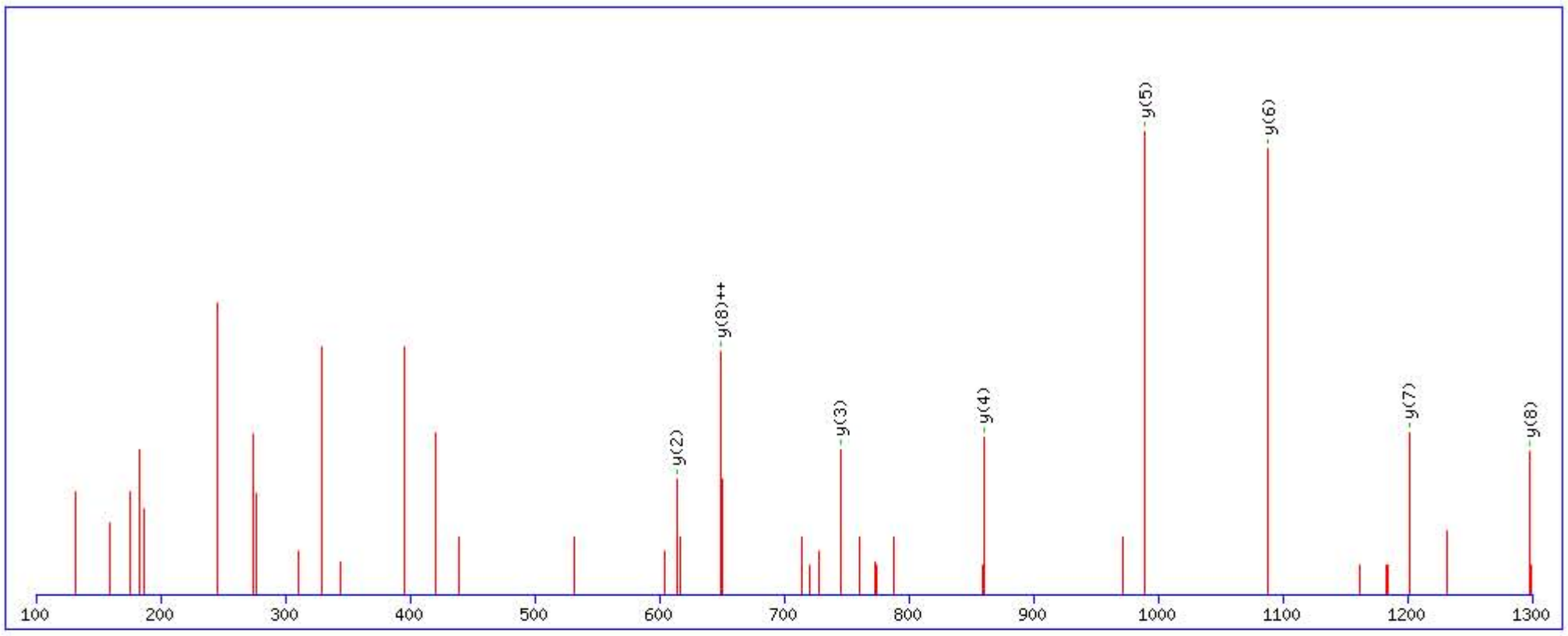
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SWFEPLVEDMQR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

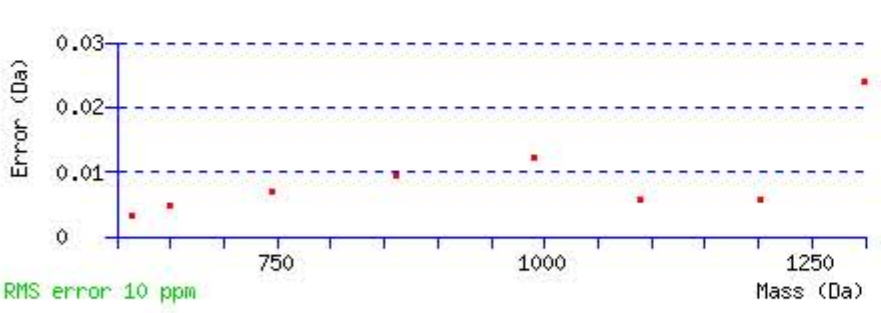
Match to Query 41189: 1846.887852 from(616.636560,3+) rtinseconds(2815) index(9962)
Title: Locus:1.1.1.2257.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

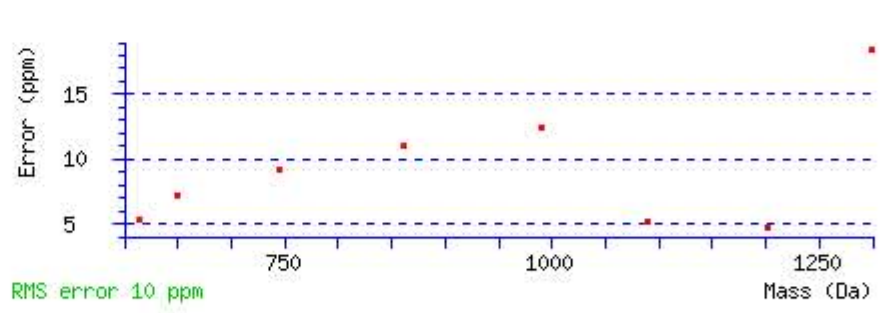
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1846.874603
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 49 **Expect:** 0.0001
**Matches :** 8/106 fragment ions using 12 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 12 |
| 2 | 274.118617 | 137.562947 | | | 256.108052 | 128.557664 | W | 1760.849861 | 880.928568 | 1743.823312 | 872.415294 | 1742.839296 | 871.923286 | 11 |
| 3 | 421.187031 | 211.097153 | | | 403.176466 | 202.091871 | F | 1574.770548 | 787.888912 | 1557.743999 | 779.375638 | 1556.759983 | 778.883629 | 10 |
| 4 | 550.229624 | 275.618450 | | | 532.219059 | 266.613168 | E | 1427.702134 | 714.354705 | 1410.675585 | 705.841431 | 1409.691569 | 705.349422 | 9 |
| 5 | 647.282388 | 324.144832 | | | 629.271823 | 315.139550 | P | *1298.659541* | 649.833409 | 1281.632992 | 641.320134 | 1280.648976 | 640.828126 | 8 |
| 6 | 760.366452 | 380.686864 | | | 742.355887 | 371.681582 | L | *1201.606777* | 601.307027 | 1184.580228 | 592.793752 | 1183.596212 | 592.301744 | 7 |
| 7 | 859.434866 | 430.221071 | | | 841.424301 | 421.215789 | V | *1088.522713* | 544.764995 | 1071.496164 | 536.251720 | 1070.512148 | 535.759712 | 6 |
| 8 | 988.477459 | 494.742368 | | | 970.466894 | 485.737085 | E | *989.454299* | 495.230788 | 972.427750 | 486.717513 | 971.443734 | 486.225505 | 5 |
| 9 | 1103.504402 | 552.255839 | | | 1085.493837 | 543.250557 | D | *860.411706* | 430.709491 | 843.385157 | 422.196216 | 842.401141 | 421.704208 | 4 |
| 10 | 1234.544887 | 617.776082 | | | 1216.534322 | 608.770799 | M | *745.384763* | 373.196020 | 728.358214 | 364.682745 | | | 3 |
| 11 | 1673.770213 | 837.388745 | 1656.743664 | 828.875470 | 1655.759648 | 828.383462 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 12 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 49.1 | 1846.874603 | 0.013249 | SWFEPLVEDMQR |
| 6.0 | 1846.866562 | 0.021290 | LCMAQPRTVQDVEER |
| 1.6 | 1846.895721 | -0.007869 | LQLEETMPSPYGR |
| 0.7 | 1846.902084 | -0.014232 | GTSRVDDKPSSPGDSSKK |
| 0.0 | 1846.895706 | -0.007854 | CFELQALLEEER |

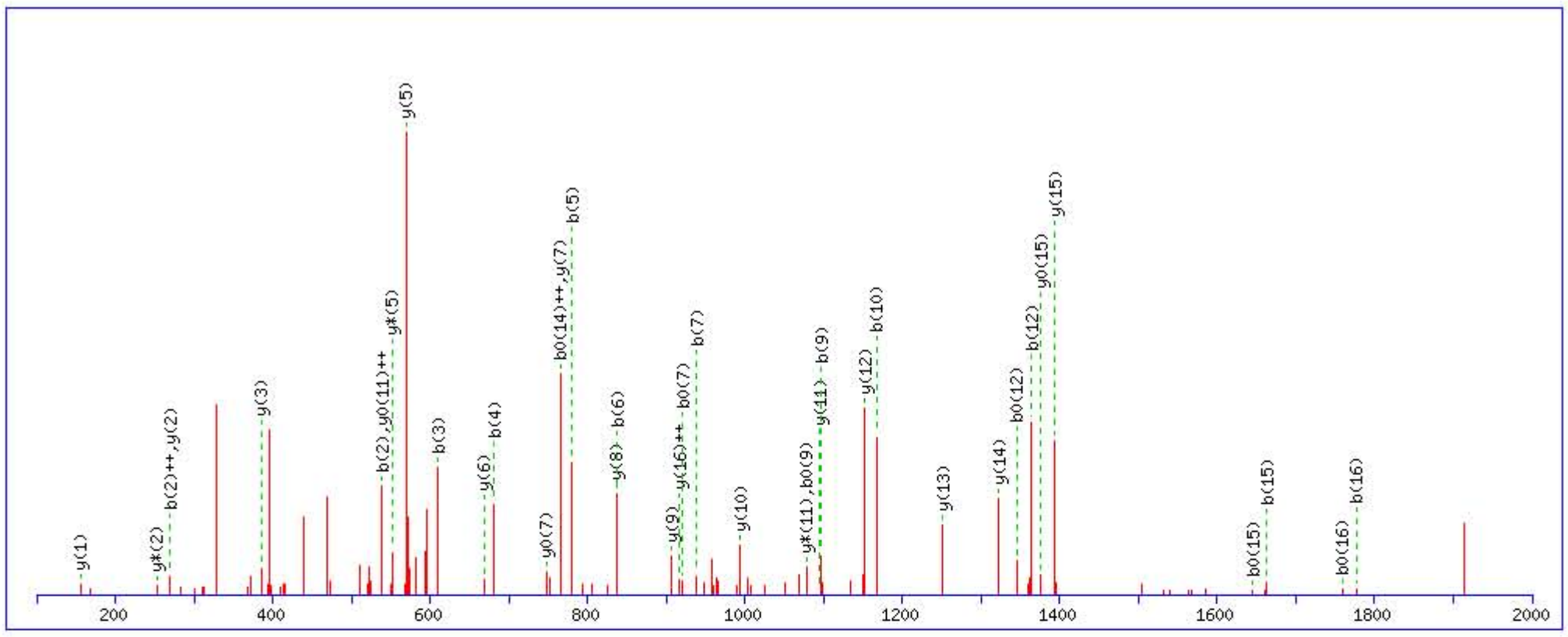
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VQAAVGTSAAPVPSDNH**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

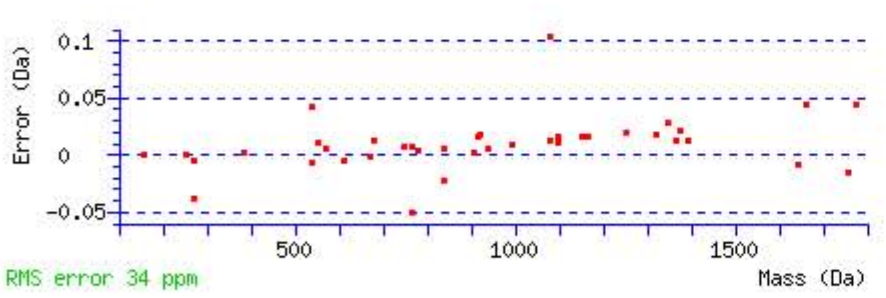
Match to Query 42718: 1930.977788 from(966.496170,2+) rtinseconds(1697) index(32258)
Title: Locus:1.1.1.699.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

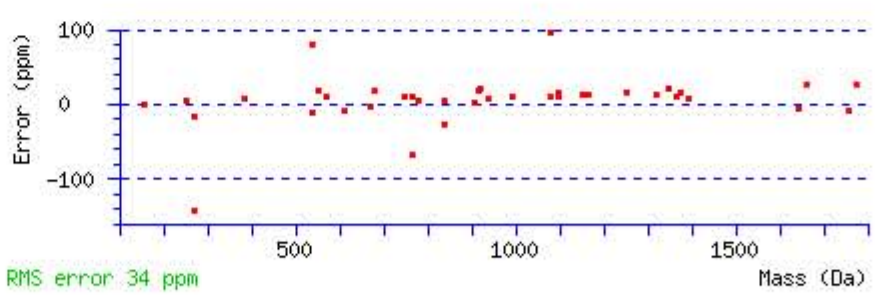
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1930.957108
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 102 **Expect:** 1.9e-009
**Matches :** 39/172 fragment ions using 59 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 17 |
| 2 | **539.301016** | 270.154146 | 522.274467 | 261.640872 | | | Q | 1832.895960 | 916.951618 | 1815.869411 | 908.438344 | 1814.885395 | 907.946336 | 16 |
| 3 | **610.338130** | 305.672703 | 593.311581 | 297.159429 | | | A | *1393.670634* | 697.338955 | 1376.644085 | 688.825681 | 1375.660069 | 688.333673 | 15 |
| 4 | **681.375244** | 341.191260 | 664.348695 | 332.677986 | | | A | *1322.633520* | 661.820398 | 1305.606971 | 653.307124 | 1304.622955 | 652.815116 | 14 |
| 5 | **780.443658** | 390.725467 | 763.417109 | 382.212193 | | | V | *1251.596406* | 626.301841 | 1234.569857 | 617.788567 | 1233.585841 | 617.296559 | 13 |
| 6 | **837.465122** | 419.236199 | 820.438573 | 410.722925 | | | G | *1152.527992* | 576.767634 | 1135.501443 | 568.254360 | 1134.517427 | 567.762352 | 12 |
| 7 | **938.512801** | 469.760039 | 921.486252 | 461.246764 | 920.502236 | 460.754756 | T | *1095.506528* | 548.256902 | 1078.479979 | 539.743628 | 1077.495963 | 539.251620 | 11 |
| 8 | 1025.544829 | 513.276053 | 1008.518280 | 504.762778 | 1007.534264 | 504.270770 | S | *994.458849* | 497.733063 | 977.432300 | 489.219788 | 976.448284 | 488.727780 | 10 |
| 9 | **1096.581943** | 548.794610 | 1079.555394 | 540.281335 | 1078.571378 | 539.789327 | A | *907.426821* | 454.217049 | 890.400272 | 445.703774 | 889.416256 | 445.211766 | 9 |
| 10 | **1167.619057** | 584.313167 | 1150.592508 | 575.799892 | 1149.608492 | 575.307884 | A | *836.389707* | 418.698492 | 819.363158 | 410.185217 | 818.379142 | 409.693209 | 8 |
| 11 | 1264.671821 | 632.839549 | 1247.645272 | 624.326274 | 1246.661256 | 623.834266 | P | *765.352593* | 383.179935 | 748.326044 | 374.666660 | 747.342028 | 374.174652 | 7 |
| 12 | **1363.740235** | 682.373756 | 1346.713686 | 673.860481 | 1345.729670 | 673.368473 | V | *668.299829* | 334.653553 | 651.273280 | 326.140278 | 650.289264 | 325.648270 | 6 |
| 13 | 1460.792999 | 730.900138 | 1443.766450 | 722.386863 | 1442.782434 | 721.894855 | P | *569.231415* | 285.119346 | 552.204866 | 276.606071 | 551.220850 | 276.114063 | 5 |
| 14 | 1547.825027 | 774.416152 | 1530.798478 | 765.902877 | 1529.814462 | 765.410869 | S | 472.178651 | 236.592964 | 455.152102 | 228.079689 | 454.168086 | 227.587681 | 4 |
| 15 | **1662.851970** | 831.929623 | 1645.825421 | 823.416349 | 1644.841405 | 822.924341 | D | *385.146623* | 193.076949 | 368.120074 | 184.563675 | 367.136058 | 184.071667 | 3 |
| 16 | **1776.894897** | 888.951087 | 1759.868348 | 880.437812 | 1758.884332 | 879.945804 | N | *270.119680* | 135.563478 | 253.093131 | 127.050203 | | | 2 |
| 17 | | | | | | | H | *156.076753* | 78.542014 | | | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 102.0 | 1930.957108 | 0.020680 | VQAAVGTSAAPVPSDNH |

**Mascot:** http://www.matrixscience.com/

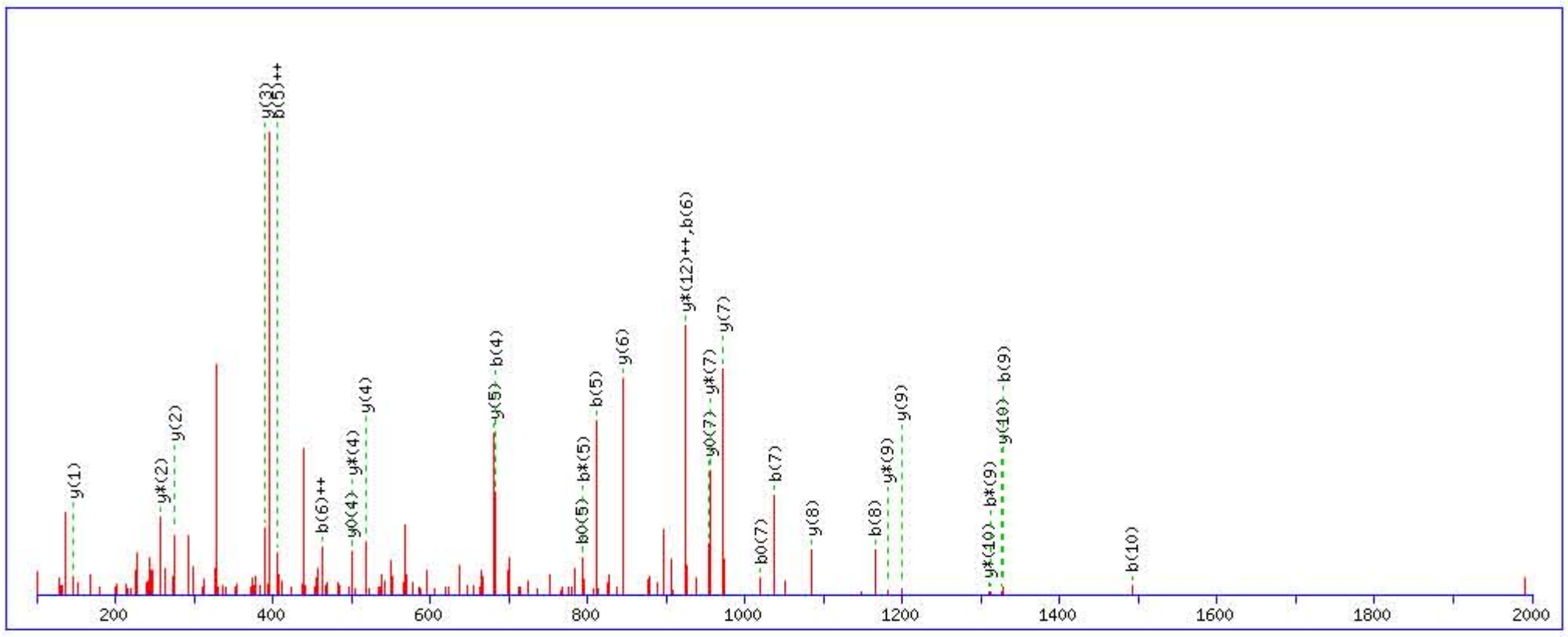
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SGVQQLIQYYQDQK**
Found in **APOF_HUMAN**, Apolipoprotein F OS=Homo sapiens GN=APOF PE=1 SV=2

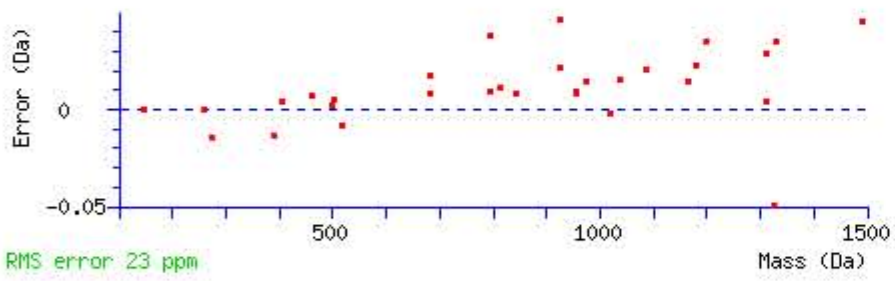
Match to Query 44879: 2008.034112 from(670.351980,3+) rtinseconds(2478) index(53228)
Title: Locus:1.1.1.2100.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

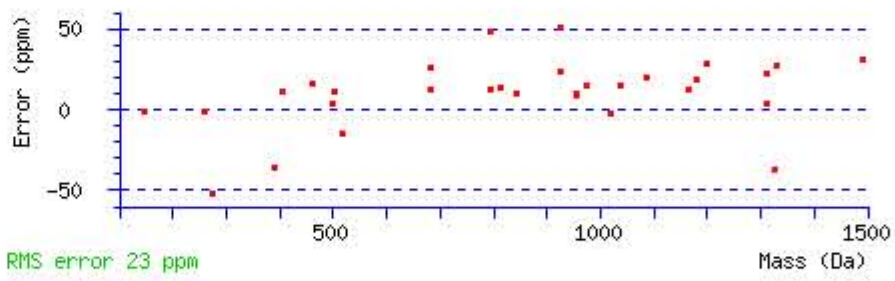
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2008.008789
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 3.8e-005
**Matches :** 31/146 fragment ions using 50 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 14 |
| 2 | 145.060768 | 73.034022 | | | 127.050203 | 64.028740 | G | 1921.984049 | 961.495663 | 1904.957500 | 952.982388 | 1903.973484 | 952.490380 | 13 |
| 3 | 244.129182 | 122.568229 | | | 226.118617 | 113.562947 | V | 1864.962585 | 932.984931 | 1847.936036 | 924.471656 | 1846.952020 | 923.979648 | 12 |
| 4 | **683.354508** | 342.180892 | 666.327959 | 333.667618 | 665.343943 | 333.175610 | Q | 1765.894171 | 883.450724 | 1748.867622 | 874.937449 | 1747.883606 | 874.445441 | 11 |
| 5 | **811.413086** | **406.210181** | 794.386537 | 397.696907 | 793.402521 | 397.204899 | Q | *1326.668845* | 663.838061 | 1309.642296 | 655.324786 | 1308.658280 | 654.832778 | 10 |
| 6 | **924.497150** | **462.752213** | 907.470601 | 454.238939 | 906.486585 | 453.746931 | L | *1198.610267* | 599.808772 | 1181.583718 | 591.295497 | 1180.599702 | 590.803489 | 9 |
| 7 | **1037.581214** | 519.294245 | 1020.554665 | 510.780971 | 1019.570649 | 510.288963 | I | *1085.526203* | 543.266740 | 1068.499654 | 534.753465 | 1067.515638 | 534.261457 | 8 |
| 8 | **1165.639792** | 583.323534 | 1148.613243 | 574.810260 | 1147.629227 | 574.318252 | Q | *972.442139* | 486.724708 | 955.415590 | 478.211433 | 954.431574 | 477.719425 | 7 |
| 9 | **1328.703121** | 664.855199 | 1311.676572 | 656.341924 | 1310.692556 | 655.849916 | Y | *844.383561* | 422.695419 | 827.357012 | 414.182144 | 826.372996 | 413.690136 | 6 |
| 10 | **1491.766450** | 746.386863 | 1474.739901 | 737.873589 | 1473.755885 | 737.381581 | Y | *681.320232* | 341.163754 | 664.293683 | 332.650480 | 663.309667 | 332.158472 | 5 |
| 11 | 1619.825028 | 810.416152 | 1602.798479 | 801.902878 | 1601.814463 | 801.410870 | Q | *518.256903* | 259.632090 | 501.230354 | 251.118815 | 500.246338 | 250.626807 | 4 |
| 12 | 1734.851971 | 867.929624 | 1717.825422 | 859.416349 | 1716.841406 | 858.924341 | D | *390.198325* | 195.602800 | 373.171776 | 187.089526 | 372.187760 | 186.597518 | 3 |
| 13 | 1862.910549 | 931.958913 | 1845.884000 | 923.445638 | 1844.899984 | 922.953630 | Q | *275.171382* | 138.089329 | 258.144833 | 129.576054 | | | 2 |
| 14 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.7 | 2008.008789 | 0.025323 | SGVQQLIQYYQDQK |
| 45.2 | 2008.008789 | 0.025323 | SGVQQLIQYYQDQK |
| 15.4 | 2008.063568 | -0.029456 | QQLEAQRAEAERLR |
| 11.1 | 2008.008789 | 0.025323 | SGVQQLIQYYQDQK |
| 6.2 | 2008.063568 | -0.029456 | QQLEAQRAEAERLR |
| 3.0 | 2008.026535 | 0.007577 | HYSNTLKALGISDEFVSK |
| 2.9 | 2008.030762 | 0.003350 | ASVMLFMKGNKQEAK |
| 1.3 | 2008.051895 | -0.017783 | MIEDTMTLLSLLGRIMR |
| 0.5 | 2008.037308 | -0.003196 | VVPVSLSELYLLQCNMK |

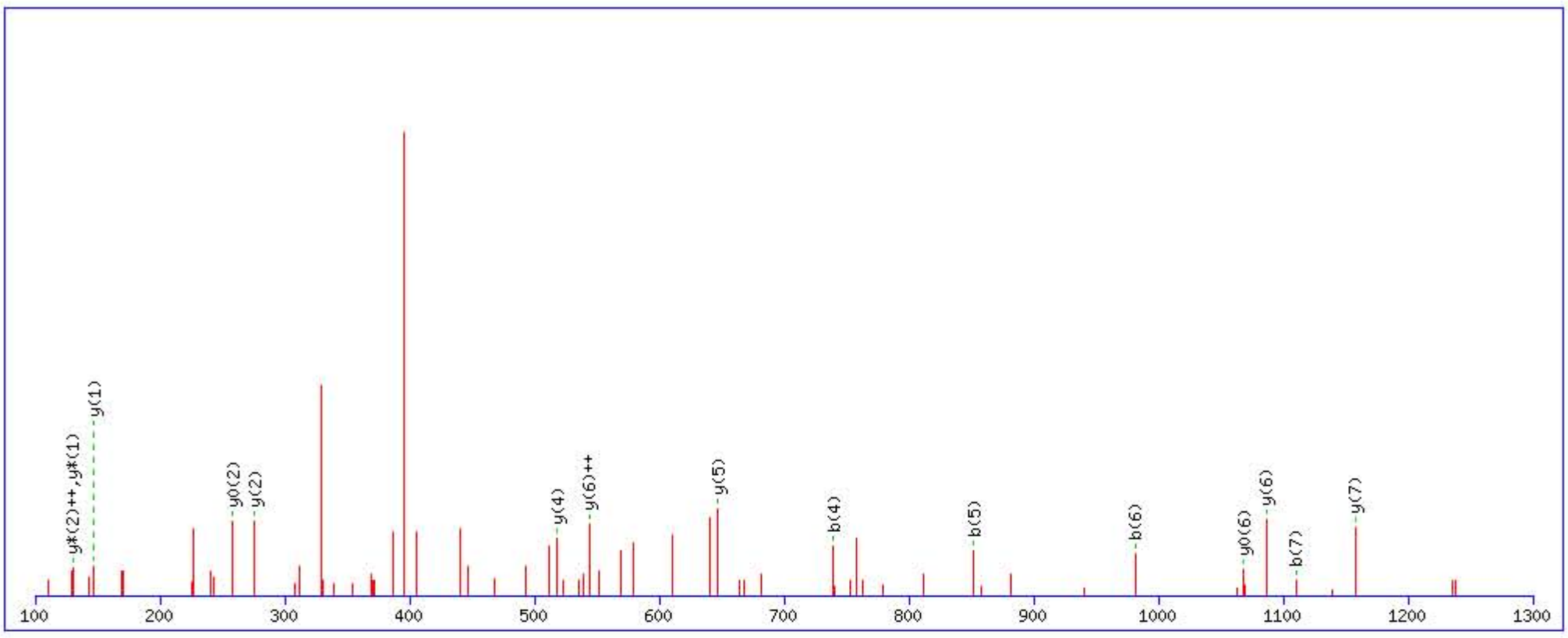
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VAQELEEK**
Found in **APOL1_HUMAN**, Apolipoprotein L1 OS=Homo sapiens GN=APOL1 PE=1 SV=5

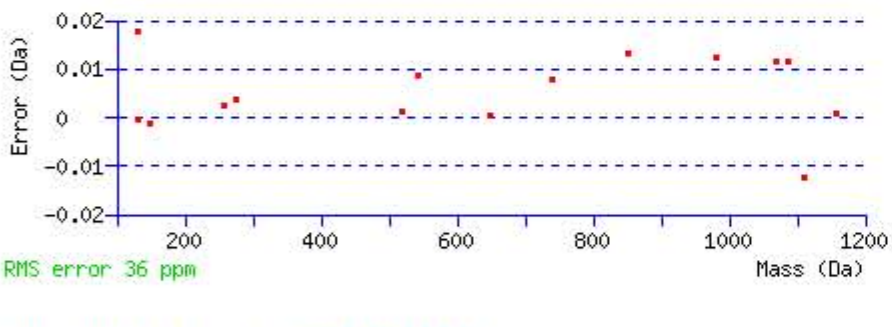
Match to Query 22050: 1255.653568 from(628.834060,2+) rtinseconds(1583) index(47492)
Title: Locus:1.1.1.1789.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

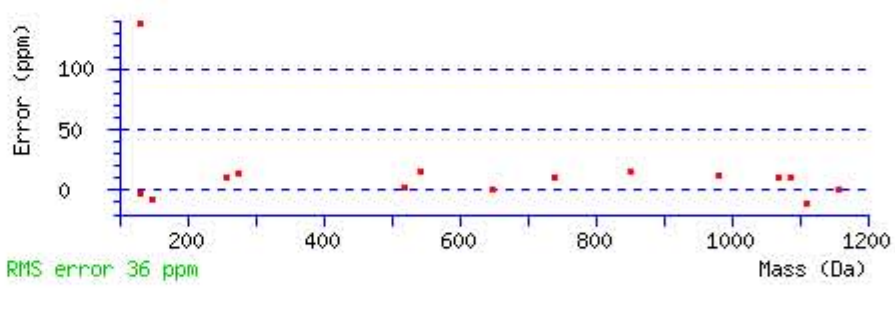
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1255.648193
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.01
**Matches :** 15/72 fragment ions using 24 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 8 |
| 2 | 171.112804 | 86.060040 | | | | | A | *1157.587087* | 579.297182 | 1140.560538 | 570.783907 | 1139.576522 | 570.291899 | 7 |
| 3 | 610.338130 | 305.672703 | 593.311581 | 297.159429 | | | Q | *1086.549973* | 543.778625 | 1069.523424 | 535.265350 | 1068.539408 | 534.773342 | 6 |
| 4 | 739.380723 | 370.194000 | 722.354174 | 361.680725 | 721.370158 | 361.188717 | E | *647.324647* | 324.165962 | 630.298098 | 315.652687 | 629.314082 | 315.160679 | 5 |
| 5 | 852.464787 | 426.736032 | 835.438238 | 418.222757 | 834.454222 | 417.730749 | L | *518.282054* | 259.644665 | 501.255505 | 251.131391 | 500.271489 | 250.639383 | 4 |
| 6 | 981.507380 | 491.257328 | 964.480831 | 482.744054 | 963.496815 | 482.252046 | E | 405.197990 | 203.102633 | 388.171441 | 194.589359 | 387.187425 | 194.097351 | 3 |
| 7 | 1110.549973 | 555.778625 | 1093.523424 | 547.265350 | 1092.539408 | 546.773342 | E | *276.155397* | 138.581336 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 8 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.5 | 1255.648193 | 0.005375 | VAQELEEK |
| 11.8 | 1255.659424 | -0.005856 | QAEKNVEK |
| 10.3 | 1255.659439 | -0.005871 | GLQGEKGEK |
| 9.1 | 1255.656067 | -0.002499 | ALPIQSFSHEK |
| 8.6 | 1255.659439 | -0.005871 | STGAQPKEK |
| 7.7 | 1255.645508 | 0.008060 | TRMIEANIHR |
| 7.2 | 1255.640793 | 0.012775 | DTHKKLEEEK |
| 6.3 | 1255.648193 | 0.005375 | EQVEIAEK |
| 6.0 | 1255.638306 | 0.015262 | FKEHQEK |
| 5.8 | 1255.659439 | -0.005871 | LLIENGVSMHK |

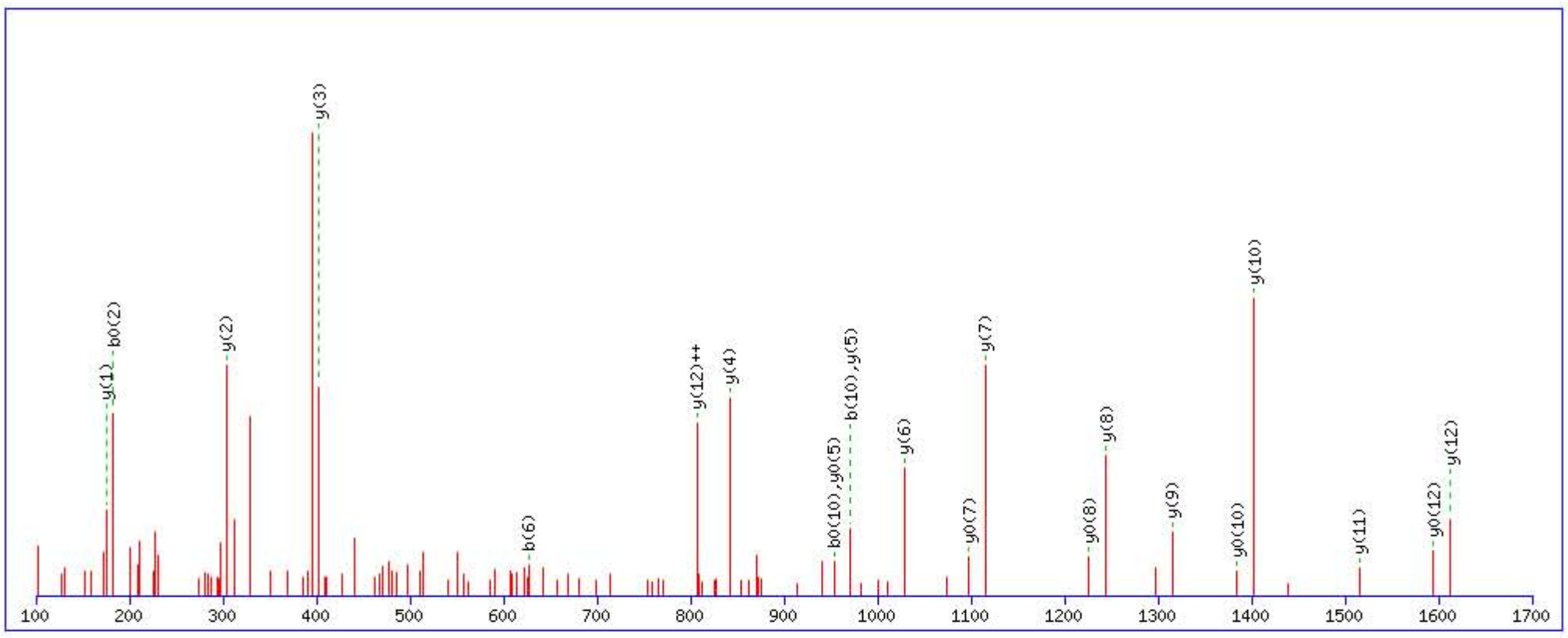
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VTEPISAESGEQVER**
Found in **APOL1_HUMAN**, Apolipoprotein L1 OS=Homo sapiens GN=APOL1 PE=1 SV=5

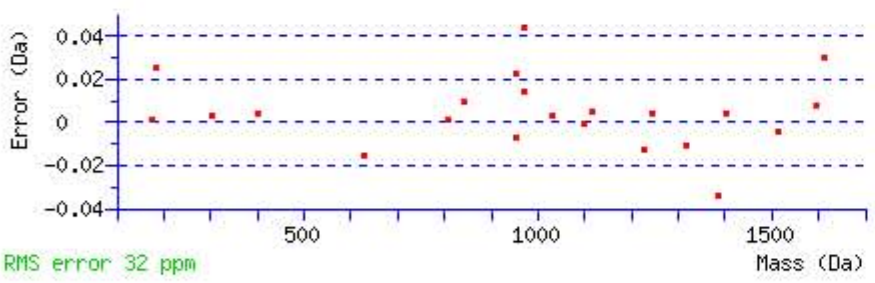
Match to Query 42942: 1940.956182 from(647.992670,3+) rtinseconds(1702) index(18248)
Title: Locus:1.1.1.2975.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

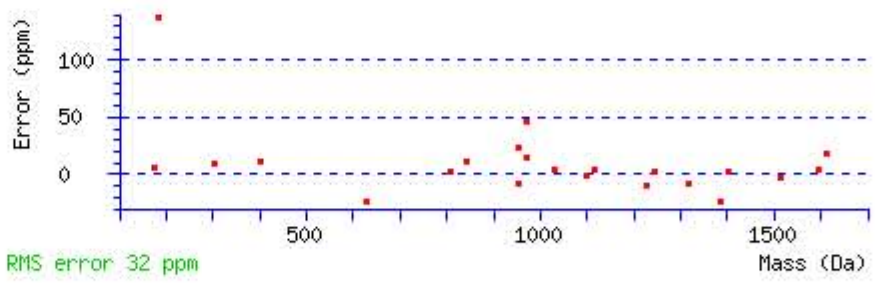
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1940.951324
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 91 **Expect:** 1.8e-008
**Matches :** 22/142 fragment ions using 30 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 15 |
| 2 | 201.123369 | 101.065322 | | | 183.112804 | 92.060040 | T | 1842.890205 | 921.948741 | 1825.863656 | 913.435466 | 1824.879640 | 912.943458 | 14 |
| 3 | 330.165962 | 165.586619 | | | 312.155397 | 156.581336 | E | 1741.842526 | 871.424901 | 1724.815977 | 862.911627 | 1723.831961 | 862.419619 | 13 |
| 4 | 427.218726 | 214.113001 | | | 409.208161 | 205.107719 | P | *1612.799933* | 806.903605 | 1595.773384 | 798.390330 | 1594.789368 | 797.898322 | 12 |
| 5 | 540.302790 | 270.655033 | | | 522.292225 | 261.649751 | I | *1515.747169* | 758.377223 | 1498.720620 | 749.863948 | 1497.736604 | 749.371940 | 11 |
| 6 | **627.334818** | 314.171047 | | | 609.324253 | 305.165765 | S | *1402.663105* | 701.835191 | 1385.636556 | 693.321916 | 1384.652540 | 692.829908 | 10 |
| 7 | 698.371932 | 349.689604 | | | 680.361367 | 340.684322 | A | *1315.631077* | 658.319177 | 1298.604528 | 649.805902 | 1297.620512 | 649.313894 | 9 |
| 8 | 827.414525 | 414.210901 | | | 809.403960 | 405.205618 | E | *1244.593963* | 622.800620 | 1227.567414 | 614.287345 | 1226.583398 | 613.795337 | 8 |
| 9 | 914.446553 | 457.726915 | | | 896.435988 | 448.721632 | S | *1115.551370* | 558.279323 | 1098.524821 | 549.766049 | 1097.540805 | 549.274041 | 7 |
| 10 | **971.468017** | 486.237647 | | | 953.457452 | 477.232364 | G | *1028.519342* | 514.763309 | 1011.492793 | 506.250035 | 1010.508777 | 505.758027 | 6 |
| 11 | 1100.510610 | 550.758943 | | | 1082.500045 | 541.753661 | E | *971.497878* | 486.252577 | 954.471329 | 477.739303 | 953.487313 | 477.247295 | 5 |
| 12 | 1539.735936 | 770.371606 | 1522.709387 | 761.858332 | 1521.725371 | 761.366324 | Q | *842.455285* | 421.731281 | 825.428736 | 413.218006 | 824.444720 | 412.725998 | 4 |
| 13 | 1638.804350 | 819.905813 | 1621.777801 | 811.392539 | 1620.793785 | 810.900531 | V | *403.229959* | 202.118617 | 386.203410 | 193.605343 | 385.219394 | 193.113335 | 3 |
| 14 | 1767.846943 | 884.427110 | 1750.820394 | 875.913835 | 1749.836378 | 875.421827 | E | *304.161545* | 152.584410 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 91.2 | 1940.951324 | 0.004858 | VTEPISAESGEQVER |
| 10.6 | 1940.962540 | -0.006358 | LLNDQEEEGTQRAK |
| 3.7 | 1940.981659 | -0.025477 | HRGYLSETVSNALGPQGR |
| 0.9 | 1940.937378 | 0.018804 | SNNLEREQEQLDR |
| 0.6 | 1940.970413 | -0.014231 | SELHQDRSSPPPPLPER |

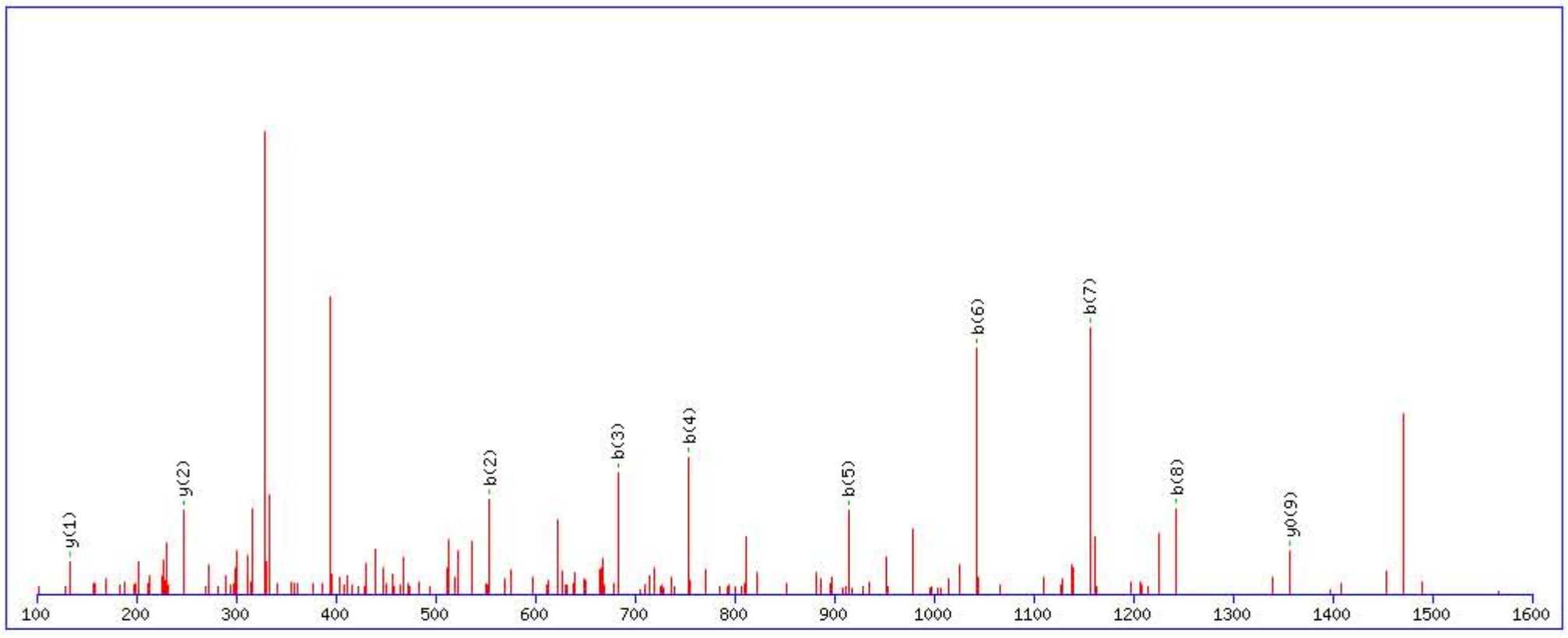
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NQEACELSNN**
Found in **APOM_HUMAN**, Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2

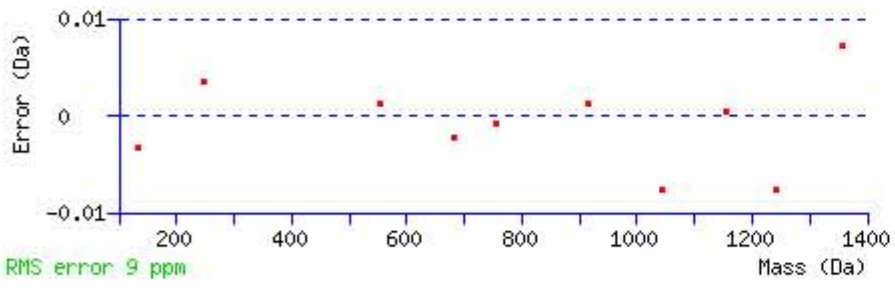
Match to Query 30730: 1488.637808 from(745.326180,2+) rtinseconds(1644) index(17839)
Title: Locus:1.1.1.2955.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

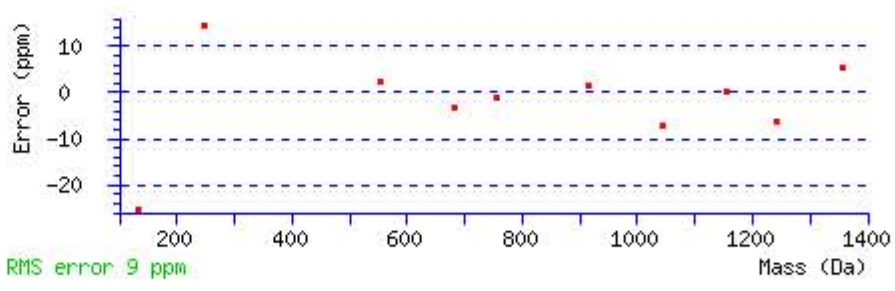
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1488.633682
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 67 **Expect:** 7.6e-007
**Matches :** 11/100 fragment ions using 14 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 10 |
| 2 | *554.275529* | 277.641403 | 537.248980 | 269.128128 | | | Q | 1375.598062 | 688.302669 | 1358.571513 | 679.789395 | 1357.587497 | 679.297387 | 9 |
| 3 | *683.318122* | 342.162699 | 666.291573 | 333.649425 | 665.307557 | 333.157417 | E | 936.372736 | 468.690006 | 919.346187 | 460.176732 | 918.362171 | 459.684724 | 8 |
| 4 | *754.355236* | 377.681256 | 737.328687 | 369.167982 | 736.344671 | 368.675974 | A | 807.330143 | 404.168710 | 790.303594 | 395.655435 | 789.319578 | 395.163427 | 7 |
| 5 | *914.385885* | 457.696581 | 897.359336 | 449.183306 | 896.375320 | 448.691298 | C | 736.293029 | 368.650153 | 719.266480 | 360.136878 | 718.282464 | 359.644870 | 6 |
| 6 | *1043.428478* | 522.217877 | 1026.401929 | 513.704603 | 1025.417913 | 513.212595 | E | 576.262380 | 288.634828 | 559.235831 | 280.121554 | 558.251815 | 279.629546 | 5 |
| 7 | *1156.512542* | 578.759909 | 1139.485993 | 570.246635 | 1138.501977 | 569.754626 | L | 447.219787 | 224.113531 | 430.193238 | 215.600257 | 429.209222 | 215.108249 | 4 |
| 8 | *1243.544570* | 622.275923 | 1226.518021 | 613.762649 | 1225.534005 | 613.270641 | S | 334.135723 | 167.571499 | 317.109174 | 159.058225 | 316.125158 | 158.566217 | 3 |
| 9 | *1357.587497* | 679.297387 | 1340.560948 | 670.784112 | 1339.576932 | 670.292104 | N | 247.103695 | 124.055485 | 230.077146 | 115.542211 | | | 2 |
| 10 | | | | | | | N | 133.060768 | 67.034022 | 116.034219 | 58.520747 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 67.4 | 1488.633682 | 0.004126 | NQEACELSNN |

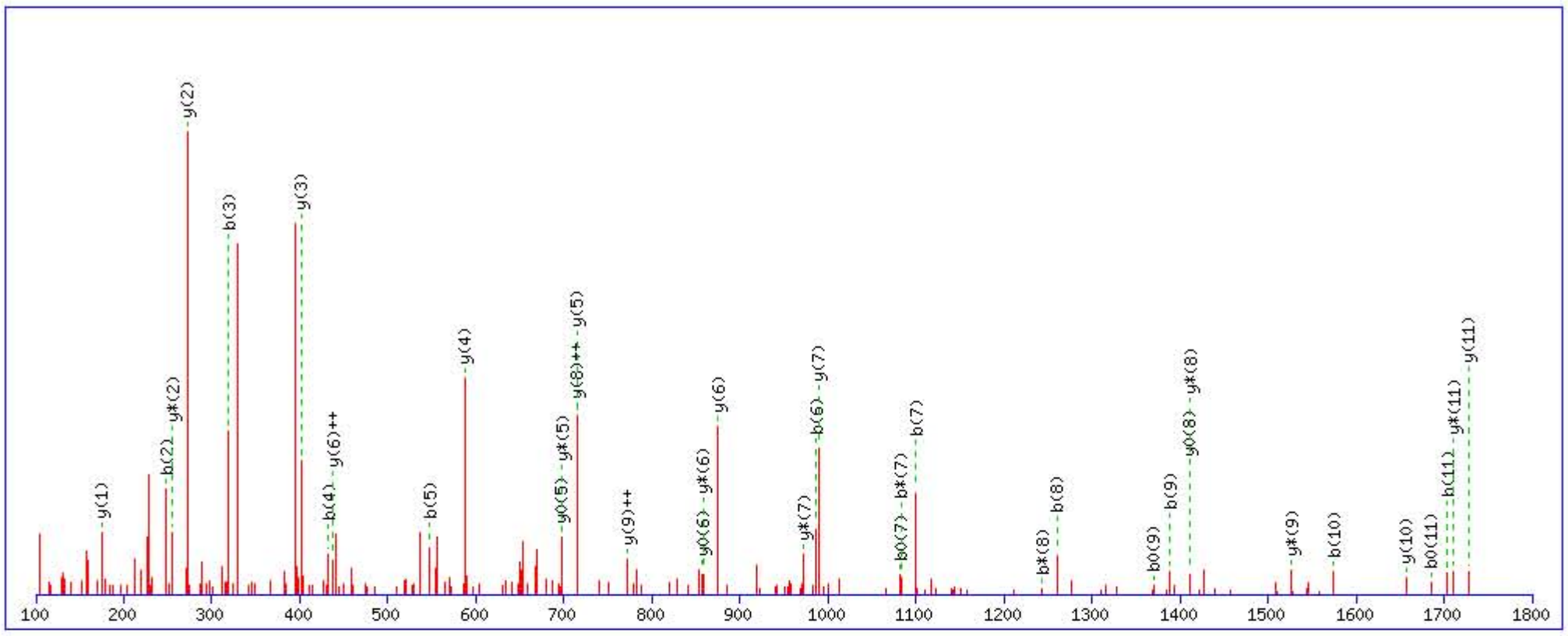
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SCALDQNCQWEPR**
Found in **ATRN_HUMAN**, Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2

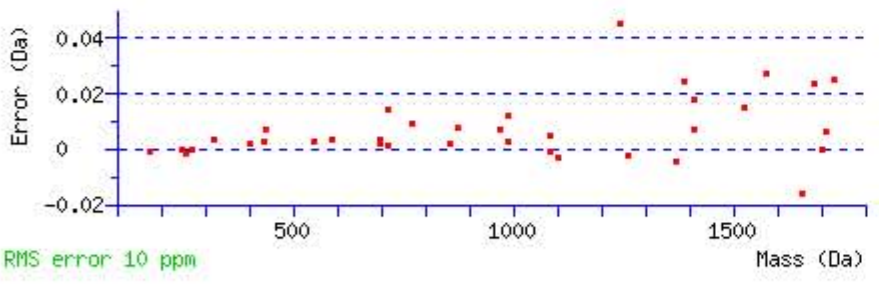
Match to Query 43642: 1973.862702 from(658.961510,3+) rtinseconds(1985) index(5557)
Title: Locus:1.1.1.1968.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

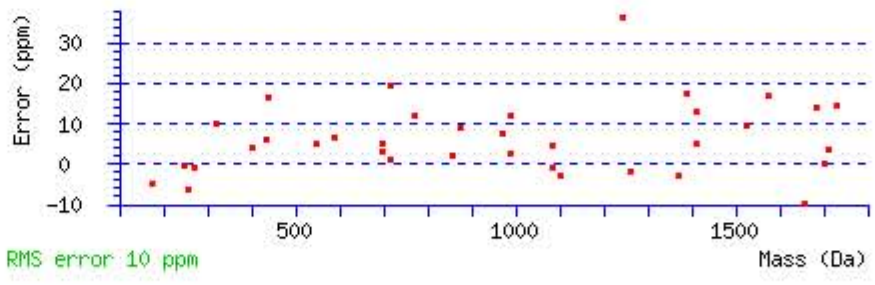
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1973.854614
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 2.5e-005
**Matches :** 37/130 fragment ions using 65 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 13 |
| 2 | *248.069953* | 124.538614 | | | 230.059388 | 115.533332 | C | 1887.829872 | 944.418574 | 1870.803323 | 935.905300 | 1869.819307 | 935.413292 | 12 |
| 3 | *319.107067* | 160.057171 | | | 301.096502 | 151.051889 | A | **1727.799223** | 864.403250 | 1710.772674 | 855.889975 | 1709.788658 | 855.397967 | 11 |
| 4 | *432.191131* | 216.599203 | | | 414.180566 | 207.593921 | L | **1656.762109** | 828.884693 | 1639.735560 | 820.371418 | 1638.751544 | 819.879410 | 10 |
| 5 | *547.218074* | 274.112675 | | | 529.207509 | 265.107393 | D | 1543.678045 | 772.342661 | 1526.651496 | 763.829386 | 1525.667480 | 763.337378 | 9 |
| 6 | *986.443400* | 493.725338 | 969.416851 | 485.212064 | 968.432835 | 484.720056 | Q | 1428.651102 | 714.829189 | 1411.624553 | 706.315915 | 1410.640537 | 705.823907 | 8 |
| 7 | *1100.486327* | 550.746802 | 1083.459778 | 542.233527 | 1082.475762 | 541.741519 | N | **989.425776** | 495.216526 | 972.399227 | 486.703252 | 971.415211 | 486.211244 | 7 |
| 8 | *1260.516976* | 630.762126 | 1243.490427 | 622.248852 | 1242.506411 | 621.756844 | C | **875.382849** | 438.195063 | 858.356300 | 429.681788 | 857.372284 | 429.189780 | 6 |
| 9 | *1388.575554* | 694.791415 | 1371.549005 | 686.278141 | 1370.564989 | 685.786133 | Q | **715.352200** | 358.179738 | 698.325651 | 349.666464 | 697.341635 | 349.174456 | 5 |
| 10 | *1574.654867* | 787.831072 | 1557.628318 | 779.317797 | 1556.644302 | 778.825789 | W | **587.293622** | 294.150449 | 570.267073 | 285.637174 | 569.283057 | 285.145166 | 4 |
| 11 | *1703.697460* | 852.352368 | 1686.670911 | 843.839094 | 1685.686895 | 843.347086 | E | **401.214309** | 201.110792 | 384.187760 | 192.597518 | 383.203744 | 192.105510 | 3 |
| 12 | 1800.750224 | 900.878750 | 1783.723675 | 892.365476 | 1782.739659 | 891.873468 | P | **272.171716** | 136.589496 | **255.145167** | 128.076221 | | | 2 |
| 13 | | | | | | | R | **175.118952** | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.9 | 1973.854614 | 0.008088 | SCALDQNCQWEPR |
| 18.5 | 1973.854614 | 0.008088 | SCALDQNCQWEPR |
| 12.9 | 1973.853729 | 0.008973 | DSPETGEEMGRAEGAWPR |

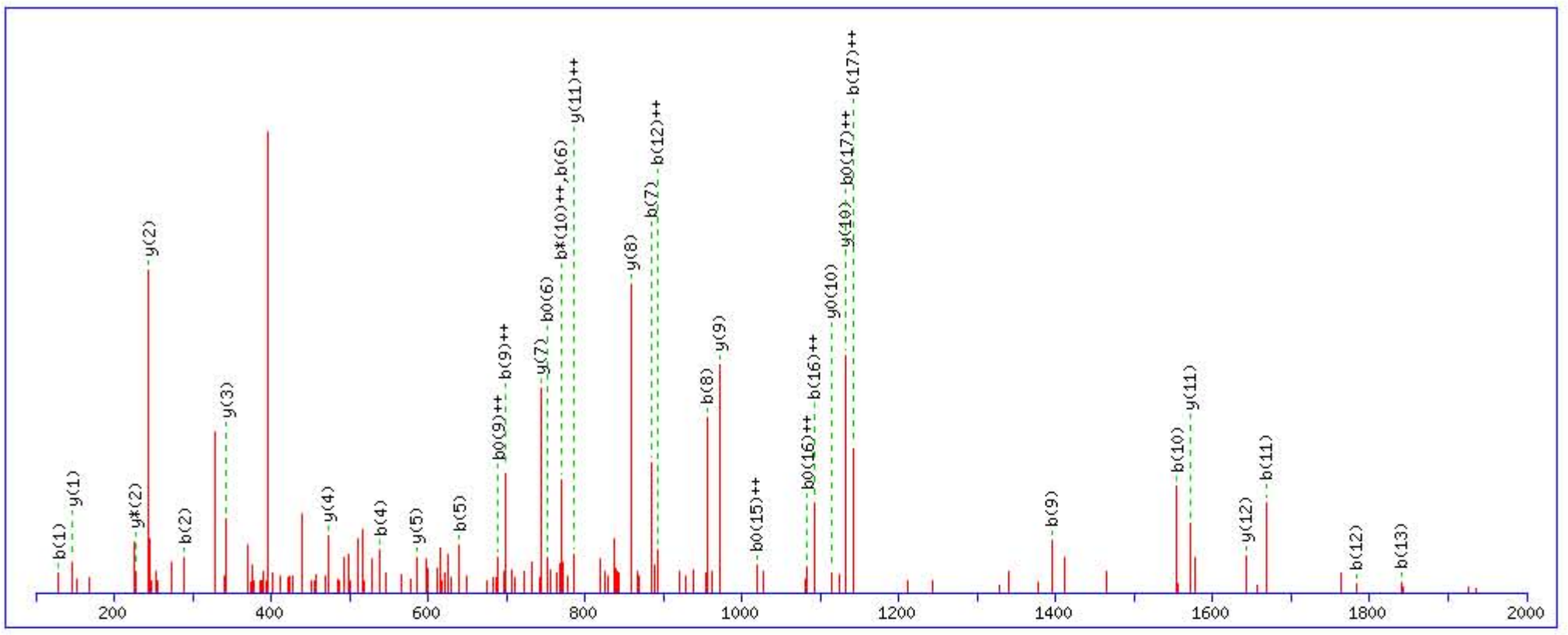
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KCSYTEDAQCIDGTIEVPK**
Found in **APOH_HUMAN**, Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3

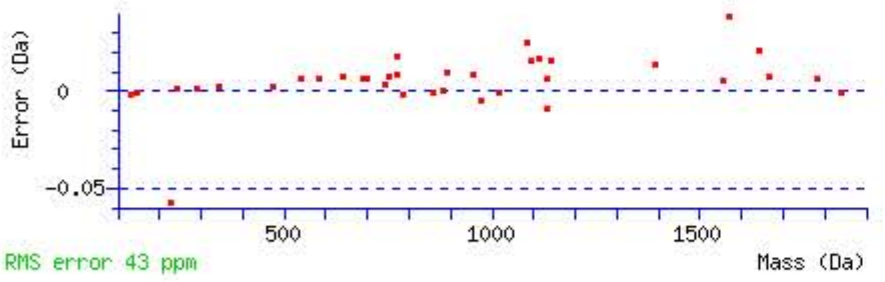
Match to Query 54713: 2524.183152 from(842.401660,3+) rtinseconds(1955) index(66164)
Title: Locus:1.1.1.1955.24 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

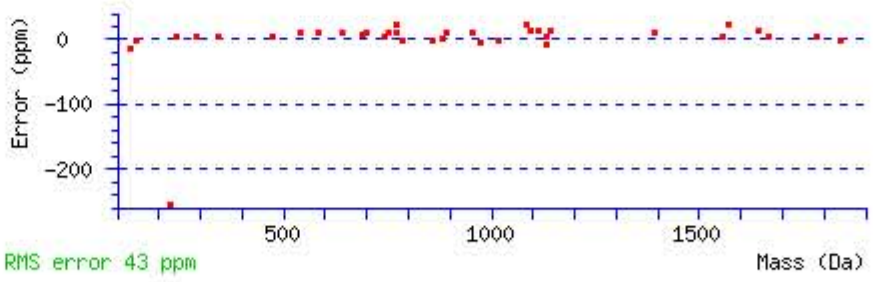
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2524.164780
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 77 **Expect:** 1.4e-007
**Matches :** 36/206 fragment ions using 65 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *129.102239* | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 19 |
| 2 | *289.132888* | 145.070082 | 272.106339 | 136.556808 | | | C | 2397.077099 | 1199.042187 | 2380.050550 | 1190.528913 | 2379.066534 | 1190.036905 | 18 |
| 3 | 376.164916 | 188.586096 | 359.138367 | 180.072822 | 358.154351 | 179.580814 | S | 2237.046450 | 1119.026863 | 2220.019901 | 1110.513588 | 2219.035885 | 1110.021580 | 17 |
| 4 | *539.228245* | 270.117761 | 522.201696 | 261.604486 | 521.217680 | 261.112478 | Y | 2150.014422 | 1075.510849 | 2132.987873 | 1066.997574 | 2132.003857 | 1066.505566 | 16 |
| 5 | *640.275924* | 320.641600 | 623.249375 | 312.128326 | 622.265359 | 311.636318 | T | 1986.951093 | 993.979185 | 1969.924544 | 985.465910 | 1968.940528 | 984.973902 | 15 |
| 6 | *769.318517* | 385.162897 | 752.291968 | 376.649622 | 751.307952 | 376.157614 | E | 1885.903414 | 943.455345 | 1868.876865 | 934.942071 | 1867.892849 | 934.450063 | 14 |
| 7 | *884.345460* | 442.676368 | 867.318911 | 434.163094 | 866.334895 | 433.671086 | D | 1756.860821 | 878.934049 | 1739.834272 | 870.420774 | 1738.850256 | 869.928766 | 13 |
| 8 | *955.382574* | 478.194925 | 938.356025 | 469.681650 | 937.372009 | 469.189642 | A | *1641.833878* | 821.420577 | 1624.807329 | 812.907303 | 1623.823313 | 812.415295 | 12 |
| 9 | *1394.607900* | **697.807588** | 1377.581351 | 689.294314 | 1376.597335 | 688.802306 | Q | *1570.796764* | 785.902020 | 1553.770215 | 777.388746 | 1552.786199 | 776.896738 | 11 |
| 10 | *1554.638549* | 777.822913 | 1537.612000 | 769.309638 | 1536.627984 | 768.817630 | C | *1131.571438* | 566.289357 | 1114.544889 | 557.776083 | 1113.560873 | 557.284075 | 10 |
| 11 | *1667.722613* | 834.364945 | 1650.696064 | 825.851670 | 1649.712048 | 825.359662 | I | *971.540789* | 486.274033 | 954.514240 | 477.760758 | 953.530224 | 477.268750 | 9 |
| 12 | *1782.749556* | **891.878416** | 1765.723007 | 883.365142 | 1764.738991 | 882.873134 | D | *858.456725* | 429.732001 | 841.430176 | 421.218726 | 840.446160 | 420.726718 | 8 |
| 13 | *1839.771020* | 920.389148 | 1822.744471 | 911.875874 | 1821.760455 | 911.383866 | G | *743.429782* | 372.218529 | 726.403233 | 363.705255 | 725.419217 | 363.213247 | 7 |
| 14 | 1940.818699 | 970.912988 | 1923.792150 | 962.399713 | 1922.808134 | 961.907705 | T | 686.408318 | 343.707797 | 669.381769 | 335.194523 | 668.397753 | 334.702515 | 6 |
| 15 | 2053.902763 | 1027.455019 | 2036.876214 | 1018.941745 | 2035.892198 | 1018.449737 | I | *585.360639* | 293.183958 | 568.334090 | 284.670683 | 567.350074 | 284.178675 | 5 |
| 16 | 2182.945356 | **1091.976316** | 2165.918807 | 1083.463041 | 2164.934791 | 1082.971034 | E | *472.276575* | 236.641925 | 455.250026 | 228.128651 | 454.266010 | 227.636643 | 4 |
| 17 | 2282.013770 | **1141.510523** | 2264.987221 | 1132.997248 | 2264.003205 | 1132.505240 | V | *343.233982* | 172.120629 | 326.207433 | 163.607354 | | | 3 |
| 18 | 2379.066534 | 1190.036905 | 2362.039985 | 1181.523630 | 2361.055969 | 1181.031622 | P | *244.165568* | 122.586422 | 227.139019 | 114.073148 | | | 2 |
| 19 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 77.3 | 2524.164780 | 0.018372 | KCSYTEDAQCIDGTIEVPK |
| 4.2 | 2524.211487 | -0.028335 | DLEITNATLQSEEDSRYMKPGK |

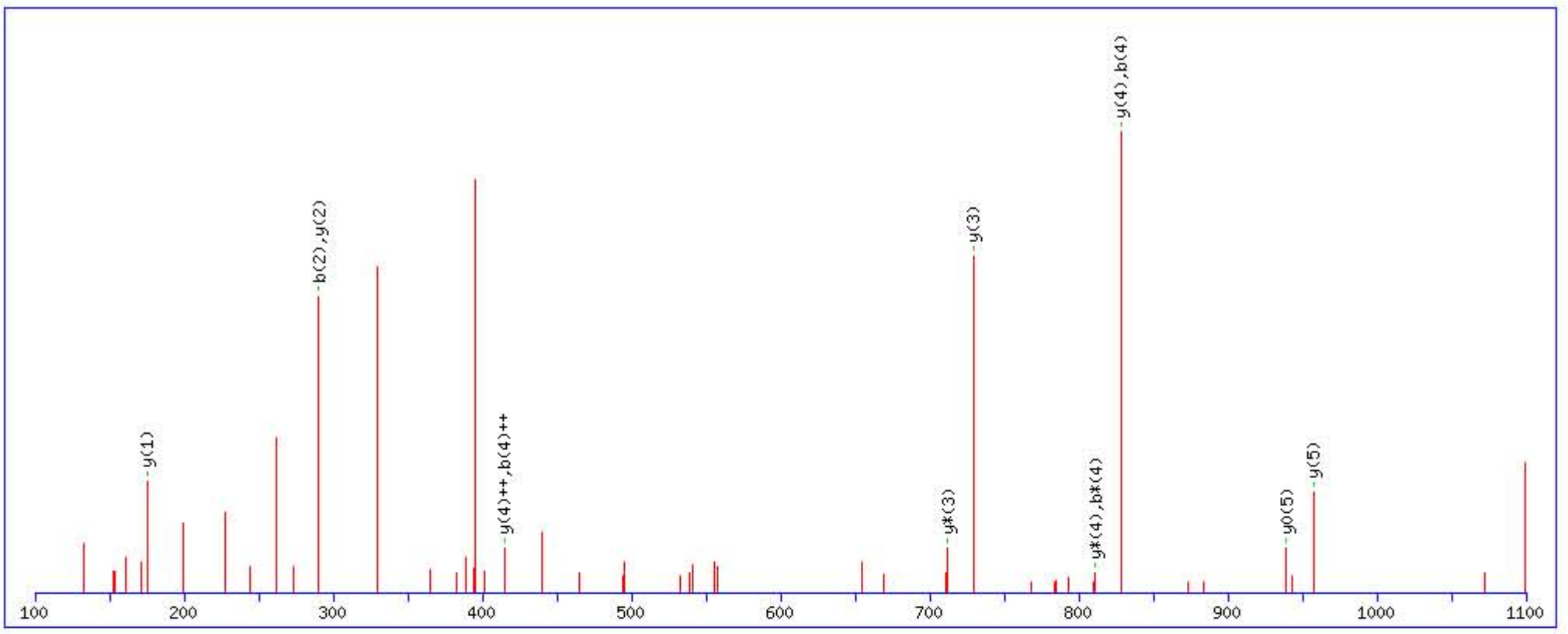
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **CEVQDR**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

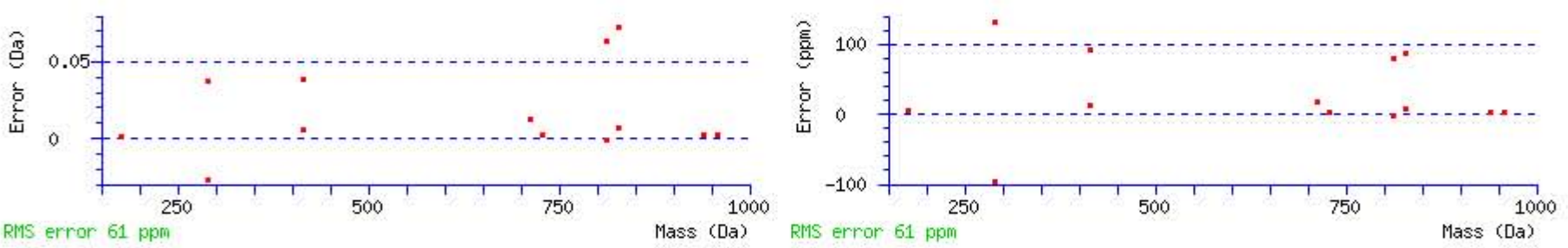
Match to Query 17156: 1116.511408 from(559.262980,2+) rtinseconds(1333) index(30064)
Title: Locus:1.1.1.572.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1116.505600
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 26 **Expect:** 0.019
**Matches :** 13/50 fragment ions using 20 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 161.037925 | 81.022600 | | | | | C | | | | | | | 6 |
| 2 | **290.080518** | 145.543897 | | | 272.069953 | 136.538615 | E | *957.482228* | 479.244752 | 940.455679 | 470.731478 | 939.471663 | 470.239470 | 5 |
| 3 | 389.148932 | 195.078104 | | | 371.138367 | 186.072822 | V | *828.439635* | 414.723456 | 811.413086 | 406.210181 | 810.429070 | 405.718173 | 4 |
| 4 | **828.374258** | 414.690767 | 811.347709 | 406.177493 | 810.363693 | 405.685485 | Q | *729.371221* | 365.189249 | 712.344672 | 356.675974 | 711.360656 | 356.183966 | 3 |
| 5 | 943.401201 | 472.204239 | 926.374652 | 463.690964 | 925.390636 | 463.198956 | D | *290.145895* | 145.576585 | 273.119346 | 137.063311 | 272.135330 | 136.571303 | 2 |
| 6 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 26.0 | 1116.505600 | 0.005808 | CEVQDR |
| 7.3 | 1116.505600 | 0.005808 | DICQDR |
| 7.3 | 1116.502228 | 0.009180 | SWDQDR |
| 6.1 | 1116.527206 | -0.015798 | TSTSGTHRDR |
| 4.8 | 1116.509644 | 0.001764 | CFSVLGFCK |
| 0.1 | 1116.504700 | 0.006708 | ELQAEQEDR |

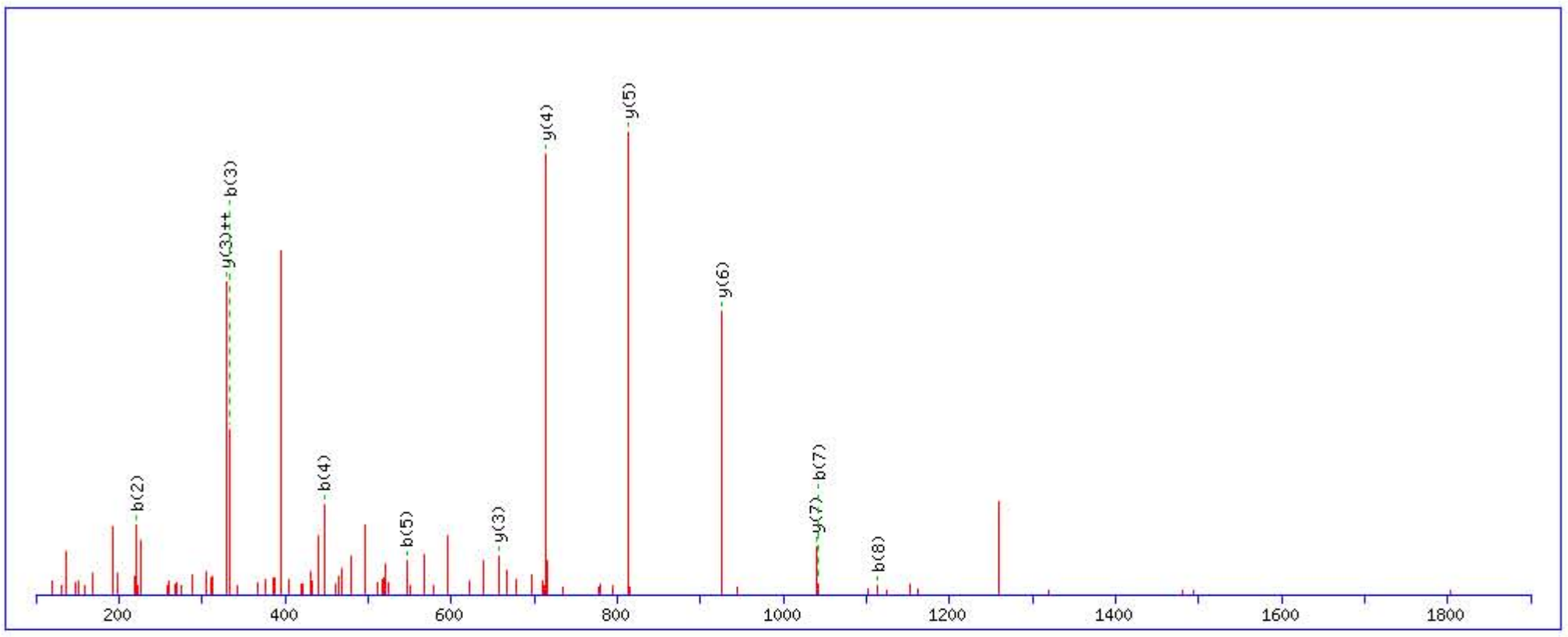
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GYILVGQAK**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

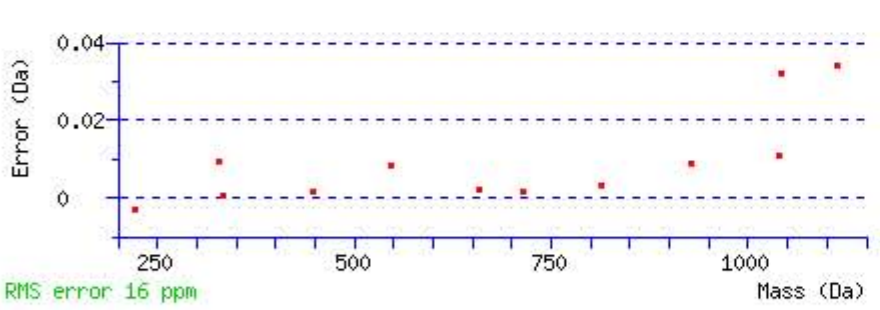
Match to Query 22096: 1258.719648 from(630.367100,2+) rtinseconds(2049) index(50637)
Title: Locus:1.1.1.1951.4 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

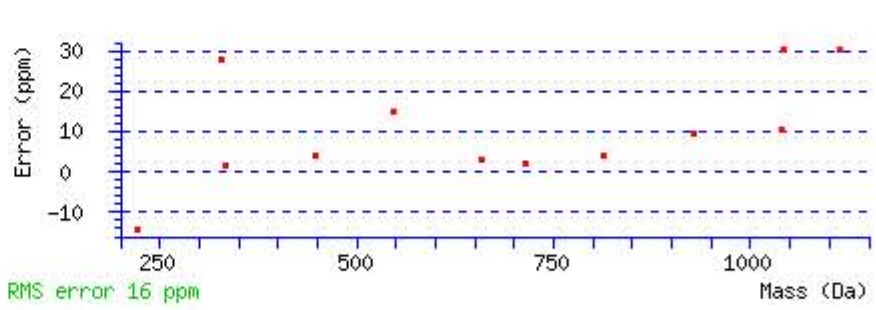
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1258.710754
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 28 **Expect:** 0.026
**Matches :** 12/52 fragment ions using 29 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | G | | | | | 9 |
| 2 | *221.092069* | 111.049673 | | | Y | 1202.696579 | 601.851928 | 1185.670030 | 593.338653 | 8 |
| 3 | *334.176133* | 167.591704 | | | I | *1039.633250* | 520.320263 | 1022.606701 | 511.806989 | 7 |
| 4 | *447.260197* | 224.133737 | | | L | *926.549186* | 463.778231 | 909.522637 | 455.264957 | 6 |
| 5 | *546.328611* | 273.667944 | | | V | *813.465122* | 407.236199 | 796.438573 | 398.722925 | 5 |
| 6 | 603.350075 | 302.178676 | | | G | *714.396708* | 357.701992 | 697.370159 | 349.188718 | 4 |
| 7 | *1042.575401* | 521.791339 | 1025.548852 | 513.278064 | Q | *657.375244* | 329.191260 | 640.348695 | 320.677986 | 3 |
| 8 | *1113.612515* | 557.309896 | 1096.585966 | 548.796621 | A | 218.149918 | 109.578597 | 201.123369 | 101.065322 | 2 |
| 9 | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 27.5 | 1258.710754 | 0.008894 | GYILVGQAK |
| 11.0 | 1258.721970 | -0.002322 | GYILQAKR |
| 8.8 | 1258.717941 | 0.001707 | RILAKVQEMR |

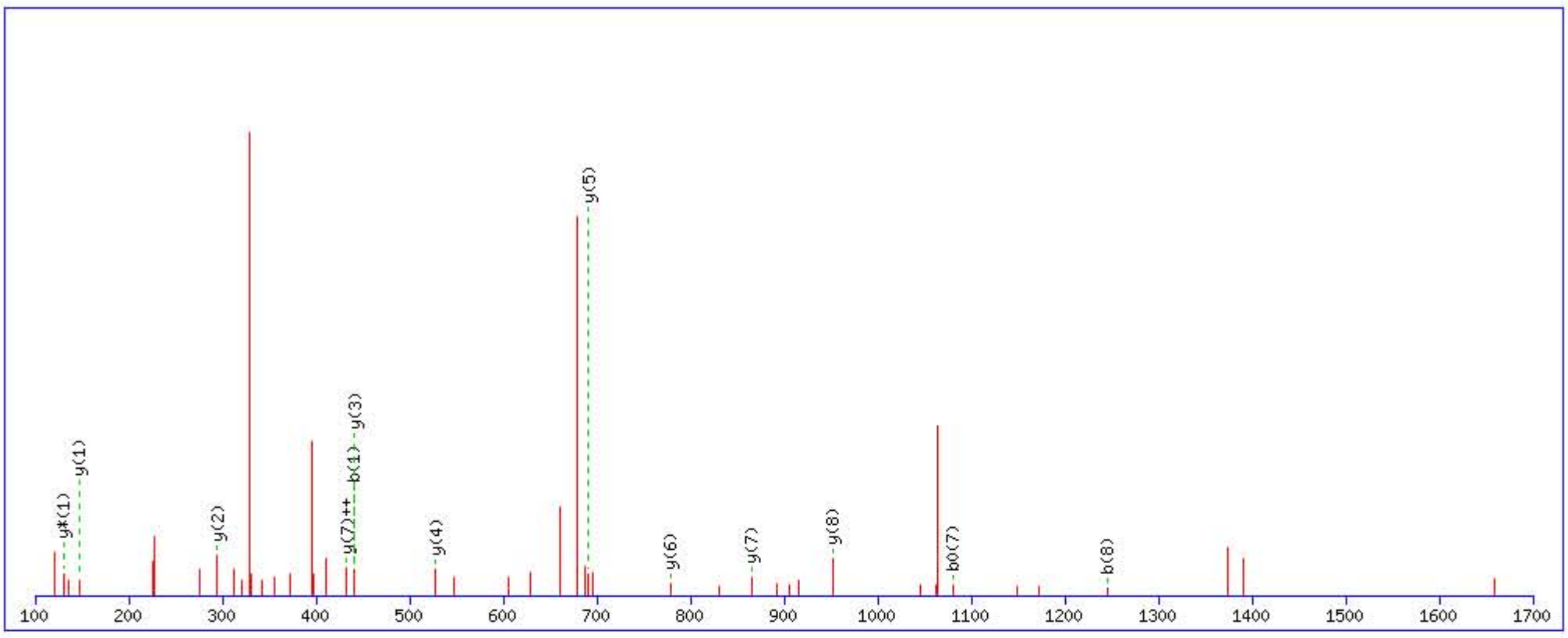
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QSSSYSFFK**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

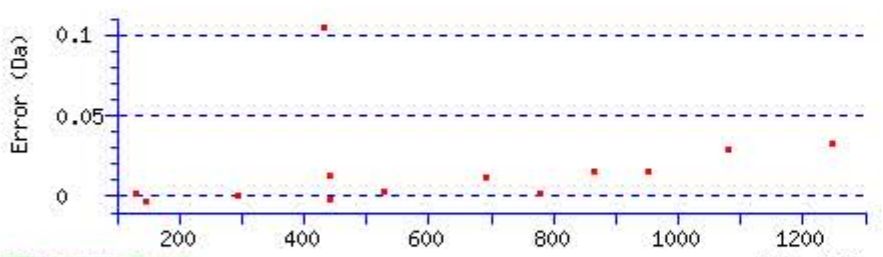
Match to Query 26925: 1390.672608 from(696.343580,2+) rtinseconds(2064) index(34651)
Title: Locus:1.1.1.827.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

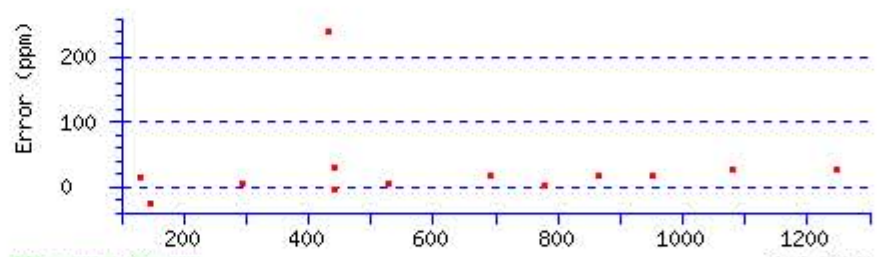
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1390.659119
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 34 **Expect:** 0.0051
**Matches** : 13/88 fragment ions using 42 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **440.232602** | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 9 |
| 2 | 527.264630 | 264.135953 | 510.238081 | 255.622679 | 509.254065 | 255.130671 | S | *952.441073* | 476.724175 | 935.414524 | 468.210900 | 934.430508 | 467.718892 | 8 |
| 3 | 614.296658 | 307.651967 | 597.270109 | 299.138692 | 596.286093 | 298.646684 | S | *865.409045* | 433.208161 | 848.382496 | 424.694886 | 847.398480 | 424.202878 | 7 |
| 4 | 701.328686 | 351.167981 | 684.302137 | 342.654706 | 683.318121 | 342.162698 | S | *778.377017* | 389.692147 | 761.350468 | 381.178872 | 760.366452 | 380.686864 | 6 |
| 5 | 864.392015 | 432.699645 | 847.365466 | 424.186371 | 846.381450 | 423.694363 | Y | *691.344989* | 346.176133 | 674.318440 | 337.662858 | 673.334424 | 337.170850 | 5 |
| 6 | 951.424043 | 476.215659 | 934.397494 | 467.702385 | 933.413478 | 467.210377 | S | *528.281660* | 264.644468 | 511.255111 | 256.131194 | 510.271095 | 255.639186 | 4 |
| 7 | 1098.492457 | 549.749866 | 1081.465908 | 541.236592 | 1080.481892 | 540.744584 | F | *441.249632* | 221.128454 | 424.223083 | 212.615180 | | | 3 |
| 8 | **1245.560871** | 623.284073 | 1228.534322 | 614.770799 | 1227.550306 | 614.278791 | F | *294.181218* | 147.594247 | 277.154669 | 139.080973 | | | 2 |
| 9 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.7 | 1390.659119 | 0.013489 | QSSSYSFFK |
| 8.8 | 1390.691467 | -0.018859 | VTKEMNEFIHK |
| 8.4 | 1390.688797 | -0.016189 | ISVNCGHPSRHK |
| 7.2 | 1390.677078 | -0.004470 | CVCNLMIKEPK |
| 6.0 | 1390.673706 | -0.001098 | TLNADLMMFAHK |
| 3.1 | 1390.669678 | 0.002930 | CAPASIRLMDNK |
| 3.1 | 1390.687424 | -0.014816 | ENTMARVDEAKK |
| 2.6 | 1390.676208 | -0.003600 | AEKSSSTDQK |
| 1.6 | 1390.684967 | -0.012359 | QCGKGFQQK |
| 1.6 | 1390.684967 | -0.012359 | QCGKGFQQK |

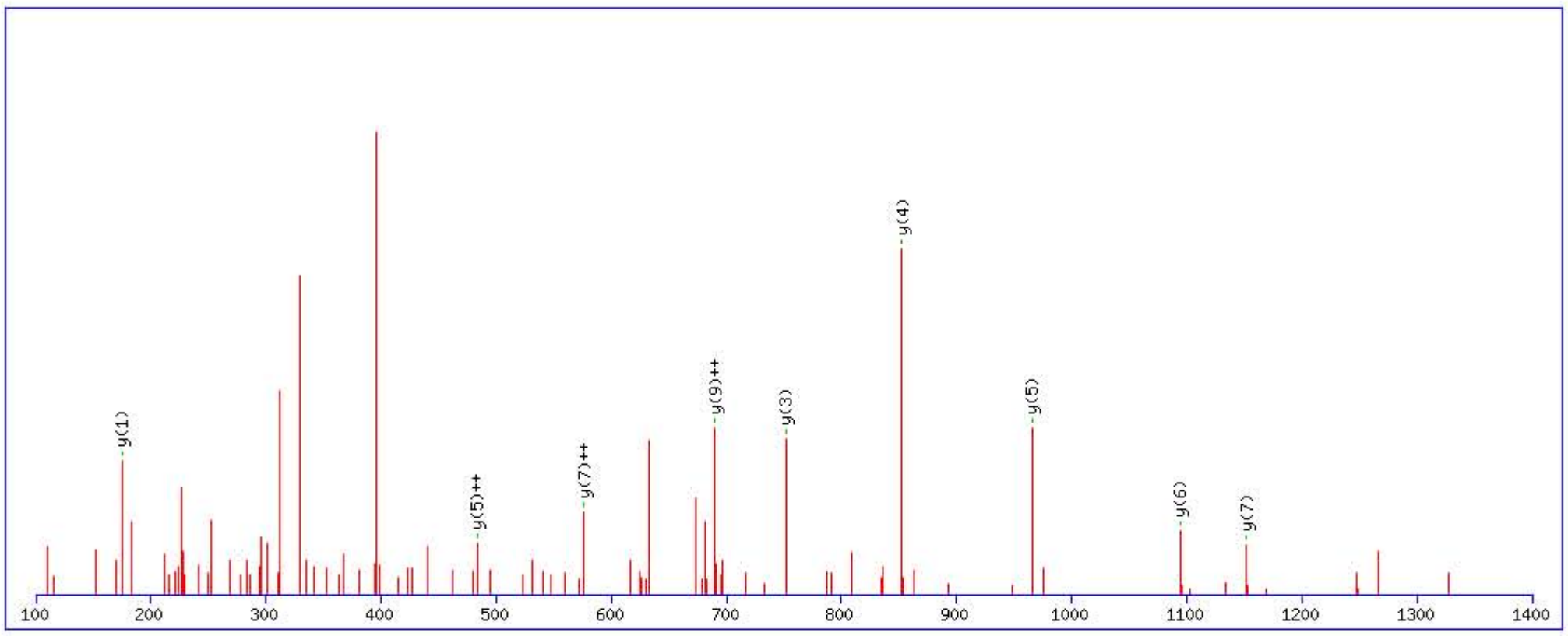
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LNNGEITQHR**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

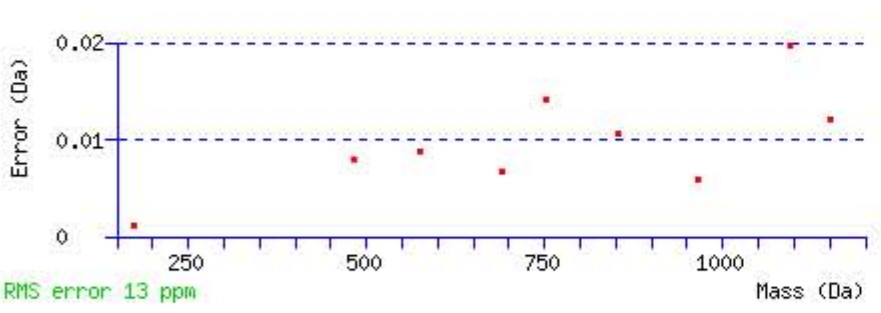
Match to Query 30840: 1491.751242 from(498.257690,3+) rtinseconds(1433) index(30608)
Title: Locus:1.1.1.607.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

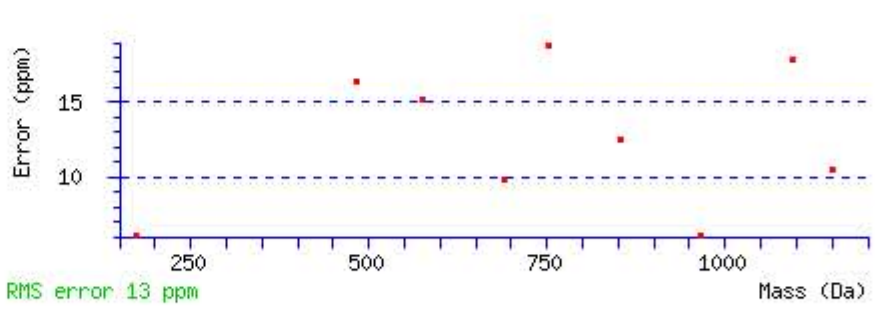
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1491.761612
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 40 **Expect:** 0.00069
**Matches :** 9/92 fragment ions using 13 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 10 |
| 2 | 228.134267 | 114.570771 | 211.107718 | 106.057497 | | | N | 1379.684844 | 690.346060 | 1362.658295 | 681.832786 | 1361.674279 | 681.340778 | 9 |
| 3 | 342.177194 | 171.592235 | 325.150645 | 163.078960 | | | N | 1265.641917 | 633.324596 | 1248.615368 | 624.811322 | 1247.631352 | 624.319314 | 8 |
| 4 | 399.198658 | 200.102967 | 382.172109 | 191.589692 | | | G | *1151.598990* | 576.303133 | 1134.572441 | 567.789859 | 1133.588425 | 567.297850 | 7 |
| 5 | 528.241251 | 264.624264 | 511.214702 | 256.110989 | 510.230686 | 255.618981 | E | *1094.577526* | 547.792401 | 1077.550977 | 539.279127 | 1076.566961 | 538.787119 | 6 |
| 6 | 641.325315 | 321.166296 | 624.298766 | 312.653021 | 623.314750 | 312.161013 | I | *965.534933* | 483.271105 | 948.508384 | 474.757830 | 947.524368 | 474.265822 | 5 |
| 7 | 742.372994 | 371.690135 | 725.346445 | 363.176861 | 724.362429 | 362.684853 | T | *852.450869* | 426.729073 | 835.424320 | 418.215798 | 834.440304 | 417.723790 | 4 |
| 8 | 1181.598320 | 591.302798 | 1164.571771 | 582.789524 | 1163.587755 | 582.297516 | Q | *751.403190* | 376.205233 | 734.376641 | 367.691959 | | | 3 |
| 9 | 1318.657232 | 659.832254 | 1301.630683 | 651.318980 | 1300.646667 | 650.826972 | H | 312.177864 | 156.592570 | 295.151315 | 148.079295 | | | 2 |
| 10 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 40.4 | 1491.761612 | -0.010370 | LNNGEITQHR |
| 6.3 | 1491.740021 | 0.011221 | LIDQFQMMR |
| 6.3 | 1491.740021 | 0.011221 | LIDQFQMMR |
| 2.9 | 1491.746338 | 0.004904 | IREMSSTLDRER |
| 1.4 | 1491.756927 | -0.005685 | IEEVIGTGSFGEVR |

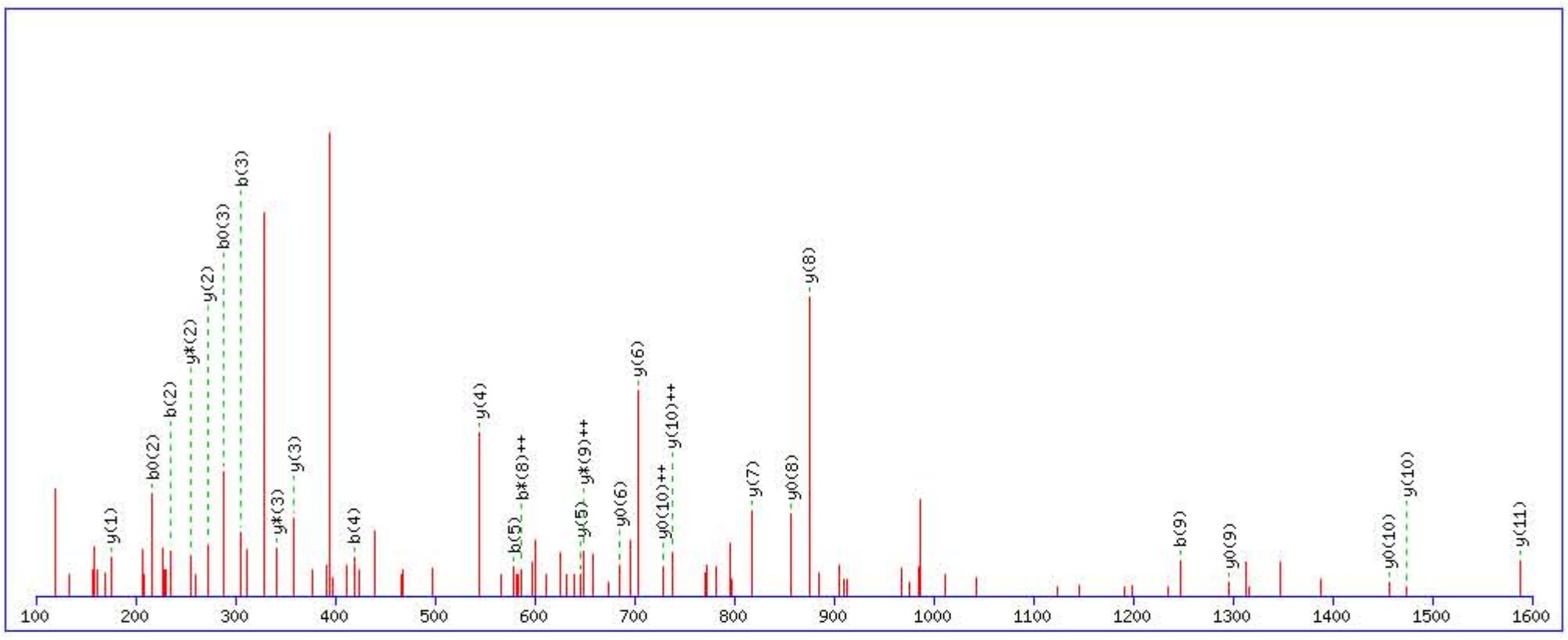
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FSAICQGDGTWSPR**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

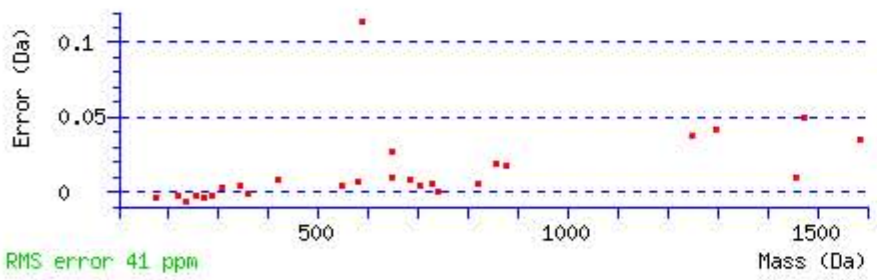
Match to Query 41981: 1891.890432 from(631.637420,3+) rtinseconds(2139) index(51278)
Title: Locus:1.1.1.1982.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

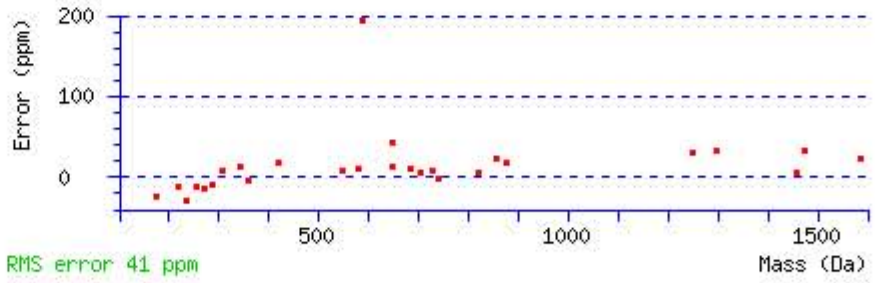
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1891.870941
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 35 **Expect:** 0.0048
**Matches :** 27/140 fragment ions using 73 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 14 |
| 2 | **235.107718** | 118.057497 | | | 217.097153 | 109.052214 | S | 1745.809788 | 873.408532 | 1728.783239 | 864.895258 | 1727.799223 | 864.403250 | 13 |
| 3 | **306.144832** | 153.576054 | | | 288.134267 | 144.570772 | A | 1658.777760 | 829.892518 | 1641.751211 | 821.379244 | 1640.767195 | 820.887236 | 12 |
| 4 | **419.228896** | 210.118086 | | | 401.218331 | 201.112804 | I | *1587.740646* | 794.373961 | 1570.714097 | 785.860687 | 1569.730081 | 785.368678 | 11 |
| 5 | **579.259545** | 290.133411 | | | 561.248980 | 281.128128 | C | *1474.656582* | 737.831929 | 1457.630033 | 729.318655 | 1456.646017 | 728.826647 | 10 |
| 6 | 1018.484871 | 509.746074 | 1001.458322 | 501.232799 | 1000.474306 | 500.740791 | Q | 1314.625933 | 657.816605 | 1297.599384 | 649.303330 | 1296.615368 | 648.811322 | 9 |
| 7 | 1075.506335 | 538.256806 | 1058.479786 | 529.743531 | 1057.495770 | 529.251523 | G | *875.400607* | 438.203942 | 858.374058 | 429.690667 | 857.390042 | 429.198659 | 8 |
| 8 | 1190.533278 | 595.770277 | 1173.506729 | 587.257003 | 1172.522713 | 586.764995 | D | *818.379143* | 409.693210 | 801.352594 | 401.179935 | 800.368578 | 400.687927 | 7 |
| 9 | **1247.554742** | 624.281009 | 1230.528193 | 615.767735 | 1229.544177 | 615.275727 | G | *703.352200* | 352.179738 | 686.325651 | 343.666464 | 685.341635 | 343.174456 | 6 |
| 10 | 1348.602421 | 674.804849 | 1331.575872 | 666.291574 | 1330.591856 | 665.799566 | T | *646.330736* | 323.669006 | 629.304187 | 315.155732 | 628.320171 | 314.663724 | 5 |
| 11 | 1534.681734 | 767.844505 | 1517.655185 | 759.331231 | 1516.671169 | 758.839223 | W | *545.283057* | 273.145167 | 528.256508 | 264.631892 | 527.272492 | 264.139884 | 4 |
| 12 | 1621.713762 | 811.360519 | 1604.687213 | 802.847245 | 1603.703197 | 802.355237 | S | *359.203744* | 180.105510 | 342.177195 | 171.592236 | 341.193179 | 171.100228 | 3 |
| 13 | 1718.766526 | 859.886901 | 1701.739977 | 851.373627 | 1700.755961 | 850.881619 | P | *272.171716* | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 14 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 35.2 | 1891.870941 | 0.019491 | FSAICQGDGTWSPR |

**Mascot:** http://www.matrixscience.com/

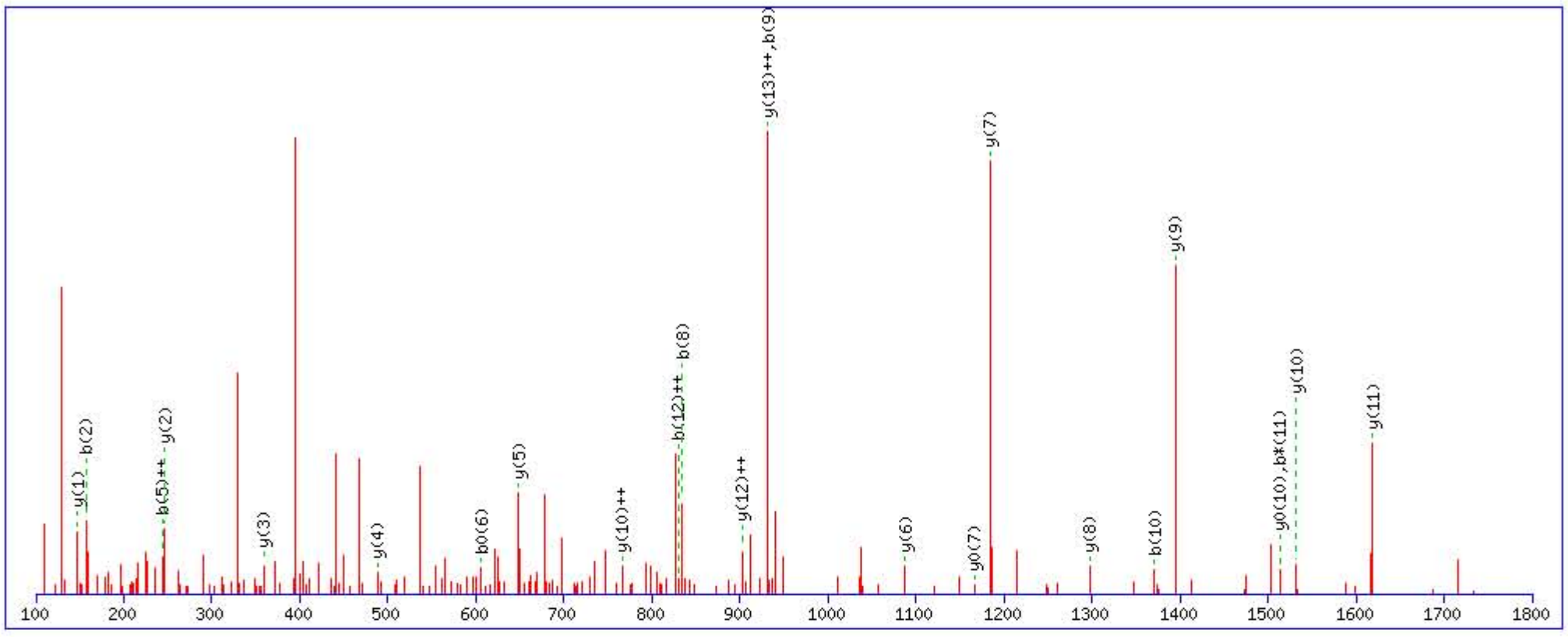
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GVGWSHPLPQCEIVK**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

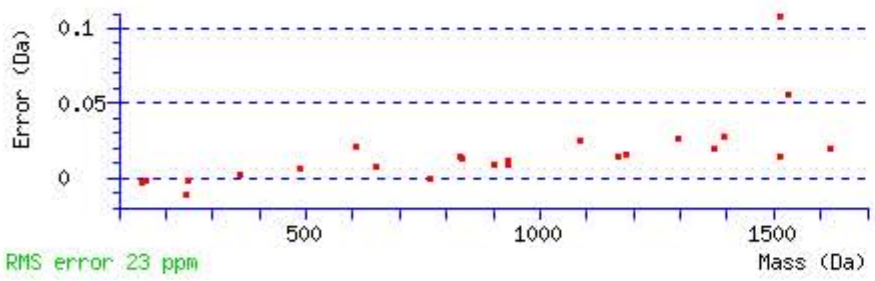
Match to Query 45024: 2017.045422 from(673.355750,3+) rtinseconds(2072) index(50800)
Title: Locus:1.1.1.1959.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

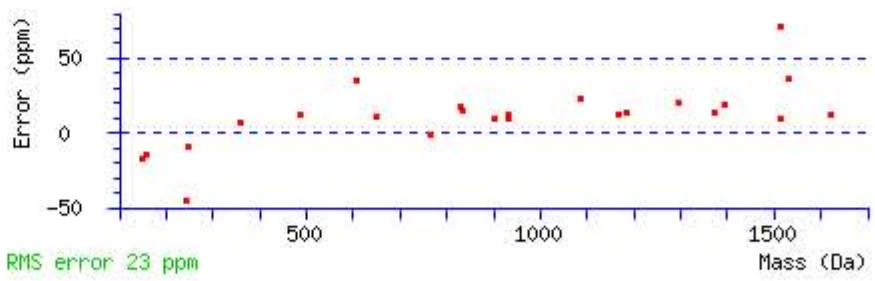
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2017.027771
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.017
**Matches :** 24/136 fragment ions using 79 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 15 |
| 2 | 157.097154 | 79.052215 | | | | | V | 1961.013573 | 981.010425 | 1943.987024 | 972.497150 | 1943.003008 | 972.005142 | 14 |
| 3 | 214.118618 | 107.562947 | | | | | G | 1861.945159 | 931.476217 | 1844.918610 | 922.962943 | 1843.934594 | 922.470935 | 13 |
| 4 | 400.197931 | 200.602603 | | | | | W | 1804.923695 | 902.965486 | 1787.897146 | 894.452211 | 1786.913130 | 893.960203 | 12 |
| 5 | 487.229959 | 244.118617 | | | 469.219394 | 235.113335 | S | *1618.844382* | 809.925829 | 1601.817833 | 801.412555 | 1600.833817 | 800.920547 | 11 |
| 6 | 624.288871 | 312.648074 | | | 606.278306 | 303.642791 | H | *1531.812354* | 766.409815 | 1514.785805 | 757.896541 | 1513.801789 | 757.404532 | 10 |
| 7 | 721.341635 | 361.174456 | | | 703.331070 | 352.169173 | P | *1394.753442* | 697.880359 | 1377.726893 | 689.367085 | 1376.742877 | 688.875076 | 9 |
| 8 | 834.425699 | 417.716488 | | | 816.415134 | 408.711205 | L | *1297.700678* | 649.353977 | 1280.674129 | 640.840703 | 1279.690113 | 640.348694 | 8 |
| 9 | 931.478463 | 466.242870 | | | 913.467898 | 457.237587 | P | *1184.616614* | 592.811945 | 1167.590065 | 584.298670 | 1166.606049 | 583.806662 | 7 |
| 10 | 1370.703789 | 685.855532 | 1353.677240 | 677.342258 | 1352.693224 | 676.850250 | Q | *1087.563850* | 544.285563 | 1070.537301 | 535.772288 | 1069.553285 | 535.280280 | 6 |
| 11 | 1530.734438 | 765.870857 | 1513.707889 | 757.357583 | 1512.723873 | 756.865574 | C | *648.338524* | 324.672900 | 631.311975 | 316.159626 | 630.327959 | 315.667618 | 5 |
| 12 | 1659.777031 | 830.392153 | 1642.750482 | 821.878879 | 1641.766466 | 821.386871 | E | *488.307875* | 244.657575 | 471.281326 | 236.144301 | 470.297310 | 235.652293 | 4 |
| 13 | 1772.861095 | 886.934185 | 1755.834546 | 878.420911 | 1754.850530 | 877.928903 | I | *359.265282* | 180.136279 | 342.238733 | 171.623004 | | | 3 |
| 14 | 1871.929509 | 936.468392 | 1854.902960 | 927.955118 | 1853.918944 | 927.463110 | V | *246.181218* | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 15 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 32.3 | 2017.027771 | 0.017651 | GVGWSHPLPQCEIVK |

**Mascot:** http://www.matrixscience.com/

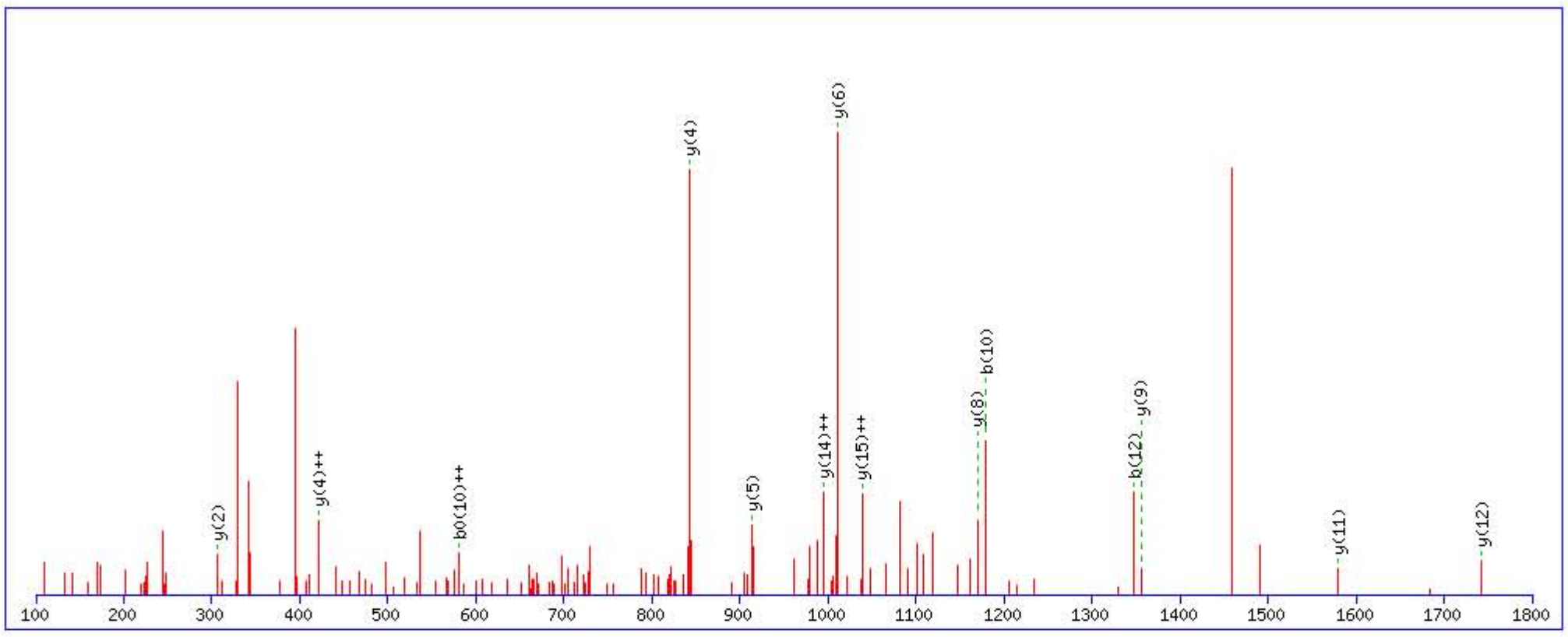
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LSCSYSHWSAPAPQCK**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

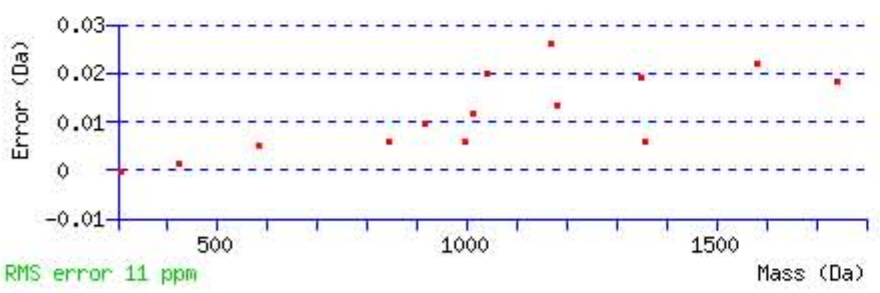
Match to Query 48275: 2189.005422 from(730.675750,3+) rtinseconds(1768) index(32719)
Title: Locus:1.1.1.724.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

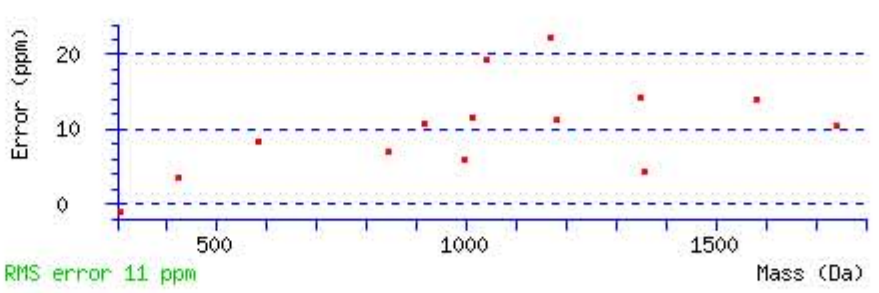
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2188.985626
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q14** : Biotin:Thermo-21345 (Q)
**Ions Score:** 35 **Expect:** 0.00058
**Matches** : 14/138 fragment ions using 31 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 16 |
| 2 | 201.123368 | 101.065322 | | | 183.112803 | 92.060039 | S | 2076.908850 | 1038.958063 | 2059.882301 | 1030.444788 | 2058.898285 | 1029.952780 | 15 |
| 3 | 361.154017 | 181.080647 | | | 343.143452 | 172.075364 | C | 1989.876822 | 995.442049 | 1972.850273 | 986.928775 | 1971.866257 | 986.436767 | 14 |
| 4 | 448.186045 | 224.596660 | | | 430.175480 | 215.591378 | S | 1829.846173 | 915.426725 | 1812.819624 | 906.913450 | 1811.835608 | 906.421442 | 13 |
| 5 | 611.249374 | 306.128325 | | | 593.238809 | 297.123043 | Y | *1742.814145* | 871.910711 | 1725.787596 | 863.397436 | 1724.803580 | 862.905428 | 12 |
| 6 | 698.281402 | 349.644339 | | | 680.270837 | 340.639056 | S | *1579.750816* | 790.379046 | 1562.724267 | 781.865772 | 1561.740251 | 781.373764 | 11 |
| 7 | 835.340314 | 418.173795 | | | 817.329749 | 409.168512 | H | 1492.718788 | 746.863032 | 1475.692239 | 738.349758 | 1474.708223 | 737.857750 | 10 |
| 8 | 1021.419627 | 511.213452 | | | 1003.409062 | 502.208169 | W | *1355.659876* | 678.333576 | 1338.633327 | 669.820302 | 1337.649311 | 669.328294 | 9 |
| 9 | 1108.451655 | 554.729466 | | | 1090.441090 | 545.724183 | S | *1169.580563* | 585.293920 | 1152.554014 | 576.780645 | 1151.569998 | 576.288637 | 8 |
| 10 | **1179.488769** | 590.248023 | | | 1161.478204 | 581.242740 | A | 1082.548535 | 541.777906 | 1065.521986 | 533.264631 | | | 7 |
| 11 | 1276.541533 | 638.774405 | | | 1258.530968 | 629.769122 | P | *1011.511421* | 506.259349 | 994.484872 | 497.746074 | | | 6 |
| 12 | **1347.578647** | 674.292962 | | | 1329.568082 | 665.287679 | A | *914.458657* | 457.732967 | 897.432108 | 449.219692 | | | 5 |
| 13 | 1444.631411 | 722.819344 | | | 1426.620846 | 713.814061 | P | *843.421543* | 422.214410 | 826.394994 | 413.701135 | | | 4 |
| 14 | 1883.856737 | 942.432007 | 1866.830188 | 933.918732 | 1865.846172 | 933.426724 | Q | 746.368779 | 373.688028 | 729.342230 | 365.174753 | | | 3 |
| 15 | 2043.887386 | 1022.447331 | 2026.860837 | 1013.934057 | 2025.876821 | 1013.442049 | C | *307.143453* | 154.075365 | 290.116904 | 145.562090 | | | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546766 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 34.8 | 2188.985626 | 0.019796 | LSCSYSHWSAPAPQCK |
| 0.2 | 2189.031891 | -0.026469 | QNYDEMSPAGQISK |

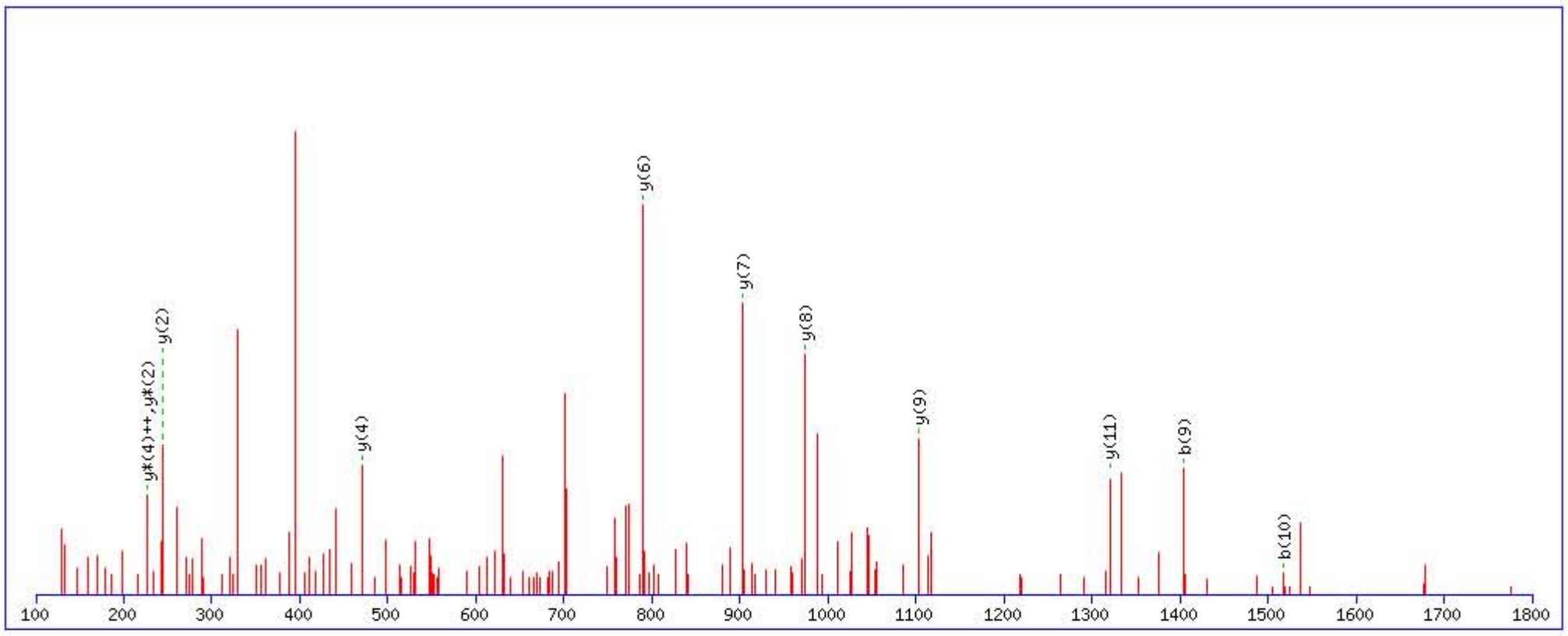
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **WTPYQGCEALCCPEPK**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

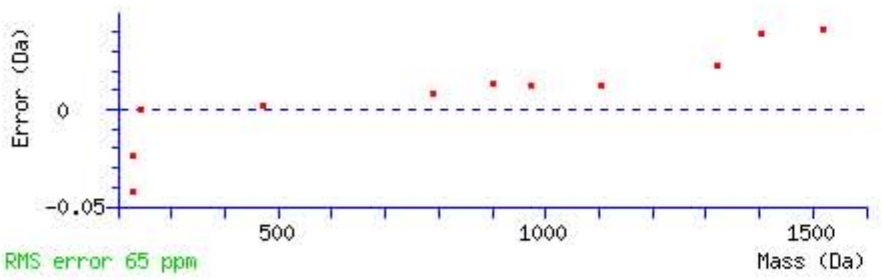
Match to Query 50643: 2306.026962 from(769.682930,3+) rtinseconds(2119) index(51136)
Title: Locus:1.1.1.1975.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

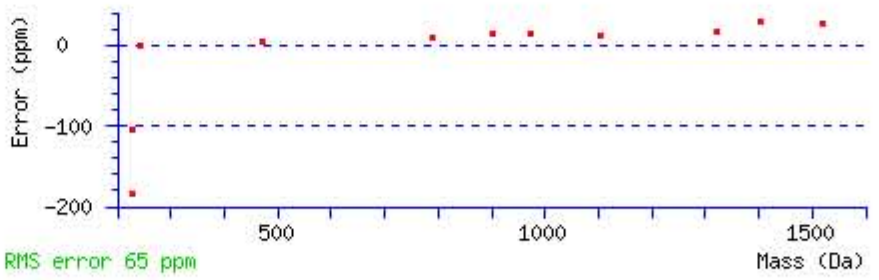
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2305.999237
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 37 **Expect:** 0.0013
**Matches :** 11/166 fragment ions using 17 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 187.086589 | 94.046932 | | | | | W | | | | | | | 16 |
| 2 | 288.134268 | 144.570772 | | | 270.123703 | 135.565490 | T | 2120.927205 | 1060.967240 | 2103.900656 | 1052.453966 | 2102.916640 | 1051.961958 | 15 |
| 3 | 385.187032 | 193.097154 | | | 367.176467 | 184.091872 | P | 2019.879526 | 1010.443401 | 2002.852977 | 1001.930127 | 2001.868961 | 1001.438119 | 14 |
| 4 | 548.250361 | 274.628819 | | | 530.239796 | 265.623536 | Y | 1922.826762 | 961.917019 | 1905.800213 | 953.403745 | 1904.816197 | 952.911737 | 13 |
| 5 | 987.475687 | 494.241482 | 970.449138 | 485.728207 | 969.465122 | 485.236199 | Q | 1759.763433 | 880.385355 | 1742.736884 | 871.872080 | 1741.752868 | 871.380072 | 12 |
| 6 | 1044.497151 | 522.752214 | 1027.470602 | 514.238939 | 1026.486586 | 513.746931 | G | *1320.538107* | 660.772692 | 1303.511558 | 652.259417 | 1302.527542 | 651.767409 | 11 |
| 7 | 1204.527800 | 602.767538 | 1187.501251 | 594.254264 | 1186.517235 | 593.762256 | C | 1263.516643 | 632.261960 | 1246.490094 | 623.748685 | 1245.506078 | 623.256677 | 10 |
| 8 | 1333.570393 | 667.288835 | 1316.543844 | 658.775560 | 1315.559828 | 658.283552 | E | *1103.485994* | 552.246635 | 1086.459445 | 543.733361 | 1085.475429 | 543.241353 | 9 |
| 9 | **1404.607507** | 702.807392 | 1387.580958 | 694.294117 | 1386.596942 | 693.802109 | A | *974.443401* | 487.725339 | 957.416852 | 479.212064 | 956.432836 | 478.720056 | 8 |
| 10 | **1517.691571** | 759.349424 | 1500.665022 | 750.836149 | 1499.681006 | 750.344141 | L | *903.406287* | 452.206782 | 886.379738 | 443.693507 | 885.395722 | 443.201499 | 7 |
| 11 | 1677.722220 | 839.364748 | 1660.695671 | 830.851474 | 1659.711655 | 830.359466 | C | *790.322223* | 395.664750 | 773.295674 | 387.151475 | 772.311658 | 386.659467 | 6 |
| 12 | 1837.752869 | 919.380073 | 1820.726320 | 910.866798 | 1819.742304 | 910.374790 | C | 630.291574 | 315.649425 | 613.265025 | 307.136151 | 612.281009 | 306.644143 | 5 |
| 13 | 1934.805633 | 967.906455 | 1917.779084 | 959.393180 | 1916.795068 | 958.901172 | P | *470.260925* | 235.634101 | 453.234376 | 227.120826 | 452.250360 | 226.628818 | 4 |
| 14 | 2063.848226 | 1032.427751 | 2046.821677 | 1023.914477 | 2045.837661 | 1023.422469 | E | 373.208161 | 187.107719 | 356.181612 | 178.594444 | 355.197596 | 178.102436 | 3 |
| 15 | 2160.900990 | 1080.954133 | 2143.874441 | 1072.440858 | 2142.890425 | 1071.948850 | P | *244.165568* | 122.586422 | 227.139019 | 114.073148 | | | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 37.5 | 2305.999237 | 0.027725 | WTPYQGCEALCCPEPK |

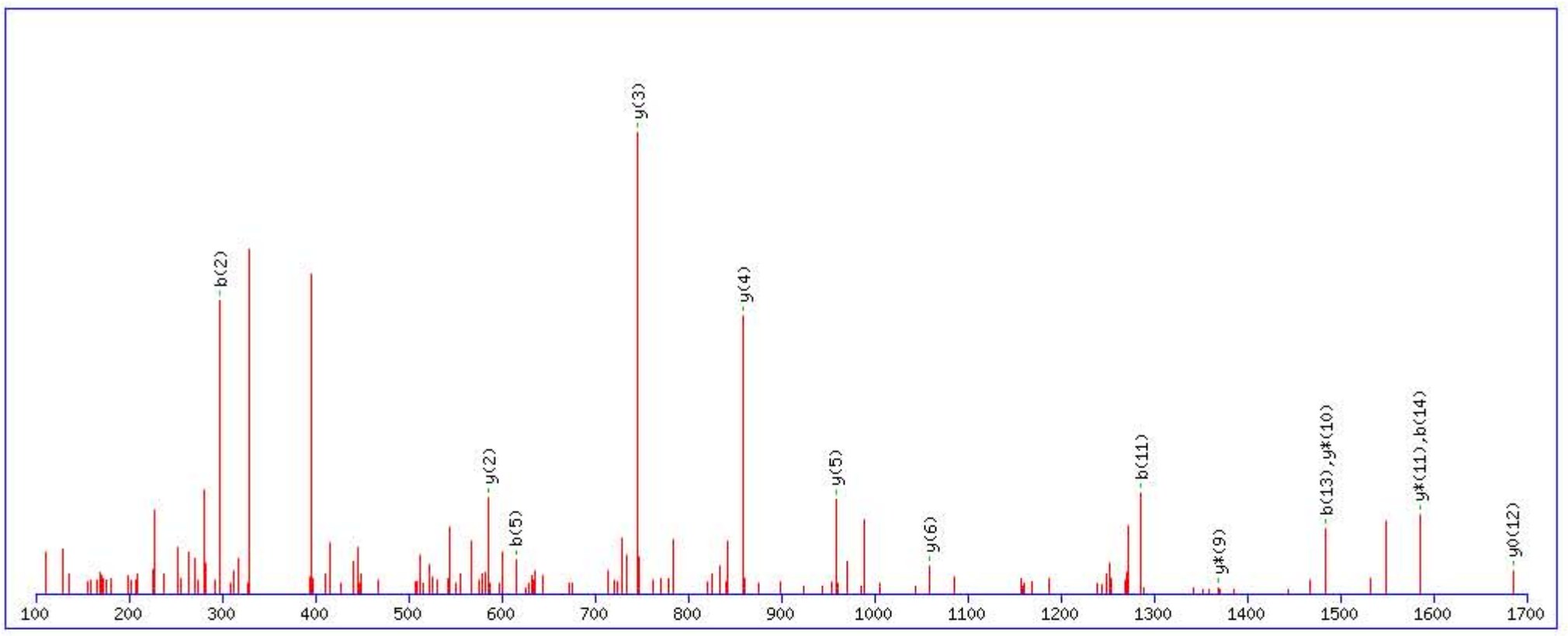
# MATRIX SCIENCE Mascot Search Results

## Peptide View

MS/MS Fragmentation of **CHPGYKPTTDEPTTVICQK**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

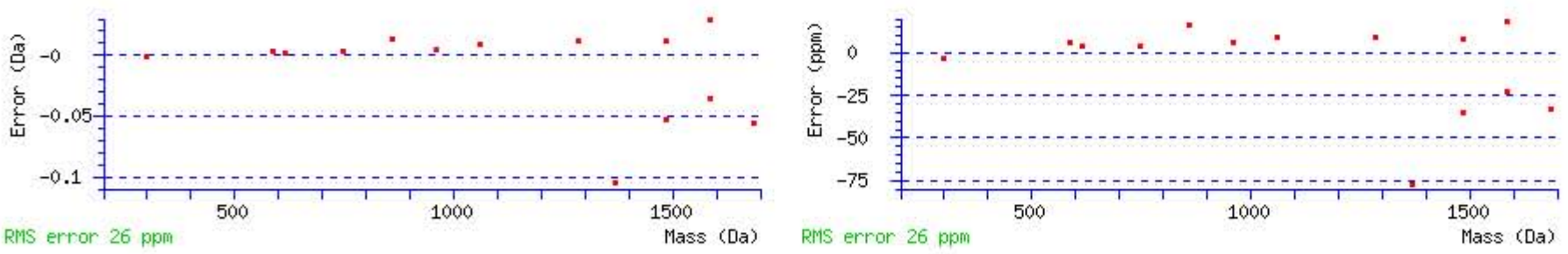
Match to Query 54899: 2542.216776 from(636.561470,4+) rtinseconds(1612) index(47736)
Title: Locus:1.1.1.1799.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2542.201859
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q18 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.00026
**Matches :** 14/182 fragment ions using 16 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 161.037925 | 81.022600 | | | | | C | | | | | | | 19 |
| 2 | *298.096837* | 149.552056 | | | | | H | 2383.178469 | 1192.092872 | 2366.151920 | 1183.579598 | 2365.167904 | 1183.087590 | 18 |
| 3 | 395.149601 | 198.078439 | | | | | P | 2246.119557 | 1123.563416 | 2229.093008 | 1115.050142 | 2228.108992 | 1114.558134 | 17 |
| 4 | 452.171065 | 226.589170 | | | | | G | 2149.066793 | 1075.037034 | 2132.040244 | 1066.523760 | 2131.056228 | 1066.031752 | 16 |
| 5 | *615.234394* | 308.120835 | | | | | Y | 2092.045329 | 1046.526302 | 2075.018780 | 1038.013028 | 2074.034764 | 1037.521020 | 15 |
| 6 | 743.329357 | 372.168317 | 726.302808 | 363.655042 | | | K | 1928.982000 | 964.994638 | 1911.955451 | 956.481364 | 1910.971435 | 955.989356 | 14 |
| 7 | 840.382121 | 420.694699 | 823.355572 | 412.181424 | | | P | 1800.887037 | 900.947157 | 1783.860488 | 892.433882 | 1782.876472 | 891.941874 | 13 |
| 8 | 941.429800 | 471.218538 | 924.403251 | 462.705264 | 923.419235 | 462.213256 | T | 1703.834273 | 852.420775 | 1686.807724 | 843.907500 | 1685.823708 | 843.415492 | 12 |
| 9 | 1042.477479 | 521.742378 | 1025.450930 | 513.229103 | 1024.466914 | 512.737095 | T | 1602.786594 | 801.896935 | 1585.760045 | 793.383661 | 1584.776029 | 792.891653 | 11 |
| 10 | 1157.504422 | 579.255849 | 1140.477873 | 570.742575 | 1139.493857 | 570.250567 | D | 1501.738915 | 751.373096 | 1484.712366 | 742.859821 | 1483.728350 | 742.367813 | 10 |
| 11 | *1286.547015* | 643.777146 | 1269.520466 | 635.263871 | 1268.536450 | 634.771863 | E | 1386.711972 | 693.859624 | 1369.685423 | 685.346350 | 1368.701407 | 684.854342 | 9 |
| 12 | 1383.599779 | 692.303528 | 1366.573230 | 683.790253 | 1365.589214 | 683.298245 | P | 1257.669379 | 629.338328 | 1240.642830 | 620.825053 | 1239.658814 | 620.333045 | 8 |
| 13 | *1484.647458* | 742.827367 | 1467.620909 | 734.314093 | 1466.636893 | 733.822085 | T | 1160.616615 | 580.811946 | 1143.590066 | 572.298671 | 1142.606050 | 571.806663 | 7 |
| 14 | *1585.695137* | 793.351207 | 1568.668588 | 784.837932 | 1567.684572 | 784.345924 | T | *1059.568936* | 530.288106 | 1042.542387 | 521.774832 | 1041.558371 | 521.282824 | 6 |
| 15 | 1684.763551 | 842.885414 | 1667.737002 | 834.372139 | 1666.752986 | 833.880131 | V | *958.521257* | 479.764267 | 941.494708 | 471.250992 | | | 5 |
| 16 | 1797.847615 | 899.427446 | 1780.821066 | 890.914171 | 1779.837050 | 890.422163 | I | *859.452843* | 430.230060 | 842.426294 | 421.716785 | | | 4 |
| 17 | 1957.878264 | 979.442770 | 1940.851715 | 970.929496 | 1939.867699 | 970.437488 | C | *746.368779* | 373.688028 | 729.342230 | 365.174753 | | | 3 |
| 18 | 2397.103590 | 1199.055433 | 2380.077041 | 1190.542158 | 2379.093025 | 1190.050151 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 19 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 39.0 | 2542.201859 | 0.014917 | CHPGYKPTTDEPTTVICQK |
| 0.9 | 2542.227280 | -0.010504 | GPGGSPGRRPSPAAPDGAPASGTSEPGR |

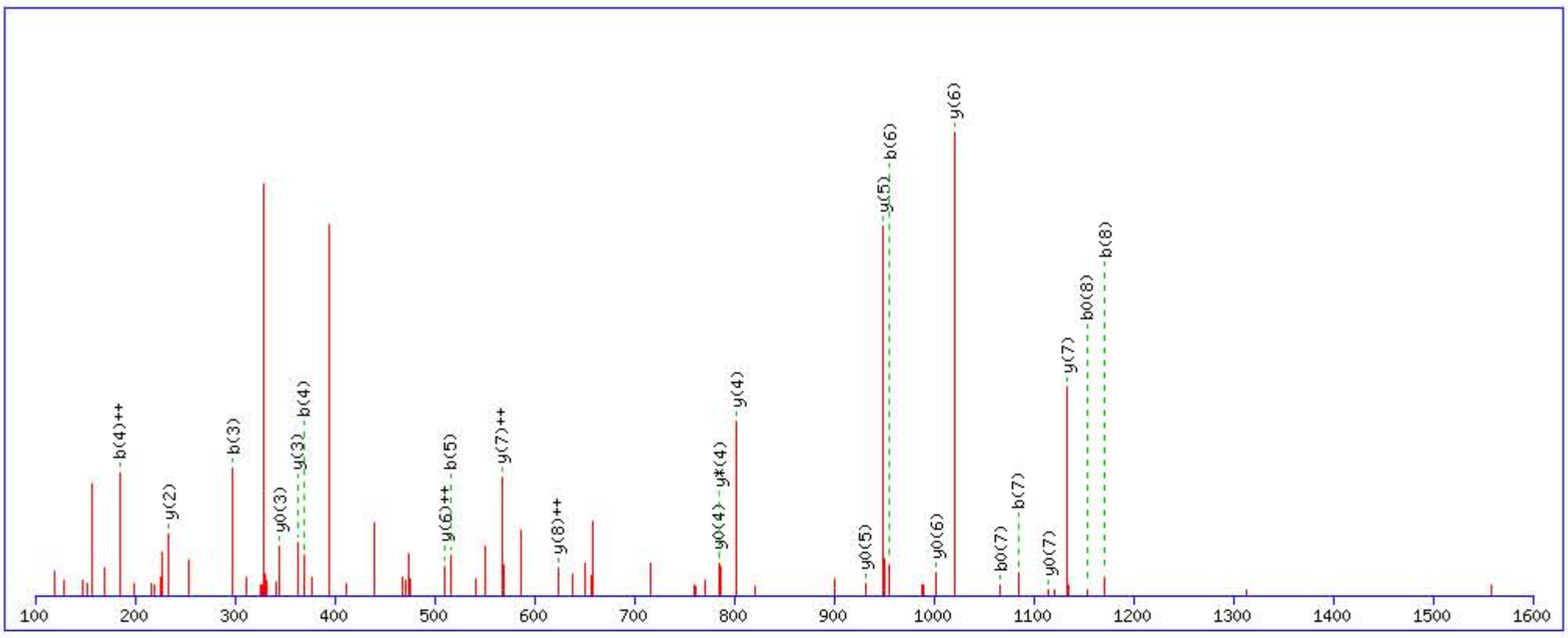
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ALLAFQESK**
Found in **C4BPB_HUMAN**, C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=1 SV=1

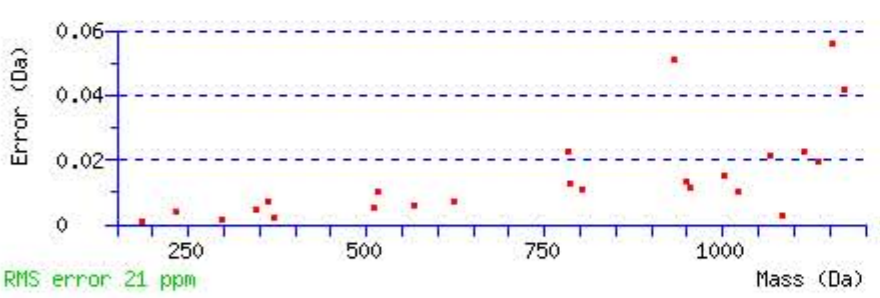
Match to Query 23620: 1316.730528 from(659.372540,2+) rtinseconds(2232) index(35656)
Title: Locus:1.1.1.886.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

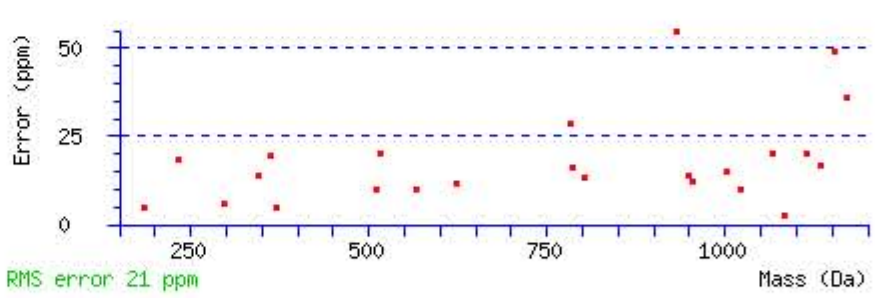
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1316.716217
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.0065
**Matches :** 25/72 fragment ions using 53 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 9 |
| 2 | *185.128454* | 93.067865 | | | | | L | 1246.686407 | 623.846842 | 1229.659858 | 615.333567 | 1228.675842 | 614.841559 | 8 |
| 3 | *298.212518* | 149.609897 | | | | | L | **1133.602343** | 567.304810 | 1116.575794 | 558.791535 | 1115.591778 | 558.299527 | 7 |
| 4 | *369.249632* | 185.128454 | | | | | A | **1020.518279** | 510.762778 | 1003.491730 | 502.249503 | 1002.507714 | 501.757495 | 6 |
| 5 | *516.318046* | 258.662661 | | | | | F | **949.481165** | 475.244221 | 932.454616 | 466.730946 | 931.470600 | 466.238938 | 5 |
| 6 | *955.543372* | 478.275324 | 938.516823 | 469.762049 | | | Q | **802.412751** | 401.710014 | 785.386202 | 393.196739 | 784.402186 | 392.704731 | 4 |
| 7 | *1084.585965* | 542.796621 | 1067.559416 | 534.283346 | 1066.575400 | 533.791338 | E | **363.187425** | 182.097351 | 346.160876 | 173.584076 | 345.176860 | 173.092068 | 3 |
| 8 | *1171.617993* | 586.312635 | 1154.591444 | 577.799360 | 1153.607428 | 577.307352 | S | **234.144832** | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 9 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 32.5 | 1316.716217 | 0.014311 | ALLAFQESK |
| 8.6 | 1316.749924 | -0.019396 | SPLIRHQR |
| 4.6 | 1316.731308 | -0.000780 | KTFPISGARGGAR |
| 2.4 | 1316.742050 | -0.011522 | AILCRKGKPMK |
| 2.1 | 1316.733994 | -0.003466 | LALVINGDFLDK |
| 2.1 | 1316.745224 | -0.014696 | SPLQLQTVIYR |
| 0.6 | 1316.729935 | 0.000593 | NTITNEELKKK |

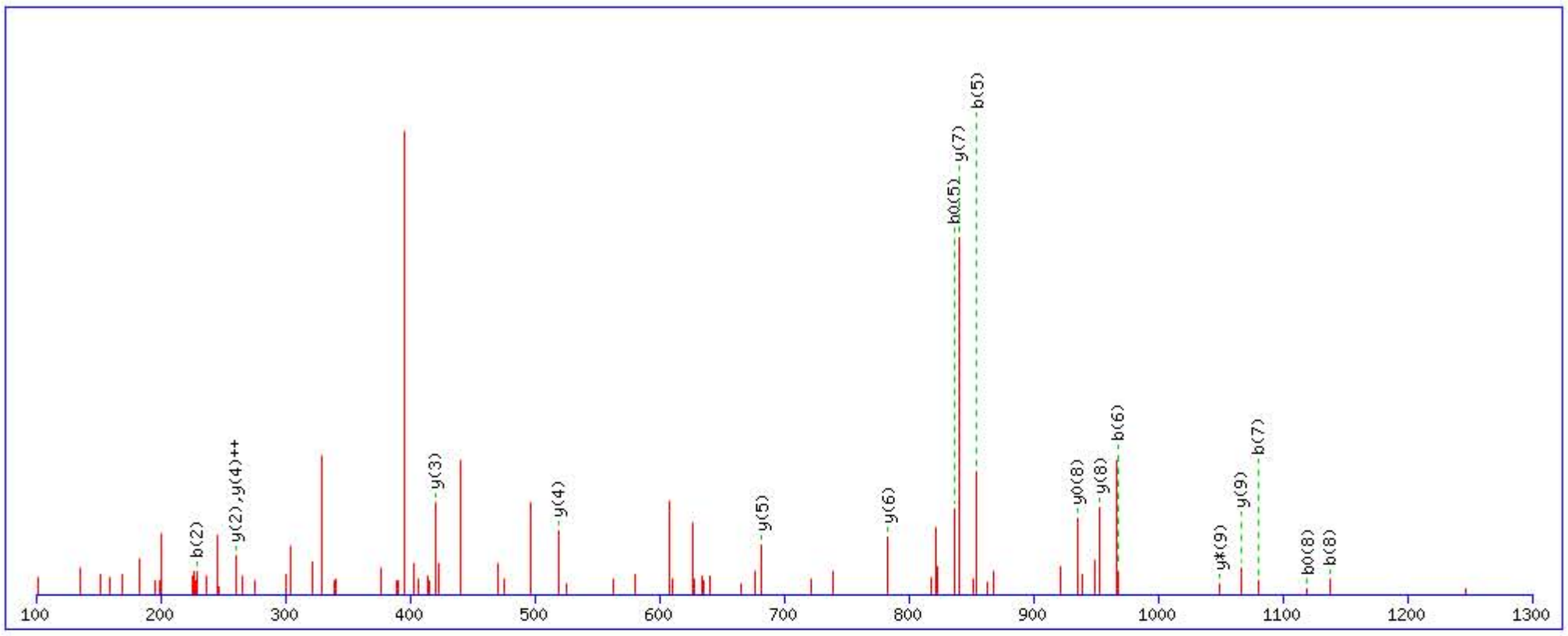
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EVEGQILGTYVCIK**
Found in **C4BPB_HUMAN**, C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=1 SV=1

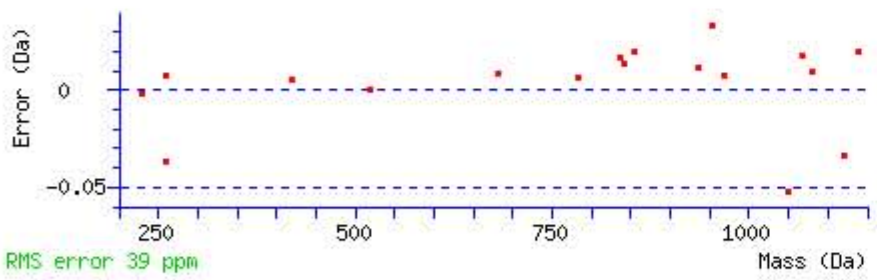
Match to Query 42495: 1919.016912 from(640.679580,3+) rtinseconds(2479) index(36913)
Title: Locus:1.1.1.972.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

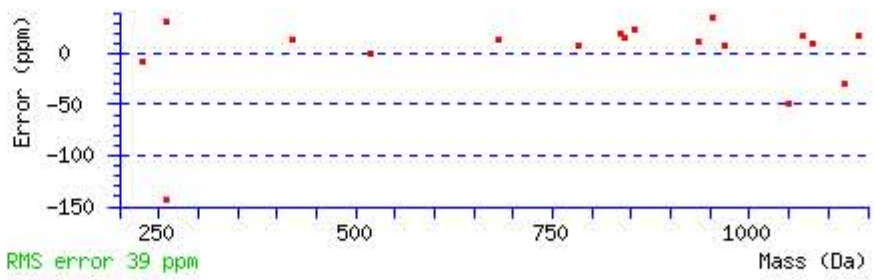
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1918.989639
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0027
**Matches :** 18/138 fragment ions using 33 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 14 |
| 2 | **229.118283** | 115.062780 | | | 211.107718 | 106.057497 | V | 1790.954328 | 895.980802 | 1773.927779 | 887.467528 | 1772.943763 | 886.975520 | 13 |
| 3 | 358.160876 | 179.584076 | | | 340.150311 | 170.578794 | E | 1691.885914 | 846.446595 | 1674.859365 | 837.933321 | 1673.875349 | 837.441313 | 12 |
| 4 | 415.182340 | 208.094808 | | | 397.171775 | 199.089526 | G | 1562.843321 | 781.925299 | 1545.816772 | 773.412024 | 1544.832756 | 772.920016 | 11 |
| 5 | **854.407666** | 427.707471 | 837.381117 | 419.194197 | 836.397101 | 418.702189 | Q | 1505.821857 | 753.414567 | 1488.795308 | 744.901292 | 1487.811292 | 744.409284 | 10 |
| 6 | **967.491730** | 484.249503 | 950.465181 | 475.736229 | 949.481165 | 475.244221 | I | *1066.596531* | 533.801904 | 1049.569982 | 525.288629 | 1048.585966 | 524.796621 | 9 |
| 7 | **1080.575794** | 540.791535 | 1063.549245 | 532.278261 | 1062.565229 | 531.786253 | L | *953.512467* | 477.259872 | 936.485918 | 468.746597 | 935.501902 | 468.254589 | 8 |
| 8 | **1137.597258** | 569.302267 | 1120.570709 | 560.788993 | 1119.586693 | 560.296985 | G | *840.428403* | 420.717840 | 823.401854 | 412.204565 | 822.417838 | 411.712557 | 7 |
| 9 | 1238.644937 | 619.826107 | 1221.618388 | 611.312832 | 1220.634372 | 610.820824 | T | *783.406939* | 392.207108 | 766.380390 | 383.693833 | 765.396374 | 383.201825 | 6 |
| 10 | 1401.708266 | 701.357771 | 1384.681717 | 692.844497 | 1383.697701 | 692.352489 | Y | *682.359260* | 341.683268 | 665.332711 | 333.169994 | | | 5 |
| 11 | 1500.776680 | 750.891978 | 1483.750131 | 742.378704 | 1482.766115 | 741.886696 | V | *519.295931* | 260.151604 | 502.269382 | 251.638329 | | | 4 |
| 12 | 1660.807329 | 830.907303 | 1643.780780 | 822.394028 | 1642.796764 | 821.902020 | C | *420.227517* | 210.617396 | 403.200968 | 202.104122 | | | 3 |
| 13 | 1773.891393 | 887.449335 | 1756.864844 | 878.936060 | 1755.880828 | 878.444052 | I | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 14 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 39.5 | 1918.989639 | 0.027273 | EVEGQILGTYVCIK |

**Mascot:** http://www.matrixscience.com/

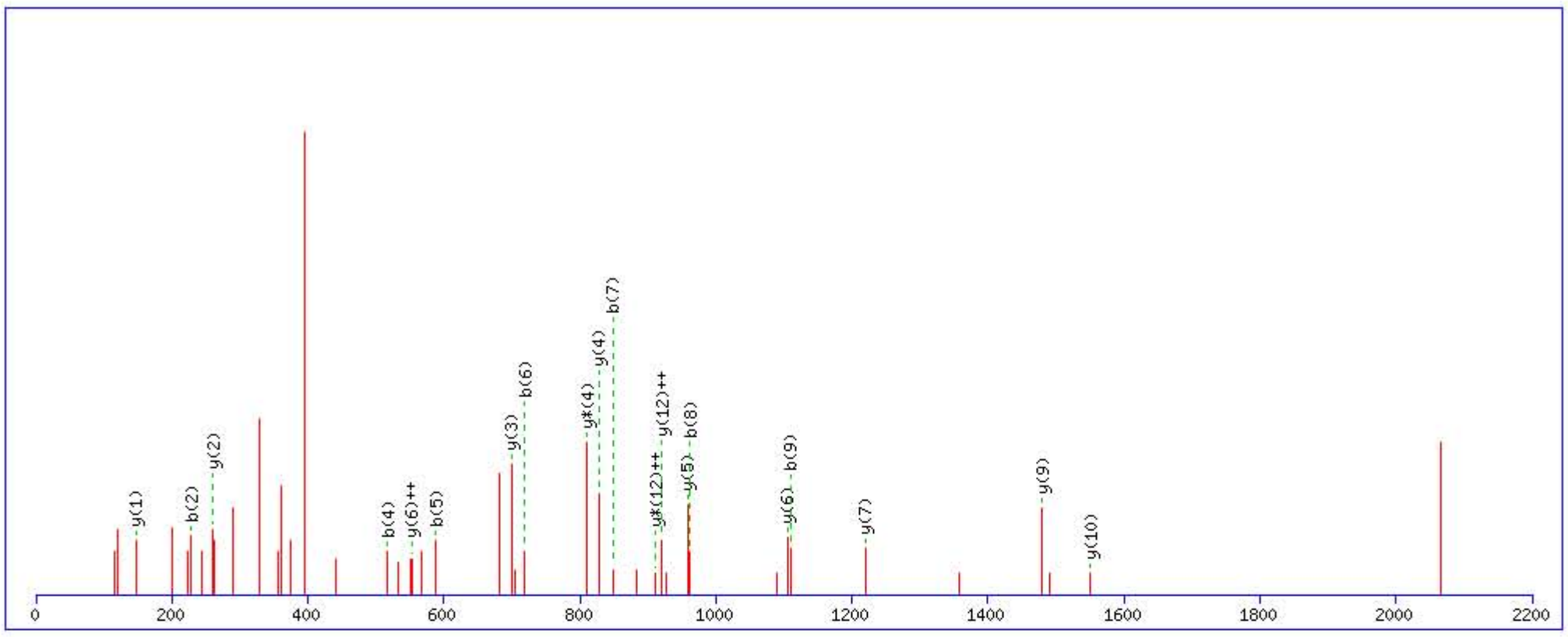
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NLCEAMENFMQQLK**
Found in **C4BPB_HUMAN**, C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=1 SV=1

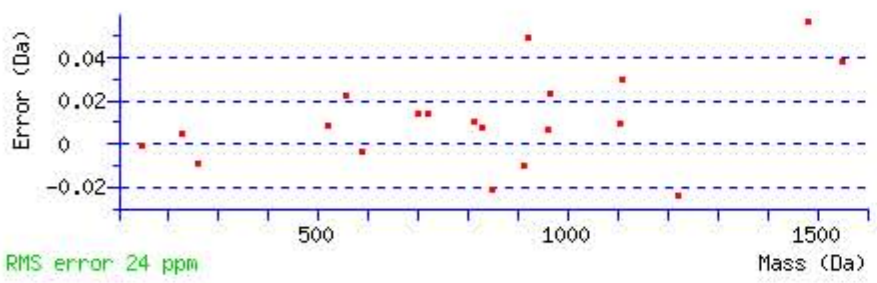
Match to Query 46042: 2065.967742 from(689.663190,3+) rtinseconds(3099) index(57706)
Title: Locus:1.1.1.2312.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

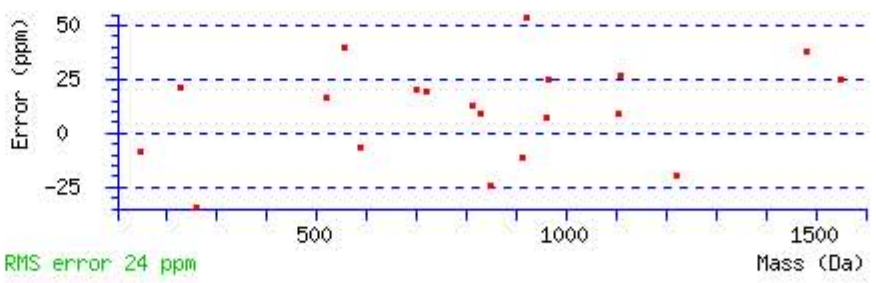
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2065.945709
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 47 **Expect:** 4.5e-005
**Matches :** 20/136 fragment ions using 40 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 14 |
| 2 | *228.134267* | 114.570771 | 211.107718 | 106.057497 | | | L | 1952.910096 | 976.958686 | 1935.883547 | 968.445412 | 1934.899531 | 967.953404 | 13 |
| 3 | 388.164916 | 194.586096 | 371.138367 | 186.072822 | | | C | 1839.826032 | 920.416654 | 1822.799483 | 911.903380 | 1821.815467 | 911.411371 | 12 |
| 4 | *517.207509* | 259.107393 | 500.180960 | 250.594118 | 499.196944 | 250.102110 | E | 1679.795383 | 840.401329 | 1662.768834 | 831.888055 | 1661.784818 | 831.396047 | 11 |
| 5 | *588.244623* | 294.625950 | 571.218074 | 286.112675 | 570.234058 | 285.620667 | A | *1550.752790* | 775.880033 | 1533.726241 | 767.366759 | 1532.742225 | 766.874751 | 10 |
| 6 | *719.285108* | 360.146192 | 702.258559 | 351.632918 | 701.274543 | 351.140910 | M | *1479.715676* | 740.361476 | 1462.689127 | 731.848202 | 1461.705111 | 731.356194 | 9 |
| 7 | *848.327701* | 424.667489 | 831.301152 | 416.154214 | 830.317136 | 415.662206 | E | 1348.675191 | 674.841234 | 1331.648642 | 666.327959 | 1330.664626 | 665.835951 | 8 |
| 8 | *962.370628* | 481.688952 | 945.344079 | 473.175678 | 944.360063 | 472.683670 | N | *1219.632598* | 610.319937 | 1202.606049 | 601.806663 | | | 7 |
| 9 | *1109.439042* | 555.223159 | 1092.412493 | 546.709885 | 1091.428477 | 546.217876 | F | *1105.589671* | 553.298474 | 1088.563122 | 544.785199 | | | 6 |
| 10 | 1240.479527 | 620.743402 | 1223.452978 | 612.230127 | 1222.468962 | 611.738119 | M | *958.521257* | 479.764267 | 941.494708 | 471.250992 | | | 5 |
| 11 | 1368.538105 | 684.772690 | 1351.511556 | 676.259416 | 1350.527540 | 675.767408 | Q | *827.480772* | 414.244024 | 810.454223 | 405.730750 | | | 4 |
| 12 | 1807.763431 | 904.385354 | 1790.736882 | 895.872079 | 1789.752866 | 895.380071 | Q | *699.422194* | 350.214735 | 682.395645 | 341.701461 | | | 3 |
| 13 | 1920.847495 | 960.927386 | 1903.820946 | 952.414111 | 1902.836930 | 951.922103 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 14 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 46.6 | 2065.945709 | 0.022033 | NLCEAMENFMQQLK |
| 38.6 | 2065.945709 | 0.022033 | NLCEAMENFMQQLK |
| 0.3 | 2065.985092 | -0.017350 | QGENSTHQQSASASVPK |
| 0.2 | 2065.966843 | 0.000899 | QEMECCLNSILKSK |

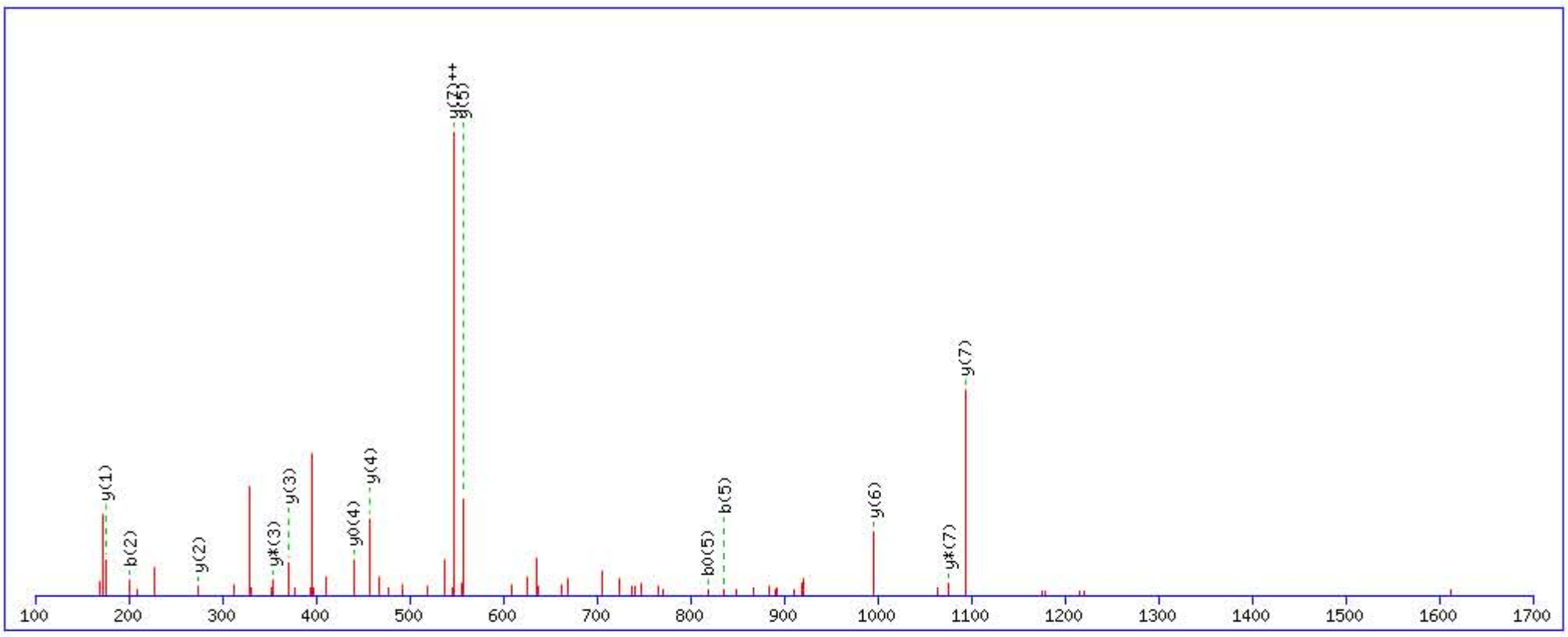
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SIPQVSPVR**
Found in **CBPN_HUMAN**, Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1

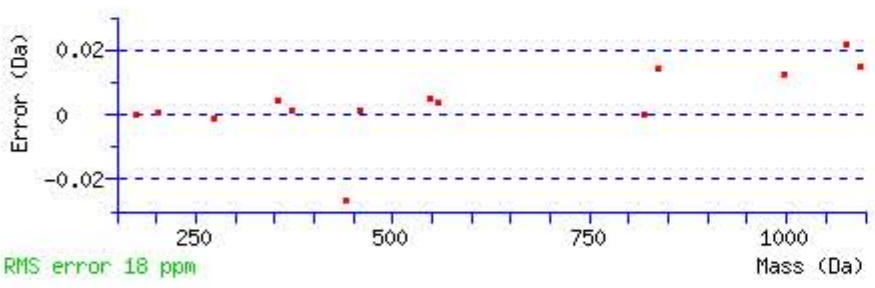
Match to Query 23221: 1292.737348 from(647.375950,2+) rtinseconds(1891) index(33388)
Title: Locus:1.1.1.767.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

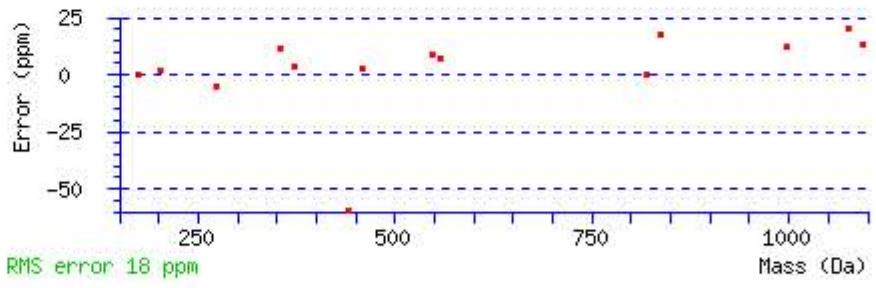
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1292.727478
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 27 **Expect:** 0.016
**Matches :** 14/84 fragment ions using 41 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 9 |
| 2 | **201.123368** | 101.065322 | | | 183.112803 | 92.060039 | I | 1206.702726 | 603.855001 | 1189.676177 | 595.341727 | 1188.692161 | 594.849718 | 8 |
| 3 | 298.176132 | 149.591704 | | | 280.165567 | 140.586422 | P | *1093.618662* | 547.312969 | 1076.592113 | 538.799695 | 1075.608097 | 538.307687 | 7 |
| 4 | 737.401458 | 369.204367 | 720.374909 | 360.691093 | 719.390893 | 360.199085 | Q | *996.565898* | 498.786587 | 979.539349 | 490.273313 | 978.555333 | 489.781305 | 6 |
| 5 | **836.469872** | 418.738574 | 819.443323 | 410.225300 | 818.459307 | 409.733292 | V | *557.340572* | 279.173924 | 540.314023 | 270.660650 | 539.330007 | 270.168642 | 5 |
| 6 | 923.501900 | 462.254588 | 906.475351 | 453.741313 | 905.491335 | 453.249305 | S | *458.272158* | 229.639717 | 441.245609 | 221.126443 | 440.261593 | 220.634435 | 4 |
| 7 | 1020.554664 | 510.780970 | 1003.528115 | 502.267696 | 1002.544099 | 501.775688 | P | *371.240130* | 186.123703 | 354.213581 | 177.610429 | | | 3 |
| 8 | 1119.623078 | 560.315177 | 1102.596529 | 551.801903 | 1101.612513 | 551.309895 | V | *274.187366* | 137.597321 | 257.160817 | 129.084047 | | | 2 |
| 9 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 27.3 | 1292.727478 | 0.009870 | SIPQVSPVR |
| 9.8 | 1292.756454 | -0.019106 | LSIPQITTKHR |
| 4.5 | 1292.756485 | -0.019137 | VTAVEVGKHVVR |
| 1.9 | 1292.756470 | -0.019122 | TVTLLSPPRPGR |
| 1.4 | 1292.745224 | -0.007876 | LSPSQHLAVLTK |

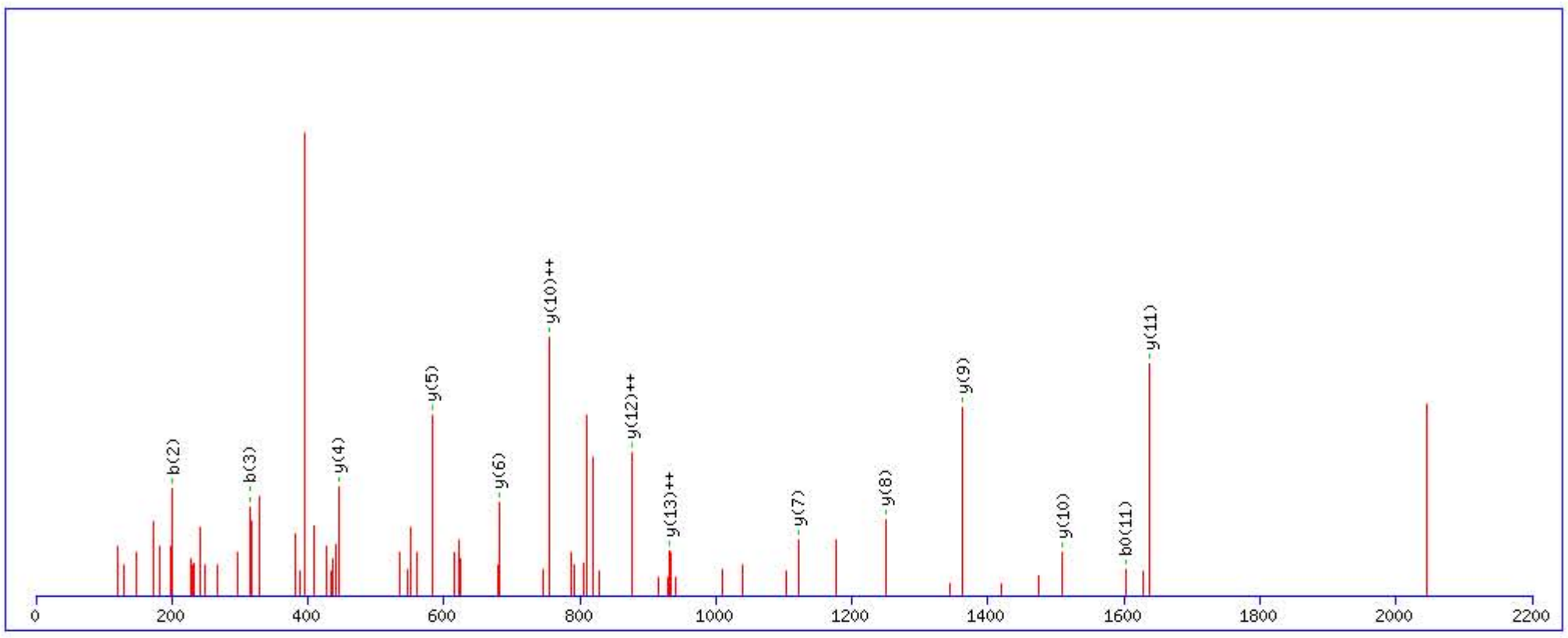
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EALIQFLEQVHQGIK**
Found in **CBPN_HUMAN**, Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1

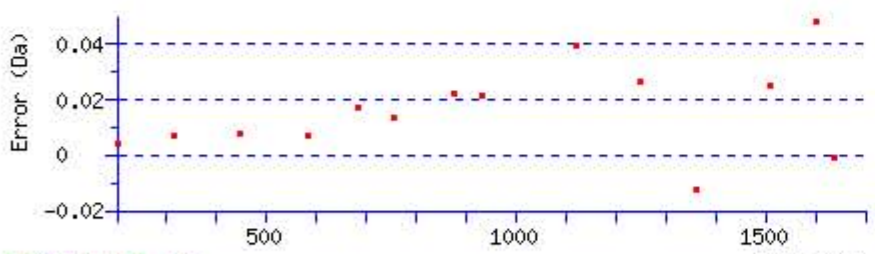
Match to Query 46015: 2063.153322 from(688.725050,3+) rtinseconds(2770) index(38920)
Title: Locus:1.1.1.1072.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

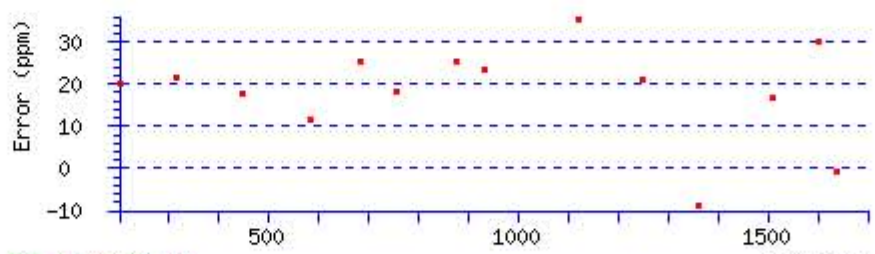
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2063.123749
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 62 **Expect:** 7.6e-006
**Matches :** 14/146 fragment ions using 17 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 15 |
| 2 | **201.086983** | 101.047130 | | | 183.076418 | 92.041847 | A | 1935.088453 | 968.047865 | 1918.061904 | 959.534590 | 1917.077888 | 959.042582 | 14 |
| 3 | **314.171047** | 157.589161 | | | 296.160482 | 148.583879 | L | 1864.051339 | 932.529307 | 1847.024790 | 924.016033 | 1846.040774 | 923.524025 | 13 |
| 4 | 427.255111 | 214.131193 | | | 409.244546 | 205.125911 | I | 1750.967275 | 875.987276 | 1733.940726 | 867.474001 | 1732.956710 | 866.981993 | 12 |
| 5 | 555.313689 | 278.160483 | 538.287140 | 269.647208 | 537.303124 | 269.155200 | Q | *1637.883211* | 819.445244 | 1620.856662 | 810.931969 | 1619.872646 | 810.439961 | 11 |
| 6 | 702.382103 | 351.694690 | 685.355554 | 343.181415 | 684.371538 | 342.689407 | F | *1509.824633* | 755.415955 | 1492.798084 | 746.902680 | 1491.814068 | 746.410672 | 10 |
| 7 | 815.466167 | 408.236722 | 798.439618 | 399.723447 | 797.455602 | 399.231439 | L | *1362.756219* | 681.881748 | 1345.729670 | 673.368473 | 1344.745654 | 672.876465 | 9 |
| 8 | 944.508760 | 472.758018 | 927.482211 | 464.244744 | 926.498195 | 463.752736 | E | *1249.672155* | 625.339716 | 1232.645606 | 616.826441 | 1231.661590 | 616.334433 | 8 |
| 9 | 1383.734086 | 692.370681 | 1366.707537 | 683.857407 | 1365.723521 | 683.365399 | Q | *1120.629562* | 560.818419 | 1103.603013 | 552.305144 | | | 7 |
| 10 | 1482.802500 | 741.904888 | 1465.775951 | 733.391614 | 1464.791935 | 732.899606 | V | *681.404236* | 341.205756 | 664.377687 | 332.692481 | | | 6 |
| 11 | 1619.861412 | 810.434344 | 1602.834863 | 801.921070 | 1601.850847 | 801.429062 | H | *582.335822* | 291.671549 | 565.309273 | 283.158274 | | | 5 |
| 12 | 1747.919990 | 874.463633 | 1730.893441 | 865.950359 | 1729.909425 | 865.458351 | Q | *445.276910* | 223.142093 | 428.250361 | 214.628818 | | | 4 |
| 13 | 1804.941454 | 902.974365 | 1787.914905 | 894.461091 | 1786.930889 | 893.969083 | G | 317.218332 | 159.112804 | 300.191783 | 150.599529 | | | 3 |
| 14 | 1918.025518 | 959.516397 | 1900.998969 | 951.003123 | 1900.014953 | 950.511114 | I | 260.196868 | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 15 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 62.2 | 2063.123749 | 0.029573 | EALIQFLEQVHQGIK |
| 25.1 | 2063.123749 | 0.029573 | EALIQFLEQVHQGIK |
| 13.5 | 2063.123749 | 0.029573 | EALIQFLEQVHQGIK |

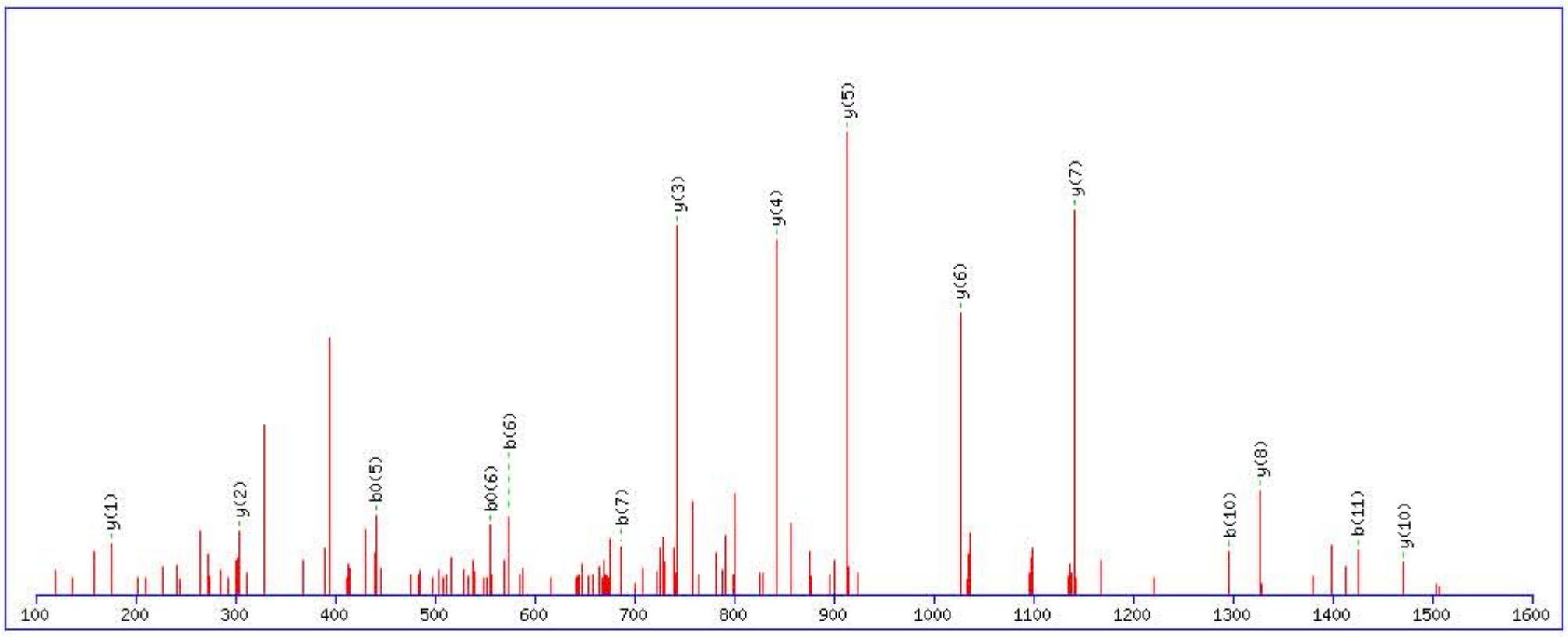
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AGGSWDLAVQER**
Found in **CPN2_HUMAN**, Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3

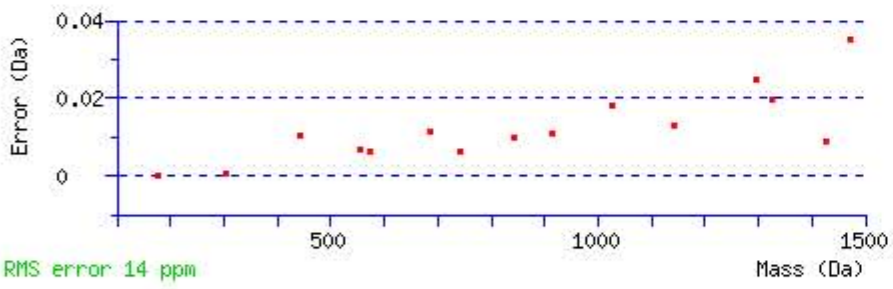
Match to Query 34671: 1598.809308 from(800.411930,2+) rtinseconds(2161) index(35223)
Title: Locus:1.1.1.861.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

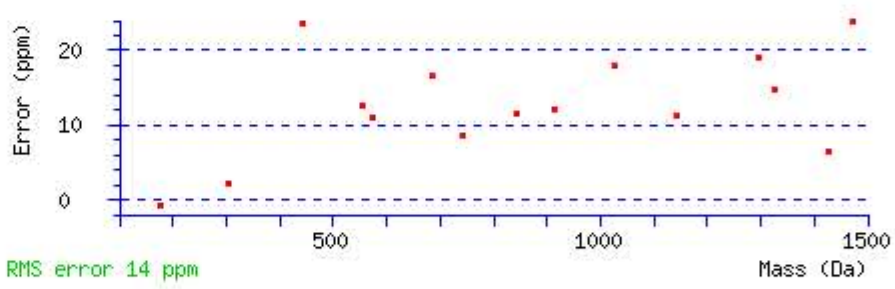
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1598.787506
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 3.3e-005
**Matches :** 15/106 fragment ions using 27 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 12 |
| 2 | 129.065854 | 65.036565 | | | | | G | 1528.757675 | 764.882476 | 1511.731126 | 756.369201 | 1510.747110 | 755.877193 | 11 |
| 3 | 186.087318 | 93.547297 | | | | | G | *1471.736211* | 736.371744 | 1454.709662 | 727.858469 | 1453.725646 | 727.366461 | 10 |
| 4 | 273.119346 | 137.063311 | | | 255.108781 | 128.058029 | S | 1414.714747 | 707.861012 | 1397.688198 | 699.347737 | 1396.704182 | 698.855729 | 9 |
| 5 | 459.198659 | 230.102968 | | | 441.188094 | 221.097685 | W | *1327.682719* | 664.344998 | 1310.656170 | 655.831723 | 1309.672154 | 655.339715 | 8 |
| 6 | **574.225602** | 287.616439 | | | 556.215037 | 278.611157 | D | *1141.603406* | 571.305341 | 1124.576857 | 562.792067 | 1123.592841 | 562.300059 | 7 |
| 7 | **687.309666** | 344.158471 | | | 669.299101 | 335.153189 | L | *1026.576463* | 513.791870 | 1009.549914 | 505.278595 | 1008.565898 | 504.786587 | 6 |
| 8 | 758.346780 | 379.677028 | | | 740.336215 | 370.671746 | A | *913.492399* | 457.249838 | 896.465850 | 448.736563 | 895.481834 | 448.244555 | 5 |
| 9 | 857.415194 | 429.211235 | | | 839.404629 | 420.205953 | V | *842.455285* | 421.731281 | 825.428736 | 413.218006 | 824.444720 | 412.725998 | 4 |
| 10 | **1296.640520** | 648.823898 | 1279.613971 | 640.310624 | 1278.629955 | 639.818616 | Q | *743.386871* | 372.197074 | 726.360322 | 363.683799 | 725.376306 | 363.191791 | 3 |
| 11 | **1425.683113** | 713.345195 | 1408.656564 | 704.831920 | 1407.672548 | 704.339912 | E | *304.161545* | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 12 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.7 | 1598.787506 | 0.021802 | AGGSWDLAVQER |
| 15.0 | 1598.797409 | 0.011899 | EDVDDLVSQLR |
| 8.8 | 1598.797379 | 0.011929 | ELDESLQVAER |
| 5.4 | 1598.797379 | 0.011929 | LEESDVLQEAR |
| 5.2 | 1598.789993 | 0.019315 | AGATSGELPVVEAENR |
| 4.1 | 1598.823883 | -0.014575 | LQISNPGFQER |
| 1.7 | 1598.791306 | 0.018002 | EREQRLEAFHER |
| 0.6 | 1598.790009 | 0.019299 | QELLEGDQDLVGQR |
| 0.6 | 1598.831100 | -0.021792 | QVETRTADGRR |

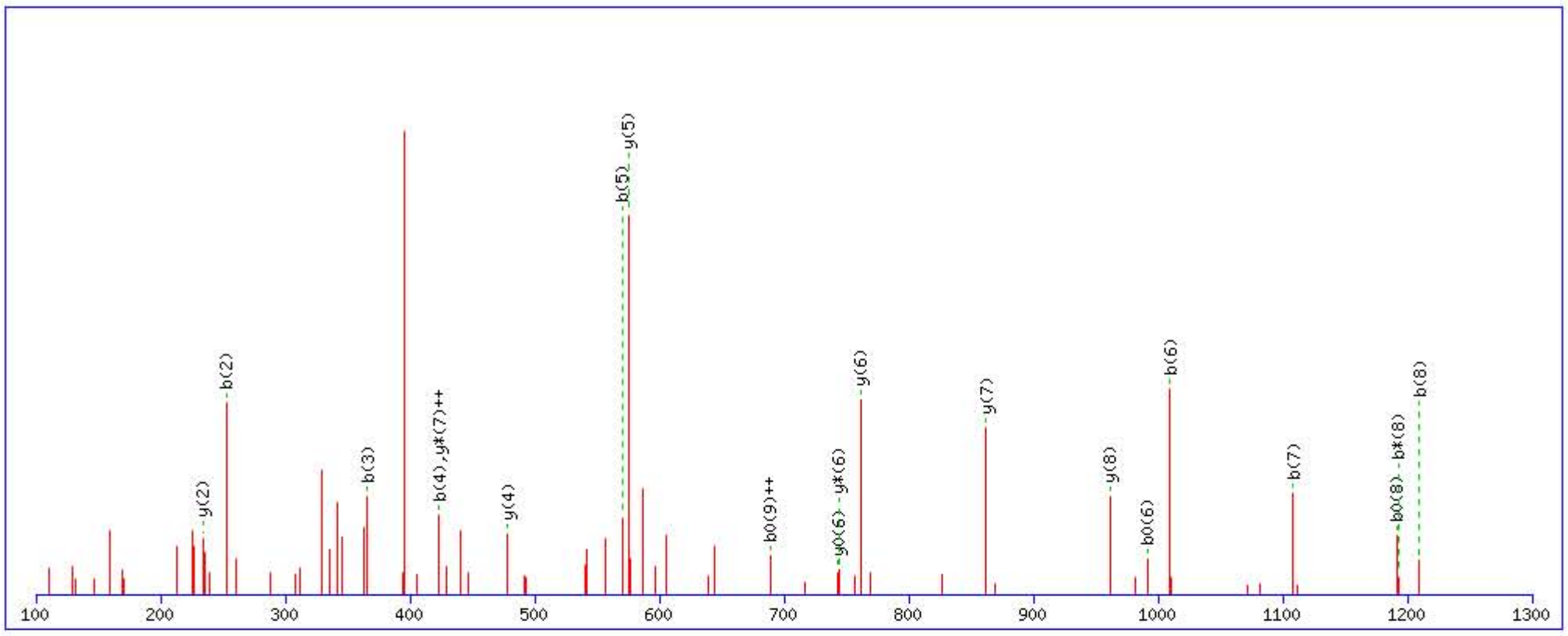
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DHLGFQVTWPDESK**
Found in **CPN2_HUMAN**, Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3

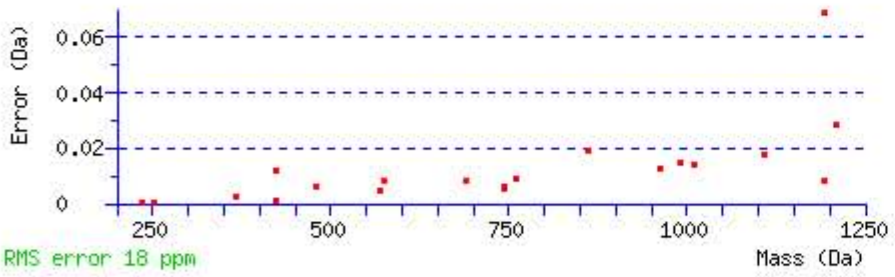
Match to Query 43556: 1968.959232 from(657.327020,3+) rtinseconds(2304) index(36070)
Title: Locus:1.1.1.911.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

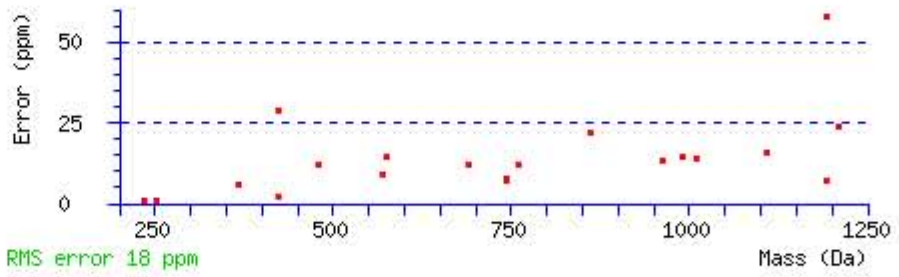
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1968.940399
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.00012
**Matches :** 20/144 fragment ions using 33 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 14 |
| 2 | *253.093131* | 127.050203 | | | 235.082566 | 118.044921 | H | 1854.920718 | 927.963997 | 1837.894169 | 919.450723 | 1836.910153 | 918.958715 | 13 |
| 3 | *366.177195* | 183.592235 | | | 348.166630 | 174.586953 | L | 1717.861806 | 859.434541 | 1700.835257 | 850.921267 | 1699.851241 | 850.429259 | 12 |
| 4 | *423.198659* | 212.102967 | | | 405.188094 | 203.097685 | G | 1604.777742 | 802.892509 | 1587.751193 | 794.379235 | 1586.767177 | 793.887227 | 11 |
| 5 | *570.267073* | 285.637175 | | | 552.256508 | 276.631892 | F | 1547.756278 | 774.381777 | 1530.729729 | 765.868503 | 1529.745713 | 765.376495 | 10 |
| 6 | *1009.492399* | 505.249838 | 992.465850 | 496.736563 | 991.481834 | 496.244555 | Q | 1400.687864 | 700.847570 | 1383.661315 | 692.334296 | 1382.677299 | 691.842288 | 9 |
| 7 | *1108.560813* | 554.784045 | 1091.534264 | 546.270770 | 1090.550248 | 545.778762 | V | *961.462538* | 481.234907 | 944.435989 | 472.721633 | 943.451973 | 472.229625 | 8 |
| 8 | *1209.608492* | 605.307884 | 1192.581943 | 596.794610 | 1191.597927 | 596.302602 | T | *862.394124* | 431.700700 | 845.367575 | 423.187426 | 844.383559 | 422.695418 | 7 |
| 9 | 1395.687805 | 698.347541 | 1378.661256 | 689.834266 | 1377.677240 | 689.342258 | W | *761.346445* | 381.176861 | 744.319896 | 372.663586 | 743.335880 | 372.171578 | 6 |
| 10 | 1492.740569 | 746.873923 | 1475.714020 | 738.360648 | 1474.730004 | 737.868640 | P | *575.267132* | 288.137204 | 558.240583 | 279.623930 | 557.256567 | 279.131922 | 5 |
| 11 | 1607.767512 | 804.387394 | 1590.740963 | 795.874120 | 1589.756947 | 795.382112 | D | *478.214368* | 239.610822 | 461.187819 | 231.097548 | 460.203803 | 230.605540 | 4 |
| 12 | 1736.810105 | 868.908691 | 1719.783556 | 860.395416 | 1718.799540 | 859.903408 | E | 363.187425 | 182.097351 | 346.160876 | 173.584076 | 345.176860 | 173.092068 | 3 |
| 13 | 1823.842133 | 912.424705 | 1806.815584 | 903.911430 | 1805.831568 | 903.419422 | S | *234.144832* | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 14 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 43.9 | 1968.940399 | 0.018833 | DHLGFQVTWPDESK |
| 1.9 | 1968.949585 | 0.009647 | EGQMESVEAAMSSKTLKK |

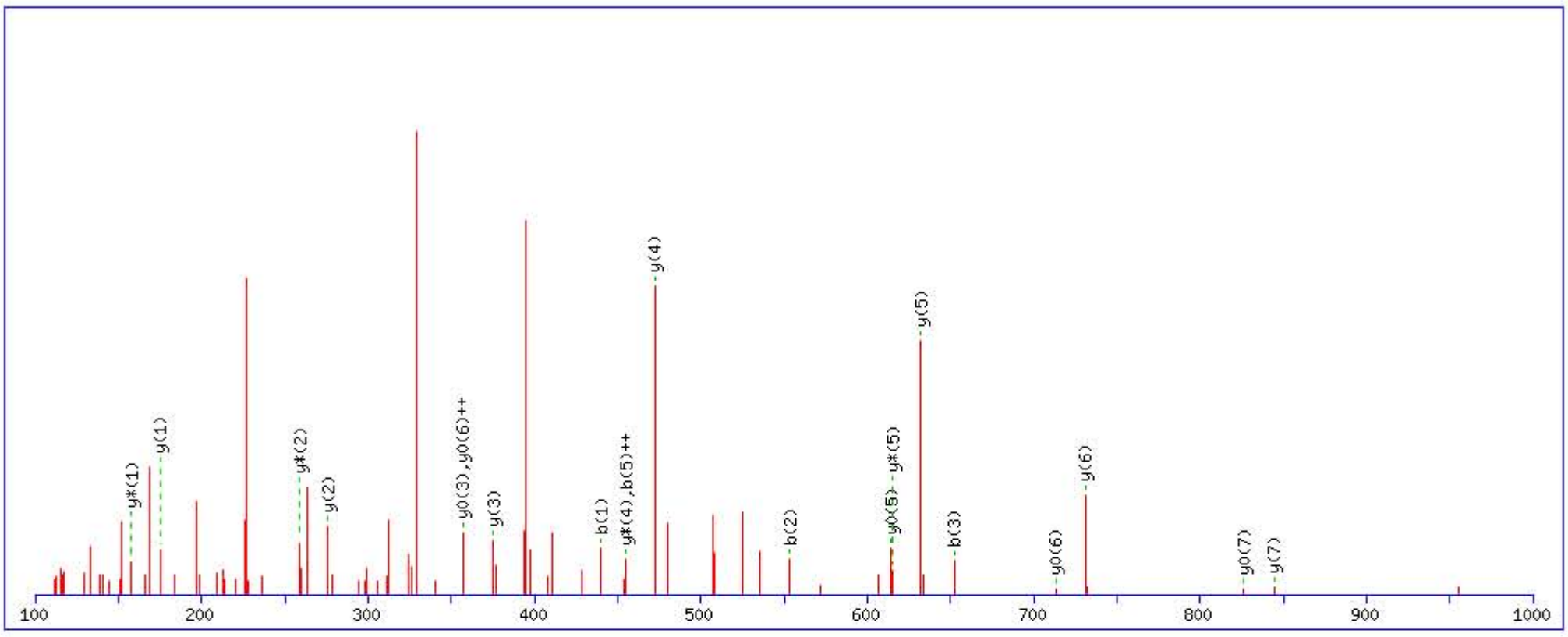
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QLVCPVTR**
Found in **CPN2_HUMAN**, Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3

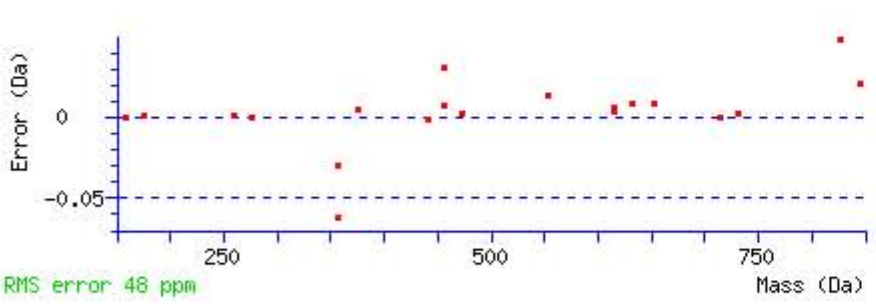
Match to Query 6799: 1282.690602 from(428.570810,3+) rtinseconds(1772) index(32751)
Title: Locus:1.1.1.726.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

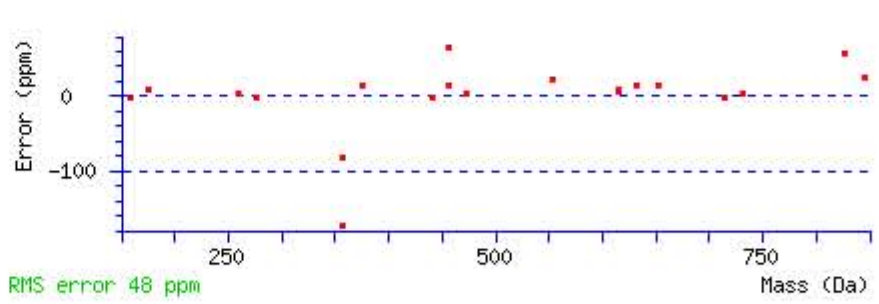
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1282.688995
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 29 **Expect:** 0.0021
**Matches** : 20/70 fragment ions using 44 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **440.232602** | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 8 |
| 2 | **553.316666** | 277.161971 | 536.290117 | 268.648697 | | | L | *844.470936* | 422.739106 | 827.444387 | 414.225831 | 826.460371 | 413.733823 | 7 |
| 3 | **652.385080** | 326.696178 | 635.358531 | 318.182904 | | | V | *731.386872* | 366.197074 | 714.360323 | 357.683799 | 713.376307 | 357.191791 | 6 |
| 4 | 812.415729 | 406.711503 | 795.389180 | 398.198228 | | | C | *632.318458* | 316.662867 | 615.291909 | 308.149592 | 614.307893 | 307.657584 | 5 |
| 5 | 909.468493 | 455.237885 | 892.441944 | 446.724610 | | | P | *472.287809* | 236.647542 | 455.261260 | 228.134268 | 454.277244 | 227.642260 | 4 |
| 6 | 1008.536907 | 504.772092 | 991.510358 | 496.258817 | | | V | *375.235045* | 188.121160 | 358.208496 | 179.607886 | 357.224480 | 179.115878 | 3 |
| 7 | 1109.584586 | 555.295931 | 1092.558037 | 546.782657 | 1091.574021 | 546.290648 | T | *276.166631* | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 29.1 | 1282.688995 | 0.001607 | QLVCPVTR |
| 0.6 | 1282.681595 | 0.009007 | KNMGGLGGLVHGK |

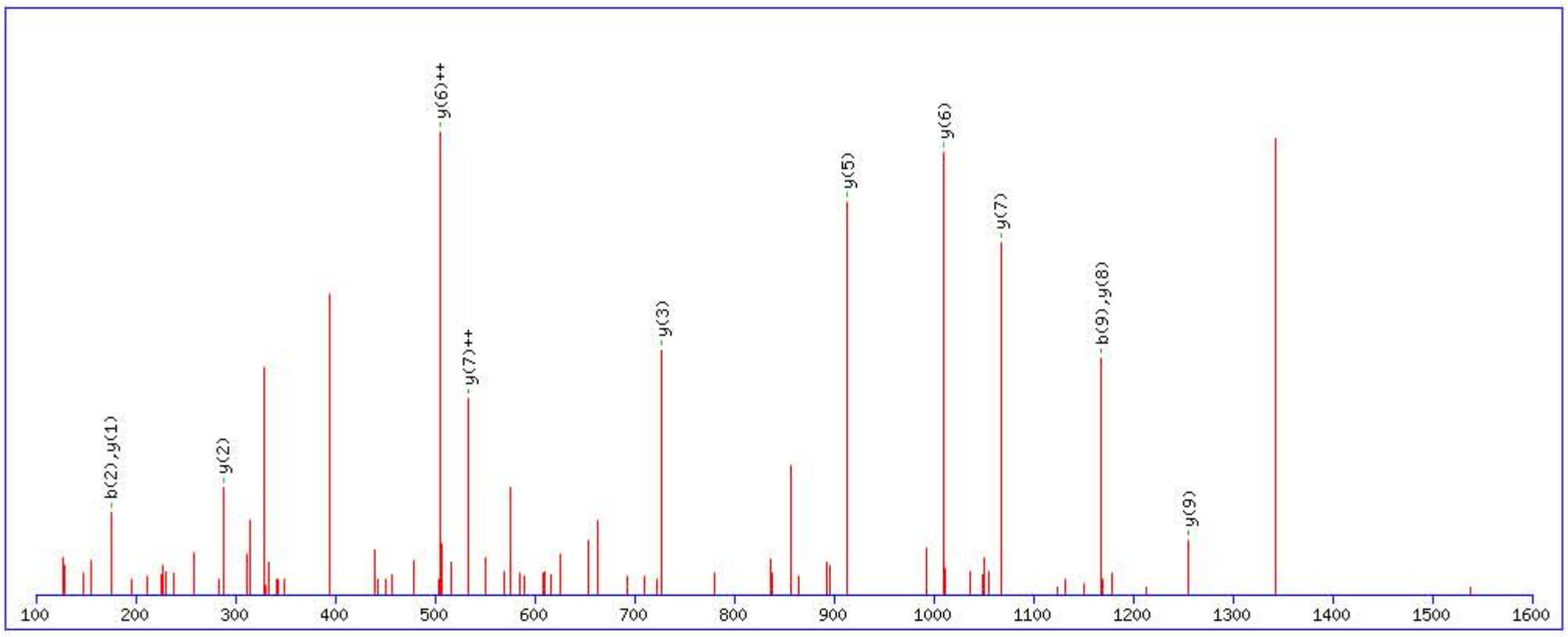
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SSTGPGEQLR**
Found in **COMP_HUMAN**, Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=1 SV=2

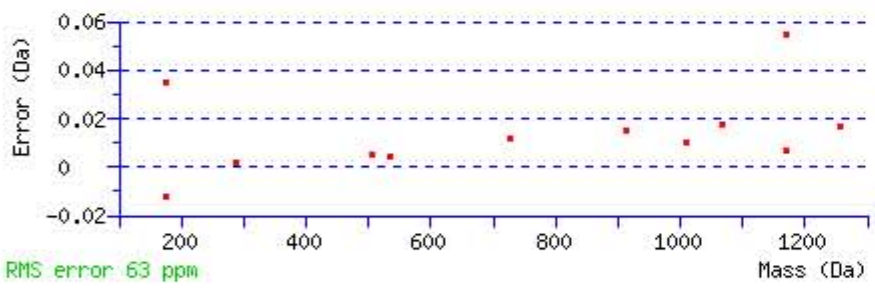
Match to Query 24163: 1341.680868 from(671.847710,2+) rtinseconds(1589) index(47545)
Title: Locus:1.1.1.1791.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

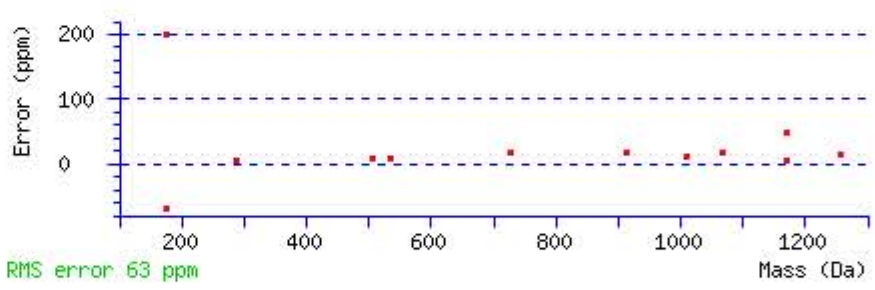
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1341.671082
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 80 **Expect:** 2.3e-007
**Matches :** 12/88 fragment ions using 12 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 10 |
| 2 | 175.071332 | 88.039304 | | | 157.060767 | 79.034021 | S | *1255.646334* | 628.326805 | 1238.619785 | 619.813530 | 1237.635769 | 619.321522 | 9 |
| 3 | 276.119011 | 138.563144 | | | 258.108446 | 129.557861 | T | *1168.614306* | 584.810791 | 1151.587757 | 576.297517 | 1150.603741 | 575.805508 | 8 |
| 4 | 333.140475 | 167.073875 | | | 315.129910 | 158.068593 | G | *1067.566627* | 534.286951 | 1050.540078 | 525.773677 | 1049.556062 | 525.281669 | 7 |
| 5 | 430.193239 | 215.600258 | | | 412.182674 | 206.594975 | P | *1010.545163* | 505.776219 | 993.518614 | 497.262945 | 992.534598 | 496.770937 | 6 |
| 6 | 487.214703 | 244.110989 | | | 469.204138 | 235.105707 | G | *913.492399* | 457.249837 | 896.465850 | 448.736563 | 895.481834 | 448.244555 | 5 |
| 7 | 616.257296 | 308.632286 | | | 598.246731 | 299.627004 | E | 856.470935 | 428.739105 | 839.444386 | 420.225831 | 838.460370 | 419.733823 | 4 |
| 8 | 1055.482622 | 528.244949 | 1038.456073 | 519.731675 | 1037.472057 | 519.239667 | Q | *727.428342* | 364.217809 | 710.401793 | 355.704534 | | | 3 |
| 9 | 1168.566686 | 584.786981 | 1151.540137 | 576.273707 | 1150.556121 | 575.781698 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 10 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 80.1 | 1341.671082 | 0.009786 | SSTGPGEQLR |
| 12.0 | 1341.663681 | 0.017187 | SSHKDSPRDVSK |
| 10.4 | 1341.674911 | 0.005957 | TSPERREPGTGR |
| 10.0 | 1341.663651 | 0.017217 | ESARDPKPEASR |
| 7.3 | 1341.697556 | -0.016688 | QASEWVRR |
| 6.7 | 1341.688828 | -0.007960 | DDAQLSGLPSALR |
| 6.4 | 1341.663696 | 0.017172 | SVGSVGDSPREPR |
| 6.4 | 1341.693512 | -0.012644 | ASEQERRR |
| 5.9 | 1341.682297 | -0.001429 | ASEQDVRAR |
| 4.9 | 1341.682327 | -0.001459 | SLHVGTQCALTR |

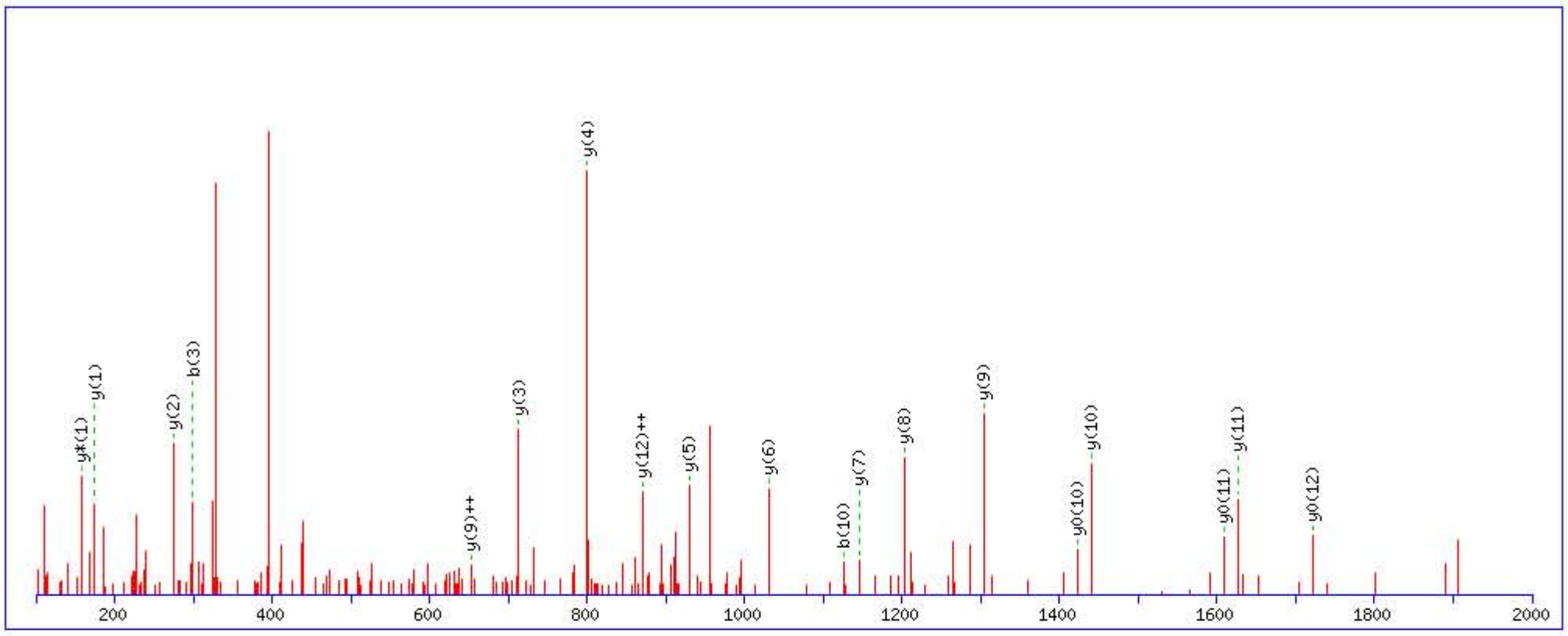
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NALWHTGDTESQVR**
Found in **COMP_HUMAN**, Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=1 SV=2

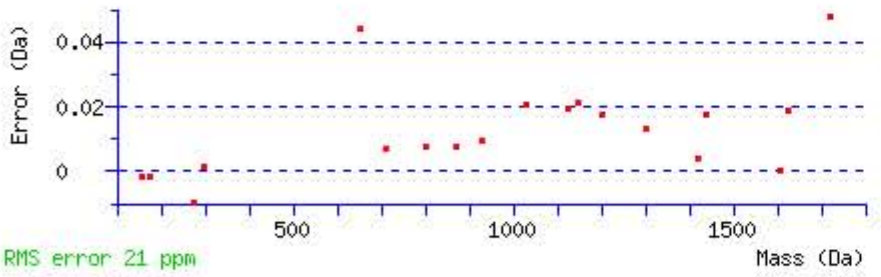
Match to Query 42602: 1923.938172 from(642.320000,3+) rtinseconds(1769) index(48776)
Title: Locus:1.1.1.1854.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

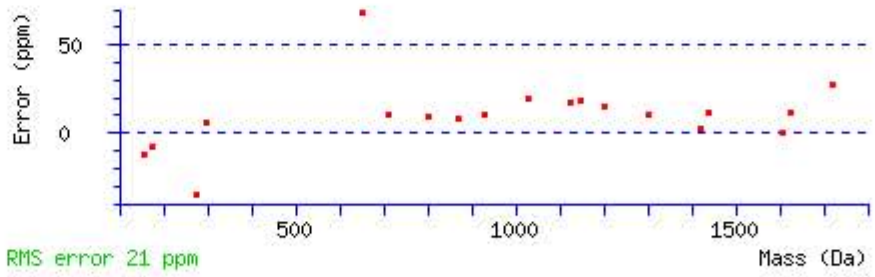
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1923.926132
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 72 **Expect:** 4.4e-007
**Matches :** 19/140 fragment ions using 36 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 14 |
| 2 | 186.087317 | 93.547296 | 169.060768 | 85.034022 | | | A | 1810.890481 | 905.948879 | 1793.863932 | 897.435604 | 1792.879916 | 896.943596 | 13 |
| 3 | 299.171381 | 150.089328 | 282.144832 | 141.576054 | | | L | 1739.853367 | 870.430322 | 1722.826818 | 861.917047 | 1721.842802 | 861.425039 | 12 |
| 4 | 485.250694 | 243.128985 | 468.224145 | 234.615711 | | | W | *1626.769303* | 813.888290 | 1609.742754 | 805.375015 | 1608.758738 | 804.883007 | 11 |
| 5 | 622.309606 | 311.658441 | 605.283057 | 303.145167 | | | H | *1440.689990* | 720.848633 | 1423.663441 | 712.335359 | 1422.679425 | 711.843351 | 10 |
| 6 | 723.357285 | 362.182281 | 706.330736 | 353.669006 | 705.346720 | 353.176998 | T | *1303.631078* | 652.319177 | 1286.604529 | 643.805903 | 1285.620513 | 643.313895 | 9 |
| 7 | 780.378749 | 390.693013 | 763.352200 | 382.179738 | 762.368184 | 381.687730 | G | *1202.583399* | 601.795338 | 1185.556850 | 593.282063 | 1184.572834 | 592.790055 | 8 |
| 8 | 895.405692 | 448.206484 | 878.379143 | 439.693210 | 877.395127 | 439.201202 | D | *1145.561935* | 573.284606 | 1128.535386 | 564.771331 | 1127.551370 | 564.279323 | 7 |
| 9 | 996.453371 | 498.730324 | 979.426822 | 490.217049 | 978.442806 | 489.725041 | T | *1030.534992* | 515.771134 | 1013.508443 | 507.257860 | 1012.524427 | 506.765852 | 6 |
| 10 | 1125.495964 | 563.251620 | 1108.469415 | 554.738346 | 1107.485399 | 554.246337 | E | *929.487313* | 465.247295 | 912.460764 | 456.734020 | 911.476748 | 456.242012 | 5 |
| 11 | 1212.527992 | 606.767634 | 1195.501443 | 598.254360 | 1194.517427 | 597.762352 | S | *800.444720* | 400.725998 | 783.418171 | 392.212724 | 782.434155 | 391.720716 | 4 |
| 12 | 1651.753318 | 826.380297 | 1634.726769 | 817.867023 | 1633.742753 | 817.375015 | Q | *713.412692* | 357.209984 | 696.386143 | 348.696710 | | | 3 |
| 13 | 1750.821732 | 875.914504 | 1733.795183 | 867.401230 | 1732.811167 | 866.909222 | V | *274.187366* | 137.597321 | 257.160817 | 129.084047 | | | 2 |
| 14 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 71.9 | 1923.926132 | 0.012040 | NALWHTGDTESQVR |
| 4.1 | 1923.909531 | 0.028641 | NLEAVETLGSTSTICSDK |

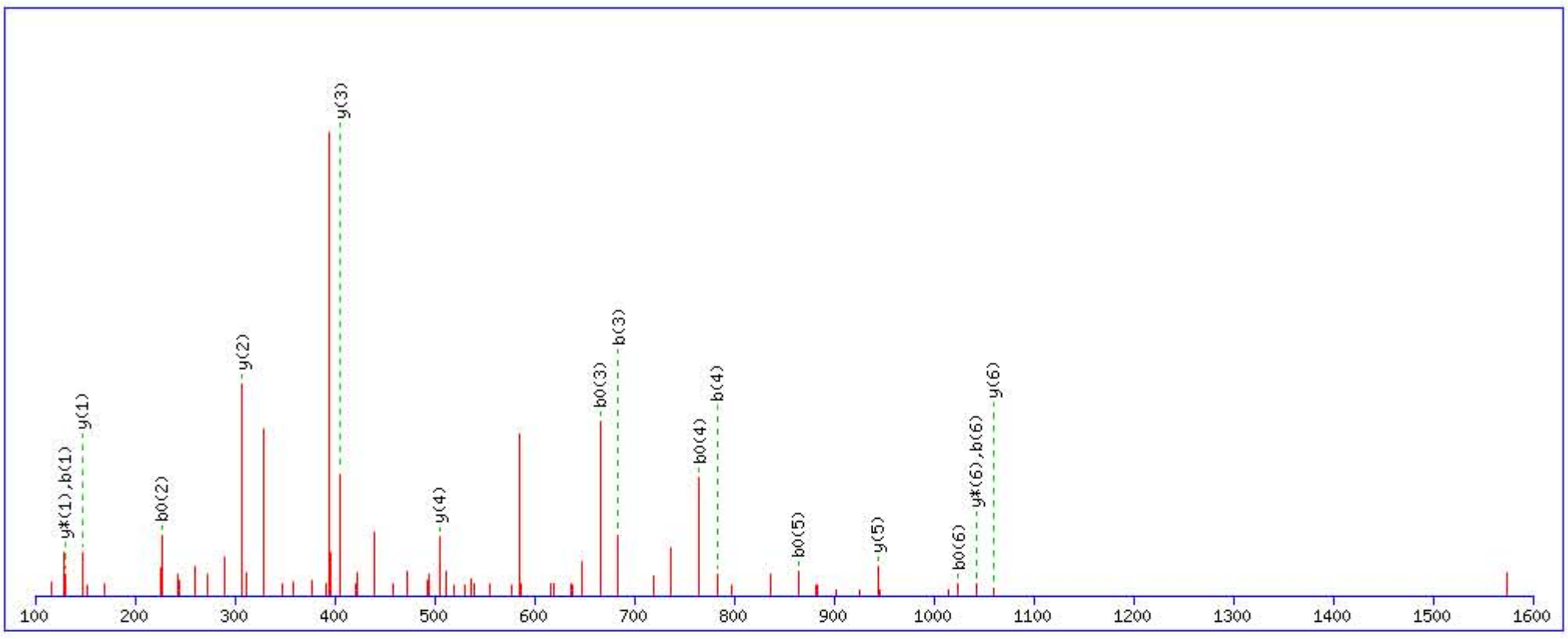
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EDQVVCK**
Found in **CD5L_HUMAN**, CD5 antigen-like OS=Homo sapiens GN=CD5L PE=1 SV=1

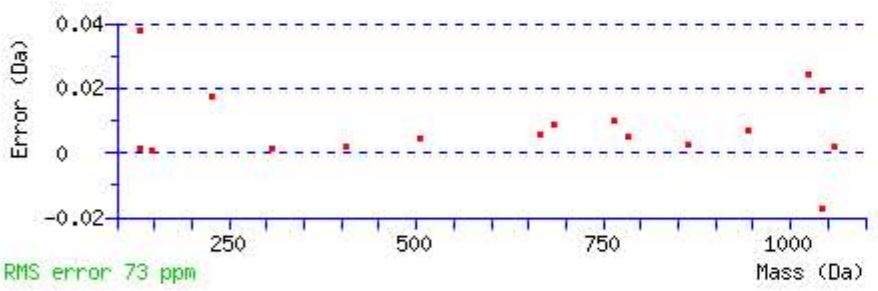
Match to Query 20223: 1187.573068 from(594.793810,2+) rtinseconds(1473) index(30889)
Title: Locus:1.1.1.621.21 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

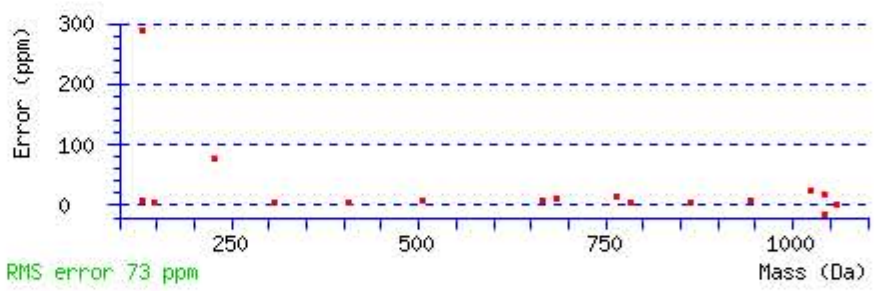
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1187.567871
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.0056
**Matches :** 17/58 fragment ions using 30 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 7 |
| 2 | 245.076812 | 123.042044 | | | 227.066247 | 114.036762 | D | *1059.532550* | 530.269913 | 1042.506001 | 521.756639 | 1041.521985 | 521.264631 | 6 |
| 3 | 684.302138 | 342.654707 | 667.275589 | 334.141433 | 666.291573 | 333.649425 | Q | *944.505607* | 472.756442 | 927.479058 | 464.243167 | | | 5 |
| 4 | 783.370552 | 392.188914 | 766.344003 | 383.675639 | 765.359987 | 383.183631 | V | *505.280281* | 253.143778 | 488.253732 | 244.630504 | | | 4 |
| 5 | 882.438966 | 441.723121 | 865.412417 | 433.209846 | 864.428401 | 432.717838 | V | *406.211867* | 203.609571 | 389.185318 | 195.096297 | | | 3 |
| 6 | 1042.469615 | 521.738446 | 1025.443066 | 513.225171 | 1024.459050 | 512.733163 | C | *307.143453* | 154.075365 | 290.116904 | 145.562090 | | | 2 |
| 7 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 32.5 | 1187.567871 | 0.005197 | EDQVVCK |
| 8.0 | 1187.585617 | -0.012549 | QEDGTSLK |
| 2.6 | 1187.585602 | -0.012534 | KIAELCDDPK |
| 2.4 | 1187.567841 | 0.005227 | QAEIECK |
| 2.4 | 1187.567841 | 0.005227 | QAIEECK |
| 2.4 | 1187.557968 | 0.015100 | QASFHCK |
| 2.3 | 1187.574371 | -0.001303 | EEEEVMVVPK |
| 0.7 | 1187.585602 | -0.012534 | EDTEKQK |
| 0.7 | 1187.586258 | -0.013190 | EFNFLDYLK |
| 0.1 | 1187.578201 | -0.005133 | EKSGSQQAEPK |

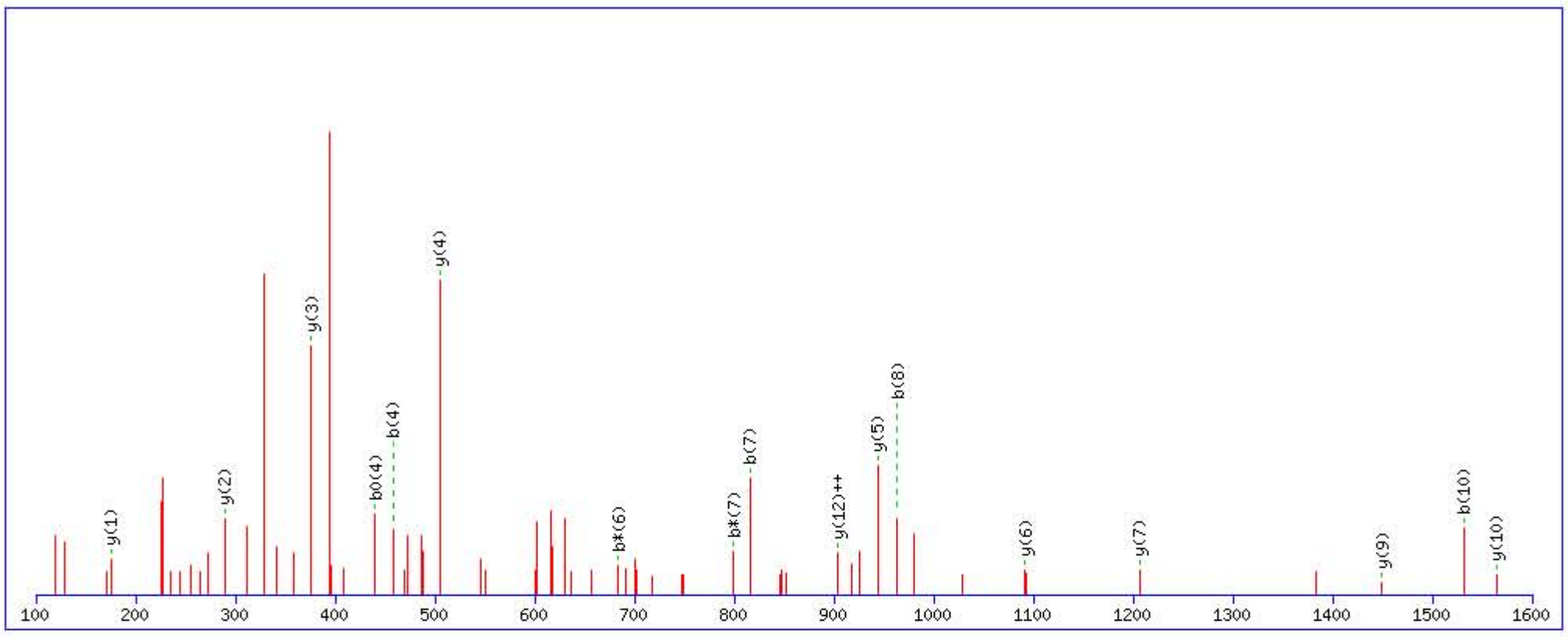
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VDKDNEDFQESNR**
Found in **CERU_HUMAN**, Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1

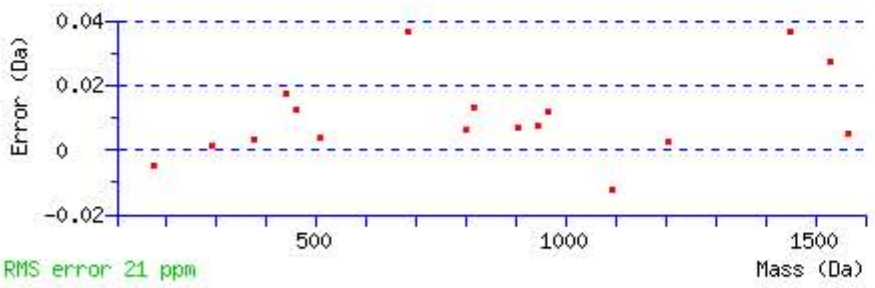
Match to Query 42193: 1905.859512 from(636.293780,3+) rtinseconds(1494) index(31034)
Title: Locus:1.1.1.628.23 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

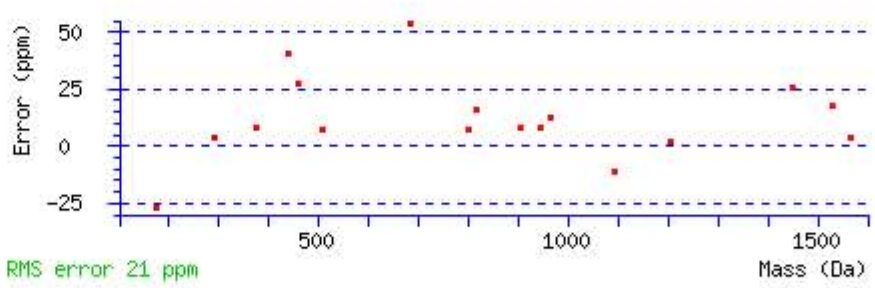
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1905.852676
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.00044
**Matches :** 17/134 fragment ions using 35 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 13 |
| 2 | 215.102633 | 108.054954 | | | 197.092068 | 99.049672 | D | 1807.791552 | 904.399414 | 1790.765003 | 895.886140 | 1789.780987 | 895.394132 | 12 |
| 3 | 343.197596 | 172.102436 | 326.171047 | 163.589162 | 325.187031 | 163.097154 | K | 1692.764609 | 846.885943 | 1675.738060 | 838.372668 | 1674.754044 | 837.880660 | 11 |
| 4 | **458.224539** | 229.615908 | 441.197990 | 221.102633 | 440.213974 | 220.610625 | D | *1564.669646* | 782.838461 | 1547.643097 | 774.325187 | 1546.659081 | 773.833179 | 10 |
| 5 | 572.267466 | 286.637371 | 555.240917 | 278.124097 | 554.256901 | 277.632089 | N | *1449.642703* | 725.324990 | 1432.616154 | 716.811715 | 1431.632138 | 716.319707 | 9 |
| 6 | 701.310059 | 351.158668 | 684.283510 | 342.645393 | 683.299494 | 342.153385 | E | 1335.599776 | 668.303526 | 1318.573227 | 659.790252 | 1317.589211 | 659.298244 | 8 |
| 7 | **816.337002** | 408.672139 | 799.310453 | 400.158865 | 798.326437 | 399.666857 | D | *1206.557183* | 603.782230 | 1189.530634 | 595.268955 | 1188.546618 | 594.776947 | 7 |
| 8 | **963.405416** | 482.206346 | 946.378867 | 473.693072 | 945.394851 | 473.201064 | F | *1091.530240* | 546.268758 | 1074.503691 | 537.755484 | 1073.519675 | 537.263476 | 6 |
| 9 | 1402.630742 | 701.819009 | 1385.604193 | 693.305735 | 1384.620177 | 692.813727 | Q | *944.461826* | 472.734551 | 927.435277 | 464.221277 | 926.451261 | 463.729269 | 5 |
| 10 | **1531.673335** | 766.340306 | 1514.646786 | 757.827031 | 1513.662770 | 757.335023 | E | *505.236500* | 253.121888 | 488.209951 | 244.608614 | 487.225935 | 244.116606 | 4 |
| 11 | 1618.705363 | 809.856320 | 1601.678814 | 801.343045 | 1600.694798 | 800.851037 | S | *376.193907* | 188.600591 | 359.167358 | 180.087317 | 358.183342 | 179.595309 | 3 |
| 12 | 1732.748290 | 866.877783 | 1715.721741 | 858.364509 | 1714.737725 | 857.872501 | N | *289.161879* | 145.084577 | 272.135330 | 136.571303 | | | 2 |
| 13 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 43.9 | 1905.852676 | 0.006836 | VDKDNEDFQESNR |

**Mascot:** http://www.matrixscience.com/

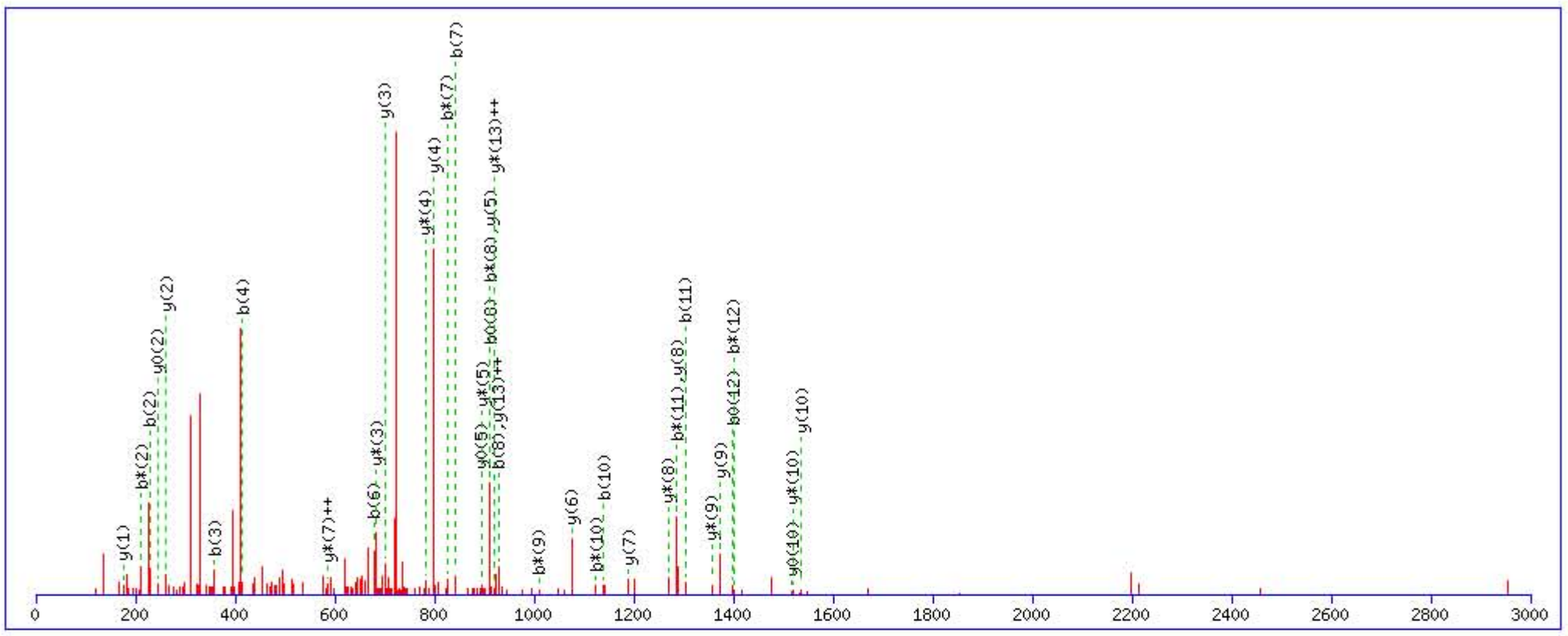
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NNEGTYYSPNYNPQSR**
Found in **CERU_HUMAN**, Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1

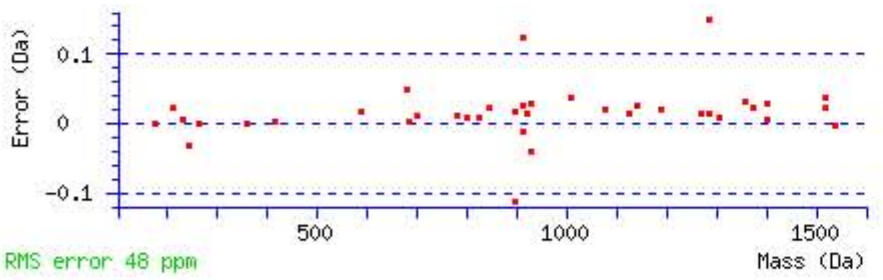
Match to Query 48730: 2213.999292 from(739.007040,3+) rtinseconds(1814) index(33006)
Title: Locus:1.1.1.740.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

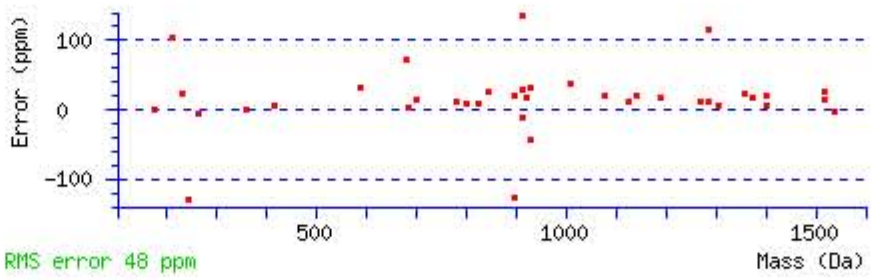
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2213.979980
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q14 : Biotin:Thermo-21345 (Q)
**Ions Score:** 34 **Expect:** 0.0035
**Matches :** 39/174 fragment ions using 95 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 16 |
| 2 | *229.093130* | 115.050203 | 212.066581 | 106.536929 | | | N | 2100.944366 | 1050.975821 | 2083.917817 | 1042.462546 | 2082.933801 | 1041.970538 | 15 |
| 3 | *358.135723* | 179.571500 | 341.109174 | 171.058225 | 340.125158 | 170.566217 | E | 1986.901439 | 993.954358 | 1969.874890 | 985.441083 | 1968.890874 | 984.949075 | 14 |
| 4 | *415.157187* | 208.082232 | 398.130638 | 199.568957 | 397.146622 | 199.076949 | G | 1857.858846 | 929.433061 | 1840.832297 | 920.919787 | 1839.848281 | 920.427779 | 13 |
| 5 | 516.204866 | 258.606071 | 499.178317 | 250.092797 | 498.194301 | 249.600789 | T | 1800.837382 | 900.922329 | 1783.810833 | 892.409055 | 1782.826817 | 891.917047 | 12 |
| 6 | *679.268195* | 340.137736 | 662.241646 | 331.624461 | 661.257630 | 331.132453 | Y | 1699.789703 | 850.398490 | 1682.763154 | 841.885215 | 1681.779138 | 841.393207 | 11 |
| 7 | *842.331524* | 421.669400 | 825.304975 | 413.156126 | 824.320959 | 412.664118 | Y | *1536.726374* | 768.866825 | 1519.699825 | 760.353551 | 1518.715809 | 759.861543 | 10 |
| 8 | *929.363552* | 465.185414 | 912.337003 | 456.672140 | 911.352987 | 456.180132 | S | *1373.663045* | 687.335161 | 1356.636496 | 678.821886 | 1355.652480 | 678.329878 | 9 |
| 9 | 1026.416316 | 513.711796 | 1009.389767 | 505.198522 | 1008.405751 | 504.706514 | P | *1286.631017* | 643.819147 | 1269.604468 | 635.305872 | 1268.620452 | 634.813864 | 8 |
| 10 | *1140.459243* | 570.733260 | 1123.432694 | 562.219985 | 1122.448678 | 561.727977 | N | *1189.578253* | 595.292765 | 1172.551704 | 586.779490 | 1171.567688 | 586.287482 | 7 |
| 11 | *1303.522572* | 652.264924 | 1286.496023 | 643.751650 | 1285.512007 | 643.259642 | Y | *1075.535326* | 538.271301 | 1058.508777 | 529.758027 | 1057.524761 | 529.266019 | 6 |
| 12 | 1417.565499 | 709.286388 | 1400.538950 | 700.773113 | 1399.554934 | 700.281105 | N | *912.471997* | 456.739637 | 895.445448 | 448.226362 | 894.461432 | 447.734354 | 5 |
| 13 | 1514.618263 | 757.812770 | 1497.591714 | 749.299495 | 1496.607698 | 748.807487 | P | *798.429070* | 399.718173 | 781.402521 | 391.204899 | 780.418505 | 390.712891 | 4 |
| 14 | 1953.843589 | 977.425433 | 1936.817040 | 968.912158 | 1935.833024 | 968.420150 | Q | *701.376306* | 351.191791 | 684.349757 | 342.678517 | 683.365741 | 342.186509 | 3 |
| 15 | 2040.875617 | 1020.941447 | 2023.849068 | 1012.428172 | 2022.865052 | 1011.936164 | S | *262.150980* | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 16 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 34.5 | 2213.979980 | 0.019312 | NNEGTYYSPNYNPQSR |

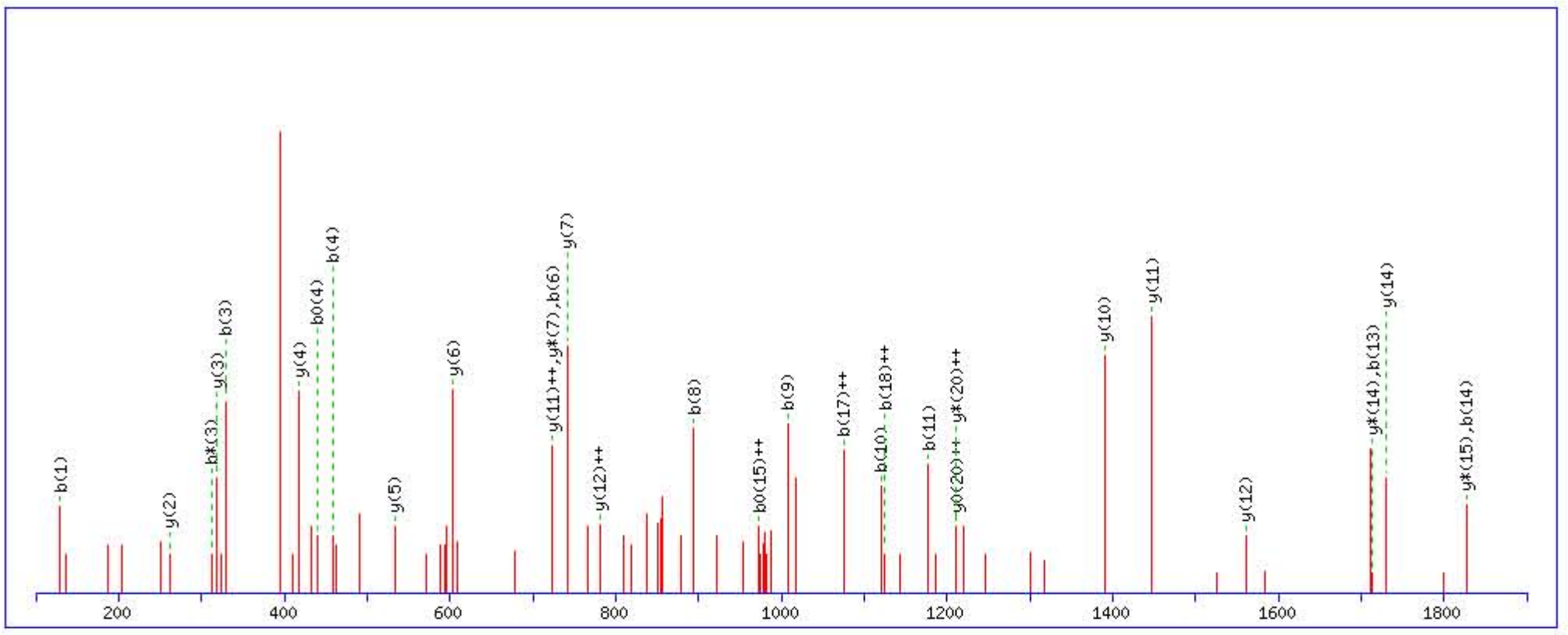
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KAEEEHLGILGPQLHADVGDK**
Found in **CERU_HUMAN**, Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1

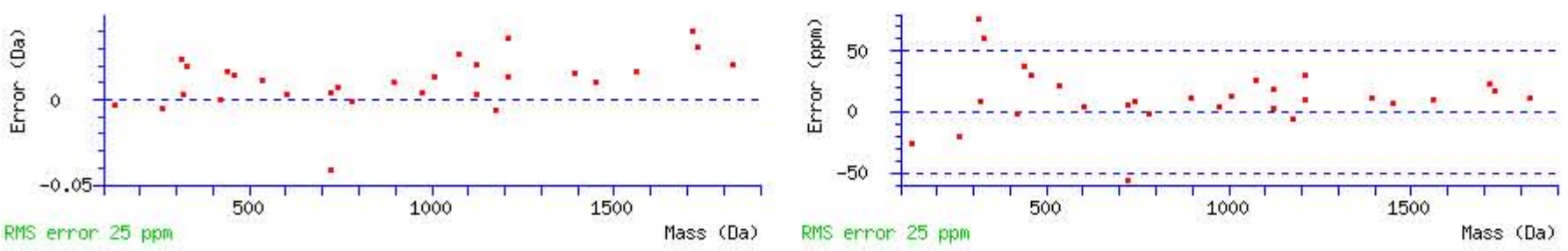
Match to Query 55103: 2566.356672 from(856.459500,3+) rtinseconds(1941) index(49922)
Title: Locus:1.1.1.1913.25 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2566.321335
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 65 **Expect:** 8e-007
**Matches :** 33/234 fragment ions using 56 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *129.102239* | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 21 |
| 2 | 200.139353 | 100.573315 | 183.112804 | 92.060040 | | | A | 2439.233673 | 1220.120474 | 2422.207124 | 1211.607200 | 2421.223108 | 1211.115192 | 20 |
| 3 | *329.181946* | 165.094611 | 312.155397 | 156.581336 | 311.171381 | 156.089328 | E | 2368.196559 | 1184.601917 | 2351.170010 | 1176.088643 | 2350.185994 | 1175.596635 | 19 |
| 4 | *458.224539* | 229.615907 | 441.197990 | 221.102633 | 440.213974 | 220.610625 | E | 2239.153966 | 1120.080621 | 2222.127417 | 1111.567346 | 2221.143401 | 1111.075338 | 18 |
| 5 | 587.267132 | 294.137204 | 570.240583 | 285.623930 | 569.256567 | 285.131922 | E | 2110.111373 | 1055.559324 | 2093.084824 | 1047.046050 | 2092.100808 | 1046.554042 | 17 |
| 6 | *724.326044* | 362.666660 | 707.299495 | 354.153386 | 706.315479 | 353.661378 | H | 1981.068780 | 991.038028 | 1964.042231 | 982.524753 | 1963.058215 | 982.032745 | 16 |
| 7 | 837.410108 | 419.208692 | 820.383559 | 410.695418 | 819.399543 | 410.203410 | L | 1844.009868 | 922.508572 | 1826.983319 | 913.995297 | 1825.999303 | 913.503289 | 15 |
| 8 | *894.431572* | 447.719424 | 877.405023 | 439.206150 | 876.421007 | 438.714142 | G | *1730.925804* | 865.966540 | 1713.899255 | 857.453265 | 1712.915239 | 856.961257 | 14 |
| 9 | *1007.515636* | 504.261456 | 990.489087 | 495.748182 | 989.505071 | 495.256174 | I | 1673.904340 | 837.455808 | 1656.877791 | 828.942533 | 1655.893775 | 828.450525 | 13 |
| 10 | *1120.599700* | 560.803488 | 1103.573151 | 552.290214 | 1102.589135 | 551.798205 | L | *1560.820276* | 780.913776 | 1543.793727 | 772.400501 | 1542.809711 | 771.908493 | 12 |
| 11 | *1177.621164* | 589.314220 | 1160.594615 | 580.800946 | 1159.610599 | 580.308937 | G | *1447.736212* | 724.371744 | 1430.709663 | 715.858469 | 1429.725647 | 715.366461 | 11 |
| 12 | 1274.673928 | 637.840602 | 1257.647379 | 629.327328 | 1256.663363 | 628.835319 | P | *1390.714748* | 695.861012 | 1373.688199 | 687.347737 | 1372.704183 | 686.855729 | 10 |
| 13 | *1713.899254* | 857.453265 | 1696.872705 | 848.939991 | 1695.888689 | 848.447983 | Q | 1293.661984 | 647.334630 | 1276.635435 | 638.821355 | 1275.651419 | 638.329347 | 9 |
| 14 | *1826.983318* | 913.995297 | 1809.956769 | 905.482023 | 1808.972753 | 904.990015 | L | 854.436658 | 427.721967 | 837.410109 | 419.208692 | 836.426093 | 418.716684 | 8 |
| 15 | 1964.042230 | 982.524753 | 1947.015681 | 974.011479 | 1946.031665 | 973.519471 | H | *741.352594* | 371.179935 | 724.326045 | 362.666660 | 723.342029 | 362.174652 | 7 |
| 16 | 2035.079344 | 1018.043310 | 2018.052795 | 1009.530036 | 2017.068779 | 1009.038028 | A | *604.293682* | 302.650479 | 587.267133 | 294.137204 | 586.283117 | 293.645196 | 6 |
| 17 | 2150.106287 | **1075.556781** | 2133.079738 | 1067.043507 | 2132.095722 | 1066.551499 | D | *533.256568* | 267.131922 | 516.230019 | 258.618647 | 515.246003 | 258.126639 | 5 |
| 18 | 2249.174701 | **1125.090988** | 2232.148152 | 1116.577714 | 2231.164136 | 1116.085706 | V | *418.229625* | 209.618450 | 401.203076 | 201.105176 | 400.219060 | 200.613168 | 4 |
| 19 | 2306.196165 | 1153.601720 | 2289.169616 | 1145.088446 | 2288.185600 | 1144.596438 | G | *319.161211* | 160.084243 | 302.134662 | 151.570969 | 301.150646 | 151.078961 | 3 |
| 20 | 2421.223108 | **1211.115192** | 2404.196559 | 1202.601917 | 2403.212543 | 1202.109909 | D | *262.139747* | 131.573511 | 245.113198 | 123.060237 | 244.129182 | 122.568229 | 2 |
| 21 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 65.1 | 2566.321335 | 0.035337 | KAEEEHLGILGPQLHADVGDK |
| 0.1 | 2566.342453 | 0.014219 | GEIQNILQKVNIPLVTNEECQK |

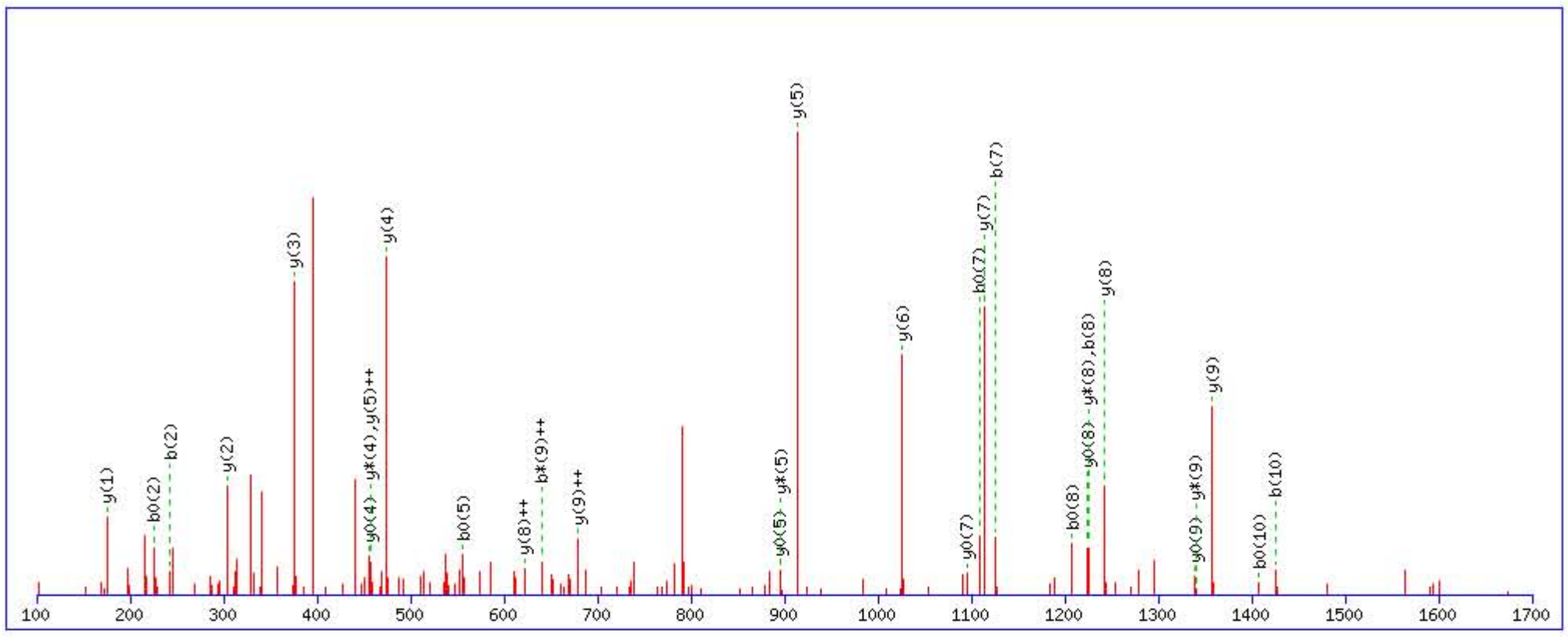
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ELDESLQVAER**
Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

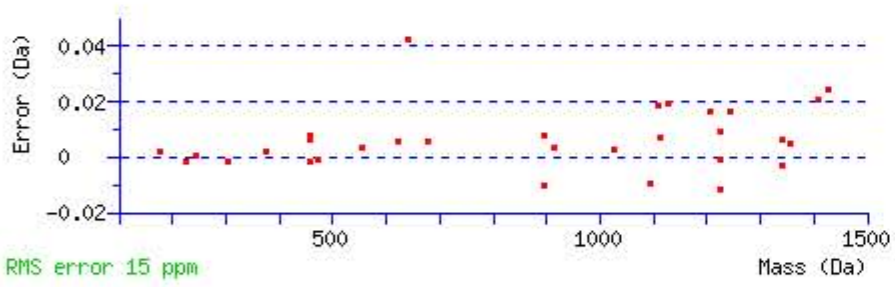
Match to Query 34668: 1598.807308 from(800.410930,2+) rtinseconds(1952) index(5396)
Title: Locus:1.1.1.1956.24 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

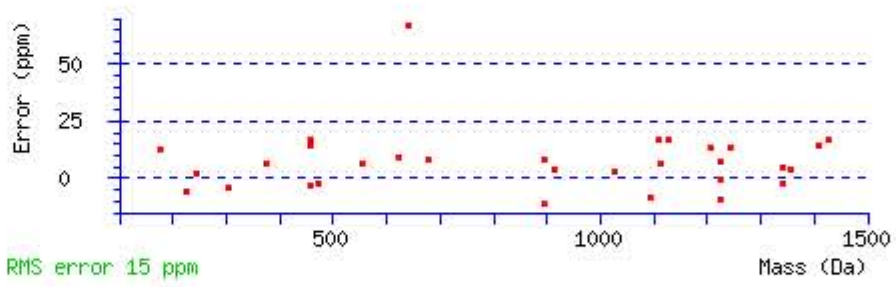
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1598.797379
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q7** : Biotin:Thermo-21345 (Q)
**Ions Score:** 50 **Expect:** 6.4e-005
**Matches** : 31/106 fragment ions using 59 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 11 |
| 2 | **243.133933** | 122.070605 | | | 225.123368 | 113.065322 | L | 1470.762091 | 735.884684 | 1453.735542 | 727.371409 | 1452.751526 | 726.879401 | 10 |
| 3 | 358.160876 | 179.584076 | | | 340.150311 | 170.578794 | D | *1357.678027* | 679.342652 | 1340.651478 | 670.829377 | 1339.667462 | 670.337369 | 9 |
| 4 | 487.203469 | 244.105373 | | | 469.192904 | 235.100090 | E | *1242.651084* | 621.829180 | 1225.624535 | 613.315906 | 1224.640519 | 612.823898 | 8 |
| 5 | 574.235497 | 287.621387 | | | 556.224932 | 278.616104 | S | *1113.608491* | 557.307884 | 1096.581942 | 548.794609 | 1095.597926 | 548.302601 | 7 |
| 6 | 687.319561 | 344.163419 | | | 669.308996 | 335.158136 | L | *1026.576463* | 513.791870 | 1009.549914 | 505.278595 | 1008.565898 | 504.786587 | 6 |
| 7 | **1126.544887** | 563.776082 | 1109.518338 | 555.262807 | 1108.534322 | 554.770799 | Q | *913.492399* | 457.249838 | 896.465850 | 448.736563 | 895.481834 | 448.244555 | 5 |
| 8 | **1225.613301** | 613.310289 | 1208.586752 | 604.797014 | 1207.602736 | 604.305006 | V | *474.267073* | 237.637175 | 457.240524 | 229.123900 | 456.256508 | 228.631892 | 4 |
| 9 | 1296.650415 | 648.828846 | 1279.623866 | 640.315571 | 1278.639850 | 639.823563 | A | *375.198659* | 188.102968 | 358.172110 | 179.589693 | 357.188094 | 179.097685 | 3 |
| 10 | **1425.693008** | 713.350142 | 1408.666459 | 704.836868 | 1407.682443 | 704.344860 | E | *304.161545* | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 49.8 | 1598.797379 | 0.009929 | ELDESLQVAER |
| 4.8 | 1598.827271 | -0.019963 | LQGQLCDVSIR |
| 4.5 | 1598.823883 | -0.016575 | TPTEKVEKMFPHR |
| 4.5 | 1598.790024 | 0.017284 | VTAEGDSHTEVVISR |
| 4.4 | 1598.797379 | 0.009929 | LEESDVLQEAR |
| 3.0 | 1598.827271 | -0.019963 | LQGQLCDVSIR |
| 2.2 | 1598.787506 | 0.019802 | AGGSWDLAVQER |
| 1.5 | 1598.789993 | 0.017315 | AGATSGELPVVEAENR |
| 1.5 | 1598.797409 | 0.009899 | EDVDDLVSQLR |
| 1.3 | 1598.817352 | -0.010044 | DRAALCQLWR |

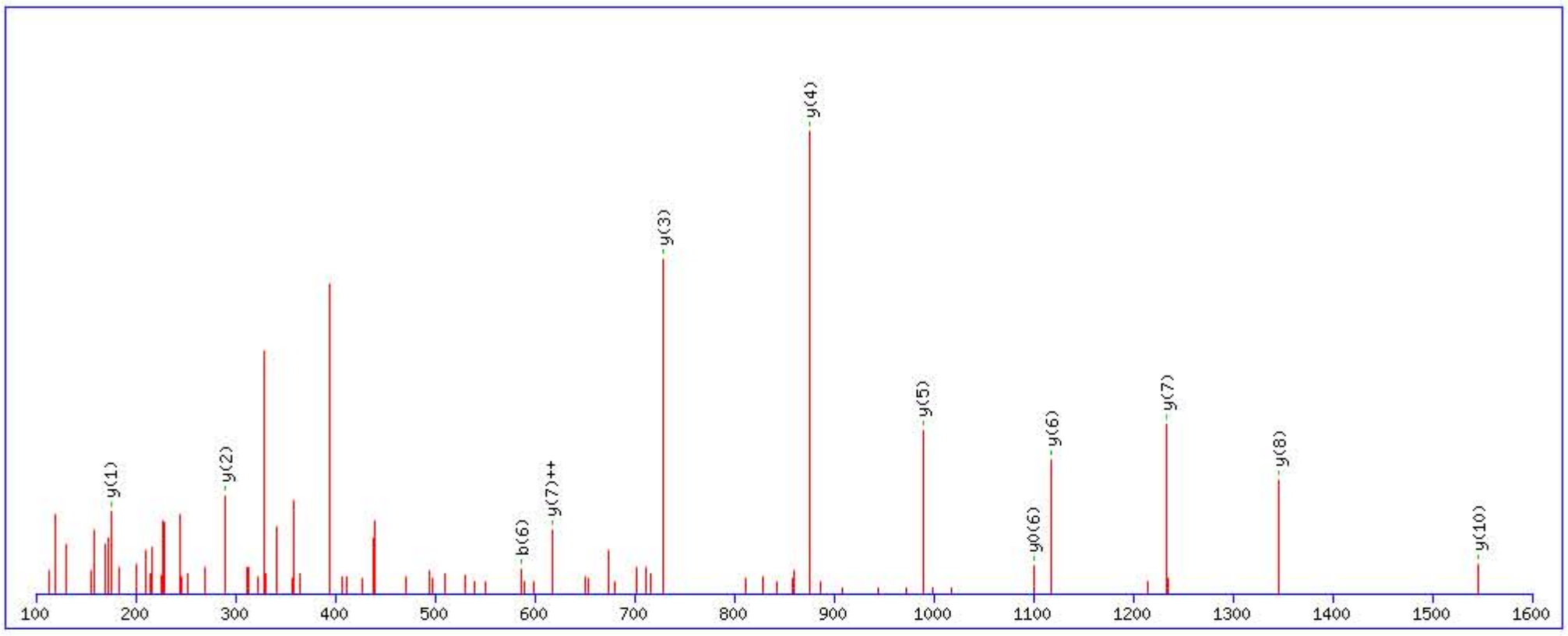
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ASSIIDELFQDR**
Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

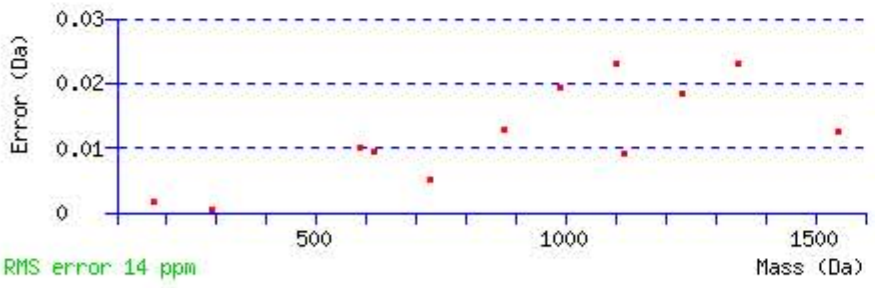
Match to Query 38064: 1703.863722 from(568.961850,3+) rtinseconds(2812) index(9935)
Title: Locus:1.1.1.2256.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

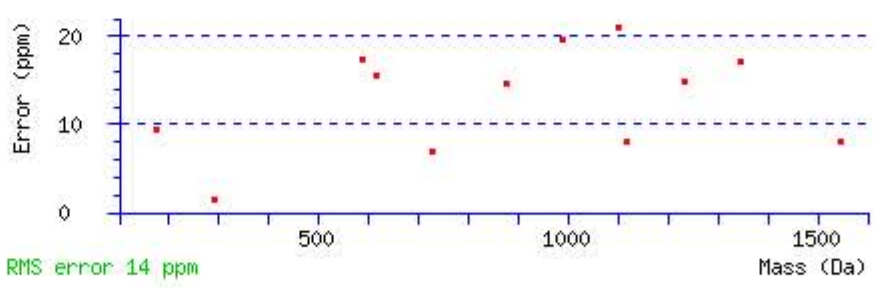
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1703.855240
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 82 **Expect:** 7e-008
**Matches :** 12/110 fragment ions using 14 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 12 |
| 2 | 159.076418 | 80.041847 | | | 141.065853 | 71.036564 | S | 1633.825419 | 817.416348 | 1616.798870 | 808.903073 | 1615.814854 | 808.411065 | 11 |
| 3 | 246.108446 | 123.557861 | | | 228.097881 | 114.552578 | S | *1546.793391* | 773.900333 | 1529.766842 | 765.387059 | 1528.782826 | 764.895051 | 10 |
| 4 | 359.192510 | 180.099893 | | | 341.181945 | 171.094610 | I | 1459.761363 | 730.384320 | 1442.734814 | 721.871045 | 1441.750798 | 721.379037 | 9 |
| 5 | 472.276574 | 236.641925 | | | 454.266009 | 227.636642 | I | *1346.677299* | 673.842288 | 1329.650750 | 665.329013 | 1328.666734 | 664.837005 | 8 |
| 6 | **587.303517** | 294.155397 | | | 569.292952 | 285.150114 | D | *1233.593235* | 617.300256 | 1216.566686 | 608.786981 | 1215.582670 | 608.294973 | 7 |
| 7 | 716.346110 | 358.676693 | | | 698.335545 | 349.671411 | E | *1118.566292* | 559.786784 | 1101.539743 | 551.273510 | 1100.555727 | 550.781501 | 6 |
| 8 | 829.430174 | 415.218725 | | | 811.419609 | 406.213443 | L | *989.523699* | 495.265488 | 972.497150 | 486.752213 | 971.513134 | 486.260205 | 5 |
| 9 | 976.498588 | 488.752932 | | | 958.488023 | 479.747650 | F | *876.439635* | 438.723456 | 859.413086 | 430.210181 | 858.429070 | 429.718173 | 4 |
| 10 | 1415.723914 | 708.365595 | 1398.697365 | 699.852321 | 1397.713349 | 699.360312 | Q | *729.371221* | 365.189249 | 712.344672 | 356.675974 | 711.360656 | 356.183966 | 3 |
| 11 | 1530.750857 | 765.879067 | 1513.724308 | 757.365792 | 1512.740292 | 756.873784 | D | *290.145895* | 145.576585 | 273.119346 | 137.063311 | 272.135330 | 136.571303 | 2 |
| 12 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 82.4 | 1703.855240 | 0.008482 | ASSIIDELFQDR |
| 6.1 | 1703.859070 | 0.004652 | RWDELETTTQAKAR |

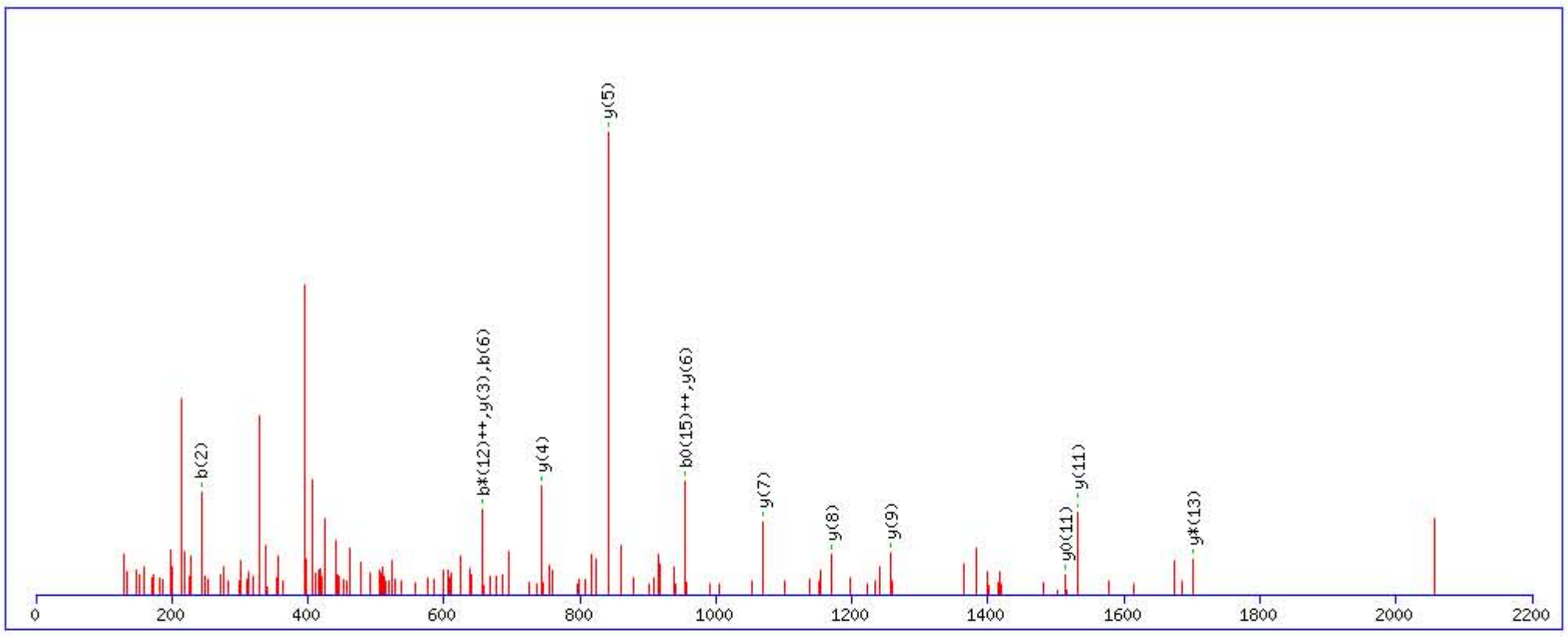
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EILSVDCSTNNPSQAK**
Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

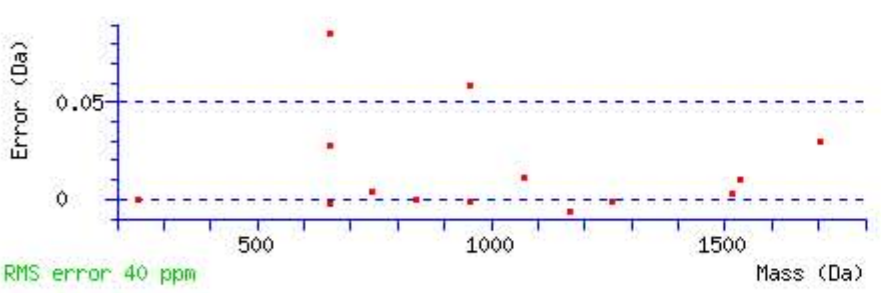
Match to Query 46129: 2072.994522 from(692.005450,3+) rtinseconds(1807) index(4382)
Title: Locus:1.1.1.1906.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

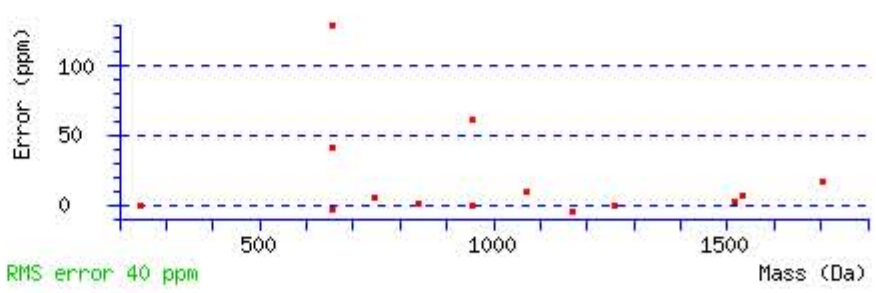
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2072.987061
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q14 : Biotin:Thermo-21345 (Q)
**Ions Score:** 55 **Expect:** 7.6e-006
**Matches :** 14/156 fragment ions using 17 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 16 |
| 2 | **243.133933** | 122.070605 | | | 225.123368 | 113.065322 | I | 1944.951759 | 972.979517 | 1927.925210 | 964.466243 | 1926.941194 | 963.974235 | 15 |
| 3 | 356.217997 | 178.612637 | | | 338.207432 | 169.607354 | L | 1831.867695 | 916.437485 | 1814.841146 | 907.924211 | 1813.857130 | 907.432203 | 14 |
| 4 | 443.250025 | 222.128650 | | | 425.239460 | 213.123368 | S | 1718.783631 | 859.895454 | 1701.757082 | 851.382179 | 1700.773066 | 850.890171 | 13 |
| 5 | 542.318439 | 271.662858 | | | 524.307874 | 262.657575 | V | 1631.751603 | 816.379439 | 1614.725054 | 807.866165 | 1613.741038 | 807.374157 | 12 |
| 6 | **657.345382** | 329.176329 | | | 639.334817 | 320.171046 | D | *1532.683189* | 766.845233 | 1515.656640 | 758.331958 | 1514.672624 | 757.839950 | 11 |
| 7 | 817.376031 | 409.191654 | | | 799.365466 | 400.186371 | C | 1417.656246 | 709.331761 | 1400.629697 | 700.818487 | 1399.645681 | 700.326479 | 10 |
| 8 | 904.408059 | 452.707668 | | | 886.397494 | 443.702385 | S | *1257.625597* | 629.316437 | 1240.599048 | 620.803162 | 1239.615032 | 620.311154 | 9 |
| 9 | 1005.455738 | 503.231507 | | | 987.445173 | 494.226225 | T | *1170.593569* | 585.800422 | 1153.567020 | 577.287148 | 1152.583004 | 576.795140 | 8 |
| 10 | 1119.498665 | 560.252971 | 1102.472116 | 551.739696 | 1101.488100 | 551.247688 | N | *1069.545890* | 535.276583 | 1052.519341 | 526.763309 | 1051.535325 | 526.271301 | 7 |
| 11 | 1233.541592 | 617.274434 | 1216.515043 | 608.761160 | 1215.531027 | 608.269152 | N | *955.502963* | 478.255119 | 938.476414 | 469.741845 | 937.492398 | 469.249837 | 6 |
| 12 | 1330.594356 | 665.800816 | 1313.567807 | 657.287542 | 1312.583791 | 656.795534 | P | *841.460036* | 421.233656 | 824.433487 | 412.720381 | 823.449471 | 412.228373 | 5 |
| 13 | 1417.626384 | 709.316830 | 1400.599835 | 700.803556 | 1399.615819 | 700.311548 | S | *744.407272* | 372.707274 | 727.380723 | 364.193999 | 726.396707 | 363.701991 | 4 |
| 14 | 1856.851710 | 928.929493 | 1839.825161 | 920.416219 | 1838.841145 | 919.924211 | Q | *657.375244* | 329.191260 | 640.348695 | 320.677985 | | | 3 |
| 15 | 1927.888824 | 964.448050 | 1910.862275 | 955.934776 | 1909.878259 | 955.442768 | A | 218.149918 | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 54.7 | 2072.987061 | 0.007461 | EILSVDCSTNNPSQAK |
| 0.1 | 2073.002747 | -0.008225 | DPQAWPSRYREALEEAR |

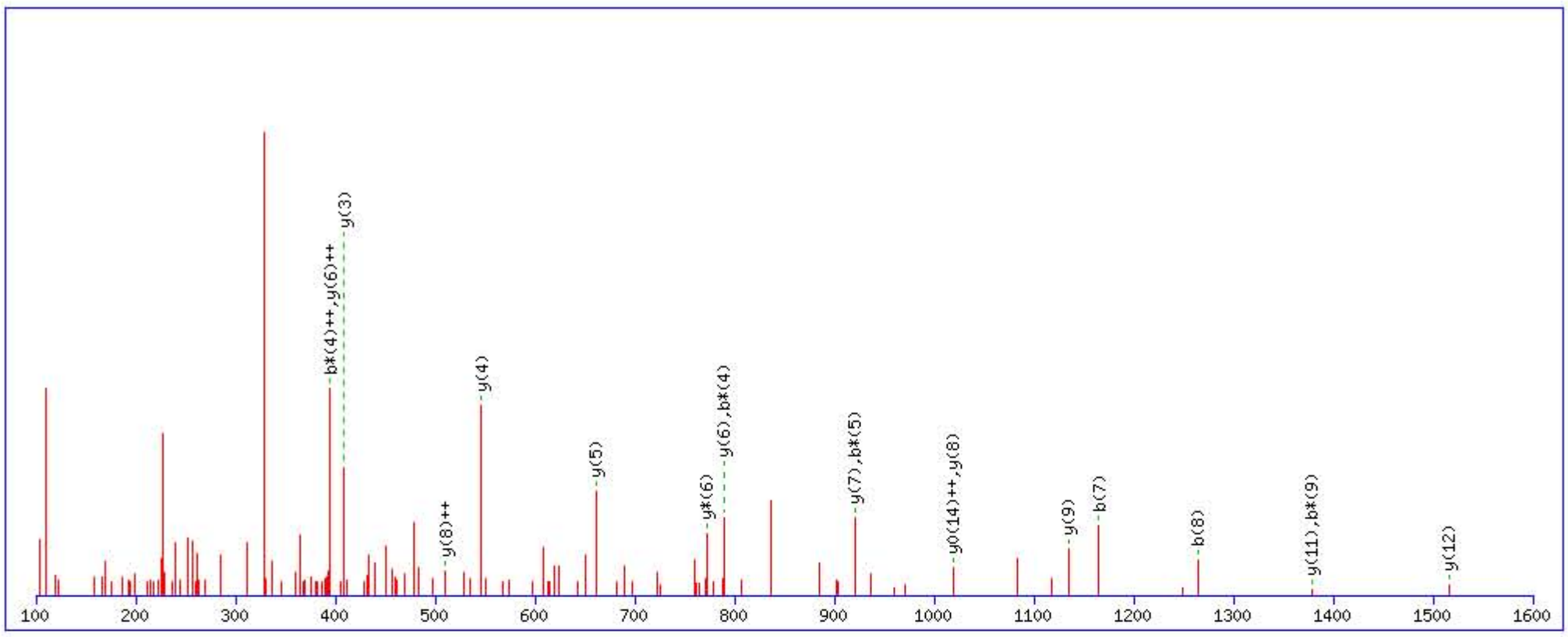
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QQTHMLDVMQDHFSR**
Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

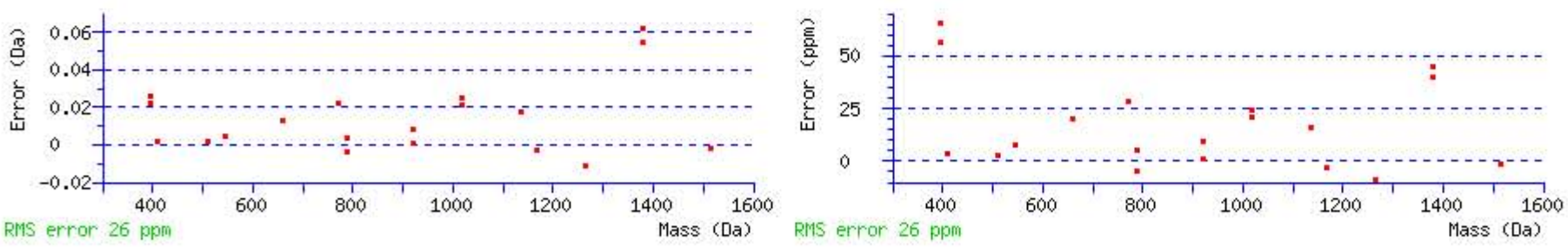
Match to Query 48132: 2183.013496 from(546.760650,4+) rtinseconds(2024) index(50490)
Title: Locus:1.1.1.1942.4 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2183.007446
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 52 **Expect:** 8.7e-005
**Matches :** 19/162 fragment ions using 26 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.065854 | 65.036565 | 112.039305 | 56.523291 | | | Q | | | | | | | 15 |
| 2 | 568.291180 | 284.649228 | 551.264631 | 276.135954 | | | Q | 2055.956135 | 1028.481705 | 2038.929586 | 1019.968431 | 2037.945570 | 1019.476423 | 14 |
| 3 | 669.338859 | 335.173068 | 652.312310 | 326.659793 | 651.328294 | 326.167785 | T | 1616.730809 | 808.869043 | 1599.704260 | 800.355768 | 1598.720244 | 799.863760 | 13 |
| 4 | 806.397771 | 403.702524 | 789.371222 | 395.189249 | 788.387206 | 394.697241 | H | *1515.683130* | 758.345203 | 1498.656581 | 749.831929 | 1497.672565 | 749.339921 | 12 |
| 5 | 937.438256 | 469.222766 | 920.411707 | 460.709492 | 919.427691 | 460.217484 | M | *1378.624218* | 689.815747 | 1361.597669 | 681.302473 | 1360.613653 | 680.810465 | 11 |
| 6 | 1050.522320 | 525.764798 | 1033.495771 | 517.251524 | 1032.511755 | 516.759516 | L | 1247.583733 | 624.295505 | 1230.557184 | 615.782230 | 1229.573168 | 615.290222 | 10 |
| 7 | 1165.549263 | 583.278270 | 1148.522714 | 574.764995 | 1147.538698 | 574.272987 | D | *1134.499669* | 567.753473 | 1117.473120 | 559.240198 | 1116.489104 | 558.748190 | 9 |
| 8 | 1264.617677 | 632.812477 | 1247.591128 | 624.299202 | 1246.607112 | 623.807194 | V | *1019.472726* | 510.240001 | 1002.446177 | 501.726727 | 1001.462161 | 501.234719 | 8 |
| 9 | 1395.658162 | 698.332719 | 1378.631613 | 689.819445 | 1377.647597 | 689.327437 | M | *920.404312* | 460.705794 | 903.377763 | 452.192520 | 902.393747 | 451.700512 | 7 |
| 10 | 1523.716740 | 762.362008 | 1506.690191 | 753.848734 | 1505.706175 | 753.356726 | Q | *789.363827* | 395.185552 | 772.337278 | 386.672277 | 771.353262 | 386.180269 | 6 |
| 11 | 1638.743683 | 819.875480 | 1621.717134 | 811.362205 | 1620.733118 | 810.870197 | D | *661.305249* | 331.156263 | 644.278700 | 322.642988 | 643.294684 | 322.150980 | 5 |
| 12 | 1775.802595 | 888.404936 | 1758.776046 | 879.891661 | 1757.792030 | 879.399653 | H | *546.278306* | 273.642791 | 529.251757 | 265.129517 | 528.267741 | 264.637509 | 4 |
| 13 | 1922.871009 | 961.939143 | 1905.844460 | 953.425868 | 1904.860444 | 952.933860 | F | *409.219394* | 205.113335 | 392.192845 | 196.600061 | 391.208829 | 196.108053 | 3 |
| 14 | 2009.903037 | 1005.455157 | 1992.876488 | 996.941882 | 1991.892472 | 996.449874 | S | 262.150980 | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 15 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 51.9 | 2183.007446 | 0.006050 | QQTHMLDVMQDHFSR |
| 51.9 | 2183.007446 | 0.006050 | QQTHMLDVMQDHFSR |

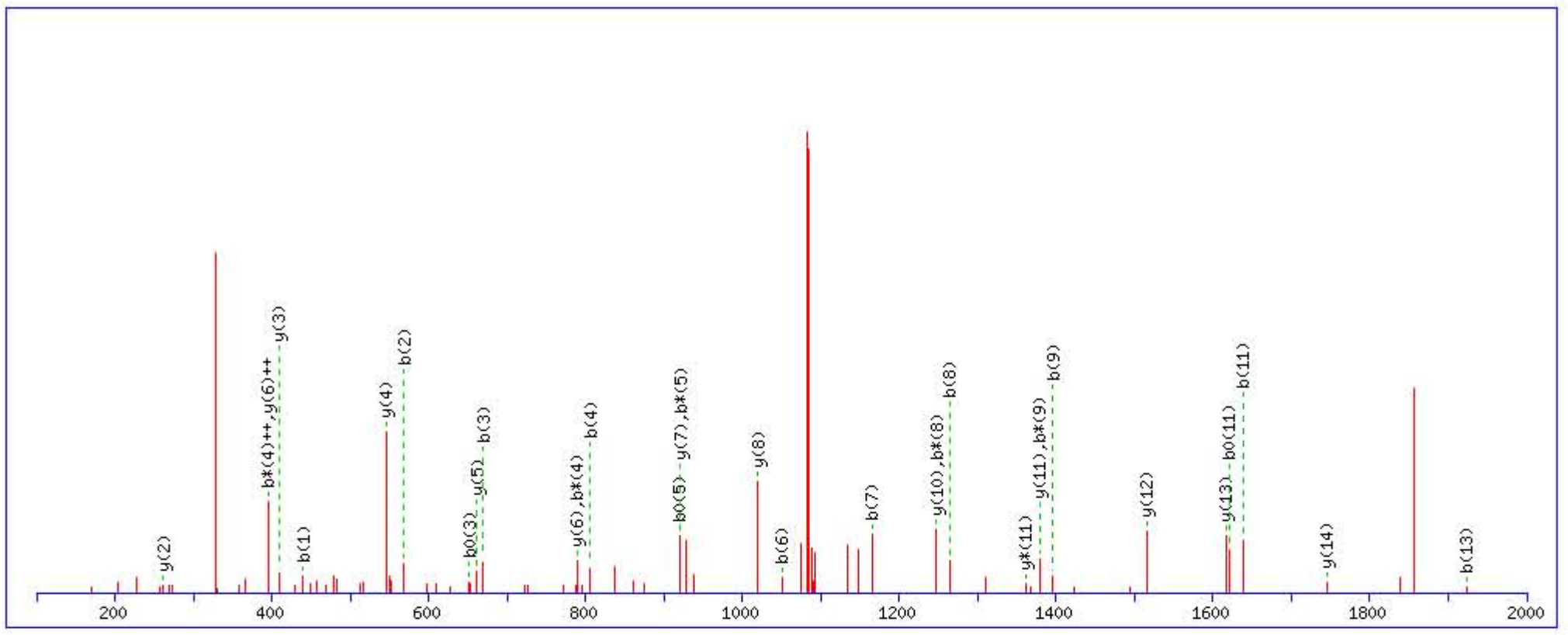
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QQTHMLDVMQDHFSR**
Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

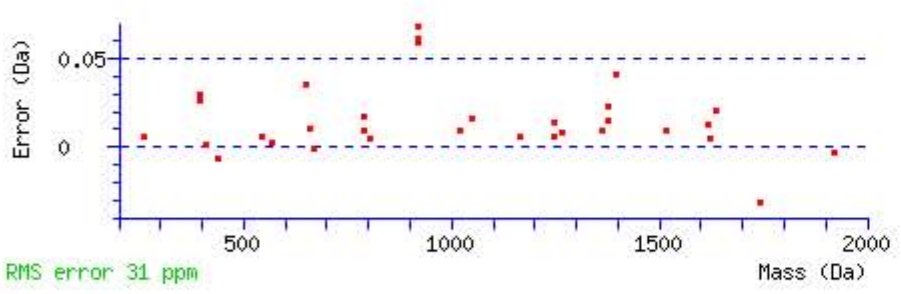
Match to Query 48139: 2183.031728 from(1092.523140,2+) rtinseconds(1988) index(20170)
Title: Locus:1.1.1.3074.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

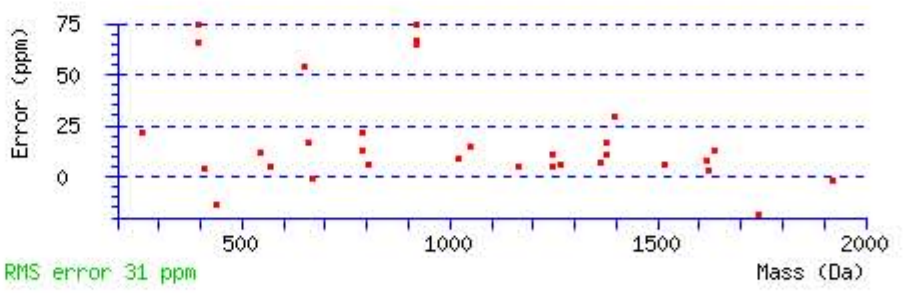
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2183.007446
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 81 **Expect:** 3.8e-008
**Matches** : 32/162 fragment ions using 46 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **440.232602** | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 15 |
| 2 | **568.291180** | 284.649228 | 551.264631 | 276.135954 | | | Q | *1744.789387* | 872.898332 | 1727.762838 | 864.385057 | 1726.778822 | 863.893049 | 14 |
| 3 | **669.338859** | 335.173068 | 652.312310 | 326.659793 | 651.328294 | 326.167785 | T | *1616.730809* | 808.869043 | 1599.704260 | 800.355768 | 1598.720244 | 799.863760 | 13 |
| 4 | **806.397771** | 403.702524 | 789.371222 | 395.189249 | 788.387206 | 394.697241 | H | *1515.683130* | 758.345203 | 1498.656581 | 749.831929 | 1497.672565 | 749.339921 | 12 |
| 5 | 937.438256 | 469.222766 | 920.411707 | 460.709492 | 919.427691 | 460.217484 | M | *1378.624218* | 689.815747 | 1361.597669 | 681.302473 | 1360.613653 | 680.810465 | 11 |
| 6 | **1050.522320** | 525.764798 | 1033.495771 | 517.251524 | 1032.511755 | 516.759516 | L | *1247.583733* | 624.295505 | 1230.557184 | 615.782230 | 1229.573168 | 615.290222 | 10 |
| 7 | **1165.549263** | 583.278270 | 1148.522714 | 574.764995 | 1147.538698 | 574.272987 | D | 1134.499669 | 567.753473 | 1117.473120 | 559.240198 | 1116.489104 | 558.748190 | 9 |
| 8 | **1264.617677** | 632.812477 | 1247.591128 | 624.299202 | 1246.607112 | 623.807194 | V | *1019.472726* | 510.240001 | 1002.446177 | 501.726727 | 1001.462161 | 501.234719 | 8 |
| 9 | **1395.658162** | 698.332719 | 1378.631613 | 689.819445 | 1377.647597 | 689.327437 | M | *920.404312* | 460.705794 | 903.377763 | 452.192520 | 902.393747 | 451.700512 | 7 |
| 10 | 1523.716740 | 762.362008 | 1506.690191 | 753.848734 | 1505.706175 | 753.356726 | Q | *789.363827* | 395.185552 | 772.337278 | 386.672277 | 771.353262 | 386.180269 | 6 |
| 11 | **1638.743683** | 819.875480 | 1621.717134 | 811.362205 | 1620.733118 | 810.870197 | D | *661.305249* | 331.156263 | 644.278700 | 322.642988 | 643.294684 | 322.150980 | 5 |
| 12 | 1775.802595 | 888.404936 | 1758.776046 | 879.891661 | 1757.792030 | 879.399653 | H | *546.278306* | 273.642791 | 529.251757 | 265.129517 | 528.267741 | 264.637509 | 4 |
| 13 | **1922.871009** | 961.939143 | 1905.844460 | 953.425868 | 1904.860444 | 952.933860 | F | *409.219394* | 205.113335 | 392.192845 | 196.600061 | 391.208829 | 196.108053 | 3 |
| 14 | 2009.903037 | 1005.455157 | 1992.876488 | 996.941882 | 1991.892472 | 996.449874 | S | *262.150980* | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 15 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 80.9 | 2183.007446 | 0.024282 | QQTHMLDVMQDHFSR |
| 66.9 | 2183.007446 | 0.024282 | QQTHMLDVMQDHFSR |
| 1.6 | 2183.007446 | 0.024282 | QQTHMLDVMQDHFSR |
| 1.6 | 2183.050842 | -0.019114 | GYGSGGGGAQQLGAGPFPAQPPGR |
| 0.9 | 2183.001816 | 0.029912 | KPYRIESDEEEDFENVGK |
| 0.8 | 2183.009933 | 0.021795 | GNDCVRISPDAPLQCAEGPK |

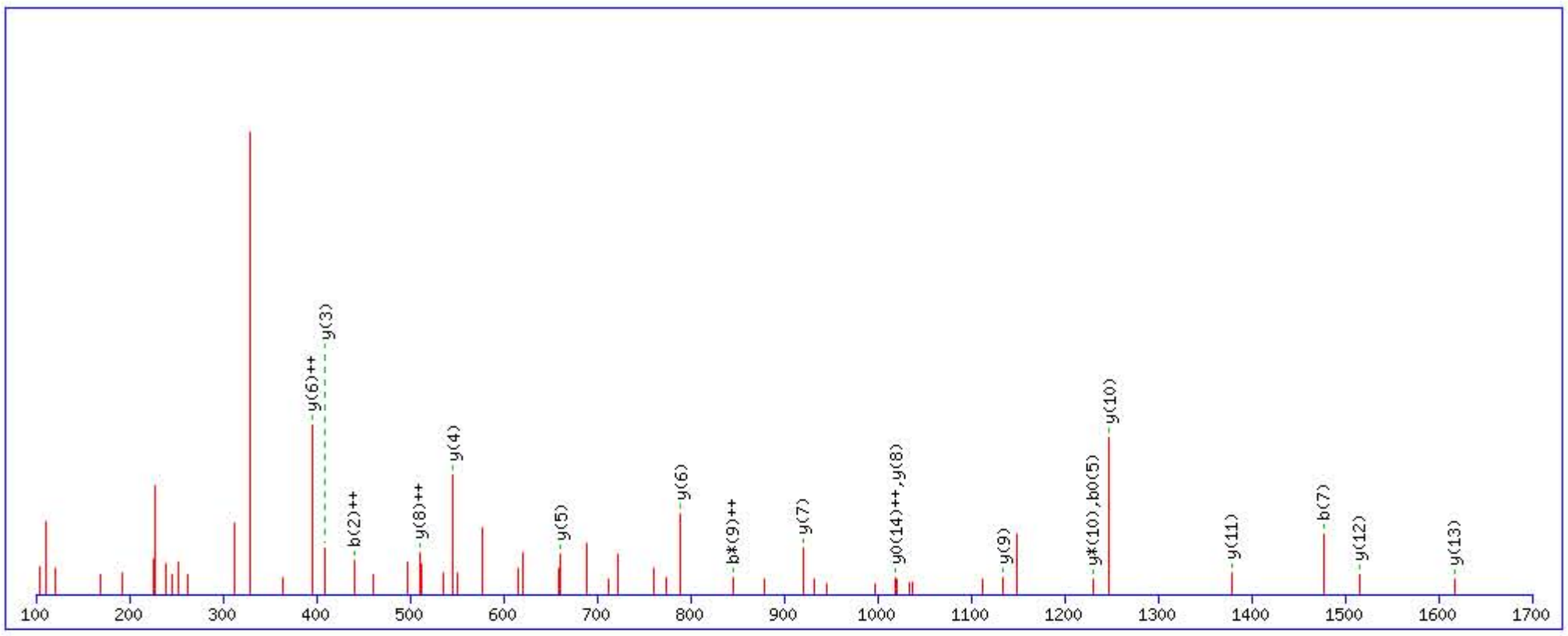
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QQTHMLDVMQDHFSR**
Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

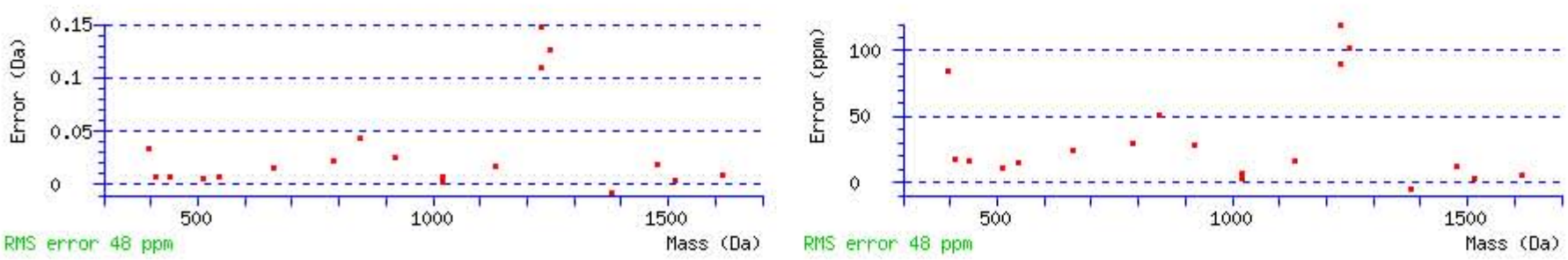
Match to Query 54235: 2494.208136 from(624.559310,4+) rtinseconds(2203) index(35486)
Title: Locus:1.1.1.876.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2494.174194
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Q2** : Biotin:Thermo-21345 (Q)
**Ions Score:** 55 **Expect:** 8.3e-005
**Matches** : 20/162 fragment ions using 39 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 15 |
| 2 | 879.457928 | 440.232602 | 862.431379 | 431.719328 | | | Q | 2055.956135 | 1028.481705 | 2038.929586 | 1019.968431 | 2037.945570 | 1019.476423 | 14 |
| 3 | 980.505607 | 490.756442 | 963.479058 | 482.243167 | 962.495042 | 481.751159 | T | *1616.730809* | 808.869043 | 1599.704260 | 800.355768 | 1598.720244 | 799.863760 | 13 |
| 4 | 1117.564519 | 559.285898 | 1100.537970 | 550.772623 | 1099.553954 | 550.280615 | H | *1515.683130* | 758.345203 | 1498.656581 | 749.831929 | 1497.672565 | 749.339921 | 12 |
| 5 | 1248.605004 | 624.806140 | 1231.578455 | 616.292866 | 1230.594439 | 615.800858 | M | *1378.624218* | 689.815747 | 1361.597669 | 681.302473 | 1360.613653 | 680.810465 | 11 |
| 6 | 1361.689068 | 681.348172 | 1344.662519 | 672.834898 | 1343.678503 | 672.342889 | L | *1247.583733* | 624.295505 | 1230.557184 | 615.782230 | 1229.573168 | 615.290222 | 10 |
| 7 | 1476.716011 | 738.861644 | 1459.689462 | 730.348369 | 1458.705446 | 729.856361 | D | *1134.499669* | 567.753473 | 1117.473120 | 559.240198 | 1116.489104 | 558.748190 | 9 |
| 8 | 1575.784425 | 788.395851 | 1558.757876 | 779.882576 | 1557.773860 | 779.390568 | V | *1019.472726* | 510.240001 | 1002.446177 | 501.726727 | 1001.462161 | 501.234719 | 8 |
| 9 | 1706.824910 | 853.916093 | 1689.798361 | 845.402819 | 1688.814345 | 844.910811 | M | *920.404312* | 460.705794 | 903.377763 | 452.192520 | 902.393747 | 451.700512 | 7 |
| 10 | 1834.883488 | 917.945382 | 1817.856939 | 909.432108 | 1816.872923 | 908.940100 | Q | *789.363827* | 395.185552 | 772.337278 | 386.672277 | 771.353262 | 386.180269 | 6 |
| 11 | 1949.910431 | 975.458854 | 1932.883882 | 966.945579 | 1931.899866 | 966.453571 | D | *661.305249* | 331.156263 | 644.278700 | 322.642988 | 643.294684 | 322.150980 | 5 |
| 12 | 2086.969343 | 1043.988310 | 2069.942794 | 1035.475035 | 2068.958778 | 1034.983027 | H | *546.278306* | 273.642791 | 529.251757 | 265.129517 | 528.267741 | 264.637509 | 4 |
| 13 | 2234.037757 | 1117.522516 | 2217.011208 | 1109.009242 | 2216.027192 | 1108.517234 | F | *409.219394* | 205.113335 | 392.192845 | 196.600060 | 391.208829 | 196.108052 | 3 |
| 14 | 2321.069785 | 1161.038531 | 2304.043236 | 1152.525256 | 2303.059220 | 1152.033248 | S | 262.150980 | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 15 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 54.7 | 2494.174194 | 0.033942 | QQTHMLDVMQDHFSR |

**Mascot:** http://www.matrixscience.com/

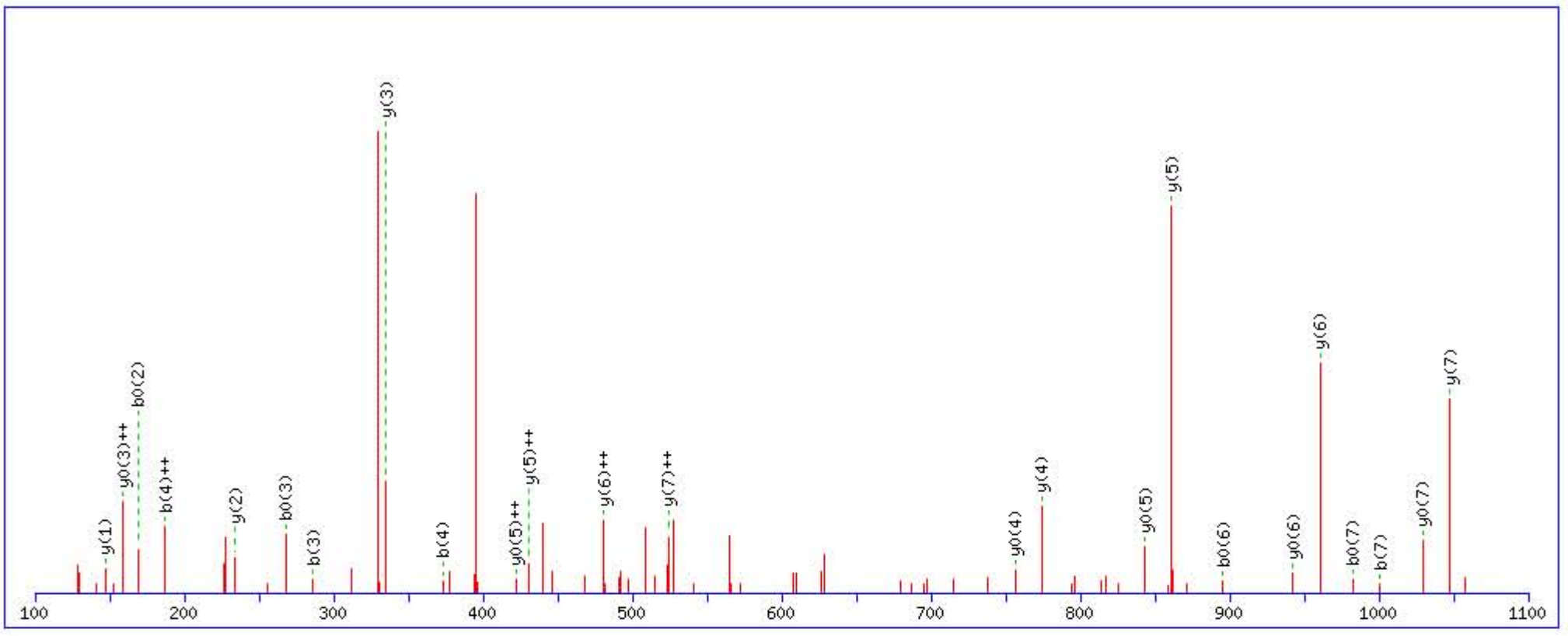
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VSVSQTSK**
Found in **FA9_HUMAN**, Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2

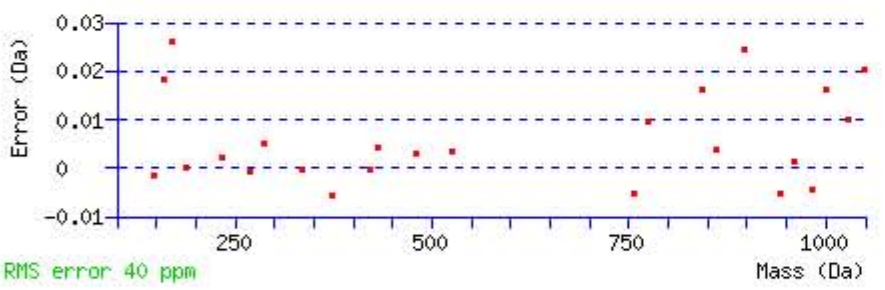
Match to Query 18811: 1145.617068 from(573.815810,2+) rtinseconds(1415) index(46433)
Title: Locus:1.1.1.1730.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

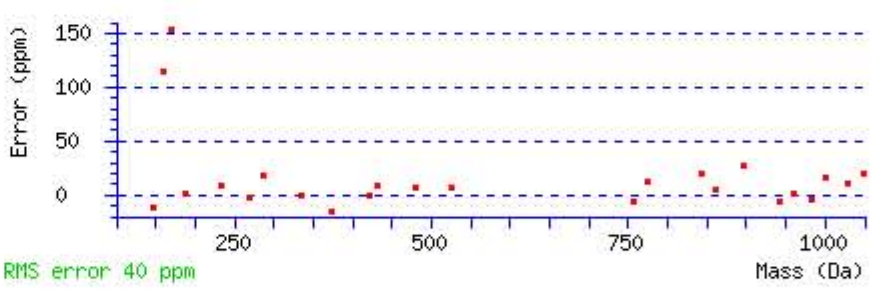
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1145.611450
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.019
**Matches :** 25/72 fragment ions using 58 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 8 |
| 2 | **187.107718** | 94.057497 | | | 169.097153 | 85.052214 | S | ***1047.550307*** | 524.278792 | 1030.523758 | 515.765517 | 1029.539742 | 515.273509 | 7 |
| 3 | **286.176132** | 143.591704 | | | 268.165567 | 134.586422 | V | ***960.518279*** | 480.762778 | 943.491730 | 472.249503 | 942.507714 | 471.757495 | 6 |
| 4 | **373.208160** | 187.107718 | | | 355.197595 | 178.102435 | S | ***861.449865*** | 431.228571 | 844.423316 | 422.715296 | 843.439300 | 422.223288 | 5 |
| 5 | 812.433486 | 406.720381 | 795.406937 | 398.207107 | 794.422921 | 397.715099 | Q | ***774.417837*** | 387.712557 | 757.391288 | 379.199282 | 756.407272 | 378.707274 | 4 |
| 6 | 913.481165 | 457.244221 | 896.454616 | 448.730946 | 895.470600 | 448.238938 | T | ***335.192511*** | 168.099893 | 318.165962 | 159.586619 | 317.181946 | 159.094611 | 3 |
| 7 | **1000.513193** | 500.760235 | 983.486644 | 492.246960 | 982.502628 | 491.754952 | S | ***234.144832*** | 117.576054 | 217.118283 | 109.062779 | 216.134267 | 108.570771 | 2 |
| 8 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.1 | 1145.611450 | 0.005618 | VSVSQTSK |
| 12.2 | 1145.611420 | 0.005648 | KSIMVQSPEK |
| 4.2 | 1145.604034 | 0.013034 | STPSSSPSLRK |
| 3.8 | 1145.629196 | -0.012128 | GEVLGLSSSLGK |
| 2.6 | 1145.623337 | -0.006269 | WVDGGKPLFK |
| 1.0 | 1145.604004 | 0.013064 | SANELLSREK |
| 0.1 | 1145.630524 | -0.013456 | VRPFSQREK |
| 0.1 | 1145.622650 | -0.005582 | VDNAMSRLLK |

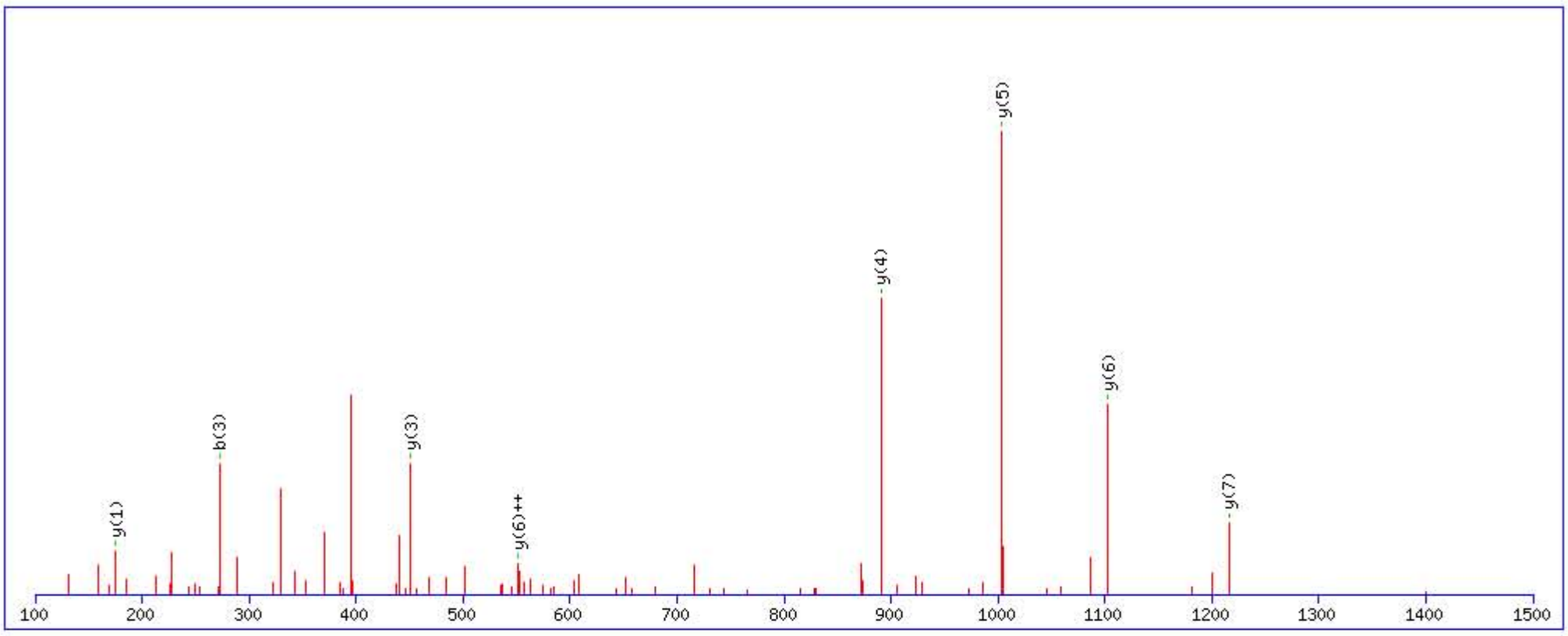
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SALVLQYLR**
Found in **FA9_HUMAN**, Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2

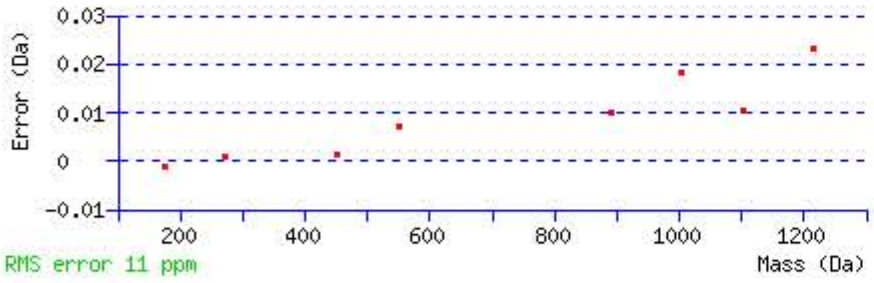
Match to Query 26346: 1372.803288 from(687.408920,2+) rtinseconds(2420) index(52971)
Title: Locus:1.1.1.2080.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

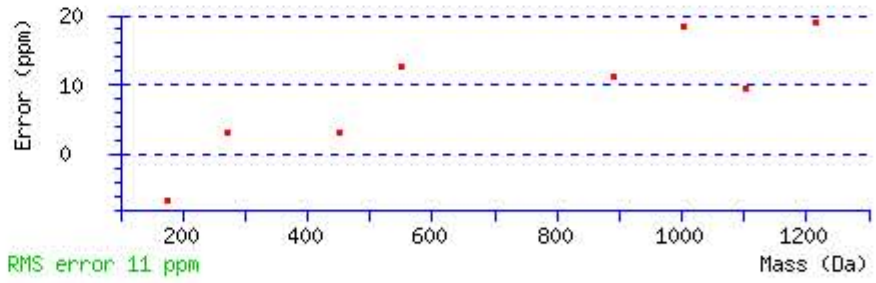
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1372.790054
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 47 **Expect:** 8.7e-005
**Matches :** 8/70 fragment ions using 11 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | 9 |
| 2 | 159.076418 | 80.041847 | | | 141.065853 | 71.036564 | A | 1286.765327 | 643.886301 | 1269.738778 | 635.373027 | 8 |
| 3 | **272.160482** | 136.583879 | | | 254.149917 | 127.578597 | L | *1215.728213* | 608.367744 | 1198.701664 | 599.854470 | 7 |
| 4 | 371.228896 | 186.118086 | | | 353.218331 | 177.112804 | V | *1102.644149* | 551.825713 | 1085.617600 | 543.312438 | 6 |
| 5 | 484.312960 | 242.660118 | | | 466.302395 | 233.654836 | L | *1003.575735* | 502.291505 | 986.549186 | 493.778231 | 5 |
| 6 | 923.538286 | 462.272781 | 906.511737 | 453.759507 | 905.527721 | 453.267499 | Q | *890.491671* | 445.749473 | 873.465122 | 437.236199 | 4 |
| 7 | 1086.601615 | 543.804446 | 1069.575066 | 535.291171 | 1068.591050 | 534.799163 | Y | *451.266345* | 226.136810 | 434.239796 | 217.623536 | 3 |
| 8 | 1199.685679 | 600.346477 | 1182.659130 | 591.833203 | 1181.675114 | 591.341195 | L | 288.203016 | 144.605146 | 271.176467 | 136.091871 | 2 |
| 9 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 46.6 | 1372.790054 | 0.013234 | SALVLQYLR |
| 3.2 | 1372.790039 | 0.013249 | KELQILYR |
| 1.3 | 1372.790039 | 0.013249 | IIEKYQLR |

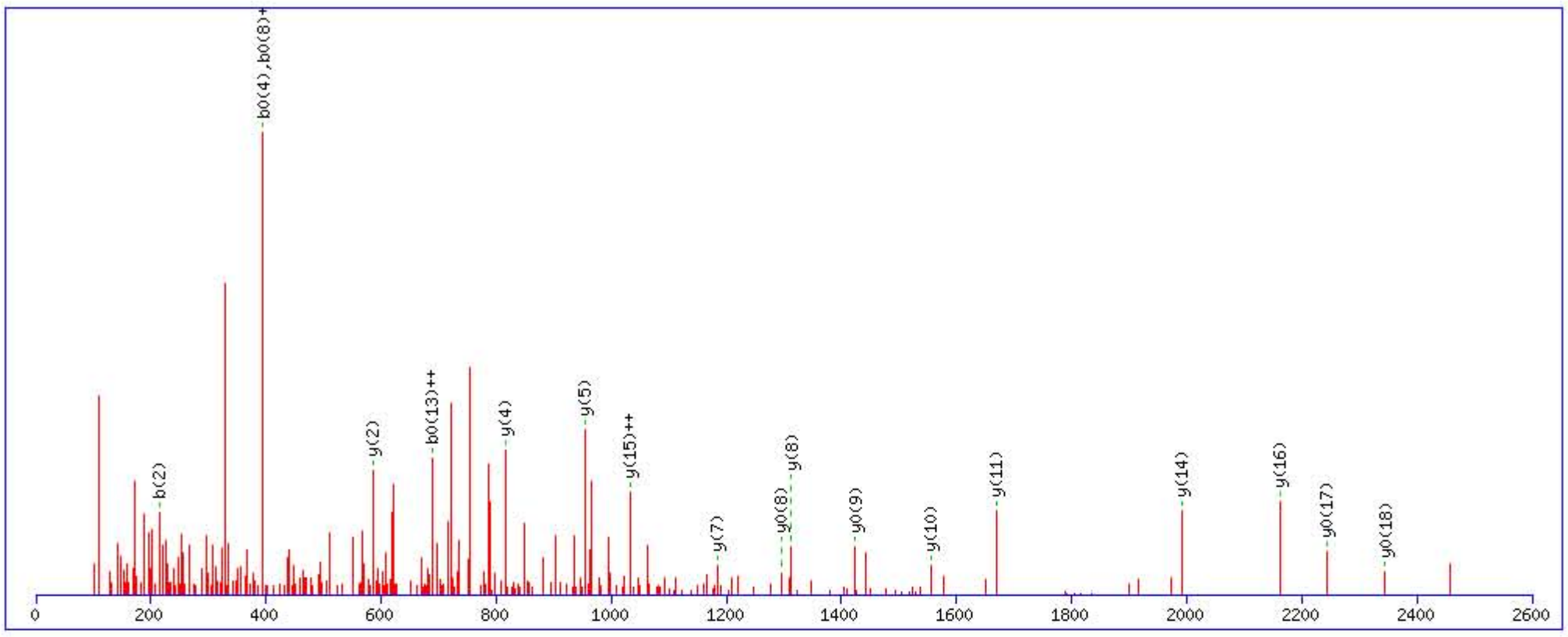
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ITVVAGEHNIEETEHTEQK**
Found in **FA9_HUMAN**, Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2

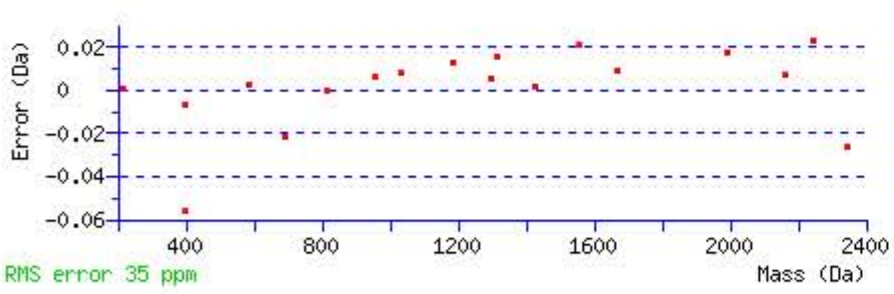
Match to Query 53602: 2474.223816 from(619.563230,4+) rtinseconds(1618) index(47771)
Title: Locus:1.1.1.1801.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

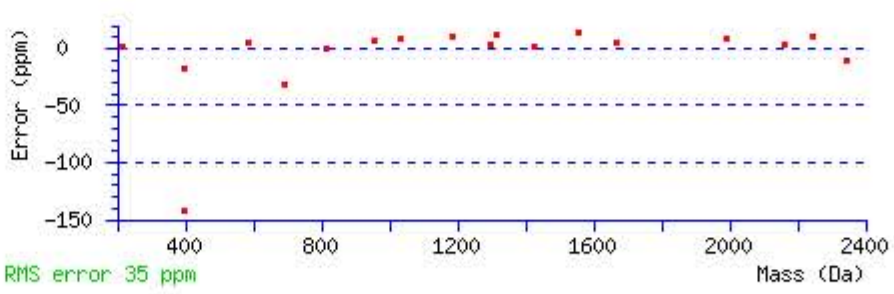
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2474.211121
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q18** : Biotin:Thermo-21345 (Q)
**Ions Score:** 52 **Expect:** 0.00017
**Matches :** 18/194 fragment ions using 23 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 19 |
| 2 | 215.139019 | 108.073147 | | | 197.128454 | 99.067865 | T | 2362.134353 | 1181.570814 | 2345.107804 | 1173.057540 | 2344.123788 | 1172.565532 | 18 |
| 3 | 314.207433 | 157.607354 | | | 296.196868 | 148.602072 | V | 2261.086674 | 1131.046975 | 2244.060125 | 1122.533700 | 2243.076109 | 1122.041692 | 17 |
| 4 | 413.275847 | 207.141561 | | | 395.265282 | 198.136279 | V | *2162.018260* | 1081.512768 | 2144.991711 | 1072.999493 | 2144.007695 | 1072.507485 | 16 |
| 5 | 484.312961 | 242.660119 | | | 466.302396 | 233.654836 | A | 2062.949846 | 1031.978561 | 2045.923297 | 1023.465286 | 2044.939281 | 1022.973278 | 15 |
| 6 | 541.334425 | 271.170851 | | | 523.323860 | 262.165568 | G | *1991.912732* | 996.460004 | 1974.886183 | 987.946730 | 1973.902167 | 987.454722 | 14 |
| 7 | 670.377018 | 335.692147 | | | 652.366453 | 326.686865 | E | 1934.891268 | 967.949272 | 1917.864719 | 959.435998 | 1916.880703 | 958.943990 | 13 |
| 8 | 807.435930 | 404.221603 | | | 789.425365 | 395.216321 | H | 1805.848675 | 903.427976 | 1788.822126 | 894.914701 | 1787.838110 | 894.422693 | 12 |
| 9 | 921.478857 | 461.243067 | 904.452308 | 452.729792 | 903.468292 | 452.237784 | N | *1668.789763* | 834.898520 | 1651.763214 | 826.385245 | 1650.779198 | 825.893237 | 11 |
| 10 | 1034.562921 | 517.785099 | 1017.536372 | 509.271824 | 1016.552356 | 508.779816 | I | *1554.746836* | 777.877056 | 1537.720287 | 769.363782 | 1536.736271 | 768.871774 | 10 |
| 11 | 1163.605514 | 582.306395 | 1146.578965 | 573.793121 | 1145.594949 | 573.301113 | E | 1441.662772 | 721.335024 | 1424.636223 | 712.821750 | 1423.652207 | 712.329742 | 9 |
| 12 | 1292.648107 | 646.827692 | 1275.621558 | 638.314417 | 1274.637542 | 637.822409 | E | *1312.620179* | 656.813728 | 1295.593630 | 648.300453 | 1294.609614 | 647.808445 | 8 |
| 13 | 1393.695786 | 697.351531 | 1376.669237 | 688.838257 | 1375.685221 | 688.346249 | T | *1183.577586* | 592.292431 | 1166.551037 | 583.779157 | 1165.567021 | 583.287149 | 7 |
| 14 | 1522.738379 | 761.872828 | 1505.711830 | 753.359553 | 1504.727814 | 752.867545 | E | 1082.529907 | 541.768592 | 1065.503358 | 533.255317 | 1064.519342 | 532.763309 | 6 |
| 15 | 1659.797291 | 830.402284 | 1642.770742 | 821.889009 | 1641.786726 | 821.397001 | H | *953.487314* | 477.247295 | 936.460765 | 468.734021 | 935.476749 | 468.242013 | 5 |
| 16 | 1760.844970 | 880.926123 | 1743.818421 | 872.412849 | 1742.834405 | 871.920841 | T | *816.428402* | 408.717839 | 799.401853 | 400.204565 | 798.417837 | 399.712557 | 4 |
| 17 | 1889.887563 | 945.447420 | 1872.861014 | 936.934145 | 1871.876998 | 936.442137 | E | 715.380723 | 358.194000 | 698.354174 | 349.680725 | 697.370158 | 349.188717 | 3 |
| 18 | 2329.112889 | 1165.060082 | 2312.086340 | 1156.546808 | 2311.102324 | 1156.054800 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 19 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.0 | 2474.211121 | 0.012695 | ITVVAGEHNIEETEHTEQK |

**Mascot:** http://www.matrixscience.com/

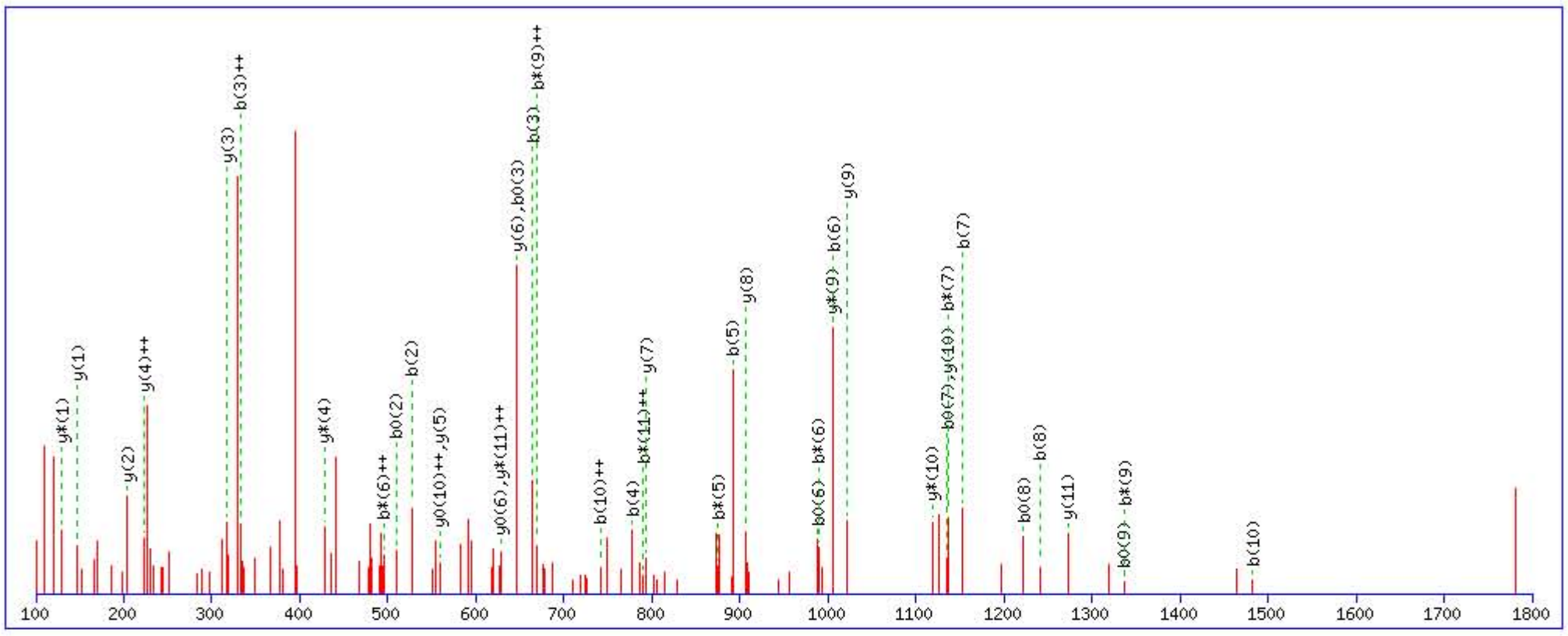
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SQHLDNFSNQIGK**
Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

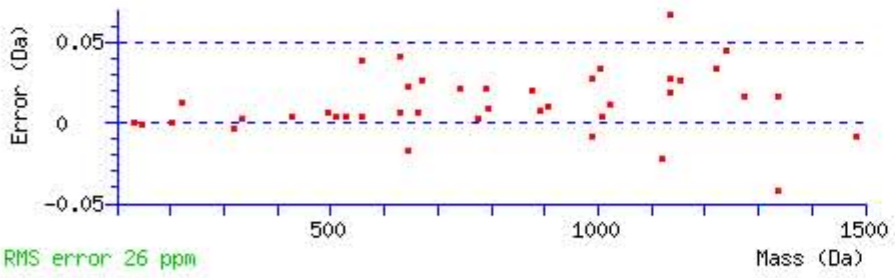
Match to Query 40210: 1797.891612 from(600.304480,3+) rtinseconds(1772) index(48802)
Title: Locus:1.1.1.1855.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

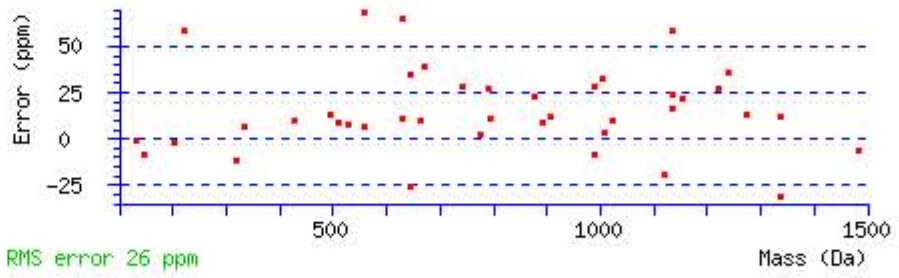
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1797.883194
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 42 **Expect:** 0.00017
**Matches :** 41/132 fragment ions using 81 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 13 |
| 2 | **527.264630** | 264.135953 | 510.238081 | 255.622679 | 509.254065 | 255.130671 | Q | 1711.858451 | 856.432863 | 1694.831902 | 847.919589 | 1693.847886 | 847.427581 | 12 |
| 3 | **664.323542** | **332.665409** | 647.296993 | 324.152134 | 646.312977 | 323.660126 | H | *1272.633125* | 636.820200 | 1255.606576 | 628.306926 | 1254.622560 | 627.814918 | 11 |
| 4 | **777.407606** | 389.207441 | 760.381057 | 380.694166 | 759.397041 | 380.202159 | L | *1135.574213* | 568.290744 | 1118.547664 | 559.777470 | 1117.563648 | 559.285462 | 10 |
| 5 | **892.434549** | 446.720913 | 875.408000 | 438.207638 | 874.423984 | 437.715630 | D | *1022.490149* | 511.748712 | 1005.463600 | 503.235438 | 1004.479584 | 502.743430 | 9 |
| 6 | **1006.477476** | 503.742376 | 989.450927 | 495.229101 | 988.466911 | 494.737093 | N | *907.463206* | 454.235241 | 890.436657 | 445.721966 | 889.452641 | 445.229958 | 8 |
| 7 | **1153.545890** | 577.276583 | 1136.519341 | 568.763308 | 1135.535325 | 568.271300 | F | *793.420279* | 397.213777 | 776.393730 | 388.700503 | 775.409714 | 388.208495 | 7 |
| 8 | **1240.577918** | 620.792597 | 1223.551369 | 612.279323 | 1222.567353 | 611.787314 | S | *646.351865* | 323.679570 | 629.325316 | 315.166296 | 628.341300 | 314.674288 | 6 |
| 9 | 1354.620845 | 677.814060 | 1337.594296 | 669.300786 | 1336.610280 | 668.808778 | N | *559.319837* | 280.163556 | 542.293288 | 271.650282 | | | 5 |
| 10 | **1482.679423** | **741.843349** | 1465.652874 | 733.330075 | 1464.668858 | 732.838067 | Q | 445.276910 | 223.142093 | 428.250361 | 214.628818 | | | 4 |
| 11 | 1595.763487 | 798.385381 | 1578.736938 | 789.872107 | 1577.752922 | 789.380099 | I | *317.218332* | 159.112804 | 300.191783 | 150.599529 | | | 3 |
| 12 | 1652.784951 | 826.896113 | 1635.758402 | 818.382839 | 1634.774386 | 817.890831 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 13 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 42.5 | 1797.883194 | 0.008418 | SQHLDNFSNQIGK |
| 2.4 | 1797.872604 | 0.019008 | KWDFSKYYVSNFSK |

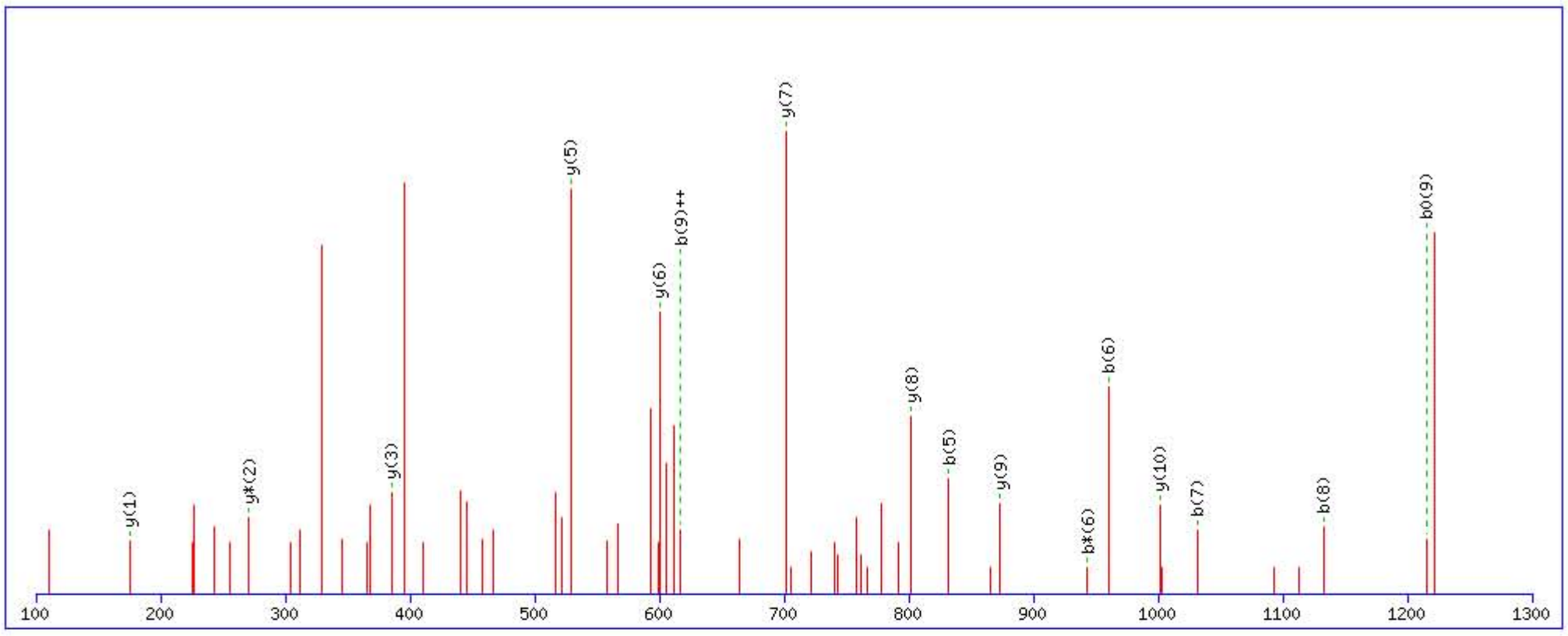
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **APSHQQATTAGSPLR**
Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

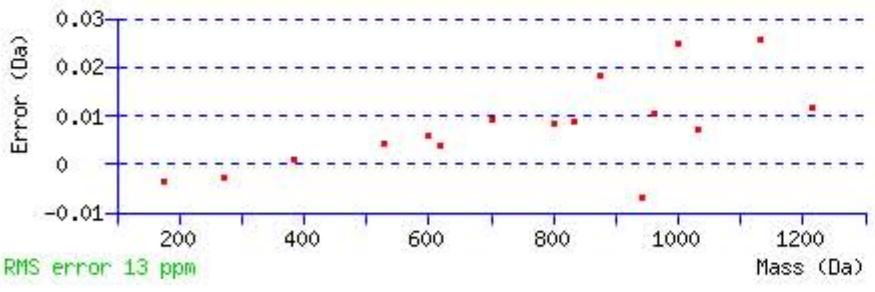
Match to Query 40924: 1831.946952 from(611.656260,3+) rtinseconds(1415) index(46435)
Title: Locus:1.1.1.1730.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

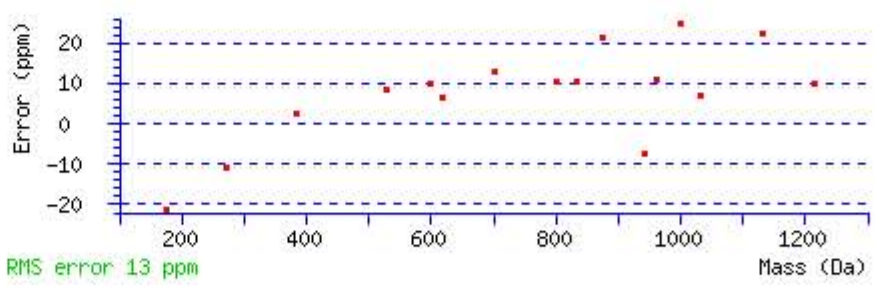
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1831.936295
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0038
**Matches :** 16/150 fragment ions using 32 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 15 |
| 2 | 169.097154 | 85.052215 | | | | | P | 1761.906466 | 881.456871 | 1744.879917 | 872.943597 | 1743.895901 | 872.451588 | 14 |
| 3 | 256.129182 | 128.568229 | | | 238.118617 | 119.562947 | S | 1664.853702 | 832.930489 | 1647.827153 | 824.417215 | 1646.843137 | 823.925206 | 13 |
| 4 | 393.188094 | 197.097685 | | | 375.177529 | 188.092402 | H | 1577.821674 | 789.414475 | 1560.795125 | 780.901200 | 1559.811109 | 780.409192 | 12 |
| 5 | **832.413420** | 416.710348 | 815.386871 | 408.197073 | 814.402855 | 407.705065 | Q | 1440.762762 | 720.885019 | 1423.736213 | 712.371744 | 1422.752197 | 711.879736 | 11 |
| 6 | **960.471998** | 480.739637 | 943.445449 | 472.226362 | 942.461433 | 471.734354 | Q | *1001.537436* | 501.272356 | 984.510887 | 492.759081 | 983.526871 | 492.267073 | 10 |
| 7 | **1031.509112** | 516.258194 | 1014.482563 | 507.744919 | 1013.498547 | 507.252911 | A | *873.478858* | 437.243067 | 856.452309 | 428.729792 | 855.468293 | 428.237784 | 9 |
| 8 | **1132.556791** | 566.782034 | 1115.530242 | 558.268759 | 1114.546226 | 557.776751 | T | *802.441744* | 401.724510 | 785.415195 | 393.211235 | 784.431179 | 392.719227 | 8 |
| 9 | 1233.604470 | 617.305873 | 1216.577921 | 608.792599 | 1215.593905 | 608.300591 | T | *701.394065* | 351.200671 | 684.367516 | 342.687396 | 683.383500 | 342.195388 | 7 |
| 10 | 1304.641584 | 652.824430 | 1287.615035 | 644.311156 | 1286.631019 | 643.819147 | A | *600.346386* | 300.676831 | 583.319837 | 292.163556 | 582.335821 | 291.671548 | 6 |
| 11 | 1361.663048 | 681.335162 | 1344.636499 | 672.821888 | 1343.652483 | 672.329879 | G | *529.309272* | 265.158274 | 512.282723 | 256.644999 | 511.298707 | 256.152991 | 5 |
| 12 | 1448.695076 | 724.851176 | 1431.668527 | 716.337902 | 1430.684511 | 715.845893 | S | 472.287808 | 236.647542 | 455.261259 | 228.134267 | 454.277243 | 227.642259 | 4 |
| 13 | 1545.747840 | 773.377558 | 1528.721291 | 764.864284 | 1527.737275 | 764.372276 | P | *385.255780* | 193.131528 | 368.229231 | 184.618253 | | | 3 |
| 14 | 1658.831904 | 829.919590 | 1641.805355 | 821.406316 | 1640.821339 | 820.914307 | L | 288.203016 | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.8 | 1831.936295 | 0.010657 | APSHQQATTAGSPLR |
| 27.3 | 1831.936295 | 0.010657 | APSHQQATTAGSPLR |

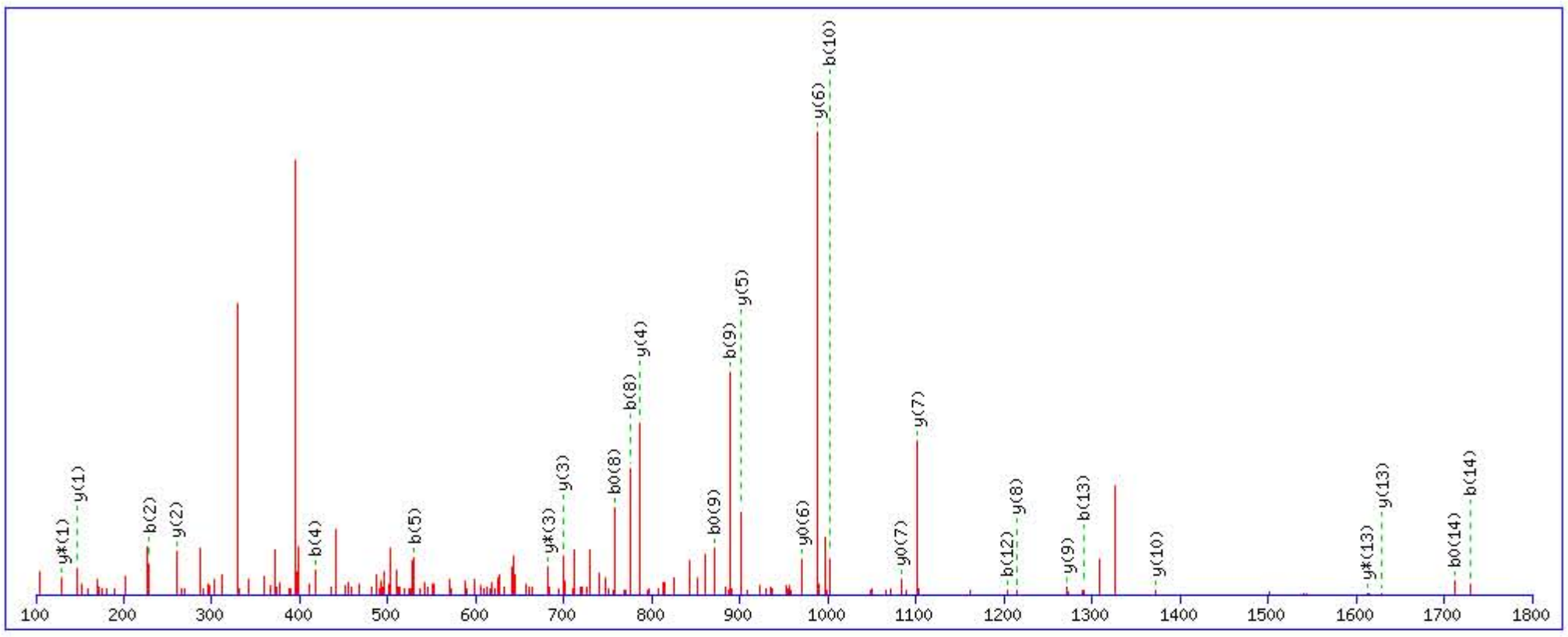
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MPMGLSTGIISDSQIK**
Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

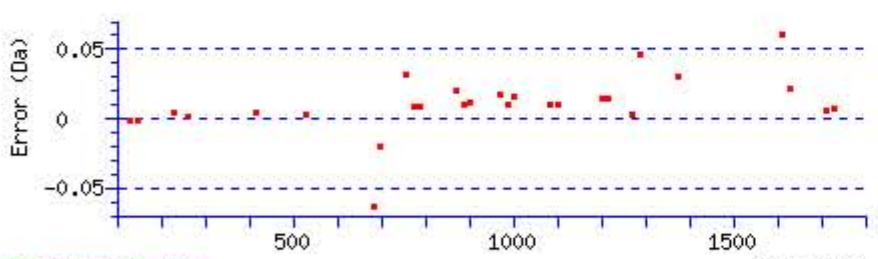
Match to Query 43878: 1988.033622 from(663.685150,3+) rtinseconds(2461) index(53154)
Title: Locus:1.1.1.2094.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

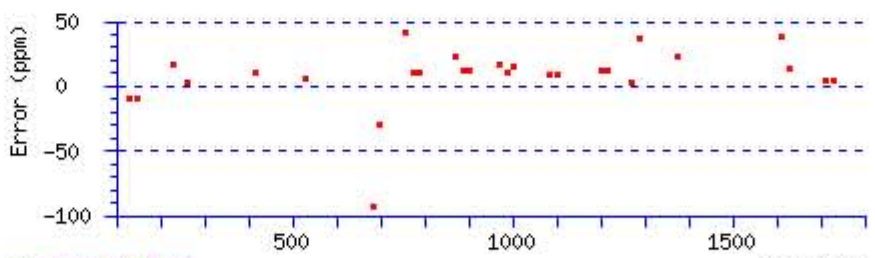
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1988.014465
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q14 : Biotin:Thermo-21345 (Q)
**Ions Score:** 64 **Expect:** 3.6e-006
**Matches :** 28/138 fragment ions using 57 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.047761 | 66.527518 | | | | | M | | | | | | | 16 |
| 2 | *229.100525* | 115.053900 | | | | | P | 1857.981269 | 929.494273 | 1840.954720 | 920.980998 | 1839.970704 | 920.488990 | 15 |
| 3 | 360.141010 | 180.574143 | | | | | M | 1760.928505 | 880.967891 | 1743.901956 | 872.454616 | 1742.917940 | 871.962608 | 14 |
| 4 | *417.162474* | 209.084875 | | | | | G | *1629.888020* | 815.447648 | 1612.861471 | 806.934374 | 1611.877455 | 806.442366 | 13 |
| 5 | *530.246538* | 265.626907 | | | | | L | 1572.866556 | 786.936916 | 1555.840007 | 778.423642 | 1554.855991 | 777.931634 | 12 |
| 6 | 617.278566 | 309.142921 | | | 599.268001 | 300.137638 | S | 1459.782492 | 730.394884 | 1442.755943 | 721.881610 | 1441.771927 | 721.389602 | 11 |
| 7 | 718.326245 | 359.666761 | | | 700.315680 | 350.661478 | T | *1372.750464* | 686.878870 | 1355.723915 | 678.365596 | 1354.739899 | 677.873588 | 10 |
| 8 | *775.347709* | 388.177493 | | | 757.337144 | 379.172210 | G | *1271.702785* | 636.355031 | 1254.676236 | 627.841756 | 1253.692220 | 627.349748 | 9 |
| 9 | *888.431773* | 444.719525 | | | 870.421208 | 435.714242 | I | *1214.681321* | 607.844299 | 1197.654772 | 599.331024 | 1196.670756 | 598.839016 | 8 |
| 10 | *1001.515837* | 501.261557 | | | 983.505272 | 492.256274 | I | *1101.597257* | 551.302267 | 1084.570708 | 542.788992 | 1083.586692 | 542.296984 | 7 |
| 11 | 1088.547865 | 544.777571 | | | 1070.537300 | 535.772288 | S | *988.513193* | 494.760235 | 971.486644 | 486.246960 | 970.502628 | 485.754952 | 6 |
| 12 | *1203.574808* | 602.291042 | | | 1185.564243 | 593.285760 | D | *901.481165* | 451.244221 | 884.454616 | 442.730946 | 883.470600 | 442.238938 | 5 |
| 13 | *1290.606836* | 645.807056 | | | 1272.596271 | 636.801774 | S | *786.454222* | 393.730749 | 769.427673 | 385.217475 | 768.443657 | 384.725467 | 4 |
| 14 | *1729.832162* | 865.419719 | 1712.805613 | 856.906445 | 1711.821597 | 856.414437 | Q | *699.422194* | 350.214735 | 682.395645 | 341.701461 | | | 3 |
| 15 | 1842.916226 | 921.961751 | 1825.889677 | 913.448477 | 1824.905661 | 912.956469 | I | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 16 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 64.0 | 1988.014465 | 0.019157 | MPMGLSTGIISDSQIK |
| 5.7 | 1988.054688 | -0.021066 | EVGKILCTDCATRPKLK |
| 4.0 | 1988.011108 | 0.022514 | QSMVNSLPTFPTDIK |
| 0.3 | 1988.051331 | -0.017709 | MTHKLVFLEDGTSQVRK |

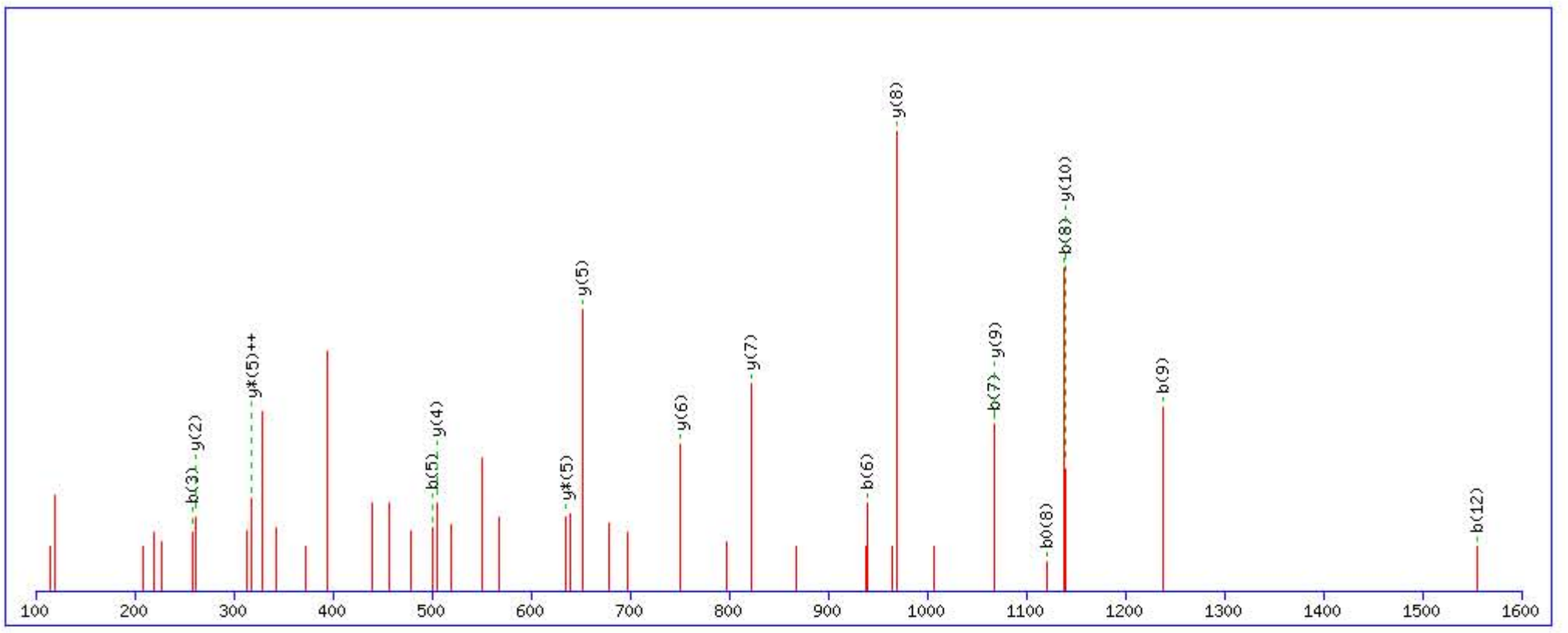
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AADIEQQAVFAVFDENK**
Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

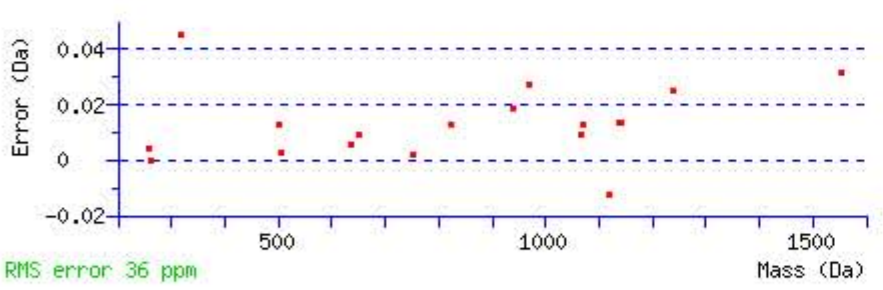
Match to Query 48539: 2205.109512 from(736.043780,3+) rtinseconds(2758) index(55184)
Title: Locus:1.1.1.2196.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

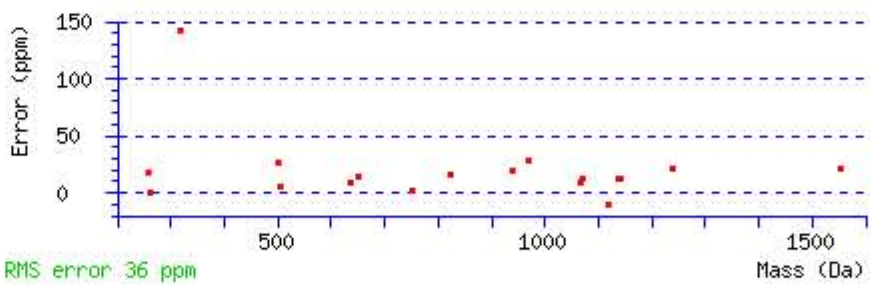
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2205.077591
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.00029
**Matches :** 18/174 fragment ions using 37 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 17 |
| 2 | 143.081504 | 72.044390 | | | | | A | 2135.047769 | 1068.027522 | 2118.021220 | 1059.514248 | 2117.037204 | 1059.022240 | 16 |
| 3 | *258.108447* | 129.557862 | | | 240.097882 | 120.552579 | D | 2064.010655 | 1032.508965 | 2046.984106 | 1023.995691 | 2046.000090 | 1023.503683 | 15 |
| 4 | 371.192511 | 186.099894 | | | 353.181946 | 177.094611 | I | 1948.983712 | 974.995494 | 1931.957163 | 966.482220 | 1930.973147 | 965.990212 | 14 |
| 5 | *500.235104* | 250.621190 | | | 482.224539 | 241.615908 | E | 1835.899648 | 918.453462 | 1818.873099 | 909.940188 | 1817.889083 | 909.448180 | 13 |
| 6 | *939.460430* | 470.233853 | 922.433881 | 461.720579 | 921.449865 | 461.228571 | Q | 1706.857055 | 853.932166 | 1689.830506 | 845.418891 | 1688.846490 | 844.926883 | 12 |
| 7 | *1067.519008* | 534.263142 | 1050.492459 | 525.749868 | 1049.508443 | 525.257860 | Q | 1267.631729 | 634.319503 | 1250.605180 | 625.806228 | 1249.621164 | 625.314220 | 11 |
| 8 | *1138.556122* | 569.781699 | 1121.529573 | 561.268425 | 1120.545557 | 560.776416 | A | *1139.573151* | 570.290214 | 1122.546602 | 561.776939 | 1121.562586 | 561.284931 | 10 |
| 9 | *1237.624536* | 619.315906 | 1220.597987 | 610.802632 | 1219.613971 | 610.310624 | V | *1068.536037* | 534.771657 | 1051.509488 | 526.258382 | 1050.525472 | 525.766374 | 9 |
| 10 | 1384.692950 | 692.850113 | 1367.666401 | 684.336839 | 1366.682385 | 683.844831 | F | *969.467623* | 485.237450 | 952.441074 | 476.724175 | 951.457058 | 476.232167 | 8 |
| 11 | 1455.730064 | 728.368670 | 1438.703515 | 719.855396 | 1437.719499 | 719.363388 | A | *822.399209* | 411.703243 | 805.372660 | 403.189968 | 804.388644 | 402.697960 | 7 |
| 12 | *1554.798478* | 777.902877 | 1537.771929 | 769.389603 | 1536.787913 | 768.897595 | V | *751.362095* | 376.184686 | 734.335546 | 367.671411 | 733.351530 | 367.179403 | 6 |
| 13 | 1701.866892 | 851.437084 | 1684.840343 | 842.923810 | 1683.856327 | 842.431802 | F | *652.293681* | 326.650479 | 635.267132 | 318.137204 | 634.283116 | 317.645196 | 5 |
| 14 | 1816.893835 | 908.950556 | 1799.867286 | 900.437281 | 1798.883270 | 899.945273 | D | *505.225267* | 253.116271 | 488.198718 | 244.602997 | 487.214702 | 244.110989 | 4 |
| 15 | 1945.936428 | 973.471852 | 1928.909879 | 964.958578 | 1927.925863 | 964.466570 | E | 390.198324 | 195.602800 | 373.171775 | 187.089525 | 372.187759 | 186.597517 | 3 |
| 16 | 2059.979355 | 1030.493315 | 2042.952806 | 1021.980041 | 2041.968790 | 1021.488033 | N | *261.155731* | 131.081503 | 244.129182 | 122.568229 | | | 2 |
| 17 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.1 | 2205.077591 | 0.031921 | AADIEQQAVFAVFDENK |
| 42.0 | 2205.077591 | 0.031921 | AADIEQQAVFAVFDENK |
| 6.9 | 2205.080063 | 0.029449 | EKENDELDIQLKVFDENK |
| 3.2 | 2205.129929 | -0.020417 | YPGRNGAQMMVHIVFKVAR |
| 0.7 | 2205.115311 | -0.005799 | FLPPPGYAPCHEAVLPRER |

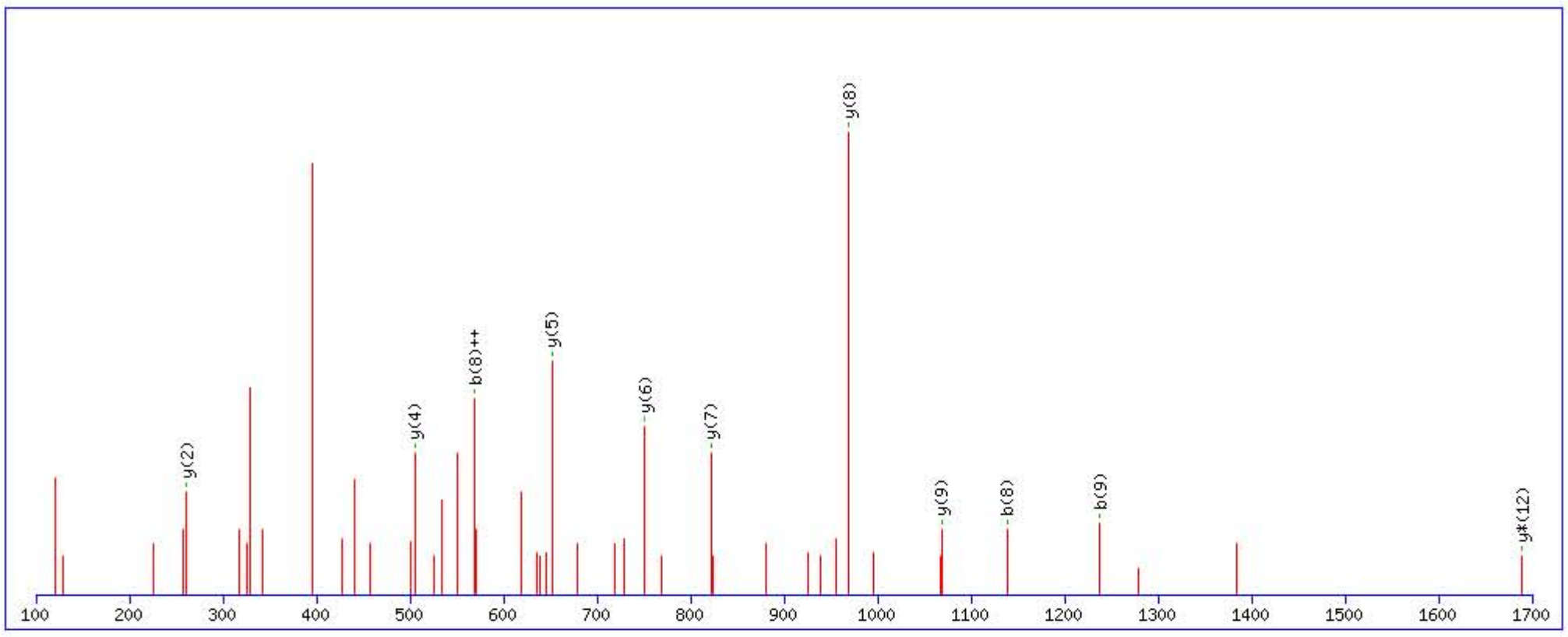
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AADIEQQAVFAVFDENK**
Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

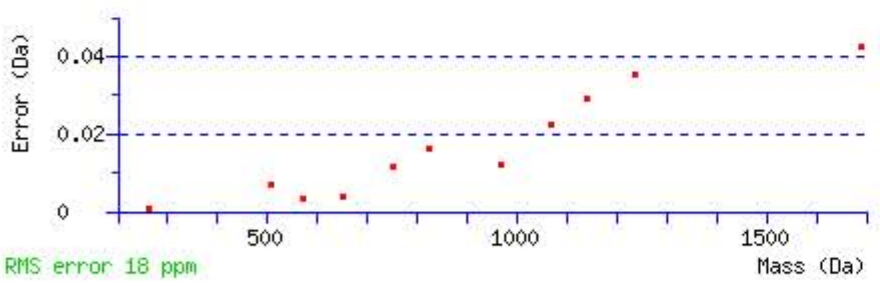
Match to Query 48540: 2205.109512 from(736.043780,3+) rtinseconds(2749) index(55104)
Title: Locus:1.1.1.2193.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

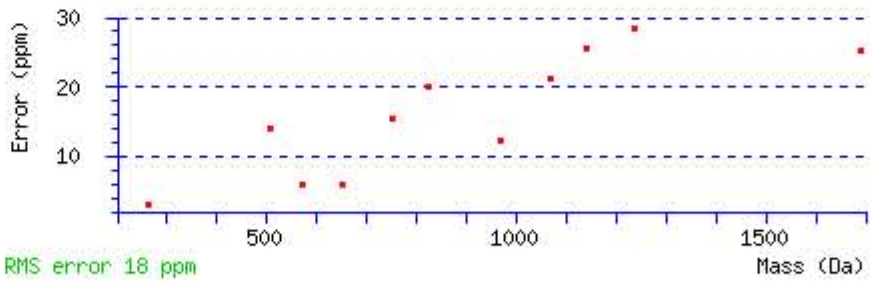
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2205.077591
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 51 **Expect:** 4.2e-005
**Matches :** 11/174 fragment ions using 14 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 17 |
| 2 | 143.081504 | 72.044390 | | | | | A | 2135.047769 | 1068.027522 | 2118.021220 | 1059.514248 | 2117.037204 | 1059.022240 | 16 |
| 3 | 258.108447 | 129.557862 | | | 240.097882 | 120.552579 | D | 2064.010655 | 1032.508965 | 2046.984106 | 1023.995691 | 2046.000090 | 1023.503683 | 15 |
| 4 | 371.192511 | 186.099894 | | | 353.181946 | 177.094611 | I | 1948.983712 | 974.995494 | 1931.957163 | 966.482220 | 1930.973147 | 965.990212 | 14 |
| 5 | 500.235104 | 250.621190 | | | 482.224539 | 241.615908 | E | 1835.899648 | 918.453462 | 1818.873099 | 909.940188 | 1817.889083 | 909.448180 | 13 |
| 6 | 628.293682 | 314.650479 | 611.267133 | 306.137205 | 610.283117 | 305.645197 | Q | 1706.857055 | 853.932166 | 1689.830506 | 845.418891 | 1688.846490 | 844.926883 | 12 |
| 7 | 1067.519008 | 534.263142 | 1050.492459 | 525.749868 | 1049.508443 | 525.257860 | Q | 1578.798477 | 789.902877 | 1561.771928 | 781.389602 | 1560.787912 | 780.897594 | 11 |
| 8 | **1138.556122** | **569.781699** | 1121.529573 | 561.268425 | 1120.545557 | 560.776416 | A | 1139.573151 | 570.290214 | 1122.546602 | 561.776939 | 1121.562586 | 561.284931 | 10 |
| 9 | **1237.624536** | 619.315906 | 1220.597987 | 610.802632 | 1219.613971 | 610.310624 | V | *1068.536037* | 534.771657 | 1051.509488 | 526.258382 | 1050.525472 | 525.766374 | 9 |
| 10 | 1384.692950 | 692.850113 | 1367.666401 | 684.336839 | 1366.682385 | 683.844831 | F | *969.467623* | 485.237450 | 952.441074 | 476.724175 | 951.457058 | 476.232167 | 8 |
| 11 | 1455.730064 | 728.368670 | 1438.703515 | 719.855396 | 1437.719499 | 719.363388 | A | *822.399209* | 411.703243 | 805.372660 | 403.189968 | 804.388644 | 402.697960 | 7 |
| 12 | 1554.798478 | 777.902877 | 1537.771929 | 769.389603 | 1536.787913 | 768.897595 | V | *751.362095* | 376.184686 | 734.335546 | 367.671411 | 733.351530 | 367.179403 | 6 |
| 13 | 1701.866892 | 851.437084 | 1684.840343 | 842.923810 | 1683.856327 | 842.431802 | F | *652.293681* | 326.650479 | 635.267132 | 318.137204 | 634.283116 | 317.645196 | 5 |
| 14 | 1816.893835 | 908.950556 | 1799.867286 | 900.437281 | 1798.883270 | 899.945273 | D | *505.225267* | 253.116271 | 488.198718 | 244.602997 | 487.214702 | 244.110989 | 4 |
| 15 | 1945.936428 | 973.471852 | 1928.909879 | 964.958578 | 1927.925863 | 964.466570 | E | 390.198324 | 195.602800 | 373.171775 | 187.089525 | 372.187759 | 186.597517 | 3 |
| 16 | 2059.979355 | 1030.493315 | 2042.952806 | 1021.980041 | 2041.968790 | 1021.488033 | N | *261.155731* | 131.081503 | 244.129182 | 122.568229 | | | 2 |
| 17 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 50.6 | 2205.077591 | 0.031921 | AADIEQQAVFAVFDENK |
| 50.6 | 2205.077591 | 0.031921 | AADIEQQAVFAVFDENK |
| 3.9 | 2205.080063 | 0.029449 | EKENDELDIQLKVFDENK |
| 3.4 | 2205.129929 | -0.020417 | YPGRNGAQMMVHIVFKVAR |

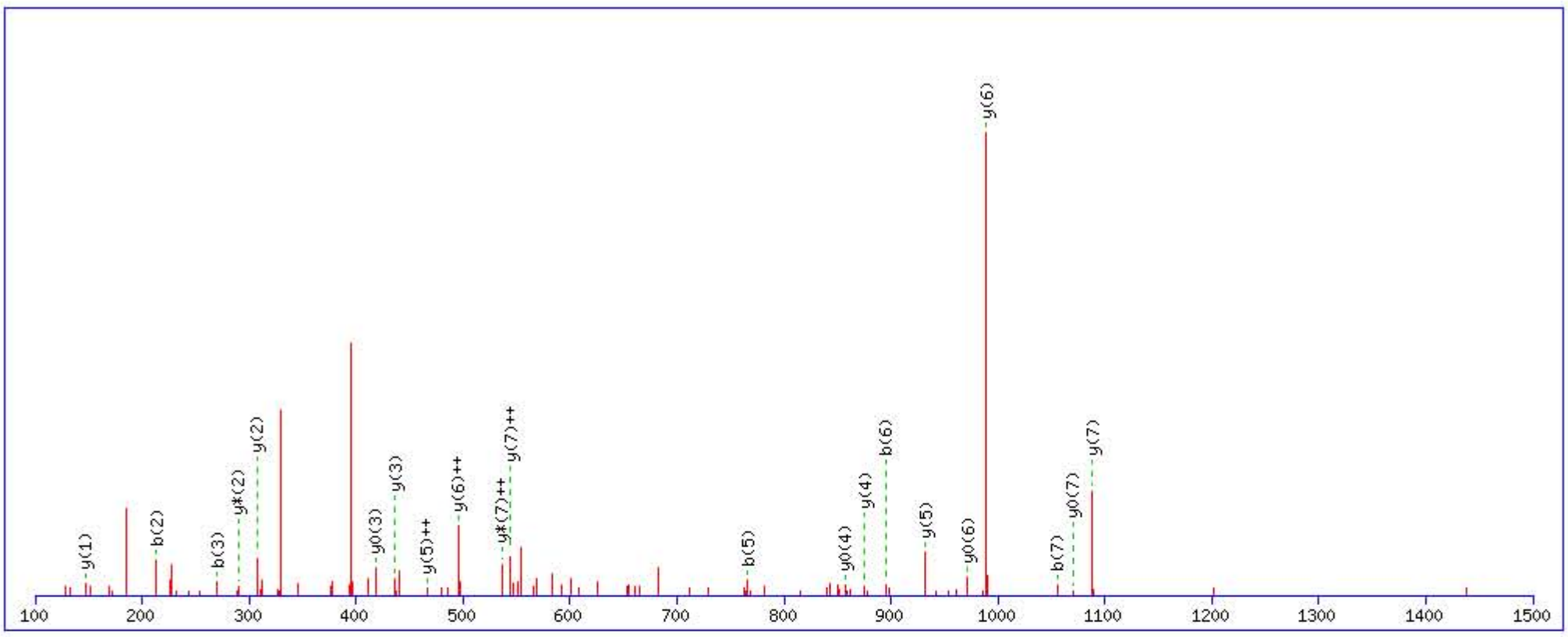
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IVGGQECK**
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

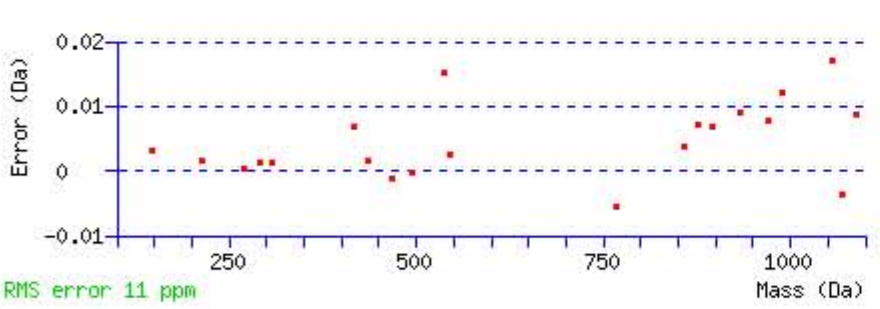
Match to Query 20552: 1200.605628 from(601.310090,2+) rtinseconds(1435) index(46572)
Title: Locus:1.1.1.1737.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

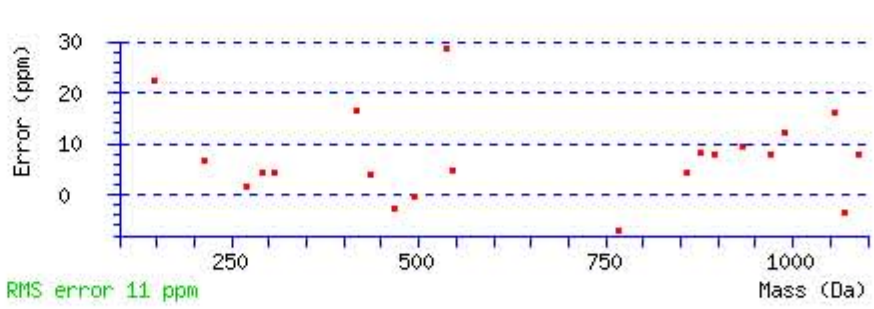
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1200.599503
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0011
**Matches :** 21/62 fragment ions using 49 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 8 |
| 2 | **213.159754** | 107.083515 | | | | | V | *1088.522714* | 544.764995 | 1071.496165 | 536.251721 | 1070.512149 | 535.759713 | 7 |
| 3 | **270.181218** | 135.594247 | | | | | G | *989.454300* | 495.230788 | 972.427751 | 486.717514 | 971.443735 | 486.225506 | 6 |
| 4 | 327.202682 | 164.104979 | | | | | G | *932.432836* | 466.720056 | 915.406287 | 458.206782 | 914.422271 | 457.714774 | 5 |
| 5 | **766.428008** | 383.717642 | 749.401459 | 375.204368 | | | Q | *875.411372* | 438.209324 | 858.384823 | 429.696050 | 857.400807 | 429.204042 | 4 |
| 6 | **895.470601** | 448.238939 | 878.444052 | 439.725664 | 877.460036 | 439.233656 | E | *436.186046* | 218.596661 | 419.159497 | 210.083386 | 418.175481 | 209.591378 | 3 |
| 7 | **1055.501250** | 528.254263 | 1038.474701 | 519.740989 | 1037.490685 | 519.248981 | C | *307.143453* | 154.075364 | 290.116904 | 145.562090 | | | 2 |
| 8 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.4 | 1200.599503 | 0.006125 | IVGGQECK |
| 1.9 | 1200.599503 | 0.006125 | LIQGDGCK |
| 1.3 | 1200.596100 | 0.009528 | LVKYMYDNR |

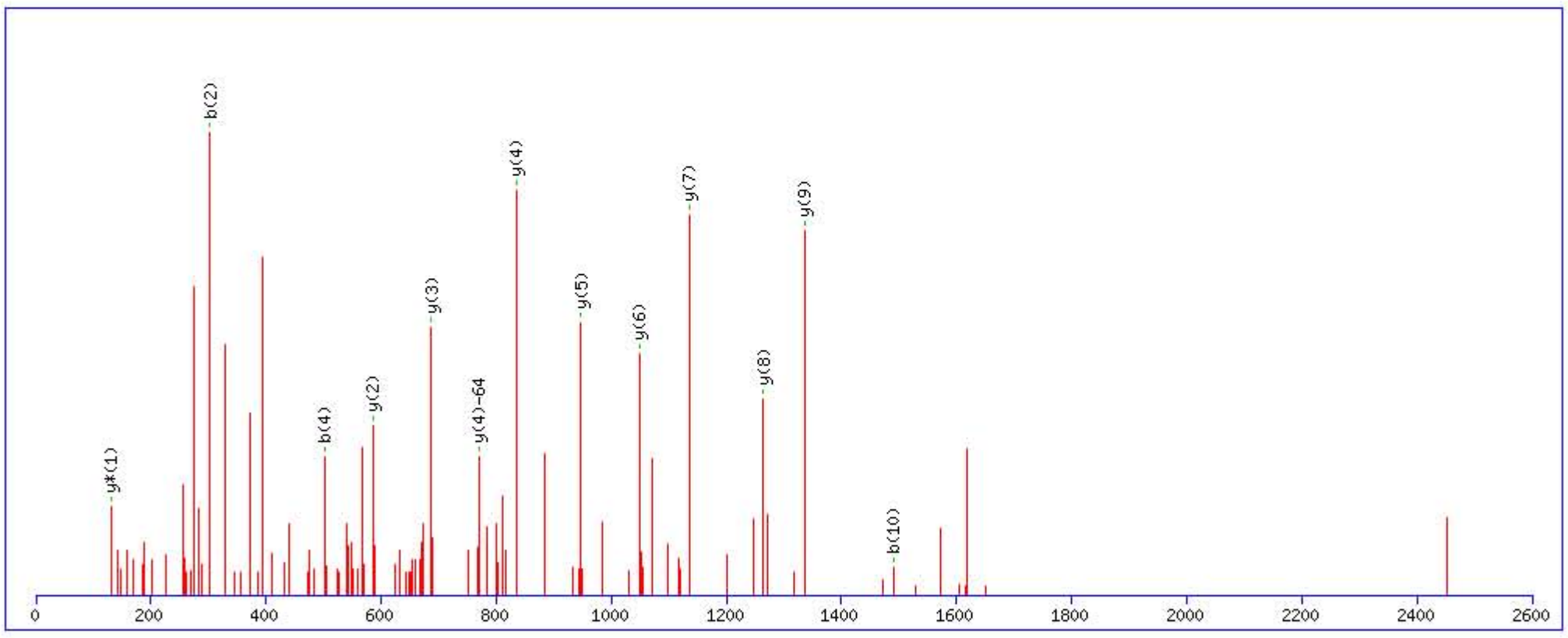
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DWAESTLMTQK**
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

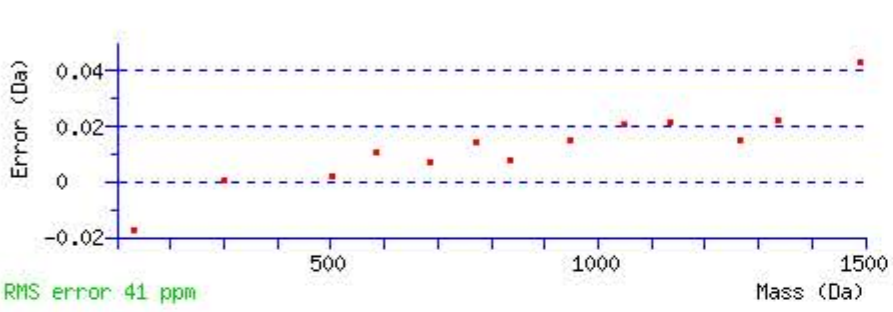
Match to Query 36517: 1635.783648 from(818.899100,2+) rtinseconds(2076) index(50824)
Title: Locus:1.1.1.1960.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

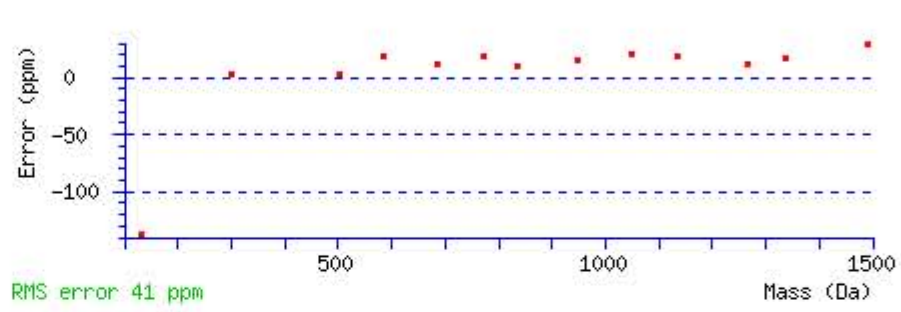
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1635.763657
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
M8 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 76 **Expect:** 1.9e-007
**Matches :** 13/154 fragment ions using 15 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 11 |
| 2 | **302.113532** | 151.560404 | | | 284.102967 | 142.555122 | W | 1521.744000 | 761.375638 | 1504.717451 | 752.862364 | 1503.733435 | 752.370356 | 10 |
| 3 | 373.150646 | 187.078961 | | | 355.140081 | 178.073679 | A | *1335.664687* | 668.335982 | 1318.638138 | 659.822707 | 1317.654122 | 659.330699 | 9 |
| 4 | **502.193239** | 251.600258 | | | 484.182674 | 242.594975 | E | *1264.627573* | 632.817425 | 1247.601024 | 624.304150 | 1246.617008 | 623.812142 | 8 |
| 5 | 589.225267 | 295.116272 | | | 571.214702 | 286.110989 | S | *1135.584980* | 568.296128 | 1118.558431 | 559.782854 | 1117.574415 | 559.290846 | 7 |
| 6 | 690.272946 | 345.640111 | | | 672.262381 | 336.634829 | T | *1048.552952* | 524.780114 | 1031.526403 | 516.266840 | 1030.542387 | 515.774832 | 6 |
| 7 | 803.357010 | 402.182143 | | | 785.346445 | 393.176861 | L | *947.505273* | 474.256275 | 930.478724 | 465.743000 | 929.494708 | 465.250992 | 5 |
| 8 | 950.392410 | 475.699843 | | | 932.381845 | 466.694561 | M | *834.421209* | 417.714243 | 817.394660 | 409.200968 | 816.410644 | 408.708960 | 4 |
| 9 | 1051.440089 | 526.223683 | | | 1033.429524 | 517.218400 | T | *687.385809* | 344.196543 | 670.359260 | 335.683268 | 669.375244 | 335.191260 | 3 |
| 10 | **1490.665415** | 745.836346 | 1473.638866 | 737.323071 | 1472.654850 | 736.831063 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 11 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 76.1 | 1635.763657 | 0.019991 | DWAESTLMTQK |
| 4.3 | 1635.789291 | -0.005643 | VSWTPPSDSVDRYK |
| 2.8 | 1635.781418 | 0.002230 | SDSPDPAPTPALPMPK |
| 2.3 | 1635.781418 | 0.002230 | EAAMWETLSVTGVDK |
| 2.2 | 1635.778259 | 0.005389 | VRVMADSMQEK |
| 0.7 | 1635.763657 | 0.019991 | AFAPDSIQDSMK |

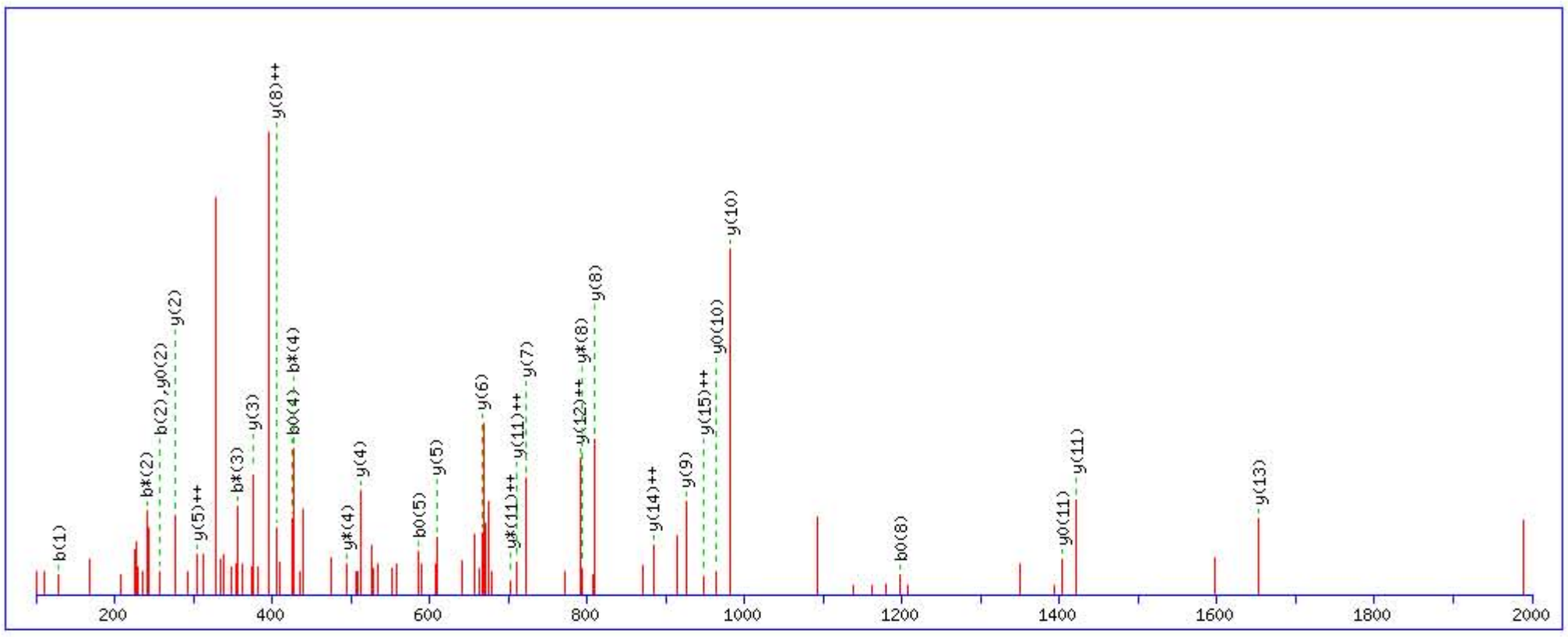
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QEDACQGDSGGPHVTR**
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

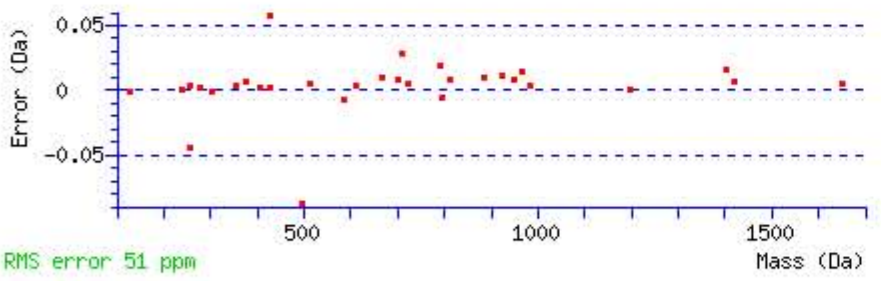
Match to Query 45122: 2023.897902 from(675.639910,3+) rtinseconds(1338) index(45991)
Title: Locus:1.1.1.1703.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

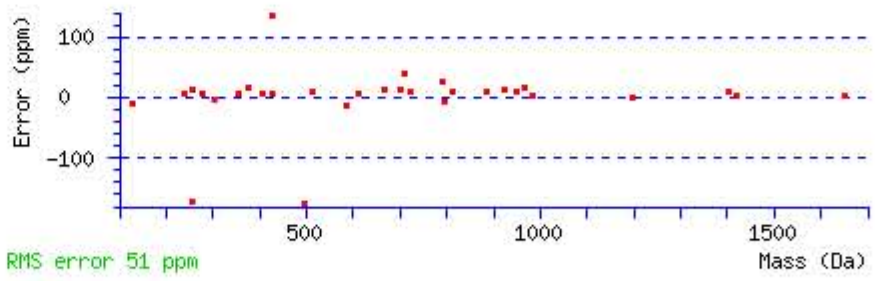
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2023.884033
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 51 **Expect:** 5.6e-005
**Matches :** 31/176 fragment ions using 68 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.065854 | 65.036565 | 112.039305 | 56.523291 | | | Q | | | | | | | 16 |
| 2 | 258.108447 | 129.557862 | 241.081898 | 121.044587 | 240.097882 | 120.552579 | E | 1896.832709 | 948.919993 | 1879.806160 | 940.406718 | 1878.822144 | 939.914710 | 15 |
| 3 | 373.135390 | 187.071333 | 356.108841 | 178.558059 | 355.124825 | 178.066051 | D | 1767.790116 | 884.398696 | 1750.763567 | 875.885422 | 1749.779551 | 875.393414 | 14 |
| 4 | 444.172504 | 222.589890 | 427.145955 | 214.076616 | 426.161939 | 213.584608 | A | *1652.763173* | 826.885225 | 1635.736624 | 818.371950 | 1634.752608 | 817.879942 | 13 |
| 5 | 604.203153 | 302.605215 | 587.176604 | 294.091940 | 586.192588 | 293.599932 | C | 1581.726059 | 791.366668 | 1564.699510 | 782.853393 | 1563.715494 | 782.361385 | 12 |
| 6 | 1043.428479 | 522.217878 | 1026.401930 | 513.704603 | 1025.417914 | 513.212595 | Q | *1421.695410* | 711.351343 | 1404.668861 | 702.838069 | 1403.684845 | 702.346061 | 11 |
| 7 | 1100.449943 | 550.728610 | 1083.423394 | 542.215335 | 1082.439378 | 541.723327 | G | *982.470084* | 491.738680 | 965.443535 | 483.225406 | 964.459519 | 482.733398 | 10 |
| 8 | 1215.476886 | 608.242081 | 1198.450337 | 599.728807 | 1197.466321 | 599.236799 | D | *925.448620* | 463.227948 | 908.422071 | 454.714674 | 907.438055 | 454.222666 | 9 |
| 9 | 1302.508914 | 651.758095 | 1285.482365 | 643.244821 | 1284.498349 | 642.752813 | S | *810.421677* | 405.714477 | 793.395128 | 397.201202 | 792.411112 | 396.709194 | 8 |
| 10 | 1359.530378 | 680.268827 | 1342.503829 | 671.755553 | 1341.519813 | 671.263545 | G | *723.389649* | 362.198463 | 706.363100 | 353.685188 | 705.379084 | 353.193180 | 7 |
| 11 | 1416.551842 | 708.779559 | 1399.525293 | 700.266285 | 1398.541277 | 699.774277 | G | *666.368185* | 333.687731 | 649.341636 | 325.174456 | 648.357620 | 324.682448 | 6 |
| 12 | 1513.604606 | 757.305941 | 1496.578057 | 748.792667 | 1495.594041 | 748.300659 | P | *609.346721* | 305.176999 | 592.320172 | 296.663724 | 591.336156 | 296.171716 | 5 |
| 13 | 1650.663518 | 825.835397 | 1633.636969 | 817.322123 | 1632.652953 | 816.830115 | H | *512.293957* | 256.650617 | 495.267408 | 248.137342 | 494.283392 | 247.645334 | 4 |
| 14 | 1749.731932 | 875.369604 | 1732.705383 | 866.856330 | 1731.721367 | 866.364322 | V | *375.235045* | 188.121161 | 358.208496 | 179.607886 | 357.224480 | 179.115878 | 3 |
| 15 | 1850.779611 | 925.893444 | 1833.753062 | 917.380169 | 1832.769046 | 916.888161 | T | *276.166631* | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 16 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 50.8 | 2023.884033 | 0.013869 | QEDACQGDSGGPHVTR |
| 18.4 | 2023.884033 | 0.013869 | QEDACQGDSGGPHVTR |

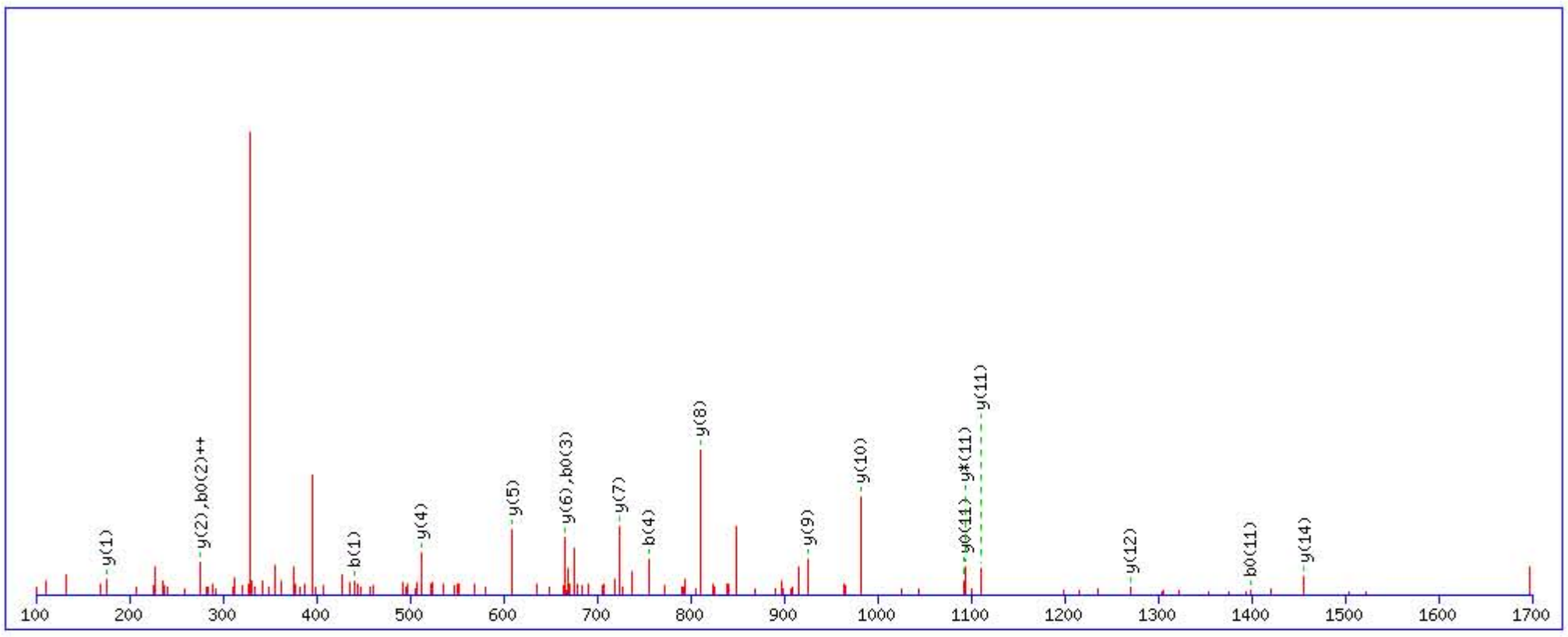
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QEDACQGDSGGPHVTR**
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

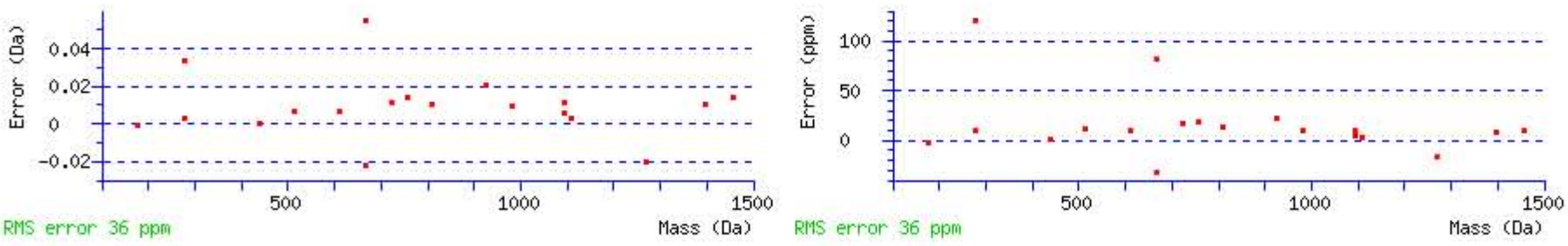
Match to Query 45124: 2023.898742 from(675.640190,3+) rtinseconds(1309) index(45788)
Title: Locus:1.1.1.1693.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2023.884033
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 80 **Expect:** 7.1e-008
**Matches** : 19/176 fragment ions using 31 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 16 |
| 2 | 569.275195 | 285.141236 | 552.248646 | 276.627961 | 551.264630 | 276.135953 | E | 1585.665961 | 793.336618 | 1568.639412 | 784.823344 | 1567.655396 | 784.331336 | 15 |
| 3 | 684.302138 | 342.654707 | 667.275589 | 334.141433 | 666.291573 | 333.649425 | D | *1456.623368* | 728.815322 | 1439.596819 | 720.302047 | 1438.612803 | 719.810039 | 14 |
| 4 | 755.339252 | 378.173264 | 738.312703 | 369.659989 | 737.328687 | 369.167982 | A | 1341.596425 | 671.301851 | 1324.569876 | 662.788576 | 1323.585860 | 662.296568 | 13 |
| 5 | 915.369901 | 458.188589 | 898.343352 | 449.675314 | 897.359336 | 449.183306 | C | *1270.559311* | 635.783294 | 1253.532762 | 627.270019 | 1252.548746 | 626.778011 | 12 |
| 6 | 1043.428479 | 522.217877 | 1026.401930 | 513.704603 | 1025.417914 | 513.212595 | Q | *1110.528662* | 555.767969 | 1093.502113 | 547.254695 | 1092.518097 | 546.762686 | 11 |
| 7 | 1100.449943 | 550.728609 | 1083.423394 | 542.215335 | 1082.439378 | 541.723327 | G | *982.470084* | 491.738680 | 965.443535 | 483.225406 | 964.459519 | 482.733398 | 10 |
| 8 | 1215.476886 | 608.242081 | 1198.450337 | 599.728807 | 1197.466321 | 599.236798 | D | *925.448620* | 463.227948 | 908.422071 | 454.714674 | 907.438055 | 454.222666 | 9 |
| 9 | 1302.508914 | 651.758095 | 1285.482365 | 643.244821 | 1284.498349 | 642.752813 | S | *810.421677* | 405.714477 | 793.395128 | 397.201202 | 792.411112 | 396.709194 | 8 |
| 10 | 1359.530378 | 680.268827 | 1342.503829 | 671.755553 | 1341.519813 | 671.263544 | G | *723.389649* | 362.198463 | 706.363100 | 353.685188 | 705.379084 | 353.193180 | 7 |
| 11 | 1416.551842 | 708.779559 | 1399.525293 | 700.266284 | 1398.541277 | 699.774276 | G | *666.368185* | 333.687731 | 649.341636 | 325.174456 | 648.357620 | 324.682448 | 6 |
| 12 | 1513.604606 | 757.305941 | 1496.578057 | 748.792667 | 1495.594041 | 748.300658 | P | *609.346721* | 305.176999 | 592.320172 | 296.663724 | 591.336156 | 296.171716 | 5 |
| 13 | 1650.663518 | 825.835397 | 1633.636969 | 817.322122 | 1632.652953 | 816.830114 | H | *512.293957* | 256.650617 | 495.267408 | 248.137342 | 494.283392 | 247.645334 | 4 |
| 14 | 1749.731932 | 875.369604 | 1732.705383 | 866.856330 | 1731.721367 | 866.364321 | V | 375.235045 | 188.121161 | 358.208496 | 179.607886 | 357.224480 | 179.115878 | 3 |
| 15 | 1850.779611 | 925.893443 | 1833.753062 | 917.380169 | 1832.769046 | 916.888161 | T | *276.166631* | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 16 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 79.8 | 2023.884033 | 0.014709 | QEDACQGDSGGPHVTR |
| 45.2 | 2023.884033 | 0.014709 | QEDACQGDSGGPHVTR |

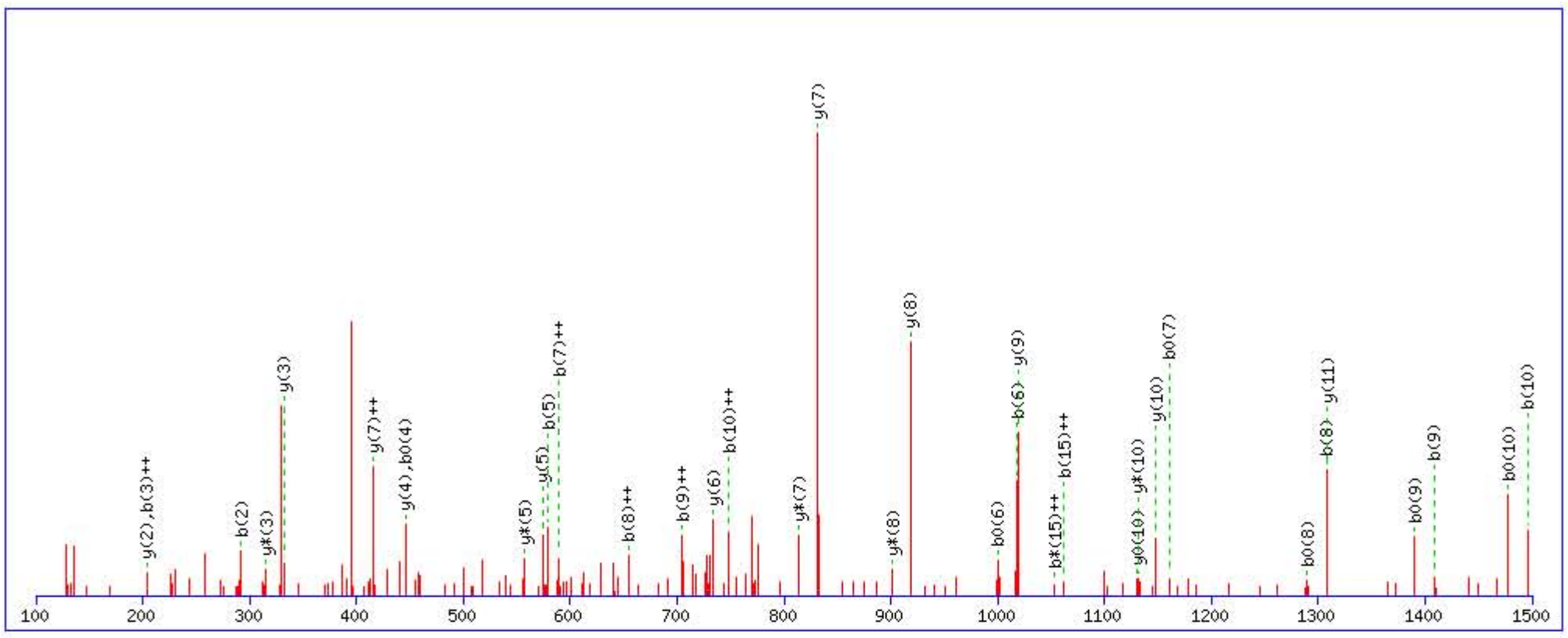
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YKDGDQCETSPCQNQGK**
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

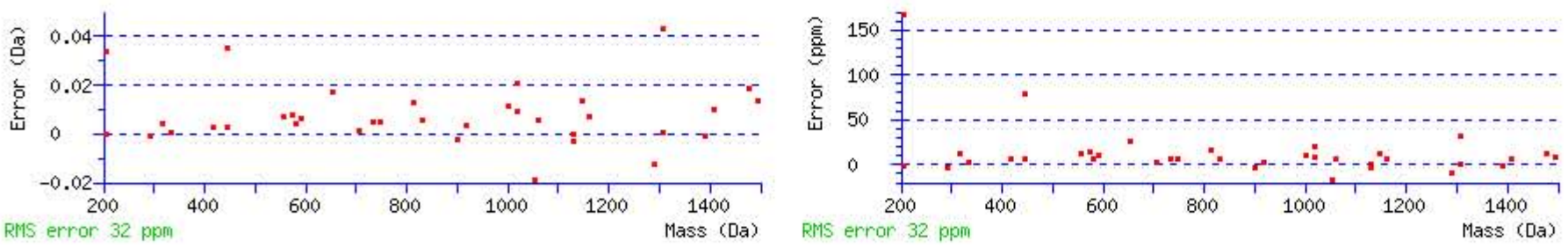
Match to Query 50989: 2325.002952 from(776.008260,3+) rtinseconds(1278) index(45600)
Title: Locus:1.1.1.1682.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2324.982407
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 2e-005
**Matches :** 36/172 fragment ions using 56 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 17 |
| 2 | **292.165568** | 146.586422 | 275.139019 | 138.073148 | | | K | 2162.926352 | 1081.966814 | 2145.899803 | 1073.453539 | 2144.915787 | 1072.961531 | 16 |
| 3 | 407.192511 | **204.099894** | 390.165962 | 195.586619 | 389.181946 | 195.094611 | D | 2034.831389 | 1017.919333 | 2017.804840 | 1009.406058 | 2016.820824 | 1008.914050 | 15 |
| 4 | 464.213975 | 232.610626 | 447.187426 | 224.097351 | 446.203410 | 223.605343 | G | 1919.804446 | 960.405861 | 1902.777897 | 951.892587 | 1901.793881 | 951.400579 | 14 |
| 5 | **579.240918** | 290.124097 | 562.214369 | 281.610823 | 561.230353 | 281.118815 | D | 1862.782982 | 931.895129 | 1845.756433 | 923.381855 | 1844.772417 | 922.889847 | 13 |
| 6 | **1018.466244** | 509.736760 | 1001.439695 | 501.223486 | 1000.455679 | 500.731478 | Q | 1747.756039 | 874.381658 | 1730.729490 | 865.868383 | 1729.745474 | 865.376375 | 12 |
| 7 | 1178.496893 | **589.752085** | 1161.470344 | 581.238810 | 1160.486328 | 580.746802 | C | *1308.530713* | 654.768995 | 1291.504164 | 646.255720 | 1290.520148 | 645.763712 | 11 |
| 8 | **1307.539486** | **654.273381** | 1290.512937 | 645.760107 | 1289.528921 | 645.268098 | E | *1148.500064* | 574.753670 | 1131.473515 | 566.240396 | 1130.489499 | 565.748388 | 10 |
| 9 | **1408.587165** | **704.797220** | 1391.560616 | 696.283946 | 1390.576600 | 695.791938 | T | *1019.457471* | 510.232374 | 1002.430922 | 501.719099 | 1001.446906 | 501.227091 | 9 |
| 10 | **1495.619193** | **748.313235** | 1478.592644 | 739.799960 | 1477.608628 | 739.307952 | S | *918.409792* | 459.708534 | 901.383243 | 451.195260 | 900.399227 | 450.703252 | 8 |
| 11 | 1592.671957 | 796.839617 | 1575.645408 | 788.326342 | 1574.661392 | 787.834334 | P | *831.377764* | 416.192520 | 814.351215 | 407.679246 | | | 7 |
| 12 | 1752.702606 | 876.854941 | 1735.676057 | 868.341667 | 1734.692041 | 867.849659 | C | *734.325000* | 367.666138 | 717.298451 | 359.152864 | | | 6 |
| 13 | 1880.761184 | 940.884230 | 1863.734635 | 932.370956 | 1862.750619 | 931.878948 | Q | *574.294351* | 287.650814 | 557.267802 | 279.137539 | | | 5 |
| 14 | 1994.804111 | 997.905694 | 1977.777562 | 989.392419 | 1976.793546 | 988.900411 | N | *446.235773* | 223.621524 | 429.209224 | 215.108250 | | | 4 |
| 15 | 2122.862689 | **1061.934982** | 2105.836140 | 1053.421708 | 2104.852124 | 1052.929700 | Q | *332.192846* | 166.600061 | 315.166297 | 158.086787 | | | 3 |
| 16 | 2179.884153 | 1090.445714 | 2162.857604 | 1081.932440 | 2161.873588 | 1081.440432 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 17 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.8 | 2324.982407 | 0.020545 | YKDGDQCETSPCQNQGK |

**Mascot:** http://www.matrixscience.com/

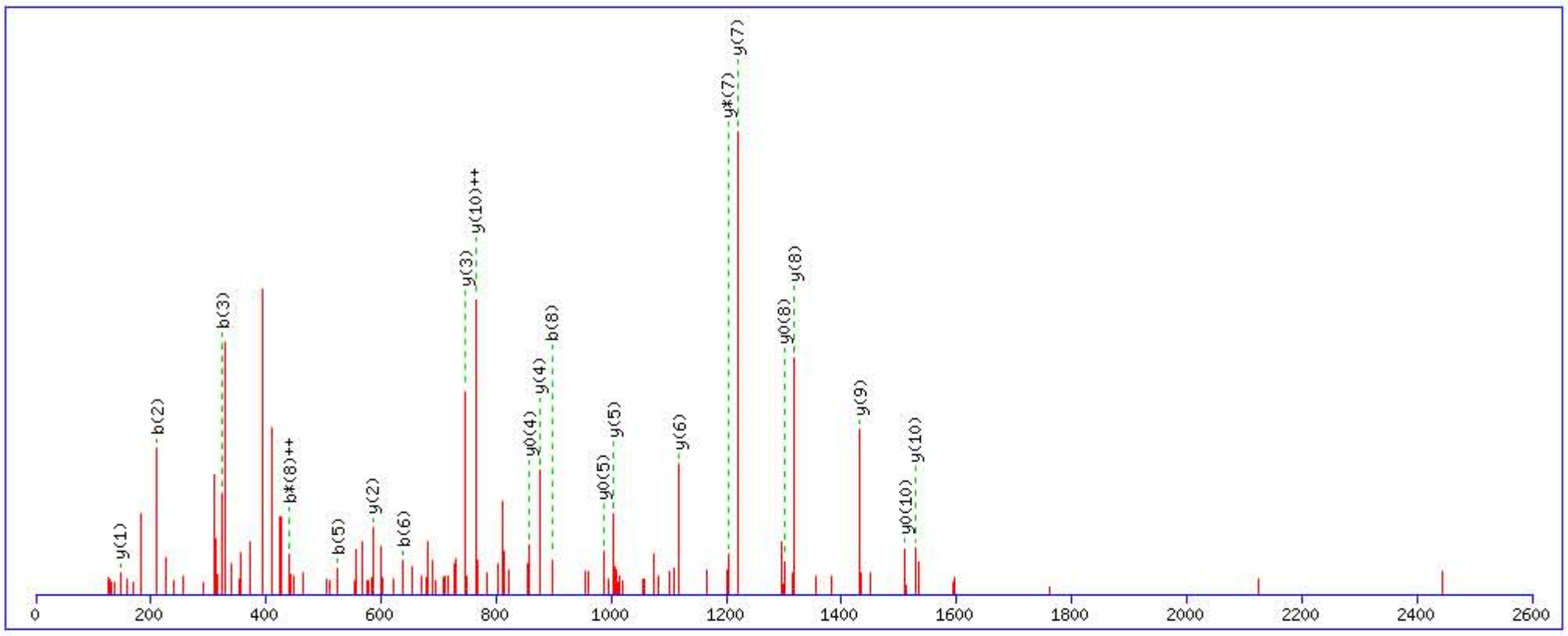
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IPLVTNEECQK**
Found in **FA11_HUMAN**, Coagulation factor XI OS=Homo sapiens GN=F11 PE=1 SV=1

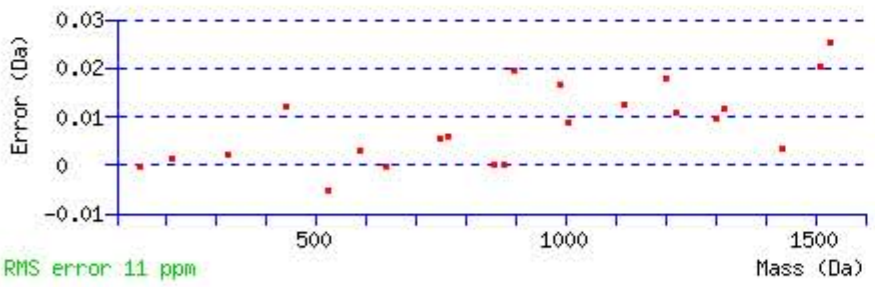
Match to Query 36696: 1640.845548 from(821.430050,2+) rtinseconds(1865) index(65428)
Title: Locus:1.1.1.1924.13 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

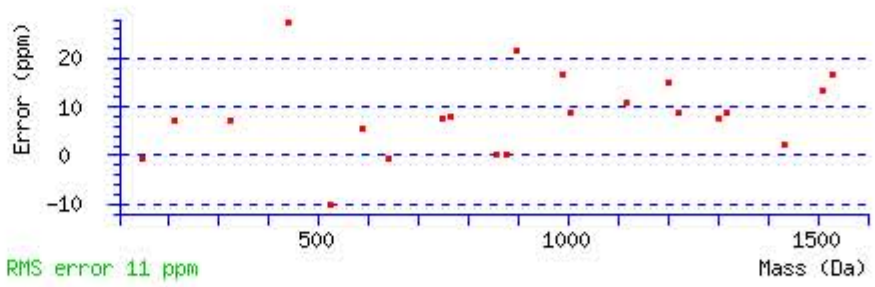
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1640.826584
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 5e-006
**Matches :** 22/96 fragment ions using 44 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 11 |
| 2 | **211.144104** | 106.075690 | | | | | P | *1528.749813* | 764.878545 | 1511.723264 | 756.365270 | 1510.739248 | 755.873262 | 10 |
| 3 | **324.228168** | 162.617722 | | | | | L | *1431.697049* | 716.352163 | 1414.670500 | 707.838888 | 1413.686484 | 707.346880 | 9 |
| 4 | 423.296582 | 212.151929 | | | | | V | *1318.612985* | 659.810131 | 1301.586436 | 651.296856 | 1300.602420 | 650.804848 | 8 |
| 5 | **524.344261** | 262.675769 | | | 506.333696 | 253.670486 | T | *1219.544571* | 610.275924 | 1202.518022 | 601.762649 | 1201.534006 | 601.270641 | 7 |
| 6 | **638.387188** | 319.697232 | 621.360639 | 311.183958 | 620.376623 | 310.691950 | N | *1118.496892* | 559.752084 | 1101.470343 | 551.238810 | 1100.486327 | 550.746802 | 6 |
| 7 | 767.429781 | 384.218529 | 750.403232 | 375.705254 | 749.419216 | 375.213246 | E | *1004.453965* | 502.730621 | 987.427416 | 494.217346 | 986.443400 | 493.725338 | 5 |
| 8 | **896.472374** | 448.739825 | 879.445825 | 440.226551 | 878.461809 | 439.734543 | E | *875.411372* | 438.209324 | 858.384823 | 429.696050 | 857.400807 | 429.204042 | 4 |
| 9 | 1056.503023 | 528.755150 | 1039.476474 | 520.241875 | 1038.492458 | 519.749867 | C | *746.368779* | 373.688028 | 729.342230 | 365.174753 | | | 3 |
| 10 | 1495.728349 | 748.367813 | 1478.701800 | 739.854538 | 1477.717784 | 739.362530 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 11 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.7 | 1640.826584 | 0.018964 | IPLVTNEECQK |
| 2.2 | 1640.862961 | -0.017413 | LPVTKMKYSGNLMK |

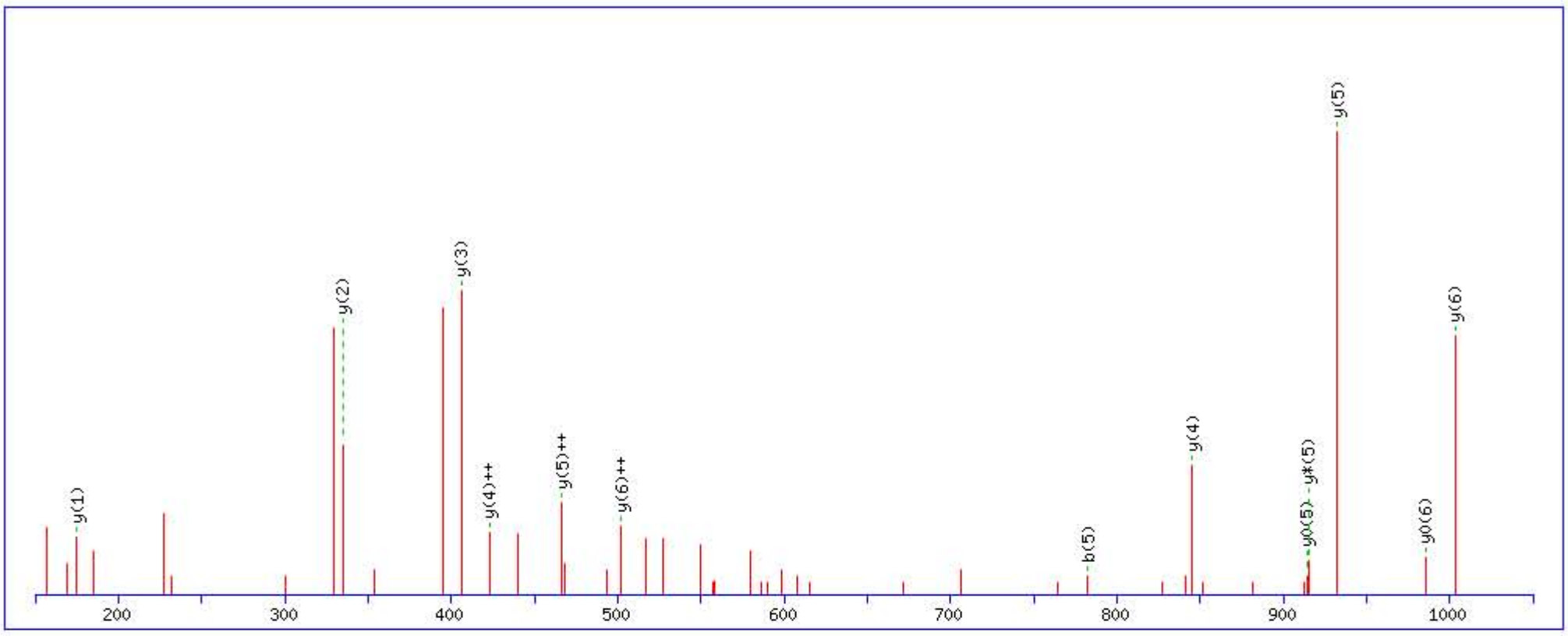
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LASQACR**
Found in **FA12_HUMAN**, Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3

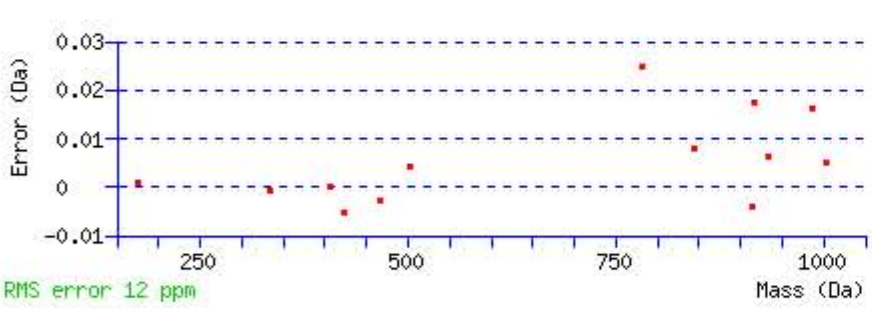
Match to Query 17133: 1115.556188 from(558.785370,2+) rtinseconds(1343) index(1572)
Title: Locus:1.1.1.1744.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

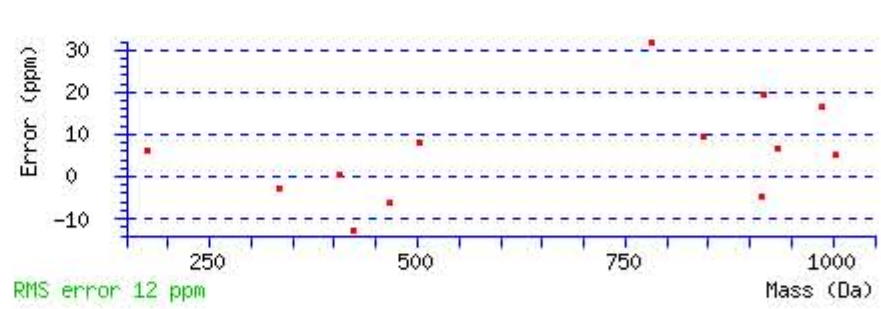
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1115.557953
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0029
**Matches :** 13/54 fragment ions using 25 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 7 |
| 2 | 185.128454 | 93.067865 | | | | | A | *1003.481183* | 502.244230 | 986.454634 | 493.730955 | 985.470618 | 493.238947 | 6 |
| 3 | 272.160482 | 136.583879 | | | 254.149917 | 127.578596 | S | *932.444069* | 466.725673 | 915.417520 | 458.212398 | 914.433504 | 457.720390 | 5 |
| 4 | 711.385808 | 356.196542 | 694.359259 | 347.683268 | 693.375243 | 347.191260 | Q | *845.412041* | 423.209659 | 828.385492 | 414.696384 | | | 4 |
| 5 | 782.422922 | 391.715099 | 765.396373 | 383.201824 | 764.412357 | 382.709816 | A | *406.186715* | 203.596995 | 389.160166 | 195.083721 | | | 3 |
| 6 | 942.453571 | 471.730424 | 925.427022 | 463.217149 | 924.443006 | 462.725141 | C | *335.149601* | 168.078438 | 318.123052 | 159.565164 | | | 2 |
| 7 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.0 | 1115.557953 | -0.001765 | LASQACR |
| 5.6 | 1115.550552 | 0.005636 | LAAGSRCPER |
| 1.0 | 1115.546722 | 0.009466 | LAQDACK |
| 0.0 | 1115.569199 | -0.013011 | QSRVCR |

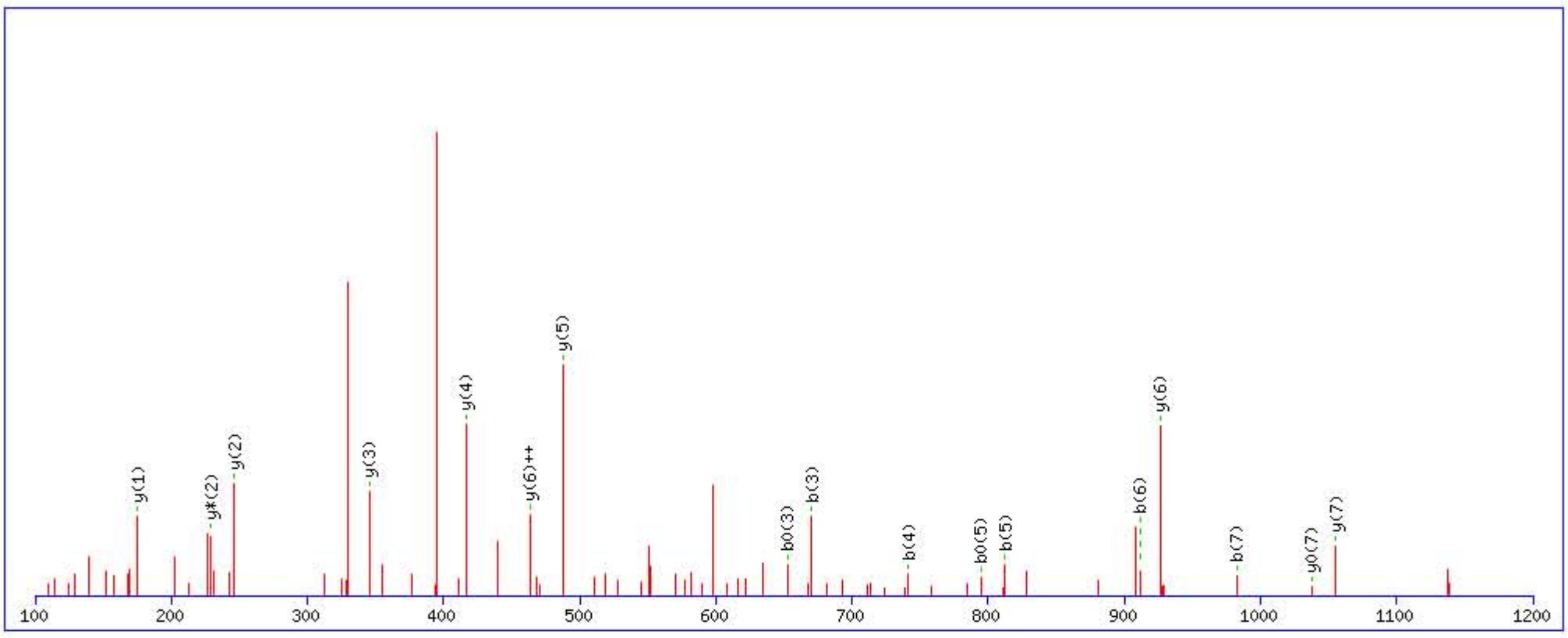
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TEQAAVAR**
Found in **FA12_HUMAN**, Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3

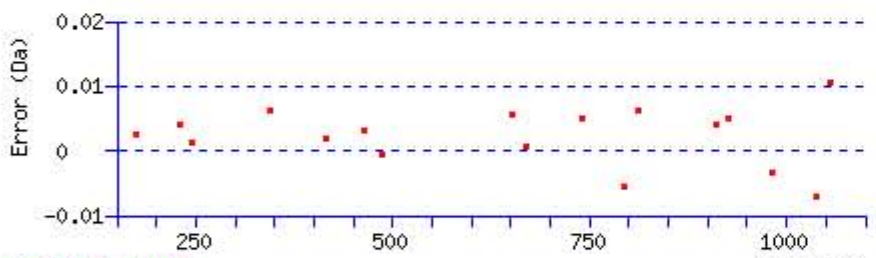
Match to Query 19101: 1155.605528 from(578.810040,2+) rtinseconds(1371) index(62575)
Title: Locus:1.1.1.1752.23 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

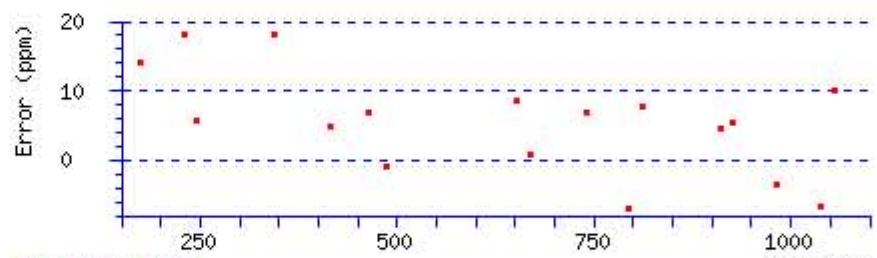
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1155.607010
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 42 **Expect:** 0.0012
**Matches :** 17/68 fragment ions using 31 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 8 |
| 2 | 231.097548 | 116.052412 | | | 213.086983 | 107.047130 | E | *1055.566627* | 528.286951 | 1038.540078 | 519.773677 | 1037.556062 | 519.281669 | 7 |
| 3 | **670.322874** | 335.665075 | 653.296325 | 327.151801 | 652.312309 | 326.659793 | Q | *926.524034* | 463.765655 | 909.497485 | 455.252380 | | | 6 |
| 4 | **741.359988** | 371.183632 | 724.333439 | 362.670358 | 723.349423 | 362.178350 | A | *487.298708* | 244.152992 | 470.272159 | 235.639717 | | | 5 |
| 5 | **812.397102** | 406.702189 | 795.370553 | 398.188915 | 794.386537 | 397.696907 | A | *416.261594* | 208.634435 | 399.235045 | 200.121160 | | | 4 |
| 6 | **911.465516** | 456.236396 | 894.438967 | 447.723121 | 893.454951 | 447.231113 | V | *345.224480* | 173.115878 | 328.197931 | 164.602603 | | | 3 |
| 7 | **982.502630** | 491.754953 | 965.476081 | 483.241678 | 964.492065 | 482.749670 | A | *246.156066* | 123.581671 | 229.129517 | 115.068396 | | | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 42.3 | 1155.607010 | -0.001482 | TEQAAVAR |
| 10.5 | 1155.588394 | 0.017134 | VEQIEAGTPGR |
| 8.2 | 1155.607025 | -0.001497 | VQDSAVAR |
| 8.1 | 1155.607025 | -0.001497 | AMAAVPQDVVR |
| 5.5 | 1155.610855 | -0.005327 | GAGAGLSRPGSAR |
| 4.7 | 1155.588379 | 0.017149 | TEVPLAENQR |
| 3.9 | 1155.599594 | 0.005934 | TKESKHEAAR |
| 3.9 | 1155.607010 | -0.001482 | QQLETAR |
| 3.7 | 1155.607010 | -0.001482 | QQLETAR |
| 3.6 | 1155.614883 | -0.009355 | RSGDWLLPGR |

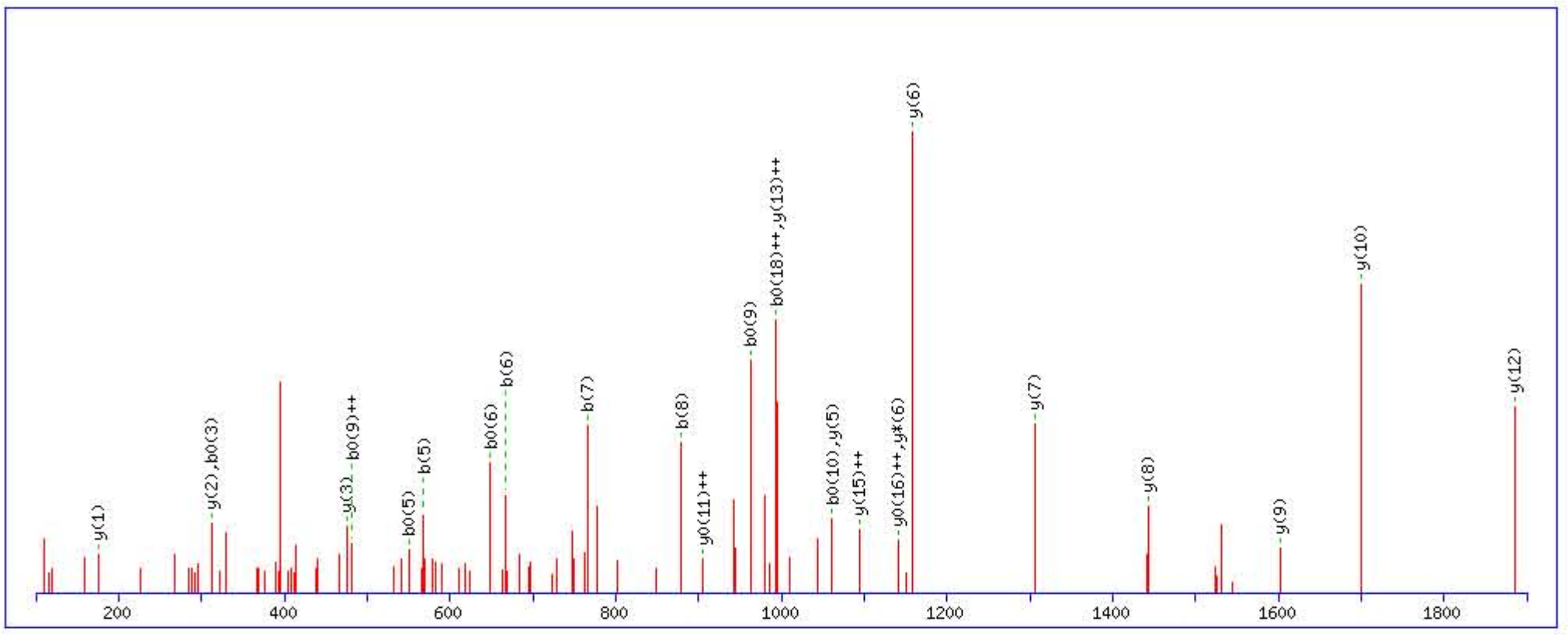
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AEEHTVVLTVTGEPCHFPFQYHR**
Found in **FA12_HUMAN**, Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3

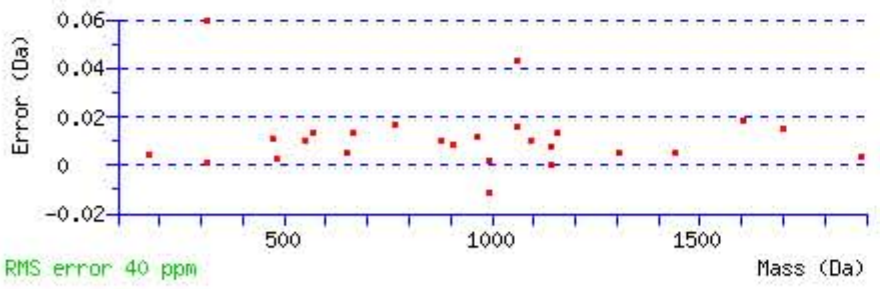
Match to Query 60577: 3064.498736 from(767.131960,4+) rtinseconds(2147) index(67300)
Title: Locus:1.1.1.2022.23 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

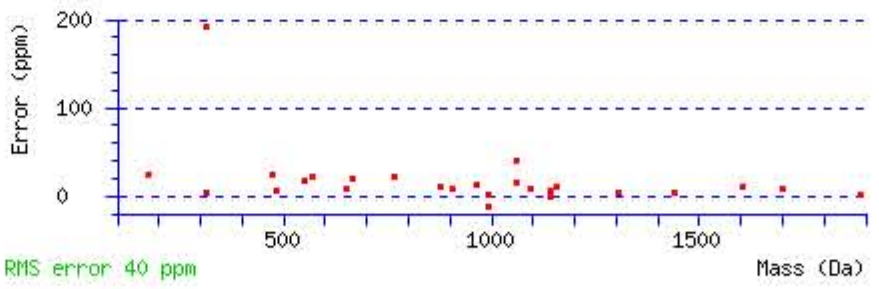
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3064.468796
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q20 : Biotin:Thermo-21345 (Q)
**Ions Score:** 63 **Expect:** 1.3e-005
**Matches** : 26/204 fragment ions using 31 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 23 |
| 2 | 201.086983 | 101.047130 | | | 183.076418 | 92.041847 | E | 2994.438934 | 1497.723105 | 2977.412385 | 1489.209830 | 2976.428369 | 1488.717822 | 22 |
| 3 | 330.129576 | 165.568426 | | | 312.119011 | 156.563144 | E | 2865.396341 | 1433.201808 | 2848.369792 | 1424.688534 | 2847.385776 | 1424.196526 | 21 |
| 4 | 467.188488 | 234.097882 | | | 449.177923 | 225.092599 | H | 2736.353748 | 1368.680512 | 2719.327199 | 1360.167237 | 2718.343183 | 1359.675229 | 20 |
| 5 | **568.236167** | 284.621722 | | | 550.225602 | 275.616439 | T | 2599.294836 | 1300.151056 | 2582.268287 | 1291.637781 | 2581.284271 | 1291.145773 | 19 |
| 6 | **667.304581** | 334.155929 | | | 649.294016 | 325.150646 | V | 2498.247157 | 1249.627216 | 2481.220608 | 1241.113942 | 2480.236592 | 1240.621934 | 18 |
| 7 | **766.372995** | 383.690136 | | | 748.362430 | 374.684853 | V | 2399.178743 | 1200.093009 | 2382.152194 | 1191.579735 | 2381.168178 | 1191.087727 | 17 |
| 8 | **879.457059** | 440.232168 | | | 861.446494 | 431.226885 | L | 2300.110329 | 1150.558802 | 2283.083780 | 1142.045528 | 2282.099764 | 1141.553520 | 16 |
| 9 | 980.504738 | 490.756007 | | | 962.494173 | 481.750724 | T | 2187.026265 | 1094.016770 | 2169.999716 | 1085.503496 | 2169.015700 | 1085.011488 | 15 |
| 10 | 1079.573152 | 540.290214 | | | 1061.562587 | 531.284931 | V | 2085.978586 | 1043.492931 | 2068.952037 | 1034.979656 | 2067.968021 | 1034.487648 | 14 |
| 11 | 1180.620831 | 590.814054 | | | 1162.610266 | 581.808771 | T | 1986.910172 | 993.958724 | 1969.883623 | 985.445450 | 1968.899607 | 984.953442 | 13 |
| 12 | 1237.642295 | 619.324785 | | | 1219.631730 | 610.319503 | G | *1885.862493* | 943.434885 | 1868.835944 | 934.921610 | 1867.851928 | 934.429602 | 12 |
| 13 | 1366.684888 | 683.846082 | | | 1348.674323 | 674.840800 | E | 1828.841029 | 914.924153 | 1811.814480 | 906.410878 | 1810.830464 | 905.918870 | 11 |
| 14 | 1463.737652 | 732.372464 | | | 1445.727087 | 723.367182 | P | *1699.798436* | 850.402856 | 1682.771887 | 841.889582 | | | 10 |
| 15 | 1623.768301 | 812.387789 | | | 1605.757736 | 803.382506 | C | *1602.745672* | 801.876474 | 1585.719123 | 793.363200 | | | 9 |
| 16 | 1760.827213 | 880.917245 | | | 1742.816648 | 871.911962 | H | *1442.715023* | 721.861150 | 1425.688474 | 713.347875 | | | 8 |
| 17 | 1907.895627 | 954.451452 | | | 1889.885062 | 945.446169 | F | *1305.656111* | 653.331694 | 1288.629562 | 644.818419 | | | 7 |
| 18 | 2004.948391 | 1002.977834 | | | 1986.937826 | 993.972551 | P | *1158.587697* | 579.797487 | 1141.561148 | 571.284212 | | | 6 |
| 19 | 2152.016805 | 1076.512040 | | | 2134.006240 | 1067.506758 | F | *1061.534933* | 531.271105 | 1044.508384 | 522.757830 | | | 5 |
| 20 | 2591.242131 | 1296.124703 | 2574.215582 | 1287.611429 | 2573.231566 | 1287.119421 | Q | 914.466519 | 457.736898 | 897.439970 | 449.223623 | | | 4 |
| 21 | 2754.305460 | 1377.656368 | 2737.278911 | 1369.143093 | 2736.294895 | 1368.651085 | Y | *475.241193* | 238.124234 | 458.214644 | 229.610960 | | | 3 |
| 22 | 2891.364372 | 1446.185824 | 2874.337823 | 1437.672549 | 2873.353807 | 1437.180541 | H | *312.177864* | 156.592570 | 295.151315 | 148.079295 | | | 2 |
| 23 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 63.1 | 3064.468796 | 0.029940 | AEEHTVVLTVTGEPCHFPFQYHR |

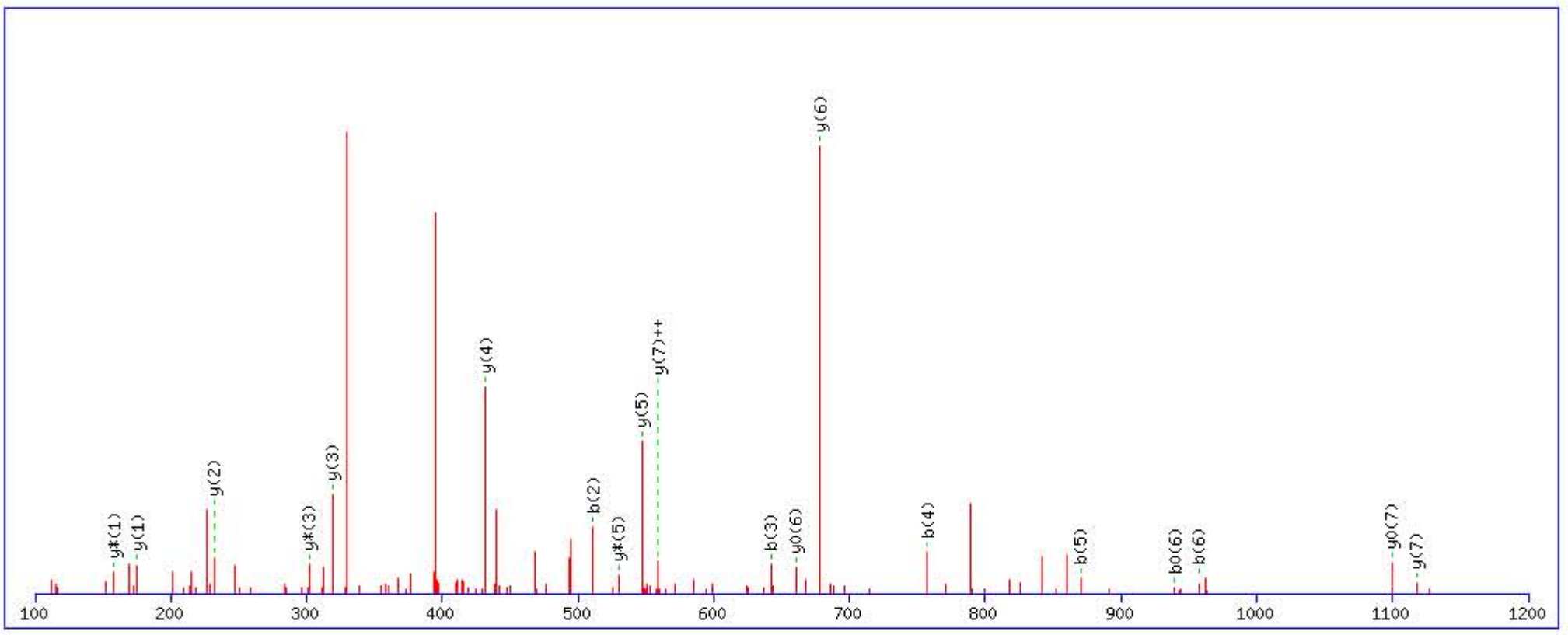
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AQMDLSGR**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

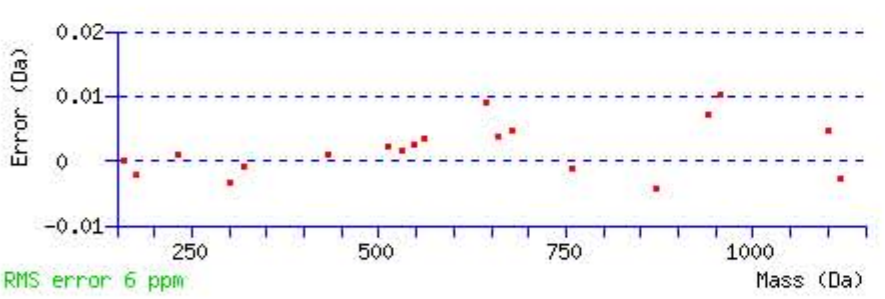
Match to Query 20228: 1187.580408 from(594.797480,2+) rtinseconds(1723) index(3908)
Title: Locus:1.1.1.1877.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

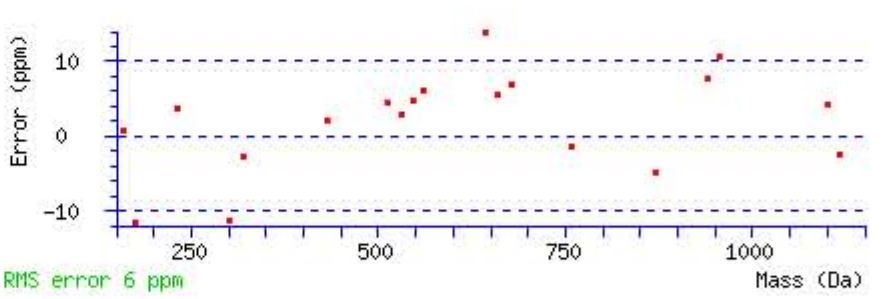
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1187.579086
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.0003
**Matches :** 19/72 fragment ions using 31 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 8 |
| 2 | **511.269716** | 256.138496 | 494.243167 | 247.625221 | | | Q | *1117.549262* | 559.278269 | 1100.522713 | 550.764995 | 1099.538697 | 550.272987 | 7 |
| 3 | **642.310201** | 321.658739 | 625.283652 | 313.145464 | | | M | *678.323936* | 339.665606 | 661.297387 | 331.152332 | 660.313371 | 330.660324 | 6 |
| 4 | **757.337144** | 379.172210 | 740.310595 | 370.658935 | 739.326579 | 370.166927 | D | *547.283451* | 274.145364 | 530.256902 | 265.632089 | 529.272886 | 265.140081 | 5 |
| 5 | **870.421208** | 435.714242 | 853.394659 | 427.200967 | 852.410643 | 426.708959 | L | *432.256508* | 216.631892 | 415.229959 | 208.118617 | 414.245943 | 207.626609 | 4 |
| 6 | **957.453236** | 479.230256 | 940.426687 | 470.716981 | 939.442671 | 470.224973 | S | *319.172444* | 160.089860 | 302.145895 | 151.576585 | 301.161879 | 151.084577 | 3 |
| 7 | 1014.474700 | 507.740988 | 997.448151 | 499.227713 | 996.464135 | 498.735705 | G | *232.140416* | 116.573846 | 215.113867 | 108.060571 | | | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 44.0 | 1187.579086 | 0.001322 | AQMDLSGR |
| 6.1 | 1187.568314 | 0.012094 | QREDIWEGR |
| 5.6 | 1187.578201 | 0.002207 | SSLENEPSLGR |
| 4.1 | 1187.579086 | 0.001322 | QAAEVMGR |
| 3.5 | 1187.593475 | -0.013067 | AESFPNTPLGR |
| 0.3 | 1187.575714 | 0.004694 | YQDAAGPR |

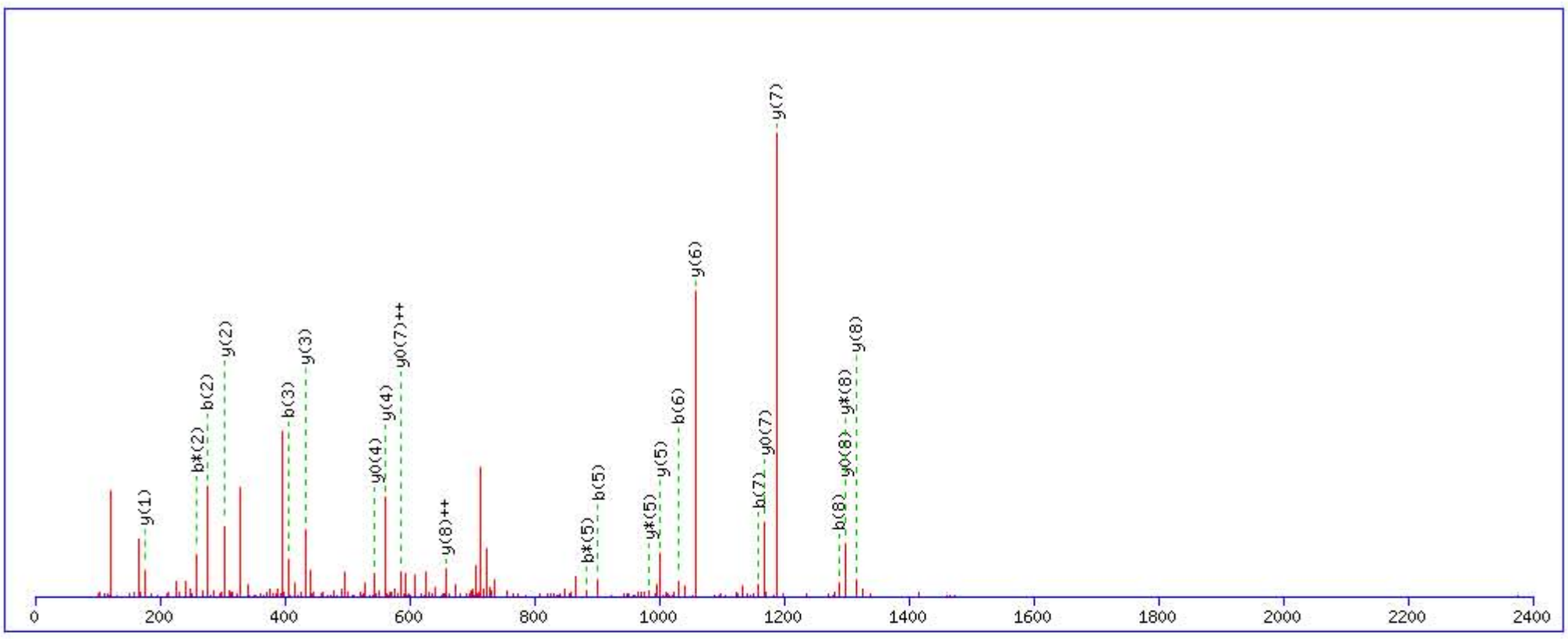
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FQEGQEEER**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

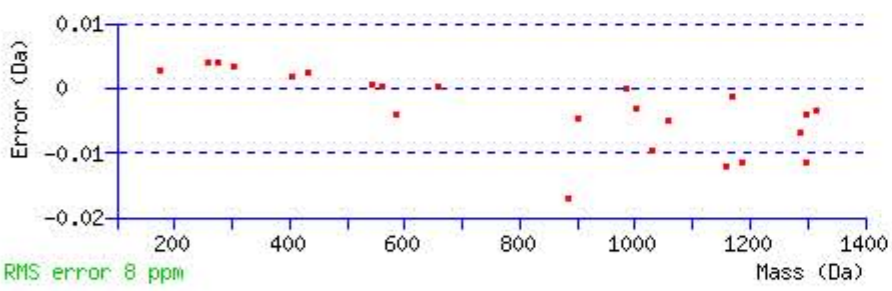
Match to Query 29976: 1461.657548 from(731.836050,2+) rtinseconds(1455) index(16593)
Title: Locus:1.1.1.2889.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

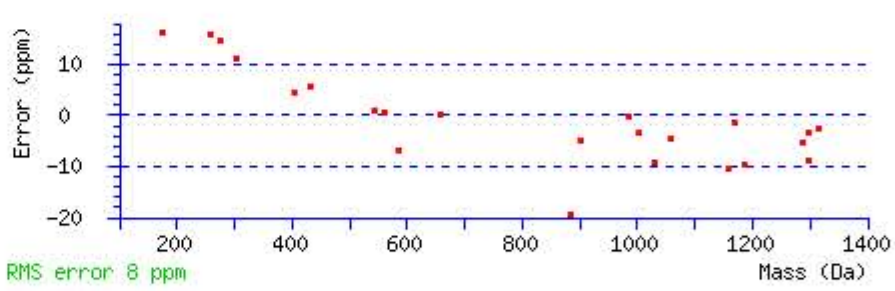
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1461.655807
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 0.00012
**Matches :** 23/88 fragment ions using 41 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 9 |
| 2 | **276.134268** | 138.570772 | 259.107719 | 130.057497 | | | Q | *1315.594692* | 658.300984 | 1298.568143 | 649.787710 | 1297.584127 | 649.295702 | 8 |
| 3 | **405.176861** | 203.092068 | 388.150312 | 194.578794 | 387.166296 | 194.086786 | E | *1187.536114* | 594.271695 | 1170.509565 | 585.758421 | 1169.525549 | 585.266413 | 7 |
| 4 | 462.198325 | 231.602800 | 445.171776 | 223.089526 | 444.187760 | 222.597518 | G | *1058.493521* | 529.750399 | 1041.466972 | 521.237124 | 1040.482956 | 520.745116 | 6 |
| 5 | **901.423651** | 451.215464 | 884.397102 | 442.702189 | 883.413086 | 442.210181 | Q | *1001.472057* | 501.239667 | 984.445508 | 492.726392 | 983.461492 | 492.234384 | 5 |
| 6 | **1030.466244** | 515.736760 | 1013.439695 | 507.223485 | 1012.455679 | 506.731477 | E | *562.246731* | 281.627004 | 545.220182 | 273.113729 | 544.236166 | 272.621721 | 4 |
| 7 | **1159.508837** | 580.258057 | 1142.482288 | 571.744782 | 1141.498272 | 571.252774 | E | *433.204138* | 217.105707 | 416.177589 | 208.592433 | 415.193573 | 208.100425 | 3 |
| 8 | **1288.551430** | 644.779353 | 1271.524881 | 636.266079 | 1270.540865 | 635.774071 | E | *304.161545* | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 9 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.1 | 1461.655807 | 0.001741 | FQEGQEEER |
| 11.5 | 1461.640564 | 0.016984 | NSGTQSDGEEK |
| 10.8 | 1461.655807 | 0.001741 | FQEGQEEER |
| 9.1 | 1461.640564 | 0.016984 | VMTDVAGNPEEER |
| 7.8 | 1461.648392 | 0.009156 | HREELSDYEER |
| 5.2 | 1461.637161 | 0.020387 | ESELQWQEEER |
| 5.1 | 1461.677811 | -0.020263 | MSQMASVPER |
| 0.8 | 1461.676956 | -0.019408 | MSGQVGDLSPSQEK |

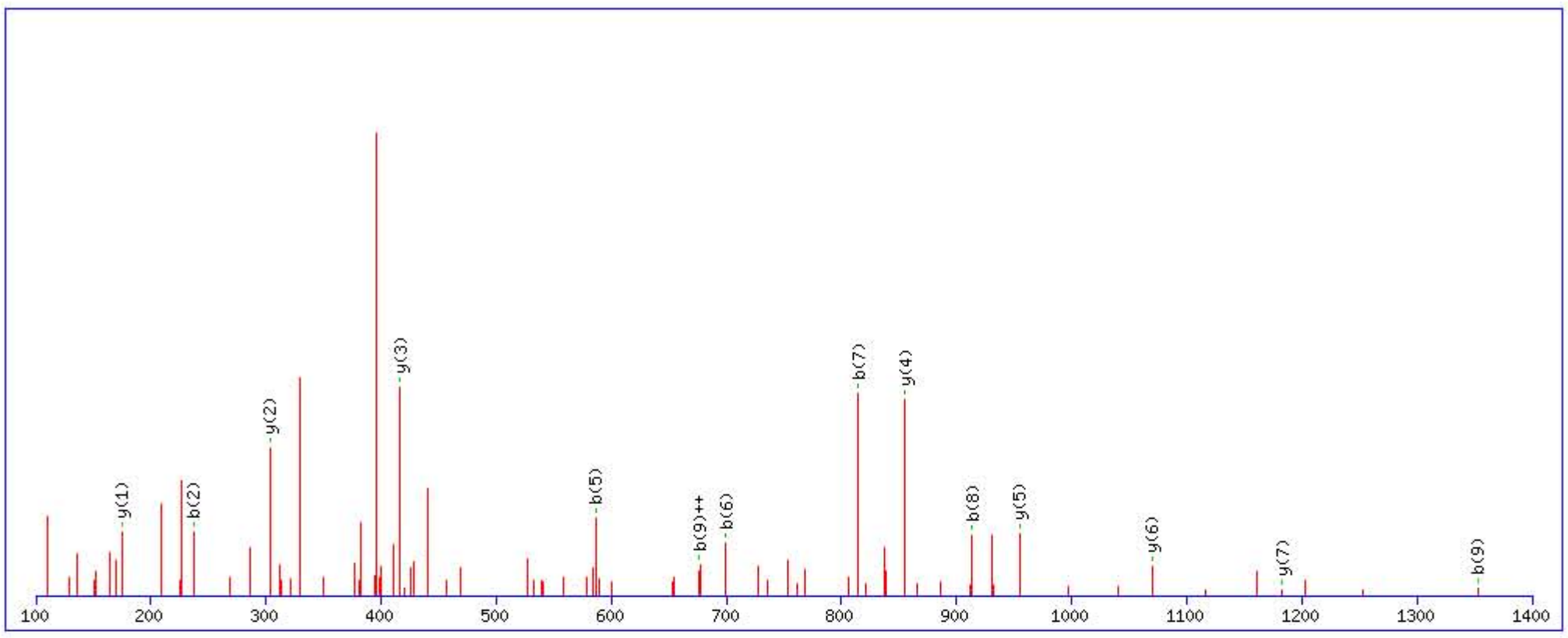
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HVYGELDVQIQR**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

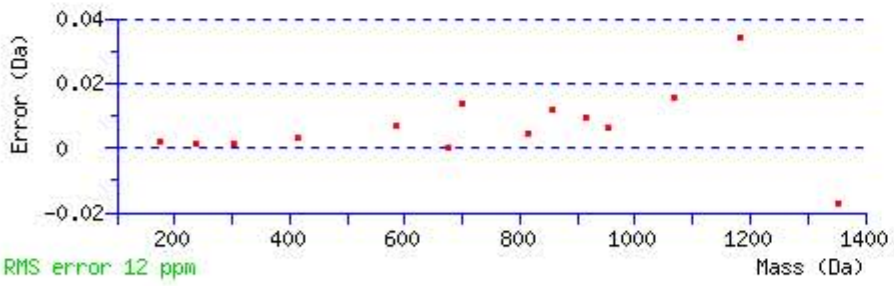
Match to Query 39506: 1766.918532 from(589.980120,3+) rtinseconds(1966) index(66259)
Title: Locus:1.1.1.1959.20 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

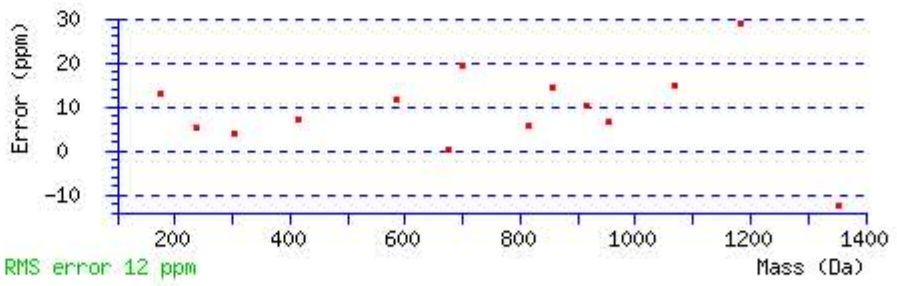
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1766.913773
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 28 **Expect:** 0.0083
**Matches :** 14/98 fragment ions using 34 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 12 |
| 2 | *237.134602* | 119.070939 | | | | | V | 1630.862141 | 815.934708 | 1613.835592 | 807.421434 | 1612.851576 | 806.929426 | 11 |
| 3 | 400.197931 | 200.602603 | | | | | Y | 1531.793727 | 766.400501 | 1514.767178 | 757.887227 | 1513.783162 | 757.395219 | 10 |
| 4 | 457.219395 | 229.113335 | | | | | G | 1368.730398 | 684.868837 | 1351.703849 | 676.355563 | 1350.719833 | 675.863554 | 9 |
| 5 | *586.261988* | 293.634632 | | | 568.251423 | 284.629349 | E | 1311.708934 | 656.358105 | 1294.682385 | 647.844830 | 1293.698369 | 647.352822 | 8 |
| 6 | *699.346052* | 350.176664 | | | 681.335487 | 341.171382 | L | *1182.666341* | 591.836808 | 1165.639792 | 583.323534 | 1164.655776 | 582.831526 | 7 |
| 7 | *814.372995* | 407.690136 | | | 796.362430 | 398.684853 | D | *1069.582277* | 535.294776 | 1052.555728 | 526.781502 | 1051.571712 | 526.289494 | 6 |
| 8 | *913.441409* | 457.224342 | | | 895.430844 | 448.219060 | V | *954.555334* | 477.781305 | 937.528785 | 469.268030 | | | 5 |
| 9 | *1352.666735* | 676.837006 | 1335.640186 | 668.323731 | 1334.656170 | 667.831723 | Q | *855.486920* | 428.247098 | 838.460371 | 419.733823 | | | 4 |
| 10 | 1465.750799 | 733.379037 | 1448.724250 | 724.865763 | 1447.740234 | 724.373755 | I | *416.261594* | 208.634435 | 399.235045 | 200.121160 | | | 3 |
| 11 | 1593.809377 | 797.408326 | 1576.782828 | 788.895052 | 1575.798812 | 788.403044 | Q | *303.177530* | 152.092403 | 286.150981 | 143.579128 | | | 2 |
| 12 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 27.6 | 1766.913773 | 0.004759 | HVYGELDVQIQR |
| 16.7 | 1766.913773 | 0.004759 | HVYGELDVQIQR |
| 5.4 | 1766.924988 | -0.006456 | GNFPVEAVKMQHAIAR |

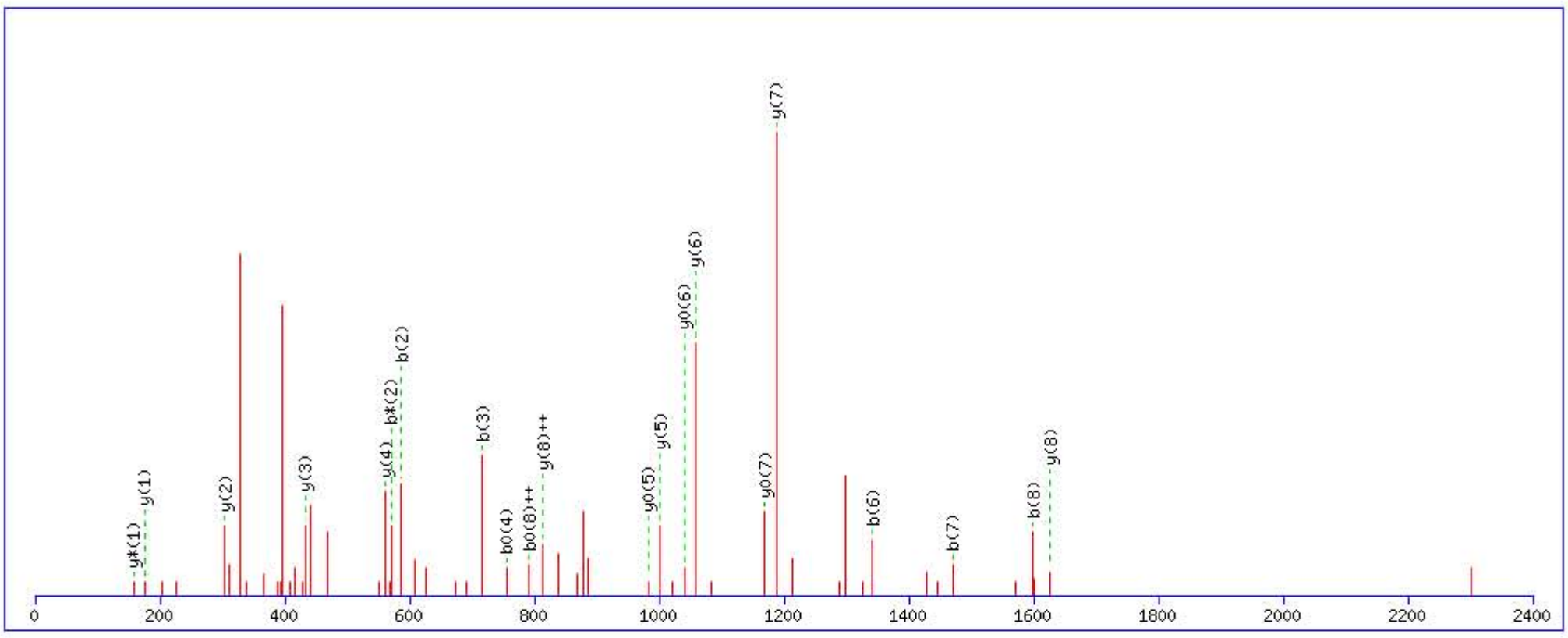
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FQEGQEEER**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

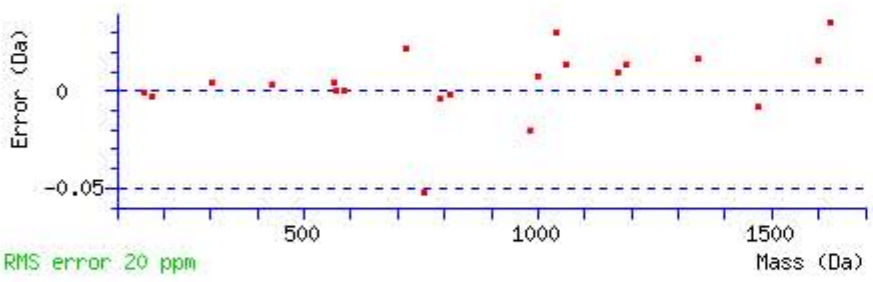
Match to Query 39703: 1772.819908 from(887.417230,2+) rtinseconds(1822) index(65262)
Title: Locus:1.1.1.1909.12 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

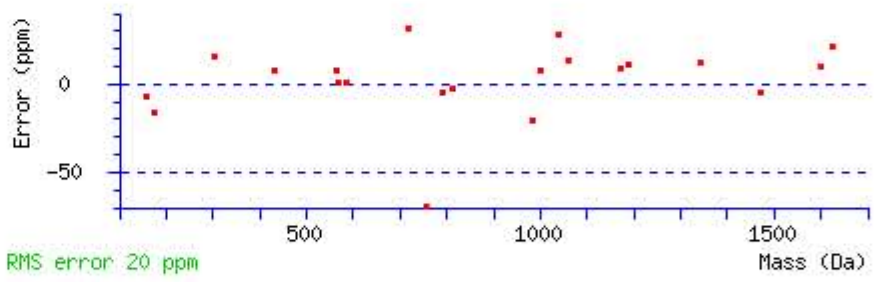
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1772.822556
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 42 **Expect:** 0.0026
**Matches :** 21/88 fragment ions using 41 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 9 |
| 2 | 587.301016 | 294.154146 | 570.274467 | 285.640872 | | | Q | *1626.761440* | 813.884358 | 1609.734891 | 805.371084 | 1608.750875 | 804.879076 | 8 |
| 3 | 716.343609 | 358.675443 | 699.317060 | 350.162168 | 698.333044 | 349.670160 | E | *1187.536114* | 594.271695 | 1170.509565 | 585.758421 | 1169.525549 | 585.266413 | 7 |
| 4 | 773.365073 | 387.186175 | 756.338524 | 378.672900 | 755.354508 | 378.180892 | G | *1058.493521* | 529.750399 | 1041.466972 | 521.237124 | 1040.482956 | 520.745116 | 6 |
| 5 | 1212.590399 | 606.798837 | 1195.563850 | 598.285563 | 1194.579834 | 597.793555 | Q | *1001.472057* | 501.239667 | 984.445508 | 492.726392 | 983.461492 | 492.234384 | 5 |
| 6 | 1341.632992 | 671.320134 | 1324.606443 | 662.806860 | 1323.622427 | 662.314852 | E | *562.246731* | 281.627004 | 545.220182 | 273.113729 | 544.236166 | 272.621721 | 4 |
| 7 | 1470.675585 | 735.841431 | 1453.649036 | 727.328156 | 1452.665020 | 726.836148 | E | *433.204138* | 217.105707 | 416.177589 | 208.592433 | 415.193573 | 208.100425 | 3 |
| 8 | 1599.718178 | 800.362727 | 1582.691629 | 791.849453 | 1581.707613 | 791.357445 | E | *304.161545* | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 9 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 42.1 | 1772.822556 | -0.002648 | FQEGQEEER |
| 24.0 | 1772.803909 | 0.015999 | ESELQWQEEER |
| 5.1 | 1772.828873 | -0.008965 | QAEQEATVAREEQER |
| 4.6 | 1772.798752 | 0.021156 | HISSCMRWPGHYSR |
| 4.3 | 1772.803909 | 0.015999 | ESELQWQEEER |
| 4.2 | 1772.836288 | -0.016380 | ADGSLTGGGLEAAAMAPER |
| 3.6 | 1772.842789 | -0.022881 | ESSPPEKEEAQEKTGK |
| 3.2 | 1772.811127 | 0.008781 | QHELSESCSASALQAR |
| 2.8 | 1772.811798 | 0.008110 | YQTPPHQNFEDLER |
| 2.3 | 1772.803909 | 0.015999 | DMASPNWSILPEEER |

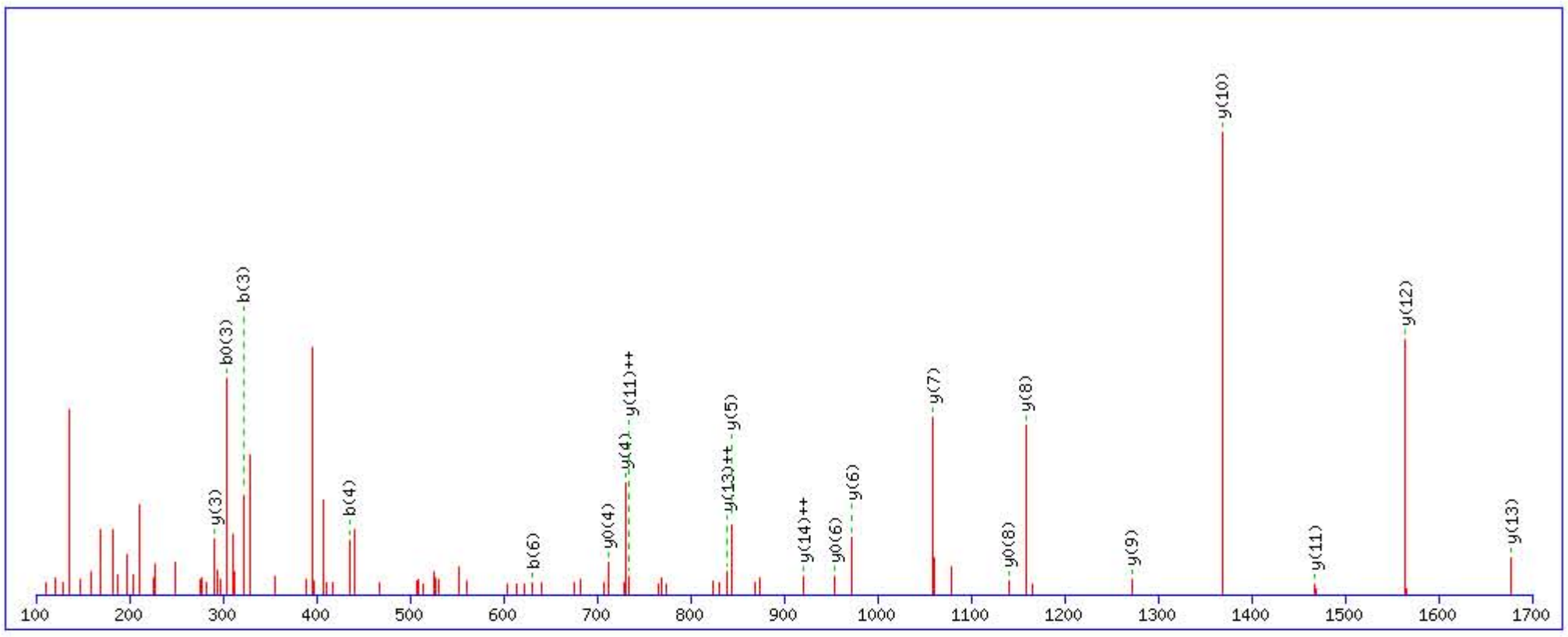
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GTYIPVPIVSELQSGK**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

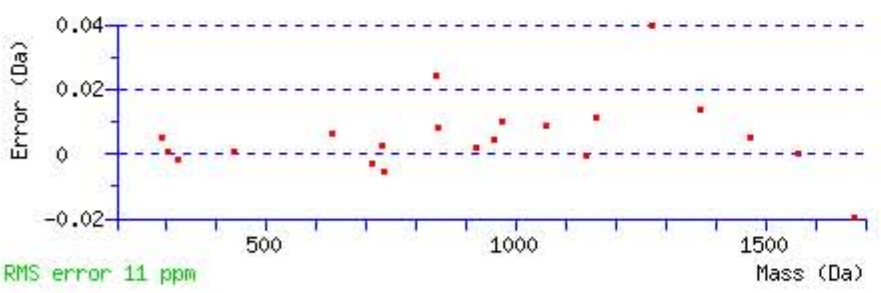
Match to Query 44070: 1998.101232 from(667.041020,3+) rtinseconds(2757) index(9675)
Title: Locus:1.1.1.2237.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

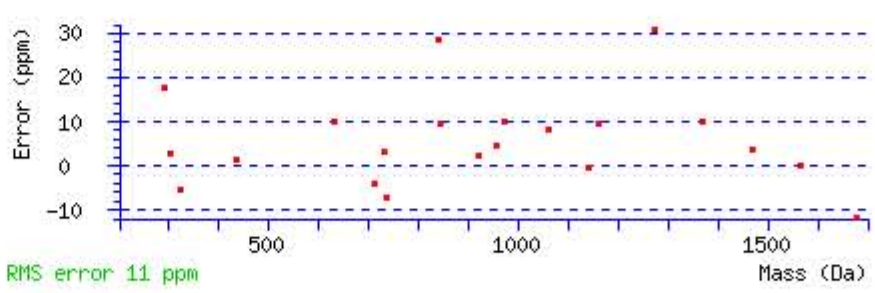
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1998.085983
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 64 **Expect:** 2.3e-006
**Matches :** 21/150 fragment ions using 41 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 16 |
| 2 | 159.076419 | 80.041847 | | | 141.065854 | 71.036565 | T | 1942.071799 | 971.539538 | 1925.045250 | 963.026263 | 1924.061234 | 962.534255 | 15 |
| 3 | **322.139748** | 161.573512 | | | 304.129183 | 152.568230 | Y | 1841.024120 | 921.015698 | 1823.997571 | 912.502424 | 1823.013555 | 912.010416 | 14 |
| 4 | **435.223812** | 218.115544 | | | 417.213247 | 209.110262 | I | *1677.960791* | 839.484034 | 1660.934242 | 830.970759 | 1659.950226 | 830.478751 | 13 |
| 5 | 532.276576 | 266.641926 | | | 514.266011 | 257.636644 | P | *1564.876727* | 782.942002 | 1547.850178 | 774.428727 | 1546.866162 | 773.936719 | 12 |
| 6 | **631.344990** | 316.176133 | | | 613.334425 | 307.170851 | V | *1467.823963* | 734.415620 | 1450.797414 | 725.902345 | 1449.813398 | 725.410337 | 11 |
| 7 | 728.397754 | 364.702515 | | | 710.387189 | 355.697233 | P | *1368.755549* | 684.881413 | 1351.729000 | 676.368138 | 1350.744984 | 675.876130 | 10 |
| 8 | 841.481818 | 421.244547 | | | 823.471253 | 412.239265 | I | *1271.702785* | 636.355031 | 1254.676236 | 627.841756 | 1253.692220 | 627.349748 | 9 |
| 9 | 940.550232 | 470.778754 | | | 922.539667 | 461.773472 | V | *1158.618721* | 579.812999 | 1141.592172 | 571.299724 | 1140.608156 | 570.807716 | 8 |
| 10 | 1027.582260 | 514.294768 | | | 1009.571695 | 505.289486 | S | *1059.550307* | 530.278792 | 1042.523758 | 521.765517 | 1041.539742 | 521.273509 | 7 |
| 11 | 1156.624853 | 578.816065 | | | 1138.614288 | 569.810782 | E | *972.518279* | 486.762777 | 955.491730 | 478.249503 | 954.507714 | 477.757495 | 6 |
| 12 | 1269.708917 | 635.358096 | | | 1251.698352 | 626.352814 | L | *843.475686* | 422.241481 | 826.449137 | 413.728207 | 825.465121 | 413.236199 | 5 |
| 13 | 1708.934243 | 854.970759 | 1691.907694 | 846.457485 | 1690.923678 | 845.965477 | Q | *730.391622* | 365.699449 | 713.365073 | 357.186175 | 712.381057 | 356.694167 | 4 |
| 14 | 1795.966271 | 898.486774 | 1778.939722 | 889.973499 | 1777.955706 | 889.481491 | S | *291.166296* | 146.086786 | 274.139747 | 137.573512 | 273.155731 | 137.081504 | 3 |
| 15 | 1852.987735 | 926.997505 | 1835.961186 | 918.484231 | 1834.977170 | 917.992223 | G | 204.134268 | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 64.1 | 1998.085983 | 0.015249 | GTYIPVPIVSELQSGK |
| 4.0 | 1998.099731 | 0.001501 | GDEVVVELVENGKKVTVGK |

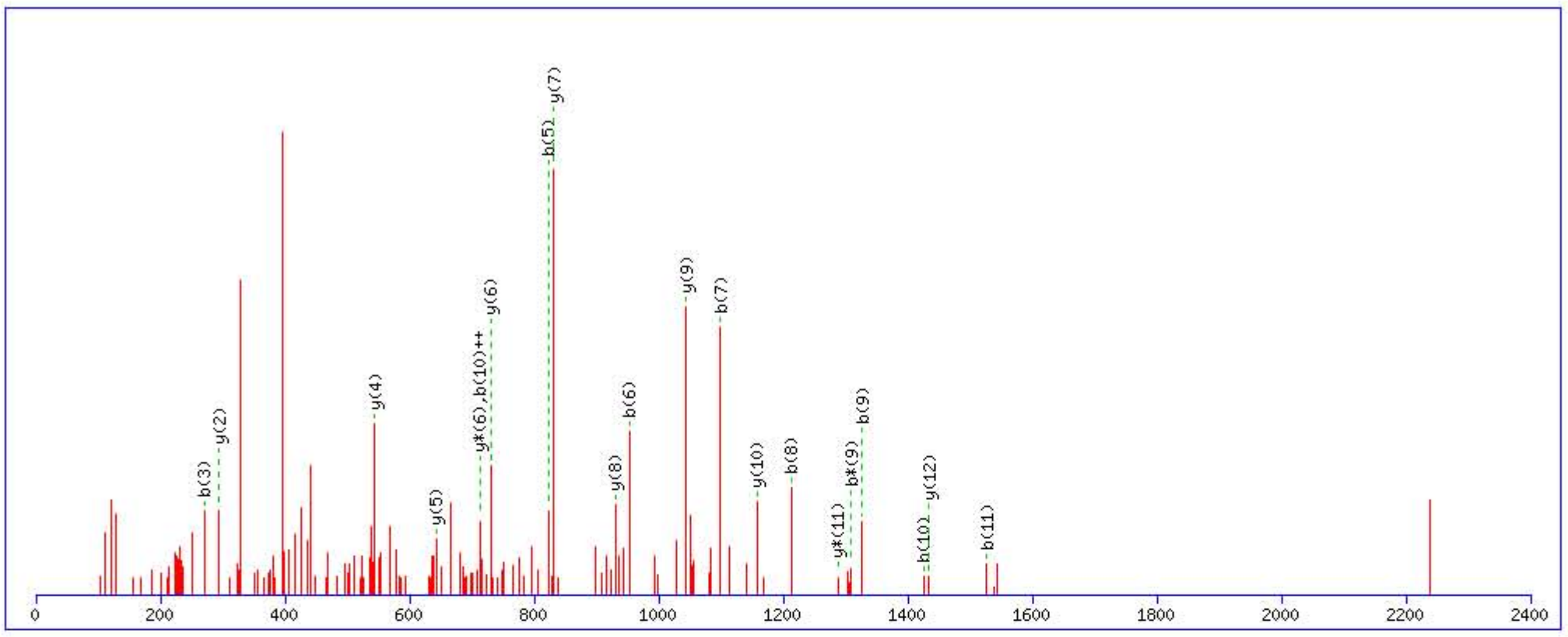
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GVNLQEFLNVTSVHLFK**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

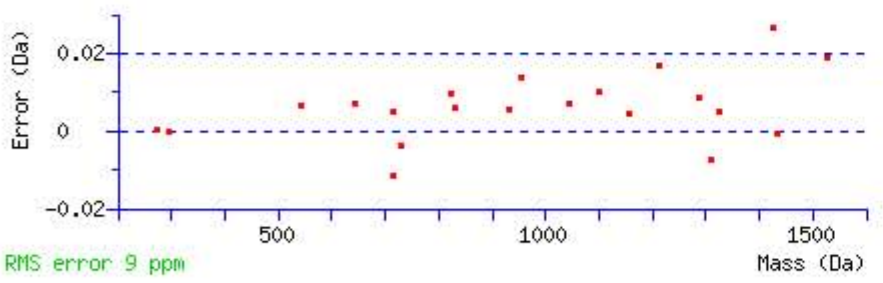
Match to Query 49543: 2255.234442 from(752.752090,3+) rtinseconds(3004) index(11297)
Title: Locus:1.1.1.2321.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

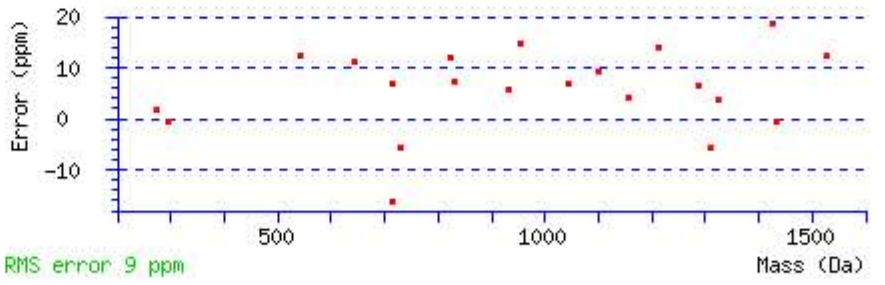
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2255.213654
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 63 **Expect:** 8.7e-006
**Matches :** 21/168 fragment ions using 31 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 17 |
| 2 | 157.097154 | 79.052215 | | | | | V | 2199.199458 | 1100.103367 | 2182.172909 | 1091.590092 | 2181.188893 | 1091.098084 | 16 |
| 3 | *271.140081* | 136.073679 | 254.113532 | 127.560404 | | | N | 2100.131044 | 1050.569160 | 2083.104495 | 1042.055885 | 2082.120479 | 1041.563877 | 15 |
| 4 | 384.224145 | 192.615711 | 367.197596 | 184.102436 | | | L | 1986.088117 | 993.547697 | 1969.061568 | 985.034422 | 1968.077552 | 984.542414 | 14 |
| 5 | *823.449471* | 412.228374 | 806.422922 | 403.715099 | | | Q | 1873.004053 | 937.005665 | 1855.977504 | 928.492390 | 1854.993488 | 928.000382 | 13 |
| 6 | *952.492064* | 476.749670 | 935.465515 | 468.236396 | 934.481499 | 467.744388 | E | *1433.778727* | 717.393002 | 1416.752178 | 708.879727 | 1415.768162 | 708.387719 | 12 |
| 7 | *1099.560478* | 550.283877 | 1082.533929 | 541.770603 | 1081.549913 | 541.278595 | F | 1304.736134 | 652.871705 | 1287.709585 | 644.358431 | 1286.725569 | 643.866423 | 11 |
| 8 | *1212.644542* | 606.825909 | 1195.617993 | 598.312635 | 1194.633977 | 597.820627 | L | *1157.667720* | 579.337498 | 1140.641171 | 570.824224 | 1139.657155 | 570.332216 | 10 |
| 9 | *1326.687469* | 663.847373 | 1309.660920 | 655.334098 | 1308.676904 | 654.842090 | N | *1044.583656* | 522.795466 | 1027.557107 | 514.282192 | 1026.573091 | 513.790184 | 9 |
| 10 | *1425.755883* | 713.381580 | 1408.729334 | 704.868305 | 1407.745318 | 704.376297 | V | *930.540729* | 465.774003 | 913.514180 | 457.260728 | 912.530164 | 456.768720 | 8 |
| 11 | *1526.803562* | 763.905419 | 1509.777013 | 755.392145 | 1508.792997 | 754.900137 | T | *831.472315* | 416.239796 | 814.445766 | 407.726521 | 813.461750 | 407.234513 | 7 |
| 12 | 1613.835590 | 807.421433 | 1596.809041 | 798.908159 | 1595.825025 | 798.416151 | S | *730.424636* | 365.715956 | 713.398087 | 357.202682 | 712.414071 | 356.710674 | 6 |
| 13 | 1712.904004 | 856.955640 | 1695.877455 | 848.442366 | 1694.893439 | 847.950358 | V | *643.392608* | 322.199942 | 626.366059 | 313.686668 | | | 5 |
| 14 | 1849.962916 | 925.485096 | 1832.936367 | 916.971822 | 1831.952351 | 916.479814 | H | *544.324194* | 272.665735 | 527.297645 | 264.152461 | | | 4 |
| 15 | 1963.046980 | 982.027128 | 1946.020431 | 973.513854 | 1945.036415 | 973.021846 | L | 407.265282 | 204.136279 | 390.238733 | 195.623004 | | | 3 |
| 16 | 2110.115394 | 1055.561335 | 2093.088845 | 1047.048060 | 2092.104829 | 1046.556052 | F | *294.181218* | 147.594247 | 277.154669 | 139.080973 | | | 2 |
| 17 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 62.9 | 2255.213654 | 0.020788 | GVNLQEFLNVTSVHLFK |

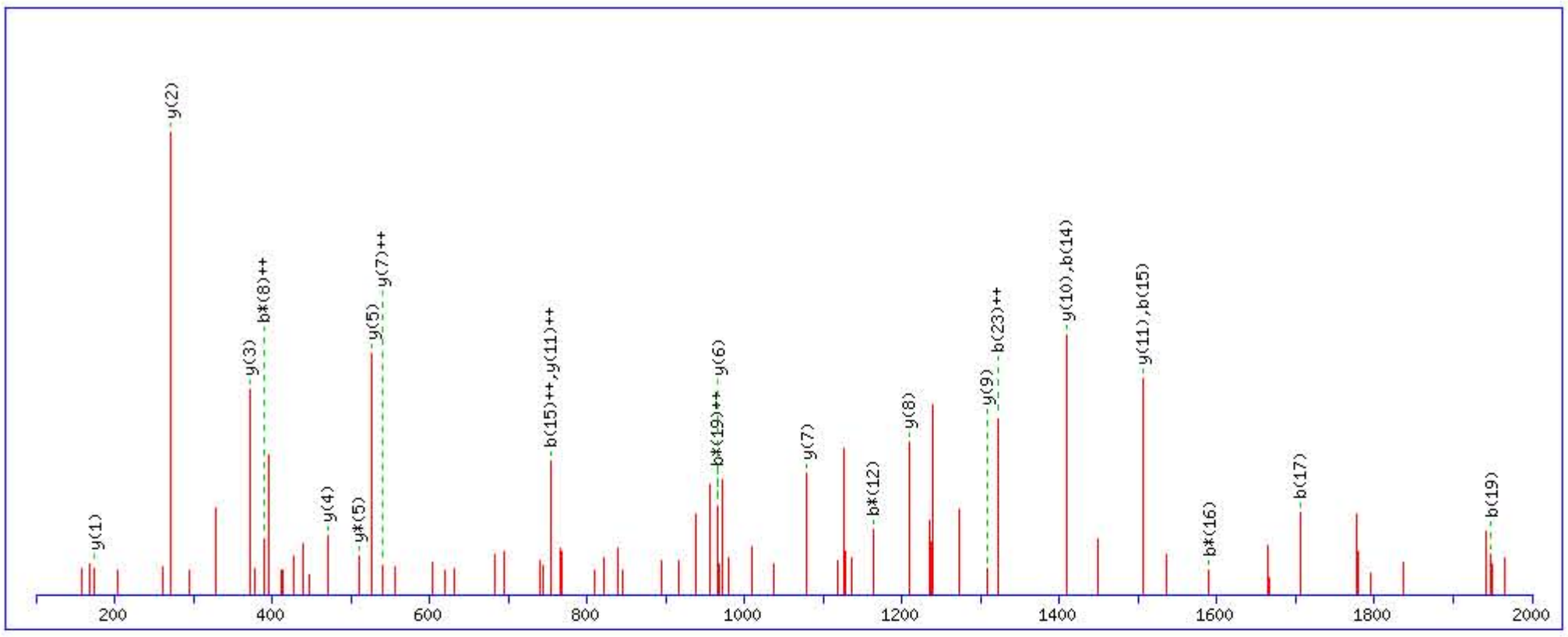
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AVPPNNSNAAEDDLPTVELQGVVPR**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

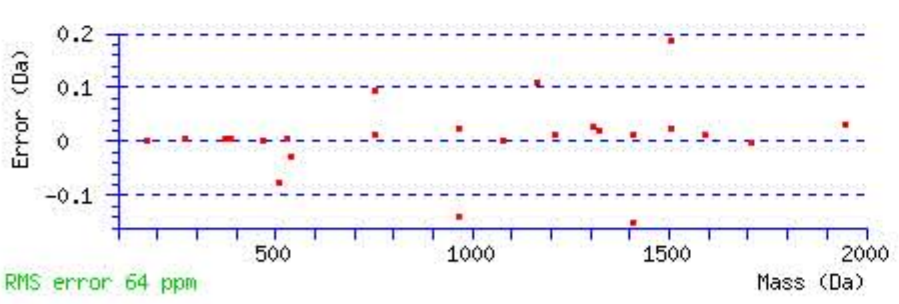
Match to Query 59186: 2912.505972 from(971.842600,3+) rtinseconds(2515) index(69421)
Title: Locus:1.1.1.2150.25 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

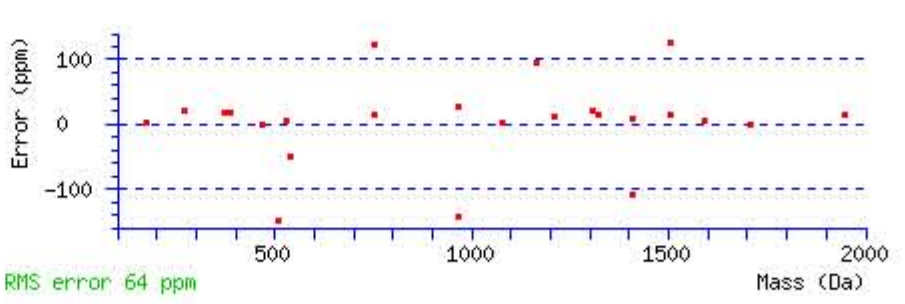
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2912.470200
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q20 : Biotin:Thermo-21345 (Q)
**Ions Score:** 34 **Expect:** 0.01
**Matches :** 24/254 fragment ions using 64 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 25 |
| 2 | 171.112804 | 86.060040 | | | | | V | 2842.440370 | 1421.723823 | 2825.413821 | 1413.210548 | 2824.429805 | 1412.718540 | 24 |
| 3 | 268.165568 | 134.586422 | | | | | P | 2743.371956 | 1372.189616 | 2726.345407 | 1363.676341 | 2725.361391 | 1363.184333 | 23 |
| 4 | 365.218332 | 183.112804 | | | | | P | 2646.319192 | 1323.663234 | 2629.292643 | 1315.149959 | 2628.308627 | 1314.657951 | 22 |
| 5 | 479.261259 | 240.134267 | 462.234710 | 231.620993 | | | N | 2549.266428 | 1275.136852 | 2532.239879 | 1266.623577 | 2531.255863 | 1266.131569 | 21 |
| 6 | 593.304186 | 297.155731 | 576.277637 | 288.642457 | | | N | 2435.223501 | 1218.115388 | 2418.196952 | 1209.602114 | 2417.212936 | 1209.110106 | 20 |
| 7 | 680.336214 | 340.671745 | 663.309665 | 332.158471 | 662.325649 | 331.666463 | S | 2321.180574 | 1161.093925 | 2304.154025 | 1152.580650 | 2303.170009 | 1152.088642 | 19 |
| 8 | 794.379141 | 397.693209 | 777.352592 | 389.179934 | 776.368576 | 388.687926 | N | 2234.148546 | 1117.577911 | 2217.121997 | 1109.064636 | 2216.137981 | 1108.572628 | 18 |
| 9 | 865.416255 | 433.211766 | 848.389706 | 424.698491 | 847.405690 | 424.206483 | A | 2120.105619 | 1060.556447 | 2103.079070 | 1052.043173 | 2102.095054 | 1051.551165 | 17 |
| 10 | 936.453369 | 468.730323 | 919.426820 | 460.217048 | 918.442804 | 459.725040 | A | 2049.068505 | 1025.037890 | 2032.041956 | 1016.524616 | 2031.057940 | 1016.032608 | 16 |
| 11 | 1065.495962 | 533.251619 | 1048.469413 | 524.738345 | 1047.485397 | 524.246336 | E | 1978.031391 | 989.519333 | 1961.004842 | 981.006059 | 1960.020826 | 980.514051 | 15 |
| 12 | 1180.522905 | 590.765091 | 1163.496356 | 582.251816 | 1162.512340 | 581.759808 | D | 1848.988798 | 924.998037 | 1831.962249 | 916.484762 | 1830.978233 | 915.992754 | 14 |
| 13 | 1295.549848 | 648.278562 | 1278.523299 | 639.765288 | 1277.539283 | 639.273280 | D | 1733.961855 | 867.484565 | 1716.935306 | 858.971291 | 1715.951290 | 858.479283 | 13 |
| 14 | **1408.633912** | 704.820594 | 1391.607363 | 696.307320 | 1390.623347 | 695.815312 | L | 1618.934912 | 809.971094 | 1601.908363 | 801.457819 | 1600.924347 | 800.965811 | 12 |
| 15 | **1505.686676** | **753.346976** | 1488.660127 | 744.833702 | 1487.676111 | 744.341694 | P | ***1505.850848*** | 753.429062 | 1488.824299 | 744.915787 | 1487.840283 | 744.423779 | 11 |
| 16 | 1606.734355 | 803.870816 | 1589.707806 | 795.357541 | 1588.723790 | 794.865533 | T | ***1408.798084*** | 704.902680 | 1391.771535 | 696.389405 | 1390.787519 | 695.897397 | 10 |
| 17 | **1705.802769** | 853.405023 | 1688.776220 | 844.891748 | 1687.792204 | 844.399740 | V | ***1307.750405*** | 654.378840 | 1290.723856 | 645.865566 | 1289.739840 | 645.373558 | 9 |
| 18 | 1834.845362 | 917.926319 | 1817.818813 | 909.413045 | 1816.834797 | 908.921037 | E | ***1208.681991*** | 604.844633 | 1191.655442 | 596.331359 | 1190.671426 | 595.839351 | 8 |
| 19 | **1947.929426** | 974.468351 | 1930.902877 | 965.955077 | 1929.918861 | 965.463069 | L | ***1079.639398*** | 540.323337 | 1062.612849 | 531.810062 | | | 7 |
| 20 | 2387.154752 | 1194.081014 | 2370.128203 | 1185.567739 | 2369.144187 | 1185.075731 | Q | ***966.555334*** | 483.781305 | 949.528785 | 475.268030 | | | 6 |
| 21 | 2444.176216 | 1222.591746 | 2427.149667 | 1214.078471 | 2426.165651 | 1213.586463 | G | ***527.330008*** | 264.168642 | 510.303459 | 255.655367 | | | 5 |
| 22 | 2543.244630 | 1272.125953 | 2526.218081 | 1263.612678 | 2525.234065 | 1263.120670 | V | ***470.308544*** | 235.657910 | 453.281995 | 227.144635 | | | 4 |
| 23 | 2642.313044 | **1321.660160** | 2625.286495 | 1313.146885 | 2624.302479 | 1312.654877 | V | ***371.240130*** | 186.123703 | 354.213581 | 177.610428 | | | 3 |
| 24 | 2739.365808 | 1370.186542 | 2722.339259 | 1361.673267 | 2721.355243 | 1361.181259 | P | ***272.171716*** | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 25 | | | | | | | R | ***175.118952*** | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 34.2 | 2912.470200 | 0.035772 | AVPPNNSNAAEDDLPTVELQGVVPR |

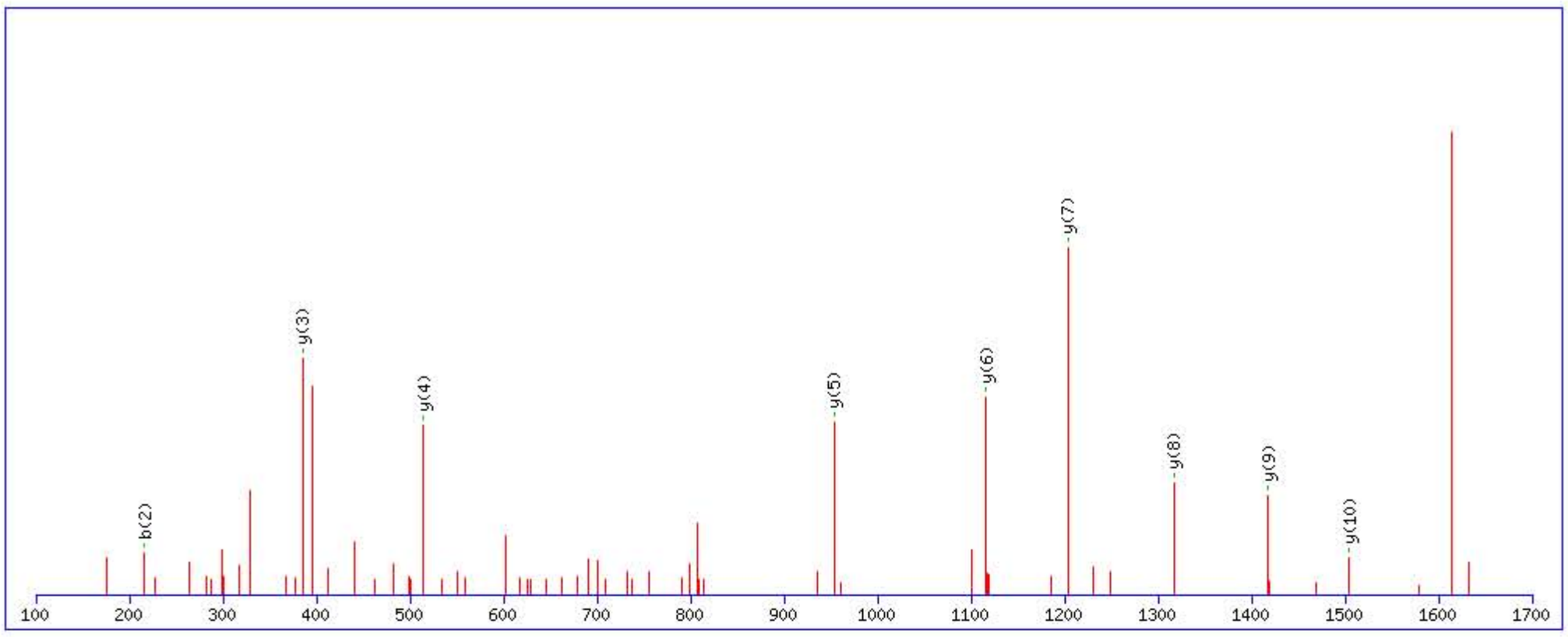
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QSTLSYQEPLR**
Found in **F13B_HUMAN**, Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3

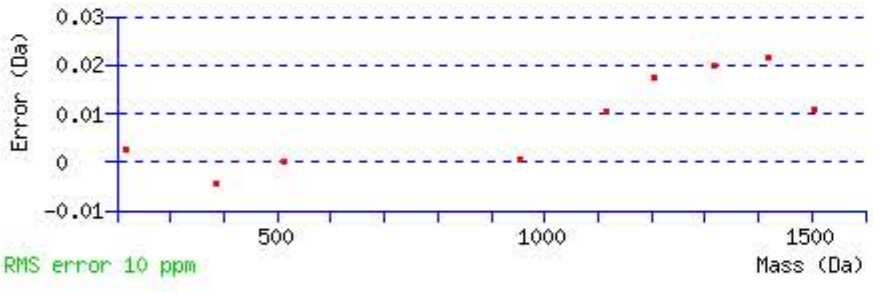
Match to Query 36406: 1631.840228 from(816.927390,2+) rtinseconds(1934) index(5246)
Title: Locus:1.1.1.1950.24 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

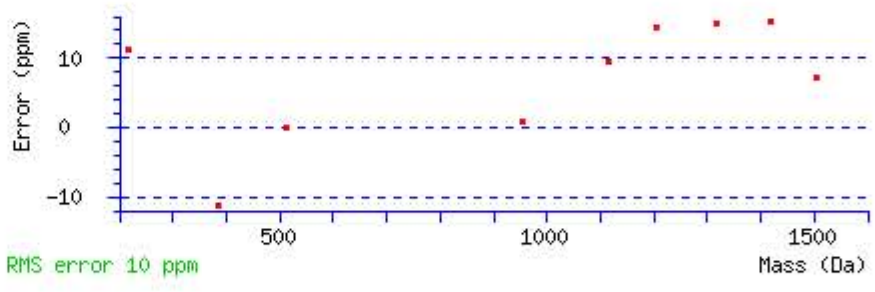
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1631.834106
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 69 **Expect:** 2.7e-006
**Matches :** 9/112 fragment ions using 14 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.065854 | 65.036565 | 112.039305 | 56.523291 | | | Q | | | | | | | 11 |
| 2 | 216.097882 | 108.552579 | 199.071333 | 100.039305 | 198.087317 | 99.547296 | S | *1504.782827* | 752.895052 | 1487.756278 | 744.381777 | 1486.772262 | 743.889769 | 10 |
| 3 | 317.145561 | 159.076418 | 300.119012 | 150.563144 | 299.134996 | 150.071136 | T | *1417.750799* | 709.379038 | 1400.724250 | 700.865763 | 1399.740234 | 700.373755 | 9 |
| 4 | 430.229625 | 215.618450 | 413.203076 | 207.105176 | 412.219060 | 206.613168 | L | *1316.703120* | 658.855198 | 1299.676571 | 650.341924 | 1298.692555 | 649.849916 | 8 |
| 5 | 517.261653 | 259.134465 | 500.235104 | 250.621190 | 499.251088 | 250.129182 | S | *1203.619056* | 602.313166 | 1186.592507 | 593.799892 | 1185.608491 | 593.307884 | 7 |
| 6 | 680.324982 | 340.666129 | 663.298433 | 332.152855 | 662.314417 | 331.660847 | Y | *1116.587028* | 558.797152 | 1099.560479 | 550.283878 | 1098.576463 | 549.791870 | 6 |
| 7 | 1119.550308 | 560.278792 | 1102.523759 | 551.765518 | 1101.539743 | 551.273510 | Q | *953.523699* | 477.265488 | 936.497150 | 468.752213 | 935.513134 | 468.260205 | 5 |
| 8 | 1248.592901 | 624.800089 | 1231.566352 | 616.286814 | 1230.582336 | 615.794806 | E | *514.298373* | 257.652825 | 497.271824 | 249.139550 | 496.287808 | 248.647542 | 4 |
| 9 | 1345.645665 | 673.326471 | 1328.619116 | 664.813196 | 1327.635100 | 664.321188 | P | *385.255780* | 193.131528 | 368.229231 | 184.618253 | | | 3 |
| 10 | 1458.729729 | 729.868503 | 1441.703180 | 721.355228 | 1440.719164 | 720.863220 | L | 288.203016 | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 11 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 68.6 | 1631.834106 | 0.006122 | QSTLSYQEPLR |
| 8.7 | 1631.863098 | -0.022870 | QLSTFEVNSINPKR |
| 6.8 | 1631.836578 | 0.003650 | NTITDEELKEKNAK |
| 6.6 | 1631.834106 | 0.006122 | QSTLSYQEPLR |
| 4.4 | 1631.822693 | 0.017535 | QGISQDLASSSRLDR |
| 4.0 | 1631.840652 | -0.000424 | KSLEGIFDDIVPDGK |
| 1.4 | 1631.838165 | 0.002063 | GASVPWDFLPGLMVK |
| 0.1 | 1631.855225 | -0.014997 | KSQMPNTTEKLLDK |

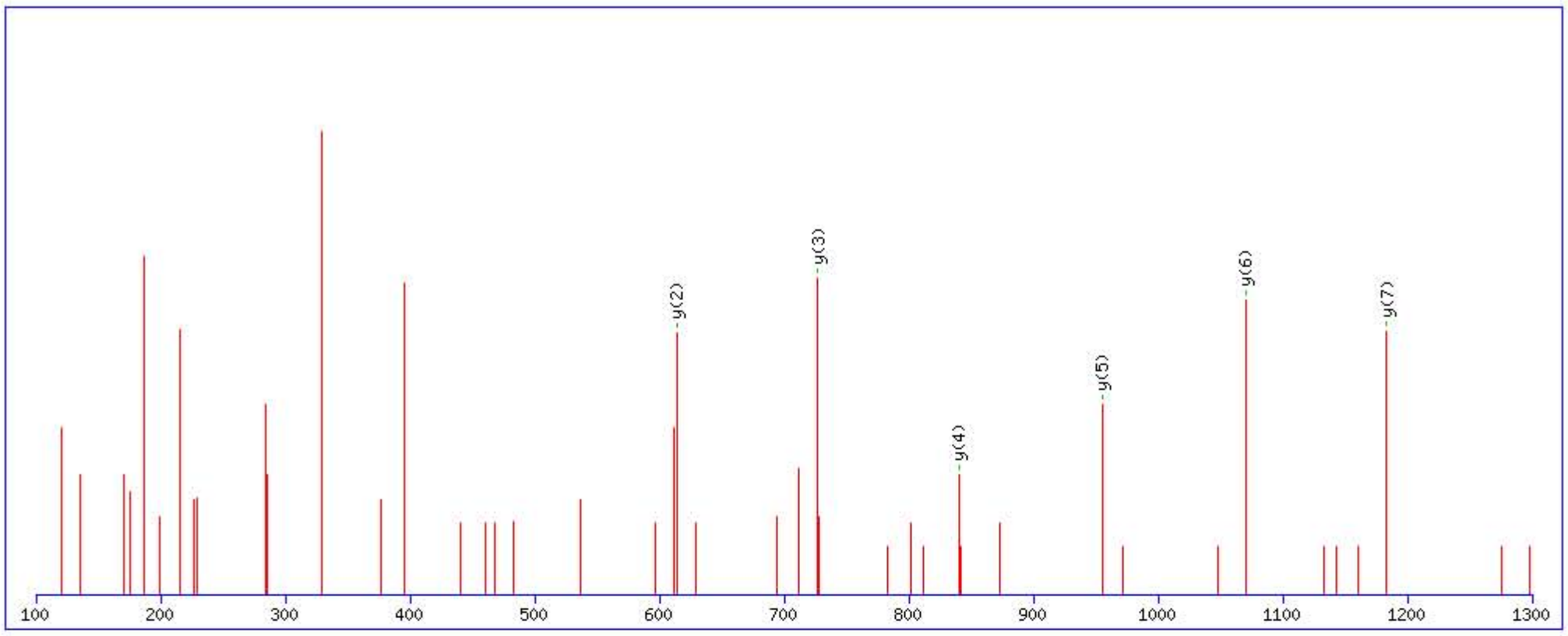
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TIAVLLDDILQR**
Found in **CC126_HUMAN**, Coiled-coil domain-containing protein 126 OS=Homo sapiens GN=CCDC126 PE=2 SV=2

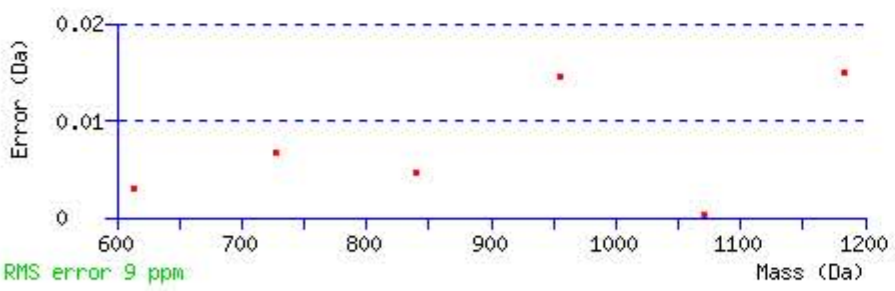
Match to Query 37542: 1679.977872 from(560.999900,3+) rtinseconds(3118) index(11741)
Title: Locus:1.1.1.2361.4 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

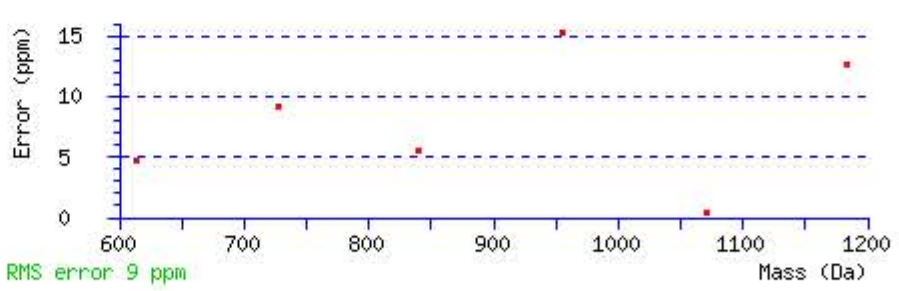
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1679.964401
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q11 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.0048
**Matches :** 6/104 fragment ions using 12 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 12 |
| 2 | 215.139019 | 108.073147 | | | 197.128454 | 99.067865 | I | 1579.924012 | 790.465644 | 1562.897463 | 781.952370 | 1561.913447 | 781.460361 | 11 |
| 3 | 286.176133 | 143.591704 | | | 268.165568 | 134.586422 | A | 1466.839948 | 733.923612 | 1449.813399 | 725.410338 | 1448.829383 | 724.918330 | 10 |
| 4 | 385.244547 | 193.125912 | | | 367.233982 | 184.120629 | V | 1395.802834 | 698.405055 | 1378.776285 | 689.891780 | 1377.792269 | 689.399772 | 9 |
| 5 | 498.328611 | 249.667944 | | | 480.318046 | 240.662661 | L | 1296.734420 | 648.870848 | 1279.707871 | 640.357574 | 1278.723855 | 639.865566 | 8 |
| 6 | 611.412675 | 306.209976 | | | 593.402110 | 297.204693 | L | *1183.650356* | 592.328816 | 1166.623807 | 583.815541 | 1165.639791 | 583.323533 | 7 |
| 7 | 726.439618 | 363.723447 | | | 708.429053 | 354.718165 | D | *1070.566292* | 535.786784 | 1053.539743 | 527.273510 | 1052.555727 | 526.781501 | 6 |
| 8 | 841.466561 | 421.236919 | | | 823.455996 | 412.231636 | D | *955.539349* | 478.273313 | 938.512800 | 469.760038 | 937.528784 | 469.268030 | 5 |
| 9 | 954.550625 | 477.778951 | | | 936.540060 | 468.773668 | I | *840.512406* | 420.759841 | 823.485857 | 412.246567 | | | 4 |
| 10 | 1067.634689 | 534.320983 | | | 1049.624124 | 525.315700 | L | *727.428342* | 364.217809 | 710.401793 | 355.704535 | | | 3 |
| 11 | 1506.860015 | 753.933646 | 1489.833466 | 745.420371 | 1488.849450 | 744.928363 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 12 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.7 | 1679.964401 | 0.013471 | TIAVLLDDILQR |

**Mascot:** http://www.matrixscience.com/

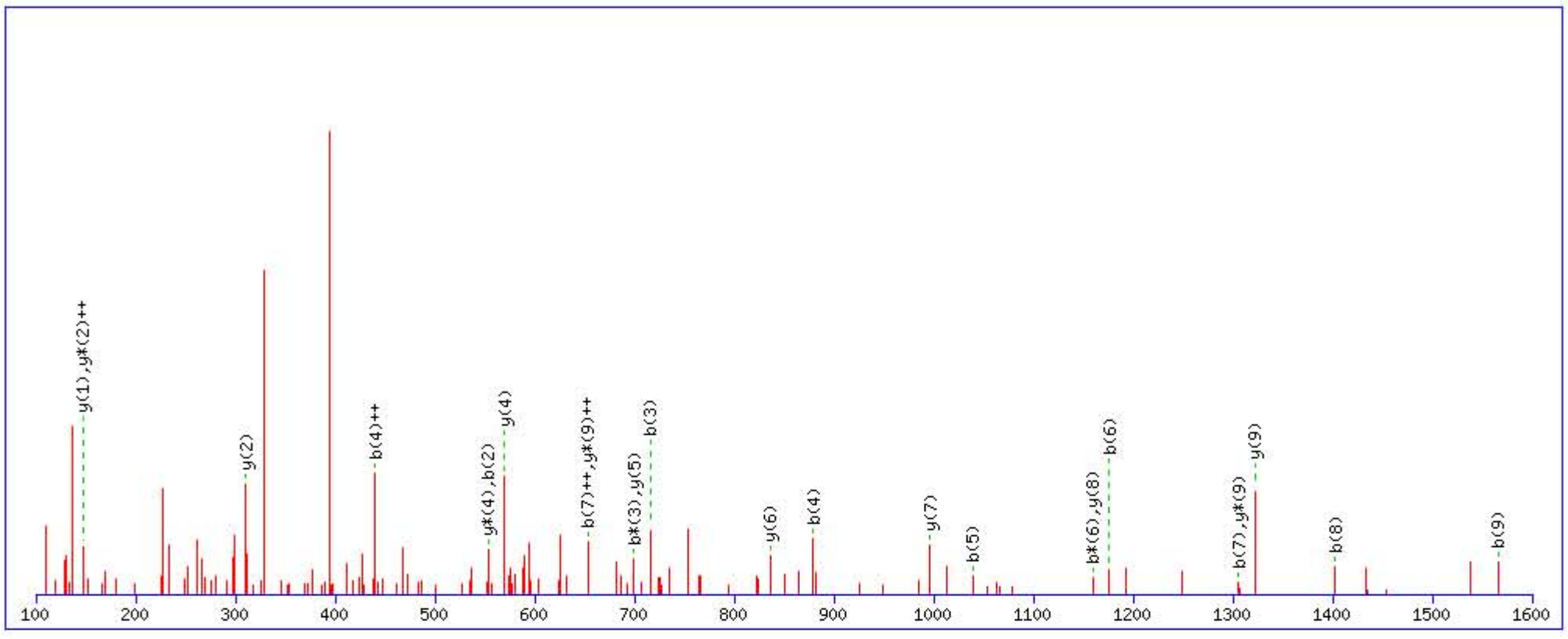
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IQYYCHEPYYK**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

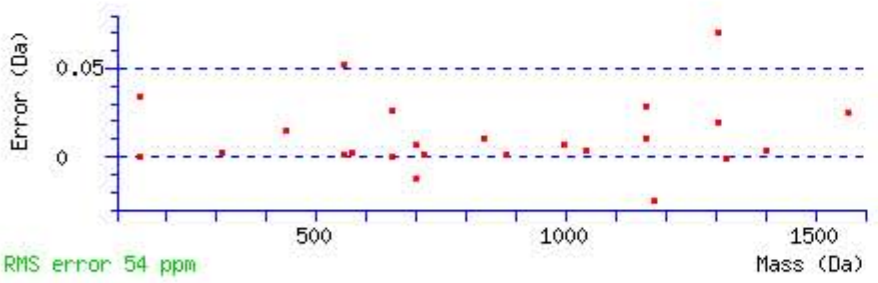
Match to Query 41764: 1873.864392 from(625.628740,3+) rtinseconds(1707) index(32312)
Title: Locus:1.1.1.703.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

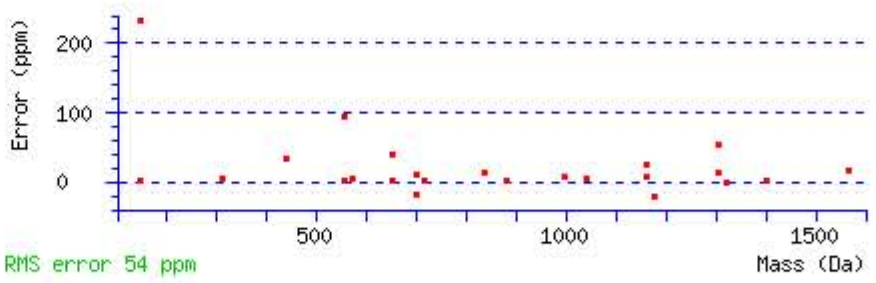
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1873.853119
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 34 **Expect:** 0.00083
**Matches :** 24/98 fragment ions using 43 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 11 |
| 2 | *553.316666* | 277.161971 | 536.290117 | 268.648697 | | | Q | 1761.776364 | 881.391820 | 1744.749815 | 872.878546 | 1743.765799 | 872.386538 | 10 |
| 3 | *716.379995* | 358.693636 | 699.353446 | 350.180361 | | | Y | *1322.551038* | 661.779157 | 1305.524489 | 653.265883 | 1304.540473 | 652.773875 | 9 |
| 4 | *879.443324* | **440.225300** | 862.416775 | 431.712026 | | | Y | *1159.487709* | 580.247493 | 1142.461160 | 571.734218 | 1141.477144 | 571.242210 | 8 |
| 5 | *1039.473973* | 520.240625 | 1022.447424 | 511.727350 | | | C | *996.424380* | 498.715828 | 979.397831 | 490.202554 | 978.413815 | 489.710546 | 7 |
| 6 | *1176.532885* | 588.770081 | 1159.506336 | 580.256806 | | | H | *836.393731* | 418.700504 | 819.367182 | 410.187229 | 818.383166 | 409.695221 | 6 |
| 7 | *1305.575478* | **653.291377** | 1288.548929 | 644.778103 | 1287.564913 | 644.286094 | E | *699.334819* | 350.171048 | 682.308270 | 341.657773 | 681.324254 | 341.165765 | 5 |
| 8 | *1402.628242* | 701.817759 | 1385.601693 | 693.304485 | 1384.617677 | 692.812477 | P | *570.292226* | 285.649751 | 553.265677 | 277.136477 | | | 4 |
| 9 | *1565.691571* | 783.349424 | 1548.665022 | 774.836149 | 1547.681006 | 774.344141 | Y | 473.239462 | 237.123369 | 456.212913 | 228.610095 | | | 3 |
| 10 | 1728.754900 | 864.881088 | 1711.728351 | 856.367814 | 1710.744335 | 855.875806 | Y | *310.176133* | 155.591705 | 293.149584 | 147.078430 | | | 2 |
| 11 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.9 | 1873.853119 | 0.011273 | IQYYCHEPYYK |
| 1.1 | 1873.873611 | -0.009219 | MTLSPSYRMDDGKMVK |

**Mascot:** http://www.matrixscience.com/

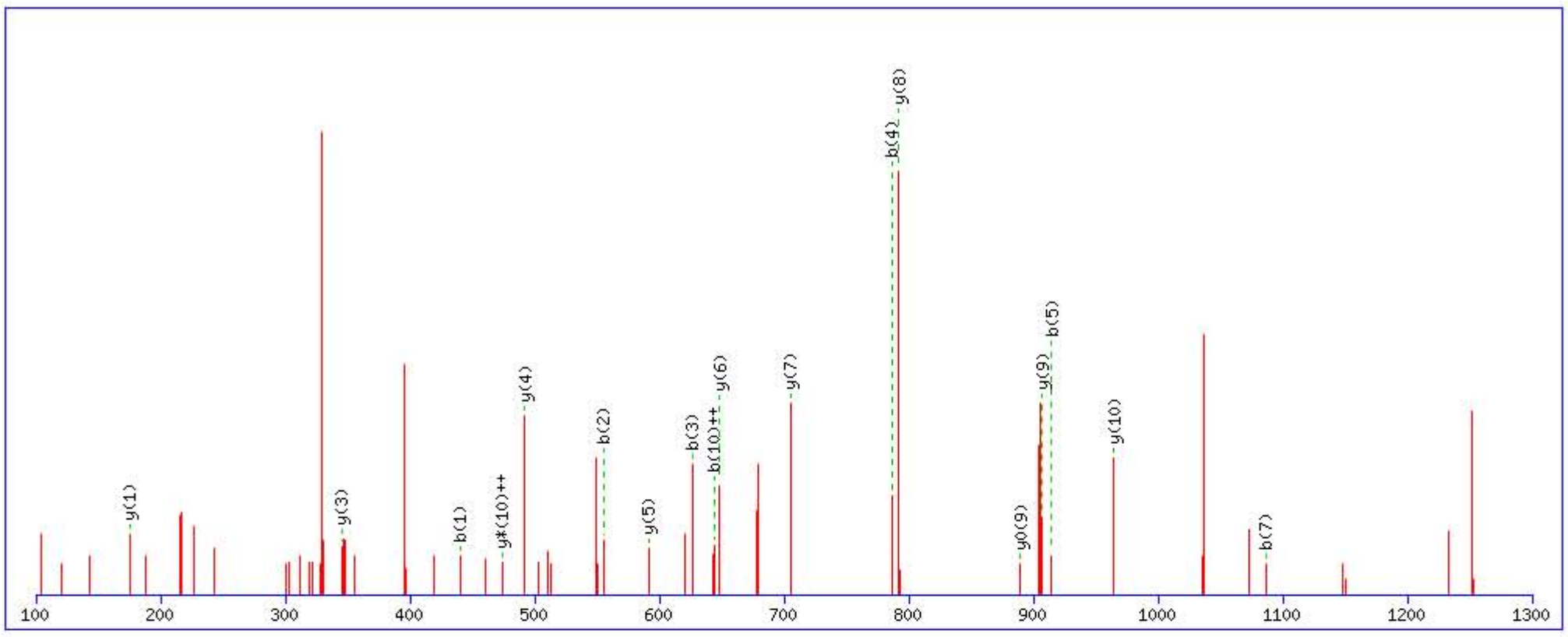
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QDACQGDSGGVFAVR**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

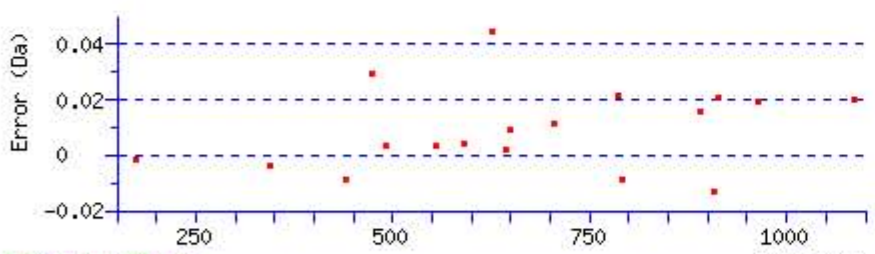
Match to Query 41810: 1876.869192 from(626.630340,3+) rtinseconds(1960) index(33982)
Title: Locus:1.1.1.791.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

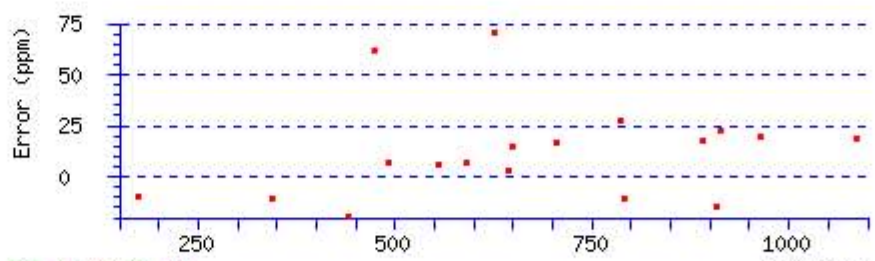
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1876.856033
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 36 **Expect:** 0.0014
**Matches** : 18/152 fragment ions using 56 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *440.232602* | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 15 |
| 2 | *555.259545* | 278.133411 | 538.232996 | 269.620136 | 537.248980 | 269.128128 | D | 1438.637955 | 719.822616 | 1421.611406 | 711.309341 | 1420.627390 | 710.817333 | 14 |
| 3 | *626.296659* | 313.651968 | 609.270110 | 305.138693 | 608.286094 | 304.646685 | A | 1323.611012 | 662.309144 | 1306.584463 | 653.795870 | 1305.600447 | 653.303862 | 13 |
| 4 | *786.327308* | 393.667292 | 769.300759 | 385.154018 | 768.316743 | 384.662010 | C | 1252.573898 | 626.790587 | 1235.547349 | 618.277313 | 1234.563333 | 617.785305 | 12 |
| 5 | *914.385886* | 457.696581 | 897.359337 | 449.183307 | 896.375321 | 448.691299 | Q | 1092.543249 | 546.775263 | 1075.516700 | 538.261988 | 1074.532684 | 537.769980 | 11 |
| 6 | 971.407350 | 486.207313 | 954.380801 | 477.694039 | 953.396785 | 477.202031 | G | *964.484671* | 482.745974 | 947.458122 | 474.232699 | 946.474106 | 473.740691 | 10 |
| 7 | *1086.434293* | 543.720785 | 1069.407744 | 535.207510 | 1068.423728 | 534.715502 | D | *907.463207* | 454.235242 | 890.436658 | 445.721967 | 889.452642 | 445.229959 | 9 |
| 8 | 1173.466321 | 587.236799 | 1156.439772 | 578.723524 | 1155.455756 | 578.231516 | S | *792.436264* | 396.721770 | 775.409715 | 388.208496 | 774.425699 | 387.716488 | 8 |
| 9 | 1230.487785 | 615.747531 | 1213.461236 | 607.234256 | 1212.477220 | 606.742248 | G | *705.404236* | 353.205756 | 688.377687 | 344.692482 | | | 7 |
| 10 | 1287.509249 | 644.258263 | 1270.482700 | 635.744988 | 1269.498684 | 635.252980 | G | *648.382772* | 324.695024 | 631.356223 | 316.181750 | | | 6 |
| 11 | 1386.577663 | 693.792470 | 1369.551114 | 685.279195 | 1368.567098 | 684.787187 | V | *591.361308* | 296.184292 | 574.334759 | 287.671018 | | | 5 |
| 12 | 1533.646077 | 767.326677 | 1516.619528 | 758.813402 | 1515.635512 | 758.321394 | F | *492.292894* | 246.650085 | 475.266345 | 238.136811 | | | 4 |
| 13 | 1604.683191 | 802.845234 | 1587.656642 | 794.331959 | 1586.672626 | 793.839951 | A | *345.224480* | 173.115878 | 328.197931 | 164.602603 | | | 3 |
| 14 | 1703.751605 | 852.379441 | 1686.725056 | 843.866166 | 1685.741040 | 843.374158 | V | 274.187366 | 137.597321 | 257.160817 | 129.084047 | | | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 36.0 | 1876.856033 | 0.013159 | QDACQGDSGGVFAVR |
| 23.7 | 1876.856033 | 0.013159 | QDACQGDSGGVFAVR |
| 5.4 | 1876.892853 | -0.023661 | SFLRDPDASPSQHQHR |

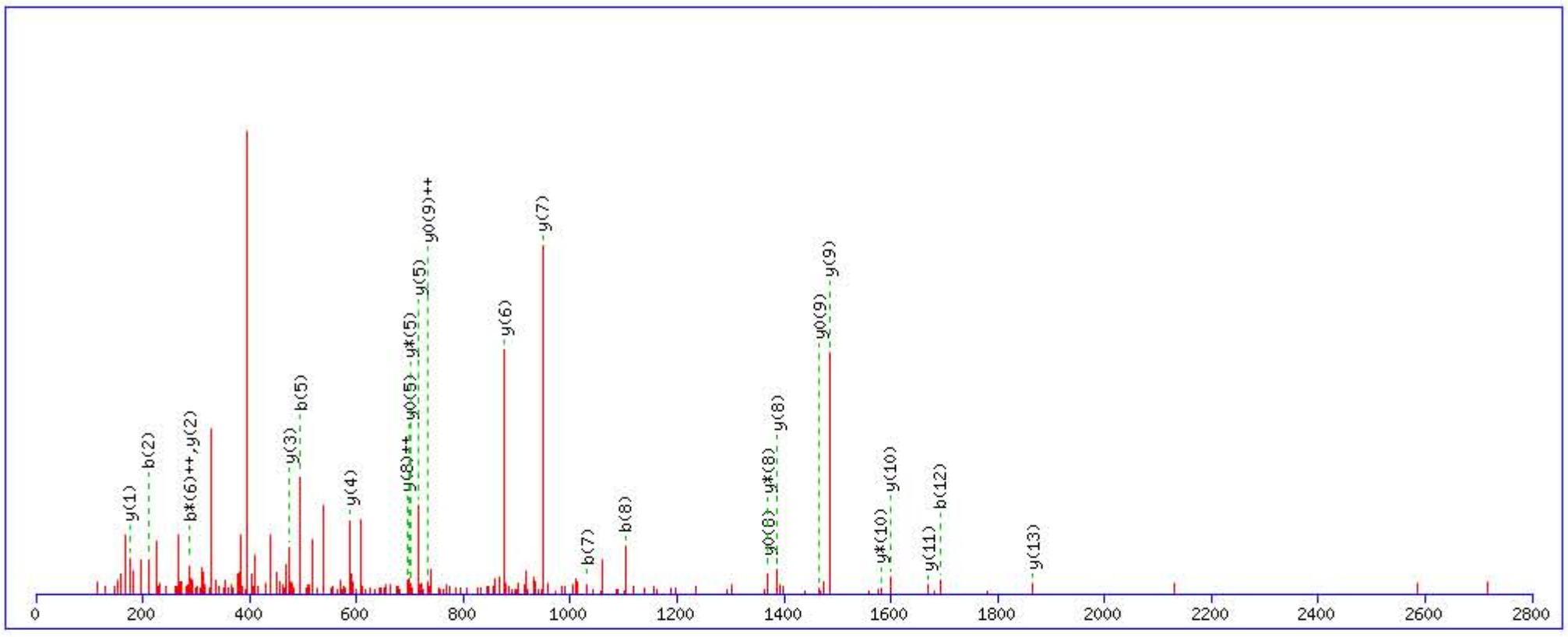
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LPVANPQACENWLR**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

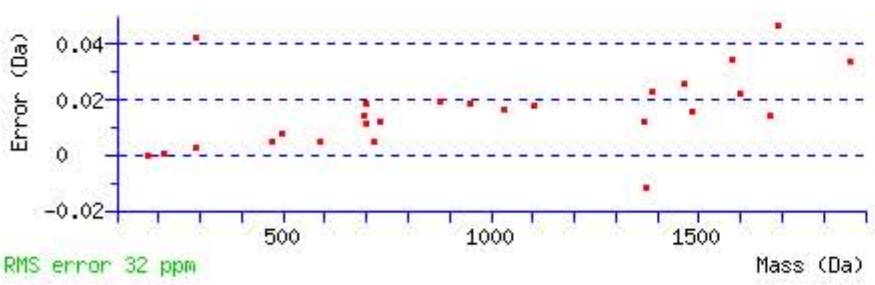
Match to Query 43714: 1978.012332 from(660.344720,3+) rtinseconds(2287) index(35979)
Title: Locus:1.1.1.905.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

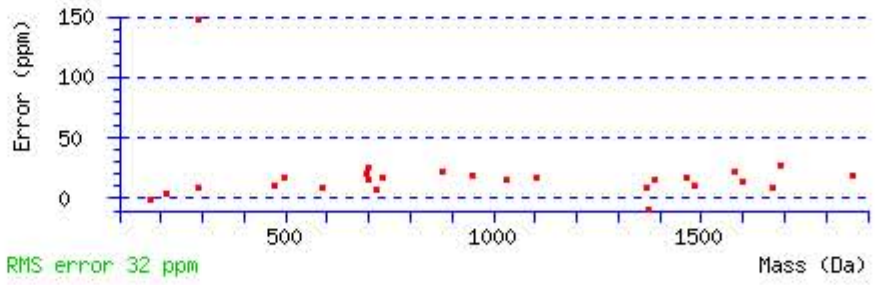
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1977.991684
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 69 **Expect:** 4.1e-007
**Matches :** 26/122 fragment ions using 50 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 14 |
| 2 | 211.144104 | 106.075690 | | | | | P | 1865.914921 | 933.461099 | 1848.888372 | 924.947824 | 1847.904356 | 924.455816 | 13 |
| 3 | 310.212518 | 155.609897 | | | | | V | 1768.862157 | 884.934717 | 1751.835608 | 876.421442 | 1750.851592 | 875.929434 | 12 |
| 4 | 381.249632 | 191.128454 | | | | | A | 1669.793743 | 835.400510 | 1652.767194 | 826.887235 | 1651.783178 | 826.395227 | 11 |
| 5 | 495.292559 | 248.149917 | 478.266010 | 239.636643 | | | N | 1598.756629 | 799.881953 | 1581.730080 | 791.368678 | 1580.746064 | 790.876670 | 10 |
| 6 | 592.345323 | 296.676300 | 575.318774 | 288.163025 | | | P | 1484.713702 | 742.860489 | 1467.687153 | 734.347215 | 1466.703137 | 733.855207 | 9 |
| 7 | 1031.570649 | 516.288963 | 1014.544100 | 507.775688 | | | Q | 1387.660938 | 694.334107 | 1370.634389 | 685.820833 | 1369.650373 | 685.328825 | 8 |
| 8 | 1102.607763 | 551.807520 | 1085.581214 | 543.294245 | | | A | 948.435612 | 474.721444 | 931.409063 | 466.208170 | 930.425047 | 465.716162 | 7 |
| 9 | 1262.638412 | 631.822844 | 1245.611863 | 623.309570 | | | C | 877.398498 | 439.202887 | 860.371949 | 430.689613 | 859.387933 | 430.197605 | 6 |
| 10 | 1391.681005 | 696.344141 | 1374.654456 | 687.830866 | 1373.670440 | 687.338858 | E | 717.367849 | 359.187563 | 700.341300 | 350.674288 | 699.357284 | 350.182280 | 5 |
| 11 | 1505.723932 | 753.365604 | 1488.697383 | 744.852330 | 1487.713367 | 744.360322 | N | 588.325256 | 294.666266 | 571.298707 | 286.152991 | | | 4 |
| 12 | 1691.803245 | 846.405261 | 1674.776696 | 837.891986 | 1673.792680 | 837.399978 | W | 474.282329 | 237.644802 | 457.255780 | 229.131528 | | | 3 |
| 13 | 1804.887309 | 902.947293 | 1787.860760 | 894.434018 | 1786.876744 | 893.942010 | L | 288.203016 | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 14 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

### All matches to this query

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 68.7 | 1977.991684 | 0.020648 | LPVANPQACENWLR |
| 0.6 | 1977.983856 | 0.028476 | VLGKGGFGEVSACQMK |

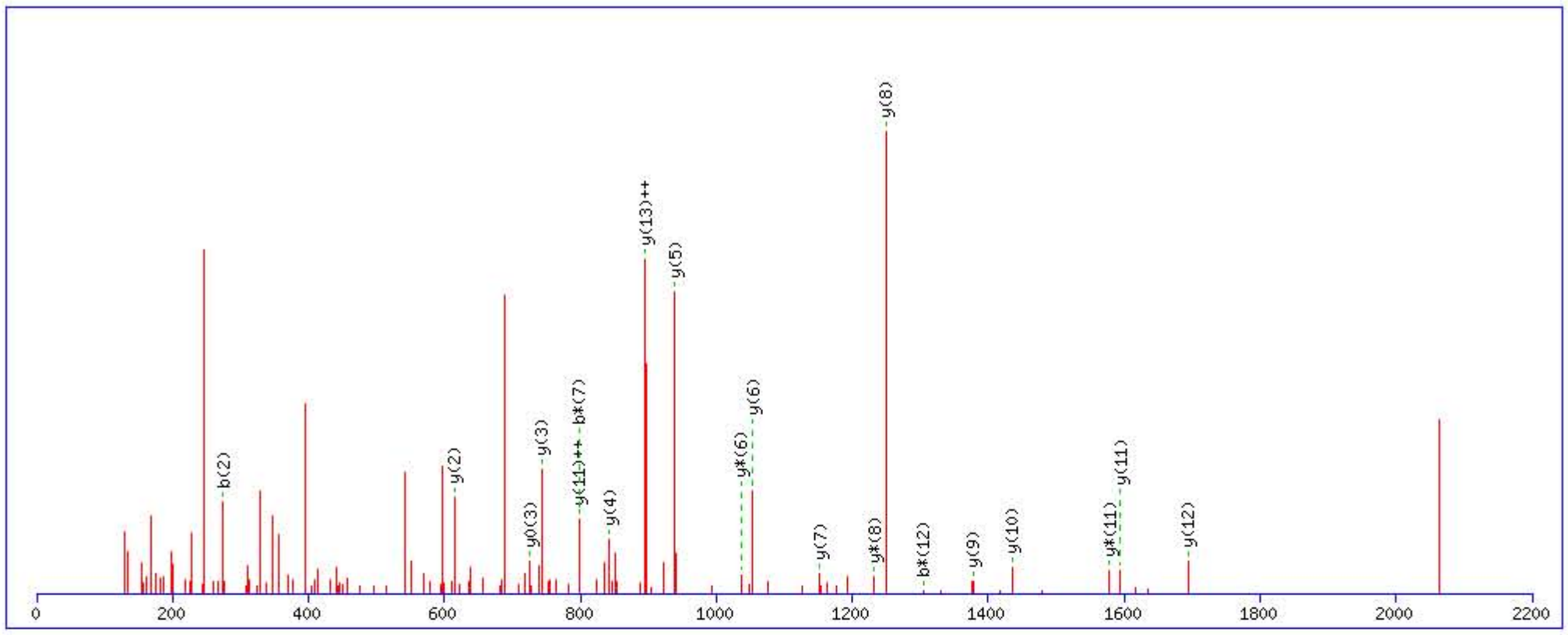
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **CLPVCGKPVNPVEQR**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

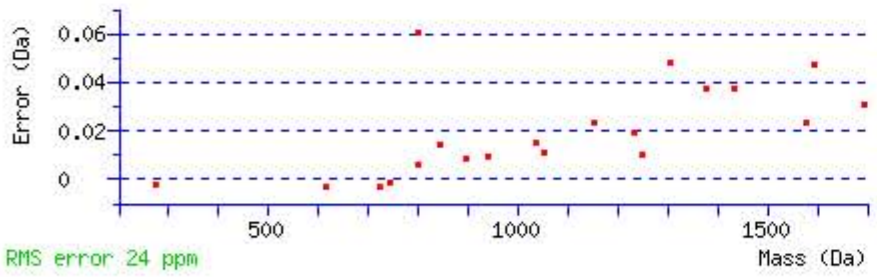
Match to Query 46014: 2063.069652 from(688.697160,3+) rtinseconds(1775) index(48822)
Title: Locus:1.1.1.1856.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

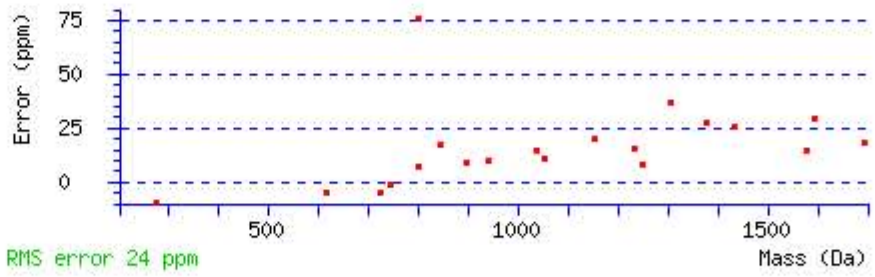
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2063.047852
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q14 : Biotin:Thermo-21345 (Q)
**Ions Score:** 49 **Expect:** 0.00038
**Matches :** 20/128 fragment ions using 47 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 161.037925 | 81.022600 | | | | | C | | | | | | | 15 |
| 2 | 274.121989 | 137.564632 | | | | | L | 1904.024472 | 952.515874 | 1886.997923 | 944.002600 | 1886.013907 | 943.510592 | 14 |
| 3 | 371.174753 | 186.091014 | | | | | P | 1790.940408 | 895.973842 | 1773.913859 | 887.460568 | 1772.929843 | 886.968560 | 13 |
| 4 | 470.243167 | 235.625221 | | | | | V | *1693.887644* | 847.447460 | 1676.861095 | 838.934186 | 1675.877079 | 838.442178 | 12 |
| 5 | 630.273816 | 315.640546 | | | | | C | *1594.819230* | 797.913253 | 1577.792681 | 789.399979 | 1576.808665 | 788.907971 | 11 |
| 6 | 687.295280 | 344.151278 | | | | | G | *1434.788581* | 717.897929 | 1417.762032 | 709.384654 | 1416.778016 | 708.892646 | 10 |
| 7 | 815.390243 | 408.198760 | 798.363694 | 399.685485 | | | K | *1377.767117* | 689.387197 | 1360.740568 | 680.873922 | 1359.756552 | 680.381914 | 9 |
| 8 | 912.443007 | 456.725142 | 895.416458 | 448.211867 | | | P | *1249.672154* | 625.339715 | 1232.645605 | 616.826441 | 1231.661589 | 616.334433 | 8 |
| 9 | 1011.511421 | 506.259349 | 994.484872 | 497.746074 | | | V | *1152.619390* | 576.813333 | 1135.592841 | 568.300059 | 1134.608825 | 567.808051 | 7 |
| 10 | 1125.554348 | 563.280812 | 1108.527799 | 554.767538 | | | N | *1053.550976* | 527.279126 | 1036.524427 | 518.765852 | 1035.540411 | 518.273844 | 6 |
| 11 | 1222.607112 | 611.807194 | 1205.580563 | 603.293920 | | | P | *939.508049* | 470.257663 | 922.481500 | 461.744388 | 921.497484 | 461.252380 | 5 |
| 12 | 1321.675526 | 661.341401 | 1304.648977 | 652.828127 | | | V | *842.455285* | 421.731281 | 825.428736 | 413.218006 | 824.444720 | 412.725998 | 4 |
| 13 | 1450.718119 | 725.862698 | 1433.691570 | 717.349423 | 1432.707554 | 716.857415 | E | *743.386871* | 372.197074 | 726.360322 | 363.683799 | 725.376306 | 363.191791 | 3 |
| 14 | 1889.943445 | 945.475361 | 1872.916896 | 936.962086 | 1871.932880 | 936.470078 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 15 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.7 | 2063.047852 | 0.021800 | CLPVCGKPVNPVEQR |

**Mascot:** http://www.matrixscience.com/

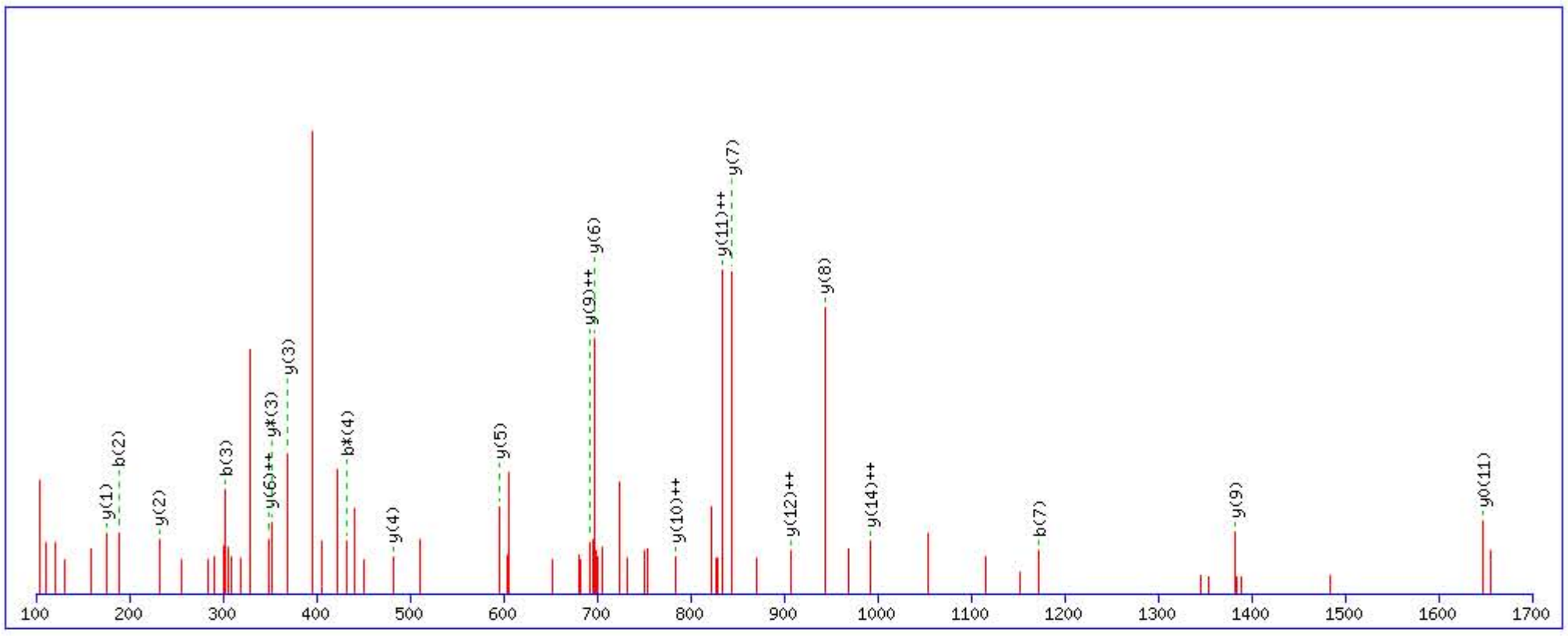
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MGNFPWQVFTNIHGR**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

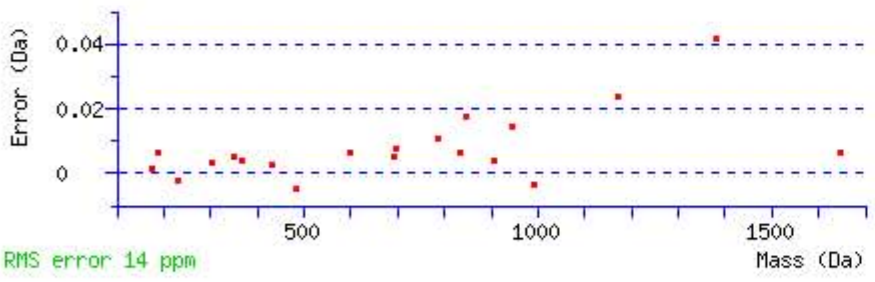
Match to Query 46818: 2114.061822 from(705.694550,3+) rtinseconds(2667) index(54419)
Title: Locus:1.1.1.2165.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

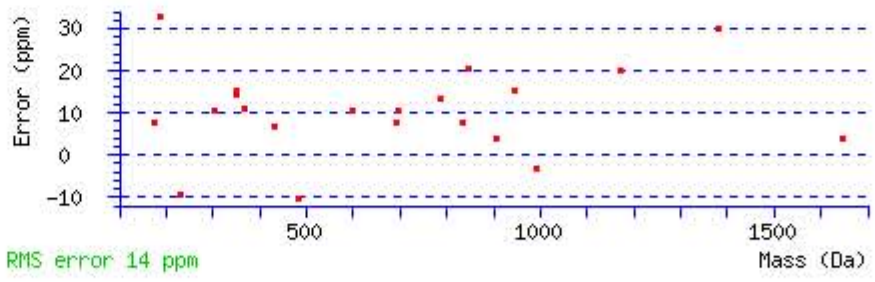
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2114.034256
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.00025
**Matches :** 21/136 fragment ions using 54 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.047761 | 66.527518 | | | | | M | | | | | | | 15 |
| 2 | **189.069225** | 95.038250 | | | | | G | 1984.001034 | 992.504155 | 1966.974485 | 983.990881 | 1965.990469 | 983.498873 | 14 |
| 3 | **303.112152** | 152.059714 | 286.085603 | 143.546439 | | | N | 1926.979570 | 963.993423 | 1909.953021 | 955.480149 | 1908.969005 | 954.988141 | 13 |
| 4 | 450.180566 | 225.593921 | 433.154017 | 217.080646 | | | F | 1812.936643 | 906.971960 | 1795.910094 | 898.458685 | 1794.926078 | 897.966677 | 12 |
| 5 | 547.233330 | 274.120303 | 530.206781 | 265.607029 | | | P | 1665.868229 | 833.437753 | 1648.841680 | 824.924478 | 1647.857664 | 824.432470 | 11 |
| 6 | 733.312643 | 367.159960 | 716.286094 | 358.646685 | | | W | 1568.815465 | 784.911371 | 1551.788916 | 776.398096 | 1550.804900 | 775.906088 | 10 |
| 7 | **1172.537969** | 586.772623 | 1155.511420 | 578.259348 | | | Q | *1382.736152* | 691.871714 | 1365.709603 | 683.358440 | 1364.725587 | 682.866432 | 9 |
| 8 | 1271.606383 | 636.306830 | 1254.579834 | 627.793555 | | | V | *943.510826* | 472.259051 | 926.484277 | 463.745777 | 925.500261 | 463.253769 | 8 |
| 9 | 1418.674797 | 709.841037 | 1401.648248 | 701.327762 | | | F | *844.442412* | 422.724844 | 827.415863 | 414.211570 | 826.431847 | 413.719562 | 7 |
| 10 | 1519.722476 | 760.364876 | 1502.695927 | 751.851602 | 1501.711911 | 751.359594 | T | *697.373998* | 349.190637 | 680.347449 | 340.677363 | 679.363433 | 340.185355 | 6 |
| 11 | 1633.765403 | 817.386340 | 1616.738854 | 808.873065 | 1615.754838 | 808.381057 | N | *596.326319* | 298.666798 | 579.299770 | 290.153523 | | | 5 |
| 12 | 1746.849467 | 873.928372 | 1729.822918 | 865.415097 | 1728.838902 | 864.923089 | I | *482.283392* | 241.645334 | 465.256843 | 233.132059 | | | 4 |
| 13 | 1883.908379 | 942.457828 | 1866.881830 | 933.944553 | 1865.897814 | 933.452545 | H | *369.199328* | 185.103302 | 352.172779 | 176.590028 | | | 3 |
| 14 | 1940.929843 | 970.968559 | 1923.903294 | 962.455285 | 1922.919278 | 961.963277 | G | *232.140416* | 116.573846 | 215.113867 | 108.060572 | | | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 39.3 | 2114.034256 | 0.027566 | MGNFPWQVFTNIHGR |
| 0.8 | 2114.079849 | -0.018027 | SHGLLPKCIMQATDIMRK |

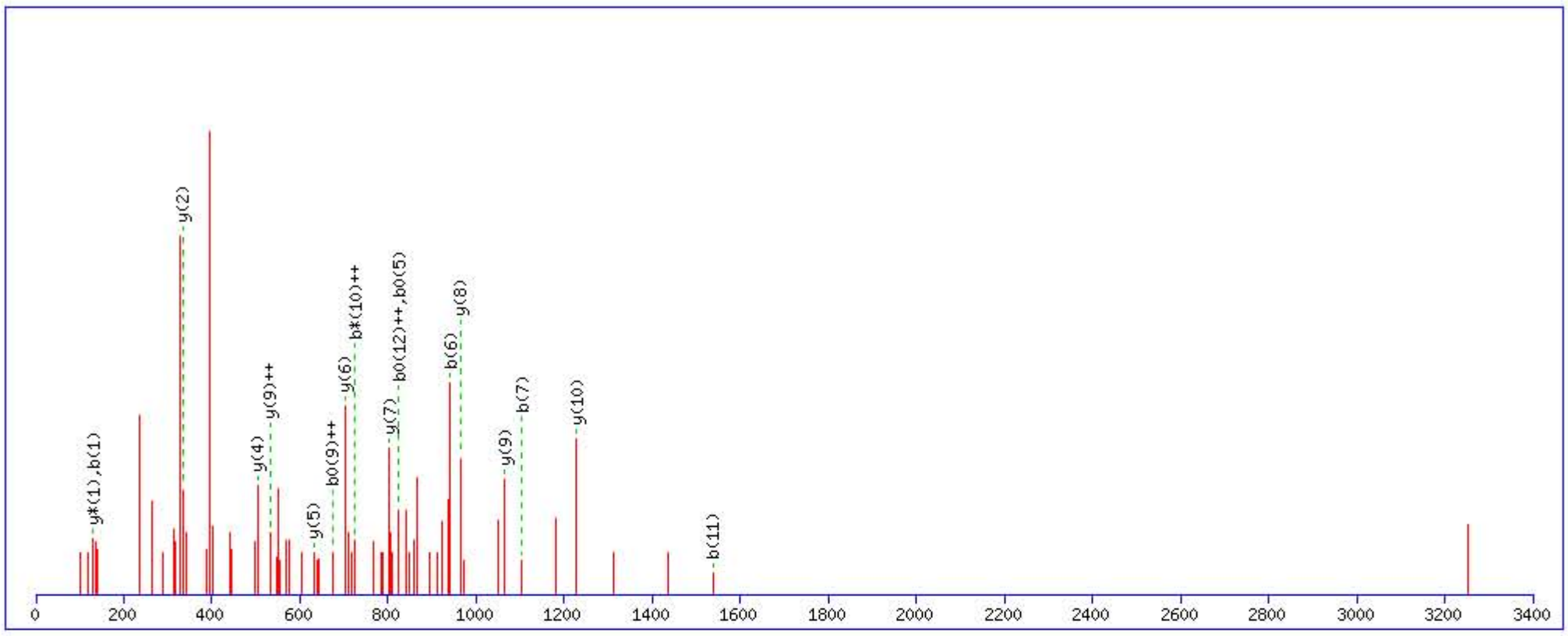
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ESEQGVYTCTAQGIWK**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

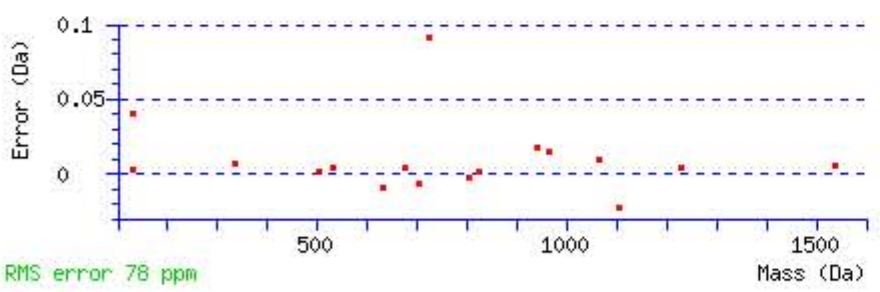
Match to Query 47768: 2167.021242 from(723.347690,3+) rtinseconds(2160) index(21272)
Title: Locus:1.1.1.3134.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

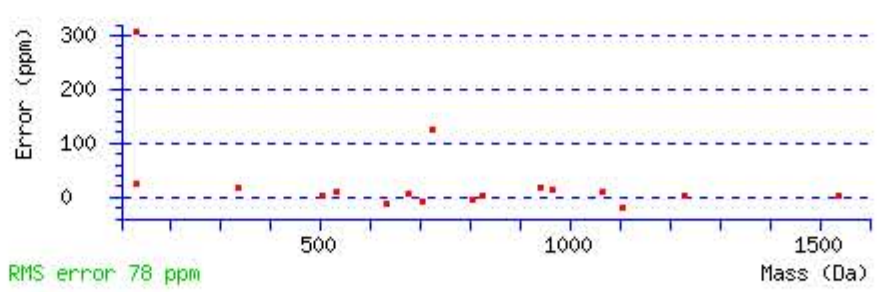
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2167.007813
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.012
**Matches :** 18/162 fragment ions using 35 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 16 |
| 2 | 217.081897 | 109.044586 | | | 199.071332 | 100.039304 | S | 2038.972498 | 1019.989887 | 2021.945949 | 1011.476613 | 2020.961933 | 1010.984604 | 15 |
| 3 | 346.124490 | 173.565883 | | | 328.113925 | 164.560600 | E | 1951.940470 | 976.473873 | 1934.913921 | 967.960599 | 1933.929905 | 967.468591 | 14 |
| 4 | 785.349816 | 393.178546 | 768.323267 | 384.665272 | 767.339251 | 384.173264 | Q | 1822.897877 | 911.952577 | 1805.871328 | 903.439302 | 1804.887312 | 902.947294 | 13 |
| 5 | 842.371280 | 421.689278 | 825.344731 | 413.176004 | 824.360715 | 412.683996 | G | 1383.672551 | 692.339913 | 1366.646002 | 683.826639 | 1365.661986 | 683.334631 | 12 |
| 6 | 941.439694 | 471.223485 | 924.413145 | 462.710211 | 923.429129 | 462.218203 | V | 1326.651087 | 663.829182 | 1309.624538 | 655.315907 | 1308.640522 | 654.823899 | 11 |
| 7 | 1104.503023 | 552.755150 | 1087.476474 | 544.241875 | 1086.492458 | 543.749867 | Y | *1227.582673* | 614.294975 | 1210.556124 | 605.781700 | 1209.572108 | 605.289692 | 10 |
| 8 | 1205.550702 | 603.278989 | 1188.524153 | 594.765715 | 1187.540137 | 594.273707 | T | *1064.519344* | 532.763310 | 1047.492795 | 524.250036 | 1046.508779 | 523.758028 | 9 |
| 9 | 1365.581351 | 683.294314 | 1348.554802 | 674.781039 | 1347.570786 | 674.289031 | C | *963.471665* | 482.239471 | 946.445116 | 473.726196 | 945.461100 | 473.234188 | 8 |
| 10 | 1466.629030 | 733.818153 | 1449.602481 | 725.304879 | 1448.618465 | 724.812871 | T | *803.441016* | 402.224146 | 786.414467 | 393.710872 | 785.430451 | 393.218864 | 7 |
| 11 | 1537.666144 | 769.336710 | 1520.639595 | 760.823436 | 1519.655579 | 760.331428 | A | *702.393337* | 351.700307 | 685.366788 | 343.187032 | | | 6 |
| 12 | 1665.724722 | 833.365999 | 1648.698173 | 824.852725 | 1647.714157 | 824.360717 | Q | *631.356223* | 316.181750 | 614.329674 | 307.668475 | | | 5 |
| 13 | 1722.746186 | 861.876731 | 1705.719637 | 853.363457 | 1704.735621 | 852.871449 | G | *503.297645* | 252.152460 | 486.271096 | 243.639186 | | | 4 |
| 14 | 1835.830250 | 918.418763 | 1818.803701 | 909.905489 | 1817.819685 | 909.413480 | I | 446.276181 | 223.641728 | 429.249632 | 215.128454 | | | 3 |
| 15 | 2021.909563 | 1011.458420 | 2004.883014 | 1002.945145 | 2003.898998 | 1002.453137 | W | *333.192117* | 167.099696 | 316.165568 | 158.586422 | | | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.7 | 2167.007813 | 0.013429 | ESEQGVYTCTAQGIWK |

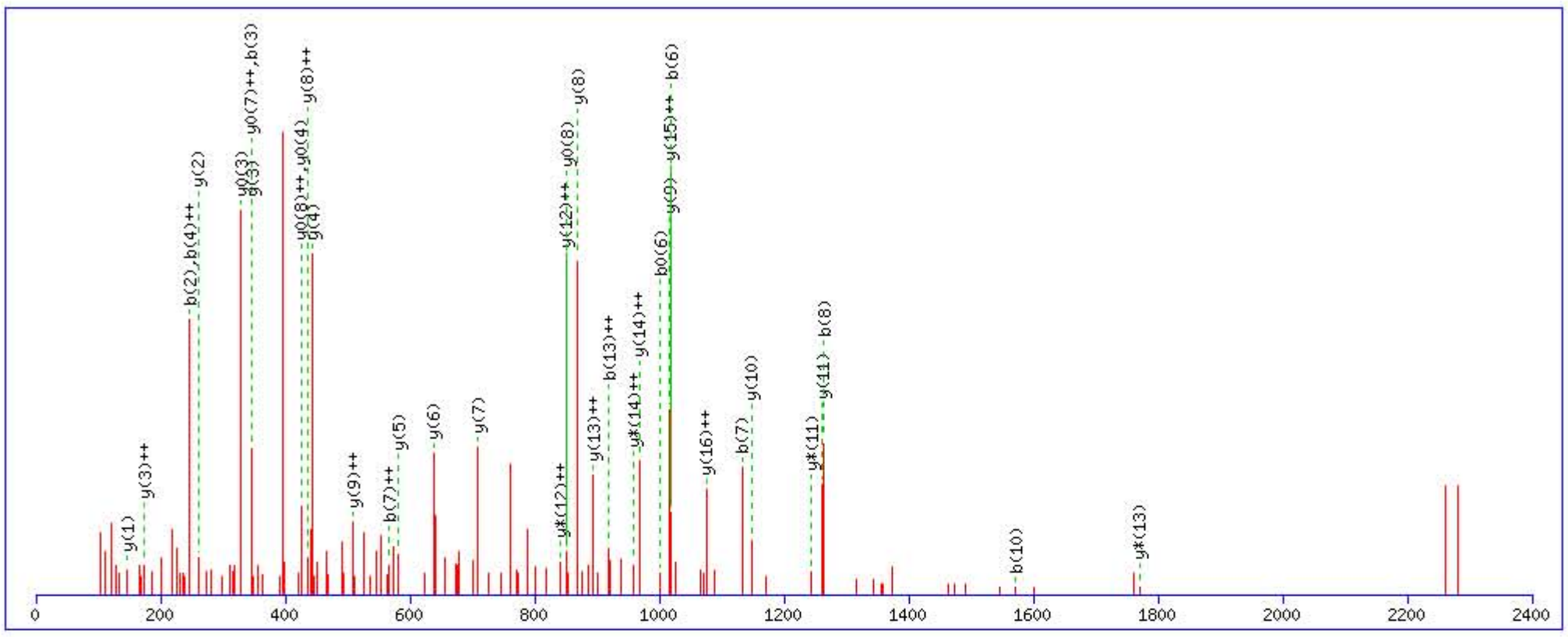
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MDVFSQNMFCAGHPSLK**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

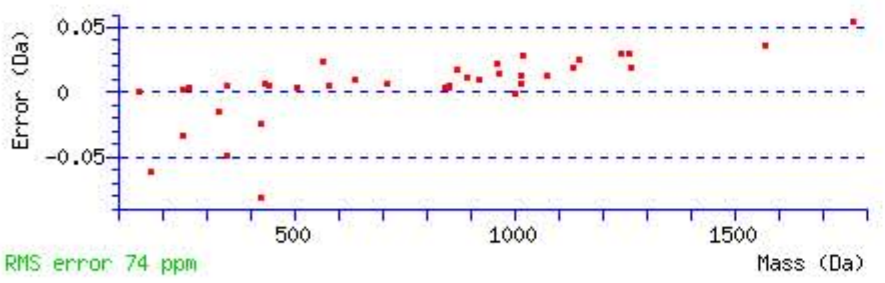
Match to Query 50142: 2279.068242 from(760.696690,3+) rtinseconds(2378) index(52730)
Title: Locus:1.1.1.2065.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

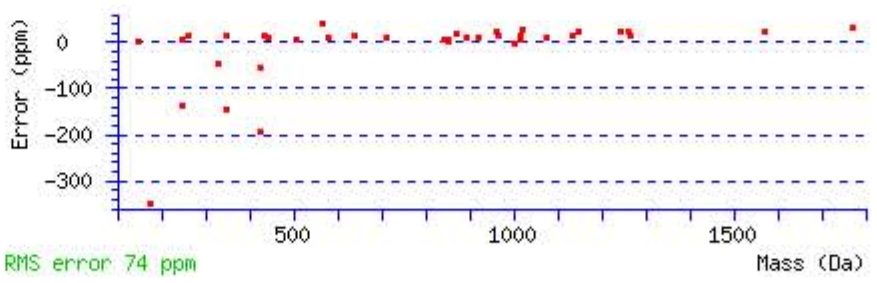
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2279.035965
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.00059
**Matches :** 38/176 fragment ions using 102 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.047761 | 66.527518 | | | | | M | | | | | | | 17 |
| 2 | **247.074704** | 124.040990 | | | 229.064139 | 115.035708 | D | 2149.002750 | 1075.005013 | 2131.976201 | 1066.491738 | 2130.992185 | 1065.999730 | 16 |
| 3 | **346.143118** | 173.575197 | | | 328.132553 | 164.569915 | V | 2033.975807 | 1017.491542 | 2016.949258 | 1008.978267 | 2015.965242 | 1008.486259 | 15 |
| 4 | 493.211532 | **247.109404** | | | 475.200967 | 238.104121 | F | 1934.907393 | 967.957335 | 1917.880844 | 959.444060 | 1916.896828 | 958.952052 | 14 |
| 5 | 580.243560 | 290.625418 | | | 562.232995 | 281.620136 | S | 1787.838979 | 894.423128 | 1770.812430 | 885.909853 | 1769.828414 | 885.417845 | 13 |
| 6 | **1019.468886** | 510.238081 | 1002.442337 | 501.724807 | 1001.458321 | 501.232799 | Q | 1700.806951 | 850.907114 | 1683.780402 | 842.393839 | 1682.796386 | 841.901831 | 12 |
| 7 | **1133.511813** | **567.259545** | 1116.485264 | 558.746270 | 1115.501248 | 558.254262 | N | *1261.581625* | 631.294451 | 1244.555076 | 622.781176 | 1243.571060 | 622.289168 | 11 |
| 8 | **1264.552298** | 632.779787 | 1247.525749 | 624.266513 | 1246.541733 | 623.774505 | M | *1147.538698* | 574.272987 | 1130.512149 | 565.759713 | 1129.528133 | 565.267705 | 10 |
| 9 | 1411.620712 | 706.313994 | 1394.594163 | 697.800720 | 1393.610147 | 697.308712 | F | *1016.498213* | 508.752745 | 999.471664 | 500.239470 | 998.487648 | 499.747462 | 9 |
| 10 | **1571.651361** | 786.329319 | 1554.624812 | 777.816044 | 1553.640796 | 777.324036 | C | *869.429799* | 435.218538 | 852.403250 | 426.705263 | 851.419234 | 426.213255 | 8 |
| 11 | 1642.688475 | 821.847876 | 1625.661926 | 813.334601 | 1624.677910 | 812.842593 | A | *709.399150* | 355.203213 | 692.372601 | 346.689939 | 691.388585 | 346.197931 | 7 |
| 12 | 1699.709939 | 850.358608 | 1682.683390 | 841.845333 | 1681.699374 | 841.353325 | G | *638.362036* | 319.684656 | 621.335487 | 311.171382 | 620.351471 | 310.679374 | 6 |
| 13 | 1836.768851 | **918.888064** | 1819.742302 | 910.374789 | 1818.758286 | 909.882781 | H | *581.340572* | 291.173924 | 564.314023 | 282.660650 | 563.330007 | 282.168642 | 5 |
| 14 | 1933.821615 | 967.414446 | 1916.795066 | 958.901171 | 1915.811050 | 958.409163 | P | *444.281660* | 222.644468 | 427.255111 | 214.131194 | 426.271095 | 213.639186 | 4 |
| 15 | 2020.853643 | 1010.930460 | 2003.827094 | 1002.417185 | 2002.843078 | 1001.925177 | S | *347.228896* | 174.118086 | 330.202347 | 165.604812 | 329.218331 | 165.112804 | 3 |
| 16 | 2133.937707 | 1067.472491 | 2116.911158 | 1058.959217 | 2115.927142 | 1058.467209 | L | *260.196868* | 130.602072 | 243.170319 | 122.088798 | | | 2 |
| 17 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 44.7 | 2279.035965 | 0.032277 | MDVFSQNMFCAGHPSLK |

**Mascot:** http://www.matrixscience.com/

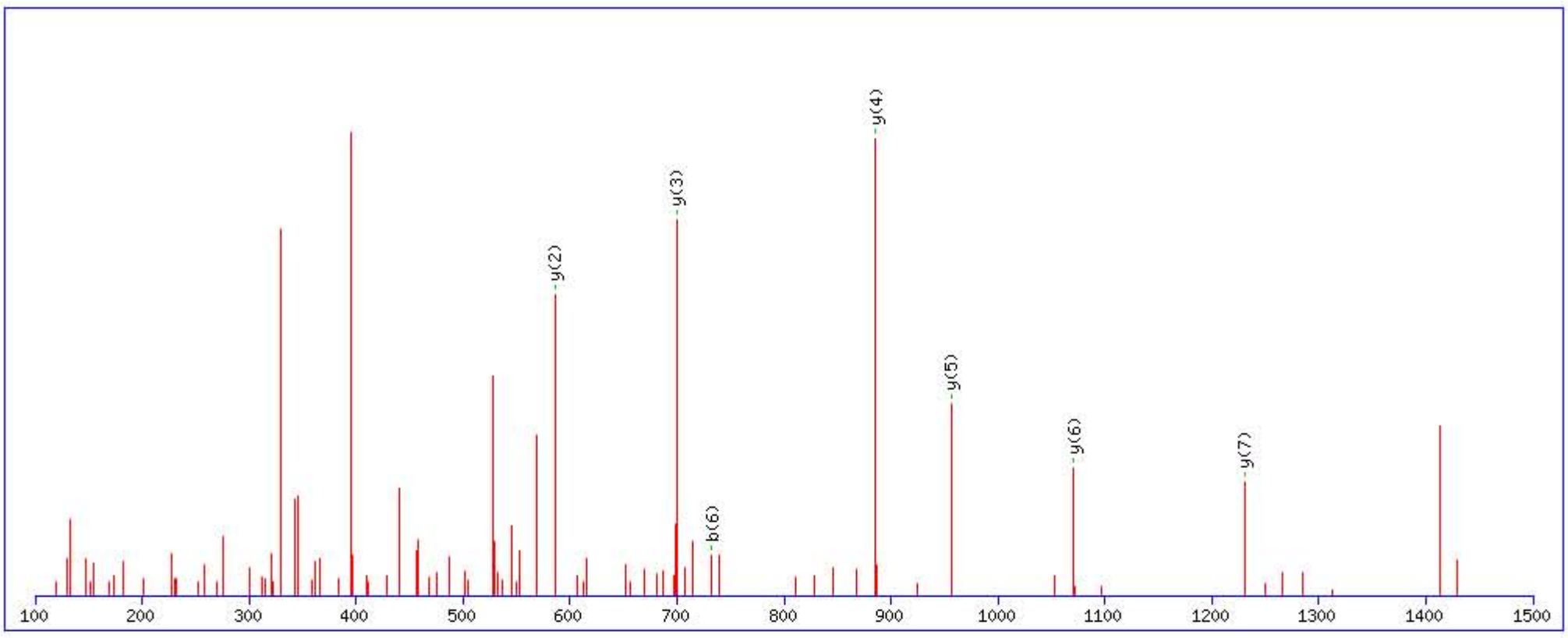
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EACNAWLQK**
Found in **C1RL_HUMAN**, Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL PE=1 SV=2

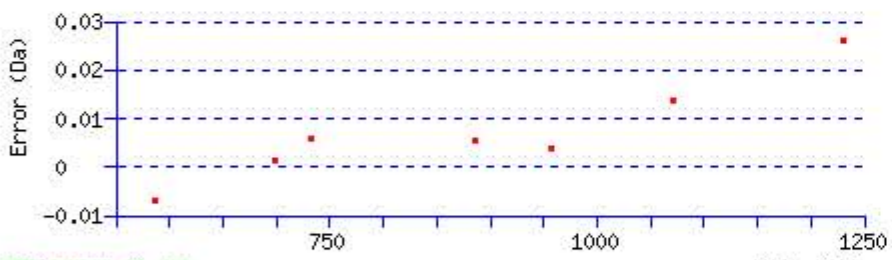
Match to Query 29036: 1429.692488 from(715.853520,2+) rtinseconds(1943) index(66066)
Title: Locus:1.1.1.1951.21 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

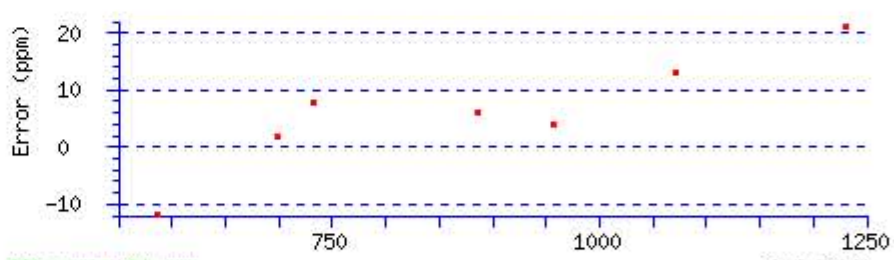
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1429.684601
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0022
**Matches :** 7/74 fragment ions using 13 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | 9 |
| 2 | 201.086983 | 101.047130 | | | 183.076418 | 92.041847 | A | 1301.649311 | 651.328293 | 1284.622762 | 642.815019 | 8 |
| 3 | 361.117632 | 181.062454 | | | 343.107067 | 172.057172 | C | *1230.612197* | 615.809736 | 1213.585648 | 607.296462 | 7 |
| 4 | 475.160559 | 238.083918 | 458.134010 | 229.570643 | 457.149994 | 229.078635 | N | *1070.581548* | 535.794412 | 1053.554999 | 527.281138 | 6 |
| 5 | 546.197673 | 273.602475 | 529.171124 | 265.089200 | 528.187108 | 264.597192 | A | *956.538621* | 478.772948 | 939.512072 | 470.259674 | 5 |
| 6 | *732.276986* | 366.642131 | 715.250437 | 358.128857 | 714.266421 | 357.636849 | W | *885.501507* | 443.254392 | 868.474958 | 434.741117 | 4 |
| 7 | 845.361050 | 423.184163 | 828.334501 | 414.670889 | 827.350485 | 414.178881 | L | *699.422194* | 350.214735 | 682.395645 | 341.701461 | 3 |
| 8 | 1284.586376 | 642.796826 | 1267.559827 | 634.283552 | 1266.575811 | 633.791543 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159428 | 2 |
| 9 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 39.4 | 1429.684601 | 0.007887 | EACNAWLQK |
| 11.2 | 1429.679886 | 0.012602 | MDDKELIEYFK |
| 11.0 | 1429.687988 | 0.004500 | CNTPAMGLQK |
| 8.6 | 1429.687119 | 0.005369 | EQHQTMDISLTK |
| 8.3 | 1429.705719 | -0.013231 | EANALAMQQK |
| 7.3 | 1429.687103 | 0.005385 | EIPDPANSTCAKK |
| 7.2 | 1429.702362 | -0.009874 | LSNWESQQK |
| 6.3 | 1429.705719 | -0.013231 | EANALAMQQK |
| 6.0 | 1429.680588 | 0.011900 | MRIHCLENVDK |
| 5.7 | 1429.687103 | 0.005385 | QSEADNNTLK |

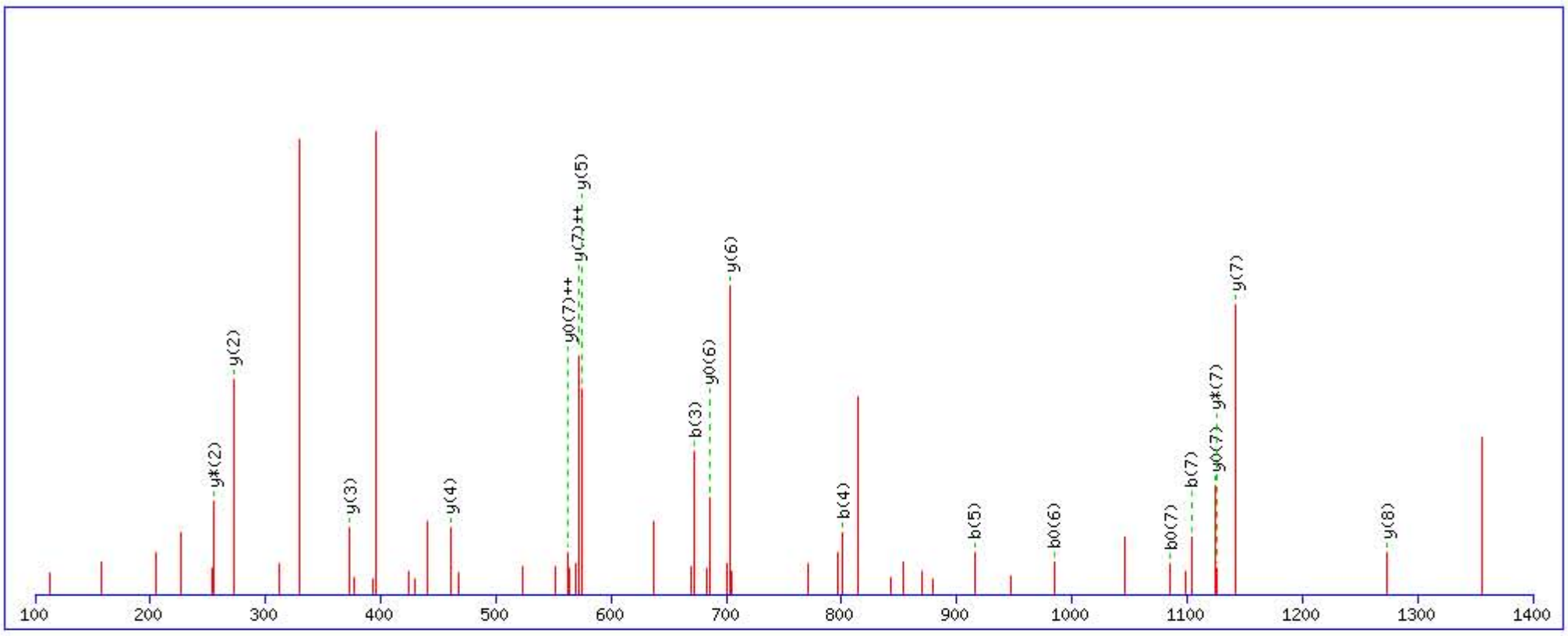
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TMQENSTPR**
Found in **C1S_HUMAN**, Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1

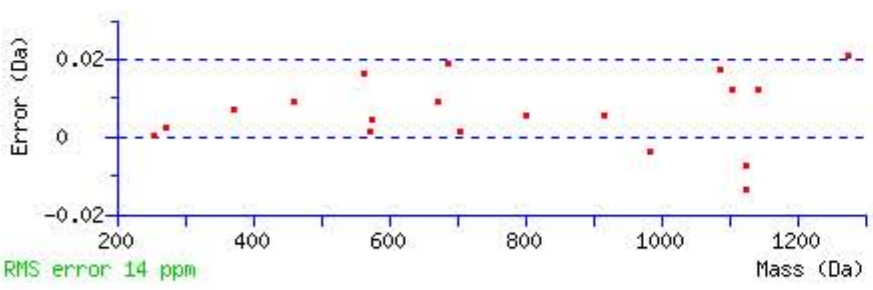
Match to Query 26357: 1373.645048 from(687.829800,2+) rtinseconds(1391) index(30376)
Title: Locus:1.1.1.592.23 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

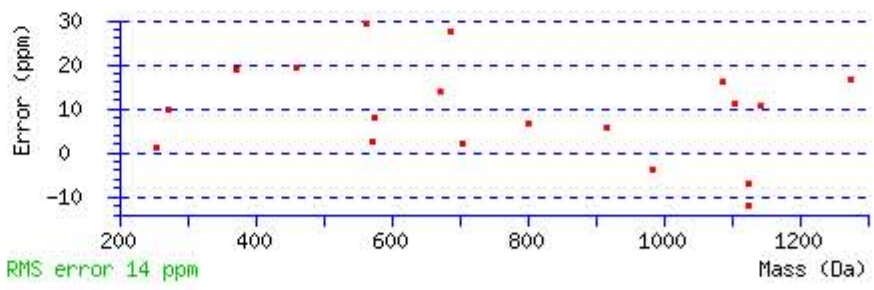
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1373.643143
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0008
**Matches :** 19/88 fragment ions using 35 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 9 |
| 2 | 233.095440 | 117.051358 | | | 215.084875 | 108.046076 | M | *1273.602754* | 637.305015 | 1256.576205 | 628.791741 | 1255.592189 | 628.299733 | 8 |
| 3 | **672.320766** | 336.664021 | 655.294217 | 328.150747 | 654.310201 | 327.658739 | Q | *1142.562269* | 571.784773 | 1125.535720 | 563.271498 | 1124.551704 | 562.779490 | 7 |
| 4 | **801.363359** | 401.185318 | 784.336810 | 392.672043 | 783.352794 | 392.180035 | E | *703.336943* | 352.172110 | 686.310394 | 343.658835 | 685.326378 | 343.166827 | 6 |
| 5 | **915.406286** | 458.206781 | 898.379737 | 449.693507 | 897.395721 | 449.201499 | N | *574.294350* | 287.650813 | 557.267801 | 279.137539 | 556.283785 | 278.645531 | 5 |
| 6 | 1002.438314 | 501.722795 | 985.411765 | 493.209521 | 984.427749 | 492.717513 | S | *460.251423* | 230.629349 | 443.224874 | 222.116075 | 442.240858 | 221.624067 | 4 |
| 7 | **1103.485993** | 552.246635 | 1086.459444 | 543.733360 | 1085.475428 | 543.241352 | T | *373.219395* | 187.113335 | 356.192846 | 178.600061 | 355.208830 | 178.108053 | 3 |
| 8 | 1200.538757 | 600.773017 | 1183.512208 | 592.259742 | 1182.528192 | 591.767734 | P | *272.171716* | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 9 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.8 | 1373.643143 | 0.001905 | TMQENSTPR |
| 5.8 | 1373.635742 | 0.009306 | DRGMPSDSPEKR |

**Mascot:** http://www.matrixscience.com/

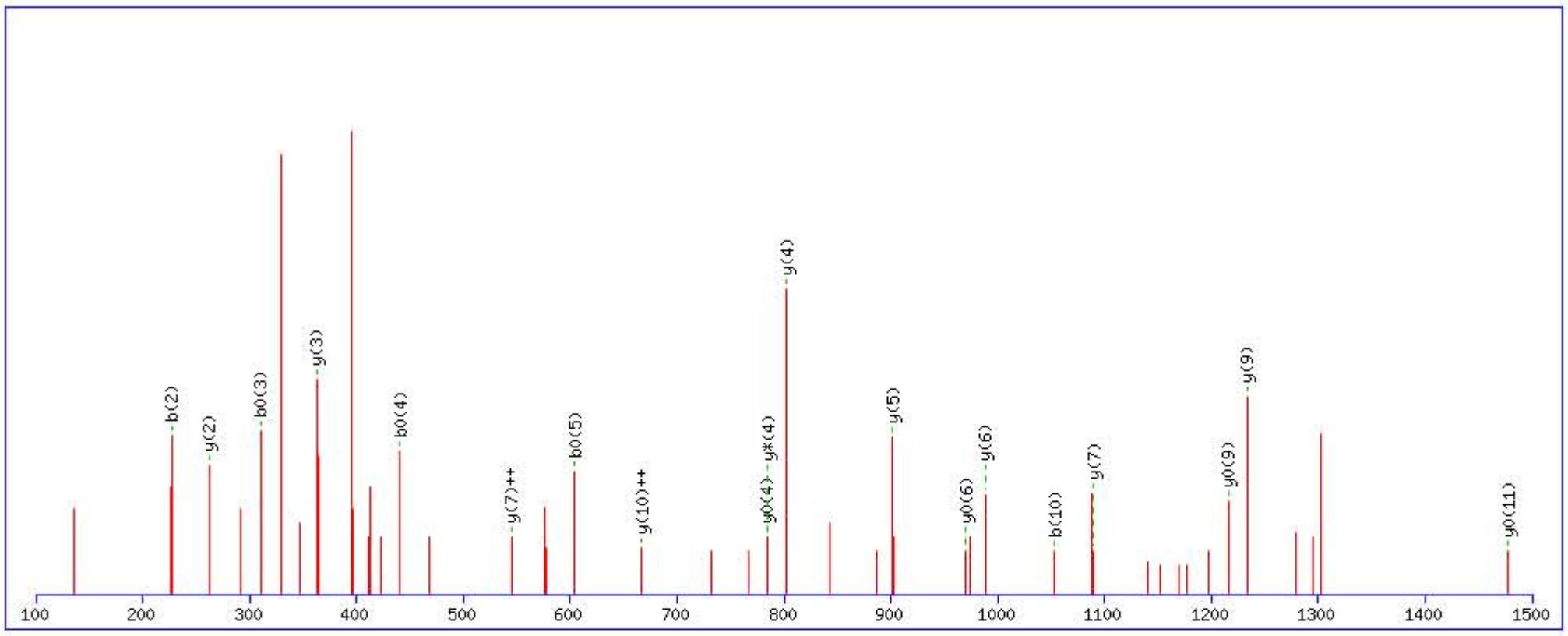
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EPTMYVGSTSVQTSR**
Found in **C1S_HUMAN**, Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1

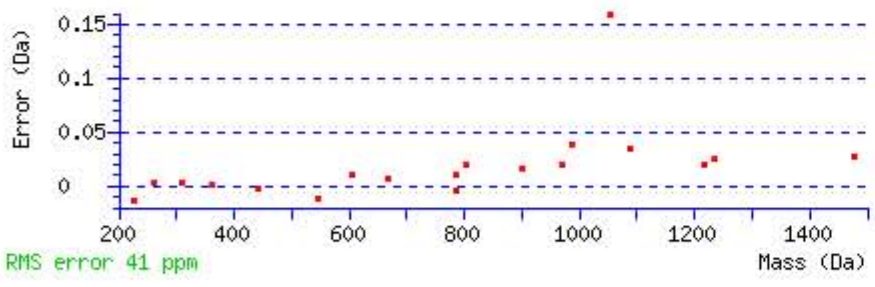
Match to Query 43162: 1952.950902 from(651.990910,3+) rtinseconds(1894) index(49514)
Title: Locus:1.1.1.1897.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

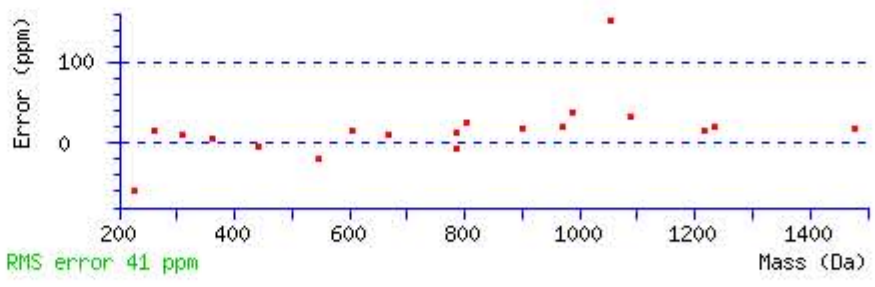
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1952.933594
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.0012
**Matches :** 19/144 fragment ions using 36 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 15 |
| 2 | 227.102633 | 114.054954 | | | 209.092068 | 105.049672 | P | 1824.898269 | 912.952773 | 1807.871720 | 904.439498 | 1806.887704 | 903.947490 | 14 |
| 3 | 328.150312 | 164.578794 | | | 310.139747 | 155.573512 | T | 1727.845505 | 864.426391 | 1710.818956 | 855.913116 | 1709.834940 | 855.421108 | 13 |
| 4 | 459.190797 | 230.099036 | | | 441.180232 | 221.093754 | M | 1626.797826 | 813.902551 | 1609.771277 | 805.389277 | 1608.787261 | 804.897269 | 12 |
| 5 | 622.254126 | 311.630701 | | | 604.243561 | 302.625419 | Y | 1495.757341 | 748.382309 | 1478.730792 | 739.869034 | 1477.746776 | 739.377026 | 11 |
| 6 | 721.322540 | 361.164908 | | | 703.311975 | 352.159626 | V | 1332.694012 | 666.850644 | 1315.667463 | 658.337370 | 1314.683447 | 657.845362 | 10 |
| 7 | 778.344004 | 389.675640 | | | 760.333439 | 380.670358 | G | *1233.625598* | 617.316437 | 1216.599049 | 608.803163 | 1215.615033 | 608.311155 | 9 |
| 8 | 865.376032 | 433.191654 | | | 847.365467 | 424.186372 | S | 1176.604134 | 588.805705 | 1159.577585 | 580.292431 | 1158.593569 | 579.800423 | 8 |
| 9 | 966.423711 | 483.715494 | | | 948.413146 | 474.710211 | T | *1089.572106* | 545.289691 | 1072.545557 | 536.776417 | 1071.561541 | 536.284409 | 7 |
| 10 | 1053.455739 | 527.231508 | | | 1035.445174 | 518.226225 | S | *988.524427* | 494.765852 | 971.497878 | 486.252577 | 970.513862 | 485.760569 | 6 |
| 11 | 1152.524153 | 576.765715 | | | 1134.513588 | 567.760432 | V | *901.492399* | 451.249838 | 884.465850 | 442.736563 | 883.481834 | 442.244555 | 5 |
| 12 | 1591.749479 | 796.378378 | 1574.722930 | 787.865103 | 1573.738914 | 787.373095 | Q | *802.423985* | 401.715631 | 785.397436 | 393.202356 | 784.413420 | 392.710348 | 4 |
| 13 | 1692.797158 | 846.902217 | 1675.770609 | 838.388943 | 1674.786593 | 837.896935 | T | *363.198659* | 182.102968 | 346.172110 | 173.589693 | 345.188094 | 173.097685 | 3 |
| 14 | 1779.829186 | 890.418231 | 1762.802637 | 881.904957 | 1761.818621 | 881.412949 | S | *262.150980* | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 15 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.5 | 1952.933594 | 0.017308 | EPTMYVGSTSVQTSR |
| 0.5 | 1952.944794 | 0.006108 | MNQVTSKYANQSAGK |

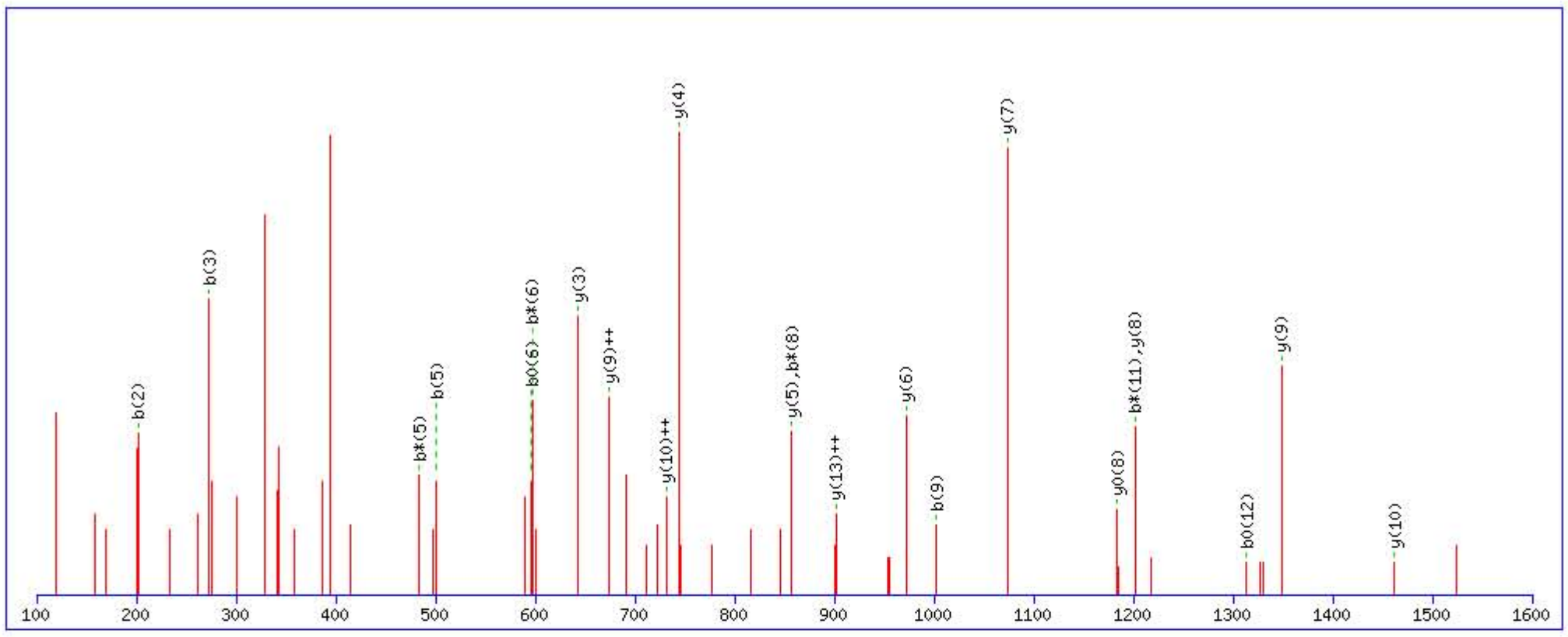
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SNALDIIFQTDLTGQK**
Found in **C1S_HUMAN**, Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1

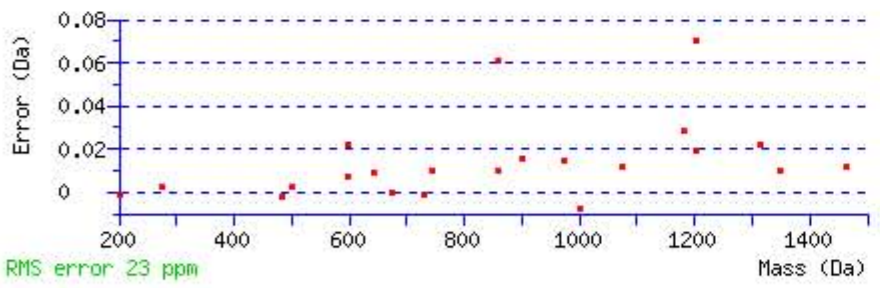
Match to Query 46167: 2074.100532 from(692.374120,3+) rtinseconds(2866) index(39587)
Title: Locus:1.1.1.1105.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

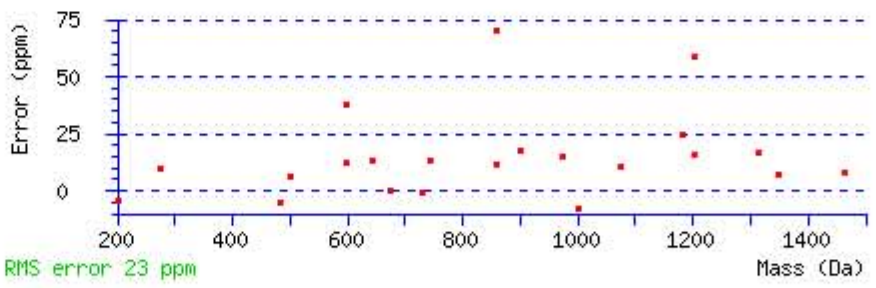
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2074.076874
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q15 : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 5.3e-006
**Matches :** 22/172 fragment ions using 26 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 16 |
| 2 | *202.082231* | 101.544753 | 185.055682 | 93.031479 | 184.071666 | 92.539471 | N | 1988.052127 | 994.529702 | 1971.025578 | 986.016427 | 1970.041562 | 985.524419 | 15 |
| 3 | *273.119345* | 137.063311 | 256.092796 | 128.550036 | 255.108780 | 128.058028 | A | 1874.009200 | 937.508238 | 1856.982651 | 928.994964 | 1855.998635 | 928.502956 | 14 |
| 4 | 386.203409 | 193.605343 | 369.176860 | 185.092068 | 368.192844 | 184.600060 | L | 1802.972086 | 901.989681 | 1785.945537 | 893.476407 | 1784.961521 | 892.984399 | 13 |
| 5 | *501.230352* | 251.118814 | 484.203803 | 242.605540 | 483.219787 | 242.113532 | D | 1689.888022 | 845.447649 | 1672.861473 | 836.934375 | 1671.877457 | 836.442367 | 12 |
| 6 | 614.314416 | 307.660846 | 597.287867 | 299.147572 | 596.303851 | 298.655564 | I | 1574.861079 | 787.934178 | 1557.834530 | 779.420903 | 1556.850514 | 778.928895 | 11 |
| 7 | 727.398480 | 364.202878 | 710.371931 | 355.689604 | 709.387915 | 355.197596 | I | *1461.777015* | 731.392146 | 1444.750466 | 722.878871 | 1443.766450 | 722.386863 | 10 |
| 8 | 874.466894 | 437.737085 | 857.440345 | 429.223811 | 856.456329 | 428.731803 | F | *1348.692951* | 674.850114 | 1331.666402 | 666.336839 | 1330.682386 | 665.844831 | 9 |
| 9 | *1002.525472* | 501.766374 | 985.498923 | 493.253100 | 984.514907 | 492.761092 | Q | *1201.624537* | 601.315907 | 1184.597988 | 592.802632 | 1183.613972 | 592.310624 | 8 |
| 10 | 1103.573151 | 552.290214 | 1086.546602 | 543.776939 | 1085.562586 | 543.284931 | T | *1073.565959* | 537.286618 | 1056.539410 | 528.773343 | 1055.555394 | 528.281335 | 7 |
| 11 | 1218.600094 | 609.803685 | 1201.573545 | 601.290411 | 1200.589529 | 600.798403 | D | *972.518280* | 486.762778 | 955.491731 | 478.249504 | 954.507715 | 477.757496 | 6 |
| 12 | 1331.684158 | 666.345717 | 1314.657609 | 657.832443 | 1313.673593 | 657.340435 | L | *857.491337* | 429.249307 | 840.464788 | 420.736032 | 839.480772 | 420.244024 | 5 |
| 13 | 1432.731837 | 716.869557 | 1415.705288 | 708.356282 | 1414.721272 | 707.864274 | T | *744.407273* | 372.707275 | 727.380724 | 364.194000 | 726.396708 | 363.701992 | 4 |
| 14 | 1489.753301 | 745.380289 | 1472.726752 | 736.867014 | 1471.742736 | 736.375006 | G | *643.359594* | 322.183435 | 626.333045 | 313.670161 | | | 3 |
| 15 | 1928.978627 | 964.992952 | 1911.952078 | 956.479677 | 1910.968062 | 955.987669 | Q | 586.338130 | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.8 | 2074.076874 | 0.023658 | SNALDIIFQTDLTGQK |
| 22.4 | 2074.076874 | 0.023658 | SNALDIIFQTDLTGQK |
| 2.5 | 2074.088104 | 0.012428 | SKGLVQNIDQLYSGGGK |

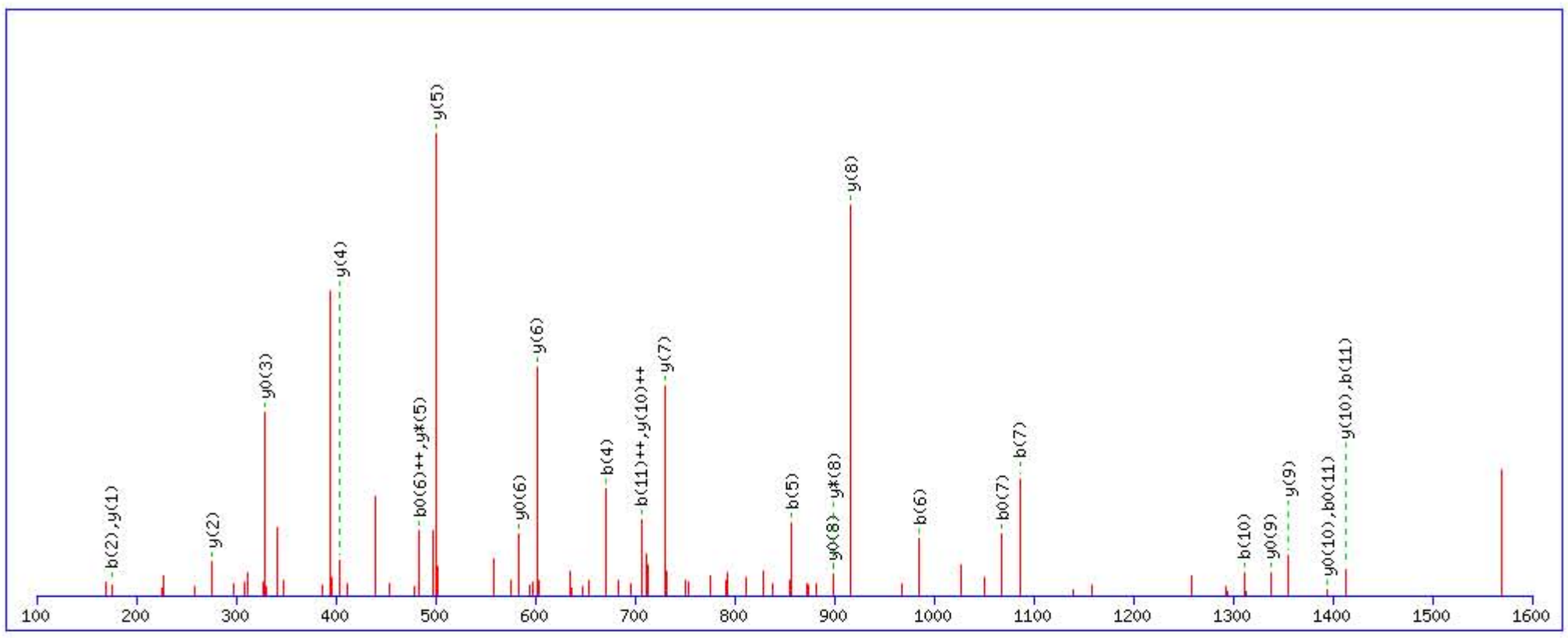
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SSGQWQTPGATR**
Found in **CO2_HUMAN**, Complement C2 OS=Homo sapiens GN=C2 PE=1 SV=2

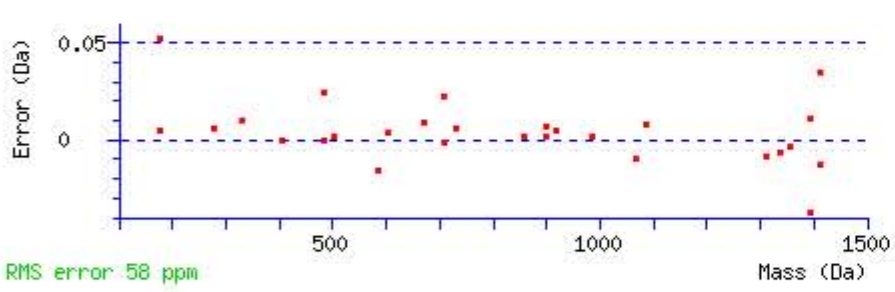
Match to Query 34012: 1585.767368 from(793.890960,2+) rtinseconds(1703) index(64586)
Title: Locus:1.1.1.1868.12 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

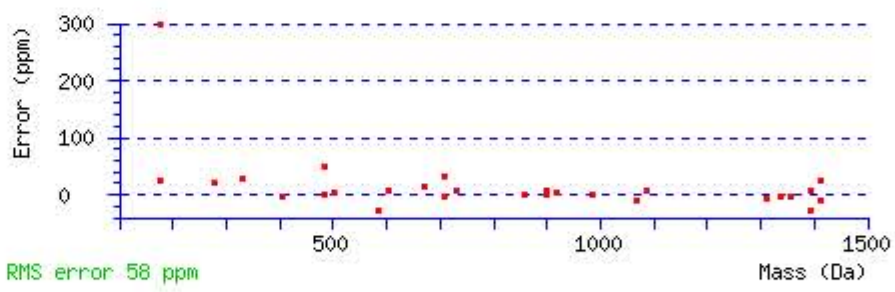
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1585.767120
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 1.8e-005
**Matches :** 28/124 fragment ions using 38 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 12 |
| 2 | 175.071332 | 88.039304 | | | 157.060767 | 79.034021 | S | 1499.742361 | 750.374818 | 1482.715812 | 741.861544 | 1481.731796 | 741.369536 | 11 |
| 3 | 232.092796 | 116.550036 | | | 214.082231 | 107.544753 | G | *1412.710333* | 706.858805 | 1395.683784 | 698.345530 | 1394.699768 | 697.853522 | 10 |
| 4 | 671.318122 | 336.162699 | 654.291573 | 327.649425 | 653.307557 | 327.157417 | Q | *1355.688869* | 678.348072 | 1338.662320 | 669.834798 | 1337.678304 | 669.342790 | 9 |
| 5 | 857.397435 | 429.202356 | 840.370886 | 420.689081 | 839.386870 | 420.197073 | W | *916.463543* | 458.735410 | 899.436994 | 450.222135 | 898.452978 | 449.730127 | 8 |
| 6 | 985.456013 | 493.231645 | 968.429464 | 484.718370 | 967.445448 | 484.226362 | Q | *730.384230* | 365.695753 | 713.357681 | 357.182478 | 712.373665 | 356.690470 | 7 |
| 7 | 1086.503692 | 543.755484 | 1069.477143 | 535.242210 | 1068.493127 | 534.750202 | T | *602.325652* | 301.666464 | 585.299103 | 293.153189 | 584.315087 | 292.661181 | 6 |
| 8 | 1183.556456 | 592.281866 | 1166.529907 | 583.768592 | 1165.545891 | 583.276584 | P | *501.277973* | 251.142624 | 484.251424 | 242.629350 | 483.267408 | 242.137342 | 5 |
| 9 | 1240.577920 | 620.792598 | 1223.551371 | 612.279324 | 1222.567355 | 611.787315 | G | *404.225209* | 202.616242 | 387.198660 | 194.102968 | 386.214644 | 193.610960 | 4 |
| 10 | 1311.615034 | 656.311155 | 1294.588485 | 647.797881 | 1293.604469 | 647.305872 | A | 347.203745 | 174.105510 | 330.177196 | 165.592236 | 329.193180 | 165.100228 | 3 |
| 11 | 1412.662713 | 706.834994 | 1395.636164 | 698.321720 | 1394.652148 | 697.829712 | T | *276.166631* | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 12 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 59.0 | 1585.767120 | 0.000248 | SSGQWQTPGATR |
| 30.1 | 1585.767120 | 0.000248 | SSGQWQTPGATR |
| 7.9 | 1585.769653 | -0.002285 | GDVGTAGSVGGTGEPGLR |
| 7.3 | 1585.769592 | -0.002224 | ETDHKSLSSSPDKR |
| 5.5 | 1585.766922 | 0.000446 | RTSNERPGSGQGQGR |
| 5.5 | 1585.767075 | 0.000293 | AWENLGEQMGKAPR |
| 5.0 | 1585.751846 | 0.015522 | LMDEPALRSPGGGDR |
| 1.8 | 1585.777863 | -0.010495 | MKQPIMADGPR |
| 0.8 | 1585.781021 | -0.013653 | IGLFYMDNDLITR |

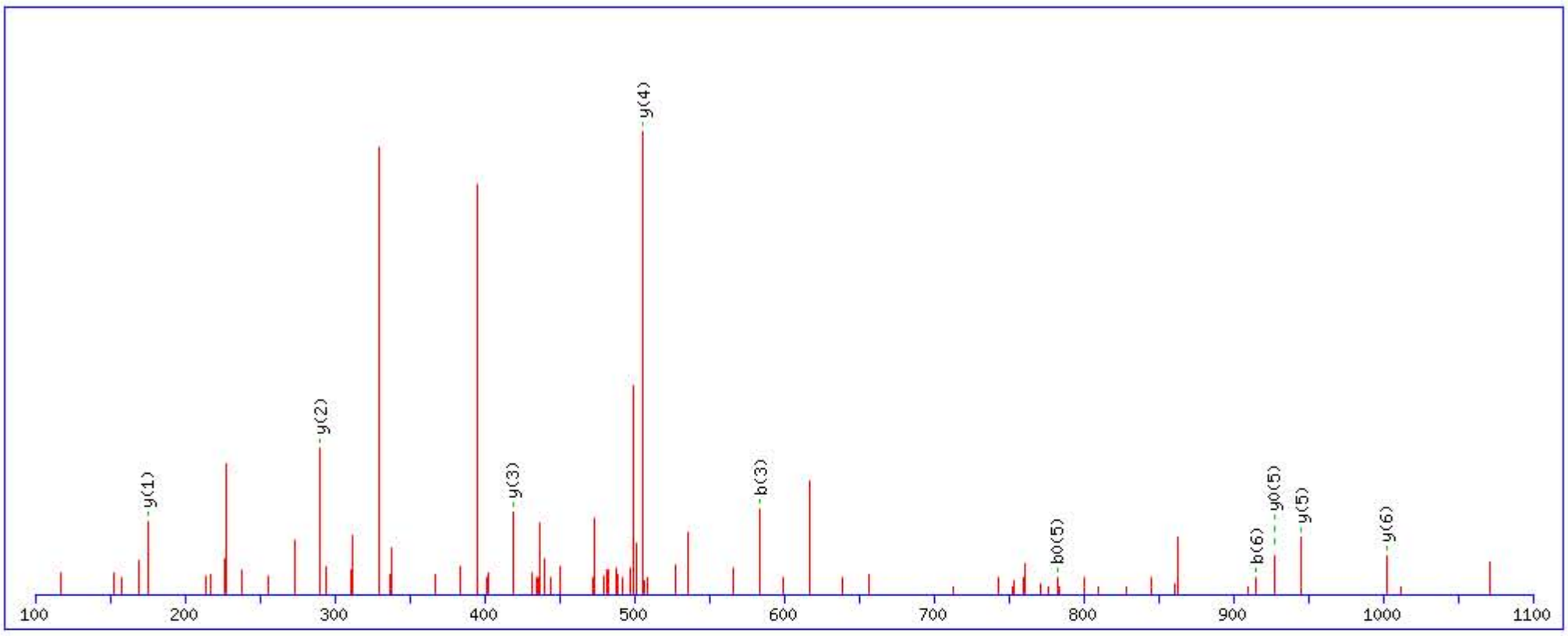
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SGQSEDR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

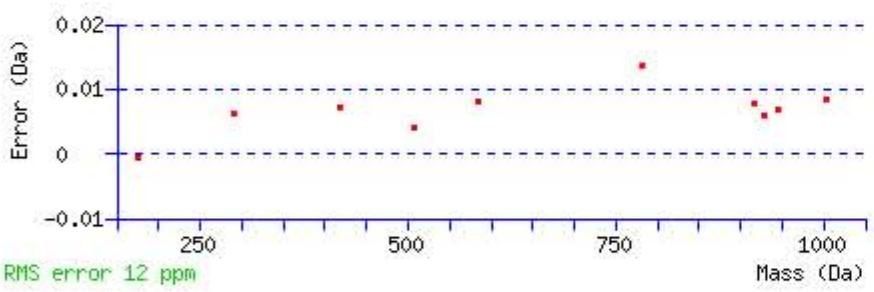
Match to Query 16029: 1088.496348 from(545.255450,2+) rtinseconds(1146) index(29319)
Title: Locus:1.1.1.507.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

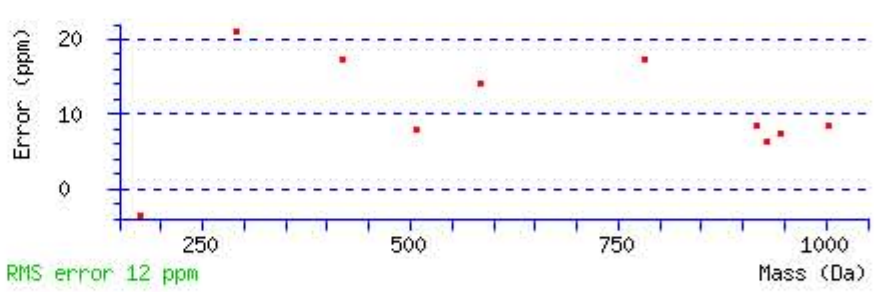
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1088.492050
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 30 **Expect:** 0.0067
**Matches :** 10/66 fragment ions using 28 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 7 |
| 2 | 145.060768 | 73.034022 | | | 127.050203 | 64.028740 | G | *1002.467306* | 501.737291 | 985.440757 | 493.224017 | 984.456741 | 492.732009 | 6 |
| 3 | **584.286094** | 292.646685 | 567.259545 | 284.133411 | 566.275529 | 283.641403 | Q | *945.445842* | 473.226559 | 928.419293 | 464.713285 | 927.435277 | 464.221277 | 5 |
| 4 | 671.318122 | 336.162699 | 654.291573 | 327.649425 | 653.307557 | 327.157417 | S | *506.220516* | 253.613896 | 489.193967 | 245.100621 | 488.209951 | 244.608613 | 4 |
| 5 | 800.360715 | 400.683996 | 783.334166 | 392.170721 | 782.350150 | 391.678713 | E | *419.188488* | 210.097882 | 402.161939 | 201.584608 | 401.177923 | 201.092600 | 3 |
| 6 | **915.387658** | 458.197467 | 898.361109 | 449.684192 | 897.377093 | 449.192185 | D | *290.145895* | 145.576585 | 273.119346 | 137.063311 | 272.135330 | 136.571303 | 2 |
| 7 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

### All matches to this query

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 30.4 | 1088.492050 | 0.004298 | SGQSEDR |
| 9.9 | 1088.509811 | -0.013463 | GAEAGSVVDER |
| 8.1 | 1088.509811 | -0.013463 | DAAPLTSSGDR |
| 4.7 | 1088.492065 | 0.004283 | LSDPAVCGDR |
| 4.3 | 1088.503265 | -0.006917 | CPAAKENGSR |
| 2.6 | 1088.510681 | -0.014333 | ATMQGDR |
| 0.9 | 1088.495880 | 0.000468 | RGEGRDEDR |

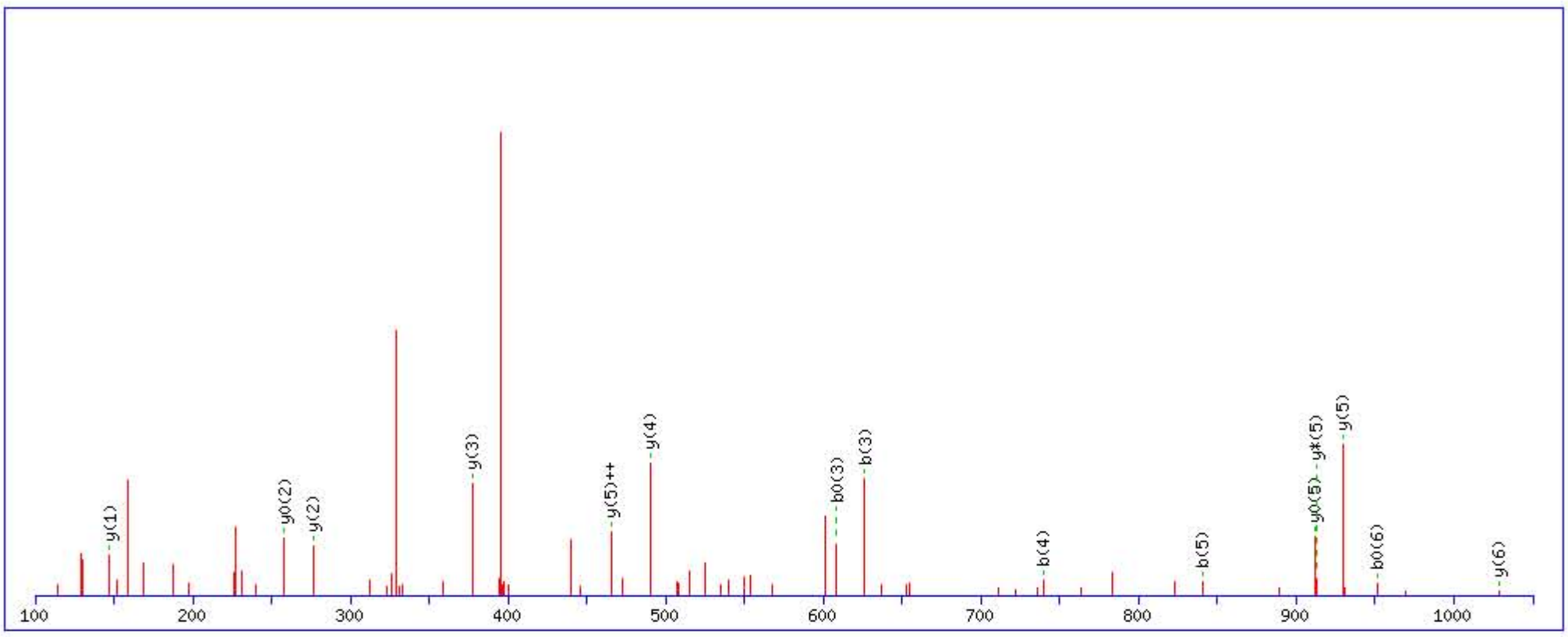
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SVQLTEK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

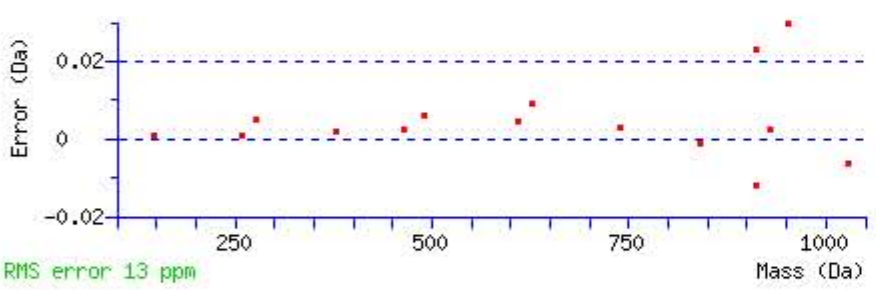
Match to Query 17111: 1114.608448 from(558.311500,2+) rtinseconds(1546) index(47249)
Title: Locus:1.1.1.1776.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

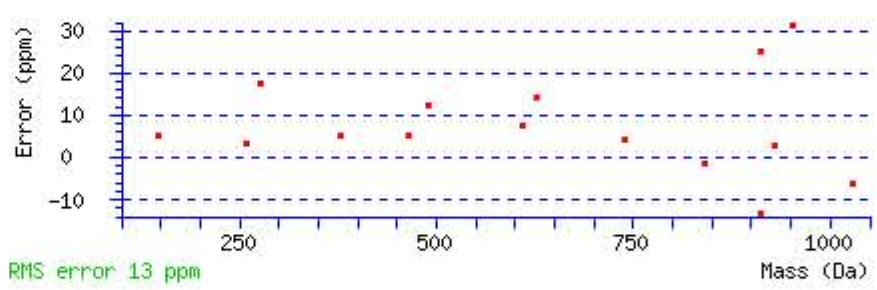
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1114.605621
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.02
**Matches :** 15/66 fragment ions using 28 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 7 |
| 2 | 187.107718 | 94.057497 | | | 169.097153 | 85.052214 | V | *1028.580880* | 514.794078 | 1011.554331 | 506.280804 | 1010.570315 | 505.788796 | 6 |
| 3 | **626.333044** | 313.670160 | 609.306495 | 305.156885 | 608.322479 | 304.664877 | Q | *929.512466* | 465.259871 | 912.485917 | 456.746597 | 911.501901 | 456.254589 | 5 |
| 4 | **739.417108** | 370.212192 | 722.390559 | 361.698917 | 721.406543 | 361.206909 | L | *490.287140* | 245.647208 | 473.260591 | 237.133934 | 472.276575 | 236.641926 | 4 |
| 5 | **840.464787** | 420.736032 | 823.438238 | 412.222757 | 822.454222 | 411.730749 | T | *377.203076* | 189.105176 | 360.176527 | 180.591902 | 359.192511 | 180.099894 | 3 |
| 6 | 969.507380 | 485.257328 | 952.480831 | 476.744054 | 951.496815 | 476.252046 | E | *276.155397* | 138.581336 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 7 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 30.8 | 1114.605621 | 0.002827 | SVQLTEK |
| 18.6 | 1114.613480 | -0.005032 | SVFAKHGLEK |
| 11.1 | 1114.623367 | -0.014919 | SIQDAELLVK |
| 7.3 | 1114.623352 | -0.014904 | ILDAIKEADK |
| 6.2 | 1114.623367 | -0.014919 | ASVGLEVLAEK |
| 6.0 | 1114.623383 | -0.014935 | QVTEAVVIEK |
| 5.2 | 1114.609451 | -0.001003 | SVARLSPETR |
| 4.8 | 1114.623352 | -0.014904 | LVEALAAATEK |
| 4.2 | 1114.609436 | -0.000988 | EGIKRQQEK |
| 3.3 | 1114.598236 | 0.010212 | SAVITSLDPGR |

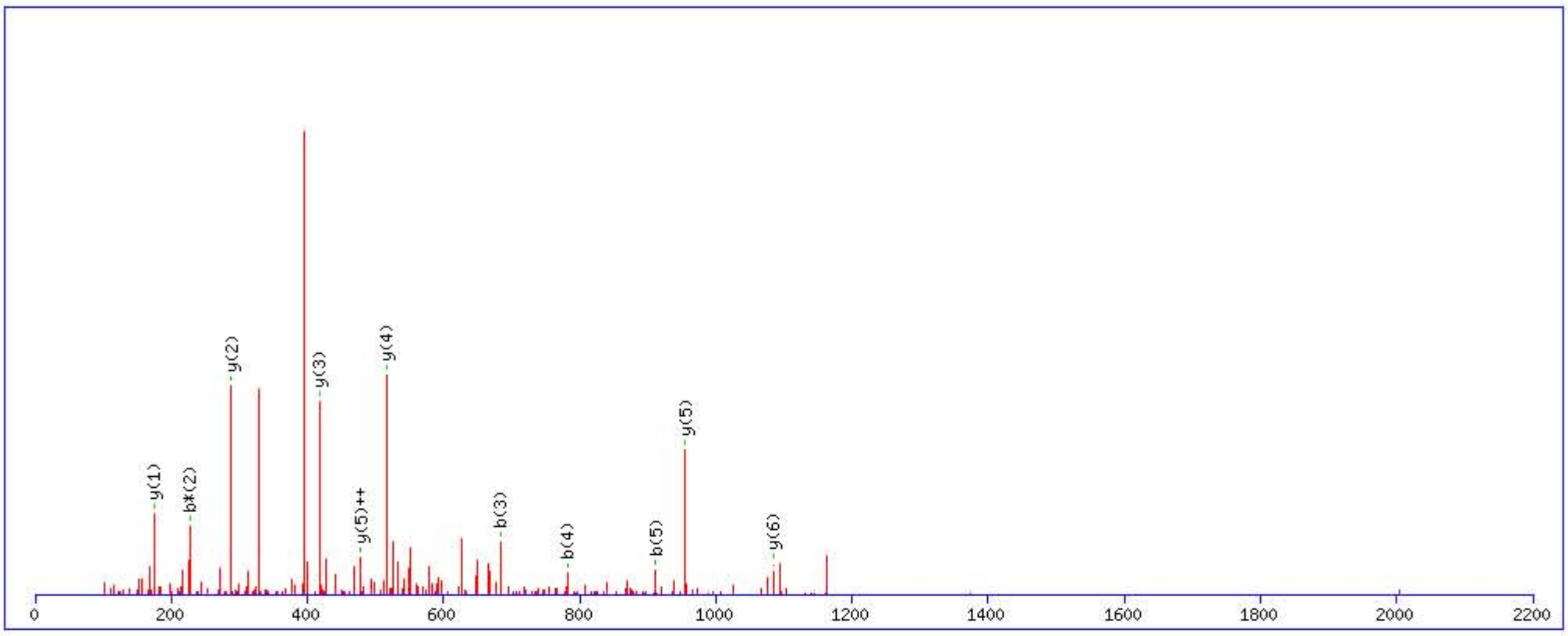
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NEQVEIR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

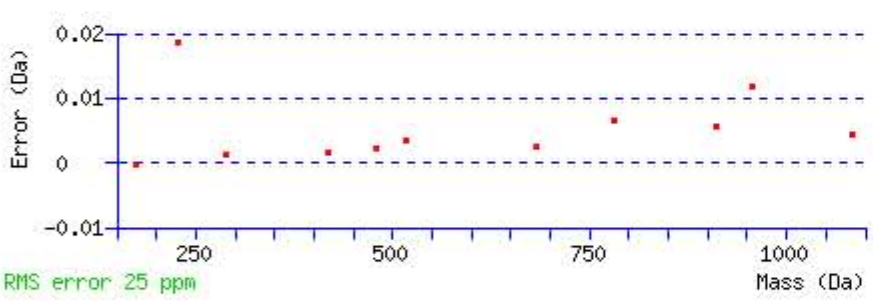
Match to Query 20497: 1197.621788 from(599.818170,2+) rtinseconds(1642) index(32007)
Title: Locus:1.1.1.680.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

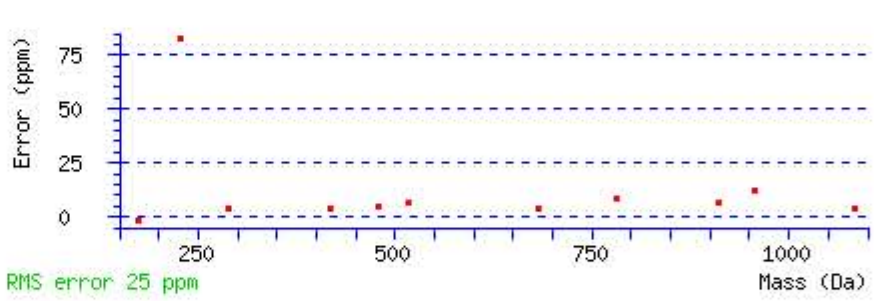
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1197.617569
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0089
**Matches :** 11/66 fragment ions using 22 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 7 |
| 2 | 244.092796 | 122.550036 | 227.066247 | 114.036762 | 226.082231 | 113.544754 | E | *1084.581942* | 542.794609 | 1067.555393 | 534.281335 | 1066.571377 | 533.789327 | 6 |
| 3 | **683.318122** | 342.162699 | 666.291573 | 333.649425 | 665.307557 | 333.157417 | Q | *955.539349* | 478.273313 | 938.512800 | 469.760038 | 937.528784 | 469.268030 | 5 |
| 4 | **782.386536** | 391.696906 | 765.359987 | 383.183632 | 764.375971 | 382.691624 | V | *516.314023* | 258.660650 | 499.287474 | 250.147375 | 498.303458 | 249.655367 | 4 |
| 5 | **911.429129** | 456.218203 | 894.402580 | 447.704928 | 893.418564 | 447.212920 | E | *417.245609* | 209.126443 | 400.219060 | 200.613168 | 399.235044 | 200.121160 | 3 |
| 6 | 1024.513193 | 512.760235 | 1007.486644 | 504.246960 | 1006.502628 | 503.754952 | I | *288.203016* | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 7 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.3 | 1197.617569 | 0.004219 | NEQVEIR |
| 14.7 | 1197.636215 | -0.014427 | GVSQMPLR |
| 10.7 | 1197.617569 | 0.004219 | NQEDLLR |
| 8.5 | 1197.617569 | 0.004219 | LQDNELR |
| 8.5 | 1197.617569 | 0.004219 | QEVNELR |
| 6.4 | 1197.621399 | 0.000389 | EKHSTQAKNR |
| 5.8 | 1197.628815 | -0.007027 | QLSMQVHALR |
| 4.8 | 1197.625443 | -0.003655 | WGSSLVKHER |
| 2.0 | 1197.635315 | -0.013527 | AAAAAETPEVLR |
| 1.5 | 1197.617584 | 0.004204 | QDLDQLR |

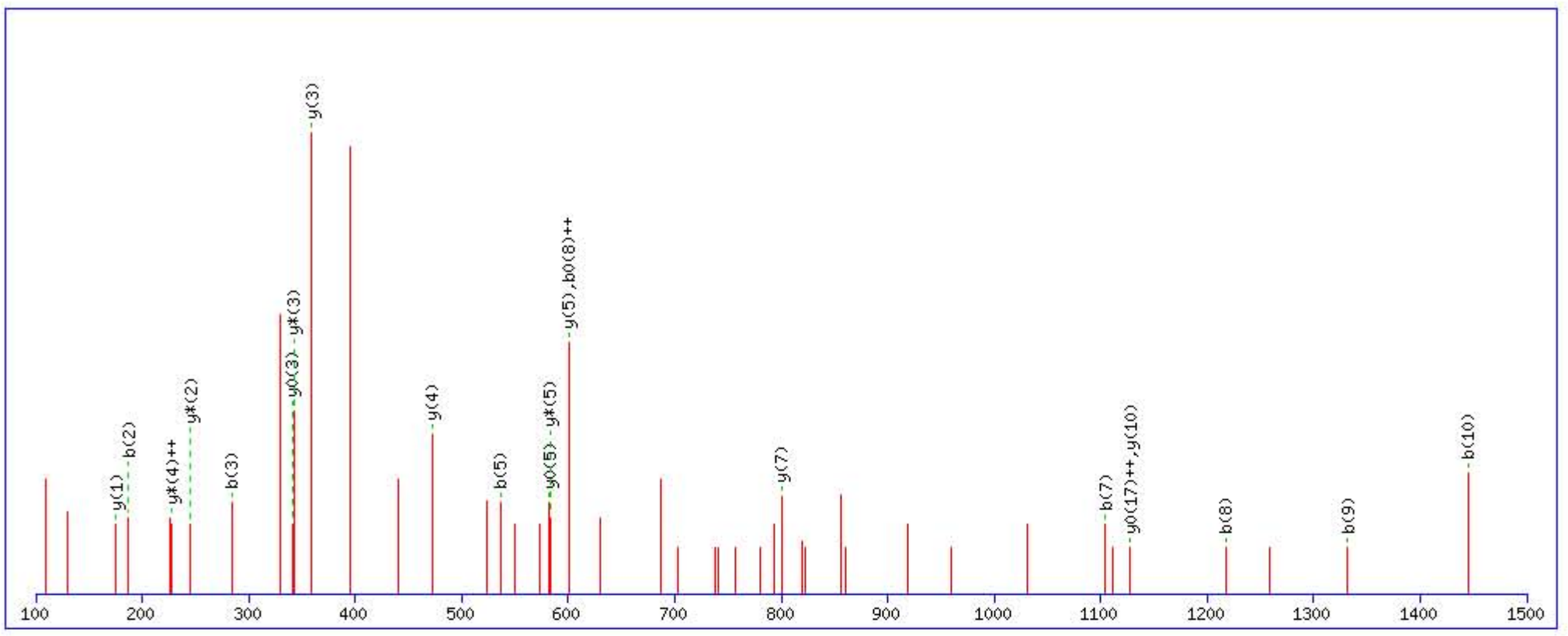
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DAPDHQELNLDVSLQLPSR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

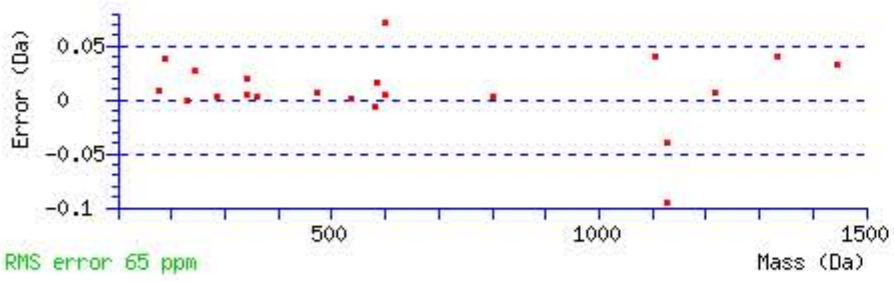
Match to Query 21236: 2457.261336 from(615.322610,4+) rtinseconds(2603) index(37719)
Title: Locus:1.1.1.1015.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

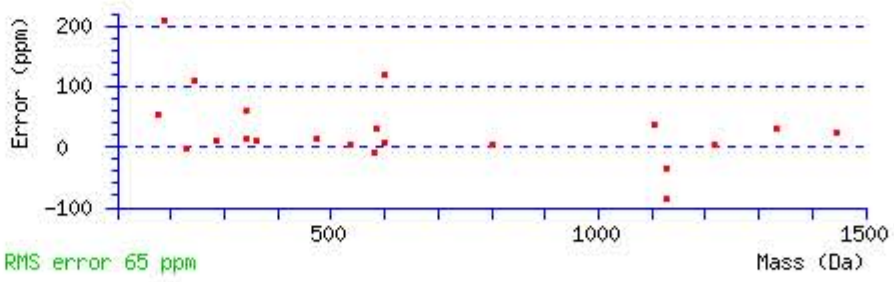
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2457.232193
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 36 **Expect:** 0.00076
**Matches :** 21/204 fragment ions using 42 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 19 |
| 2 | *187.071333* | 94.039304 | | | 169.060768 | 85.034022 | A | 2343.212542 | 1172.109909 | 2326.185993 | 1163.596634 | 2325.201977 | 1163.104626 | 18 |
| 3 | *284.124097* | 142.565686 | | | 266.113532 | 133.560404 | P | 2272.175428 | 1136.591352 | 2255.148879 | 1128.078077 | 2254.164863 | 1127.586069 | 17 |
| 4 | 399.151040 | 200.079158 | | | 381.140475 | 191.073875 | D | 2175.122664 | 1088.064970 | 2158.096115 | 1079.551695 | 2157.112099 | 1079.059687 | 16 |
| 5 | *536.209952* | 268.608614 | | | 518.199387 | 259.603332 | H | 2060.095721 | 1030.551498 | 2043.069172 | 1022.038224 | 2042.085156 | 1021.546216 | 15 |
| 6 | 975.435278 | 488.221277 | 958.408729 | 479.708003 | 957.424713 | 479.215995 | Q | 1923.036809 | 962.022043 | 1906.010260 | 953.508768 | 1905.026244 | 953.016760 | 14 |
| 7 | *1104.477871* | 552.742574 | 1087.451322 | 544.229299 | 1086.467306 | 543.737291 | E | 1483.811483 | 742.409380 | 1466.784934 | 733.896105 | 1465.800918 | 733.404097 | 13 |
| 8 | *1217.561935* | 609.284606 | 1200.535386 | 600.771331 | 1199.551370 | 600.279323 | L | 1354.768890 | 677.888083 | 1337.742341 | 669.374809 | 1336.758325 | 668.882801 | 12 |
| 9 | *1331.604862* | 666.306069 | 1314.578313 | 657.792795 | 1313.594297 | 657.300786 | N | 1241.684826 | 621.346051 | 1224.658277 | 612.832777 | 1223.674261 | 612.340769 | 11 |
| 10 | *1444.688926* | 722.848101 | 1427.662377 | 714.334826 | 1426.678361 | 713.842818 | L | *1127.641899* | 564.324588 | 1110.615350 | 555.811313 | 1109.631334 | 555.319305 | 10 |
| 11 | 1559.715869 | 780.361572 | 1542.689320 | 771.848298 | 1541.705304 | 771.356290 | D | 1014.557835 | 507.782556 | 997.531286 | 499.269281 | 996.547270 | 498.777273 | 9 |
| 12 | 1658.784283 | 829.895780 | 1641.757734 | 821.382505 | 1640.773718 | 820.890497 | V | 899.530892 | 450.269084 | 882.504343 | 441.755810 | 881.520327 | 441.263802 | 8 |
| 13 | 1745.816311 | 873.411794 | 1728.789762 | 864.898519 | 1727.805746 | 864.406511 | S | *800.462478* | 400.734877 | 783.435929 | 392.221603 | 782.451913 | 391.729595 | 7 |
| 14 | 1858.900375 | 929.953825 | 1841.873826 | 921.440551 | 1840.889810 | 920.948543 | L | 713.430450 | 357.218863 | 696.403901 | 348.705589 | 695.419885 | 348.213581 | 6 |
| 15 | 1986.958953 | 993.983115 | 1969.932404 | 985.469840 | 1968.948388 | 984.977832 | Q | *600.346386* | 300.676831 | 583.319837 | 292.163557 | 582.335821 | 291.671549 | 5 |
| 16 | 2100.043017 | 1050.525146 | 2083.016468 | 1042.011872 | 2082.032452 | 1041.519864 | L | *472.287808* | 236.647542 | 455.261259 | 228.134268 | 454.277243 | 227.642260 | 4 |
| 17 | 2197.095781 | 1099.051528 | 2180.069232 | 1090.538254 | 2179.085216 | 1090.046246 | P | *359.203744* | 180.105510 | 342.177195 | 171.592236 | 341.193179 | 171.100228 | 3 |
| 18 | 2284.127809 | 1142.567542 | 2267.101260 | 1134.054268 | 2266.117244 | 1133.562260 | S | 262.150980 | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 19 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 36.3 | 2457.232193 | 0.029143 | DAPDHQELNLDVSLQLPSR |
| 9.6 | 2457.232193 | 0.029143 | DAPDHQELNLDVSLQLPSR |
| 3.0 | 2457.243423 | 0.017913 | TGLSDAFMILNPSPDVPESRRR |

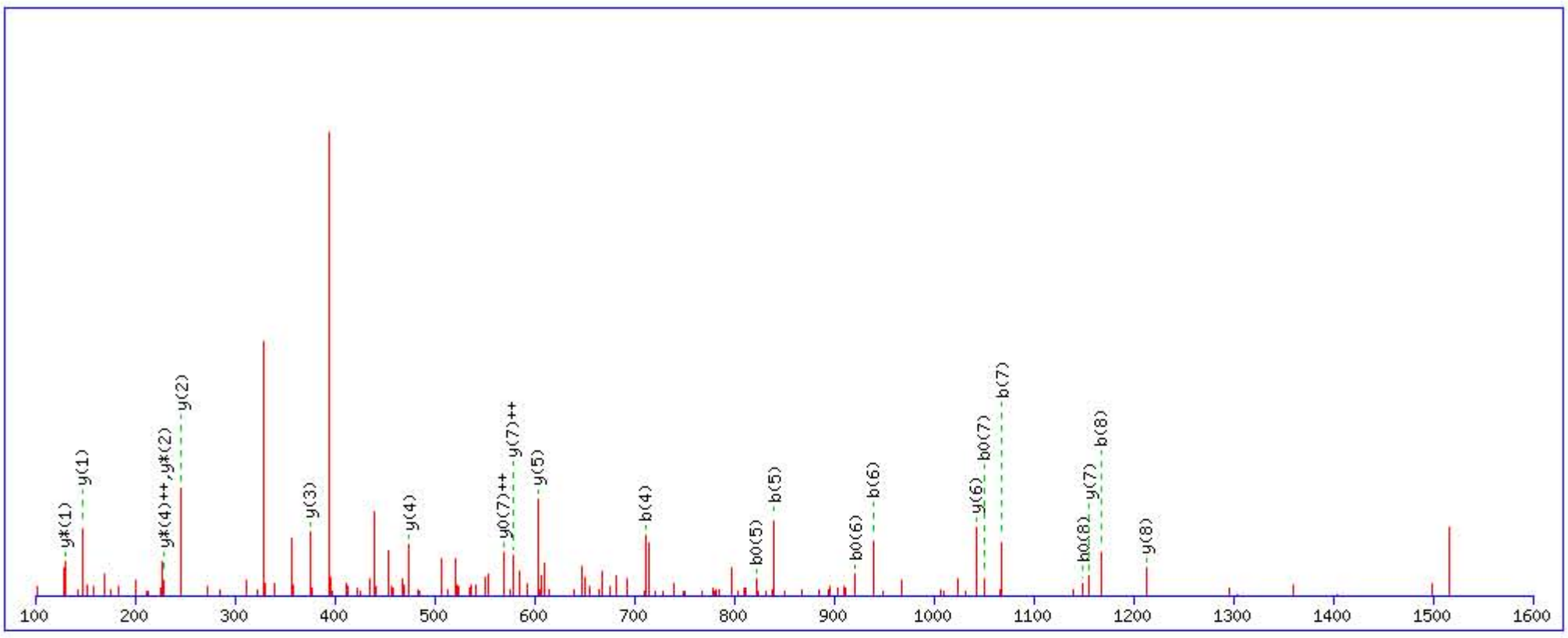
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TGLQEVEVK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

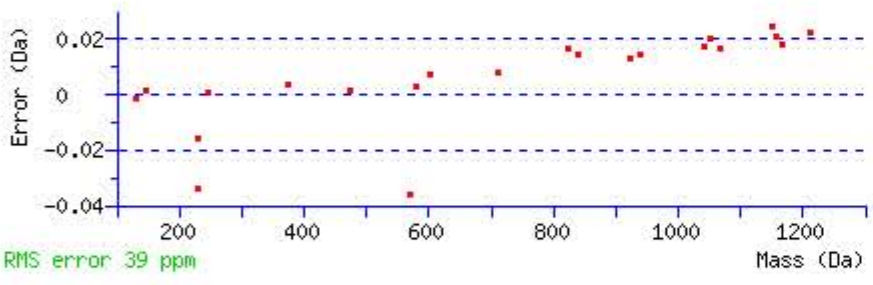
Match to Query 23551: 1312.717528 from(657.366040,2+) rtinseconds(1822) index(33051)
Title: Locus:1.1.1.743.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

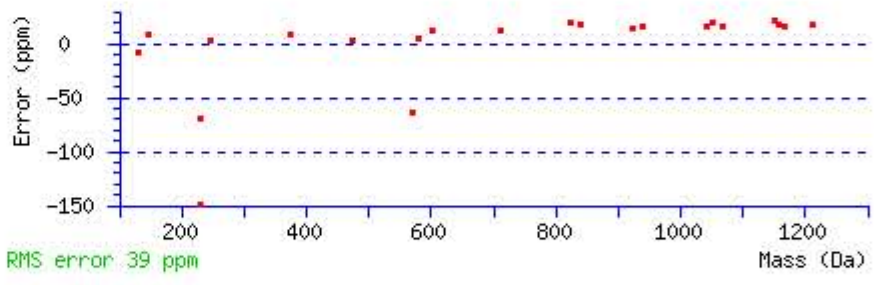
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1312.706070
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 52 **Expect:** 0.00014
**Matches :** 22/86 fragment ions using 36 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | $y^{*}$ | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 9 |
| 2 | 159.076419 | 80.041847 | | | 141.065854 | 71.036565 | G | *1212.665672* | 606.836474 | 1195.639123 | 598.323200 | 1194.655107 | 597.831192 | 8 |
| 3 | 272.160483 | 136.583879 | | | 254.149918 | 127.578597 | L | *1155.644208* | 578.325742 | 1138.617659 | 569.812468 | 1137.633643 | 569.320460 | 7 |
| 4 | **711.385809** | 356.196543 | 694.359260 | 347.683268 | 693.375244 | 347.191260 | Q | *1042.560144* | 521.783710 | 1025.533595 | 513.270436 | 1024.549579 | 512.778428 | 6 |
| 5 | **840.428402** | 420.717839 | 823.401853 | 412.204565 | 822.417837 | 411.712557 | E | *603.334818* | 302.171047 | 586.308269 | 293.657773 | 585.324253 | 293.165765 | 5 |
| 6 | **939.496816** | 470.252046 | 922.470267 | 461.738772 | 921.486251 | 461.246764 | V | *474.292225* | 237.649751 | 457.265676 | 229.136476 | 456.281660 | 228.644468 | 4 |
| 7 | **1068.539409** | 534.773343 | 1051.512860 | 526.260068 | 1050.528844 | 525.768060 | E | *375.223811* | 188.115544 | 358.197262 | 179.602269 | 357.213246 | 179.110261 | 3 |
| 8 | **1167.607823** | 584.307550 | 1150.581274 | 575.794275 | 1149.597258 | 575.302267 | V | *246.181218* | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 9 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.3 | 1312.706070 | 0.011458 | TGLQEVEVK |
| 14.7 | 1312.713913 | 0.003615 | KVFEKYTTAAR |
| 10.2 | 1312.699524 | 0.018004 | TIMHLMINNVK |
| 9.2 | 1312.735077 | -0.017549 | TSQGGAGVSPLLVK |
| 6.1 | 1312.721130 | -0.003602 | QVEVLTNQRAR |
| 5.7 | 1312.717300 | 0.000228 | ASLQTVDIR |
| 5.3 | 1312.728546 | -0.011018 | QGSRGTAVVK |
| 3.7 | 1312.728516 | -0.010988 | KPQRGMPKVEK |
| 3.5 | 1312.735031 | -0.017503 | DIALQIREDIK |
| 3.2 | 1312.732346 | -0.014818 | QRKRPESGSIR |

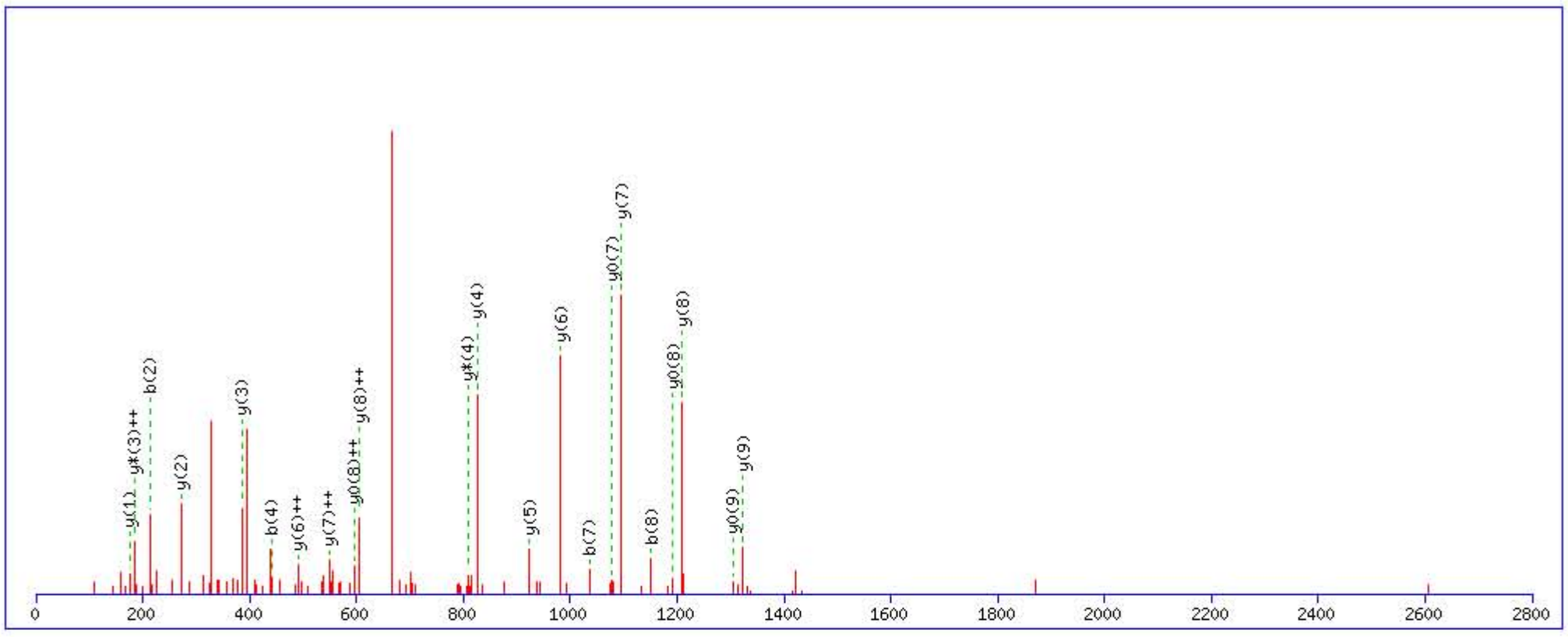
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VLLDGVQNPR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

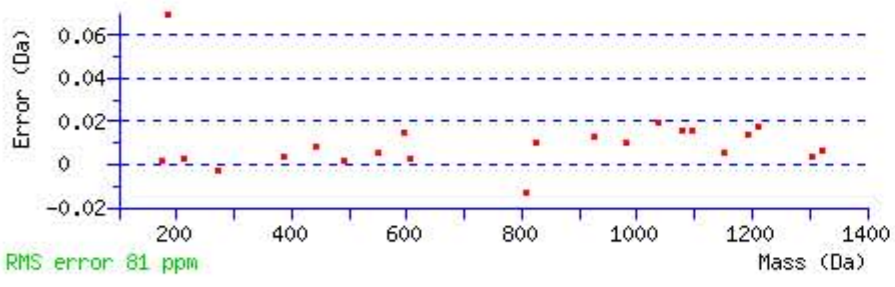
Match to Query 28409: 1420.803348 from(711.408950,2+) rtinseconds(1989) index(34221)
Title: Locus:1.1.1.801.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

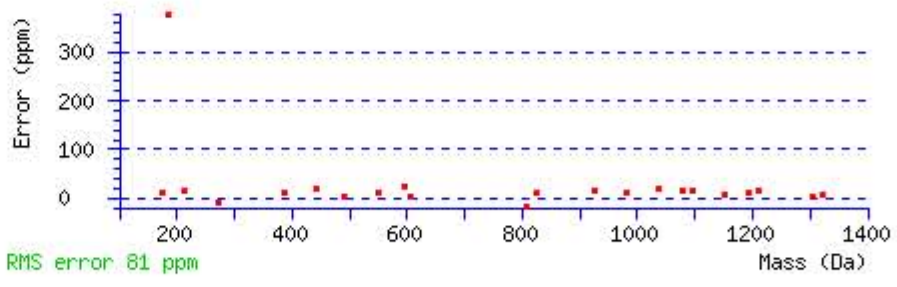
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1420.786057
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 62 **Expect:** 7e-006
**Matches :** 22/78 fragment ions using 39 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 10 |
| 2 | **213.159754** | 107.083515 | | | | | L | *1322.724918* | 661.866097 | 1305.698369 | 653.352823 | 1304.714353 | 652.860814 | 9 |
| 3 | 326.243818 | 163.625547 | | | | | L | *1209.640854* | 605.324065 | 1192.614305 | 596.810791 | 1191.630289 | 596.318783 | 8 |
| 4 | **441.270761** | 221.139018 | | | 423.260196 | 212.133736 | D | *1096.556790* | 548.782033 | 1079.530241 | 540.268758 | 1078.546225 | 539.776750 | 7 |
| 5 | 498.292225 | 249.649750 | | | 480.281660 | 240.644468 | G | *981.529847* | 491.268562 | 964.503298 | 482.755287 | | | 6 |
| 6 | 597.360639 | 299.183958 | | | 579.350074 | 290.178675 | V | *924.508383* | 462.757830 | 907.481834 | 454.244555 | | | 5 |
| 7 | **1036.585965** | 518.796621 | 1019.559416 | 510.283346 | 1018.575400 | 509.791338 | Q | *825.439969* | 413.223623 | 808.413420 | 404.710348 | | | 4 |
| 8 | **1150.628892** | 575.818084 | 1133.602343 | 567.304810 | 1132.618327 | 566.812801 | N | *386.214643* | 193.610959 | 369.188094 | 185.097685 | | | 3 |
| 9 | 1247.681656 | 624.344466 | 1230.655107 | 615.831192 | 1229.671091 | 615.339183 | P | *272.171716* | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 10 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 62.2 | 1420.786057 | 0.017291 | VLLDGVQNPR |

**Mascot:** http://www.matrixscience.com/

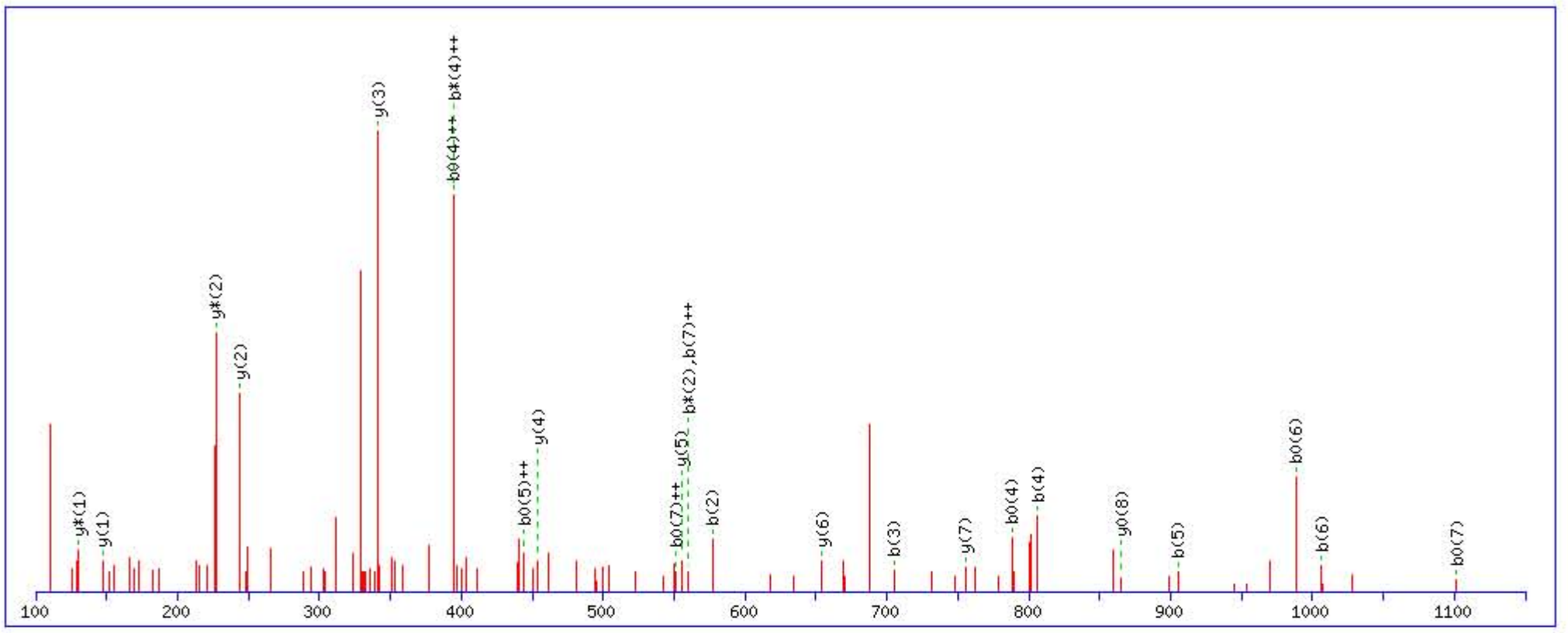
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HQQTVTIPPK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

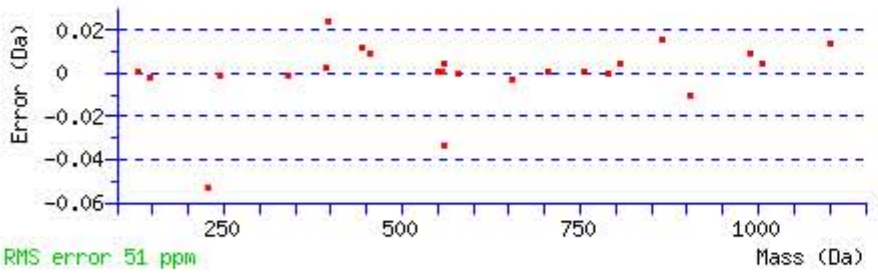
Match to Query 29915: 1458.800382 from(487.274070,3+) rtinseconds(1561) index(31459)
Title: Locus:1.1.1.652.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

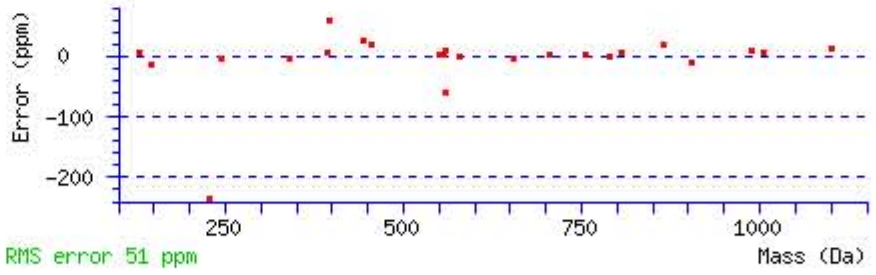
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1458.801712
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 27 **Expect:** 0.047
**Matches :** 24/92 fragment ions using 55 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 10 |
| 2 | **577.291514** | 289.149395 | 560.264965 | 280.636121 | | | Q | 1322.750072 | 661.878674 | 1305.723523 | 653.365400 | 1304.739507 | 652.873392 | 9 |
| 3 | **705.350092** | 353.178684 | 688.323543 | 344.665410 | | | Q | 883.524746 | 442.266011 | 866.498197 | 433.752737 | 865.514181 | 433.260729 | 8 |
| 4 | **806.397771** | 403.702524 | 789.371222 | 395.189249 | 788.387206 | 394.697241 | T | ***755.466168*** | 378.236722 | 738.439619 | 369.723448 | 737.455603 | 369.231440 | 7 |
| 5 | **905.466185** | 453.236731 | 888.439636 | 444.723456 | 887.455620 | 444.231448 | V | ***654.418489*** | 327.712883 | 637.391940 | 319.199608 | 636.407924 | 318.707600 | 6 |
| 6 | **1006.513864** | 503.760570 | 989.487315 | 495.247296 | 988.503299 | 494.755288 | T | ***555.350075*** | 278.178676 | 538.323526 | 269.665401 | 537.339510 | 269.173393 | 5 |
| 7 | 1119.597928 | 560.302602 | 1102.571379 | 551.789328 | 1101.587363 | 551.297319 | I | ***454.302396*** | 227.654836 | 437.275847 | 219.141561 | | | 4 |
| 8 | 1216.650692 | 608.828984 | 1199.624143 | 600.315710 | 1198.640127 | 599.823701 | P | ***341.218332*** | 171.112804 | 324.191783 | 162.599530 | | | 3 |
| 9 | 1313.703456 | 657.355366 | 1296.676907 | 648.842092 | 1295.692891 | 648.350083 | P | ***244.165568*** | 122.586422 | 227.139019 | 114.073148 | | | 2 |
| 10 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 26.6 | 1458.801712 | -0.001330 | HQQTVTIPPK |
| 25.7 | 1458.801712 | -0.001330 | HQQTVTIPPK |

**Mascot:** http://www.matrixscience.com/

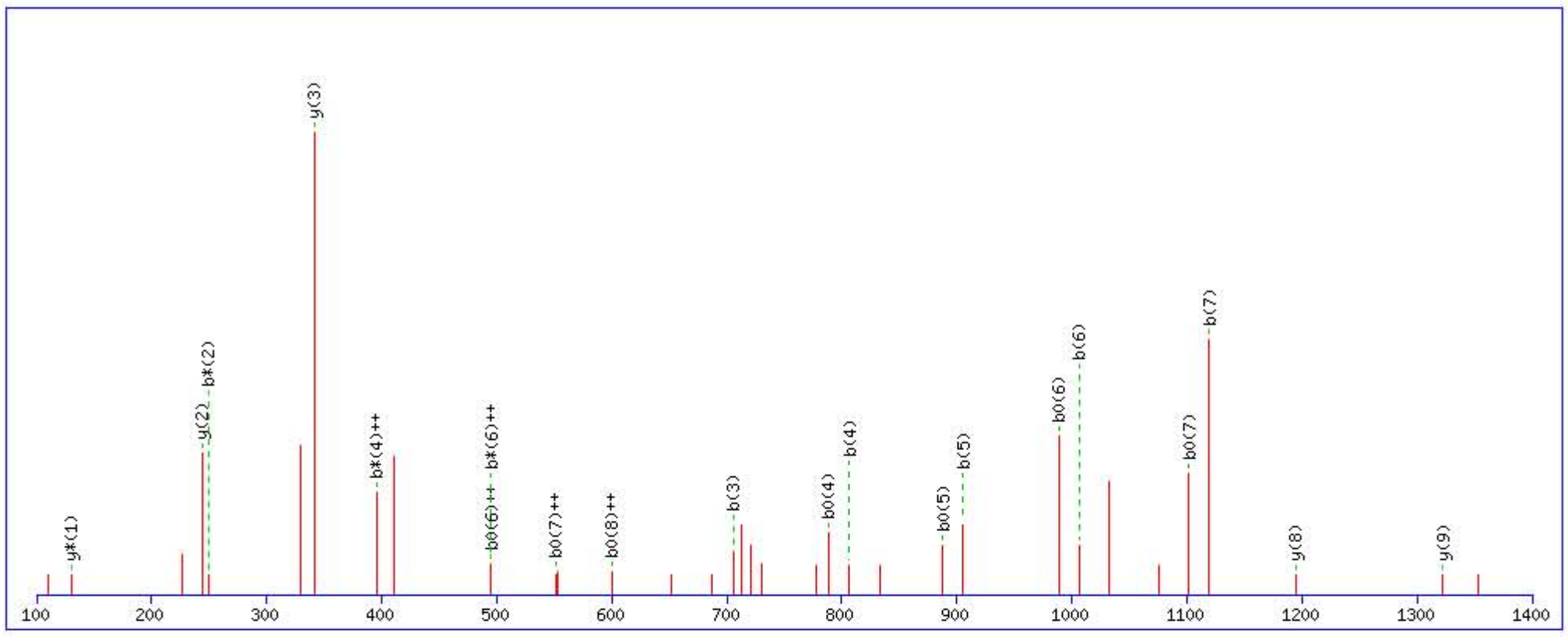
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HQQTVTIPPK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

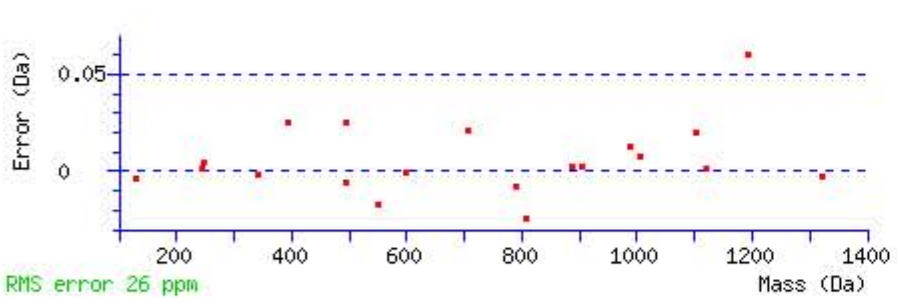
Match to Query 29937: 1458.807008 from(730.410780,2+) rtinseconds(1576) index(31548)
Title: Locus:1.1.1.657.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

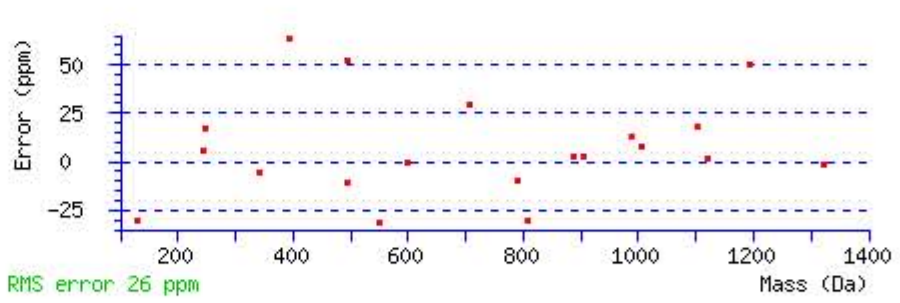
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1458.801712
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0028
**Matches :** 20/92 fragment ions using 36 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 10 |
| 2 | 266.124766 | 133.566021 | 249.098217 | 125.052746 | | | Q | *1322.750072* | 661.878674 | 1305.723523 | 653.365400 | 1304.739507 | 652.873392 | 9 |
| 3 | *705.350092* | 353.178684 | 688.323543 | 344.665410 | | | Q | *1194.691494* | 597.849385 | 1177.664945 | 589.336111 | 1176.680929 | 588.844102 | 8 |
| 4 | *806.397771* | 403.702524 | 789.371222 | 395.189249 | 788.387206 | 394.697241 | T | 755.466168 | 378.236722 | 738.439619 | 369.723448 | 737.455603 | 369.231440 | 7 |
| 5 | *905.466185* | 453.236731 | 888.439636 | 444.723456 | 887.455620 | 444.231448 | V | 654.418489 | 327.712883 | 637.391940 | 319.199608 | 636.407924 | 318.707600 | 6 |
| 6 | *1006.513864* | 503.760570 | 989.487315 | 495.247296 | 988.503299 | 494.755288 | T | 555.350075 | 278.178676 | 538.323526 | 269.665401 | 537.339510 | 269.173393 | 5 |
| 7 | *1119.597928* | 560.302602 | 1102.571379 | 551.789328 | 1101.587363 | 551.297319 | I | 454.302396 | 227.654836 | 437.275847 | 219.141561 | | | 4 |
| 8 | 1216.650692 | 608.828984 | 1199.624143 | 600.315710 | 1198.640127 | 599.823701 | P | *341.218332* | 171.112804 | 324.191783 | 162.599530 | | | 3 |
| 9 | 1313.703456 | 657.355366 | 1296.676907 | 648.842092 | 1295.692891 | 648.350083 | P | *244.165568* | 122.586422 | 227.139019 | 114.073148 | | | 2 |
| 10 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 32.6 | 1458.801712 | 0.005296 | HQQTVTIPPK |
| 24.8 | 1458.801712 | 0.005296 | HQQTVTIPPK |
| 5.1 | 1458.826859 | -0.019851 | VGALLVQSFSK |
| 1.0 | 1458.822800 | -0.015792 | DKMSKDLLLGIAR |
| 0.2 | 1458.790466 | 0.016542 | GIMDGHTIYLVIK |

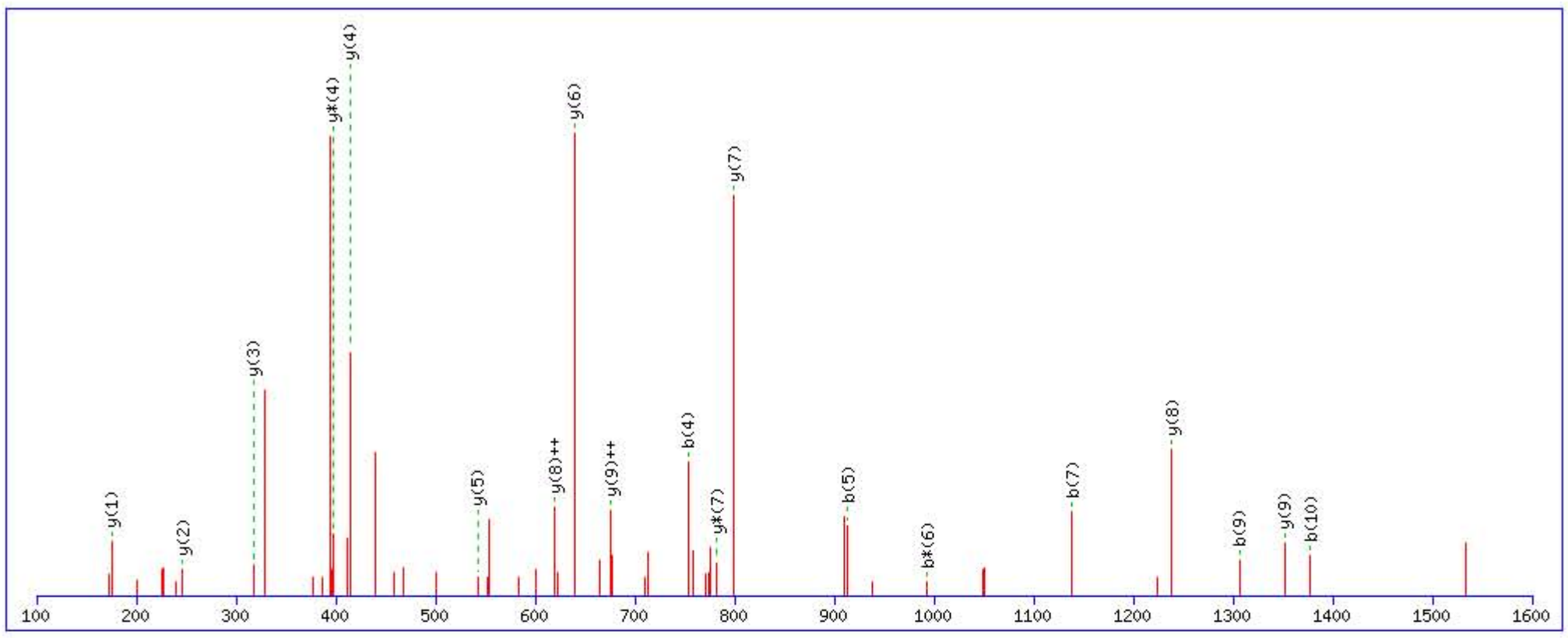
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AELQCPQPAAR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

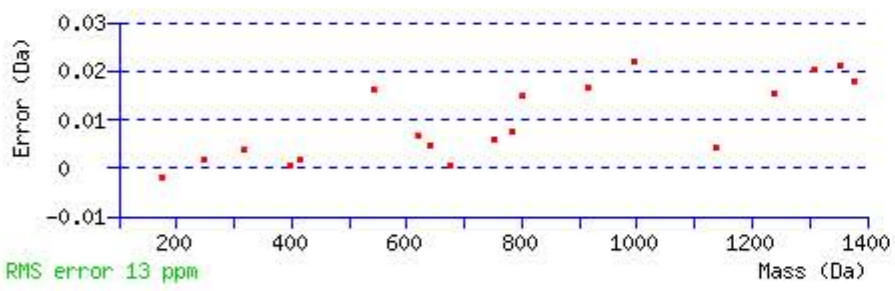
Match to Query 32523: 1550.780248 from(776.397400,2+) rtinseconds(1585) index(31607)
Title: Locus:1.1.1.660.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

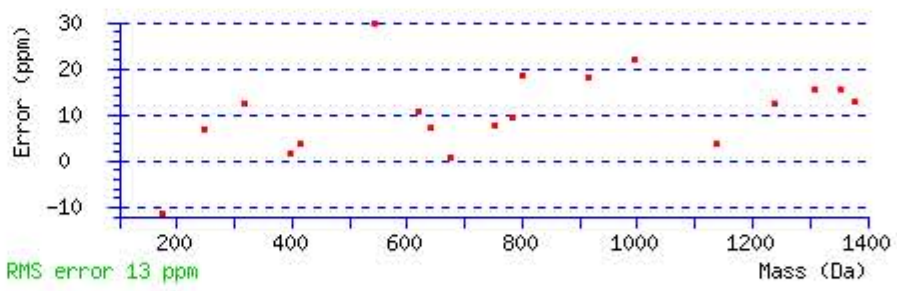
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1550.769730
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 54 **Expect:** 8.4e-005
**Matches** : 19/94 fragment ions using 40 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 11 |
| 2 | 201.086983 | 101.047130 | | | 183.076418 | 92.041847 | E | 1480.739918 | 740.873597 | 1463.713369 | 732.360323 | 1462.729353 | 731.868315 | 10 |
| 3 | 314.171047 | 157.589161 | | | 296.160482 | 148.583879 | L | *1351.697325* | 676.352301 | 1334.670776 | 667.839026 | | | 9 |
| 4 | **753.396373** | 377.201825 | 736.369824 | 368.688550 | 735.385808 | 368.196542 | Q | *1238.613261* | 619.810269 | 1221.586712 | 611.296994 | | | 8 |
| 5 | **913.427022** | 457.217149 | 896.400473 | 448.703875 | 895.416457 | 448.211867 | C | *799.387935* | 400.197606 | 782.361386 | 391.684331 | | | 7 |
| 6 | 1010.479786 | 505.743531 | 993.453237 | 497.230257 | 992.469221 | 496.738249 | P | *639.357286* | 320.182281 | 622.330737 | 311.669007 | | | 6 |
| 7 | **1138.538364** | 569.772820 | 1121.511815 | 561.259546 | 1120.527799 | 560.767538 | Q | *542.304522* | 271.655899 | 525.277973 | 263.142625 | | | 5 |
| 8 | 1235.591128 | 618.299202 | 1218.564579 | 609.785928 | 1217.580563 | 609.293920 | P | *414.245944* | 207.626610 | 397.219395 | 199.113335 | | | 4 |
| 9 | **1306.628242** | 653.817759 | 1289.601693 | 645.304485 | 1288.617677 | 644.812477 | A | *317.193180* | 159.100228 | 300.166631 | 150.586953 | | | 3 |
| 10 | **1377.665356** | 689.336316 | 1360.638807 | 680.823042 | 1359.654791 | 680.331034 | A | *246.156066* | 123.581671 | 229.129517 | 115.068396 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 54.4 | 1550.769730 | 0.010518 | AELQCPQPAAR |
| 17.0 | 1550.769730 | 0.010518 | AELQCPQPAAR |
| 10.6 | 1550.780121 | 0.000127 | GSSPGPRPVEGTPASR |
| 8.6 | 1550.768845 | 0.011403 | SLGKRDLYDEAER |
| 7.7 | 1550.761856 | 0.018392 | MCSLMLSKELPAR |
| 6.7 | 1550.780975 | -0.000727 | AANGQGQQR |
| 6.7 | 1550.780975 | -0.000727 | AANGQGQQR |
| 6.3 | 1550.780945 | -0.000697 | EAIREHQMAR |
| 3.9 | 1550.770218 | 0.010030 | NFSNGHQLTIHQR |
| 3.5 | 1550.761856 | 0.018392 | MCSLMLSKELPAR |

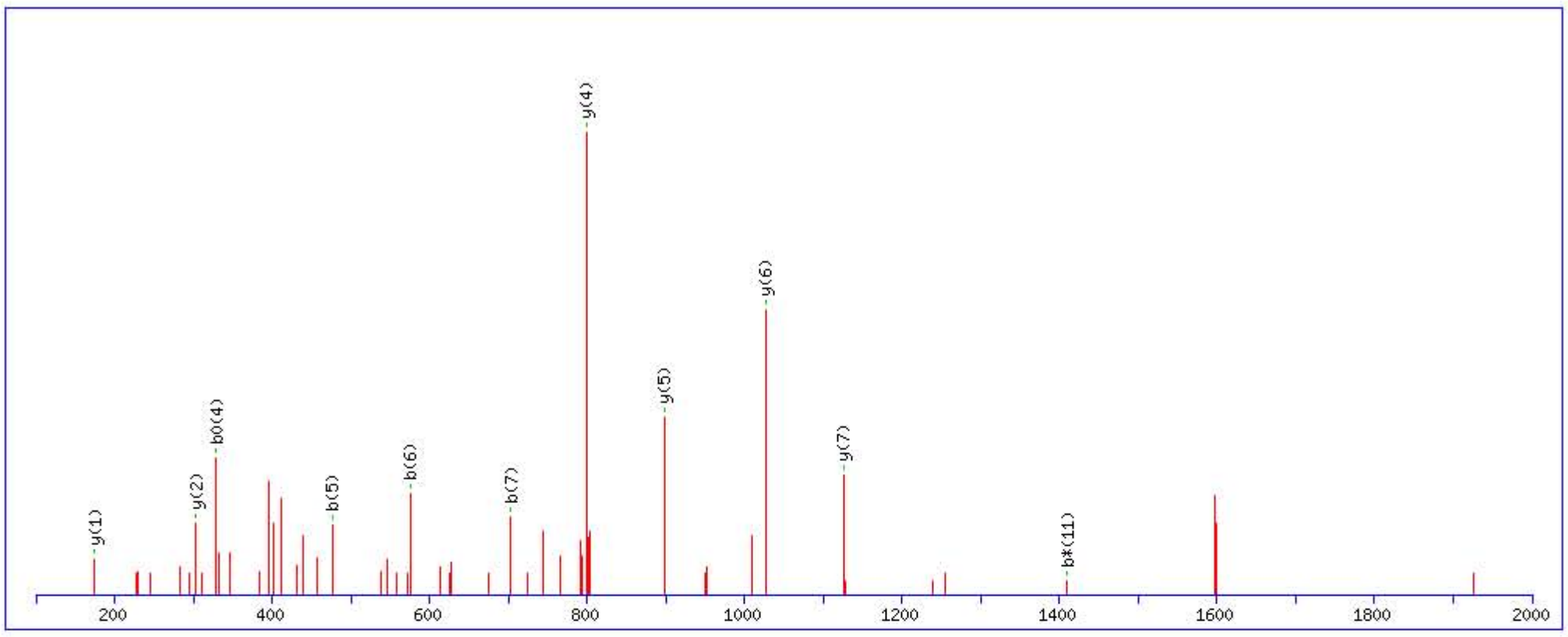
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SGSDEVQVGQQR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

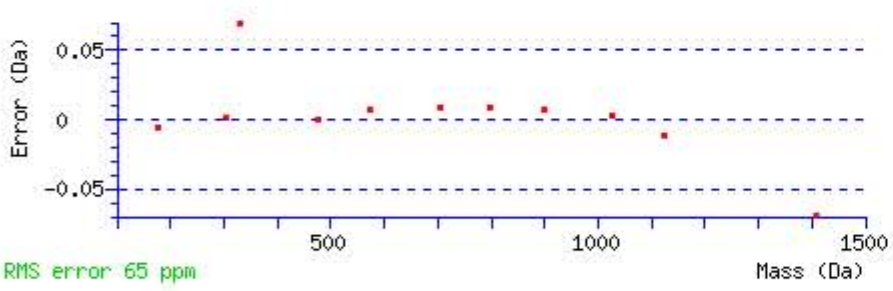
Match to Query 34701: 1599.782788 from(800.898670,2+) rtinseconds(1576) index(31551)
Title: Locus:1.1.1.657.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

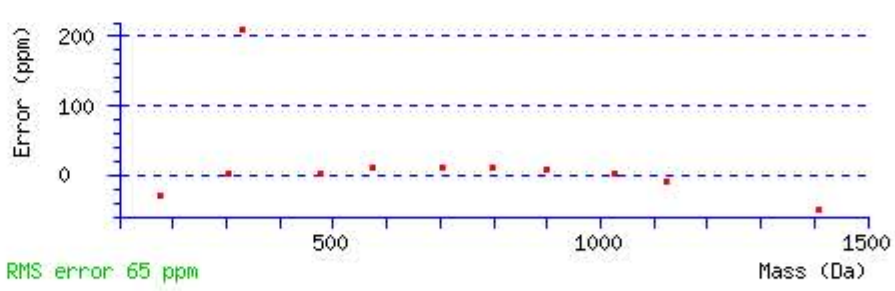
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1599.767517
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 26 **Expect:** 0.028
**Matches :** 11/106 fragment ions using 25 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 12 |
| 2 | 145.060768 | 73.034022 | | | 127.050203 | 64.028740 | G | 1513.742754 | 757.375015 | 1496.716205 | 748.861741 | 1495.732189 | 748.369733 | 11 |
| 3 | 232.092796 | 116.550036 | | | 214.082231 | 107.544753 | S | 1456.721290 | 728.864283 | 1439.694741 | 720.351009 | 1438.710725 | 719.859001 | 10 |
| 4 | 347.119739 | 174.063507 | | | 329.109174 | 165.058225 | D | 1369.689262 | 685.348269 | 1352.662713 | 676.834995 | 1351.678697 | 676.342987 | 9 |
| 5 | **476.162332** | 238.584804 | | | 458.151767 | 229.579522 | E | 1254.662319 | 627.834798 | 1237.635770 | 619.321523 | 1236.651754 | 618.829515 | 8 |
| 6 | **575.230746** | 288.119011 | | | 557.220181 | 279.113729 | V | *1125.619726* | 563.313501 | 1108.593177 | 554.800227 | | | 7 |
| 7 | **703.289324** | 352.148300 | 686.262775 | 343.635026 | 685.278759 | 343.143018 | Q | *1026.551312* | 513.779294 | 1009.524763 | 505.266020 | | | 6 |
| 8 | 802.357738 | 401.682507 | 785.331189 | 393.169233 | 784.347173 | 392.677225 | V | *898.492734* | 449.750005 | 881.466185 | 441.236731 | | | 5 |
| 9 | 859.379202 | 430.193239 | 842.352653 | 421.679965 | 841.368637 | 421.187957 | G | *799.424320* | 400.215798 | 782.397771 | 391.702524 | | | 4 |
| 10 | 1298.604528 | 649.805902 | 1281.577979 | 641.292628 | 1280.593963 | 640.800620 | Q | 742.402856 | 371.705066 | 725.376307 | 363.191792 | | | 3 |
| 11 | 1426.663106 | 713.835191 | 1409.636557 | 705.321917 | 1408.652541 | 704.829909 | Q | *303.177530* | 152.092403 | 286.150981 | 143.579129 | | | 2 |
| 12 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.9 | 1599.767517 | 0.015271 | SGSDEVQVGQQR |
| 23.7 | 1599.767517 | 0.015271 | SGSDEVQVGQQR |
| 8.8 | 1599.767471 | 0.015317 | AMNAANLNIPPSDTR |
| 8.5 | 1599.767517 | 0.015271 | SGSDEVQVGQQR |
| 2.9 | 1599.779388 | 0.003400 | RFPDFSYITQNGR |
| 0.8 | 1599.793961 | -0.011173 | VGAPAWREAAQAMAR |

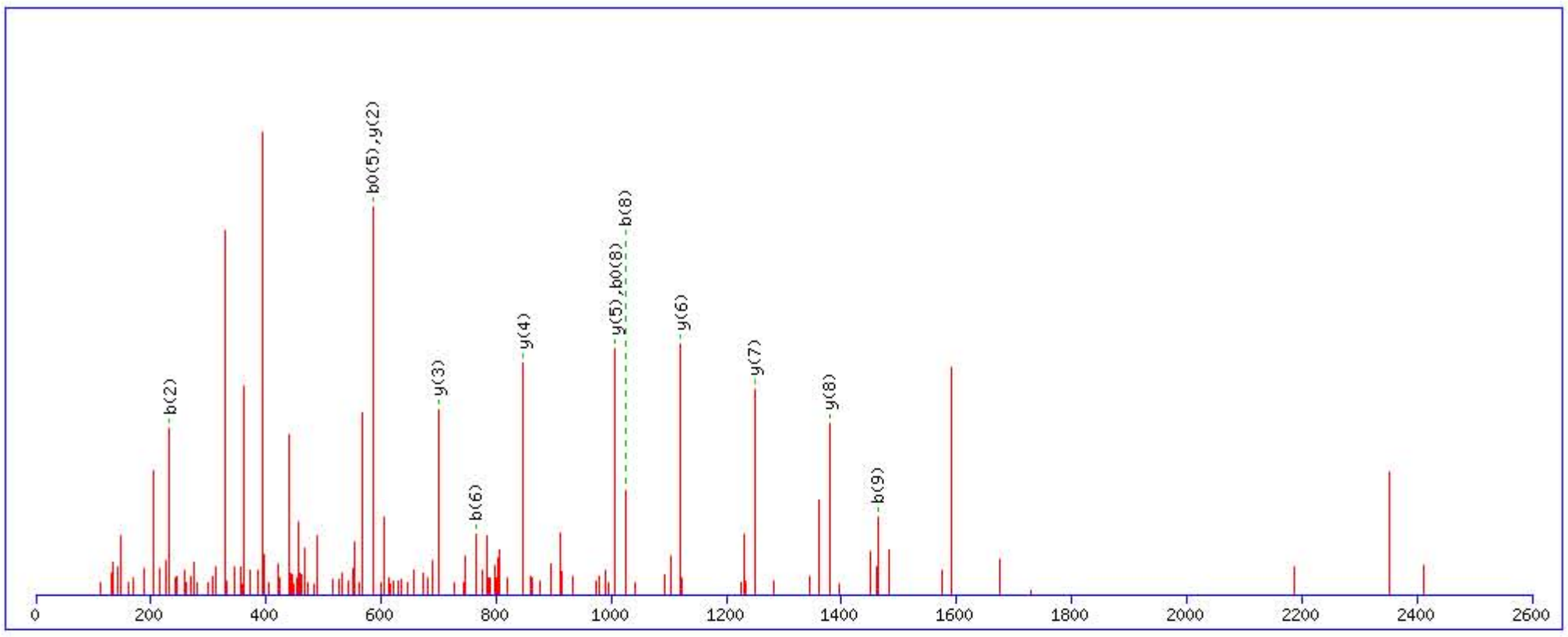
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **CAEENCFIQK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

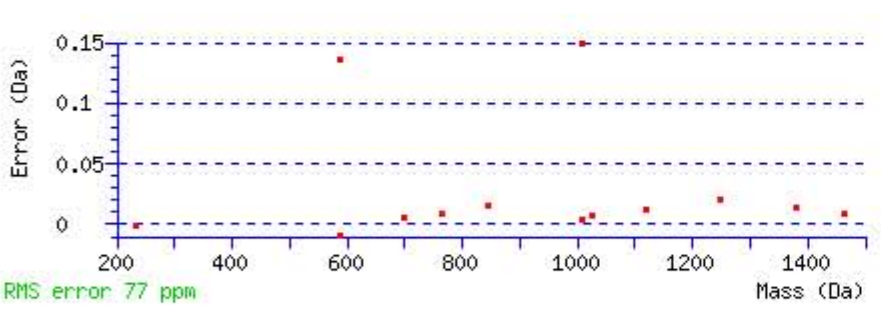
Match to Query 34957: 1608.729108 from(805.371830,2+) rtinseconds(1794) index(32893)
Title: Locus:1.1.1.733.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

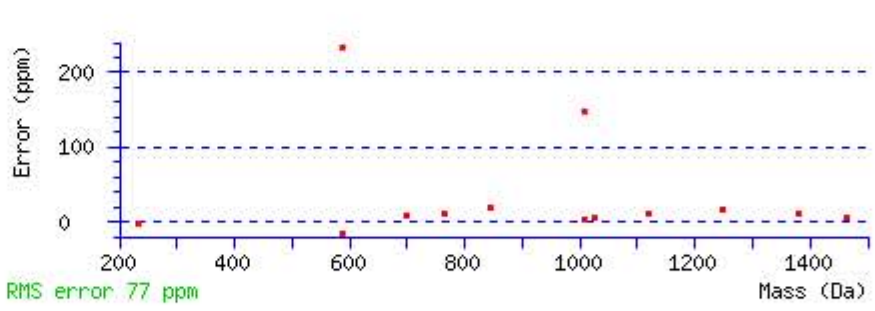
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1608.709839
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 55 **Expect:** 2.7e-005
**Matches :** 13/84 fragment ions using 15 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 161.037925 | 81.022600 | | | | | C | | | | | | | 10 |
| 2 | **232.075039** | 116.541158 | | | | | A | 1449.686484 | 725.346880 | 1432.659935 | 716.833606 | 1431.675919 | 716.341598 | 9 |
| 3 | 361.117632 | 181.062454 | | | 343.107067 | 172.057172 | E | *1378.649370* | 689.828323 | 1361.622821 | 681.315049 | 1360.638805 | 680.823041 | 8 |
| 4 | 490.160225 | 245.583751 | | | 472.149660 | 236.578468 | E | *1249.606777* | 625.307027 | 1232.580228 | 616.793752 | 1231.596212 | 616.301744 | 7 |
| 5 | 604.203152 | 302.605214 | 587.176603 | 294.091940 | 586.192587 | 293.599932 | N | *1120.564184* | 560.785730 | 1103.537635 | 552.272456 | | | 6 |
| 6 | **764.233801** | 382.620539 | 747.207252 | 374.107264 | 746.223236 | 373.615256 | C | *1006.521257* | 503.764267 | 989.494708 | 495.250992 | | | 5 |
| 7 | 911.302215 | 456.154746 | 894.275666 | 447.641471 | 893.291650 | 447.149463 | F | *846.490608* | 423.748942 | 829.464059 | 415.235668 | | | 4 |
| 8 | **1024.386279** | 512.696777 | 1007.359730 | 504.183503 | 1006.375714 | 503.691495 | I | *699.422194* | 350.214735 | 682.395645 | 341.701461 | | | 3 |
| 9 | **1463.611605** | 732.309441 | 1446.585056 | 723.796166 | 1445.601040 | 723.304158 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 10 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 55.2 | 1608.709839 | 0.019269 | CAEENCFIQK |
| 6.2 | 1608.721085 | 0.008023 | CNECGKGFAQK |
| 4.1 | 1608.750107 | -0.020999 | CPACFVGTITGDRR |
| 2.2 | 1608.753220 | -0.024112 | QEEAQKSFVDSWR |
| 2.1 | 1608.726746 | 0.002362 | TENGTLFEDQNVDK |
| 0.9 | 1608.731461 | -0.002353 | ELGCGGPQQPDPAAGR |

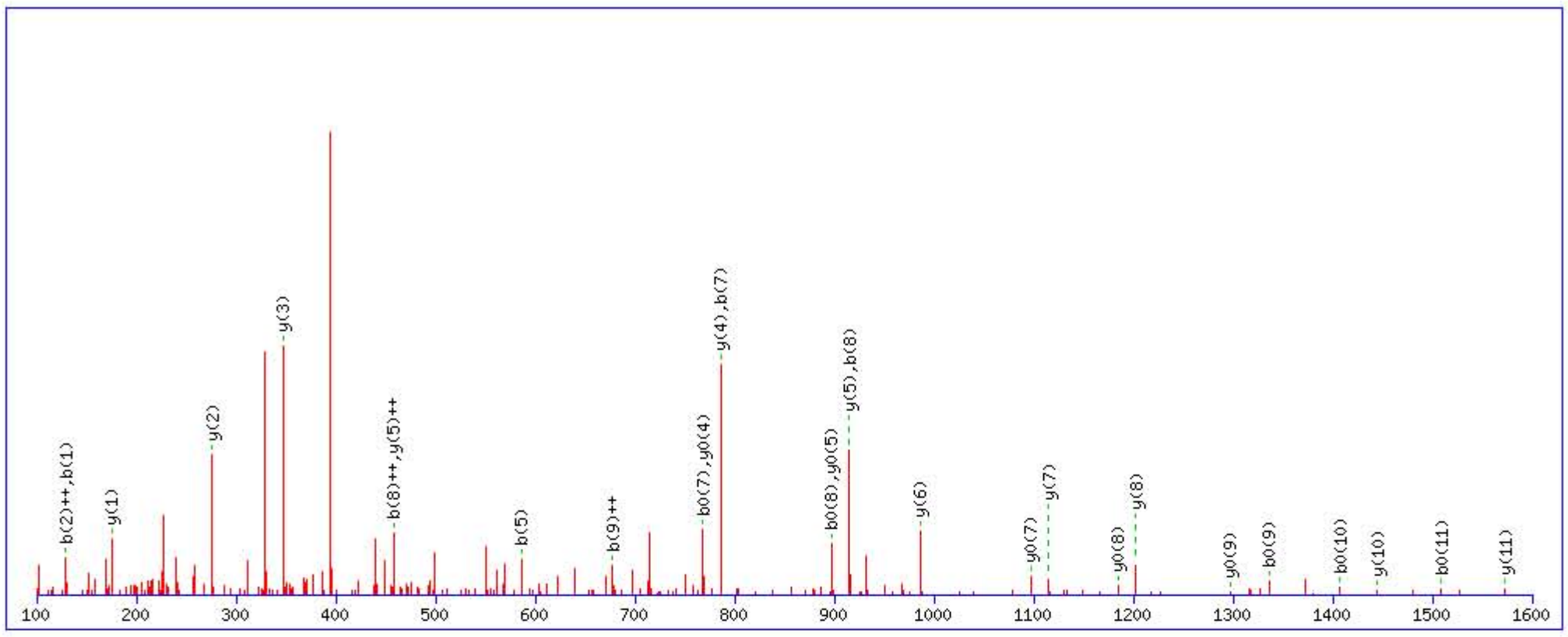
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KQELSEAEQATR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

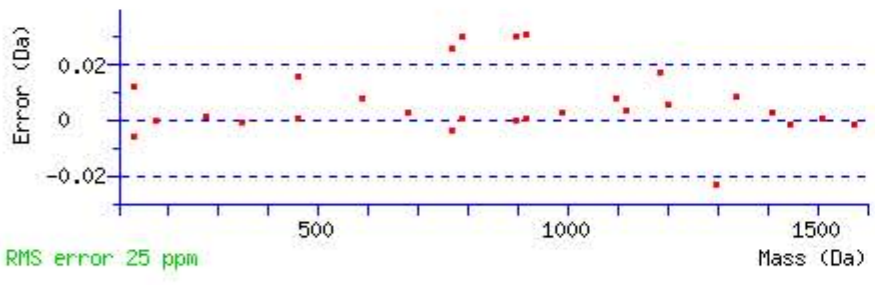
Match to Query 37938: 1699.862562 from(567.628130,3+) rtinseconds(1414) index(30532)
Title: Locus:1.1.1.600.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

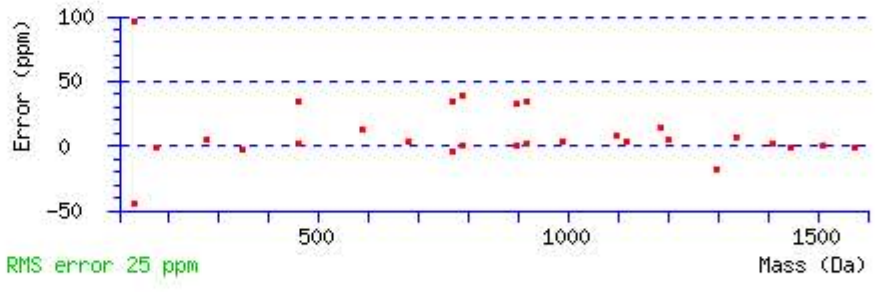
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1699.856277
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 78 **Expect:** 4.2e-007
**Matches :** 28/126 fragment ions using 30 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **129.102239** | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 12 |
| 2 | 257.160817 | **129.084047** | 240.134268 | 120.570772 | | | Q | *1572.768634* | 786.887955 | 1555.742085 | 778.374681 | 1554.758069 | 777.882673 | 11 |
| 3 | 386.203410 | 193.605343 | 369.176861 | 185.092069 | 368.192845 | 184.600061 | E | *1444.710056* | 722.858666 | 1427.683507 | 714.345392 | 1426.699491 | 713.853384 | 10 |
| 4 | 499.287474 | 250.147375 | 482.260925 | 241.634101 | 481.276909 | 241.142093 | L | 1315.667463 | 658.337370 | 1298.640914 | 649.824095 | 1297.656898 | 649.332087 | 9 |
| 5 | **586.319502** | 293.663389 | 569.292953 | 285.150115 | 568.308937 | 284.658107 | S | *1202.583399* | 601.795338 | 1185.556850 | 593.282063 | 1184.572834 | 592.790055 | 8 |
| 6 | 715.362095 | 358.184686 | 698.335546 | 349.671411 | 697.351530 | 349.179403 | E | *1115.551371* | 558.279324 | 1098.524822 | 549.766049 | 1097.540806 | 549.274041 | 7 |
| 7 | **786.399209** | 393.703243 | 769.372660 | 385.189968 | 768.388644 | 384.697960 | A | *986.508778* | 493.758027 | 969.482229 | 485.244753 | 968.498213 | 484.752745 | 6 |
| 8 | **915.441802** | **458.224539** | 898.415253 | 449.711265 | 897.431237 | 449.219257 | E | *915.471664* | 458.239470 | 898.445115 | 449.726196 | 897.461099 | 449.234188 | 5 |
| 9 | 1354.667128 | **677.837202** | 1337.640579 | 669.323928 | 1336.656563 | 668.831920 | Q | *786.429071* | 393.718174 | 769.402522 | 385.204899 | 768.418506 | 384.712891 | 4 |
| 10 | 1425.704242 | 713.355759 | 1408.677693 | 704.842485 | 1407.693677 | 704.350477 | A | *347.203745* | 174.105510 | 330.177196 | 165.592236 | 329.193180 | 165.100228 | 3 |
| 11 | 1526.751921 | 763.879599 | 1509.725372 | 755.366324 | 1508.741356 | 754.874316 | T | *276.166631* | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 12 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 78.1 | 1699.856277 | 0.006285 | KQELSEAEQATR |
| 22.1 | 1699.856277 | 0.006285 | KQELSEAEQATR |
| 9.6 | 1699.874039 | -0.011477 | KEISVNDLNESSIPR |
| 9.6 | 1699.849792 | 0.012770 | QEMRTTQLGPGR |
| 9.4 | 1699.849792 | 0.012770 | QEMRTTQLGPGR |
| 8.6 | 1699.845932 | 0.016630 | QAMQEQLSK |
| 8.0 | 1699.881424 | -0.018862 | LSSKELQEQAEK |
| 7.0 | 1699.882813 | -0.020250 | IMVHPHVTAVSEQPR |
| 6.3 | 1699.843735 | 0.018827 | QFNRQRGVSHAMGGR |
| 6.1 | 1699.863678 | -0.001116 | AGMQLNLEELQK |

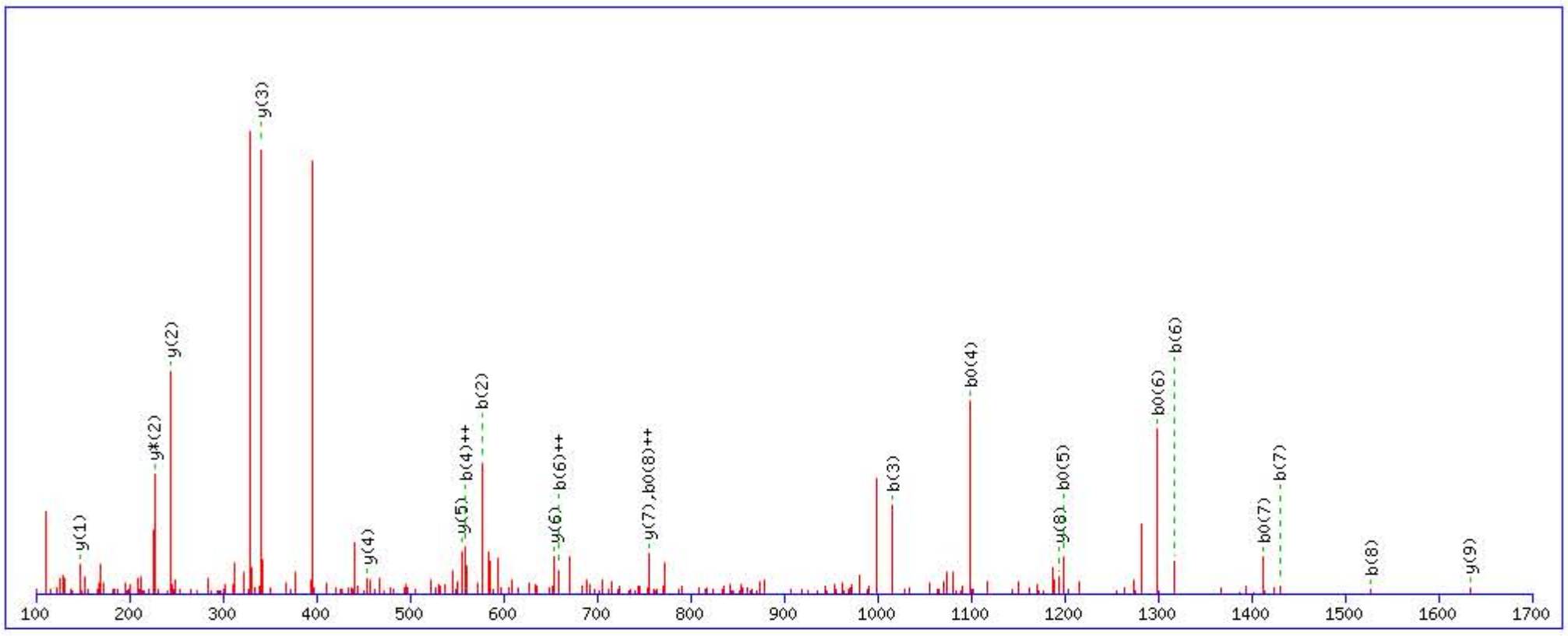
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HQQTVTIPPK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

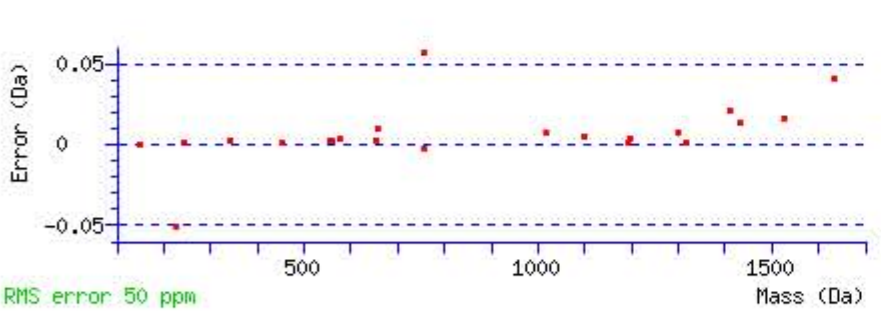
Match to Query 39642: 1769.977002 from(590.999610,3+) rtinseconds(1842) index(33140)
Title: Locus:1.1.1.750.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

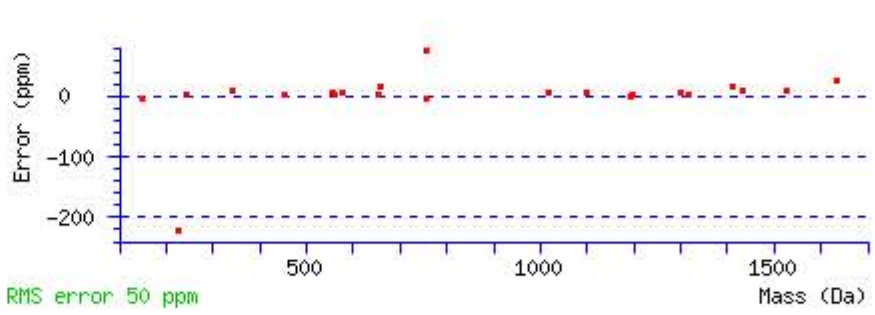
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1769.968460
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.00056
**Matches :** 22/92 fragment ions using 45 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 10 |
| 2 | **577.291514** | 289.149395 | 560.264965 | 280.636121 | | | Q | *1633.916820* | 817.462048 | 1616.890271 | 808.948774 | 1615.906255 | 808.456766 | 9 |
| 3 | **1016.516840** | 508.762058 | 999.490291 | 500.248784 | | | Q | *1194.691494* | 597.849385 | 1177.664945 | 589.336111 | 1176.680929 | 588.844103 | 8 |
| 4 | 1117.564519 | **559.285898** | 1100.537970 | 550.772623 | 1099.553954 | 550.280615 | T | *755.466168* | 378.236722 | 738.439619 | 369.723448 | 737.455603 | 369.231440 | 7 |
| 5 | 1216.632933 | 608.820105 | 1199.606384 | 600.306830 | 1198.622368 | 599.814822 | V | *654.418489* | 327.712883 | 637.391940 | 319.199608 | 636.407924 | 318.707600 | 6 |
| 6 | **1317.680612** | **659.343944** | 1300.654063 | 650.830670 | 1299.670047 | 650.338662 | T | *555.350075* | 278.178676 | 538.323526 | 269.665401 | 537.339510 | 269.173393 | 5 |
| 7 | **1430.764676** | 715.885976 | 1413.738127 | 707.372702 | 1412.754111 | 706.880694 | I | *454.302396* | 227.654836 | 437.275847 | 219.141561 | | | 4 |
| 8 | **1527.817440** | 764.412358 | 1510.790891 | 755.899084 | 1509.806875 | 755.407076 | P | *341.218332* | 171.112804 | 324.191783 | 162.599530 | | | 3 |
| 9 | 1624.870204 | 812.938740 | 1607.843655 | 804.425466 | 1606.859639 | 803.933458 | P | *244.165568* | 122.586422 | 227.139019 | 114.073148 | | | 2 |
| 10 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 44.4 | 1769.968460 | 0.008542 | HQQTVTIPPK |
| 9.2 | 1769.961029 | 0.015973 | WMLSRDRASTLPLPK |
| 0.9 | 1769.997437 | -0.020435 | AVPPRMPAVNLGQVPPK |

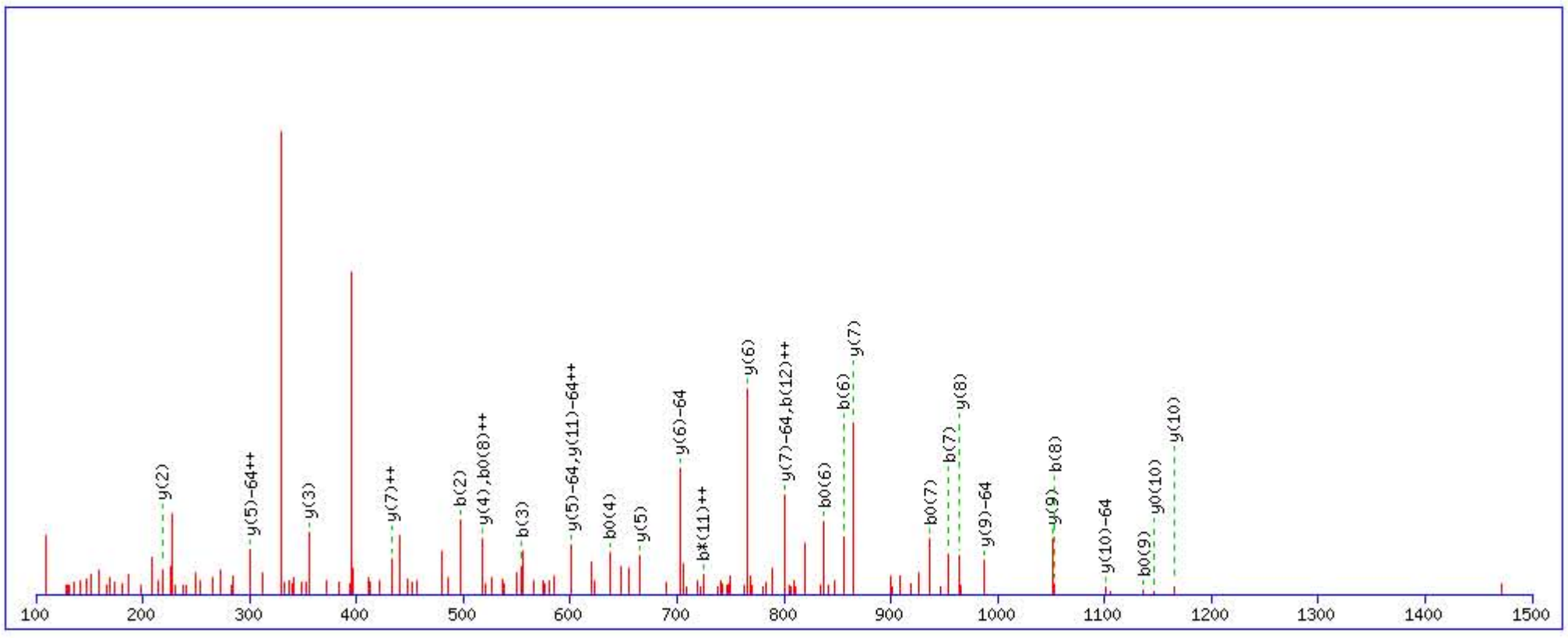
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GQGTLSVVTMYHAK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

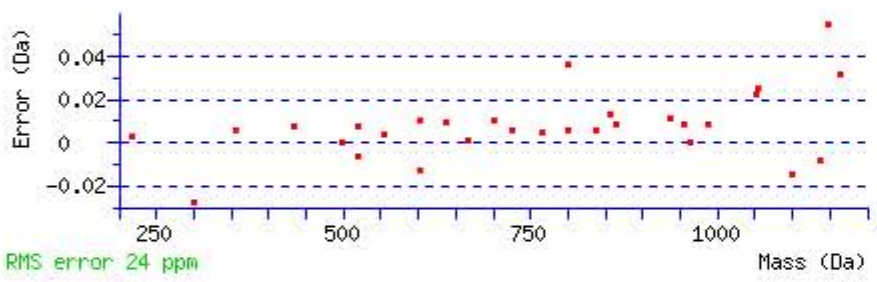
Match to Query 40691: 1817.928342 from(606.983390,3+) rtinseconds(1828) index(33081)
Title: Locus:1.1.1.745.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

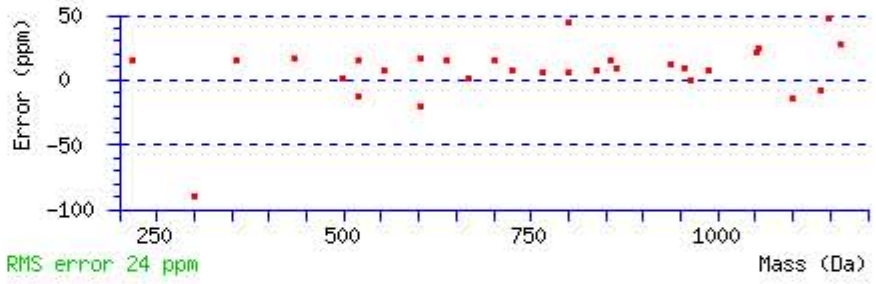
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1817.916824
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
M10 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
**Ions Score:** 51 **Expect:** 0.00022
**Matches :** 30/214 fragment ions using 44 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 14 |
| 2 | **497.254066** | 249.130671 | 480.227517 | 240.617397 | | | Q | 1761.902627 | 881.454952 | 1744.876078 | 872.941677 | 1743.892062 | 872.449669 | 13 |
| 3 | **554.275530** | 277.641403 | 537.248981 | 269.128129 | | | G | 1322.677301 | 661.842289 | 1305.650752 | 653.329014 | 1304.666736 | 652.837006 | 12 |
| 4 | 655.323209 | 328.165243 | 638.296660 | 319.651968 | 637.312644 | 319.159960 | T | 1265.655837 | 633.331557 | 1248.629288 | 624.818282 | 1247.645272 | 624.326274 | 11 |
| 5 | 768.407273 | 384.707275 | 751.380724 | 376.194000 | 750.396708 | 375.701992 | L | ***1164.608158*** | 582.807717 | 1147.581609 | 574.294443 | 1146.597593 | 573.802435 | 10 |
| 6 | **855.439301** | 428.223289 | 838.412752 | 419.710014 | 837.428736 | 419.218006 | S | ***1051.524094*** | 526.265685 | 1034.497545 | 517.752411 | 1033.513529 | 517.260403 | 9 |
| 7 | **954.507715** | 477.757496 | 937.481166 | 469.244221 | 936.497150 | 468.752213 | V | ***964.492066*** | 482.749671 | 947.465517 | 474.236397 | 946.481501 | 473.744389 | 8 |
| 8 | **1053.576129** | 527.291703 | 1036.549580 | 518.778428 | 1035.565564 | 518.286420 | V | ***865.423652*** | 433.215464 | 848.397103 | 424.702190 | 847.413087 | 424.210182 | 7 |
| 9 | 1154.623808 | 577.815542 | 1137.597259 | 569.302268 | 1136.613243 | 568.810260 | T | ***766.355238*** | 383.681257 | 749.328689 | 375.167983 | 748.344673 | 374.675975 | 6 |
| 10 | 1301.659208 | 651.333242 | 1284.632659 | 642.819968 | 1283.648643 | 642.327960 | M | ***665.307559*** | 333.157418 | 648.281010 | 324.644143 | | | 5 |
| 11 | 1464.722537 | 732.864907 | 1447.695988 | 724.351632 | 1446.711972 | 723.859624 | Y | ***518.272159*** | 259.639718 | 501.245610 | 251.126443 | | | 4 |
| 12 | 1601.781449 | 801.394363 | 1584.754900 | 792.881088 | 1583.770884 | 792.389080 | H | ***355.208830*** | 178.108053 | 338.182281 | 169.594778 | | | 3 |
| 13 | 1672.818563 | 836.912920 | 1655.792014 | 828.399645 | 1654.807998 | 827.907637 | A | ***218.149918*** | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 14 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 51.0 | 1817.916824 | 0.011518 | GQGTLSVVTMYHAK |

**Mascot:** http://www.matrixscience.com/

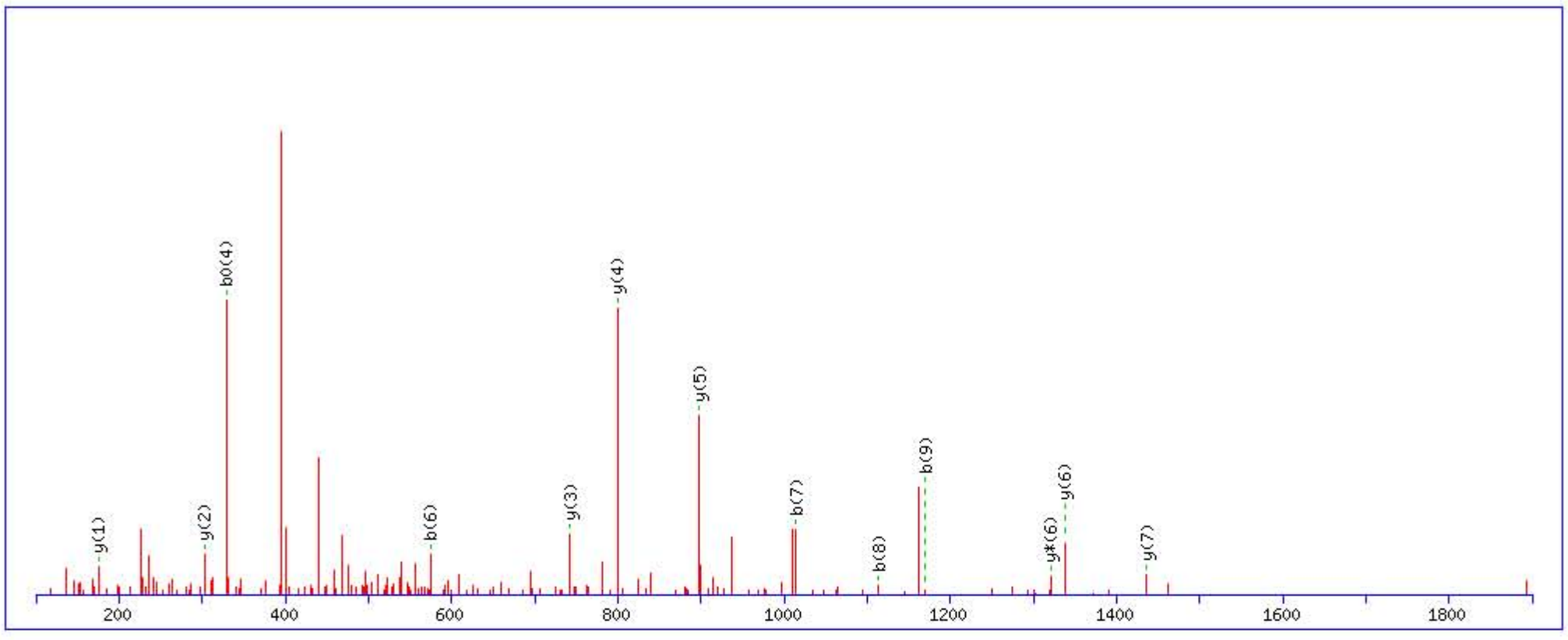
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SGSDEVQVGQQR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

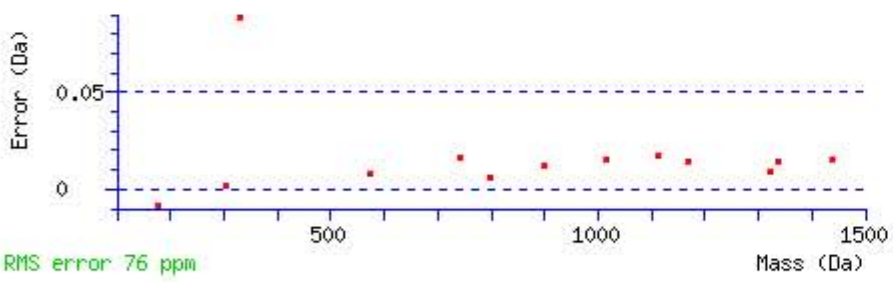
Match to Query 42357: 1910.947692 from(637.989840,3+) rtinseconds(1882) index(33320)
Title: Locus:1.1.1.764.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

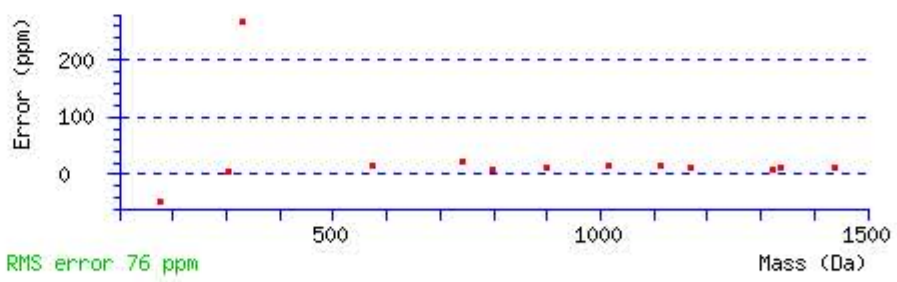
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1910.934265
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.019
**Matches** : 13/106 fragment ions using 29 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 12 |
| 2 | 145.060768 | 73.034022 | | | 127.050203 | 64.028740 | G | 1824.909502 | 912.958389 | 1807.882953 | 904.445115 | 1806.898937 | 903.953107 | 11 |
| 3 | 232.092796 | 116.550036 | | | 214.082231 | 107.544753 | S | 1767.888038 | 884.447657 | 1750.861489 | 875.934383 | 1749.877473 | 875.442375 | 10 |
| 4 | 347.119739 | 174.063507 | | | 329.109174 | 165.058225 | D | 1680.856010 | 840.931643 | 1663.829461 | 832.418369 | 1662.845445 | 831.926361 | 9 |
| 5 | 476.162332 | 238.584804 | | | 458.151767 | 229.579522 | E | 1565.829067 | 783.418172 | 1548.802518 | 774.904897 | 1547.818502 | 774.412889 | 8 |
| 6 | **575.230746** | 288.119011 | | | 557.220181 | 279.113729 | V | *1436.786474* | 718.896875 | 1419.759925 | 710.383601 | | | 7 |
| 7 | **1014.456072** | 507.731674 | 997.429523 | 499.218400 | 996.445507 | 498.726392 | Q | *1337.718060* | 669.362668 | 1320.691511 | 660.849394 | | | 6 |
| 8 | **1113.524486** | 557.265881 | 1096.497937 | 548.752607 | 1095.513921 | 548.260599 | V | *898.492734* | 449.750005 | 881.466185 | 441.236731 | | | 5 |
| 9 | **1170.545950** | 585.776613 | 1153.519401 | 577.263339 | 1152.535385 | 576.771330 | G | *799.424320* | 400.215798 | 782.397771 | 391.702524 | | | 4 |
| 10 | 1609.771276 | 805.389276 | 1592.744727 | 796.876002 | 1591.760711 | 796.383994 | Q | *742.402856* | 371.705066 | 725.376307 | 363.191792 | | | 3 |
| 11 | 1737.829854 | 869.418565 | 1720.803305 | 860.905291 | 1719.819289 | 860.413283 | Q | *303.177530* | 152.092403 | 286.150981 | 143.579129 | | | 2 |
| 12 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.9 | 1910.938263 | 0.009429 | YVTSAPMPEPQAPGR |
| 30.9 | 1910.934265 | 0.013427 | SGSDEVQVGQQR |
| 21.9 | 1910.934265 | 0.013427 | SGSDEVQVGQQR |
| 1.6 | 1910.971970 | -0.024278 | KAPMGTARFGHHMAVLR |

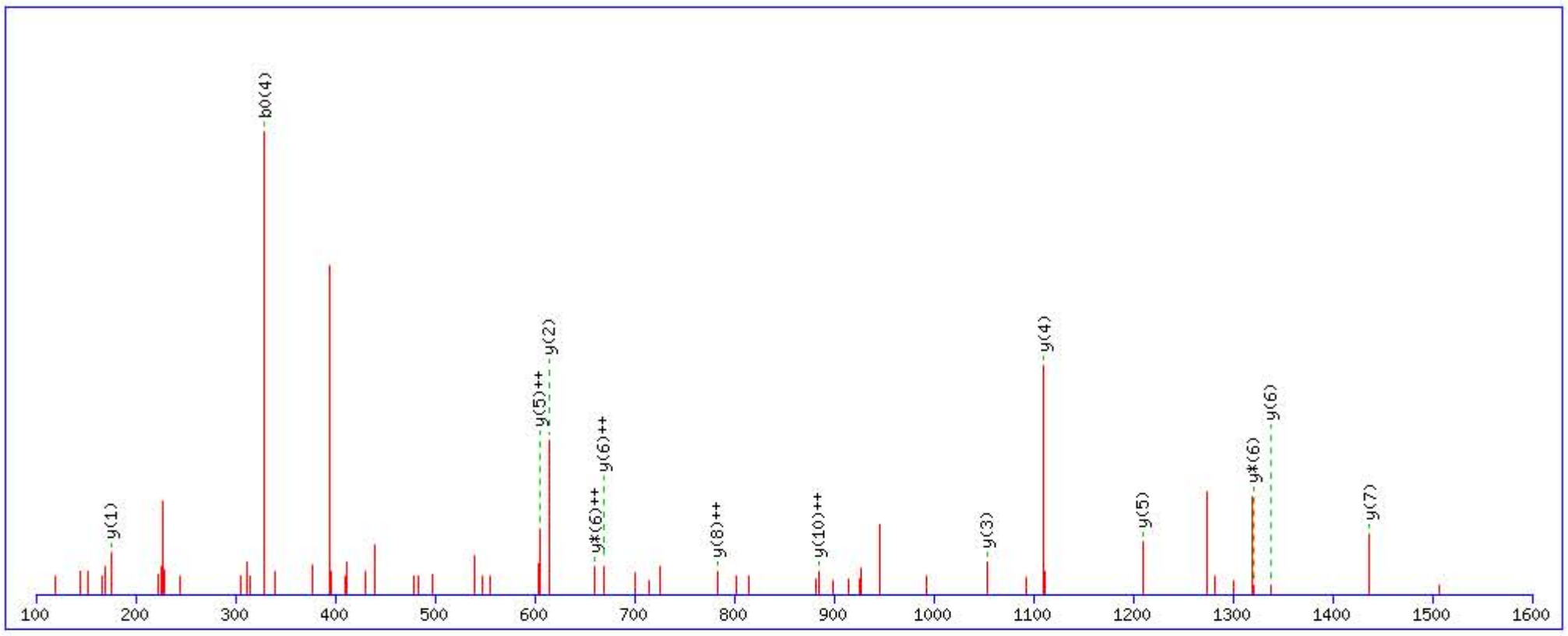
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SGSDEVQVGQQR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

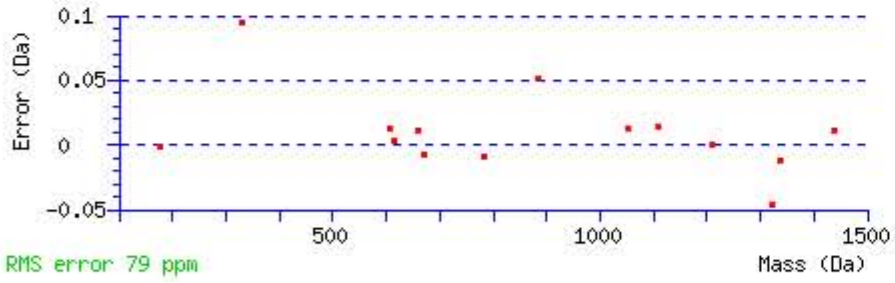
Match to Query 42358: 1910.949072 from(637.990300,3+) rtinseconds(1940) index(33807)
Title: Locus:1.1.1.784.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

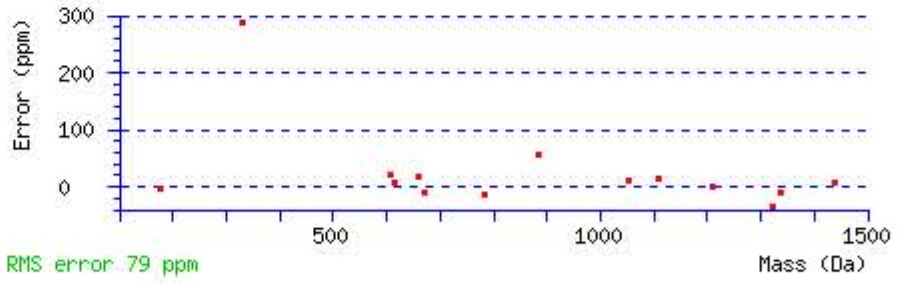
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1910.934265
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q10** : Biotin:Thermo-21345 (Q)
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.0017
**Matches** : 14/106 fragment ions using 28 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 12 |
| 2 | 145.060768 | 73.034022 | | | 127.050203 | 64.028740 | G | 1824.909502 | 912.958389 | 1807.882953 | 904.445115 | 1806.898937 | 903.953107 | 11 |
| 3 | 232.092796 | 116.550036 | | | 214.082231 | 107.544753 | S | 1767.888038 | 884.447657 | 1750.861489 | 875.934383 | 1749.877473 | 875.442375 | 10 |
| 4 | 347.119739 | 174.063507 | | | 329.109174 | 165.058225 | D | 1680.856010 | 840.931643 | 1663.829461 | 832.418369 | 1662.845445 | 831.926361 | 9 |
| 5 | 476.162332 | 238.584804 | | | 458.151767 | 229.579522 | E | 1565.829067 | 783.418172 | 1548.802518 | 774.904897 | 1547.818502 | 774.412889 | 8 |
| 6 | 575.230746 | 288.119011 | | | 557.220181 | 279.113729 | V | *1436.786474* | 718.896875 | 1419.759925 | 710.383601 | | | 7 |
| 7 | 703.289324 | 352.148300 | 686.262775 | 343.635026 | 685.278759 | 343.143018 | Q | *1337.718060* | 669.362668 | 1320.691511 | 660.849394 | | | 6 |
| 8 | 802.357738 | 401.682507 | 785.331189 | 393.169233 | 784.347173 | 392.677225 | V | *1209.659482* | 605.333379 | 1192.632933 | 596.820105 | | | 5 |
| 9 | 859.379202 | 430.193239 | 842.352653 | 421.679965 | 841.368637 | 421.187957 | G | *1110.591068* | 555.799172 | 1093.564519 | 547.285898 | | | 4 |
| 10 | 1298.604528 | 649.805902 | 1281.577979 | 641.292628 | 1280.593963 | 640.800620 | Q | *1053.569604* | 527.288440 | 1036.543055 | 518.775166 | | | 3 |
| 11 | 1737.829854 | 869.418565 | 1720.803305 | 860.905291 | 1719.819289 | 860.413283 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 12 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.6 | 1910.934265 | 0.014807 | SGSDEVQVGQQR |
| 6.7 | 1910.934265 | 0.014807 | SGSDEVQVGQQR |
| 2.0 | 1910.960709 | -0.011637 | VGAPAWREAAQAMAR |
| 0.5 | 1910.934265 | 0.014807 | SGSDEVQVGQQR |

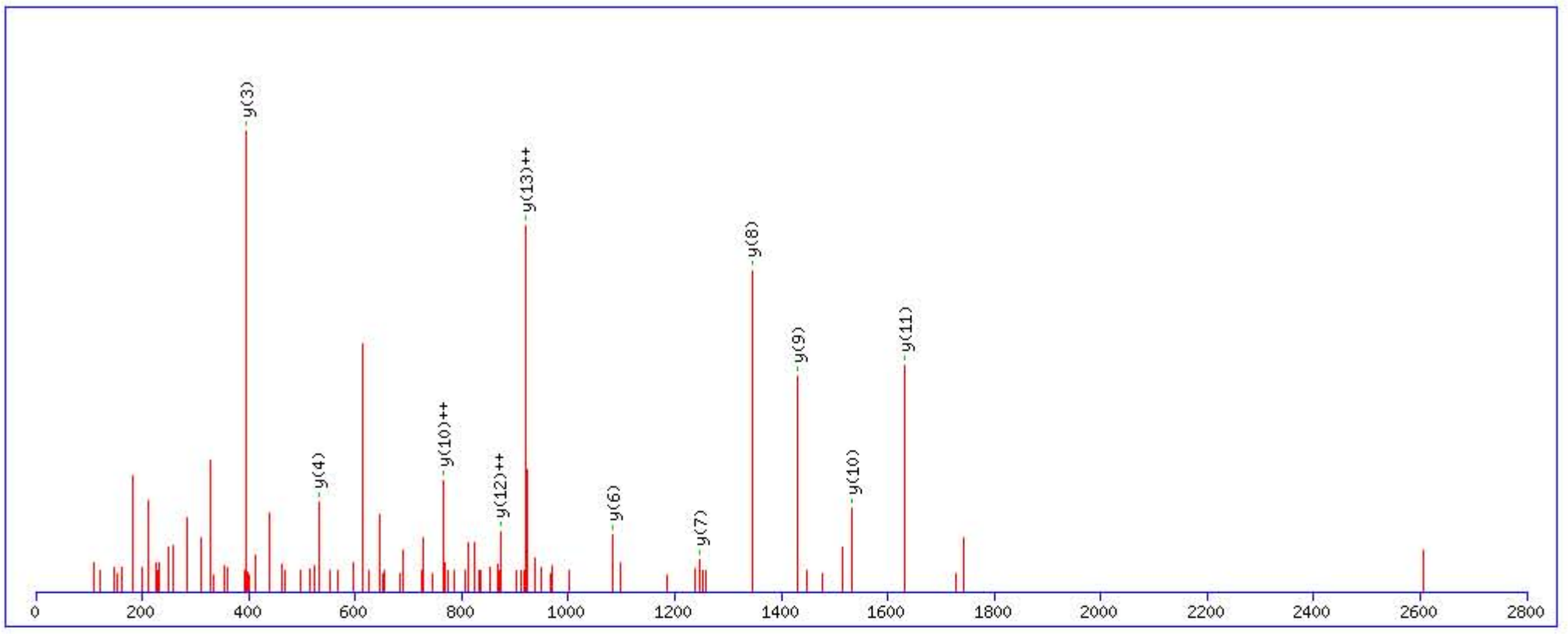
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SGIPIVTSPYQIHFTK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

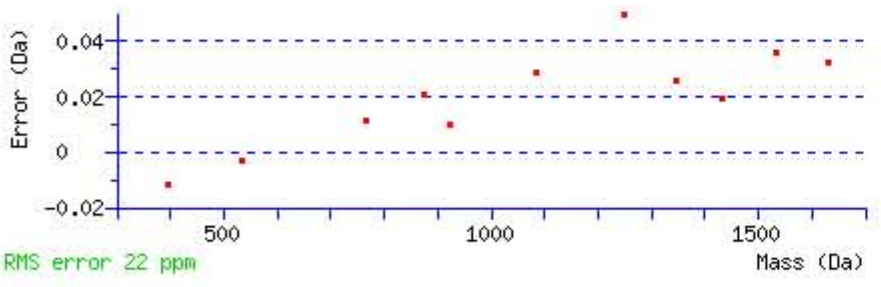
Match to Query 46561: 2098.151022 from(700.390950,3+) rtinseconds(2325) index(52399)
Title: Locus:1.1.1.2047.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

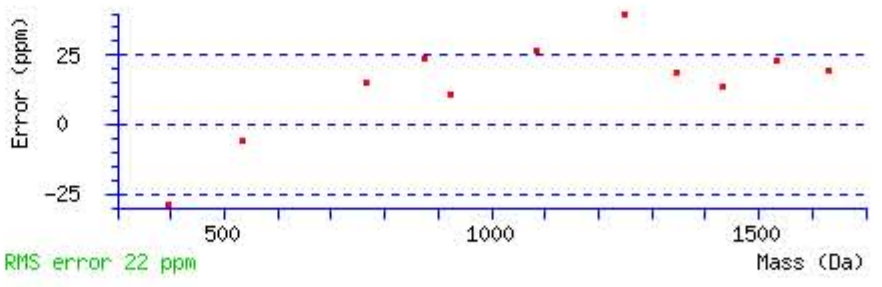
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2098.128525
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 7.5e-005
**Matches** : 11/158 fragment ions using 17 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 16 |
| 2 | 145.060768 | 73.034022 | | | 127.050203 | 64.028740 | G | 2012.103769 | 1006.555523 | 1995.077220 | 998.042248 | 1994.093204 | 997.550240 | 15 |
| 3 | 258.144832 | 129.576054 | | | 240.134267 | 120.570772 | I | 1955.082305 | 978.044791 | 1938.055756 | 969.531516 | 1937.071740 | 969.039508 | 14 |
| 4 | 355.197596 | 178.102436 | | | 337.187031 | 169.097154 | P | 1841.998241 | 921.502759 | 1824.971692 | 912.989484 | 1823.987676 | 912.497476 | 13 |
| 5 | 468.281660 | 234.644468 | | | 450.271095 | 225.639186 | I | 1744.945477 | 872.976377 | 1727.918928 | 864.463102 | 1726.934912 | 863.971094 | 12 |
| 6 | 567.350074 | 284.178675 | | | 549.339509 | 275.173393 | V | *1631.861413* | 816.434345 | 1614.834864 | 807.921070 | 1613.850848 | 807.429062 | 11 |
| 7 | 668.397753 | 334.702515 | | | 650.387188 | 325.697232 | T | *1532.792999* | 766.900138 | 1515.766450 | 758.386863 | 1514.782434 | 757.894855 | 10 |
| 8 | 755.429781 | 378.218529 | | | 737.419216 | 369.213246 | S | *1431.745320* | 716.376298 | 1414.718771 | 707.863024 | 1413.734755 | 707.371016 | 9 |
| 9 | 852.482545 | 426.744911 | | | 834.471980 | 417.739628 | P | *1344.713292* | 672.860284 | 1327.686743 | 664.347010 | 1326.702727 | 663.855002 | 8 |
| 10 | 1015.545874 | 508.276575 | | | 997.535309 | 499.271293 | Y | *1247.660528* | 624.333902 | 1230.633979 | 615.820628 | 1229.649963 | 615.328620 | 7 |
| 11 | 1454.771200 | 727.889238 | 1437.744651 | 719.375964 | 1436.760635 | 718.883956 | Q | *1084.597199* | 542.802238 | 1067.570650 | 534.288963 | 1066.586634 | 533.796955 | 6 |
| 12 | 1567.855264 | 784.431270 | 1550.828715 | 775.917996 | 1549.844699 | 775.425988 | I | 645.371873 | 323.189574 | 628.345324 | 314.676300 | 627.361308 | 314.184292 | 5 |
| 13 | 1704.914176 | 852.960726 | 1687.887627 | 844.447452 | 1686.903611 | 843.955444 | H | *532.287809* | 266.647542 | 515.261260 | 258.134268 | 514.277244 | 257.642260 | 4 |
| 14 | 1851.982590 | 926.494933 | 1834.956041 | 917.981659 | 1833.972025 | 917.489651 | F | *395.228897* | 198.118086 | 378.202348 | 189.604812 | 377.218332 | 189.112804 | 3 |
| 15 | 1953.030269 | 977.018773 | 1936.003720 | 968.505498 | 1935.019704 | 968.013490 | T | 248.160483 | 124.583879 | 231.133934 | 116.070605 | 230.149918 | 115.578597 | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 53.3 | 2098.128525 | 0.022497 | SGIPIVTSPYQIHFTK |

**Mascot:** http://www.matrixscience.com/

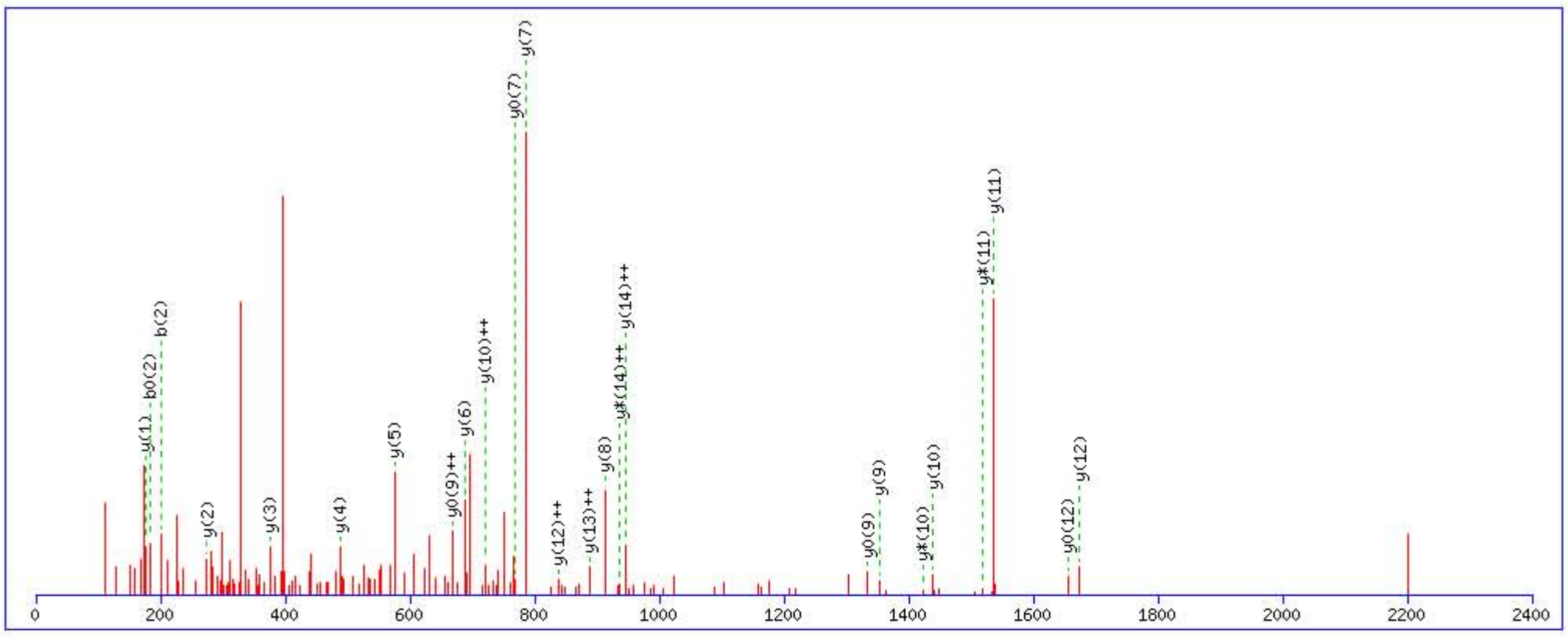
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LSINTHPSQKPLSITVR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

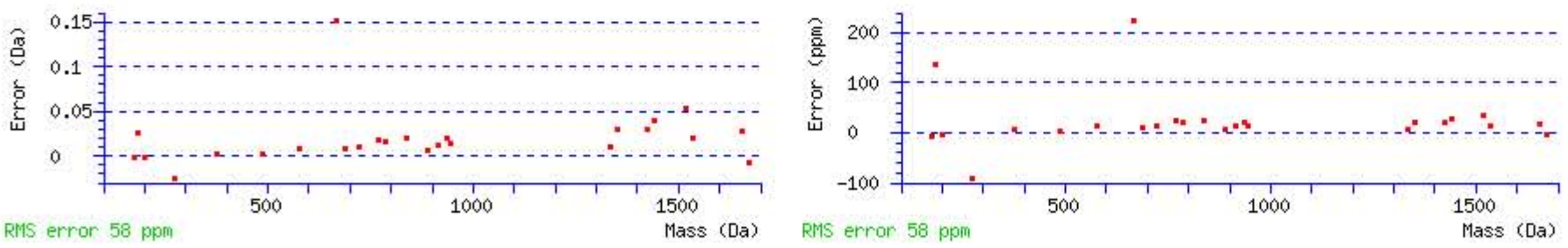
Match to Query 48477: 2201.244696 from(551.318450,4+) rtinseconds(1896) index(33428)
Title: Locus:1.1.1.769.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2201.235428
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 46 **Expect:** 0.0002
**Matches :** 25/180 fragment ions using 69 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 17 |
| 2 | 201.123368 | 101.065322 | | | 183.112803 | 92.060039 | S | 2089.158656 | 1045.082966 | 2072.132107 | 1036.569691 | 2071.148091 | 1036.077683 | 16 |
| 3 | 314.207432 | 157.607354 | | | 296.196867 | 148.602071 | I | 2002.126628 | 1001.566952 | 1985.100079 | 993.053678 | 1984.116063 | 992.561669 | 15 |
| 4 | 428.250359 | 214.628818 | 411.223810 | 206.115543 | 410.239794 | 205.623535 | N | 1889.042564 | 945.024920 | 1872.016015 | 936.511646 | 1871.031999 | 936.019638 | 14 |
| 5 | 529.298038 | 265.152657 | 512.271489 | 256.639383 | 511.287473 | 256.147375 | T | 1774.999637 | 888.003456 | 1757.973088 | 879.490182 | 1756.989072 | 878.998174 | 13 |
| 6 | 666.356950 | 333.682113 | 649.330401 | 325.168838 | 648.346385 | 324.676830 | H | *1673.951958* | 837.479617 | 1656.925409 | 828.966343 | 1655.941393 | 828.474334 | 12 |
| 7 | 763.409714 | 382.208495 | 746.383165 | 373.695221 | 745.399149 | 373.203213 | P | *1536.893046* | 768.950161 | 1519.866497 | 760.436887 | 1518.882481 | 759.944878 | 11 |
| 8 | 850.441742 | 425.724509 | 833.415193 | 417.211234 | 832.431177 | 416.719226 | S | *1439.840282* | 720.423779 | 1422.813733 | 711.910505 | 1421.829717 | 711.418496 | 10 |
| 9 | 1289.667068 | 645.337172 | 1272.640519 | 636.823898 | 1271.656503 | 636.331889 | Q | *1352.808254* | 676.907765 | 1335.781705 | 668.394491 | 1334.797689 | 667.902483 | 9 |
| 10 | 1417.762031 | 709.384654 | 1400.735482 | 700.871379 | 1399.751466 | 700.379371 | K | *913.582928* | 457.295102 | 896.556379 | 448.781828 | 895.572363 | 448.289820 | 8 |
| 11 | 1514.814795 | 757.911036 | 1497.788246 | 749.397761 | 1496.804230 | 748.905753 | P | *785.487965* | 393.247621 | 768.461416 | 384.734346 | 767.477400 | 384.242338 | 7 |
| 12 | 1627.898859 | 814.453067 | 1610.872310 | 805.939793 | 1609.888294 | 805.447785 | L | *688.435201* | 344.721239 | 671.408652 | 336.207964 | 670.424636 | 335.715956 | 6 |
| 13 | 1714.930887 | 857.969082 | 1697.904338 | 849.455807 | 1696.920322 | 848.963799 | S | *575.351137* | 288.179207 | 558.324588 | 279.665932 | 557.340572 | 279.173924 | 5 |
| 14 | 1828.014951 | 914.511113 | 1810.988402 | 905.997839 | 1810.004386 | 905.505831 | I | *488.319109* | 244.663192 | 471.292560 | 236.149918 | 470.308544 | 235.657910 | 4 |
| 15 | 1929.062630 | 965.034953 | 1912.036081 | 956.521679 | 1911.052065 | 956.029670 | T | *375.235045* | 188.121161 | 358.208496 | 179.607886 | 357.224480 | 179.115878 | 3 |
| 16 | 2028.131044 | 1014.569160 | 2011.104495 | 1006.055886 | 2010.120479 | 1005.563878 | V | *274.187366* | 137.597321 | 257.160817 | 129.084047 | | | 2 |
| 17 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.7 | 2201.235428 | 0.009268 | LSINTHPSQKPLSITVR |

**Mascot:** http://www.matrixscience.com/

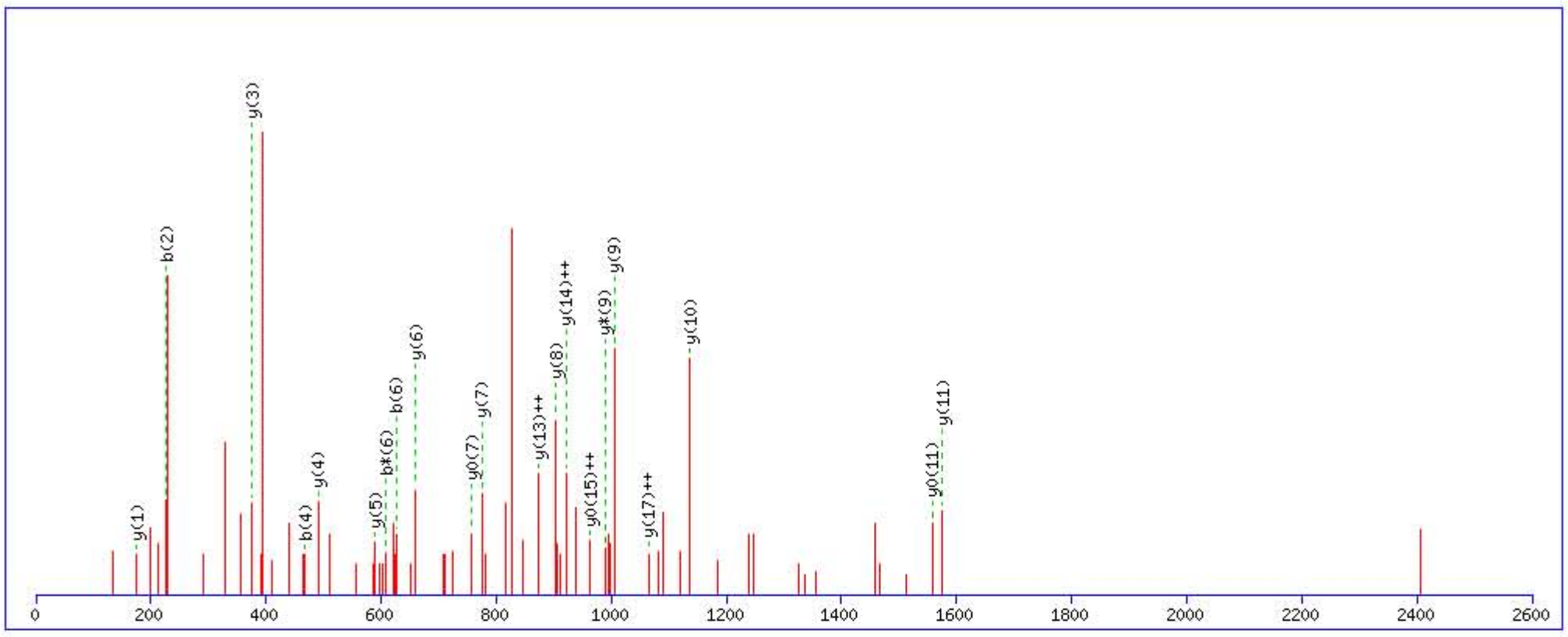
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ILLQGTPVAQMTEDAVDAER**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

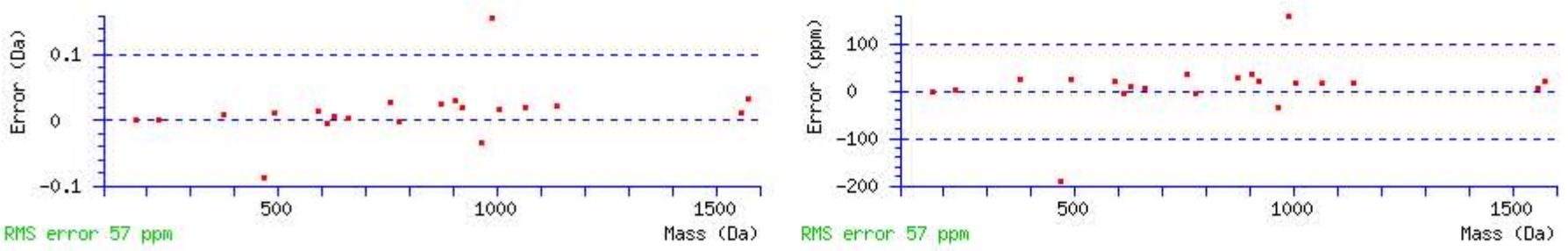
Match to Query 53415: 2467.265682 from(823.429170,3+) rtinseconds(2726) index(38549)
Title: Locus:1.1.1.1057.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2467.245071
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 27 **Expect:** 0.061
**Matches :** 21/210 fragment ions using 68 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 20 |
| 2 | **227.175404** | 114.091340 | | | | | L | 2355.168297 | 1178.087786 | 2338.141748 | 1169.574512 | 2337.157732 | 1169.082504 | 19 |
| 3 | 340.259468 | 170.633372 | | | | | L | 2242.084233 | 1121.545754 | 2225.057684 | 1113.032480 | 2224.073668 | 1112.540472 | 18 |
| 4 | **468.318046** | 234.662661 | 451.291497 | 226.149386 | | | Q | 2129.000169 | 1065.003722 | 2111.973620 | 1056.490448 | 2110.989604 | 1055.998440 | 17 |
| 5 | 525.339510 | 263.173393 | 508.312961 | 254.660119 | | | G | 2000.941591 | 1000.974434 | 1983.915042 | 992.461159 | 1982.931026 | 991.969151 | 16 |
| 6 | **626.387189** | 313.697233 | 609.360640 | 305.183958 | 608.376624 | 304.691950 | T | 1943.920127 | 972.463702 | 1926.893578 | 963.950427 | 1925.909562 | 963.458419 | 15 |
| 7 | 723.439953 | 362.223615 | 706.413404 | 353.710340 | 705.429388 | 353.218332 | P | 1842.872448 | 921.939862 | 1825.845899 | 913.426588 | 1824.861883 | 912.934580 | 14 |
| 8 | 822.508367 | 411.757822 | 805.481818 | 403.244547 | 804.497802 | 402.752539 | V | 1745.819684 | 873.413480 | 1728.793135 | 864.900206 | 1727.809119 | 864.408198 | 13 |
| 9 | 893.545481 | 447.276379 | 876.518932 | 438.763104 | 875.534916 | 438.271096 | A | 1646.751270 | 823.879273 | 1629.724721 | 815.365999 | 1628.740705 | 814.873991 | 12 |
| 10 | 1332.770807 | 666.889042 | 1315.744258 | 658.375767 | 1314.760242 | 657.883759 | Q | *1575.714156* | 788.360716 | 1558.687607 | 779.847442 | 1557.703591 | 779.355434 | 11 |
| 11 | 1463.811292 | 732.409284 | 1446.784743 | 723.896010 | 1445.800727 | 723.404002 | M | *1136.488830* | 568.748053 | 1119.462281 | 560.234779 | 1118.478265 | 559.742771 | 10 |
| 12 | 1564.858971 | 782.933124 | 1547.832422 | 774.419849 | 1546.848406 | 773.927841 | T | *1005.448345* | 503.227811 | 988.421796 | 494.714536 | 987.437780 | 494.222528 | 9 |
| 13 | 1693.901564 | 847.454420 | 1676.875015 | 838.941146 | 1675.890999 | 838.449138 | E | *904.400666* | 452.703971 | 887.374117 | 444.190697 | 886.390101 | 443.698689 | 8 |
| 14 | 1808.928507 | 904.967892 | 1791.901958 | 896.454617 | 1790.917942 | 895.962609 | D | *775.358073* | 388.182675 | 758.331524 | 379.669400 | 757.347508 | 379.177392 | 7 |
| 15 | 1879.965621 | 940.486449 | 1862.939072 | 931.973174 | 1861.955056 | 931.481166 | A | *660.331130* | 330.669203 | 643.304581 | 322.155929 | 642.320565 | 321.663921 | 6 |
| 16 | 1979.034035 | 990.020656 | 1962.007486 | 981.507381 | 1961.023470 | 981.015373 | V | *589.294016* | 295.150646 | 572.267467 | 286.637372 | 571.283451 | 286.145364 | 5 |
| 17 | 2094.060978 | 1047.534127 | 2077.034429 | 1039.020852 | 2076.050413 | 1038.528844 | D | *490.225602* | 245.616439 | 473.199053 | 237.103165 | 472.215037 | 236.611157 | 4 |
| 18 | 2165.098092 | 1083.052684 | 2148.071543 | 1074.539409 | 2147.087527 | 1074.047402 | A | *375.198659* | 188.102968 | 358.172110 | 179.589693 | 357.188094 | 179.097685 | 3 |
| 19 | 2294.140685 | 1147.573981 | 2277.114136 | 1139.060706 | 2276.130120 | 1138.568698 | E | 304.161545 | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 20 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 26.6 | 2467.245071 | 0.020611 | ILLQGTPVAQMTEDAVDAER |
| 22.7 | 2467.245071 | 0.020611 | ILLQGTPVAQMTEDAVDAER |

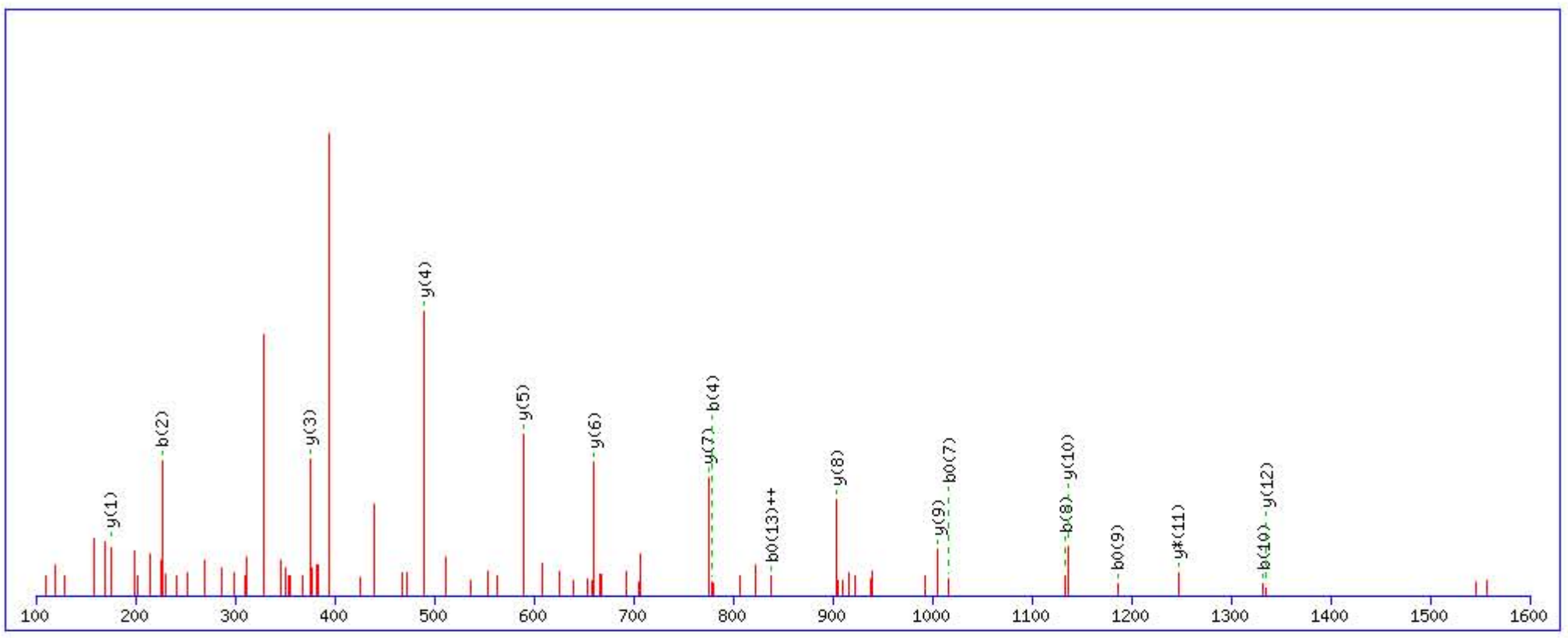
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ILLQGTPVAQMTEDAVDAER**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

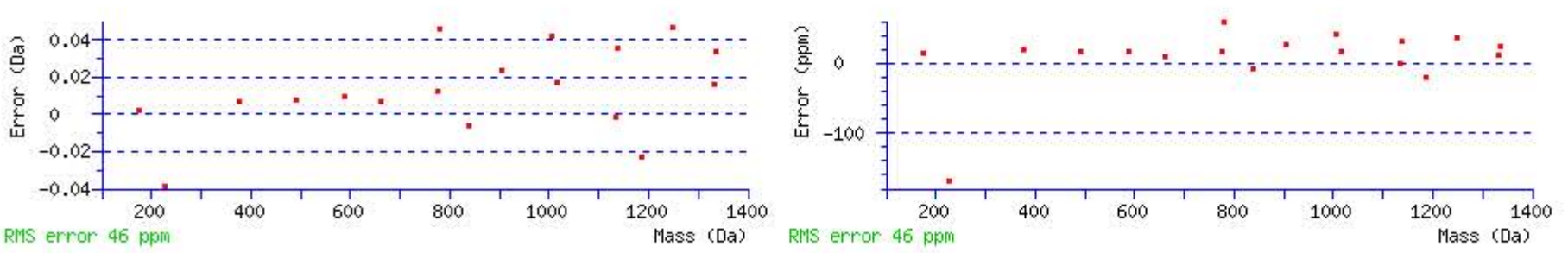
Match to Query 53417: 2467.275096 from(617.826050,4+) rtinseconds(2675) index(38137)
Title: Locus:1.1.1.1040.4 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2467.245071
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 50 **Expect:** 0.0003
**Matches :** 18/210 fragment ions using 36 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 20 |
| 2 | 227.175404 | 114.091340 | | | | | L | 2355.168297 | 1178.087786 | 2338.141748 | 1169.574512 | 2337.157732 | 1169.082504 | 19 |
| 3 | 340.259468 | 170.633372 | | | | | L | 2242.084233 | 1121.545754 | 2225.057684 | 1113.032480 | 2224.073668 | 1112.540472 | 18 |
| 4 | 779.484794 | 390.246035 | 762.458245 | 381.732760 | | | Q | 2129.000169 | 1065.003722 | 2111.973620 | 1056.490448 | 2110.989604 | 1055.998440 | 17 |
| 5 | 836.506258 | 418.756767 | 819.479709 | 410.243493 | | | G | 1689.774843 | 845.391060 | 1672.748294 | 836.877785 | 1671.764278 | 836.385777 | 16 |
| 6 | 937.553937 | 469.280607 | 920.527388 | 460.767332 | 919.543372 | 460.275324 | T | 1632.753379 | 816.880328 | 1615.726830 | 808.367053 | 1614.742814 | 807.875045 | 15 |
| 7 | 1034.606701 | 517.806988 | 1017.580152 | 509.293714 | 1016.596136 | 508.801706 | P | 1531.705700 | 766.356488 | 1514.679151 | 757.843214 | 1513.695135 | 757.351206 | 14 |
| 8 | 1133.675115 | 567.341196 | 1116.648566 | 558.827921 | 1115.664550 | 558.335913 | V | 1434.652936 | 717.830106 | 1417.626387 | 709.316832 | 1416.642371 | 708.824824 | 13 |
| 9 | 1204.712229 | 602.859753 | 1187.685680 | 594.346478 | 1186.701664 | 593.854470 | A | *1335.584522* | 668.295899 | 1318.557973 | 659.782625 | 1317.573957 | 659.290617 | 12 |
| 10 | 1332.770807 | 666.889042 | 1315.744258 | 658.375767 | 1314.760242 | 657.883759 | Q | 1264.547408 | 632.777342 | 1247.520859 | 624.264068 | 1246.536843 | 623.772060 | 11 |
| 11 | 1463.811292 | 732.409284 | 1446.784743 | 723.896010 | 1445.800727 | 723.404002 | M | *1136.488830* | 568.748053 | 1119.462281 | 560.234779 | 1118.478265 | 559.742771 | 10 |
| 12 | 1564.858971 | 782.933124 | 1547.832422 | 774.419849 | 1546.848406 | 773.927841 | T | *1005.448345* | 503.227811 | 988.421796 | 494.714536 | 987.437780 | 494.222528 | 9 |
| 13 | 1693.901564 | 847.454420 | 1676.875015 | 838.941146 | 1675.890999 | 838.449138 | E | *904.400666* | 452.703971 | 887.374117 | 444.190697 | 886.390101 | 443.698689 | 8 |
| 14 | 1808.928507 | 904.967892 | 1791.901958 | 896.454617 | 1790.917942 | 895.962609 | D | *775.358073* | 388.182675 | 758.331524 | 379.669400 | 757.347508 | 379.177392 | 7 |
| 15 | 1879.965621 | 940.486449 | 1862.939072 | 931.973174 | 1861.955056 | 931.481166 | A | *660.331130* | 330.669203 | 643.304581 | 322.155929 | 642.320565 | 321.663921 | 6 |
| 16 | 1979.034035 | 990.020656 | 1962.007486 | 981.507381 | 1961.023470 | 981.015373 | V | *589.294016* | 295.150646 | 572.267467 | 286.637372 | 571.283451 | 286.145364 | 5 |
| 17 | 2094.060978 | 1047.534127 | 2077.034429 | 1039.020852 | 2076.050413 | 1038.528844 | D | *490.225602* | 245.616439 | 473.199053 | 237.103165 | 472.215037 | 236.611157 | 4 |
| 18 | 2165.098092 | 1083.052684 | 2148.071543 | 1074.539409 | 2147.087527 | 1074.047402 | A | *375.198659* | 188.102968 | 358.172110 | 179.589693 | 357.188094 | 179.097685 | 3 |
| 19 | 2294.140685 | 1147.573981 | 2277.114136 | 1139.060706 | 2276.130120 | 1138.568698 | E | 304.161545 | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 20 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 49.9 | 2467.245071 | 0.030025 | ILLQGTPVAQMTEDAVDAER |
| 44.1 | 2467.245071 | 0.030025 | ILLQGTPVAQMTEDAVDAER |

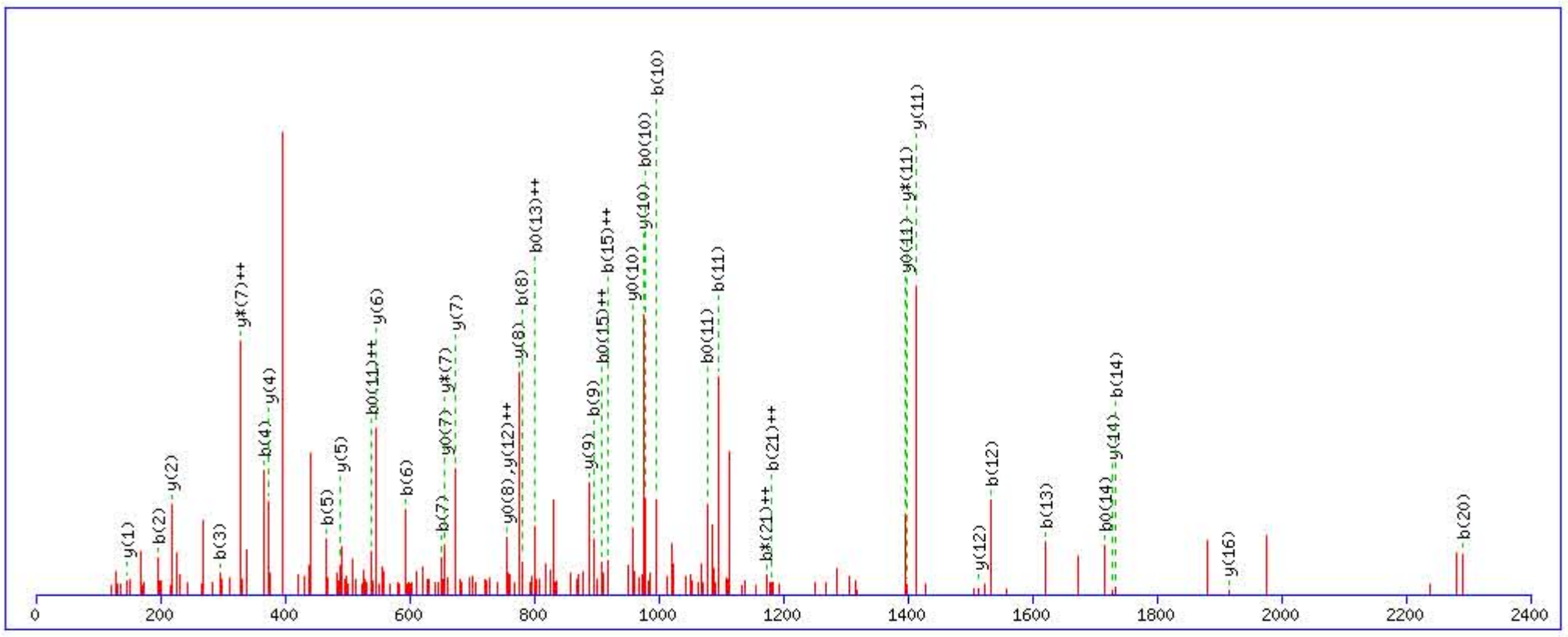
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VPVAVQGEDTVQSLTQGDGVAK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

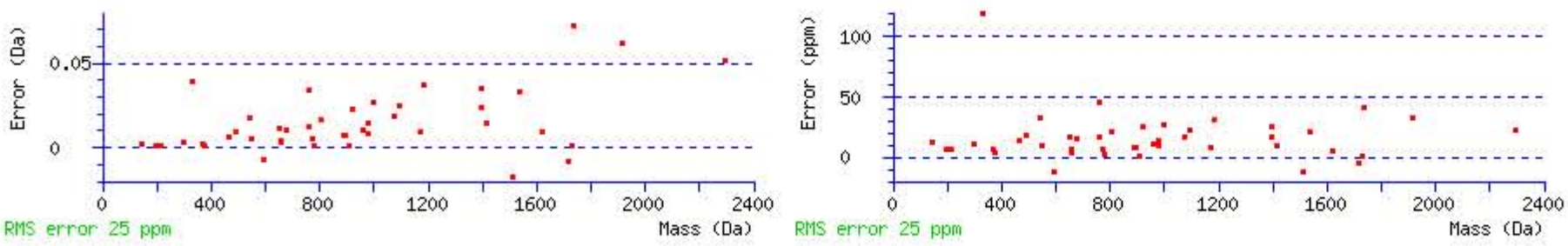
Match to Query 54514: 2508.326952 from(837.116260,3+) rtinseconds(2245) index(35726)
Title: Locus:1.1.1.890.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2508.289429
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 81 **Expect:** 2.8e-008
**Matches :** 44/220 fragment ions using 93 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 22 |
| 2 | *197.128454* | 99.067865 | | | | | P | 2410.228255 | 1205.617765 | 2393.201706 | 1197.104491 | 2392.217690 | 1196.612483 | 21 |
| 3 | *296.196868* | 148.602072 | | | | | V | 2313.175491 | 1157.091383 | 2296.148942 | 1148.578109 | 2295.164926 | 1148.086101 | 20 |
| 4 | *367.233982* | 184.120629 | | | | | A | 2214.107077 | 1107.557176 | 2197.080528 | 1099.043902 | 2196.096512 | 1098.551894 | 19 |
| 5 | *466.302396* | 233.654836 | | | | | V | 2143.069963 | 1072.038619 | 2126.043414 | 1063.525345 | 2125.059398 | 1063.033337 | 18 |
| 6 | *594.360974* | 297.684125 | 577.334425 | 289.170851 | | | Q | 2044.001549 | 1022.504413 | 2026.975000 | 1013.991138 | 2025.990984 | 1013.499130 | 17 |
| 7 | *651.382438* | 326.194857 | 634.355889 | 317.681583 | | | G | *1915.942971* | 958.475124 | 1898.916422 | 949.961849 | 1897.932406 | 949.469841 | 16 |
| 8 | *780.425031* | 390.716154 | 763.398482 | 382.202879 | 762.414466 | 381.710871 | E | 1858.921507 | 929.964391 | 1841.894958 | 921.451117 | 1840.910942 | 920.959109 | 15 |
| 9 | *895.451974* | 448.229625 | 878.425425 | 439.716351 | 877.441409 | 439.224343 | D | *1729.878914* | 865.443095 | 1712.852365 | 856.929821 | 1711.868349 | 856.437812 | 14 |
| 10 | *996.499653* | 498.753465 | 979.473104 | 490.240190 | 978.489088 | 489.748182 | T | 1614.851971 | 807.929623 | 1597.825422 | 799.416349 | 1596.841406 | 798.924341 | 13 |
| 11 | *1095.568067* | 548.287672 | 1078.541518 | 539.774397 | 1077.557502 | 539.282389 | V | *1513.804292* | 757.405784 | 1496.777743 | 748.892510 | 1495.793727 | 748.400502 | 12 |
| 12 | *1534.793393* | 767.900335 | 1517.766844 | 759.387060 | 1516.782828 | 758.895052 | Q | *1414.735878* | 707.871577 | 1397.709329 | 699.358303 | 1396.725313 | 698.866294 | 11 |
| 13 | *1621.825421* | 811.416349 | 1604.798872 | 802.903074 | 1603.814856 | 802.411066 | S | *975.510552* | 488.258914 | 958.484003 | 479.745639 | 957.499987 | 479.253631 | 10 |
| 14 | *1734.909485* | 867.958381 | 1717.882936 | 859.445106 | 1716.898920 | 858.953098 | L | *888.478524* | 444.742900 | 871.451975 | 436.229625 | 870.467959 | 435.737617 | 9 |
| 15 | 1835.957164 | **918.482220** | 1818.930615 | 909.968946 | 1817.946599 | 909.476938 | T | *775.394460* | 388.200868 | 758.367911 | 379.687593 | 757.383895 | 379.195585 | 8 |
| 16 | 1964.015742 | 982.511509 | 1946.989193 | 973.998235 | 1946.005177 | 973.506227 | Q | *674.346781* | 337.677029 | 657.320232 | 329.163754 | 656.336216 | 328.671746 | 7 |
| 17 | 2021.037206 | 1011.022241 | 2004.010657 | 1002.508967 | 2003.026641 | 1002.016959 | G | *546.288203* | 273.647739 | 529.261654 | 265.134465 | 528.277638 | 264.642457 | 6 |
| 18 | 2136.064149 | 1068.535712 | 2119.037600 | 1060.022438 | 2118.053584 | 1059.530430 | D | *489.266739* | 245.137007 | 472.240190 | 236.623733 | 471.256174 | 236.131725 | 5 |
| 19 | 2193.085613 | 1097.046444 | 2176.059064 | 1088.533170 | 2175.075048 | 1088.041162 | G | *374.239796* | 187.623536 | 357.213247 | 179.110261 | | | 4 |
| 20 | *2292.154027* | 1146.580651 | 2275.127478 | 1138.067377 | 2274.143462 | 1137.575369 | V | 317.218332 | 159.112804 | 300.191783 | 150.599530 | | | 3 |
| 21 | 2363.191141 | **1182.099208** | 2346.164592 | 1173.585934 | 2345.180576 | 1173.093926 | A | *218.149918* | 109.578597 | 201.123369 | 101.065323 | | | 2 |
| 22 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 81.4 | 2508.289429 | 0.037523 | VPVAVQGEDTVQSLTQGDGVAK |
| 47.5 | 2508.289429 | 0.037523 | VPVAVQGEDTVQSLTQGDGVAK |
| 26.9 | 2508.289429 | 0.037523 | VPVAVQGEDTVQSLTQGDGVAK |
| 0.8 | 2508.336960 | -0.010008 | QKQAEQALQELRDLLTEGK |

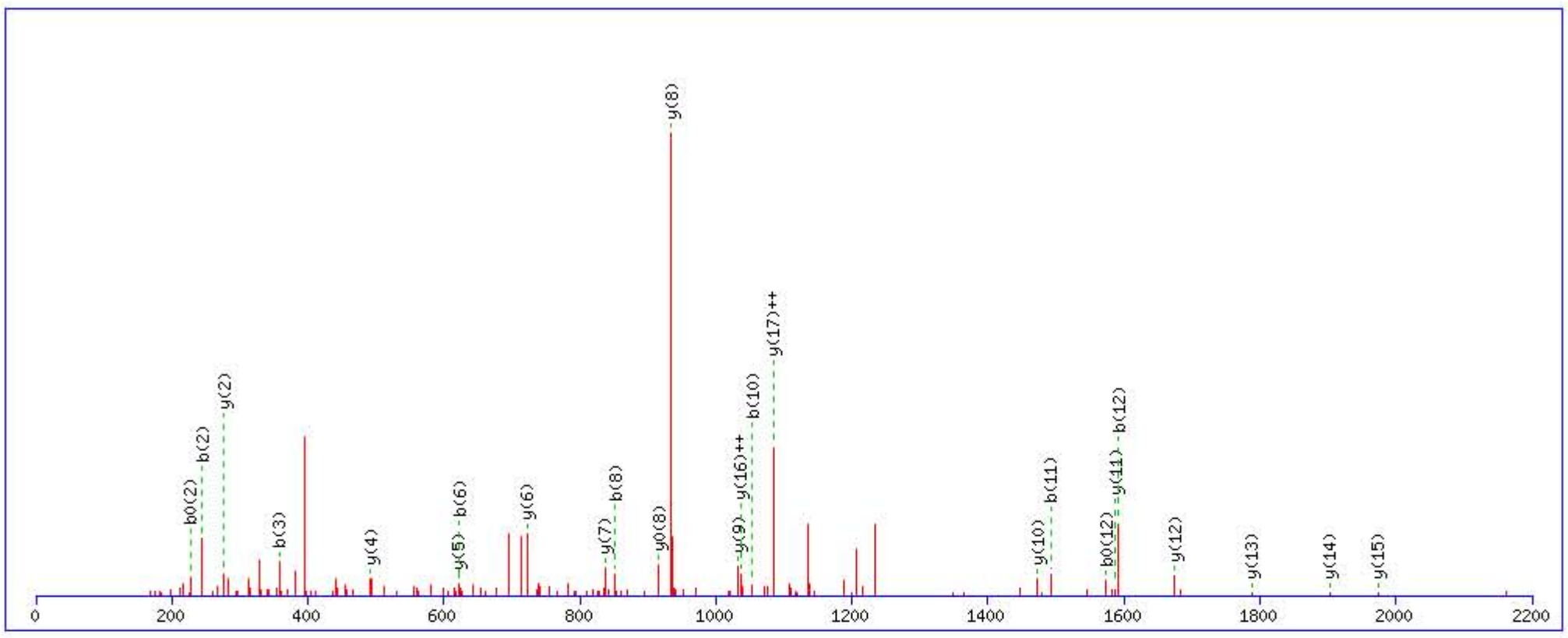
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EDIPPADLSDQVPDTESETR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

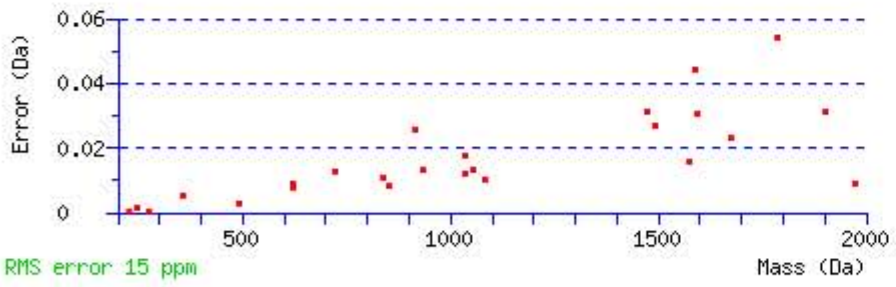
Match to Query 54715: 2524.198932 from(842.406920,3+) rtinseconds(2095) index(34836)
Title: Locus:1.1.1.838.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

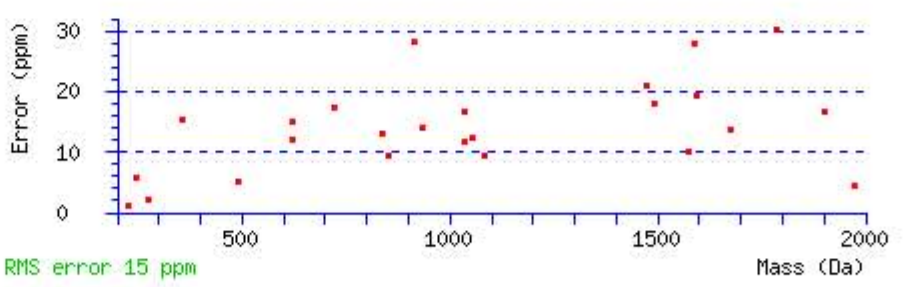
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2524.163910
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 72 **Expect:** 1.2e-006
**Matches** : 25/206 fragment ions using 50 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 20 |
| 2 | **245.076812** | 123.042044 | | | 227.066247 | 114.036762 | D | 2396.128598 | 1198.567937 | 2379.102049 | 1190.054662 | 2378.118033 | 1189.562654 | 19 |
| 3 | **358.160876** | 179.584076 | | | 340.150311 | 170.578794 | I | 2281.101655 | 1141.054465 | 2264.075106 | 1132.541191 | 2263.091090 | 1132.049183 | 18 |
| 4 | 455.213640 | 228.110458 | | | 437.203075 | 219.105176 | P | 2168.017591 | 1084.512433 | 2150.991042 | 1075.999159 | 2150.007026 | 1075.507151 | 17 |
| 5 | 552.266404 | 276.636840 | | | 534.255839 | 267.631558 | P | 2070.964827 | 1035.986051 | 2053.938278 | 1027.472777 | 2052.954262 | 1026.980769 | 16 |
| 6 | **623.303518** | 312.155397 | | | 605.292953 | 303.150115 | A | *1973.912063* | 987.459670 | 1956.885514 | 978.946395 | 1955.901498 | 978.454387 | 15 |
| 7 | 738.330461 | 369.668869 | | | 720.319896 | 360.663586 | D | *1902.874949* | 951.941113 | 1885.848400 | 943.427838 | 1884.864384 | 942.935830 | 14 |
| 8 | **851.414525** | 426.210901 | | | 833.403960 | 417.205618 | L | *1787.848006* | 894.427641 | 1770.821457 | 885.914367 | 1769.837441 | 885.422359 | 13 |
| 9 | 938.446553 | 469.726915 | | | 920.435988 | 460.721632 | S | *1674.763942* | 837.885609 | 1657.737393 | 829.372335 | 1656.753377 | 828.880327 | 12 |
| 10 | **1053.473496** | 527.240386 | | | 1035.462931 | 518.235104 | D | *1587.731914* | 794.369595 | 1570.705365 | 785.856321 | 1569.721349 | 785.364313 | 11 |
| 11 | **1492.698822** | 746.853049 | 1475.672273 | 738.339775 | 1474.688257 | 737.847767 | Q | *1472.704971* | 736.856124 | 1455.678422 | 728.342849 | 1454.694406 | 727.850841 | 10 |
| 12 | **1591.767236** | 796.387256 | 1574.740687 | 787.873982 | 1573.756671 | 787.381974 | V | *1033.479645* | 517.243461 | 1016.453096 | 508.730186 | 1015.469080 | 508.238178 | 9 |
| 13 | 1688.820000 | 844.913638 | 1671.793451 | 836.400364 | 1670.809435 | 835.908356 | P | *934.411231* | 467.709254 | 917.384682 | 459.195979 | 916.400666 | 458.703971 | 8 |
| 14 | 1803.846943 | 902.427110 | 1786.820394 | 893.913835 | 1785.836378 | 893.421827 | D | *837.358467* | 419.182872 | 820.331918 | 410.669597 | 819.347902 | 410.177589 | 7 |
| 15 | 1904.894622 | 952.950949 | 1887.868073 | 944.437675 | 1886.884057 | 943.945667 | T | *722.331524* | 361.669400 | 705.304975 | 353.156125 | 704.320959 | 352.664117 | 6 |
| 16 | 2033.937215 | 1017.472246 | 2016.910666 | 1008.958971 | 2015.926650 | 1008.466963 | E | *621.283845* | 311.145560 | 604.257296 | 302.632286 | 603.273280 | 302.140278 | 5 |
| 17 | 2120.969243 | 1060.988259 | 2103.942694 | 1052.474985 | 2102.958678 | 1051.982977 | S | *492.241252* | 246.624264 | 475.214703 | 238.110989 | 474.230687 | 237.618981 | 4 |
| 18 | 2250.011836 | 1125.509556 | 2232.985287 | 1116.996281 | 2232.001271 | 1116.504274 | E | 405.209224 | 203.108250 | 388.182675 | 194.594975 | 387.198659 | 194.102967 | 3 |
| 19 | 2351.059515 | 1176.033395 | 2334.032966 | 1167.520121 | 2333.048950 | 1167.028113 | T | *276.166631* | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 20 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 72.3 | 2524.163910 | 0.035022 | EDIPPADLSDQVPDTESETR |

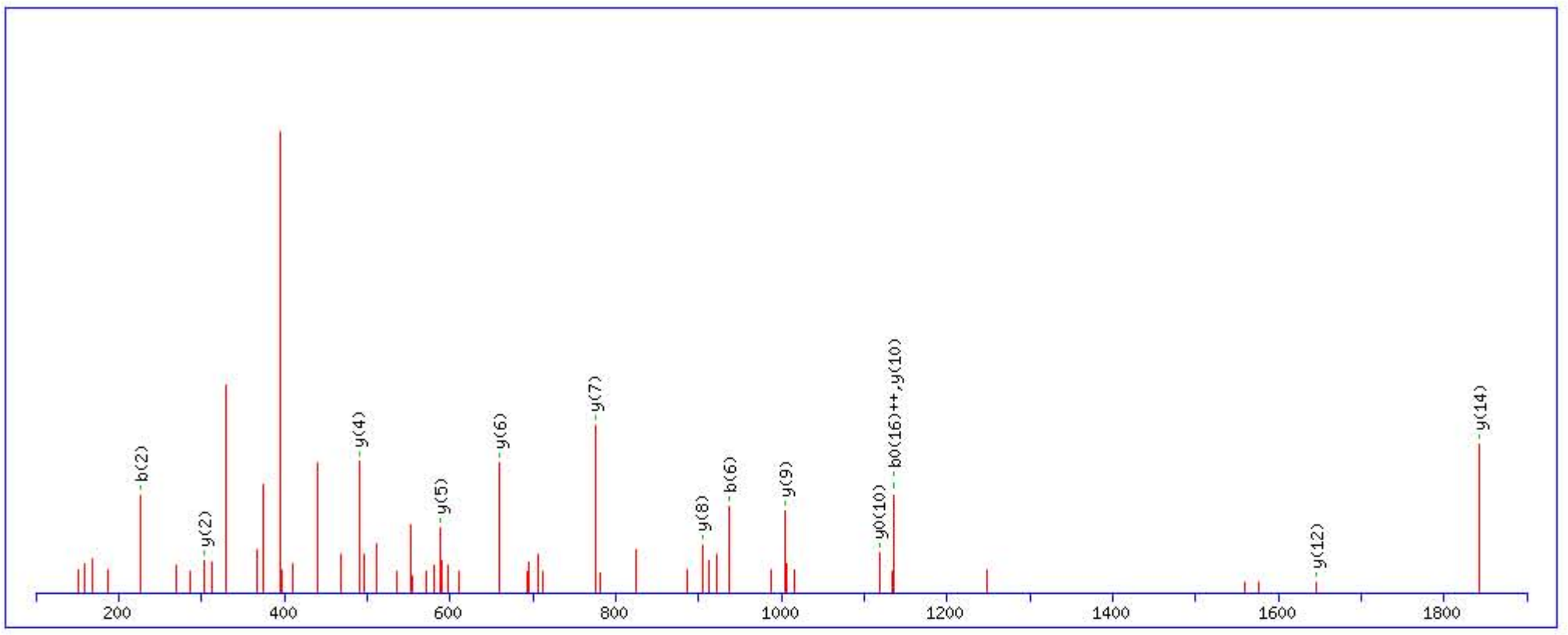
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ILLQGTPVAQMTEDAVDAER**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

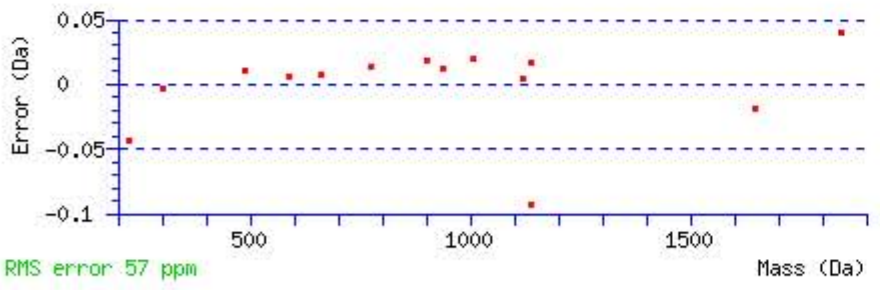
Match to Query 57266: 2778.452456 from(695.620390,4+) rtinseconds(2788) index(39070)
Title: Locus:1.1.1.1078.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

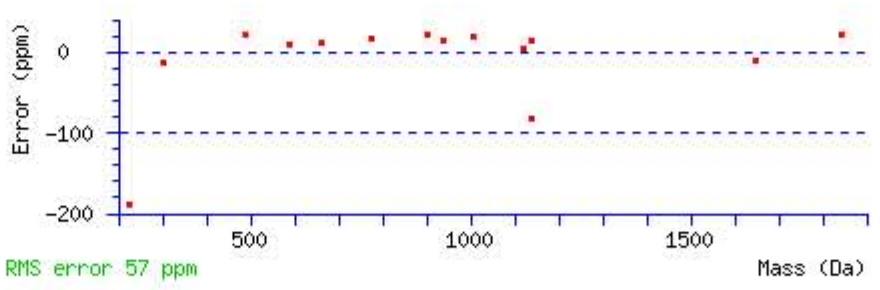
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2778.411819
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 55 **Expect:** 7.5e-005
**Matches :** 14/210 fragment ions using 24 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 20 |
| 2 | **227.175404** | 114.091340 | | | | | L | 2666.335045 | 1333.671160 | 2649.308496 | 1325.157886 | 2648.324480 | 1324.665878 | 19 |
| 3 | 340.259468 | 170.633372 | | | | | L | 2553.250981 | 1277.129128 | 2536.224432 | 1268.615854 | 2535.240416 | 1268.123846 | 18 |
| 4 | 779.484794 | 390.246035 | 762.458245 | 381.732760 | | | Q | 2440.166917 | 1220.587096 | 2423.140368 | 1212.073822 | 2422.156352 | 1211.581814 | 17 |
| 5 | 836.506258 | 418.756767 | 819.479709 | 410.243493 | | | G | 2000.941591 | 1000.974434 | 1983.915042 | 992.461159 | 1982.931026 | 991.969151 | 16 |
| 6 | **937.553937** | 469.280607 | 920.527388 | 460.767332 | 919.543372 | 460.275324 | T | 1943.920127 | 972.463702 | 1926.893578 | 963.950427 | 1925.909562 | 963.458419 | 15 |
| 7 | 1034.606701 | 517.806988 | 1017.580152 | 509.293714 | 1016.596136 | 508.801706 | P | *1842.872448* | 921.939862 | 1825.845899 | 913.426588 | 1824.861883 | 912.934580 | 14 |
| 8 | 1133.675115 | 567.341196 | 1116.648566 | 558.827921 | 1115.664550 | 558.335913 | V | 1745.819684 | 873.413480 | 1728.793135 | 864.900206 | 1727.809119 | 864.408198 | 13 |
| 9 | 1204.712229 | 602.859753 | 1187.685680 | 594.346478 | 1186.701664 | 593.854470 | A | *1646.751270* | 823.879273 | 1629.724721 | 815.365999 | 1628.740705 | 814.873991 | 12 |
| 10 | 1643.937555 | 822.472416 | 1626.911006 | 813.959141 | 1625.926990 | 813.467133 | Q | 1575.714156 | 788.360716 | 1558.687607 | 779.847442 | 1557.703591 | 779.355434 | 11 |
| 11 | 1774.978040 | 887.992658 | 1757.951491 | 879.479384 | 1756.967475 | 878.987376 | M | *1136.488830* | 568.748053 | 1119.462281 | 560.234779 | 1118.478265 | 559.742771 | 10 |
| 12 | 1876.025719 | 938.516498 | 1858.999170 | 930.003223 | 1858.015154 | 929.511215 | T | *1005.448345* | 503.227811 | 988.421796 | 494.714536 | 987.437780 | 494.222528 | 9 |
| 13 | 2005.068312 | 1003.037794 | 1988.041763 | 994.524520 | 1987.057747 | 994.032512 | E | *904.400666* | 452.703971 | 887.374117 | 444.190697 | 886.390101 | 443.698689 | 8 |
| 14 | 2120.095255 | 1060.551265 | 2103.068706 | 1052.037991 | 2102.084690 | 1051.545983 | D | *775.358073* | 388.182675 | 758.331524 | 379.669400 | 757.347508 | 379.177392 | 7 |
| 15 | 2191.132369 | 1096.069822 | 2174.105820 | 1087.556548 | 2173.121804 | 1087.064540 | A | *660.331130* | 330.669203 | 643.304581 | 322.155929 | 642.320565 | 321.663921 | 6 |
| 16 | 2290.200783 | 1145.604029 | 2273.174234 | 1137.090755 | 2272.190218 | 1136.598747 | V | *589.294016* | 295.150646 | 572.267467 | 286.637372 | 571.283451 | 286.145364 | 5 |
| 17 | 2405.227726 | 1203.117501 | 2388.201177 | 1194.604226 | 2387.217161 | 1194.112218 | D | *490.225602* | 245.616439 | 473.199053 | 237.103165 | 472.215037 | 236.611157 | 4 |
| 18 | 2476.264840 | 1238.636058 | 2459.238291 | 1230.122783 | 2458.254275 | 1229.630775 | A | 375.198659 | 188.102968 | 358.172110 | 179.589693 | 357.188094 | 179.097685 | 3 |
| 19 | 2605.307433 | 1303.157354 | 2588.280884 | 1294.644080 | 2587.296868 | 1294.152072 | E | *304.161545* | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 20 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 55.4 | 2778.411819 | 0.040637 | ILLQGTPVAQMTEDAVDAER |

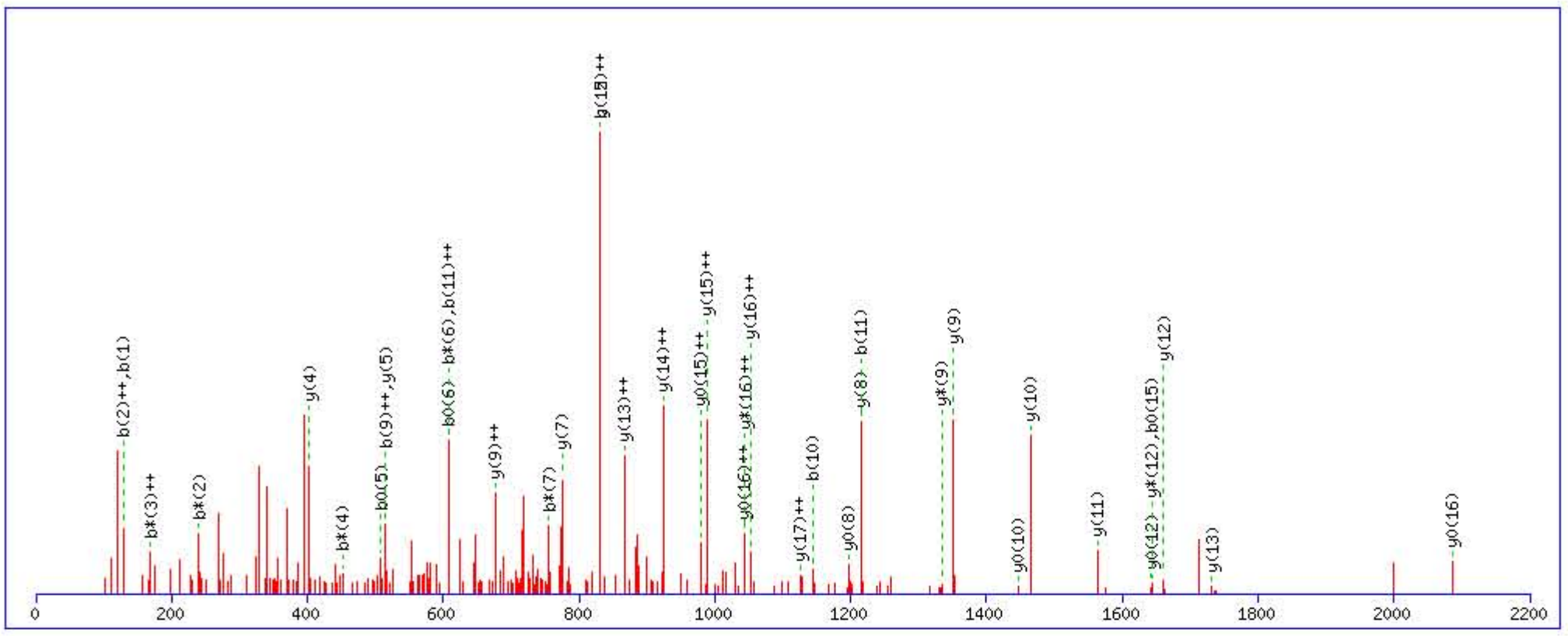
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QKPDGVFQEDAPVIHQEMIGGLR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

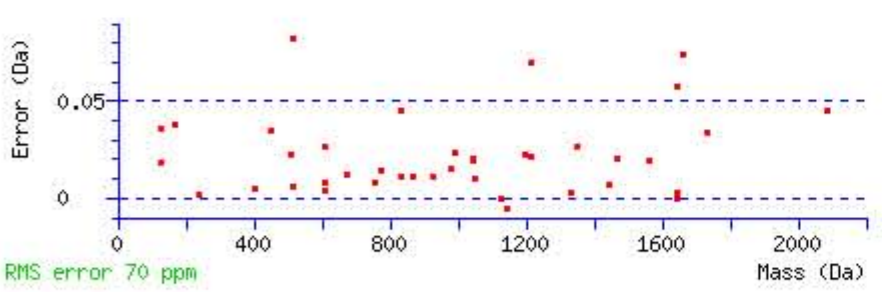
Match to Query 58871: 2874.488216 from(719.629330,4+) rtinseconds(2238) index(35689)
Title: Locus:1.1.1.888.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

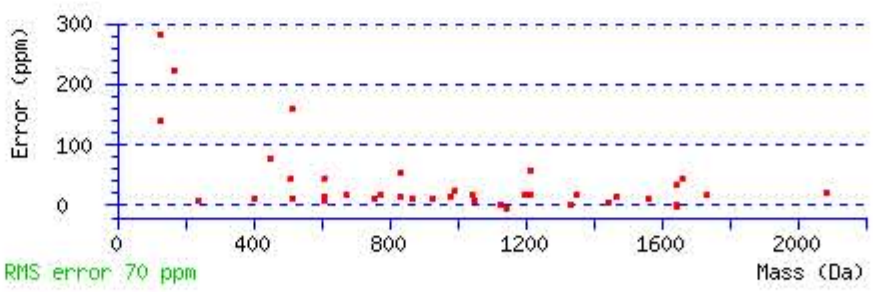
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2874.452057
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q16 : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 1.5e-005
**Matches :** 40/246 fragment ions using 52 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.065854 | 65.036565 | 112.039305 | 56.523291 | | | Q | | | | | | | 23 |
| 2 | 257.160817 | 129.084047 | 240.134268 | 120.570772 | | | K | 2747.400756 | 1374.204016 | 2730.374207 | 1365.690741 | 2729.390191 | 1365.198733 | 22 |
| 3 | 354.213581 | 177.610429 | 337.187032 | 169.097154 | | | P | 2619.305793 | 1310.156534 | 2602.279244 | 1301.643260 | 2601.295228 | 1301.151252 | 21 |
| 4 | 469.240524 | 235.123900 | 452.213975 | 226.610626 | 451.229959 | 226.118618 | D | 2522.253029 | 1261.630152 | 2505.226480 | 1253.116878 | 2504.242464 | 1252.624870 | 20 |
| 5 | 526.261988 | 263.634632 | 509.235439 | 255.121358 | 508.251423 | 254.629350 | G | 2407.226086 | 1204.116681 | 2390.199537 | 1195.603406 | 2389.215521 | 1195.111398 | 19 |
| 6 | 625.330402 | 313.168839 | 608.303853 | 304.655565 | 607.319837 | 304.163557 | V | 2350.204622 | 1175.605949 | 2333.178073 | 1167.092674 | 2332.194057 | 1166.600666 | 18 |
| 7 | 772.398816 | 386.703046 | 755.372267 | 378.189772 | 754.388251 | 377.697764 | F | 2251.136208 | 1126.071742 | 2234.109659 | 1117.558467 | 2233.125643 | 1117.066459 | 17 |
| 8 | 900.457394 | 450.732335 | 883.430845 | 442.219061 | 882.446829 | 441.727053 | Q | 2104.067794 | 1052.537535 | 2087.041245 | 1044.024260 | 2086.057229 | 1043.532252 | 16 |
| 9 | 1029.499987 | 515.253631 | 1012.473438 | 506.740357 | 1011.489422 | 506.248349 | E | 1976.009216 | 988.508246 | 1958.982667 | 979.994972 | 1957.998651 | 979.502964 | 15 |
| 10 | 1144.526930 | 572.767103 | 1127.500381 | 564.253829 | 1126.516365 | 563.761821 | D | 1846.966623 | 923.986950 | 1829.940074 | 915.473675 | 1828.956058 | 914.981667 | 14 |
| 11 | 1215.564044 | 608.285660 | 1198.537495 | 599.772386 | 1197.553479 | 599.280377 | A | *1731.939680* | 866.473478 | 1714.913131 | 857.960204 | 1713.929115 | 857.468196 | 13 |
| 12 | 1312.616808 | 656.812042 | 1295.590259 | 648.298768 | 1294.606243 | 647.806760 | P | *1660.902566* | 830.954921 | 1643.876017 | 822.441647 | 1642.892001 | 821.949639 | 12 |
| 13 | 1411.685222 | 706.346249 | 1394.658673 | 697.832975 | 1393.674657 | 697.340967 | V | *1563.849802* | 782.428539 | 1546.823253 | 773.915265 | 1545.839237 | 773.423257 | 11 |
| 14 | 1524.769286 | 762.888281 | 1507.742737 | 754.375007 | 1506.758721 | 753.882998 | I | *1464.781388* | 732.894332 | 1447.754839 | 724.381058 | 1446.770823 | 723.889050 | 10 |
| 15 | 1661.828198 | 831.417737 | 1644.801649 | 822.904463 | 1643.817633 | 822.412454 | H | *1351.697324* | 676.352300 | 1334.670775 | 667.839026 | 1333.686759 | 667.347018 | 9 |
| 16 | 2101.053524 | 1051.030400 | 2084.026975 | 1042.517125 | 2083.042959 | 1042.025117 | Q | *1214.638412* | 607.822844 | 1197.611863 | 599.309570 | 1196.627847 | 598.817562 | 8 |
| 17 | 2230.096117 | 1115.551696 | 2213.069568 | 1107.038422 | 2212.085552 | 1106.546414 | E | *775.413086* | 388.210181 | 758.386537 | 379.696907 | 757.402521 | 379.204899 | 7 |
| 18 | 2361.136602 | 1181.071939 | 2344.110053 | 1172.558664 | 2343.126037 | 1172.066656 | M | 646.370493 | 323.688885 | 629.343944 | 315.175610 | | | 6 |
| 19 | 2474.220666 | 1237.613971 | 2457.194117 | 1229.100696 | 2456.210101 | 1228.608689 | I | *515.330008* | 258.168642 | 498.303459 | 249.655368 | | | 5 |
| 20 | 2531.242130 | 1266.124703 | 2514.215581 | 1257.611428 | 2513.231565 | 1257.119420 | G | *402.245944* | 201.626610 | 385.219395 | 193.113335 | | | 4 |
| 21 | 2588.263594 | 1294.635435 | 2571.237045 | 1286.122160 | 2570.253029 | 1285.630152 | G | 345.224480 | 173.115878 | 328.197931 | 164.602603 | | | 3 |
| 22 | 2701.347658 | 1351.177467 | 2684.321109 | 1342.664192 | 2683.337093 | 1342.172185 | L | 288.203016 | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 23 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 53.4 | 2874.452057 | 0.036159 | QKPDGVFQEDAPVIHQEMIGGLR |
| 4.3 | 2874.452057 | 0.036159 | QKPDGVFQEDAPVIHQEMIGGLR |
| 2.0 | 2874.452026 | 0.036190 | QPIQYCVVINKEHNFKSLCAVEAK |

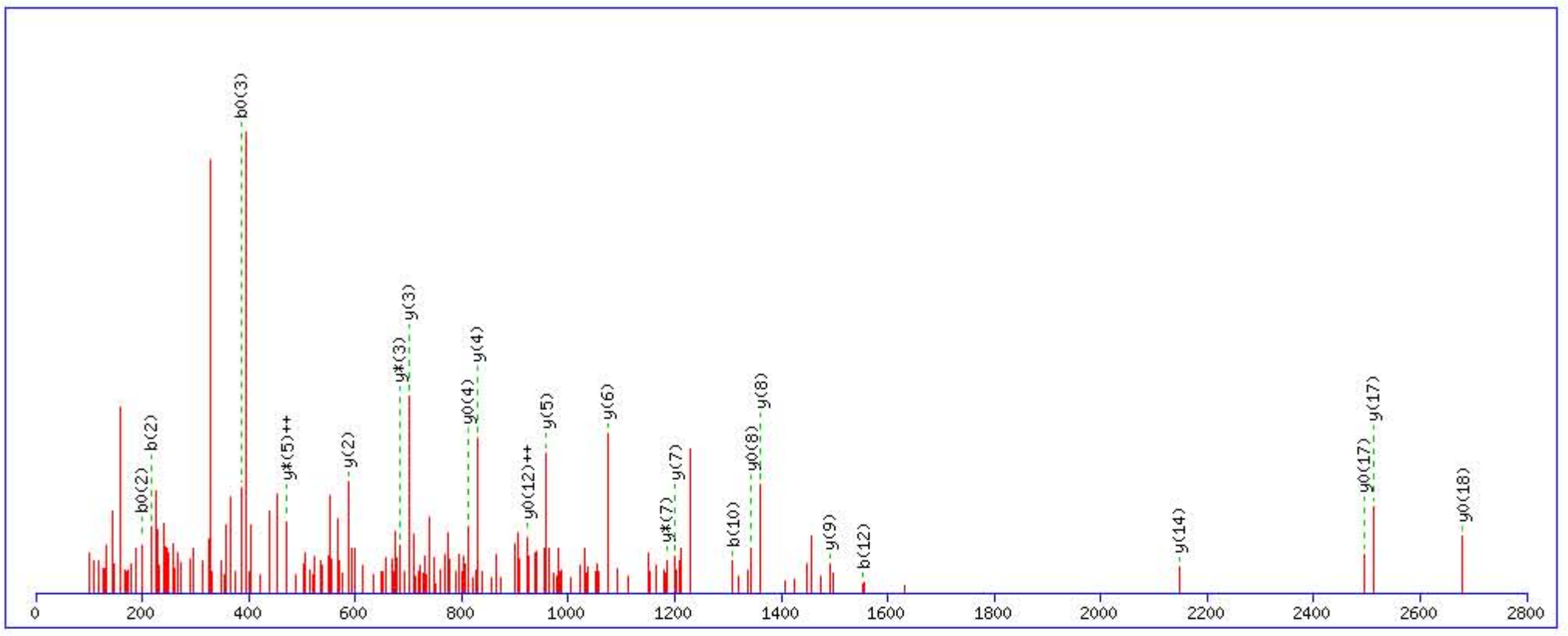
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DTWVEHWPEEDECQDEENQK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

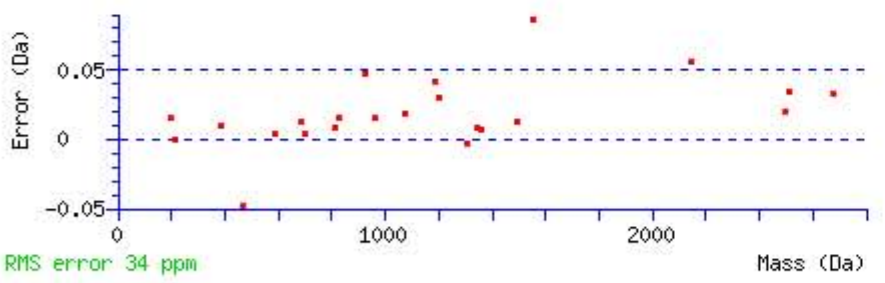
Match to Query 59217: 2913.221936 from(729.312760,4+) rtinseconds(2107) index(51037)
Title: Locus:1.1.1.1971.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

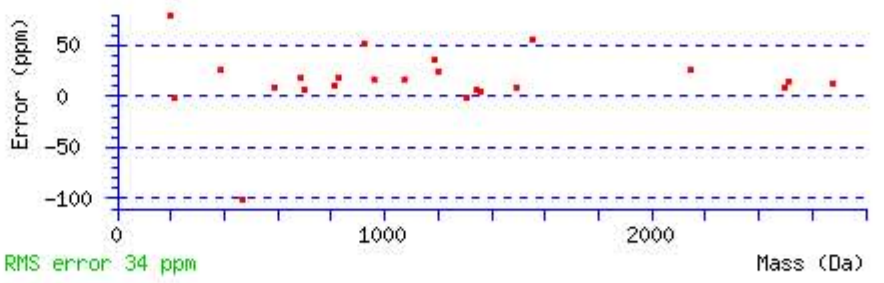
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2913.185776
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q19 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.00025
**Matches :** 23/196 fragment ions using 49 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 20 |
| 2 | **217.081898** | 109.044587 | | | 199.071333 | 100.039304 | T | 2799.166123 | 1400.086699 | 2782.139574 | 1391.573425 | 2781.155558 | 1391.081417 | 19 |
| 3 | 403.161211 | 202.084244 | | | 385.150646 | 193.078961 | W | 2698.118444 | 1349.562860 | 2681.091895 | 1341.049585 | 2680.107879 | 1340.557577 | 18 |
| 4 | 502.229625 | 251.618451 | | | 484.219060 | 242.613168 | V | ***2512.039131*** | 1256.523203 | 2495.012582 | 1248.009929 | 2494.028566 | 1247.517921 | 17 |
| 5 | 631.272218 | 316.139747 | | | 613.261653 | 307.134465 | E | 2412.970717 | 1206.988996 | 2395.944168 | 1198.475722 | 2394.960152 | 1197.983714 | 16 |
| 6 | 768.331130 | 384.669203 | | | 750.320565 | 375.663921 | H | 2283.928124 | 1142.467700 | 2266.901575 | 1133.954425 | 2265.917559 | 1133.462417 | 15 |
| 7 | 954.410443 | 477.708860 | | | 936.399878 | 468.703577 | W | ***2146.869212*** | 1073.938244 | 2129.842663 | 1065.424969 | 2128.858647 | 1064.932961 | 14 |
| 8 | 1051.463207 | 526.235242 | | | 1033.452642 | 517.229959 | P | 1960.789899 | 980.898588 | 1943.763350 | 972.385313 | 1942.779334 | 971.893305 | 13 |
| 9 | 1180.505800 | 590.756538 | | | 1162.495235 | 581.751256 | E | 1863.737135 | 932.372206 | 1846.710586 | 923.858931 | 1845.726570 | 923.366923 | 12 |
| 10 | **1309.548393** | 655.277835 | | | 1291.537828 | 646.272552 | E | 1734.694542 | 867.850909 | 1717.667993 | 859.337635 | 1716.683977 | 858.845627 | 11 |
| 11 | 1424.575336 | 712.791306 | | | 1406.564771 | 703.786024 | D | 1605.651949 | 803.329613 | 1588.625400 | 794.816338 | 1587.641384 | 794.324330 | 10 |
| 12 | **1553.617929** | 777.312603 | | | 1535.607364 | 768.307320 | E | ***1490.625006*** | 745.816141 | 1473.598457 | 737.302867 | 1472.614441 | 736.810859 | 9 |
| 13 | 1713.648578 | 857.327927 | | | 1695.638013 | 848.322645 | C | ***1361.582413*** | 681.294845 | 1344.555864 | 672.781570 | 1343.571848 | 672.289562 | 8 |
| 14 | 1841.707156 | 921.357216 | 1824.680607 | 912.843942 | 1823.696591 | 912.351934 | Q | ***1201.551764*** | 601.279520 | 1184.525215 | 592.766246 | 1183.541199 | 592.274238 | 7 |
| 15 | 1956.734099 | 978.870688 | 1939.707550 | 970.357413 | 1938.723534 | 969.865405 | D | ***1073.493186*** | 537.250231 | 1056.466637 | 528.736957 | 1055.482621 | 528.244949 | 6 |
| 16 | 2085.776692 | 1043.391984 | 2068.750143 | 1034.878709 | 2067.766127 | 1034.386701 | E | ***958.466243*** | 479.736760 | 941.439694 | 471.223485 | 940.455678 | 470.731477 | 5 |
| 17 | 2214.819285 | 1107.913280 | 2197.792736 | 1099.400006 | 2196.808720 | 1098.907998 | E | ***829.423650*** | 415.215463 | 812.397101 | 406.702189 | 811.413085 | 406.210181 | 4 |
| 18 | 2328.862212 | 1164.934744 | 2311.835663 | 1156.421469 | 2310.851647 | 1155.929461 | N | ***700.381057*** | 350.694167 | 683.354508 | 342.180892 | | | 3 |
| 19 | 2768.087538 | 1384.547407 | 2751.060989 | 1376.034132 | 2750.076973 | 1375.542125 | Q | ***586.338130*** | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 20 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 39.4 | 2913.185776 | 0.036160 | DTWVEHWPEEDECQDEENQK |
| 10.1 | 2913.185776 | 0.036160 | DTWVEHWPEEDECQDEENQK |

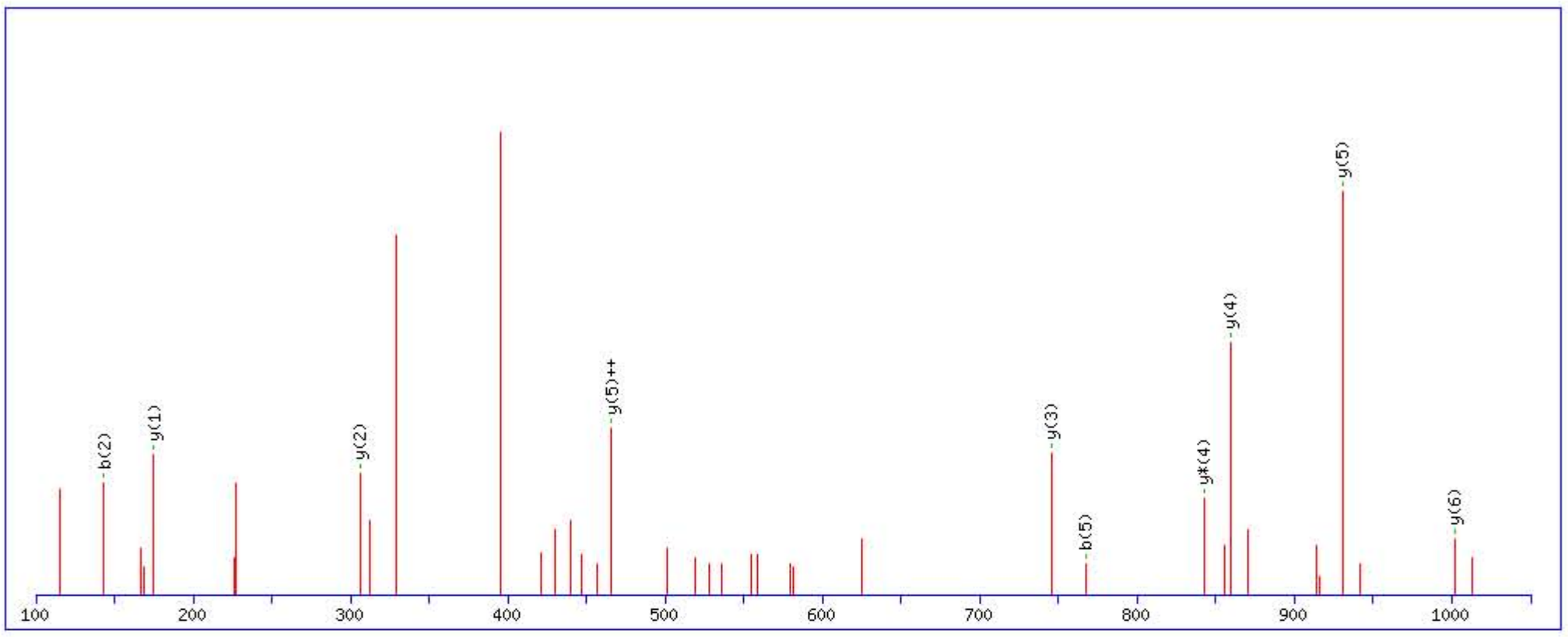
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AAANQMR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

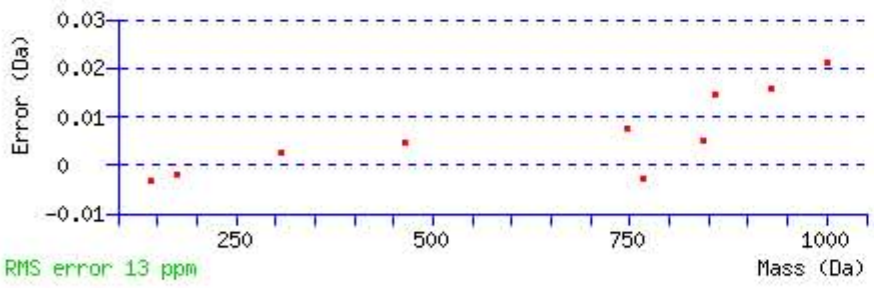
Match to Query 15686: 1071.535968 from(536.775260,2+) rtinseconds(1375) index(30281)
Title: Locus:1.1.1.587.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

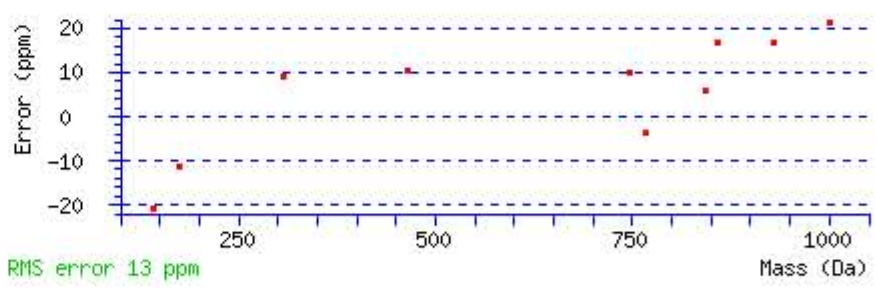
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1071.531723
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0026
**Matches :** 10/42 fragment ions using 17 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | A | | | | | 7 |
| 2 | **143.081504** | 72.044390 | | | A | ***1001.501918*** | 501.254597 | 984.475369 | 492.741323 | 6 |
| 3 | 214.118618 | 107.562947 | | | A | ***930.464804*** | 465.736040 | 913.438255 | 457.222766 | 5 |
| 4 | 328.161545 | 164.584410 | 311.134996 | 156.071136 | N | ***859.427690*** | 430.217483 | 842.401141 | 421.704209 | 4 |
| 5 | **767.386871** | 384.197074 | 750.360322 | 375.683799 | Q | ***745.384763*** | 373.196020 | 728.358214 | 364.682745 | 3 |
| 6 | 898.427356 | 449.717316 | 881.400807 | 441.204042 | M | ***306.159437*** | 153.583357 | 289.132888 | 145.070082 | 2 |
| 7 | | | | | R | ***175.118952*** | 88.063114 | 158.092403 | 79.549840 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.7 | 1071.531723 | 0.004245 | AAANQMR |
| 19.7 | 1071.530853 | 0.005115 | AAEESGAKGPR |

**Mascot:** http://www.matrixscience.com/

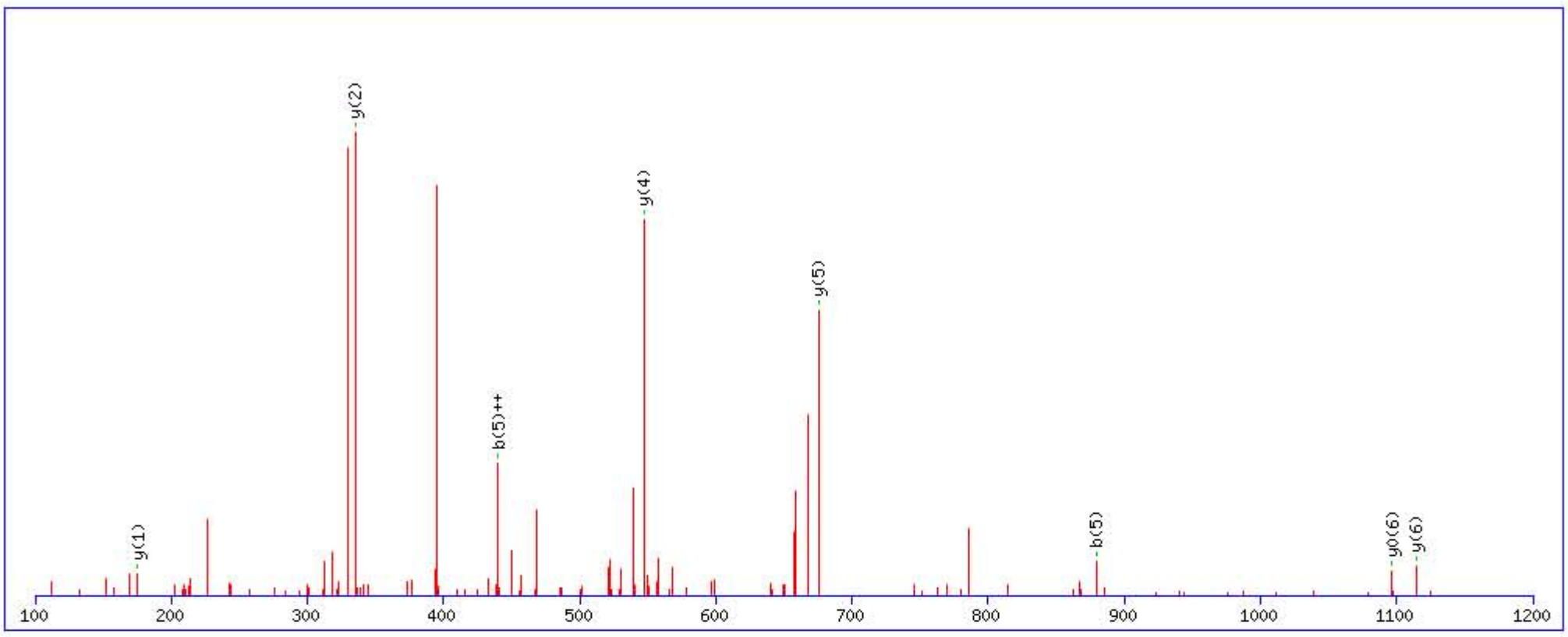
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VQQPDCR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

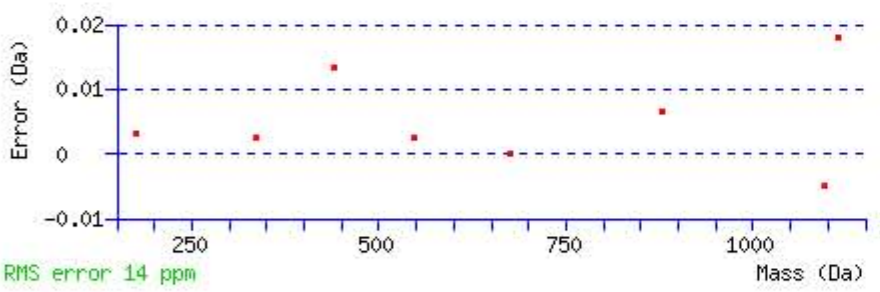
Match to Query 20808: 1212.580108 from(607.297330,2+) rtinseconds(1289) index(45674)
Title: Locus:1.1.1.1686.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

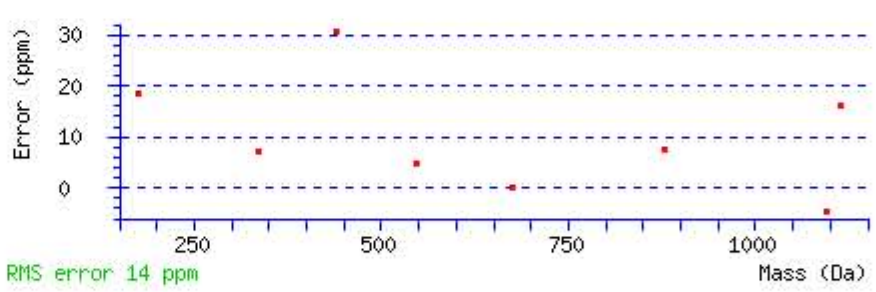
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1212.574356
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 36 **Expect:** 0.003
**Matches :** 8/58 fragment ions using 11 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 7 |
| 2 | 539.301016 | 270.154146 | 522.274467 | 261.640872 | | | Q | *1114.513212* | 557.760244 | 1097.486663 | 549.246970 | 1096.502647 | 548.754962 | 6 |
| 3 | 667.359594 | 334.183435 | 650.333045 | 325.670161 | | | Q | *675.287886* | 338.147581 | 658.261337 | 329.634307 | 657.277321 | 329.142299 | 5 |
| 4 | 764.412358 | 382.709817 | 747.385809 | 374.196543 | | | P | *547.229308* | 274.118292 | 530.202759 | 265.605018 | 529.218743 | 265.113010 | 4 |
| 5 | **879.439301** | **440.223289** | 862.412752 | 431.710014 | 861.428736 | 431.218006 | D | 450.176544 | 225.591910 | 433.149995 | 217.078635 | 432.165979 | 216.586627 | 3 |
| 6 | 1039.469950 | 520.238613 | 1022.443401 | 511.725339 | 1021.459385 | 511.233331 | C | *335.149601* | 168.078438 | 318.123052 | 159.565164 | | | 2 |
| 7 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 36.4 | 1212.574356 | 0.005752 | VQQPDCR |
| 22.6 | 1212.574356 | 0.005752 | VQQPDCR |
| 11.5 | 1212.596115 | -0.016007 | YFVEAGAMAVR |
| 4.5 | 1212.592102 | -0.011994 | VQEDQQR |
| 1.1 | 1212.592758 | -0.012650 | IYYVDHFTR |
| 0.8 | 1212.562241 | 0.017867 | TTAQYDQASTK |
| 0.6 | 1212.582199 | -0.002091 | GRMPPSEFHR |

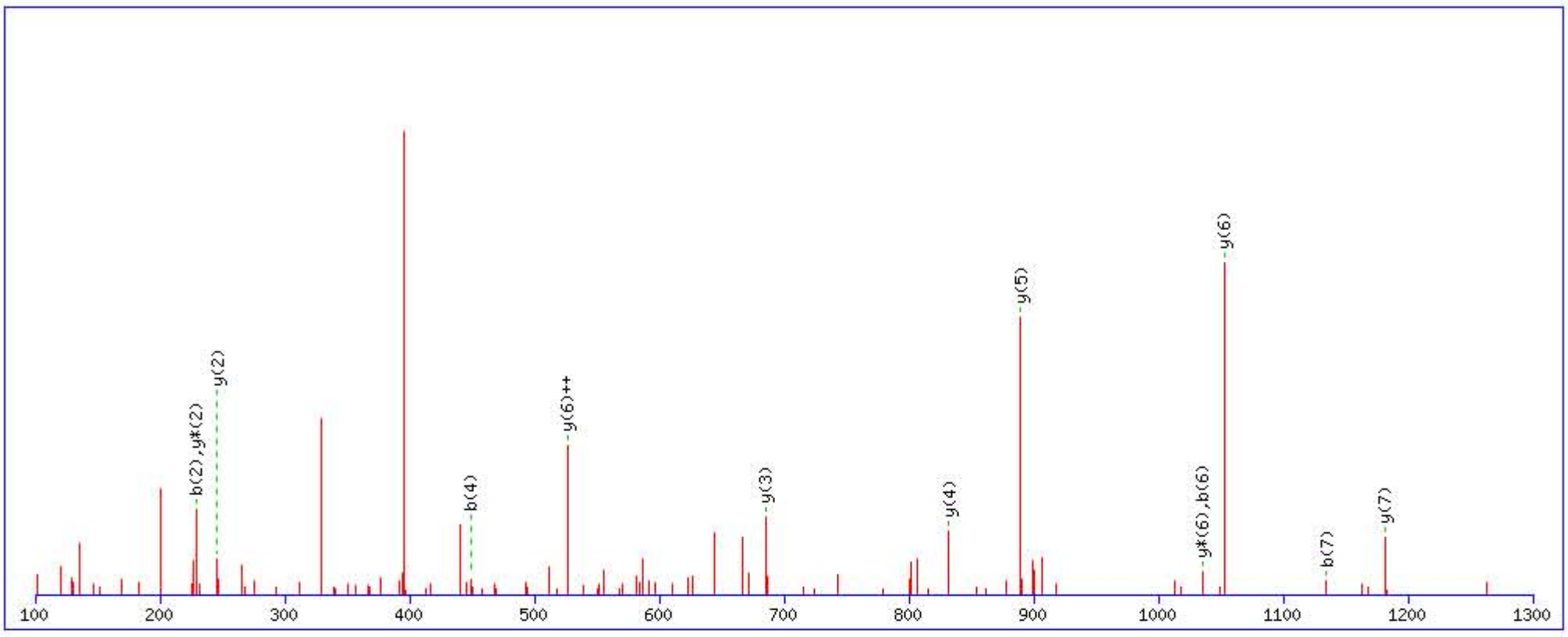
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VEYGFQVK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

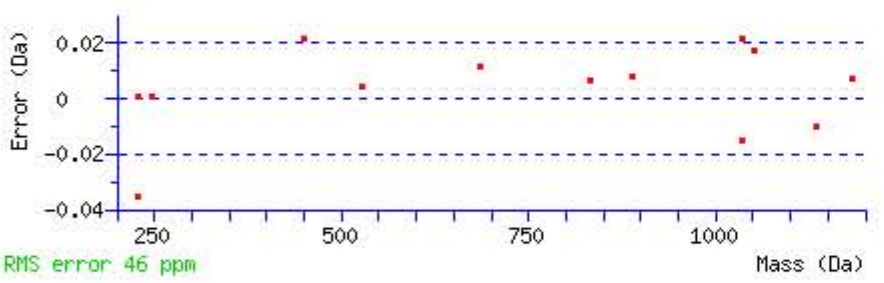
Match to Query 22737: 1279.673408 from(640.843980,2+) rtinseconds(1984) index(34172)
Title: Locus:1.1.1.799.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

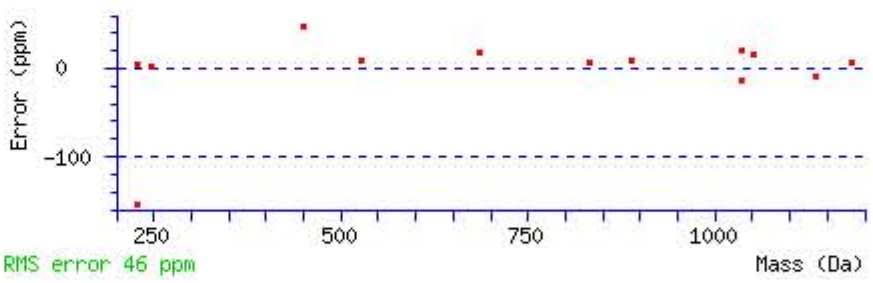
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1279.663483
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.016
**Matches :** 13/60 fragment ions using 23 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 8 |
| 2 | **229.118283** | 115.062780 | | | 211.107718 | 106.057497 | E | ***1181.602344*** | 591.304810 | 1164.575795 | 582.791536 | 1163.591779 | 582.299528 | 7 |
| 3 | 392.181612 | 196.594444 | | | 374.171047 | 187.589162 | Y | ***1052.559751*** | 526.783514 | 1035.533202 | 518.270239 | | | 6 |
| 4 | **449.203076** | 225.105176 | | | 431.192511 | 216.099894 | G | ***889.496422*** | 445.251849 | 872.469873 | 436.738575 | | | 5 |
| 5 | 596.271490 | 298.639383 | | | 578.260925 | 289.634101 | F | ***832.474958*** | 416.741117 | 815.448409 | 408.227843 | | | 4 |
| 6 | **1035.496816** | 518.252046 | 1018.470267 | 509.738772 | 1017.486251 | 509.246764 | Q | ***685.406544*** | 343.206910 | 668.379995 | 334.693636 | | | 3 |
| 7 | **1134.565230** | 567.786253 | 1117.538681 | 559.272979 | 1116.554665 | 558.780971 | V | ***246.181218*** | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 8 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 30.6 | 1279.663483 | 0.009925 | VEYGFQVK |
| 12.3 | 1279.663483 | 0.009925 | QFVGYLDK |
| 7.1 | 1279.659470 | 0.013938 | VCSFGKQVVEK |
| 3.3 | 1279.684601 | -0.011193 | TKPLMTEFSVK |
| 3.1 | 1279.684601 | -0.011193 | MSASAVFILDVK |
| 3.0 | 1279.681229 | -0.007821 | EVTVKEWYVK |
| 0.9 | 1279.670670 | 0.002738 | VEHKSNQK |
| 0.6 | 1279.677200 | -0.003792 | EYVGKTSLVER |

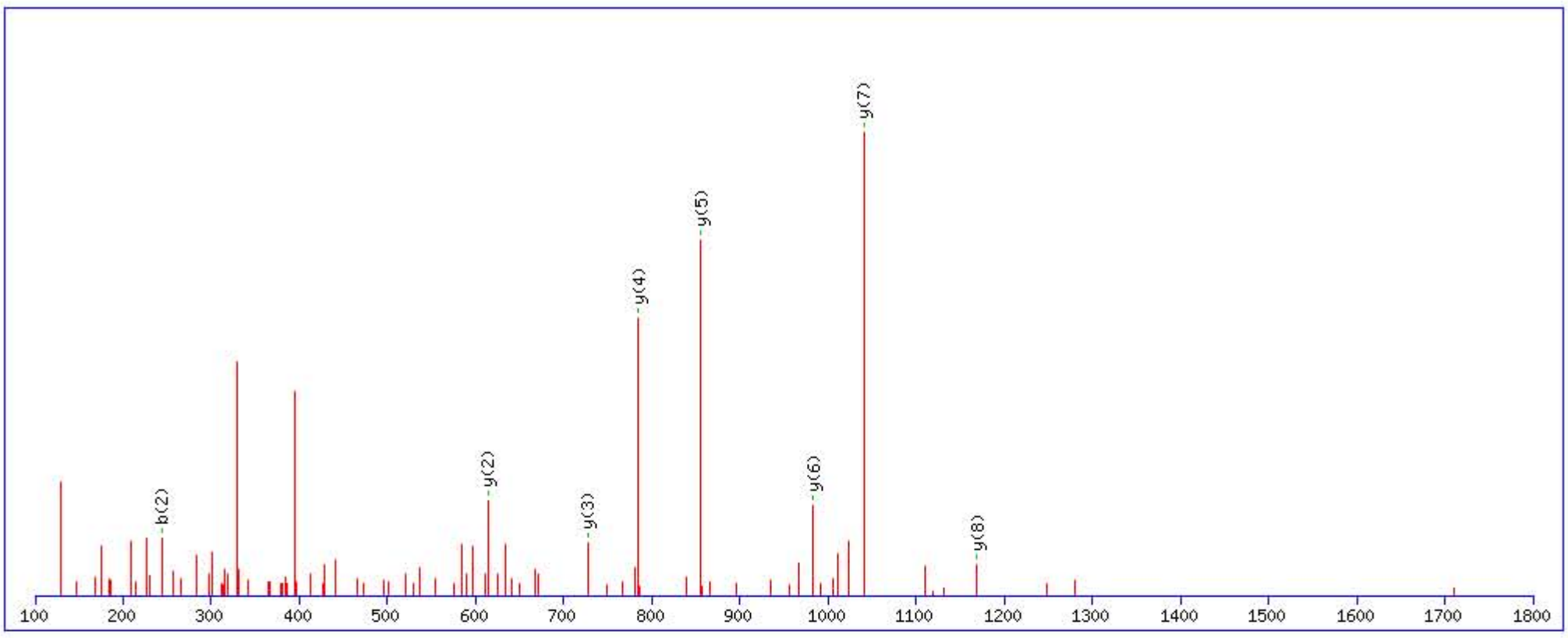
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DKGQAGLQR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

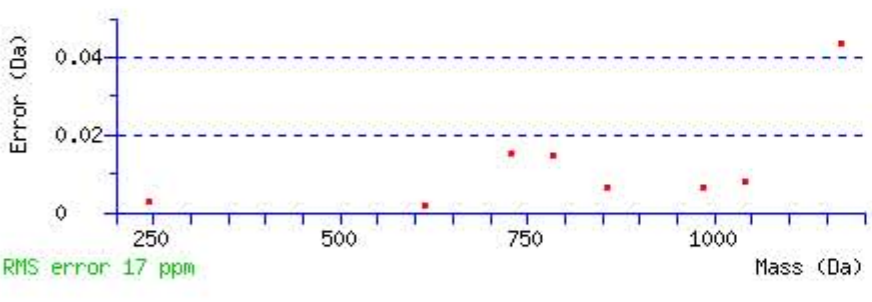
Match to Query 22931: 1282.691548 from(642.353050,2+) rtinseconds(1340) index(46002)
Title: Locus:1.1.1.1704.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

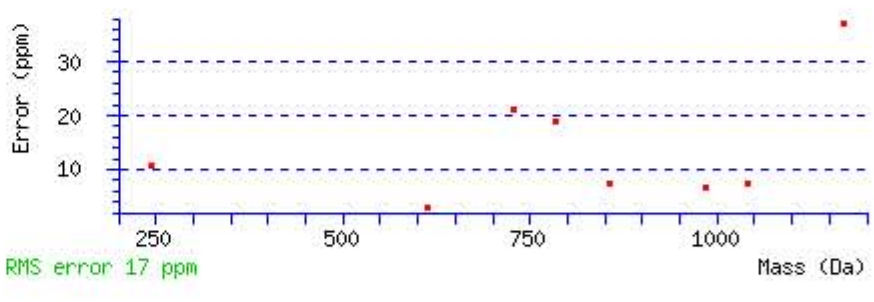
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1282.681580
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 55 **Expect:** 6.8e-005
**Matches :** 8/78 fragment ions using 12 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | 9 |
| 2 | **244.129182** | 122.568229 | 227.102633 | 114.054955 | 226.118617 | 113.562947 | K | *1168.661925* | 584.834600 | 1151.635376 | 576.321326 | 8 |
| 3 | 301.150646 | 151.078961 | 284.124097 | 142.565687 | 283.140081 | 142.073679 | G | *1040.566962* | 520.787119 | 1023.540413 | 512.273844 | 7 |
| 4 | 429.209224 | 215.108250 | 412.182675 | 206.594976 | 411.198659 | 206.102968 | Q | *983.545498* | 492.276387 | 966.518949 | 483.763112 | 6 |
| 5 | 500.246338 | 250.626807 | 483.219789 | 242.113532 | 482.235773 | 241.621524 | A | *855.486920* | 428.247098 | 838.460371 | 419.733823 | 5 |
| 6 | 557.267802 | 279.137539 | 540.241253 | 270.624265 | 539.257237 | 270.132257 | G | *784.449806* | 392.728541 | 767.423257 | 384.215266 | 4 |
| 7 | 670.351866 | 335.679571 | 653.325317 | 327.166297 | 652.341301 | 326.674289 | L | *727.428342* | 364.217809 | 710.401793 | 355.704534 | 3 |
| 8 | 1109.577192 | 555.292234 | 1092.550643 | 546.778960 | 1091.566627 | 546.286951 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162502 | 2 |
| 9 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 55.1 | 1282.681580 | 0.009968 | DKGQAGLQR |
| 15.1 | 1282.674194 | 0.017354 | QGEGQSRLVPGR |
| 12.0 | 1282.706711 | -0.015163 | KDIAELQR |
| 7.6 | 1282.681580 | 0.009968 | DKGQAGLQR |
| 7.4 | 1282.706711 | -0.015163 | DKALQELR |
| 6.6 | 1282.706726 | -0.015178 | ELGISVAQR |
| 4.7 | 1282.674164 | 0.017384 | NEGGKLGNPKNR |
| 3.7 | 1282.688095 | 0.003453 | KPTKPESQSPGK |
| 3.3 | 1282.706711 | -0.015163 | DKLQAIER |
| 2.9 | 1282.676834 | 0.014714 | KALEDEKPEPK |

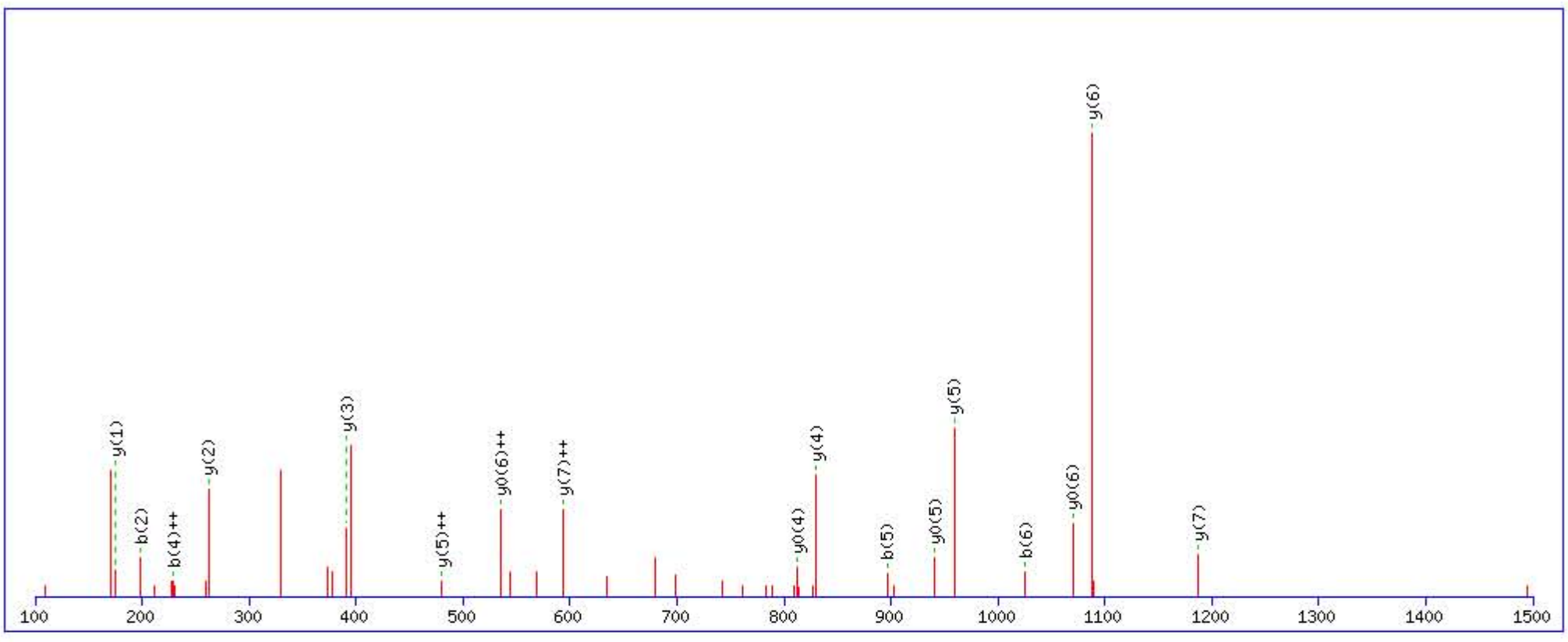
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VVEEQESR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

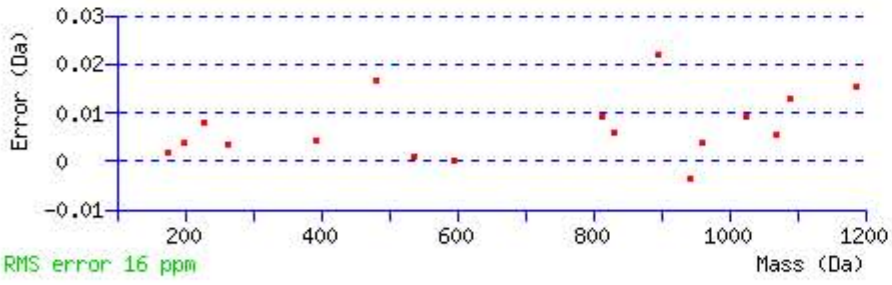
Match to Query 23024: 1285.640788 from(643.827670,2+) rtinseconds(1376) index(30286)
Title: Locus:1.1.1.587.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

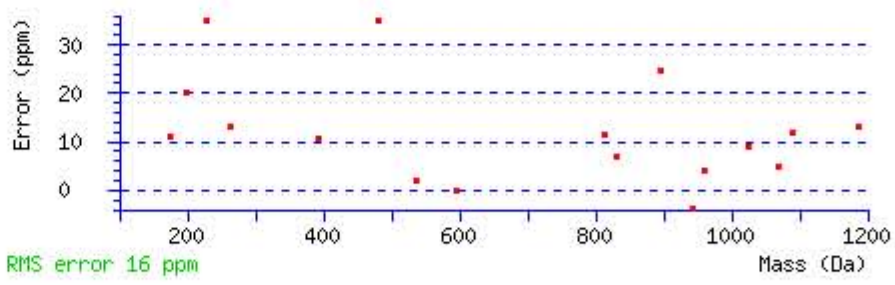
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1285.633621
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 47 **Expect:** 0.00042
**Matches :** 17/70 fragment ions using 28 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 8 |
| 2 | **199.144104** | 100.075690 | | | | | V | *1187.572499* | 594.289888 | 1170.545950 | 585.776613 | 1169.561934 | 585.284605 | 7 |
| 3 | 328.186697 | 164.596987 | | | 310.176132 | 155.591704 | E | *1088.504085* | 544.755681 | 1071.477536 | 536.242406 | 1070.493520 | 535.750398 | 6 |
| 4 | 457.229290 | 229.118283 | | | 439.218725 | 220.113001 | E | *959.461492* | 480.234384 | 942.434943 | 471.721110 | 941.450927 | 471.229102 | 5 |
| 5 | **896.454616** | 448.730946 | 879.428067 | 440.217672 | 878.444051 | 439.725664 | Q | *830.418899* | 415.713088 | 813.392350 | 407.199813 | 812.408334 | 406.707805 | 4 |
| 6 | **1025.497209** | 513.252243 | 1008.470660 | 504.738968 | 1007.486644 | 504.246960 | E | *391.193573* | 196.100425 | 374.167024 | 187.587150 | 373.183008 | 187.095142 | 3 |
| 7 | 1112.529237 | 556.768257 | 1095.502688 | 548.254982 | 1094.518672 | 547.762974 | S | *262.150980* | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 46.8 | 1285.633621 | 0.007167 | VVEEQESR |

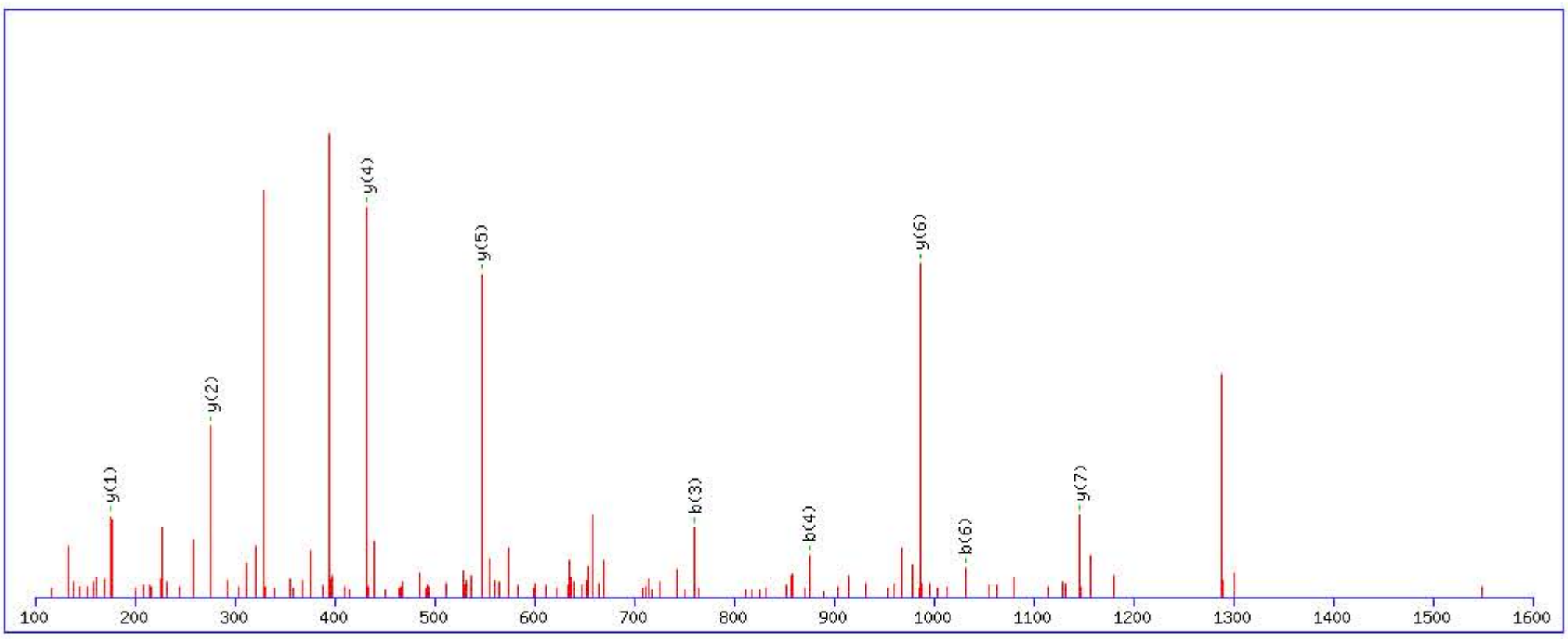
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **CCQDGVTR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

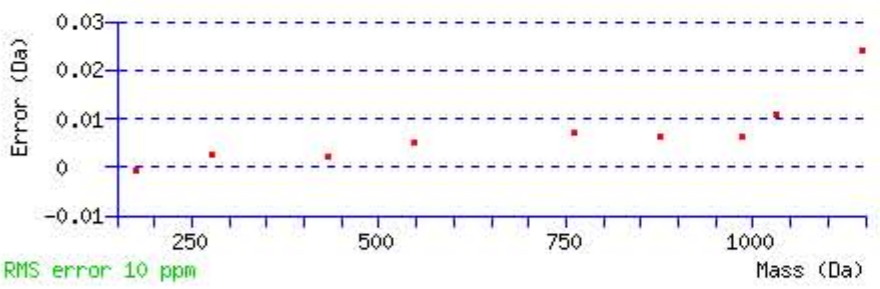
Match to Query 23417: 1305.571108 from(653.792830,2+) rtinseconds(1381) index(46230)
Title: Locus:1.1.1.1718.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

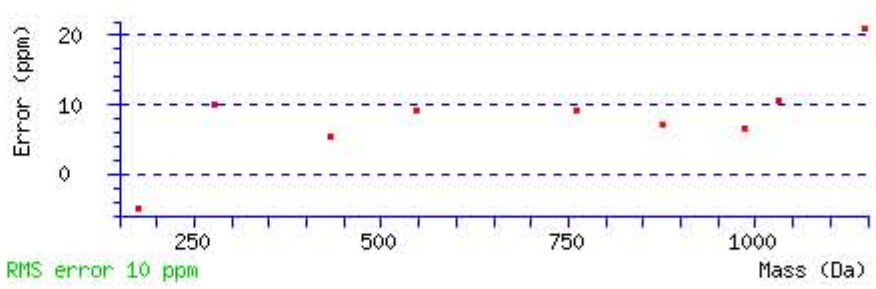
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1305.562820
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 50 **Expect:** 4.4e-005
**Matches :** 9/72 fragment ions using 12 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 161.037925 | 81.022600 | | | | | C | | | | | | | 8 |
| 2 | 321.068574 | 161.037925 | | | | | C | *1146.539427* | 573.773352 | 1129.512878 | 565.260077 | 1128.528862 | 564.768069 | 7 |
| 3 | **760.293900** | 380.650588 | 743.267351 | 372.137314 | | | Q | *986.508778* | 493.758027 | 969.482229 | 485.244753 | 968.498213 | 484.752745 | 6 |
| 4 | **875.320843** | 438.164060 | 858.294294 | 429.650785 | 857.310278 | 429.158777 | D | *547.283452* | 274.145364 | 530.256903 | 265.632090 | 529.272887 | 265.140082 | 5 |
| 5 | 932.342307 | 466.674792 | 915.315758 | 458.161517 | 914.331742 | 457.669509 | G | *432.256509* | 216.631893 | 415.229960 | 208.118618 | 414.245944 | 207.626610 | 4 |
| 6 | **1031.410721** | 516.208999 | 1014.384172 | 507.695724 | 1013.400156 | 507.203716 | V | 375.235045 | 188.121161 | 358.208496 | 179.607886 | 357.224480 | 179.115878 | 3 |
| 7 | 1132.458400 | 566.732838 | 1115.431851 | 558.219564 | 1114.447835 | 557.727556 | T | *276.166631* | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 50.4 | 1305.562820 | 0.008288 | CCQDGVTR |
| 19.7 | 1305.588409 | -0.017301 | CRSSTPADAWR |
| 9.1 | 1305.577194 | -0.006086 | CDAGWLADGSVR |
| 5.1 | 1305.562805 | 0.008303 | CCTSPSQR |
| 1.6 | 1305.556061 | 0.015047 | CSFSPWTEHR |
| 0.3 | 1305.583679 | -0.012571 | EQEPDFEEKR |
| 0.1 | 1305.588409 | -0.017301 | DGMEDFKRHR |

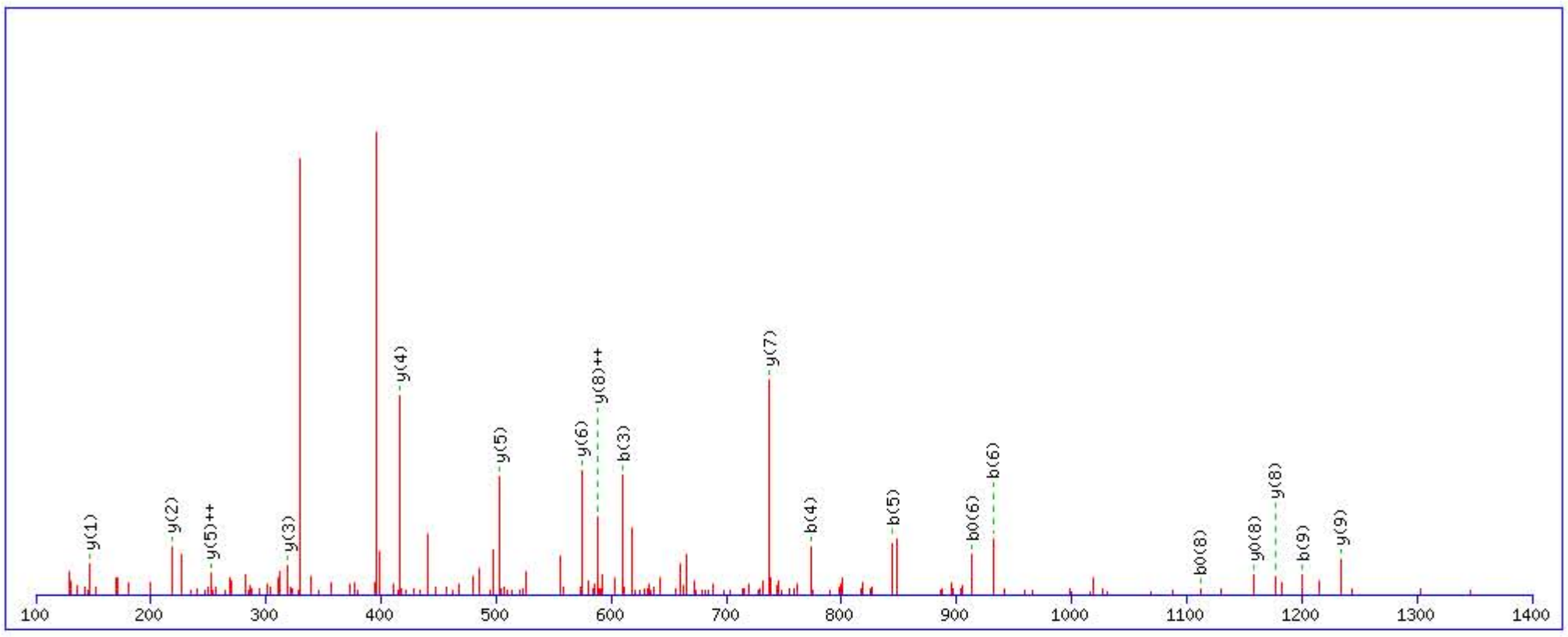
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LGQYASPTAK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

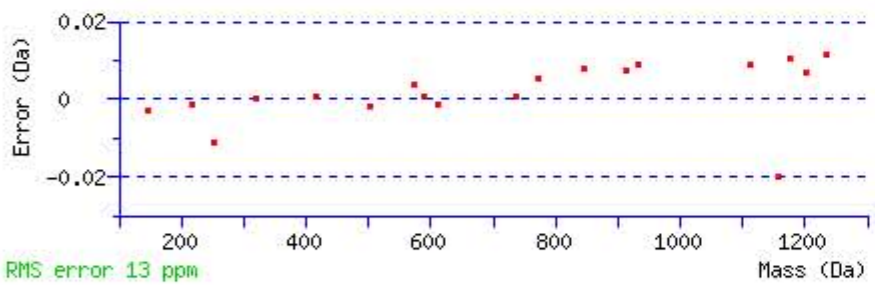
Match to Query 24292: 1345.715168 from(673.864860,2+) rtinseconds(1618) index(47773)
Title: Locus:1.1.1.1801.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

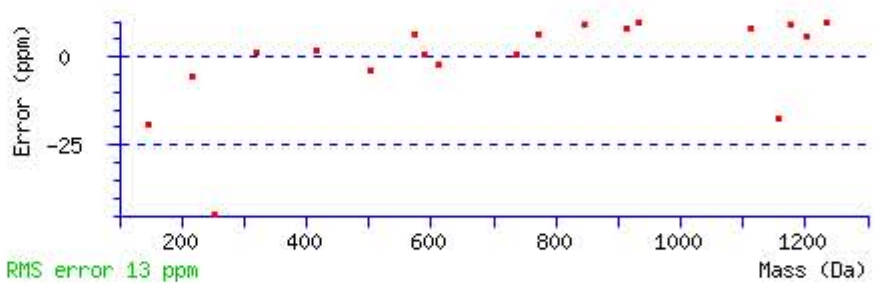
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1345.706390
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 3.9e-005
**Matches :** 19/90 fragment ions using 36 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 10 |
| 2 | 171.112804 | 86.060040 | | | | | G | *1233.629622* | 617.318449 | 1216.603073 | 608.805175 | 1215.619057 | 608.313167 | 9 |
| 3 | **610.338130** | 305.672703 | 593.311581 | 297.159429 | | | Q | *1176.608158* | 588.807717 | 1159.581609 | 580.294443 | 1158.597593 | 579.802435 | 8 |
| 4 | **773.401459** | 387.204368 | 756.374910 | 378.691093 | | | Y | *737.382832* | 369.195054 | 720.356283 | 360.681780 | 719.372267 | 360.189772 | 7 |
| 5 | **844.438573** | 422.722925 | 827.412024 | 414.209650 | | | A | *574.319503* | 287.663389 | 557.292954 | 279.150115 | 556.308938 | 278.658107 | 6 |
| 6 | **931.470601** | 466.238939 | 914.444052 | 457.725664 | 913.460036 | 457.233656 | S | *503.282389* | 252.144832 | 486.255840 | 243.631558 | 485.271824 | 243.139550 | 5 |
| 7 | 1028.523365 | 514.765321 | 1011.496816 | 506.252046 | 1010.512800 | 505.760038 | P | *416.250361* | 208.628818 | 399.223812 | 200.115544 | 398.239796 | 199.623536 | 4 |
| 8 | 1129.571044 | 565.289160 | 1112.544495 | 556.775886 | 1111.560479 | 556.283878 | T | *319.197597* | 160.102436 | 302.171048 | 151.589162 | 301.187032 | 151.097154 | 3 |
| 9 | **1200.608158** | 600.807717 | 1183.581609 | 592.294443 | 1182.597593 | 591.802435 | A | *218.149918* | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 10 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.1 | 1345.706390 | 0.008778 | LGQYASPTAK |
| 11.1 | 1345.706390 | 0.008778 | LGQYDQALK |
| 10.1 | 1345.724182 | -0.009014 | LGAVPATSGPTTFK |
| 9.0 | 1345.727509 | -0.012341 | DKLKMEVDQLK |
| 8.2 | 1345.727509 | -0.012341 | LGLMDNEIKVAK |
| 7.9 | 1345.706406 | 0.008762 | QGLYTPQTK |
| 2.5 | 1345.724152 | -0.008984 | QPLQTDIYGLAK |
| 1.7 | 1345.717636 | -0.002468 | QMPQPTFTLRK |
| 1.3 | 1345.713608 | 0.001560 | NGMLLTGGGKDRK |
| 0.7 | 1345.720993 | -0.005825 | QVGMICERLLK |

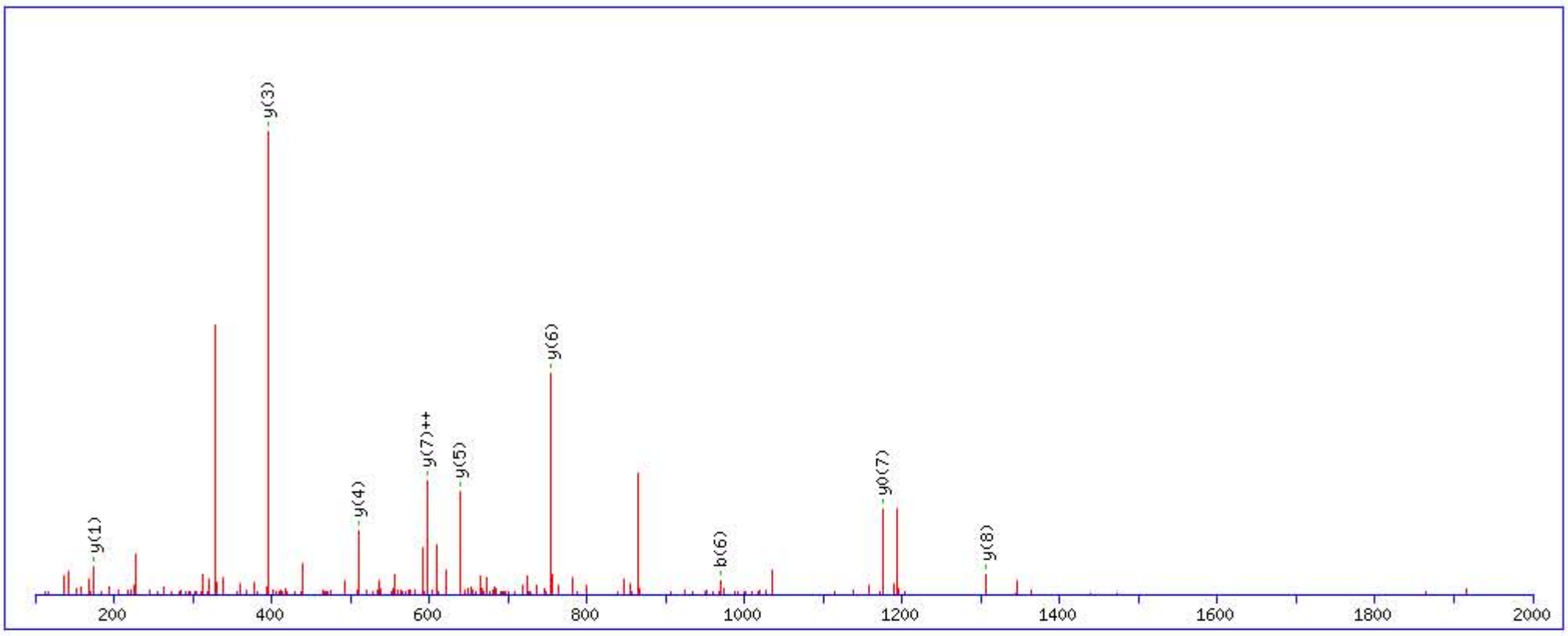
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GLQDEDGYR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

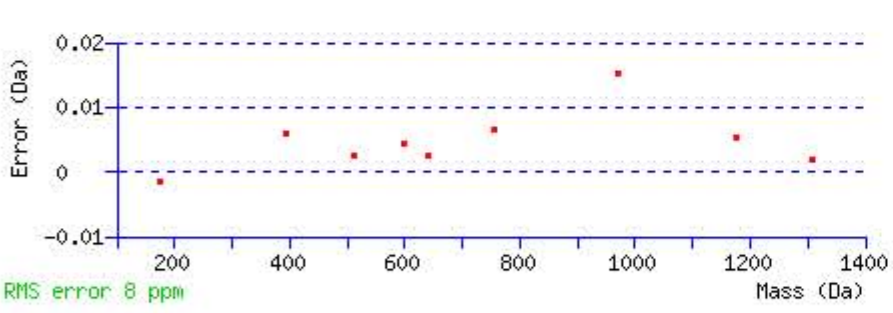
Match to Query 25943: 1362.632588 from(682.323570,2+) rtinseconds(1718) index(48398)
Title: Locus:1.1.1.1836.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

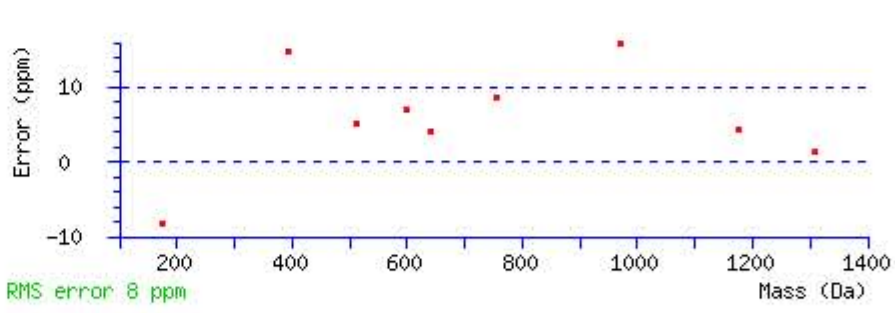
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1362.623795
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 47 **Expect:** 0.00014
**Matches :** 9/80 fragment ions using 13 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 9 |
| 2 | 171.112804 | 86.060040 | | | | | L | *1306.609614* | 653.808445 | 1289.583065 | 645.295171 | 1288.599049 | 644.803163 | 8 |
| 3 | 610.338130 | 305.672703 | 593.311581 | 297.159429 | | | Q | 1193.525550 | *597.266413* | 1176.499001 | 588.753139 | *1175.514985* | 588.261131 | 7 |
| 4 | 725.365073 | 363.186175 | 708.338524 | 354.672900 | 707.354508 | 354.180892 | D | *754.300224* | 377.653750 | 737.273675 | 369.140476 | 736.289659 | 368.648468 | 6 |
| 5 | 854.407666 | 427.707471 | 837.381117 | 419.194197 | 836.397101 | 418.702189 | E | *639.273281* | 320.140279 | 622.246732 | 311.627004 | 621.262716 | 311.134996 | 5 |
| 6 | **969.434609** | 485.220943 | 952.408060 | 476.707668 | 951.424044 | 476.215660 | D | *510.230688* | 255.618982 | 493.204139 | 247.105707 | 492.220123 | 246.613700 | 4 |
| 7 | 1026.456073 | 513.731675 | 1009.429524 | 505.218400 | 1008.445508 | 504.726392 | G | *395.203745* | 198.105511 | 378.177196 | 189.592236 | | | 3 |
| 8 | 1189.519402 | 595.263339 | 1172.492853 | 586.750065 | 1171.508837 | 586.258057 | Y | 338.182281 | 169.594778 | 321.155732 | 161.081504 | | | 2 |
| 9 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 46.8 | 1362.623795 | 0.008793 | GLQDEDGYR |
| 5.3 | 1362.652756 | -0.020168 | GLAADERAEFER |
| 3.0 | 1362.642883 | -0.010295 | GDRVYSPYNHR |
| 2.2 | 1362.623795 | 0.008793 | TGFLEIDEHMR |
| 0.6 | 1362.623795 | 0.008793 | GPAFPGMGSEELR |

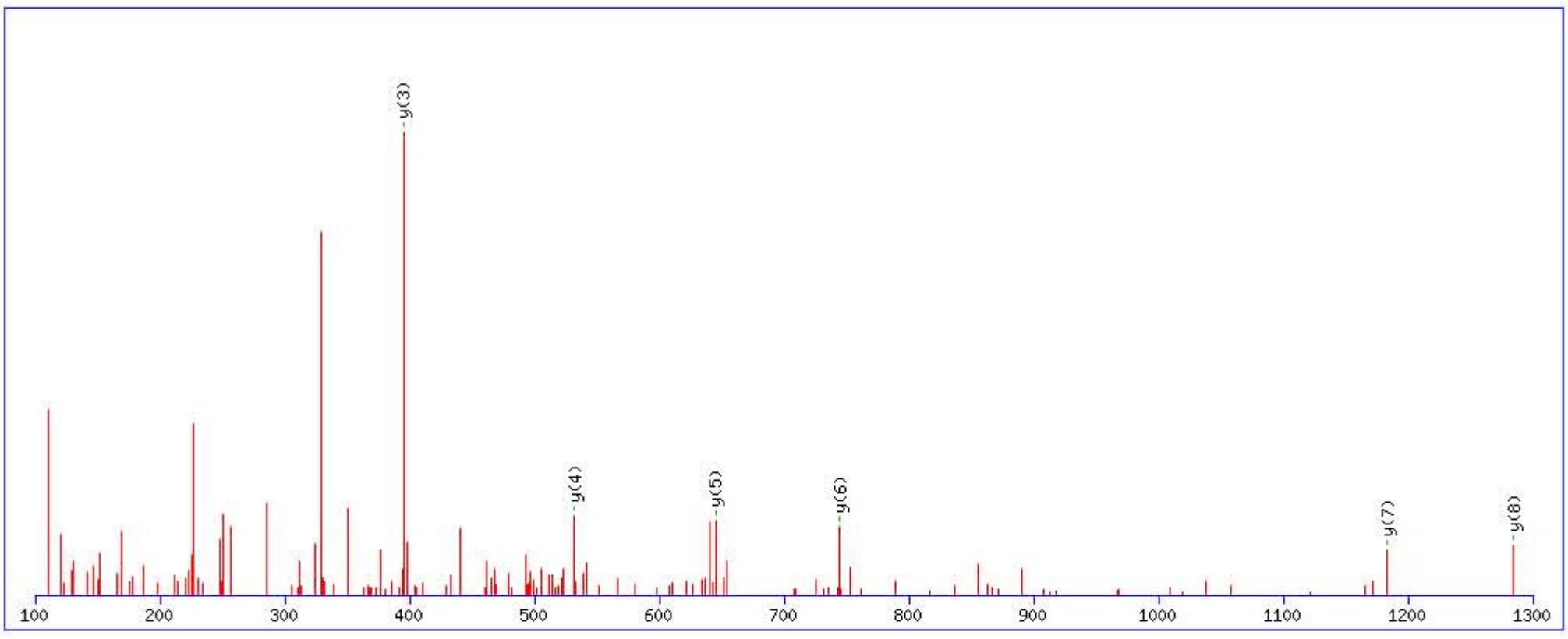
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ITQVLHFTK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

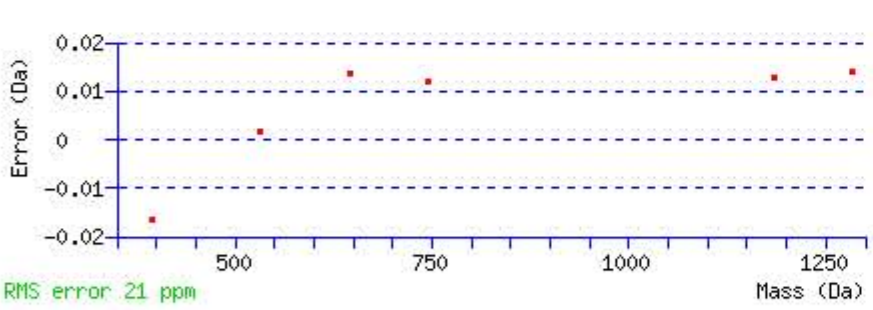
Match to Query 27226: 1396.790862 from(466.604230,3+) rtinseconds(1948) index(49973)
Title: Locus:1.1.1.1916.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

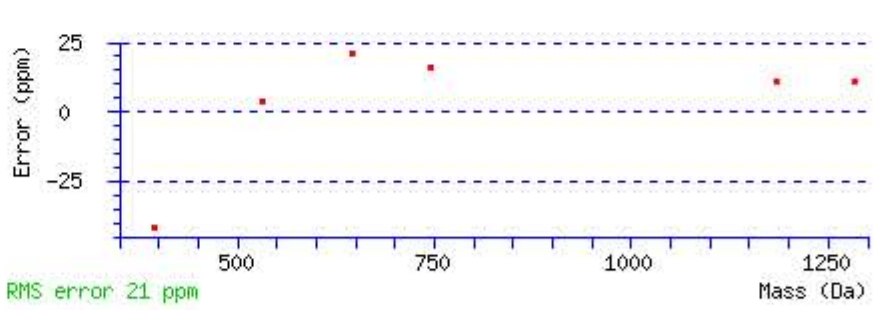
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1396.790085
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 34 **Expect:** 0.0015
**Matches :** 6/88 fragment ions using 12 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 9 |
| 2 | 215.139019 | 108.073147 | | | 197.128454 | 99.067865 | T | *1284.713292* | 642.860284 | 1267.686743 | 634.347010 | 1266.702727 | 633.855002 | 8 |
| 3 | 654.364345 | 327.685811 | 637.337796 | 319.172536 | 636.353780 | 318.680528 | Q | *1183.665613* | 592.336445 | 1166.639064 | 583.823170 | 1165.655048 | 583.331162 | 7 |
| 4 | 753.432759 | 377.220018 | 736.406210 | 368.706743 | 735.422194 | 368.214735 | V | *744.440287* | 372.723782 | 727.413738 | 364.210507 | 726.429722 | 363.718499 | 6 |
| 5 | 866.516823 | 433.762050 | 849.490274 | 425.248775 | 848.506258 | 424.756767 | L | *645.371873* | 323.189575 | 628.345324 | 314.676300 | 627.361308 | 314.184292 | 5 |
| 6 | 1003.575735 | 502.291506 | 986.549186 | 493.778231 | 985.565170 | 493.286223 | H | *532.287809* | 266.647543 | 515.261260 | 258.134268 | 514.277244 | 257.642260 | 4 |
| 7 | 1150.644149 | 575.825713 | 1133.617600 | 567.312438 | 1132.633584 | 566.820430 | F | *395.228897* | 198.118086 | 378.202348 | 189.604812 | 377.218332 | 189.112804 | 3 |
| 8 | 1251.691828 | 626.349552 | 1234.665279 | 617.836278 | 1233.681263 | 617.344270 | T | 248.160483 | 124.583879 | 231.133934 | 116.070605 | 230.149918 | 115.578597 | 2 |
| 9 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.7 | 1396.790085 | 0.000777 | ITQVLHFTK |
| 3.5 | 1396.792557 | -0.001695 | LLGELQEQIVQK |
| 1.8 | 1396.774796 | 0.016066 | LLQEGIAQSK |
| 1.2 | 1396.778625 | 0.012237 | ILIENGVAERQR |

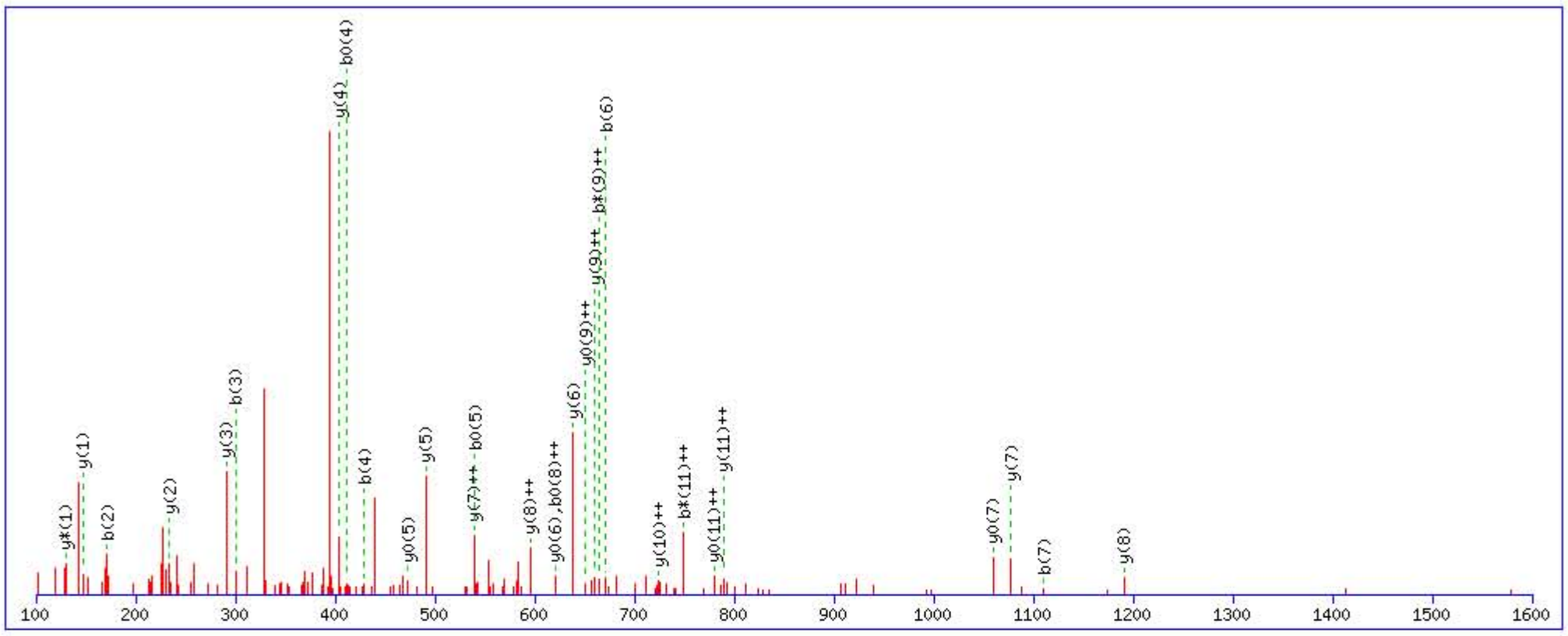
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GLEEELQFSLGSK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

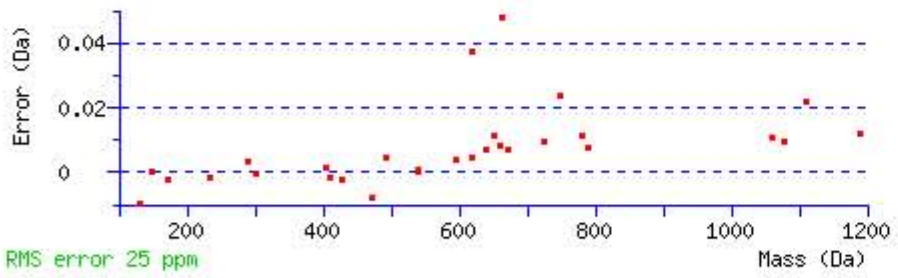
Match to Query 39030: 1746.901002 from(583.307610,3+) rtinseconds(2544) index(53587)
Title: Locus:1.1.1.2123.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

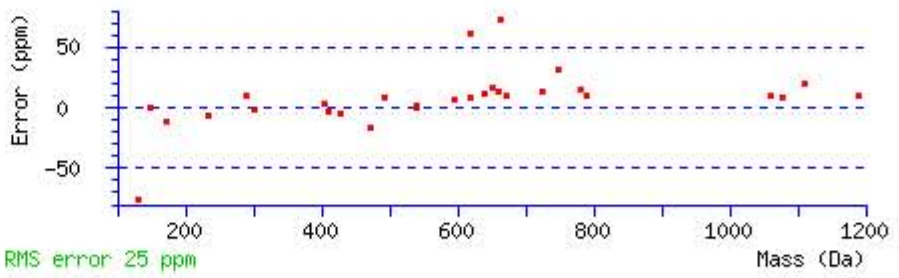
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1746.886200
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 29 **Expect:** 0.038
**Matches :** 29/126 fragment ions using 74 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 13 |
| 2 | *171.112804* | 86.060040 | | | | | L | 1690.872035 | 845.939656 | 1673.845486 | 837.426381 | 1672.861470 | 836.934373 | 12 |
| 3 | *300.155397* | 150.581336 | | | 282.144832 | 141.576054 | E | 1577.787971 | 789.397624 | 1560.761422 | 780.884349 | 1559.777406 | 780.392341 | 11 |
| 4 | *429.197990* | 215.102633 | | | 411.187425 | 206.097351 | E | 1448.745378 | 724.876327 | 1431.718829 | 716.363053 | 1430.734813 | 715.871045 | 10 |
| 5 | 558.240583 | 279.623930 | | | 540.230018 | 270.618647 | E | 1319.702785 | 660.355031 | 1302.676236 | 651.841756 | 1301.692220 | 651.349748 | 9 |
| 6 | *671.324647* | 336.165962 | | | 653.314082 | 327.160679 | L | *1190.660192* | 595.833734 | 1173.633643 | 587.320460 | 1172.649627 | 586.828452 | 8 |
| 7 | *1110.549973* | 555.778624 | 1093.523424 | 547.265350 | 1092.539408 | 546.773342 | Q | *1077.576128* | 539.291702 | 1060.549579 | 530.778428 | 1059.565563 | 530.286419 | 7 |
| 8 | 1257.618387 | 629.312832 | 1240.591838 | 620.799557 | 1239.607822 | 620.307549 | F | *638.350802* | 319.679039 | 621.324253 | 311.165765 | 620.340237 | 310.673757 | 6 |
| 9 | 1344.650415 | 672.828846 | 1327.623866 | 664.315571 | 1326.639850 | 663.823563 | S | *491.282388* | 246.144832 | 474.255839 | 237.631557 | 473.271823 | 237.139549 | 5 |
| 10 | 1457.734479 | 729.370878 | 1440.707930 | 720.857603 | 1439.723914 | 720.365595 | L | *404.250360* | 202.628818 | 387.223811 | 194.115543 | 386.239795 | 193.623535 | 4 |
| 11 | 1514.755943 | 757.881609 | 1497.729394 | 749.368335 | 1496.745378 | 748.876327 | G | *291.166296* | 146.086786 | 274.139747 | 137.573512 | 273.155731 | 137.081504 | 3 |
| 12 | 1601.787971 | 801.397624 | 1584.761422 | 792.884349 | 1583.777406 | 792.392341 | S | *234.144832* | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 13 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 28.6 | 1746.886200 | 0.014802 | GLEEELQFSLGSK |

**Mascot:** http://www.matrixscience.com/

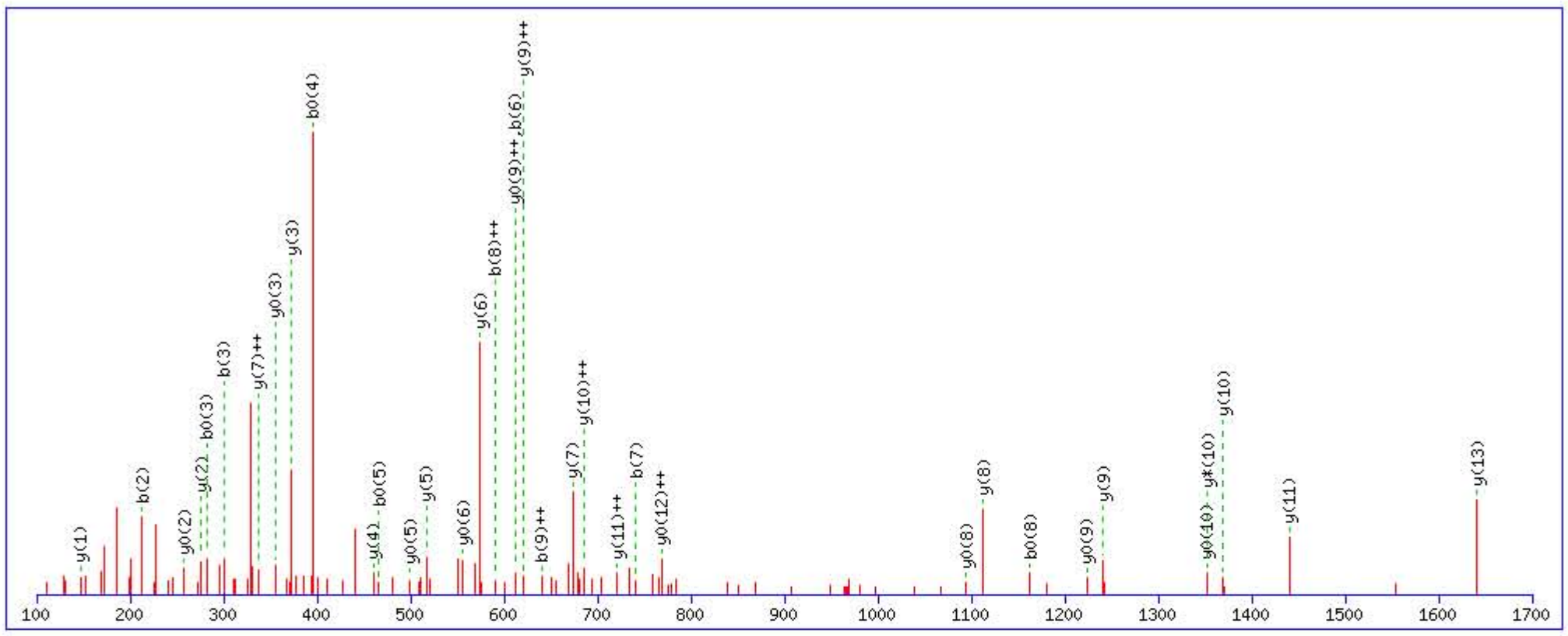
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VLSLAQEQVGGSPEK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

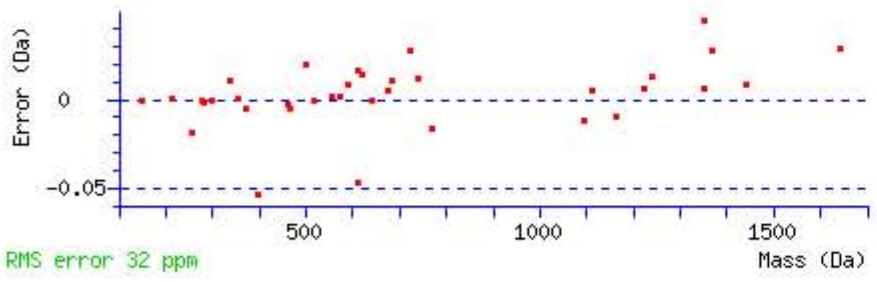
Match to Query 41289: 1851.988242 from(618.336690,3+) rtinseconds(1981) index(50251)
Title: Locus:1.1.1.1927.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

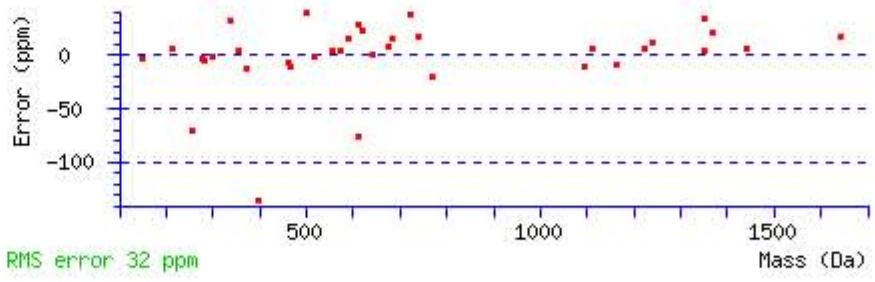
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1851.976425
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 3.5e-005
**Matches :** 36/152 fragment ions using 83 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 15 |
| 2 | **213.159754** | 107.083515 | | | | | L | 1753.915298 | 877.461287 | 1736.888749 | 868.948013 | 1735.904733 | 868.456004 | 14 |
| 3 | **300.191782** | 150.599529 | | | 282.181217 | 141.594247 | S | *1640.831234* | 820.919255 | 1623.804685 | 812.405981 | 1622.820669 | 811.913973 | 13 |
| 4 | 413.275846 | 207.141561 | | | 395.265281 | 198.136279 | L | 1553.799206 | 777.403241 | 1536.772657 | 768.889967 | 1535.788641 | 768.397958 | 12 |
| 5 | 484.312960 | 242.660118 | | | 466.302395 | 233.654836 | A | *1440.715142* | 720.861209 | 1423.688593 | 712.347935 | 1422.704577 | 711.855927 | 11 |
| 6 | **612.371538** | 306.689407 | 595.344989 | 298.176133 | 594.360973 | 297.684125 | Q | *1369.678028* | 685.342652 | 1352.651479 | 676.829378 | 1351.667463 | 676.337370 | 10 |
| 7 | **741.414131** | 371.210704 | 724.387582 | 362.697429 | 723.403566 | 362.205421 | E | *1241.619450* | 621.313363 | 1224.592901 | 612.800089 | 1223.608885 | 612.308080 | 9 |
| 8 | 1180.639457 | **590.823367** | 1163.612908 | 582.310092 | 1162.628892 | 581.818084 | Q | *1112.576857* | 556.792066 | 1095.550308 | 548.278792 | 1094.566292 | 547.786784 | 8 |
| 9 | 1279.707871 | **640.357574** | 1262.681322 | 631.844299 | 1261.697306 | 631.352291 | V | *673.351531* | 337.179404 | 656.324982 | 328.666129 | 655.340966 | 328.174121 | 7 |
| 10 | 1336.729335 | 668.868306 | 1319.702786 | 660.355031 | 1318.718770 | 659.863023 | G | *574.283117* | 287.645197 | 557.256568 | 279.131922 | 556.272552 | 278.639914 | 6 |
| 11 | 1393.750799 | 697.379037 | 1376.724250 | 688.865763 | 1375.740234 | 688.373755 | G | *517.261653* | 259.134465 | 500.235104 | 250.621190 | 499.251088 | 250.129182 | 5 |
| 12 | 1480.782827 | 740.895052 | 1463.756278 | 732.381777 | 1462.772262 | 731.889769 | S | *460.240189* | 230.623732 | 443.213640 | 222.110458 | 442.229624 | 221.618450 | 4 |
| 13 | 1577.835591 | 789.421434 | 1560.809042 | 780.908159 | 1559.825026 | 780.416151 | P | *373.208161* | 187.107718 | 356.181612 | 178.594444 | 355.197596 | 178.102436 | 3 |
| 14 | 1706.878184 | 853.942730 | 1689.851635 | 845.429456 | 1688.867619 | 844.937447 | E | *276.155397* | 138.581336 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 15 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.2 | 1851.976425 | 0.011817 | VLSLAQEQVGGSPEK |
| 35.4 | 1851.976425 | 0.011817 | VLSLAQEQVGGSPEK |

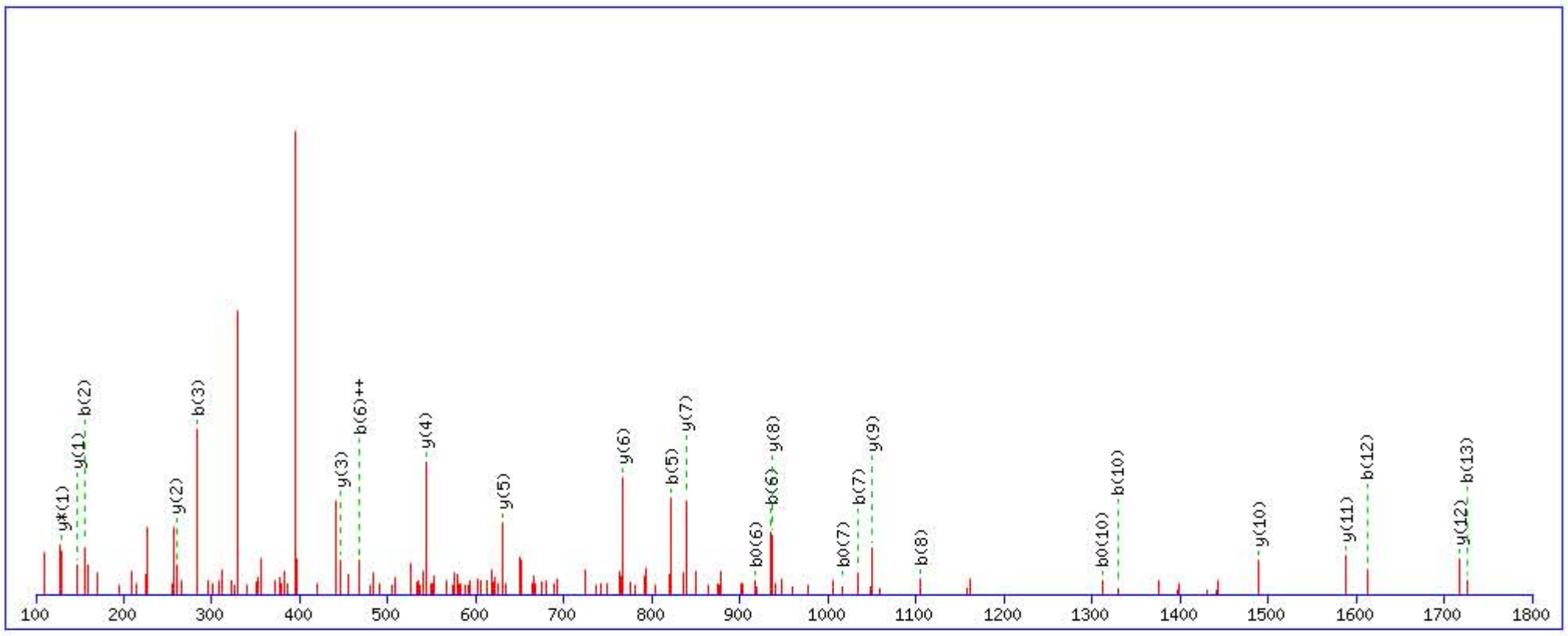
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GPEVQLVAHSPWLK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

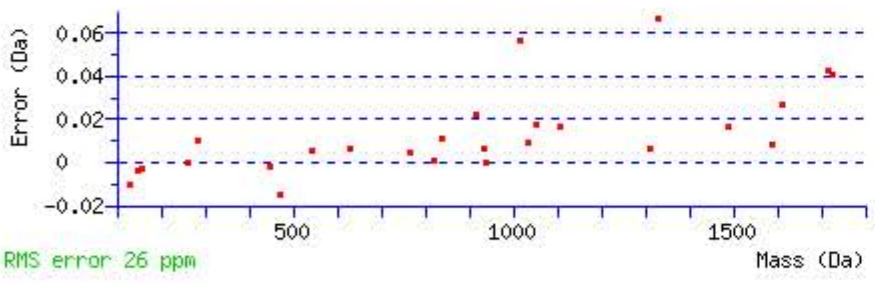
Match to Query 41721: 1871.029962 from(624.683930,3+) rtinseconds(2228) index(51842)
Title: Locus:1.1.1.2013.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

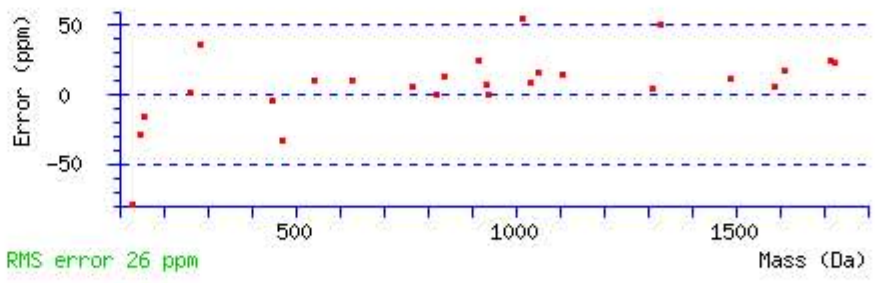
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1871.012756
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 57 **Expect:** 6.9e-006
**Matches** : 26/136 fragment ions using 65 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 14 |
| 2 | **155.081504** | 78.044390 | | | | | P | 1814.998574 | 908.002925 | 1797.972025 | 899.489651 | 1796.988009 | 898.997643 | 13 |
| 3 | **284.124097** | 142.565687 | | | 266.113532 | 133.560404 | E | *1717.945810* | 859.476543 | 1700.919261 | 850.963269 | 1699.935245 | 850.471261 | 12 |
| 4 | 383.192511 | 192.099894 | | | 365.181946 | 183.094611 | V | *1588.903217* | 794.955247 | 1571.876668 | 786.441972 | 1570.892652 | 785.949964 | 11 |
| 5 | **822.417837** | 411.712557 | 805.391288 | 403.199282 | 804.407272 | 402.707274 | Q | *1489.834803* | 745.421040 | 1472.808254 | 736.907765 | 1471.824238 | 736.415757 | 10 |
| 6 | **935.501901** | 468.254589 | 918.475352 | 459.741314 | 917.491336 | 459.249306 | L | *1050.609477* | 525.808377 | 1033.582928 | 517.295102 | 1032.598912 | 516.803094 | 9 |
| 7 | **1034.570315** | 517.788796 | 1017.543766 | 509.275521 | 1016.559750 | 508.783513 | V | *937.525413* | 469.266345 | 920.498864 | 460.753070 | 919.514848 | 460.261062 | 8 |
| 8 | **1105.607429** | 553.307353 | 1088.580880 | 544.794078 | 1087.596864 | 544.302070 | A | *838.456999* | 419.732138 | 821.430450 | 411.218863 | 820.446434 | 410.726855 | 7 |
| 9 | 1242.666341 | 621.836809 | 1225.639792 | 613.323534 | 1224.655776 | 612.831526 | H | *767.419885* | 384.213581 | 750.393336 | 375.700306 | 749.409320 | 375.208298 | 6 |
| 10 | **1329.698369** | 665.352823 | 1312.671820 | 656.839548 | 1311.687804 | 656.347540 | S | *630.360973* | 315.684125 | 613.334424 | 307.170850 | 612.350408 | 306.678842 | 5 |
| 11 | 1426.751133 | 713.879205 | 1409.724584 | 705.365930 | 1408.740568 | 704.873922 | P | *543.328945* | 272.168111 | 526.302396 | 263.654836 | | | 4 |
| 12 | **1612.830446** | 806.918861 | 1595.803897 | 798.405587 | 1594.819881 | 797.913579 | W | *446.276181* | 223.641728 | 429.249632 | 215.128454 | | | 3 |
| 13 | **1725.914510** | 863.460893 | 1708.887961 | 854.947619 | 1707.903945 | 854.455611 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 14 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 57.1 | 1871.012756 | 0.017206 | GPEVQLVAHSPWLK |
| 1.9 | 1871.037231 | -0.007269 | ISKLLMICQNAGISVPK |
| 0.1 | 1871.037689 | -0.007727 | ILRPDATKNARNDFLK |

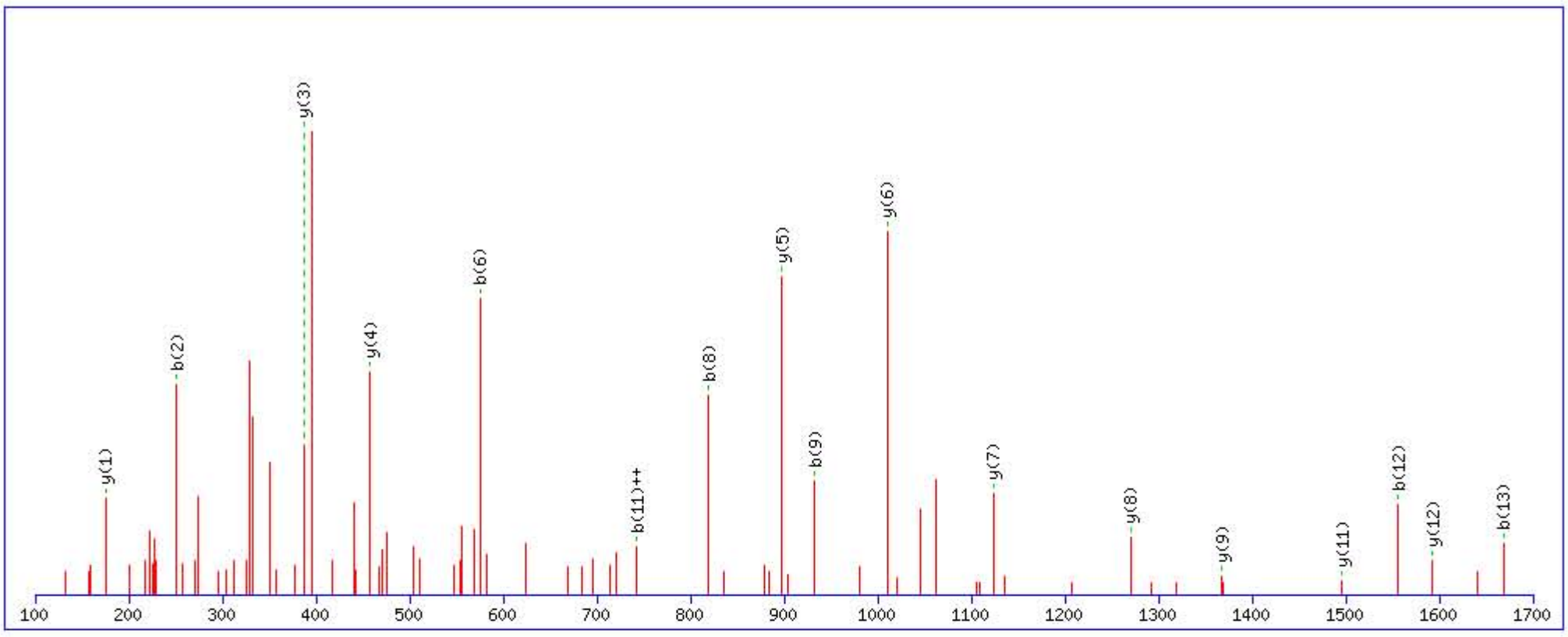
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HLVPGAPFLLQALVR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

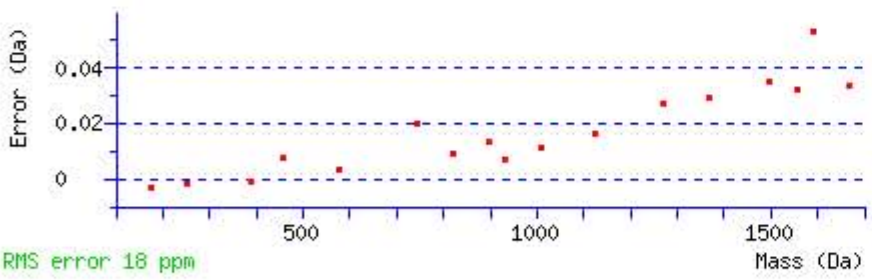
Match to Query 42959: 1941.162702 from(648.061510,3+) rtinseconds(2855) index(55999)
Title: Locus:1.1.1.2229.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

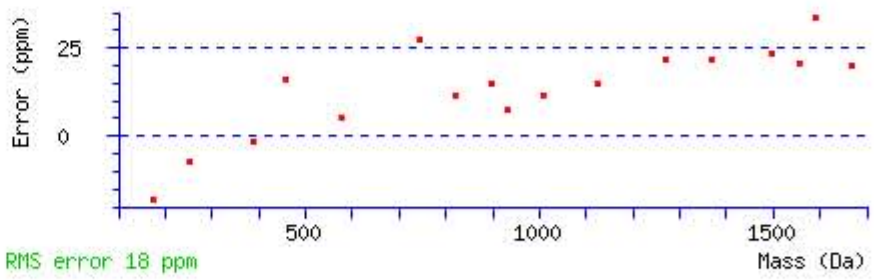
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1941.138626
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q11 : Biotin:Thermo-21345 (Q)
**Ions Score:** 60 **Expect:** 1.5e-006
**Matches :** 17/92 fragment ions using 31 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | H | | | | | 15 |
| 2 | **251.150252** | 126.078764 | | | L | 1805.086996 | 903.047136 | 1788.060447 | 894.533862 | 14 |
| 3 | 350.218666 | 175.612971 | | | V | 1692.002932 | 846.505104 | 1674.976383 | 837.991830 | 13 |
| 4 | 447.271430 | 224.139353 | | | P | *1592.934518* | 796.970897 | 1575.907969 | 788.457623 | 12 |
| 5 | 504.292894 | 252.650085 | | | G | *1495.881754* | 748.444515 | 1478.855205 | 739.931241 | 11 |
| 6 | **575.330008** | 288.168642 | | | A | 1438.860290 | 719.933783 | 1421.833741 | 711.420509 | 10 |
| 7 | 672.382772 | 336.695024 | | | P | *1367.823176* | 684.415226 | 1350.796627 | 675.901952 | 9 |
| 8 | **819.451186** | 410.229231 | | | F | *1270.770412* | 635.888844 | 1253.743863 | 627.375570 | 8 |
| 9 | **932.535250** | 466.771263 | | | L | *1123.701998* | 562.354637 | 1106.675449 | 553.841363 | 7 |
| 10 | 1045.619314 | 523.313295 | | | L | *1010.617934* | 505.812605 | 993.591385 | 497.299331 | 6 |
| 11 | 1484.844640 | 742.925958 | 1467.818091 | 734.412684 | Q | *897.533870* | 449.270573 | 880.507321 | 440.757298 | 5 |
| 12 | **1555.881754** | 778.444515 | 1538.855205 | 769.931241 | A | *458.308544* | 229.657910 | 441.281995 | 221.144635 | 4 |
| 13 | **1668.965818** | 834.986547 | 1651.939269 | 826.473273 | L | *387.271430* | 194.139353 | 370.244881 | 185.626078 | 3 |
| 14 | 1768.034232 | 884.520754 | 1751.007683 | 876.007480 | V | 274.187366 | 137.597321 | 257.160817 | 129.084047 | 2 |
| 15 | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 59.8 | 1941.138626 | 0.024076 | HLVPGAPFLLQALVR |

**Mascot:** http://www.matrixscience.com/

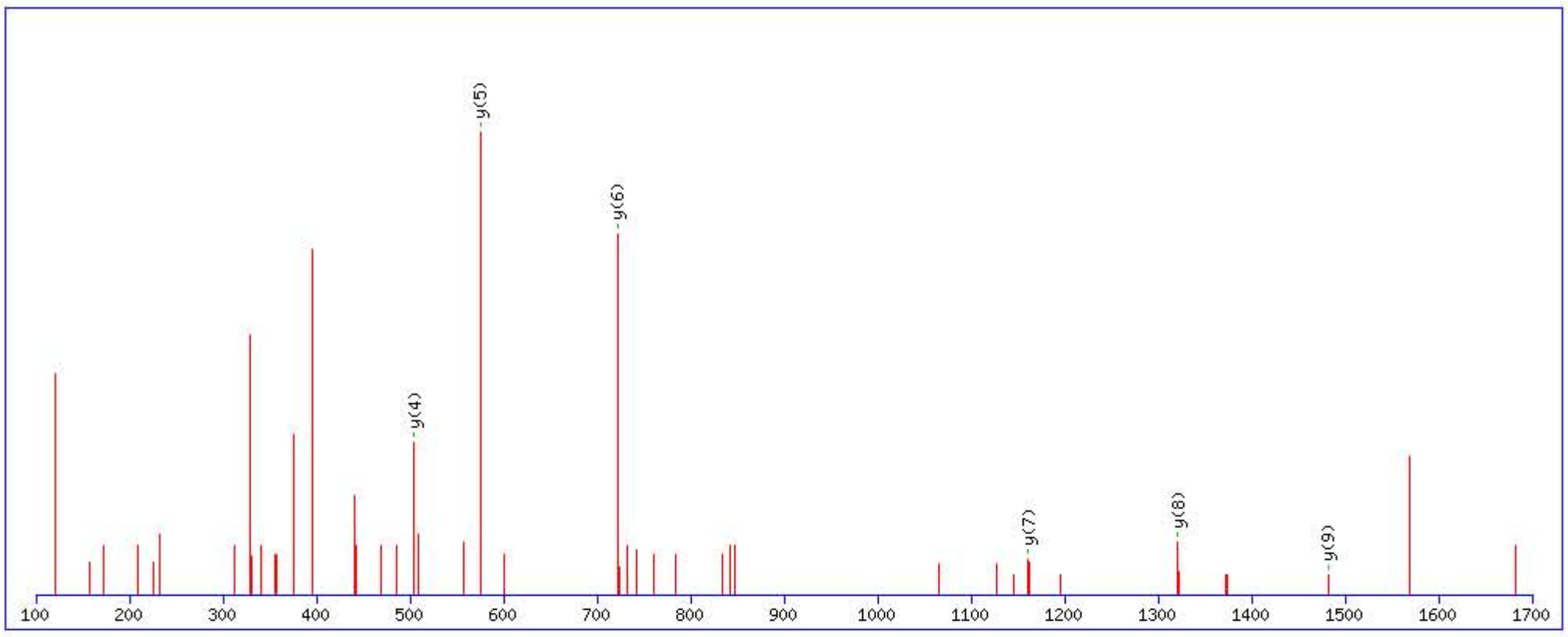
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EPFLSCCQFAESLR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

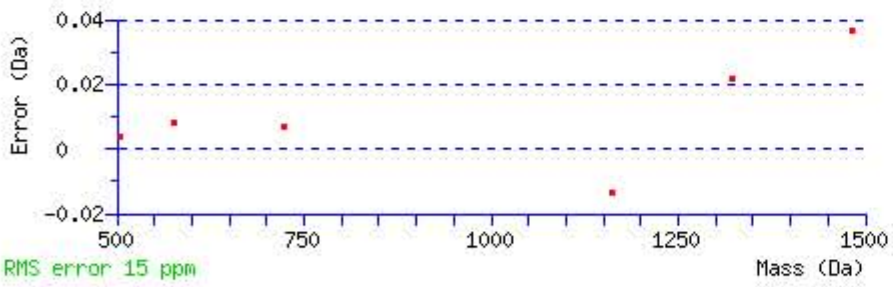
Match to Query 45812: 2053.967652 from(685.663160,3+) rtinseconds(2491) index(37010)
Title: Locus:1.1.1.976.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

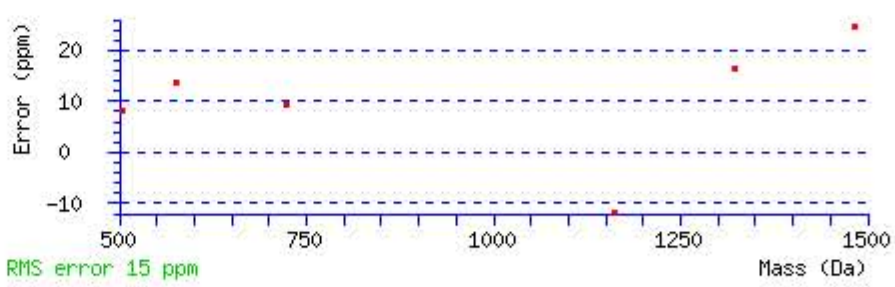
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2053.942368
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 28 **Expect:** 0.025
**Matches :** 6/138 fragment ions using 13 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 14 |
| 2 | 227.102633 | 114.054954 | | | 209.092068 | 105.049672 | P | 1925.907059 | 963.457168 | 1908.880510 | 954.943893 | 1907.896494 | 954.451885 | 13 |
| 3 | 374.171047 | 187.589161 | | | 356.160482 | 178.583879 | F | 1828.854295 | 914.930786 | 1811.827746 | 906.417511 | 1810.843730 | 905.925503 | 12 |
| 4 | 487.255111 | 244.131193 | | | 469.244546 | 235.125911 | L | 1681.785881 | 841.396579 | 1664.759332 | 832.883304 | 1663.775316 | 832.391296 | 11 |
| 5 | 574.287139 | 287.647208 | | | 556.276574 | 278.641925 | S | 1568.701817 | 784.854547 | 1551.675268 | 776.341272 | 1550.691252 | 775.849264 | 10 |
| 6 | 734.317788 | 367.662532 | | | 716.307223 | 358.657250 | C | *1481.669789* | 741.338533 | 1464.643240 | 732.825258 | 1463.659224 | 732.333250 | 9 |
| 7 | 894.348437 | 447.677857 | | | 876.337872 | 438.672574 | C | *1321.639140* | 661.323208 | 1304.612591 | 652.809934 | 1303.628575 | 652.317926 | 8 |
| 8 | 1333.573763 | 667.290520 | 1316.547214 | 658.777245 | 1315.563198 | 658.285237 | Q | *1161.608491* | 581.307884 | 1144.581942 | 572.794609 | 1143.597926 | 572.302601 | 7 |
| 9 | 1480.642177 | 740.824727 | 1463.615628 | 732.311452 | 1462.631612 | 731.819444 | F | *722.383165* | 361.695221 | 705.356616 | 353.181946 | 704.372600 | 352.689938 | 6 |
| 10 | 1551.679291 | 776.343284 | 1534.652742 | 767.830009 | 1533.668726 | 767.338001 | A | *575.314751* | 288.161014 | 558.288202 | 279.647739 | 557.304186 | 279.155731 | 5 |
| 11 | 1680.721884 | 840.864580 | 1663.695335 | 832.351306 | 1662.711319 | 831.859298 | E | *504.277637* | 252.642457 | 487.251088 | 244.129182 | 486.267072 | 243.637174 | 4 |
| 12 | 1767.753912 | 884.380594 | 1750.727363 | 875.867320 | 1749.743347 | 875.375312 | S | 375.235044 | 188.121160 | 358.208495 | 179.607885 | 357.224479 | 179.115877 | 3 |
| 13 | 1880.837976 | 940.922626 | 1863.811427 | 932.409352 | 1862.827411 | 931.917344 | L | 288.203016 | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 14 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 28.3 | 2053.942368 | 0.025284 | EPFLSCCQFAESLR |

**Mascot:** http://www.matrixscience.com/

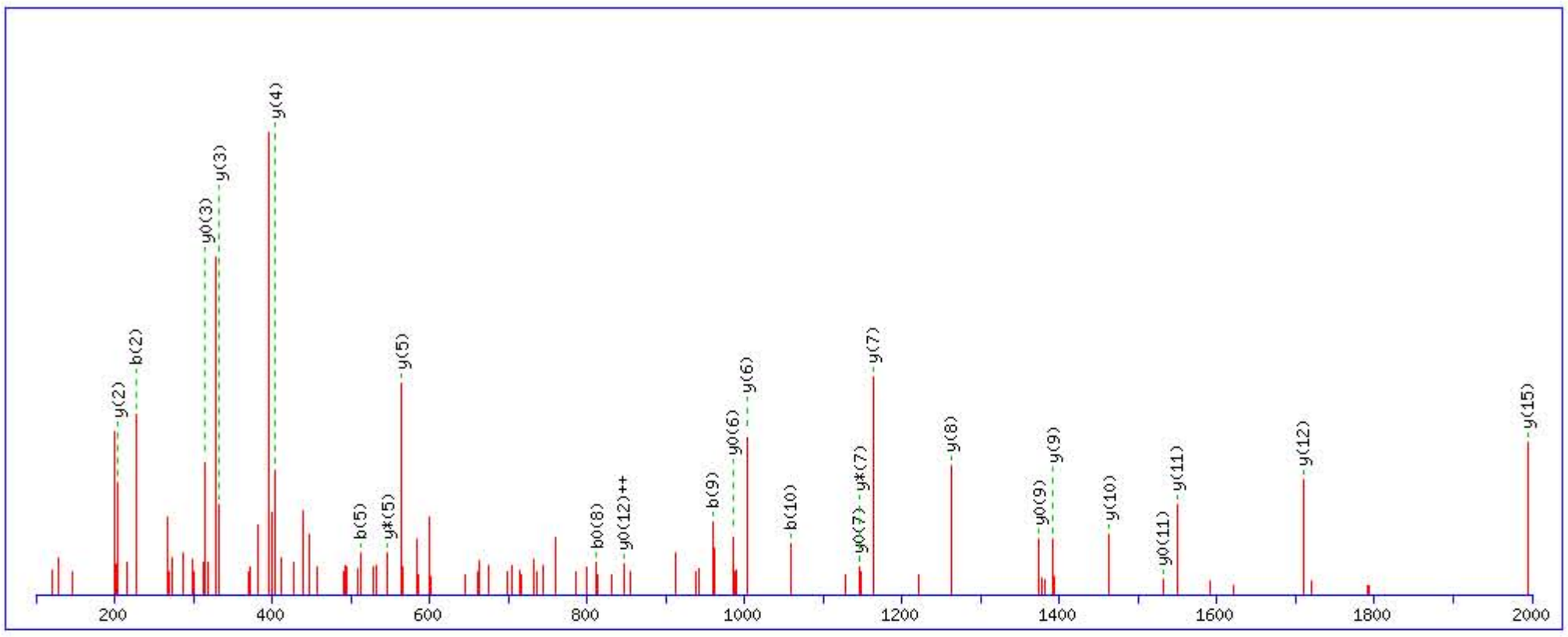
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LLATLCSAEVCQCAEGK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

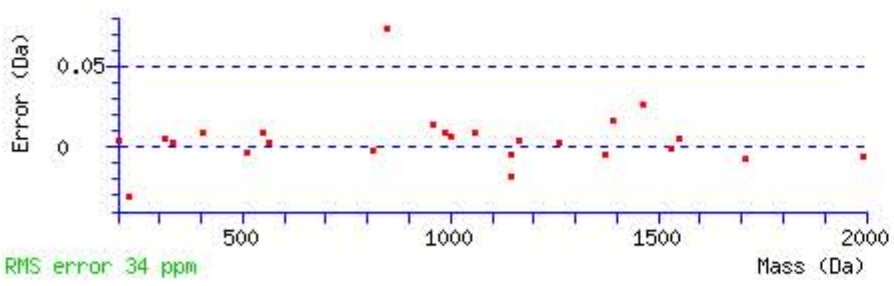
Match to Query 48946: 2220.056982 from(741.026270,3+) rtinseconds(2115) index(67084)
Title: Locus:1.1.1.2011.11 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

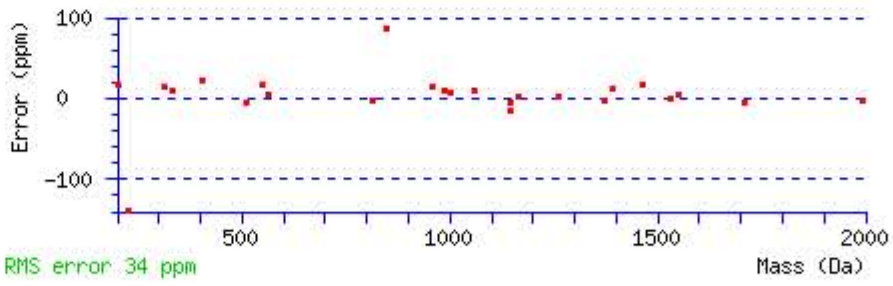
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2220.041092
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 55 **Expect:** 2e-005
**Matches :** 25/160 fragment ions using 60 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 17 |
| 2 | **227.175404** | 114.091340 | | | | | L | 2107.964318 | 1054.485797 | 2090.937769 | 1045.972522 | 2089.953753 | 1045.480514 | 16 |
| 3 | 298.212518 | 149.609897 | | | | | A | *1994.880254* | 997.943765 | 1977.853705 | 989.430491 | 1976.869689 | 988.938483 | 15 |
| 4 | 399.260197 | 200.133737 | | | 381.249632 | 191.128454 | T | 1923.843140 | 962.425208 | 1906.816591 | 953.911934 | 1905.832575 | 953.419926 | 14 |
| 5 | **512.344261** | 256.675769 | | | 494.333696 | 247.670486 | L | 1822.795461 | 911.901369 | 1805.768912 | 903.388094 | 1804.784896 | 902.896086 | 13 |
| 6 | 672.374910 | 336.691093 | | | 654.364345 | 327.685811 | C | *1709.711397* | 855.359337 | 1692.684848 | 846.846062 | 1691.700832 | 846.354054 | 12 |
| 7 | 759.406938 | 380.207107 | | | 741.396373 | 371.201825 | S | *1549.680748* | 775.344012 | 1532.654199 | 766.830738 | 1531.670183 | 766.338730 | 11 |
| 8 | 830.444052 | 415.725664 | | | 812.433487 | 406.720382 | A | *1462.648720* | 731.827998 | 1445.622171 | 723.314724 | 1444.638155 | 722.822716 | 10 |
| 9 | **959.486645** | 480.246961 | | | 941.476080 | 471.241678 | E | *1391.611606* | 696.309441 | 1374.585057 | 687.796167 | 1373.601041 | 687.304159 | 9 |
| 10 | **1058.555059** | 529.781168 | | | 1040.544494 | 520.775885 | V | *1262.569013* | 631.788145 | 1245.542464 | 623.274870 | 1244.558448 | 622.782862 | 8 |
| 11 | 1218.585708 | 609.796492 | | | 1200.575143 | 600.791210 | C | *1163.500599* | 582.253938 | 1146.474050 | 573.740663 | 1145.490034 | 573.248655 | 7 |
| 12 | 1657.811034 | 829.409155 | 1640.784485 | 820.895881 | 1639.800469 | 820.403873 | Q | *1003.469950* | 502.238613 | 986.443401 | 493.725339 | 985.459385 | 493.233331 | 6 |
| 13 | 1817.841683 | 909.424480 | 1800.815134 | 900.911205 | 1799.831118 | 900.419197 | C | *564.244624* | 282.625950 | 547.218075 | 274.112676 | 546.234059 | 273.620668 | 5 |
| 14 | 1888.878797 | 944.943037 | 1871.852248 | 936.429762 | 1870.868232 | 935.937754 | A | *404.213975* | 202.610626 | 387.187426 | 194.097351 | 386.203410 | 193.605343 | 4 |
| 15 | 2017.921390 | 1009.464333 | 2000.894841 | 1000.951059 | 1999.910825 | 1000.459051 | E | *333.176861* | 167.092069 | 316.150312 | 158.578794 | 315.166296 | 158.086786 | 3 |
| 16 | 2074.942854 | 1037.975065 | 2057.916305 | 1029.461790 | 2056.932289 | 1028.969782 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 17 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 54.6 | 2220.041092 | 0.015890 | LLATLCSAEVCQCAEGK |
| 4.5 | 2220.048080 | 0.008902 | EPQEGAELPEATGTTSHR |

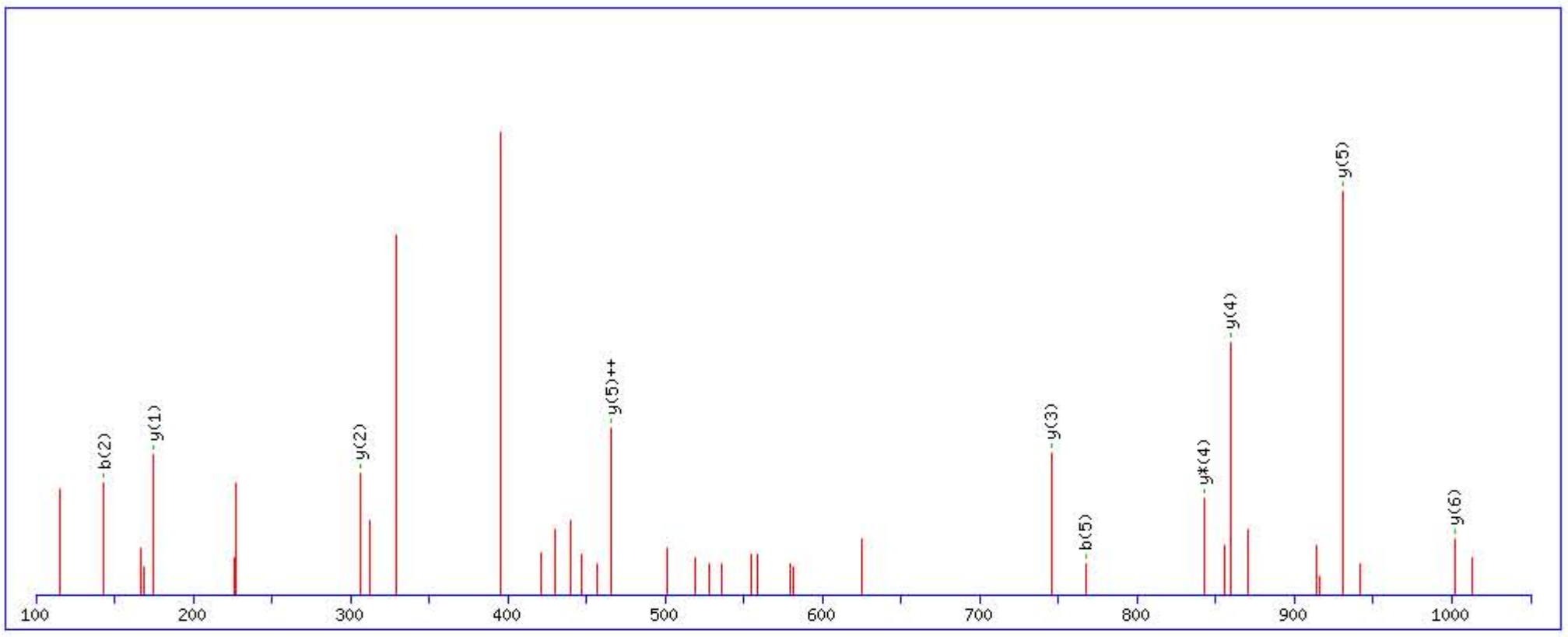
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AAANQMR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

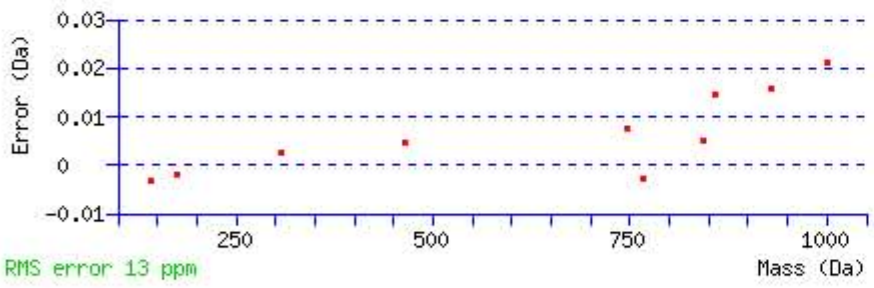
Match to Query 15686: 1071.535968 from(536.775260,2+) rtinseconds(1375) index(30281)
Title: Locus:1.1.1.587.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

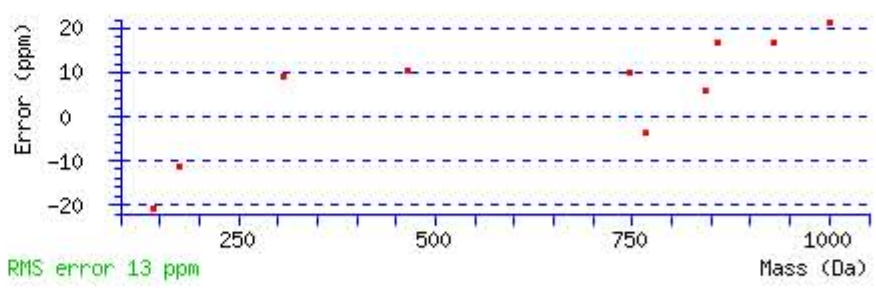
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1071.531723
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0026
**Matches :** 10/42 fragment ions using 17 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | A | | | | | 7 |
| 2 | **143.081504** | 72.044390 | | | A | ***1001.501918*** | 501.254597 | 984.475369 | 492.741323 | 6 |
| 3 | 214.118618 | 107.562947 | | | A | ***930.464804*** | 465.736040 | 913.438255 | 457.222766 | 5 |
| 4 | 328.161545 | 164.584410 | 311.134996 | 156.071136 | N | ***859.427690*** | 430.217483 | 842.401141 | 421.704209 | 4 |
| 5 | **767.386871** | 384.197074 | 750.360322 | 375.683799 | Q | ***745.384763*** | 373.196020 | 728.358214 | 364.682745 | 3 |
| 6 | 898.427356 | 449.717316 | 881.400807 | 441.204042 | M | ***306.159437*** | 153.583357 | 289.132888 | 145.070082 | 2 |
| 7 | | | | | R | ***175.118952*** | 88.063114 | 158.092403 | 79.549840 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.7 | 1071.531723 | 0.004245 | AAANQMR |
| 19.7 | 1071.530853 | 0.005115 | AAEESGAKGPR |

**Mascot:** http://www.matrixscience.com/

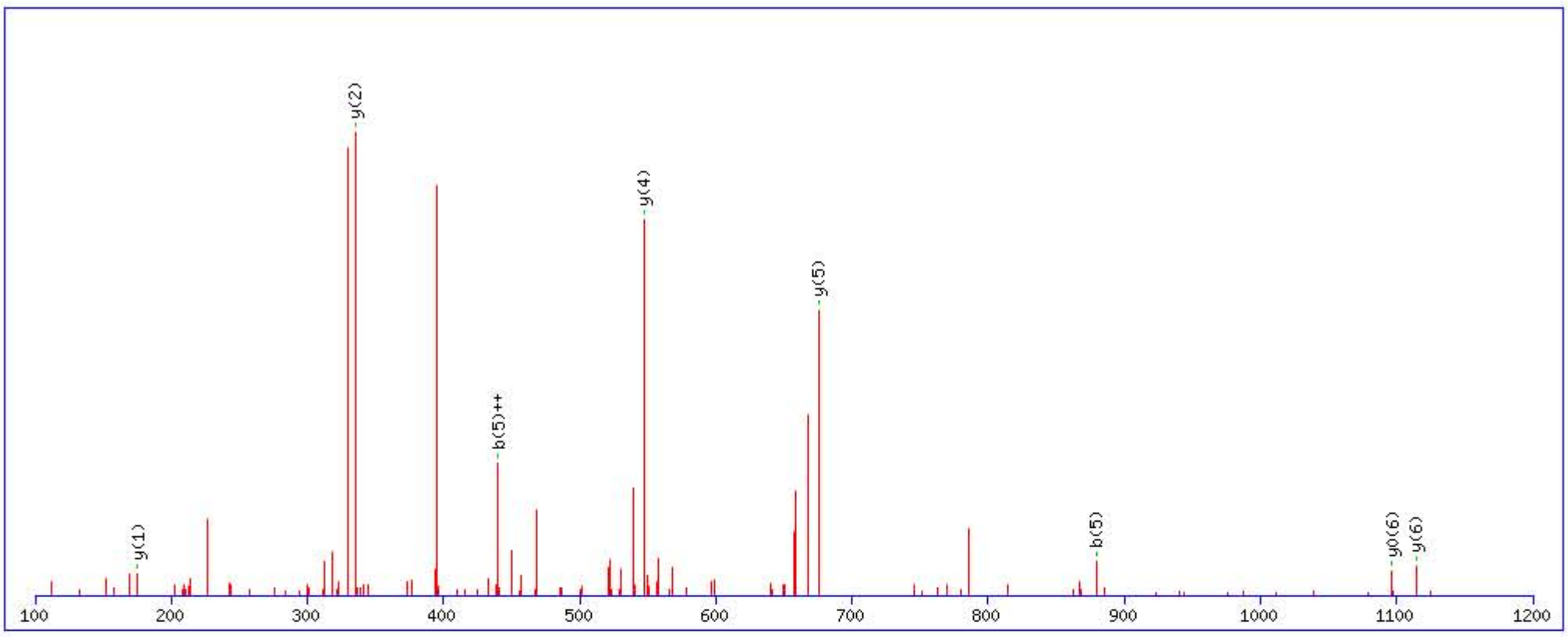
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VQQPDCR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

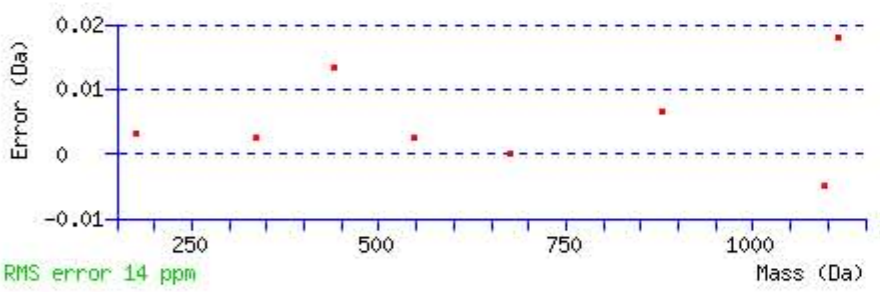
Match to Query 20808: 1212.580108 from(607.297330,2+) rtinseconds(1289) index(45674)
Title: Locus:1.1.1.1686.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

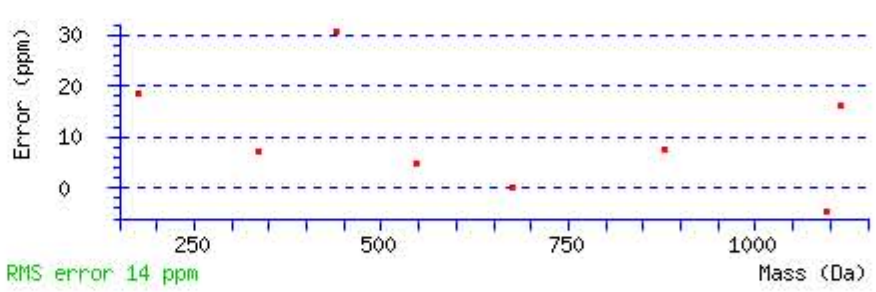
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1212.574356
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 36 **Expect:** 0.003
**Matches :** 8/58 fragment ions using 11 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 7 |
| 2 | 539.301016 | 270.154146 | 522.274467 | 261.640872 | | | Q | *1114.513212* | 557.760244 | 1097.486663 | 549.246970 | 1096.502647 | 548.754962 | 6 |
| 3 | 667.359594 | 334.183435 | 650.333045 | 325.670161 | | | Q | *675.287886* | 338.147581 | 658.261337 | 329.634307 | 657.277321 | 329.142299 | 5 |
| 4 | 764.412358 | 382.709817 | 747.385809 | 374.196543 | | | P | *547.229308* | 274.118292 | 530.202759 | 265.605018 | 529.218743 | 265.113010 | 4 |
| 5 | **879.439301** | **440.223289** | 862.412752 | 431.710014 | 861.428736 | 431.218006 | D | 450.176544 | 225.591910 | 433.149995 | 217.078635 | 432.165979 | 216.586627 | 3 |
| 6 | 1039.469950 | 520.238613 | 1022.443401 | 511.725339 | 1021.459385 | 511.233331 | C | *335.149601* | 168.078438 | 318.123052 | 159.565164 | | | 2 |
| 7 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 36.4 | 1212.574356 | 0.005752 | VQQPDCR |
| 22.6 | 1212.574356 | 0.005752 | VQQPDCR |
| 11.5 | 1212.596115 | -0.016007 | YFVEAGAMAVR |
| 4.5 | 1212.592102 | -0.011994 | VQEDQQR |
| 1.1 | 1212.592758 | -0.012650 | IYYVDHFTR |
| 0.8 | 1212.562241 | 0.017867 | TTAQYDQASTK |
| 0.6 | 1212.582199 | -0.002091 | GRMPPSEFHR |

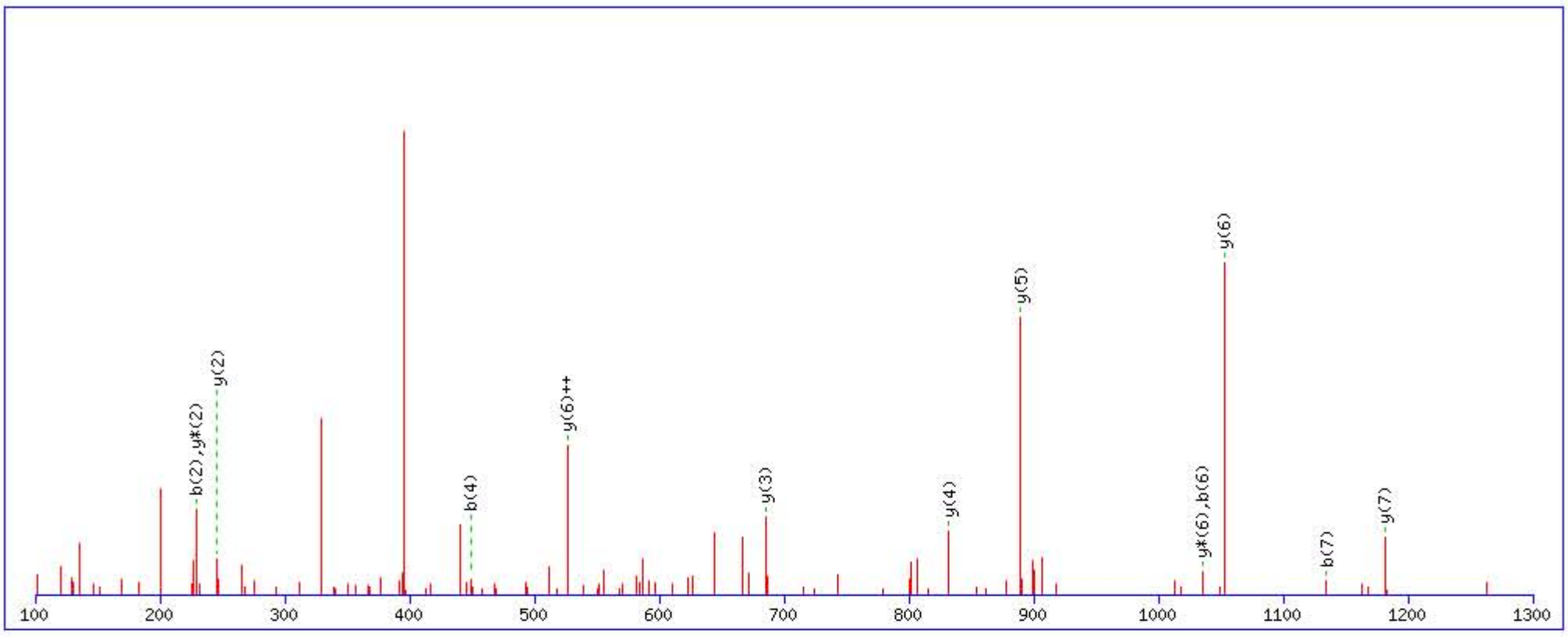
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VEYGFQVK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

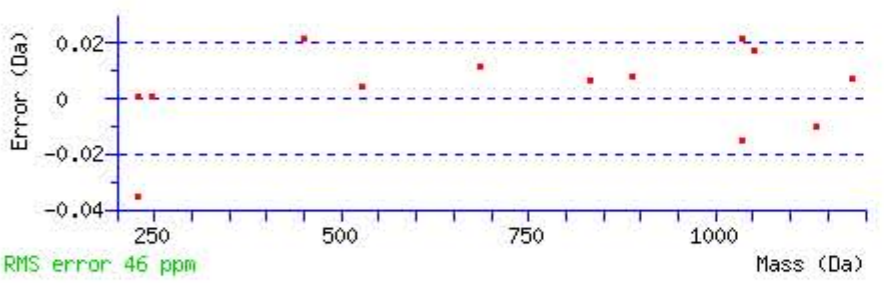
Match to Query 22737: 1279.673408 from(640.843980,2+) rtinseconds(1984) index(34172)
Title: Locus:1.1.1.799.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

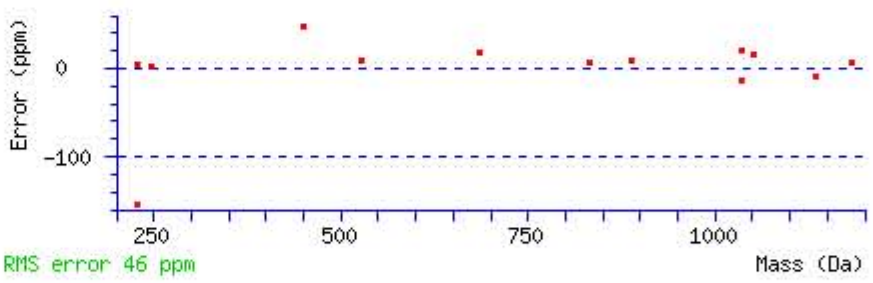
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1279.663483
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.016
**Matches :** 13/60 fragment ions using 23 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 8 |
| 2 | **229.118283** | 115.062780 | | | 211.107718 | 106.057497 | E | ***1181.602344*** | 591.304810 | 1164.575795 | 582.791536 | 1163.591779 | 582.299528 | 7 |
| 3 | 392.181612 | 196.594444 | | | 374.171047 | 187.589162 | Y | ***1052.559751*** | 526.783514 | 1035.533202 | 518.270239 | | | 6 |
| 4 | **449.203076** | 225.105176 | | | 431.192511 | 216.099894 | G | ***889.496422*** | 445.251849 | 872.469873 | 436.738575 | | | 5 |
| 5 | 596.271490 | 298.639383 | | | 578.260925 | 289.634101 | F | ***832.474958*** | 416.741117 | 815.448409 | 408.227843 | | | 4 |
| 6 | **1035.496816** | 518.252046 | 1018.470267 | 509.738772 | 1017.486251 | 509.246764 | Q | ***685.406544*** | 343.206910 | 668.379995 | 334.693636 | | | 3 |
| 7 | **1134.565230** | 567.786253 | 1117.538681 | 559.272979 | 1116.554665 | 558.780971 | V | ***246.181218*** | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 8 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 30.6 | 1279.663483 | 0.009925 | VEYGFQVK |
| 12.3 | 1279.663483 | 0.009925 | QFVGYLDK |
| 7.1 | 1279.659470 | 0.013938 | VCSFGKQVVEK |
| 3.3 | 1279.684601 | -0.011193 | TKPLMTEFSVK |
| 3.1 | 1279.684601 | -0.011193 | MSASAVFILDVK |
| 3.0 | 1279.681229 | -0.007821 | EVTVKEWYVK |
| 0.9 | 1279.670670 | 0.002738 | VEHKSNQK |
| 0.6 | 1279.677200 | -0.003792 | EYVGKTSLVER |

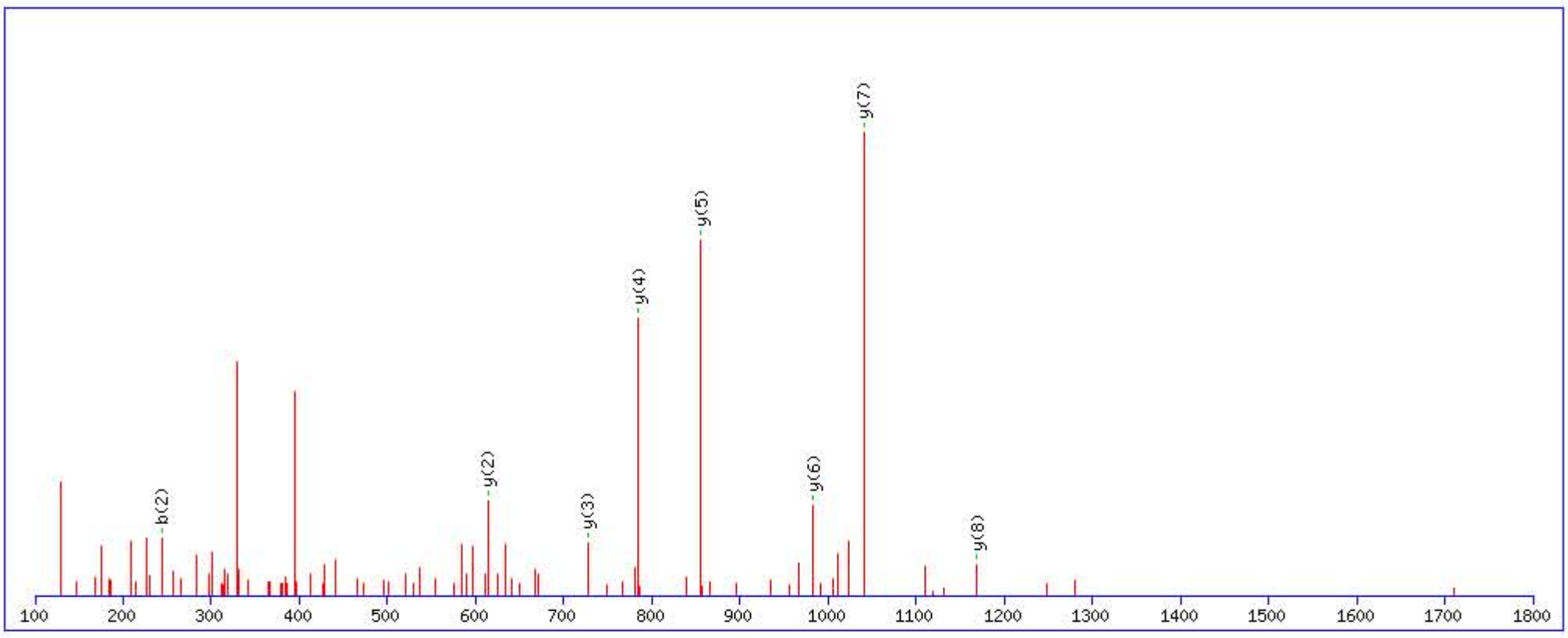
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DKGQAGLQR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

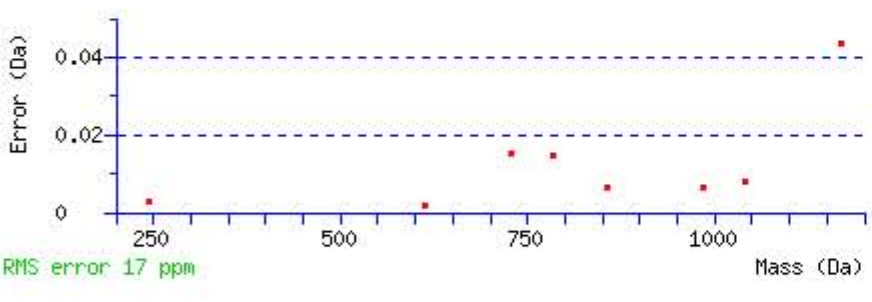
Match to Query 22931: 1282.691548 from(642.353050,2+) rtinseconds(1340) index(46002)
Title: Locus:1.1.1.1704.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

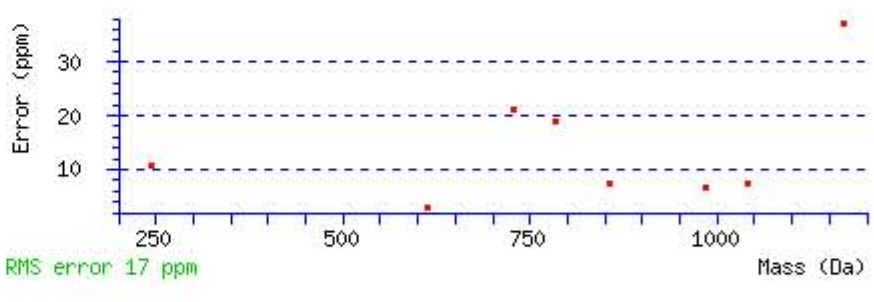
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1282.681580
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 55 **Expect:** 6.8e-005
**Matches :** 8/78 fragment ions using 12 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | 9 |
| 2 | **244.129182** | 122.568229 | 227.102633 | 114.054955 | 226.118617 | 113.562947 | K | *1168.661925* | 584.834600 | 1151.635376 | 576.321326 | 8 |
| 3 | 301.150646 | 151.078961 | 284.124097 | 142.565687 | 283.140081 | 142.073679 | G | *1040.566962* | 520.787119 | 1023.540413 | 512.273844 | 7 |
| 4 | 429.209224 | 215.108250 | 412.182675 | 206.594976 | 411.198659 | 206.102968 | Q | *983.545498* | 492.276387 | 966.518949 | 483.763112 | 6 |
| 5 | 500.246338 | 250.626807 | 483.219789 | 242.113532 | 482.235773 | 241.621524 | A | *855.486920* | 428.247098 | 838.460371 | 419.733823 | 5 |
| 6 | 557.267802 | 279.137539 | 540.241253 | 270.624265 | 539.257237 | 270.132257 | G | *784.449806* | 392.728541 | 767.423257 | 384.215266 | 4 |
| 7 | 670.351866 | 335.679571 | 653.325317 | 327.166297 | 652.341301 | 326.674289 | L | *727.428342* | 364.217809 | 710.401793 | 355.704534 | 3 |
| 8 | 1109.577192 | 555.292234 | 1092.550643 | 546.778960 | 1091.566627 | 546.286951 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162502 | 2 |
| 9 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 55.1 | 1282.681580 | 0.009968 | DKGQAGLQR |
| 15.1 | 1282.674194 | 0.017354 | QGEGQSRLVPGR |
| 12.0 | 1282.706711 | -0.015163 | KDIAELQR |
| 7.6 | 1282.681580 | 0.009968 | DKGQAGLQR |
| 7.4 | 1282.706711 | -0.015163 | DKALQELR |
| 6.6 | 1282.706726 | -0.015178 | ELGISVAQR |
| 4.7 | 1282.674164 | 0.017384 | NEGGKLGNPKNR |
| 3.7 | 1282.688095 | 0.003453 | KPTKPESQSPGK |
| 3.3 | 1282.706711 | -0.015163 | DKLQAIER |
| 2.9 | 1282.676834 | 0.014714 | KALEDEKPEPK |

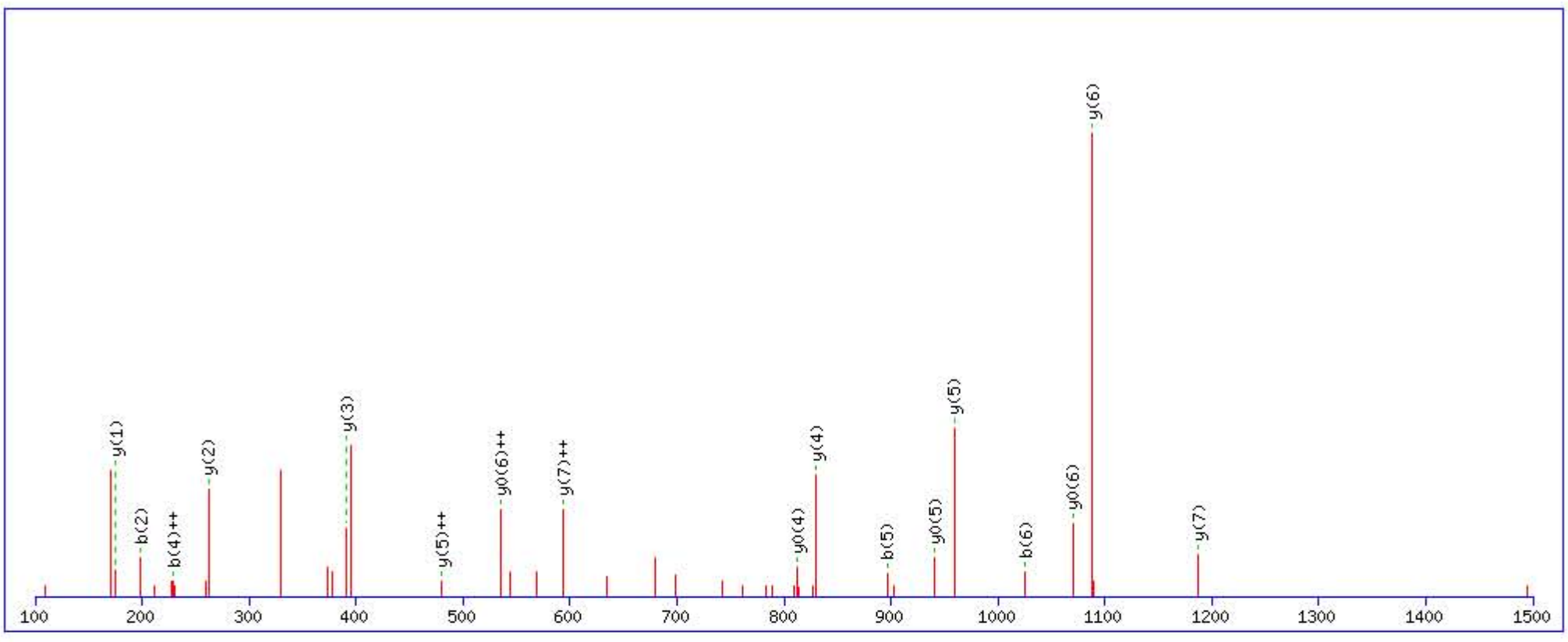
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VVEEQESR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

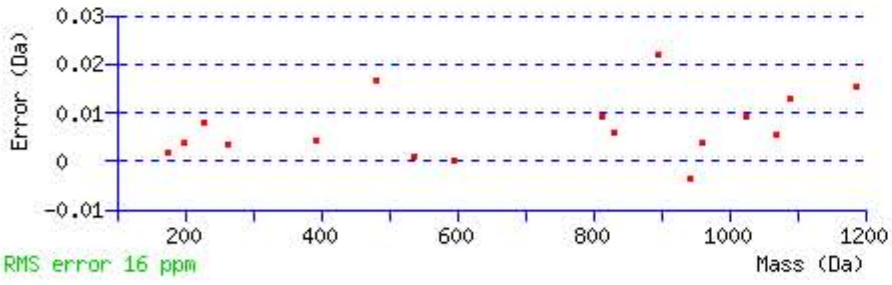
Match to Query 23024: 1285.640788 from(643.827670,2+) rtinseconds(1376) index(30286)
Title: Locus:1.1.1.587.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

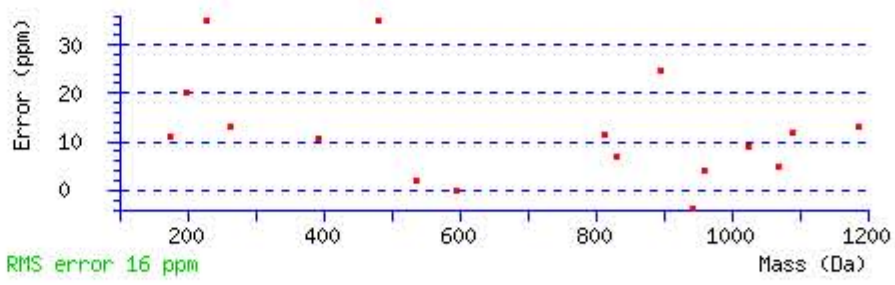
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1285.633621
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 47 **Expect:** 0.00042
**Matches :** 17/70 fragment ions using 28 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 8 |
| 2 | **199.144104** | 100.075690 | | | | | V | *1187.572499* | 594.289888 | 1170.545950 | 585.776613 | 1169.561934 | 585.284605 | 7 |
| 3 | 328.186697 | 164.596987 | | | 310.176132 | 155.591704 | E | *1088.504085* | 544.755681 | 1071.477536 | 536.242406 | 1070.493520 | 535.750398 | 6 |
| 4 | 457.229290 | 229.118283 | | | 439.218725 | 220.113001 | E | *959.461492* | 480.234384 | 942.434943 | 471.721110 | 941.450927 | 471.229102 | 5 |
| 5 | **896.454616** | 448.730946 | 879.428067 | 440.217672 | 878.444051 | 439.725664 | Q | *830.418899* | 415.713088 | 813.392350 | 407.199813 | 812.408334 | 406.707805 | 4 |
| 6 | **1025.497209** | 513.252243 | 1008.470660 | 504.738968 | 1007.486644 | 504.246960 | E | *391.193573* | 196.100425 | 374.167024 | 187.587150 | 373.183008 | 187.095142 | 3 |
| 7 | 1112.529237 | 556.768257 | 1095.502688 | 548.254982 | 1094.518672 | 547.762974 | S | *262.150980* | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 46.8 | 1285.633621 | 0.007167 | VVEEQESR |

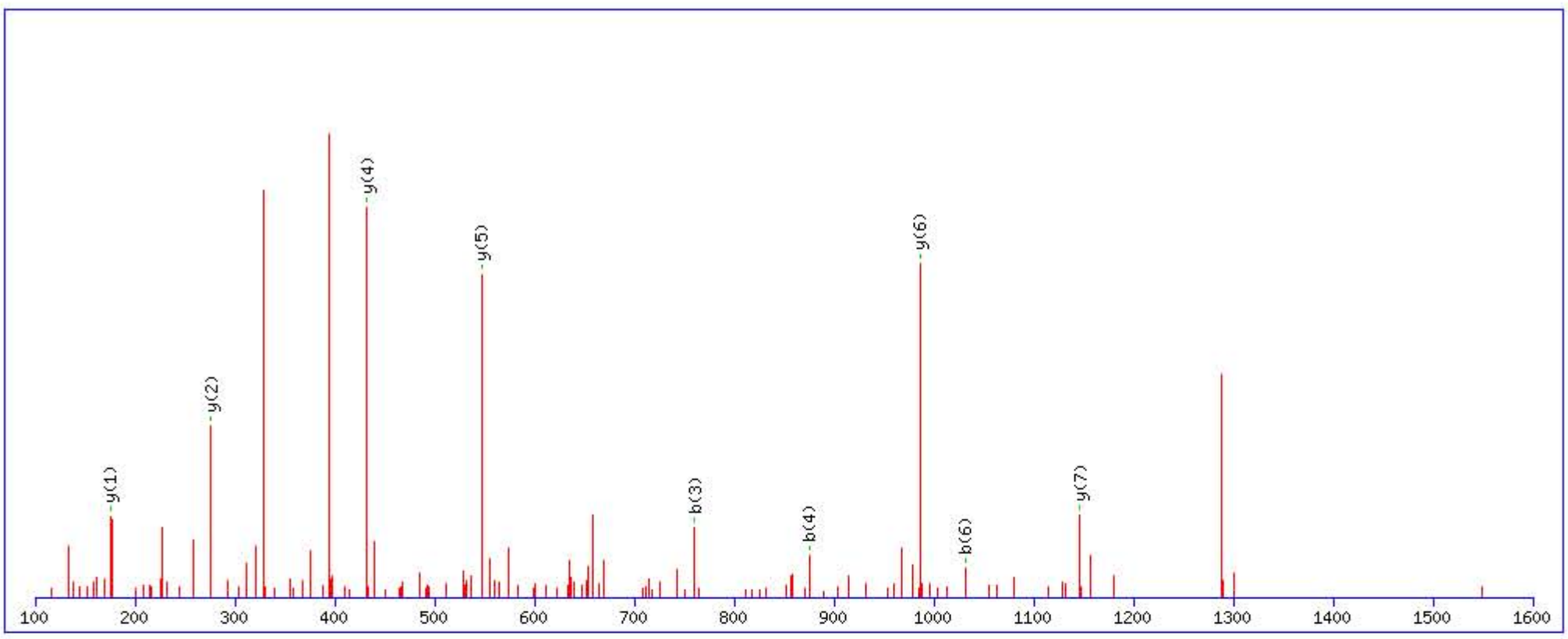
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **CCQDGVTR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

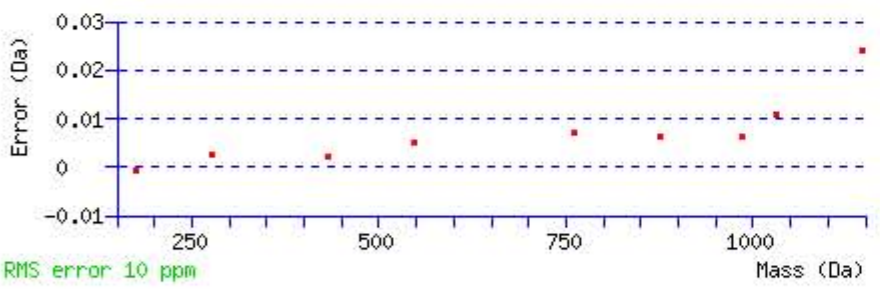
Match to Query 23417: 1305.571108 from(653.792830,2+) rtinseconds(1381) index(46230)
Title: Locus:1.1.1.1718.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

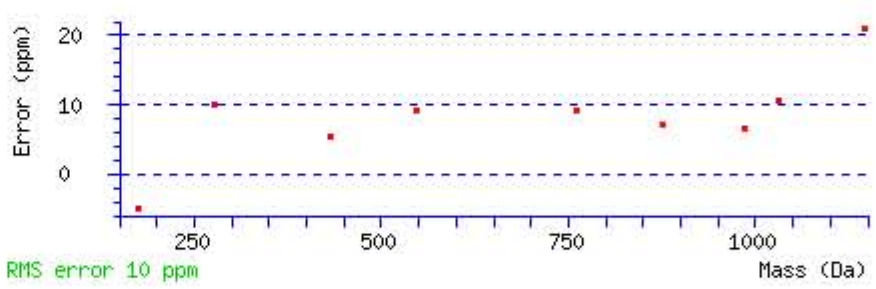
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1305.562820
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 50 **Expect:** 4.4e-005
**Matches :** 9/72 fragment ions using 12 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 161.037925 | 81.022600 | | | | | C | | | | | | | 8 |
| 2 | 321.068574 | 161.037925 | | | | | C | *1146.539427* | 573.773352 | 1129.512878 | 565.260077 | 1128.528862 | 564.768069 | 7 |
| 3 | **760.293900** | 380.650588 | 743.267351 | 372.137314 | | | Q | *986.508778* | 493.758027 | 969.482229 | 485.244753 | 968.498213 | 484.752745 | 6 |
| 4 | **875.320843** | 438.164060 | 858.294294 | 429.650785 | 857.310278 | 429.158777 | D | *547.283452* | 274.145364 | 530.256903 | 265.632090 | 529.272887 | 265.140082 | 5 |
| 5 | 932.342307 | 466.674792 | 915.315758 | 458.161517 | 914.331742 | 457.669509 | G | *432.256509* | 216.631893 | 415.229960 | 208.118618 | 414.245944 | 207.626610 | 4 |
| 6 | **1031.410721** | 516.208999 | 1014.384172 | 507.695724 | 1013.400156 | 507.203716 | V | 375.235045 | 188.121161 | 358.208496 | 179.607886 | 357.224480 | 179.115878 | 3 |
| 7 | 1132.458400 | 566.732838 | 1115.431851 | 558.219564 | 1114.447835 | 557.727556 | T | *276.166631* | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 50.4 | 1305.562820 | 0.008288 | CCQDGVTR |
| 19.7 | 1305.588409 | -0.017301 | CRSSTPADAWR |
| 9.1 | 1305.577194 | -0.006086 | CDAGWLADGSVR |
| 5.1 | 1305.562805 | 0.008303 | CCTSPSQR |
| 1.6 | 1305.556061 | 0.015047 | CSFSPWTEHR |
| 0.3 | 1305.583679 | -0.012571 | EQEPDFEEKR |
| 0.1 | 1305.588409 | -0.017301 | DGMEDFKRHR |

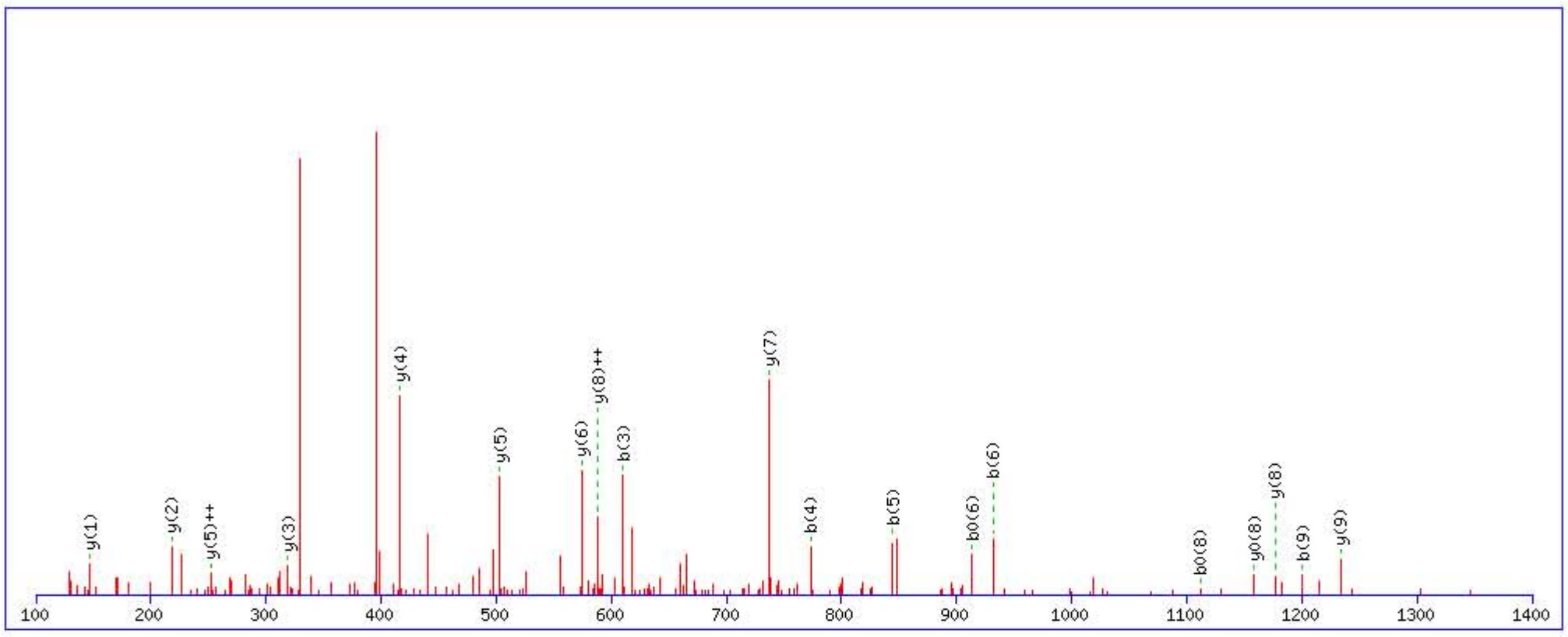
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LGQYASPTAK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

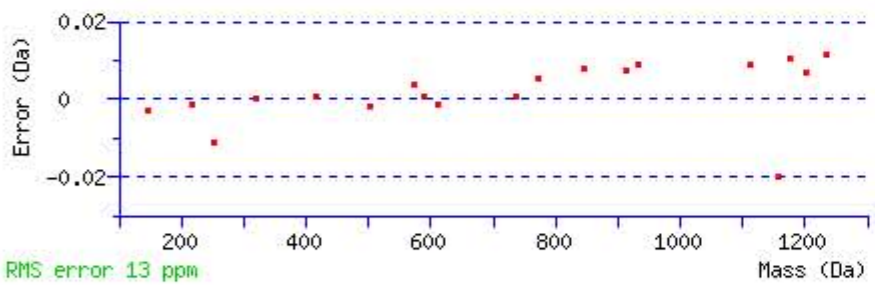
Match to Query 24292: 1345.715168 from(673.864860,2+) rtinseconds(1618) index(47773)
Title: Locus:1.1.1.1801.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

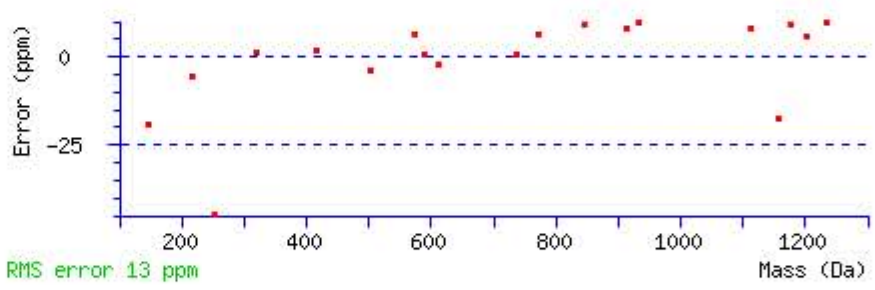
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1345.706390
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 3.9e-005
**Matches :** 19/90 fragment ions using 36 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 10 |
| 2 | 171.112804 | 86.060040 | | | | | G | *1233.629622* | 617.318449 | 1216.603073 | 608.805175 | 1215.619057 | 608.313167 | 9 |
| 3 | **610.338130** | 305.672703 | 593.311581 | 297.159429 | | | Q | *1176.608158* | 588.807717 | 1159.581609 | 580.294443 | 1158.597593 | 579.802435 | 8 |
| 4 | **773.401459** | 387.204368 | 756.374910 | 378.691093 | | | Y | *737.382832* | 369.195054 | 720.356283 | 360.681780 | 719.372267 | 360.189772 | 7 |
| 5 | **844.438573** | 422.722925 | 827.412024 | 414.209650 | | | A | *574.319503* | 287.663389 | 557.292954 | 279.150115 | 556.308938 | 278.658107 | 6 |
| 6 | **931.470601** | 466.238939 | 914.444052 | 457.725664 | 913.460036 | 457.233656 | S | *503.282389* | 252.144832 | 486.255840 | 243.631558 | 485.271824 | 243.139550 | 5 |
| 7 | 1028.523365 | 514.765321 | 1011.496816 | 506.252046 | 1010.512800 | 505.760038 | P | *416.250361* | 208.628818 | 399.223812 | 200.115544 | 398.239796 | 199.623536 | 4 |
| 8 | 1129.571044 | 565.289160 | 1112.544495 | 556.775886 | 1111.560479 | 556.283878 | T | *319.197597* | 160.102436 | 302.171048 | 151.589162 | 301.187032 | 151.097154 | 3 |
| 9 | **1200.608158** | 600.807717 | 1183.581609 | 592.294443 | 1182.597593 | 591.802435 | A | *218.149918* | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 10 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.1 | 1345.706390 | 0.008778 | LGQYASPTAK |
| 11.1 | 1345.706390 | 0.008778 | LGQYDQALK |
| 10.1 | 1345.724182 | -0.009014 | LGAVPATSGPTTFK |
| 9.0 | 1345.727509 | -0.012341 | DKLKMEVDQLK |
| 8.2 | 1345.727509 | -0.012341 | LGLMDNEIKVAK |
| 7.9 | 1345.706406 | 0.008762 | QGLYTPQTK |
| 2.5 | 1345.724152 | -0.008984 | QPLQTDIYGLAK |
| 1.7 | 1345.717636 | -0.002468 | QMPQPTFTLRK |
| 1.3 | 1345.713608 | 0.001560 | NGMLLTGGGKDRK |
| 0.7 | 1345.720993 | -0.005825 | QVGMICERLLK |

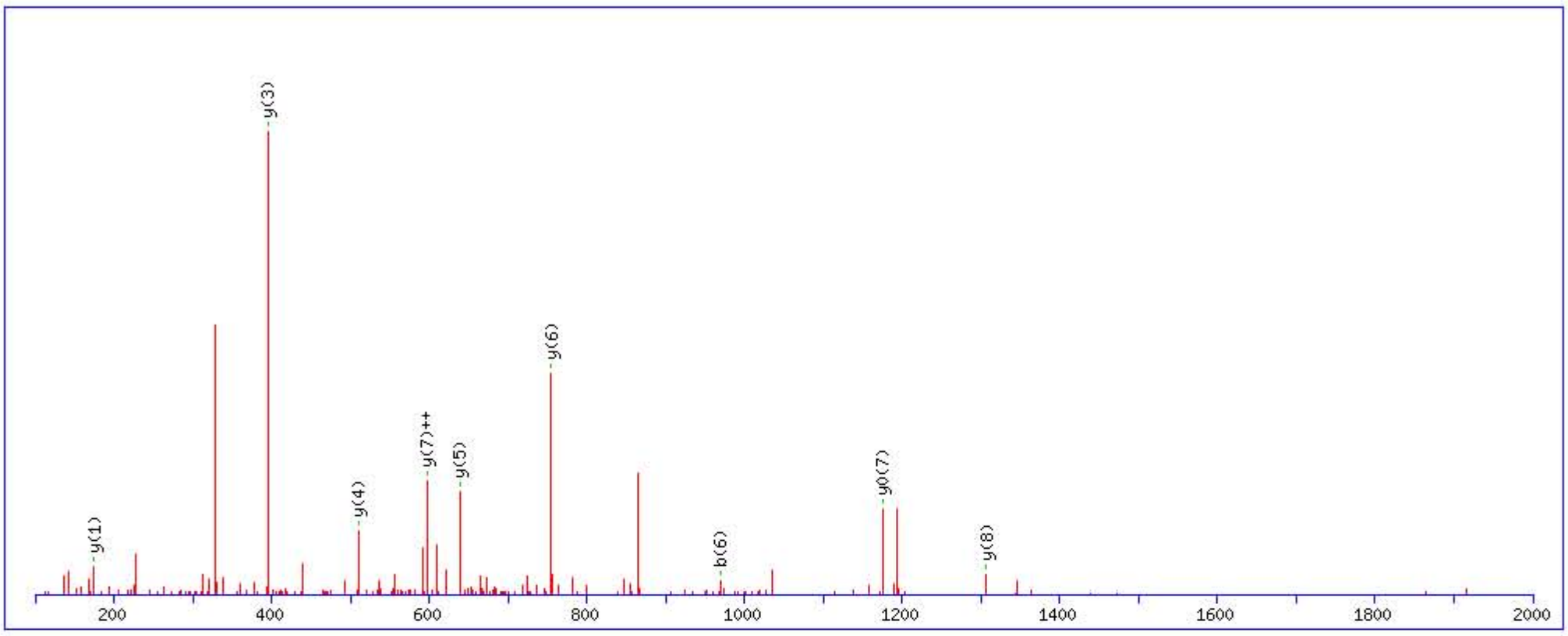
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GLQDEDGYR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

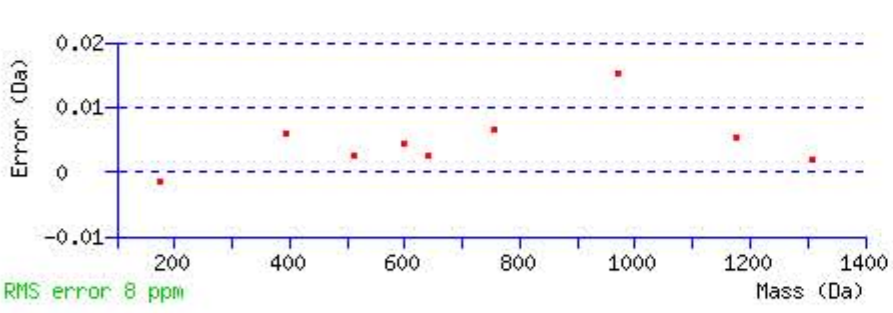
Match to Query 25943: 1362.632588 from(682.323570,2+) rtinseconds(1718) index(48398)
Title: Locus:1.1.1.1836.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

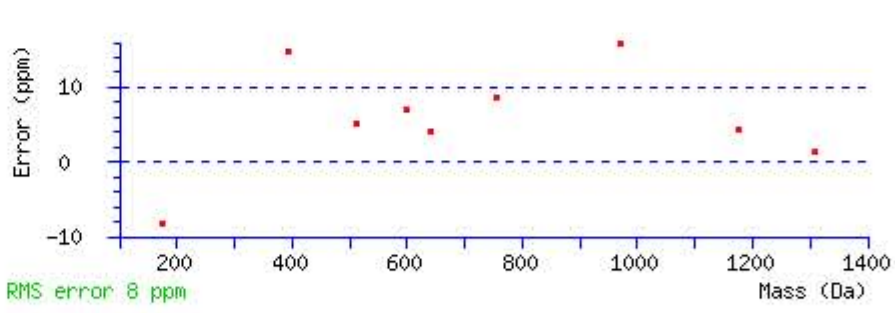
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1362.623795
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 47 **Expect:** 0.00014
**Matches :** 9/80 fragment ions using 13 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 9 |
| 2 | 171.112804 | 86.060040 | | | | | L | *1306.609614* | 653.808445 | 1289.583065 | 645.295171 | 1288.599049 | 644.803163 | 8 |
| 3 | 610.338130 | 305.672703 | 593.311581 | 297.159429 | | | Q | 1193.525550 | *597.266413* | 1176.499001 | 588.753139 | *1175.514985* | 588.261131 | 7 |
| 4 | 725.365073 | 363.186175 | 708.338524 | 354.672900 | 707.354508 | 354.180892 | D | *754.300224* | 377.653750 | 737.273675 | 369.140476 | 736.289659 | 368.648468 | 6 |
| 5 | 854.407666 | 427.707471 | 837.381117 | 419.194197 | 836.397101 | 418.702189 | E | *639.273281* | 320.140279 | 622.246732 | 311.627004 | 621.262716 | 311.134996 | 5 |
| 6 | **969.434609** | 485.220943 | 952.408060 | 476.707668 | 951.424044 | 476.215660 | D | *510.230688* | 255.618982 | 493.204139 | 247.105707 | 492.220123 | 246.613700 | 4 |
| 7 | 1026.456073 | 513.731675 | 1009.429524 | 505.218400 | 1008.445508 | 504.726392 | G | *395.203745* | 198.105511 | 378.177196 | 189.592236 | | | 3 |
| 8 | 1189.519402 | 595.263339 | 1172.492853 | 586.750065 | 1171.508837 | 586.258057 | Y | 338.182281 | 169.594778 | 321.155732 | 161.081504 | | | 2 |
| 9 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 46.8 | 1362.623795 | 0.008793 | GLQDEDGYR |
| 5.3 | 1362.652756 | -0.020168 | GLAADERAEFER |
| 3.0 | 1362.642883 | -0.010295 | GDRVYSPYNHR |
| 2.2 | 1362.623795 | 0.008793 | TGFLEIDEHMR |
| 0.6 | 1362.623795 | 0.008793 | GPAFPGMGSEELR |

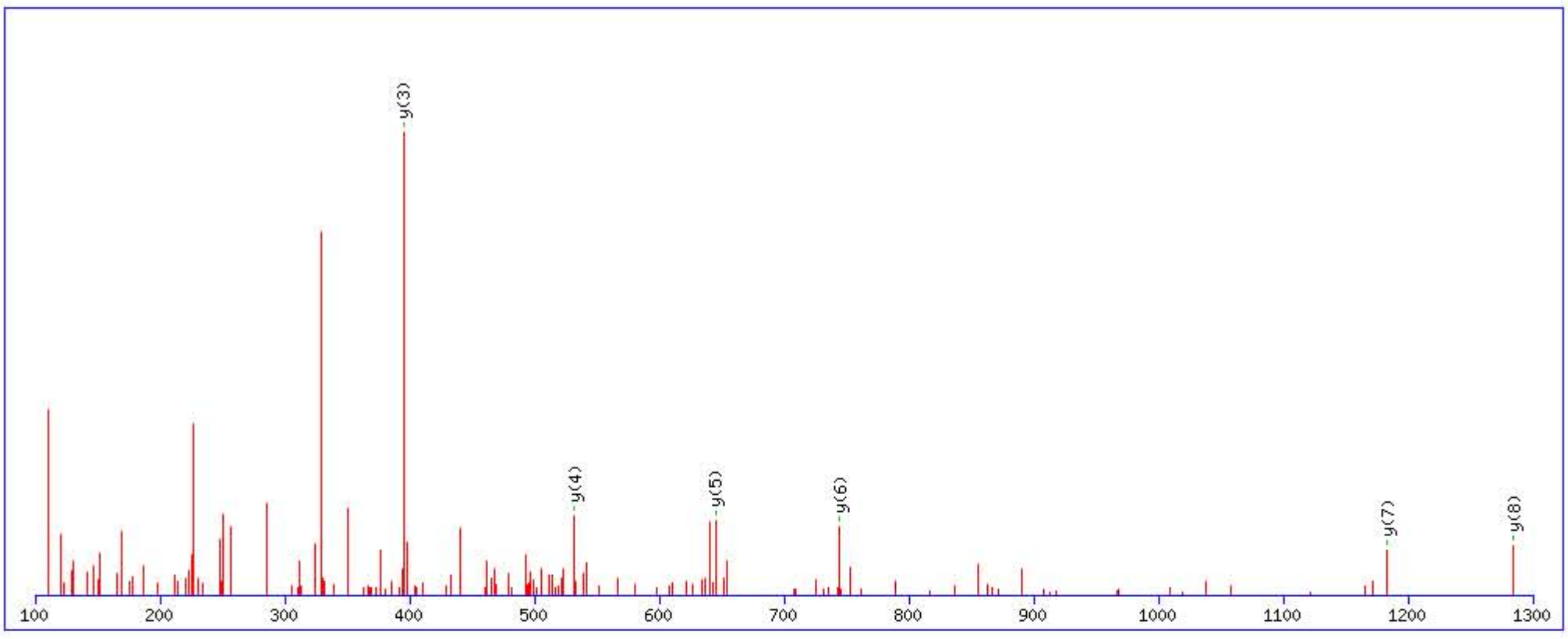
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ITQVLHFTK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

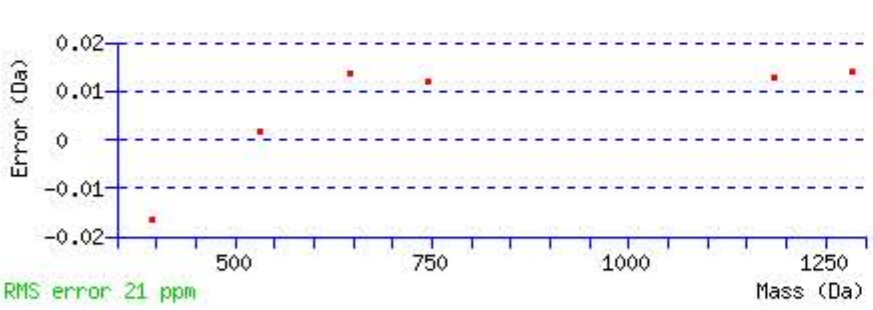
Match to Query 27226: 1396.790862 from(466.604230,3+) rtinseconds(1948) index(49973)
Title: Locus:1.1.1.1916.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

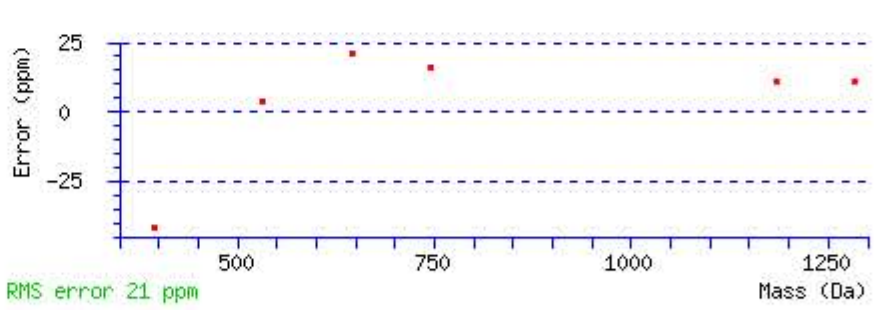
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1396.790085
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 34 **Expect:** 0.0015
**Matches :** 6/88 fragment ions using 12 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 9 |
| 2 | 215.139019 | 108.073147 | | | 197.128454 | 99.067865 | T | *1284.713292* | 642.860284 | 1267.686743 | 634.347010 | 1266.702727 | 633.855002 | 8 |
| 3 | 654.364345 | 327.685811 | 637.337796 | 319.172536 | 636.353780 | 318.680528 | Q | *1183.665613* | 592.336445 | 1166.639064 | 583.823170 | 1165.655048 | 583.331162 | 7 |
| 4 | 753.432759 | 377.220018 | 736.406210 | 368.706743 | 735.422194 | 368.214735 | V | *744.440287* | 372.723782 | 727.413738 | 364.210507 | 726.429722 | 363.718499 | 6 |
| 5 | 866.516823 | 433.762050 | 849.490274 | 425.248775 | 848.506258 | 424.756767 | L | *645.371873* | 323.189575 | 628.345324 | 314.676300 | 627.361308 | 314.184292 | 5 |
| 6 | 1003.575735 | 502.291506 | 986.549186 | 493.778231 | 985.565170 | 493.286223 | H | *532.287809* | 266.647543 | 515.261260 | 258.134268 | 514.277244 | 257.642260 | 4 |
| 7 | 1150.644149 | 575.825713 | 1133.617600 | 567.312438 | 1132.633584 | 566.820430 | F | *395.228897* | 198.118086 | 378.202348 | 189.604812 | 377.218332 | 189.112804 | 3 |
| 8 | 1251.691828 | 626.349552 | 1234.665279 | 617.836278 | 1233.681263 | 617.344270 | T | 248.160483 | 124.583879 | 231.133934 | 116.070605 | 230.149918 | 115.578597 | 2 |
| 9 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.7 | 1396.790085 | 0.000777 | ITQVLHFTK |
| 3.5 | 1396.792557 | -0.001695 | LLGELQEQIVQK |
| 1.8 | 1396.774796 | 0.016066 | LLQEGIAQSK |
| 1.2 | 1396.778625 | 0.012237 | ILIENGVAERQR |

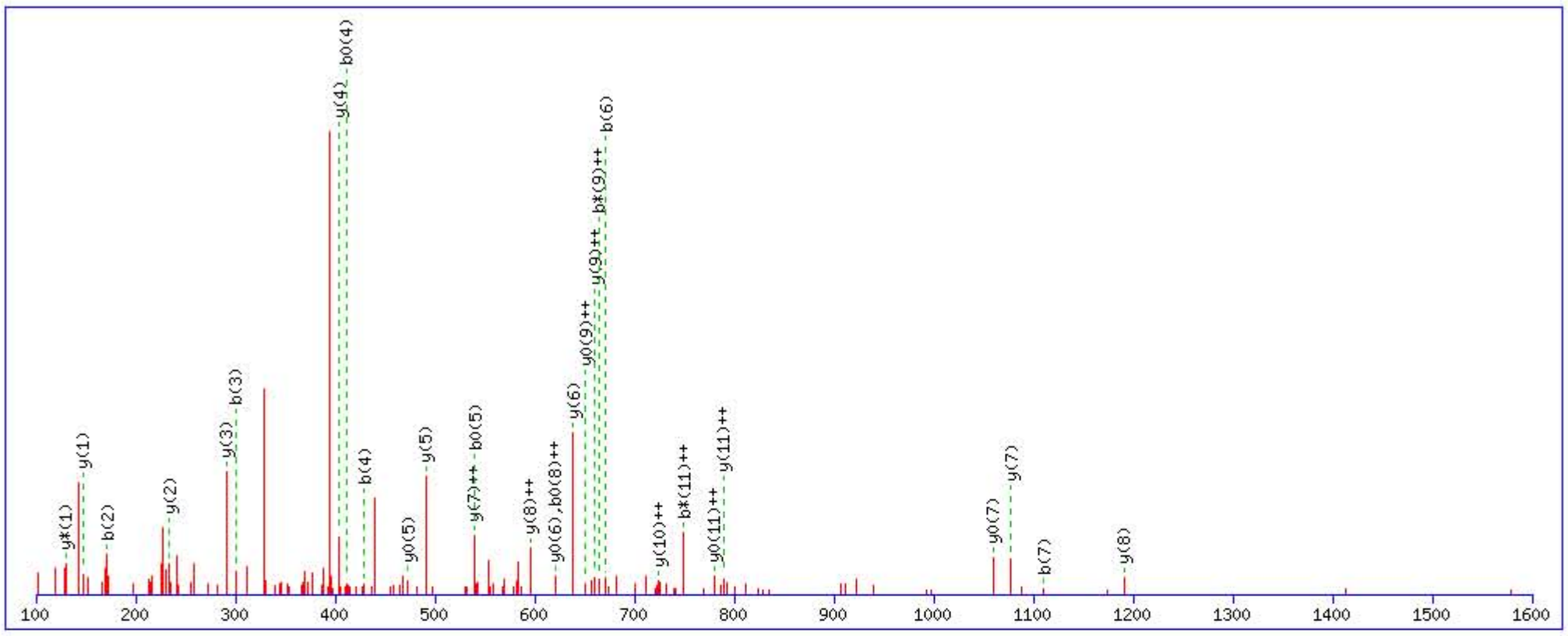
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GLEEELQFSLGSK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

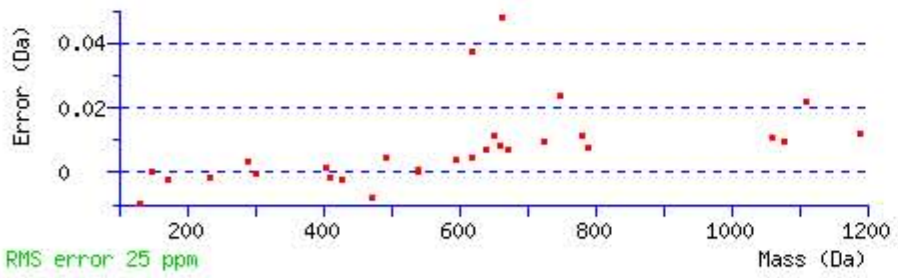
Match to Query 39030: 1746.901002 from(583.307610,3+) rtinseconds(2544) index(53587)
Title: Locus:1.1.1.2123.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

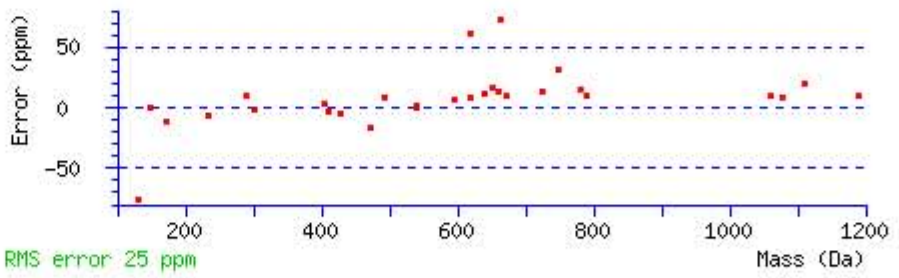
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1746.886200
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 29 **Expect:** 0.038
**Matches :** 29/126 fragment ions using 74 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 13 |
| 2 | *171.112804* | 86.060040 | | | | | L | 1690.872035 | 845.939656 | 1673.845486 | 837.426381 | 1672.861470 | 836.934373 | 12 |
| 3 | *300.155397* | 150.581336 | | | 282.144832 | 141.576054 | E | 1577.787971 | 789.397624 | 1560.761422 | 780.884349 | 1559.777406 | 780.392341 | 11 |
| 4 | *429.197990* | 215.102633 | | | 411.187425 | 206.097351 | E | 1448.745378 | 724.876327 | 1431.718829 | 716.363053 | 1430.734813 | 715.871045 | 10 |
| 5 | 558.240583 | 279.623930 | | | 540.230018 | 270.618647 | E | 1319.702785 | 660.355031 | 1302.676236 | 651.841756 | 1301.692220 | 651.349748 | 9 |
| 6 | *671.324647* | 336.165962 | | | 653.314082 | 327.160679 | L | *1190.660192* | 595.833734 | 1173.633643 | 587.320460 | 1172.649627 | 586.828452 | 8 |
| 7 | *1110.549973* | 555.778624 | 1093.523424 | 547.265350 | 1092.539408 | 546.773342 | Q | *1077.576128* | 539.291702 | 1060.549579 | 530.778428 | 1059.565563 | 530.286419 | 7 |
| 8 | 1257.618387 | 629.312832 | 1240.591838 | 620.799557 | 1239.607822 | 620.307549 | F | *638.350802* | 319.679039 | 621.324253 | 311.165765 | 620.340237 | 310.673757 | 6 |
| 9 | 1344.650415 | 672.828846 | 1327.623866 | 664.315571 | 1326.639850 | 663.823563 | S | *491.282388* | 246.144832 | 474.255839 | 237.631557 | 473.271823 | 237.139549 | 5 |
| 10 | 1457.734479 | 729.370878 | 1440.707930 | 720.857603 | 1439.723914 | 720.365595 | L | *404.250360* | 202.628818 | 387.223811 | 194.115543 | 386.239795 | 193.623535 | 4 |
| 11 | 1514.755943 | 757.881609 | 1497.729394 | 749.368335 | 1496.745378 | 748.876327 | G | *291.166296* | 146.086786 | 274.139747 | 137.573512 | 273.155731 | 137.081504 | 3 |
| 12 | 1601.787971 | 801.397624 | 1584.761422 | 792.884349 | 1583.777406 | 792.392341 | S | *234.144832* | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 13 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 28.6 | 1746.886200 | 0.014802 | GLEEELQFSLGSK |

**Mascot:** http://www.matrixscience.com/

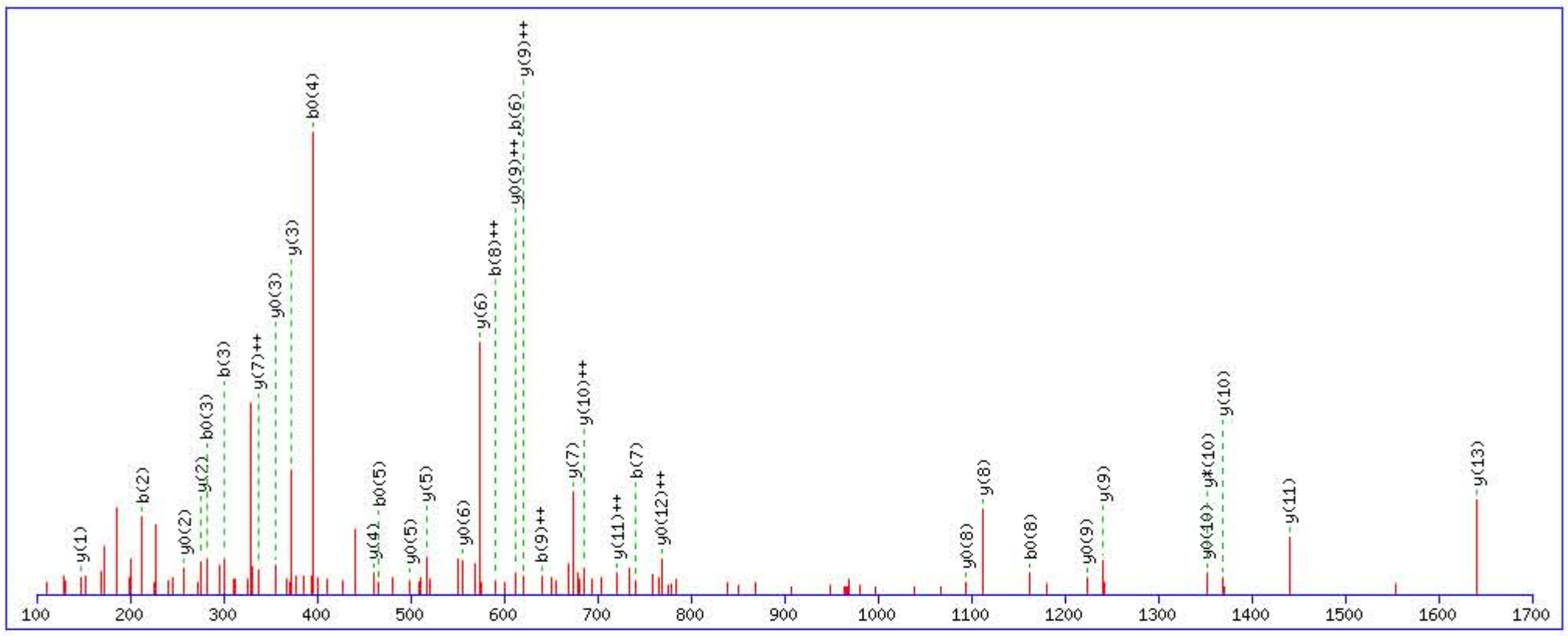
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VLSLAQEQVGGSPEK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

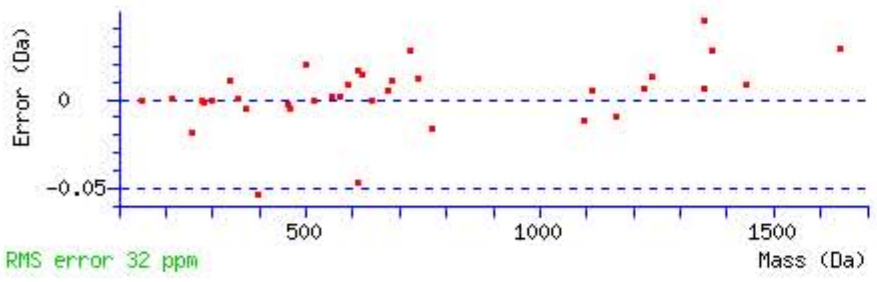
Match to Query 41289: 1851.988242 from(618.336690,3+) rtinseconds(1981) index(50251)
Title: Locus:1.1.1.1927.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

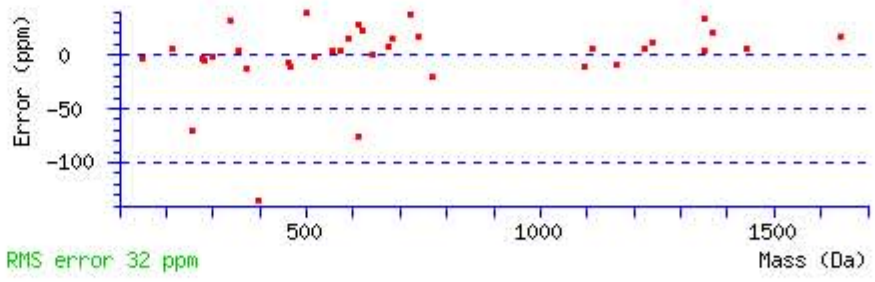
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1851.976425
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 3.5e-005
**Matches :** 36/152 fragment ions using 83 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 15 |
| 2 | **213.159754** | 107.083515 | | | | | L | 1753.915298 | 877.461287 | 1736.888749 | 868.948013 | 1735.904733 | 868.456004 | 14 |
| 3 | **300.191782** | 150.599529 | | | 282.181217 | 141.594247 | S | *1640.831234* | 820.919255 | 1623.804685 | 812.405981 | 1622.820669 | 811.913973 | 13 |
| 4 | 413.275846 | 207.141561 | | | 395.265281 | 198.136279 | L | 1553.799206 | 777.403241 | 1536.772657 | 768.889967 | 1535.788641 | 768.397958 | 12 |
| 5 | 484.312960 | 242.660118 | | | 466.302395 | 233.654836 | A | *1440.715142* | 720.861209 | 1423.688593 | 712.347935 | 1422.704577 | 711.855927 | 11 |
| 6 | **612.371538** | 306.689407 | 595.344989 | 298.176133 | 594.360973 | 297.684125 | Q | *1369.678028* | 685.342652 | 1352.651479 | 676.829378 | 1351.667463 | 676.337370 | 10 |
| 7 | **741.414131** | 371.210704 | 724.387582 | 362.697429 | 723.403566 | 362.205421 | E | *1241.619450* | 621.313363 | 1224.592901 | 612.800089 | 1223.608885 | 612.308080 | 9 |
| 8 | 1180.639457 | **590.823367** | 1163.612908 | 582.310092 | 1162.628892 | 581.818084 | Q | *1112.576857* | 556.792066 | 1095.550308 | 548.278792 | 1094.566292 | 547.786784 | 8 |
| 9 | 1279.707871 | **640.357574** | 1262.681322 | 631.844299 | 1261.697306 | 631.352291 | V | *673.351531* | 337.179404 | 656.324982 | 328.666129 | 655.340966 | 328.174121 | 7 |
| 10 | 1336.729335 | 668.868306 | 1319.702786 | 660.355031 | 1318.718770 | 659.863023 | G | *574.283117* | 287.645197 | 557.256568 | 279.131922 | 556.272552 | 278.639914 | 6 |
| 11 | 1393.750799 | 697.379037 | 1376.724250 | 688.865763 | 1375.740234 | 688.373755 | G | *517.261653* | 259.134465 | 500.235104 | 250.621190 | 499.251088 | 250.129182 | 5 |
| 12 | 1480.782827 | 740.895052 | 1463.756278 | 732.381777 | 1462.772262 | 731.889769 | S | *460.240189* | 230.623732 | 443.213640 | 222.110458 | 442.229624 | 221.618450 | 4 |
| 13 | 1577.835591 | 789.421434 | 1560.809042 | 780.908159 | 1559.825026 | 780.416151 | P | *373.208161* | 187.107718 | 356.181612 | 178.594444 | 355.197596 | 178.102436 | 3 |
| 14 | 1706.878184 | 853.942730 | 1689.851635 | 845.429456 | 1688.867619 | 844.937447 | E | *276.155397* | 138.581336 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 15 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.2 | 1851.976425 | 0.011817 | VLSLAQEQVGGSPEK |
| 35.4 | 1851.976425 | 0.011817 | VLSLAQEQVGGSPEK |

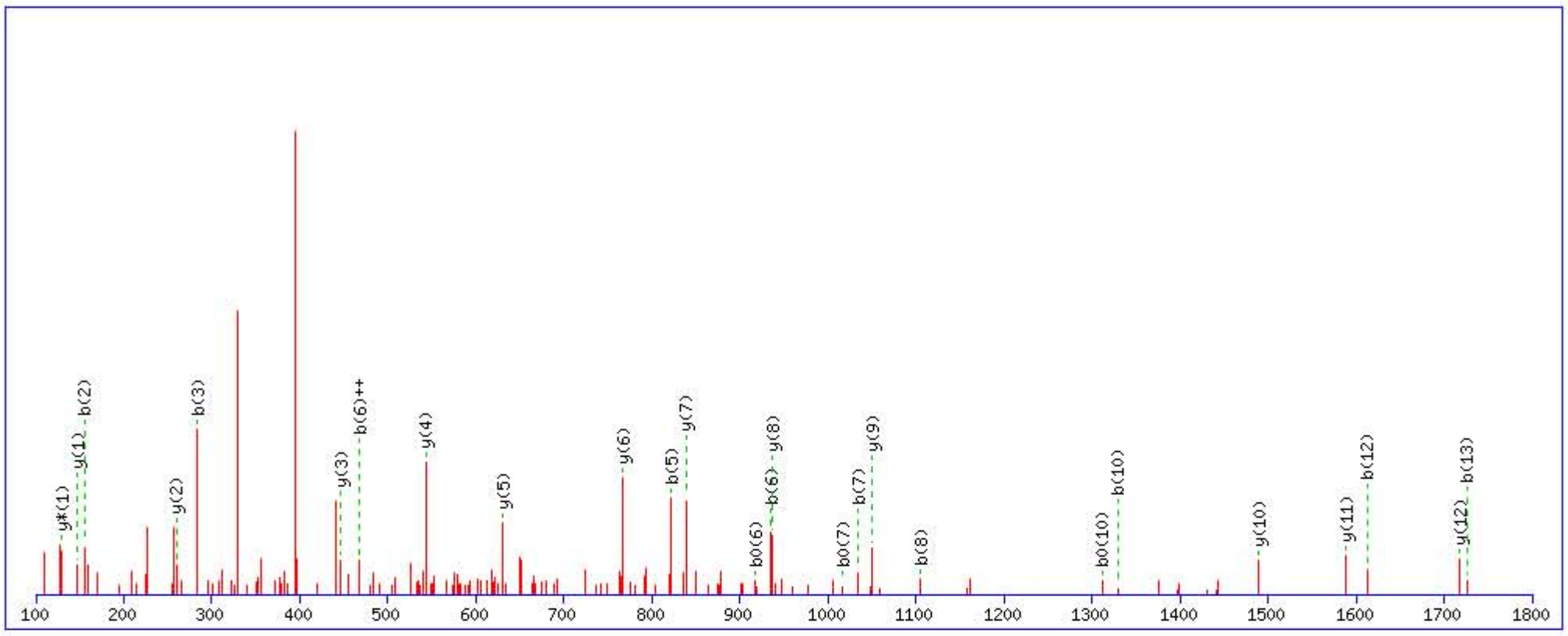
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GPEVQLVAHSPWLK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

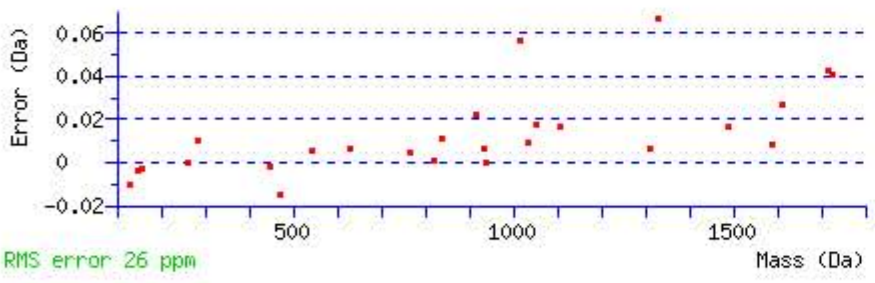
Match to Query 41721: 1871.029962 from(624.683930,3+) rtinseconds(2228) index(51842)
Title: Locus:1.1.1.2013.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

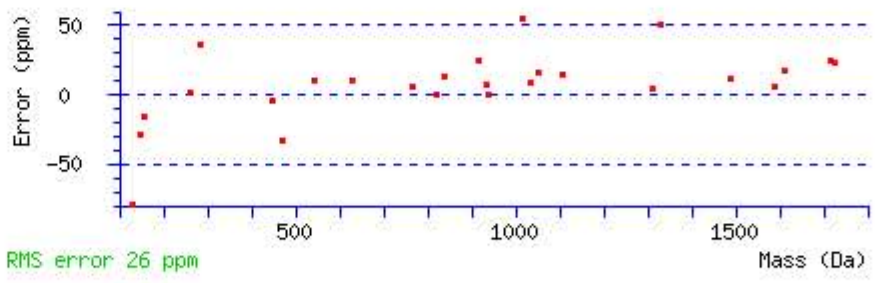
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1871.012756
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 57 **Expect:** 6.9e-006
**Matches** : 26/136 fragment ions using 65 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 14 |
| 2 | **155.081504** | 78.044390 | | | | | P | 1814.998574 | 908.002925 | 1797.972025 | 899.489651 | 1796.988009 | 898.997643 | 13 |
| 3 | **284.124097** | 142.565687 | | | 266.113532 | 133.560404 | E | *1717.945810* | 859.476543 | 1700.919261 | 850.963269 | 1699.935245 | 850.471261 | 12 |
| 4 | 383.192511 | 192.099894 | | | 365.181946 | 183.094611 | V | *1588.903217* | 794.955247 | 1571.876668 | 786.441972 | 1570.892652 | 785.949964 | 11 |
| 5 | **822.417837** | 411.712557 | 805.391288 | 403.199282 | 804.407272 | 402.707274 | Q | *1489.834803* | 745.421040 | 1472.808254 | 736.907765 | 1471.824238 | 736.415757 | 10 |
| 6 | **935.501901** | 468.254589 | 918.475352 | 459.741314 | 917.491336 | 459.249306 | L | *1050.609477* | 525.808377 | 1033.582928 | 517.295102 | 1032.598912 | 516.803094 | 9 |
| 7 | **1034.570315** | 517.788796 | 1017.543766 | 509.275521 | 1016.559750 | 508.783513 | V | *937.525413* | 469.266345 | 920.498864 | 460.753070 | 919.514848 | 460.261062 | 8 |
| 8 | **1105.607429** | 553.307353 | 1088.580880 | 544.794078 | 1087.596864 | 544.302070 | A | *838.456999* | 419.732138 | 821.430450 | 411.218863 | 820.446434 | 410.726855 | 7 |
| 9 | 1242.666341 | 621.836809 | 1225.639792 | 613.323534 | 1224.655776 | 612.831526 | H | *767.419885* | 384.213581 | 750.393336 | 375.700306 | 749.409320 | 375.208298 | 6 |
| 10 | **1329.698369** | 665.352823 | 1312.671820 | 656.839548 | 1311.687804 | 656.347540 | S | *630.360973* | 315.684125 | 613.334424 | 307.170850 | 612.350408 | 306.678842 | 5 |
| 11 | 1426.751133 | 713.879205 | 1409.724584 | 705.365930 | 1408.740568 | 704.873922 | P | *543.328945* | 272.168111 | 526.302396 | 263.654836 | | | 4 |
| 12 | **1612.830446** | 806.918861 | 1595.803897 | 798.405587 | 1594.819881 | 797.913579 | W | *446.276181* | 223.641728 | 429.249632 | 215.128454 | | | 3 |
| 13 | **1725.914510** | 863.460893 | 1708.887961 | 854.947619 | 1707.903945 | 854.455611 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 14 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 57.1 | 1871.012756 | 0.017206 | GPEVQLVAHSPWLK |
| 1.9 | 1871.037231 | -0.007269 | ISKLLMICQNAGISVPK |
| 0.1 | 1871.037689 | -0.007727 | ILRPDATKNARNDFLK |

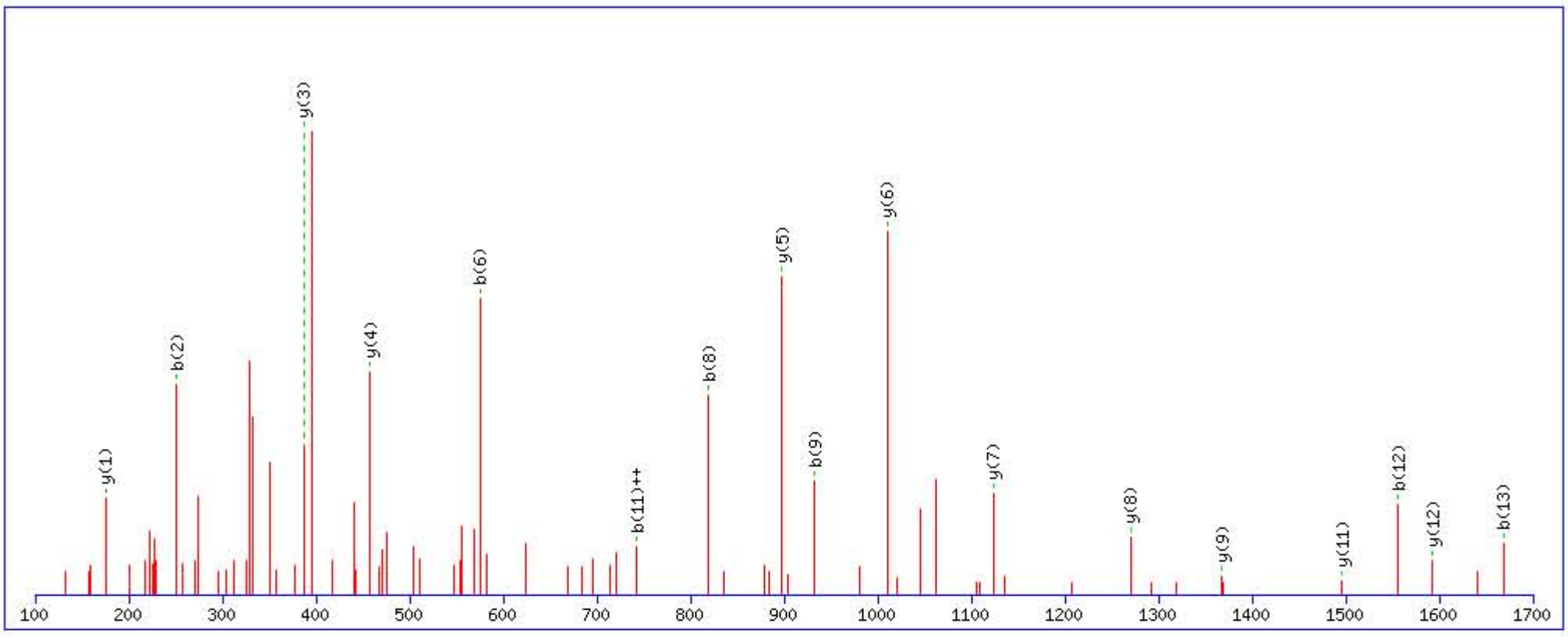
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HLVPGAPFLLQALVR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

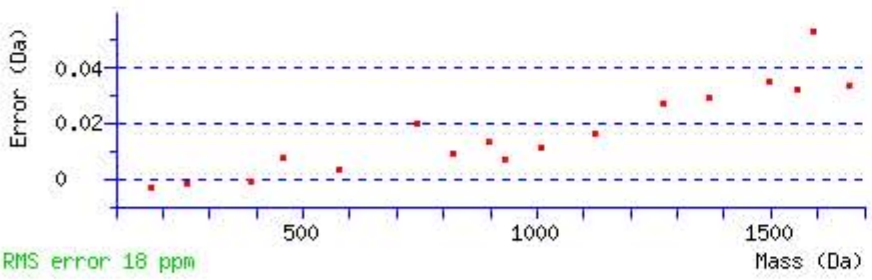
Match to Query 42959: 1941.162702 from(648.061510,3+) rtinseconds(2855) index(55999)
Title: Locus:1.1.1.2229.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

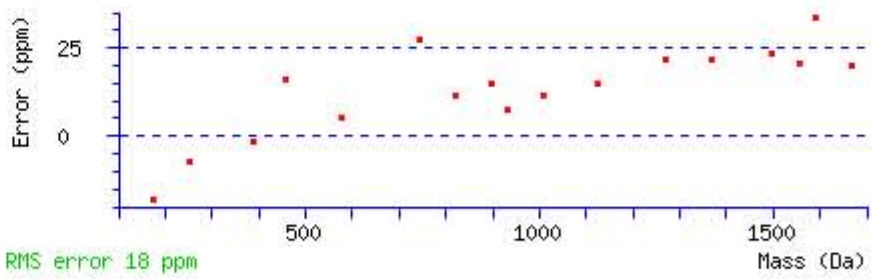
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1941.138626
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q11 : Biotin:Thermo-21345 (Q)
**Ions Score:** 60 **Expect:** 1.5e-006
**Matches :** 17/92 fragment ions using 31 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | H | | | | | 15 |
| 2 | **251.150252** | 126.078764 | | | L | 1805.086996 | 903.047136 | 1788.060447 | 894.533862 | 14 |
| 3 | 350.218666 | 175.612971 | | | V | 1692.002932 | 846.505104 | 1674.976383 | 837.991830 | 13 |
| 4 | 447.271430 | 224.139353 | | | P | *1592.934518* | 796.970897 | 1575.907969 | 788.457623 | 12 |
| 5 | 504.292894 | 252.650085 | | | G | *1495.881754* | 748.444515 | 1478.855205 | 739.931241 | 11 |
| 6 | **575.330008** | 288.168642 | | | A | 1438.860290 | 719.933783 | 1421.833741 | 711.420509 | 10 |
| 7 | 672.382772 | 336.695024 | | | P | *1367.823176* | 684.415226 | 1350.796627 | 675.901952 | 9 |
| 8 | **819.451186** | 410.229231 | | | F | *1270.770412* | 635.888844 | 1253.743863 | 627.375570 | 8 |
| 9 | **932.535250** | 466.771263 | | | L | *1123.701998* | 562.354637 | 1106.675449 | 553.841363 | 7 |
| 10 | 1045.619314 | 523.313295 | | | L | *1010.617934* | 505.812605 | 993.591385 | 497.299331 | 6 |
| 11 | 1484.844640 | 742.925958 | 1467.818091 | 734.412684 | Q | *897.533870* | 449.270573 | 880.507321 | 440.757298 | 5 |
| 12 | **1555.881754** | 778.444515 | 1538.855205 | 769.931241 | A | *458.308544* | 229.657910 | 441.281995 | 221.144635 | 4 |
| 13 | **1668.965818** | 834.986547 | 1651.939269 | 826.473273 | L | *387.271430* | 194.139353 | 370.244881 | 185.626078 | 3 |
| 14 | 1768.034232 | 884.520754 | 1751.007683 | 876.007480 | V | 274.187366 | 137.597321 | 257.160817 | 129.084047 | 2 |
| 15 | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 59.8 | 1941.138626 | 0.024076 | HLVPGAPFLLQALVR |

**Mascot:** http://www.matrixscience.com/

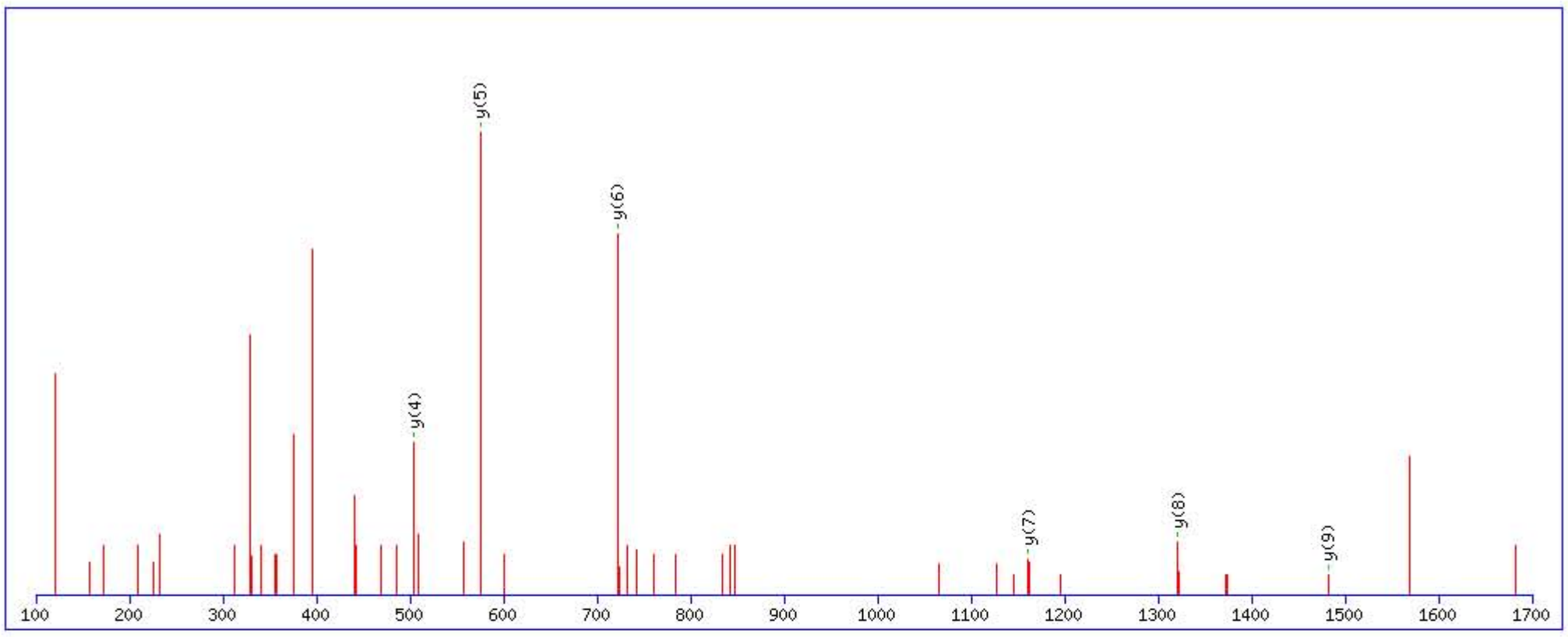
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EPFLSCCQFAESLR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

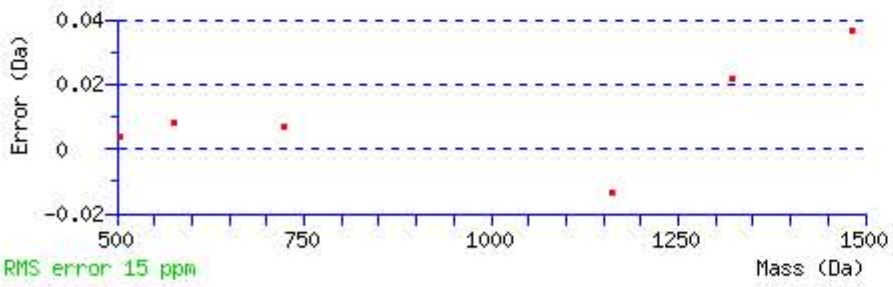
Match to Query 45812: 2053.967652 from(685.663160,3+) rtinseconds(2491) index(37010)
Title: Locus:1.1.1.976.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

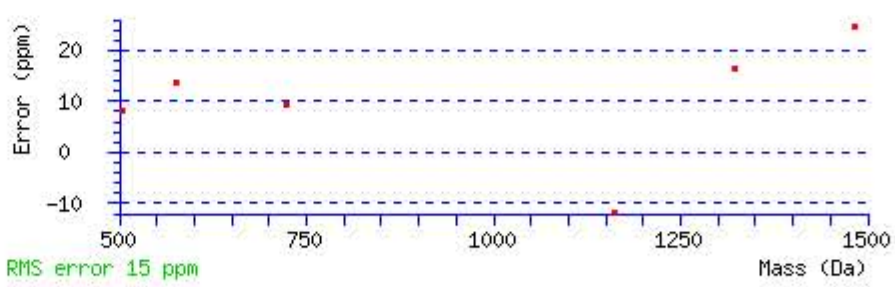
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2053.942368
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 28 **Expect:** 0.025
**Matches :** 6/138 fragment ions using 13 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 14 |
| 2 | 227.102633 | 114.054954 | | | 209.092068 | 105.049672 | P | 1925.907059 | 963.457168 | 1908.880510 | 954.943893 | 1907.896494 | 954.451885 | 13 |
| 3 | 374.171047 | 187.589161 | | | 356.160482 | 178.583879 | F | 1828.854295 | 914.930786 | 1811.827746 | 906.417511 | 1810.843730 | 905.925503 | 12 |
| 4 | 487.255111 | 244.131193 | | | 469.244546 | 235.125911 | L | 1681.785881 | 841.396579 | 1664.759332 | 832.883304 | 1663.775316 | 832.391296 | 11 |
| 5 | 574.287139 | 287.647208 | | | 556.276574 | 278.641925 | S | 1568.701817 | 784.854547 | 1551.675268 | 776.341272 | 1550.691252 | 775.849264 | 10 |
| 6 | 734.317788 | 367.662532 | | | 716.307223 | 358.657250 | C | *1481.669789* | 741.338533 | 1464.643240 | 732.825258 | 1463.659224 | 732.333250 | 9 |
| 7 | 894.348437 | 447.677857 | | | 876.337872 | 438.672574 | C | *1321.639140* | 661.323208 | 1304.612591 | 652.809934 | 1303.628575 | 652.317926 | 8 |
| 8 | 1333.573763 | 667.290520 | 1316.547214 | 658.777245 | 1315.563198 | 658.285237 | Q | *1161.608491* | 581.307884 | 1144.581942 | 572.794609 | 1143.597926 | 572.302601 | 7 |
| 9 | 1480.642177 | 740.824727 | 1463.615628 | 732.311452 | 1462.631612 | 731.819444 | F | *722.383165* | 361.695221 | 705.356616 | 353.181946 | 704.372600 | 352.689938 | 6 |
| 10 | 1551.679291 | 776.343284 | 1534.652742 | 767.830009 | 1533.668726 | 767.338001 | A | *575.314751* | 288.161014 | 558.288202 | 279.647739 | 557.304186 | 279.155731 | 5 |
| 11 | 1680.721884 | 840.864580 | 1663.695335 | 832.351306 | 1662.711319 | 831.859298 | E | *504.277637* | 252.642457 | 487.251088 | 244.129182 | 486.267072 | 243.637174 | 4 |
| 12 | 1767.753912 | 884.380594 | 1750.727363 | 875.867320 | 1749.743347 | 875.375312 | S | 375.235044 | 188.121160 | 358.208495 | 179.607885 | 357.224479 | 179.115877 | 3 |
| 13 | 1880.837976 | 940.922626 | 1863.811427 | 932.409352 | 1862.827411 | 931.917344 | L | 288.203016 | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 14 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 28.3 | 2053.942368 | 0.025284 | EPFLSCCQFAESLR |

**Mascot:** http://www.matrixscience.com/

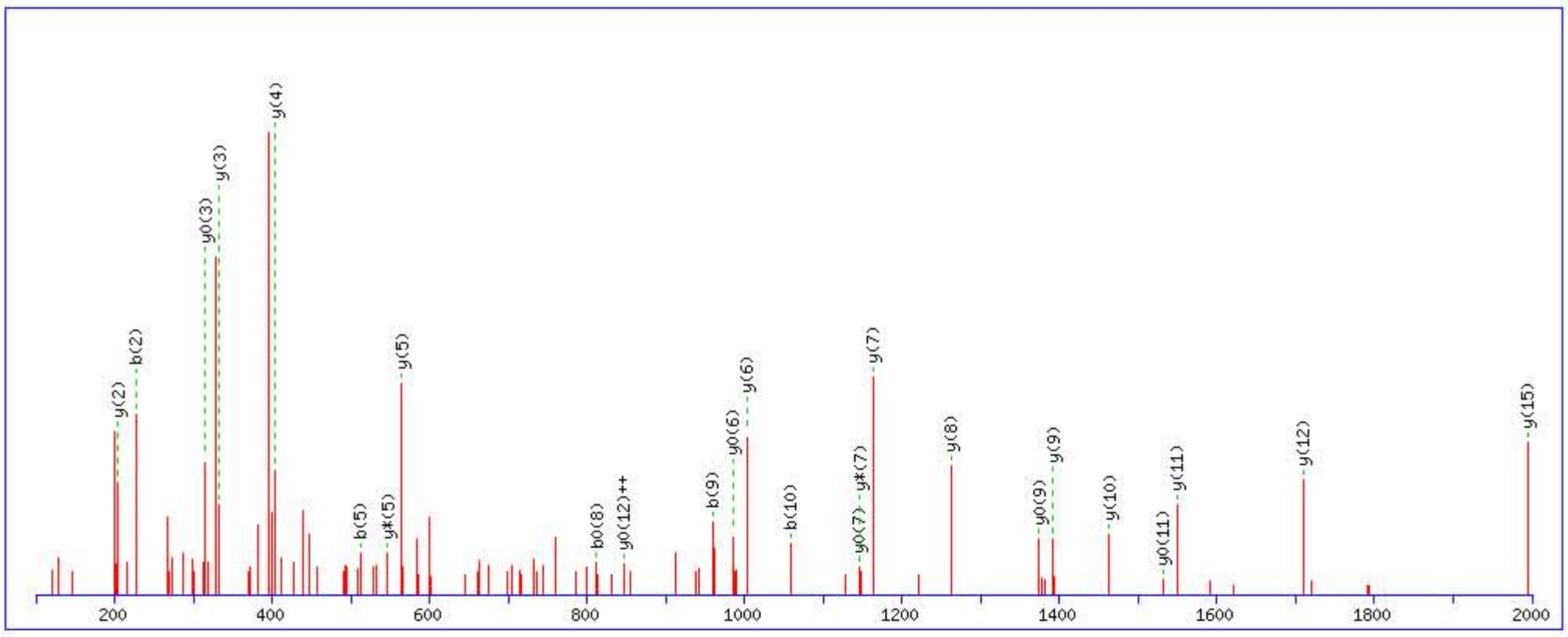
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LLATLCSAEVCQCAEGK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

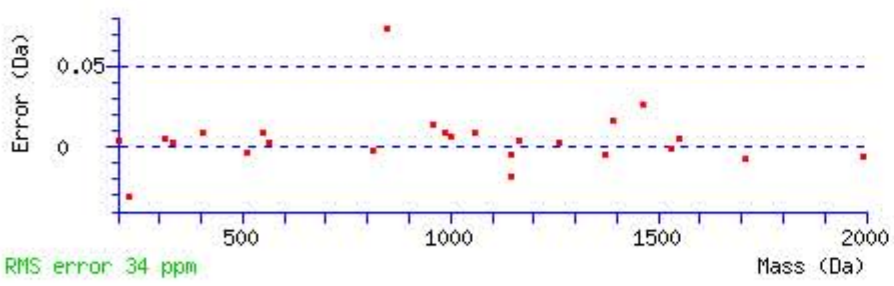
Match to Query 48946: 2220.056982 from(741.026270,3+) rtinseconds(2115) index(67084)
Title: Locus:1.1.1.2011.11 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

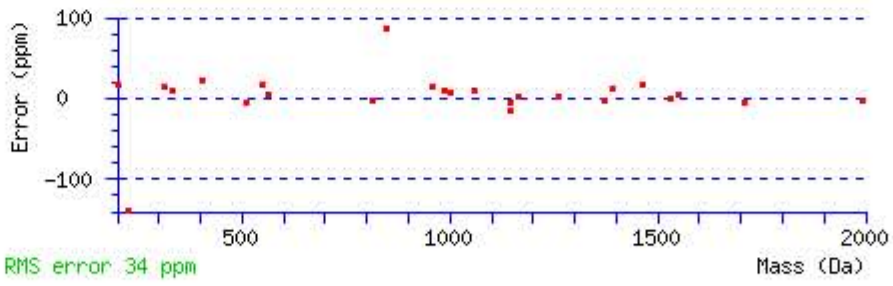
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2220.041092
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 55 **Expect:** 2e-005
**Matches :** 25/160 fragment ions using 60 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 17 |
| 2 | **227.175404** | 114.091340 | | | | | L | 2107.964318 | 1054.485797 | 2090.937769 | 1045.972522 | 2089.953753 | 1045.480514 | 16 |
| 3 | 298.212518 | 149.609897 | | | | | A | *1994.880254* | 997.943765 | 1977.853705 | 989.430491 | 1976.869689 | 988.938483 | 15 |
| 4 | 399.260197 | 200.133737 | | | 381.249632 | 191.128454 | T | 1923.843140 | 962.425208 | 1906.816591 | 953.911934 | 1905.832575 | 953.419926 | 14 |
| 5 | **512.344261** | 256.675769 | | | 494.333696 | 247.670486 | L | 1822.795461 | 911.901369 | 1805.768912 | 903.388094 | 1804.784896 | 902.896086 | 13 |
| 6 | 672.374910 | 336.691093 | | | 654.364345 | 327.685811 | C | *1709.711397* | 855.359337 | 1692.684848 | 846.846062 | 1691.700832 | 846.354054 | 12 |
| 7 | 759.406938 | 380.207107 | | | 741.396373 | 371.201825 | S | *1549.680748* | 775.344012 | 1532.654199 | 766.830738 | 1531.670183 | 766.338730 | 11 |
| 8 | 830.444052 | 415.725664 | | | 812.433487 | 406.720382 | A | *1462.648720* | 731.827998 | 1445.622171 | 723.314724 | 1444.638155 | 722.822716 | 10 |
| 9 | **959.486645** | 480.246961 | | | 941.476080 | 471.241678 | E | *1391.611606* | 696.309441 | 1374.585057 | 687.796167 | 1373.601041 | 687.304159 | 9 |
| 10 | **1058.555059** | 529.781168 | | | 1040.544494 | 520.775885 | V | *1262.569013* | 631.788145 | 1245.542464 | 623.274870 | 1244.558448 | 622.782862 | 8 |
| 11 | 1218.585708 | 609.796492 | | | 1200.575143 | 600.791210 | C | *1163.500599* | 582.253938 | 1146.474050 | 573.740663 | 1145.490034 | 573.248655 | 7 |
| 12 | 1657.811034 | 829.409155 | 1640.784485 | 820.895881 | 1639.800469 | 820.403873 | Q | *1003.469950* | 502.238613 | 986.443401 | 493.725339 | 985.459385 | 493.233331 | 6 |
| 13 | 1817.841683 | 909.424480 | 1800.815134 | 900.911205 | 1799.831118 | 900.419197 | C | *564.244624* | 282.625950 | 547.218075 | 274.112676 | 546.234059 | 273.620668 | 5 |
| 14 | 1888.878797 | 944.943037 | 1871.852248 | 936.429762 | 1870.868232 | 935.937754 | A | *404.213975* | 202.610626 | 387.187426 | 194.097351 | 386.203410 | 193.605343 | 4 |
| 15 | 2017.921390 | 1009.464333 | 2000.894841 | 1000.951059 | 1999.910825 | 1000.459051 | E | *333.176861* | 167.092069 | 316.150312 | 158.578794 | 315.166296 | 158.086786 | 3 |
| 16 | 2074.942854 | 1037.975065 | 2057.916305 | 1029.461790 | 2056.932289 | 1028.969782 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 17 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 54.6 | 2220.041092 | 0.015890 | LLATLCSAEVCQCAEGK |
| 4.5 | 2220.048080 | 0.008902 | EPQEGAELPEATGTTSHR |

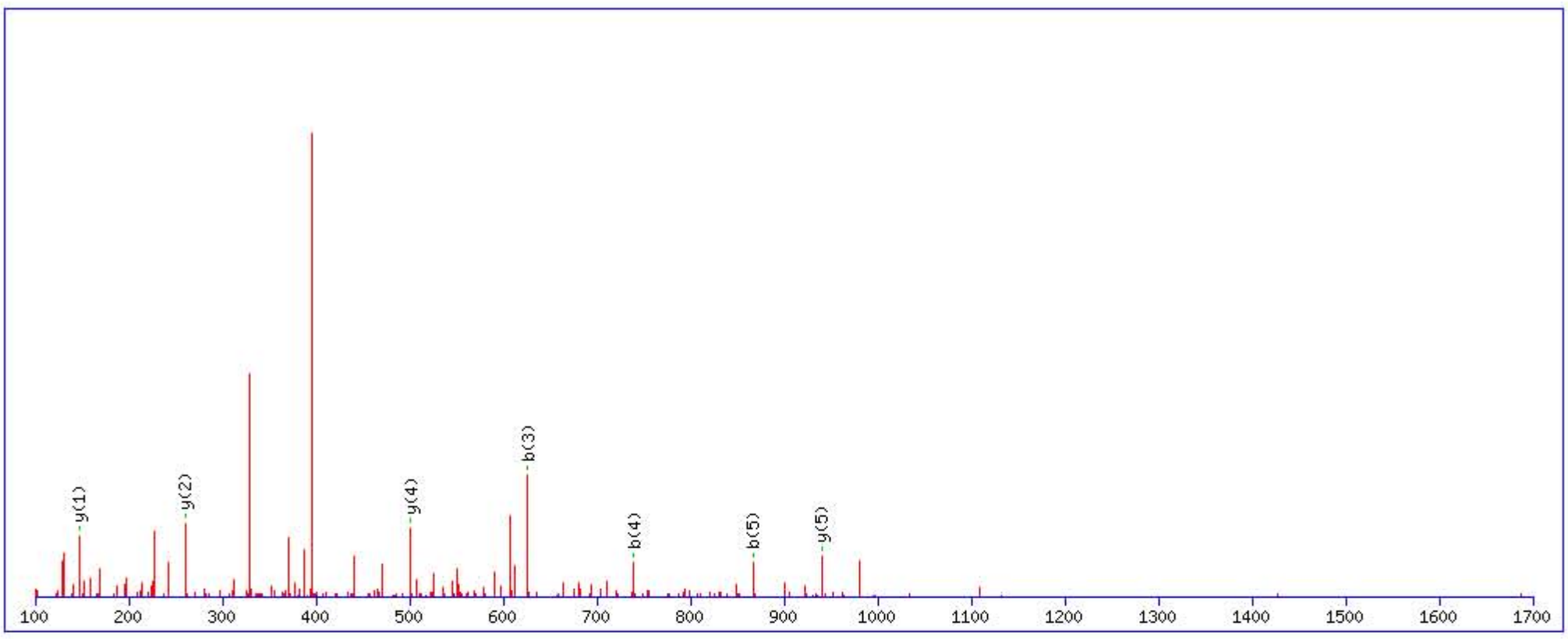
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GEQIQLK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

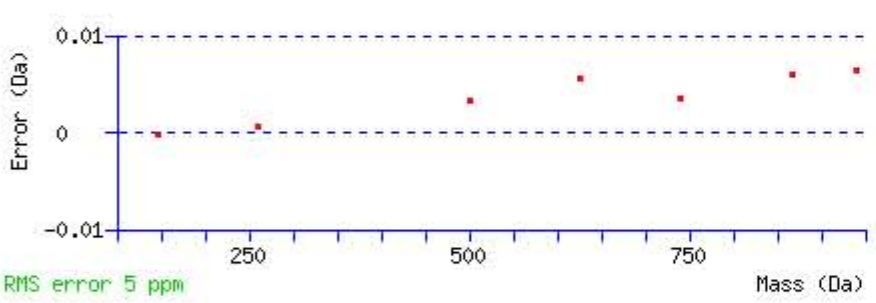
Match to Query 17487: 1125.627408 from(563.820980,2+) rtinseconds(1761) index(32668)
Title: Locus:1.1.1.722.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

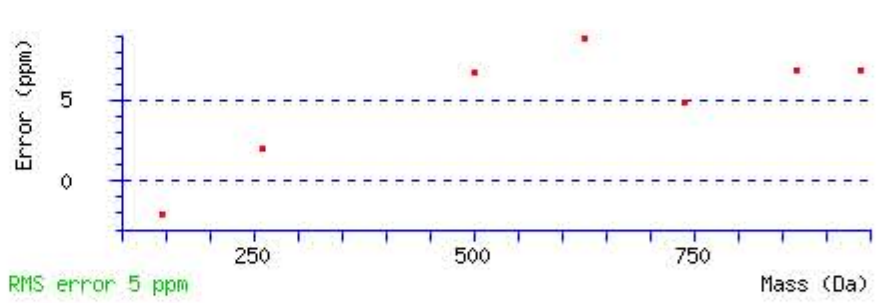
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1125.621597
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 25 **Expect:** 0.055
**Matches :** 7/56 fragment ions using 11 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 7 |
| 2 | 187.071333 | 94.039305 | | | 169.060768 | 85.034022 | E | 1069.607429 | 535.307353 | 1052.580880 | 526.794078 | 1051.596864 | 526.302070 | 6 |
| 3 | *626.296659* | 313.651968 | 609.270110 | 305.138693 | 608.286094 | 304.646685 | Q | *940.564836* | 470.786056 | 923.538287 | 462.272782 | | | 5 |
| 4 | *739.380723* | 370.194000 | 722.354174 | 361.680725 | 721.370158 | 361.188717 | I | *501.339510* | 251.173393 | 484.312961 | 242.660119 | | | 4 |
| 5 | *867.439301* | 434.223289 | 850.412752 | 425.710014 | 849.428736 | 425.218006 | Q | 388.255446 | 194.631361 | 371.228897 | 186.118087 | | | 3 |
| 6 | 980.523365 | 490.765321 | 963.496816 | 482.252046 | 962.512800 | 481.760038 | L | *260.196868* | 130.602072 | 243.170319 | 122.088798 | | | 2 |
| 7 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546766 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.2 | 1125.621597 | 0.005811 | GEQIQLK |
| 11.1 | 1125.632828 | -0.005420 | KLCLSHLQK |
| 9.9 | 1125.621597 | 0.005811 | EQVAQLK |
| 9.6 | 1125.632813 | -0.005404 | EQAARLK |
| 8.8 | 1125.636856 | -0.009448 | WAAQVIK |
| 7.0 | 1125.629486 | -0.002078 | RVDGWPVGLK |
| 5.8 | 1125.644073 | -0.016665 | MKRVVQHTK |
| 5.6 | 1125.621597 | 0.005811 | GEQIQLK |
| 5.6 | 1125.633499 | -0.006091 | VSHFLPWIK |
| 5.3 | 1125.621597 | 0.005811 | GQELIQK |

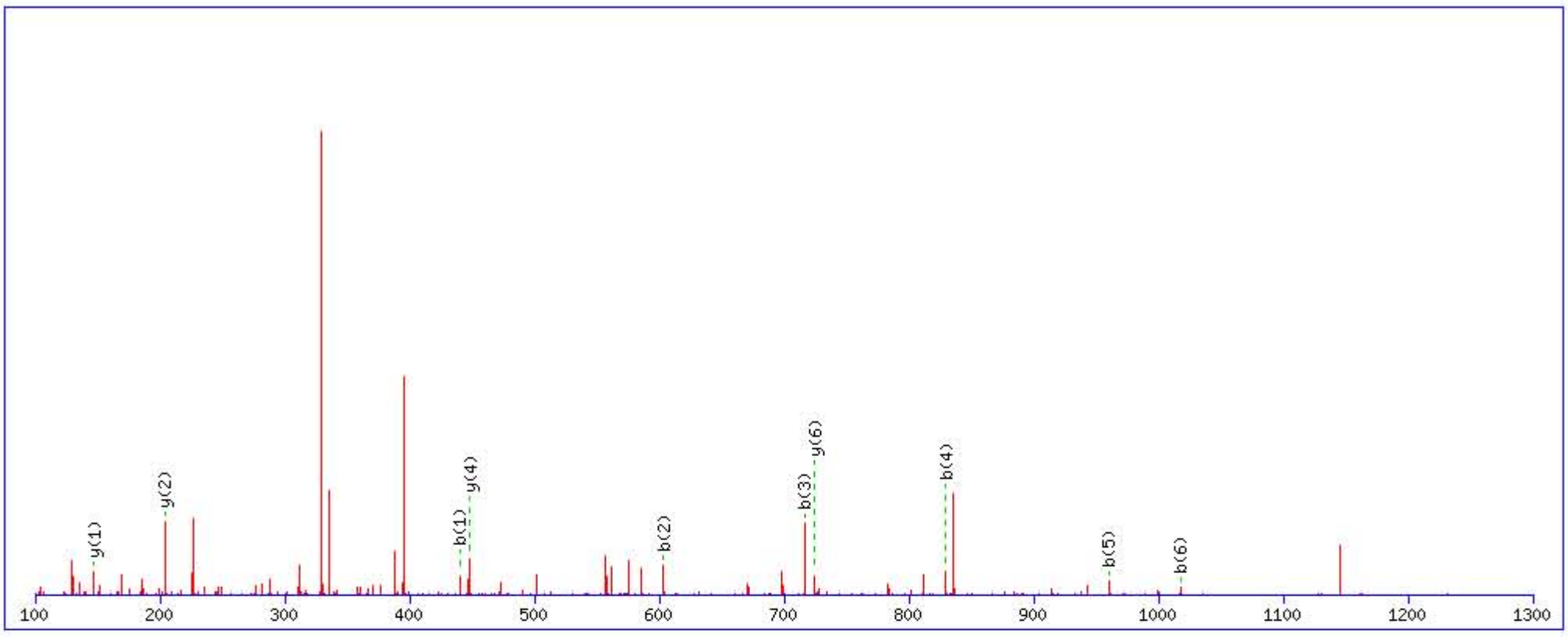
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QYLIMGK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

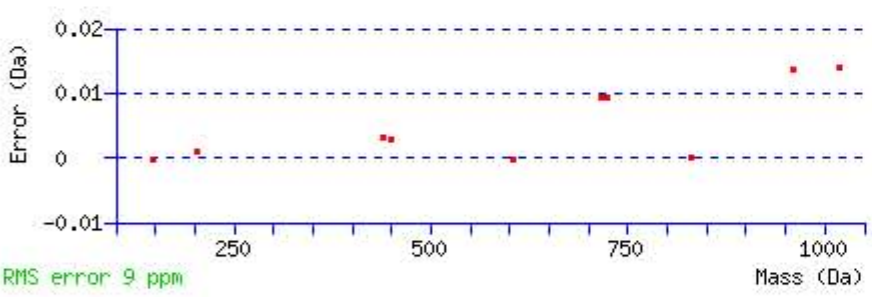
Match to Query 19345: 1162.631648 from(582.323100,2+) rtinseconds(2109) index(34909)
Title: Locus:1.1.1.843.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

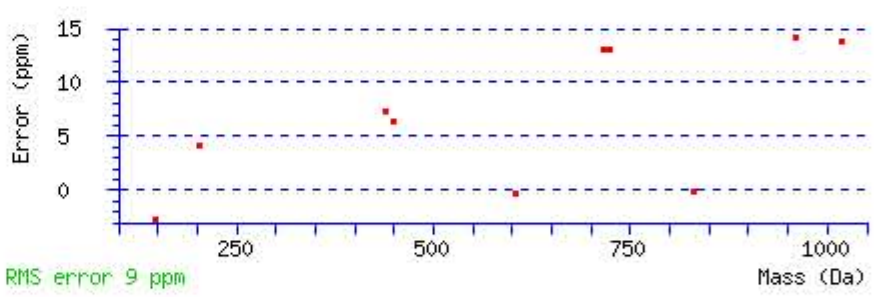
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1162.624237
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 30 **Expect:** 0.015
**Matches** : 10/48 fragment ions using 22 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *440.232602* | 220.619939 | 423.206053 | 212.106664 | Q | | | | | 7 |
| 2 | *603.295931* | 302.151604 | 586.269382 | 293.638329 | Y | 724.406210 | 362.706743 | 707.379661 | 354.193469 | 6 |
| 3 | *716.379995* | 358.693636 | 699.353446 | 350.180361 | L | 561.342881 | 281.175079 | 544.316332 | 272.661804 | 5 |
| 4 | *829.464059* | 415.235668 | 812.437510 | 406.722393 | I | 448.258817 | 224.633046 | 431.232268 | 216.119772 | 4 |
| 5 | *960.504544* | 480.755910 | 943.477995 | 472.242636 | M | 335.174753 | 168.091014 | 318.148204 | 159.577740 | 3 |
| 6 | *1017.526008* | 509.266642 | 1000.499459 | 500.753368 | G | 204.134268 | 102.570772 | 187.107719 | 94.057497 | 2 |
| 7 | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 30.1 | 1162.624237 | 0.007411 | QYLIMGK |
| 14.9 | 1162.641998 | -0.010350 | QYLTSLK |
| 5.6 | 1162.634598 | -0.002950 | YRVLAIGDEK |
| 5.3 | 1162.624069 | 0.007579 | VGRCRSLSTK |
| 5.2 | 1162.626724 | 0.004924 | KVEIAEMSLK |
| 4.8 | 1162.623383 | 0.008265 | FDGLQLELTK |
| 4.5 | 1162.639313 | -0.007665 | QRHLNGK |
| 4.1 | 1162.616852 | 0.014796 | QKAQSMPVFK |
| 3.8 | 1162.626740 | 0.004908 | EVLKMDTSIK |
| 3.4 | 1162.635956 | -0.004308 | WGGFLGRRSK |

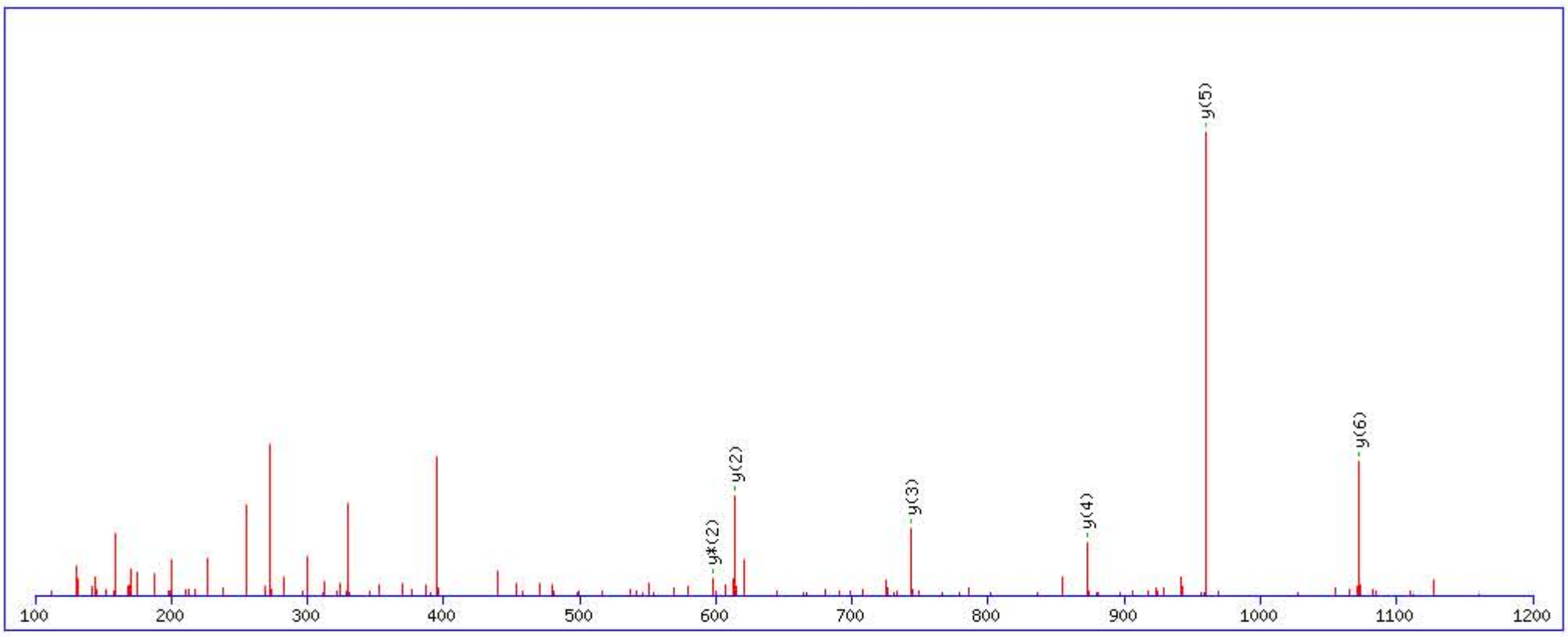
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **WLSEEQR**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

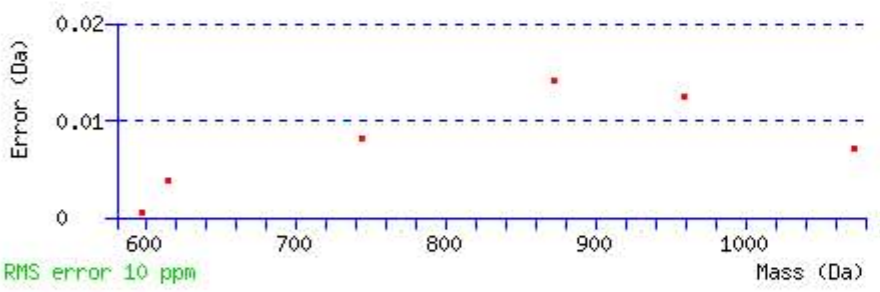
Match to Query 22085: 1257.625908 from(629.820230,2+) rtinseconds(1813) index(33000)
Title: Locus:1.1.1.740.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

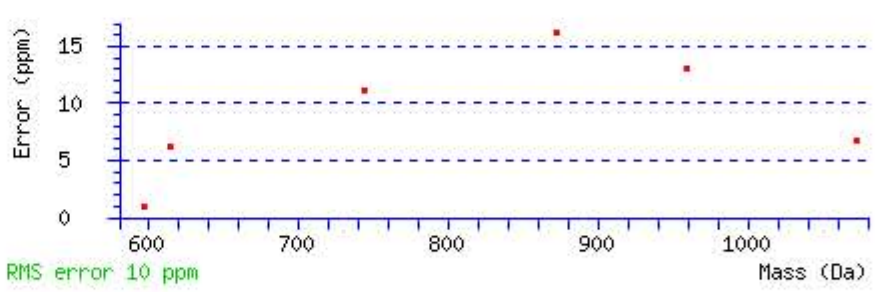
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1257.617569
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 30 **Expect:** 0.0073
**Matches :** 6/54 fragment ions using 11 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 187.086589 | 94.046932 | | | | | W | | | | | | | 7 |
| 2 | 300.170653 | 150.588965 | | | | | L | *1072.545556* | 536.776416 | 1055.519007 | 528.263142 | 1054.534991 | 527.771134 | 6 |
| 3 | 387.202681 | 194.104979 | | | 369.192116 | 185.099696 | S | *959.461492* | 480.234384 | 942.434943 | 471.721109 | 941.450927 | 471.229101 | 5 |
| 4 | 516.245274 | 258.626275 | | | 498.234709 | 249.620993 | E | *872.429464* | 436.718370 | 855.402915 | 428.205095 | 854.418899 | 427.713087 | 4 |
| 5 | 645.287867 | 323.147572 | | | 627.277302 | 314.142289 | E | *743.386871* | 372.197073 | 726.360322 | 363.683799 | 725.376306 | 363.191791 | 3 |
| 6 | 1084.513193 | 542.760235 | 1067.486644 | 534.246960 | 1066.502628 | 533.754952 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162502 | | | 2 |
| 7 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 29.6 | 1257.617569 | 0.008339 | WLSEEQR |
| 6.5 | 1257.620071 | 0.005837 | EGLEEGDQILR |
| 3.2 | 1257.617584 | 0.008324 | SVMEAPFPAPGR |
| 2.3 | 1257.638687 | -0.012779 | EGEMALLSKHK |
| 1.3 | 1257.613541 | 0.012367 | DHVKAMEERK |
| 1.1 | 1257.617599 | 0.008309 | QADVFPDR |

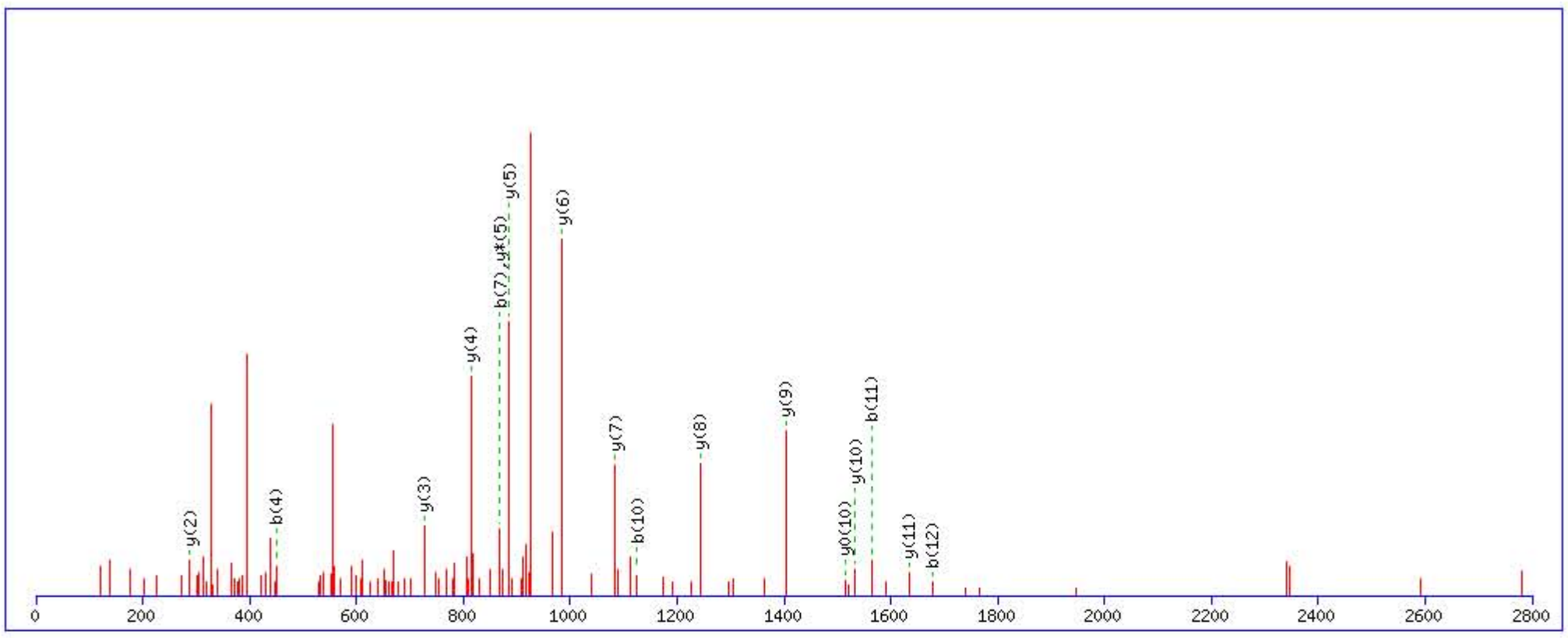
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AFTECCVVASQLR**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

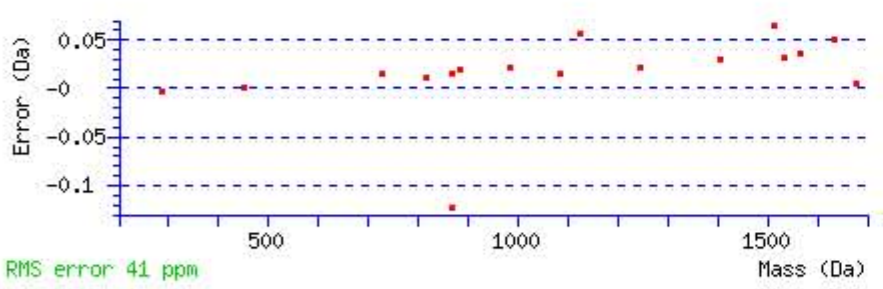
Match to Query 41277: 1850.906468 from(926.460510,2+) rtinseconds(2172) index(51552)
Title: Locus:1.1.1.1993.21 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

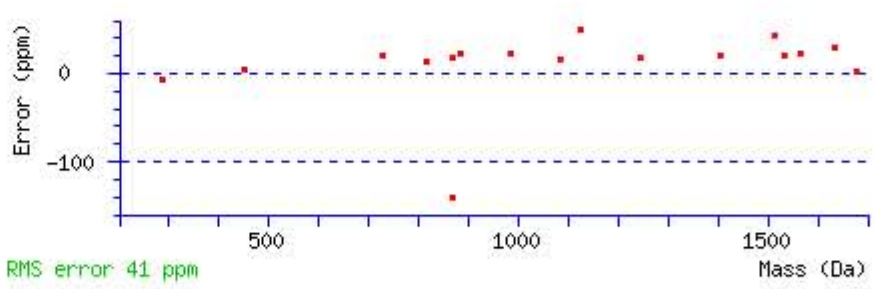
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1850.884140
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q11 : Biotin:Thermo-21345 (Q)
**Ions Score:** 57 **Expect:** 4.9e-005
**Matches :** 17/114 fragment ions using 33 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 13 |
| 2 | 219.112804 | 110.060040 | | | | | F | 1780.854296 | 890.930786 | 1763.827747 | 882.417512 | 1762.843731 | 881.925504 | 12 |
| 3 | 320.160483 | 160.583879 | | | 302.149918 | 151.578597 | T | *1633.785882* | 817.396579 | 1616.759333 | 808.883305 | 1615.775317 | 808.391297 | 11 |
| 4 | **449.203076** | 225.105176 | | | 431.192511 | 216.099894 | E | *1532.738203* | 766.872740 | 1515.711654 | 758.359465 | 1514.727638 | 757.867457 | 10 |
| 5 | 609.233725 | 305.120501 | | | 591.223160 | 296.115218 | C | *1403.695610* | 702.351443 | 1386.669061 | 693.838169 | 1385.685045 | 693.346161 | 9 |
| 6 | 769.264374 | 385.135825 | | | 751.253809 | 376.130543 | C | *1243.664961* | 622.336119 | 1226.638412 | 613.822844 | 1225.654396 | 613.330836 | 8 |
| 7 | **868.332788** | 434.670032 | | | 850.322223 | 425.664750 | V | *1083.634312* | 542.320794 | 1066.607763 | 533.807520 | 1065.623747 | 533.315512 | 7 |
| 8 | 967.401202 | 484.204239 | | | 949.390637 | 475.198957 | V | *984.565898* | 492.786587 | 967.539349 | 484.273313 | 966.555333 | 483.781305 | 6 |
| 9 | 1038.438316 | 519.722796 | | | 1020.427751 | 510.717514 | A | *885.497484* | 443.252380 | 868.470935 | 434.739106 | 867.486919 | 434.247098 | 5 |
| 10 | **1125.470344** | 563.238810 | | | 1107.459779 | 554.233528 | S | *814.460370* | 407.733823 | 797.433821 | 399.220549 | 796.449805 | 398.728541 | 4 |
| 11 | **1564.695670** | 782.851473 | 1547.669121 | 774.338199 | 1546.685105 | 773.846191 | Q | *727.428342* | 364.217809 | 710.401793 | 355.704535 | | | 3 |
| 12 | **1677.779734** | 839.393505 | 1660.753185 | 830.880231 | 1659.769169 | 830.388223 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 13 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 57.3 | 1850.884140 | 0.022328 | AFTECCVVASQLR |
| 10.7 | 1850.901901 | 0.004567 | QDDSGQDVPLR |
| 2.5 | 1850.920303 | -0.013835 | EDYFVTADQLWVPLR |
| 2.1 | 1850.930847 | -0.024379 | DQAPAEDARGEIIR |

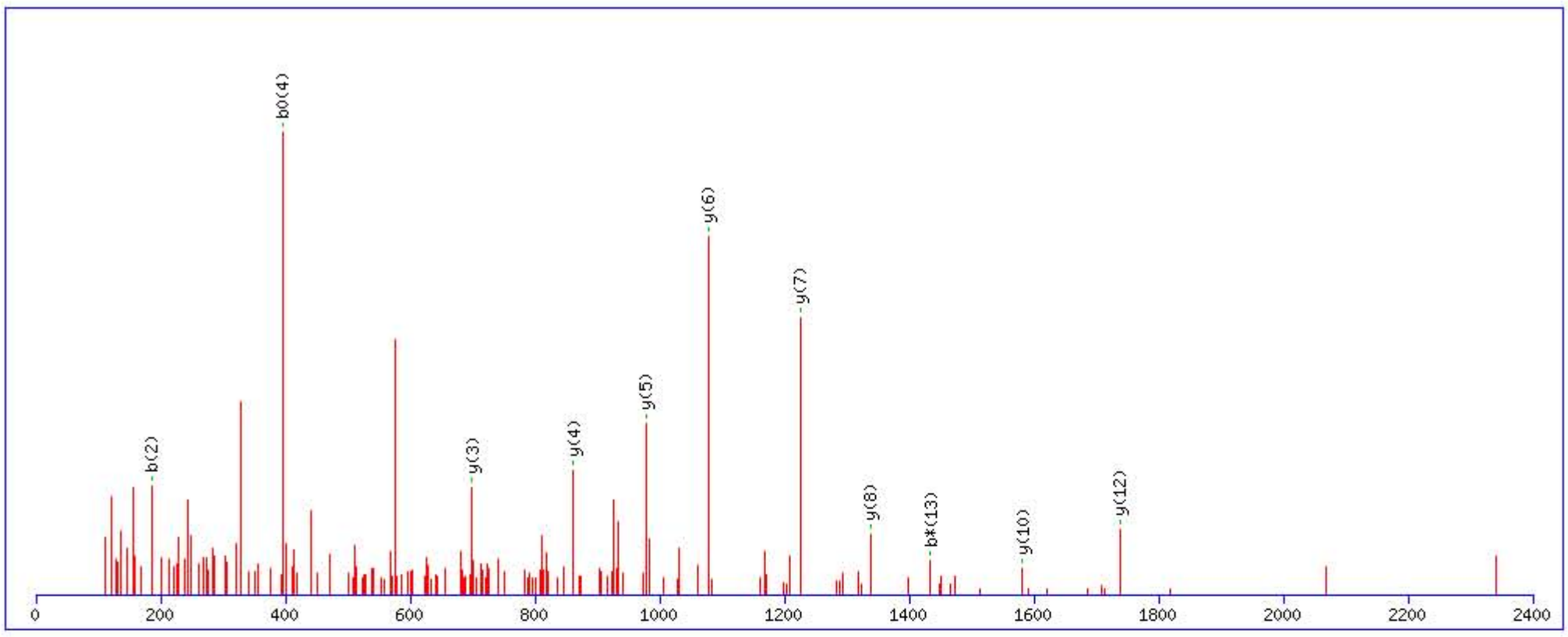
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ALVEGVDQLFTDYQIK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

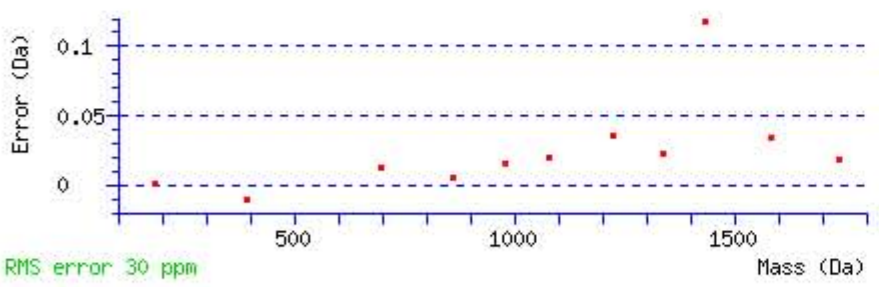
Match to Query 47393: 2149.144902 from(717.388910,3+) rtinseconds(2846) index(39431)
Title: Locus:1.1.1.1098.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

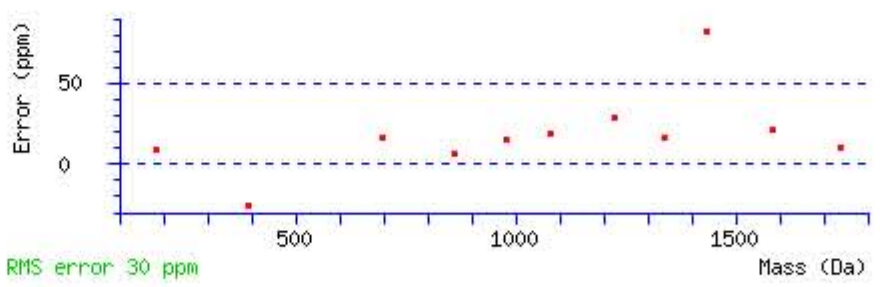
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2149.112930
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q14 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0033
**Matches :** 11/152 fragment ions using 19 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 16 |
| 2 | 185.128454 | 93.067865 | | | | | L | 2079.083093 | 1040.045184 | 2062.056544 | 1031.531910 | 2061.072528 | 1031.039902 | 15 |
| 3 | 284.196868 | 142.602072 | | | | | V | 1965.999029 | 983.503153 | 1948.972480 | 974.989878 | 1947.988464 | 974.497870 | 14 |
| 4 | 413.239461 | 207.123369 | | | 395.228896 | 198.118086 | E | 1866.930615 | 933.968946 | 1849.904066 | 925.455671 | 1848.920050 | 924.963663 | 13 |
| 5 | 470.260925 | 235.634100 | | | 452.250360 | 226.628818 | G | *1737.888022* | 869.447649 | 1720.861473 | 860.934375 | 1719.877457 | 860.442367 | 12 |
| 6 | 569.329339 | 285.168308 | | | 551.318774 | 276.163025 | V | 1680.866558 | 840.936917 | 1663.840009 | 832.423643 | 1662.855993 | 831.931635 | 11 |
| 7 | 684.356282 | 342.681779 | | | 666.345717 | 333.676496 | D | *1581.798144* | 791.402710 | 1564.771595 | 782.889436 | 1563.787579 | 782.397428 | 10 |
| 8 | 812.414860 | 406.711068 | 795.388311 | 398.197793 | 794.404295 | 397.705785 | Q | 1466.771201 | 733.889239 | 1449.744652 | 725.375964 | 1448.760636 | 724.883956 | 9 |
| 9 | 925.498924 | 463.253100 | 908.472375 | 454.739825 | 907.488359 | 454.247818 | L | *1338.712623* | 669.859950 | 1321.686074 | 661.346675 | 1320.702058 | 660.854667 | 8 |
| 10 | 1072.567338 | 536.787307 | 1055.540789 | 528.274033 | 1054.556773 | 527.782025 | F | *1225.628559* | 613.317918 | 1208.602010 | 604.804643 | 1207.617994 | 604.312635 | 7 |
| 11 | 1173.615017 | 587.311147 | 1156.588468 | 578.797872 | 1155.604452 | 578.305864 | T | *1078.560145* | 539.783711 | 1061.533596 | 531.270436 | 1060.549580 | 530.778428 | 6 |
| 12 | 1288.641960 | 644.824618 | 1271.615411 | 636.311344 | 1270.631395 | 635.819336 | D | *977.512466* | 489.259871 | 960.485917 | 480.746597 | 959.501901 | 480.254589 | 5 |
| 13 | 1451.705289 | 726.356283 | 1434.678740 | 717.843008 | 1433.694724 | 717.351000 | Y | *862.485523* | 431.746400 | 845.458974 | 423.233125 | | | 4 |
| 14 | 1890.930615 | 945.968946 | 1873.904066 | 937.455671 | 1872.920050 | 936.963663 | Q | *699.422194* | 350.214735 | 682.395645 | 341.701461 | | | 3 |
| 15 | 2004.014679 | 1002.510978 | 1986.988130 | 993.997703 | 1986.004114 | 993.505695 | I | 260.196868 | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.5 | 2149.112930 | 0.031972 | ALVEGVDQLFTDYQIK |
| 2.6 | 2149.112930 | 0.031972 | ALVEGVDQLFTDYQIK |

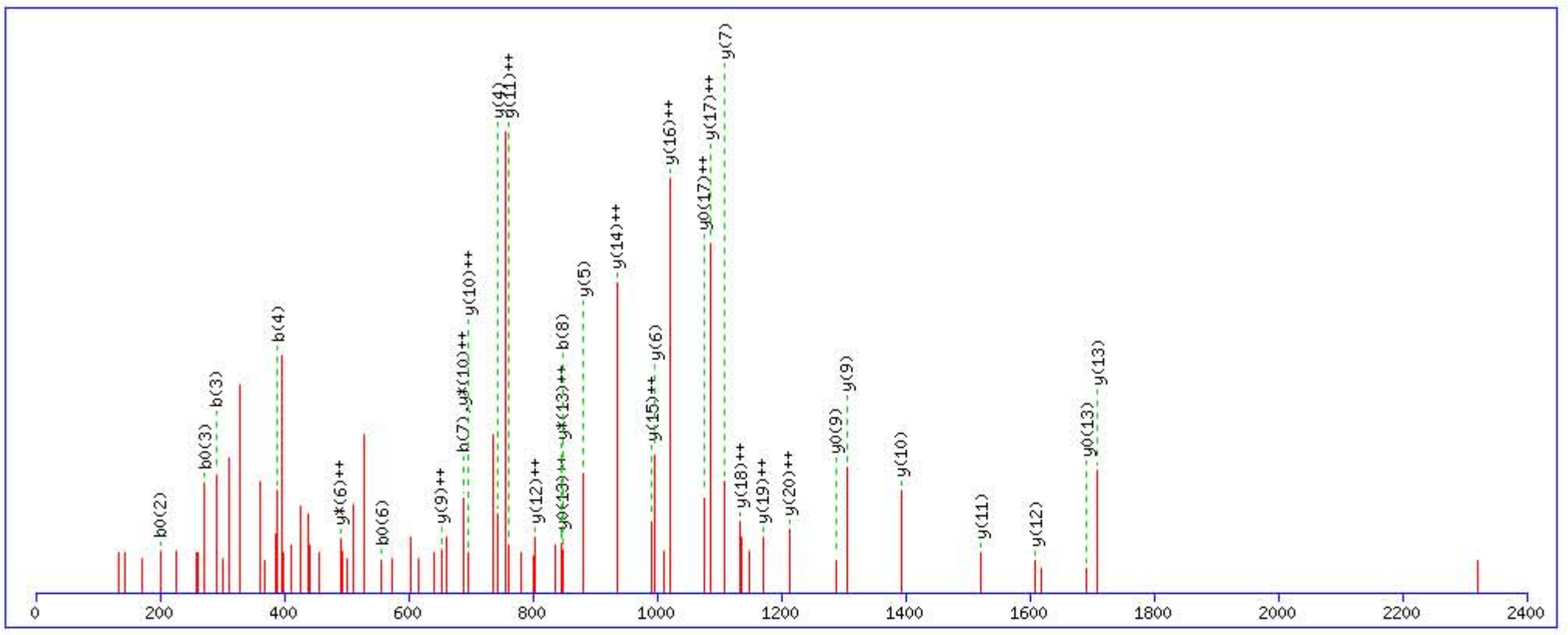
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MSAVEGICTSESPVIDHQGTK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

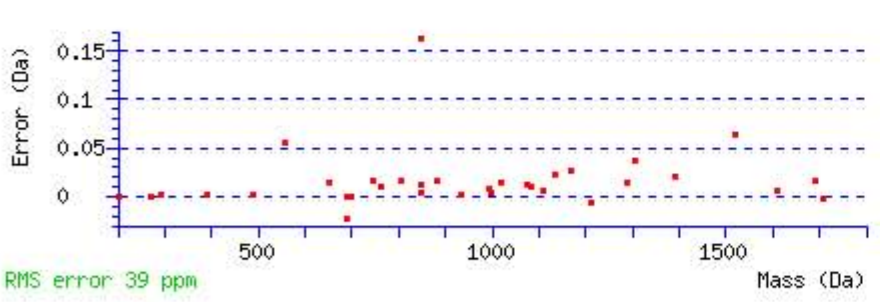
Match to Query 55016: 2556.232092 from(853.084640,3+) rtinseconds(1952) index(33917)
Title: Locus:1.1.1.788.24 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

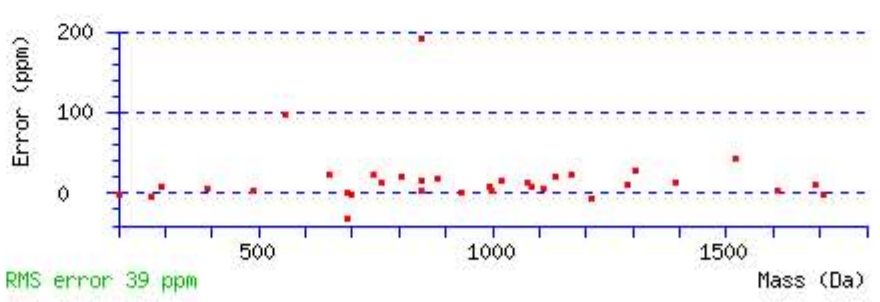
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2556.202240
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q18 : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 4e-005
**Matches :** 34/202 fragment ions using 70 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.047761 | 66.527518 | | | | | M | | | | | | | 21 |
| 2 | 219.079789 | 110.043532 | | | 201.069224 | 101.038250 | S | 2426.169024 | 1213.588150 | 2409.142475 | 1205.074875 | 2408.158459 | 1204.582867 | 20 |
| 3 | **290.116903** | 145.562089 | | | 272.106338 | 136.556807 | A | 2339.136996 | 1170.072136 | 2322.110447 | 1161.558861 | 2321.126431 | 1161.066853 | 19 |
| 4 | **389.185317** | 195.096296 | | | 371.174752 | 186.091014 | V | 2268.099882 | 1134.553579 | 2251.073333 | 1126.040304 | 2250.089317 | 1125.548296 | 18 |
| 5 | 518.227910 | 259.617593 | | | 500.217345 | 250.612311 | E | 2169.031468 | 1085.019372 | 2152.004919 | 1076.506097 | 2151.020903 | 1076.014089 | 17 |
| 6 | 575.249374 | 288.128325 | | | 557.238809 | 279.123043 | G | 2039.988875 | 1020.498076 | 2022.962326 | 1011.984801 | 2021.978310 | 1011.492793 | 16 |
| 7 | **688.333438** | 344.670357 | | | 670.322873 | 335.665075 | I | 1982.967411 | 991.987343 | 1965.940862 | 983.474069 | 1964.956846 | 982.982061 | 15 |
| 8 | **848.364087** | 424.685682 | | | 830.353522 | 415.680399 | C | 1869.883347 | 935.445312 | 1852.856798 | 926.932037 | 1851.872782 | 926.440029 | 14 |
| 9 | 949.411766 | 475.209521 | | | 931.401201 | 466.204239 | T | *1709.852698* | 855.429987 | 1692.826149 | 846.916713 | 1691.842133 | 846.424704 | 13 |
| 10 | 1036.443794 | 518.725535 | | | 1018.433229 | 509.720253 | S | *1608.805019* | 804.906147 | 1591.778470 | 796.392873 | 1590.794454 | 795.900865 | 12 |
| 11 | 1165.486387 | 583.246832 | | | 1147.475822 | 574.241549 | E | *1521.772991* | 761.390133 | 1504.746442 | 752.876859 | 1503.762426 | 752.384851 | 11 |
| 12 | 1252.518415 | 626.762846 | | | 1234.507850 | 617.757563 | S | *1392.730398* | 696.868837 | 1375.703849 | 688.355563 | 1374.719833 | 687.863554 | 10 |
| 13 | 1349.571179 | 675.289228 | | | 1331.560614 | 666.283945 | P | *1305.698370* | 653.352823 | 1288.671821 | 644.839548 | 1287.687805 | 644.347540 | 9 |
| 14 | 1448.639593 | 724.823435 | | | 1430.629028 | 715.818152 | V | 1208.645606 | 604.826441 | 1191.619057 | 596.313166 | 1190.635041 | 595.821158 | 8 |
| 15 | 1561.723657 | 781.365467 | | | 1543.713092 | 772.360184 | I | *1109.577192* | 555.292234 | 1092.550643 | 546.778959 | 1091.566627 | 546.286951 | 7 |
| 16 | 1676.750600 | 838.878938 | | | 1658.740035 | 829.873656 | D | *996.493128* | 498.750202 | 979.466579 | 490.236927 | 978.482563 | 489.744919 | 6 |
| 17 | 1813.809512 | 907.408394 | | | 1795.798947 | 898.403112 | H | *881.466185* | 441.236730 | 864.439636 | 432.723456 | 863.455620 | 432.231448 | 5 |
| 18 | 2253.034838 | 1127.021057 | 2236.008289 | 1118.507782 | 2235.024273 | 1118.015774 | Q | *744.407273* | 372.707274 | 727.380724 | 364.194000 | 726.396708 | 363.701992 | 4 |
| 19 | 2310.056302 | 1155.531789 | 2293.029753 | 1147.018514 | 2292.045737 | 1146.526506 | G | 305.181947 | 153.094611 | 288.155398 | 144.581337 | 287.171382 | 144.089329 | 3 |
| 20 | 2411.103981 | 1206.055628 | 2394.077432 | 1197.542354 | 2393.093416 | 1197.050346 | T | 248.160483 | 124.583879 | 231.133934 | 116.070605 | 230.149918 | 115.578597 | 2 |
| 21 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 57.8 | 2556.202240 | 0.029852 | MSAVEGICTSESPVIDHQGTK |

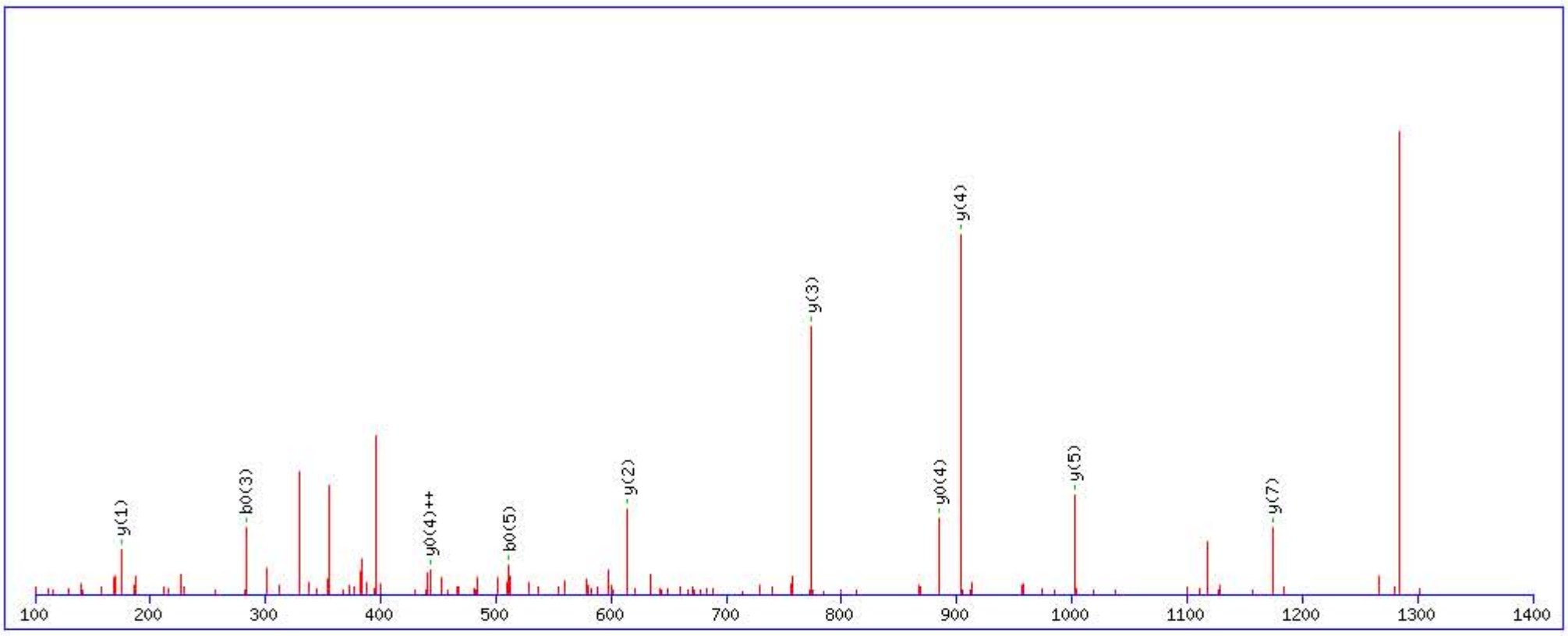
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QGDVECQR**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

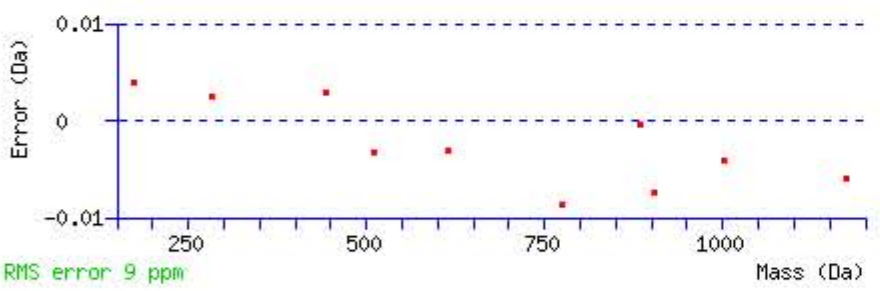
Match to Query 23357: 1301.592968 from(651.803760,2+) rtinseconds(1332) index(15745)
Title: Locus:1.1.1.2846.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

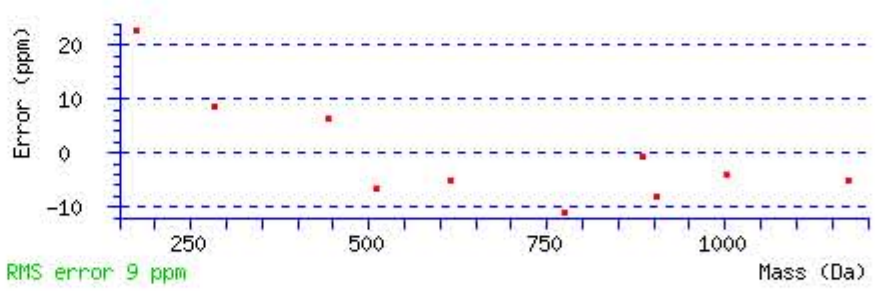
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1301.585648
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 49 **Expect:** 0.0002
**Matches :** 10/74 fragment ions using 12 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.065854 | 65.036565 | 112.039305 | 56.523291 | | | Q | | | | | | | 8 |
| 2 | 186.087318 | 93.547297 | 169.060769 | 85.034023 | | | G | *1174.534341* | 587.770809 | 1157.507792 | 579.257534 | 1156.523776 | 578.765526 | 7 |
| 3 | 301.114261 | 151.060768 | 284.087712 | 142.547494 | 283.103696 | 142.055486 | D | 1117.512877 | 559.260077 | 1100.486328 | 550.746802 | 1099.502312 | 550.254794 | 6 |
| 4 | 400.182675 | 200.594976 | 383.156126 | 192.081701 | 382.172110 | 191.589693 | V | *1002.485934* | 501.746605 | 985.459385 | 493.233331 | 984.475369 | 492.741323 | 5 |
| 5 | 529.225268 | 265.116272 | 512.198719 | 256.602998 | 511.214703 | 256.110990 | E | *903.417520* | 452.212398 | 886.390971 | 443.699124 | 885.406955 | 443.207116 | 4 |
| 6 | 689.255917 | 345.131597 | 672.229368 | 336.618322 | 671.245352 | 336.126314 | C | *774.374927* | 387.691102 | 757.348378 | 379.177827 | | | 3 |
| 7 | 1128.481243 | 564.744260 | 1111.454694 | 556.230985 | 1110.470678 | 555.738977 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.5 | 1301.585648 | 0.007320 | QGDVECQR |
| 8.0 | 1301.584747 | 0.008221 | QESPSQENIDR |
| 7.1 | 1301.584763 | 0.008205 | KATEDAEGGDGPR |
| 6.4 | 1301.604721 | -0.011753 | QSSTYHRHMR |
| 6.2 | 1301.609894 | -0.016926 | GAAEELASTPNDK |
| 5.9 | 1301.604263 | -0.011295 | CPAAMTVMHLR |
| 5.9 | 1301.604263 | -0.011295 | CPAAMTVMHLR |

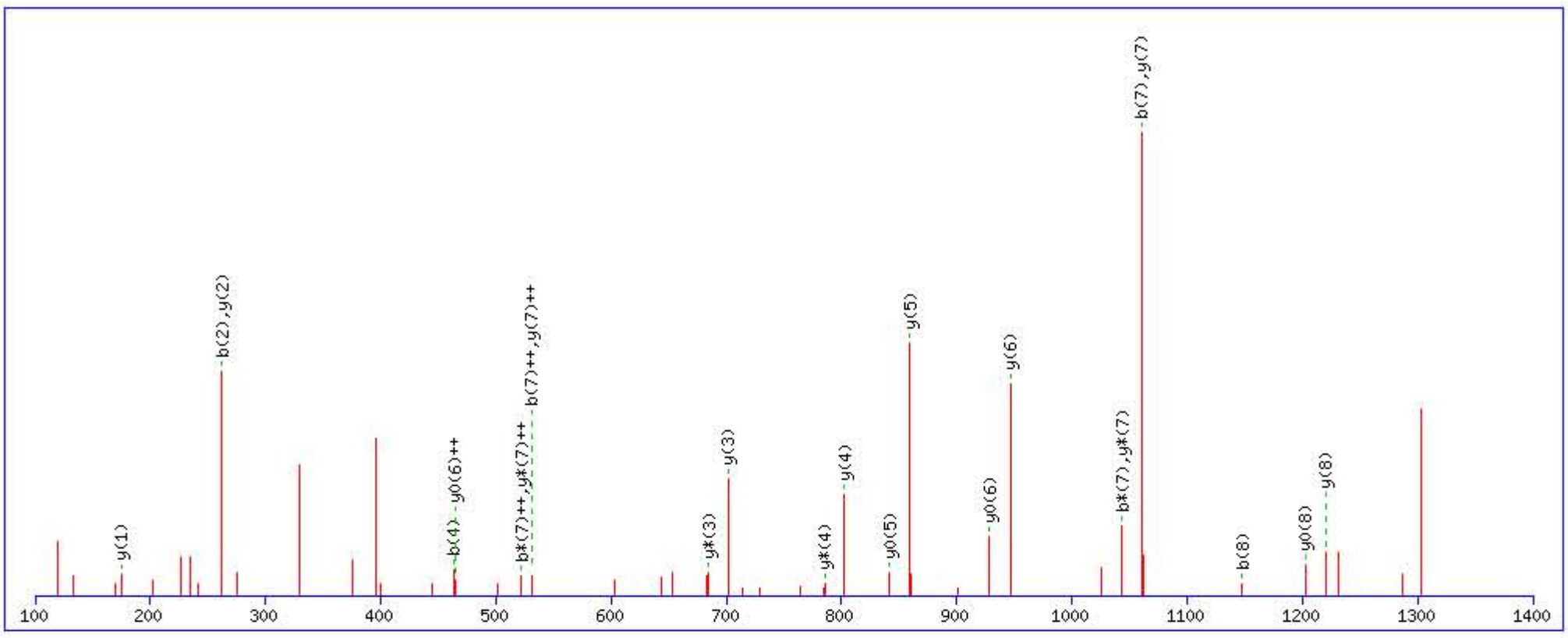
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TCNSGTQSR**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

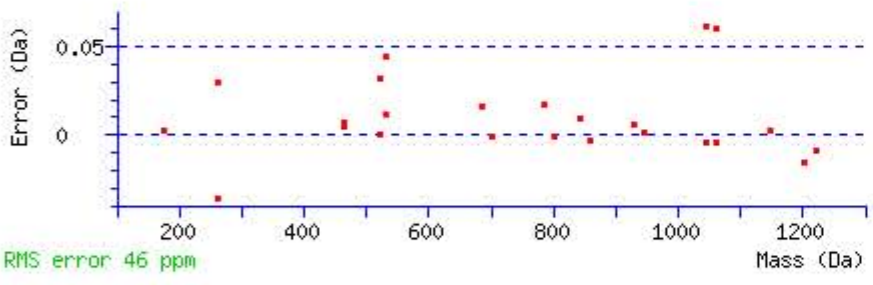
Match to Query 23654: 1320.591408 from(661.302980,2+) rtinseconds(1067) index(14687)
Title: Locus:1.1.1.2753.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

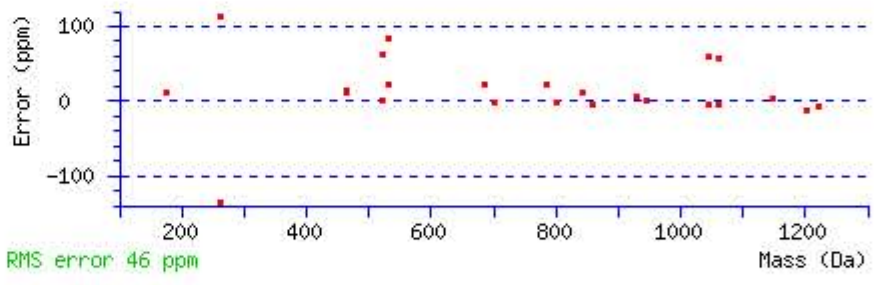
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1320.591461
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 70 **Expect:** 6.7e-007
**Matches :** 24/90 fragment ions using 24 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 9 |
| 2 | **262.085604** | 131.546440 | | | 244.075039 | 122.541158 | C | *1220.551053* | 610.779165 | 1203.524504 | 602.265890 | 1202.540488 | 601.773882 | 8 |
| 3 | 376.128531 | 188.567904 | 359.101982 | 180.054629 | 358.117966 | 179.562621 | N | *1060.520404* | 530.763840 | 1043.493855 | 522.250566 | 1042.509839 | 521.758558 | 7 |
| 4 | **463.160559** | 232.083917 | 446.134010 | 223.570643 | 445.149994 | 223.078635 | S | *946.477477* | 473.742377 | 929.450928 | 465.229102 | 928.466912 | 464.737094 | 6 |
| 5 | 520.182023 | 260.594650 | 503.155474 | 252.081375 | 502.171458 | 251.589367 | G | *859.445449* | 430.226363 | 842.418900 | 421.713088 | 841.434884 | 421.221080 | 5 |
| 6 | 621.229702 | 311.118489 | 604.203153 | 302.605215 | 603.219137 | 302.113207 | T | *802.423985* | 401.715631 | 785.397436 | 393.202356 | 784.413420 | 392.710348 | 4 |
| 7 | **1060.455028** | 530.731152 | 1043.428479 | 522.217878 | 1042.444463 | 521.725870 | Q | *701.376306* | 351.191791 | 684.349757 | 342.678517 | 683.365741 | 342.186509 | 3 |
| 8 | **1147.487056** | 574.247166 | 1130.460507 | 565.733892 | 1129.476491 | 565.241884 | S | *262.150980* | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 9 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 70.4 | 1320.591461 | -0.000053 | TCNSGTQSR |
| 10.5 | 1320.599289 | -0.007881 | NELPMHHNSSR |
| 10.4 | 1320.609192 | -0.017784 | MTSERAPSPSSR |
| 9.7 | 1320.584045 | 0.007363 | SQGCSREASPSR |
| 9.0 | 1320.597946 | -0.006538 | LMNTNDLEESR |
| 6.8 | 1320.605804 | -0.014396 | TSAHYEENKSR |
| 2.1 | 1320.605835 | -0.014427 | EDTWSSRTPSR |
| 1.6 | 1320.587616 | 0.003792 | MTCVEQDK |
| 1.3 | 1320.579330 | 0.012078 | DSDLENSEGLSR |
| 1.2 | 1320.605362 | -0.013954 | SSSDMDLQK |

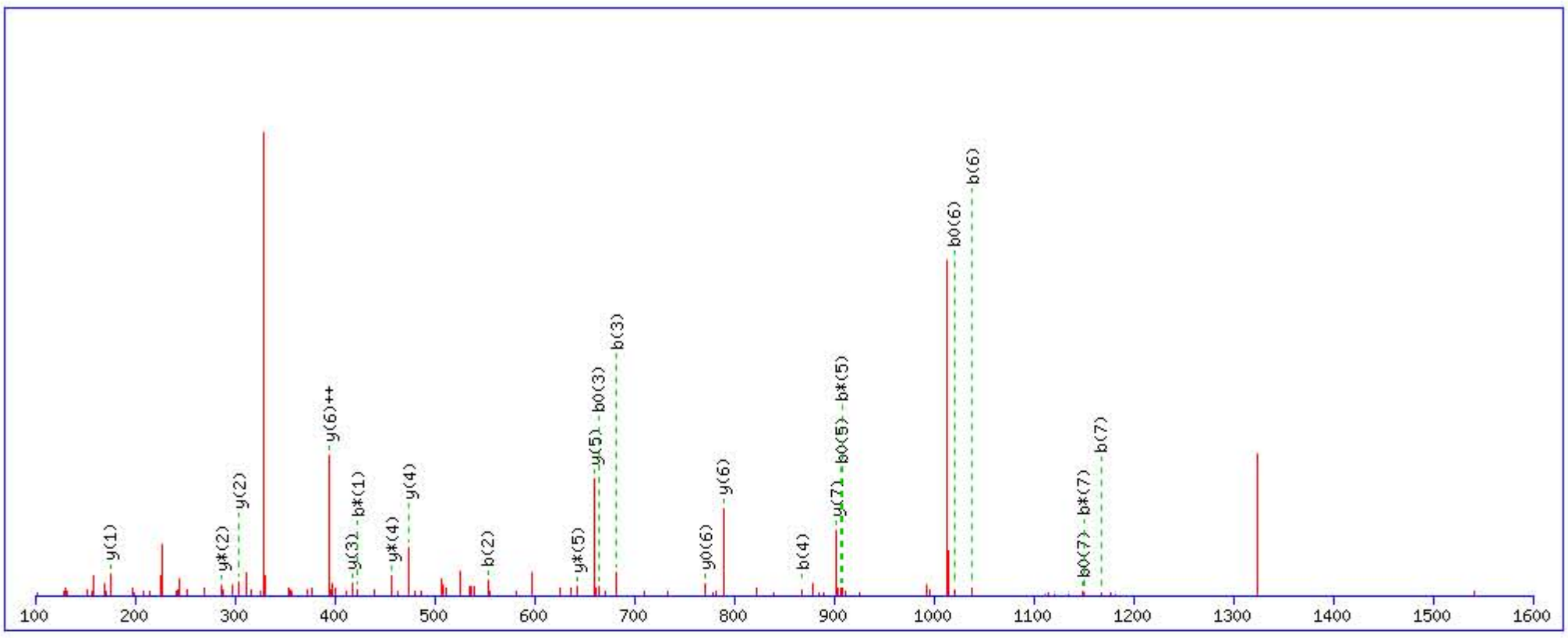
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QLEWGLER**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

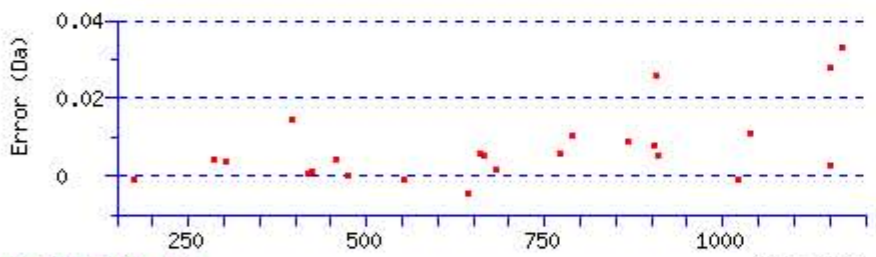
Match to Query 24137: 1340.699648 from(671.357100,2+) rtinseconds(2225) index(21636)
Title: Locus:1.1.1.3157.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

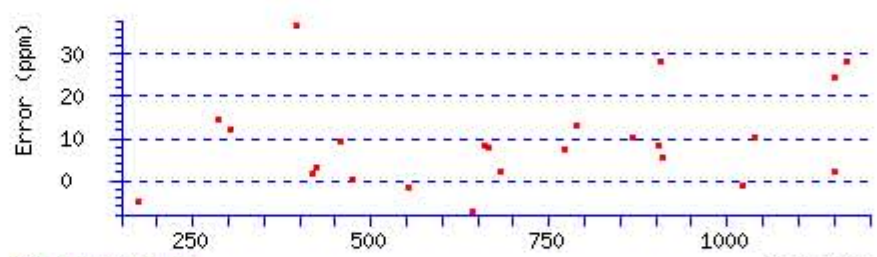
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1340.691071
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 27 **Expect:** 0.044
**Matches** : 24/78 fragment ions using 55 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 8 |
| 2 | **553.316666** | 277.161971 | 536.290117 | 268.648697 | | | L | *902.473043* | 451.740160 | 885.446494 | 443.226885 | 884.462478 | 442.734877 | 7 |
| 3 | **682.359259** | 341.683268 | 665.332710 | 333.169993 | 664.348694 | 332.677985 | E | *789.388979* | 395.198128 | 772.362430 | 386.684853 | 771.378414 | 386.192845 | 6 |
| 4 | **868.438572** | 434.722924 | 851.412023 | 426.209650 | 850.428007 | 425.717642 | W | *660.346386* | 330.676831 | 643.319837 | 322.163556 | 642.335821 | 321.671548 | 5 |
| 5 | 925.460036 | 463.233656 | 908.433487 | 454.720382 | 907.449471 | 454.228374 | G | *474.267073* | 237.637174 | 457.240524 | 229.123900 | 456.256508 | 228.631892 | 4 |
| 6 | **1038.544100** | 519.775688 | 1021.517551 | 511.262414 | 1020.533535 | 510.770406 | L | *417.245609* | 209.126442 | 400.219060 | 200.613168 | 399.235044 | 200.121160 | 3 |
| 7 | **1167.586693** | 584.296985 | 1150.560144 | 575.783710 | 1149.576128 | 575.291702 | E | *304.161545* | 152.584410 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 27.4 | 1340.691071 | 0.008577 | QLEWGLER |
| 18.7 | 1340.712204 | -0.012556 | QLDSLLGER |
| 9.8 | 1340.687042 | 0.012606 | QINDSANLR |
| 7.0 | 1340.687057 | 0.012591 | GSSPKQSPSR |
| 5.0 | 1340.687027 | 0.012621 | QEIEERAR |
| 4.9 | 1340.716019 | -0.016371 | EAKAQALQAQQR |
| 4.7 | 1340.683655 | 0.015993 | IYYLSQERNR |
| 4.6 | 1340.687027 | 0.012621 | QLREEAER |
| 4.5 | 1340.690872 | 0.008776 | SSEHRLAGSRNK |
| 4.0 | 1340.691071 | 0.008577 | QWLEDALR |

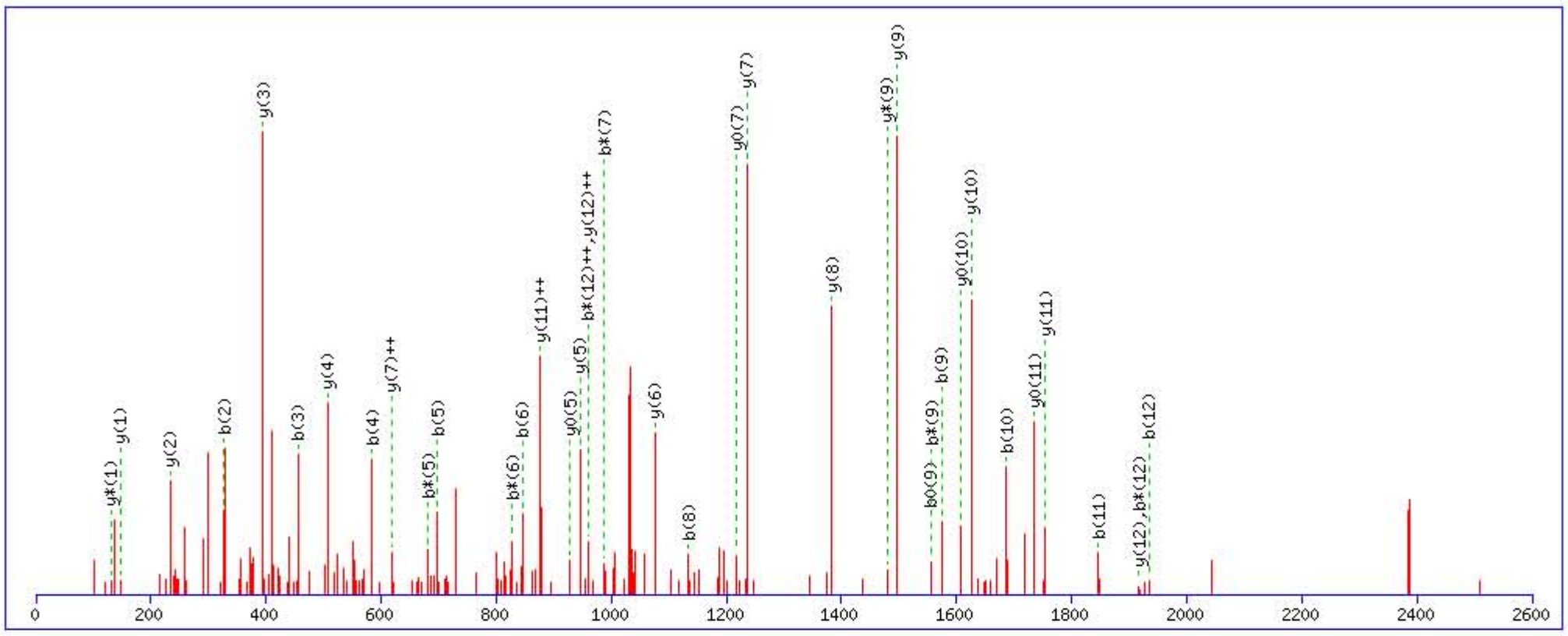
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YYQENFCEQICSK**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

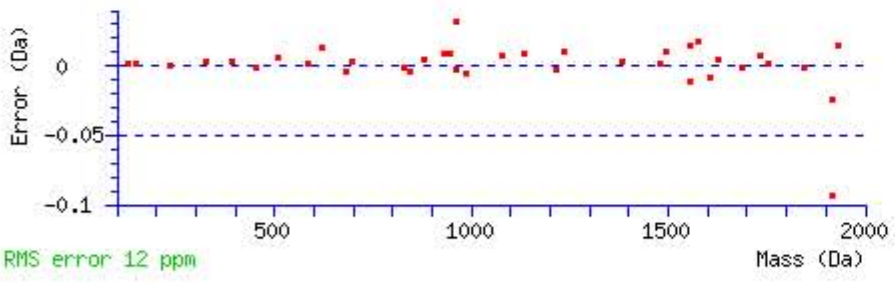
Match to Query 46225: 2078.912288 from(1040.463420,2+) rtinseconds(2022) index(20369)
Title: Locus:1.1.1.3086.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

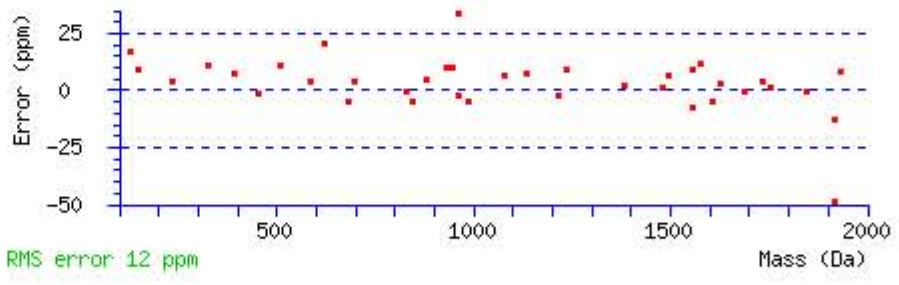
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2078.889984
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 64 **Expect:** 2.2e-006
**Matches :** 38/132 fragment ions using 75 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 13 |
| 2 | **327.133934** | 164.070605 | | | | | Y | *1916.833954* | 958.920615 | 1899.807405 | 950.407341 | 1898.823389 | 949.915333 | 12 |
| 3 | **455.192512** | 228.099894 | 438.165963 | 219.586620 | | | Q | *1753.770625* | 877.388951 | 1736.744076 | 868.875676 | 1735.760060 | 868.383668 | 11 |
| 4 | **584.235105** | 292.621191 | 567.208556 | 284.107916 | 566.224540 | 283.615908 | E | *1625.712047* | 813.359662 | 1608.685498 | 804.846387 | 1607.701482 | 804.354379 | 10 |
| 5 | **698.278032** | 349.642654 | 681.251483 | 341.129380 | 680.267467 | 340.637372 | N | *1496.669454* | 748.838365 | 1479.642905 | 740.325091 | 1478.658889 | 739.833083 | 9 |
| 6 | **845.346446** | 423.176861 | 828.319897 | 414.663587 | 827.335881 | 414.171579 | F | *1382.626527* | 691.816902 | 1365.599978 | 683.303627 | 1364.615962 | 682.811619 | 8 |
| 7 | 1005.377095 | 503.192186 | 988.350546 | 494.678911 | 987.366530 | 494.186903 | C | *1235.558113* | 618.282695 | 1218.531564 | 609.769420 | 1217.547548 | 609.277412 | 7 |
| 8 | **1134.419688** | 567.713482 | 1117.393139 | 559.200208 | 1116.409123 | 558.708200 | E | *1075.527464* | 538.267370 | 1058.500915 | 529.754096 | 1057.516899 | 529.262088 | 6 |
| 9 | **1573.645014** | 787.326145 | 1556.618465 | 778.812871 | 1555.634449 | 778.320863 | Q | *946.484871* | 473.746074 | 929.458322 | 465.232799 | 928.474306 | 464.740791 | 5 |
| 10 | **1686.729078** | 843.868177 | 1669.702529 | 835.354903 | 1668.718513 | 834.862895 | I | *507.259545* | 254.133411 | 490.232996 | 245.620136 | 489.248980 | 245.128128 | 4 |
| 11 | **1846.759727** | 923.883502 | 1829.733178 | 915.370227 | 1828.749162 | 914.878219 | C | *394.175481* | 197.591379 | 377.148932 | 189.078104 | 376.164916 | 188.586096 | 3 |
| 12 | **1933.791755** | 967.399516 | 1916.765206 | 958.886241 | 1915.781190 | 958.394233 | S | *234.144832* | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 13 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 64.4 | 2078.889984 | 0.022304 | YYQENFCEQICSK |
| 10.4 | 2078.889984 | 0.022304 | YYQENFCEQICSK |
| 4.9 | 2078.932907 | -0.020619 | EYTLQSFGEMADSFK |

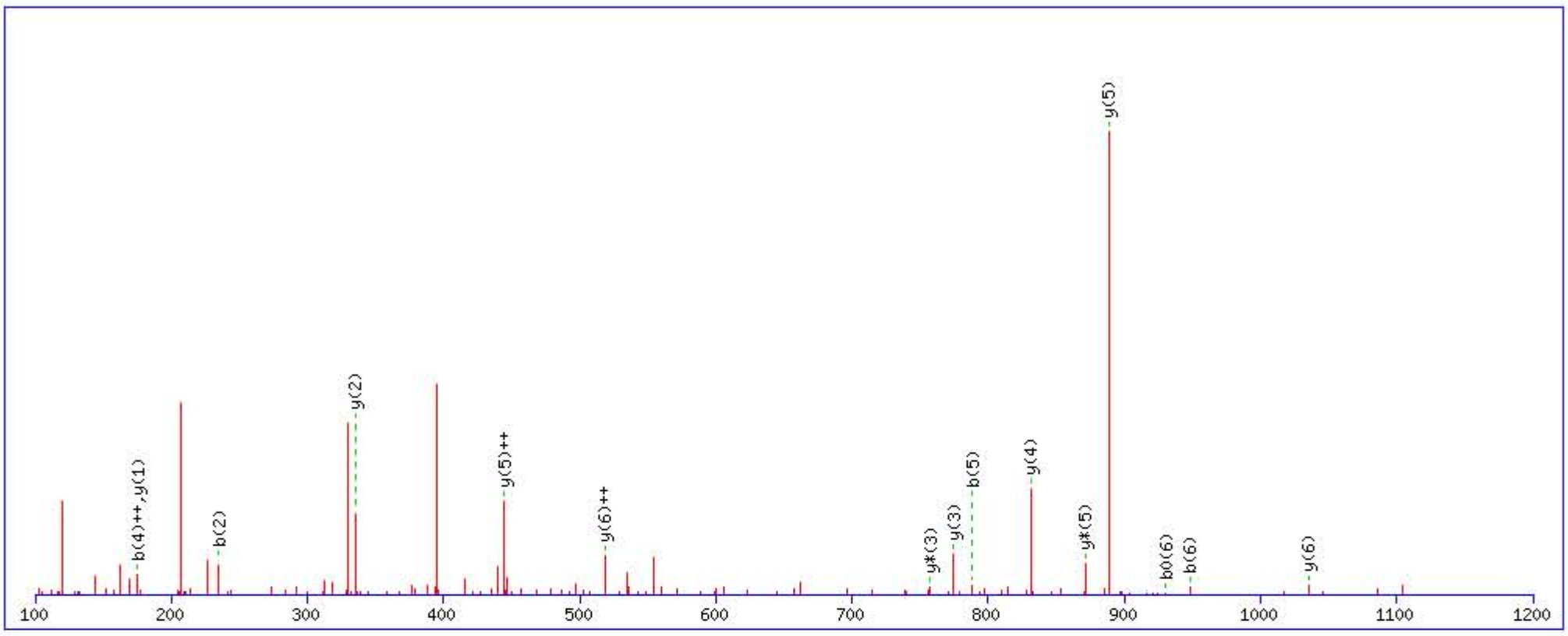
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SFGGQCR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

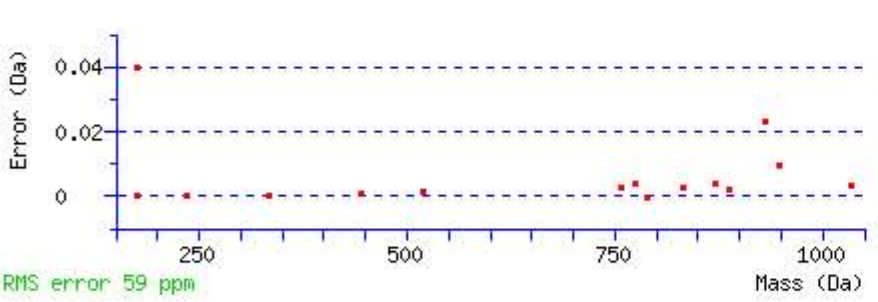
Match to Query 17383: 1121.512888 from(561.763720,2+) rtinseconds(1509) index(2693)
Title: Locus:1.1.1.1802.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

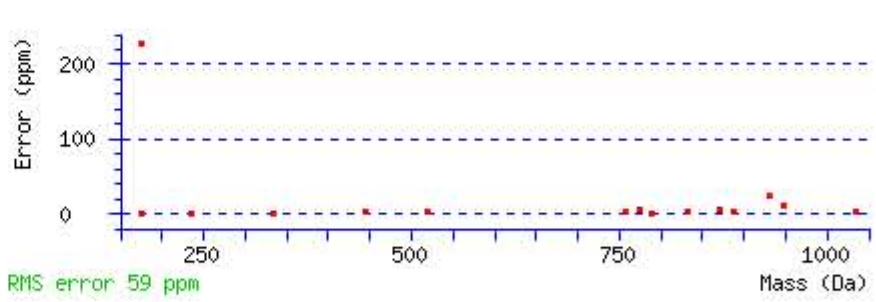
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1121.511032
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.0029
**Matches :** 15/52 fragment ions using 31 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | 7 |
| 2 | **235.107718** | 118.057497 | | | 217.097153 | 109.052214 | F | *1035.486269* | 518.246773 | 1018.459720 | 509.733498 | 6 |
| 3 | 292.129182 | 146.568229 | | | 274.118617 | 137.562946 | G | *888.417855* | 444.712566 | 871.391306 | 436.199291 | 5 |
| 4 | 349.150646 | 175.078961 | | | 331.140081 | 166.073678 | G | *831.396391* | 416.201834 | 814.369842 | 407.688559 | 4 |
| 5 | **788.375972** | 394.691624 | 771.349423 | 386.178350 | 770.365407 | 385.686342 | Q | *774.374927* | 387.691102 | 757.348378 | 379.177827 | 3 |
| 6 | **948.406621** | 474.706949 | 931.380072 | 466.193674 | 930.396056 | 465.701666 | C | *335.149601* | 168.078438 | 318.123052 | 159.565164 | 2 |
| 7 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.6 | 1121.511032 | 0.001856 | SFGGQCR |
| 4.3 | 1121.500259 | 0.012629 | HPGFHQEDR |
| 2.1 | 1121.502274 | 0.010614 | MSVEEQIDR |

**Mascot:** http://www.matrixscience.com/

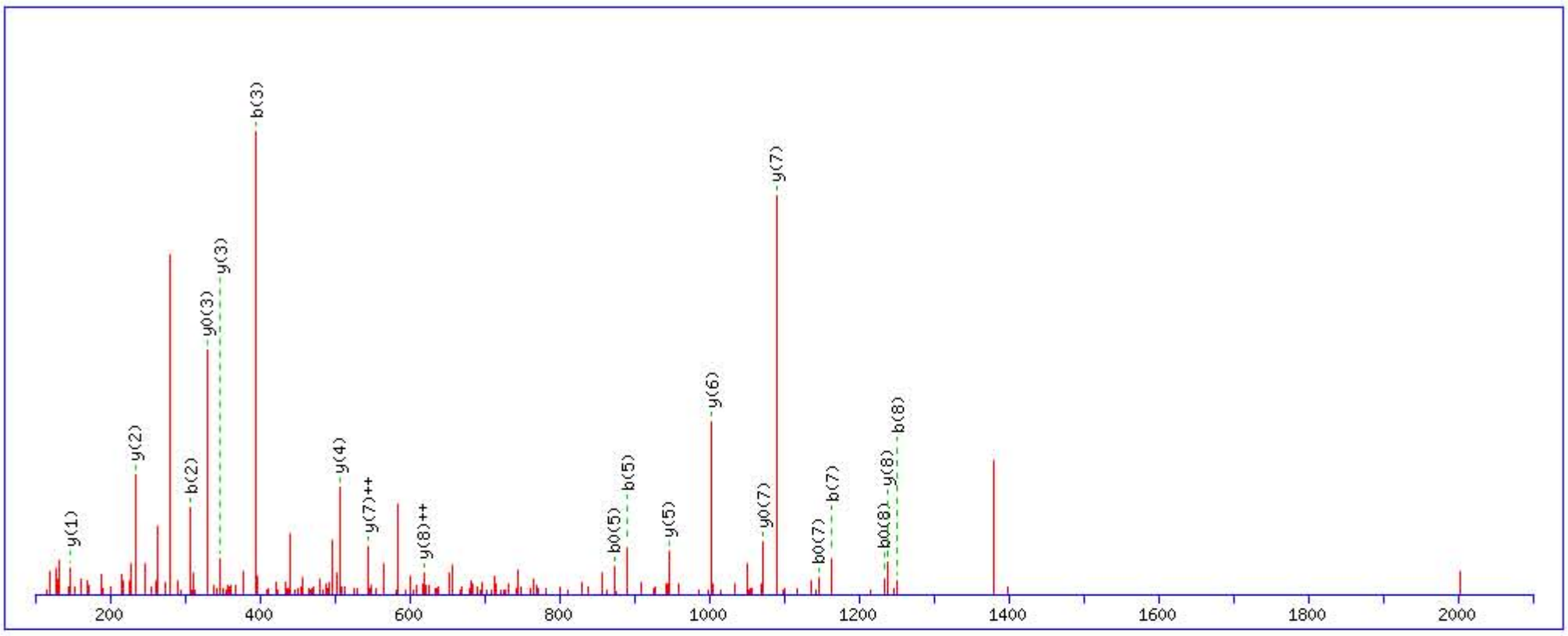
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **CFSGQCISK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

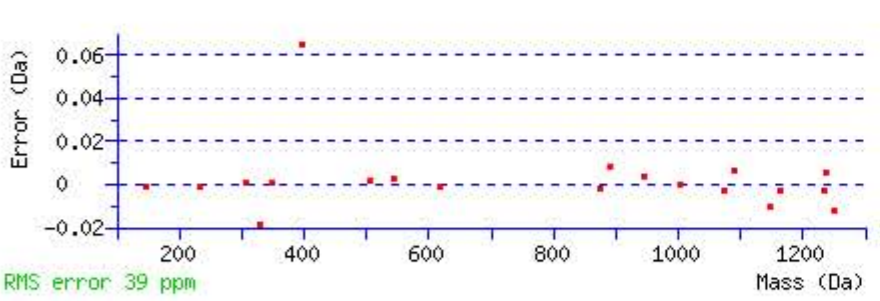
Match to Query 27214: 1396.634528 from(699.324540,2+) rtinseconds(1627) index(3407)
Title: Locus:1.1.1.1843.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

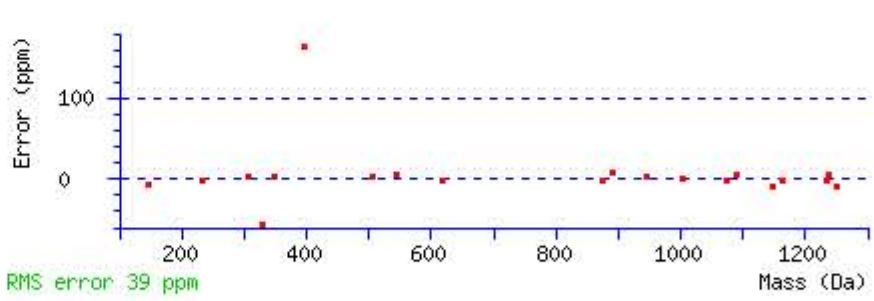
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1396.630157
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 49 **Expect:** 9.7e-005
**Matches :** 20/82 fragment ions using 37 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 161.037925 | 81.022600 | | | | | C | | | | | | | 9 |
| 2 | **308.106339** | 154.556807 | | | | | F | *1237.606777* | 619.307027 | 1220.580228 | 610.793752 | 1219.596212 | 610.301744 | 8 |
| 3 | **395.138367** | 198.072821 | | | 377.127802 | 189.067539 | S | *1090.538363* | 545.772819 | 1073.511814 | 537.259545 | 1072.527798 | 536.767537 | 7 |
| 4 | 452.159831 | 226.583553 | | | 434.149266 | 217.578271 | G | *1003.506335* | 502.256806 | 986.479786 | 493.743531 | 985.495770 | 493.251523 | 6 |
| 5 | **891.385157** | 446.196217 | 874.358608 | 437.682942 | 873.374592 | 437.190934 | Q | *946.484871* | 473.746074 | 929.458322 | 465.232799 | 928.474306 | 464.740791 | 5 |
| 6 | 1051.415806 | 526.211541 | 1034.389257 | 517.698267 | 1033.405241 | 517.206258 | C | *507.259545* | 254.133410 | 490.232996 | 245.620136 | 489.248980 | 245.128128 | 4 |
| 7 | **1164.499870** | 582.753573 | 1147.473321 | 574.240298 | 1146.489305 | 573.748290 | I | *347.228896* | 174.118086 | 330.202347 | 165.604811 | 329.218331 | 165.112803 | 3 |
| 8 | **1251.531898** | 626.269587 | 1234.505349 | 617.756313 | 1233.521333 | 617.264304 | S | *234.144832* | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 9 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 49.5 | 1396.630157 | 0.004371 | CFSGQCISK |
| 17.9 | 1396.629272 | 0.005256 | QLSQAEATDFCK |
| 2.5 | 1396.629257 | 0.005271 | FDNLMNQKEDK |

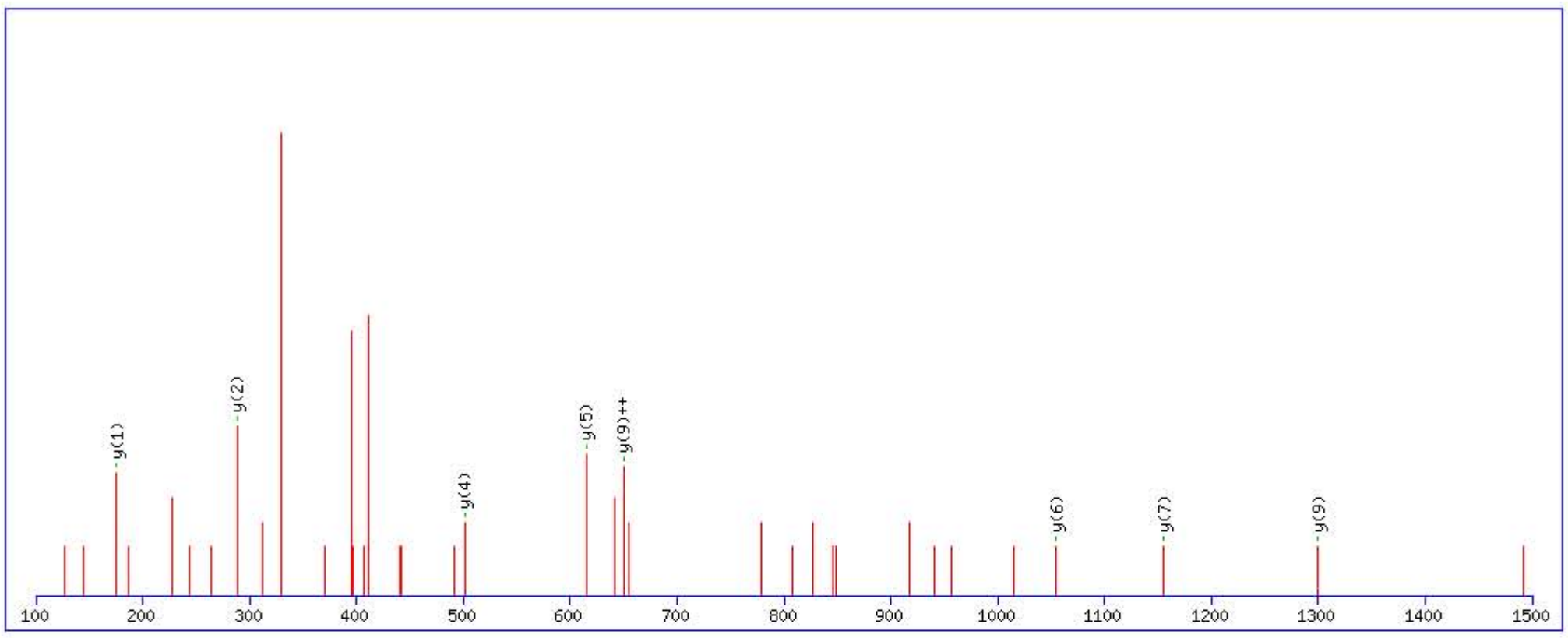
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AASGTQNNVLR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

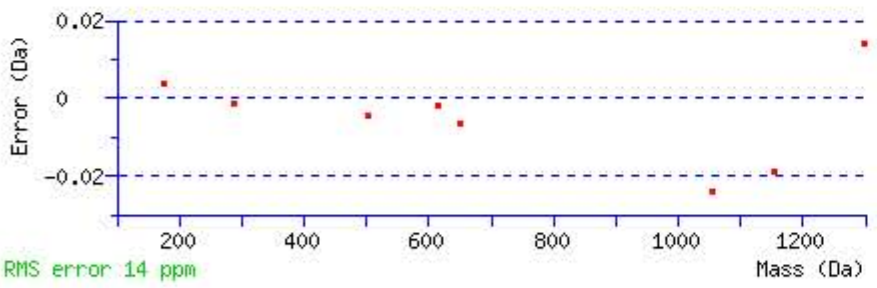
Match to Query 29389: 1440.752748 from(721.383650,2+) rtinseconds(1571) index(17434)
Title: Locus:1.1.1.2929.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

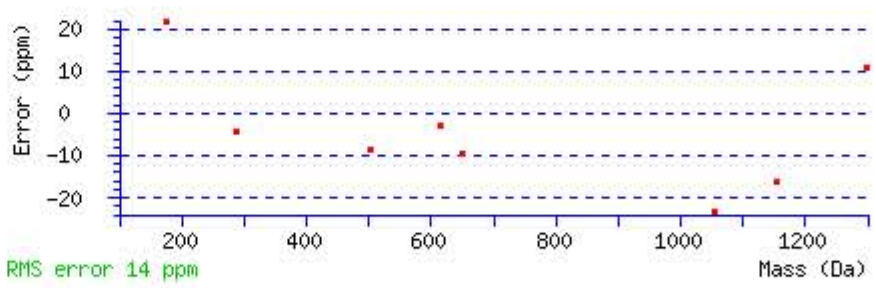
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1440.750717
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q6** : Biotin:Thermo-21345 (Q)
**Ions Score:** 51 **Expect:** 4.1e-005
**Matches** : 8/94 fragment ions using 12 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 11 |
| 2 | 143.081504 | 72.044390 | | | | | A | 1370.720895 | 685.864086 | 1353.694346 | 677.350811 | 1352.710330 | 676.858803 | 10 |
| 3 | 230.113532 | 115.560404 | | | 212.102967 | 106.555121 | S | *1299.683781* | 650.345529 | 1282.657232 | 641.832254 | 1281.673216 | 641.340246 | 9 |
| 4 | 287.134996 | 144.071136 | | | 269.124431 | 135.065854 | G | 1212.651753 | 606.829515 | 1195.625204 | 598.316240 | 1194.641188 | 597.824232 | 8 |
| 5 | 388.182675 | 194.594976 | | | 370.172110 | 185.589693 | T | *1155.630289* | 578.318783 | 1138.603740 | 569.805508 | 1137.619724 | 569.313500 | 7 |
| 6 | 827.408001 | 414.207639 | 810.381452 | 405.694364 | 809.397436 | 405.202356 | Q | *1054.582610* | 527.794943 | 1037.556061 | 519.281669 | | | 6 |
| 7 | 941.450928 | 471.229102 | 924.424379 | 462.715828 | 923.440363 | 462.223820 | N | *615.357284* | 308.182280 | 598.330735 | 299.669006 | | | 5 |
| 8 | 1055.493855 | 528.250566 | 1038.467306 | 519.737291 | 1037.483290 | 519.245283 | N | *501.314357* | 251.160816 | 484.287808 | 242.647542 | | | 4 |
| 9 | 1154.562269 | 577.784773 | 1137.535720 | 569.271498 | 1136.551704 | 568.779490 | V | 387.271430 | 194.139353 | 370.244881 | 185.626078 | | | 3 |
| 10 | 1267.646333 | 634.326805 | 1250.619784 | 625.813530 | 1249.635768 | 625.321522 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 51.3 | 1440.750717 | 0.002031 | AASGTQNNVLR |
| 4.5 | 1440.739487 | 0.013261 | AAVTGQDEAIR |

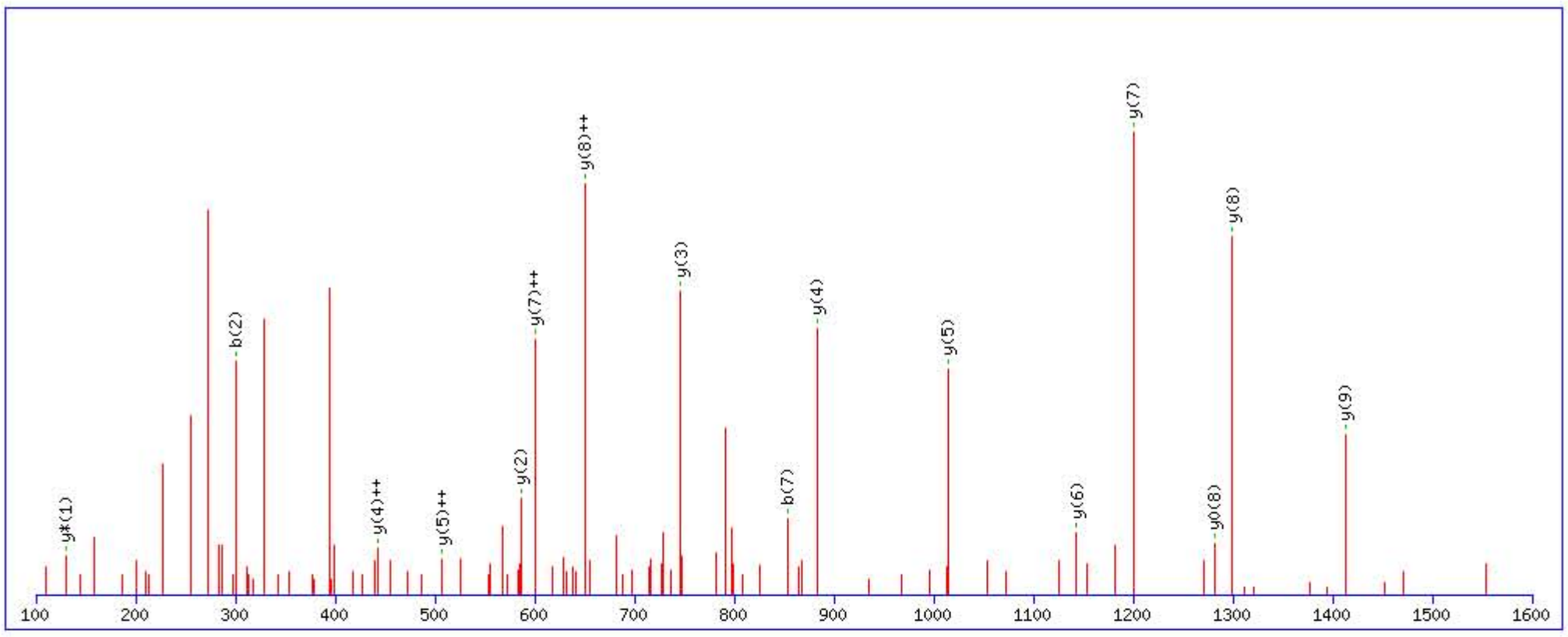
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **WLVGEMHCQK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

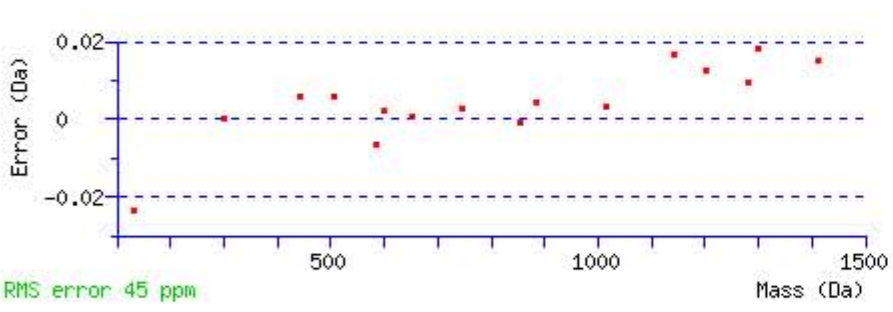
Match to Query 34632: 1597.775528 from(799.895040,2+) rtinseconds(1874) index(4726)
Title: Locus:1.1.1.1929.25 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

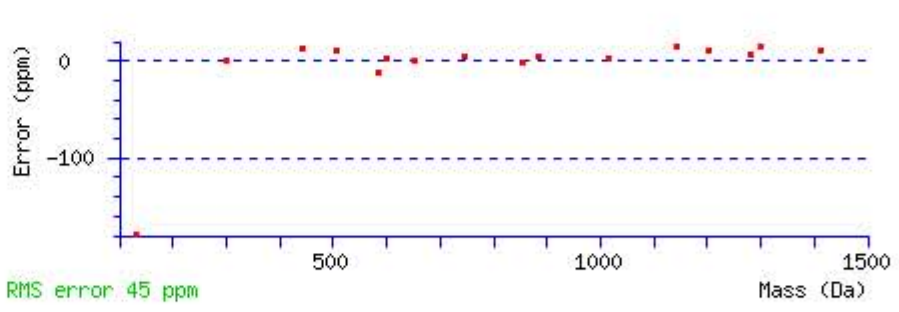
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1597.756744
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 50 **Expect:** 9.5e-005
**Matches :** 16/74 fragment ions using 29 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 187.086589 | 94.046932 | | | | | W | | | | | | | 10 |
| 2 | **300.170653** | 150.588965 | | | | | L | *1412.684711* | 706.845994 | 1395.658162 | 698.332719 | 1394.674146 | 697.840711 | 9 |
| 3 | 399.239067 | 200.123172 | | | | | V | *1299.600647* | 650.303962 | 1282.574098 | 641.790687 | 1281.590082 | 641.298679 | 8 |
| 4 | 456.260531 | 228.633904 | | | | | G | *1200.532233* | 600.769755 | 1183.505684 | 592.256480 | 1182.521668 | 591.764472 | 7 |
| 5 | 585.303124 | 293.155200 | | | 567.292559 | 284.149918 | E | *1143.510769* | 572.259023 | 1126.484220 | 563.745748 | 1125.500204 | 563.253740 | 6 |
| 6 | 716.343609 | 358.675443 | | | 698.333044 | 349.670160 | M | *1014.468176* | 507.737726 | 997.441627 | 499.224452 | | | 5 |
| 7 | **853.402521** | 427.204899 | | | 835.391956 | 418.199616 | H | *883.427691* | 442.217484 | 866.401142 | 433.704209 | | | 4 |
| 8 | 1013.433170 | 507.220223 | | | 995.422605 | 498.214941 | C | *746.368779* | 373.688028 | 729.342230 | 365.174753 | | | 3 |
| 9 | 1452.658496 | 726.832886 | 1435.631947 | 718.319612 | 1434.647931 | 717.827604 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 10 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 49.7 | 1597.756744 | 0.018784 | WLVGEMHCQK |
| 6.4 | 1597.763718 | 0.011810 | LWKDEGRWEHDK |
| 4.9 | 1597.751846 | 0.023682 | NPEDDGCLLKQGPR |
| 3.5 | 1597.763062 | 0.012466 | RDAELIQAGHMDSR |
| 0.5 | 1597.784393 | -0.008865 | GAMGIMLVYDITNGK |

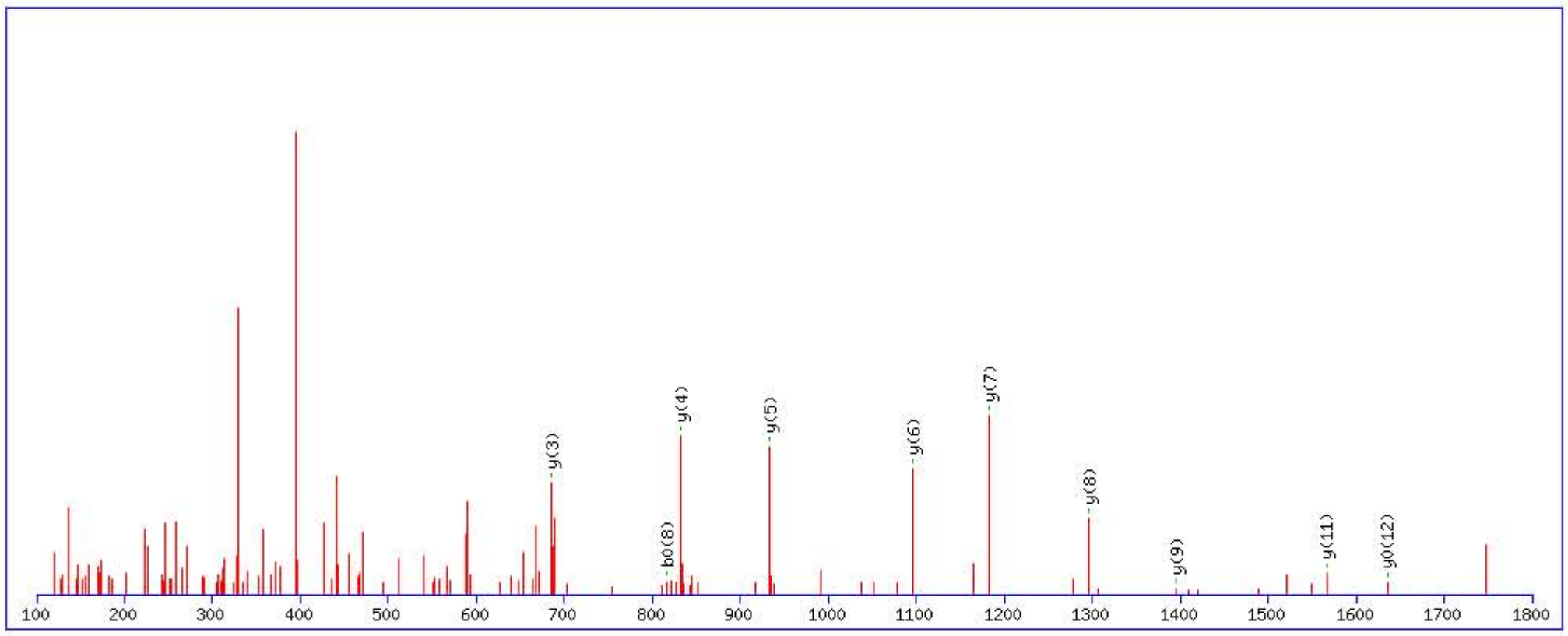
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LSGNVLSYTFQVK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

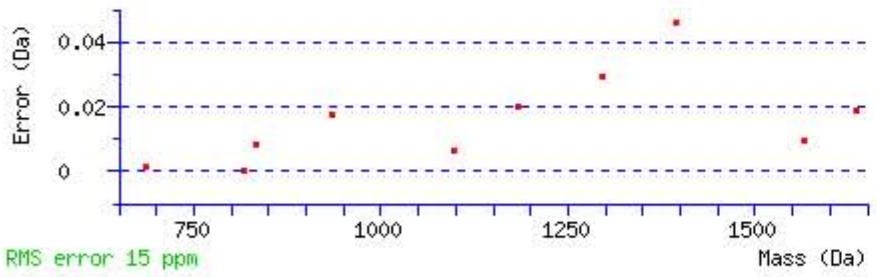
Match to Query 39470: 1765.952742 from(589.658190,3+) rtinseconds(2481) index(8193)
Title: Locus:1.1.1.2141.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

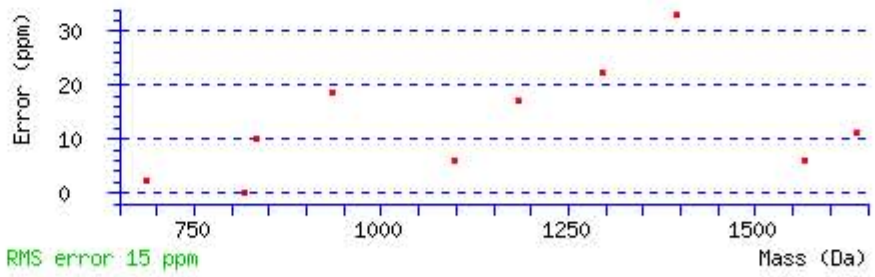
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1765.943680
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 3.5e-005
**Matches :** 10/128 fragment ions using 17 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 13 |
| 2 | 201.123368 | 101.065322 | | | 183.112803 | 92.060039 | S | 1653.866891 | 827.437084 | 1636.840342 | 818.923809 | 1635.856326 | 818.431801 | 12 |
| 3 | 258.144832 | 129.576054 | | | 240.134267 | 120.570771 | G | *1566.834863* | 783.921070 | 1549.808314 | 775.407795 | 1548.824298 | 774.915787 | 11 |
| 4 | 372.187759 | 186.597517 | 355.161210 | 178.084243 | 354.177194 | 177.592235 | N | 1509.813399 | 755.410338 | 1492.786850 | 746.897063 | 1491.802834 | 746.405055 | 10 |
| 5 | 471.256173 | 236.131724 | 454.229624 | 227.618450 | 453.245608 | 227.126442 | V | *1395.770472* | 698.388874 | 1378.743923 | 689.875600 | 1377.759907 | 689.383592 | 9 |
| 6 | 584.340237 | 292.673757 | 567.313688 | 284.160482 | 566.329672 | 283.668474 | L | *1296.702058* | 648.854667 | 1279.675509 | 640.341393 | 1278.691493 | 639.849385 | 8 |
| 7 | 671.372265 | 336.189771 | 654.345716 | 327.676496 | 653.361700 | 327.184488 | S | *1183.617994* | 592.312635 | 1166.591445 | 583.799361 | 1165.607429 | 583.307353 | 7 |
| 8 | 834.435594 | 417.721435 | 817.409045 | 409.208161 | 816.425029 | 408.716153 | Y | *1096.585966* | 548.796621 | 1079.559417 | 540.283347 | 1078.575401 | 539.791339 | 6 |
| 9 | 935.483273 | 468.245275 | 918.456724 | 459.732000 | 917.472708 | 459.239992 | T | *933.522637* | 467.264957 | 916.496088 | 458.751682 | 915.512072 | 458.259674 | 5 |
| 10 | 1082.551687 | 541.779482 | 1065.525138 | 533.266207 | 1064.541122 | 532.774199 | F | *832.474958* | 416.741117 | 815.448409 | 408.227843 | | | 4 |
| 11 | 1521.777013 | 761.392145 | 1504.750464 | 752.878870 | 1503.766448 | 752.386862 | Q | *685.406544* | 343.206910 | 668.379995 | 334.693636 | | | 3 |
| 12 | 1620.845427 | 810.926352 | 1603.818878 | 802.413077 | 1602.834862 | 801.921069 | V | 246.181218 | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 13 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 47.7 | 1765.943680 | 0.009062 | LSGNVLSYTFQVK |
| 0.2 | 1765.950882 | 0.001860 | VTGNVSKKTNYLVMGR |

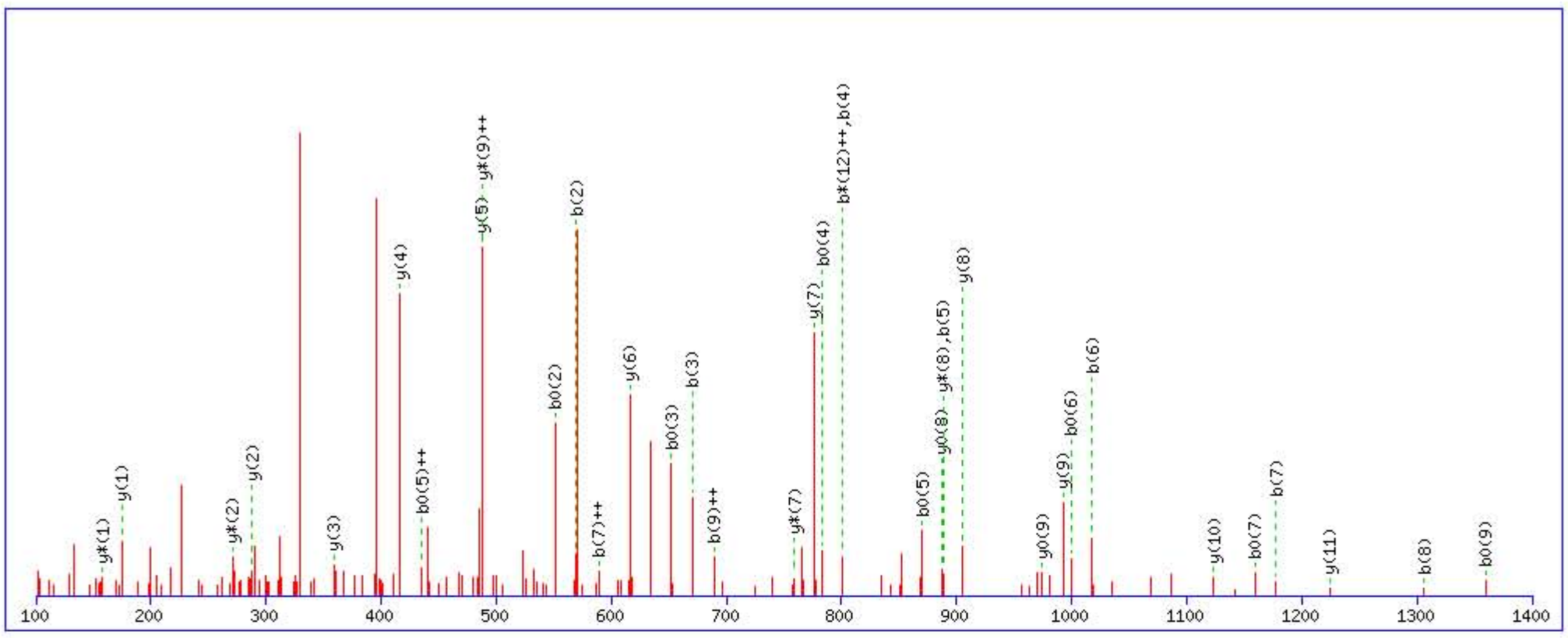
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EQTMSECEAGALR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

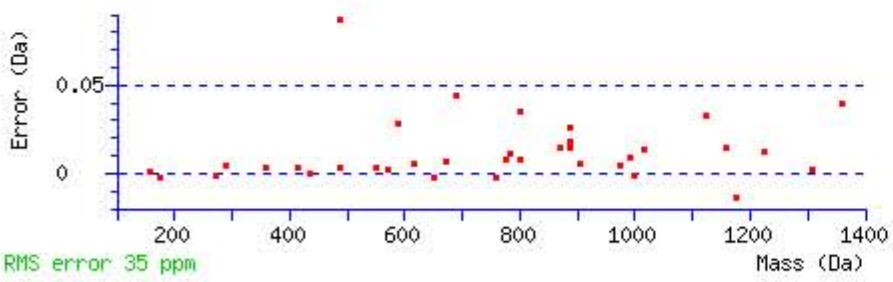
Match to Query 40100: 1791.798102 from(598.273310,3+) rtinseconds(1752) index(4102)
Title: Locus:1.1.1.1887.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

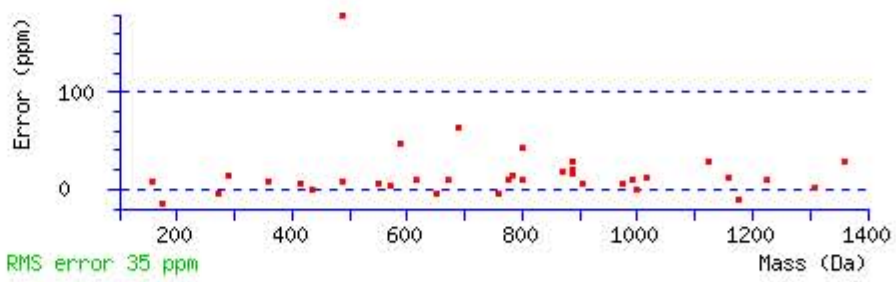
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1791.795349
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 9.2e-006
**Matches :** 36/132 fragment ions using 66 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 13 |
| 2 | **569.275195** | 285.141236 | 552.248646 | 276.627961 | 551.264630 | 276.135953 | Q | 1663.760061 | 832.383668 | 1646.733512 | 823.870394 | 1645.749496 | 823.378386 | 12 |
| 3 | **670.322874** | 335.665075 | 653.296325 | 327.151801 | 652.312309 | 326.659793 | T | *1224.534735* | 612.771005 | 1207.508186 | 604.257731 | 1206.524170 | 603.765723 | 11 |
| 4 | **801.363359** | 401.185318 | 784.336810 | 392.672043 | 783.352794 | 392.180035 | M | *1123.487056* | 562.247166 | 1106.460507 | 553.733891 | 1105.476491 | 553.241883 | 10 |
| 5 | **888.395387** | 444.701332 | 871.368838 | 436.188057 | 870.384822 | 435.696049 | S | *992.446571* | 496.726923 | 975.420022 | 488.213649 | 974.436006 | 487.721641 | 9 |
| 6 | **1017.437980** | 509.222628 | 1000.411431 | 500.709354 | 999.427415 | 500.217346 | E | *905.414543* | 453.210909 | 888.387994 | 444.697635 | 887.403978 | 444.205627 | 8 |
| 7 | **1177.468629** | **589.237953** | 1160.442080 | 580.724678 | 1159.458064 | 580.232670 | C | *776.371950* | 388.689613 | 759.345401 | 380.176338 | 758.361385 | 379.684330 | 7 |
| 8 | **1306.511222** | 653.759249 | 1289.484673 | 645.245974 | 1288.500657 | 644.753966 | E | *616.341301* | 308.674288 | 599.314752 | 300.161014 | 598.330736 | 299.669006 | 6 |
| 9 | 1377.548336 | **689.277806** | 1360.521787 | 680.764531 | 1359.537771 | 680.272523 | A | *487.298708* | 244.152992 | 470.272159 | 235.639717 | | | 5 |
| 10 | 1434.569800 | 717.788538 | 1417.543251 | 709.275263 | 1416.559235 | 708.783255 | G | *416.261594* | 208.634435 | 399.235045 | 200.121160 | | | 4 |
| 11 | 1505.606914 | 753.307095 | 1488.580365 | 744.793820 | 1487.596349 | 744.301812 | A | *359.240130* | 180.123703 | 342.213581 | 171.610428 | | | 3 |
| 12 | 1618.690978 | 809.849127 | 1601.664429 | 801.335852 | 1600.680413 | 800.843844 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 13 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 59.4 | 1791.795349 | 0.002753 | EQTMSECEAGALR |

**Mascot:** http://www.matrixscience.com/

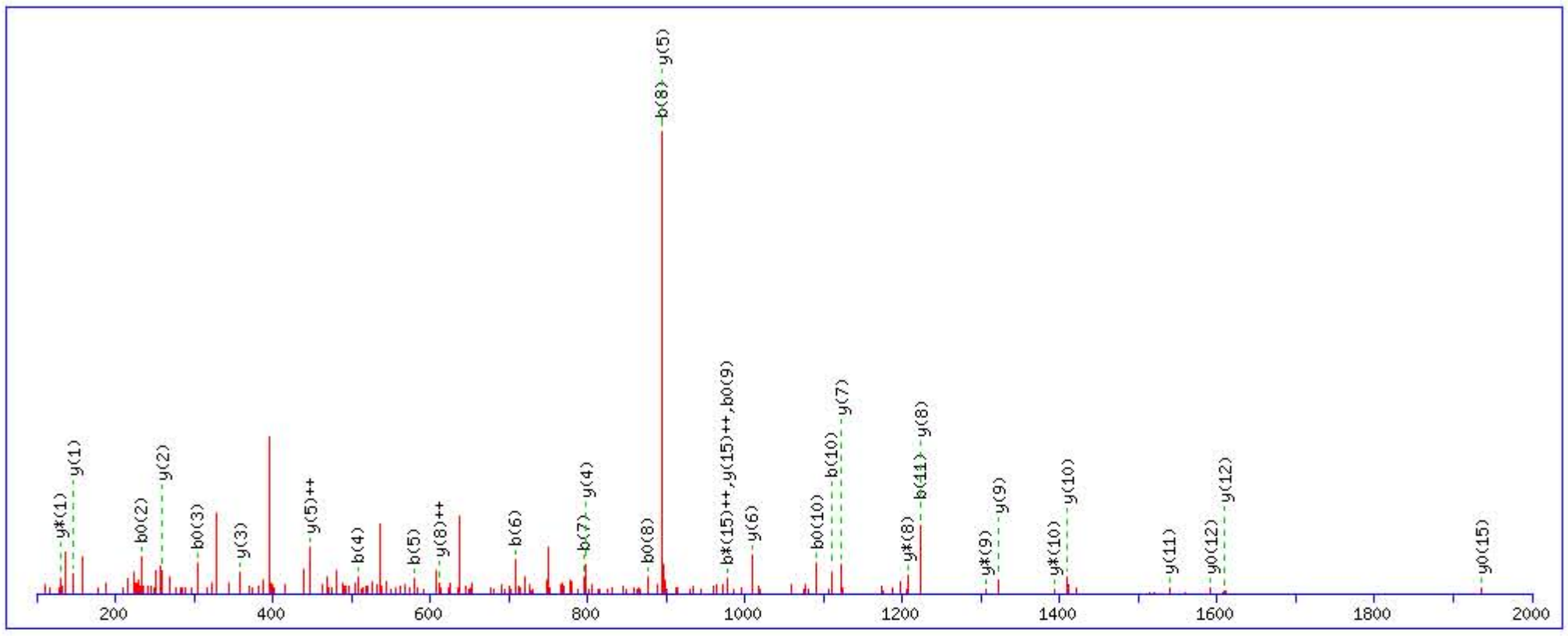
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YSAWAESVTNLPQVIK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

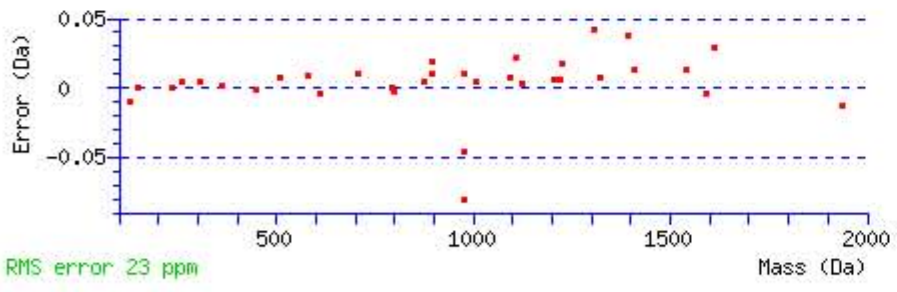
Match to Query 46851: 2116.115262 from(706.379030,3+) rtinseconds(2593) index(8710)
Title: Locus:1.1.1.2180.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

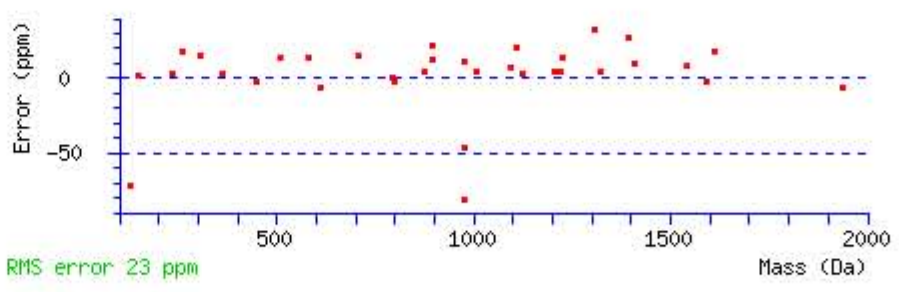
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2116.102676
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 68 **Expect:** 4.3e-006
**Matches :** 34/146 fragment ions using 59 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 16 |
| 2 | 251.102633 | 126.054954 | | | 233.092068 | 117.049672 | S | 1954.046646 | 977.526961 | 1937.020097 | 969.013687 | 1936.036081 | 968.521679 | 15 |
| 3 | 322.139747 | 161.573512 | | | 304.129182 | 152.568229 | A | 1867.014618 | 934.010947 | 1849.988069 | 925.497673 | 1849.004053 | 925.005665 | 14 |
| 4 | **508.219060** | 254.613168 | | | 490.208495 | 245.607886 | W | 1795.977504 | 898.492390 | 1778.950955 | 889.979116 | 1777.966939 | 889.487108 | 13 |
| 5 | **579.256174** | 290.131725 | | | 561.245609 | 281.126443 | A | ***1609.898191*** | 805.452734 | 1592.871642 | 796.939459 | 1591.887626 | 796.447451 | 12 |
| 6 | **708.298767** | 354.653022 | | | 690.288202 | 345.647739 | E | ***1538.861077*** | 769.934177 | 1521.834528 | 761.420902 | 1520.850512 | 760.928894 | 11 |
| 7 | **795.330795** | 398.169036 | | | 777.320230 | 389.163753 | S | ***1409.818484*** | 705.412880 | 1392.791935 | 696.899606 | 1391.807919 | 696.407598 | 10 |
| 8 | **894.399209** | 447.703243 | | | 876.388644 | 438.697960 | V | ***1322.786456*** | 661.896866 | 1305.759907 | 653.383592 | 1304.775891 | 652.891584 | 9 |
| 9 | 995.446888 | 498.227082 | | | 977.436323 | 489.221800 | T | ***1223.718042*** | 612.362659 | 1206.691493 | 603.849385 | 1205.707477 | 603.357377 | 8 |
| 10 | **1109.489815** | 555.248546 | 1092.463266 | 546.735271 | 1091.479250 | 546.243263 | N | ***1122.670363*** | 561.838820 | 1105.643814 | 553.325545 | | | 7 |
| 11 | **1222.573879** | 611.790578 | 1205.547330 | 603.277303 | 1204.563314 | 602.785295 | L | ***1008.627436*** | 504.817356 | 991.600887 | 496.304082 | | | 6 |
| 12 | 1319.626643 | 660.316960 | 1302.600094 | 651.803685 | 1301.616078 | 651.311677 | P | ***895.543372*** | 448.275324 | 878.516823 | 439.762050 | | | 5 |
| 13 | 1758.851969 | 879.929623 | 1741.825420 | 871.416348 | 1740.841404 | 870.924340 | Q | ***798.490608*** | 399.748942 | 781.464059 | 391.235668 | | | 4 |
| 14 | 1857.920383 | 929.463830 | 1840.893834 | 920.950555 | 1839.909818 | 920.458547 | V | ***359.265282*** | 180.136279 | 342.238733 | 171.623004 | | | 3 |
| 15 | 1971.004447 | 986.005862 | 1953.977898 | 977.492587 | 1952.993882 | 977.000579 | I | ***260.196868*** | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 16 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 67.9 | 2116.102676 | 0.012586 | YSAWAESVTNLPQVIK |

**Mascot:** http://www.matrixscience.com/

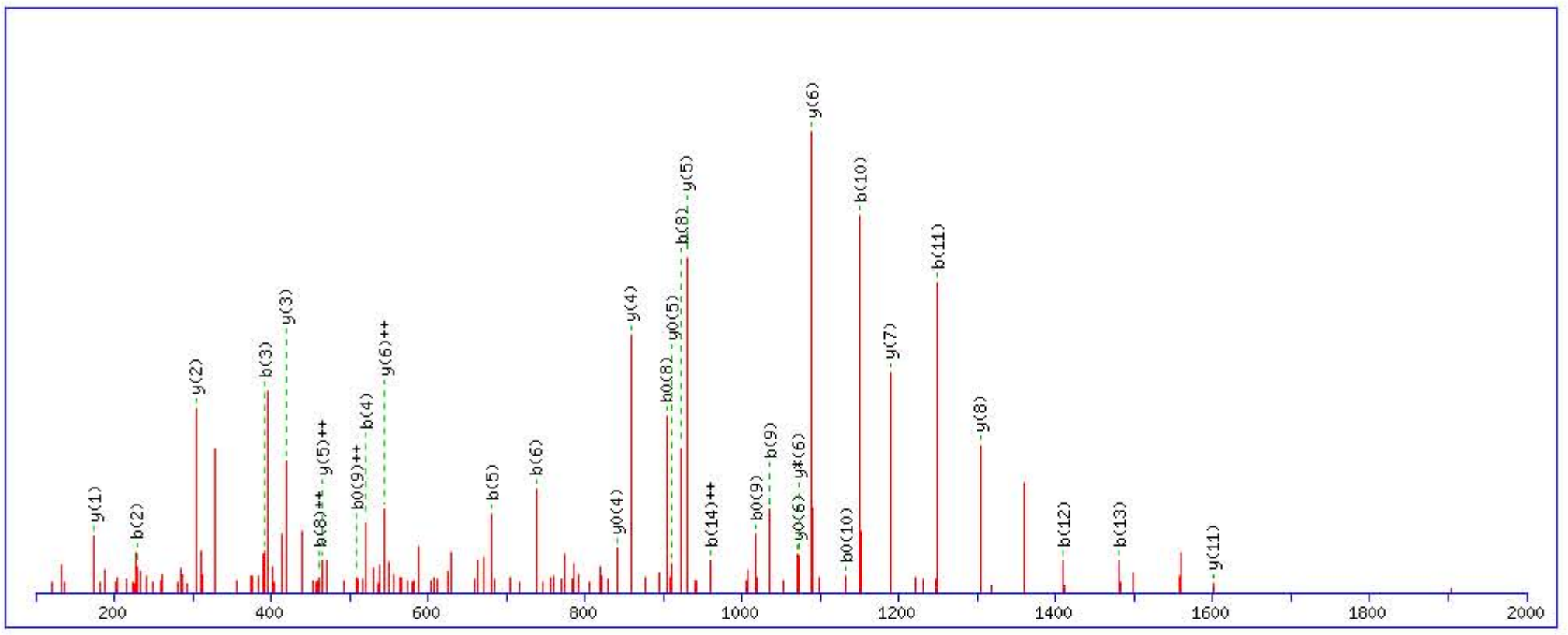
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MPYECGPSLDVCAQDER**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

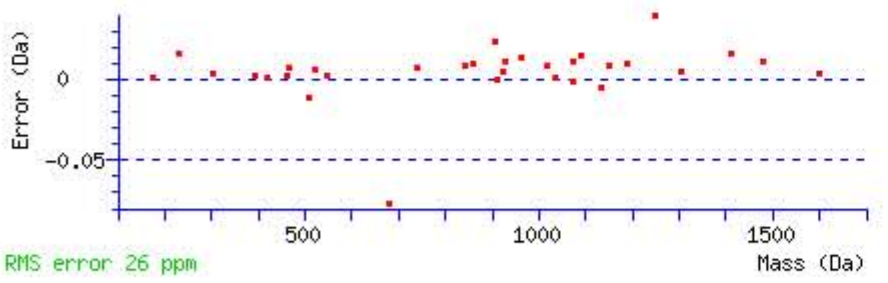
Match to Query 51199: 2337.007482 from(780.009770,3+) rtinseconds(2112) index(6252)
Title: Locus:1.1.1.2012.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

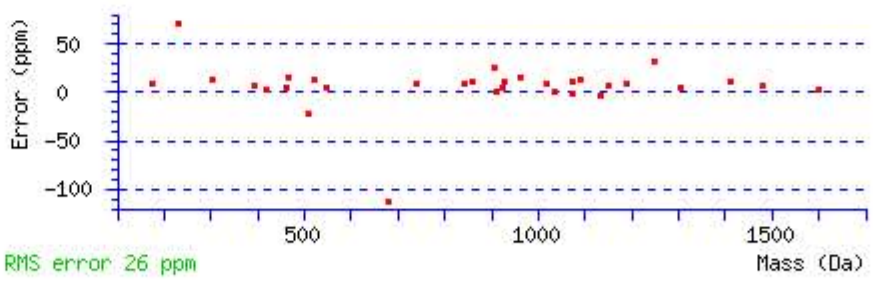
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2336.989792
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q14 : Biotin:Thermo-21345 (Q)
**Ions Score:** 55 **Expect:** 1.4e-005
**Matches :** 32/158 fragment ions using 69 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.047761 | 66.527518 | | | | | M | | | | | | | 17 |
| 2 | *229.100525* | 115.053900 | | | | | P | 2206.956589 | 1103.981932 | 2189.930040 | 1095.468658 | 2188.946024 | 1094.976650 | 16 |
| 3 | *392.163854* | 196.585565 | | | | | Y | 2109.903825 | 1055.455550 | 2092.877276 | 1046.942276 | 2091.893260 | 1046.450268 | 15 |
| 4 | *521.206447* | 261.106862 | | | 503.195882 | 252.101579 | E | 1946.840496 | 973.923886 | 1929.813947 | 965.410612 | 1928.829931 | 964.918604 | 14 |
| 5 | *681.237096* | 341.122186 | | | 663.226531 | 332.116904 | C | 1817.797903 | 909.402590 | 1800.771354 | 900.889315 | 1799.787338 | 900.397307 | 13 |
| 6 | *738.258560* | 369.632918 | | | 720.247995 | 360.627636 | G | 1657.767254 | 829.387265 | 1640.740705 | 820.873991 | 1639.756689 | 820.381983 | 12 |
| 7 | 835.311324 | 418.159300 | | | 817.300759 | 409.154018 | P | *1600.745790* | 800.876533 | 1583.719241 | 792.363259 | 1582.735225 | 791.871251 | 11 |
| 8 | *922.343352* | **461.675314** | | | 904.332787 | 452.670032 | S | 1503.693026 | 752.350151 | 1486.666477 | 743.836877 | 1485.682461 | 743.344869 | 10 |
| 9 | *1035.427416* | 518.217346 | | | 1017.416851 | 509.212064 | L | 1416.660998 | 708.834137 | 1399.634449 | 700.320863 | 1398.650433 | 699.828855 | 9 |
| 10 | *1150.454359* | 575.730818 | | | 1132.443794 | 566.725535 | D | *1303.576934* | 652.292105 | 1286.550385 | 643.778831 | 1285.566369 | 643.286823 | 8 |
| 11 | *1249.522773* | 625.265025 | | | 1231.512208 | 616.259742 | V | *1188.549991* | 594.778634 | 1171.523442 | 586.265359 | 1170.539426 | 585.773351 | 7 |
| 12 | *1409.553422* | 705.280349 | | | 1391.542857 | 696.275067 | C | *1089.481577* | 545.244427 | 1072.455028 | 536.731152 | 1071.471012 | 536.239144 | 6 |
| 13 | *1480.590536* | 740.798906 | | | 1462.579971 | 731.793624 | A | *929.450928* | 465.229102 | 912.424379 | 456.715827 | 911.440363 | 456.223819 | 5 |
| 14 | 1919.815862 | **960.411569** | 1902.789313 | 951.898295 | 1901.805297 | 951.406287 | Q | *858.413814* | 429.710545 | 841.387265 | 421.197271 | 840.403249 | 420.705263 | 4 |
| 15 | 2034.842805 | 1017.925041 | 2017.816256 | 1009.411766 | 2016.832240 | 1008.919758 | D | *419.188488* | 210.097882 | 402.161939 | 201.584607 | 401.177923 | 201.092599 | 3 |
| 16 | 2163.885398 | 1082.446337 | 2146.858849 | 1073.933062 | 2145.874833 | 1073.441054 | E | *304.161545* | 152.584410 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 17 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 54.6 | 2336.989792 | 0.017690 | MPYECGPSLDVCAQDER |

**Mascot:** http://www.matrixscience.com/

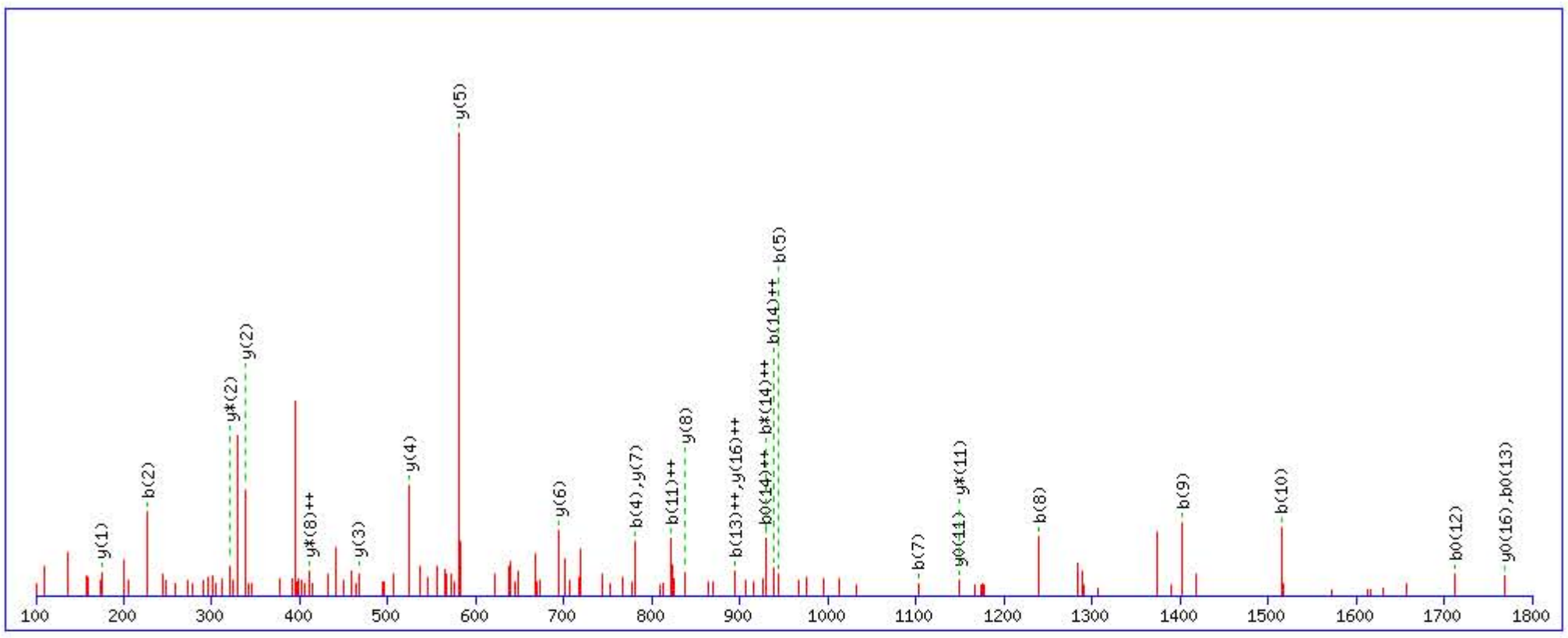
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LIDQYGTHYLQSGSLGGEYR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

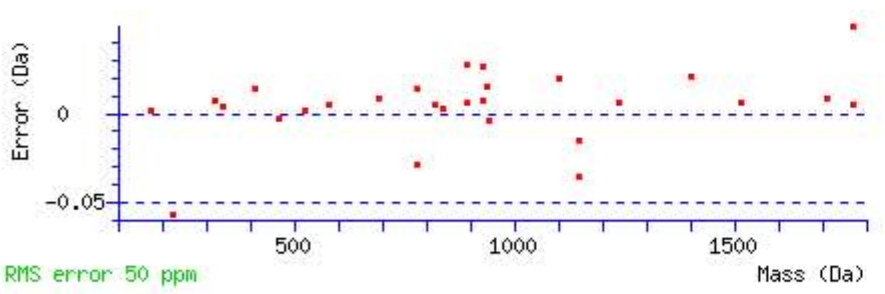
Match to Query 55108: 2567.271176 from(642.825070,4+) rtinseconds(2123) index(6302)
Title: Locus:1.1.1.2016.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

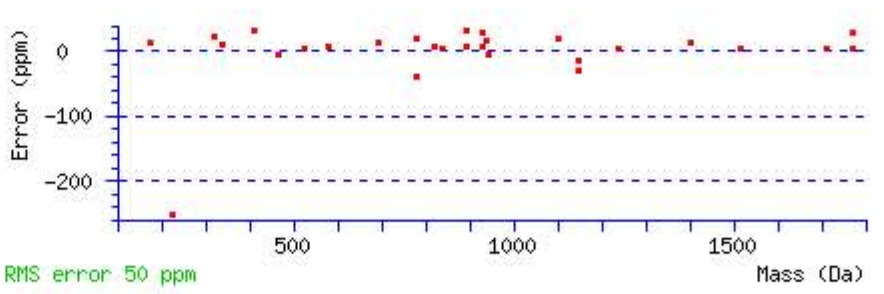
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2567.247849
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.004
**Matches :** 28/214 fragment ions using 60 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 20 |
| 2 | *227.175404* | 114.091340 | | | | | I | 2455.171074 | 1228.089175 | 2438.144525 | 1219.575900 | 2437.160509 | 1219.083892 | 19 |
| 3 | 342.202347 | 171.604811 | | | 324.191782 | 162.599529 | D | 2342.087010 | 1171.547143 | 2325.060461 | 1163.033868 | 2324.076445 | 1162.541860 | 18 |
| 4 | *781.427673* | 391.217475 | 764.401124 | 382.704200 | 763.417108 | 382.212192 | Q | 2227.060067 | 1114.033671 | 2210.033518 | 1105.520397 | 2209.049502 | 1105.028389 | 17 |
| 5 | *944.491002* | 472.749139 | 927.464453 | 464.235864 | 926.480437 | 463.743856 | Y | 1787.834741 | 894.421009 | 1770.808192 | 885.907734 | 1769.824176 | 885.415726 | 16 |
| 6 | 1001.512466 | 501.259871 | 984.485917 | 492.746597 | 983.501901 | 492.254589 | G | 1624.771412 | 812.889344 | 1607.744863 | 804.376070 | 1606.760847 | 803.884062 | 15 |
| 7 | *1102.560145* | 551.783710 | 1085.533596 | 543.270436 | 1084.549580 | 542.778428 | T | 1567.749948 | 784.378612 | 1550.723399 | 775.865338 | 1549.739383 | 775.373330 | 14 |
| 8 | *1239.619057* | 620.313166 | 1222.592508 | 611.799892 | 1221.608492 | 611.307884 | H | 1466.702269 | 733.854773 | 1449.675720 | 725.341498 | 1448.691704 | 724.849490 | 13 |
| 9 | *1402.682386* | 701.844831 | 1385.655837 | 693.331557 | 1384.671821 | 692.839548 | Y | 1329.643357 | 665.325317 | 1312.616808 | 656.812042 | 1311.632792 | 656.320034 | 12 |
| 10 | *1515.766450* | 758.386863 | 1498.739901 | 749.873588 | 1497.755885 | 749.381580 | L | 1166.580028 | 583.793652 | 1149.553479 | 575.280378 | 1148.569463 | 574.788370 | 11 |
| 11 | 1643.825028 | **822.416152** | 1626.798479 | 813.902878 | 1625.814463 | 813.410869 | Q | 1053.495964 | 527.251620 | 1036.469415 | 518.738346 | 1035.485399 | 518.246338 | 10 |
| 12 | 1730.857056 | 865.932166 | 1713.830507 | 857.418892 | 1712.846491 | 856.926884 | S | 925.437386 | 463.222331 | 908.410837 | 454.709057 | 907.426821 | 454.217049 | 9 |
| 13 | 1787.878520 | **894.442898** | 1770.851971 | 885.929624 | 1769.867955 | 885.437615 | G | *838.405358* | 419.706317 | 821.378809 | 411.193043 | 820.394793 | 410.701035 | 8 |
| 14 | 1874.910548 | **937.958912** | 1857.883999 | 929.445638 | 1856.899983 | 928.953630 | S | *781.383894* | 391.195585 | 764.357345 | 382.682311 | 763.373329 | 382.190303 | 7 |
| 15 | 1987.994612 | 994.500944 | 1970.968063 | 985.987670 | 1969.984047 | 985.495661 | L | *694.351866* | 347.679571 | 677.325317 | 339.166297 | 676.341301 | 338.674289 | 6 |
| 16 | 2045.016076 | 1023.011676 | 2027.989527 | 1014.498402 | 2027.005511 | 1014.006393 | G | *581.267802* | 291.137539 | 564.241253 | 282.624265 | 563.257237 | 282.132257 | 5 |
| 17 | 2102.037540 | 1051.522408 | 2085.010991 | 1043.009133 | 2084.026975 | 1042.517125 | G | *524.246338* | 262.626807 | 507.219789 | 254.113533 | 506.235773 | 253.621525 | 4 |
| 18 | 2231.080133 | 1116.043704 | 2214.053584 | 1107.530430 | 2213.069568 | 1107.038422 | E | *467.224874* | 234.116075 | 450.198325 | 225.602801 | 449.214309 | 225.110793 | 3 |
| 19 | 2394.143462 | 1197.575369 | 2377.116913 | 1189.062094 | 2376.132897 | 1188.570086 | Y | *338.182281* | 169.594778 | 321.155732 | 161.081504 | | | 2 |
| 20 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.3 | 2567.247849 | 0.023327 | LIDQYGTHYLQSGSLGGEYR |
| 12.0 | 2567.247849 | 0.023327 | LIDQYGTHYLQSGSLGGEYR |

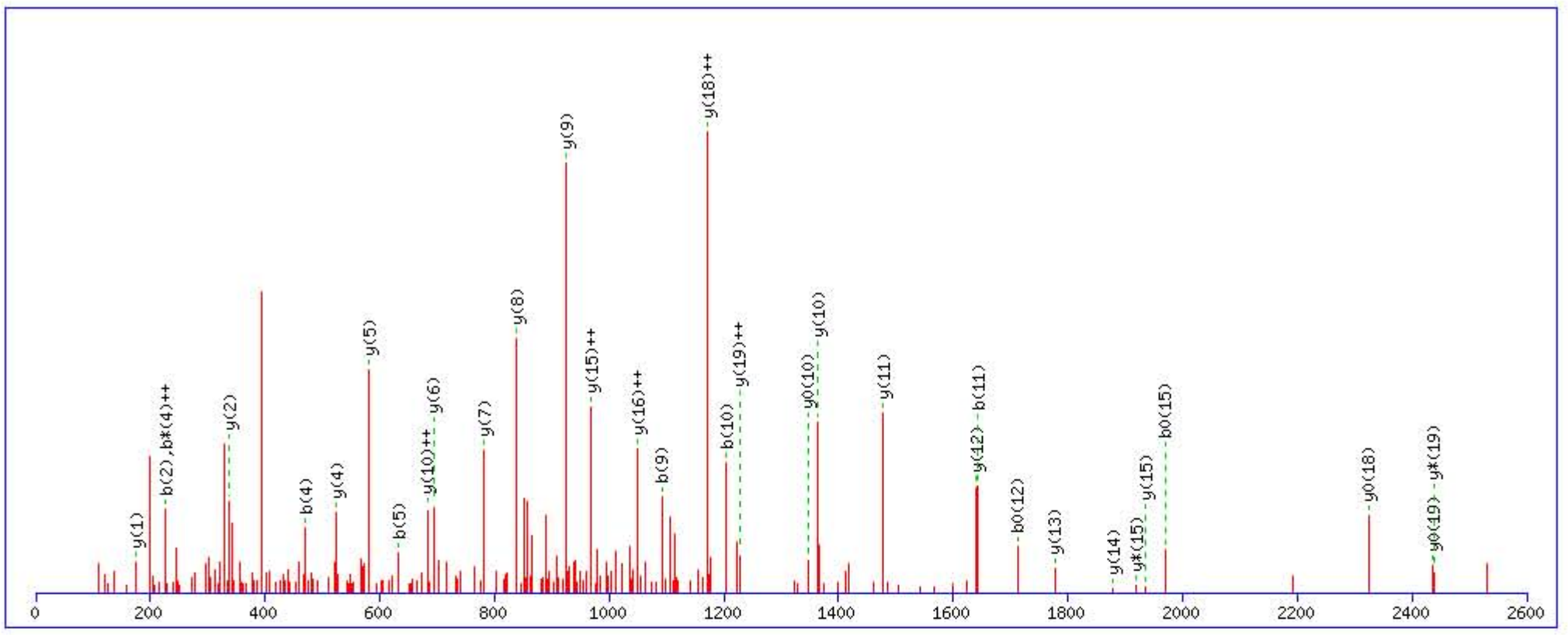
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LIDQYGTHYLQSGSLGGEYR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

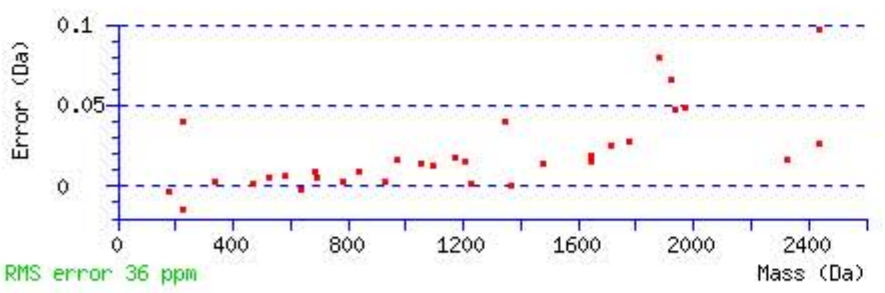
Match to Query 55109: 2567.275902 from(856.765910,3+) rtinseconds(2104) index(6210)
Title: Locus:1.1.1.2009.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

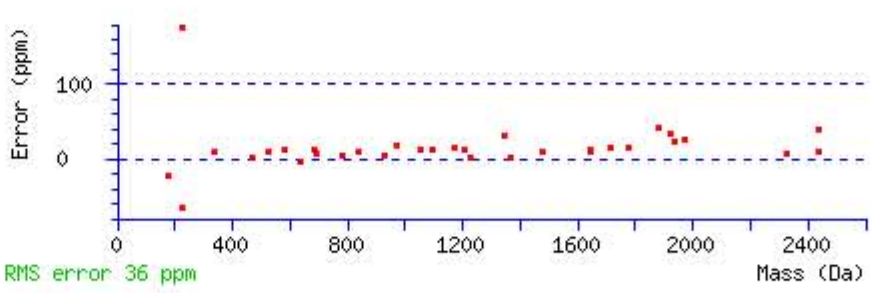
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2567.247849
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q11 : Biotin:Thermo-21345 (Q)
**Ions Score:** 82 **Expect:** 1.9e-007
**Matches :** 33/214 fragment ions using 60 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 20 |
| 2 | 227.175404 | 114.091340 | | | | | I | 2455.171074 | 1228.089175 | 2438.144525 | 1219.575900 | 2437.160509 | 1219.083892 | 19 |
| 3 | 342.202347 | 171.604811 | | | 324.191782 | 162.599529 | D | 2342.087010 | 1171.547143 | 2325.060461 | 1163.033868 | 2324.076445 | 1162.541860 | 18 |
| 4 | 470.260925 | 235.634100 | 453.234376 | 227.120826 | 452.250360 | 226.628818 | Q | 2227.060067 | 1114.033671 | 2210.033518 | 1105.520397 | 2209.049502 | 1105.028389 | 17 |
| 5 | 633.324254 | 317.165765 | 616.297705 | 308.652491 | 615.313689 | 308.160483 | Y | 2099.001489 | 1050.004382 | 2081.974940 | 1041.491108 | 2080.990924 | 1040.999100 | 16 |
| 6 | 690.345718 | 345.676497 | 673.319169 | 337.163223 | 672.335153 | 336.671215 | G | *1935.938160* | 968.472718 | 1918.911611 | 959.959444 | 1917.927595 | 959.467436 | 15 |
| 7 | 791.393397 | 396.200337 | 774.366848 | 387.687062 | 773.382832 | 387.195054 | T | *1878.916696* | 939.961986 | 1861.890147 | 931.448712 | 1860.906131 | 930.956704 | 14 |
| 8 | 928.452309 | 464.729793 | 911.425760 | 456.216518 | 910.441744 | 455.724510 | H | *1777.869017* | 889.438147 | 1760.842468 | 880.924872 | 1759.858452 | 880.432864 | 13 |
| 9 | 1091.515638 | 546.261457 | 1074.489089 | 537.748183 | 1073.505073 | 537.256175 | Y | *1640.810105* | 820.908691 | 1623.783556 | 812.395416 | 1622.799540 | 811.903408 | 12 |
| 10 | 1204.599702 | 602.803489 | 1187.573153 | 594.290215 | 1186.589137 | 593.798206 | L | *1477.746776* | 739.377026 | 1460.720227 | 730.863752 | 1459.736211 | 730.371744 | 11 |
| 11 | 1643.825028 | 822.416152 | 1626.798479 | 813.902878 | 1625.814463 | 813.410869 | Q | *1364.662712* | 682.834994 | 1347.636163 | 674.321720 | 1346.652147 | 673.829712 | 10 |
| 12 | 1730.857056 | 865.932166 | 1713.830507 | 857.418892 | 1712.846491 | 856.926884 | S | *925.437386* | 463.222331 | 908.410837 | 454.709057 | 907.426821 | 454.217049 | 9 |
| 13 | 1787.878520 | 894.442898 | 1770.851971 | 885.929624 | 1769.867955 | 885.437615 | G | *838.405358* | 419.706317 | 821.378809 | 411.193043 | 820.394793 | 410.701035 | 8 |
| 14 | 1874.910548 | 937.958912 | 1857.883999 | 929.445638 | 1856.899983 | 928.953630 | S | *781.383894* | 391.195585 | 764.357345 | 382.682311 | 763.373329 | 382.190303 | 7 |
| 15 | 1987.994612 | 994.500944 | 1970.968063 | 985.987670 | 1969.984047 | 985.495661 | L | *694.351866* | 347.679571 | 677.325317 | 339.166297 | 676.341301 | 338.674289 | 6 |
| 16 | 2045.016076 | 1023.011676 | 2027.989527 | 1014.498402 | 2027.005511 | 1014.006393 | G | *581.267802* | 291.137539 | 564.241253 | 282.624265 | 563.257237 | 282.132257 | 5 |
| 17 | 2102.037540 | 1051.522408 | 2085.010991 | 1043.009133 | 2084.026975 | 1042.517125 | G | *524.246338* | 262.626807 | 507.219789 | 254.113533 | 506.235773 | 253.621525 | 4 |
| 18 | 2231.080133 | 1116.043704 | 2214.053584 | 1107.530430 | 2213.069568 | 1107.038422 | E | 467.224874 | 234.116075 | 450.198325 | 225.602801 | 449.214309 | 225.110793 | 3 |
| 19 | 2394.143462 | 1197.575369 | 2377.116913 | 1189.062094 | 2376.132897 | 1188.570086 | Y | *338.182281* | 169.594778 | 321.155732 | 161.081504 | | | 2 |
| 20 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 81.6 | 2567.247849 | 0.028053 | LIDQYGTHYLQSGSLGGEYR |
| 20.5 | 2567.247849 | 0.028053 | LIDQYGTHYLQSGSLGGEYR |

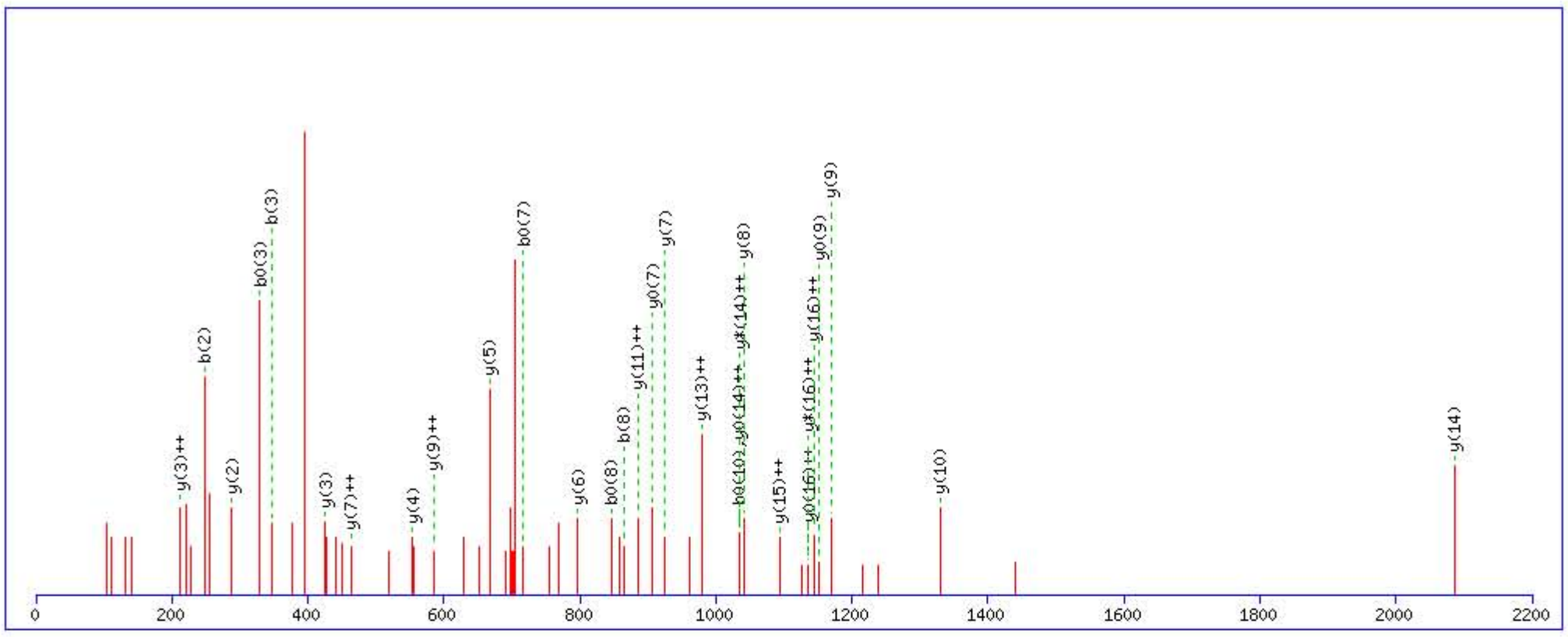
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SCVGETTESTQCEDEELEHLR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

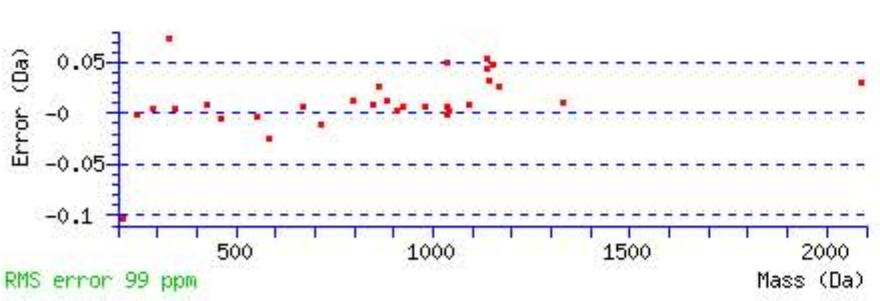
Match to Query 57841: 2819.219936 from(705.812260,4+) rtinseconds(1896) index(4924)
Title: Locus:1.1.1.1937.24 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

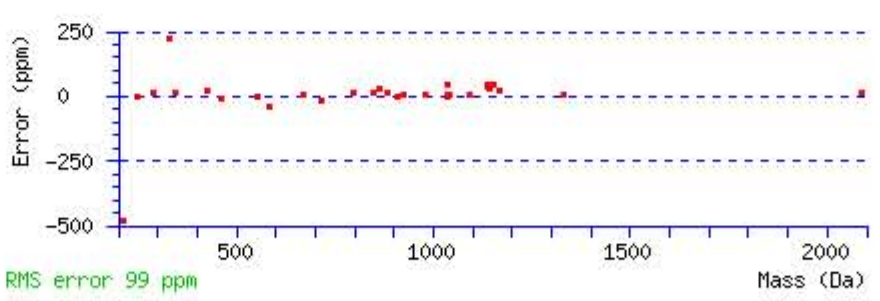
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2819.204803
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.00016
**Matches :** 30/214 fragment ions using 62 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 21 |
| 2 | **248.069953** | 124.538614 | | | 230.059388 | 115.533332 | C | 2733.180060 | 1367.093668 | 2716.153511 | 1358.580393 | 2715.169495 | 1358.088385 | 20 |
| 3 | **347.138367** | 174.072822 | | | 329.127802 | 165.067539 | V | 2573.149411 | 1287.078343 | 2556.122862 | 1278.565069 | 2555.138846 | 1278.073061 | 19 |
| 4 | 404.159831 | 202.583553 | | | 386.149266 | 193.578271 | G | 2474.080997 | 1237.544136 | 2457.054448 | 1229.030862 | 2456.070432 | 1228.538854 | 18 |
| 5 | 533.202424 | 267.104850 | | | 515.191859 | 258.099568 | E | 2417.059533 | 1209.033404 | 2400.032984 | 1200.520130 | 2399.048968 | 1200.028122 | 17 |
| 6 | 634.250103 | 317.628690 | | | 616.239538 | 308.623407 | T | 2288.016940 | 1144.512108 | 2270.990391 | 1135.998833 | 2270.006375 | 1135.506825 | 16 |
| 7 | 735.297782 | 368.152529 | | | 717.287217 | 359.147247 | T | 2186.969261 | 1093.988268 | 2169.942712 | 1085.474994 | 2168.958696 | 1084.982986 | 15 |
| 8 | **864.340375** | 432.673826 | | | 846.329810 | 423.668543 | E | ***2085.921582*** | 1043.464429 | 2068.895033 | 1034.951154 | 2067.911017 | 1034.459146 | 14 |
| 9 | 951.372403 | 476.189840 | | | 933.361838 | 467.184557 | S | 1956.878989 | 978.943133 | 1939.852440 | 970.429858 | 1938.868424 | 969.937850 | 13 |
| 10 | 1052.420082 | 526.713679 | | | 1034.409517 | 517.708397 | T | 1869.846961 | 935.427119 | 1852.820412 | 926.913844 | 1851.836396 | 926.421836 | 12 |
| 11 | 1491.645408 | 746.326342 | 1474.618859 | 737.813068 | 1473.634843 | 737.321060 | Q | 1768.799282 | 884.903279 | 1751.772733 | 876.390005 | 1750.788717 | 875.897997 | 11 |
| 12 | 1651.676057 | 826.341667 | 1634.649508 | 817.828392 | 1633.665492 | 817.336384 | C | ***1329.573956*** | 665.290616 | 1312.547407 | 656.777342 | 1311.563391 | 656.285334 | 10 |
| 13 | 1780.718650 | 890.862963 | 1763.692101 | 882.349689 | 1762.708085 | 881.857681 | E | ***1169.543307*** | 585.275292 | 1152.516758 | 576.762017 | 1151.532742 | 576.270009 | 9 |
| 14 | 1895.745593 | 948.376435 | 1878.719044 | 939.863160 | 1877.735028 | 939.371152 | D | ***1040.500714*** | 520.753995 | 1023.474165 | 512.240721 | 1022.490149 | 511.748713 | 8 |
| 15 | 2024.788186 | 1012.897731 | 2007.761637 | 1004.384457 | 2006.777621 | 1003.892449 | E | ***925.473771*** | 463.240524 | 908.447222 | 454.727249 | 907.463206 | 454.235241 | 7 |
| 16 | 2153.830779 | 1077.419027 | 2136.804230 | 1068.905753 | 2135.820214 | 1068.413745 | E | ***796.431178*** | 398.719227 | 779.404629 | 390.205953 | 778.420613 | 389.713945 | 6 |
| 17 | 2266.914843 | 1133.961059 | 2249.888294 | 1125.447785 | 2248.904278 | 1124.955777 | L | ***667.388585*** | 334.197931 | 650.362036 | 325.684656 | 649.378020 | 325.192648 | 5 |
| 18 | 2395.957436 | 1198.482356 | 2378.930887 | 1189.969081 | 2377.946871 | 1189.477074 | E | ***554.304521*** | 277.655899 | 537.277972 | 269.142624 | 536.293956 | 268.650616 | 4 |
| 19 | 2533.016348 | 1267.011812 | 2515.989799 | 1258.498537 | 2515.005783 | 1258.006529 | H | ***425.261928*** | 213.134602 | 408.235379 | 204.621328 | | | 3 |
| 20 | 2646.100412 | 1323.553844 | 2629.073863 | 1315.040569 | 2628.089847 | 1314.548562 | L | ***288.203016*** | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 21 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 44.3 | 2819.204803 | 0.015133 | SCVGETTESTQCEDEELEHLR |

**Mascot:** http://www.matrixscience.com/

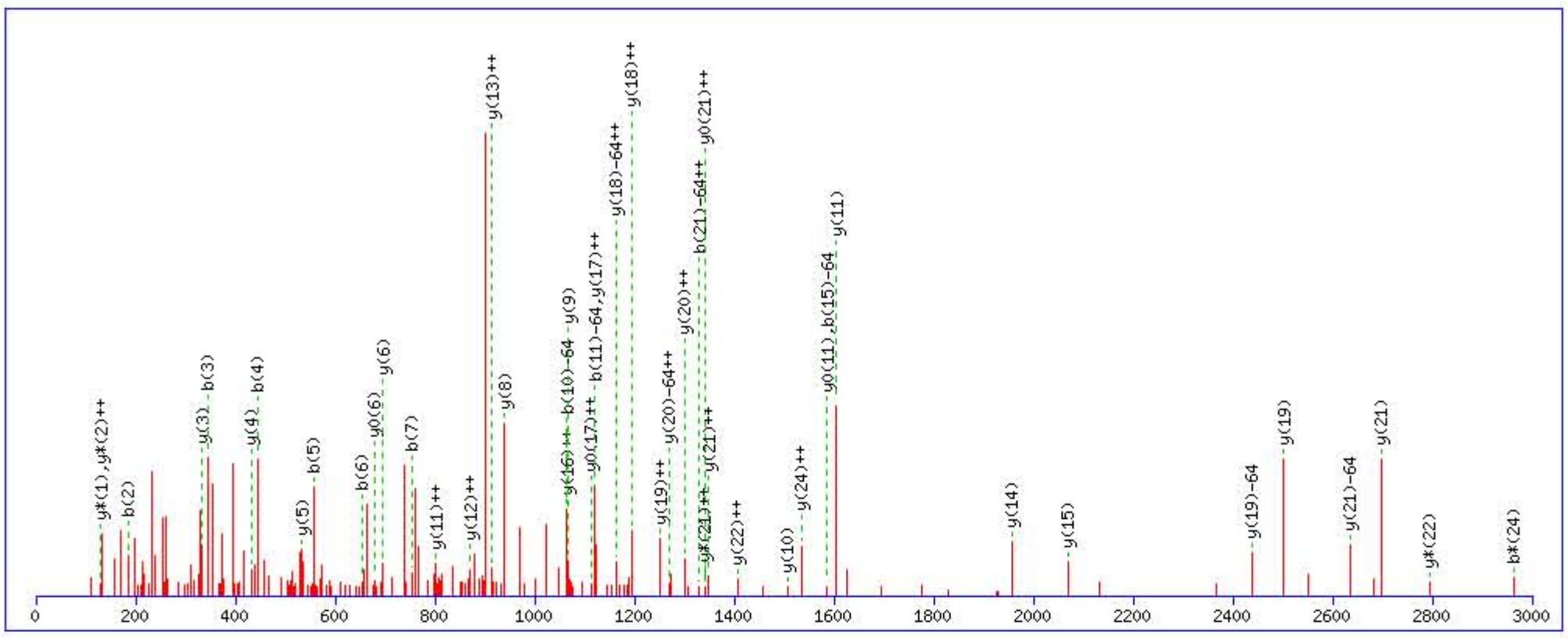
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IACVLPVLMDGIQSHPQKPFYTVGEK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

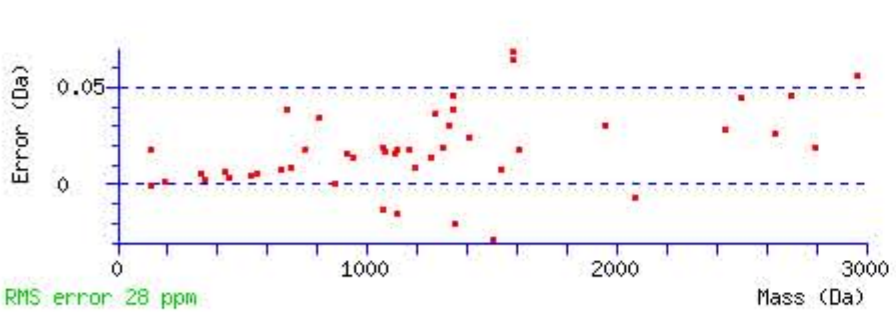
Match to Query 63493: 3253.703736 from(814.433210,4+) rtinseconds(2379) index(7730)
Title: Locus:1.1.1.2105.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

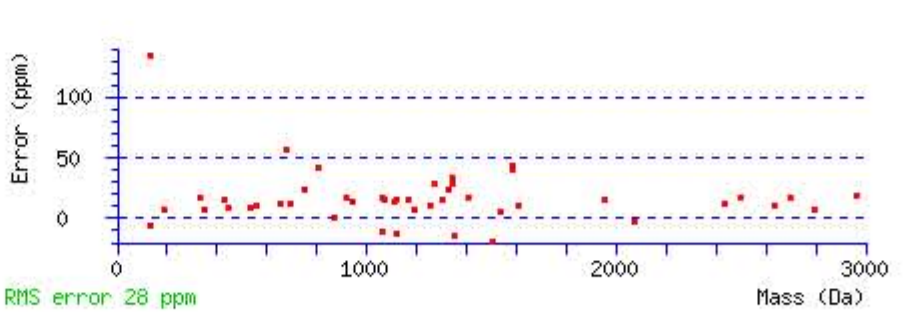
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3253.670181
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
M9 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q17 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.00083
**Matches :** 46/396 fragment ions using 127 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 26 |
| 2 | **185.128454** | 93.067865 | | | | | A | 3141.593386 | 1571.300331 | 3124.566837 | 1562.787056 | 3123.582821 | 1562.295048 | 25 |
| 3 | **345.159103** | 173.083190 | | | | | C | 3070.556272 | 1535.781774 | 3053.529723 | 1527.268499 | 3052.545707 | 1526.776491 | 24 |
| 4 | **444.227517** | 222.617397 | | | | | V | 2910.525623 | 1455.766449 | 2893.499074 | 1447.253175 | 2892.515058 | 1446.761167 | 23 |
| 5 | **557.311581** | 279.159429 | | | | | L | 2811.457209 | 1406.232242 | 2794.430660 | 1397.718968 | 2793.446644 | 1397.226960 | 22 |
| 6 | **654.364345** | 327.685811 | | | | | P | *2698.373145* | 1349.690210 | 2681.346596 | 1341.176936 | 2680.362580 | 1340.684928 | 21 |
| 7 | **753.432759** | 377.220018 | | | | | V | 2601.320381 | 1301.163828 | 2584.293832 | 1292.650554 | 2583.309816 | 1292.158546 | 20 |
| 8 | 866.516823 | 433.762050 | | | | | L | *2502.251967* | 1251.629621 | 2485.225418 | 1243.116347 | 2484.241402 | 1242.624339 | 19 |
| 9 | 1013.552223 | 507.279750 | | | | | M | 2389.167903 | 1195.087589 | 2372.141354 | 1186.574315 | 2371.157338 | 1186.082307 | 18 |
| 10 | 1128.579166 | 564.793221 | | | 1110.568601 | 555.787939 | D | 2242.132503 | 1121.569889 | 2225.105954 | 1113.056615 | 2224.121938 | 1112.564607 | 17 |
| 11 | 1185.600630 | 593.303953 | | | 1167.590065 | 584.298670 | G | 2127.105560 | 1064.056418 | 2110.079011 | 1055.543143 | 2109.094995 | 1055.051135 | 16 |
| 12 | 1298.684694 | 649.845985 | | | 1280.674129 | 640.840702 | I | *2070.084096* | 1035.545686 | 2053.057547 | 1027.032411 | 2052.073531 | 1026.540403 | 15 |
| 13 | 1426.743272 | 713.875274 | 1409.716723 | 705.362000 | 1408.732707 | 704.869991 | Q | *1957.000032* | 979.003654 | 1939.973483 | 970.490380 | 1938.989467 | 969.998372 | 14 |
| 14 | 1513.775300 | 757.391288 | 1496.748751 | 748.878014 | 1495.764735 | 748.386006 | S | 1828.941454 | 914.974365 | 1811.914905 | 906.461091 | 1810.930889 | 905.969083 | 13 |
| 15 | 1650.834212 | 825.920744 | 1633.807663 | 817.407470 | 1632.823647 | 816.915461 | H | 1741.909426 | 871.458351 | 1724.882877 | 862.945077 | 1723.898861 | 862.453068 | 12 |
| 16 | 1747.886976 | 874.447126 | 1730.860427 | 865.933852 | 1729.876411 | 865.441844 | P | *1604.850514* | 802.928895 | 1587.823965 | 794.415621 | 1586.839949 | 793.923612 | 11 |
| 17 | 2187.112302 | 1094.059789 | 2170.085753 | 1085.546514 | 2169.101737 | 1085.054506 | Q | *1507.797750* | 754.402513 | 1490.771201 | 745.889239 | 1489.787185 | 745.397230 | 10 |
| 18 | 2315.207265 | 1158.107270 | 2298.180716 | 1149.593996 | 2297.196700 | 1149.101988 | K | *1068.572424* | 534.789850 | 1051.545875 | 526.276575 | 1050.561859 | 525.784567 | 9 |
| 19 | 2412.260029 | 1206.633652 | 2395.233480 | 1198.120378 | 2394.249464 | 1197.628370 | P | *940.477461* | 470.742368 | 923.450912 | 462.229094 | 922.466896 | 461.737086 | 8 |
| 20 | 2559.328443 | 1280.167859 | 2542.301894 | 1271.654585 | 2541.317878 | 1271.162577 | F | 843.424697 | 422.215986 | 826.398148 | 413.702712 | 825.414132 | 413.210704 | 7 |
| 21 | 2722.391772 | 1361.699524 | 2705.365223 | 1353.186249 | 2704.381207 | 1352.694241 | Y | *696.356283* | 348.681779 | 679.329734 | 340.168505 | 678.345718 | 339.676497 | 6 |
| 22 | 2823.439451 | 1412.223363 | 2806.412902 | 1403.710089 | 2805.428886 | 1403.218081 | T | *533.292954* | 267.150115 | 516.266405 | 258.636840 | 515.282389 | 258.144832 | 5 |
| 23 | 2922.507865 | 1461.757570 | 2905.481316 | 1453.244296 | 2904.497300 | 1452.752288 | V | *432.245275* | 216.626275 | 415.218726 | 208.113001 | 414.234710 | 207.620993 | 4 |
| 24 | 2979.529329 | 1490.268302 | 2962.502780 | 1481.755028 | 2961.518764 | 1481.263020 | G | *333.176861* | 167.092069 | 316.150312 | 158.578794 | 315.166296 | 158.086786 | 3 |
| 25 | 3108.571922 | 1554.789599 | 3091.545373 | 1546.276324 | 3090.561357 | 1545.784316 | E | 276.155397 | 138.581337 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 26 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 44.2 | 3253.670181 | 0.033555 | IACVLPVLMDGIQSHPQKPFYTVGEK |
| 26.1 | 3253.670181 | 0.033555 | IACVLPVLMDGIQSHPQKPFYTVGEK |

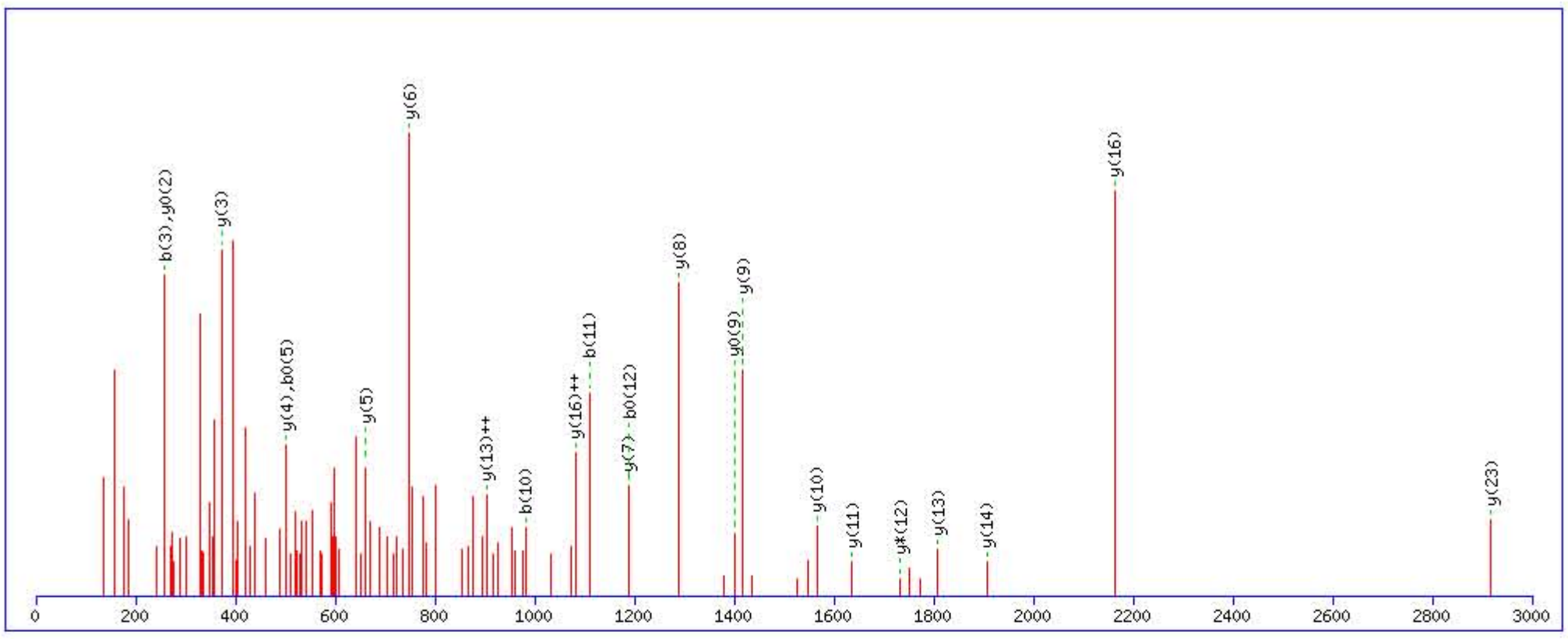
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SVAVYGQYGGQPCVGNAFETQSCEPTR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

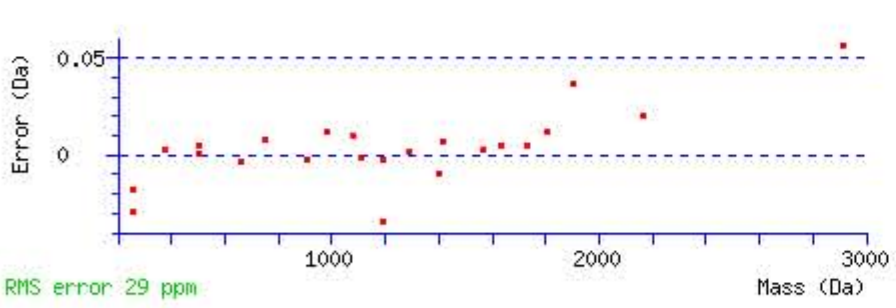
Match to Query 63987: 3272.493816 from(819.130730,4+) rtinseconds(2163) index(6560)
Title: Locus:1.1.1.2030.21 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

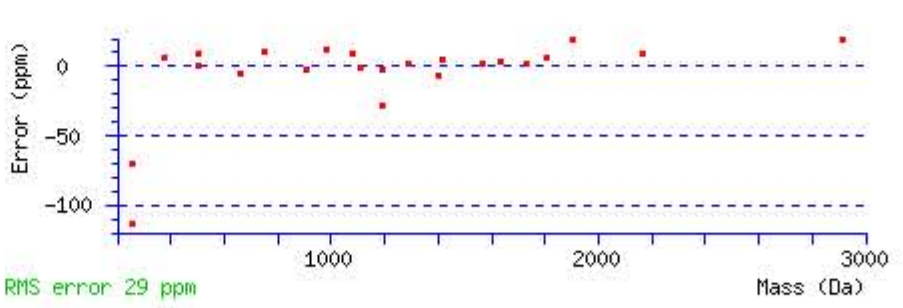
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3272.468933
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q21 : Biotin:Thermo-21345 (Q)
**Ions Score:** 76 **Expect:** 2.7e-007
**Matches :** 23/298 fragment ions using 36 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 27 |
| 2 | 187.107718 | 94.057497 | | | 169.097153 | 85.052214 | V | 3186.444157 | 1593.725716 | 3169.417608 | 1585.212442 | 3168.433592 | 1584.720434 | 26 |
| 3 | **258.144832** | 129.576054 | | | 240.134267 | 120.570772 | A | 3087.375743 | 1544.191509 | 3070.349194 | 1535.678235 | 3069.365178 | 1535.186227 | 25 |
| 4 | 357.213246 | 179.110261 | | | 339.202681 | 170.104979 | V | 3016.338629 | 1508.672952 | 2999.312080 | 1500.159678 | 2998.328064 | 1499.667670 | 24 |
| 5 | 520.276575 | 260.641926 | | | 502.266010 | 251.636643 | Y | *2917.270215* | 1459.138745 | 2900.243666 | 1450.625471 | 2899.259650 | 1450.133463 | 23 |
| 6 | 577.298039 | 289.152658 | | | 559.287474 | 280.147375 | G | 2754.206886 | 1377.607081 | 2737.180337 | 1369.093806 | 2736.196321 | 1368.601798 | 22 |
| 7 | 705.356617 | 353.181947 | 688.330068 | 344.668672 | 687.346052 | 344.176664 | Q | 2697.185422 | 1349.096349 | 2680.158873 | 1340.583074 | 2679.174857 | 1340.091066 | 21 |
| 8 | 868.419946 | 434.713611 | 851.393397 | 426.200337 | 850.409381 | 425.708329 | Y | 2569.126844 | 1285.067060 | 2552.100295 | 1276.553785 | 2551.116279 | 1276.061777 | 20 |
| 9 | 925.441410 | 463.224343 | 908.414861 | 454.711069 | 907.430845 | 454.219061 | G | 2406.063515 | 1203.535395 | 2389.036966 | 1195.022121 | 2388.052950 | 1194.530113 | 19 |
| 10 | **982.462874** | 491.735075 | 965.436325 | 483.221801 | 964.452309 | 482.729793 | G | 2349.042051 | 1175.024663 | 2332.015502 | 1166.511389 | 2331.031486 | 1166.019381 | 18 |
| 11 | **1110.521452** | 555.764364 | 1093.494903 | 547.251090 | 1092.510887 | 546.759082 | Q | 2292.020587 | 1146.513931 | 2274.994038 | 1138.000657 | 2274.010022 | 1137.508649 | 17 |
| 12 | 1207.574216 | 604.290746 | 1190.547667 | 595.777472 | 1189.563651 | 595.285464 | P | *2163.962009* | 1082.484642 | 2146.935460 | 1073.971368 | 2145.951444 | 1073.479360 | 16 |
| 13 | 1367.604865 | 684.306071 | 1350.578316 | 675.792796 | 1349.594300 | 675.300788 | C | 2066.909245 | 1033.958260 | 2049.882696 | 1025.444986 | 2048.898680 | 1024.952978 | 15 |
| 14 | 1466.673279 | 733.840278 | 1449.646730 | 725.327003 | 1448.662714 | 724.834995 | V | *1906.878596* | 953.942936 | 1889.852047 | 945.429662 | 1888.868031 | 944.937654 | 14 |
| 15 | 1523.694743 | 762.351010 | 1506.668194 | 753.837735 | 1505.684178 | 753.345727 | G | *1807.810182* | 904.408729 | 1790.783633 | 895.895455 | 1789.799617 | 895.403446 | 13 |
| 16 | 1637.737670 | 819.372473 | 1620.711121 | 810.859199 | 1619.727105 | 810.367191 | N | 1750.788718 | 875.897997 | 1733.762169 | 867.384723 | 1732.778153 | 866.892715 | 12 |
| 17 | 1708.774784 | 854.891030 | 1691.748235 | 846.377756 | 1690.764219 | 845.885748 | A | *1636.745791* | 818.876534 | 1619.719242 | 810.363259 | 1618.735226 | 809.871251 | 11 |
| 18 | 1855.843198 | 928.425237 | 1838.816649 | 919.911963 | 1837.832633 | 919.419955 | F | *1565.708677* | 783.357977 | 1548.682128 | 774.844702 | 1547.698112 | 774.352694 | 10 |
| 19 | 1984.885791 | 992.946534 | 1967.859242 | 984.433259 | 1966.875226 | 983.941251 | E | *1418.640263* | 709.823770 | 1401.613714 | 701.310495 | 1400.629698 | 700.818487 | 9 |
| 20 | 2085.933470 | 1043.470373 | 2068.906921 | 1034.957098 | 2067.922905 | 1034.465090 | T | *1289.597670* | 645.302473 | 1272.571121 | 636.789199 | 1271.587105 | 636.297190 | 8 |
| 21 | 2525.158796 | 1263.083036 | 2508.132247 | 1254.569761 | 2507.148231 | 1254.077754 | Q | *1188.549991* | 594.778634 | 1171.523442 | 586.265359 | 1170.539426 | 585.773351 | 7 |
| 22 | 2612.190824 | 1306.599050 | 2595.164275 | 1298.085776 | 2594.180259 | 1297.593768 | S | *749.324665* | 375.165970 | 732.298116 | 366.652696 | 731.314100 | 366.160688 | 6 |
| 23 | 2772.221473 | 1386.614374 | 2755.194924 | 1378.101100 | 2754.210908 | 1377.609092 | C | *662.292637* | 331.649956 | 645.266088 | 323.136682 | 644.282072 | 322.644674 | 5 |
| 24 | 2901.264066 | 1451.135671 | 2884.237517 | 1442.622396 | 2883.253501 | 1442.130389 | E | *502.261988* | 251.634632 | 485.235439 | 243.121357 | 484.251423 | 242.629349 | 4 |
| 25 | 2998.316830 | 1499.662053 | 2981.290281 | 1491.148778 | 2980.306265 | 1490.656771 | P | *373.219395* | 187.113335 | 356.192846 | 178.600061 | 355.208830 | 178.108053 | 3 |
| 26 | 3099.364509 | 1550.185892 | 3082.337960 | 1541.672618 | 3081.353944 | 1541.180610 | T | 276.166631 | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 27 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 76.2 | 3272.468933 | 0.024883 | SVAVYGQYGGQPCVGNAFETQSCEPTR |
| 10.0 | 3272.468933 | 0.024883 | SVAVYGQYGGQPCVGNAFETQSCEPTR |
| 2.0 | 3272.468933 | 0.024883 | SVAVYGQYGGQPCVGNAFETQSCEPTR |

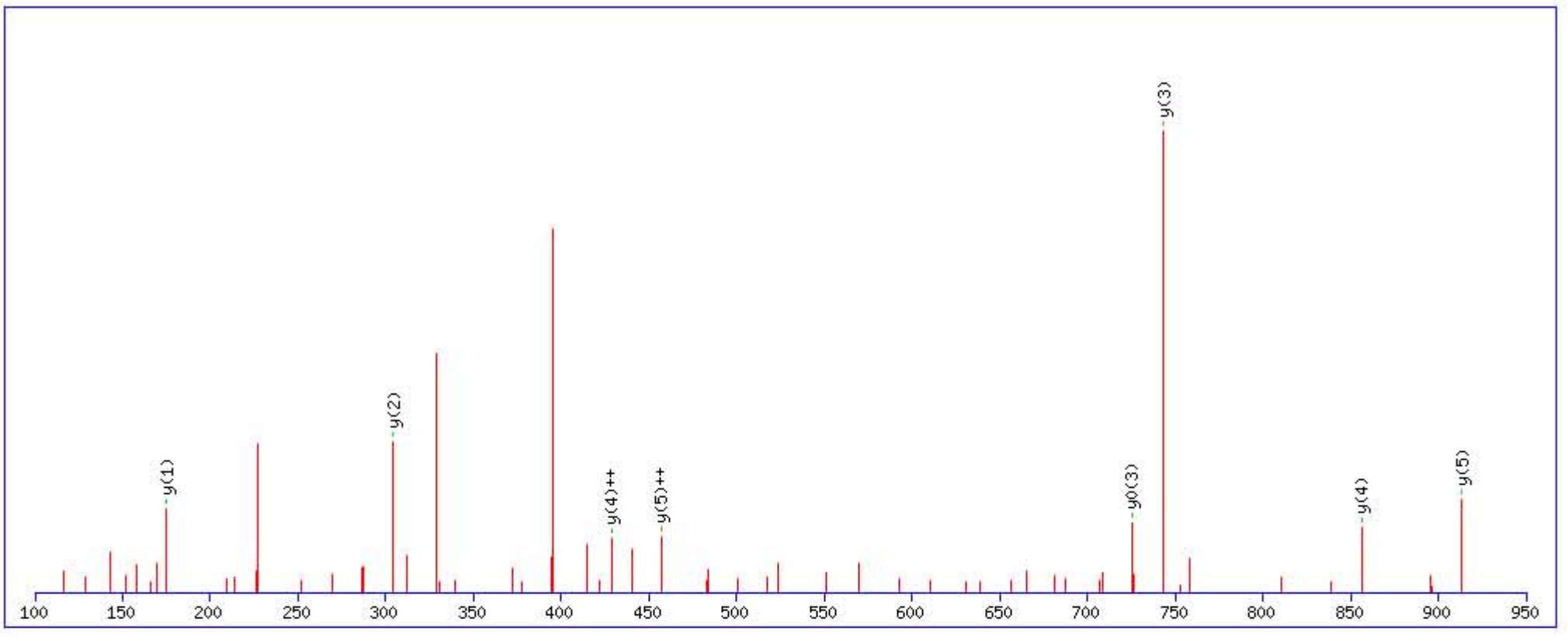
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AGIQER**
Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

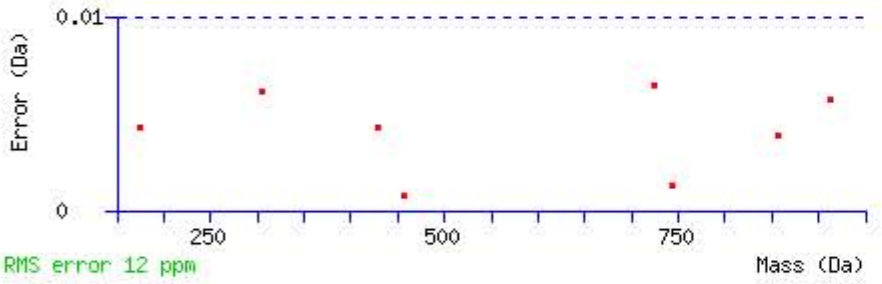
Match to Query 13178: 983.522828 from(492.768690,2+) rtinseconds(1400) index(16257)
Title: Locus:1.1.1.2870.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

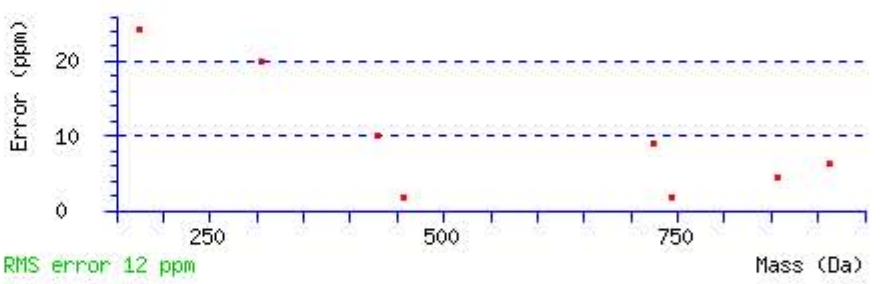
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 983.522217
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 29 **Expect:** 0.024
**Matches :** 8/44 fragment ions using 16 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 6 |
| 2 | 129.065854 | 65.036565 | | | | | G | *913.492399* | 457.249838 | 896.465850 | 448.736563 | 895.481834 | 448.244555 | 5 |
| 3 | 242.149918 | 121.578597 | | | | | I | *856.470935* | 428.739106 | 839.444386 | 420.225831 | 838.460370 | 419.733823 | 4 |
| 4 | 681.375244 | 341.191260 | 664.348695 | 332.677986 | | | Q | *743.386871* | 372.197074 | 726.360322 | 363.683799 | 725.376306 | 363.191791 | 3 |
| 5 | 810.417837 | 405.712557 | 793.391288 | 397.199282 | 792.407272 | 396.707274 | E | *304.161545* | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 6 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

### All matches to this query

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 29.1 | 983.522217 | 0.000611 | AGIQER |
| 17.5 | 983.522217 | 0.000611 | AGLEQR |
| 14.0 | 983.522217 | 0.000611 | QIQER |
| 14.0 | 983.522217 | 0.000611 | QLQER |
| 10.8 | 983.522217 | 0.000611 | IQQER |
| 10.8 | 983.522217 | 0.000611 | LQQER |
| 10.5 | 983.522217 | 0.000611 | AAQVER |
| 9.5 | 983.514816 | 0.008012 | QPVREAER |
| 5.9 | 983.522202 | 0.000626 | KLMENPPR |
| 5.7 | 983.522217 | 0.000611 | QLEQR |

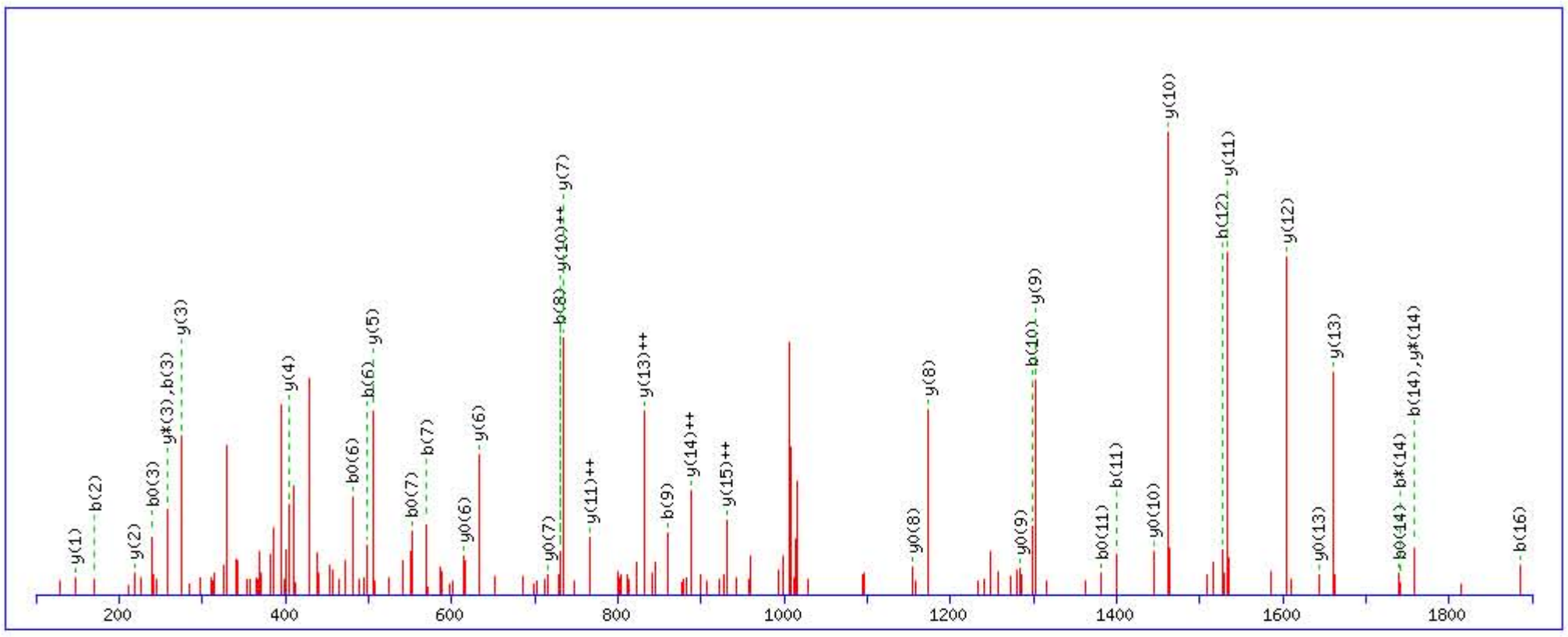
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LGSLGAACEQTQTEGAK**
Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

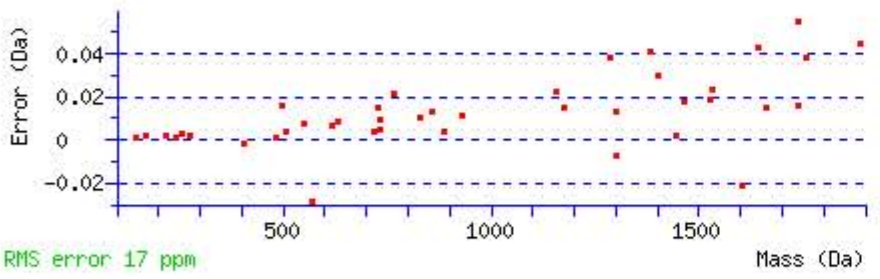
Match to Query 45284: 2031.005628 from(1016.510090,2+) rtinseconds(1727) index(32450)
Title: Locus:1.1.1.710.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

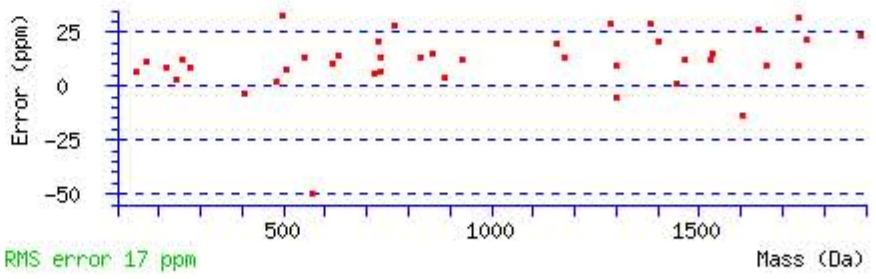
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2030.976501
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 90 **Expect:** 1.1e-008
**Matches :** 43/164 fragment ions using 66 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 17 |
| 2 | *171.112804* | 86.060040 | | | | | G | 1918.899727 | 959.953502 | 1901.873178 | 951.440227 | 1900.889162 | 950.948219 | 16 |
| 3 | *258.144832* | 129.576054 | | | 240.134267 | 120.570772 | S | 1861.878263 | 931.442770 | 1844.851714 | 922.929495 | 1843.867698 | 922.437487 | 15 |
| 4 | 371.228896 | 186.118086 | | | 353.218331 | 177.112804 | L | 1774.846235 | 887.926756 | 1757.819686 | 879.413481 | 1756.835670 | 878.921473 | 14 |
| 5 | 428.250360 | 214.628818 | | | 410.239795 | 205.623536 | G | *1661.762171* | 831.384724 | 1644.735622 | 822.871449 | 1643.751606 | 822.379441 | 13 |
| 6 | *499.287474* | 250.147375 | | | 481.276909 | 241.142093 | A | *1604.740707* | 802.873992 | 1587.714158 | 794.360717 | 1586.730142 | 793.868709 | 12 |
| 7 | *570.324588* | 285.665932 | | | 552.314023 | 276.660650 | A | *1533.703593* | 767.355435 | 1516.677044 | 758.842160 | 1515.693028 | 758.350152 | 11 |
| 8 | *730.355237* | 365.681257 | | | 712.344672 | 356.675974 | C | *1462.666479* | 731.836878 | 1445.639930 | 723.323603 | 1444.655914 | 722.831595 | 10 |
| 9 | *859.397830* | 430.202553 | | | 841.387265 | 421.197271 | E | *1302.635830* | 651.821553 | 1285.609281 | 643.308279 | 1284.625265 | 642.816270 | 9 |
| 10 | *1298.623156* | 649.815216 | 1281.596607 | 641.301942 | 1280.612591 | 640.809934 | Q | *1173.593237* | 587.300257 | 1156.566688 | 578.786982 | 1155.582672 | 578.294974 | 8 |
| 11 | *1399.670835* | 700.339056 | 1382.644286 | 691.825781 | 1381.660270 | 691.333773 | T | *734.367911* | 367.687594 | 717.341362 | 359.174319 | 716.357346 | 358.682311 | 7 |
| 12 | *1527.729413* | 764.368345 | 1510.702864 | 755.855070 | 1509.718848 | 755.363062 | Q | *633.320232* | 317.163754 | 616.293683 | 308.650480 | 615.309667 | 308.158472 | 6 |
| 13 | 1628.777092 | 814.892184 | 1611.750543 | 806.378910 | 1610.766527 | 805.886902 | T | *505.261654* | 253.134465 | 488.235105 | 244.621190 | 487.251089 | 244.129182 | 5 |
| 14 | *1757.819685* | 879.413481 | 1740.793136 | 870.900206 | 1739.809120 | 870.408198 | E | *404.213975* | 202.610625 | 387.187426 | 194.097351 | 386.203410 | 193.605343 | 4 |
| 15 | 1814.841149 | 907.924213 | 1797.814600 | 899.410938 | 1796.830584 | 898.918930 | G | *275.171382* | 138.089329 | 258.144833 | 129.576054 | | | 3 |
| 16 | *1885.878263* | 943.442770 | 1868.851714 | 934.929495 | 1867.867698 | 934.437487 | A | *218.149918* | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 17 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 89.8 | 2030.976501 | 0.029127 | LGSLGAACEQTQTEGAK |
| 59.6 | 2030.976501 | 0.029127 | LGSLGAACEQTQTEGAK |
| 4.7 | 2031.000748 | 0.004880 | LEQQVEDLESSLEQEKK |
| 3.8 | 2031.012863 | -0.007235 | KLETLLHSMEVAQNGMAK |

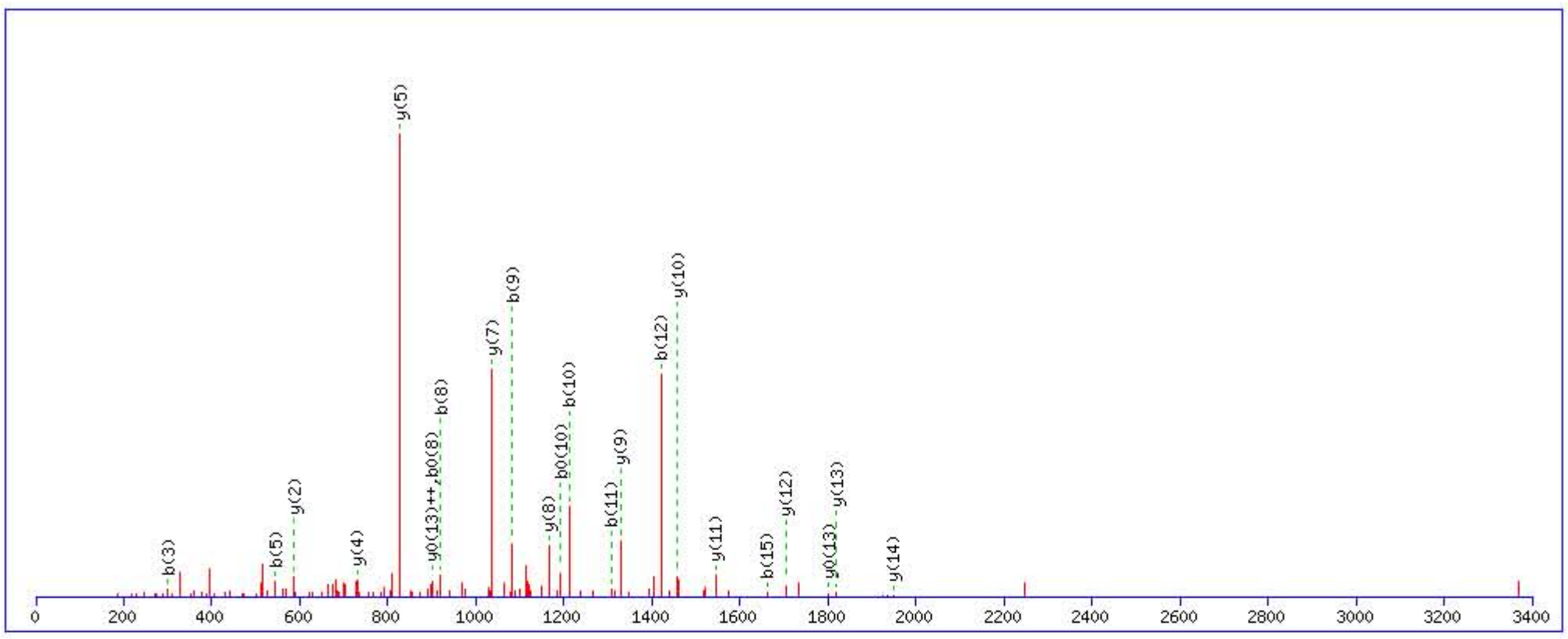
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AIDEDCSQYEPIPGSQK**
Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

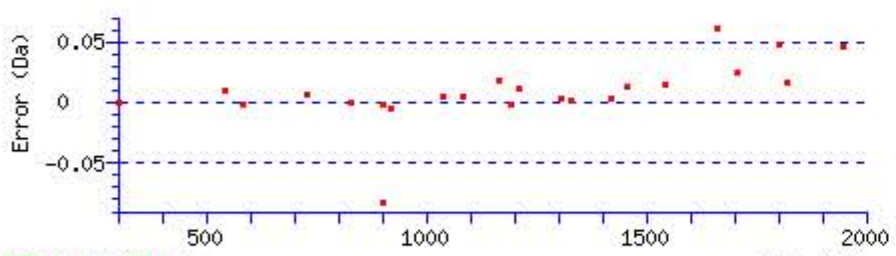
Match to Query 49399: 2247.050268 from(1124.532410,2+) rtinseconds(1893) index(19546)
Title: Locus:1.1.1.3041.26 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

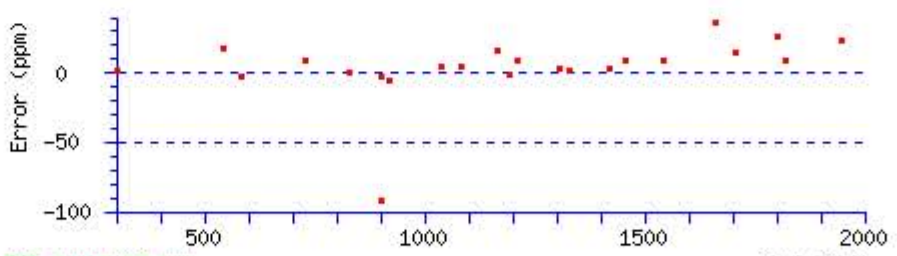
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2247.018753
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q16** : Biotin:Thermo-21345 (Q)
**Ions Score:** 76 **Expect:** 2e-007
**Matches** : 23/170 fragment ions using 35 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 17 |
| 2 | 185.128454 | 93.067865 | | | | | I | 2176.988934 | 1088.998105 | 2159.962385 | 1080.484830 | 2158.978369 | 1079.992822 | 16 |
| 3 | **300.155397** | 150.581336 | | | 282.144832 | 141.576054 | D | 2063.904870 | 1032.456073 | 2046.878321 | 1023.942798 | 2045.894305 | 1023.450790 | 15 |
| 4 | 429.197990 | 215.102633 | | | 411.187425 | 206.097351 | E | *1948.877927* | 974.942602 | 1931.851378 | 966.429327 | 1930.867362 | 965.937319 | 14 |
| 5 | **544.224933** | 272.616105 | | | 526.214368 | 263.610822 | D | *1819.835334* | 910.421305 | 1802.808785 | 901.908031 | 1801.824769 | 901.416022 | 13 |
| 6 | 704.255582 | 352.631429 | | | 686.245017 | 343.626147 | C | *1704.808391* | 852.907833 | 1687.781842 | 844.394559 | 1686.797826 | 843.902551 | 12 |
| 7 | 791.287610 | 396.147443 | | | 773.277045 | 387.142161 | S | *1544.777742* | 772.892509 | 1527.751193 | 764.379235 | 1526.767177 | 763.887227 | 11 |
| 8 | **919.346188** | 460.176732 | 902.319639 | 451.663458 | 901.335623 | 451.171450 | Q | *1457.745714* | 729.376495 | 1440.719165 | 720.863221 | 1439.735149 | 720.371212 | 10 |
| 9 | **1082.409517** | 541.708397 | 1065.382968 | 533.195122 | 1064.398952 | 532.703114 | Y | *1329.687136* | 665.347206 | 1312.660587 | 656.833931 | 1311.676571 | 656.341923 | 9 |
| 10 | **1211.452110** | 606.229693 | 1194.425561 | 597.716419 | 1193.441545 | 597.224410 | E | *1166.623807* | 583.815541 | 1149.597258 | 575.302267 | 1148.613242 | 574.810259 | 8 |
| 11 | **1308.504874** | 654.756075 | 1291.478325 | 646.242801 | 1290.494309 | 645.750792 | P | *1037.581214* | 519.294245 | 1020.554665 | 510.780971 | 1019.570649 | 510.288963 | 7 |
| 12 | **1421.588938** | 711.298107 | 1404.562389 | 702.784832 | 1403.578373 | 702.292824 | I | 940.528450 | 470.767863 | 923.501901 | 462.254589 | 922.517885 | 461.762581 | 6 |
| 13 | 1518.641702 | 759.824489 | 1501.615153 | 751.311215 | 1500.631137 | 750.819206 | P | *827.444386* | 414.225831 | 810.417837 | 405.712557 | 809.433821 | 405.220549 | 5 |
| 14 | 1575.663166 | 788.335221 | 1558.636617 | 779.821946 | 1557.652601 | 779.329938 | G | *730.391622* | 365.699449 | 713.365073 | 357.186175 | 712.381057 | 356.694167 | 4 |
| 15 | **1662.695194** | 831.851235 | 1645.668645 | 823.337961 | 1644.684629 | 822.845952 | S | 673.370158 | 337.188717 | 656.343609 | 328.675443 | 655.359593 | 328.183435 | 3 |
| 16 | 2101.920520 | 1051.463898 | 2084.893971 | 1042.950623 | 2083.909955 | 1042.458615 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 17 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 75.8 | 2247.018753 | 0.031515 | AIDEDCSQYEPIPGSQK |
| 17.4 | 2247.018753 | 0.031515 | AIDEDCSQYEPIPGSQK |
| 4.1 | 2247.051773 | -0.001505 | EVMQDYRDELKDFFAVDK |
| 0.3 | 2247.063034 | -0.012766 | VTDANDNPPVFSQDVYR |

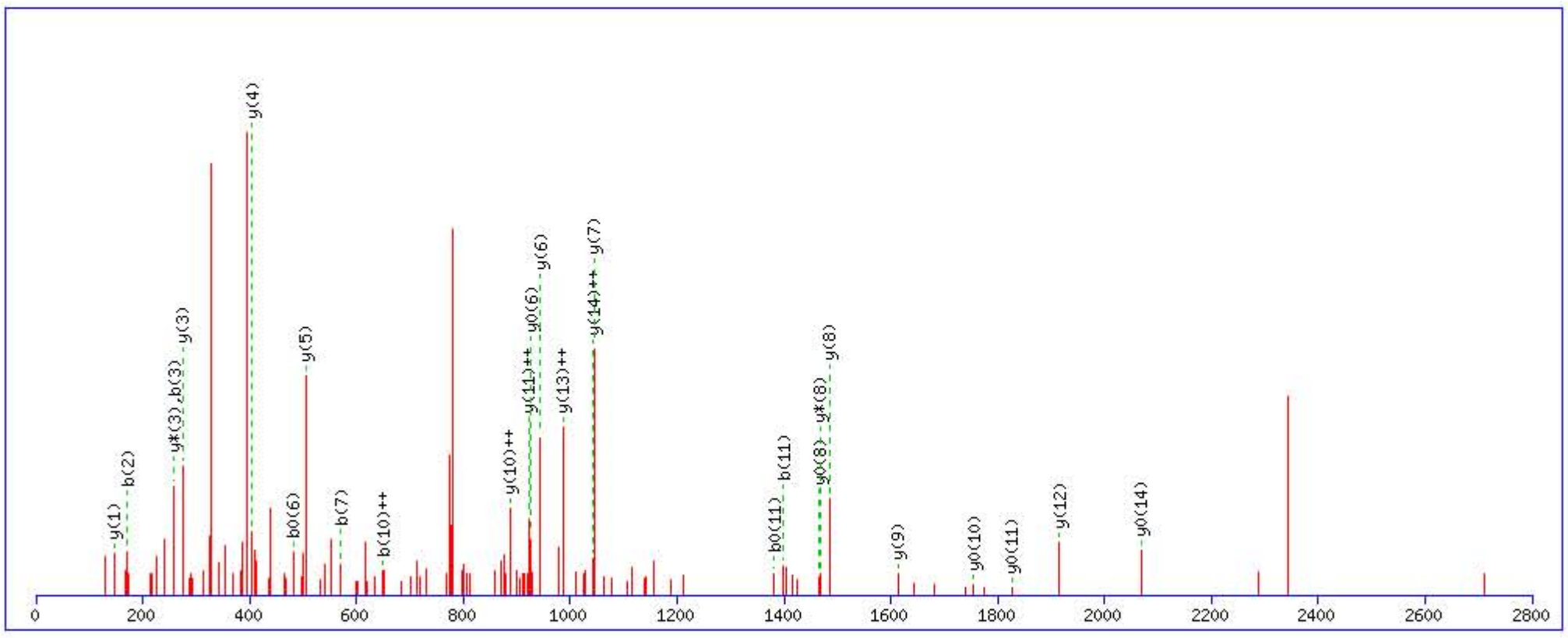
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LGSLGAACEQTQTEGAK**
Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

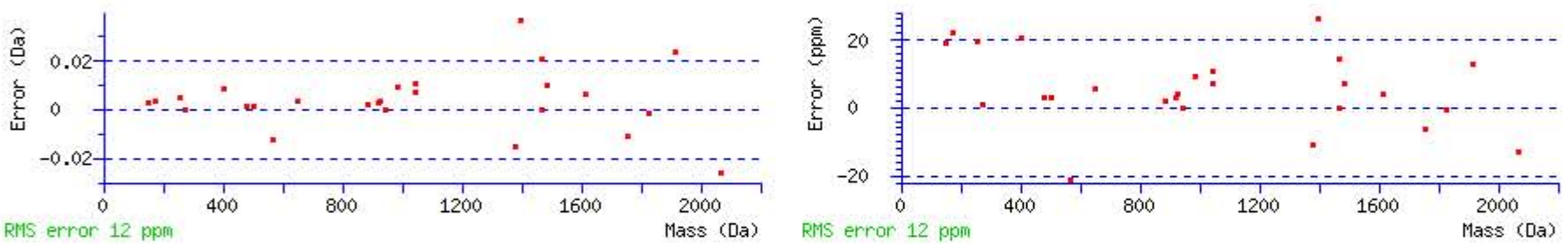
Match to Query 51246: 2342.159352 from(781.727060,3+) rtinseconds(1995) index(20210)
Title: Locus:1.1.1.3077.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2342.143250
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 42 **Expect:** 0.0017
**Matches :** 27/164 fragment ions using 48 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 17 |
| 2 | **171.112804** | 86.060040 | | | | | G | 2230.066475 | 1115.536875 | 2213.039926 | 1107.023601 | 2212.055910 | 1106.531593 | 16 |
| 3 | **258.144832** | 129.576054 | | | 240.134267 | 120.570772 | S | 2173.045011 | 1087.026143 | 2156.018462 | 1078.512869 | 2155.034446 | 1078.020861 | 15 |
| 4 | 371.228896 | 186.118086 | | | 353.218331 | 177.112804 | L | 2086.012983 | 1043.510129 | 2068.986434 | 1034.996855 | 2068.002418 | 1034.504847 | 14 |
| 5 | 428.250360 | 214.628818 | | | 410.239795 | 205.623536 | G | 1972.928919 | 986.968098 | 1955.902370 | 978.454823 | 1954.918354 | 977.962815 | 13 |
| 6 | 499.287474 | 250.147375 | | | 481.276909 | 241.142093 | A | *1915.907455* | 958.457366 | 1898.880906 | 949.944091 | 1897.896890 | 949.452083 | 12 |
| 7 | **570.324588** | 285.665932 | | | 552.314023 | 276.660650 | A | 1844.870341 | 922.938809 | 1827.843792 | 914.425534 | 1826.859776 | 913.933526 | 11 |
| 8 | 730.355237 | 365.681257 | | | 712.344672 | 356.675974 | C | 1773.833227 | 887.420252 | 1756.806678 | 878.906977 | 1755.822662 | 878.414969 | 10 |
| 9 | 859.397830 | 430.202553 | | | 841.387265 | 421.197271 | E | *1613.802578* | 807.404927 | 1596.776029 | 798.891653 | 1595.792013 | 798.399645 | 9 |
| 10 | 1298.623156 | 649.815216 | 1281.596607 | 641.301942 | 1280.612591 | 640.809934 | Q | *1484.759985* | 742.883631 | 1467.733436 | 734.370356 | 1466.749420 | 733.878348 | 8 |
| 11 | **1399.670835** | 700.339056 | 1382.644286 | 691.825781 | 1381.660270 | 691.333773 | T | *1045.534659* | 523.270968 | 1028.508110 | 514.757693 | 1027.524094 | 514.265685 | 7 |
| 12 | 1838.896161 | 919.951719 | 1821.869612 | 911.438444 | 1820.885596 | 910.946436 | Q | *944.486980* | 472.747128 | 927.460431 | 464.233854 | 926.476415 | 463.741846 | 6 |
| 13 | 1939.943840 | 970.475558 | 1922.917291 | 961.962284 | 1921.933275 | 961.470276 | T | *505.261654* | 253.134465 | 488.235105 | 244.621191 | 487.251089 | 244.129183 | 5 |
| 14 | 2068.986433 | 1034.996854 | 2051.959884 | 1026.483580 | 2050.975868 | 1025.991572 | E | *404.213975* | 202.610626 | 387.187426 | 194.097351 | 386.203410 | 193.605343 | 4 |
| 15 | 2126.007897 | 1063.507586 | 2108.981348 | 1054.994312 | 2107.997332 | 1054.502304 | G | *275.171382* | 138.089329 | 258.144833 | 129.576055 | | | 3 |
| 16 | 2197.045011 | 1099.026144 | 2180.018462 | 1090.512869 | 2179.034446 | 1090.020861 | A | 218.149918 | 109.578597 | 201.123369 | 101.065323 | | | 2 |
| 17 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 42.4 | 2342.143250 | 0.016102 | LGSLGAACEQTQTEGAK |

**Mascot:** http://www.matrixscience.com/

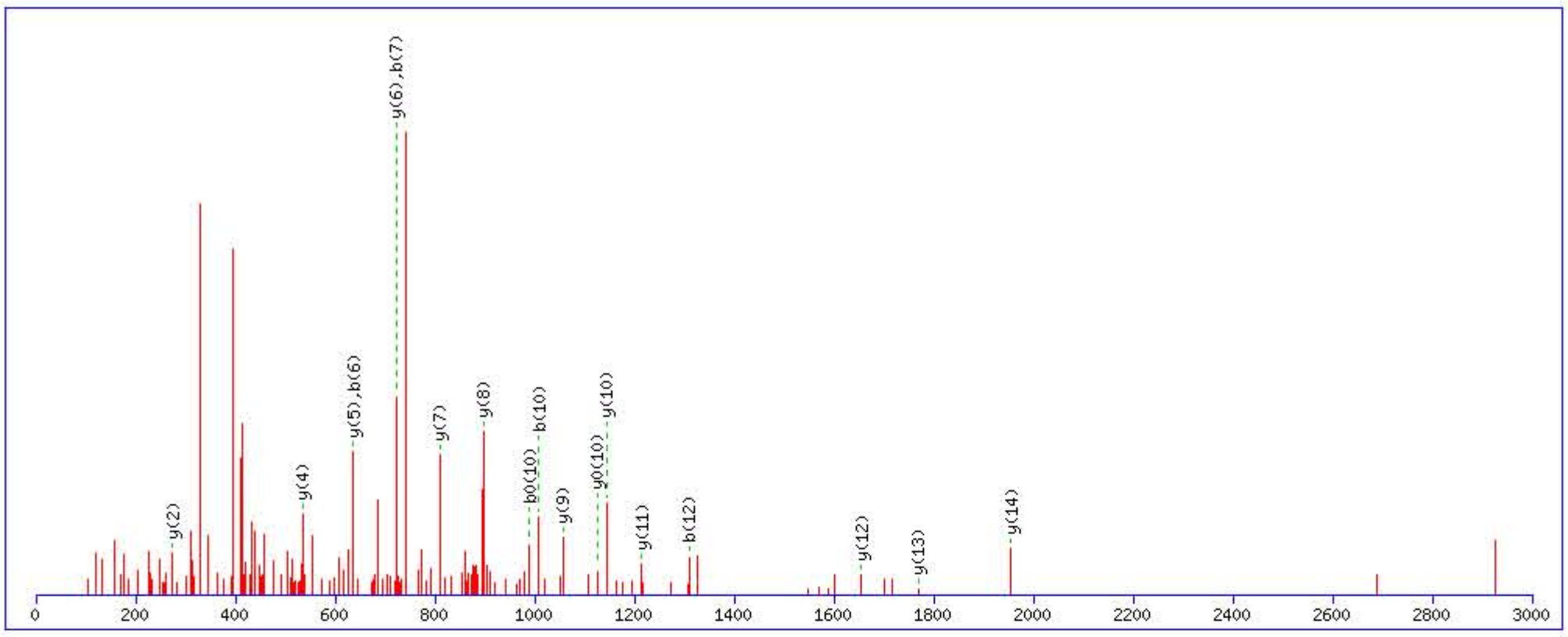
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FGGTICSGDIWDQASCSSSTTCVR**
Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

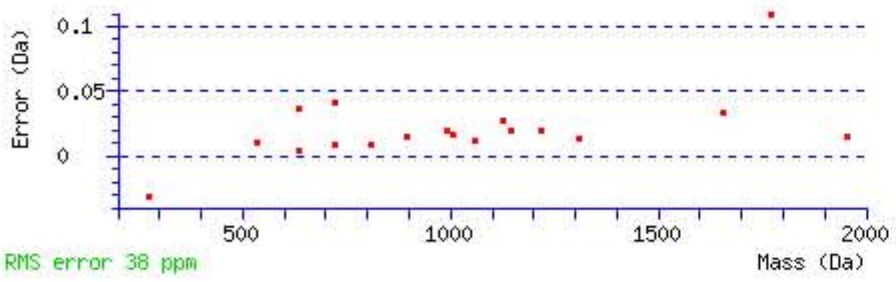
Match to Query 59805: 2962.315696 from(741.586200,4+) rtinseconds(2373) index(36446)
Title: Locus:1.1.1.935.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

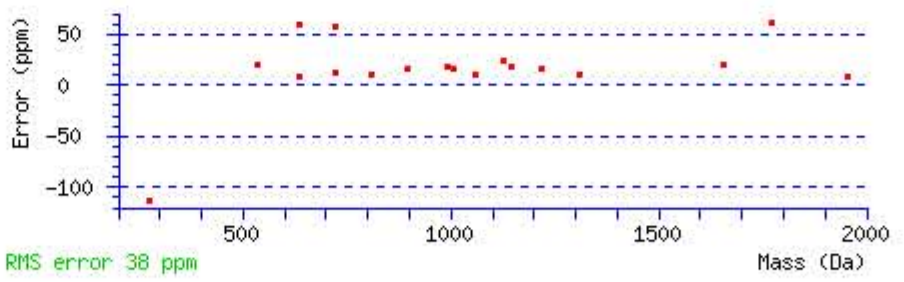
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2962.271835
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 60 **Expect:** 7.1e-006
**Matches :** 18/240 fragment ions using 35 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 24 |
| 2 | 205.097154 | 103.052215 | | | | | G | 2816.210649 | 1408.608962 | 2799.184100 | 1400.095688 | 2798.200084 | 1399.603680 | 23 |
| 3 | 262.118618 | 131.562947 | | | | | G | 2759.189185 | 1380.098230 | 2742.162636 | 1371.584956 | 2741.178620 | 1371.092948 | 22 |
| 4 | 363.166297 | 182.086786 | | | 345.155732 | 173.081504 | T | 2702.167721 | 1351.587498 | 2685.141172 | 1343.074224 | 2684.157156 | 1342.582216 | 21 |
| 5 | 476.250361 | 238.628818 | | | 458.239796 | 229.623536 | I | 2601.120042 | 1301.063659 | 2584.093493 | 1292.550384 | 2583.109477 | 1292.058376 | 20 |
| 6 | **636.281010** | 318.644143 | | | 618.270445 | 309.638861 | C | 2488.035978 | 1244.521627 | 2471.009429 | 1236.008352 | 2470.025413 | 1235.516344 | 19 |
| 7 | **723.313038** | 362.160157 | | | 705.302473 | 353.154875 | S | 2328.005329 | 1164.506302 | 2310.978780 | 1155.993028 | 2309.994764 | 1155.501020 | 18 |
| 8 | 780.334502 | 390.670889 | | | 762.323937 | 381.665607 | G | 2240.973301 | 1120.990288 | 2223.946752 | 1112.477014 | 2222.962736 | 1111.985006 | 17 |
| 9 | 895.361445 | 448.184361 | | | 877.350880 | 439.179078 | D | 2183.951837 | 1092.479556 | 2166.925288 | 1083.966282 | 2165.941272 | 1083.474274 | 16 |
| 10 | **1008.445509** | 504.726393 | | | 990.434944 | 495.721110 | I | 2068.924894 | 1034.966085 | 2051.898345 | 1026.452810 | 2050.914329 | 1025.960802 | 15 |
| 11 | 1194.524822 | 597.766049 | | | 1176.514257 | 588.760767 | W | *1955.840830* | 978.424053 | 1938.814281 | 969.910778 | 1937.830265 | 969.418770 | 14 |
| 12 | **1309.551765** | 655.279521 | | | 1291.541200 | 646.274238 | D | *1769.761517* | 885.384396 | 1752.734968 | 876.871122 | 1751.750952 | 876.379114 | 13 |
| 13 | 1748.777091 | 874.892184 | 1731.750542 | 866.378909 | 1730.766526 | 865.886901 | Q | *1654.734574* | 827.870925 | 1637.708025 | 819.357650 | 1636.724009 | 818.865642 | 12 |
| 14 | 1819.814205 | 910.410741 | 1802.787656 | 901.897466 | 1801.803640 | 901.405458 | A | *1215.509248* | 608.258262 | 1198.482699 | 599.744987 | 1197.498683 | 599.252979 | 11 |
| 15 | 1906.846233 | 953.926755 | 1889.819684 | 945.413480 | 1888.835668 | 944.921472 | S | *1144.472134* | 572.739705 | 1127.445585 | 564.226430 | 1126.461569 | 563.734422 | 10 |
| 16 | 2066.876882 | 1033.942079 | 2049.850333 | 1025.428804 | 2048.866317 | 1024.936796 | C | *1057.440106* | 529.223691 | 1040.413557 | 520.710416 | 1039.429541 | 520.218408 | 9 |
| 17 | 2153.908910 | 1077.458093 | 2136.882361 | 1068.944818 | 2135.898345 | 1068.452810 | S | *897.409457* | 449.208366 | 880.382908 | 440.695092 | 879.398892 | 440.203084 | 8 |
| 18 | 2240.940938 | 1120.974107 | 2223.914389 | 1112.460832 | 2222.930373 | 1111.968825 | S | *810.377429* | 405.692352 | 793.350880 | 397.179078 | 792.366864 | 396.687070 | 7 |
| 19 | 2327.972966 | 1164.490121 | 2310.946417 | 1155.976847 | 2309.962401 | 1155.484839 | S | *723.345401* | 362.176338 | 706.318852 | 353.663064 | 705.334836 | 353.171056 | 6 |
| 20 | 2429.020645 | 1215.013960 | 2411.994096 | 1206.500686 | 2411.010080 | 1206.008678 | T | *636.313373* | 318.660324 | 619.286824 | 310.147050 | 618.302808 | 309.655042 | 5 |
| 21 | 2530.068324 | 1265.537800 | 2513.041775 | 1257.024525 | 2512.057759 | 1256.532517 | T | *535.265694* | 268.136485 | 518.239145 | 259.623210 | 517.255129 | 259.131202 | 4 |
| 22 | 2690.098973 | 1345.553124 | 2673.072424 | 1337.039850 | 2672.088408 | 1336.547842 | C | 434.218015 | 217.612645 | 417.191466 | 209.099371 | | | 3 |
| 23 | 2789.167387 | 1395.087331 | 2772.140838 | 1386.574057 | 2771.156822 | 1386.082049 | V | *274.187366* | 137.597321 | 257.160817 | 129.084046 | | | 2 |
| 24 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 60.5 | 2962.271835 | 0.043861 | FGGTICSGDIWDQASCSSSTTCVR |

**Mascot:** http://www.matrixscience.com/

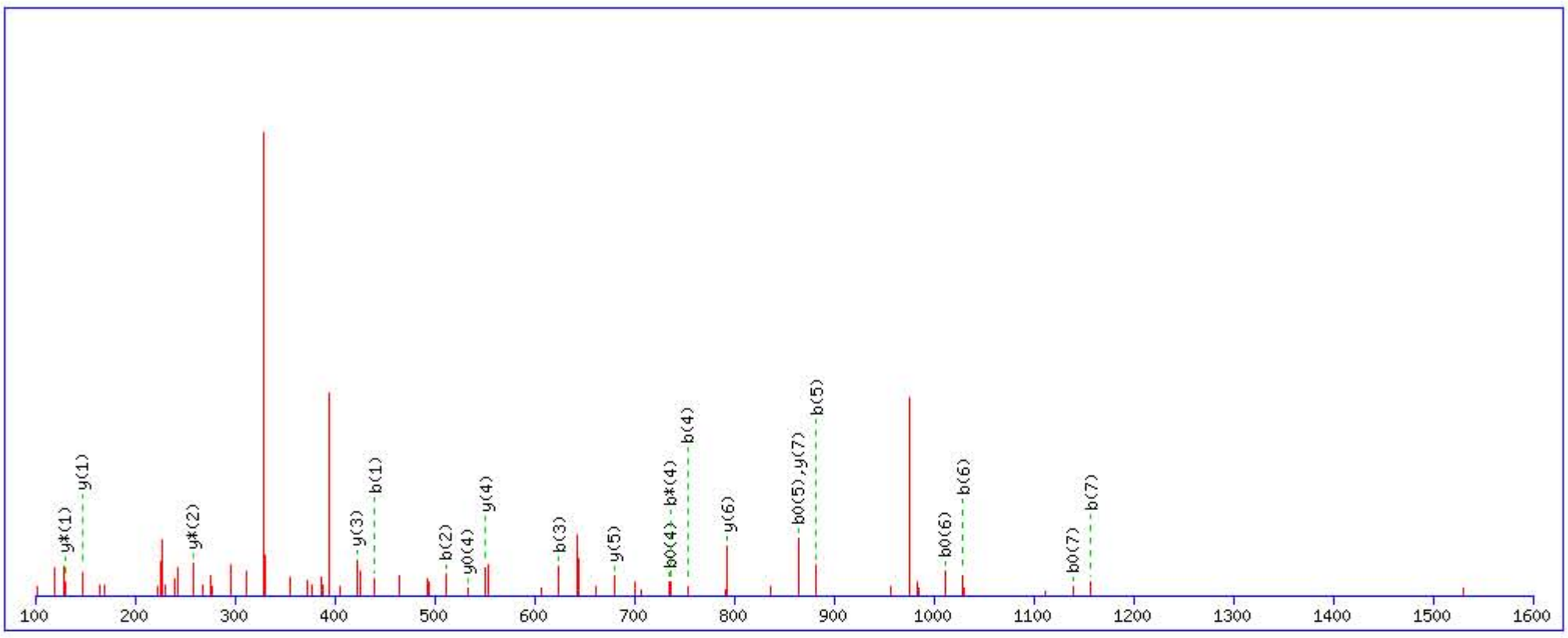
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QALEEFQK**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

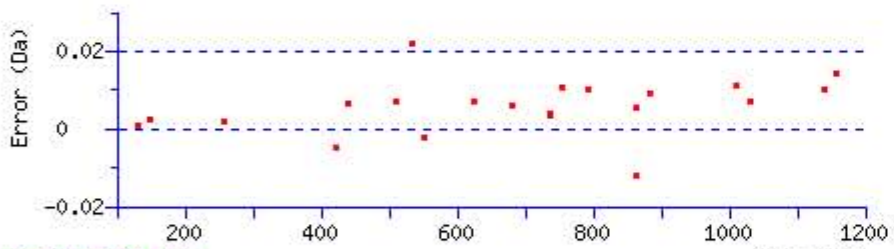
Match to Query 23374: 1302.666908 from(652.340730,2+) rtinseconds(1874) index(19378)
Title: Locus:1.1.1.3035.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

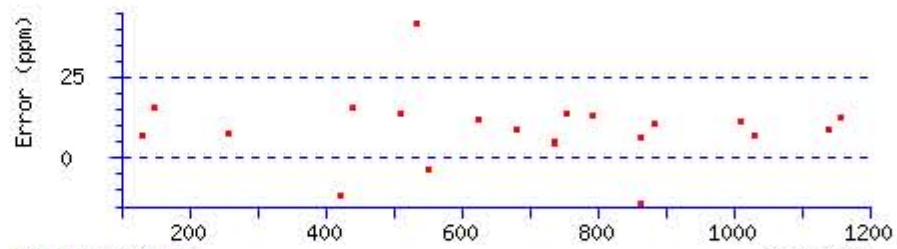
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1302.664185
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q1 : Biotin:Thermo-21345 (Q)
**Ions Score:** 35 **Expect:** 0.0072
**Matches :** 21/72 fragment ions using 41 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *440.232602* | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 8 |
| 2 | *511.269716* | 256.138496 | 494.243167 | 247.625221 | | | A | **864.446160** | 432.726718 | 847.419611 | 424.213443 | 846.435595 | 423.721435 | 7 |
| 3 | *624.353780* | 312.680528 | 607.327231 | 304.167254 | | | L | **793.409046** | 397.208161 | 776.382497 | 388.694887 | 775.398481 | 388.202879 | 6 |
| 4 | *753.396373* | 377.201825 | 736.369824 | 368.688550 | 735.385808 | 368.196542 | E | **680.324982** | 340.666129 | 663.298433 | 332.152854 | 662.314417 | 331.660846 | 5 |
| 5 | *882.438966* | 441.723121 | 865.412417 | 433.209847 | 864.428401 | 432.717839 | E | **551.282389** | 276.144833 | 534.255840 | 267.631558 | 533.271824 | 267.139550 | 4 |
| 6 | *1029.507380* | 515.257328 | 1012.480831 | 506.744054 | 1011.496815 | 506.252046 | F | **422.239796** | 211.623536 | 405.213247 | 203.110261 | | | 3 |
| 7 | *1157.565958* | 579.286617 | 1140.539409 | 570.773343 | 1139.555393 | 570.281334 | Q | 275.171382 | 138.089329 | 258.144833 | 129.576054 | | | 2 |
| 8 | | | | | | | K | **147.112804** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 35.4 | 1302.664185 | 0.002723 | QALEEFQK |
| 12.8 | 1302.667542 | -0.000634 | KEALMQEK |
| 9.6 | 1302.666641 | 0.000267 | EKEAELKEAEK |
| 8.4 | 1302.660141 | 0.006767 | EAEGKLAAQMQK |
| 8.2 | 1302.668045 | -0.001137 | QPAGPASATPPGPR |
| 7.1 | 1302.649582 | 0.017326 | FYSLLDPSYAK |
| 6.5 | 1302.666672 | 0.000236 | AQEELEKVTEK |
| 5.7 | 1302.667542 | -0.000634 | QKEMESLK |
| 5.1 | 1302.677917 | -0.011009 | SSATIQNETPKK |
| 4.5 | 1302.656799 | 0.010109 | QSIEPPSGIYGR |

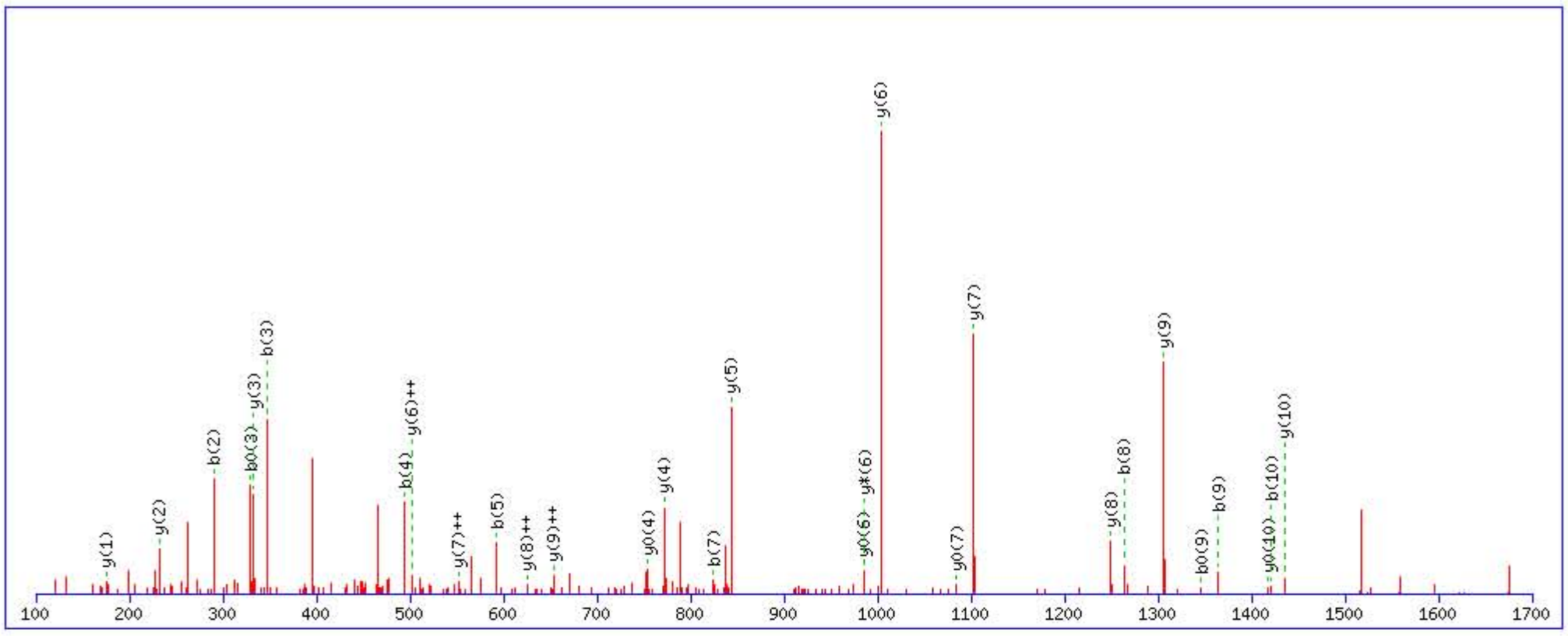
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **CEGFVCAQTGR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

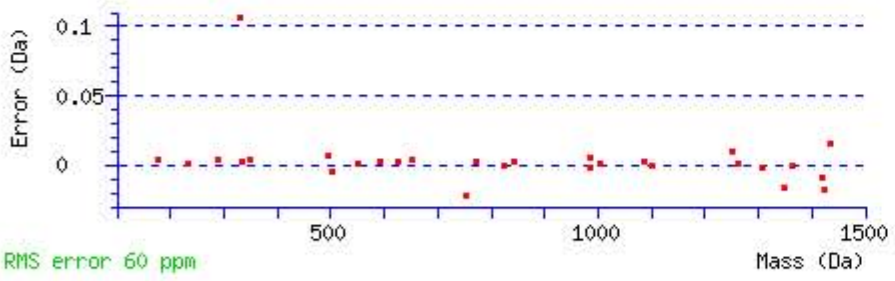
Match to Query 34383: 1594.711728 from(798.363140,2+) rtinseconds(1772) index(18698)
Title: Locus:1.1.1.2999.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

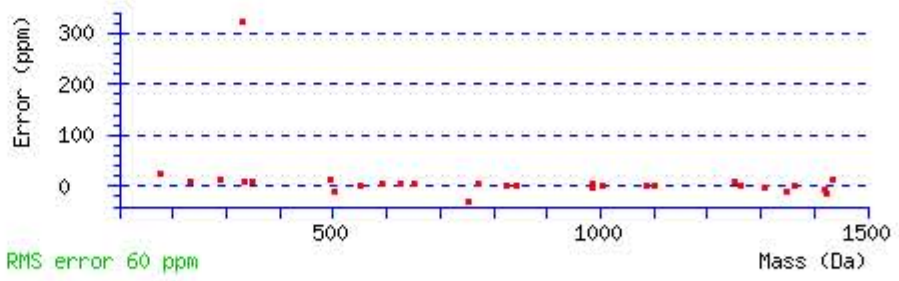
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1594.705460
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 1.2e-005
**Matches :** 29/100 fragment ions using 60 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 161.037925 | 81.022600 | | | | | C | | | | | | | 11 |
| 2 | **290.080518** | 145.543897 | | | 272.069953 | 136.538615 | E | *1435.682069* | 718.344673 | 1418.655520 | 709.831398 | 1417.671504 | 709.339390 | 10 |
| 3 | **347.101982** | 174.054629 | | | 329.091417 | 165.049347 | G | *1306.639476* | 653.823376 | 1289.612927 | 645.310102 | 1288.628911 | 644.818094 | 9 |
| 4 | **494.170396** | 247.588836 | | | 476.159831 | 238.583554 | F | *1249.618012* | 625.312644 | 1232.591463 | 616.799370 | 1231.607447 | 616.307361 | 8 |
| 5 | **593.238810** | 297.123043 | | | 575.228245 | 288.117761 | V | *1102.549598* | 551.778437 | 1085.523049 | 543.265162 | 1084.539033 | 542.773154 | 7 |
| 6 | 753.269459 | 377.138368 | | | 735.258894 | 368.133085 | C | *1003.481184* | 502.244230 | 986.454635 | 493.730955 | 985.470619 | 493.238947 | 6 |
| 7 | **824.306573** | 412.656925 | | | 806.296008 | 403.651642 | A | *843.450535* | 422.228906 | 826.423986 | 413.715631 | 825.439970 | 413.223623 | 5 |
| 8 | **1263.531899** | 632.269588 | 1246.505350 | 623.756313 | 1245.521334 | 623.264305 | Q | *772.413421* | 386.710349 | 755.386872 | 378.197074 | 754.402856 | 377.705066 | 4 |
| 9 | **1364.579578** | 682.793427 | 1347.553029 | 674.280153 | 1346.569013 | 673.788145 | T | *333.188095* | 167.097685 | 316.161546 | 158.584411 | 315.177530 | 158.092403 | 3 |
| 10 | **1421.601042** | 711.304159 | 1404.574493 | 702.790885 | 1403.590477 | 702.298877 | G | *232.140416* | 116.573846 | 215.113867 | 108.060571 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 57.8 | 1594.705460 | 0.006268 | CEGFVCAQTGR |

**Mascot:** http://www.matrixscience.com/

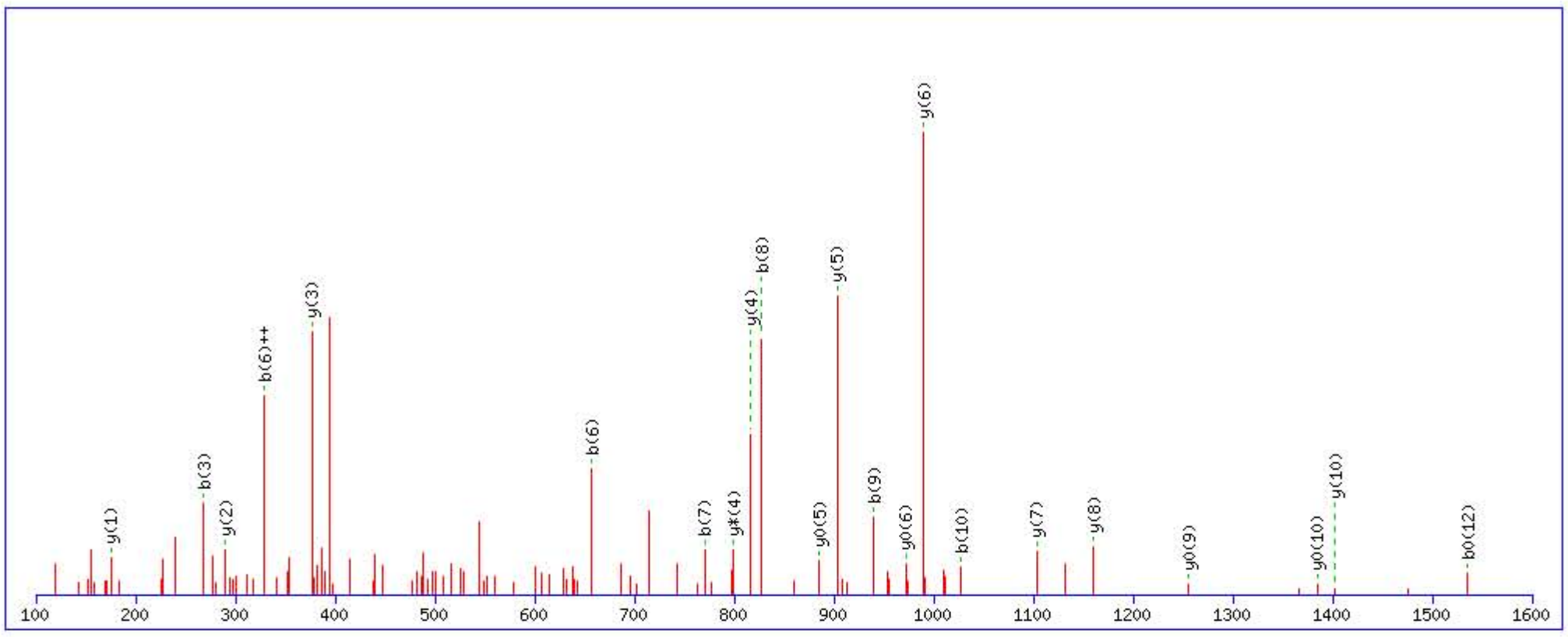
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IPGIFELGISSQSDR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

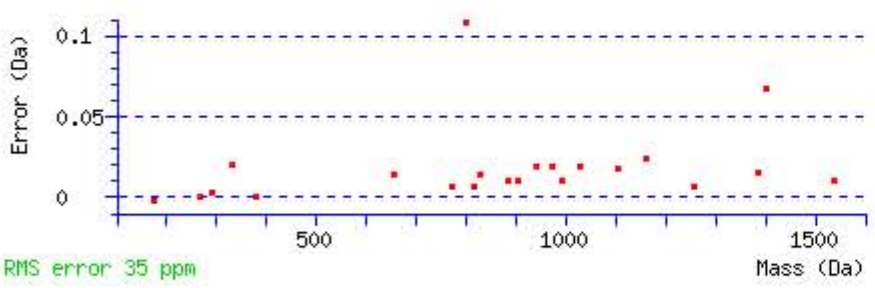
Match to Query 42694: 1929.023022 from(644.014950,3+) rtinseconds(2683) index(24160)
Title: Locus:1.1.1.3316.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

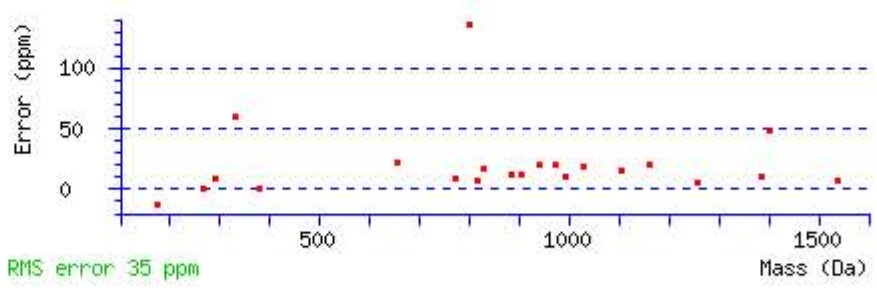
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1929.002975
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 52 **Expect:** 7.5e-005
**Matches :** 22/134 fragment ions using 37 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 15 |
| 2 | 211.144104 | 106.075690 | | | | | P | 1816.926196 | 908.966736 | 1799.899647 | 900.453462 | 1798.915631 | 899.961454 | 14 |
| 3 | *268.165568* | 134.586422 | | | | | G | 1719.873432 | 860.440354 | 1702.846883 | 851.927080 | 1701.862867 | 851.435072 | 13 |
| 4 | 381.249632 | 191.128454 | | | | | I | 1662.851968 | 831.929622 | 1645.825419 | 823.416348 | 1644.841403 | 822.924340 | 12 |
| 5 | 528.318046 | 264.662661 | | | | | F | 1549.767904 | 775.387590 | 1532.741355 | 766.874316 | 1531.757339 | 766.382308 | 11 |
| 6 | *657.360639* | 329.183958 | | | 639.350074 | 320.178675 | E | *1402.699490* | 701.853383 | 1385.672941 | 693.340109 | 1384.688925 | 692.848101 | 10 |
| 7 | *770.444703* | 385.725990 | | | 752.434138 | 376.720707 | L | 1273.656897 | 637.332087 | 1256.630348 | 628.818812 | 1255.646332 | 628.326804 | 9 |
| 8 | *827.466167* | 414.236722 | | | 809.455602 | 405.231439 | G | *1160.572833* | 580.790055 | 1143.546284 | 572.276780 | 1142.562268 | 571.784772 | 8 |
| 9 | *940.550231* | 470.778754 | | | 922.539666 | 461.773471 | I | *1103.551369* | 552.279323 | 1086.524820 | 543.766048 | 1085.540804 | 543.274040 | 7 |
| 10 | *1027.582259* | 514.294768 | | | 1009.571694 | 505.289485 | S | *990.467305* | 495.737291 | 973.440756 | 487.224016 | 972.456740 | 486.732008 | 6 |
| 11 | 1114.614287 | 557.810782 | | | 1096.603722 | 548.805499 | S | *903.435277* | 452.221277 | 886.408728 | 443.708002 | 885.424712 | 443.215994 | 5 |
| 12 | 1553.839613 | 777.423445 | 1536.813064 | 768.910170 | 1535.829048 | 768.418162 | Q | *816.403249* | 408.705263 | 799.376700 | 400.191988 | 798.392684 | 399.699980 | 4 |
| 13 | 1640.871641 | 820.939459 | 1623.845092 | 812.426184 | 1622.861076 | 811.934176 | S | *377.177923* | 189.092600 | 360.151374 | 180.579325 | 359.167358 | 180.087317 | 3 |
| 14 | 1755.898584 | 878.452930 | 1738.872035 | 869.939656 | 1737.888019 | 869.447648 | D | *290.145895* | 145.576585 | 273.119346 | 137.063311 | 272.135330 | 136.571303 | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.1 | 1929.002975 | 0.020047 | IPGIFELGISSQSDR |
| 7.7 | 1929.041840 | -0.018818 | ADEVLAEVTVSAQASAKIK |
| 7.5 | 1929.018219 | 0.004803 | LPEFLVQLYSYMRVR |
| 7.0 | 1928.996445 | 0.026577 | QCQVILNFLAAEGR |
| 1.9 | 1929.012833 | 0.010189 | EMEERTITIEIPEVLK |
| 1.3 | 1929.020721 | 0.002301 | RELEELSVGSDGVLIWK |

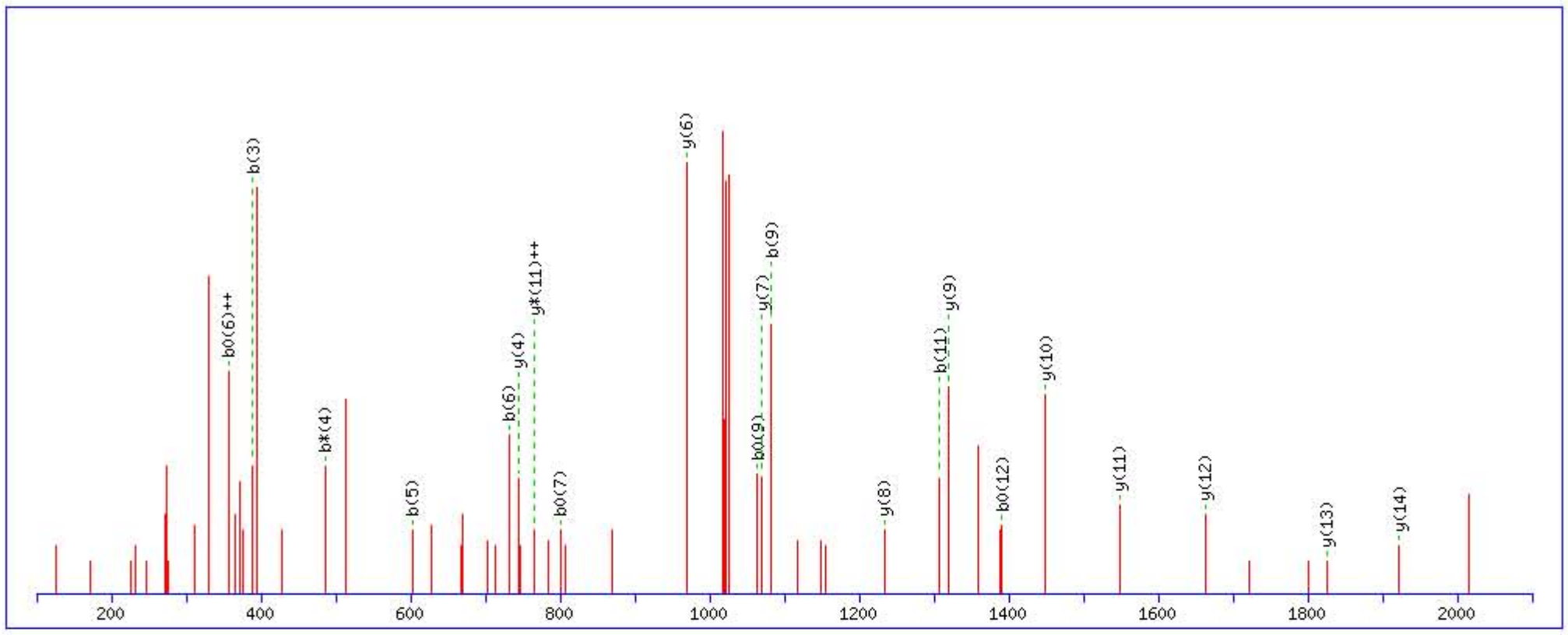
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KPYNVESYTPQTQGK**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

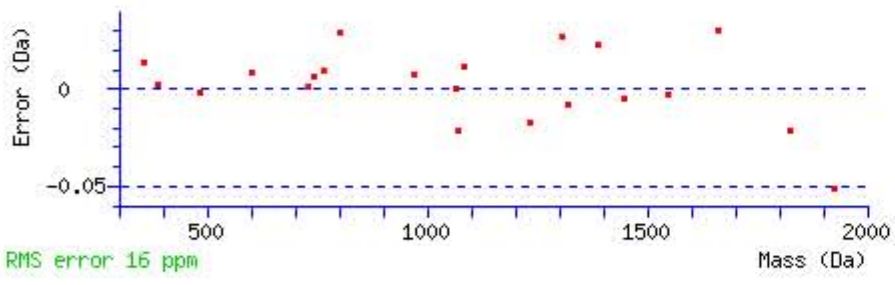
Match to Query 45758: 2050.024068 from(1026.019310,2+) rtinseconds(1600) index(17615)
Title: Locus:1.1.1.2939.22 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

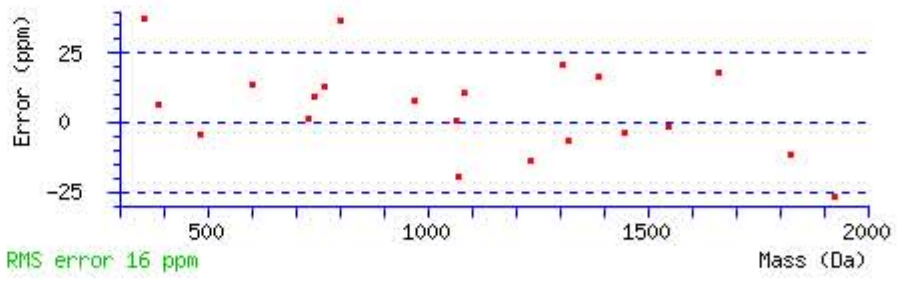
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2050.019348
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 50 **Expect:** 0.00025
**Matches :** 21/152 fragment ions using 47 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.102239 | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 15 |
| 2 | 226.155003 | 113.581139 | 209.128454 | 105.067865 | | | P | *1922.931678* | 961.969477 | 1905.905129 | 953.456203 | 1904.921113 | 952.964195 | 14 |
| 3 | **389.218332** | 195.112804 | 372.191783 | 186.599529 | | | Y | *1825.878914* | 913.443095 | 1808.852365 | 904.929821 | 1807.868349 | 904.437813 | 13 |
| 4 | 503.261259 | 252.134267 | 486.234710 | 243.620993 | | | N | *1662.815585* | 831.911431 | 1645.789036 | 823.398156 | 1644.805020 | 822.906148 | 12 |
| 5 | **602.329673** | 301.668475 | 585.303124 | 293.155200 | | | V | *1548.772658* | 774.889967 | 1531.746109 | 766.376693 | 1530.762093 | 765.884685 | 11 |
| 6 | **731.372266** | 366.189771 | 714.345717 | 357.676497 | 713.361701 | 357.184489 | E | *1449.704244* | 725.355760 | 1432.677695 | 716.842486 | 1431.693679 | 716.350478 | 10 |
| 7 | 818.404294 | 409.705785 | 801.377745 | 401.192511 | 800.393729 | 400.700503 | S | *1320.661651* | 660.834464 | 1303.635102 | 652.321189 | 1302.651086 | 651.829181 | 9 |
| 8 | 981.467623 | 491.237450 | 964.441074 | 482.724175 | 963.457058 | 482.232167 | Y | *1233.629623* | 617.318450 | 1216.603074 | 608.805175 | 1215.619058 | 608.313167 | 8 |
| 9 | **1082.515302** | 541.761289 | 1065.488753 | 533.248015 | 1064.504737 | 532.756007 | T | *1070.566294* | 535.786785 | 1053.539745 | 527.273511 | 1052.555729 | 526.781503 | 7 |
| 10 | 1179.568066 | 590.287671 | 1162.541517 | 581.774397 | 1161.557501 | 581.282389 | P | *969.518615* | 485.262946 | 952.492066 | 476.749671 | 951.508050 | 476.257663 | 6 |
| 11 | **1307.626644** | 654.316960 | 1290.600095 | 645.803686 | 1289.616079 | 645.311678 | Q | 872.465851 | 436.736564 | 855.439302 | 428.223289 | 854.455286 | 427.731281 | 5 |
| 12 | 1408.674323 | 704.840800 | 1391.647774 | 696.327525 | 1390.663758 | 695.835517 | T | *744.407273* | 372.707275 | 727.380724 | 364.194000 | 726.396708 | 363.701992 | 4 |
| 13 | 1847.899649 | 924.453463 | 1830.873100 | 915.940188 | 1829.889084 | 915.448180 | Q | 643.359594 | 322.183435 | 626.333045 | 313.670161 | | | 3 |
| 14 | 1904.921113 | 952.964195 | 1887.894564 | 944.450920 | 1886.910548 | 943.958912 | G | 204.134268 | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 15 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 50.2 | 2050.019348 | 0.004720 | KPYNVESYTPQTQGK |
| 37.2 | 2050.019348 | 0.004720 | KPYNVESYTPQTQGK |

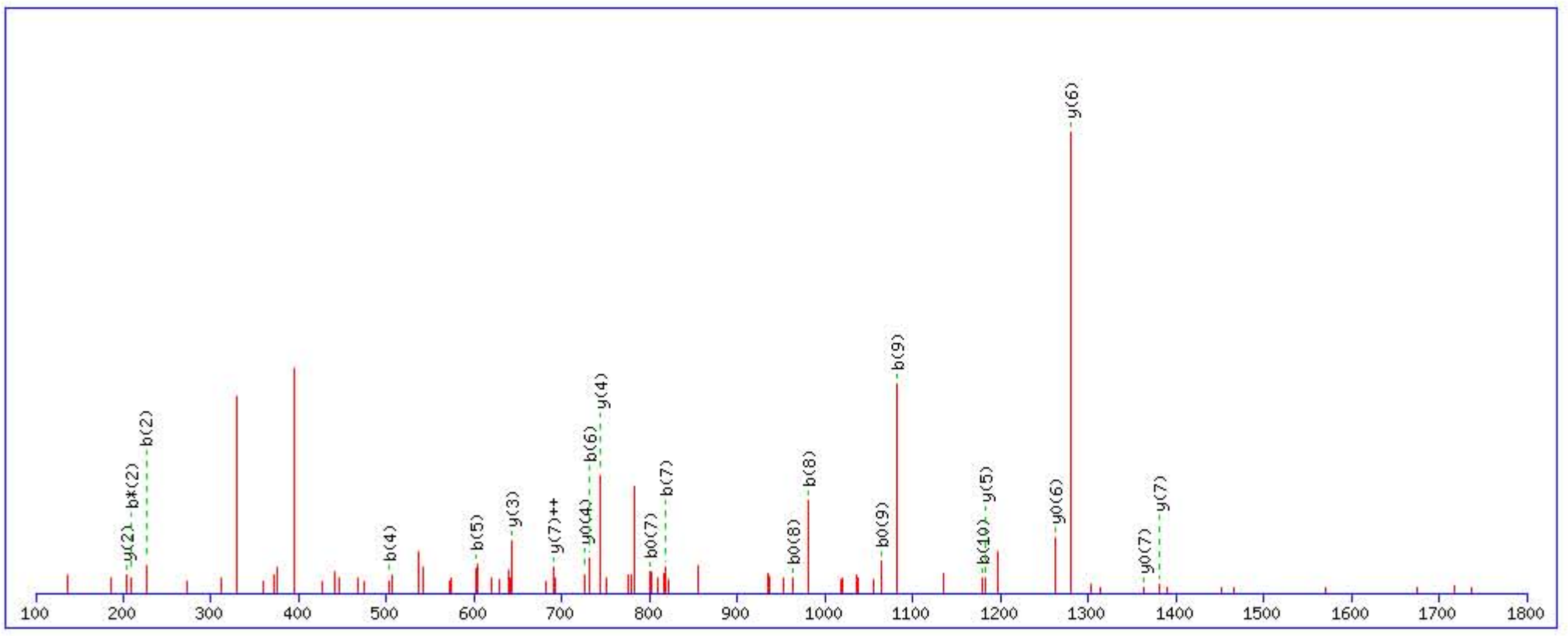
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KPYNVESYTPQTQGK**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

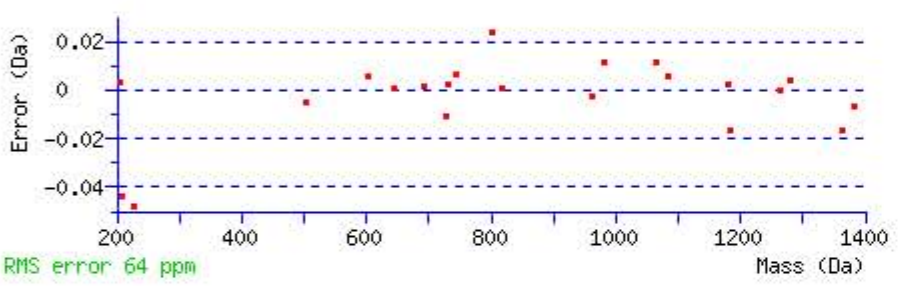
Match to Query 51470: 2361.190872 from(788.070900,3+) rtinseconds(1901) index(19610)
Title: Locus:1.1.1.3044.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

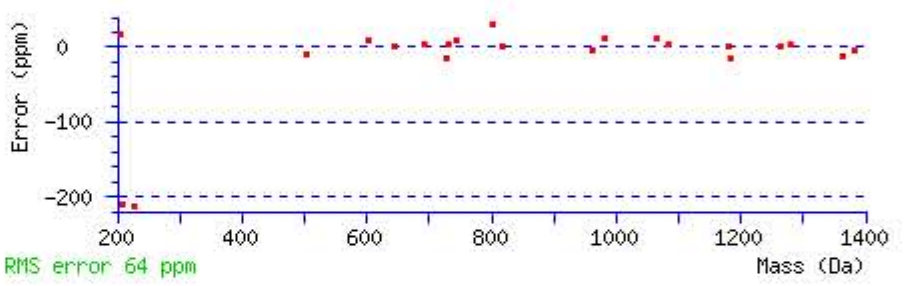
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2361.186096
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Q13** : Biotin:Thermo-21345 (Q)
**Ions Score:** 25 **Expect:** 0.0067
**Matches** : 22/152 fragment ions using 61 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.102239 | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 15 |
| 2 | *226.155003* | 113.581139 | 209.128454 | 105.067865 | | | P | 2234.098426 | 1117.552851 | 2217.071877 | 1109.039576 | 2216.087861 | 1108.547568 | 14 |
| 3 | 389.218332 | 195.112804 | 372.191783 | 186.599529 | | | Y | 2137.045662 | 1069.026469 | 2120.019113 | 1060.513194 | 2119.035097 | 1060.021186 | 13 |
| 4 | *503.261259* | 252.134267 | 486.234710 | 243.620993 | | | N | 1973.982333 | 987.494805 | 1956.955784 | 978.981530 | 1955.971768 | 978.489522 | 12 |
| 5 | *602.329673* | 301.668475 | 585.303124 | 293.155200 | | | V | 1859.939406 | 930.473341 | 1842.912857 | 921.960067 | 1841.928841 | 921.468059 | 11 |
| 6 | *731.372266* | 366.189771 | 714.345717 | 357.676497 | 713.361701 | 357.184489 | E | 1760.870992 | 880.939134 | 1743.844443 | 872.425860 | 1742.860427 | 871.933852 | 10 |
| 7 | *818.404294* | 409.705785 | 801.377745 | 401.192511 | 800.393729 | 400.700503 | S | 1631.828399 | 816.417838 | 1614.801850 | 807.904563 | 1613.817834 | 807.412555 | 9 |
| 8 | *981.467623* | 491.237450 | 964.441074 | 482.724175 | 963.457058 | 482.232167 | Y | 1544.796371 | 772.901824 | 1527.769822 | 764.388549 | 1526.785806 | 763.896541 | 8 |
| 9 | *1082.515302* | 541.761289 | 1065.488753 | 533.248015 | 1064.504737 | 532.756007 | T | *1381.733042* | 691.370159 | 1364.706493 | 682.856885 | 1363.722477 | 682.364877 | 7 |
| 10 | *1179.568066* | 590.287671 | 1162.541517 | 581.774397 | 1161.557501 | 581.282389 | P | *1280.685363* | 640.846320 | 1263.658814 | 632.333045 | 1262.674798 | 631.841037 | 6 |
| 11 | 1618.793392 | 809.900334 | 1601.766843 | 801.387060 | 1600.782827 | 800.895052 | Q | *1183.632599* | 592.319938 | 1166.606050 | 583.806663 | 1165.622034 | 583.314655 | 5 |
| 12 | 1719.841071 | 860.424174 | 1702.814522 | 851.910899 | 1701.830506 | 851.418891 | T | *744.407273* | 372.707275 | 727.380724 | 364.194000 | 726.396708 | 363.701992 | 4 |
| 13 | 2159.066397 | 1080.036836 | 2142.039848 | 1071.523562 | 2141.055832 | 1071.031554 | Q | *643.359594* | 322.183435 | 626.333045 | 313.670161 | | | 3 |
| 14 | 2216.087861 | 1108.547568 | 2199.061312 | 1100.034294 | 2198.077296 | 1099.542286 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 15 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.3 | 2361.186096 | 0.004776 | KPYNVESYTPQTQGK |
| 2.1 | 2361.199814 | -0.008942 | AAQALAKLTITSNPEMTFPGER |
| 1.8 | 2361.203217 | -0.012345 | SVLDDLTSCTTSLRQINK |

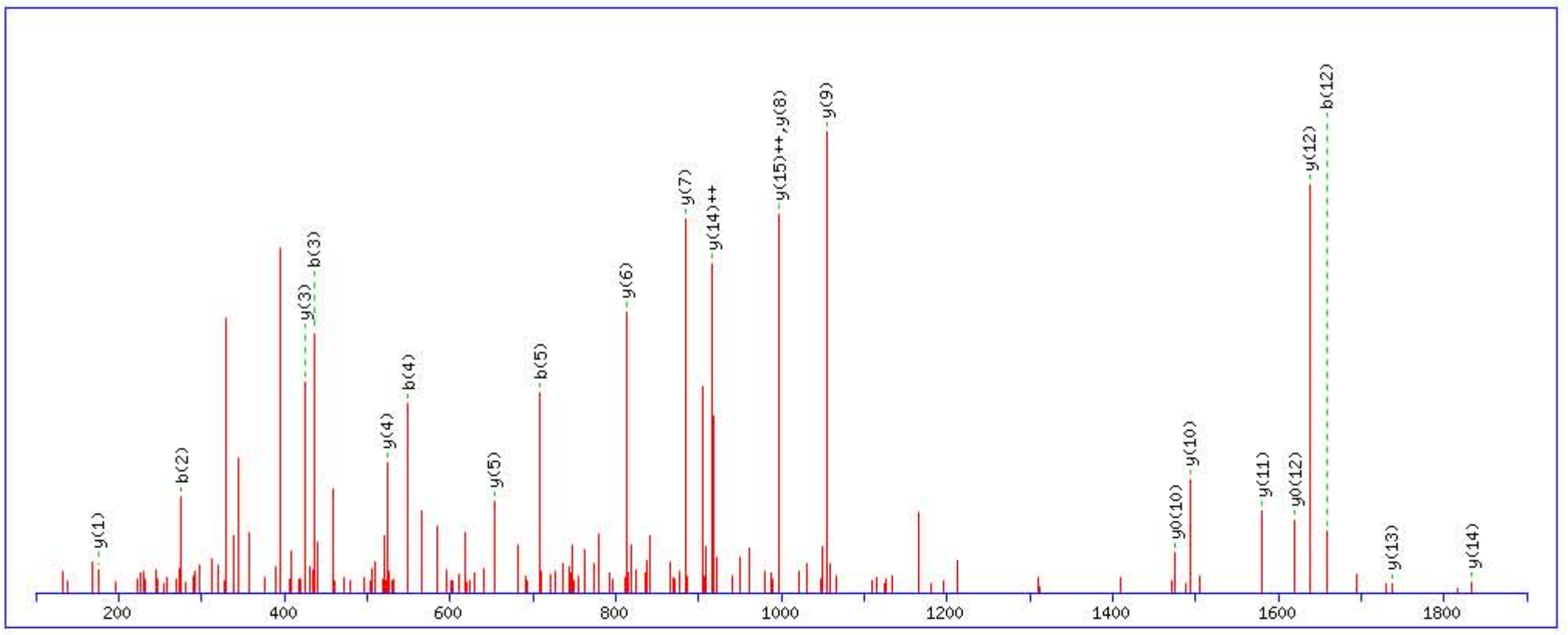
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **CDCICPVGSQGLACEVSYR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

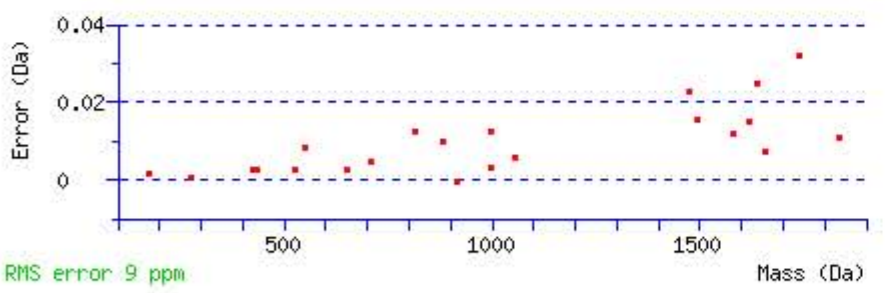
Match to Query 54890: 2541.117102 from(848.046310,3+) rtinseconds(2154) index(21227)
Title: Locus:1.1.1.3132.22 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

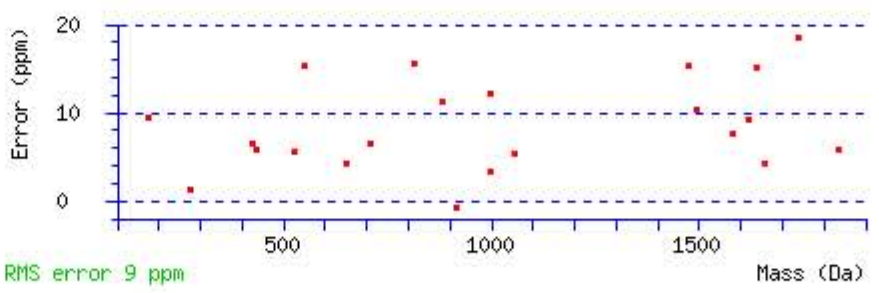
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2541.094299
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 90 **Expect:** 5.6e-009
**Matches :** 22/192 fragment ions using 34 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 161.037925 | 81.022600 | | | | | C | | | | | | | 19 |
| 2 | 276.064868 | 138.536072 | | | 258.054303 | 129.530790 | D | 2382.070908 | 1191.539092 | 2365.044359 | 1183.025817 | 2364.060343 | 1182.533809 | 18 |
| 3 | 436.095517 | 218.551397 | | | 418.084952 | 209.546114 | C | 2267.043965 | 1134.025620 | 2250.017416 | 1125.512346 | 2249.033400 | 1125.020338 | 17 |
| 4 | 549.179581 | 275.093429 | | | 531.169016 | 266.088146 | I | 2107.013316 | 1054.010296 | 2089.986767 | 1045.497021 | 2089.002751 | 1045.005013 | 16 |
| 5 | 709.210230 | 355.108753 | | | 691.199665 | 346.103471 | C | 1993.929252 | 997.468264 | 1976.902703 | 988.954990 | 1975.918687 | 988.462982 | 15 |
| 6 | 806.262994 | 403.635135 | | | 788.252429 | 394.629853 | P | *1833.898603* | 917.452940 | 1816.872054 | 908.939665 | 1815.888038 | 908.447657 | 14 |
| 7 | 905.331408 | 453.169342 | | | 887.320843 | 444.164060 | V | *1736.845839* | 868.926558 | 1719.819290 | 860.413283 | 1718.835274 | 859.921275 | 13 |
| 8 | 962.352872 | 481.680074 | | | 944.342307 | 472.674792 | G | *1637.777425* | 819.392351 | 1620.750876 | 810.879076 | 1619.766860 | 810.387068 | 12 |
| 9 | 1049.384900 | 525.196088 | | | 1031.374335 | 516.190806 | S | *1580.755961* | 790.881619 | 1563.729412 | 782.368344 | 1562.745396 | 781.876336 | 11 |
| 10 | 1488.610226 | 744.808751 | 1471.583677 | 736.295477 | 1470.599661 | 735.803469 | Q | *1493.723933* | 747.365605 | 1476.697384 | 738.852330 | 1475.713368 | 738.360322 | 10 |
| 11 | 1545.631690 | 773.319483 | 1528.605141 | 764.806209 | 1527.621125 | 764.314201 | G | *1054.498607* | 527.752941 | 1037.472058 | 519.239667 | 1036.488042 | 518.747659 | 9 |
| 12 | 1658.715754 | 829.861515 | 1641.689205 | 821.348241 | 1640.705189 | 820.856233 | L | *997.477143* | 499.242209 | 980.450594 | 490.728935 | 979.466578 | 490.236927 | 8 |
| 13 | 1729.752868 | 865.380072 | 1712.726319 | 856.866798 | 1711.742303 | 856.374790 | A | *884.393079* | 442.700178 | 867.366530 | 434.186903 | 866.382514 | 433.694895 | 7 |
| 14 | 1889.783517 | 945.395397 | 1872.756968 | 936.882122 | 1871.772952 | 936.390114 | C | *813.355965* | 407.181621 | 796.329416 | 398.668346 | 795.345400 | 398.176338 | 6 |
| 15 | 2018.826110 | 1009.916693 | 2001.799561 | 1001.403419 | 2000.815545 | 1000.911411 | E | *653.325316* | 327.166296 | 636.298767 | 318.653021 | 635.314751 | 318.161013 | 5 |
| 16 | 2117.894524 | 1059.450900 | 2100.867975 | 1050.937625 | 2099.883959 | 1050.445617 | V | *524.282723* | 262.645000 | 507.256174 | 254.131725 | 506.272158 | 253.639717 | 4 |
| 17 | 2204.926552 | 1102.966914 | 2187.900003 | 1094.453639 | 2186.915987 | 1093.961631 | S | *425.214309* | 213.110793 | 408.187760 | 204.597518 | 407.203744 | 204.105510 | 3 |
| 18 | 2367.989881 | 1184.498578 | 2350.963332 | 1175.985304 | 2349.979316 | 1175.493296 | Y | 338.182281 | 169.594778 | 321.155732 | 161.081504 | | | 2 |
| 19 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 90.2 | 2541.094299 | 0.022803 | CDCICPVGSQGLACEVSYR |

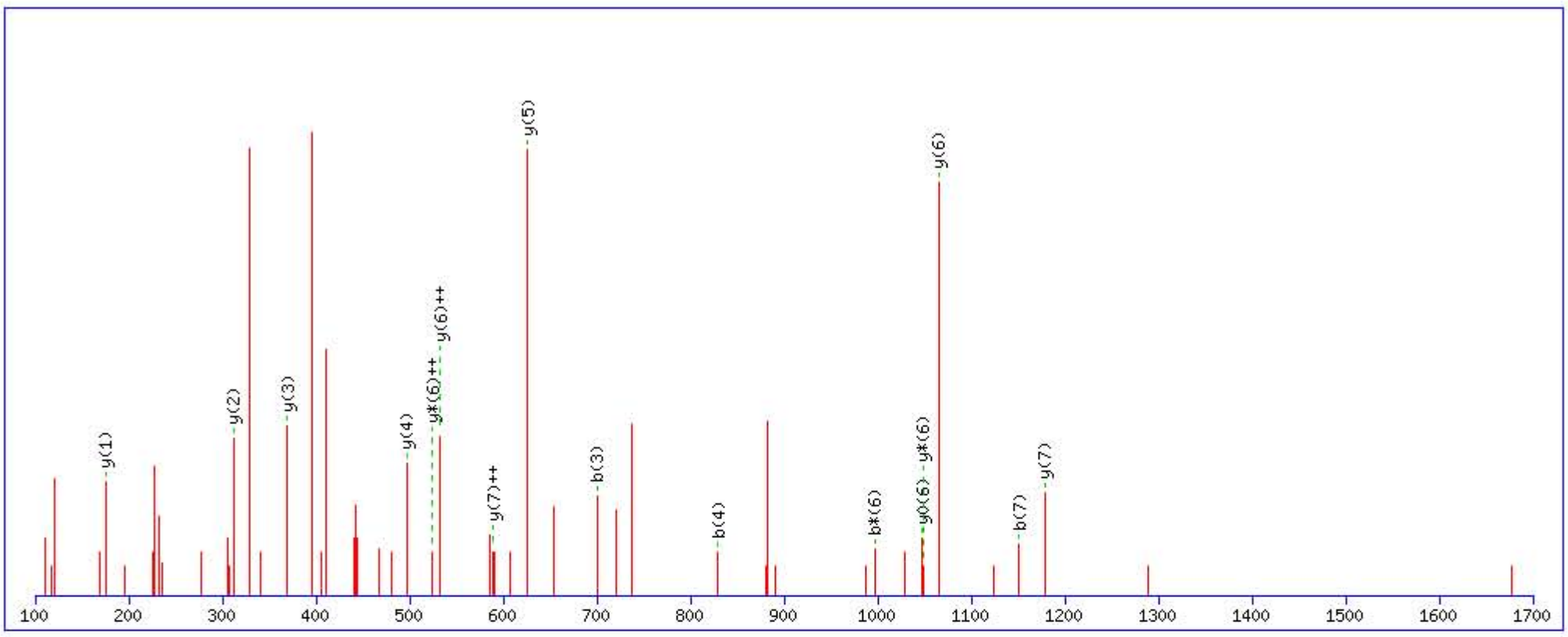
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FLQEQGHR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

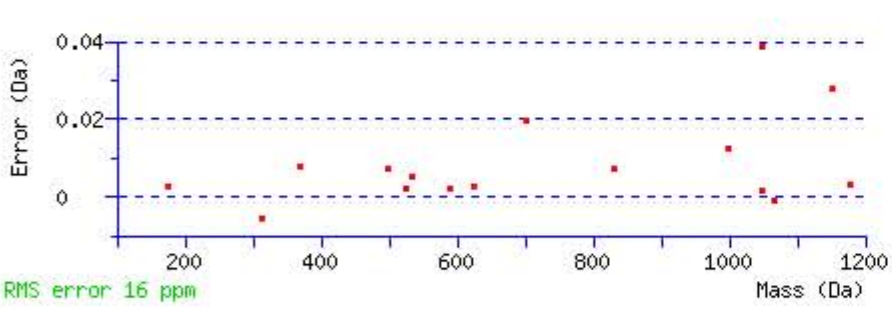
Match to Query 23757: 1324.680428 from(663.347490,2+) rtinseconds(1524) index(31225)
Title: Locus:1.1.1.639.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

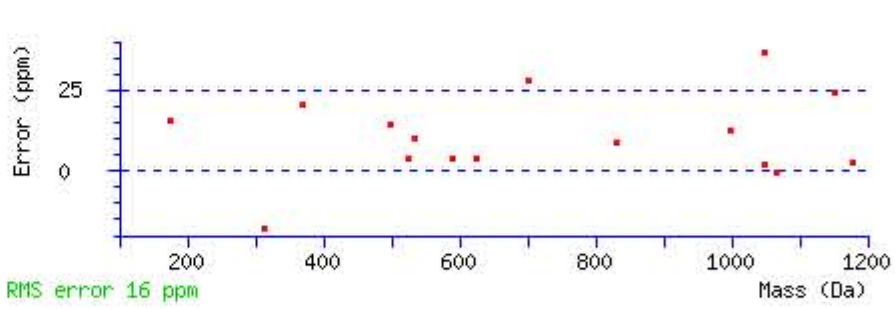
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1324.671021
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 34 **Expect:** 0.0039
**Matches :** 16/66 fragment ions using 39 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 8 |
| 2 | 261.159754 | 131.083515 | | | | | L | *1178.609889* | 589.808583 | 1161.583340 | 581.295308 | 1160.599324 | 580.803300 | 7 |
| 3 | **700.385080** | 350.696178 | 683.358531 | 342.182904 | | | Q | *1065.525825* | 533.266551 | 1048.499276 | 524.753276 | 1047.515260 | 524.261268 | 6 |
| 4 | **829.427673** | 415.217475 | 812.401124 | 406.704200 | 811.417108 | 406.212192 | E | *626.300499* | 313.653888 | 609.273950 | 305.140613 | 608.289934 | 304.648605 | 5 |
| 5 | 957.486251 | 479.246764 | 940.459702 | 470.733489 | 939.475686 | 470.241481 | Q | *497.257906* | 249.132591 | 480.231357 | 240.619317 | | | 4 |
| 6 | 1014.507715 | 507.757496 | 997.481166 | 499.244221 | 996.497150 | 498.752213 | G | *369.199328* | 185.103302 | 352.172779 | 176.590028 | | | 3 |
| 7 | **1151.566627** | 576.286952 | 1134.540078 | 567.773677 | 1133.556062 | 567.281669 | H | *312.177864* | 156.592570 | 295.151315 | 148.079296 | | | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 34.3 | 1324.671021 | 0.009407 | FLQEQGHR |
| 10.4 | 1324.671021 | 0.009407 | FLQEQGHR |
| 8.3 | 1324.669647 | 0.010781 | MKEIAEAYLGGK |
| 3.3 | 1324.692795 | -0.012367 | YLDFSLFKHR |

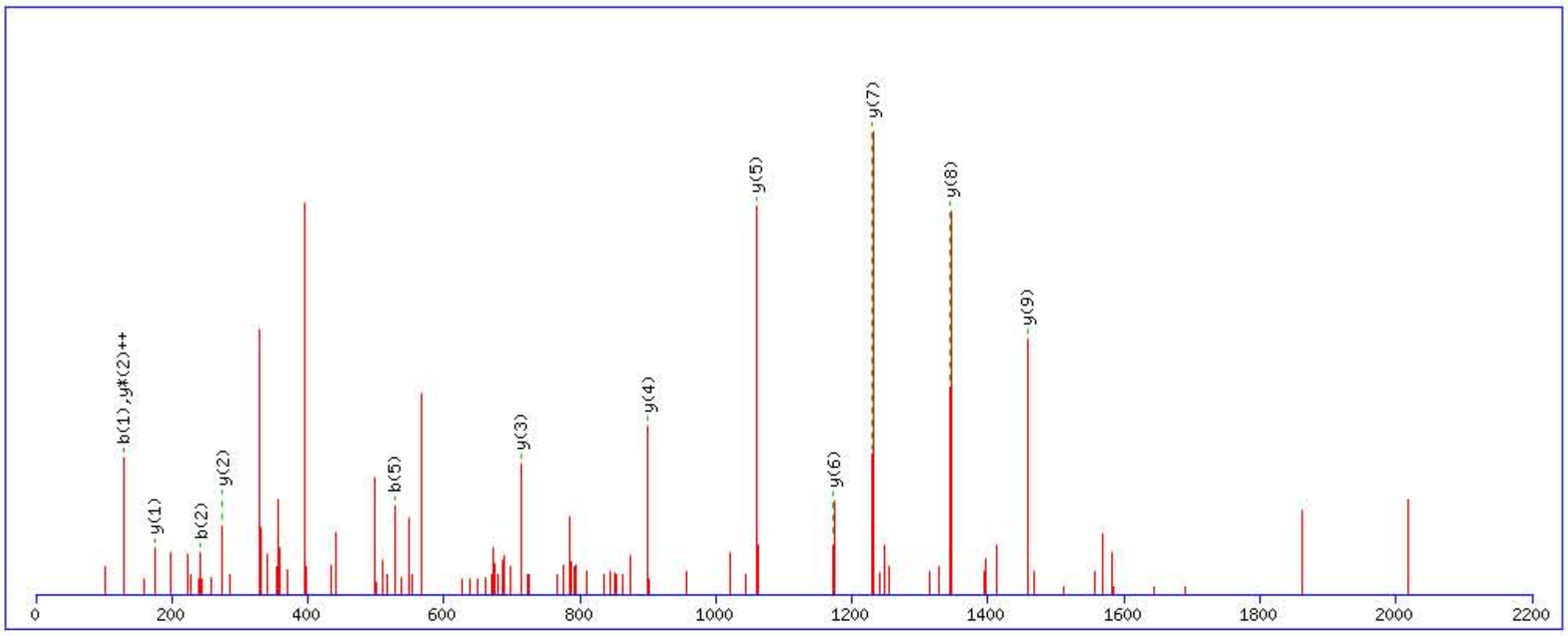
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KLDGICWQVR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

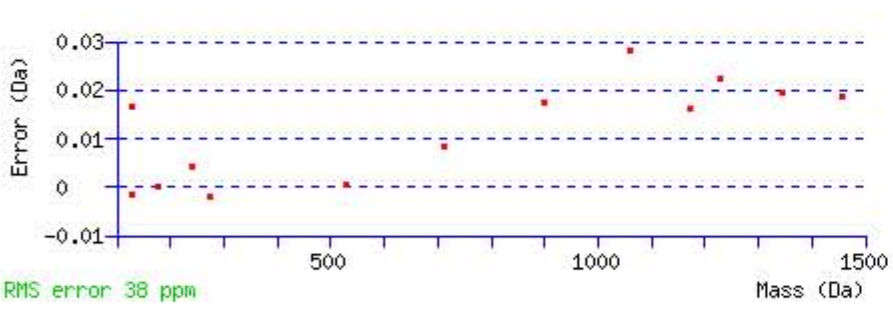
Match to Query 33984: 1584.845828 from(793.430190,2+) rtinseconds(2084) index(34759)
Title: Locus:1.1.1.834.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

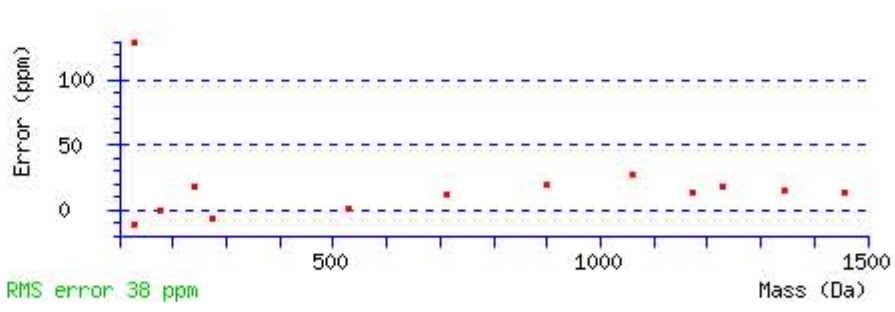
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1584.826874
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 47 **Expect:** 0.00049
**Matches :** 13/90 fragment ions using 30 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.102239 | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 10 |
| 2 | 242.186303 | 121.596790 | 225.159754 | 113.083515 | | | L | *1457.739189* | 729.373233 | 1440.712640 | 720.859958 | 1439.728624 | 720.367950 | 9 |
| 3 | 357.213246 | 179.110261 | 340.186697 | 170.596987 | 339.202681 | 170.104979 | D | *1344.655125* | 672.831201 | 1327.628576 | 664.317926 | 1326.644560 | 663.825918 | 8 |
| 4 | 414.234710 | 207.620993 | 397.208161 | 199.107719 | 396.224145 | 198.615711 | G | *1229.628182* | 615.317729 | 1212.601633 | 606.804455 | | | 7 |
| 5 | 527.318774 | 264.163025 | 510.292225 | 255.649751 | 509.308209 | 255.157743 | I | *1172.606718* | 586.806997 | 1155.580169 | 578.293723 | | | 6 |
| 6 | 687.349423 | 344.178350 | 670.322874 | 335.665075 | 669.338858 | 335.173067 | C | *1059.522654* | 530.264965 | 1042.496105 | 521.751691 | | | 5 |
| 7 | 873.428736 | 437.218006 | 856.402187 | 428.704732 | 855.418171 | 428.212724 | W | *899.492005* | 450.249641 | 882.465456 | 441.736366 | | | 4 |
| 8 | 1312.654062 | 656.830669 | 1295.627513 | 648.317395 | 1294.643497 | 647.825387 | Q | *713.412692* | 357.209984 | 696.386143 | 348.696710 | | | 3 |
| 9 | 1411.722476 | 706.364876 | 1394.695927 | 697.851602 | 1393.711911 | 697.359594 | V | *274.187366* | 137.597321 | 257.160817 | 129.084047 | | | 2 |
| 10 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

### All matches to this query

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 46.7 | 1584.826874 | 0.018954 | KLDGICWQVR |
| 10.9 | 1584.858353 | -0.012525 | QLDGLAGLKGEGSRGK |
| 4.2 | 1584.865738 | -0.019910 | KLNMDQVLDQILR |
| 3.2 | 1584.858337 | -0.012509 | LKSNDGEERLAVVR |
| 2.9 | 1584.822830 | 0.022998 | QLDQKCKQAR |

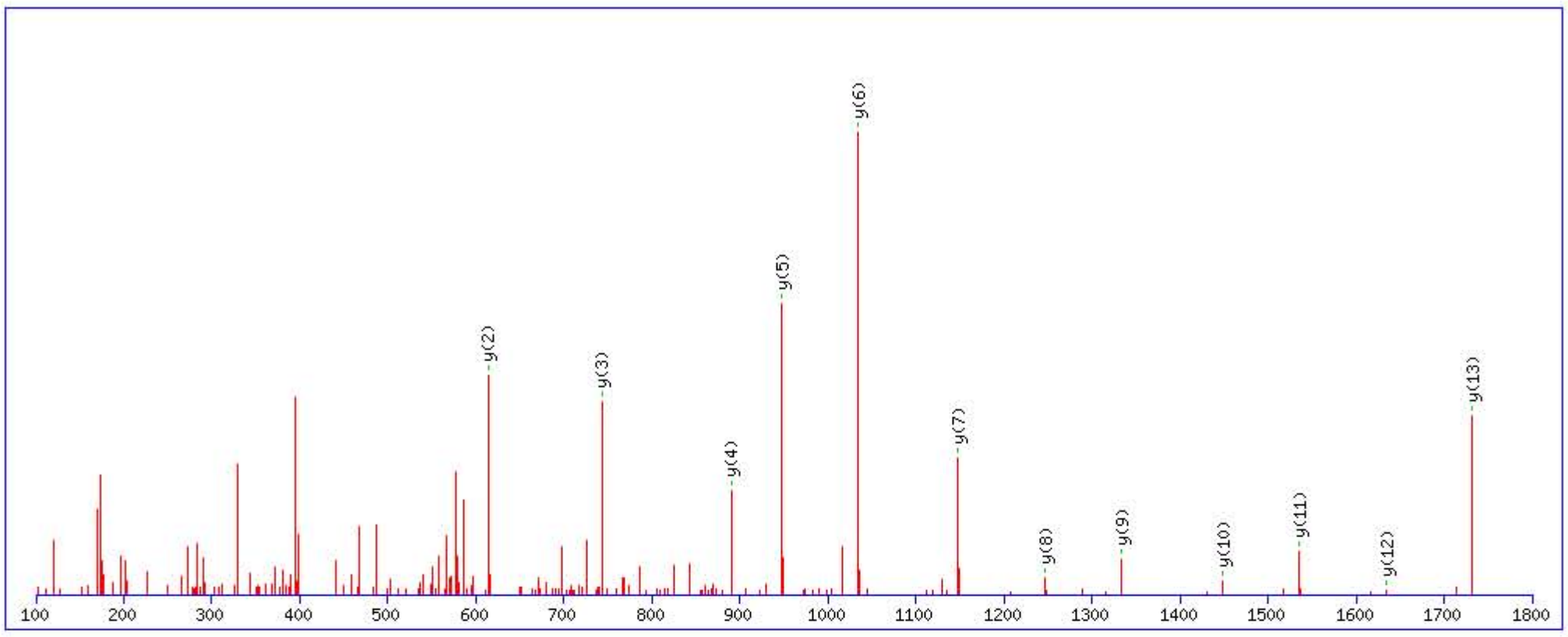
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SLPVSDSVLSGFEQR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

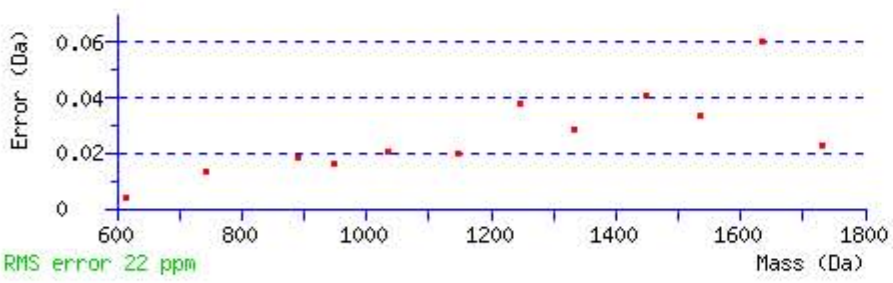
Match to Query 42720: 1931.002752 from(644.674860,3+) rtinseconds(2512) index(23248)
Title: Locus:1.1.1.3257.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

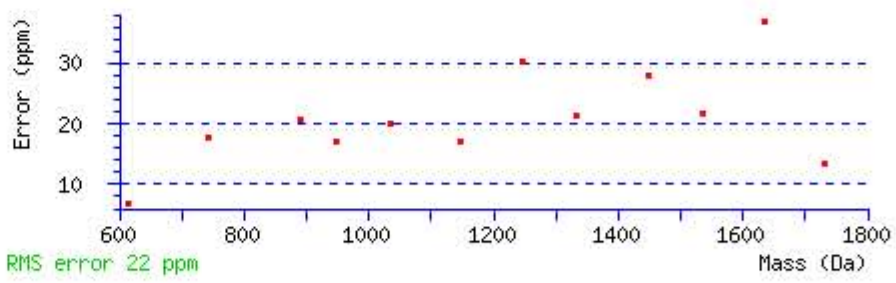
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1930.982254
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q14 : Biotin:Thermo-21345 (Q)
**Ions Score:** 104 **Expect:** 2.8e-010
**Matches :** 12/138 fragment ions using 17 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 15 |
| 2 | 201.123368 | 101.065322 | | | 183.112803 | 92.060039 | L | 1844.957496 | 922.982386 | 1827.930947 | 914.469112 | 1826.946931 | 913.977104 | 14 |
| 3 | 298.176132 | 149.591704 | | | 280.165567 | 140.586422 | P | *1731.873432* | 866.440354 | 1714.846883 | 857.927080 | 1713.862867 | 857.435072 | 13 |
| 4 | 397.244546 | 199.125911 | | | 379.233981 | 190.120629 | V | *1634.820668* | 817.913972 | 1617.794119 | 809.400698 | 1616.810103 | 808.908690 | 12 |
| 5 | 484.276574 | 242.641925 | | | 466.266009 | 233.636643 | S | *1535.752254* | 768.379765 | 1518.725705 | 759.866491 | 1517.741689 | 759.374483 | 11 |
| 6 | 599.303517 | 300.155397 | | | 581.292952 | 291.150114 | D | *1448.720226* | 724.863751 | 1431.693677 | 716.350477 | 1430.709661 | 715.858469 | 10 |
| 7 | 686.335545 | 343.671411 | | | 668.324980 | 334.666128 | S | *1333.693283* | 667.350280 | 1316.666734 | 658.837005 | 1315.682718 | 658.344997 | 9 |
| 8 | 785.403959 | 393.205618 | | | 767.393394 | 384.200335 | V | *1246.661255* | 623.834266 | 1229.634706 | 615.320991 | 1228.650690 | 614.828983 | 8 |
| 9 | 898.488023 | 449.747650 | | | 880.477458 | 440.742367 | L | *1147.592841* | 574.300059 | 1130.566292 | 565.786784 | 1129.582276 | 565.294776 | 7 |
| 10 | 985.520051 | 493.263664 | | | 967.509486 | 484.258381 | S | *1034.508777* | 517.758027 | 1017.482228 | 509.244752 | 1016.498212 | 508.752744 | 6 |
| 11 | 1042.541515 | 521.774395 | | | 1024.530950 | 512.769113 | G | *947.476749* | 474.242013 | 930.450200 | 465.728738 | 929.466184 | 465.236730 | 5 |
| 12 | 1189.609929 | 595.308603 | | | 1171.599364 | 586.303320 | F | *890.455285* | 445.731281 | 873.428736 | 437.218006 | 872.444720 | 436.725998 | 4 |
| 13 | 1318.652522 | 659.829899 | | | 1300.641957 | 650.824617 | E | *743.386871* | 372.197074 | 726.360322 | 363.683799 | 725.376306 | 363.191791 | 3 |
| 14 | 1757.877848 | 879.442562 | 1740.851299 | 870.929288 | 1739.867283 | 870.437280 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 15 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 104.2 | 1930.982254 | 0.020498 | SLPVSDSVLSGFEQR |
| 2.2 | 1930.978195 | 0.024557 | VALSNISKDGNLMETAPR |
| 1.5 | 1931.000885 | 0.001867 | LSPVTACAGQTLQFK |
| 0.4 | 1930.989410 | 0.013342 | EAQSQLIKSDEMQRLR |

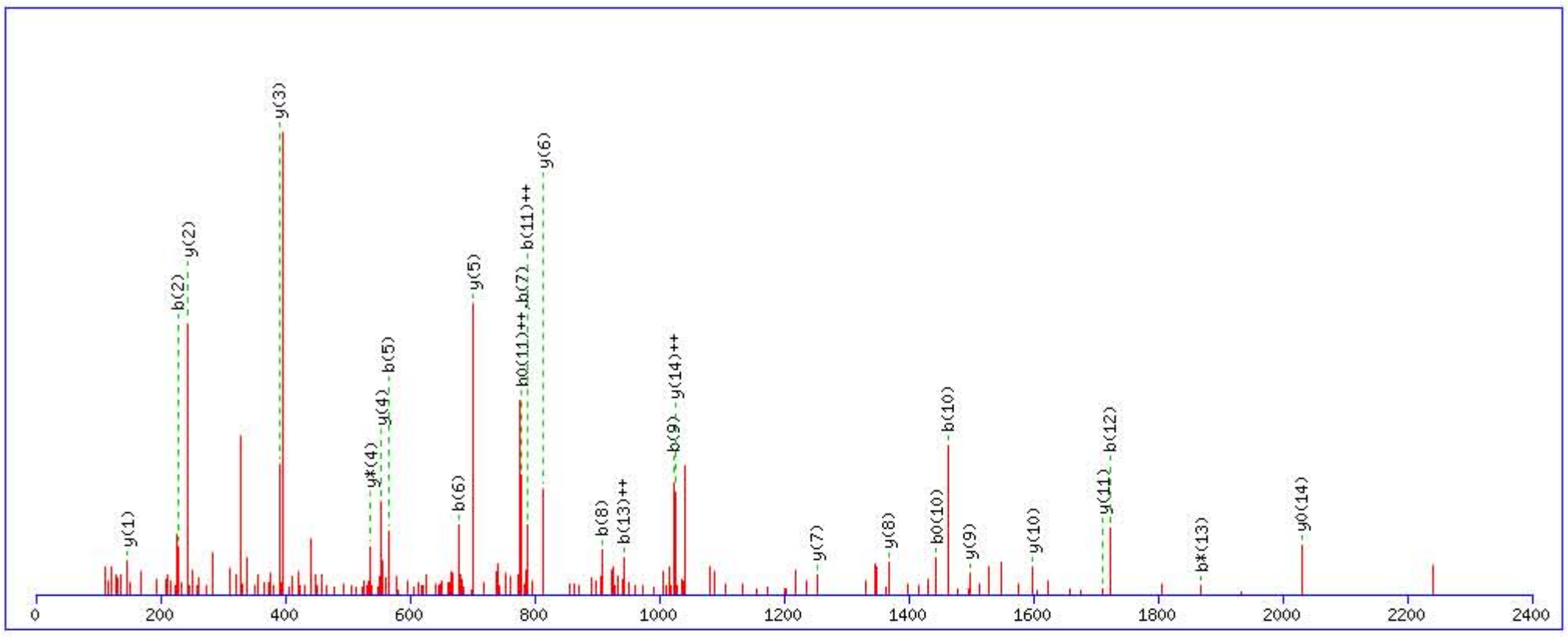
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VQEAHLTEDQIFYFPK**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

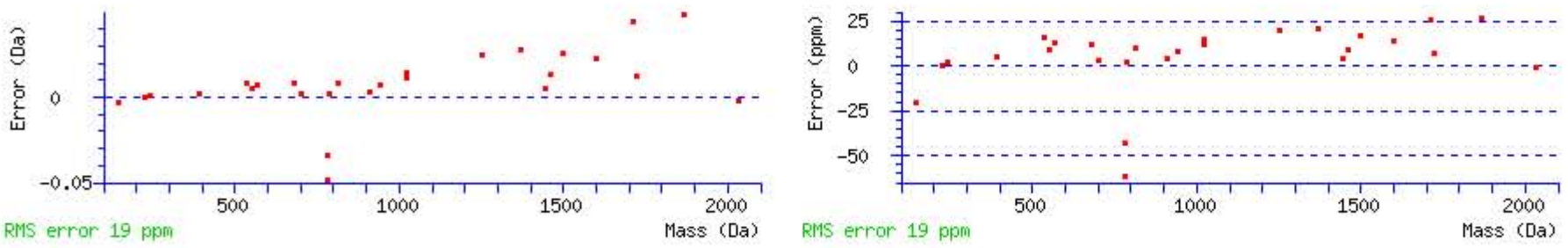
Match to Query 50078: 2275.161492 from(759.394440,3+) rtinseconds(2378) index(22503)
Title: Locus:1.1.1.3210.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2275.134720
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 52 **Expect:** 1.4e-005
**Matches :** 27/160 fragment ions using 55 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 16 |
| 2 | **228.134268** | 114.570772 | 211.107719 | 106.057498 | | | Q | 2177.073591 | 1089.040433 | 2160.047042 | 1080.527159 | 2159.063026 | 1080.035151 | 15 |
| 3 | 357.176861 | 179.092069 | 340.150312 | 170.578794 | 339.166296 | 170.086786 | E | 2049.015013 | 1025.011144 | 2031.988464 | 1016.497870 | 2031.004448 | 1016.005862 | 14 |
| 4 | 428.213975 | 214.610626 | 411.187426 | 206.097351 | 410.203410 | 205.605343 | A | 1919.972420 | 960.489848 | 1902.945871 | 951.976573 | 1901.961855 | 951.484565 | 13 |
| 5 | **565.272887** | 283.140082 | 548.246338 | 274.626807 | 547.262322 | 274.134799 | H | 1848.935306 | 924.971291 | 1831.908757 | 916.458016 | 1830.924741 | 915.966008 | 12 |
| 6 | **678.356951** | 339.682114 | 661.330402 | 331.168839 | 660.346386 | 330.676831 | L | *1711.876394* | 856.441835 | 1694.849845 | 847.928561 | 1693.865829 | 847.436552 | 11 |
| 7 | **779.404630** | 390.205953 | 762.378081 | 381.692679 | 761.394065 | 381.200671 | T | *1598.792330* | 799.899803 | 1581.765781 | 791.386529 | 1580.781765 | 790.894521 | 10 |
| 8 | **908.447223** | 454.727250 | 891.420674 | 446.213975 | 890.436658 | 445.721967 | E | *1497.744651* | 749.375963 | 1480.718102 | 740.862689 | 1479.734086 | 740.370681 | 9 |
| 9 | **1023.474166** | 512.240721 | 1006.447617 | 503.727447 | 1005.463601 | 503.235439 | D | *1368.702058* | 684.854667 | 1351.675509 | 676.341392 | 1350.691493 | 675.849384 | 8 |
| 10 | **1462.699492** | 731.853384 | 1445.672943 | 723.340110 | 1444.688927 | 722.848101 | Q | *1253.675115* | 627.341195 | 1236.648566 | 618.827921 | | | 7 |
| 11 | 1575.783556 | **788.395416** | 1558.757007 | 779.882141 | 1557.772991 | 779.390133 | I | *814.449789* | 407.728533 | 797.423240 | 399.215258 | | | 6 |
| 12 | **1722.851970** | 861.929623 | 1705.825421 | 853.416349 | 1704.841405 | 852.924340 | F | *701.365725* | 351.186501 | 684.339176 | 342.673226 | | | 5 |
| 13 | 1885.915299 | **943.461288** | 1868.888750 | 934.948013 | 1867.904734 | 934.456005 | Y | *554.297311* | 277.652294 | 537.270762 | 269.139019 | | | 4 |
| 14 | 2032.983713 | 1016.995495 | 2015.957164 | 1008.482220 | 2014.973148 | 1007.990212 | F | *391.233982* | 196.120629 | 374.207433 | 187.607354 | | | 3 |
| 15 | 2130.036477 | 1065.521876 | 2113.009928 | 1057.008602 | 2112.025912 | 1056.516594 | P | *244.165568* | 122.586422 | 227.139019 | 114.073147 | | | 2 |
| 16 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.4 | 2275.134720 | 0.026772 | VQEAHLTEDQIFYFPK |
| 16.1 | 2275.134720 | 0.026772 | VQEAHLTEDQIFYFPK |
| 0.8 | 2275.160538 | 0.000954 | VLPYCWKGMTPEQQAAIRK |

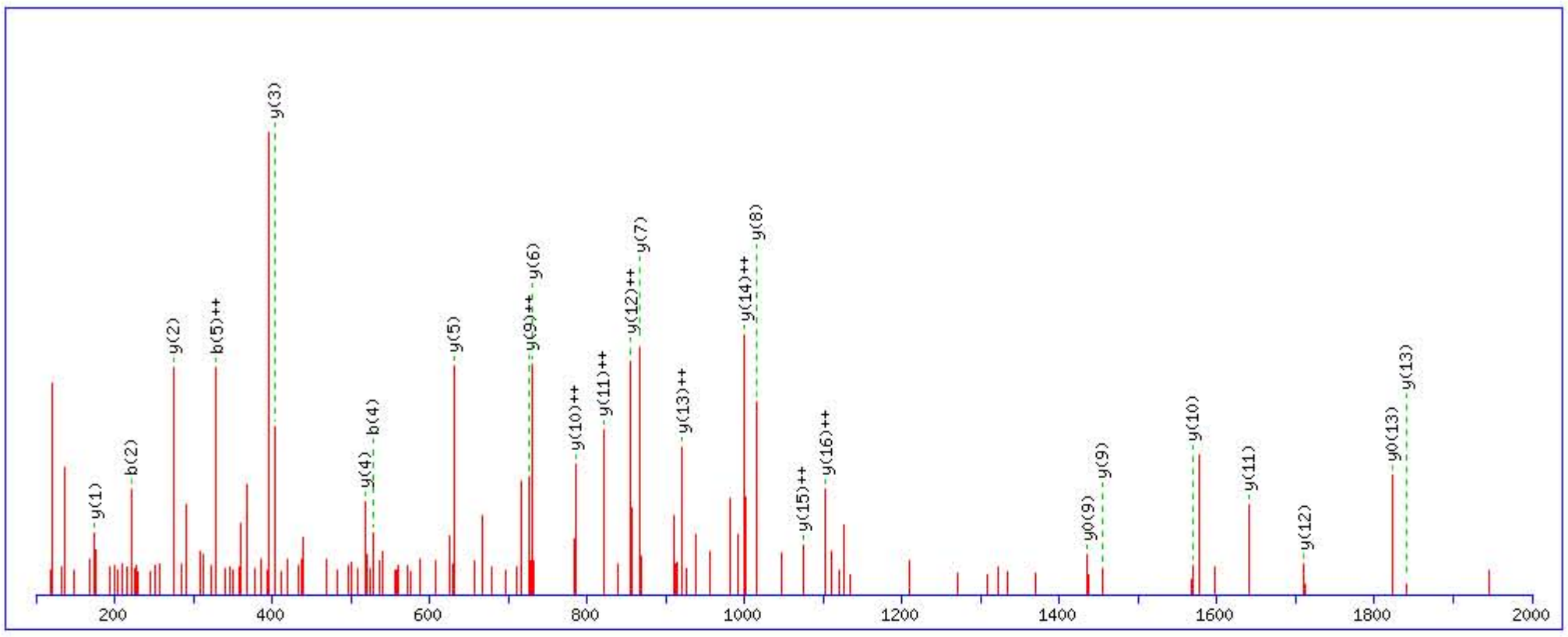
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YGFCEAADQFHVLDEVR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

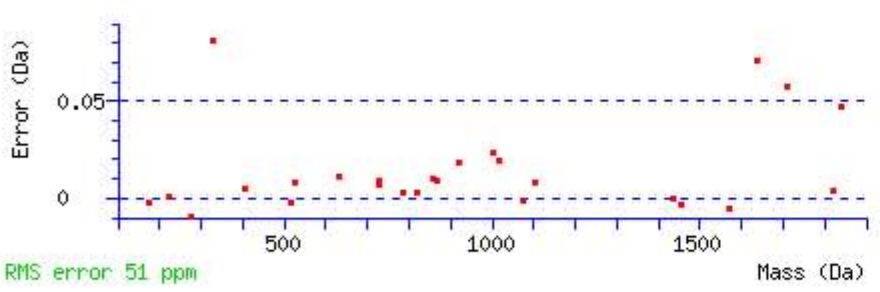
Match to Query 51513: 2366.115132 from(789.712320,3+) rtinseconds(2568) index(23538)
Title: Locus:1.1.1.3276.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

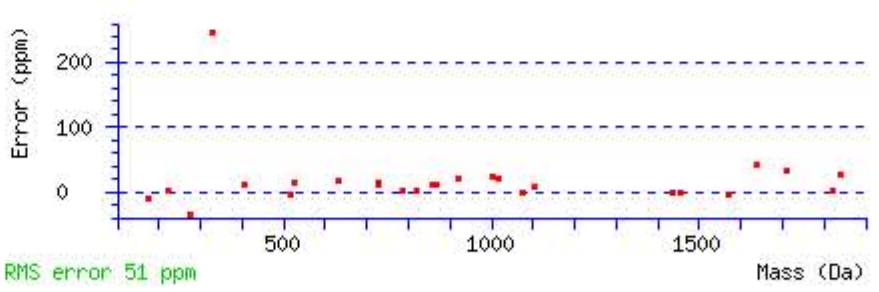
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2366.082382
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 73 **Expect:** 2.3e-007
**Matches :** 26/164 fragment ions using 50 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 17 |
| 2 | **221.092069** | 111.049673 | | | | | G | 2204.026323 | 1102.516799 | 2186.999774 | 1094.003525 | 2186.015758 | 1093.511517 | 16 |
| 3 | 368.160483 | 184.583879 | | | | | F | 2147.004859 | 1074.006067 | 2129.978310 | 1065.492793 | 2128.994294 | 1065.000785 | 15 |
| 4 | **528.191132** | 264.599204 | | | | | C | 1999.936445 | 1000.471860 | 1982.909896 | 991.958586 | 1981.925880 | 991.466578 | 14 |
| 5 | 657.233725 | 329.120501 | | | 639.223160 | 320.115218 | E | ***1839.905796*** | 920.456536 | 1822.879247 | 911.943261 | ***1821.895231*** | 911.451253 | 13 |
| 6 | 728.270839 | 364.639058 | | | 710.260274 | 355.633775 | A | ***1710.863203*** | 855.935239 | 1693.836654 | 847.421965 | 1692.852638 | 846.929957 | 12 |
| 7 | 799.307953 | 400.157615 | | | 781.297388 | 391.152332 | A | ***1639.826089*** | 820.416682 | 1622.799540 | 811.903408 | 1621.815524 | 811.411400 | 11 |
| 8 | 914.334896 | 457.671086 | | | 896.324331 | 448.665803 | D | ***1568.788975*** | 784.898125 | 1551.762426 | 776.384851 | 1550.778410 | 775.892843 | 10 |
| 9 | 1353.560222 | 677.283749 | 1336.533673 | 668.770474 | 1335.549657 | 668.278466 | Q | ***1453.762032*** | 727.384654 | 1436.735483 | 718.871379 | ***1435.751467*** | 718.379371 | 9 |
| 10 | 1500.628636 | 750.817956 | 1483.602087 | 742.304682 | 1482.618071 | 741.812673 | F | ***1014.536706*** | 507.771991 | 997.510157 | 499.258717 | 996.526141 | 498.766709 | 8 |
| 11 | 1637.687548 | 819.347412 | 1620.660999 | 810.834138 | 1619.676983 | 810.342129 | H | ***867.468292*** | 434.237784 | 850.441743 | 425.724510 | 849.457727 | 425.232502 | 7 |
| 12 | 1736.755962 | 868.881619 | 1719.729413 | 860.368345 | 1718.745397 | 859.876336 | V | ***730.409380*** | 365.708328 | 713.382831 | 357.195054 | 712.398815 | 356.703046 | 6 |
| 13 | 1849.840026 | 925.423651 | 1832.813477 | 916.910376 | 1831.829461 | 916.418368 | L | ***631.340966*** | 316.174121 | 614.314417 | 307.660846 | 613.330401 | 307.168838 | 5 |
| 14 | 1964.866969 | 982.937122 | 1947.840420 | 974.423848 | 1946.856404 | 973.931840 | D | ***518.256902*** | 259.632089 | 501.230353 | 251.118815 | 500.246337 | 250.626807 | 4 |
| 15 | 2093.909562 | 1047.458419 | 2076.883013 | 1038.945144 | 2075.898997 | 1038.453136 | E | ***403.229959*** | 202.118617 | 386.203410 | 193.605343 | 385.219394 | 193.113335 | 3 |
| 16 | 2192.977976 | 1096.992626 | 2175.951427 | 1088.479351 | 2174.967411 | 1087.987343 | V | ***274.187366*** | 137.597321 | 257.160817 | 129.084046 | | | 2 |
| 17 | | | | | | | R | ***175.118952*** | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 73.5 | 2366.082382 | 0.032750 | YGFCEAADQFHVLDEVR |
| 2.7 | 2366.109802 | 0.005330 | EEAETPAEATGKPQRDEAGPQR |

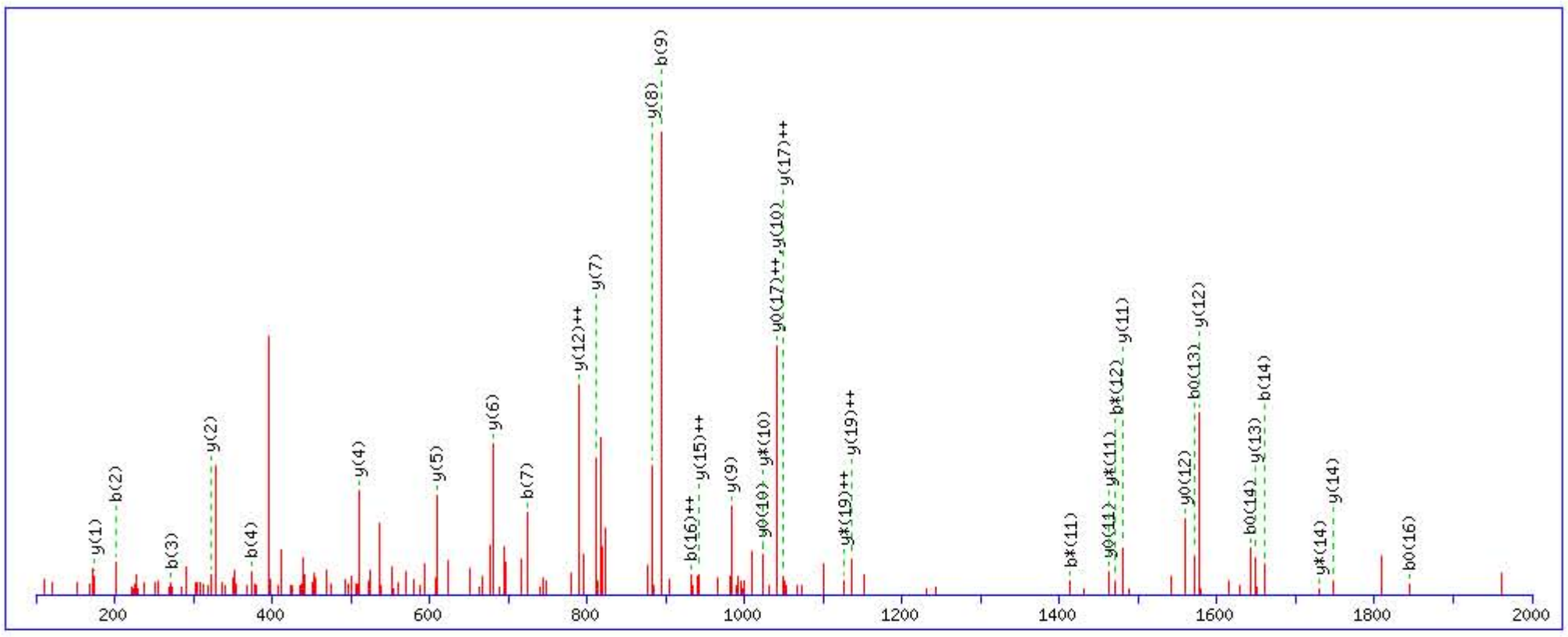
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AEATTLHVAPQGTAMAVSTFR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

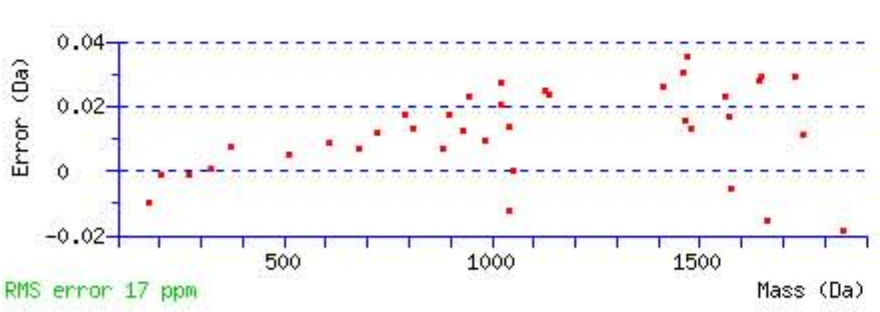
Match to Query 53464: 2469.287562 from(824.103130,3+) rtinseconds(2128) index(21038)
Title: Locus:1.1.1.3123.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

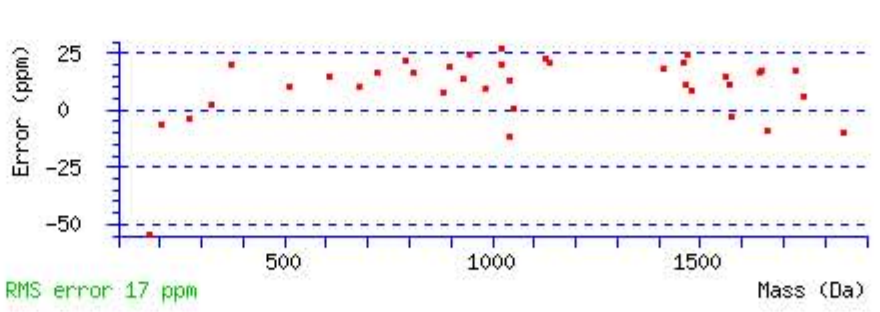
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2469.250839
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 3.6e-005
**Matches :** 37/214 fragment ions using 78 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 21 |
| 2 | **201.086983** | 101.047130 | | | 183.076418 | 92.041847 | E | 2399.221002 | 1200.114139 | 2382.194453 | 1191.600864 | 2381.210437 | 1191.108856 | 20 |
| 3 | **272.124097** | 136.565687 | | | 254.113532 | 127.560404 | A | 2270.178409 | 1135.592842 | 2253.151860 | 1127.079568 | 2252.167844 | 1126.587560 | 19 |
| 4 | **373.171776** | 187.089526 | | | 355.161211 | 178.084244 | T | 2199.141295 | 1100.074285 | 2182.114746 | 1091.561011 | 2181.130730 | 1091.069003 | 18 |
| 5 | 474.219455 | 237.613366 | | | 456.208890 | 228.608083 | T | 2098.093616 | 1049.550446 | 2081.067067 | 1041.037171 | 2080.083051 | 1040.545163 | 17 |
| 6 | 587.303519 | 294.155398 | | | 569.292954 | 285.150115 | L | 1997.045937 | 999.026606 | 1980.019388 | 990.513332 | 1979.035372 | 990.021324 | 16 |
| 7 | **724.362431** | 362.684854 | | | 706.351866 | 353.679571 | H | 1883.961873 | 942.484574 | 1866.935324 | 933.971300 | 1865.951308 | 933.479292 | 15 |
| 8 | 823.430845 | 412.219061 | | | 805.420280 | 403.213778 | V | *1746.902961* | 873.955118 | 1729.876412 | 865.441844 | 1728.892396 | 864.949836 | 14 |
| 9 | **894.467959** | 447.737618 | | | 876.457394 | 438.732335 | A | *1647.834547* | 824.420911 | 1630.807998 | 815.907637 | 1629.823982 | 815.415629 | 13 |
| 10 | 991.520723 | 496.264000 | | | 973.510158 | 487.258717 | P | *1576.797433* | 788.902355 | 1559.770884 | 780.389080 | 1558.786868 | 779.897072 | 12 |
| 11 | 1430.746049 | 715.876663 | 1413.719500 | 707.363388 | 1412.735484 | 706.871380 | Q | *1479.744669* | 740.375972 | 1462.718120 | 731.862698 | 1461.734104 | 731.370690 | 11 |
| 12 | 1487.767513 | 744.387395 | 1470.740964 | 735.874120 | 1469.756948 | 735.382112 | G | *1040.519343* | 520.763309 | 1023.492794 | 512.250035 | 1022.508778 | 511.758027 | 10 |
| 13 | 1588.815192 | 794.911234 | 1571.788643 | 786.397960 | 1570.804627 | 785.905952 | T | *983.497879* | 492.252577 | 966.471330 | 483.739303 | 965.487314 | 483.247295 | 9 |
| 14 | **1659.852306** | 830.429791 | 1642.825757 | 821.916517 | 1641.841741 | 821.424509 | A | *882.450200* | 441.728738 | 865.423651 | 433.215463 | 864.439635 | 432.723455 | 8 |
| 15 | 1790.892791 | 895.950034 | 1773.866242 | 887.436759 | 1772.882226 | 886.944751 | M | *811.413086* | 406.210181 | 794.386537 | 397.696906 | 793.402521 | 397.204898 | 7 |
| 16 | 1861.929905 | 931.468591 | 1844.903356 | 922.955316 | 1843.919340 | 922.463308 | A | *680.372601* | 340.689938 | 663.346052 | 332.176664 | 662.362036 | 331.684656 | 6 |
| 17 | 1960.998319 | 981.002798 | 1943.971770 | 972.489523 | 1942.987754 | 971.997515 | V | *609.335487* | 305.171381 | 592.308938 | 296.658107 | 591.324922 | 296.166099 | 5 |
| 18 | 2048.030347 | 1024.518812 | 2031.003798 | 1016.005537 | 2030.019782 | 1015.513529 | S | *510.267073* | 255.637174 | 493.240524 | 247.123900 | 492.256508 | 246.631892 | 4 |
| 19 | 2149.078026 | 1075.042651 | 2132.051477 | 1066.529376 | 2131.067461 | 1066.037368 | T | 423.235045 | 212.121160 | 406.208496 | 203.607886 | 405.224480 | 203.115878 | 3 |
| 20 | 2296.146440 | 1148.576858 | 2279.119891 | 1140.063583 | 2278.135875 | 1139.571575 | F | *322.187366* | 161.597321 | 305.160817 | 153.084046 | | | 2 |
| 21 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.9 | 2469.250839 | 0.036723 | AEATTLHVAPQGTAMAVSTFR |

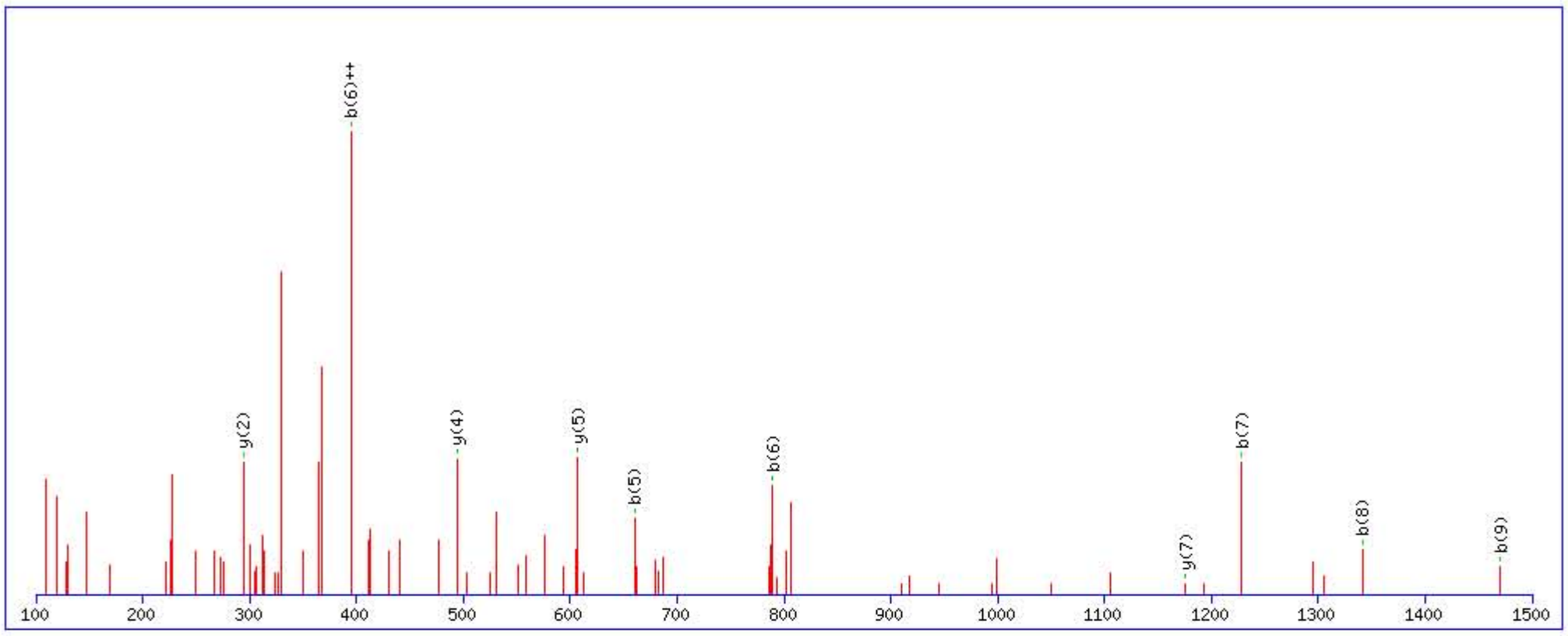
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TEHYEEQIEAFK**
Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

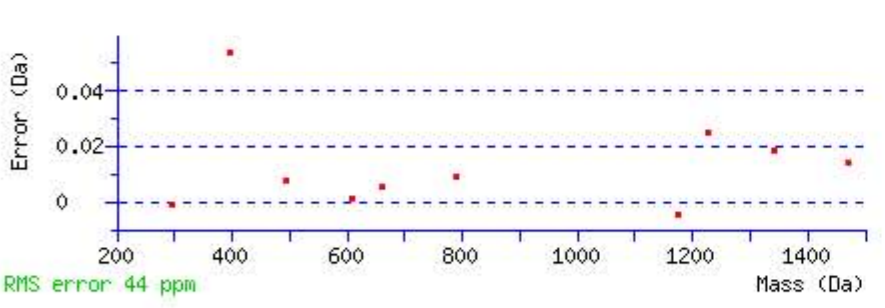
Match to Query 40951: 1833.873192 from(612.298340,3+) rtinseconds(1978) index(50226)
Title: Locus:1.1.1.1926.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

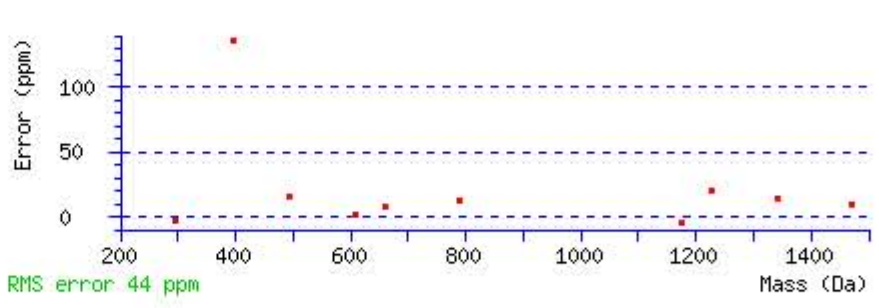
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1833.860703
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 34 **Expect:** 0.0008
**Matches :** 10/114 fragment ions using 13 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 12 |
| 2 | 231.097548 | 116.052412 | | | 213.086983 | 107.047130 | E | 1733.820335 | 867.413805 | 1716.793786 | 858.900531 | 1715.809770 | 858.408523 | 11 |
| 3 | 368.156460 | 184.581868 | | | 350.145895 | 175.576585 | H | 1604.777742 | 802.892509 | 1587.751193 | 794.379235 | 1586.767177 | 793.887227 | 10 |
| 4 | 531.219789 | 266.113533 | | | 513.209224 | 257.108250 | Y | 1467.718830 | 734.363053 | 1450.692281 | 725.849779 | 1449.708265 | 725.357771 | 9 |
| 5 | *660.262382* | 330.634829 | | | 642.251817 | 321.629547 | E | 1304.655501 | 652.831389 | 1287.628952 | 644.318114 | 1286.644936 | 643.826106 | 8 |
| 6 | *789.304975* | **395.156126** | | | 771.294410 | 386.150843 | E | *1175.612908* | 588.310092 | 1158.586359 | 579.796817 | 1157.602343 | 579.304809 | 7 |
| 7 | *1228.530301* | 614.768789 | 1211.503752 | 606.255514 | 1210.519736 | 605.763506 | Q | 1046.570315 | 523.788795 | 1029.543766 | 515.275521 | 1028.559750 | 514.783513 | 6 |
| 8 | *1341.614365* | 671.310820 | 1324.587816 | 662.797546 | 1323.603800 | 662.305538 | I | *607.344989* | 304.176132 | 590.318440 | 295.662858 | 589.334424 | 295.170850 | 5 |
| 9 | *1470.656958* | 735.832117 | 1453.630409 | 727.318842 | 1452.646393 | 726.826834 | E | *494.260925* | 247.634100 | 477.234376 | 239.120826 | 476.250360 | 238.628818 | 4 |
| 10 | 1541.694072 | 771.350674 | 1524.667523 | 762.837399 | 1523.683507 | 762.345391 | A | 365.218332 | 183.112804 | 348.191783 | 174.599530 | | | 3 |
| 11 | 1688.762486 | 844.884881 | 1671.735937 | 836.371606 | 1670.751921 | 835.879598 | F | *294.181218* | 147.594247 | 277.154669 | 139.080973 | | | 2 |
| 12 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 34.5 | 1833.860703 | 0.012489 | TEHYEEQIEAFK |
| 1.4 | 1833.878510 | -0.005318 | EGSGYFFLNTSTADVVK |
| 1.2 | 1833.881805 | -0.008613 | EAYDQKIAEEEAK |
| 1.1 | 1833.848831 | 0.024361 | IIQDESTQEDAMK |

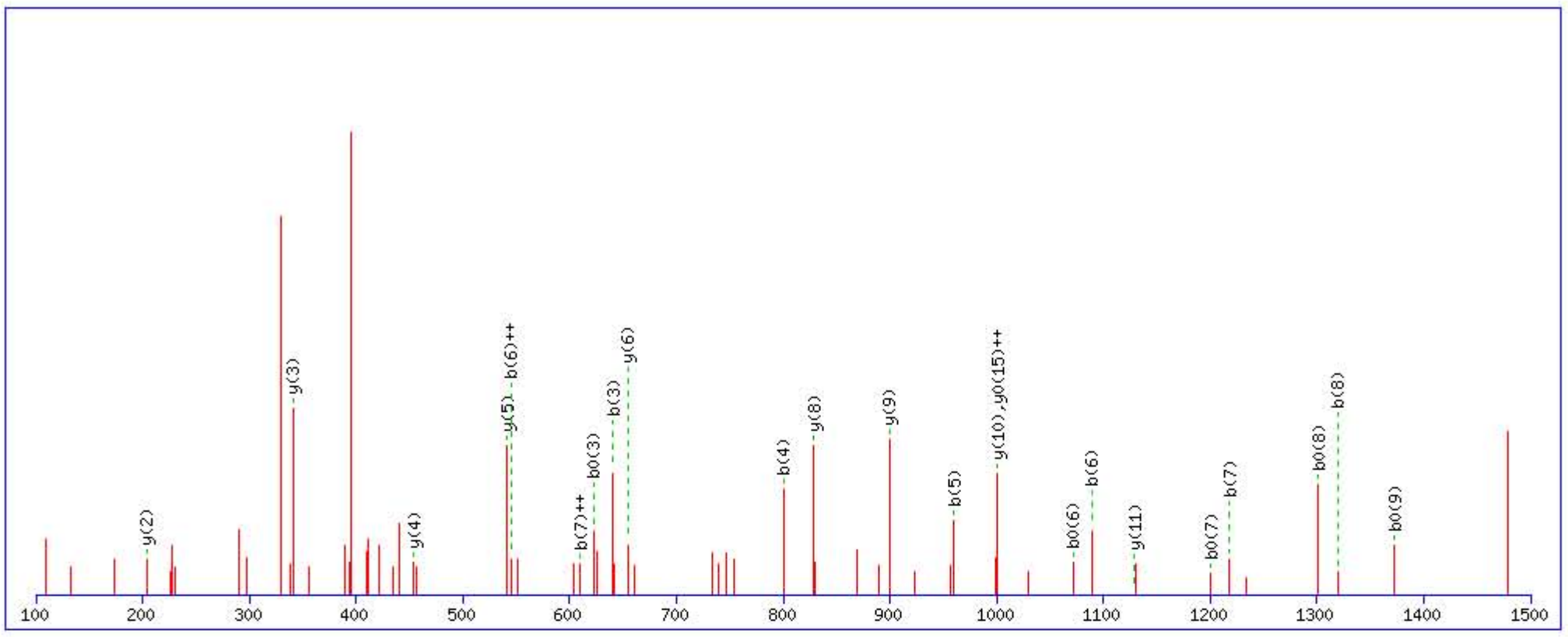
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AEQCCEETASSISLHGK**
Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

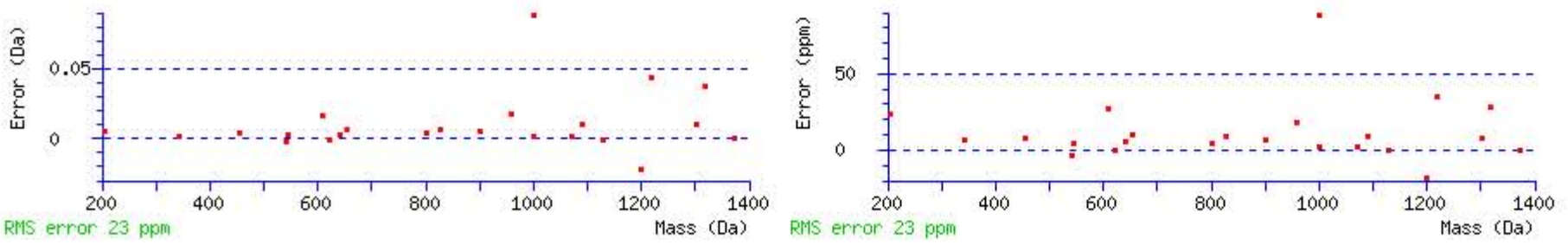
Match to Query 48860: 2217.002382 from(740.008070,3+) rtinseconds(1611) index(31820)
Title: Locus:1.1.1.669.23 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2216.986404
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 43 **Expect:** 0.00063
**Matches :** 23/178 fragment ions using 47 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 17 |
| 2 | 201.086983 | 101.047130 | | | 183.076418 | 92.041847 | E | 2146.956588 | 1073.981932 | 2129.930039 | 1065.468657 | 2128.946023 | 1064.976649 | 16 |
| 3 | *640.312309* | 320.659793 | 623.285760 | 312.146518 | 622.301744 | 311.654510 | Q | 2017.913995 | 1009.460636 | 2000.887446 | 1000.947361 | 1999.903430 | 1000.455353 | 15 |
| 4 | *800.342958* | 400.675117 | 783.316409 | 392.161843 | 782.332393 | 391.669835 | C | 1578.688669 | 789.847972 | 1561.662120 | 781.334698 | 1560.678104 | 780.842690 | 14 |
| 5 | *960.373607* | 480.690442 | 943.347058 | 472.177167 | 942.363042 | 471.685159 | C | 1418.658020 | 709.832648 | 1401.631471 | 701.319374 | 1400.647455 | 700.827366 | 13 |
| 6 | *1089.416200* | *545.211738* | 1072.389651 | 536.698464 | 1071.405635 | 536.206456 | E | 1258.627371 | 629.817323 | 1241.600822 | 621.304049 | 1240.616806 | 620.812041 | 12 |
| 7 | *1218.458793* | *609.733035* | 1201.432244 | 601.219760 | 1200.448228 | 600.727752 | E | *1129.584778* | 565.296027 | 1112.558229 | 556.782753 | 1111.574213 | 556.290744 | 11 |
| 8 | *1319.506472* | 660.256874 | 1302.479923 | 651.743600 | 1301.495907 | 651.251592 | T | *1000.542185* | 500.774731 | 983.515636 | 492.261456 | 982.531620 | 491.769448 | 10 |
| 9 | 1390.543586 | 695.775431 | 1373.517037 | 687.262157 | 1372.533021 | 686.770149 | A | *899.494506* | 450.250891 | 882.467957 | 441.737617 | 881.483941 | 441.245609 | 9 |
| 10 | 1477.575614 | 739.291445 | 1460.549065 | 730.778171 | 1459.565049 | 730.286163 | S | *828.457392* | 414.732334 | 811.430843 | 406.219060 | 810.446827 | 405.727052 | 8 |
| 11 | 1564.607642 | 782.807459 | 1547.581093 | 774.294185 | 1546.597077 | 773.802177 | S | 741.425364 | 371.216320 | 724.398815 | 362.703045 | 723.414799 | 362.211037 | 7 |
| 12 | 1677.691706 | 839.349491 | 1660.665157 | 830.836217 | 1659.681141 | 830.344209 | I | *654.393336* | 327.700306 | 637.366787 | 319.187031 | 636.382771 | 318.695023 | 6 |
| 13 | 1764.723734 | 882.865505 | 1747.697185 | 874.352231 | 1746.713169 | 873.860223 | S | *541.309272* | 271.158274 | 524.282723 | 262.644999 | 523.298707 | 262.152991 | 5 |
| 14 | 1877.807798 | 939.407537 | 1860.781249 | 930.894263 | 1859.797233 | 930.402255 | L | *454.277244* | 227.642260 | 437.250695 | 219.128985 | | | 4 |
| 15 | 2014.866710 | 1007.936993 | 1997.840161 | 999.423719 | 1996.856145 | 998.931711 | H | *341.193180* | 171.100228 | 324.166631 | 162.586953 | | | 3 |
| 16 | 2071.888174 | 1036.447725 | 2054.861625 | 1027.934450 | 2053.877609 | 1027.442442 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 17 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 42.7 | 2216.986404 | 0.015978 | AEQCCEETASSISLHGK |

**Mascot:** http://www.matrixscience.com/

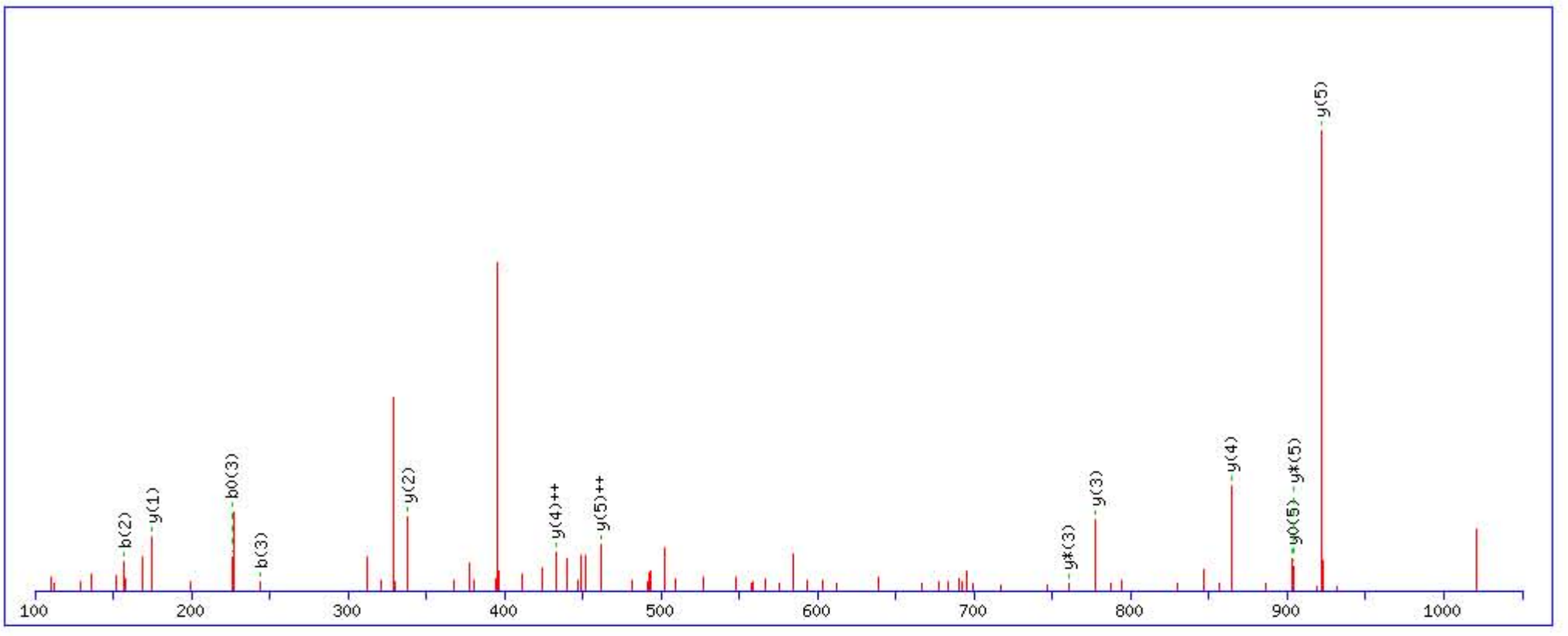
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VGSQYR**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

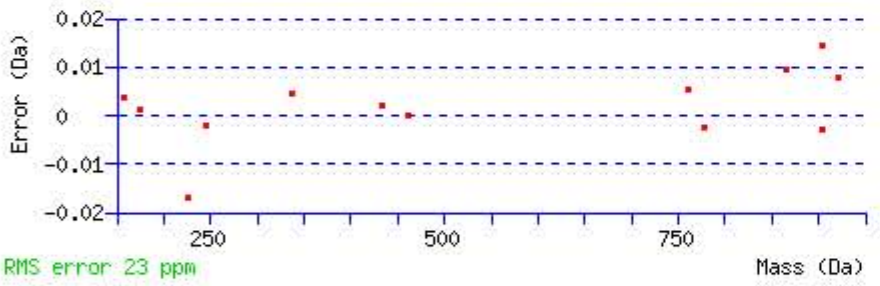
Match to Query 14271: 1019.521628 from(510.768090,2+) rtinseconds(1376) index(62617)
Title: Locus:1.1.1.1754.15 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

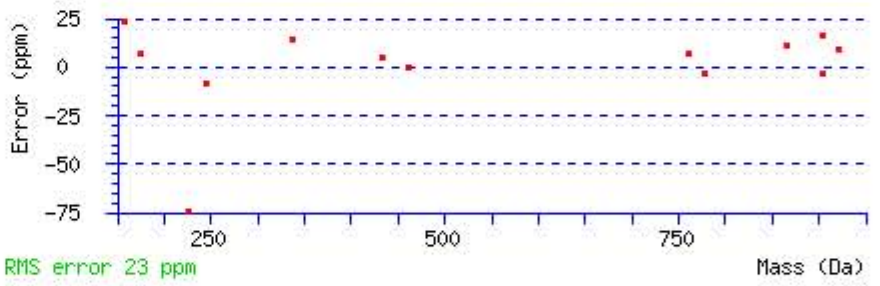
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1019.522232
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 25 **Expect:** 0.06
**Matches :** 13/44 fragment ions using 27 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 6 |
| 2 | 157.097154 | 79.052215 | | | | | G | *921.461099* | 461.234188 | 904.434550 | 452.720913 | 903.450534 | 452.228905 | 5 |
| 3 | 244.129182 | 122.568229 | | | 226.118617 | 113.562946 | S | *864.439635* | 432.723456 | 847.413086 | 424.210181 | 846.429070 | 423.718173 | 4 |
| 4 | 683.354508 | 342.180892 | 666.327959 | 333.667618 | 665.343943 | 333.175610 | Q | *777.407607* | 389.207442 | 760.381058 | 380.694167 | | | 3 |
| 5 | 846.417837 | 423.712557 | 829.391288 | 415.199282 | 828.407272 | 414.707274 | Y | *338.182281* | 169.594778 | 321.155732 | 161.081504 | | | 2 |
| 6 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

### All matches to this query

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.1 | 1019.522232 | -0.000604 | VGSQYR |
| 11.3 | 1019.510818 | 0.010810 | RSSVSSGGAGR |
| 10.3 | 1019.533447 | -0.011819 | RSQYR |
| 6.1 | 1019.512146 | 0.009482 | RSRGHHDR |
| 5.6 | 1019.506973 | 0.014655 | SSMPVIQSR |
| 2.7 | 1019.533463 | -0.011835 | VSLMWRGR |
| 2.5 | 1019.526047 | -0.004419 | SRERGPYR |
| 2.1 | 1019.506973 | 0.014655 | TLLAQGMDR |
| 1.3 | 1019.526077 | -0.004449 | VPQAGGQHAR |
| 0.6 | 1019.506989 | 0.014639 | SVGEVMGIGR |

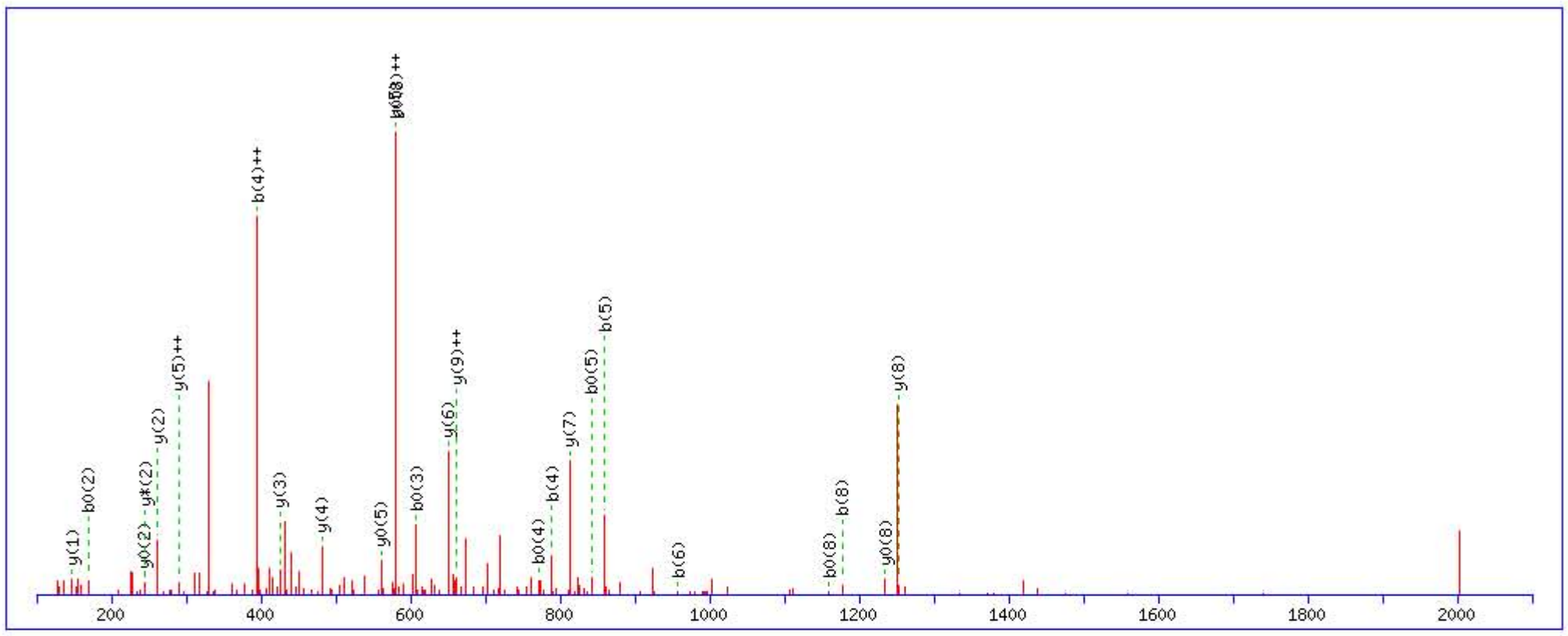
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DAQYAPGYDK**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

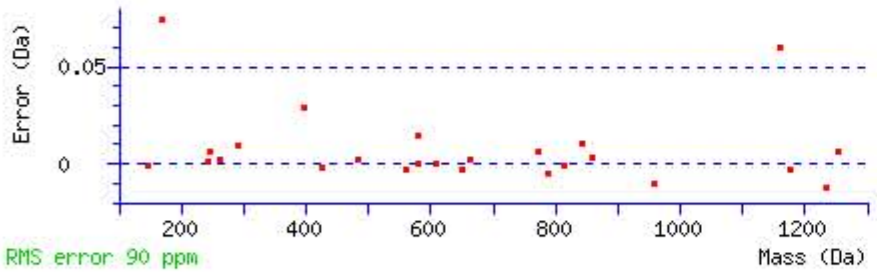
Match to Query 29294: 1437.659868 from(719.837210,2+) rtinseconds(1627) index(64215)
Title: Locus:1.1.1.1841.9 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

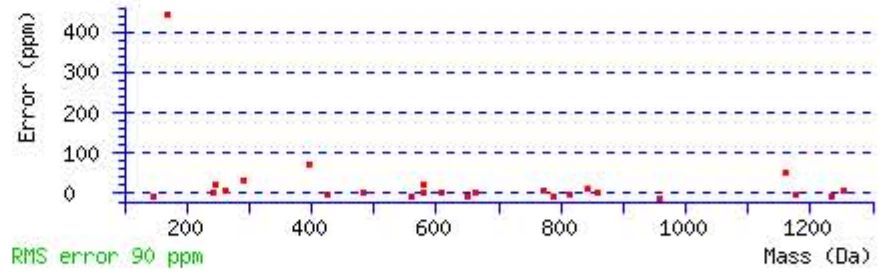
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1437.659836
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.012
**Matches :** 25/102 fragment ions using 67 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 10 |
| 2 | 187.071333 | 94.039304 | | | 169.060768 | 85.034022 | A | 1323.640187 | 662.323732 | 1306.613638 | 653.810457 | 1305.629622 | 653.318449 | 9 |
| 3 | 626.296659 | 313.651968 | 609.270110 | 305.138693 | 608.286094 | 304.646685 | Q | *1252.603073* | 626.805175 | 1235.576524 | 618.291900 | 1234.592508 | 617.799892 | 8 |
| 4 | **789.359988** | 395.183632 | 772.333439 | 386.670358 | 771.349423 | 386.178350 | Y | *813.377747* | 407.192512 | 796.351198 | 398.679237 | 795.367182 | 398.187229 | 7 |
| 5 | **860.397102** | 430.702189 | 843.370553 | 422.188915 | 842.386537 | 421.696907 | A | *650.314418* | 325.660847 | 633.287869 | 317.147573 | 632.303853 | 316.655565 | 6 |
| 6 | **957.449866** | 479.228571 | 940.423317 | 470.715297 | 939.439301 | 470.223289 | P | *579.277304* | 290.142290 | 562.250755 | 281.629016 | 561.266739 | 281.137008 | 5 |
| 7 | 1014.471330 | 507.739303 | 997.444781 | 499.226029 | 996.460765 | 498.734021 | G | *482.224540* | 241.615908 | 465.197991 | 233.102634 | 464.213975 | 232.610626 | 4 |
| 8 | **1177.534659** | 589.270968 | 1160.508110 | 580.757693 | 1159.524094 | 580.265685 | Y | *425.203076* | 213.105176 | 408.176527 | 204.591902 | 407.192511 | 204.099894 | 3 |
| 9 | 1292.561602 | 646.784439 | 1275.535053 | 638.271165 | 1274.551037 | 637.779157 | D | *262.139747* | 131.573512 | 245.113198 | 123.060237 | 244.129182 | 122.568229 | 2 |
| 10 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 32.3 | 1437.659836 | 0.000032 | DAQYAPGYDK |
| 11.7 | 1437.659164 | 0.000704 | LAEAEQMALMGSR |
| 3.3 | 1437.647064 | 0.012804 | ASSDLSIASSEEDK |

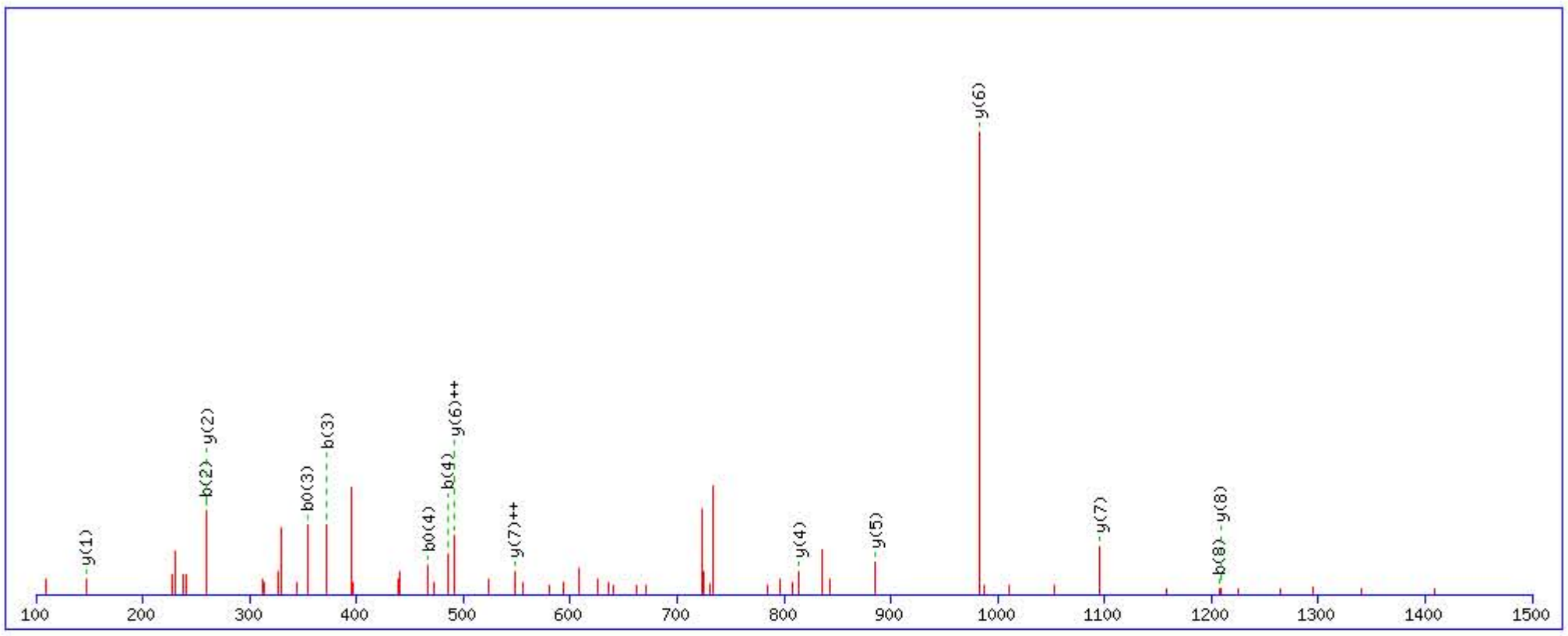
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EELLPAQDIK**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

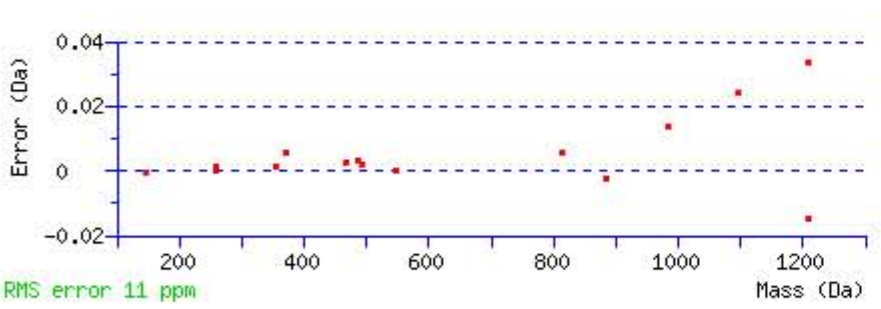
Match to Query 30136: 1465.798708 from(733.906630,2+) rtinseconds(2152) index(6462)
Title: Locus:1.1.1.2026.23 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

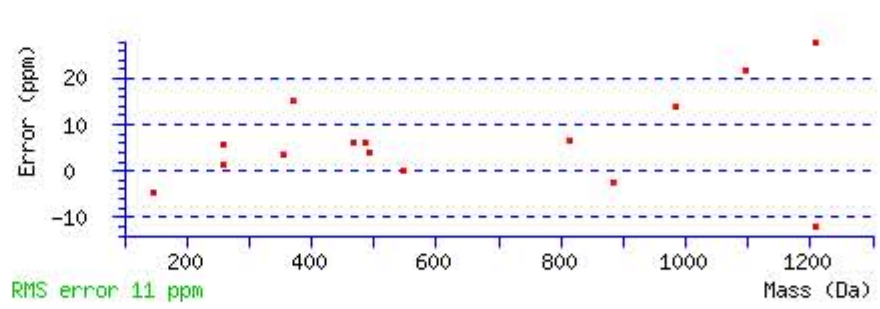
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1465.785019
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.0023
**Matches :** 15/92 fragment ions using 37 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 10 |
| 2 | **259.092462** | 130.049869 | | | 241.081897 | 121.044587 | E | 1337.749736 | 669.378506 | 1320.723187 | 660.865232 | 1319.739171 | 660.373223 | 9 |
| 3 | **372.176526** | 186.591901 | | | 354.165961 | 177.586619 | L | *1208.707143* | 604.857210 | 1191.680594 | 596.343935 | 1190.696578 | 595.851927 | 8 |
| 4 | **485.260590** | 243.133933 | | | 467.250025 | 234.128651 | L | *1095.623079* | 548.315178 | 1078.596530 | 539.801903 | 1077.612514 | 539.309895 | 7 |
| 5 | 582.313354 | 291.660315 | | | 564.302789 | 282.655033 | P | *982.539015* | 491.773146 | 965.512466 | 483.259871 | 964.528450 | 482.767863 | 6 |
| 6 | 653.350468 | 327.178872 | | | 635.339903 | 318.173590 | A | *885.486251* | 443.246764 | 868.459702 | 434.733489 | 867.475686 | 434.241481 | 5 |
| 7 | 1092.575794 | 546.791535 | 1075.549245 | 538.278261 | 1074.565229 | 537.786253 | Q | *814.449137* | 407.728207 | 797.422588 | 399.214932 | 796.438572 | 398.722924 | 4 |
| 8 | **1207.602737** | 604.305007 | 1190.576188 | 595.791732 | 1189.592172 | 595.299724 | D | 375.223811 | 188.115543 | 358.197262 | 179.602269 | 357.213246 | 179.110261 | 3 |
| 9 | 1320.686801 | 660.847039 | 1303.660252 | 652.333764 | 1302.676236 | 651.841756 | I | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 10 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.5 | 1465.785019 | 0.013689 | EELLPAQDIK |
| 3.2 | 1465.789734 | 0.008974 | TAAALGMHQKK |
| 0.1 | 1465.794235 | 0.004473 | KWGIGYHLSLHR |

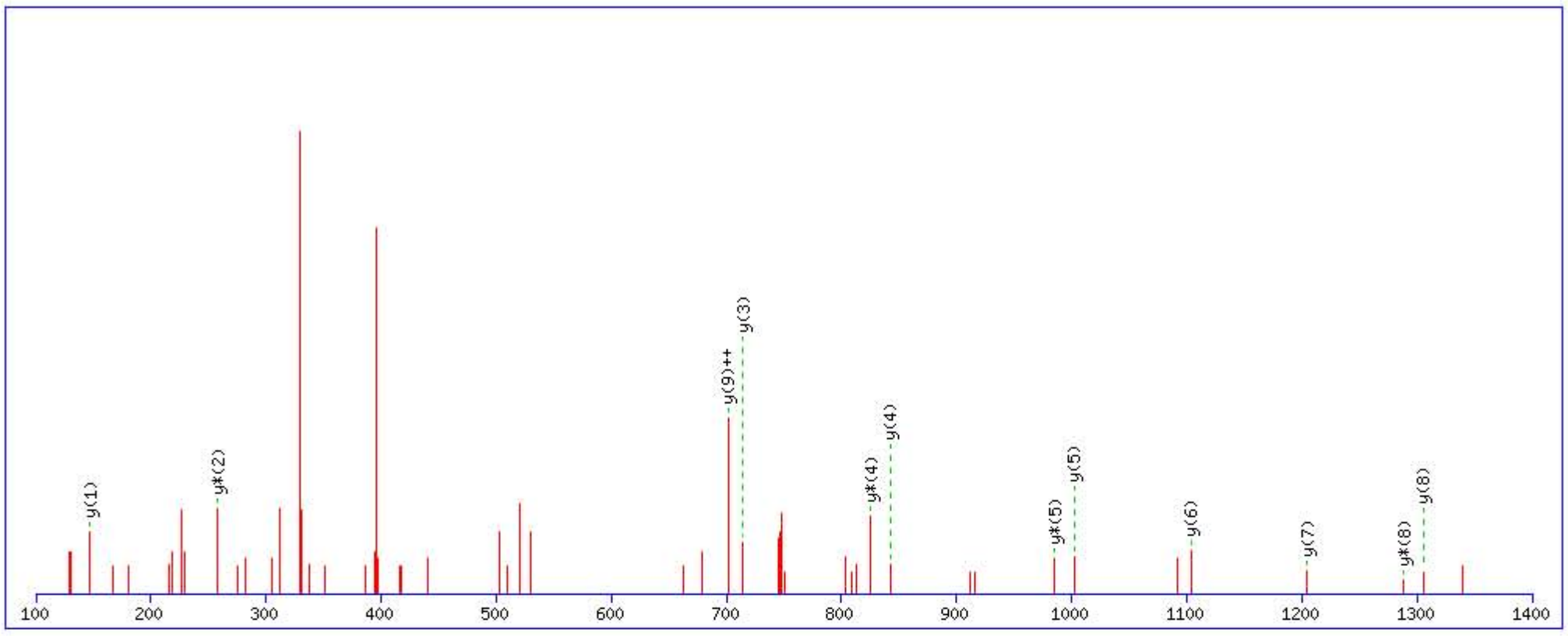
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LPPTTTCQQQK**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

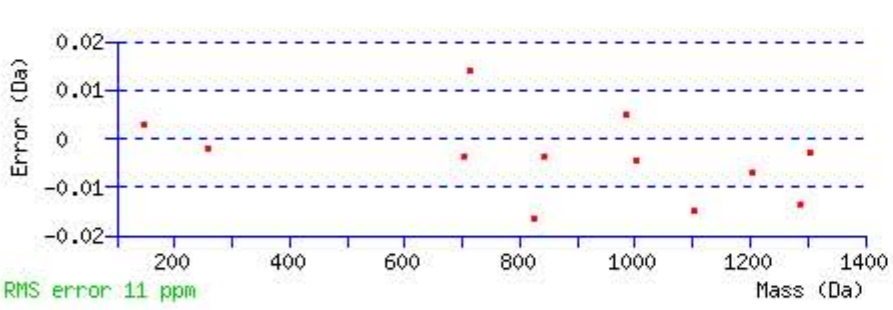
Match to Query 35191: 1611.808932 from(538.276920,3+) rtinseconds(1420) index(62950)
Title: Locus:1.1.1.1769.18 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

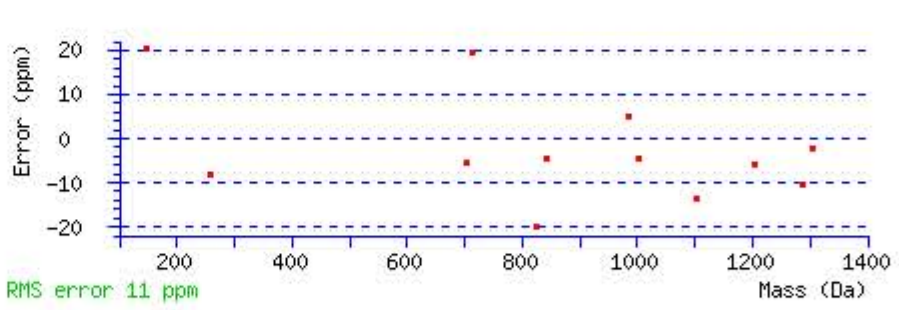
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1611.811295
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.006
**Matches :** 12/90 fragment ions using 24 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 11 |
| 2 | 211.144104 | 106.075690 | | | | | P | 1499.734500 | 750.370888 | 1482.707951 | 741.857614 | 1481.723935 | 741.365606 | 10 |
| 3 | 308.196868 | 154.602072 | | | | | P | 1402.681736 | 701.844506 | 1385.655187 | 693.331232 | 1384.671171 | 692.839224 | 9 |
| 4 | 409.244547 | 205.125911 | | | 391.233982 | 196.120629 | T | *1305.628972* | 653.318124 | 1288.602423 | 644.804850 | 1287.618407 | 644.312842 | 8 |
| 5 | 510.292226 | 255.649751 | | | 492.281661 | 246.644468 | T | *1204.581293* | 602.794285 | 1187.554744 | 594.281010 | 1186.570728 | 593.789002 | 7 |
| 6 | 611.339905 | 306.173591 | | | 593.329340 | 297.168308 | T | *1103.533614* | 552.270445 | 1086.507065 | 543.757171 | 1085.523049 | 543.265163 | 6 |
| 7 | 771.370554 | 386.188915 | | | 753.359989 | 377.183633 | C | *1002.485935* | 501.746606 | 985.459386 | 493.233331 | | | 5 |
| 8 | 899.429132 | 450.218204 | 882.402583 | 441.704930 | 881.418567 | 441.212922 | Q | *842.455286* | 421.731281 | 825.428737 | 413.218007 | | | 4 |
| 9 | 1338.654458 | 669.830867 | 1321.627909 | 661.317593 | 1320.643893 | 660.825585 | Q | *714.396708* | 357.701992 | 697.370159 | 349.188718 | | | 3 |
| 10 | 1466.713036 | 733.860156 | 1449.686487 | 725.346882 | 1448.702471 | 724.854874 | Q | 275.171382 | 138.089329 | 258.144833 | 129.576055 | | | 2 |
| 11 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 32.2 | 1611.811295 | -0.002363 | LPPTTTCQQQK |
| 29.6 | 1611.811295 | -0.002363 | LPPTTTCQQQK |
| 21.9 | 1611.811295 | -0.002363 | LPPTTTCQQQK |
| 8.2 | 1611.803406 | 0.005526 | TPIKMGISASTMTMK |
| 5.0 | 1611.803406 | 0.005526 | TPIKMGISASTMTMK |
| 3.4 | 1611.815094 | -0.006162 | NDVEGAKMHLRQAK |

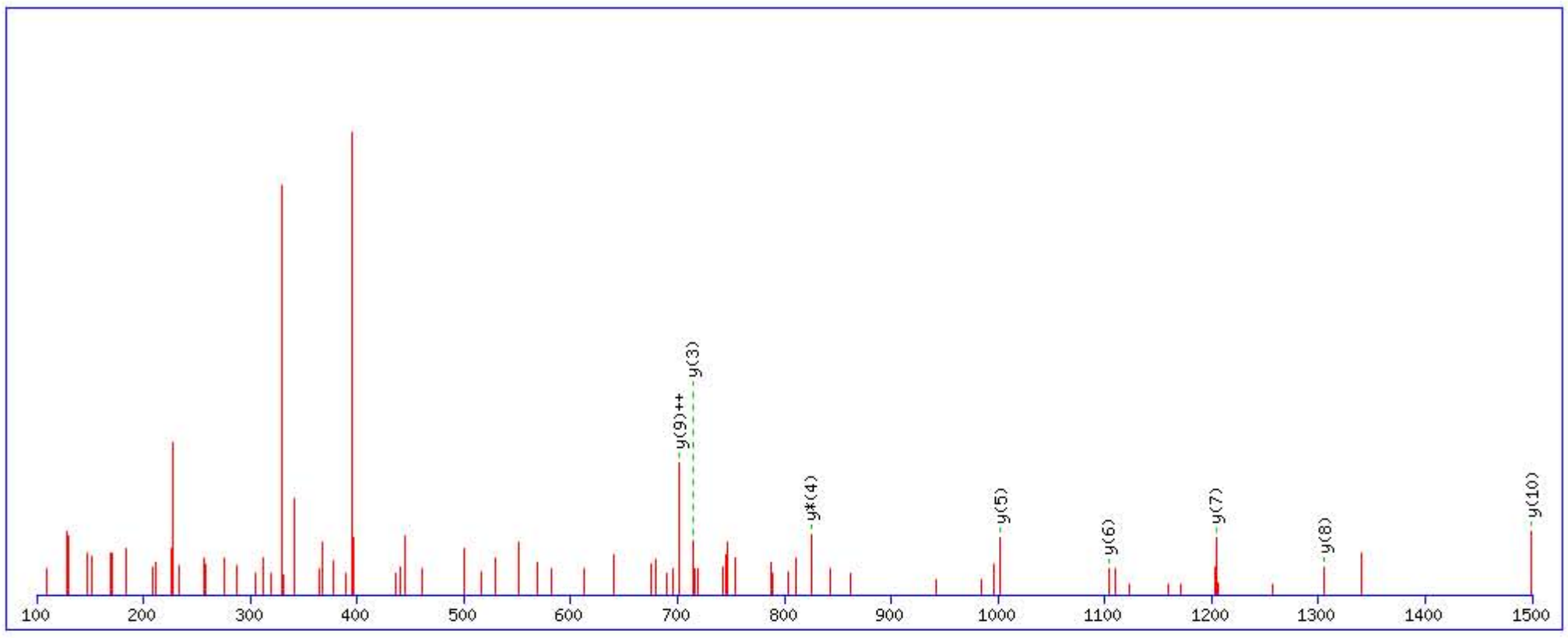
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LPPTTTCQQQK**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

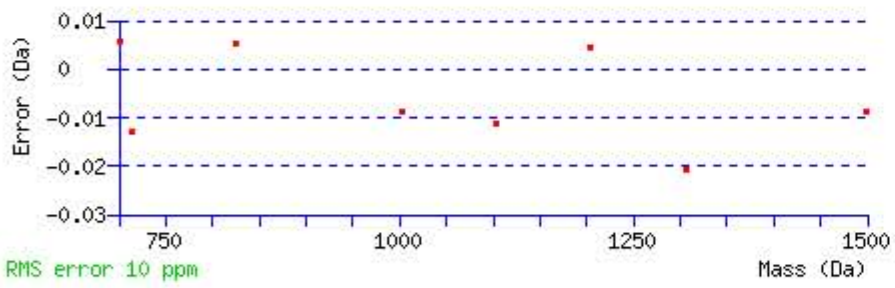
Match to Query 35196: 1611.812292 from(538.278040,3+) rtinseconds(1438) index(2236)
Title: Locus:1.1.1.1777.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

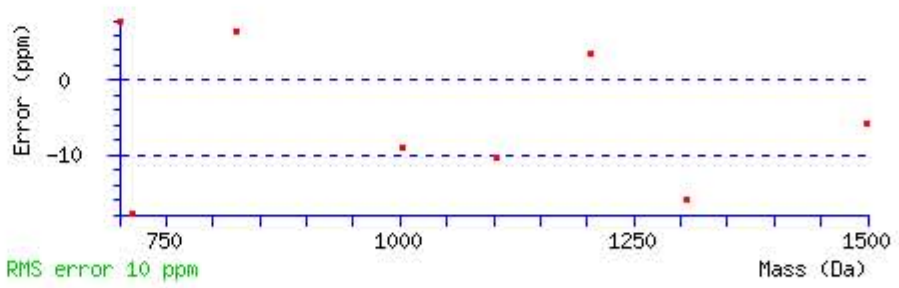
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1611.811295
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.021
**Matches :** 8/90 fragment ions using 14 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 11 |
| 2 | 211.144104 | 106.075690 | | | | | P | *1499.734500* | 750.370888 | 1482.707951 | 741.857614 | 1481.723935 | 741.365606 | 10 |
| 3 | 308.196868 | 154.602072 | | | | | P | 1402.681736 | 701.844506 | 1385.655187 | 693.331232 | 1384.671171 | 692.839224 | 9 |
| 4 | 409.244547 | 205.125911 | | | 391.233982 | 196.120629 | T | *1305.628972* | 653.318124 | 1288.602423 | 644.804850 | 1287.618407 | 644.312842 | 8 |
| 5 | 510.292226 | 255.649751 | | | 492.281661 | 246.644468 | T | *1204.581293* | 602.794285 | 1187.554744 | 594.281010 | 1186.570728 | 593.789002 | 7 |
| 6 | 611.339905 | 306.173591 | | | 593.329340 | 297.168308 | T | *1103.533614* | 552.270445 | 1086.507065 | 543.757171 | 1085.523049 | 543.265163 | 6 |
| 7 | 771.370554 | 386.188915 | | | 753.359989 | 377.183633 | C | *1002.485935* | 501.746606 | 985.459386 | 493.233331 | | | 5 |
| 8 | 899.429132 | 450.218204 | 882.402583 | 441.704930 | 881.418567 | 441.212922 | Q | 842.455286 | 421.731281 | 825.428737 | 413.218007 | | | 4 |
| 9 | 1027.487710 | 514.247493 | 1010.461161 | 505.734219 | 1009.477145 | 505.242211 | Q | *714.396708* | 357.701992 | 697.370159 | 349.188718 | | | 3 |
| 10 | 1466.713036 | 733.860156 | 1449.686487 | 725.346882 | 1448.702471 | 724.854874 | Q | 586.338130 | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 11 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.0 | 1611.811295 | 0.000997 | LPPTTTCQQQK |
| 31.0 | 1611.811295 | 0.000997 | LPPTTTCQQQK |
| 19.3 | 1611.811295 | 0.000997 | LPPTTTCQQQK |

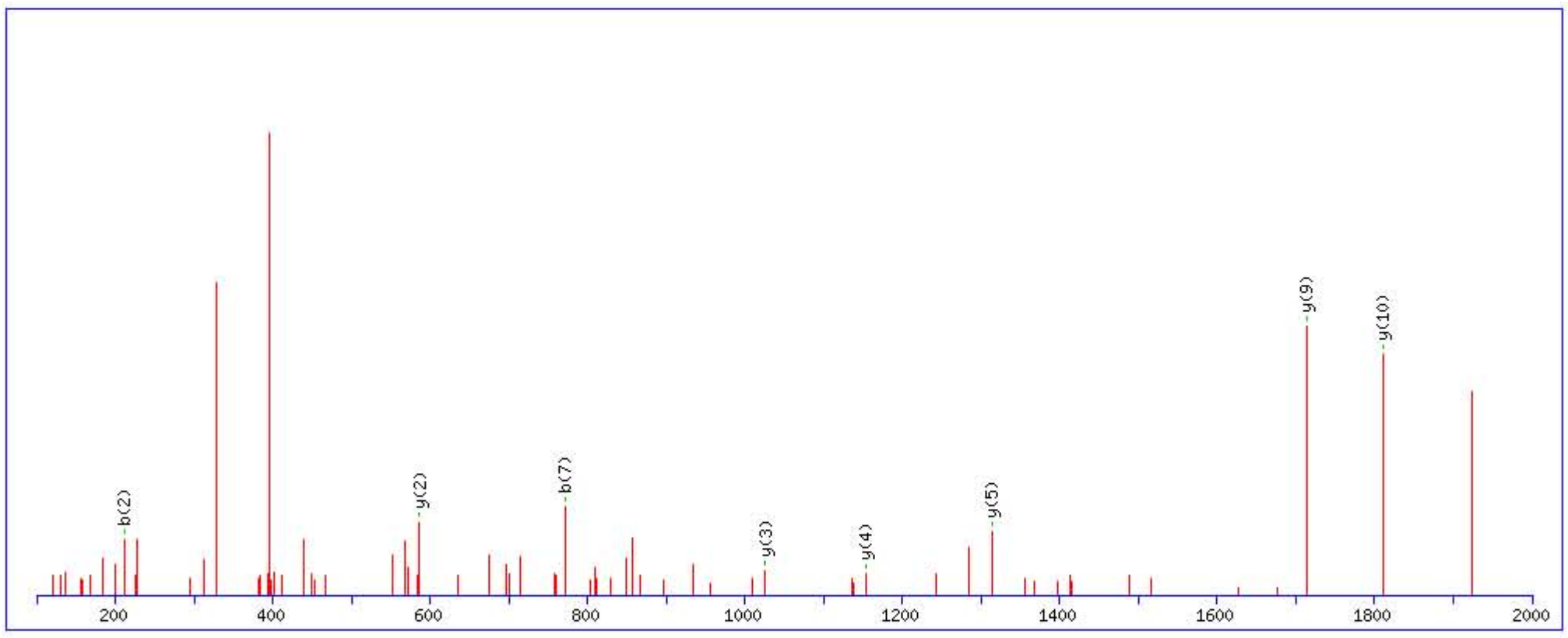
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LPPTTTCQQQK**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

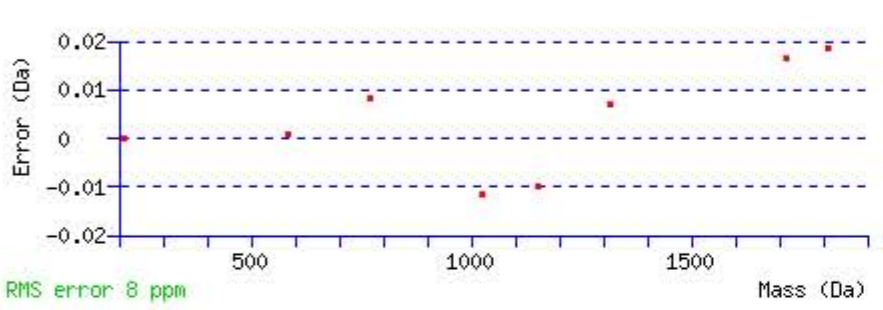
Match to Query 42579: 1922.981682 from(642.001170,3+) rtinseconds(1772) index(65025)
Title: Locus:1.1.1.1892.13 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

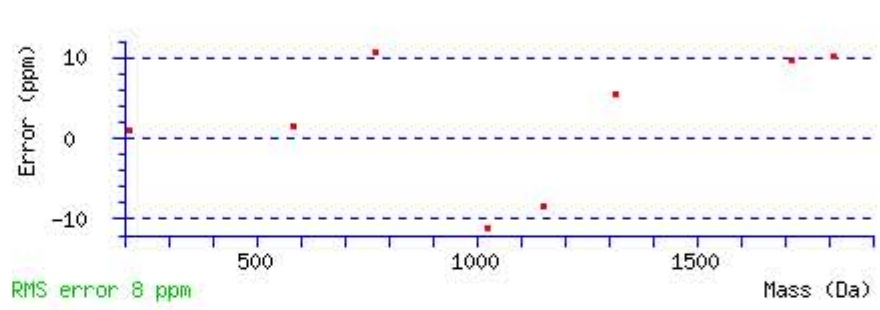
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1922.978043
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 28 **Expect:** 0.024
**Matches :** 8/90 fragment ions using 16 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 11 |
| 2 | 211.144104 | 106.075690 | | | | | P | *1810.901248* | 905.954262 | 1793.874699 | 897.440988 | 1792.890683 | 896.948980 | 10 |
| 3 | 308.196868 | 154.602072 | | | | | P | *1713.848484* | 857.427880 | 1696.821935 | 848.914606 | 1695.837919 | 848.422598 | 9 |
| 4 | 409.244547 | 205.125911 | | | 391.233982 | 196.120629 | T | 1616.795720 | 808.901498 | 1599.769171 | 800.388224 | 1598.785155 | 799.896216 | 8 |
| 5 | 510.292226 | 255.649751 | | | 492.281661 | 246.644468 | T | 1515.748041 | 758.377659 | 1498.721492 | 749.864384 | 1497.737476 | 749.372376 | 7 |
| 6 | 611.339905 | 306.173591 | | | 593.329340 | 297.168308 | T | 1414.700362 | 707.853819 | 1397.673813 | 699.340545 | 1396.689797 | 698.848537 | 6 |
| 7 | 771.370554 | 386.188915 | | | 753.359989 | 377.183633 | C | *1313.652683* | 657.329980 | 1296.626134 | 648.816705 | | | 5 |
| 8 | 899.429132 | 450.218204 | 882.402583 | 441.704930 | 881.418567 | 441.212922 | Q | *1153.622034* | 577.314655 | 1136.595485 | 568.801381 | | | 4 |
| 9 | 1338.654458 | 669.830867 | 1321.627909 | 661.317593 | 1320.643893 | 660.825585 | Q | *1025.563456* | 513.285366 | 1008.536907 | 504.772092 | | | 3 |
| 10 | 1777.879784 | 889.443530 | 1760.853235 | 880.930256 | 1759.869219 | 880.438248 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 11 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 28.3 | 1922.978043 | 0.003639 | LPPTTTCQQQK |
| 24.6 | 1922.978043 | 0.003639 | LPPTTTCQQQK |
| 16.5 | 1922.978043 | 0.003639 | LPPTTTCQQQK |
| 10.4 | 1922.981842 | -0.000160 | NDVEGAKMHLRQAK |
| 1.6 | 1922.970612 | 0.011070 | HQEMEDVIRLAQK |
| 0.9 | 1923.003632 | -0.021950 | AKELHVQNVHMYLPTK |

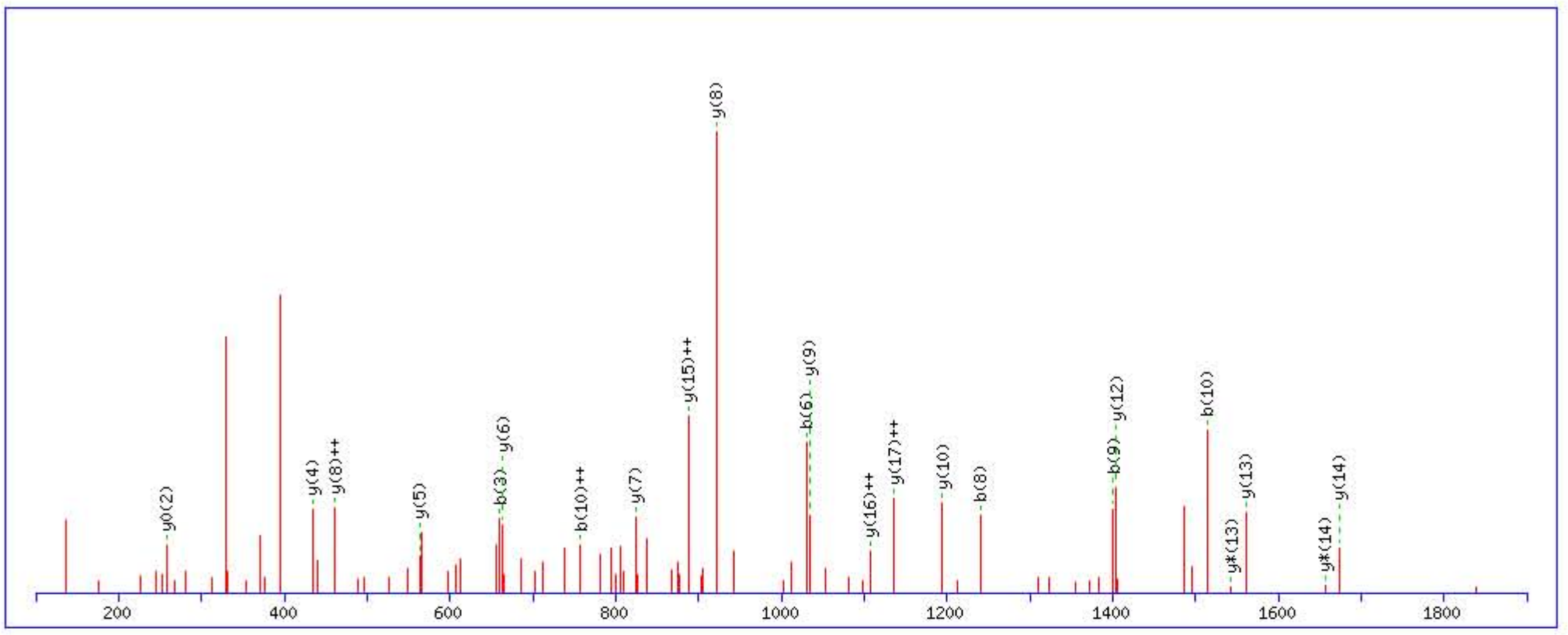
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YGQTIRPICLPCTEGTTR**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

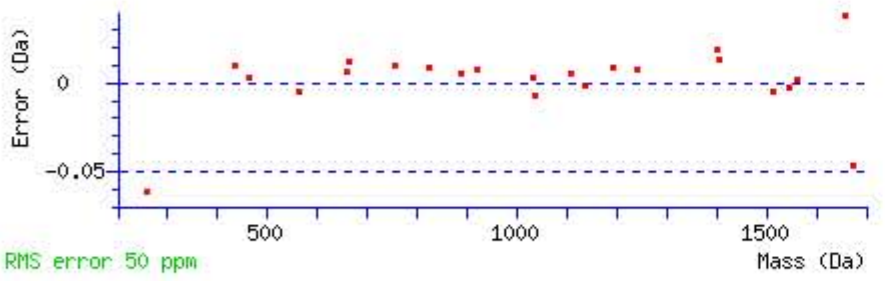
Match to Query 52704: 2433.212802 from(812.078210,3+) rtinseconds(2066) index(66815)
Title: Locus:1.1.1.1994.10 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

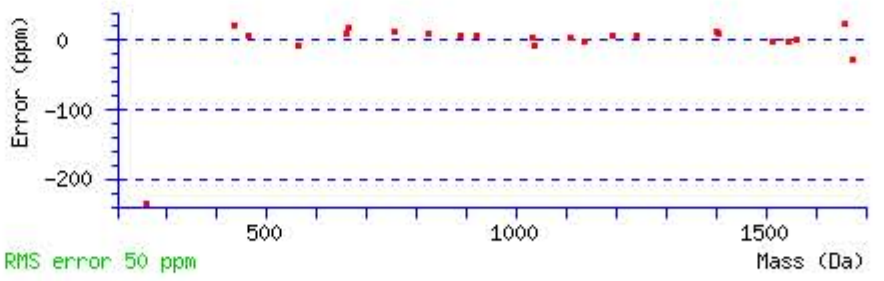
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2433.196701
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 65 **Expect:** 1e-005
**Matches :** 23/192 fragment ions using 33 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 18 |
| 2 | 221.092069 | 111.049673 | | | | | G | 2271.140644 | 1136.073960 | 2254.114095 | 1127.560685 | 2253.130079 | 1127.068677 | 17 |
| 3 | **660.317395** | 330.662336 | 643.290846 | 322.149061 | | | Q | 2214.119180 | 1107.563228 | 2197.092631 | 1099.049953 | 2196.108615 | 1098.557945 | 16 |
| 4 | 761.365074 | 381.186175 | 744.338525 | 372.672901 | 743.354509 | 372.180893 | T | 1774.893854 | 887.950565 | 1757.867305 | 879.437290 | 1756.883289 | 878.945282 | 15 |
| 5 | 874.449138 | 437.728207 | 857.422589 | 429.214933 | 856.438573 | 428.722925 | I | *1673.846175* | 837.426725 | *1656.819626* | 828.913451 | 1655.835610 | 828.421443 | 14 |
| 6 | **1030.550249** | 515.778763 | 1013.523700 | 507.265488 | 1012.539684 | 506.773480 | R | *1560.762111* | 780.884693 | 1543.735562 | 772.371419 | 1542.751546 | 771.879411 | 13 |
| 7 | 1127.603013 | 564.305145 | 1110.576464 | 555.791870 | 1109.592448 | 555.299862 | P | *1404.661000* | 702.834138 | 1387.634451 | 694.320863 | 1386.650435 | 693.828855 | 12 |
| 8 | **1240.687077** | 620.847177 | 1223.660528 | 612.333902 | 1222.676512 | 611.841894 | I | 1307.608236 | 654.307756 | 1290.581687 | 645.794481 | 1289.597671 | 645.302473 | 11 |
| 9 | **1400.717726** | 700.862501 | 1383.691177 | 692.349227 | 1382.707161 | 691.857219 | C | *1194.524172* | 597.765724 | 1177.497623 | 589.252449 | 1176.513607 | 588.760441 | 10 |
| 10 | **1513.801790** | 757.404533 | 1496.775241 | 748.891259 | 1495.791225 | 748.399250 | L | *1034.493523* | 517.750399 | 1017.466974 | 509.237125 | 1016.482958 | 508.745117 | 9 |
| 11 | 1610.854554 | 805.930915 | 1593.828005 | 797.417641 | 1592.843989 | 796.925633 | P | *921.409459* | 461.208367 | 904.382910 | 452.695093 | 903.398894 | 452.203085 | 8 |
| 12 | 1770.885203 | 885.946240 | 1753.858654 | 877.432965 | 1752.874638 | 876.940957 | C | *824.356695* | 412.681985 | 807.330146 | 404.168711 | 806.346130 | 403.676703 | 7 |
| 13 | 1871.932882 | 936.470079 | 1854.906333 | 927.956805 | 1853.922317 | 927.464797 | T | *664.326046* | 332.666661 | 647.299497 | 324.153386 | 646.315481 | 323.661378 | 6 |
| 14 | 2000.975475 | 1000.991376 | 1983.948926 | 992.478101 | 1982.964910 | 991.986093 | E | *563.278367* | 282.142821 | 546.251818 | 273.629547 | 545.267802 | 273.137539 | 5 |
| 15 | 2057.996939 | 1029.502107 | 2040.970390 | 1020.988833 | 2039.986374 | 1020.496825 | G | *434.235774* | 217.621525 | 417.209225 | 209.108250 | 416.225209 | 208.616242 | 4 |
| 16 | 2159.044618 | 1080.025947 | 2142.018069 | 1071.512672 | 2141.034053 | 1071.020664 | T | 377.214310 | 189.110793 | 360.187761 | 180.597518 | 359.203745 | 180.105510 | 3 |
| 17 | 2260.092297 | 1130.549786 | 2243.065748 | 1122.036512 | 2242.081732 | 1121.544504 | T | 276.166631 | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 18 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 64.6 | 2433.196701 | 0.016101 | YGQTIRPICLPCTEGTTR |

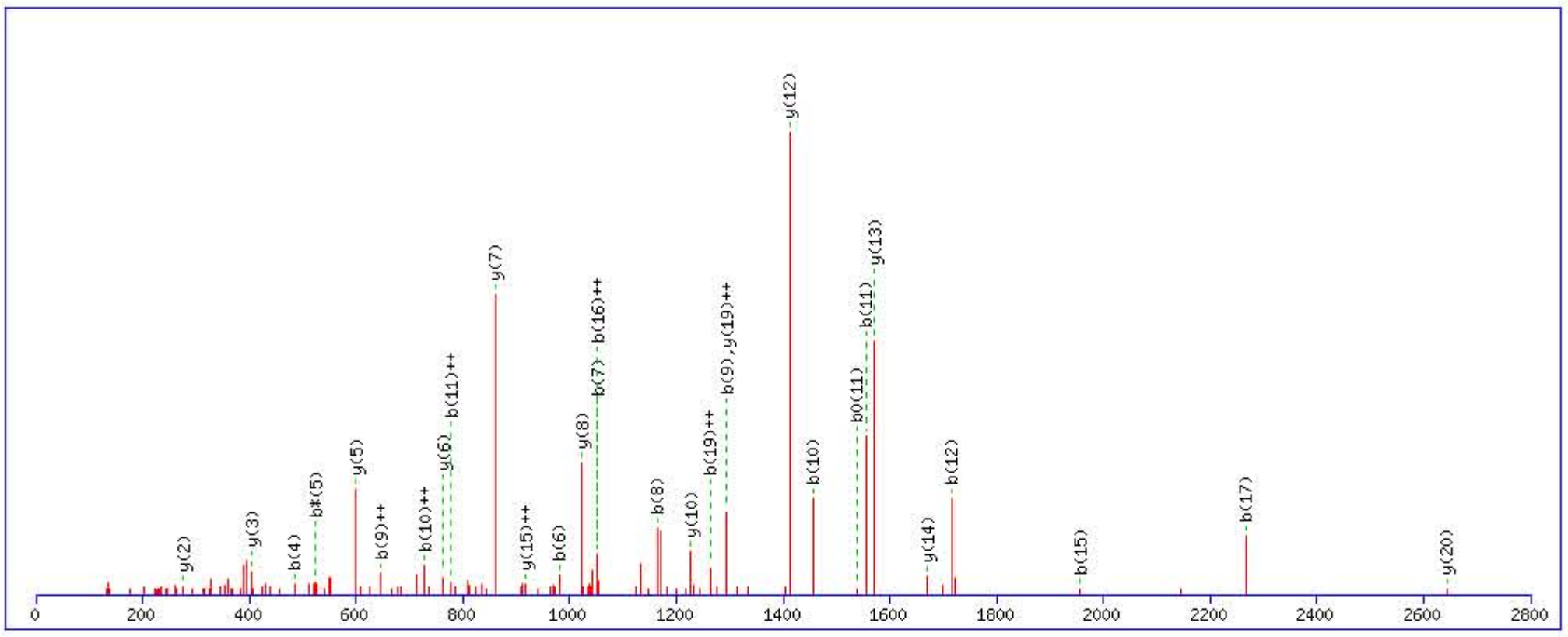
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LLQEGQALEYVCPSGFYPYPVQTR**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

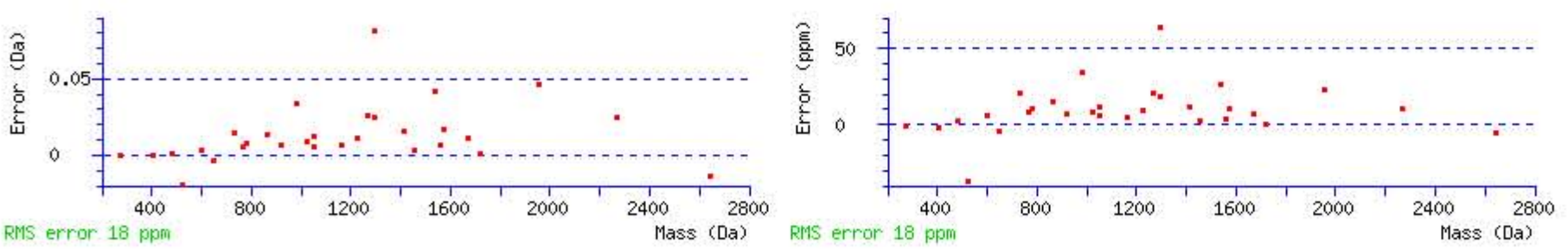
Match to Query 61045: 3125.570382 from(1042.864070,3+) rtinseconds(2669) index(9074)
Title: Locus:1.1.1.2206.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3125.535446
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 66 **Expect:** 7.1e-006
**Matches** : 30/264 fragment ions using 52 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 24 |
| 2 | 227.175404 | 114.091340 | | | | | L | 3013.458667 | 1507.232971 | 2996.432118 | 1498.719697 | 2995.448102 | 1498.227689 | 23 |
| 3 | 355.233982 | 178.120629 | 338.207433 | 169.607355 | | | Q | 2900.374603 | 1450.690939 | 2883.348054 | 1442.177665 | 2882.364038 | 1441.685657 | 22 |
| 4 | *484.276575* | 242.641926 | 467.250026 | 234.128651 | 466.266010 | 233.636643 | E | 2772.316025 | 1386.661650 | 2755.289476 | 1378.148376 | 2754.305460 | 1377.656368 | 21 |
| 5 | 541.298039 | 271.152658 | 524.271490 | 262.639383 | 523.287474 | 262.147375 | G | *2643.273432* | 1322.140354 | 2626.246883 | 1313.627079 | 2625.262867 | 1313.135071 | 20 |
| 6 | *980.523365* | 490.765321 | 963.496816 | 482.252046 | 962.512800 | 481.760038 | Q | 2586.251968 | 1293.629622 | 2569.225419 | 1285.116347 | 2568.241403 | 1284.624339 | 19 |
| 7 | *1051.560479* | 526.283878 | 1034.533930 | 517.770603 | 1033.549914 | 517.278595 | A | 2147.026642 | 1074.016959 | 2130.000093 | 1065.503684 | 2129.016077 | 1065.011676 | 18 |
| 8 | *1164.644543* | 582.825910 | 1147.617994 | 574.312635 | 1146.633978 | 573.820627 | L | 2075.989528 | 1038.498402 | 2058.962979 | 1029.985127 | 2057.978963 | 1029.493119 | 17 |
| 9 | *1293.687136* | *647.347206* | 1276.660587 | 638.833932 | 1275.676571 | 638.341924 | E | 1962.905464 | 981.956370 | 1945.878915 | 973.443096 | 1944.894899 | 972.951088 | 16 |
| 10 | *1456.750465* | *728.878871* | 1439.723916 | 720.365596 | 1438.739900 | 719.873588 | Y | 1833.862871 | 917.435074 | 1816.836322 | 908.921799 | 1815.852306 | 908.429791 | 15 |
| 11 | *1555.818879* | *778.413078* | 1538.792330 | 769.899803 | 1537.808314 | 769.407795 | V | *1670.799542* | 835.903409 | 1653.772993 | 827.390135 | 1652.788977 | 826.898126 | 14 |
| 12 | *1715.849528* | 858.428402 | 1698.822979 | 849.915128 | 1697.838963 | 849.423120 | C | *1571.731128* | 786.369202 | 1554.704579 | 777.855928 | 1553.720563 | 777.363919 | 13 |
| 13 | 1812.902292 | 906.954784 | 1795.875743 | 898.441510 | 1794.891727 | 897.949502 | P | *1411.700479* | 706.353877 | 1394.673930 | 697.840603 | 1393.689914 | 697.348595 | 12 |
| 14 | 1899.934320 | 950.470798 | 1882.907771 | 941.957524 | 1881.923755 | 941.465516 | S | 1314.647715 | 657.827495 | 1297.621166 | 649.314221 | 1296.637150 | 648.822213 | 11 |
| 15 | *1956.955784* | 978.981530 | 1939.929235 | 970.468256 | 1938.945219 | 969.976248 | G | *1227.615687* | 614.311481 | 1210.589138 | 605.798207 | 1209.605122 | 605.306199 | 10 |
| 16 | 2104.024198 | *1052.515737* | 2086.997649 | 1044.002462 | 2086.013633 | 1043.510454 | F | 1170.594223 | 585.800749 | 1153.567674 | 577.287475 | 1152.583658 | 576.795467 | 9 |
| 17 | *2267.087527* | 1134.047402 | 2250.060978 | 1125.534127 | 2249.076962 | 1125.042119 | Y | *1023.525809* | 512.266543 | 1006.499260 | 503.753268 | 1005.515244 | 503.261260 | 8 |
| 18 | 2364.140291 | 1182.573784 | 2347.113742 | 1174.060509 | 2346.129726 | 1173.568501 | P | *860.462480* | 430.734878 | 843.435931 | 422.221603 | 842.451915 | 421.729595 | 7 |
| 19 | 2527.203620 | *1264.105448* | 2510.177071 | 1255.592173 | 2509.193055 | 1255.100166 | Y | *763.409716* | 382.208496 | 746.383167 | 373.695221 | 745.399151 | 373.203213 | 6 |
| 20 | 2624.256384 | 1312.631830 | 2607.229835 | 1304.118556 | 2606.245819 | 1303.626548 | P | *600.346387* | 300.676831 | 583.319838 | 292.163557 | 582.335822 | 291.671549 | 5 |
| 21 | 2723.324798 | 1362.166037 | 2706.298249 | 1353.652762 | 2705.314233 | 1353.160754 | V | 503.293623 | 252.150449 | 486.267074 | 243.637175 | 485.283058 | 243.145167 | 4 |
| 22 | 2851.383376 | 1426.195326 | 2834.356827 | 1417.682051 | 2833.372811 | 1417.190044 | Q | *404.225209* | 202.616242 | 387.198660 | 194.102968 | 386.214644 | 193.610960 | 3 |
| 23 | 2952.431055 | 1476.719165 | 2935.404506 | 1468.205891 | 2934.420490 | 1467.713883 | T | *276.166631* | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 24 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 66.1 | 3125.535446 | 0.034936 | LLQEGQALEYVCPSGFYPYPVQTR |
| 57.3 | 3125.535446 | 0.034936 | LLQEGQALEYVCPSGFYPYPVQTR |
| 5.3 | 3125.535446 | 0.034936 | LLQEGQALEYVCPSGFYPYPVQTR |

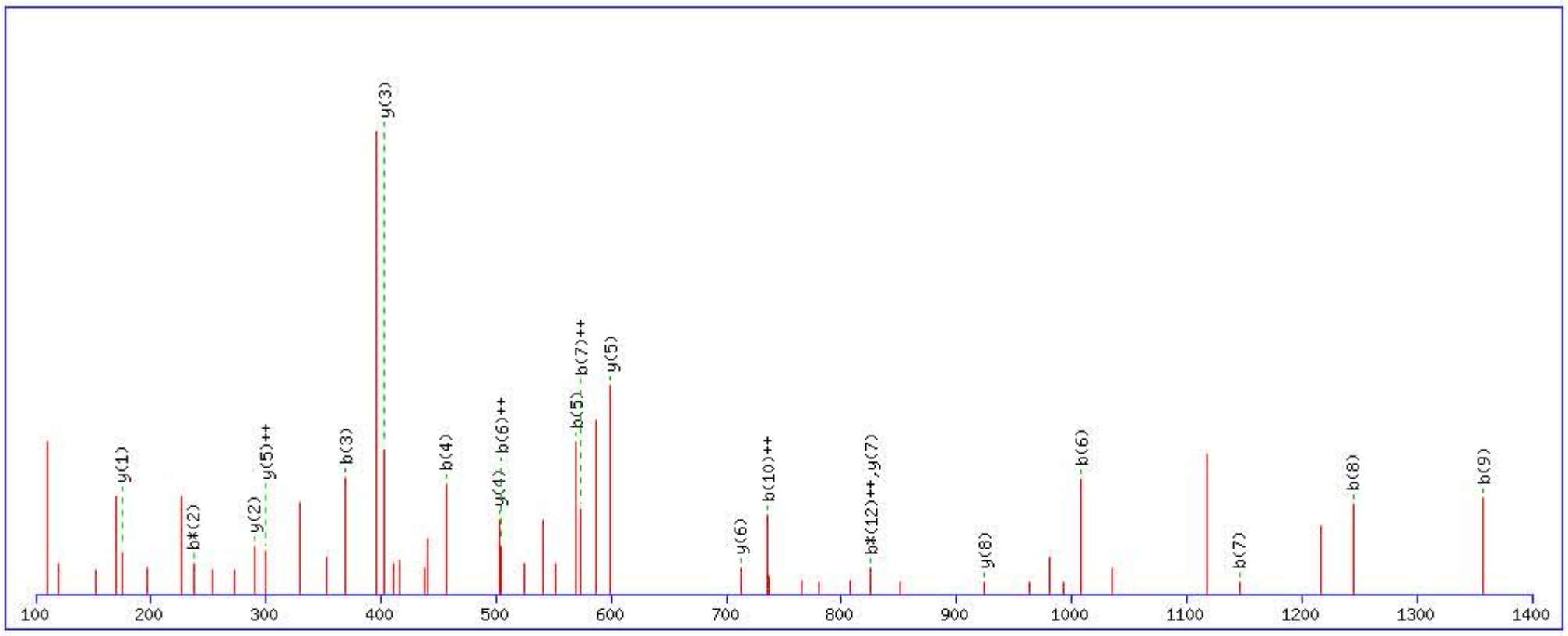
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **RPDSLQHVLLPVLDR**
Found in **CFAD_HUMAN**, Complement factor D OS=Homo sapiens GN=CFD PE=1 SV=5

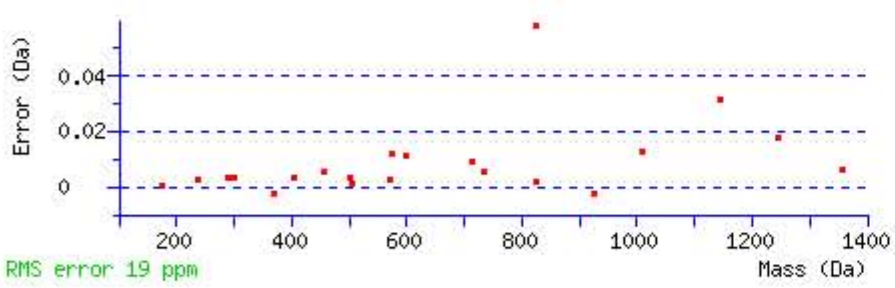
Match to Query 46056: 2068.175056 from(518.051040,4+) rtinseconds(2372) index(68592)
Title: Locus:1.1.1.2101.5 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

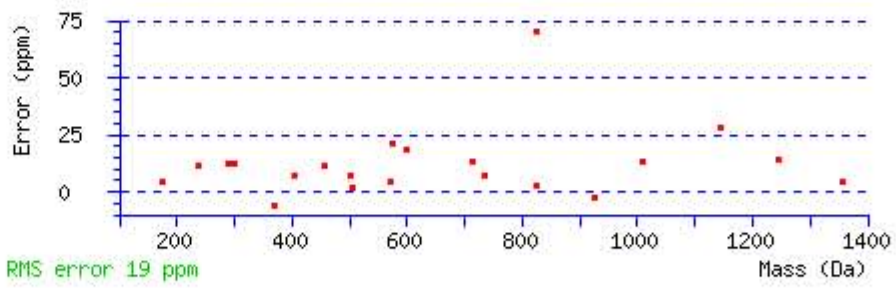
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2068.161545
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 52 **Expect:** 5.3e-005
**Matches :** 21/162 fragment ions using 36 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 157.108387 | 79.057831 | 140.081838 | 70.544557 | | | R | | | | | | | 15 |
| 2 | 254.161151 | 127.584213 | 237.134602 | 119.070939 | | | P | 1913.067716 | 957.037496 | 1896.041167 | 948.524222 | 1895.057151 | 948.032214 | 14 |
| 3 | *369.188094* | 185.097685 | 352.161545 | 176.584410 | 351.177529 | 176.092402 | D | 1816.014952 | 908.511114 | 1798.988403 | 899.997840 | 1798.004387 | 899.505832 | 13 |
| 4 | *456.220122* | 228.613699 | 439.193573 | 220.100425 | 438.209557 | 219.608417 | S | 1700.988009 | 850.997643 | 1683.961460 | 842.484368 | 1682.977444 | 841.992360 | 12 |
| 5 | *569.304186* | 285.155731 | 552.277637 | 276.642457 | 551.293621 | 276.150449 | L | 1613.955981 | 807.481629 | 1596.929432 | 798.968354 | 1595.945416 | 798.476346 | 11 |
| 6 | *1008.529512* | **504.768394** | 991.502963 | 496.255120 | 990.518947 | 495.763112 | Q | 1500.871917 | 750.939597 | 1483.845368 | 742.426322 | 1482.861352 | 741.934314 | 10 |
| 7 | *1145.588424* | **573.297850** | 1128.561875 | 564.784576 | 1127.577859 | 564.292568 | H | 1061.646591 | 531.326934 | 1044.620042 | 522.813659 | 1043.636026 | 522.321651 | 9 |
| 8 | *1244.656838* | 622.832057 | 1227.630289 | 614.318783 | 1226.646273 | 613.826775 | V | *924.587679* | 462.797478 | 907.561130 | 454.284203 | 906.577114 | 453.792195 | 8 |
| 9 | *1357.740902* | 679.374089 | 1340.714353 | 670.860815 | 1339.730337 | 670.368807 | L | *825.519265* | 413.263271 | 808.492716 | 404.749996 | 807.508700 | 404.257988 | 7 |
| 10 | 1470.824966 | **735.916121** | 1453.798417 | 727.402847 | 1452.814401 | 726.910838 | L | *712.435201* | 356.721239 | 695.408652 | 348.207964 | 694.424636 | 347.715956 | 6 |
| 11 | 1567.877730 | 784.442503 | 1550.851181 | 775.929229 | 1549.867165 | 775.437220 | P | *599.351137* | 300.179207 | 582.324588 | 291.665932 | 581.340572 | 291.173924 | 5 |
| 12 | 1666.946144 | 833.976710 | 1649.919595 | 825.463436 | 1648.935579 | 824.971428 | V | *502.298373* | 251.652825 | 485.271824 | 243.139550 | 484.287808 | 242.647542 | 4 |
| 13 | 1780.030208 | 890.518742 | 1763.003659 | 882.005468 | 1762.019643 | 881.513459 | L | *403.229959* | 202.118618 | 386.203410 | 193.605343 | 385.219394 | 193.113335 | 3 |
| 14 | 1895.057151 | 948.032214 | 1878.030602 | 939.518939 | 1877.046586 | 939.026931 | D | *290.145895* | 145.576586 | 273.119346 | 137.063311 | 272.135330 | 136.571303 | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 51.7 | 2068.161545 | 0.013511 | RPDSLQHVLLPVLDR |

**Mascot:** http://www.matrixscience.com/

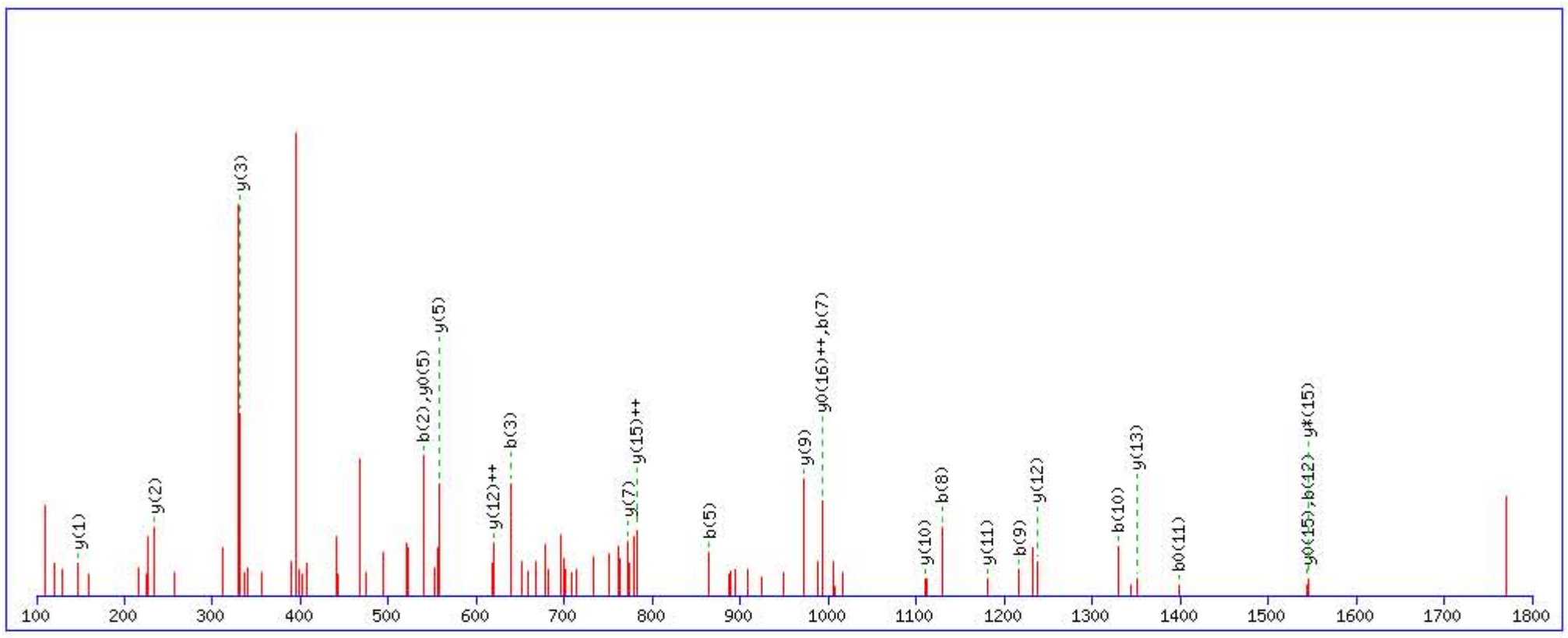
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VQVLLGAHSLSQPEPSK**
Found in **CFAD_HUMAN**, Complement factor D OS=Homo sapiens GN=CFD PE=1 SV=5

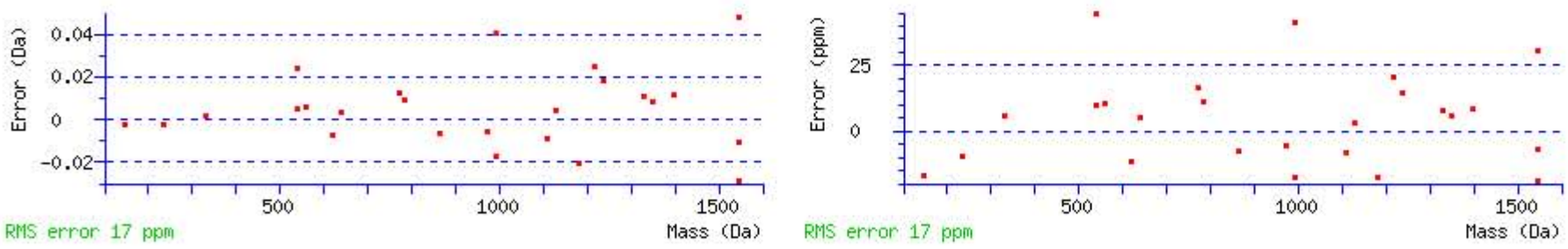
Match to Query 46596: 2100.152202 from(701.058010,3+) rtinseconds(1963) index(66234)
Title: Locus:1.1.1.1958.20 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2100.140137
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 61 **Expect:** 1.3e-005
**Matches :** 25/172 fragment ions using 41 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 17 |
| 2 | *539.301016* | 270.154146 | 522.274467 | 261.640872 | | | Q | 2002.079009 | 1001.543143 | 1985.052460 | 993.029868 | 1984.068444 | 992.537860 | 16 |
| 3 | *638.369430* | 319.688353 | 621.342881 | 311.175079 | | | V | 1562.853683 | 781.930480 | 1545.827134 | 773.417205 | 1544.843118 | 772.925197 | 15 |
| 4 | 751.453494 | 376.230385 | 734.426945 | 367.717111 | | | L | 1463.785269 | 732.396273 | 1446.758720 | 723.882998 | 1445.774704 | 723.390990 | 14 |
| 5 | *864.537558* | 432.772417 | 847.511009 | 424.259143 | | | L | *1350.701205* | 675.854241 | 1333.674656 | 667.340966 | 1332.690640 | 666.848958 | 13 |
| 6 | 921.559022 | 461.283149 | 904.532473 | 452.769875 | | | G | *1237.617141* | 619.312209 | 1220.590592 | 610.798934 | 1219.606576 | 610.306926 | 12 |
| 7 | *992.596136* | 496.801706 | 975.569587 | 488.288432 | | | A | *1180.595677* | 590.801477 | 1163.569128 | 582.288202 | 1162.585112 | 581.796194 | 11 |
| 8 | *1129.655048* | 565.331162 | 1112.628499 | 556.817888 | | | H | *1109.558563* | 555.282920 | 1092.532014 | 546.769645 | 1091.547998 | 546.277637 | 10 |
| 9 | *1216.687076* | 608.847176 | 1199.660527 | 600.333902 | 1198.676511 | 599.841894 | S | *972.499651* | 486.753464 | 955.473102 | 478.240189 | 954.489086 | 477.748181 | 9 |
| 10 | *1329.771140* | 665.389208 | 1312.744591 | 656.875934 | 1311.760575 | 656.383926 | L | 885.467623 | 443.237450 | 868.441074 | 434.724175 | 867.457058 | 434.232167 | 8 |
| 11 | 1416.803168 | 708.905222 | 1399.776619 | 700.391948 | 1398.792603 | 699.899940 | S | *772.383559* | 386.695418 | 755.357010 | 378.182143 | 754.372994 | 377.690135 | 7 |
| 12 | *1544.861746* | 772.934511 | 1527.835197 | 764.421237 | 1526.851181 | 763.929229 | Q | 685.351531 | 343.179404 | 668.324982 | 334.666129 | 667.340966 | 334.174121 | 6 |
| 13 | 1641.914510 | 821.460893 | 1624.887961 | 812.947619 | 1623.903945 | 812.455611 | P | *557.292953* | 279.150115 | 540.266404 | 270.636840 | 539.282388 | 270.144832 | 5 |
| 14 | 1770.957103 | 885.982190 | 1753.930554 | 877.468915 | 1752.946538 | 876.976907 | E | 460.240189 | 230.623733 | 443.213640 | 222.110458 | 442.229624 | 221.618450 | 4 |
| 15 | 1868.009867 | 934.508572 | 1850.983318 | 925.995297 | 1849.999302 | 925.503289 | P | *331.197596* | 166.102436 | 314.171047 | 157.589162 | 313.187031 | 157.097154 | 3 |
| 16 | 1955.041895 | 978.024586 | 1938.015346 | 969.511311 | 1937.031330 | 969.019303 | S | *234.144832* | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 17 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 61.0 | 2100.140137 | 0.012065 | VQVLLGAHSLSQPEPSK |

**Mascot:** http://www.matrixscience.com/

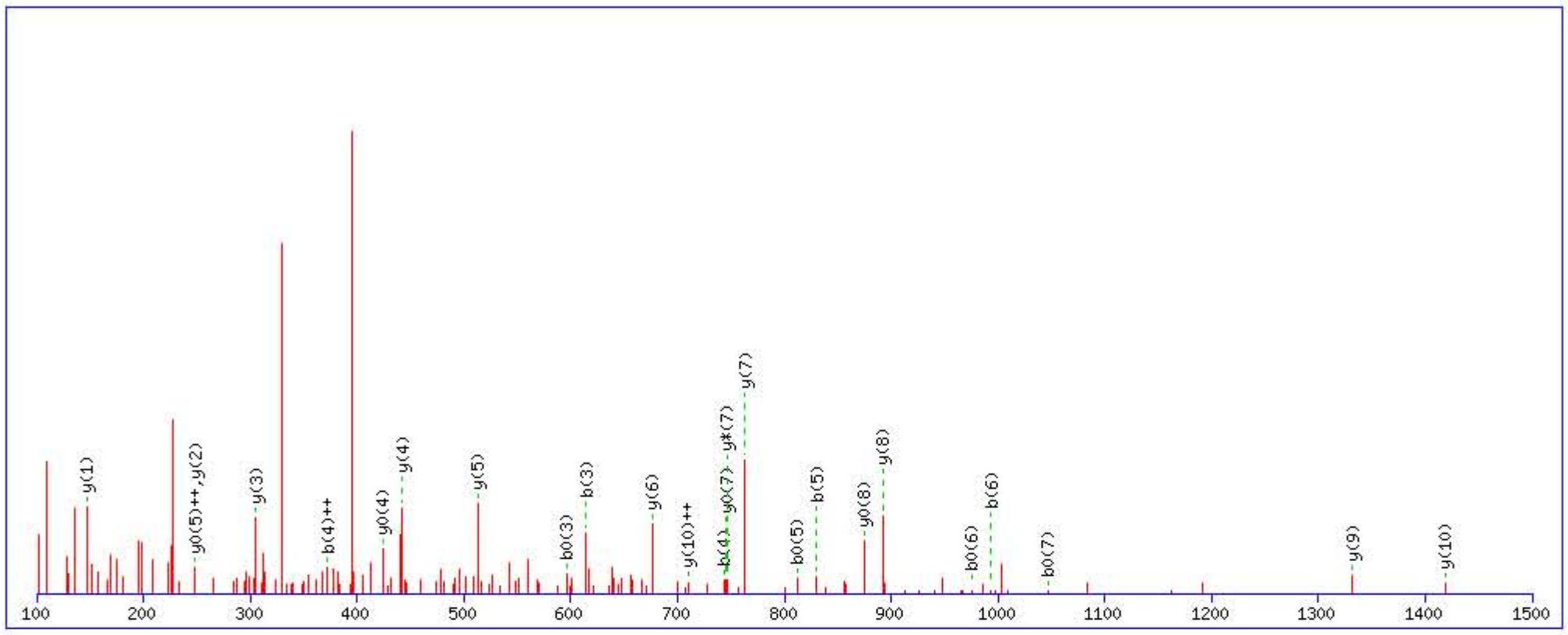
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SSQESYAHGTK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

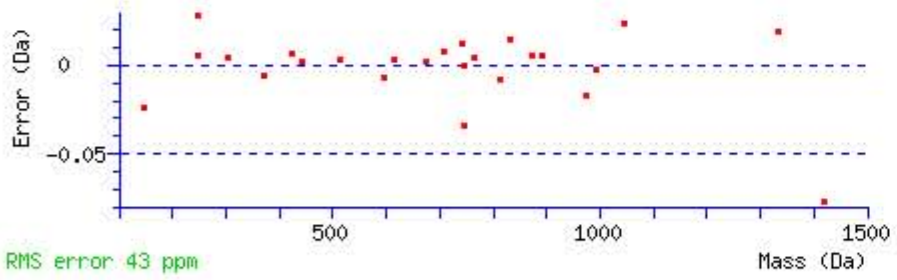
Match to Query 31209: 1504.698042 from(502.573290,3+) rtinseconds(1201) index(15147)
Title: Locus:1.1.1.2800.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

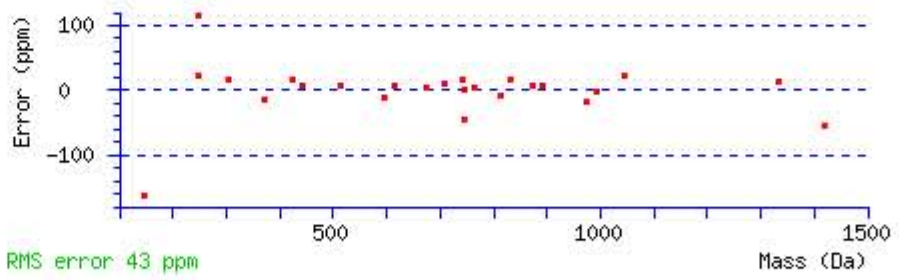
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1504.698013
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 50 **Expect:** 0.00015
**Matches :** 25/114 fragment ions using 53 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 11 |
| 2 | 175.071332 | 88.039304 | | | 157.060767 | 79.034021 | S | *1418.673277* | 709.840276 | 1401.646728 | 701.327002 | 1400.662712 | 700.834994 | 10 |
| 3 | **614.296658** | 307.651967 | 597.270109 | 299.138692 | 596.286093 | 298.646684 | Q | *1331.641249* | 666.324263 | 1314.614700 | 657.810988 | 1313.630684 | 657.318980 | 9 |
| 4 | **743.339251** | 372.173264 | 726.312702 | 363.659989 | 725.328686 | 363.167981 | E | *892.415923* | 446.711600 | 875.389374 | 438.198325 | 874.405358 | 437.706317 | 8 |
| 5 | **830.371279** | 415.689278 | 813.344730 | 407.176003 | 812.360714 | 406.683995 | S | *763.373330* | 382.190303 | 746.346781 | 373.677029 | 745.362765 | 373.185021 | 7 |
| 6 | **993.434608** | 497.220942 | 976.408059 | 488.707668 | 975.424043 | 488.215660 | Y | *676.341302* | 338.674289 | 659.314753 | 330.161015 | 658.330737 | 329.669007 | 6 |
| 7 | 1064.471722 | 532.739499 | 1047.445173 | 524.226225 | 1046.461157 | 523.734217 | A | *513.277973* | 257.142625 | 496.251424 | 248.629350 | 495.267408 | 248.137342 | 5 |
| 8 | 1201.530634 | 601.268955 | 1184.504085 | 592.755681 | 1183.520069 | 592.263672 | H | *442.240859* | 221.624067 | 425.214310 | 213.110793 | 424.230294 | 212.618785 | 4 |
| 9 | 1258.552098 | 629.779687 | 1241.525549 | 621.266413 | 1240.541533 | 620.774404 | G | *305.181947* | 153.094611 | 288.155398 | 144.581337 | 287.171382 | 144.089329 | 3 |
| 10 | 1359.599777 | 680.303526 | 1342.573228 | 671.790252 | 1341.589212 | 671.298244 | T | *248.160483* | 124.583879 | 231.133934 | 116.070605 | 230.149918 | 115.578597 | 2 |
| 11 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 49.7 | 1504.698013 | 0.000029 | SSQESYAHGTK |

**Mascot:** http://www.matrixscience.com/

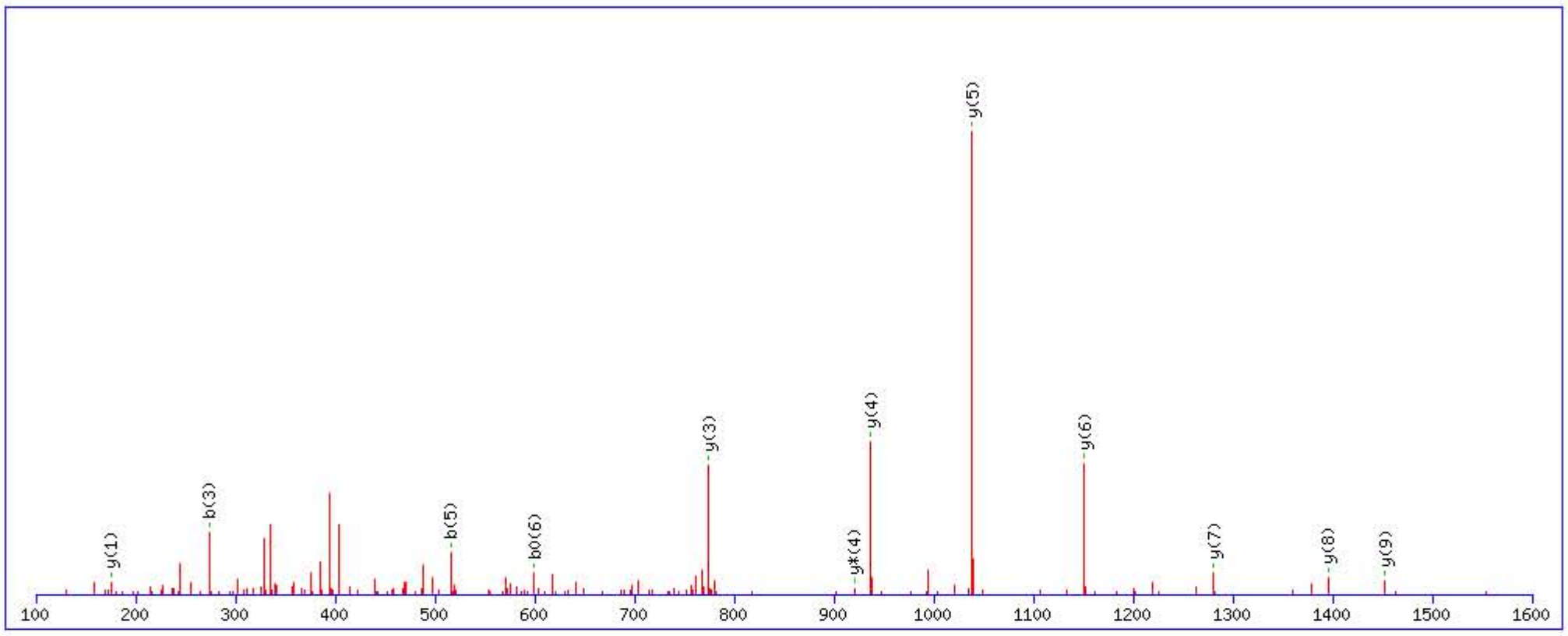
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TGDEITYQCR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

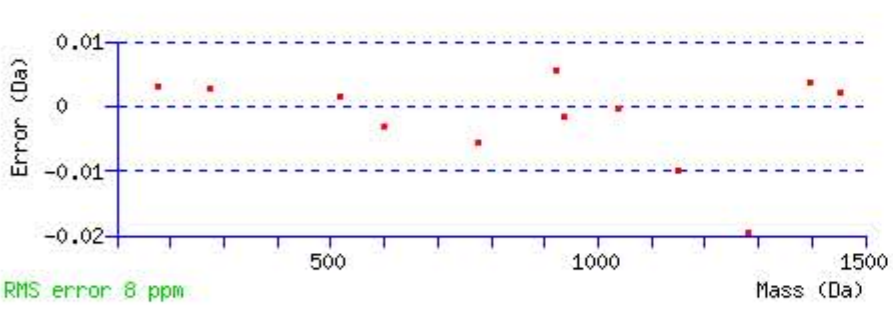
Match to Query 32540: 1552.704428 from(777.359490,2+) rtinseconds(1673) index(18041)
Title: Locus:1.1.1.2965.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

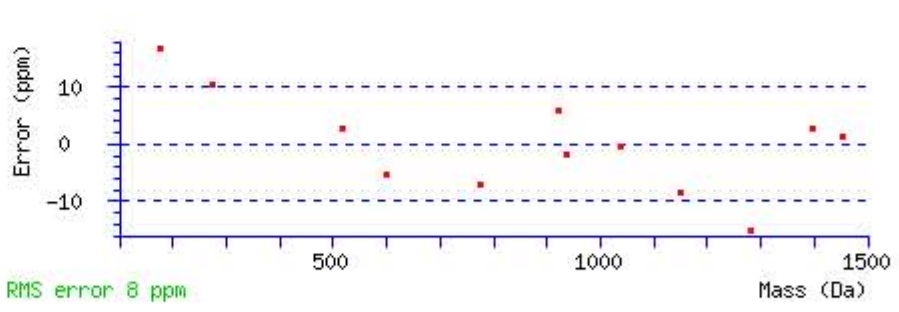
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1552.701401
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 74 **Expect:** 4e-007
**Matches :** 12/86 fragment ions using 14 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 10 |
| 2 | 159.076419 | 80.041847 | | | 141.065854 | 71.036565 | G | *1452.660999* | 726.834138 | 1435.634450 | 718.320863 | 1434.650434 | 717.828855 | 9 |
| 3 | **274.103362** | 137.555319 | | | 256.092797 | 128.550037 | D | *1395.639535* | 698.323406 | 1378.612986 | 689.810131 | 1377.628970 | 689.318123 | 8 |
| 4 | 403.145955 | 202.076616 | | | 385.135390 | 193.071333 | E | *1280.612592* | 640.809934 | 1263.586043 | 632.296660 | 1262.602027 | 631.804652 | 7 |
| 5 | **516.230019** | 258.618648 | | | 498.219454 | 249.613365 | I | *1151.569999* | 576.288638 | 1134.543450 | 567.775363 | 1133.559434 | 567.283355 | 6 |
| 6 | 617.277698 | 309.142487 | | | 599.267133 | 300.137205 | T | *1038.485935* | 519.746606 | 1021.459386 | 511.233331 | 1020.475370 | 510.741323 | 5 |
| 7 | 780.341027 | 390.674152 | | | 762.330462 | 381.668869 | Y | *937.438256* | 469.222766 | 920.411707 | 460.709492 | | | 4 |
| 8 | 1219.566353 | 610.286815 | 1202.539804 | 601.773540 | 1201.555788 | 601.281532 | Q | *774.374927* | 387.691102 | 757.348378 | 379.177827 | | | 3 |
| 9 | 1379.597002 | 690.302139 | 1362.570453 | 681.788865 | 1361.586437 | 681.296857 | C | 335.149601 | 168.078438 | 318.123052 | 159.565164 | | | 2 |
| 10 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 73.7 | 1552.701401 | 0.003027 | TGDEITYQCR |
| 9.1 | 1552.715149 | -0.010721 | LTNGSSSCSGTVEVR |
| 7.3 | 1552.712616 | -0.008188 | NVGMPVAHMESPER |
| 6.8 | 1552.715820 | -0.011392 | AVFDALDGDGDGFVR |
| 6.1 | 1552.716629 | -0.012201 | NEQPYLYCR |

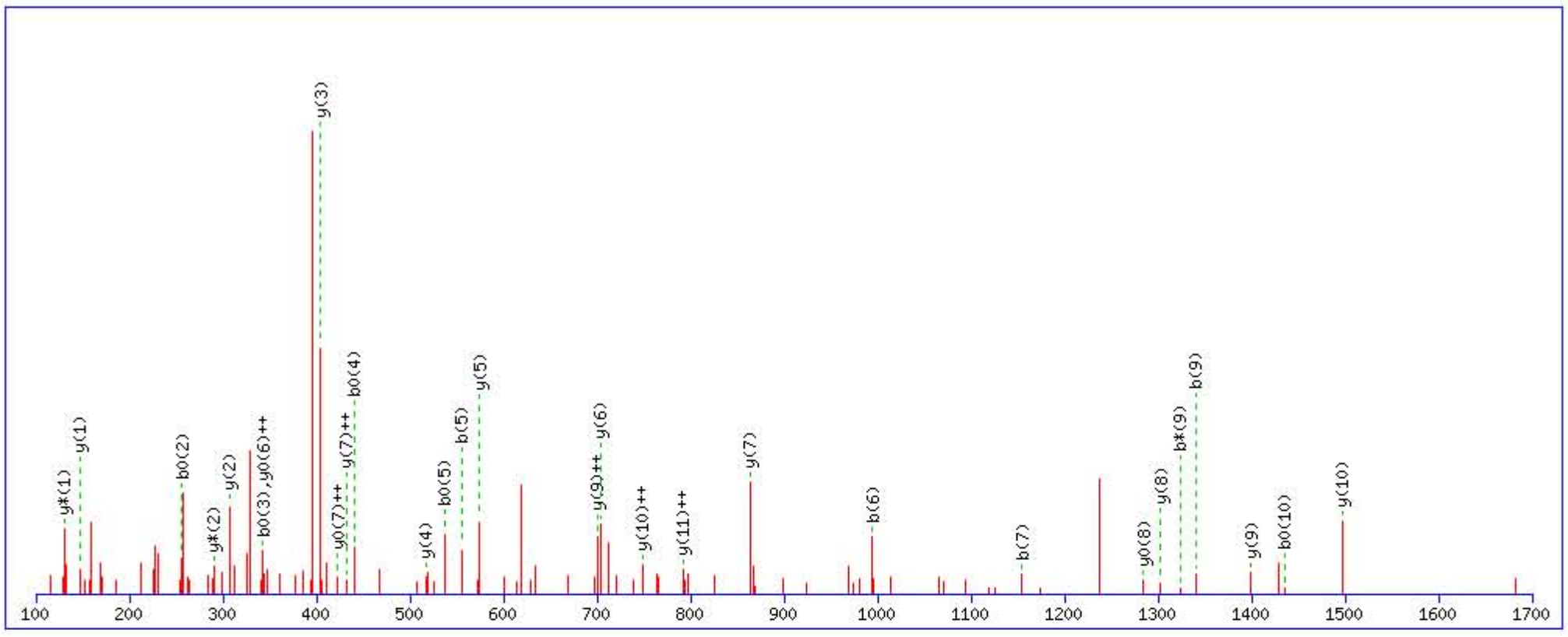
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **WSSPPQCEGLPCK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

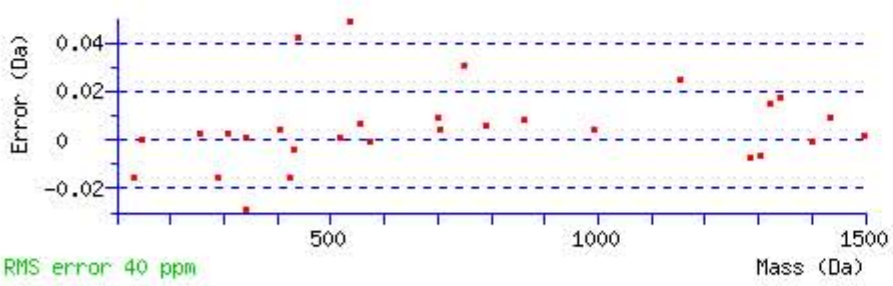
Match to Query 41487: 1855.851282 from(619.624370,3+) rtinseconds(1915) index(19735)
Title: Locus:1.1.1.3049.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

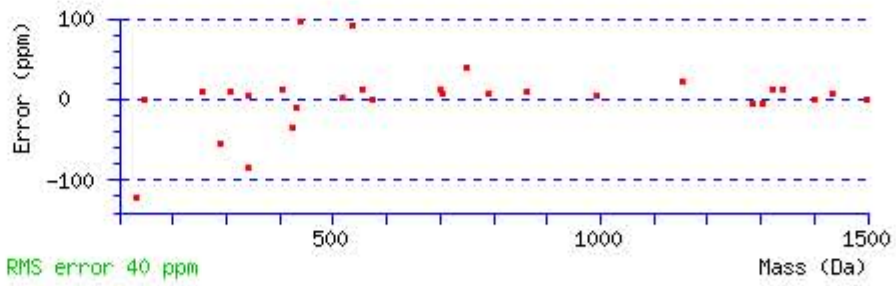
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1855.841934
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 40 **Expect:** 0.0012
**Matches :** 29/122 fragment ions using 71 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 187.086589 | 94.046932 | | | | | W | | | | | | | 13 |
| 2 | 274.118617 | 137.562947 | | | 256.108052 | 128.557664 | S | 1670.769897 | 835.888587 | 1653.743348 | 827.375312 | 1652.759332 | 826.883304 | 12 |
| 3 | 361.150645 | 181.078960 | | | 343.140080 | 172.073678 | S | 1583.737869 | 792.372573 | 1566.711320 | 783.859298 | 1565.727304 | 783.367290 | 11 |
| 4 | 458.203409 | 229.605343 | | | 440.192844 | 220.600060 | P | *1496.705841* | 748.856559 | 1479.679292 | 740.343284 | 1478.695276 | 739.851276 | 10 |
| 5 | **555.256173** | 278.131725 | | | 537.245608 | 269.126442 | P | *1399.653077* | 700.330177 | 1382.626528 | 691.816902 | 1381.642512 | 691.324894 | 9 |
| 6 | **994.481499** | 497.744388 | 977.454950 | 489.231113 | 976.470934 | 488.739105 | Q | *1302.600313* | 651.803795 | 1285.573764 | 643.290520 | 1284.589748 | 642.798512 | 8 |
| 7 | **1154.512148** | 577.759712 | 1137.485599 | 569.246438 | 1136.501583 | 568.754430 | C | *863.374987* | 432.191132 | 846.348438 | 423.677857 | 845.364422 | 423.185849 | 7 |
| 8 | 1283.554741 | 642.281009 | 1266.528192 | 633.767734 | 1265.544176 | 633.275726 | E | *703.344338* | 352.175807 | 686.317789 | 343.662533 | 685.333773 | 343.170525 | 6 |
| 9 | **1340.576205** | 670.791741 | 1323.549656 | 662.278466 | 1322.565640 | 661.786458 | G | *574.301745* | 287.654511 | 557.275196 | 279.141236 | | | 5 |
| 10 | 1453.660269 | 727.333773 | 1436.633720 | 718.820498 | 1435.649704 | 718.328490 | L | *517.280281* | 259.143779 | 500.253732 | 250.630504 | | | 4 |
| 11 | 1550.713033 | 775.860155 | 1533.686484 | 767.346880 | 1532.702468 | 766.854872 | P | *404.196217* | 202.601747 | 387.169668 | 194.088472 | | | 3 |
| 12 | 1710.743682 | 855.875479 | 1693.717133 | 847.362205 | 1692.733117 | 846.870197 | C | *307.143453* | 154.075365 | 290.116904 | 145.562090 | | | 2 |
| 13 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 39.6 | 1855.841934 | 0.009348 | WSSPPQCEGLPCK |

**Mascot:** http://www.matrixscience.com/

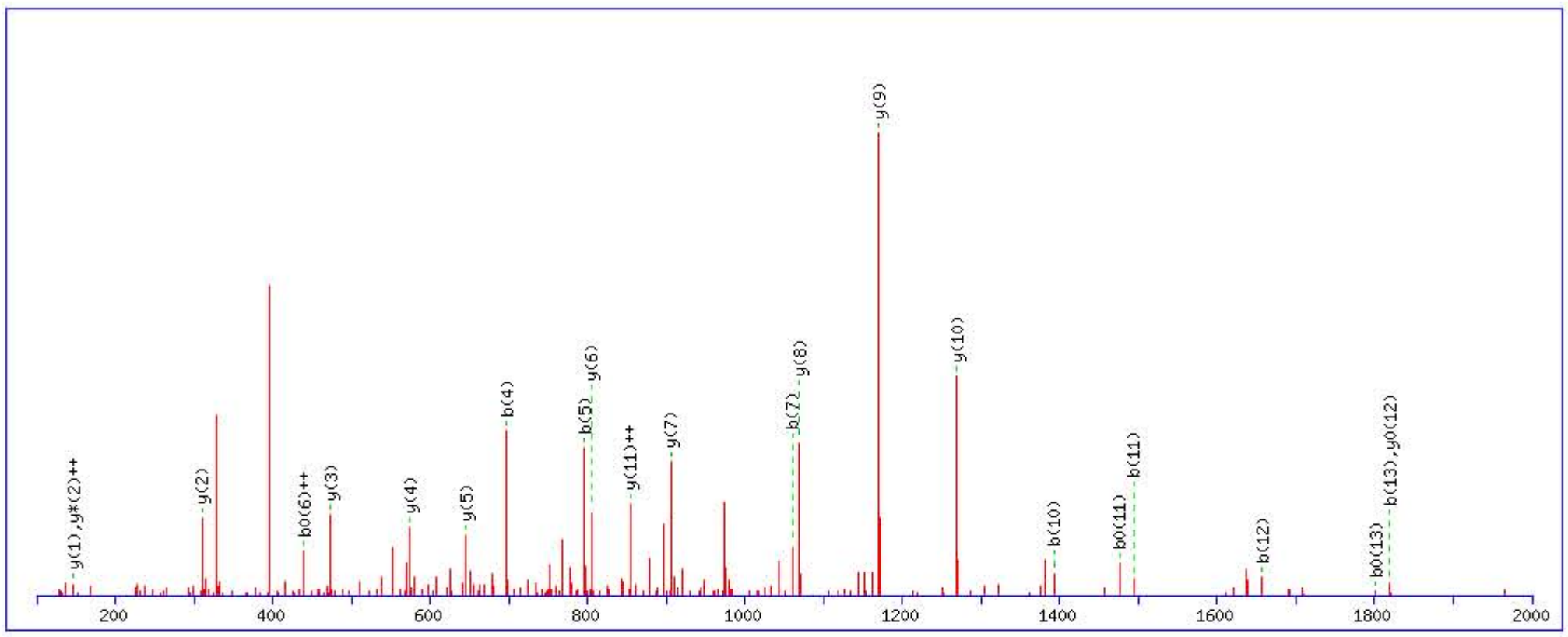
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AGEQVTYTCATYYK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

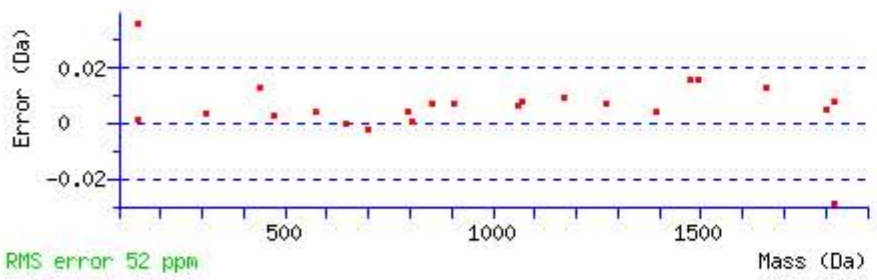
Match to Query 43462: 1964.919168 from(983.466860,2+) rtinseconds(1858) index(19254)
Title: Locus:1.1.1.3029.25 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

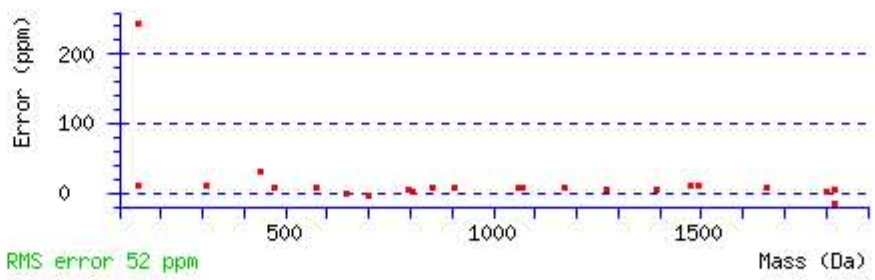
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1964.901215
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 66 **Expect:** 3.3e-006
**Matches :** 23/140 fragment ions using 35 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 14 |
| 2 | 129.065854 | 65.036565 | | | | | G | 1894.871388 | 947.939332 | 1877.844839 | 939.426058 | 1876.860823 | 938.934050 | 13 |
| 3 | 258.108447 | 129.557862 | | | 240.097882 | 120.552579 | E | 1837.849924 | 919.428600 | 1820.823375 | 910.915326 | 1819.839359 | 910.423318 | 12 |
| 4 | 697.333773 | 349.170525 | 680.307224 | 340.657250 | 679.323208 | 340.165242 | Q | 1708.807331 | 854.907304 | 1691.780782 | 846.394029 | 1690.796766 | 845.902021 | 11 |
| 5 | 796.402187 | 398.704732 | 779.375638 | 390.191457 | 778.391622 | 389.699449 | V | *1269.582005* | 635.294641 | 1252.555456 | 626.781366 | 1251.571440 | 626.289358 | 10 |
| 6 | 897.449866 | 449.228571 | 880.423317 | 440.715297 | 879.439301 | 440.223289 | T | *1170.513591* | 585.760434 | 1153.487042 | 577.247159 | 1152.503026 | 576.755151 | 9 |
| 7 | 1060.513195 | 530.760236 | 1043.486646 | 522.246961 | 1042.502630 | 521.754953 | Y | *1069.465912* | 535.236594 | 1052.439363 | 526.723320 | 1051.455347 | 526.231312 | 8 |
| 8 | 1161.560874 | 581.284075 | 1144.534325 | 572.770801 | 1143.550309 | 572.278793 | T | *906.402583* | 453.704930 | 889.376034 | 445.191655 | 888.392018 | 444.699647 | 7 |
| 9 | 1321.591523 | 661.299400 | 1304.564974 | 652.786125 | 1303.580958 | 652.294117 | C | *805.354904* | 403.181090 | 788.328355 | 394.667816 | 787.344339 | 394.175808 | 6 |
| 10 | 1392.628637 | 696.817957 | 1375.602088 | 688.304682 | 1374.618072 | 687.812674 | A | *645.324255* | 323.165766 | 628.297706 | 314.652491 | 627.313690 | 314.160483 | 5 |
| 11 | 1493.676316 | 747.341796 | 1476.649767 | 738.828522 | 1475.665751 | 738.336514 | T | *574.287141* | 287.647209 | 557.260592 | 279.133934 | 556.276576 | 278.641926 | 4 |
| 12 | 1656.739645 | 828.873461 | 1639.713096 | 820.360186 | 1638.729080 | 819.868178 | Y | *473.239462* | 237.123369 | 456.212913 | 228.610095 | | | 3 |
| 13 | 1819.802974 | 910.405125 | 1802.776425 | 901.891851 | 1801.792409 | 901.399843 | Y | *310.176133* | 155.591705 | 293.149584 | 147.078430 | | | 2 |
| 14 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 66.4 | 1964.901215 | 0.017953 | AGEQVTYTCATYYK |

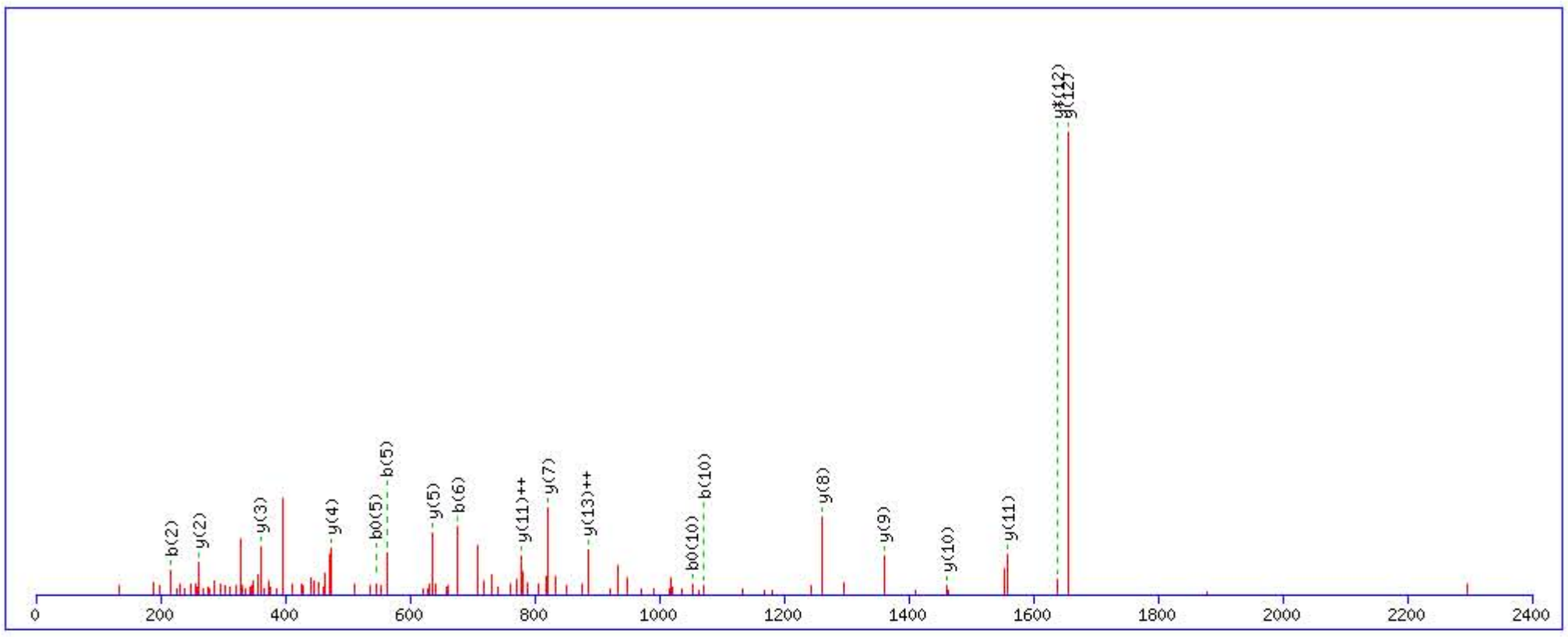
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DTSCVNPPTVQNAYIVSR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

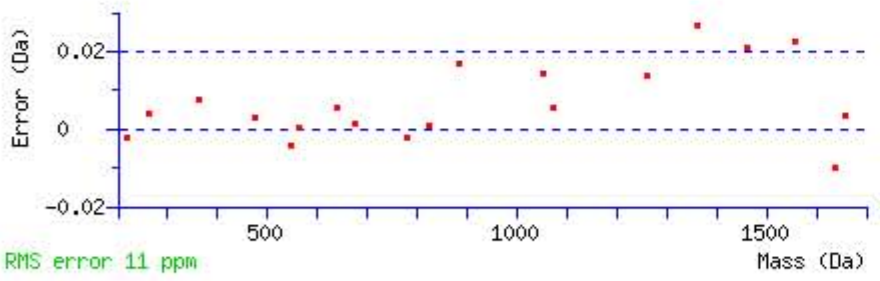
Match to Query 51112: 2331.158352 from(778.060060,3+) rtinseconds(2111) index(20911)
Title: Locus:1.1.1.3117.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

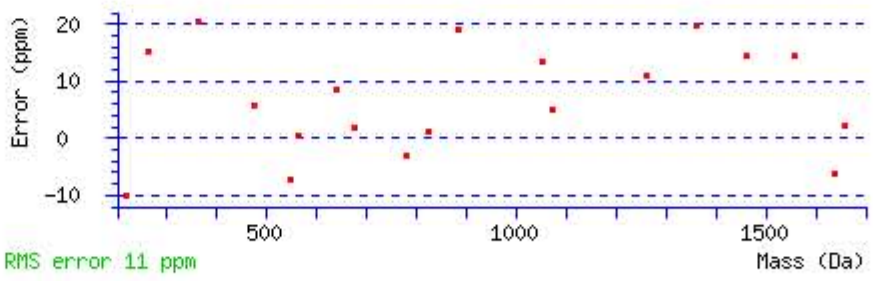
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2331.135147
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 3.3e-005
**Matches :** 19/192 fragment ions using 34 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 18 |
| 2 | **217.081898** | 109.044587 | | | 199.071333 | 100.039304 | T | 2217.115472 | 1109.061374 | 2200.088923 | 1100.548099 | 2199.104907 | 1100.056091 | 17 |
| 3 | 304.113926 | 152.560601 | | | 286.103361 | 143.555319 | S | 2116.067793 | 1058.537534 | 2099.041244 | 1050.024260 | 2098.057228 | 1049.532252 | 16 |
| 4 | 464.144575 | 232.575925 | | | 446.134010 | 223.570643 | C | 2029.035765 | 1015.021521 | 2012.009216 | 1006.508246 | 2011.025200 | 1006.016238 | 15 |
| 5 | **563.212989** | 282.110133 | | | 545.202424 | 273.104850 | V | 1869.005116 | 935.006196 | 1851.978567 | 926.492922 | 1850.994551 | 926.000914 | 14 |
| 6 | **677.255916** | 339.131596 | 660.229367 | 330.618321 | 659.245351 | 330.126313 | N | 1769.936702 | 885.471989 | 1752.910153 | 876.958715 | 1751.926137 | 876.466707 | 13 |
| 7 | 774.308680 | 387.657978 | 757.282131 | 379.144703 | 756.298115 | 378.652695 | P | *1655.893775* | 828.450526 | 1638.867226 | 819.937251 | 1637.883210 | 819.445243 | 12 |
| 8 | 871.361444 | 436.184360 | 854.334895 | 427.671086 | 853.350879 | 427.179078 | P | *1558.841011* | 779.924144 | 1541.814462 | 771.410869 | 1540.830446 | 770.918861 | 11 |
| 9 | 972.409123 | 486.708200 | 955.382574 | 478.194925 | 954.398558 | 477.702917 | T | *1461.788247* | 731.397762 | 1444.761698 | 722.884487 | 1443.777682 | 722.392479 | 10 |
| 10 | **1071.477537** | 536.242407 | 1054.450988 | 527.729132 | 1053.466972 | 527.237124 | V | *1360.740568* | 680.873922 | 1343.714019 | 672.360648 | 1342.730003 | 671.868639 | 9 |
| 11 | 1510.702863 | 755.855070 | 1493.676314 | 747.341795 | 1492.692298 | 746.849787 | Q | *1261.672154* | 631.339715 | 1244.645605 | 622.826441 | 1243.661589 | 622.334433 | 8 |
| 12 | 1624.745790 | 812.876533 | 1607.719241 | 804.363259 | 1606.735225 | 803.871251 | N | *822.446828* | 411.727052 | 805.420279 | 403.213777 | 804.436263 | 402.721769 | 7 |
| 13 | 1695.782904 | 848.395090 | 1678.756355 | 839.881816 | 1677.772339 | 839.389808 | A | 708.403901 | 354.705588 | 691.377352 | 346.192314 | 690.393336 | 345.700306 | 6 |
| 14 | 1858.846233 | 929.926755 | 1841.819684 | 921.413480 | 1840.835668 | 920.921472 | Y | *637.366787* | 319.187031 | 620.340238 | 310.673757 | 619.356222 | 310.181749 | 5 |
| 15 | 1971.930297 | 986.468787 | 1954.903748 | 977.955512 | 1953.919732 | 977.463504 | I | *474.303458* | 237.655367 | 457.276909 | 229.142092 | 456.292893 | 228.650084 | 4 |
| 16 | 2070.998711 | 1036.002993 | 2053.972162 | 1027.489719 | 2052.988146 | 1026.997711 | V | *361.219394* | 181.113335 | 344.192845 | 172.600060 | 343.208829 | 172.108052 | 3 |
| 17 | 2158.030739 | 1079.519007 | 2141.004190 | 1071.005733 | 2140.020174 | 1070.513725 | S | *262.150980* | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 18 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 59.2 | 2331.135147 | 0.023205 | DTSCVNPPTVQNAYIVSR |

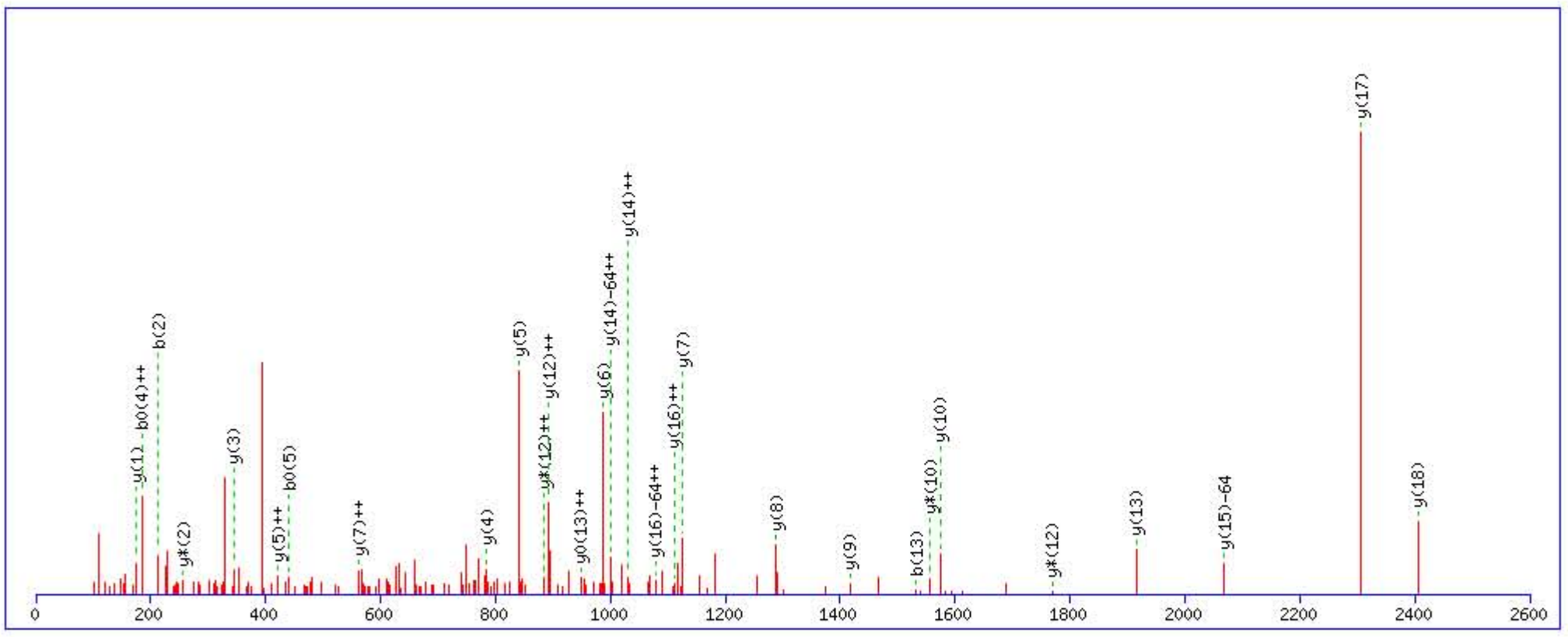
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IVSSAMEPDREYHFGQAVR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

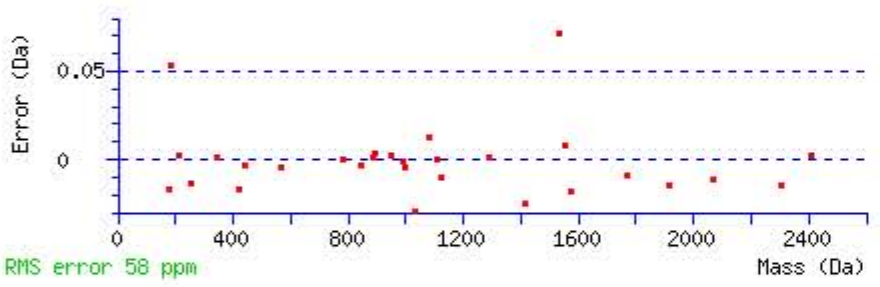
Match to Query 54663: 2518.210856 from(630.559990,4+) rtinseconds(1673) index(18039)
Title: Locus:1.1.1.2965.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

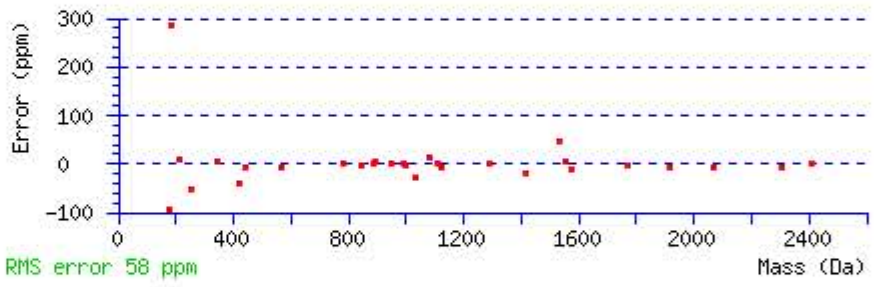
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2518.209686
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**M6** : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
**Q16** : Biotin:Thermo-21345 (Q)
**Ions Score:** 47 **Expect:** 0.00051
**Matches :** 29/278 fragment ions using 74 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 19 |
| 2 | 213.159754 | 107.083515 | | | | | V | 2406.132913 | 1203.570094 | 2389.106364 | 1195.056820 | 2388.122348 | 1194.564812 | 18 |
| 3 | 300.191782 | 150.599529 | | | 282.181217 | 141.594247 | S | 2307.064499 | 1154.035887 | 2290.037950 | 1145.522613 | 2289.053934 | 1145.030605 | 17 |
| 4 | 387.223810 | 194.115543 | | | 369.213245 | 185.110261 | S | 2220.032471 | 1110.519873 | 2203.005922 | 1102.006599 | 2202.021906 | 1101.514591 | 16 |
| 5 | 458.260924 | 229.634100 | | | 440.250359 | 220.628818 | A | 2133.000443 | 1067.003859 | 2115.973894 | 1058.490585 | 2114.989878 | 1057.998577 | 15 |
| 6 | 605.296324 | 303.151800 | | | 587.285759 | 294.146518 | M | 2061.963329 | 1031.485302 | 2044.936780 | 1022.972028 | 2043.952764 | 1022.480020 | 14 |
| 7 | 734.338917 | 367.673097 | | | 716.328352 | 358.667814 | E | 1914.927929 | 957.967603 | 1897.901380 | 949.454328 | 1896.917364 | 948.962320 | 13 |
| 8 | 831.391681 | 416.199479 | | | 813.381116 | 407.194196 | P | 1785.885336 | 893.446306 | 1768.858787 | 884.933032 | 1767.874771 | 884.441024 | 12 |
| 9 | 946.418624 | 473.712950 | | | 928.408059 | 464.707668 | D | 1688.832572 | 844.919924 | 1671.806023 | 836.406650 | 1670.822007 | 835.914642 | 11 |
| 10 | 1102.519735 | 551.763506 | 1085.493186 | 543.250231 | 1084.509170 | 542.758223 | R | 1573.805629 | 787.406453 | 1556.779080 | 778.893178 | 1555.795064 | 778.401170 | 10 |
| 11 | 1231.562328 | 616.284802 | 1214.535779 | 607.771528 | 1213.551763 | 607.279520 | E | 1417.704518 | 709.355897 | 1400.677969 | 700.842623 | 1399.693953 | 700.350615 | 9 |
| 12 | 1394.625657 | 697.816467 | 1377.599108 | 689.303192 | 1376.615092 | 688.811184 | Y | 1288.661925 | 644.834601 | 1271.635376 | 636.321326 | | | 8 |
| 13 | 1531.684569 | 766.345923 | 1514.658020 | 757.832648 | 1513.674004 | 757.340640 | H | 1125.598596 | 563.302936 | 1108.572047 | 554.789662 | | | 7 |
| 14 | 1678.752983 | 839.880130 | 1661.726434 | 831.366855 | 1660.742418 | 830.874847 | F | 988.539684 | 494.773480 | 971.513135 | 486.260206 | | | 6 |
| 15 | 1735.774447 | 868.390862 | 1718.747898 | 859.877587 | 1717.763882 | 859.385579 | G | 841.471270 | 421.239273 | 824.444721 | 412.725999 | | | 5 |
| 16 | 2174.999773 | 1088.003524 | 2157.973224 | 1079.490250 | 2156.989208 | 1078.998242 | Q | 784.449806 | 392.728541 | 767.423257 | 384.215267 | | | 4 |
| 17 | 2246.036887 | 1123.522082 | 2229.010338 | 1115.008807 | 2228.026322 | 1114.516799 | A | 345.224480 | 173.115878 | 328.197931 | 164.602603 | | | 3 |
| 18 | 2345.105301 | 1173.056288 | 2328.078752 | 1164.543014 | 2327.094736 | 1164.051006 | V | 274.187366 | 137.597321 | 257.160817 | 129.084046 | | | 2 |
| 19 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 46.7 | 2518.209686 | 0.001170 | IVSSAMEPDREYHFGQAVR |

**Mascot:** http://www.matrixscience.com/

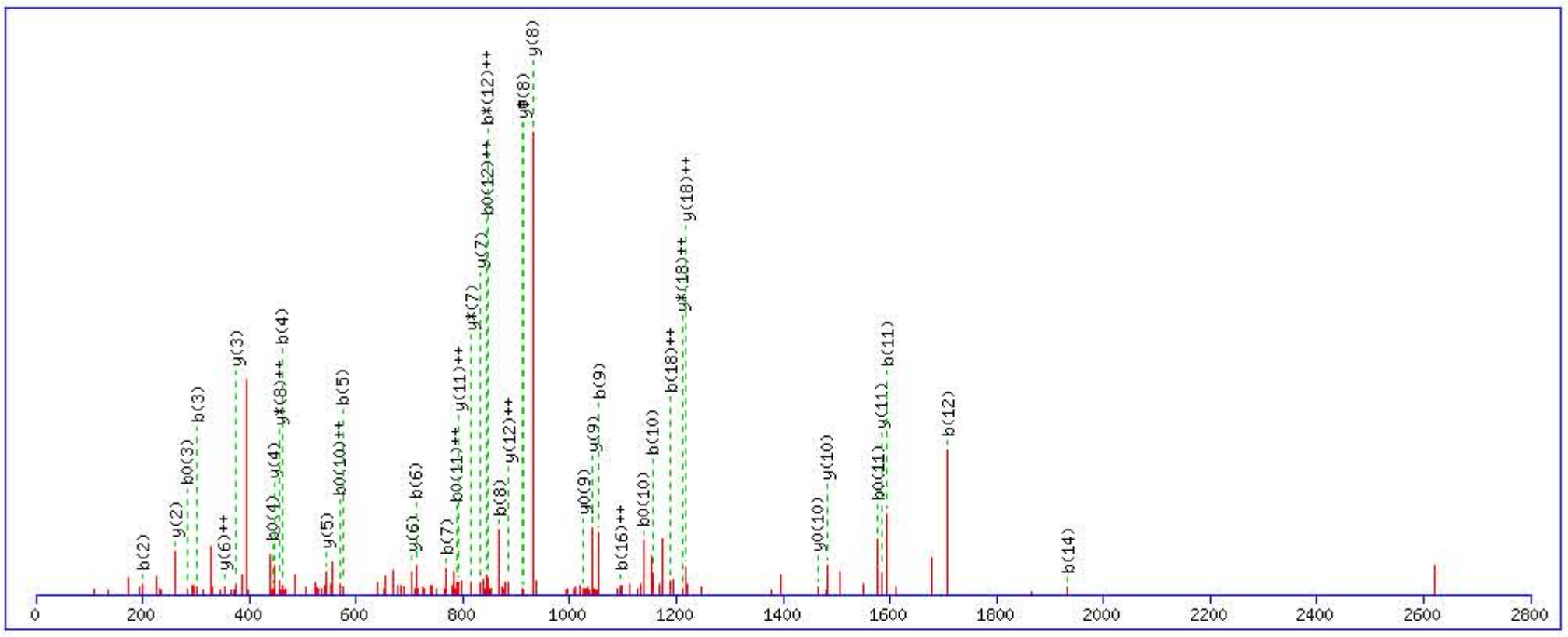
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SITCIHGVWTQLPQCVAIDK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

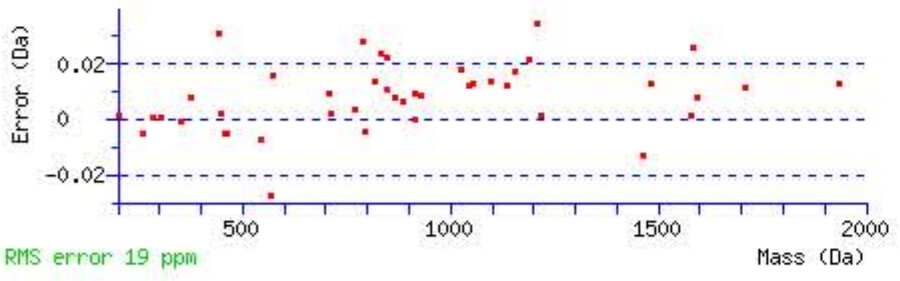
Match to Query 55804: 2636.363742 from(879.795190,3+) rtinseconds(2353) index(22365)
Title: Locus:1.1.1.3201.24 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

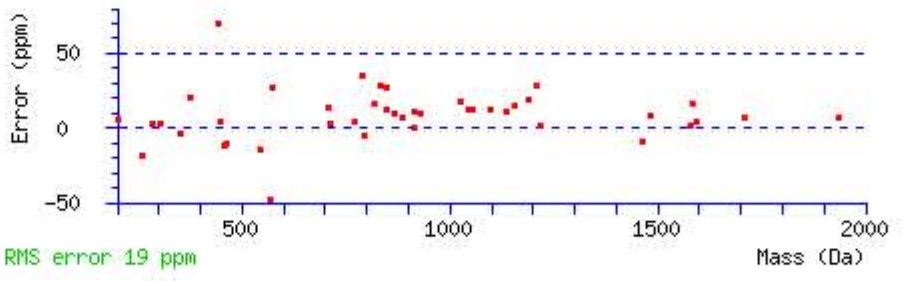
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2636.327728
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q11 : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 1.9e-005
**Matches :** 43/206 fragment ions using 106 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 20 |
| 2 | *201.123368* | 101.065322 | | | 183.112803 | 92.060039 | I | 2550.302958 | 1275.655117 | 2533.276409 | 1267.141842 | 2532.292393 | 1266.649834 | 19 |
| 3 | *302.171047* | 151.589161 | | | 284.160482 | 142.583879 | T | 2437.218894 | 1219.113085 | 2420.192345 | 1210.599810 | 2419.208329 | 1210.107802 | 18 |
| 4 | *462.201696* | 231.604486 | | | 444.191131 | 222.599204 | C | 2336.171215 | 1168.589245 | 2319.144666 | 1160.075971 | 2318.160650 | 1159.583963 | 17 |
| 5 | *575.285760* | 288.146518 | | | 557.275195 | 279.141236 | I | 2176.140566 | 1088.573921 | 2159.114017 | 1080.060646 | 2158.130001 | 1079.568638 | 16 |
| 6 | *712.344672* | 356.675974 | | | 694.334107 | 347.670692 | H | 2063.056502 | 1032.031889 | 2046.029953 | 1023.518614 | 2045.045937 | 1023.026606 | 15 |
| 7 | *769.366136* | 385.186706 | | | 751.355571 | 376.181424 | G | 1925.997590 | 963.502433 | 1908.971041 | 954.989159 | 1907.987025 | 954.497151 | 14 |
| 8 | *868.434550* | 434.720913 | | | 850.423985 | 425.715631 | V | 1868.976126 | 934.991701 | 1851.949577 | 926.478427 | 1850.965561 | 925.986419 | 13 |
| 9 | *1054.513863* | 527.760570 | | | 1036.503298 | 518.755287 | W | 1769.907712 | 885.457494 | 1752.881163 | 876.944220 | 1751.897147 | 876.452211 | 12 |
| 10 | *1155.561542* | 578.284409 | | | 1137.550977 | 569.279127 | T | *1583.828399* | 792.417838 | 1566.801850 | 783.904563 | 1565.817834 | 783.412555 | 11 |
| 11 | *1594.786868* | 797.897072 | 1577.760319 | 789.383798 | 1576.776303 | 788.891790 | Q | *1482.780720* | 741.893998 | 1465.754171 | 733.380724 | 1464.770155 | 732.888715 | 10 |
| 12 | *1707.870932* | 854.439104 | 1690.844383 | 845.925830 | 1689.860367 | 845.433822 | L | *1043.555394* | 522.281335 | 1026.528845 | 513.768060 | 1025.544829 | 513.276052 | 9 |
| 13 | 1804.923696 | 902.965486 | 1787.897147 | 894.452212 | 1786.913131 | 893.960204 | P | *930.471330* | 465.739303 | 913.444781 | 457.226028 | 912.460765 | 456.734020 | 8 |
| 14 | *1932.982274* | 966.994775 | 1915.955725 | 958.481501 | 1914.971709 | 957.989493 | Q | *833.418566* | 417.212921 | 816.392017 | 408.699646 | 815.408001 | 408.207638 | 7 |
| 15 | 2093.012923 | 1047.010099 | 2075.986374 | 1038.496825 | 2075.002358 | 1038.004817 | C | *705.359988* | 353.183632 | 688.333439 | 344.670357 | 687.349423 | 344.178349 | 6 |
| 16 | 2192.081337 | **1096.544306** | 2175.054788 | 1088.031032 | 2174.070772 | 1087.539024 | V | *545.329339* | 273.168308 | 528.302790 | 264.655033 | 527.318774 | 264.163025 | 5 |
| 17 | 2263.118451 | 1132.062863 | 2246.091902 | 1123.549589 | 2245.107886 | 1123.057581 | A | *446.260925* | 223.634101 | 429.234376 | 215.120826 | 428.250360 | 214.628818 | 4 |
| 18 | 2376.202515 | **1188.604895** | 2359.175966 | 1180.091621 | 2358.191950 | 1179.599613 | I | *375.223811* | 188.115543 | 358.197262 | 179.602269 | 357.213246 | 179.110261 | 3 |
| 19 | 2491.229458 | 1246.118367 | 2474.202909 | 1237.605092 | 2473.218893 | 1237.113084 | D | *262.139747* | 131.573511 | 245.113198 | 123.060237 | 244.129182 | 122.568229 | 2 |
| 20 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 53.4 | 2636.327728 | 0.036014 | SITCIHGVWTQLPQCVAIDK |
| 23.2 | 2636.327728 | 0.036014 | SITCIHGVWTQLPQCVAIDK |
| 2.8 | 2636.344574 | 0.019168 | IEGWELTTEPSLTHNSSGLLSPLR |
| 1.1 | 2636.338226 | 0.025516 | QFQSLKEFYETEIPQK |
| 1.0 | 2636.346130 | 0.017612 | QRGAGSNAGASQSTQRK |
| 0.2 | 2636.376648 | -0.012906 | FHTIYRQLHSLCQRR |

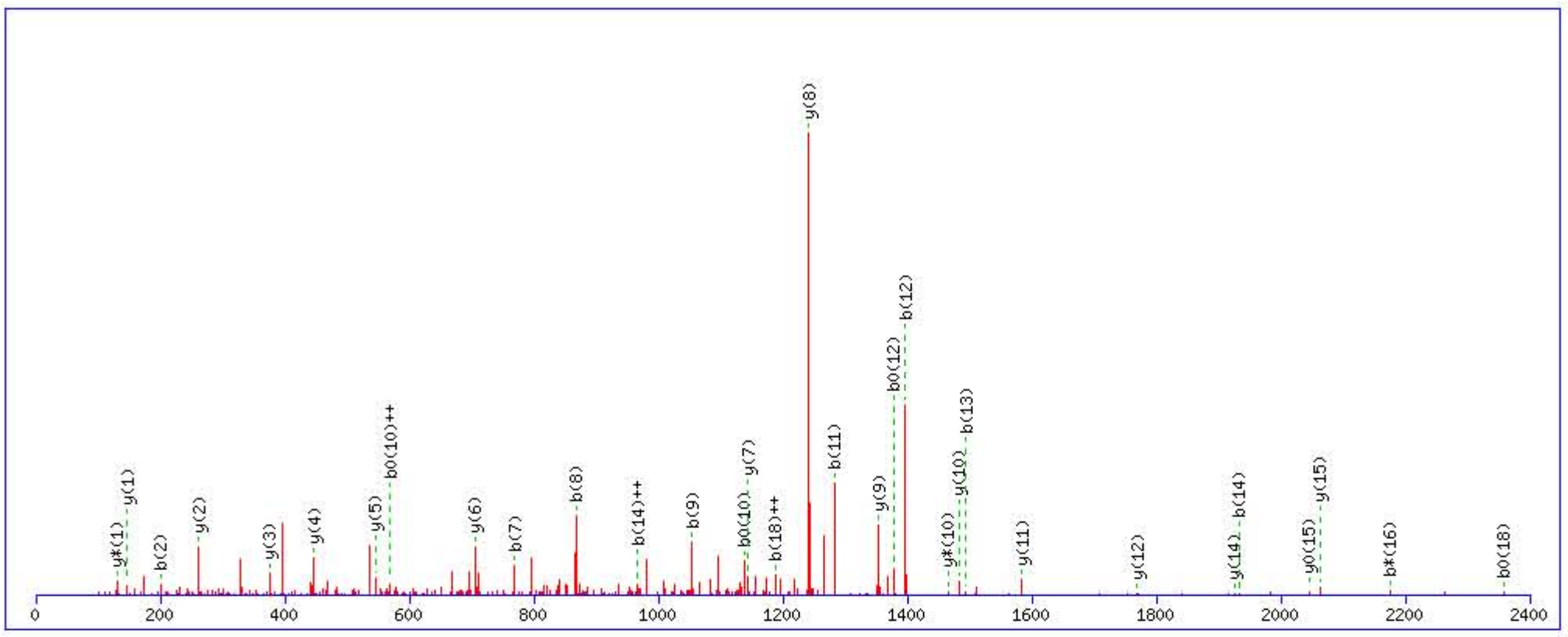
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SITCIHGVWTQLPQCVAIDK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

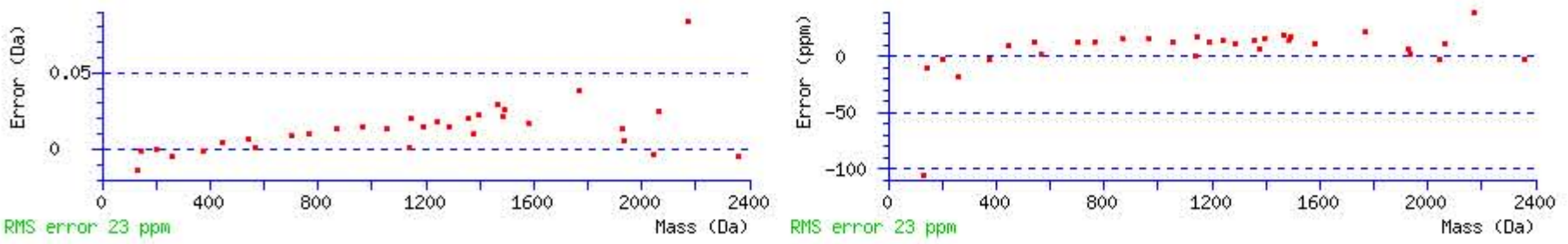
Match to Query 55808: 2636.366502 from(879.796110,3+) rtinseconds(2387) index(22577)
Title: Locus:1.1.1.3213.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2636.327728
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q14 : Biotin:Thermo-21345 (Q)
**Ions Score:** 84 **Expect:** 1.6e-008
**Matches :** 32/206 fragment ions using 57 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 20 |
| 2 | **201.123368** | 101.065322 | | | 183.112803 | 92.060039 | I | 2550.302958 | 1275.655117 | 2533.276409 | 1267.141842 | 2532.292393 | 1266.649834 | 19 |
| 3 | 302.171047 | 151.589161 | | | 284.160482 | 142.583879 | T | 2437.218894 | 1219.113085 | 2420.192345 | 1210.599810 | 2419.208329 | 1210.107802 | 18 |
| 4 | 462.201696 | 231.604486 | | | 444.191131 | 222.599204 | C | 2336.171215 | 1168.589245 | 2319.144666 | 1160.075971 | 2318.160650 | 1159.583963 | 17 |
| 5 | 575.285760 | 288.146518 | | | 557.275195 | 279.141236 | I | 2176.140566 | 1088.573921 | 2159.114017 | 1080.060646 | 2158.130001 | 1079.568638 | 16 |
| 6 | 712.344672 | 356.675974 | | | 694.334107 | 347.670692 | H | *2063.056502* | 1032.031889 | 2046.029953 | 1023.518614 | 2045.045937 | 1023.026606 | 15 |
| 7 | **769.366136** | 385.186706 | | | 751.355571 | 376.181424 | G | *1925.997590* | 963.502433 | 1908.971041 | 954.989159 | 1907.987025 | 954.497151 | 14 |
| 8 | **868.434550** | 434.720913 | | | 850.423985 | 425.715631 | V | 1868.976126 | 934.991701 | 1851.949577 | 926.478427 | 1850.965561 | 925.986419 | 13 |
| 9 | **1054.513863** | 527.760570 | | | 1036.503298 | 518.755287 | W | *1769.907712* | 885.457494 | 1752.881163 | 876.944220 | 1751.897147 | 876.452211 | 12 |
| 10 | 1155.561542 | 578.284409 | | | 1137.550977 | 569.279127 | T | *1583.828399* | 792.417838 | 1566.801850 | 783.904563 | 1565.817834 | 783.412555 | 11 |
| 11 | **1283.620120** | 642.313698 | 1266.593571 | 633.800424 | 1265.609555 | 633.308416 | Q | *1482.780720* | 741.893998 | 1465.754171 | 733.380724 | 1464.770155 | 732.888715 | 10 |
| 12 | **1396.704184** | 698.855730 | 1379.677635 | 690.342456 | 1378.693619 | 689.850448 | L | *1354.722142* | 677.864709 | 1337.695593 | 669.351434 | 1336.711577 | 668.859426 | 9 |
| 13 | **1493.756948** | 747.382112 | 1476.730399 | 738.868838 | 1475.746383 | 738.376830 | P | *1241.638078* | 621.322677 | 1224.611529 | 612.809403 | 1223.627513 | 612.317394 | 8 |
| 14 | **1932.982274** | **966.994775** | 1915.955725 | 958.481501 | 1914.971709 | 957.989493 | Q | *1144.585314* | 572.796295 | 1127.558765 | 564.283021 | 1126.574749 | 563.791012 | 7 |
| 15 | 2093.012923 | 1047.010099 | 2075.986374 | 1038.496825 | 2075.002358 | 1038.004817 | C | *705.359988* | 353.183632 | 688.333439 | 344.670357 | 687.349423 | 344.178349 | 6 |
| 16 | 2192.081337 | 1096.544306 | 2175.054788 | 1088.031032 | 2174.070772 | 1087.539024 | V | *545.329339* | 273.168308 | 528.302790 | 264.655033 | 527.318774 | 264.163025 | 5 |
| 17 | 2263.118451 | 1132.062863 | 2246.091902 | 1123.549589 | 2245.107886 | 1123.057581 | A | *446.260925* | 223.634101 | 429.234376 | 215.120826 | 428.250360 | 214.628818 | 4 |
| 18 | 2376.202515 | **1188.604895** | 2359.175966 | 1180.091621 | 2358.191950 | 1179.599613 | I | *375.223811* | 188.115543 | 358.197262 | 179.602269 | 357.213246 | 179.110261 | 3 |
| 19 | 2491.229458 | 1246.118367 | 2474.202909 | 1237.605092 | 2473.218893 | 1237.113084 | D | *262.139747* | 131.573511 | 245.113198 | 123.060237 | 244.129182 | 122.568229 | 2 |
| 20 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 84.1 | 2636.327728 | 0.038774 | SITCIHGVWTQLPQCVAIDK |
| 43.5 | 2636.327728 | 0.038774 | SITCIHGVWTQLPQCVAIDK |
| 1.1 | 2636.366592 | -0.000090 | ASKTTDLRIPASVCTMFNVLVDAK |

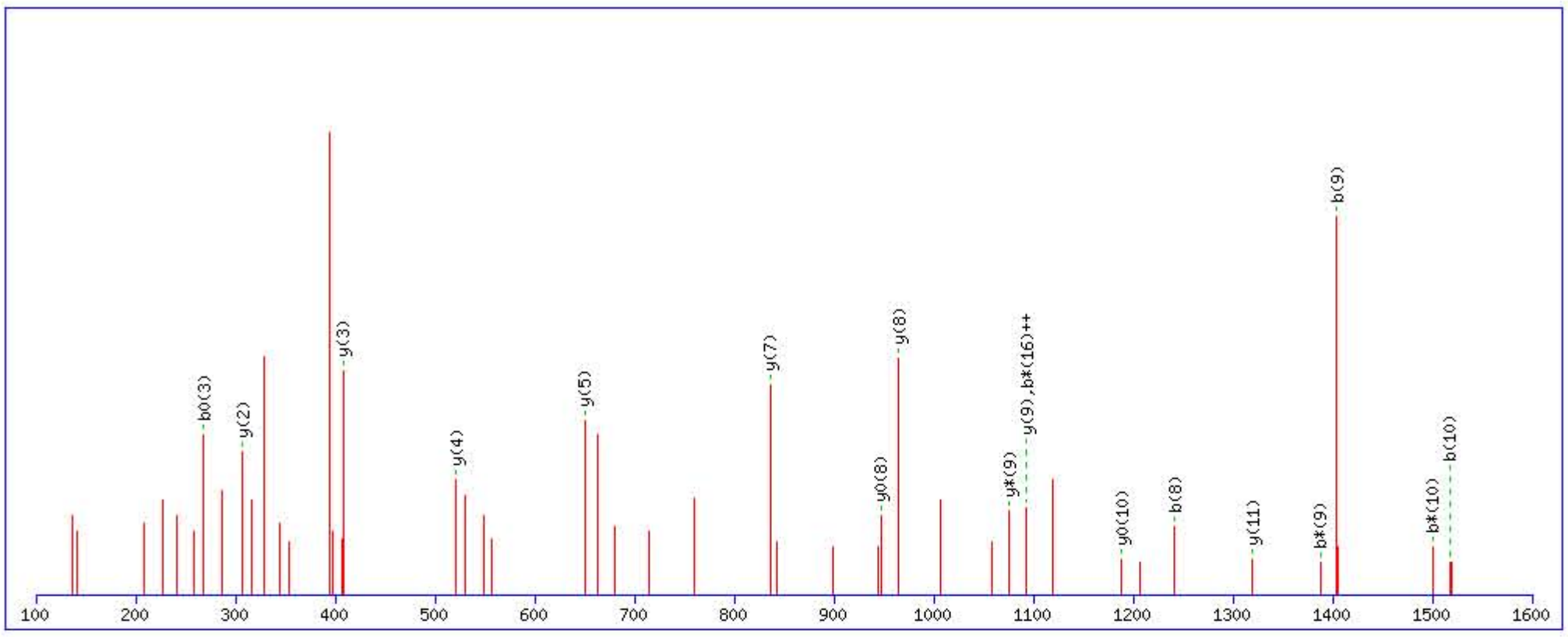
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VSVLCQENYLIQEGEEITCK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

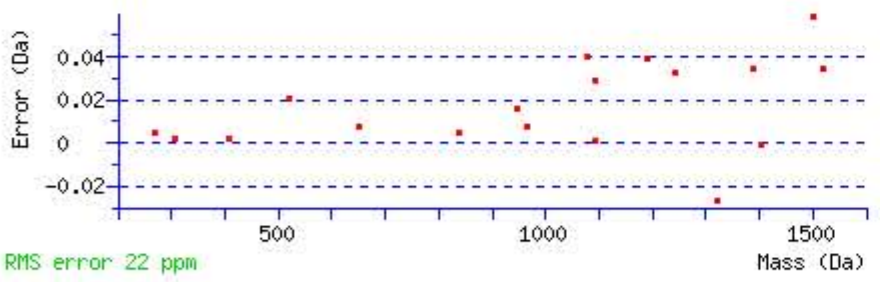
Match to Query 56621: 2722.328776 from(681.589470,4+) rtinseconds(2757) index(24785)
Title: Locus:1.1.1.3341.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

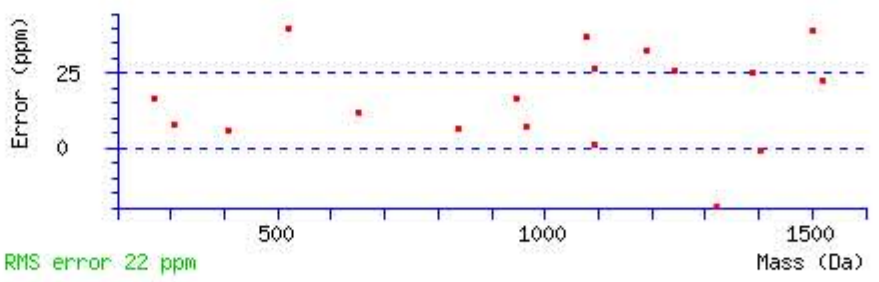
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2722.301590
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.0021
**Matches** : 18/212 fragment ions using 36 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 20 |
| 2 | 187.107718 | 94.057497 | | | 169.097153 | 85.052214 | S | 2624.240475 | 1312.623875 | 2607.213926 | 1304.110601 | 2606.229910 | 1303.618593 | 19 |
| 3 | 286.176132 | 143.591704 | | | 268.165567 | 134.586422 | V | 2537.208447 | 1269.107861 | 2520.181898 | 1260.594587 | 2519.197882 | 1260.102579 | 18 |
| 4 | 399.260196 | 200.133736 | | | 381.249631 | 191.128454 | L | 2438.140033 | 1219.573654 | 2421.113484 | 1211.060380 | 2420.129468 | 1210.568372 | 17 |
| 5 | 559.290845 | 280.149061 | | | 541.280280 | 271.143778 | C | 2325.055969 | 1163.031622 | 2308.029420 | 1154.518348 | 2307.045404 | 1154.026340 | 16 |
| 6 | 998.516171 | 499.761724 | 981.489622 | 491.248449 | 980.505606 | 490.756441 | Q | 2165.025320 | 1083.016298 | 2147.998771 | 1074.503023 | 2147.014755 | 1074.011015 | 15 |
| 7 | 1127.558764 | 564.283020 | 1110.532215 | 555.769746 | 1109.548199 | 555.277738 | E | 1725.799994 | 863.403635 | 1708.773445 | 854.890361 | 1707.789429 | 854.398353 | 14 |
| 8 | 1241.601691 | 621.304484 | 1224.575142 | 612.791209 | 1223.591126 | 612.299201 | N | 1596.757401 | 798.882339 | 1579.730852 | 790.369064 | 1578.746836 | 789.877056 | 13 |
| 9 | 1404.665020 | 702.836148 | 1387.638471 | 694.322874 | 1386.654455 | 693.830866 | Y | 1482.714474 | 741.860875 | 1465.687925 | 733.347601 | 1464.703909 | 732.855593 | 12 |
| 10 | 1517.749084 | 759.378180 | 1500.722535 | 750.864906 | 1499.738519 | 750.372898 | L | *1319.651145* | 660.329211 | 1302.624596 | 651.815936 | 1301.640580 | 651.323928 | 11 |
| 11 | 1630.833148 | 815.920212 | 1613.806599 | 807.406938 | 1612.822583 | 806.914929 | I | 1206.567081 | 603.787179 | 1189.540532 | 595.273904 | 1188.556516 | 594.781896 | 10 |
| 12 | 1758.891726 | 879.949501 | 1741.865177 | 871.436227 | 1740.881161 | 870.944219 | Q | *1093.483017* | 547.245147 | 1076.456468 | 538.731872 | 1075.472452 | 538.239864 | 9 |
| 13 | 1887.934319 | 944.470798 | 1870.907770 | 935.957523 | 1869.923754 | 935.465515 | E | *965.424439* | 483.215858 | 948.397890 | 474.702583 | 947.413874 | 474.210575 | 8 |
| 14 | 1944.955783 | 972.981530 | 1927.929234 | 964.468255 | 1926.945218 | 963.976247 | G | *836.381846* | 418.694561 | 819.355297 | 410.181287 | 818.371281 | 409.689279 | 7 |
| 15 | 2073.998376 | 1037.502826 | 2056.971827 | 1028.989551 | 2055.987811 | 1028.497543 | E | 779.360382 | 390.183829 | 762.333833 | 381.670555 | 761.349817 | 381.178547 | 6 |
| 16 | 2203.040969 | 1102.024123 | 2186.014420 | 1093.510848 | 2185.030404 | 1093.018840 | E | *650.317789* | 325.662533 | 633.291240 | 317.149258 | 632.307224 | 316.657250 | 5 |
| 17 | 2316.125033 | 1158.566155 | 2299.098484 | 1150.052880 | 2298.114468 | 1149.560872 | I | *521.275196* | 261.141236 | 504.248647 | 252.627961 | 503.264631 | 252.135953 | 4 |
| 18 | 2417.172712 | 1209.089994 | 2400.146163 | 1200.576719 | 2399.162147 | 1200.084711 | T | *408.191132* | 204.599204 | 391.164583 | 196.085929 | 390.180567 | 195.593921 | 3 |
| 19 | 2577.203361 | 1289.105318 | 2560.176812 | 1280.592044 | 2559.192796 | 1280.100036 | C | *307.143453* | 154.075364 | 290.116904 | 145.562090 | | | 2 |
| 20 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.7 | 2722.301590 | 0.027186 | VSVLCQENYLIQEGEEITCK |
| 30.1 | 2722.301590 | 0.027186 | VSVLCQENYLIQEGEEITCK |
| 3.0 | 2722.309433 | 0.019343 | GMNWLANLYEQGINGILADEMGLGK |

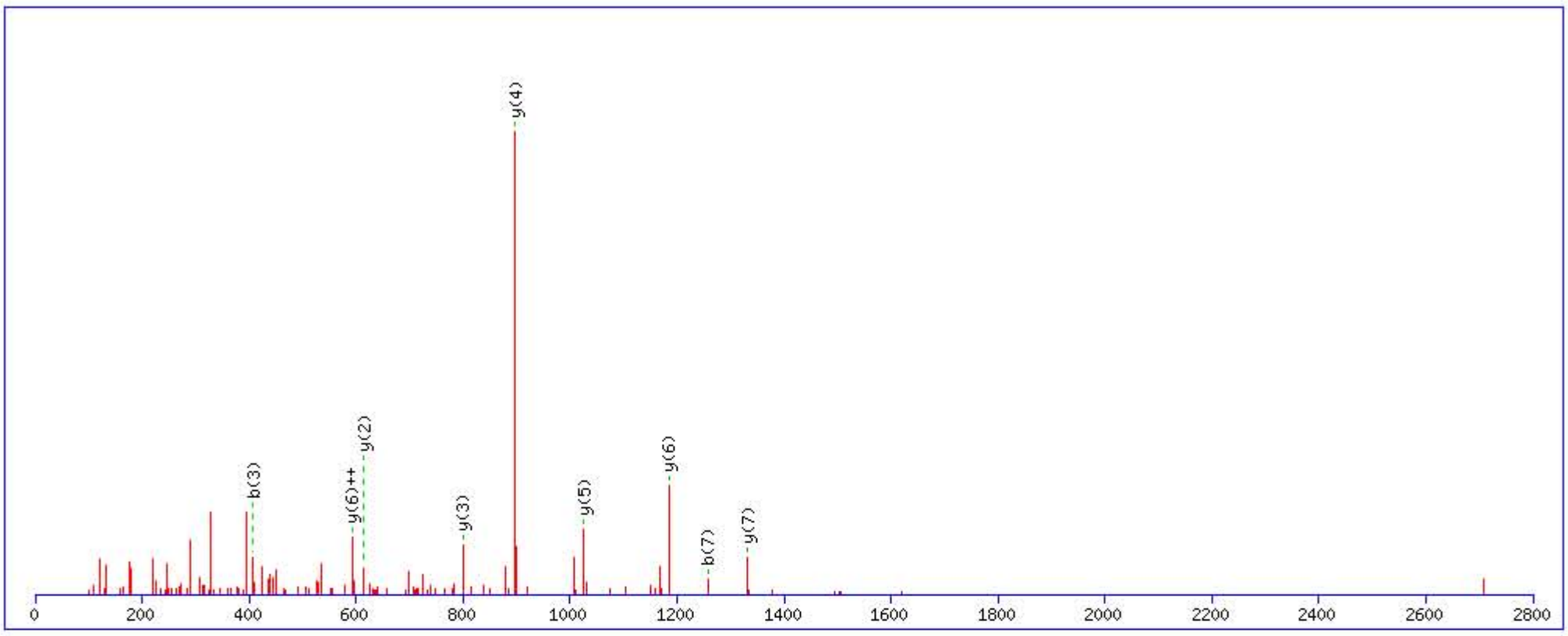
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VFCQPWQR**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

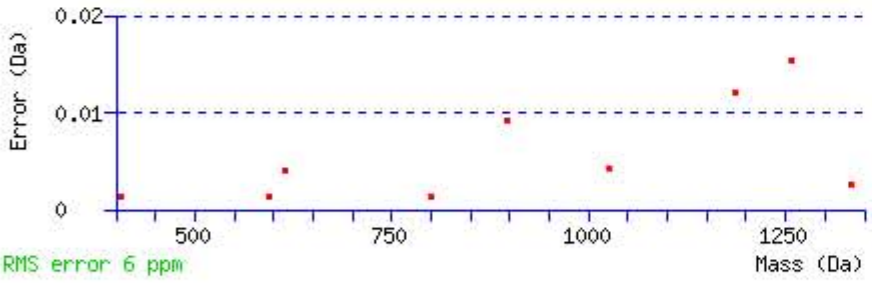
Match to Query 29075: 1430.703788 from(716.359170,2+) rtinseconds(2034) index(66613)
Title: Locus:1.1.1.1983.9 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

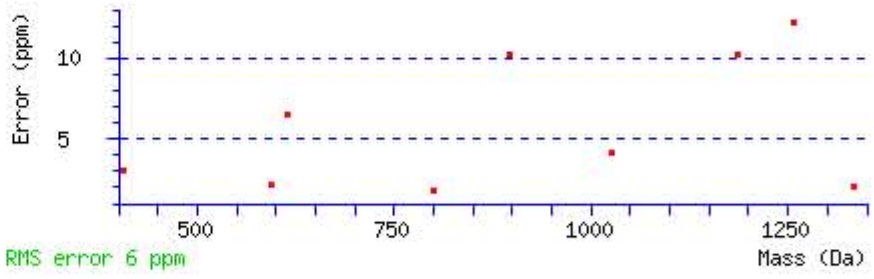
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1430.695145
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 43 **Expect:** 0.00032
**Matches :** 9/50 fragment ions using 13 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | V | | | | | 8 |
| 2 | 247.144104 | 124.075690 | | | F | *1332.633996* | 666.820636 | 1315.607447 | 658.307362 | 7 |
| 3 | **407.174753** | 204.091014 | | | C | *1185.565582* | 593.286429 | 1168.539033 | 584.773155 | 6 |
| 4 | 535.233331 | 268.120304 | 518.206782 | 259.607029 | Q | *1025.534933* | 513.271105 | 1008.508384 | 504.757830 | 5 |
| 5 | 632.286095 | 316.646686 | 615.259546 | 308.133411 | P | *897.476355* | 449.241816 | 880.449806 | 440.728541 | 4 |
| 6 | 818.365408 | 409.686342 | 801.338859 | 401.173068 | W | *800.423591* | 400.715434 | 783.397042 | 392.202159 | 3 |
| 7 | **1257.590734** | 629.299005 | 1240.564185 | 620.785731 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | 2 |
| 8 | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 43.2 | 1430.695145 | 0.008643 | VFCQPWQR |
| 7.3 | 1430.695145 | 0.008643 | VFCQPWQR |
| 5.5 | 1430.700989 | 0.002799 | NMPQADAMVLVAR |
| 3.4 | 1430.693619 | 0.010169 | QLQTLSMPGGGGNR |
| 0.1 | 1430.711319 | -0.007531 | RAKAEDENETLR |

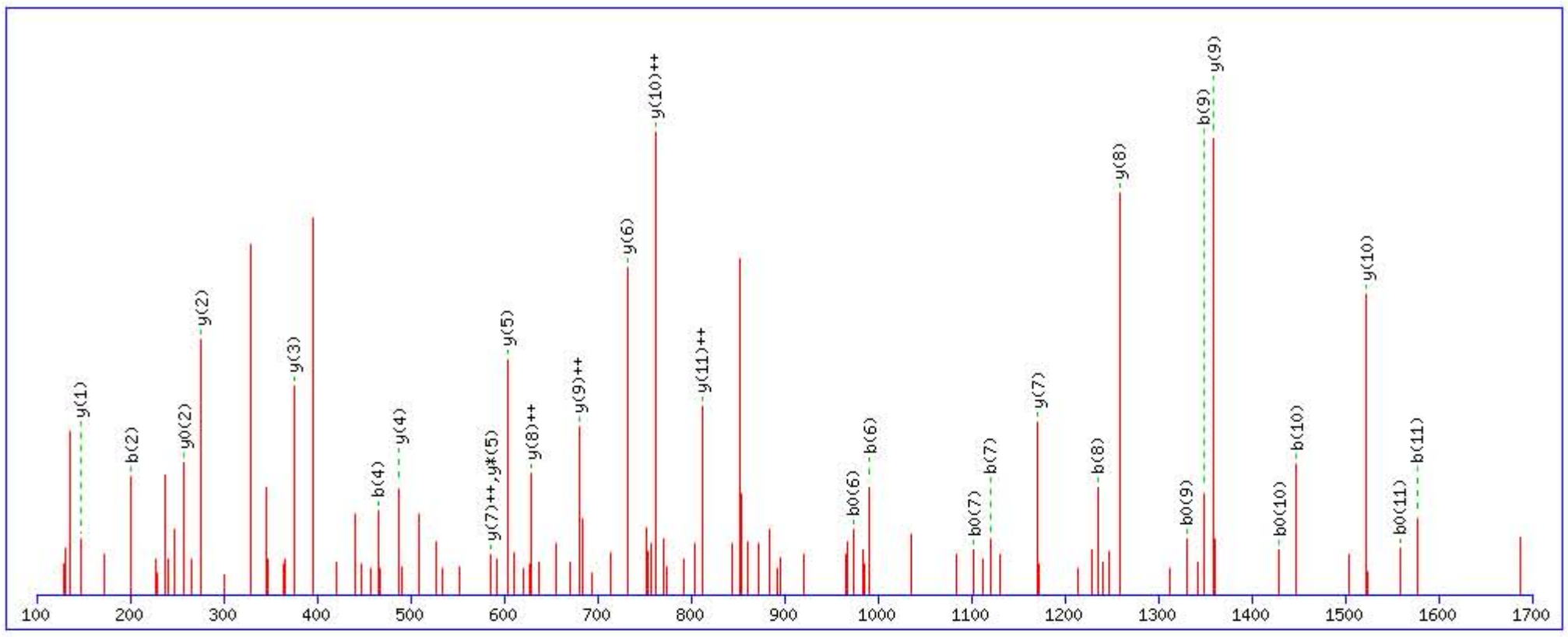
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VTYTSQEDLVEK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

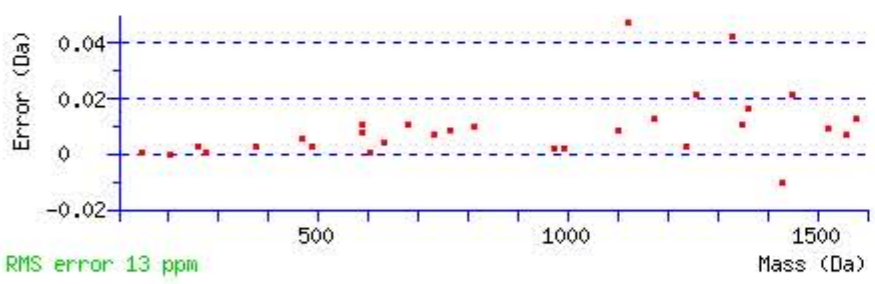
Match to Query 38440: 1721.870868 from(861.942710,2+) rtinseconds(1879) index(65521)
Title: Locus:1.1.1.1929.26 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

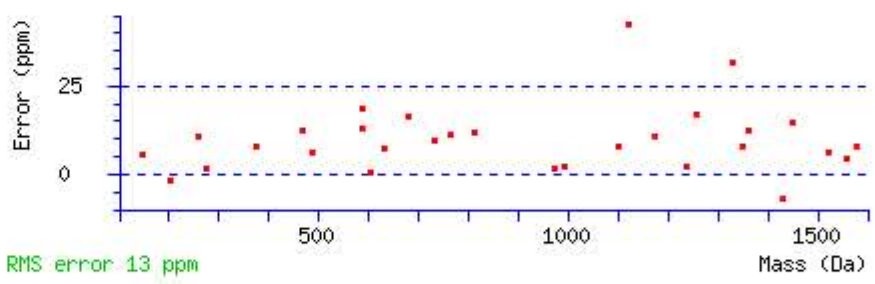
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1721.854584
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 73 **Expect:** 1.8e-006
**Matches :** 30/118 fragment ions using 45 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 12 |
| 2 | **201.123369** | 101.065322 | | | 183.112804 | 92.060040 | T | 1623.793452 | 812.400364 | 1606.766903 | 803.887090 | 1605.782887 | 803.395081 | 11 |
| 3 | 364.186698 | 182.596987 | | | 346.176133 | 173.591705 | Y | *1522.745773* | 761.876524 | 1505.719224 | 753.363250 | 1504.735208 | 752.871242 | 10 |
| 4 | **465.234377** | 233.120827 | | | 447.223812 | 224.115544 | T | *1359.682444* | 680.344860 | 1342.655895 | 671.831585 | 1341.671879 | 671.339577 | 9 |
| 5 | 552.266405 | 276.636841 | | | 534.255840 | 267.631558 | S | *1258.634765* | 629.821021 | 1241.608216 | 621.307746 | 1240.624200 | 620.815738 | 8 |
| 6 | **991.491731** | 496.249504 | 974.465182 | 487.736229 | 973.481166 | 487.244221 | Q | *1171.602737* | 586.305006 | 1154.576188 | 577.791732 | 1153.592172 | 577.299724 | 7 |
| 7 | **1120.534324** | 560.770800 | 1103.507775 | 552.257526 | 1102.523759 | 551.765517 | E | *732.377411* | 366.692343 | 715.350862 | 358.179069 | 714.366846 | 357.687061 | 6 |
| 8 | **1235.561267** | 618.284272 | 1218.534718 | 609.770997 | 1217.550702 | 609.278989 | D | *603.334818* | 302.171047 | 586.308269 | 293.657773 | 585.324253 | 293.165765 | 5 |
| 9 | **1348.645331** | 674.826303 | 1331.618782 | 666.313029 | 1330.634766 | 665.821021 | L | *488.307875* | 244.657575 | 471.281326 | 236.144301 | 470.297310 | 235.652293 | 4 |
| 10 | **1447.713745** | 724.360511 | 1430.687196 | 715.847236 | 1429.703180 | 715.355228 | V | *375.223811* | 188.115543 | 358.197262 | 179.602269 | 357.213246 | 179.110261 | 3 |
| 11 | **1576.756338** | 788.881807 | 1559.729789 | 780.368533 | 1558.745773 | 779.876524 | E | *276.155397* | 138.581336 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 12 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 72.7 | 1721.854584 | 0.016284 | VTYTSQEDLVEK |
| 10.7 | 1721.883560 | -0.012692 | SLPPADISDIIHSTEK |
| 7.5 | 1721.858414 | 0.012454 | DRVYQVTEQQISEK |
| 3.2 | 1721.858414 | 0.012454 | ESEKPVDSLHPGAGTAK |
| 3.1 | 1721.847122 | 0.023746 | EAYDQKIAEEEAKAK |
| 2.7 | 1721.850510 | 0.020358 | LLEAMGTSKKNEEEK |
| 2.5 | 1721.888275 | -0.017407 | DVMRETFRNLASVGK |
| 2.0 | 1721.869186 | 0.001682 | CDVTLTLKELQQMK |
| 1.7 | 1721.859283 | 0.011585 | SLRTMEQQFQK |

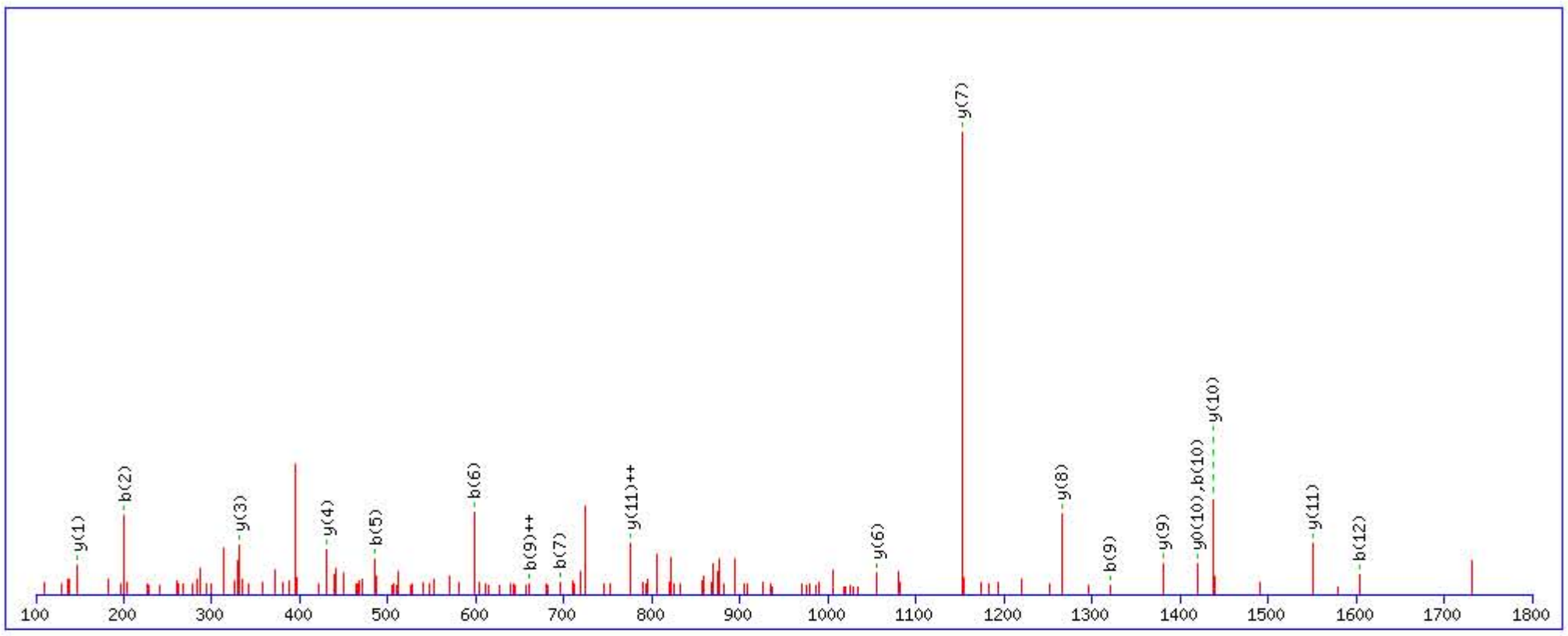
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AQLGDLPWQVAIK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

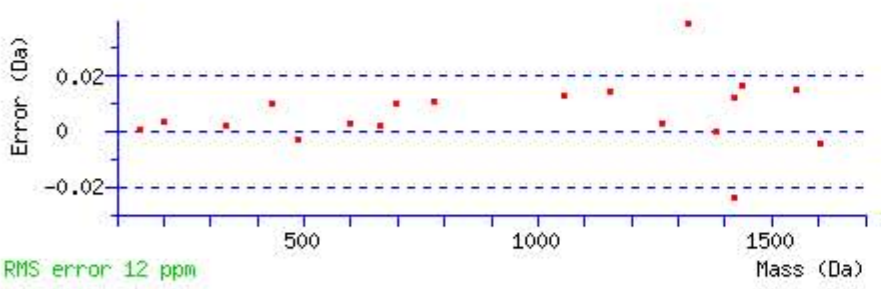
Match to Query 39079: 1748.990488 from(875.502520,2+) rtinseconds(2656) index(70203)
Title: Locus:1.1.1.2200.9 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

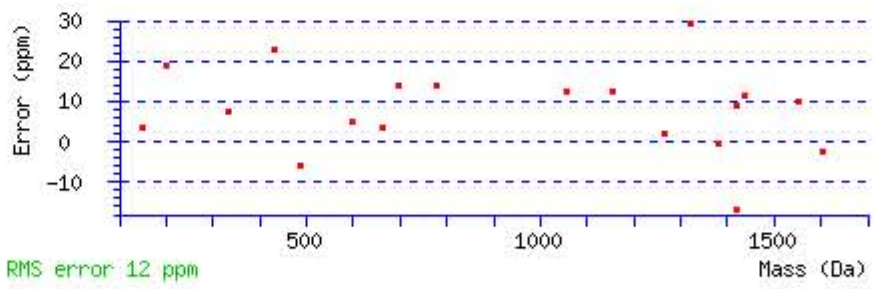
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1748.964737
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 55 **Expect:** 1.4e-005
**Matches :** 19/118 fragment ions using 31 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 13 |
| 2 | **200.102968** | 100.555122 | 183.076419 | 92.041848 | | | Q | 1678.934912 | 839.971094 | 1661.908363 | 831.457820 | 1660.924347 | 830.965812 | 12 |
| 3 | 313.187032 | 157.097154 | 296.160483 | 148.583879 | | | L | *1550.876334* | 775.941805 | 1533.849785 | 767.428531 | 1532.865769 | 766.936523 | 11 |
| 4 | 370.208496 | 185.607886 | 353.181947 | 177.094611 | | | G | *1437.792270* | 719.399773 | 1420.765721 | 710.886499 | 1419.781705 | 710.394491 | 10 |
| 5 | **485.235439** | 243.121357 | 468.208890 | 234.608083 | 467.224874 | 234.116075 | D | *1380.770806* | 690.889041 | 1363.744257 | 682.375767 | 1362.760241 | 681.883759 | 9 |
| 6 | **598.319503** | 299.663390 | 581.292954 | 291.150115 | 580.308938 | 290.658107 | L | *1265.743863* | 633.375570 | 1248.717314 | 624.862295 | | | 8 |
| 7 | **695.372267** | 348.189772 | 678.345718 | 339.676497 | 677.361702 | 339.184489 | P | *1152.659799* | 576.833538 | 1135.633250 | 568.320263 | | | 7 |
| 8 | 881.451580 | 441.229428 | 864.425031 | 432.716154 | 863.441015 | 432.224146 | W | *1055.607035* | 528.307156 | 1038.580486 | 519.793881 | | | 6 |
| 9 | **1320.676906** | 660.842091 | 1303.650357 | 652.328817 | 1302.666341 | 651.836809 | Q | 869.527722 | 435.267499 | 852.501173 | 426.754225 | | | 5 |
| 10 | **1419.745320** | 710.376298 | 1402.718771 | 701.863024 | 1401.734755 | 701.371016 | V | *430.302396* | 215.654836 | 413.275847 | 207.141561 | | | 4 |
| 11 | 1490.782434 | 745.894855 | 1473.755885 | 737.381581 | 1472.771869 | 736.889573 | A | *331.233982* | 166.120629 | 314.207433 | 157.607354 | | | 3 |
| 12 | **1603.866498** | 802.436887 | 1586.839949 | 793.923613 | 1585.855933 | 793.431605 | I | 260.196868 | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 13 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 54.8 | 1748.964737 | 0.025751 | AQLGDLPWQVAIK |
| 5.6 | 1748.964737 | 0.025751 | AQLGDLPWQVAIK |
| 2.9 | 1748.978500 | 0.011988 | VSAPGVQGDVKGPQVALK |
| 1.1 | 1748.978439 | 0.012049 | YARKISGTTALQEALK |

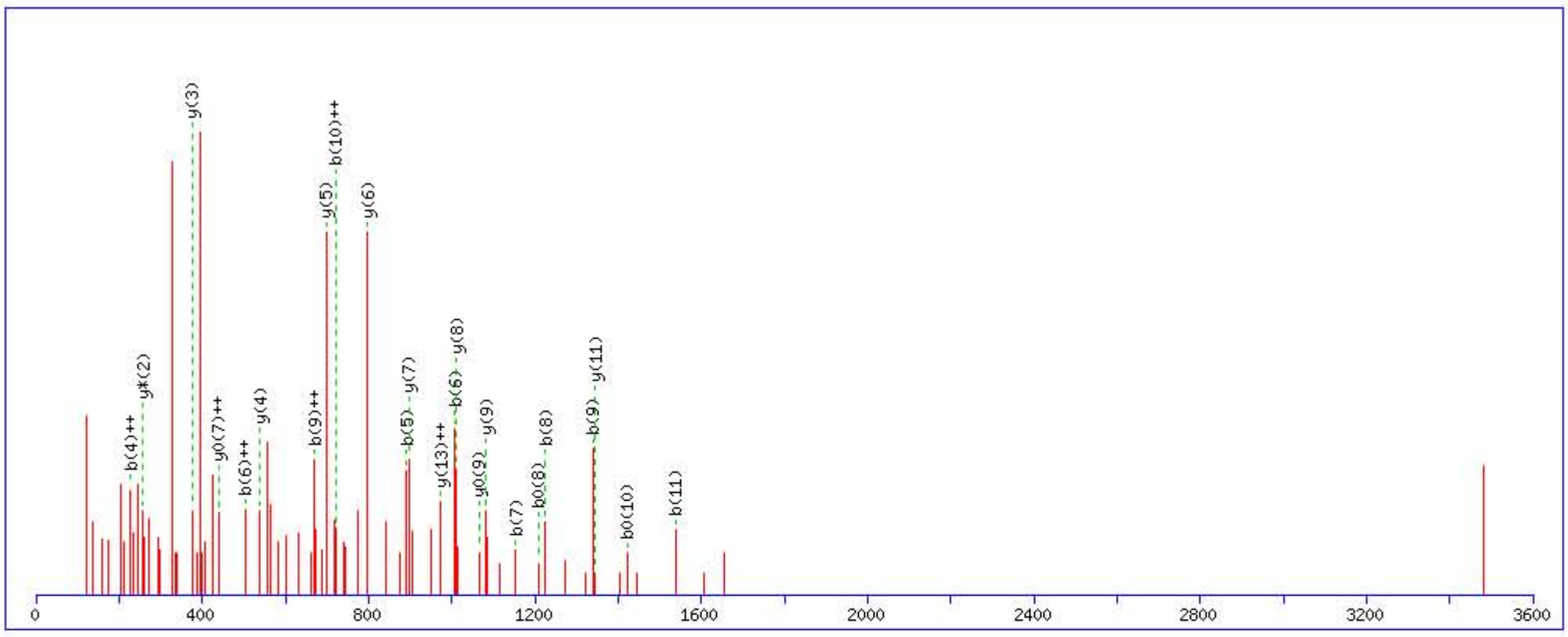
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TMGYQDFADVVCYTQK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

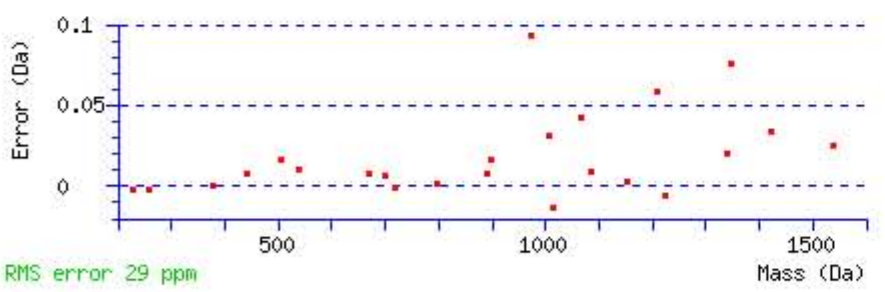
Match to Query 49227: 2236.024542 from(746.348790,3+) rtinseconds(2514) index(69413)
Title: Locus:1.1.1.2150.17 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

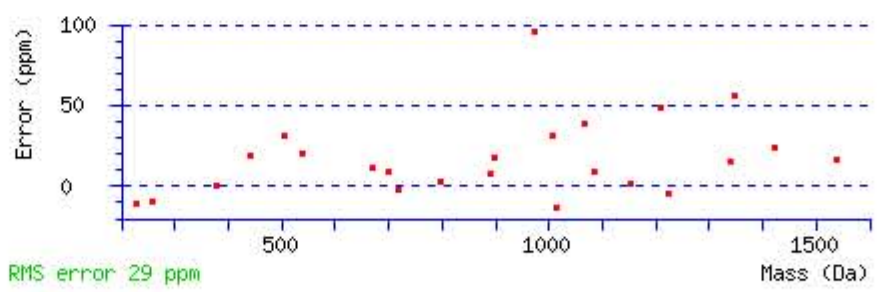
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2236.000305
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 36 **Expect:** 0.0029
**Matches :** 24/168 fragment ions using 42 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 16 |
| 2 | 233.095440 | 117.051358 | | | 215.084875 | 108.046076 | M | 2135.959885 | 1068.483580 | 2118.933336 | 1059.970306 | 2117.949320 | 1059.478298 | 15 |
| 3 | 290.116904 | 145.562090 | | | 272.106339 | 136.556807 | G | 2004.919400 | 1002.963338 | 1987.892851 | 994.450064 | 1986.908835 | 993.958056 | 14 |
| 4 | 453.180233 | 227.093754 | | | 435.169668 | 218.088472 | Y | 1947.897936 | 974.452606 | 1930.871387 | 965.939332 | 1929.887371 | 965.447324 | 13 |
| 5 | 892.405559 | 446.706418 | 875.379010 | 438.193143 | 874.394994 | 437.701135 | Q | 1784.834607 | 892.920942 | 1767.808058 | 884.407667 | 1766.824042 | 883.915659 | 12 |
| 6 | 1007.432502 | 504.219889 | 990.405953 | 495.706615 | 989.421937 | 495.214607 | D | *1345.609281* | 673.308279 | 1328.582732 | 664.795004 | 1327.598716 | 664.302996 | 11 |
| 7 | 1154.500916 | 577.754096 | 1137.474367 | 569.240822 | 1136.490351 | 568.748813 | F | 1230.582338 | 615.794807 | 1213.555789 | 607.281533 | 1212.571773 | 606.789525 | 10 |
| 8 | 1225.538030 | 613.272653 | 1208.511481 | 604.759379 | 1207.527465 | 604.267370 | A | *1083.513924* | 542.260600 | 1066.487375 | 533.747326 | 1065.503359 | 533.255318 | 9 |
| 9 | 1340.564973 | 670.786125 | 1323.538424 | 662.272850 | 1322.554408 | 661.780842 | D | *1012.476810* | 506.742043 | 995.450261 | 498.228769 | 994.466245 | 497.736761 | 8 |
| 10 | 1439.633387 | 720.320332 | 1422.606838 | 711.807057 | 1421.622822 | 711.315049 | V | *897.449867* | 449.228572 | 880.423318 | 440.715297 | 879.439302 | 440.223289 | 7 |
| 11 | 1538.701801 | 769.854539 | 1521.675252 | 761.341264 | 1520.691236 | 760.849256 | V | *798.381453* | 399.694365 | 781.354904 | 391.181090 | 780.370888 | 390.689082 | 6 |
| 12 | 1698.732450 | 849.869863 | 1681.705901 | 841.356589 | 1680.721885 | 840.864581 | C | *699.313039* | 350.160158 | 682.286490 | 341.646883 | 681.302474 | 341.154875 | 5 |
| 13 | 1861.795779 | 931.401528 | 1844.769230 | 922.888253 | 1843.785214 | 922.396245 | Y | *539.282390* | 270.144833 | 522.255841 | 261.631559 | 521.271825 | 261.139551 | 4 |
| 14 | 1962.843458 | 981.925367 | 1945.816909 | 973.412093 | 1944.832893 | 972.920085 | T | *376.219061* | 188.613168 | 359.192512 | 180.099894 | 358.208496 | 179.607886 | 3 |
| 15 | 2090.902036 | 1045.954656 | 2073.875487 | 1037.441381 | 2072.891471 | 1036.949373 | Q | 275.171382 | 138.089329 | 258.144833 | 129.576054 | | | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 36.1 | 2236.000305 | 0.024237 | TMGYQDFADVVCYTQK |

**Mascot:** http://www.matrixscience.com/

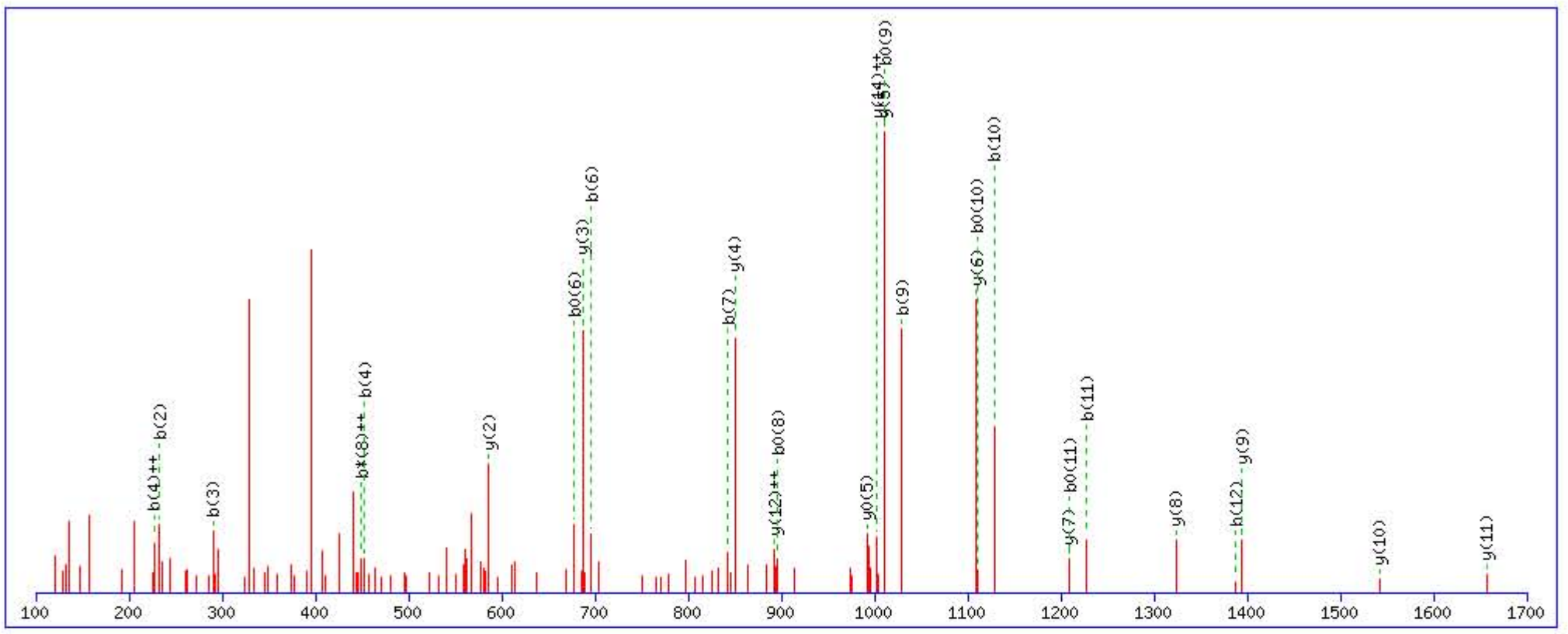
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TMGYQDFADVVCYTQK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

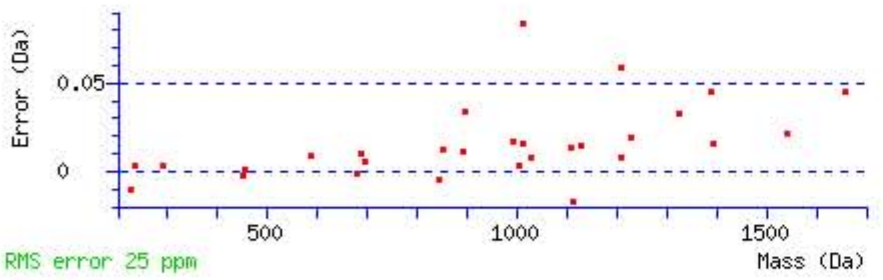
Match to Query 49229: 2236.031442 from(746.351090,3+) rtinseconds(2574) index(69653)
Title: Locus:1.1.1.2172.8 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

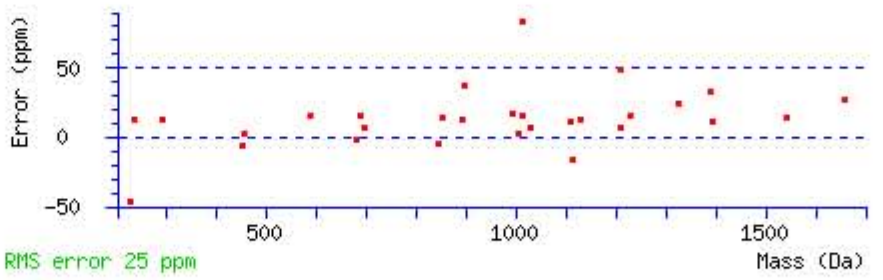
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2236.000305
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q15 : Biotin:Thermo-21345 (Q)
**Ions Score:** 62 **Expect:** 7.2e-006
**Matches :** 29/168 fragment ions using 49 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 16 |
| 2 | *233.095440* | 117.051358 | | | 215.084875 | 108.046076 | M | 2135.959885 | 1068.483580 | 2118.933336 | 1059.970306 | 2117.949320 | 1059.478298 | 15 |
| 3 | *290.116904* | 145.562090 | | | 272.106339 | 136.556807 | G | 2004.919400 | 1002.963338 | 1987.892851 | 994.450064 | 1986.908835 | 993.958056 | 14 |
| 4 | *453.180233* | 227.093754 | | | 435.169668 | 218.088472 | Y | 1947.897936 | 974.452606 | 1930.871387 | 965.939332 | 1929.887371 | 965.447324 | 13 |
| 5 | 581.238811 | 291.123044 | 564.212262 | 282.609769 | 563.228246 | 282.117761 | Q | 1784.834607 | 892.920942 | 1767.808058 | 884.407667 | 1766.824042 | 883.915659 | 12 |
| 6 | *696.265754* | 348.636515 | 679.239205 | 340.123241 | 678.255189 | 339.631233 | D | *1656.776029* | 828.891653 | 1639.749480 | 820.378378 | 1638.765464 | 819.886370 | 11 |
| 7 | *843.334168* | 422.170722 | 826.307619 | 413.657447 | 825.323603 | 413.165439 | F | *1541.749086* | 771.378181 | 1524.722537 | 762.864907 | 1523.738521 | 762.372899 | 10 |
| 8 | 914.371282 | 457.689279 | 897.344733 | 449.176004 | 896.360717 | 448.683996 | A | *1394.680672* | 697.843974 | 1377.654123 | 689.330700 | 1376.670107 | 688.838692 | 9 |
| 9 | *1029.398225* | 515.202750 | 1012.371676 | 506.689476 | 1011.387660 | 506.197468 | D | *1323.643558* | 662.325417 | 1306.617009 | 653.812143 | 1305.632993 | 653.320135 | 8 |
| 10 | *1128.466639* | 564.736958 | 1111.440090 | 556.223683 | 1110.456074 | 555.731675 | V | *1208.616615* | 604.811946 | 1191.590066 | 596.298671 | 1190.606050 | 595.806663 | 7 |
| 11 | *1227.535053* | 614.271165 | 1210.508504 | 605.757890 | 1209.524488 | 605.265882 | V | *1109.548201* | 555.277739 | 1092.521652 | 546.764464 | 1091.537636 | 546.272456 | 6 |
| 12 | *1387.565702* | 694.286489 | 1370.539153 | 685.773215 | 1369.555137 | 685.281207 | C | *1010.479787* | 505.743532 | 993.453238 | 497.230257 | 992.469222 | 496.738249 | 5 |
| 13 | 1550.629031 | 775.818154 | 1533.602482 | 767.304879 | 1532.618466 | 766.812871 | Y | *850.449138* | 425.728207 | 833.422589 | 417.214933 | 832.438573 | 416.722925 | 4 |
| 14 | 1651.676710 | 826.341993 | 1634.650161 | 817.828719 | 1633.666145 | 817.336711 | T | *687.385809* | 344.196543 | 670.359260 | 335.683268 | 669.375244 | 335.191260 | 3 |
| 15 | 2090.902036 | 1045.954656 | 2073.875487 | 1037.441381 | 2072.891471 | 1036.949373 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 62.5 | 2236.000305 | 0.031137 | TMGYQDFADVVCYTQK |

**Mascot:** http://www.matrixscience.com/

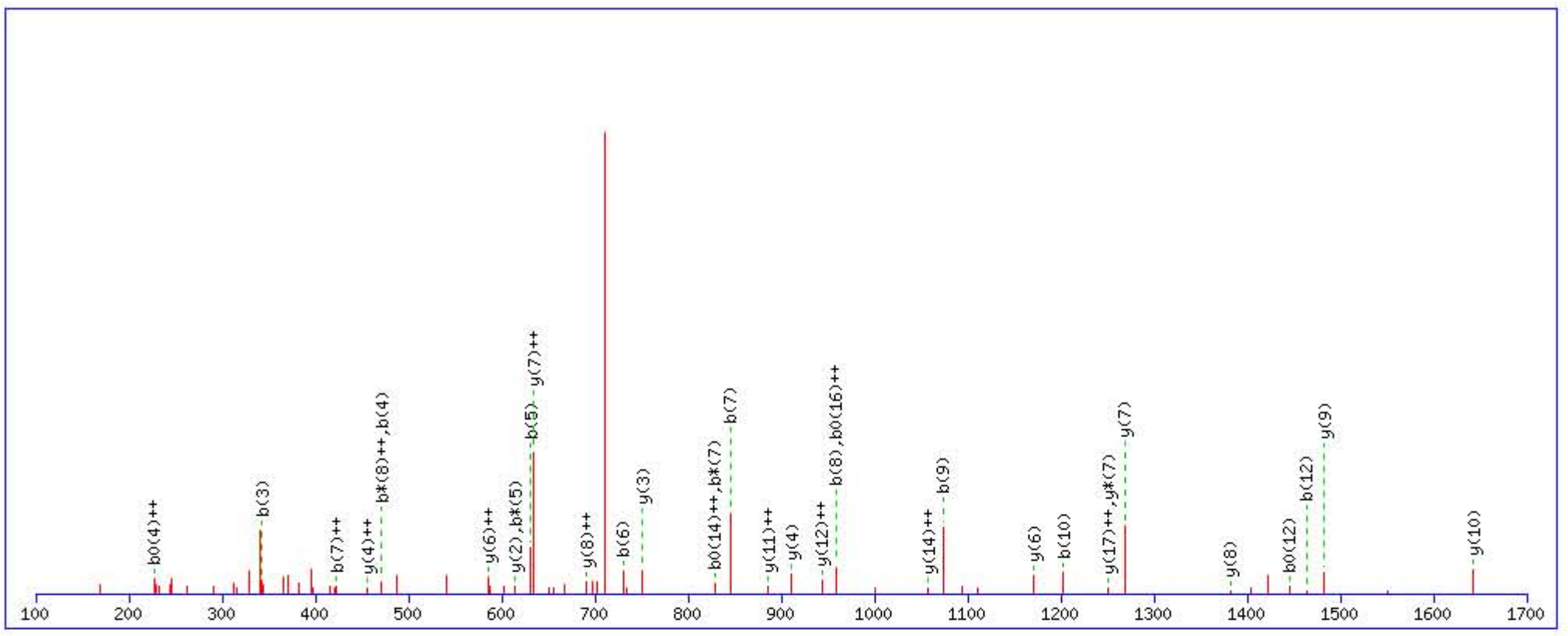
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **RGEQCVDIDECTIPPYCHQR**
Found in **FBLN3_HUMAN**, EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2

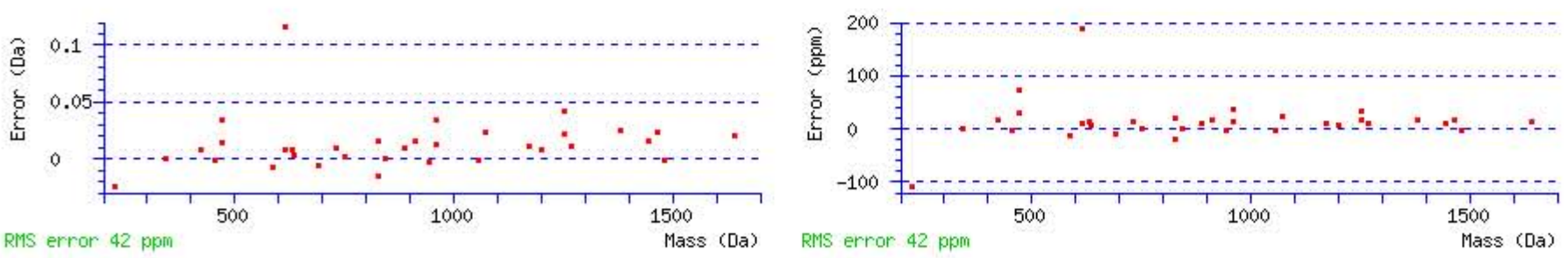
Match to Query 28447: 2843.269016 from(711.824530,4+) rtinseconds(1777) index(32785)
Title: Locus:1.1.1.727.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2843.261169
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q19 : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 7.4e-005
**Matches :** 34/208 fragment ions using 57 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 157.108387 | 79.057831 | 140.081838 | 70.544557 | | | R | | | | | | | 20 |
| 2 | 214.129851 | 107.568564 | 197.103302 | 99.055289 | | | G | 2688.167329 | 1344.587302 | 2671.140780 | 1336.074028 | 2670.156764 | 1335.582020 | 19 |
| 3 | *343.172444* | 172.089860 | 326.145895 | 163.576585 | 325.161879 | 163.084577 | E | 2631.145865 | 1316.076570 | 2614.119316 | 1307.563296 | 2613.135300 | 1307.071288 | 18 |
| 4 | *471.231022* | 236.119149 | 454.204473 | 227.605875 | 453.220457 | 227.113867 | Q | 2502.103272 | 1251.555274 | 2485.076723 | 1243.041999 | 2484.092707 | 1242.549991 | 17 |
| 5 | *631.261671* | 316.134474 | 614.235122 | 307.621199 | 613.251106 | 307.129191 | C | 2374.044694 | 1187.525985 | 2357.018145 | 1179.012710 | 2356.034129 | 1178.520702 | 16 |
| 6 | *730.330085* | 365.668681 | 713.303536 | 357.155406 | 712.319520 | 356.663398 | V | 2214.014045 | 1107.510660 | 2196.987496 | 1098.997386 | 2196.003480 | 1098.505378 | 15 |
| 7 | *845.357028* | 423.182152 | 828.330479 | 414.668878 | 827.346463 | 414.176870 | D | 2114.945631 | 1057.976453 | 2097.919082 | 1049.463179 | 2096.935066 | 1048.971171 | 14 |
| 8 | *958.441092* | 479.724184 | 941.414543 | 471.210910 | 940.430527 | 470.718902 | I | 1999.918688 | 1000.462982 | 1982.892139 | 991.949708 | 1981.908123 | 991.457700 | 13 |
| 9 | *1073.468035* | 537.237656 | 1056.441486 | 528.724381 | 1055.457470 | 528.232373 | D | 1886.834624 | 943.920950 | 1869.808075 | 935.407676 | 1868.824059 | 934.915668 | 12 |
| 10 | *1202.510628* | 601.758952 | 1185.484079 | 593.245678 | 1184.500063 | 592.753670 | E | 1771.807681 | 886.407479 | 1754.781132 | 877.894204 | 1753.797116 | 877.402196 | 11 |
| 11 | 1362.541277 | 681.774277 | 1345.514728 | 673.261002 | 1344.530712 | 672.768994 | C | *1642.765088* | 821.886182 | 1625.738539 | 813.372908 | 1624.754523 | 812.880900 | 10 |
| 12 | *1463.588956* | 732.298116 | 1446.562407 | 723.784842 | 1445.578391 | 723.292834 | T | *1482.734439* | 741.870858 | 1465.707890 | 733.357583 | 1464.723874 | 732.865575 | 9 |
| 13 | 1576.673020 | 788.840148 | 1559.646471 | 780.326874 | 1558.662455 | 779.834866 | I | *1381.686760* | 691.347018 | 1364.660211 | 682.833744 | | | 8 |
| 14 | 1673.725784 | 837.366530 | 1656.699235 | 828.853256 | 1655.715219 | 828.361248 | P | *1268.602696* | 634.804986 | 1251.576147 | 626.291712 | | | 7 |
| 15 | 1770.778548 | 885.892912 | 1753.751999 | 877.379638 | 1752.767983 | 876.887630 | P | *1171.549932* | 586.278604 | 1154.523383 | 577.765330 | | | 6 |
| 16 | 1933.841877 | 967.424577 | 1916.815328 | 958.911302 | 1915.831312 | 958.419294 | Y | 1074.497168 | 537.752222 | 1057.470619 | 529.238948 | | | 5 |
| 17 | 2093.872526 | 1047.439901 | 2076.845977 | 1038.926626 | 2075.861961 | 1038.434618 | C | *911.433839* | 456.220558 | 894.407290 | 447.707283 | | | 4 |
| 18 | 2230.931438 | 1115.969357 | 2213.904889 | 1107.456082 | 2212.920873 | 1106.964074 | H | *751.403190* | 376.205233 | 734.376641 | 367.691959 | | | 3 |
| 19 | 2670.156764 | 1335.582020 | 2653.130215 | 1327.068746 | 2652.146199 | 1326.576738 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 20 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.8 | 2843.261169 | 0.007847 | RGEQCVDIDECTIPPYCHQR |

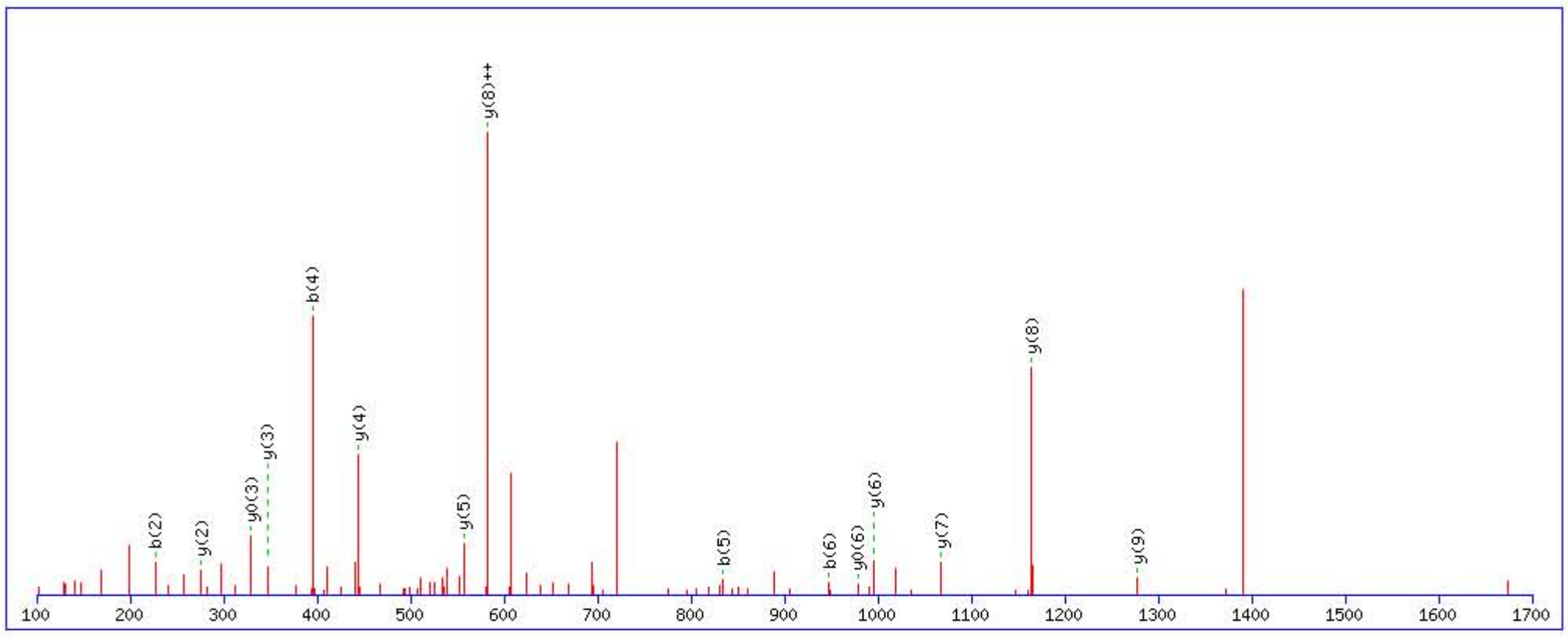
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LLPAQLPAEK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

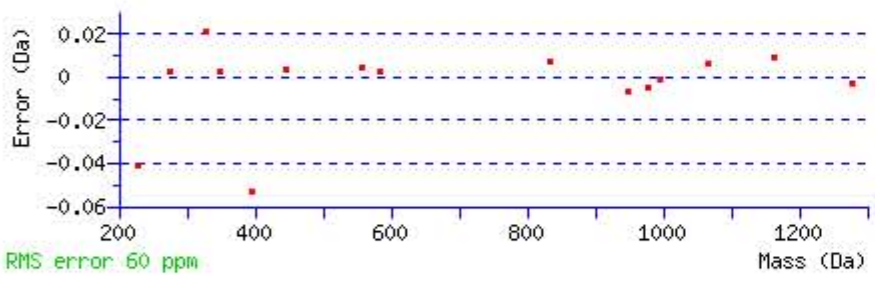
Match to Query 26911: 1389.811268 from(695.912910,2+) rtinseconds(2004) index(20271)
Title: Locus:1.1.1.3080.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

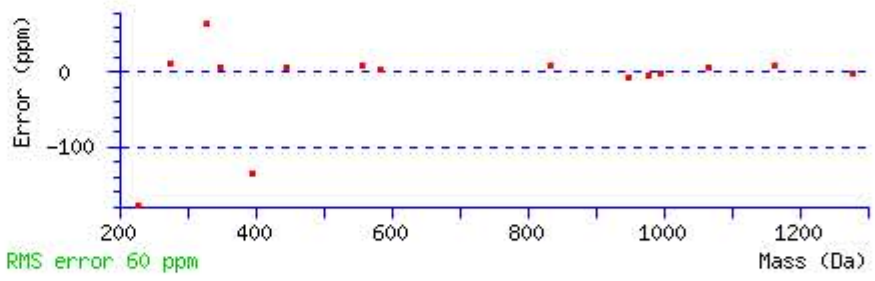
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1389.805359
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 42 **Expect:** 0.00039
**Matches :** 15/82 fragment ions using 35 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 10 |
| 2 | ***227.175404*** | 114.091340 | | | | | L | *1277.728607* | 639.367942 | 1260.702058 | 630.854667 | 1259.718042 | 630.362659 | 9 |
| 3 | 324.228168 | 162.617722 | | | | | P | *1164.644543* | 582.825909 | 1147.617994 | 574.312635 | 1146.633978 | 573.820627 | 8 |
| 4 | ***395.265282*** | 198.136279 | | | | | A | *1067.591779* | 534.299527 | 1050.565230 | 525.786253 | 1049.581214 | 525.294245 | 7 |
| 5 | ***834.490608*** | 417.748942 | 817.464059 | 409.235668 | | | Q | *996.554665* | 498.780970 | 979.528116 | 490.267696 | 978.544100 | 489.775688 | 6 |
| 6 | ***947.574672*** | 474.290974 | 930.548123 | 465.777700 | | | L | *557.329339* | 279.168307 | 540.302790 | 270.655033 | 539.318774 | 270.163025 | 5 |
| 7 | 1044.627436 | 522.817356 | 1027.600887 | 514.304082 | | | P | *444.245275* | 222.626275 | 427.218726 | 214.113001 | 426.234710 | 213.620993 | 4 |
| 8 | 1115.664550 | 558.335913 | 1098.638001 | 549.822639 | | | A | *347.192511* | 174.099893 | 330.165962 | 165.586619 | 329.181946 | 165.094611 | 3 |
| 9 | 1244.707143 | 622.857209 | 1227.680594 | 614.343935 | 1226.696578 | 613.851927 | E | *276.155397* | 138.581336 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 10 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 42.4 | 1389.805359 | 0.005909 | LLPAQLPAEK |
| 10.3 | 1389.809189 | 0.002079 | LIKRLDLSYNR |
| 2.6 | 1389.820450 | -0.009182 | LINRTHATVPIR |
| 1.5 | 1389.823135 | -0.011867 | ILIVITDGQKYK |
| 1.5 | 1389.813232 | -0.001964 | LIQAPSKFAFLR |
| 1.5 | 1389.797989 | 0.013279 | LLNLQSLFVTSR |
| 1.4 | 1389.816605 | -0.005337 | ILGPLPKHMIQK |
| 0.3 | 1389.797974 | 0.013294 | ILLYRGADKDVK |
| 0.3 | 1389.805359 | 0.005909 | LLSSYLQKK |
| 0.3 | 1389.809204 | 0.002064 | LLTYLRLQSQR |

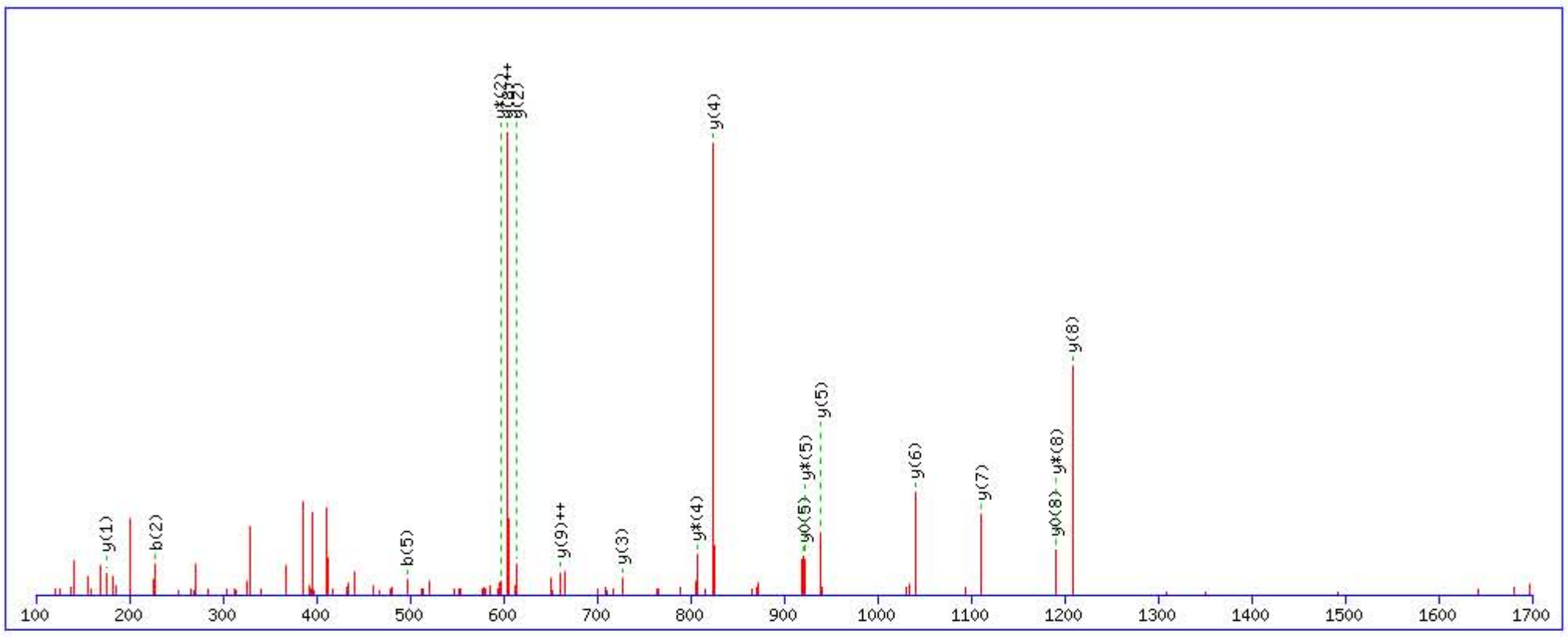
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NLPATDPLQR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

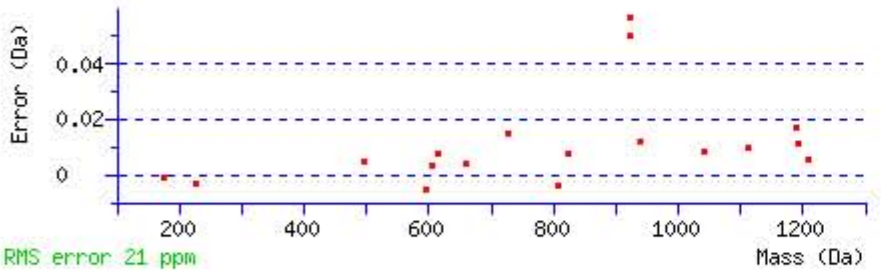
Match to Query 29253: 1434.769288 from(718.391920,2+) rtinseconds(1991) index(5582)
Title: Locus:1.1.1.1970.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

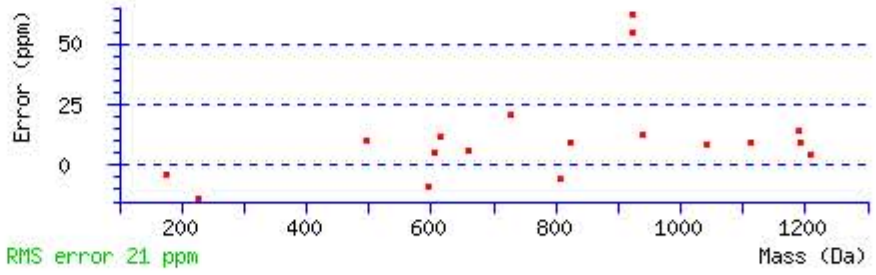
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1434.765305
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.0011
**Matches :** 18/92 fragment ions using 46 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 10 |
| 2 | **228.134267** | 114.570771 | 211.107718 | 106.057497 | | | L | 1321.729670 | 661.368473 | 1304.703121 | 652.855199 | 1303.719105 | 652.363190 | 9 |
| 3 | 325.187031 | 163.097153 | 308.160482 | 154.583879 | | | P | *1208.645606* | 604.826441 | 1191.619057 | 596.313166 | 1190.635041 | 595.821158 | 8 |
| 4 | 396.224145 | 198.615710 | 379.197596 | 190.102436 | | | A | *1111.592842* | 556.300059 | 1094.566293 | 547.786784 | 1093.582277 | 547.294776 | 7 |
| 5 | **497.271824** | 249.139550 | 480.245275 | 240.626275 | 479.261259 | 240.134267 | T | *1040.555728* | 520.781502 | 1023.529179 | 512.268227 | 1022.545163 | 511.776220 | 6 |
| 6 | 612.298767 | 306.653022 | 595.272218 | 298.139747 | 594.288202 | 297.647739 | D | *939.508049* | 470.257662 | 922.481500 | 461.744388 | 921.497484 | 461.252380 | 5 |
| 7 | 709.351531 | 355.179404 | 692.324982 | 346.666129 | 691.340966 | 346.174121 | P | *824.481106* | 412.744191 | 807.454557 | 404.230916 | | | 4 |
| 8 | 822.435595 | 411.721436 | 805.409046 | 403.208161 | 804.425030 | 402.716153 | L | *727.428342* | 364.217809 | 710.401793 | 355.704534 | | | 3 |
| 9 | 1261.660921 | 631.334098 | 1244.634372 | 622.820824 | 1243.650356 | 622.328816 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162502 | | | 2 |
| 10 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.2 | 1434.765305 | 0.003983 | NLPATDPLQR |
| 6.1 | 1434.757889 | 0.011399 | NLIRQISSGEYR |
| 0.1 | 1434.761932 | 0.007356 | NLDYPFGNVLRK |

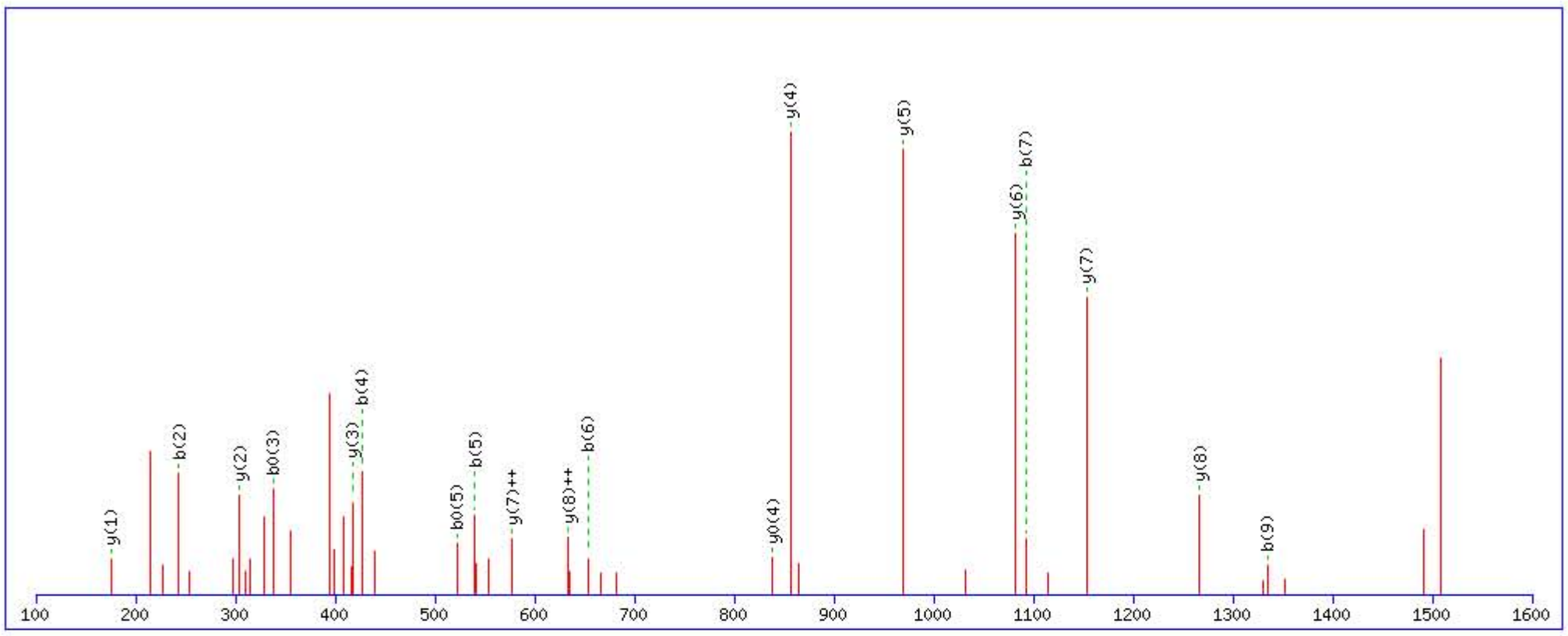
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ELLALIQLER**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

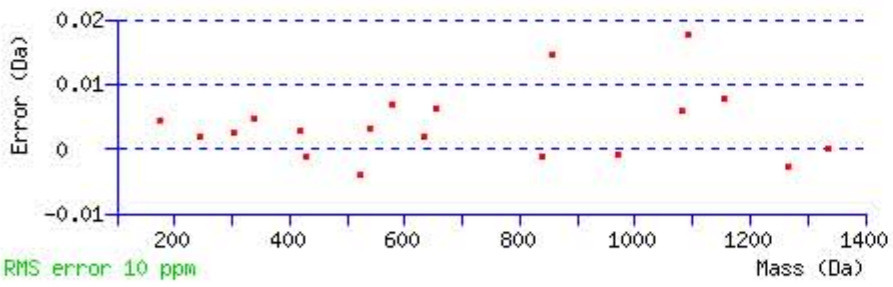
Match to Query 31405: 1507.895268 from(754.954910,2+) rtinseconds(2746) index(9580)
Title: Locus:1.1.1.2233.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

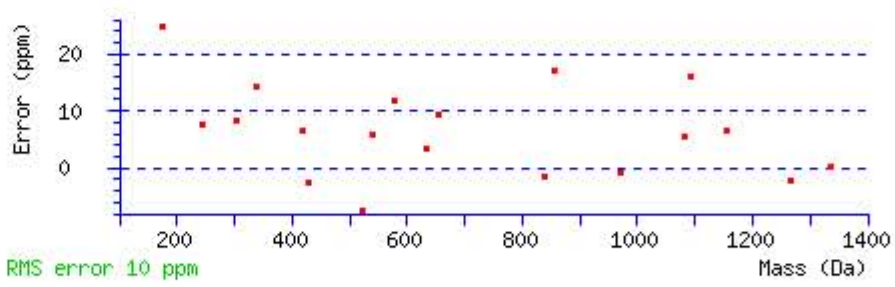
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1507.879578
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 3.4e-006
**Matches :** 19/94 fragment ions using 29 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 10 |
| 2 | **243.133933** | 122.070605 | | | 225.123368 | 113.065322 | L | 1379.844305 | 690.425790 | 1362.817756 | 681.912516 | 1361.833740 | 681.420508 | 9 |
| 3 | 356.217997 | 178.612637 | | | 338.207432 | 169.607354 | L | *1266.760241* | 633.883759 | 1249.733692 | 625.370484 | 1248.749676 | 624.878476 | 8 |
| 4 | **427.255111** | 214.131193 | | | 409.244546 | 205.125911 | A | *1153.676177* | 577.341727 | 1136.649628 | 568.828452 | 1135.665612 | 568.336444 | 7 |
| 5 | **540.339175** | 270.673226 | | | 522.328610 | 261.667943 | L | *1082.639063* | 541.823169 | 1065.612514 | 533.309895 | 1064.628498 | 532.817887 | 6 |
| 6 | **653.423239** | 327.215258 | | | 635.412674 | 318.209975 | I | *969.554999* | 485.281138 | 952.528450 | 476.767863 | 951.544434 | 476.275855 | 5 |
| 7 | **1092.648565** | 546.827921 | 1075.622016 | 538.314646 | 1074.638000 | 537.822638 | Q | *856.470935* | 428.739105 | 839.444386 | 420.225831 | 838.460370 | 419.733823 | 4 |
| 8 | 1205.732629 | 603.369953 | 1188.706080 | 594.856678 | 1187.722064 | 594.364670 | L | *417.245609* | 209.126442 | 400.219060 | 200.613168 | 399.235044 | 200.121160 | 3 |
| 9 | **1334.775222** | 667.891249 | 1317.748673 | 659.377975 | 1316.764657 | 658.885966 | E | *304.161545* | 152.584410 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 10 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.8 | 1507.879578 | 0.015690 | ELLALIQLER |
| 0.4 | 1507.879608 | 0.015660 | LVVELVQELR |

**Mascot:** http://www.matrixscience.com/

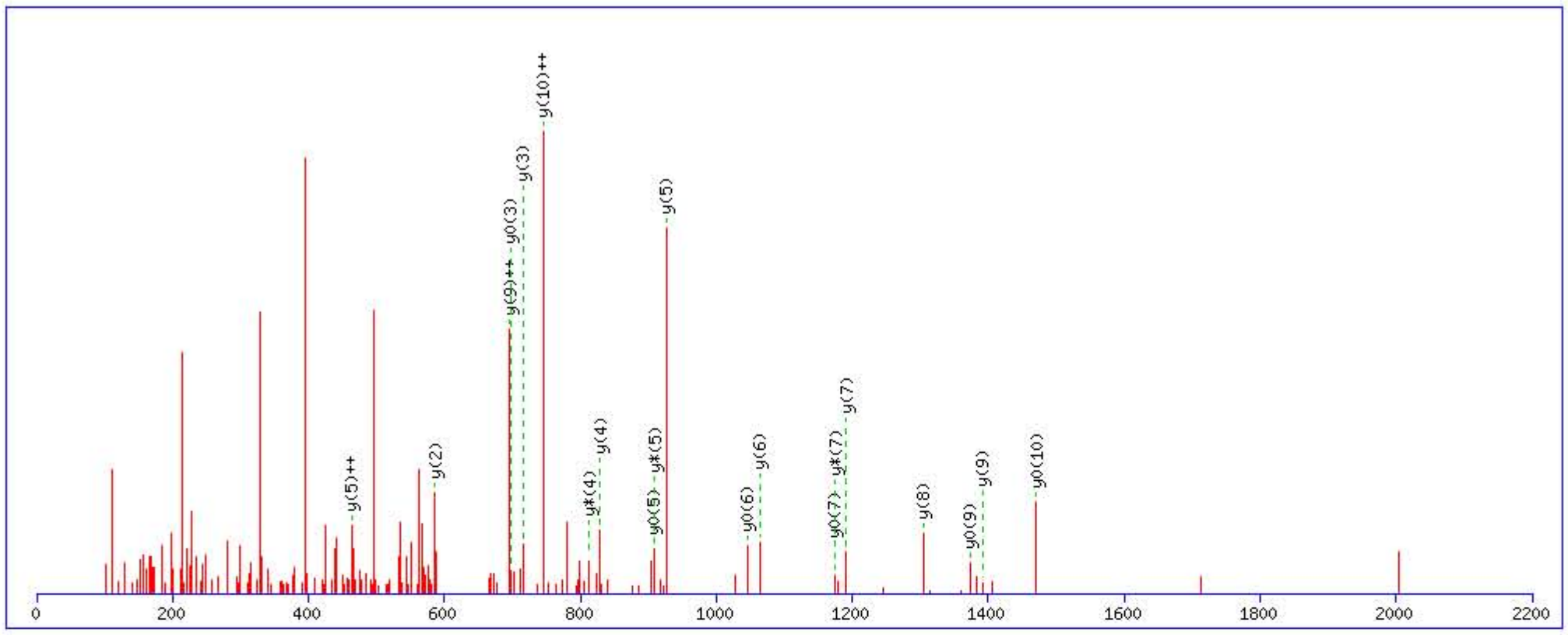
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ELPSLQHPNEQK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

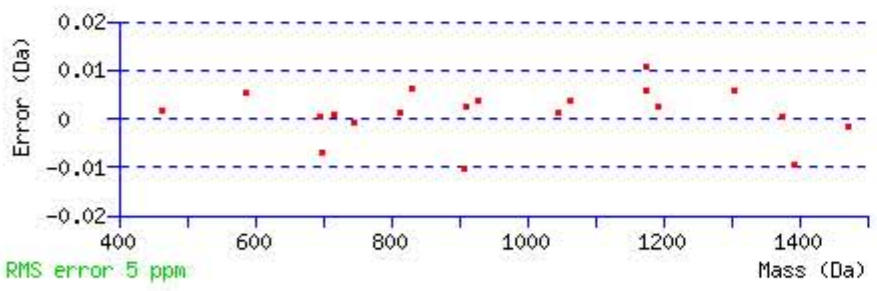
Match to Query 38609: 1729.882542 from(577.634790,3+) rtinseconds(1624) index(3397)
Title: Locus:1.1.1.1842.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

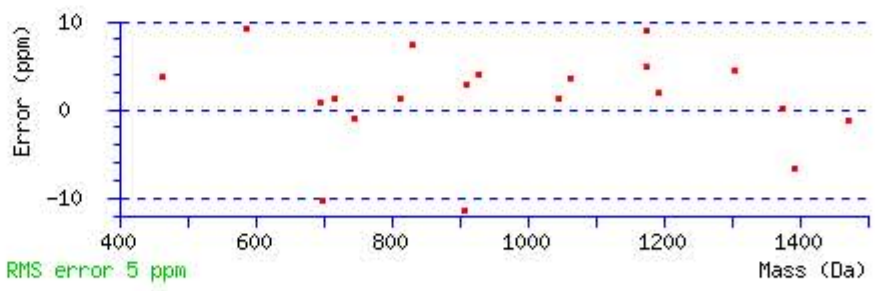
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1729.882111
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q11 : Biotin:Thermo-21345 (Q)
**Ions Score:** 30 **Expect:** 0.03
**Matches :** 20/118 fragment ions using 52 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 12 |
| 2 | 243.133933 | 122.070605 | | | 225.123368 | 113.065322 | L | 1601.846824 | 801.427050 | 1584.820275 | 792.913776 | 1583.836259 | 792.421767 | 11 |
| 3 | 340.186697 | 170.596987 | | | 322.176132 | 161.591704 | P | 1488.762760 | 744.885018 | 1471.736211 | 736.371744 | 1470.752195 | 735.879736 | 10 |
| 4 | 427.218725 | 214.113001 | | | 409.208160 | 205.107718 | S | *1391.709996* | 696.358636 | 1374.683447 | 687.845362 | 1373.699431 | 687.353354 | 9 |
| 5 | 540.302789 | 270.655033 | | | 522.292224 | 261.649750 | L | *1304.677968* | 652.842622 | 1287.651419 | 644.329348 | 1286.667403 | 643.837340 | 8 |
| 6 | 668.361367 | 334.684322 | 651.334818 | 326.171047 | 650.350802 | 325.679039 | Q | *1191.593904* | 596.300590 | 1174.567355 | 587.787316 | 1173.583339 | 587.295308 | 7 |
| 7 | 805.420279 | 403.213778 | 788.393730 | 394.700503 | 787.409714 | 394.208495 | H | *1063.535326* | 532.271301 | 1046.508777 | 523.758027 | 1045.524761 | 523.266018 | 6 |
| 8 | 902.473043 | 451.740160 | 885.446494 | 443.226885 | 884.462478 | 442.734877 | P | *926.476414* | 463.741845 | 909.449865 | 455.228571 | 908.465849 | 454.736563 | 5 |
| 9 | 1016.515970 | 508.761623 | 999.489421 | 500.248349 | 998.505405 | 499.756341 | N | *829.423650* | 415.215463 | 812.397101 | 406.702189 | 811.413085 | 406.210181 | 4 |
| 10 | 1145.558563 | 573.282920 | 1128.532014 | 564.769645 | 1127.547998 | 564.277637 | E | *715.380723* | 358.194000 | 698.354174 | 349.680725 | 697.370158 | 349.188717 | 3 |
| 11 | 1584.783889 | 792.895583 | 1567.757340 | 784.382308 | 1566.773324 | 783.890300 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 12 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 29.8 | 1729.882111 | 0.000431 | ELPSLQHPNEQK |
| 2.8 | 1729.882111 | 0.000431 | ELPSLQHPNEQK |

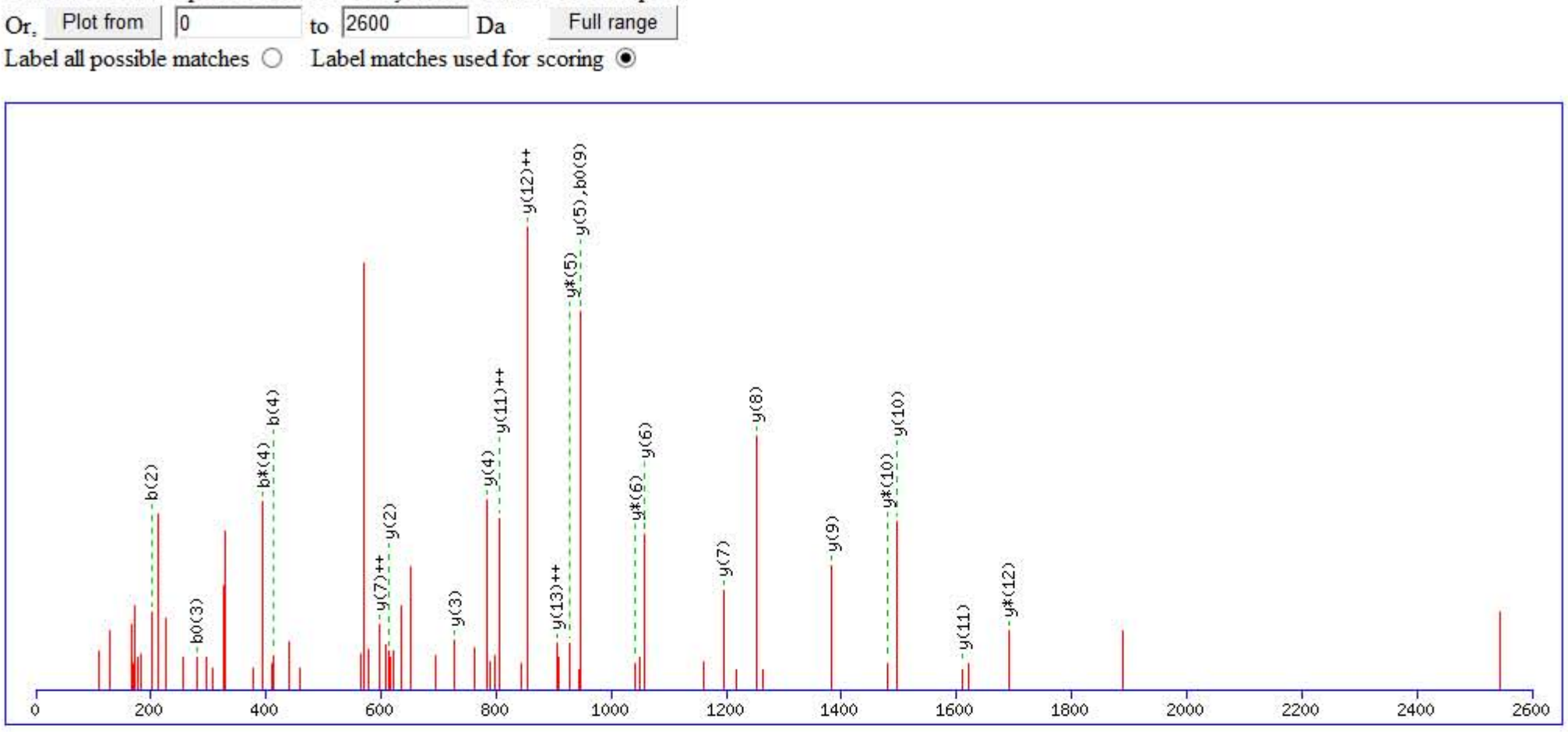
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VTPNLMGHLCGNQR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

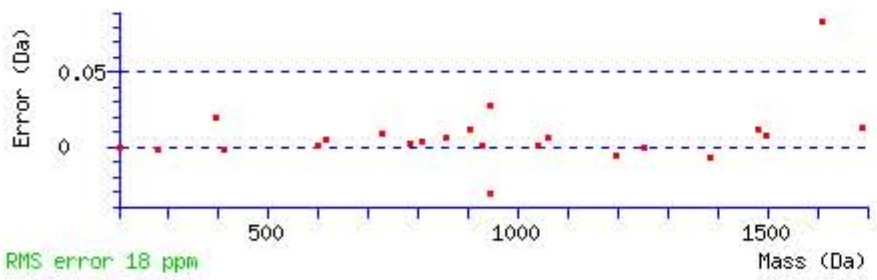
Match to Query 42265: 1906.939272 from(636.653700,3+) rtinseconds(1887) index(4843)
Title: Locus:1.1.1.1934.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

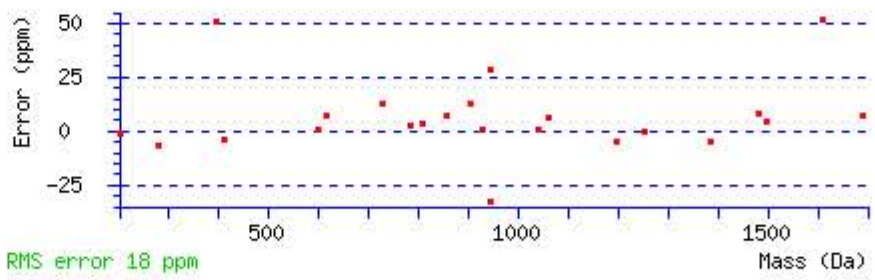
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1906.932816
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 0.00034
**Matches :** 23/124 fragment ions using 51 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 14 |
| 2 | **201.123369** | 101.065322 | | | 183.112804 | 92.060040 | T | 1808.871677 | 904.939477 | 1791.845128 | 896.426202 | 1790.861112 | 895.934194 | 13 |
| 3 | 298.176133 | 149.591704 | | | 280.165568 | 140.586422 | P | 1707.823998 | 854.415637 | 1690.797449 | 845.902363 | | | 12 |
| 4 | **412.219060** | 206.613168 | 395.192511 | 198.099894 | 394.208495 | 197.607886 | N | *1610.771234* | 805.889255 | 1593.744685 | 797.375981 | | | 11 |
| 5 | 525.303124 | 263.155200 | 508.276575 | 254.641926 | 507.292559 | 254.149918 | L | *1496.728307* | 748.867792 | 1479.701758 | 740.354517 | | | 10 |
| 6 | 656.343609 | 328.675443 | 639.317060 | 320.162168 | 638.333044 | 319.670160 | M | *1383.644243* | 692.325760 | 1366.617694 | 683.812485 | | | 9 |
| 7 | 713.365073 | 357.186175 | 696.338524 | 348.672900 | 695.354508 | 348.180892 | G | *1252.603758* | 626.805517 | 1235.577209 | 618.292243 | | | 8 |
| 8 | 850.423985 | 425.715631 | 833.397436 | 417.202356 | 832.413420 | 416.710348 | H | *1195.582294* | 598.294785 | 1178.555745 | 589.781511 | | | 7 |
| 9 | 963.508049 | 482.257663 | 946.481500 | 473.744388 | 945.497484 | 473.252380 | L | *1058.523382* | 529.765329 | 1041.496833 | 521.252055 | | | 6 |
| 10 | 1123.538698 | 562.272987 | 1106.512149 | 553.759713 | 1105.528133 | 553.267705 | C | *945.439318* | 473.223297 | 928.412769 | 464.710023 | | | 5 |
| 11 | 1180.560162 | 590.783719 | 1163.533613 | 582.270445 | 1162.549597 | 581.778437 | G | *785.408669* | 393.207973 | 768.382120 | 384.694698 | | | 4 |
| 12 | 1294.603089 | 647.805183 | 1277.576540 | 639.291908 | 1276.592524 | 638.799900 | N | *728.387205* | 364.697241 | 711.360656 | 356.183966 | | | 3 |
| 13 | 1733.828415 | 867.417846 | 1716.801866 | 858.904571 | 1715.817850 | 858.412563 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 14 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.4 | 1906.932816 | 0.006456 | VTPNLMGHLCGNQR |

**Mascot:** http://www.matrixscience.com/

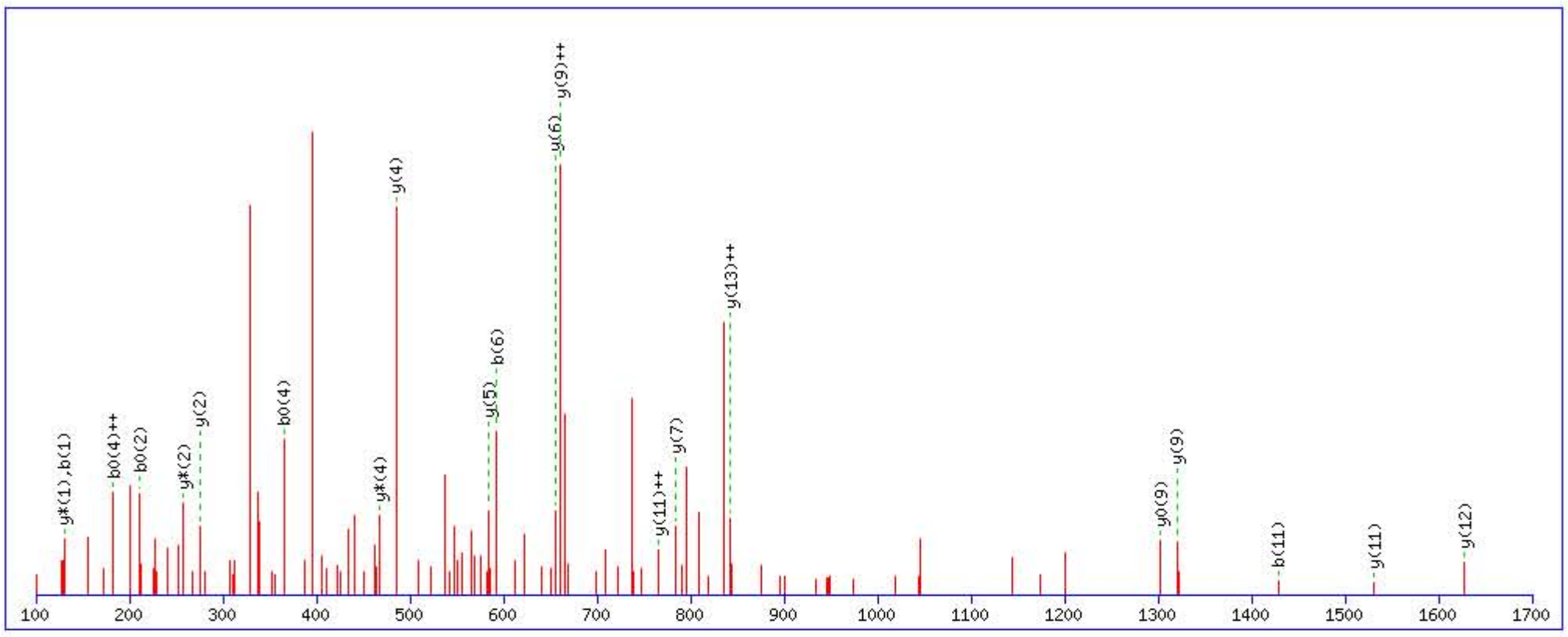
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EVGPPLPQEAVPLQK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

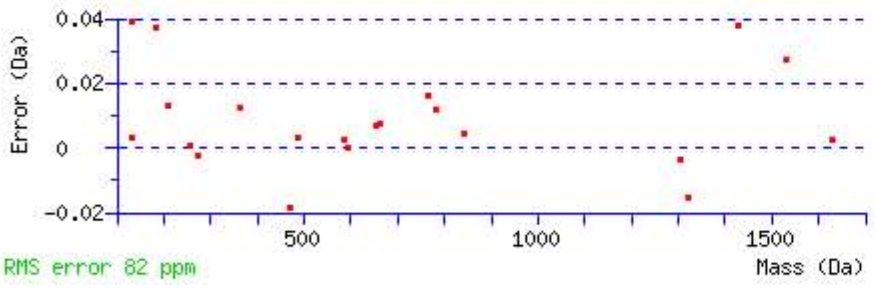
Match to Query 42406: 1912.058742 from(638.360190,3+) rtinseconds(2216) index(6832)
Title: Locus:1.1.1.2049.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

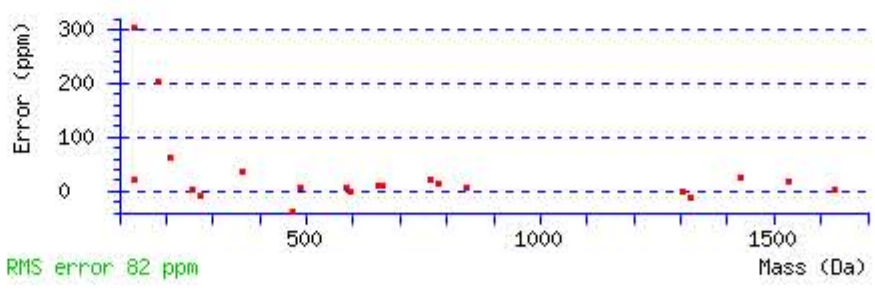
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1912.049194
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 29 **Expect:** 0.018
**Matches :** 21/142 fragment ions using 48 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 15 |
| 2 | 229.118283 | 115.062780 | | | 211.107718 | 106.057497 | V | 1784.013891 | 892.510583 | 1766.987342 | 883.997309 | 1766.003326 | 883.505301 | 14 |
| 3 | 286.139747 | 143.573512 | | | 268.129182 | 134.568229 | G | 1684.945477 | 842.976377 | 1667.918928 | 834.463102 | 1666.934912 | 833.971094 | 13 |
| 4 | 383.192511 | 192.099894 | | | 365.181946 | 183.094611 | P | *1627.924013* | 814.465645 | 1610.897464 | 805.952370 | 1609.913448 | 805.460362 | 12 |
| 5 | 480.245275 | 240.626276 | | | 462.234710 | 231.620993 | P | *1530.871249* | 765.939263 | 1513.844700 | 757.425988 | 1512.860684 | 756.933980 | 11 |
| 6 | 593.329339 | 297.168308 | | | 575.318774 | 288.163025 | L | 1433.818485 | 717.412881 | 1416.791936 | 708.899606 | 1415.807920 | 708.407598 | 10 |
| 7 | 690.382103 | 345.694690 | | | 672.371538 | 336.689407 | P | *1320.734421* | 660.870848 | 1303.707872 | 652.357574 | 1302.723856 | 651.865566 | 9 |
| 8 | 1129.607429 | 565.307353 | 1112.580880 | 556.794078 | 1111.596864 | 556.302070 | Q | 1223.681657 | 612.344466 | 1206.655108 | 603.831192 | 1205.671092 | 603.339184 | 8 |
| 9 | 1258.650022 | 629.828649 | 1241.623473 | 621.315375 | 1240.639457 | 620.823367 | E | *784.456331* | 392.731803 | 767.429782 | 384.218529 | 766.445766 | 383.726521 | 7 |
| 10 | 1329.687136 | 665.347206 | 1312.660587 | 656.833932 | 1311.676571 | 656.341924 | A | *655.413738* | 328.210507 | 638.387189 | 319.697232 | | | 6 |
| 11 | 1428.755550 | 714.881413 | 1411.729001 | 706.368139 | 1410.744985 | 705.876131 | V | *584.376624* | 292.691950 | 567.350075 | 284.178676 | | | 5 |
| 12 | 1525.808314 | 763.407795 | 1508.781765 | 754.894521 | 1507.797749 | 754.402513 | P | *485.308210* | 243.157743 | 468.281661 | 234.644468 | | | 4 |
| 13 | 1638.892378 | 819.949827 | 1621.865829 | 811.436553 | 1620.881813 | 810.944545 | L | 388.255446 | 194.631361 | 371.228897 | 186.118086 | | | 3 |
| 14 | 1766.950956 | 883.979116 | 1749.924407 | 875.465842 | 1748.940391 | 874.973833 | Q | *275.171382* | 138.089329 | 258.144833 | 129.576054 | | | 2 |
| 15 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 29.4 | 1912.049194 | 0.009548 | EVGPPLPQEAVPLQK |
| 10.8 | 1912.049194 | 0.009548 | EVGPPLPQEAVPLQK |

**Mascot:** http://www.matrixscience.com/

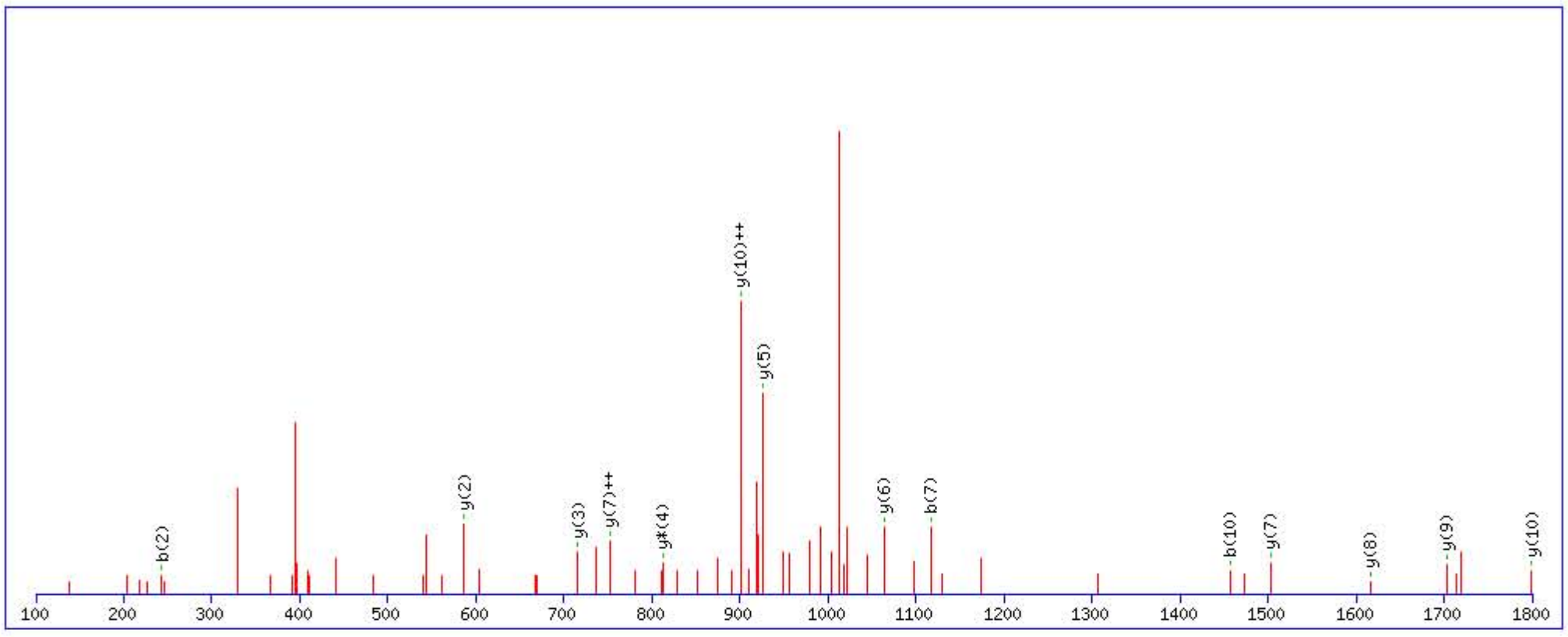
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ELPSLQHPNEQK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

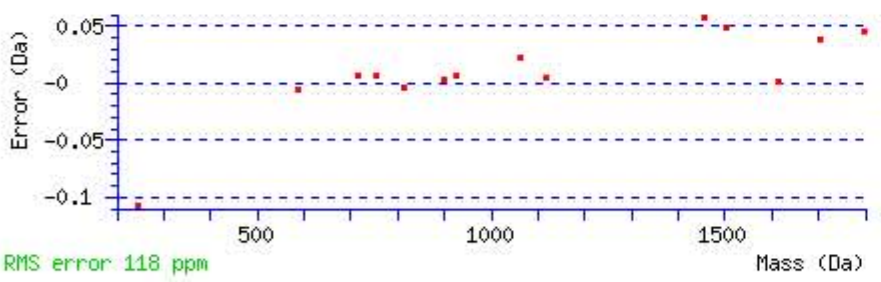
Match to Query 45487: 2041.064148 from(1021.539350,2+) rtinseconds(1986) index(5564)
Title: Locus:1.1.1.1968.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

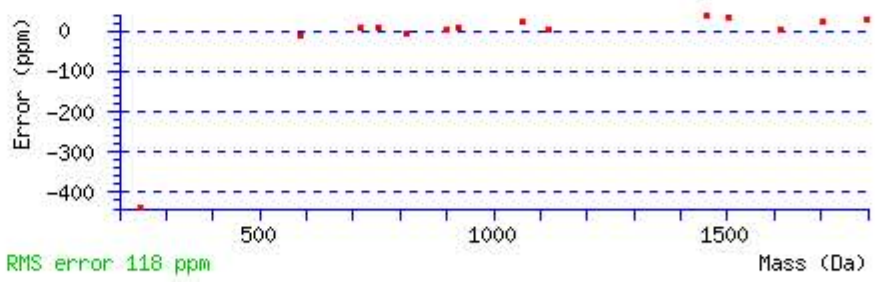
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2041.048859
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
Q11 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 6.5e-005
**Matches** : 14/118 fragment ions using 28 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 12 |
| 2 | **243.133933** | 122.070605 | | | 225.123368 | 113.065322 | L | 1913.013572 | 957.010424 | 1895.987023 | 948.497150 | 1895.003007 | 948.005142 | 11 |
| 3 | 340.186697 | 170.596987 | | | 322.176132 | 161.591704 | P | *1799.929508* | 900.468392 | 1782.902959 | 891.955118 | 1781.918943 | 891.463110 | 10 |
| 4 | 427.218725 | 214.113001 | | | 409.208160 | 205.107718 | S | *1702.876744* | 851.942010 | 1685.850195 | 843.428736 | 1684.866179 | 842.936728 | 9 |
| 5 | 540.302789 | 270.655033 | | | 522.292224 | 261.649750 | L | *1615.844716* | 808.425996 | 1598.818167 | 799.912722 | 1597.834151 | 799.420714 | 8 |
| 6 | 979.528115 | 490.267696 | 962.501566 | 481.754421 | 961.517550 | 481.262413 | Q | *1502.760652* | 751.883964 | 1485.734103 | 743.370690 | 1484.750087 | 742.878682 | 7 |
| 7 | **1116.587027** | 558.797152 | 1099.560478 | 550.283877 | 1098.576462 | 549.791869 | H | *1063.535326* | 532.271301 | 1046.508777 | 523.758027 | 1045.524761 | 523.266019 | 6 |
| 8 | 1213.639791 | 607.323534 | 1196.613242 | 598.810259 | 1195.629226 | 598.318251 | P | *926.476414* | 463.741845 | 909.449865 | 455.228571 | 908.465849 | 454.736563 | 5 |
| 9 | 1327.682718 | 664.344997 | 1310.656169 | 655.831723 | 1309.672153 | 655.339715 | N | 829.423650 | 415.215463 | 812.397101 | 406.702189 | 811.413085 | 406.210181 | 4 |
| 10 | **1456.725311** | 728.866293 | 1439.698762 | 720.353019 | 1438.714746 | 719.861011 | E | *715.380723* | 358.194000 | 698.354174 | 349.680725 | 697.370158 | 349.188717 | 3 |
| 11 | 1895.950637 | 948.478957 | 1878.924088 | 939.965682 | 1877.940072 | 939.473674 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 12 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 44.8 | 2041.048859 | 0.015289 | ELPSLQHPNEQK |
| 0.2 | 2041.044830 | 0.019318 | ELTEMRLQDQQLAR |
| 0.2 | 2041.044830 | 0.019318 | ELTEMRLQDQQLAR |
| 0.1 | 2041.094269 | -0.030121 | KPITKSSPSLLIESDSPDK |

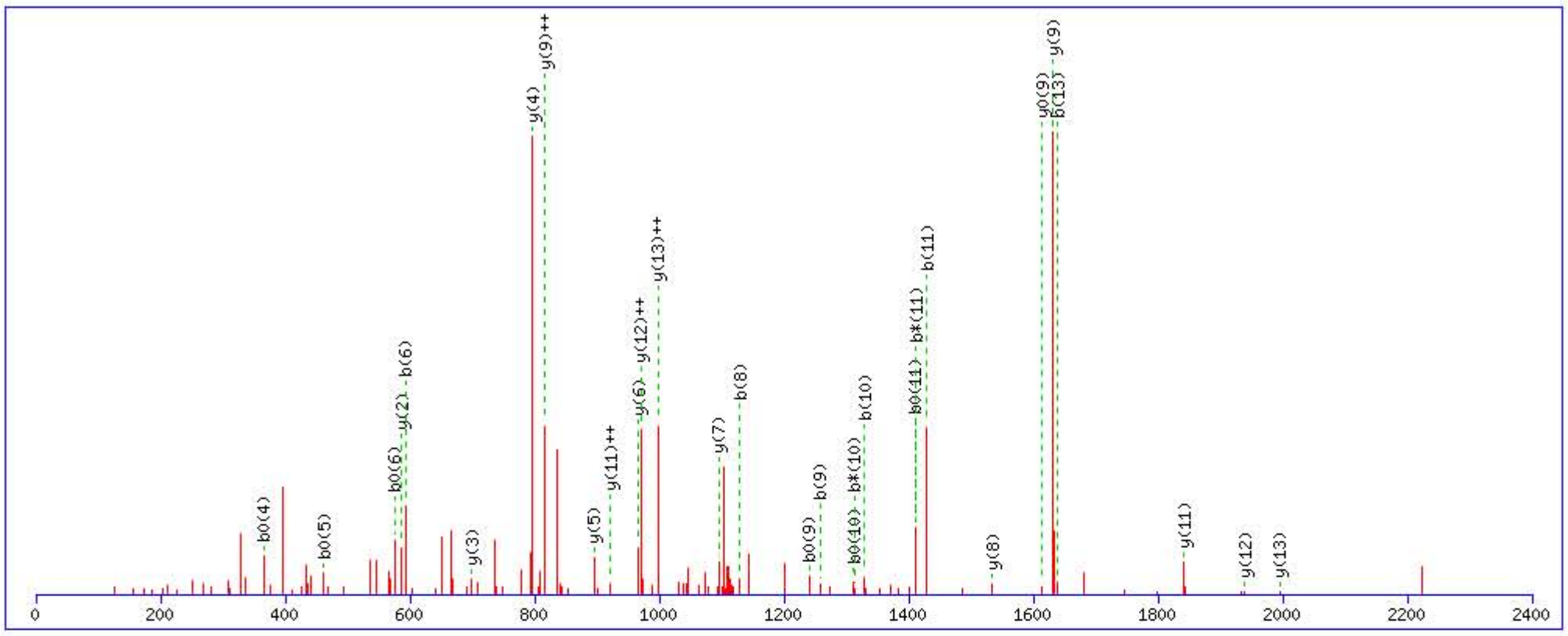
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EVGPPLPQEAVPLQK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

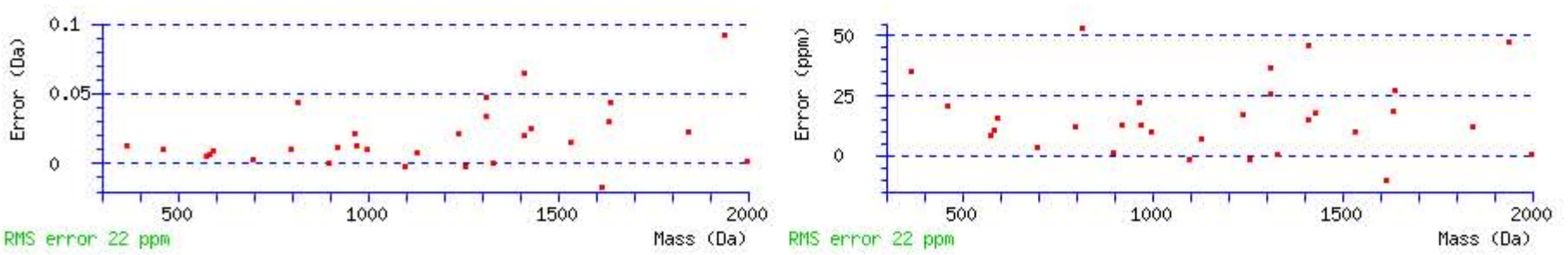
Match to Query 49010: 2223.237048 from(1112.625800,2+) rtinseconds(2453) index(8095)
Title: Locus:1.1.1.2131.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2223.215942
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
Q14 : Biotin:Thermo-21345 (Q)
**Ions Score:** 42 **Expect:** 0.0012
**Matches :** 30/142 fragment ions using 80 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 15 |
| 2 | 229.118283 | 115.062780 | | | 211.107718 | 106.057497 | V | 2095.180639 | 1048.093957 | 2078.154090 | 1039.580683 | 2077.170074 | 1039.088675 | 14 |
| 3 | 286.139747 | 143.573512 | | | 268.129182 | 134.568229 | G | *1996.112225* | 998.559751 | 1979.085676 | 990.046476 | 1978.101660 | 989.554468 | 13 |
| 4 | 383.192511 | 192.099894 | | | 365.181946 | 183.094611 | P | *1939.090761* | 970.049019 | 1922.064212 | 961.535744 | 1921.080196 | 961.043736 | 12 |
| 5 | 480.245275 | 240.626276 | | | 462.234710 | 231.620993 | P | *1842.037997* | 921.522637 | 1825.011448 | 913.009362 | 1824.027432 | 912.517354 | 11 |
| 6 | **593.329339** | 297.168308 | | | 575.318774 | 288.163025 | L | 1744.985233 | 872.996255 | 1727.958684 | 864.482980 | 1726.974668 | 863.990972 | 10 |
| 7 | 690.382103 | 345.694690 | | | 672.371538 | 336.689407 | P | *1631.901169* | 816.454223 | 1614.874620 | 807.940948 | 1613.890604 | 807.448940 | 9 |
| 8 | **1129.607429** | 565.307353 | 1112.580880 | 556.794078 | 1111.596864 | 556.302070 | Q | *1534.848405* | 767.927841 | 1517.821856 | 759.414566 | 1516.837840 | 758.922558 | 8 |
| 9 | **1258.650022** | 629.828649 | 1241.623473 | 621.315375 | 1240.639457 | 620.823367 | E | *1095.623079* | 548.315178 | 1078.596530 | 539.801903 | 1077.612514 | 539.309895 | 7 |
| 10 | **1329.687136** | 665.347206 | 1312.660587 | 656.833932 | 1311.676571 | 656.341924 | A | *966.580486* | 483.793881 | 949.553937 | 475.280607 | | | 6 |
| 11 | **1428.755550** | 714.881413 | 1411.729001 | 706.368139 | 1410.744985 | 705.876131 | V | *895.543372* | 448.275324 | 878.516823 | 439.762050 | | | 5 |
| 12 | 1525.808314 | 763.407795 | 1508.781765 | 754.894521 | 1507.797749 | 754.402513 | P | *796.474958* | 398.741117 | 779.448409 | 390.227843 | | | 4 |
| 13 | **1638.892378** | 819.949827 | 1621.865829 | 811.436553 | 1620.881813 | 810.944545 | L | *699.422194* | 350.214735 | 682.395645 | 341.701461 | | | 3 |
| 14 | 2078.117704 | 1039.562490 | 2061.091155 | 1031.049215 | 2060.107139 | 1030.557207 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 15 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 42.1 | 2223.215942 | 0.021106 | EVGPPLPQEAVPLQK |

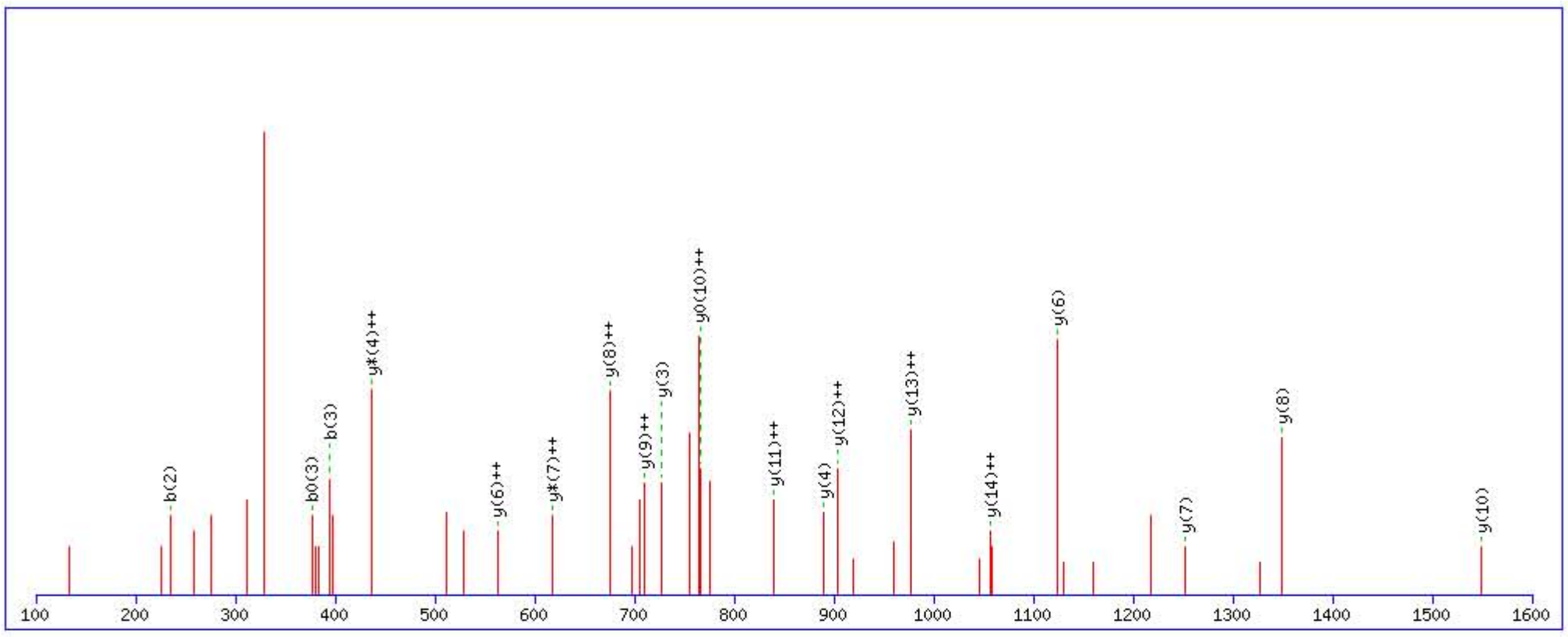
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FSCFQEEAPQPHYQLR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

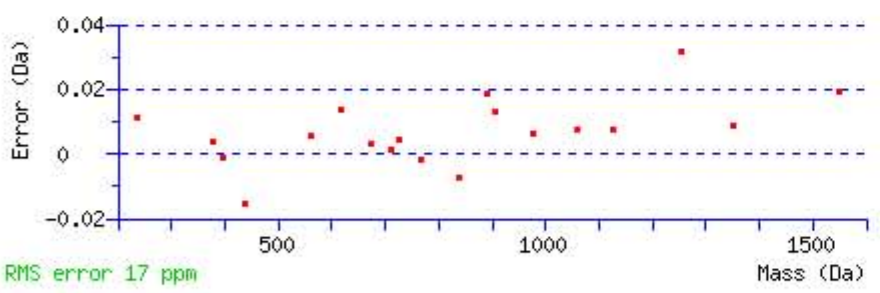
Match to Query 51296: 2347.101462 from(783.374430,3+) rtinseconds(1946) index(5348)
Title: Locus:1.1.1.1954.26 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

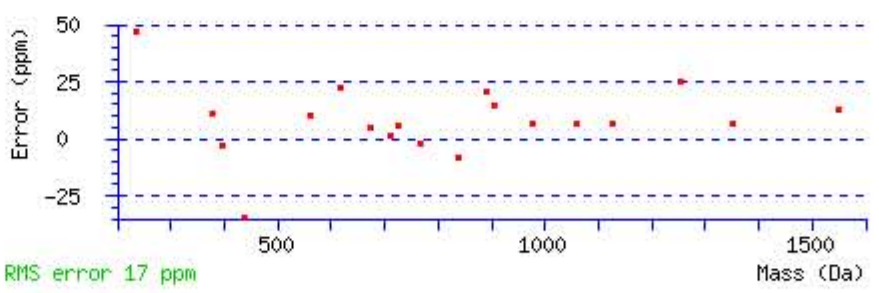
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2347.087784
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q14** : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.00068
**Matches :** 19/152 fragment ions using 33 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 16 |
| 2 | 235.107718 | 118.057497 | | | 217.097153 | 109.052214 | S | 2201.026658 | 1101.016967 | 2184.000109 | 1092.503692 | 2183.016093 | 1092.011684 | 15 |
| 3 | 395.138367 | 198.072821 | | | 377.127802 | 189.067539 | C | 2113.994630 | 1057.500953 | 2096.968081 | 1048.987678 | 2095.984065 | 1048.495670 | 14 |
| 4 | 542.206781 | 271.607029 | | | 524.196216 | 262.601746 | F | 1953.963981 | 977.485629 | 1936.937432 | 968.972354 | 1935.953416 | 968.480346 | 13 |
| 5 | 670.265359 | 335.636318 | 653.238810 | 327.123043 | 652.254794 | 326.631035 | Q | 1806.895567 | 903.951422 | 1789.869018 | 895.438147 | 1788.885002 | 894.946139 | 12 |
| 6 | 799.307952 | 400.157614 | 782.281403 | 391.644340 | 781.297387 | 391.152332 | E | 1678.836989 | 839.922133 | 1661.810440 | 831.408858 | 1660.826424 | 830.916850 | 11 |
| 7 | 928.350545 | 464.678911 | 911.323996 | 456.165636 | 910.339980 | 455.673628 | E | *1549.794396* | 775.400836 | 1532.767847 | 766.887562 | 1531.783831 | 766.395554 | 10 |
| 8 | 999.387659 | 500.197468 | 982.361110 | 491.684193 | 981.377094 | 491.192185 | A | 1420.751803 | 710.879540 | 1403.725254 | 702.366265 | | | 9 |
| 9 | 1096.440423 | 548.723850 | 1079.413874 | 540.210575 | 1078.429858 | 539.718567 | P | *1349.714689* | 675.360983 | 1332.688140 | 666.847708 | | | 8 |
| 10 | 1224.499001 | 612.753138 | 1207.472452 | 604.239864 | 1206.488436 | 603.747856 | Q | *1252.661925* | 626.834601 | 1235.635376 | 618.321326 | | | 7 |
| 11 | 1321.551765 | 661.279520 | 1304.525216 | 652.766246 | 1303.541200 | 652.274238 | P | *1124.603347* | 562.805312 | 1107.576798 | 554.292037 | | | 6 |
| 12 | 1458.610677 | 729.808976 | 1441.584128 | 721.295702 | 1440.600112 | 720.803694 | H | 1027.550583 | 514.278930 | 1010.524034 | 505.765655 | | | 5 |
| 13 | 1621.674006 | 811.340641 | 1604.647457 | 802.827367 | 1603.663441 | 802.335358 | Y | *890.491671* | 445.749474 | 873.465122 | 437.236199 | | | 4 |
| 14 | 2060.899332 | 1030.953304 | 2043.872783 | 1022.440030 | 2042.888767 | 1021.948022 | Q | *727.428342* | 364.217809 | 710.401793 | 355.704535 | | | 3 |
| 15 | 2173.983396 | 1087.495336 | 2156.956847 | 1078.982061 | 2155.972831 | 1078.490053 | L | 288.203016 | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 16 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 44.0 | 2347.087784 | 0.013678 | FSCFQEEAPQPHYQLR |
| 21.0 | 2347.087784 | 0.013678 | FSCFQEEAPQPHYQLR |

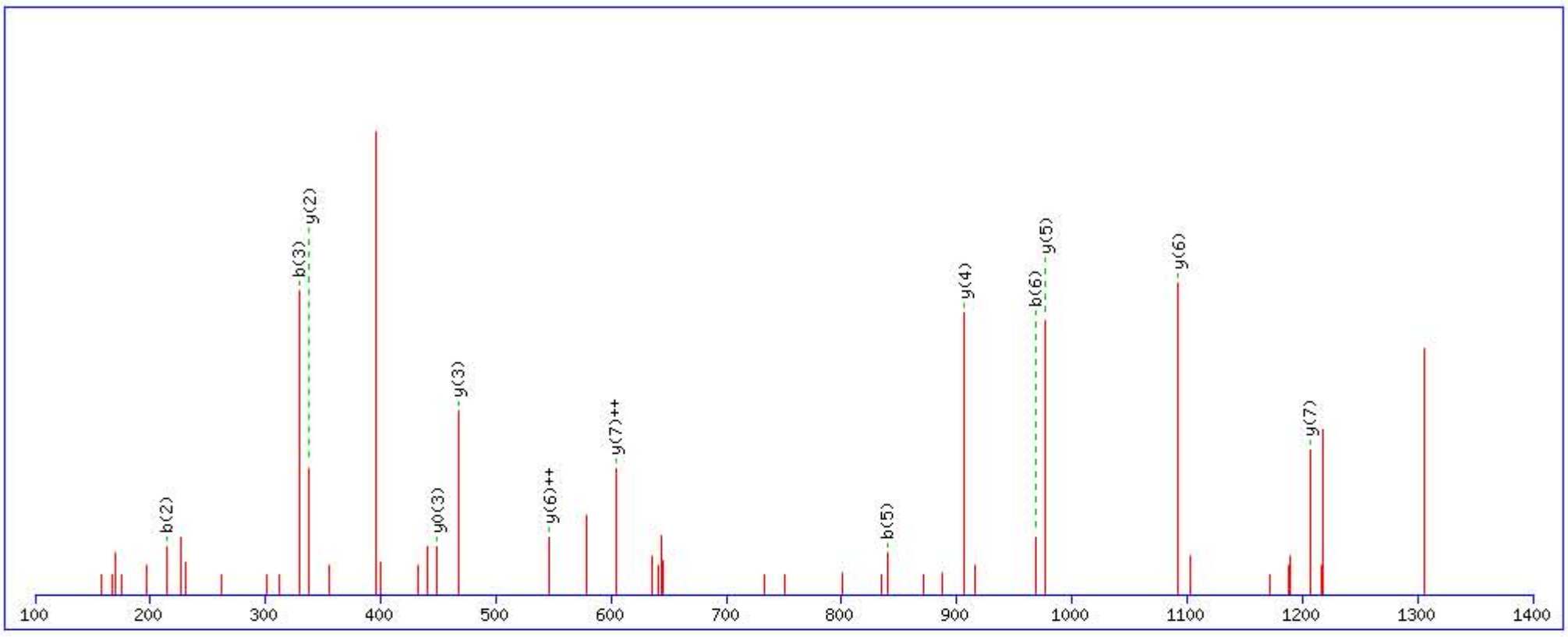
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VNDAQEYR**
Found in **FETUB_HUMAN**, Fetuin-B OS=Homo sapiens GN=FETUB PE=1 SV=2

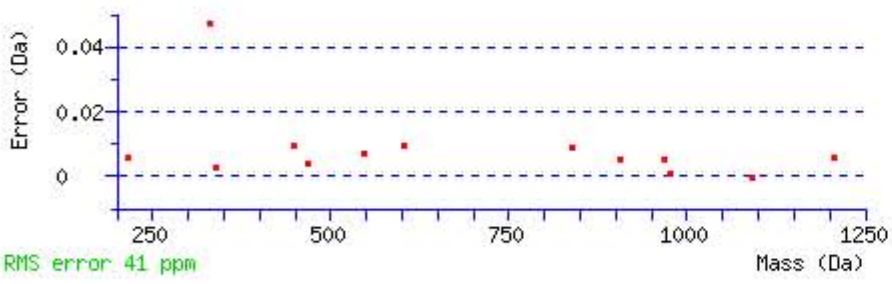
Match to Query 23404: 1304.619188 from(653.316870,2+) rtinseconds(1458) index(63247)
Title: Locus:1.1.1.1782.24 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

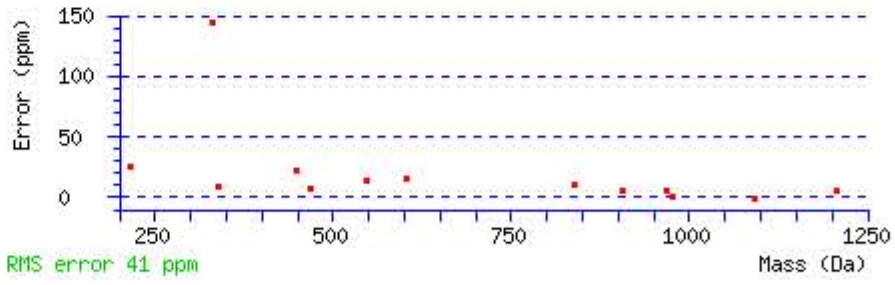
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1304.618301
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 37 **Expect:** 0.0026
**Matches :** 13/74 fragment ions using 22 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 8 |
| 2 | 214.118617 | 107.562947 | 197.092068 | 99.049672 | | | N | *1206.557184* | 603.782230 | 1189.530635 | 595.268956 | 1188.546619 | 594.776948 | 7 |
| 3 | 329.145560 | 165.076418 | 312.119011 | 156.563144 | 311.134995 | 156.071136 | D | *1092.514257* | 546.760767 | 1075.487708 | 538.247492 | 1074.503692 | 537.755484 | 6 |
| 4 | 400.182674 | 200.594975 | 383.156125 | 192.081700 | 382.172109 | 191.589692 | A | *977.487314* | 489.247295 | 960.460765 | 480.734021 | 959.476749 | 480.242013 | 5 |
| 5 | 839.408000 | 420.207638 | 822.381451 | 411.694364 | 821.397435 | 411.202356 | Q | *906.450200* | 453.728738 | 889.423651 | 445.215464 | 888.439635 | 444.723456 | 4 |
| 6 | 968.450593 | 484.728935 | 951.424044 | 476.215660 | 950.440028 | 475.723652 | E | *467.224874* | 234.116075 | 450.198325 | 225.602801 | 449.214309 | 225.110793 | 3 |
| 7 | 1131.513922 | 566.260599 | 1114.487373 | 557.747325 | 1113.503357 | 557.255317 | Y | *338.182281* | 169.594778 | 321.155732 | 161.081504 | | | 2 |
| 8 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 37.4 | 1304.618301 | 0.000887 | VNDAQEYR |

**Mascot:** http://www.matrixscience.com/

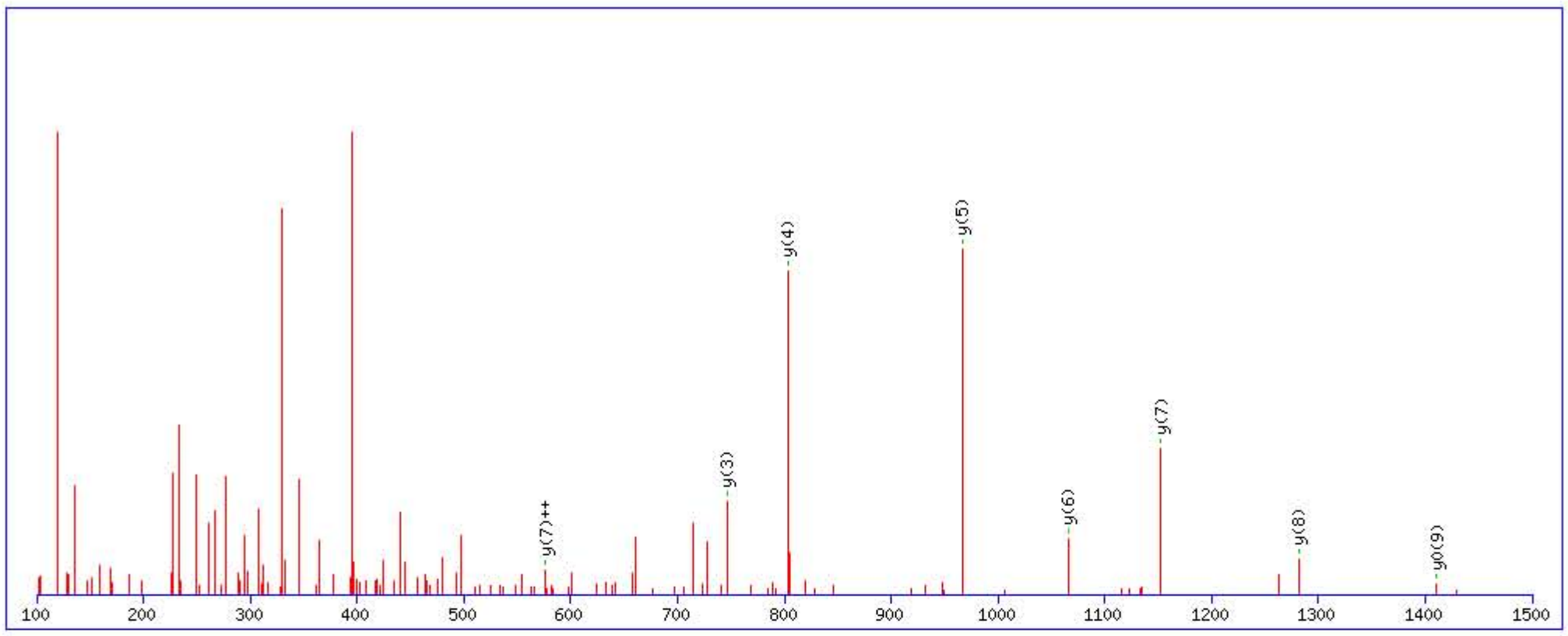
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IFFESVYGQCK**
Found in **FETUB_HUMAN**, Fetuin-B OS=Homo sapiens GN=FETUB PE=1 SV=2

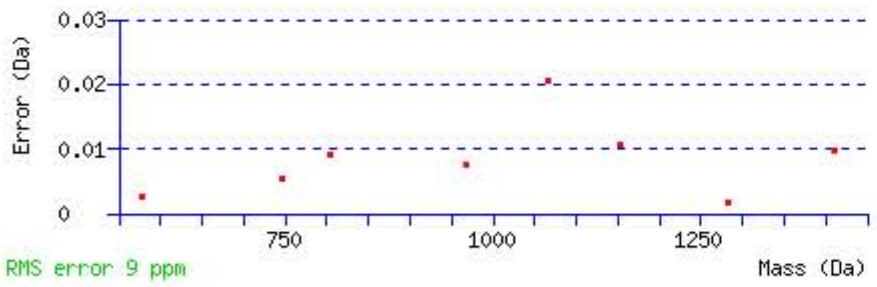
Match to Query 37707: 1687.821012 from(563.614280,3+) rtinseconds(2319) index(68258)
Title: Locus:1.1.1.2082.9 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

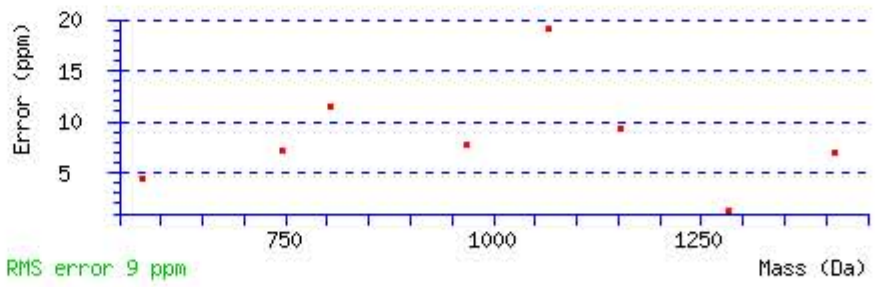
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1687.810226
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 35 **Expect:** 0.0073
**Matches :** 8/86 fragment ions using 13 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 11 |
| 2 | 261.159754 | 131.083515 | | | | | F | 1575.733435 | 788.370356 | 1558.706886 | 779.857081 | 1557.722870 | 779.365073 | 10 |
| 3 | 408.228168 | 204.617722 | | | | | F | 1428.665021 | 714.836149 | 1411.638472 | 706.322874 | 1410.654456 | 705.830866 | 9 |
| 4 | 537.270761 | 269.139019 | | | 519.260196 | 260.133736 | E | *1281.596607* | 641.301942 | 1264.570058 | 632.788667 | 1263.586042 | 632.296659 | 8 |
| 5 | 624.302789 | 312.655033 | | | 606.292224 | 303.649750 | S | *1152.554014* | 576.780645 | 1135.527465 | 568.267371 | 1134.543449 | 567.775363 | 7 |
| 6 | 723.371203 | 362.189239 | | | 705.360638 | 353.183957 | V | *1065.521986* | 533.264631 | 1048.495437 | 524.751357 | | | 6 |
| 7 | 886.434532 | 443.720904 | | | 868.423967 | 434.715622 | Y | *966.453572* | 483.730424 | 949.427023 | 475.217150 | | | 5 |
| 8 | 943.455996 | 472.231636 | | | 925.445431 | 463.226354 | G | *803.390243* | 402.198760 | 786.363694 | 393.685485 | | | 4 |
| 9 | 1382.681322 | 691.844299 | 1365.654773 | 683.331025 | 1364.670757 | 682.839017 | Q | *746.368779* | 373.688028 | 729.342230 | 365.174753 | | | 3 |
| 10 | 1542.711971 | 771.859624 | 1525.685422 | 763.346349 | 1524.701406 | 762.854341 | C | 307.143453 | 154.075365 | 290.116904 | 145.562090 | | | 2 |
| 11 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 34.6 | 1687.810226 | 0.010786 | IFFESVYGQCK |

**Mascot:** http://www.matrixscience.com/

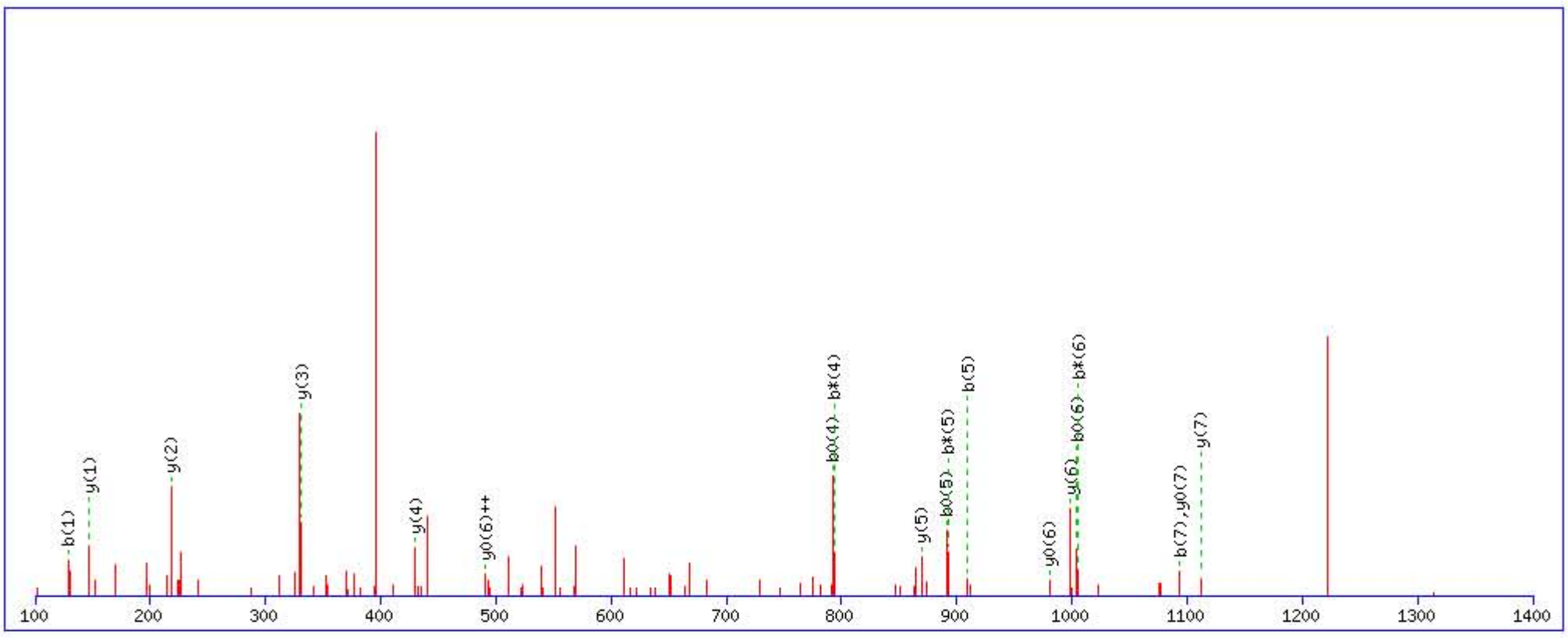
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QLEQVIAK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

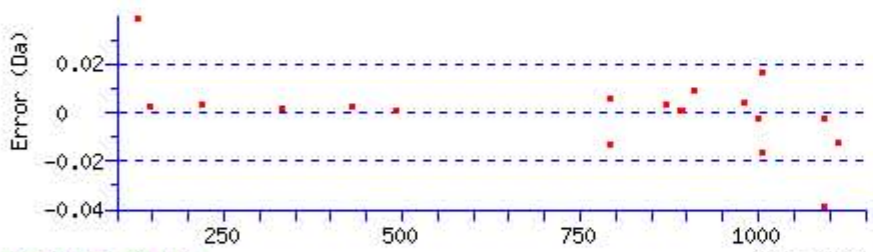
Match to Query 21515: 1238.706568 from(620.360560,2+) rtinseconds(1756) index(18604)
Title: Locus:1.1.1.2994.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

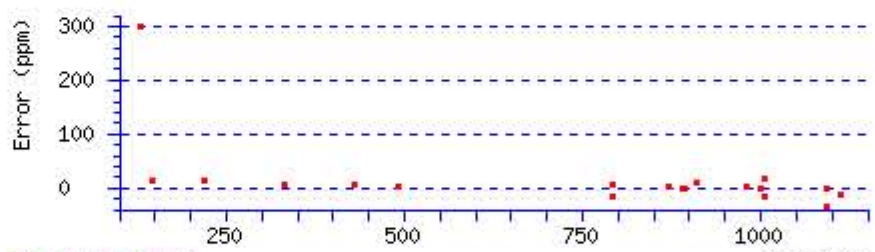
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1238.705658
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.0006
**Matches :** 19/70 fragment ions using 32 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.065854 | 65.036565 | 112.039305 | 56.523291 | | | Q | | | | | | | 8 |
| 2 | 242.149918 | 121.578597 | 225.123369 | 113.065323 | | | L | *1111.654379* | 556.330828 | 1094.627830 | 547.817553 | 1093.643814 | 547.325545 | 7 |
| 3 | 371.192511 | 186.099894 | 354.165962 | 177.586619 | 353.181946 | 177.094611 | E | *998.570315* | 499.788796 | 981.543766 | 491.275521 | 980.559750 | 490.783513 | 6 |
| 4 | 810.417837 | 405.712557 | 793.391288 | 397.199282 | 792.407272 | 396.707274 | Q | *869.527722* | 435.267499 | 852.501173 | 426.754225 | | | 5 |
| 5 | 909.486251 | 455.246764 | 892.459702 | 446.733489 | 891.475686 | 446.241481 | V | *430.302396* | 215.654836 | 413.275847 | 207.141562 | | | 4 |
| 6 | 1022.570315 | 511.788796 | 1005.543766 | 503.275521 | 1004.559750 | 502.783513 | I | *331.233982* | 166.120629 | 314.207433 | 157.607355 | | | 3 |
| 7 | 1093.607429 | 547.307353 | 1076.580880 | 538.794078 | 1075.596864 | 538.302070 | A | *218.149918* | 109.578597 | 201.123369 | 101.065323 | | | 2 |
| 8 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 44.1 | 1238.705658 | 0.000910 | QLEQVIAK |
| 13.6 | 1238.705658 | 0.000910 | QLEQVIAK |
| 11.3 | 1238.698257 | 0.008311 | IHADASSKVLAK |
| 10.8 | 1238.716904 | -0.010336 | DRVQVAIK |
| 6.3 | 1238.705658 | 0.000910 | QIAQEIVK |
| 5.5 | 1238.698273 | 0.008295 | GHVTQLKESLK |
| 5.4 | 1238.702301 | 0.004267 | DVFKKGFSIAK |
| 5.3 | 1238.716888 | -0.010320 | KRILCPLDPK |
| 4.8 | 1238.709473 | -0.002905 | NDLRPANKLAK |
| 3.3 | 1238.691040 | 0.015528 | LYKEFIDLAK |

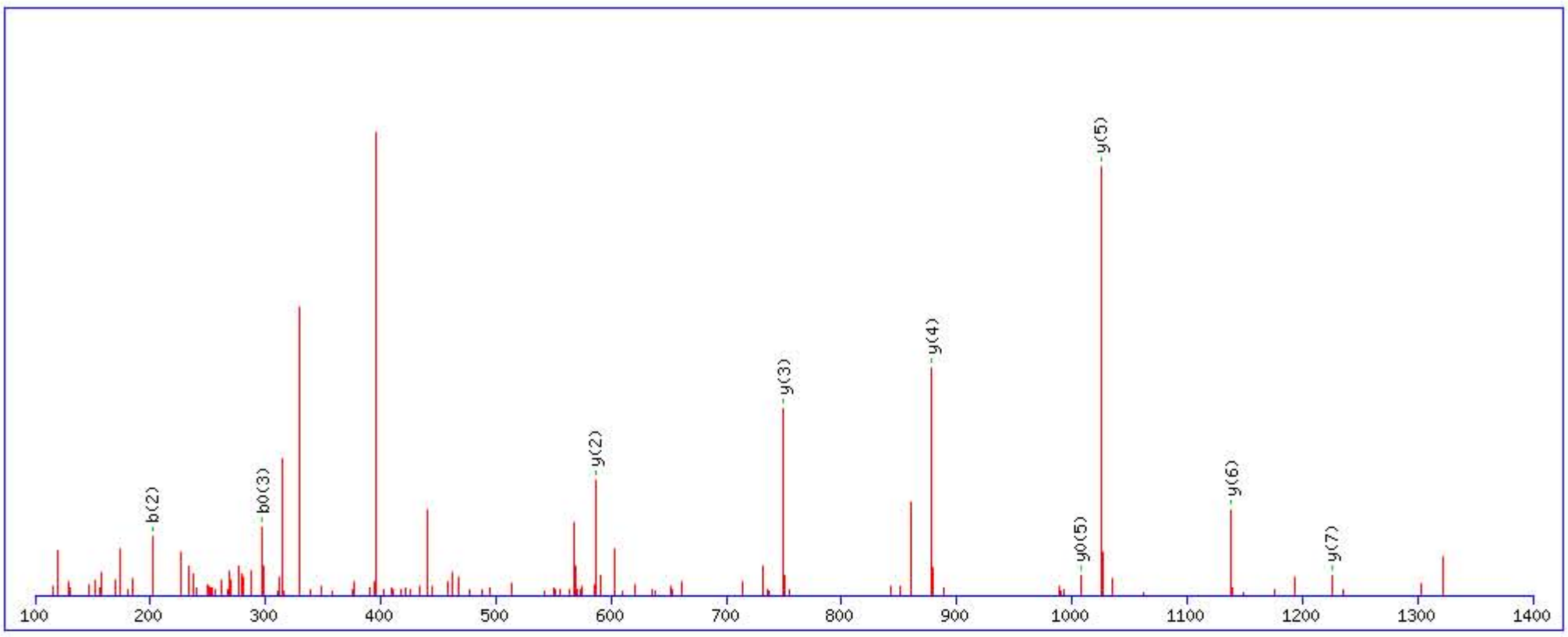
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NSLFEYQK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

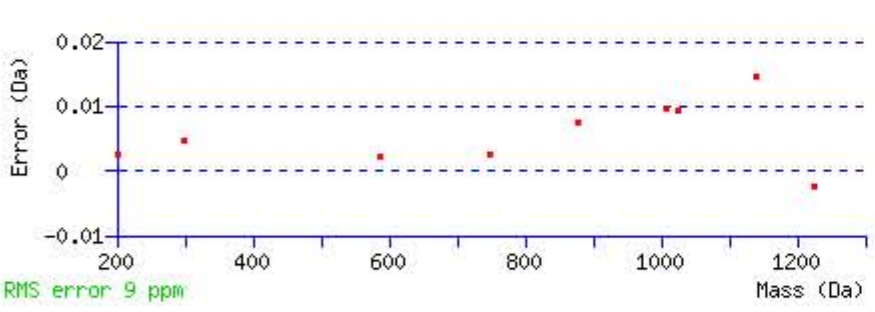
Match to Query 24061: 1338.672688 from(670.343620,2+) rtinseconds(2044) index(20483)
Title: Locus:1.1.1.3094.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

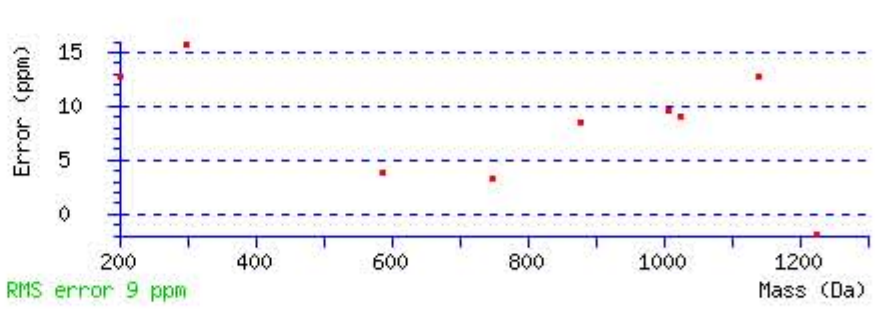
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1338.664185
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 49 **Expect:** 0.00023
**Matches :** 9/76 fragment ions using 13 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 8 |
| 2 | **202.082231** | 101.544753 | 185.055682 | 93.031479 | 184.071666 | 92.539471 | S | *1225.628558* | 613.317917 | 1208.602009 | 604.804643 | 1207.617993 | 604.312635 | 7 |
| 3 | 315.166295 | 158.086785 | 298.139746 | 149.573511 | 297.155730 | 149.081503 | L | *1138.596530* | 569.801903 | 1121.569981 | 561.288629 | 1120.585965 | 560.796621 | 6 |
| 4 | 462.234709 | 231.620993 | 445.208160 | 223.107718 | 444.224144 | 222.615710 | F | *1025.512466* | 513.259871 | 1008.485917 | 504.746597 | 1007.501901 | 504.254589 | 5 |
| 5 | 591.277302 | 296.142289 | 574.250753 | 287.629015 | 573.266737 | 287.137007 | E | *878.444052* | 439.725664 | 861.417503 | 431.212390 | 860.433487 | 430.720382 | 4 |
| 6 | 754.340631 | 377.673954 | 737.314082 | 369.160679 | 736.330066 | 368.668671 | Y | *749.401459* | 375.204368 | 732.374910 | 366.691093 | | | 3 |
| 7 | 1193.565957 | 597.286617 | 1176.539408 | 588.773342 | 1175.555392 | 588.281334 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 8 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 49.1 | 1338.664185 | 0.008503 | NSLFEYQK |
| 11.2 | 1338.660172 | 0.012516 | NSMFTAGKGVAEK |
| 8.0 | 1338.660172 | 0.012516 | BTVYLQMBSLR |
| 2.4 | 1338.682632 | -0.009944 | NLSRMQSRFGK |
| 1.5 | 1338.686188 | -0.013500 | TVKMMYQK |

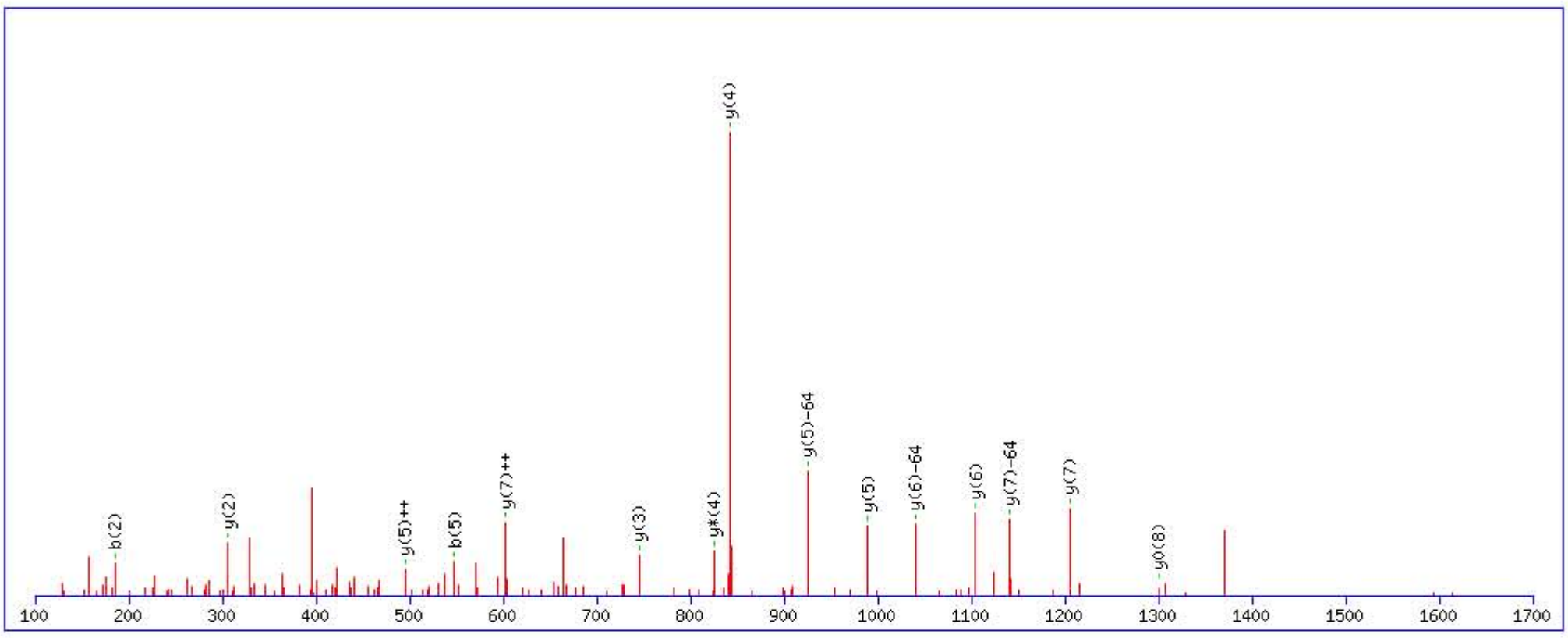
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ALTDMPQMR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

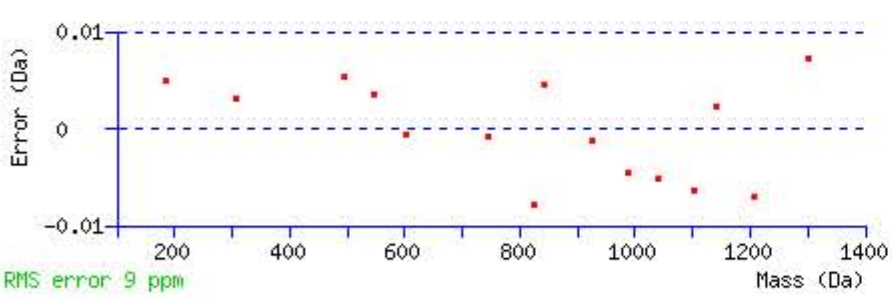
Match to Query 26760: 1388.662008 from(695.338280,2+) rtinseconds(1659) index(17930)
Title: Locus:1.1.1.2960.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

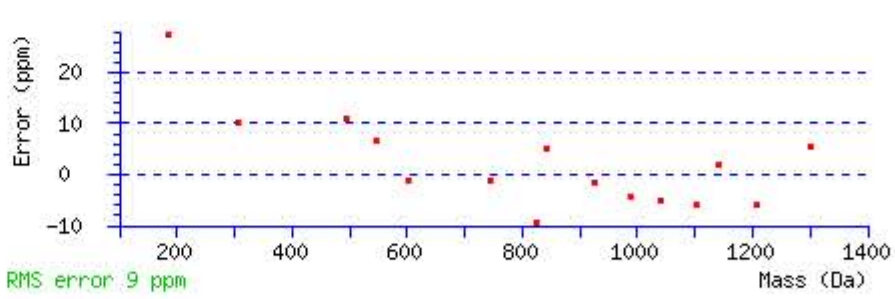
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1388.661438
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
M5 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 41 **Expect:** 0.00031
**Matches :** 15/112 fragment ions using 25 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 9 |
| 2 | **185.128454** | 93.067865 | | | | | L | 1318.631613 | 659.819445 | 1301.605064 | 651.306170 | 1300.621048 | 650.814162 | 8 |
| 3 | 286.176133 | 143.591704 | | | 268.165568 | 134.586422 | T | *1205.547549* | 603.277413 | 1188.521000 | 594.764138 | 1187.536984 | 594.272130 | 7 |
| 4 | 401.203076 | 201.105176 | | | 383.192511 | 192.099894 | D | *1104.499870* | 552.753573 | 1087.473321 | 544.240298 | 1086.489305 | 543.748290 | 6 |
| 5 | **548.238476** | 274.622876 | | | 530.227911 | 265.617594 | M | *989.472927* | 495.240102 | 972.446378 | 486.726827 | | | 5 |
| 6 | 645.291240 | 323.149258 | | | 627.280675 | 314.143976 | P | *842.437527* | 421.722402 | 825.410978 | 413.209127 | | | 4 |
| 7 | 1084.516566 | 542.761921 | 1067.490017 | 534.248647 | 1066.506001 | 533.756639 | Q | *745.384763* | 373.196020 | 728.358214 | 364.682745 | | | 3 |
| 8 | 1215.557051 | 608.282164 | 1198.530502 | 599.768889 | 1197.546486 | 599.276881 | M | *306.159437* | 153.583356 | 289.132888 | 145.070082 | | | 2 |
| 9 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 40.9 | 1388.661438 | 0.000570 | ALTDMPQMR |
| 9.2 | 1388.661438 | 0.000570 | ALTDMPQMR |

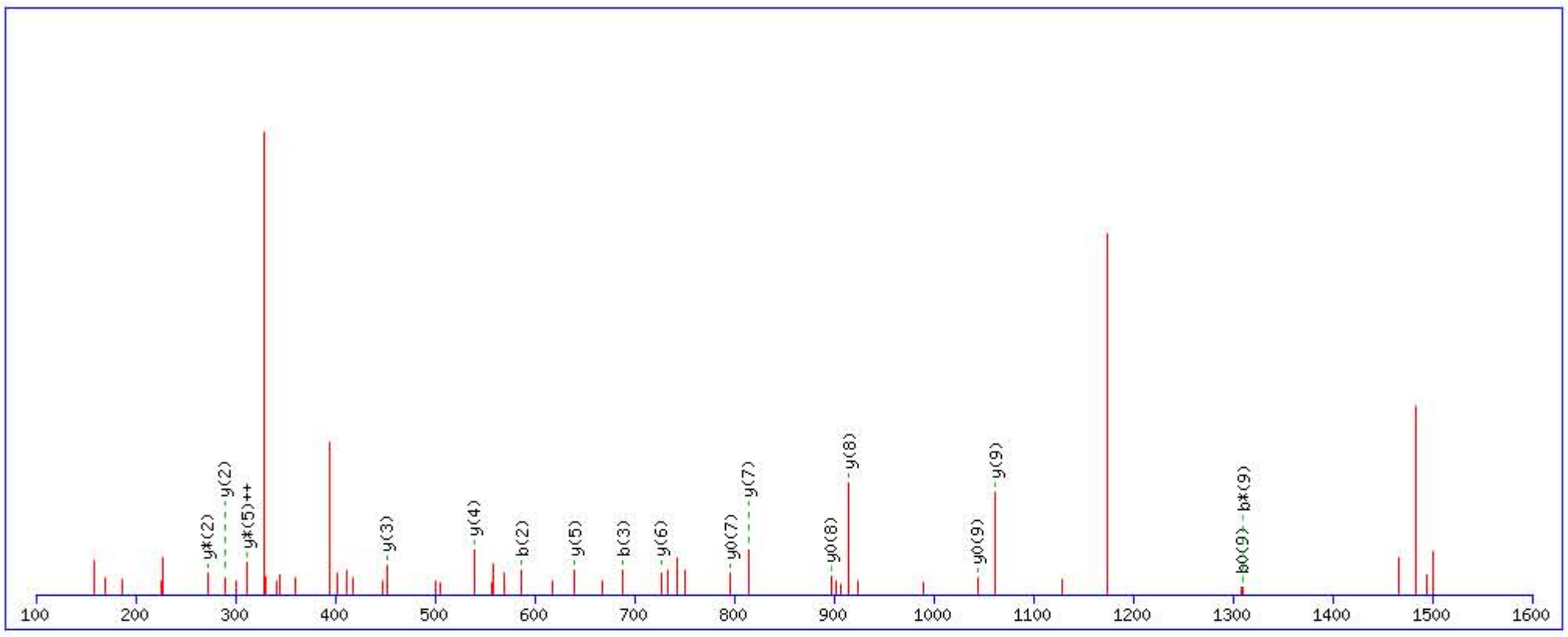
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QFTSSTSYNR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

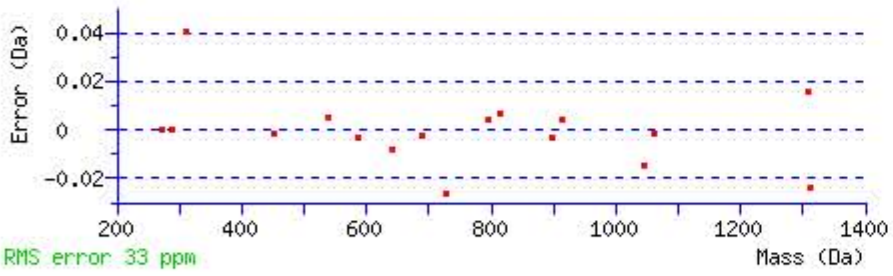
Match to Query 31048: 1500.706068 from(751.360310,2+) rtinseconds(1570) index(63947)
Title: Locus:1.1.1.1821.19 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

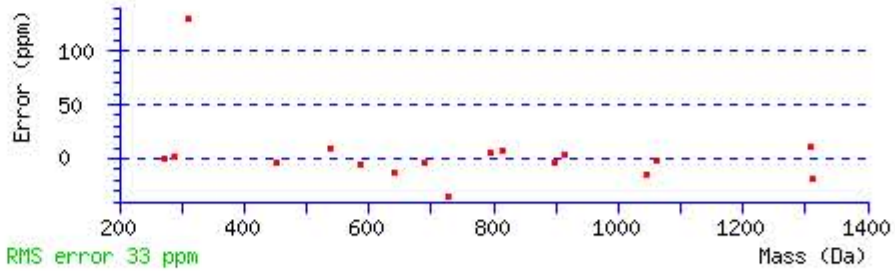
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1500.703110
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0015
**Matches :** 17/98 fragment ions using 52 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 10 |
| 2 | 587.301016 | 294.154146 | 570.274467 | 285.640872 | | | F | *1062.485064* | 531.746170 | 1045.458515 | 523.232896 | 1044.474499 | 522.740887 | 9 |
| 3 | 688.348695 | 344.677986 | 671.322146 | 336.164711 | 670.338130 | 335.672703 | T | *915.416650* | 458.211963 | 898.390101 | 449.698689 | 897.406085 | 449.206681 | 8 |
| 4 | 775.380723 | 388.194000 | 758.354174 | 379.680725 | 757.370158 | 379.188717 | S | *814.368971* | 407.688124 | 797.342422 | 399.174849 | 796.358406 | 398.682841 | 7 |
| 5 | 862.412751 | 431.710014 | 845.386202 | 423.196739 | 844.402186 | 422.704731 | S | *727.336943* | 364.172110 | 710.310394 | 355.658835 | 709.326378 | 355.166827 | 6 |
| 6 | 963.460430 | 482.233853 | 946.433881 | 473.720578 | 945.449865 | 473.228570 | T | *640.304915* | 320.656096 | 623.278366 | 312.142821 | 622.294350 | 311.650813 | 5 |
| 7 | 1050.492458 | 525.749867 | 1033.465909 | 517.236593 | 1032.481893 | 516.744584 | S | *539.257236* | 270.132256 | 522.230687 | 261.618982 | 521.246671 | 261.126974 | 4 |
| 8 | 1213.555787 | 607.281532 | 1196.529238 | 598.768257 | 1195.545222 | 598.276249 | Y | *452.225208* | 226.616242 | 435.198659 | 218.102967 | | | 3 |
| 9 | 1327.598714 | 664.302995 | 1310.572165 | 655.789721 | 1309.588149 | 655.297712 | N | *289.161879* | 145.084577 | 272.135330 | 136.571303 | | | 2 |
| 10 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 32.6 | 1500.703110 | 0.002958 | QFTSSTSYNR |
| 2.6 | 1500.724869 | -0.018801 | SKIEDYFPEFAR |

**Mascot:** http://www.matrixscience.com/

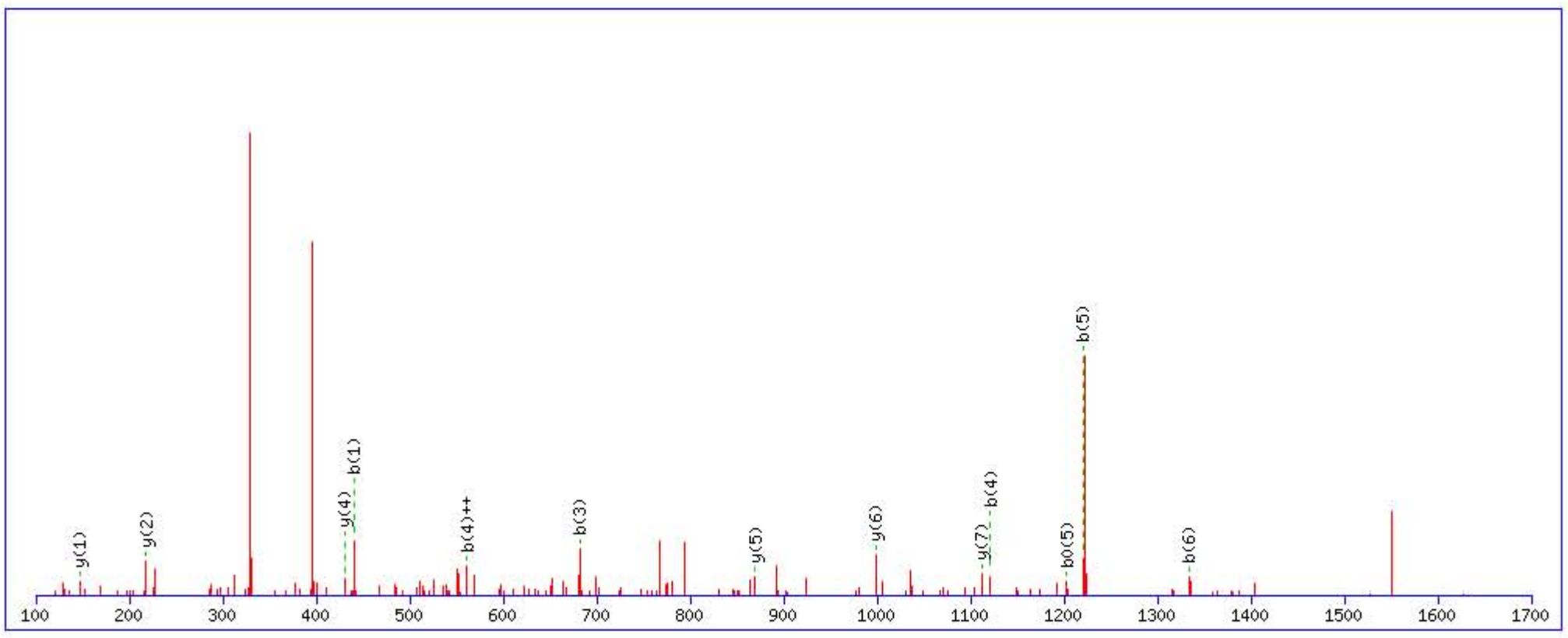
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QLEQVIAK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

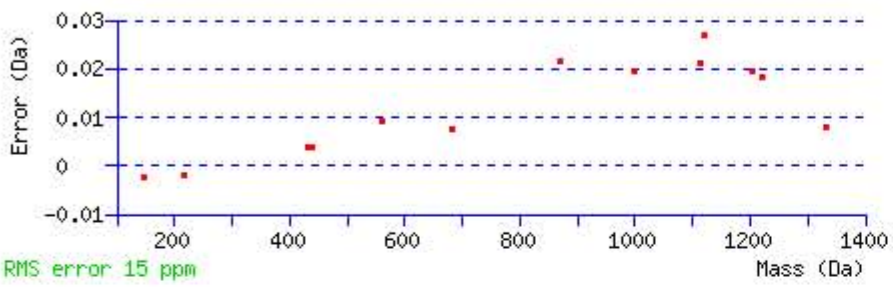
Match to Query 32511: 1549.859708 from(775.937130,2+) rtinseconds(2117) index(51117)
Title: Locus:1.1.1.1974.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

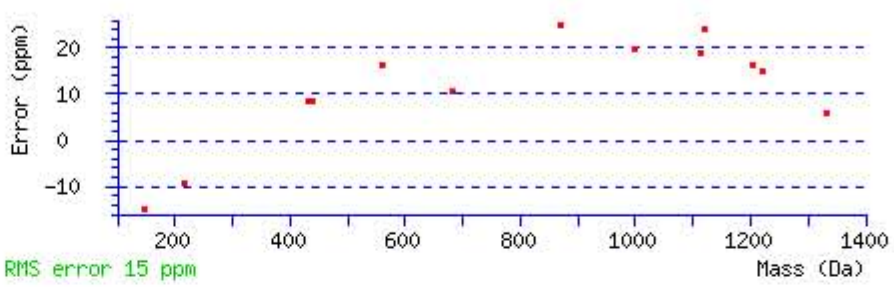
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1549.872406
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Q4** : Biotin:Thermo-21345 (Q)
**Ions Score:** 25 **Expect:** 0.015
**Matches** : 13/70 fragment ions using 27 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *440.232602* | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 8 |
| 2 | 553.316666 | 277.161971 | 536.290117 | 268.648697 | | | L | *1111.654379* | 556.330828 | 1094.627830 | 547.817553 | 1093.643814 | 547.325545 | 7 |
| 3 | *682.359259* | 341.683268 | 665.332710 | 333.169993 | 664.348694 | 332.677985 | E | *998.570315* | 499.788796 | 981.543766 | 491.275521 | 980.559750 | 490.783513 | 6 |
| 4 | *1121.584585* | 561.295931 | 1104.558036 | 552.782656 | 1103.574020 | 552.290648 | Q | *869.527722* | 435.267499 | 852.501173 | 426.754225 | | | 5 |
| 5 | *1220.652999* | 610.830138 | 1203.626450 | 602.316863 | 1202.642434 | 601.824855 | V | *430.302396* | 215.654836 | 413.275847 | 207.141561 | | | 4 |
| 6 | *1333.737063* | 667.372170 | 1316.710514 | 658.858895 | 1315.726498 | 658.366887 | I | 331.233982 | 166.120629 | 314.207433 | 157.607354 | | | 3 |
| 7 | 1404.774177 | 702.890727 | 1387.747628 | 694.377452 | 1386.763612 | 693.885444 | A | *218.149918* | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 8 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.4 | 1549.872406 | -0.012698 | QLEQVIAK |
| 5.5 | 1549.861633 | -0.001925 | KLSRPFQSEIFAK |
| 4.2 | 1549.865005 | -0.005297 | KSLAGMLTPYVARK |
| 3.6 | 1549.846359 | 0.013349 | ATEQLETYRKLAK |
| 2.3 | 1549.857605 | 0.002103 | RIEVENKEVLHGK |
| 1.3 | 1549.861618 | -0.001910 | TAEKLYRTAWIAK |
| 0.9 | 1549.855148 | 0.004560 | QSFVPVRPGPR |
| 0.9 | 1549.862991 | -0.003283 | AAWLRVFQHLGPR |
| 0.0 | 1549.857620 | 0.002088 | TRAADLLVNPLDPR |

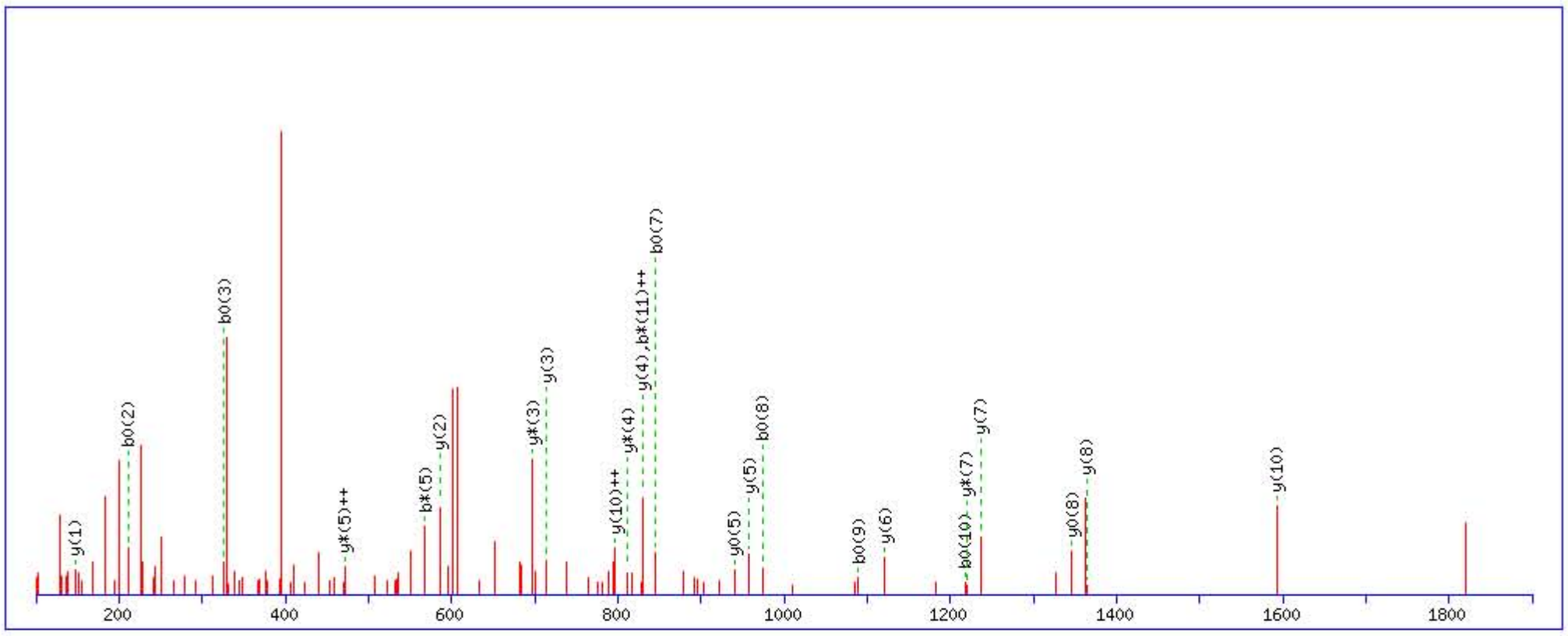
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EVDLKDYEDQQK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

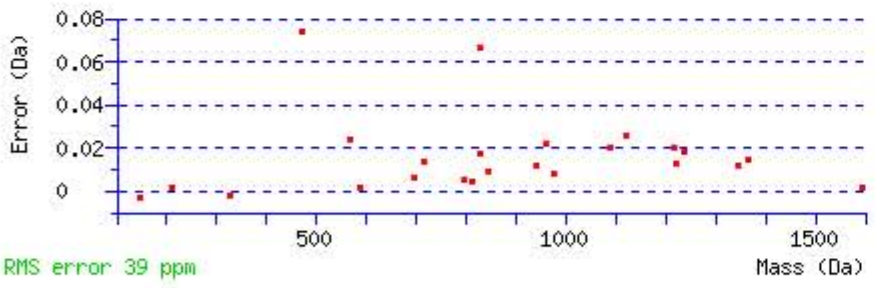
Match to Query 40727: 1819.877982 from(607.633270,3+) rtinseconds(1781) index(48861)
Title: Locus:1.1.1.1858.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

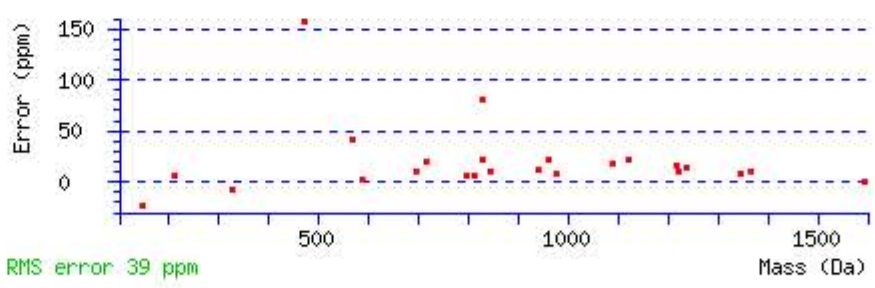
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1819.866196
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 29 **Expect:** 0.026
**Matches** : 24/118 fragment ions using 49 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 12 |
| 2 | 229.118283 | 115.062780 | | | 211.107718 | 106.057497 | V | 1691.830900 | 846.419088 | 1674.804351 | 837.905814 | 1673.820335 | 837.413806 | 11 |
| 3 | 344.145226 | 172.576251 | | | 326.134661 | 163.570969 | D | *1592.762486* | 796.884881 | 1575.735937 | 788.371607 | 1574.751921 | 787.879599 | 10 |
| 4 | 457.229290 | 229.118283 | | | 439.218725 | 220.113001 | L | 1477.735543 | 739.371410 | 1460.708994 | 730.858135 | 1459.724978 | 730.366127 | 9 |
| 5 | 585.324253 | 293.165765 | 568.297704 | 284.652490 | 567.313688 | 284.160482 | K | *1364.651479* | 682.829378 | 1347.624930 | 674.316103 | 1346.640914 | 673.824095 | 8 |
| 6 | 700.351196 | 350.679236 | 683.324647 | 342.165962 | 682.340631 | 341.673954 | D | *1236.556516* | 618.781896 | 1219.529967 | 610.268622 | 1218.545951 | 609.776614 | 7 |
| 7 | 863.414525 | 432.210901 | 846.387976 | 423.697626 | 845.403960 | 423.205618 | Y | *1121.529573* | 561.268425 | 1104.503024 | 552.755150 | 1103.519008 | 552.263142 | 6 |
| 8 | 992.457118 | 496.732197 | 975.430569 | 488.218923 | 974.446553 | 487.726915 | E | *958.466244* | 479.736760 | 941.439695 | 471.223486 | 940.455679 | 470.731478 | 5 |
| 9 | 1107.484061 | 554.245669 | 1090.457512 | 545.732394 | 1089.473496 | 545.240386 | D | *829.423651* | 415.215464 | 812.397102 | 406.702189 | 811.413086 | 406.210181 | 4 |
| 10 | 1235.542639 | 618.274958 | 1218.516090 | 609.761683 | 1217.532074 | 609.269675 | Q | *714.396708* | 357.701992 | 697.370159 | 349.188718 | | | 3 |
| 11 | 1674.767965 | 837.887621 | 1657.741416 | 829.374346 | 1656.757400 | 828.882338 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 12 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 29.0 | 1819.866196 | 0.011786 | EVDLKDYEDQQK |
| 20.6 | 1819.866196 | 0.011786 | EVDLKDYEDQQK |

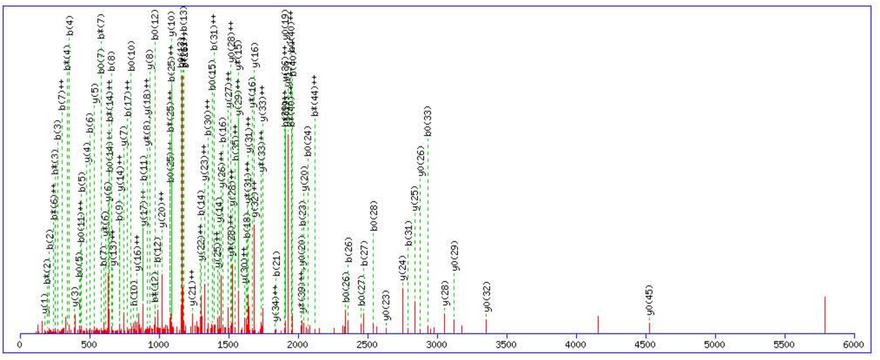
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPRPGSTGTWNPGSSER
Found in FIBA_HUMAN, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

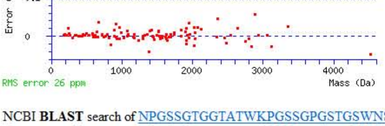
Match to Query 74930: 5844.652720 from(1169.937820,5+) rtinseconds(1758) index(18615)
Title: Locus:1.1.1.2994.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

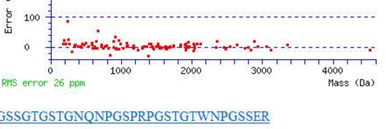
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 6000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



**Monoisotopic mass of neutral peptide Mr(calc):** 5844.608032
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q39 : Biotin:Thermo-21345 (Q)
**Ions Score:** 120 **Expect:** 5.7e-012
**Matches :** 107/688 fragment ions using 204 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^0$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^0$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 59 |
| 2 | *212.102967* | 106.555121 | 195.076418 | 98.041847 | | | P | 5731.572302 | 2866.289789 | 5714.545753 | 2857.776515 | 5713.561737 | 2857.284507 | 58 |
| 3 | *269.124431* | 135.065853 | 252.097882 | 126.552579 | | | G | 5634.519538 | 2817.763407 | 5617.492989 | 2809.250133 | 5616.508973 | 2808.758125 | 57 |
| 4 | *356.156459* | 178.581867 | 339.129910 | 170.068593 | 338.145894 | 169.576585 | S | 5577.498074 | 2789.252675 | 5560.471525 | 2780.739401 | 5559.487509 | 2780.247393 | 56 |
| 5 | *443.188487* | 222.097881 | 426.161938 | 213.584607 | 425.177922 | 213.092599 | S | 5490.466046 | 2745.736661 | 5473.439497 | 2737.223387 | 5472.455481 | 2736.731379 | 55 |
| 6 | *500.209951* | 250.608613 | 483.183402 | 242.095339 | 482.199386 | 241.603331 | G | 5403.434018 | 2702.220647 | 5386.407469 | 2693.707373 | 5385.423453 | 2693.215365 | 54 |
| 7 | *601.257630* | **301.132453** | 584.231081 | 292.619178 | 583.247065 | 292.127170 | T | 5346.412554 | 2673.709915 | 5329.386005 | 2665.196641 | 5328.401989 | 2664.704633 | 53 |
| 8 | *658.279094* | 329.643185 | 641.252545 | 321.129910 | 640.268529 | 320.637903 | G | 5245.364875 | 2623.186076 | 5228.338326 | 2614.672801 | 5227.354310 | 2614.180793 | 52 |
| 9 | *715.300558* | 358.153917 | 698.274009 | 349.640643 | 697.289993 | 349.148635 | G | 5188.343411 | 2594.675344 | 5171.316862 | 2586.162069 | 5170.332846 | 2585.670061 | 51 |
| 10 | *816.348237* | 408.677757 | 799.321688 | 400.164482 | 798.337672 | 399.672474 | T | 5131.321947 | 2566.164612 | 5114.295398 | 2557.651337 | 5113.311382 | 2557.159329 | 50 |
| 11 | *887.385351* | 444.196314 | 870.358802 | 435.683039 | 869.374786 | 435.191031 | A | 5030.274268 | 2515.640772 | 5013.247719 | 2507.127498 | 5012.263703 | 2506.635490 | 49 |
| 12 | *988.433030* | 494.720153 | 971.406481 | 486.206879 | 970.422465 | 485.714871 | T | 4959.237154 | 2480.122215 | 4942.210605 | 2471.608941 | 4941.226589 | 2471.116933 | 48 |
| 13 | *1174.512343* | 587.759810 | 1157.485794 | 579.246535 | 1156.501778 | 578.754527 | W | 4858.189475 | 2429.598376 | 4841.162926 | 2421.085101 | 4840.178910 | 2420.593093 | 47 |
| 14 | *1302.607306* | 651.807291 | 1285.580757 | 643.294017 | 1284.596741 | 642.802009 | K | 4672.110162 | 2336.558719 | 4655.083613 | 2328.045445 | 4654.099597 | 2327.553437 | 46 |
| 15 | 1399.660070 | 700.333673 | 1382.633521 | 691.820399 | 1381.649505 | 691.328391 | P | 4544.015199 | 2272.511238 | 4526.988650 | 2263.997963 | 4526.004634 | 2263.505955 | 45 |
| 16 | *1456.681534* | 728.844405 | 1439.654985 | 720.331131 | 1438.670969 | 719.839123 | G | 4446.962435 | 2223.984856 | 4429.935886 | 2215.471581 | 4428.951870 | 2214.979573 | 44 |
| 17 | 1543.713562 | **772.360419** | 1526.687013 | 763.847145 | 1525.702997 | 763.355137 | S | 4389.940971 | 2195.474124 | 4372.914422 | 2186.960849 | 4371.930406 | 2186.468841 | 43 |
| 18 | *1630.745590* | 815.876433 | 1613.719041 | 807.363159 | 1612.735025 | 806.871151 | S | 4302.908943 | 2151.958110 | 4285.882394 | 2143.444835 | 4284.898378 | 2142.952827 | 42 |
| 19 | 1687.767054 | 844.387165 | 1670.740505 | 835.873891 | 1669.756489 | 835.381883 | G | 4215.876915 | 2108.442096 | 4198.850366 | 2099.928821 | 4197.866350 | 2099.436813 | 41 |
| 20 | 1784.819818 | 892.913547 | 1767.793269 | 884.400273 | 1766.809253 | 883.908265 | P | 4158.855451 | 2079.931364 | 4141.828902 | 2071.418089 | 4140.844886 | 2070.926081 | 40 |
| 21 | *1841.841282* | 921.424279 | 1824.814733 | 912.911005 | 1823.830717 | 912.418997 | G | 4061.802687 | 2031.404982 | 4044.776138 | 2022.891707 | 4043.792122 | 2022.399699 | 39 |
| 22 | 1928.873310 | 964.940293 | 1911.846761 | 956.427019 | 1910.862745 | 955.935011 | S | 4004.781223 | 2002.894250 | 3987.754674 | 1994.380975 | 3986.770658 | 1993.888967 | 38 |
| 23 | *2029.920989* | 1015.464133 | 2012.894440 | 1006.950858 | 2011.910424 | 1006.458850 | T | 3917.749195 | 1959.378236 | 3900.722646 | 1950.864961 | 3899.738630 | 1950.372953 | 37 |
| 24 | 2086.942453 | 1043.974865 | 2069.915904 | 1035.461590 | 2068.931888 | 1034.969582 | G | 3816.701516 | 1908.854396 | 3799.674967 | 1900.341122 | 3798.690951 | 1899.849114 | 36 |
| 25 | 2173.974481 | **1087.490879** | 2156.947932 | 1078.977604 | 2155.963916 | 1078.485596 | S | 3759.680052 | 1880.343664 | 3742.653503 | 1871.830389 | 3741.669487 | 1871.338382 | 35 |
| 26 | *2360.053794* | **1180.530535** | 2343.027245 | 1172.017261 | 2342.043229 | 1171.525253 | W | 3672.648024 | 1836.827650 | 3655.621475 | 1828.314375 | 3654.637459 | 1827.822367 | 34 |
| 27 | *2474.096721* | 1237.551999 | 2457.070172 | 1229.038724 | 2456.086156 | 1228.546716 | N | 3486.568711 | 1743.787993 | 3469.542162 | 1735.274719 | 3468.558146 | 1734.782711 | 33 |
| 28 | 2561.128749 | 1281.068013 | 2544.102200 | 1272.554738 | 2543.118184 | 1272.062730 | S | 3372.525784 | 1686.766530 | 3355.499235 | 1678.253255 | 3354.515219 | 1677.761247 | 32 |
| 29 | 2618.150213 | 1309.578745 | 2601.123664 | 1301.065470 | 2600.139648 | 1300.573462 | G | 3285.493756 | 1643.250516 | 3268.467207 | 1634.737241 | 3267.483191 | 1634.245233 | 31 |
| 30 | 2705.182241 | **1353.094759** | 2688.155692 | 1344.581484 | 2687.171676 | 1344.089476 | S | 3228.472292 | 1614.739784 | 3211.445743 | 1606.226509 | 3210.461727 | 1605.734501 | 30 |
| 31 | *2792.214269* | **1396.610773** | 2775.187720 | 1388.097498 | 2774.203704 | 1387.605490 | S | 3141.440264 | 1571.223770 | 3124.413715 | 1562.710495 | 3123.429699 | 1562.218487 | 29 |
| 32 | 2849.235733 | 1425.121505 | 2832.209184 | 1416.608230 | 2831.225168 | 1416.116222 | G | *3054.408236* | 1527.707756 | 3037.381687 | 1519.194481 | 3036.397671 | 1518.702473 | 28 |
| 33 | 2950.283412 | 1475.645344 | 2933.256863 | 1467.132069 | 2932.272847 | 1466.640062 | T | 2997.386772 | 1499.197024 | 2980.360223 | 1490.683749 | 2979.376207 | 1490.191741 | 27 |
| 34 | 3007.304876 | 1504.156076 | 2990.278327 | 1495.642801 | 2989.294311 | 1495.150794 | G | 2896.339093 | 1448.673184 | 2879.312544 | 1440.159910 | 2878.328528 | 1439.667902 | 26 |
| 35 | 3094.336904 | **1547.672090** | 3077.310355 | 1539.158815 | 3076.326339 | 1538.666808 | S | *2839.317629* | 1420.162453 | 2822.291080 | 1411.649178 | 2821.307064 | 1411.157170 | 25 |
| 36 | 3195.384583 | 1598.195929 | 3178.358034 | 1589.682655 | 3177.374018 | 1589.190647 | T | *2752.285601* | 1376.646438 | 2735.259052 | 1368.133164 | 2734.275036 | 1367.641156 | 24 |
| 37 | 3252.406047 | 1626.706661 | 3235.379498 | 1618.193387 | 3234.395482 | 1617.701379 | G | 2651.237922 | 1326.122599 | 2634.211373 | 1317.609325 | 2633.227357 | 1317.117317 | 23 |
| 38 | 3366.448974 | 1683.728125 | 3349.422425 | 1675.214850 | 3348.438409 | 1674.722842 | N | 2594.216458 | 1297.611867 | 2577.189909 | 1289.098593 | 2576.205893 | 1288.606585 | 22 |
| 39 | 3805.674300 | **1903.340788** | 3788.647751 | 1894.827513 | 3787.663735 | 1894.335506 | Q | 2480.173531 | 1240.590404 | 2463.146982 | 1232.077129 | 2462.162966 | 1231.585121 | 21 |
| 40 | 3919.717227 | **1960.362252** | 3902.690678 | *1951.848977* | 3901.706662 | *1951.356969* | N | *2040.948205* | 1020.977741 | 2023.921656 | 1012.464466 | 2022.937640 | 1011.972458 | 20 |
| 41 | 4016.769991 | 2008.888634 | 3999.743442 | 2000.375359 | 3998.759426 | 1999.883351 | P | *1926.905278* | 963.956277 | 1909.878729 | 955.443003 | 1908.894713 | 954.950995 | 19 |
| 42 | 4073.791455 | 2037.399365 | 4056.764906 | 2028.886091 | 4055.780890 | 2028.394083 | G | 1829.852514 | 915.429895 | 1812.825965 | 906.916621 | 1811.841949 | 906.424613 | 18 |
| 43 | 4160.823483 | 2080.915380 | 4143.796934 | 2072.402105 | 4142.812918 | 2071.910097 | S | 1772.831050 | 886.919163 | 1755.804501 | 878.405889 | 1754.820485 | 877.913881 | 17 |
| 44 | 4257.876247 | 2129.441762 | 4240.849698 | 2120.928487 | 4239.865682 | 2120.436479 | P | *1685.799022* | 843.403149 | 1668.772473 | 834.889875 | 1667.788457 | 834.397867 | 16 |
| 45 | 4413.977358 | 2207.492317 | 4396.950809 | 2198.979043 | 4395.966793 | 2198.487035 | R | 1588.746258 | 794.876767 | 1571.719709 | 786.363493 | 1570.735693 | 785.871485 | 15 |
| 46 | 4511.030122 | 2256.018699 | 4494.003573 | 2247.505425 | 4493.019557 | 2247.013417 | P | *1432.645147* | 716.826212 | 1415.618598 | 708.312937 | 1414.634582 | 707.820929 | 14 |
| 47 | 4568.051586 | 2284.529431 | 4551.025037 | 2276.016157 | 4550.041021 | 2275.524149 | G | 1335.592383 | 668.299830 | 1318.565834 | 659.786555 | 1317.581818 | 659.294547 | 13 |
| 48 | 4655.083614 | 2328.045445 | 4638.057065 | 2319.532171 | 4637.073049 | 2319.040163 | S | 1278.570919 | 639.789098 | 1261.544370 | 631.275823 | 1260.560354 | 630.783815 | 12 |
| 49 | 4756.131293 | 2378.569285 | 4739.104744 | 2370.056010 | 4738.120728 | 2369.564002 | T | 1191.538891 | 596.273084 | *1174.512342* | 587.759809 | 1173.528326 | 587.267801 | 11 |
| 50 | 4813.152757 | 2407.080017 | 4796.126208 | 2398.566742 | 4795.142192 | 2398.074734 | G | *1090.491212* | 545.749244 | 1073.464663 | 537.235970 | 1072.480647 | 536.743962 | 10 |
| 51 | 4914.200436 | 2457.603856 | 4897.173887 | 2449.090582 | 4896.189871 | 2448.598574 | T | 1033.469748 | 517.238512 | 1016.443199 | 508.725238 | 1015.459183 | 508.233230 | 9 |
| 52 | 5100.279749 | 2550.643513 | 5083.253200 | 2542.130238 | 5082.269184 | 2541.638230 | W | *932.422069* | 466.714673 | 915.395520 | 458.201398 | 914.411504 | 457.709390 | 8 |
| 53 | 5214.322676 | 2607.664976 | 5197.296127 | 2599.151702 | 5196.312111 | 2598.659694 | N | *746.342756* | 373.675016 | 729.316207 | 365.161742 | 728.332191 | 364.669734 | 7 |
| 54 | 5311.375440 | 2656.191358 | 5294.348891 | 2647.678084 | 5293.364875 | 2647.186076 | P | *632.299829* | 316.653552 | 615.273280 | 308.140278 | 614.289264 | 307.648270 | 6 |
| 55 | 5368.396904 | 2684.702090 | 5351.370355 | 2676.188816 | 5350.386339 | 2675.696808 | G | *535.247065* | 268.127170 | 518.220516 | 259.613896 | 517.236500 | 259.121888 | 5 |
| 56 | 5455.428932 | 2728.218104 | 5438.402383 | 2719.704830 | 5437.418367 | 2719.212822 | S | *478.225601* | 239.616438 | 461.199052 | 231.103164 | 460.215036 | 230.611156 | 4 |
| 57 | 5542.460960 | 2771.734118 | 5525.434411 | 2763.220844 | 5524.450395 | 2762.728836 | S | *391.193573* | 196.100424 | 374.167024 | 187.587150 | 373.183008 | 187.095142 | 3 |
| 58 | 5671.503553 | 2836.255415 | 5654.477004 | 2827.742140 | 5653.492988 | 2827.250132 | E | 304.161545 | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 59 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 119.6 | 5844.608032 | 0.044688 | NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPRPGSTGTWNPGSSER |

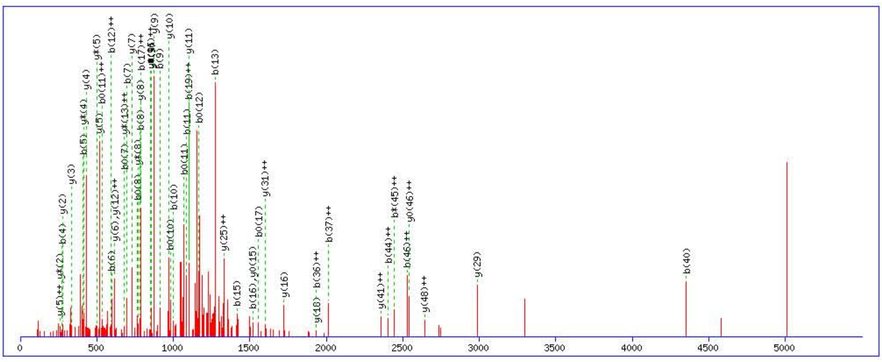
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GSAGHWTSESSVSGSTGQWHSESGSFRPDSPGSGNARPNNPDWGTFEEVSGNVSPGTR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

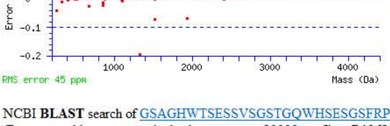
Match to Query 75121: 6284.847264 from(1048.481820,6+) rtinseconds(2044) index(66674)
Title: Locus:1.1.1.1986.17 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

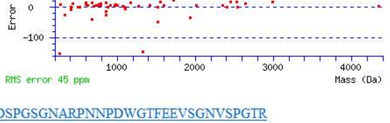
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 5500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 6284.792847
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q18** : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 8.2e-005
**Matches :** 56/646 fragment ions using 128 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 58 |
| 2 | 145.060768 | 73.034022 | | | 127.050203 | 64.028740 | S | 6228.778603 | 3114.892940 | 6211.752054 | 3106.379665 | 6210.768038 | 3105.887657 | 57 |
| 3 | 216.097882 | 108.552579 | | | 198.087317 | 99.547296 | A | 6141.746575 | 3071.376926 | 6124.720026 | 3062.863651 | 6123.736010 | 3062.371643 | 56 |
| 4 | *273.119346* | 137.063311 | | | 255.108781 | 128.058029 | G | 6070.709461 | 3035.858369 | 6053.682912 | 3027.345094 | 6052.698896 | 3026.853086 | 55 |
| 5 | *410.178258* | 205.592767 | | | 392.167693 | 196.587484 | H | 6013.687997 | 3007.347637 | 5996.661448 | 2998.834362 | 5995.677432 | 2998.342354 | 54 |
| 6 | *596.257571* | 298.632424 | | | 578.247006 | 289.627141 | W | 5876.629085 | 2938.818181 | 5859.602536 | 2930.304906 | 5858.618520 | 2929.812898 | 53 |
| 7 | *697.305250* | 349.156263 | | | 679.294685 | 340.150981 | T | 5690.549772 | 2845.778524 | 5673.523223 | 2837.265250 | 5672.539207 | 2836.773242 | 52 |
| 8 | *784.337278* | 392.672277 | | | 766.326713 | 383.666995 | S | 5589.502093 | 2795.254685 | 5572.475544 | 2786.741410 | 5571.491528 | 2786.249402 | 51 |
| 9 | *913.379871* | 457.193574 | | | 895.369306 | 448.188291 | E | 5502.470065 | 2751.738671 | 5485.443516 | 2743.225396 | 5484.459500 | 2742.733388 | 50 |
| 10 | *1000.411899* | 500.709588 | | | 982.401334 | 491.704305 | S | 5373.427472 | 2687.217374 | 5356.400923 | 2678.704100 | 5355.416907 | 2678.212092 | 49 |
| 11 | *1087.443927* | 544.225602 | | | 1069.433362 | *535.220319* | S | 5286.395444 | *2643.701360* | 5269.368895 | 2635.188086 | 5268.384879 | 2634.696078 | 48 |
| 12 | 1186.512341 | *593.759809* | | | 1168.501776 | 584.754526 | V | 5199.363416 | 2600.185346 | 5182.336867 | 2591.672072 | 5181.352851 | 2591.180064 | 47 |
| 13 | *1273.544369* | 637.275823 | | | 1255.533804 | 628.270540 | S | 5100.295002 | 2550.651139 | 5083.268453 | 2542.137865 | 5082.284437 | *2541.645857* | 46 |
| 14 | 1330.565833 | 665.786555 | | | 1312.555268 | 656.781272 | G | 5013.262974 | 2507.135125 | 4996.236425 | 2498.621851 | 4995.252409 | 2498.129843 | 45 |
| 15 | *1417.597861* | 709.302569 | | | 1399.587296 | 700.297286 | S | 4956.241510 | 2478.624393 | 4939.214961 | 2470.111119 | 4938.230945 | 2469.619111 | 44 |
| 16 | *1518.645540* | 759.826408 | | | 1500.634975 | 750.821126 | T | 4869.209482 | 2435.108379 | 4852.182933 | 2426.595105 | 4851.198917 | 2426.103097 | 43 |
| 17 | 1575.667004 | *788.337140* | | | *1557.656439* | 779.331858 | G | 4768.161803 | 2384.584540 | 4751.135254 | 2376.071265 | 4750.151238 | 2375.579257 | 42 |
| 18 | 2014.892330 | 1007.949803 | 1997.865781 | 999.436529 | 1996.881765 | 998.944521 | Q | 4711.140339 | *2356.073808* | 4694.113790 | 2347.560533 | 4693.129774 | 2347.068525 | 41 |
| 19 | 2200.971643 | *1100.989460* | 2183.945094 | 1092.476185 | 2182.961078 | 1091.984177 | W | 4271.915013 | 2136.461145 | 4254.888464 | 2127.947870 | 4253.904448 | 2127.455862 | 40 |
| 20 | 2338.030555 | 1169.518916 | 2321.004006 | 1161.005641 | 2320.019990 | 1160.513633 | H | 4085.835700 | 2043.421488 | 4068.809151 | 2034.908214 | 4067.825135 | 2034.416206 | 39 |
| 21 | 2425.062583 | 1213.034930 | 2408.036034 | 1204.521655 | 2407.052018 | 1204.029647 | S | 3948.776788 | 1974.892032 | 3931.750239 | 1966.378758 | 3930.766223 | 1965.886750 | 38 |
| 22 | 2554.105176 | 1277.556226 | 2537.078627 | 1269.042952 | 2536.094611 | 1268.550944 | E | 3861.744760 | 1931.376018 | 3844.718211 | 1922.862744 | 3843.734195 | 1922.370736 | 37 |
| 23 | 2641.137204 | 1321.072240 | 2624.110655 | 1312.558966 | 2623.126639 | 1312.066958 | S | 3732.702167 | 1866.854722 | 3715.675618 | 1858.341447 | 3714.691602 | 1857.849439 | 36 |
| 24 | 2698.158668 | 1349.582972 | 2681.132119 | 1341.069698 | 2680.148103 | 1340.577690 | G | 3645.670139 | 1823.338708 | 3628.643590 | 1814.825433 | 3627.659574 | 1814.333425 | 35 |
| 25 | 2785.190696 | 1393.098986 | 2768.164147 | 1384.585712 | 2767.180131 | 1384.093704 | S | 3588.648675 | 1794.827976 | 3571.622126 | 1786.314701 | 3570.638110 | 1785.822693 | 34 |
| 26 | 2932.259110 | 1466.633193 | 2915.232561 | 1458.119919 | 2914.248545 | 1457.627911 | F | 3501.616647 | 1751.311962 | 3484.590098 | 1742.798687 | 3483.606082 | 1742.306679 | 33 |
| 27 | 3088.360221 | 1544.683749 | 3071.333672 | 1536.170474 | 3070.349656 | 1535.678466 | R | 3354.548233 | 1677.777755 | 3337.521684 | 1669.264480 | 3336.537668 | 1668.772472 | 32 |
| 28 | 3185.412985 | 1593.210131 | 3168.386436 | 1584.696856 | 3167.402420 | 1584.204848 | P | 3198.447122 | *1599.727199* | 3181.420573 | 1591.213925 | 3180.436557 | 1590.721917 | 31 |
| 29 | 3300.439928 | 1650.723602 | 3283.413379 | 1642.210327 | 3282.429363 | 1641.718320 | D | 3101.394358 | 1551.200817 | 3084.367809 | 1542.687543 | 3083.383793 | 1542.195535 | 30 |
| 30 | 3387.471956 | 1694.239616 | 3370.445407 | 1685.726342 | 3369.461391 | 1685.234334 | S | *2986.367415* | 1493.687346 | 2969.340866 | 1485.174071 | 2968.356850 | 1484.682063 | 29 |
| 31 | 3484.524720 | 1742.765998 | 3467.498171 | 1734.252724 | 3466.514155 | 1733.760716 | P | 2899.335387 | 1450.171332 | 2882.308838 | 1441.658057 | 2881.324822 | 1441.166049 | 28 |
| 32 | 3541.546184 | 1771.276730 | 3524.519635 | 1762.763456 | 3523.535619 | 1762.271448 | G | 2802.282623 | 1401.644950 | 2785.256074 | 1393.131675 | 2784.272058 | 1392.639667 | 27 |
| 33 | 3628.578212 | 1814.792744 | 3611.551663 | 1806.279470 | 3610.567647 | 1805.787462 | S | 2745.261159 | 1373.134218 | 2728.234610 | 1364.620943 | 2727.250594 | 1364.128935 | 26 |
| 34 | 3685.599676 | 1843.303476 | 3668.573127 | 1834.790202 | 3667.589111 | 1834.298194 | G | 2658.229131 | *1329.618204* | 2641.202582 | 1321.104929 | 2640.218566 | 1320.612921 | 25 |
| 35 | 3799.642603 | 1900.324940 | 3782.616054 | 1891.811665 | 3781.632038 | 1891.319657 | N | 2601.207667 | 1301.107472 | 2584.181118 | 1292.594197 | 2583.197102 | 1292.102189 | 24 |
| 36 | 3870.679717 | *1935.843497* | 3853.653168 | 1927.330222 | 3852.669152 | 1926.838214 | A | 2487.164740 | 1244.086008 | 2470.138191 | 1235.572734 | 2469.154175 | 1235.080726 | 23 |
| 37 | 4026.780828 | *2013.894052* | 4009.754279 | 2005.380778 | 4008.770263 | 2004.888770 | R | 2416.127626 | 1208.567451 | 2399.101077 | 1200.054177 | 2398.117061 | 1199.562169 | 22 |
| 38 | 4123.833592 | 2062.420434 | 4106.807043 | 2053.907160 | 4105.823027 | 2053.415152 | P | 2260.026515 | 1130.516896 | 2242.999966 | 1122.003621 | 2242.015950 | 1121.511613 | 21 |
| 39 | 4237.876519 | 2119.441898 | 4220.849970 | 2110.928623 | 4219.865954 | 2110.436615 | N | 2162.973751 | 1081.990514 | 2145.947202 | 1073.477239 | 2144.963186 | 1072.985231 | 20 |
| 40 | *4351.919446* | 2176.463361 | 4334.892897 | 2167.950087 | 4333.908881 | 2167.458079 | N | 2048.930824 | 1024.969050 | 2031.904275 | 1016.455776 | 2030.920259 | 1015.963768 | 19 |
| 41 | 4448.972210 | 2224.989743 | 4431.945661 | 2216.476469 | 4430.961645 | 2215.984461 | P | *1934.887897* | 967.947587 | 1917.861348 | 959.434312 | 1916.877332 | 958.942304 | 18 |
| 42 | 4563.999153 | 2282.503215 | 4546.972604 | 2273.989940 | 4545.988588 | 2273.497932 | D | 1837.835133 | 919.421205 | 1820.808584 | 910.907930 | 1819.824568 | 910.415922 | 17 |
| 43 | 4750.078466 | 2375.542871 | 4733.051917 | 2367.029597 | 4732.067901 | 2366.537589 | W | *1722.808190* | 861.907733 | 1705.781641 | *853.394459* | 1704.797625 | 852.902451 | 16 |
| 44 | 4807.099930 | *2404.053603* | 4790.073381 | 2395.540329 | 4789.089365 | 2395.048321 | G | 1536.728877 | 768.868077 | 1519.702328 | 760.354802 | *1518.718312* | 759.862794 | 15 |
| 45 | 4908.147609 | 2454.577443 | 4891.121060 | *2446.064168* | 4890.137044 | 2445.572160 | T | 1479.707413 | 740.357345 | 1462.680864 | 731.844070 | 1461.696848 | 731.352062 | 14 |
| 46 | 5055.216023 | *2528.111650* | 5038.189474 | 2519.598375 | 5037.205458 | 2519.106367 | F | 1378.659734 | 689.833505 | 1361.633185 | *681.320231* | 1360.649169 | 680.828223 | 13 |
| 47 | 5184.258616 | 2592.632946 | 5167.232067 | 2584.119672 | 5166.248051 | 2583.627664 | E | 1231.591320 | *616.299298* | 1214.564771 | 607.786024 | 1213.580755 | 607.294016 | 12 |
| 48 | 5313.301209 | 2657.154243 | 5296.274660 | 2648.640968 | 5295.290644 | 2648.148960 | E | *1102.548727* | 551.778002 | 1085.522178 | 543.264727 | 1084.538162 | 542.772719 | 11 |
| 49 | 5412.369623 | 2706.688450 | 5395.343074 | 2698.175175 | 5394.359058 | 2697.683167 | V | *973.506134* | 487.256705 | 956.479585 | 478.743431 | 955.495569 | 478.251423 | 10 |
| 50 | 5499.401651 | 2750.204464 | 5482.375102 | 2741.691189 | 5481.391086 | 2741.199181 | S | *874.437720* | 437.722498 | *857.411171* | 429.209224 | *856.427155* | 428.717216 | 9 |
| 51 | 5556.423115 | 2778.715196 | 5539.396566 | 2770.201921 | 5538.412550 | 2769.709913 | G | *787.405692* | 394.206484 | *770.379143* | 385.693210 | 769.395127 | 385.201202 | 8 |
| 52 | 5670.466042 | 2835.736659 | 5653.439493 | 2827.223385 | 5652.455477 | 2826.731377 | N | *730.384228* | 365.695752 | 713.357679 | 357.182478 | 712.373663 | 356.690470 | 7 |
| 53 | 5769.534456 | 2885.270866 | 5752.507907 | 2876.757592 | 5751.523891 | 2876.265584 | V | *616.341301* | 308.674289 | 599.314752 | 300.161014 | 598.330736 | 299.669006 | 6 |
| 54 | 5856.566484 | 2928.786880 | 5839.539935 | 2920.273606 | 5838.555919 | 2919.781598 | S | *517.272887* | *259.140082* | *500.246338* | 250.626807 | 499.262322 | 250.134799 | 5 |
| 55 | 5953.619248 | 2977.313262 | 5936.592699 | 2968.799988 | 5935.608683 | 2968.307980 | P | *430.240859* | 215.624068 | *413.214310* | 207.110793 | 412.230294 | 206.618785 | 4 |
| 56 | 6010.640712 | 3005.823994 | 5993.614163 | 2997.310720 | 5992.630147 | 2996.818712 | G | *333.188095* | 167.097686 | 316.161546 | 158.584411 | 315.177530 | 158.092403 | 3 |
| 57 | 6111.688391 | 3056.347834 | 6094.661842 | 3047.834559 | 6093.677826 | 3047.342551 | T | *276.166631* | 138.586954 | *259.140082* | 130.073679 | 258.156066 | 129.581671 | 2 |
| 58 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.3 | 6284.792847 | 0.054417 | GSAGHWTSESSVSGSTGQWHSESGSFRPDSPGSGNARPNNPDWGTFEEVSGNVSPGTR |

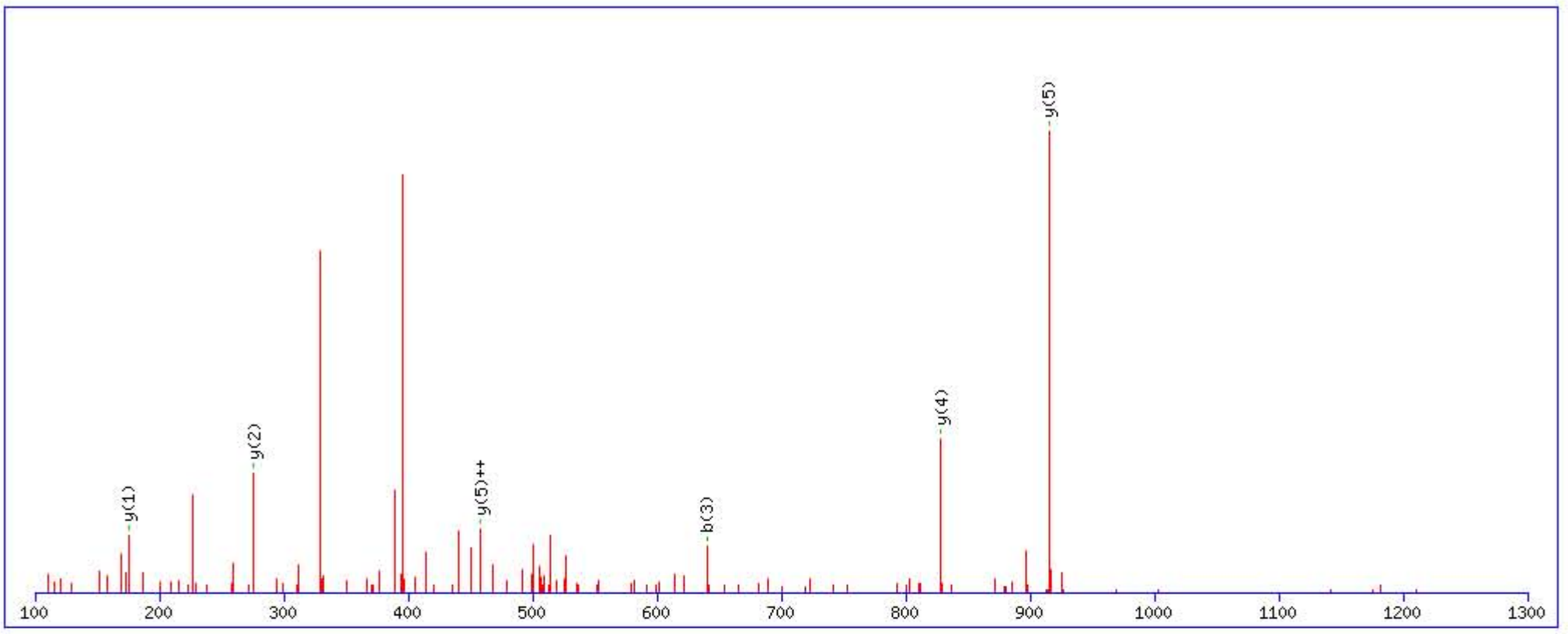
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ISQLTR**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

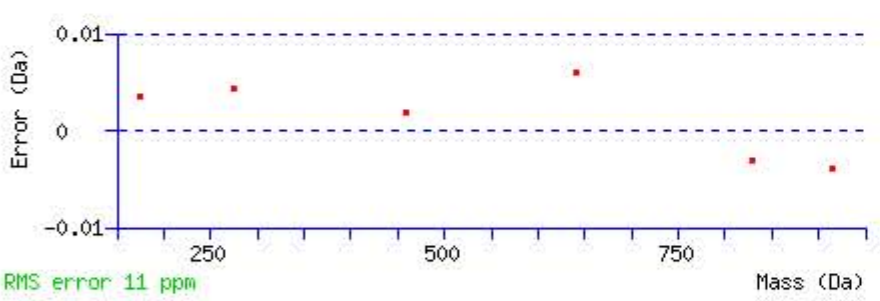
Match to Query 14528: 1027.585328 from(514.799940,2+) rtinseconds(1581) index(17491)
Title: Locus:1.1.1.2933.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

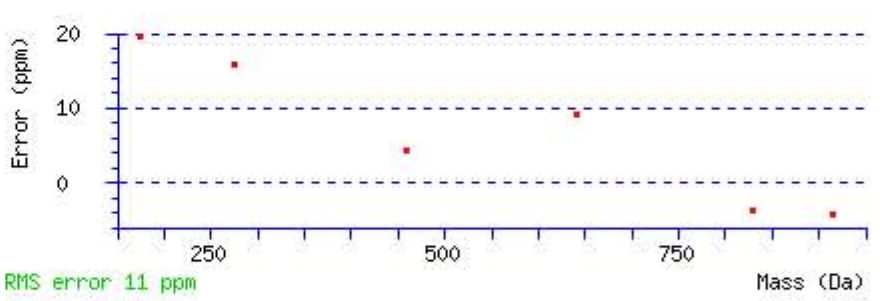
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1027.584824
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 25 **Expect:** 0.061
**Matches :** 6/52 fragment ions using 9 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 6 |
| 2 | 201.123368 | 101.065322 | | | 183.112803 | 92.060039 | S | *915.508049* | 458.257663 | 898.481500 | 449.744388 | 897.497484 | 449.252380 | 5 |
| 3 | **640.348694** | 320.677985 | 623.322145 | 312.164711 | 622.338129 | 311.672703 | Q | *828.476021* | 414.741649 | 811.449472 | 406.228374 | 810.465456 | 405.736366 | 4 |
| 4 | 753.432758 | 377.220017 | 736.406209 | 368.706743 | 735.422193 | 368.214735 | L | 389.250695 | 195.128986 | 372.224146 | 186.615711 | 371.240130 | 186.123703 | 3 |
| 5 | 854.480437 | 427.743857 | 837.453888 | 419.230582 | 836.469872 | 418.738574 | T | *276.166631* | 138.586954 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 6 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.2 | 1027.584824 | 0.000504 | ISQLTR |
| 21.4 | 1027.584824 | 0.000504 | ILSQTR |
| 13.4 | 1027.573578 | 0.011750 | ISQLEK |
| 10.6 | 1027.584839 | 0.000489 | LQTVTR |
| 10.6 | 1027.592682 | -0.007354 | LRLSWPTR |
| 10.4 | 1027.584824 | 0.000504 | IISTQR |
| 10.3 | 1027.573578 | 0.011750 | ILQVPAMEK |
| 10.3 | 1027.573578 | 0.011750 | ILSQEK |
| 10.3 | 1027.573578 | 0.011750 | LLSQEK |
| 9.9 | 1027.592667 | -0.007339 | IIYQAHKR |

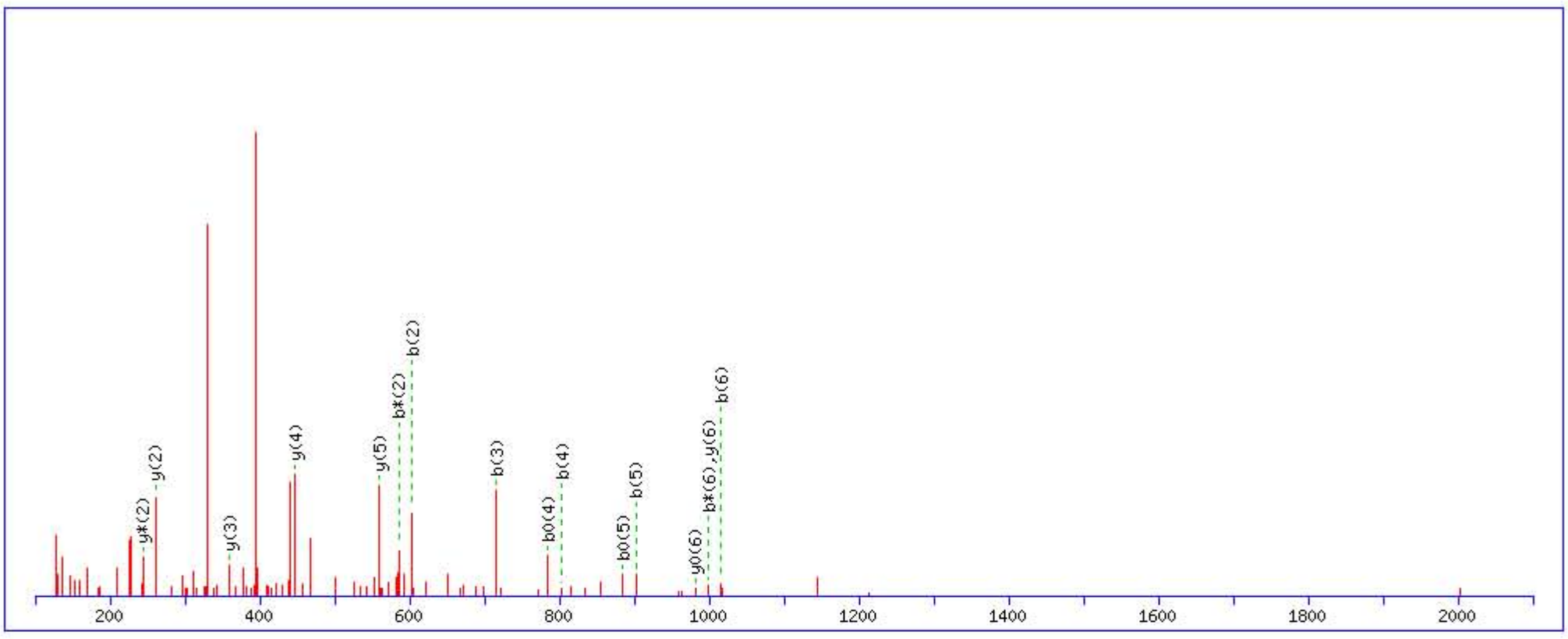
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YQISVNK**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

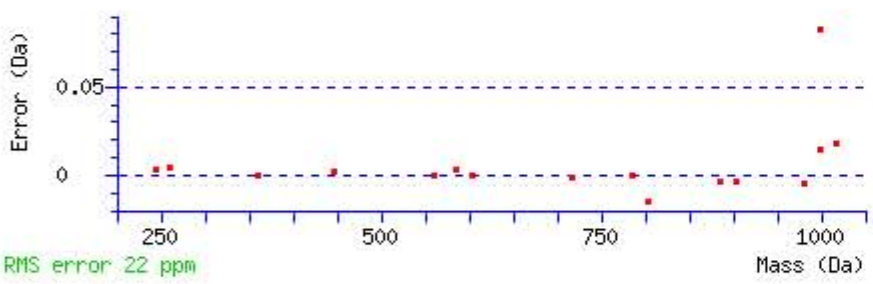
Match to Query 19317: 1161.623408 from(581.818980,2+) rtinseconds(1670) index(18016)
Title: Locus:1.1.1.2964.4 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

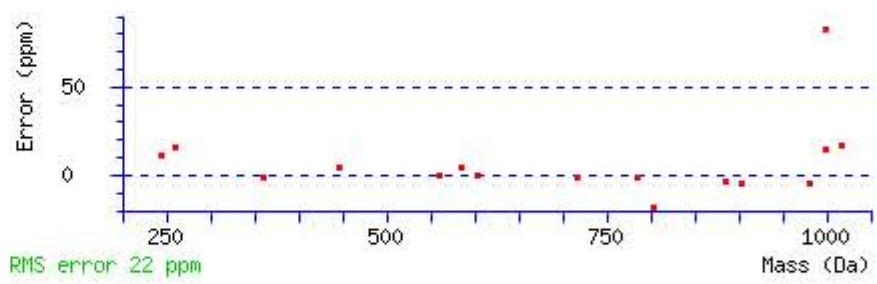
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1161.621597
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 27 **Expect:** 0.012
**Matches :** 16/58 fragment ions using 28 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 7 |
| 2 | *603.295931* | 302.151604 | 586.269382 | 293.638329 | | | Q | *999.565563* | 500.286419 | 982.539014 | 491.773145 | 981.554998 | 491.281137 | 6 |
| 3 | *716.379995* | 358.693636 | 699.353446 | 350.180361 | | | I | *560.340237* | 280.673756 | 543.313688 | 272.160482 | 542.329672 | 271.668474 | 5 |
| 4 | *803.412023* | 402.209650 | 786.385474 | 393.696375 | 785.401458 | 393.204367 | S | *447.256173* | 224.131724 | 430.229624 | 215.618450 | 429.245608 | 215.126442 | 4 |
| 5 | *902.480437* | 451.743857 | 885.453888 | 443.230582 | 884.469872 | 442.738574 | V | *360.224145* | 180.615710 | 343.197596 | 172.102436 | | | 3 |
| 6 | *1016.523364* | 508.765320 | 999.496815 | 500.252046 | 998.512799 | 499.760038 | N | *261.155731* | 131.081503 | 244.129182 | 122.568229 | | | 2 |
| 7 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 27.4 | 1161.621597 | 0.001811 | YQISVNK |
| 26.1 | 1161.629456 | -0.006048 | DFALRLWNK |
| 6.4 | 1161.606323 | 0.017085 | MEIKGEQISK |
| 6.2 | 1161.639359 | -0.015951 | FLDKDGLINK |
| 4.5 | 1161.611694 | 0.011714 | WMIRNWIK |
| 4.4 | 1161.614197 | 0.009211 | YDISVKPANR |
| 4.2 | 1161.610168 | 0.013240 | RATESRDLSK |
| 2.8 | 1161.625443 | -0.002035 | ENVIHLPGQR |
| 2.7 | 1161.635330 | -0.011922 | IESVLSSSGKR |
| 1.7 | 1161.628128 | -0.004720 | LESLDIPFTK |

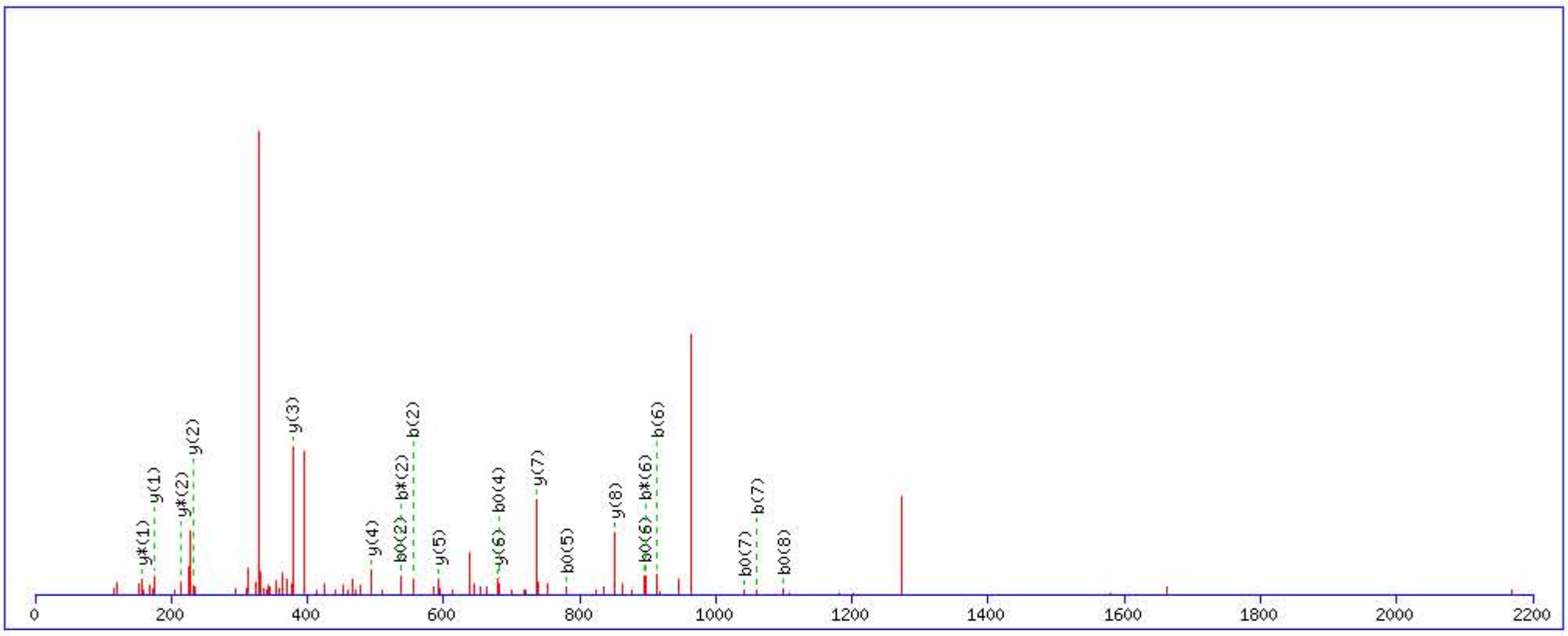
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QDGSVDFGR**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

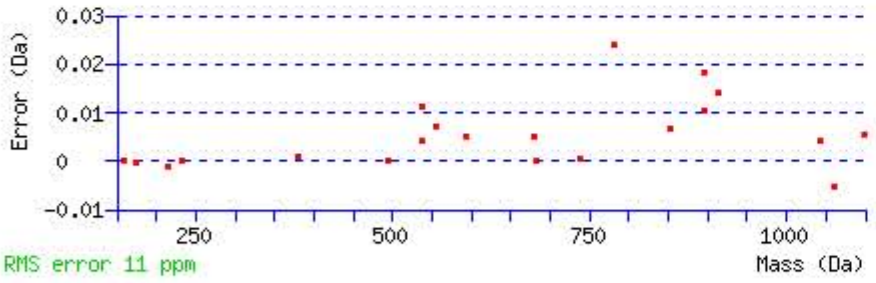
Match to Query 23167: 1290.615128 from(646.314840,2+) rtinseconds(1778) index(48843)
Title: Locus:1.1.1.1857.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

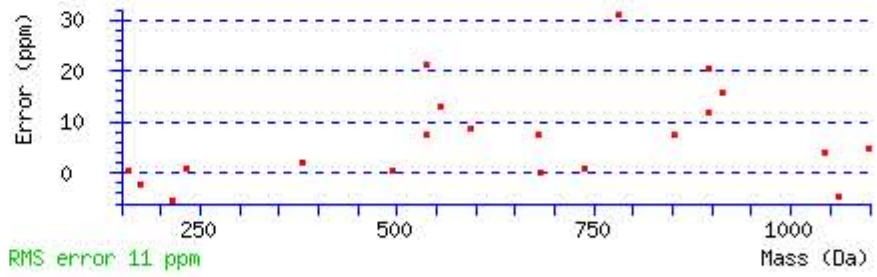
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1290.602692
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q1 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.00036
**Matches :** 21/88 fragment ions using 43 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 9 |
| 2 | **555.259545** | 278.133411 | 538.232996 | 269.620136 | 537.248980 | 269.128128 | D | *852.384622* | 426.695949 | 835.358073 | 418.182674 | 834.374057 | 417.690666 | 8 |
| 3 | 612.281009 | 306.644143 | 595.254460 | 298.130868 | 594.270444 | 297.638860 | G | *737.357679* | 369.182477 | 720.331130 | 360.669203 | 719.347114 | 360.177195 | 7 |
| 4 | 699.313037 | 350.160157 | 682.286488 | 341.646882 | 681.302472 | 341.154874 | S | *680.336215* | 340.671745 | 663.309666 | 332.158471 | 662.325650 | 331.666463 | 6 |
| 5 | 798.381451 | 399.694364 | 781.354902 | 391.181089 | 780.370886 | 390.689081 | V | *593.304187* | 297.155731 | 576.277638 | 288.642457 | 575.293622 | 288.150449 | 5 |
| 6 | **913.408394** | 457.207835 | 896.381845 | 448.694560 | 895.397829 | 448.202552 | D | *494.235773* | 247.621524 | 477.209224 | 239.108250 | 476.225208 | 238.616242 | 4 |
| 7 | **1060.476808** | 530.742042 | 1043.450259 | 522.228768 | 1042.466243 | 521.736759 | F | *379.208830* | 190.108053 | 362.182281 | 181.594778 | | | 3 |
| 8 | 1117.498272 | 559.252774 | 1100.471723 | 550.739499 | 1099.487707 | 550.247491 | G | *232.140416* | 116.573846 | 215.113867 | 108.060571 | | | 2 |
| 9 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

### All matches to this query

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.4 | 1290.602692 | 0.012436 | QDGSVDFGR |
| 8.3 | 1290.631668 | -0.016540 | GAKGEPGPDGPPGR |
| 3.4 | 1290.632507 | -0.017379 | RGDNWMLMLR |

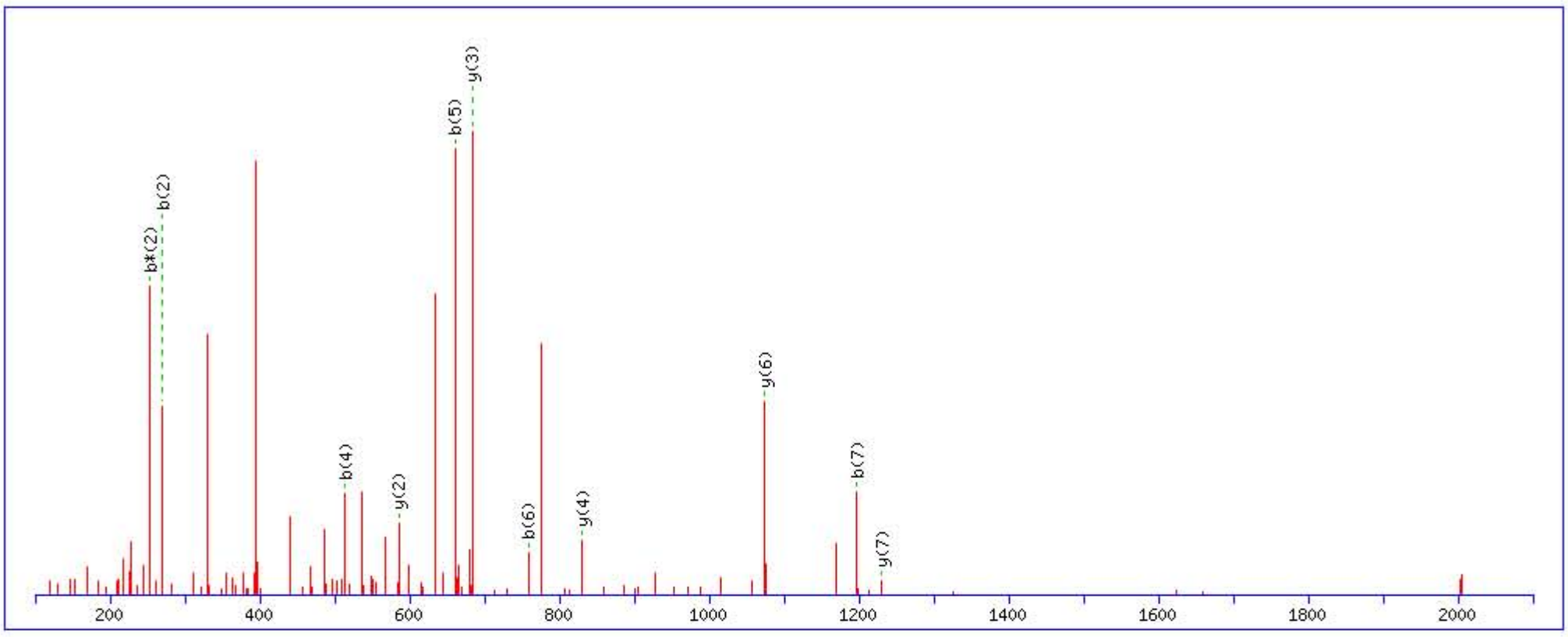
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IRPFFPQQ**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

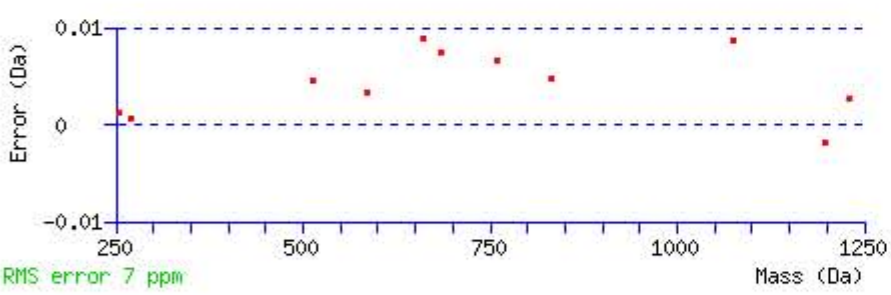
Match to Query 24179: 1342.732848 from(672.373700,2+) rtinseconds(2279) index(7203)
Title: Locus:1.1.1.2071.4 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

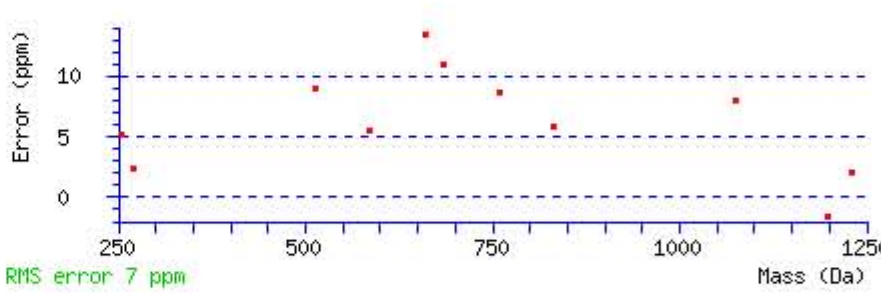
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1342.722000
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 26 **Expect:** 0.017
**Matches :** 11/54 fragment ions using 24 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | I | | | | | 8 |
| 2 | *270.192451* | 135.599864 | 253.165902 | 127.086589 | R | *1230.645212* | 615.826244 | 1213.618663 | 607.312970 | 7 |
| 3 | 367.245215 | 184.126245 | 350.218666 | 175.612971 | P | *1074.544101* | 537.775689 | 1057.517552 | 529.262414 | 6 |
| 4 | *514.313629* | 257.660453 | 497.287080 | 249.147178 | F | 977.491337 | 489.249307 | 960.464788 | 480.736032 | 5 |
| 5 | *661.382043* | 331.194660 | 644.355494 | 322.681385 | F | *830.422923* | 415.715100 | 813.396374 | 407.201825 | 4 |
| 6 | *758.434807* | 379.721042 | 741.408258 | 371.207767 | P | *683.354509* | 342.180893 | 666.327960 | 333.667618 | 3 |
| 7 | *1197.660133* | 599.333705 | 1180.633584 | 590.820430 | Q | *586.301745* | 293.654511 | 569.275196 | 285.141236 | 2 |
| 8 | | | | | Q | 147.076419 | 74.041848 | 130.049870 | 65.528573 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 26.4 | 1342.722000 | 0.010848 | IRPFFPQQ |
| 20.8 | 1342.722000 | 0.010848 | IRPFFPQQ |
| 7.2 | 1342.716629 | 0.016219 | LLSVTEDQK |
| 5.9 | 1342.746918 | -0.014070 | RIYNNIPANLR |
| 5.2 | 1342.743103 | -0.010255 | IRYVPEQK |
| 5.0 | 1342.727829 | 0.005019 | LNPASAEIMLLR |
| 2.5 | 1342.729187 | 0.003661 | QPHRPIER |

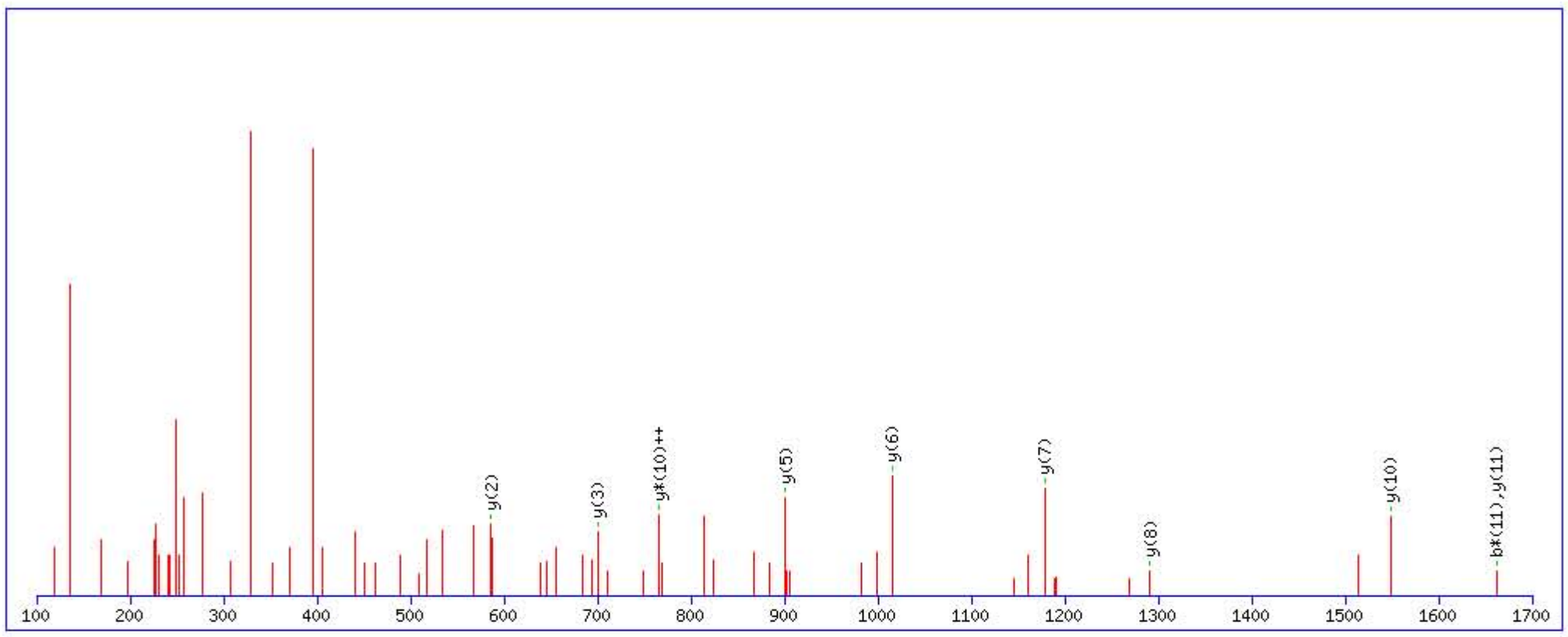
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YLQEIYNSNNQK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

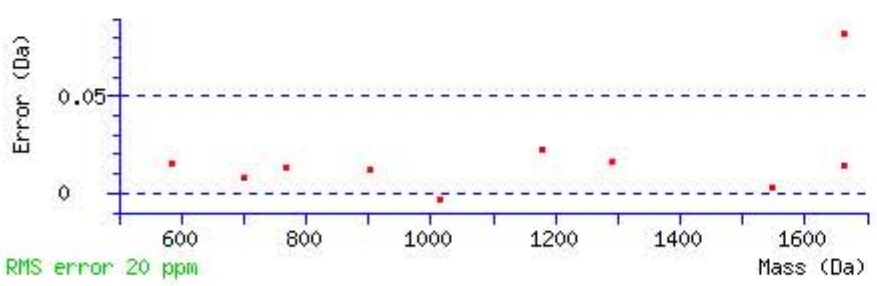
Match to Query 40782: 1823.897262 from(608.973030,3+) rtinseconds(1852) index(49258)
Title: Locus:1.1.1.1883.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

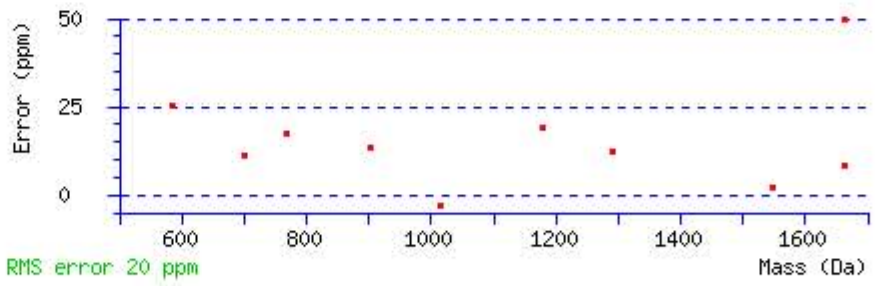
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1823.887573
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 0.00011
**Matches :** 10/114 fragment ions using 14 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 12 |
| 2 | 277.154669 | 139.080973 | | | | | L | *1661.831567* | 831.419422 | 1644.805018 | 822.906147 | 1643.821002 | 822.414139 | 11 |
| 3 | 405.213247 | 203.110262 | 388.186698 | 194.596987 | | | Q | *1548.747503* | 774.877390 | 1531.720954 | 766.364115 | 1530.736938 | 765.872107 | 10 |
| 4 | 534.255840 | 267.631558 | 517.229291 | 259.118284 | 516.245275 | 258.626276 | E | 1420.688925 | 710.848100 | 1403.662376 | 702.334826 | 1402.678360 | 701.842818 | 9 |
| 5 | 647.339904 | 324.173590 | 630.313355 | 315.660316 | 629.329339 | 315.168308 | I | *1291.646332* | 646.326804 | 1274.619783 | 637.813530 | 1273.635767 | 637.321522 | 8 |
| 6 | 810.403233 | 405.705255 | 793.376684 | 397.191980 | 792.392668 | 396.699972 | Y | *1178.562268* | 589.784772 | 1161.535719 | 581.271498 | 1160.551703 | 580.779489 | 7 |
| 7 | 924.446160 | 462.726718 | 907.419611 | 454.213443 | 906.435595 | 453.721435 | N | *1015.498939* | 508.253108 | 998.472390 | 499.739833 | 997.488374 | 499.247825 | 6 |
| 8 | 1011.478188 | 506.242732 | 994.451639 | 497.729457 | 993.467623 | 497.237449 | S | *901.456012* | 451.231644 | 884.429463 | 442.718370 | 883.445447 | 442.226362 | 5 |
| 9 | 1125.521115 | 563.264196 | 1108.494566 | 554.750921 | 1107.510550 | 554.258913 | N | 814.423984 | 407.715630 | 797.397435 | 399.202356 | | | 4 |
| 10 | 1239.564042 | 620.285659 | 1222.537493 | 611.772385 | 1221.553477 | 611.280376 | N | *700.381057* | 350.694167 | 683.354508 | 342.180892 | | | 3 |
| 11 | 1678.789368 | 839.898322 | 1661.762819 | 831.385048 | 1660.778803 | 830.893039 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 12 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 53.0 | 1823.887573 | 0.009689 | YLQEIYNSNNQK |

**Mascot:** http://www.matrixscience.com/

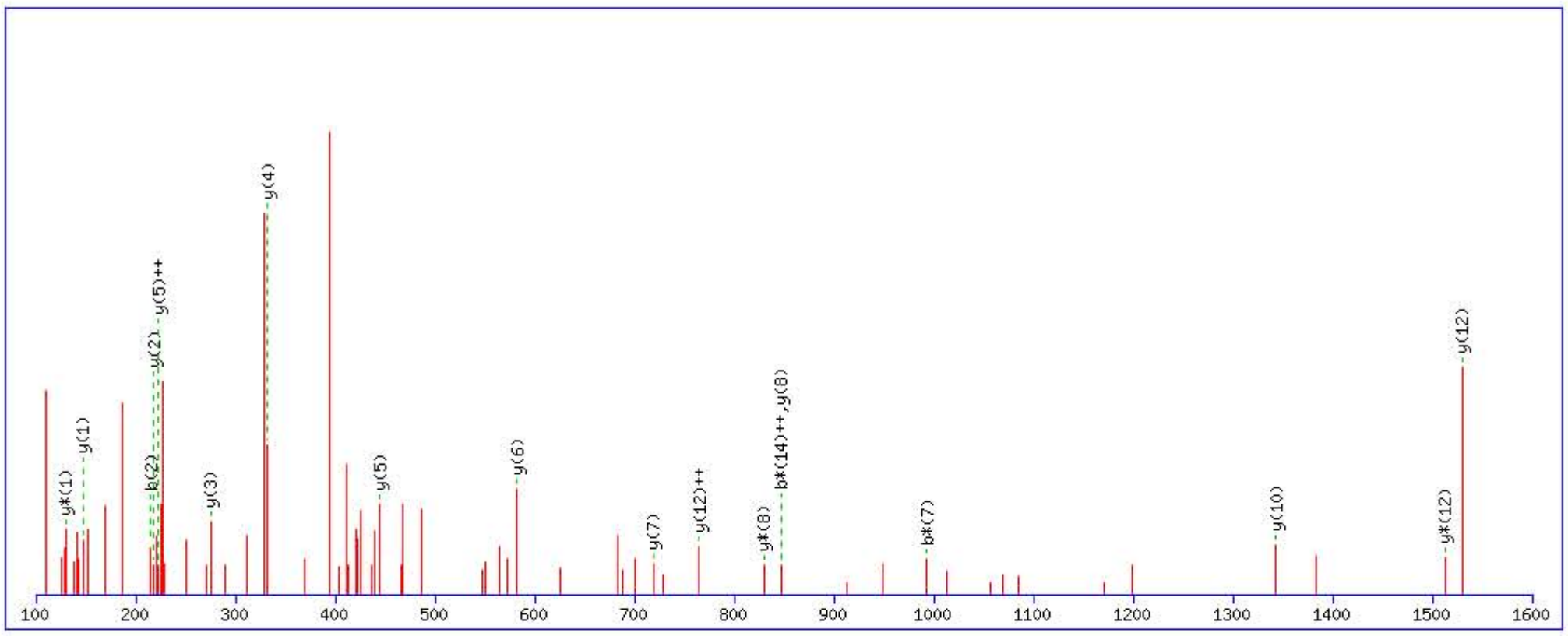
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

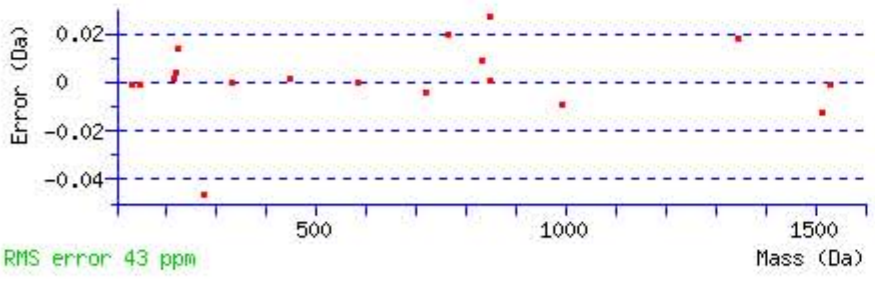
Match to Query 41495: 1855.970656 from(464.999940,4+) rtinseconds(1503) index(2658)
Title: Locus:1.1.1.1800.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

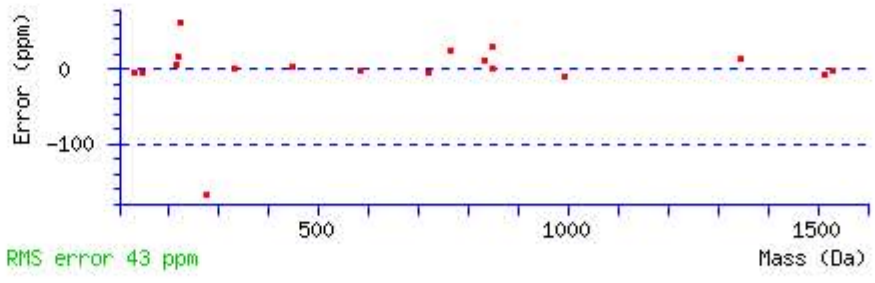
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1855.972687
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 28 **Expect:** 0.046
**Matches :** 18/134 fragment ions using 61 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 15 |
| 2 | 215.139019 | 108.073147 | | | 197.128454 | 99.067865 | T | 1743.895902 | 872.451589 | 1726.869353 | 863.938314 | 1725.885337 | 863.446306 | 14 |
| 3 | 328.223083 | 164.615179 | | | 310.212518 | 155.609897 | I | 1642.848223 | 821.927749 | 1625.821674 | 813.414475 | 1624.837658 | 812.922467 | 13 |
| 4 | 385.244547 | 193.125911 | | | 367.233982 | 184.120629 | G | *1529.764159* | 765.385717 | 1512.737610 | 756.872443 | 1511.753594 | 756.380435 | 12 |
| 5 | 514.287140 | 257.647208 | | | 496.276575 | 248.641926 | E | 1472.742695 | 736.874985 | 1455.716146 | 728.361711 | 1454.732130 | 727.869703 | 11 |
| 6 | 571.308604 | 286.157940 | | | 553.298039 | 277.152658 | G | *1343.700102* | 672.353689 | 1326.673553 | 663.840414 | | | 10 |
| 7 | 1010.533930 | 505.770603 | 993.507381 | 497.257329 | 992.523365 | 496.765321 | Q | 1286.678638 | 643.842957 | 1269.652089 | 635.329682 | | | 9 |
| 8 | 1138.592508 | 569.799892 | 1121.565959 | 561.286618 | 1120.581943 | 560.794609 | Q | *847.453312* | 424.230294 | 830.426763 | 415.717019 | | | 8 |
| 9 | 1275.651420 | 638.329348 | 1258.624871 | 629.816074 | 1257.640855 | 629.324065 | H | *719.394734* | 360.201005 | 702.368185 | 351.687730 | | | 7 |
| 10 | 1412.710332 | 706.858804 | 1395.683783 | 698.345530 | 1394.699767 | 697.853521 | H | *582.335822* | 291.671549 | 565.309273 | 283.158274 | | | 6 |
| 11 | 1525.794396 | 763.400836 | 1508.767847 | 754.887561 | 1507.783831 | 754.395553 | L | *445.276910* | 223.142093 | 428.250361 | 214.628818 | | | 5 |
| 12 | 1582.815860 | 791.911568 | 1565.789311 | 783.398293 | 1564.805295 | 782.906285 | G | *332.192846* | 166.600061 | 315.166297 | 158.086786 | | | 4 |
| 13 | 1639.837324 | 820.422300 | 1622.810775 | 811.909025 | 1621.826759 | 811.417017 | G | *275.171382* | 138.089329 | 258.144833 | 129.576054 | | | 3 |
| 14 | 1710.874438 | 855.940857 | 1693.847889 | 847.427582 | 1692.863873 | 846.935574 | A | *218.149918* | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 15 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 27.8 | 1855.972687 | -0.002031 | LTIGEGQQHHLGGAK |
| 18.8 | 1855.972687 | -0.002031 | LTIGEGQQHHLGGAK |

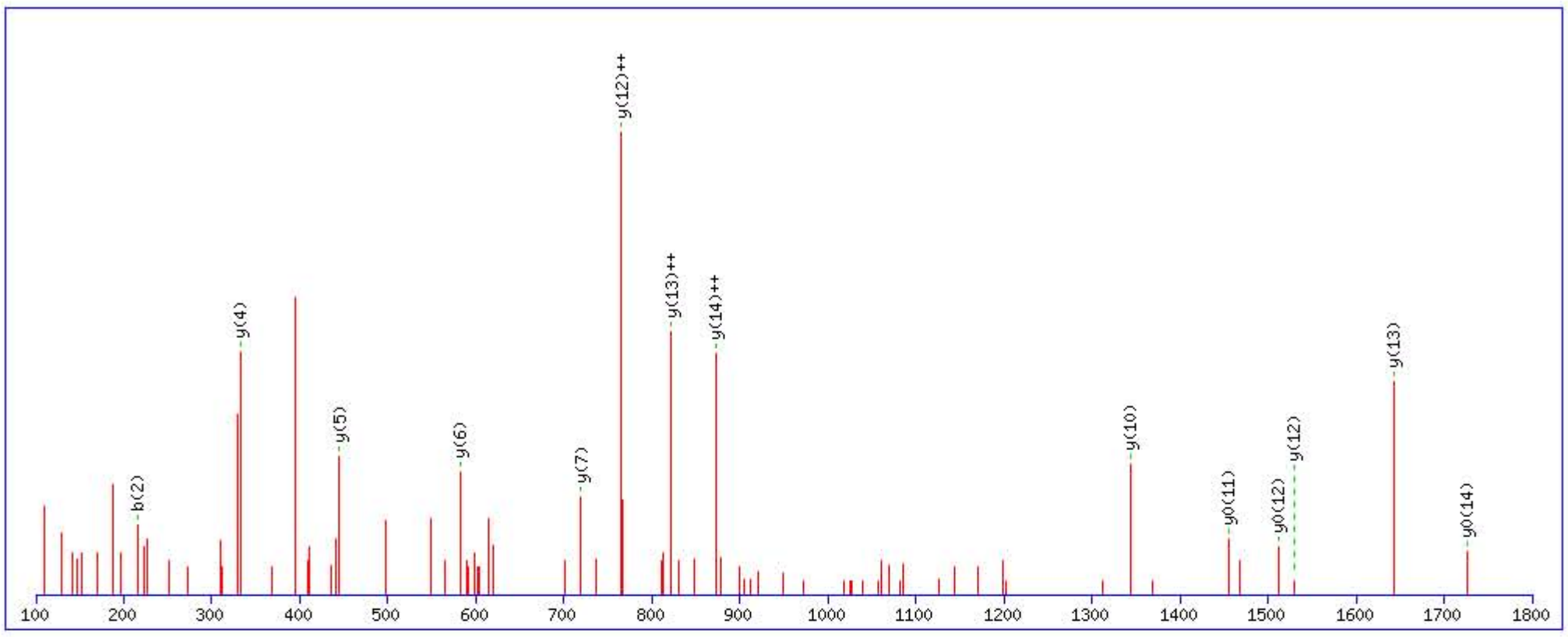
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

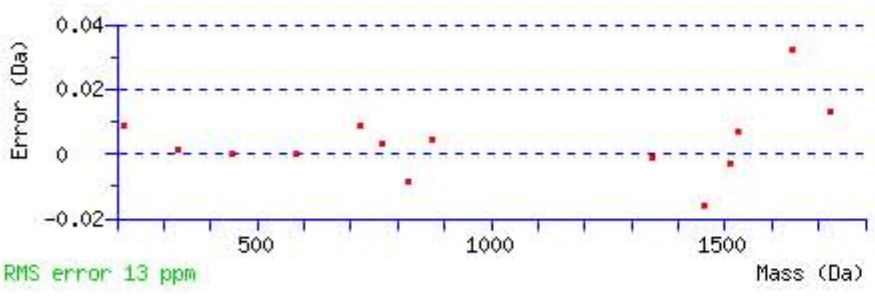
Match to Query 41508: 1855.975032 from(619.665620,3+) rtinseconds(1503) index(2662)
Title: Locus:1.1.1.1800.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

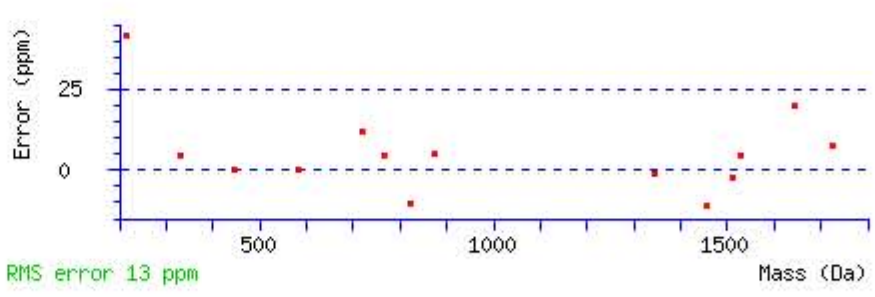
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1855.972687
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.0011
**Matches :** 14/134 fragment ions using 30 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 15 |
| 2 | 215.139019 | 108.073147 | | | 197.128454 | 99.067865 | T | 1743.895902 | 872.451589 | 1726.869353 | 863.938314 | 1725.885337 | 863.446306 | 14 |
| 3 | 328.223083 | 164.615179 | | | 310.212518 | 155.609897 | I | *1642.848223* | 821.927749 | 1625.821674 | 813.414475 | 1624.837658 | 812.922467 | 13 |
| 4 | 385.244547 | 193.125911 | | | 367.233982 | 184.120629 | G | *1529.764159* | 765.385717 | 1512.737610 | 756.872443 | 1511.753594 | 756.380435 | 12 |
| 5 | 514.287140 | 257.647208 | | | 496.276575 | 248.641926 | E | 1472.742695 | 736.874985 | 1455.716146 | 728.361711 | 1454.732130 | 727.869703 | 11 |
| 6 | 571.308604 | 286.157940 | | | 553.298039 | 277.152658 | G | *1343.700102* | 672.353689 | 1326.673553 | 663.840414 | | | 10 |
| 7 | 699.367182 | 350.187229 | 682.340633 | 341.673955 | 681.356617 | 341.181947 | Q | 1286.678638 | 643.842957 | 1269.652089 | 635.329682 | | | 9 |
| 8 | 1138.592508 | 569.799892 | 1121.565959 | 561.286618 | 1120.581943 | 560.794609 | Q | 1158.620060 | 579.813668 | 1141.593511 | 571.300393 | | | 8 |
| 9 | 1275.651420 | 638.329348 | 1258.624871 | 629.816074 | 1257.640855 | 629.324065 | H | *719.394734* | 360.201005 | 702.368185 | 351.687730 | | | 7 |
| 10 | 1412.710332 | 706.858804 | 1395.683783 | 698.345530 | 1394.699767 | 697.853521 | H | *582.335822* | 291.671549 | 565.309273 | 283.158274 | | | 6 |
| 11 | 1525.794396 | 763.400836 | 1508.767847 | 754.887561 | 1507.783831 | 754.395553 | L | *445.276910* | 223.142093 | 428.250361 | 214.628818 | | | 5 |
| 12 | 1582.815860 | 791.911568 | 1565.789311 | 783.398293 | 1564.805295 | 782.906285 | G | *332.192846* | 166.600061 | 315.166297 | 158.086786 | | | 4 |
| 13 | 1639.837324 | 820.422300 | 1622.810775 | 811.909025 | 1621.826759 | 811.417017 | G | 275.171382 | 138.089329 | 258.144833 | 129.576054 | | | 3 |
| 14 | 1710.874438 | 855.940857 | 1693.847889 | 847.427582 | 1692.863873 | 846.935574 | A | 218.149918 | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 15 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.7 | 1855.972687 | 0.002345 | LTIGEGQQHHLGGAK |
| 31.7 | 1855.972687 | 0.002345 | LTIGEGQQHHLGGAK |
| 0.0 | 1855.979202 | -0.004170 | ITIVENVGSVEGLAYHR |

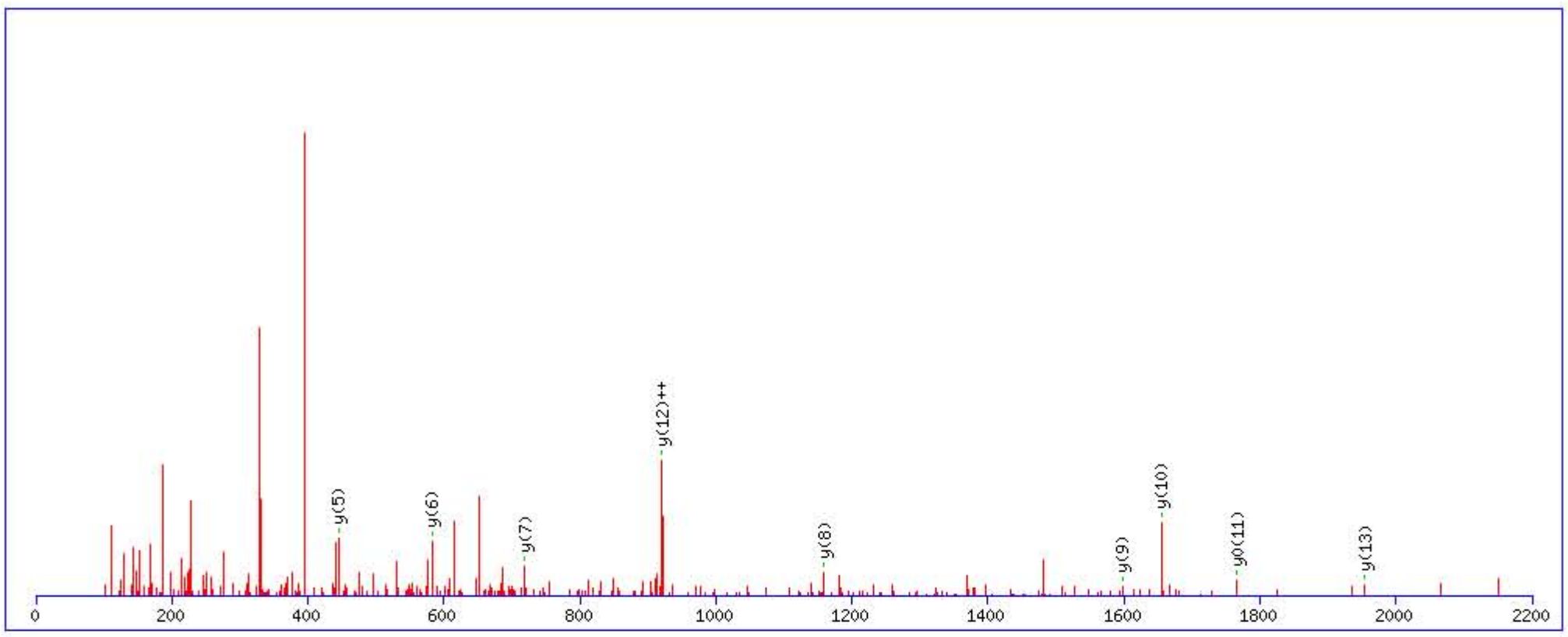
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

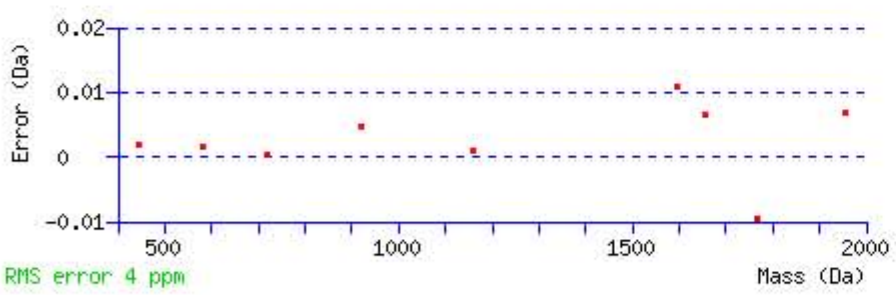
Match to Query 47801: 2167.140936 from(542.792510,4+) rtinseconds(1790) index(4320)
Title: Locus:1.1.1.1900.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

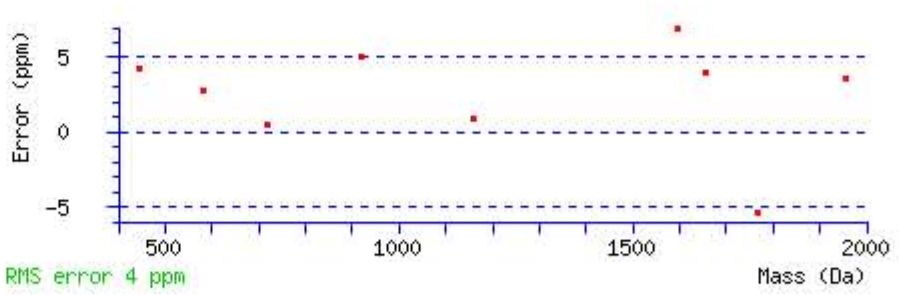
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2167.139435
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 26 **Expect:** 0.065
**Matches** : 9/134 fragment ions using 21 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 15 |
| 2 | 215.139019 | 108.073147 | | | 197.128454 | 99.067865 | T | 2055.062650 | 1028.034963 | 2038.036101 | 1019.521688 | 2037.052085 | 1019.029680 | 14 |
| 3 | 328.223083 | 164.615179 | | | 310.212518 | 155.609897 | I | *1954.014971* | 977.511123 | 1936.988422 | 968.997849 | 1936.004406 | 968.505841 | 13 |
| 4 | 385.244547 | 193.125911 | | | 367.233982 | 184.120629 | G | 1840.930907 | 920.969091 | 1823.904358 | 912.455817 | 1822.920342 | 911.963809 | 12 |
| 5 | 514.287140 | 257.647208 | | | 496.276575 | 248.641926 | E | 1783.909443 | 892.458359 | 1766.882894 | 883.945085 | 1765.898878 | 883.453077 | 11 |
| 6 | 571.308604 | 286.157940 | | | 553.298039 | 277.152658 | G | *1654.866850* | 827.937063 | 1637.840301 | 819.423788 | | | 10 |
| 7 | 1010.533930 | 505.770603 | 993.507381 | 497.257329 | 992.523365 | 496.765321 | Q | *1597.845386* | 799.426331 | 1580.818837 | 790.913056 | | | 9 |
| 8 | 1449.759256 | 725.383266 | 1432.732707 | 716.869992 | 1431.748691 | 716.377984 | Q | *1158.620060* | 579.813668 | 1141.593511 | 571.300393 | | | 8 |
| 9 | 1586.818168 | 793.912722 | 1569.791619 | 785.399448 | 1568.807603 | 784.907440 | H | *719.394734* | 360.201005 | 702.368185 | 351.687730 | | | 7 |
| 10 | 1723.877080 | 862.442178 | 1706.850531 | 853.928904 | 1705.866515 | 853.436895 | H | *582.335822* | 291.671549 | 565.309273 | 283.158274 | | | 6 |
| 11 | 1836.961144 | 918.984210 | 1819.934595 | 910.470936 | 1818.950579 | 909.978927 | L | *445.276910* | 223.142093 | 428.250361 | 214.628818 | | | 5 |
| 12 | 1893.982608 | 947.494942 | 1876.956059 | 938.981667 | 1875.972043 | 938.489659 | G | 332.192846 | 166.600061 | 315.166297 | 158.086786 | | | 4 |
| 13 | 1951.004072 | 976.005674 | 1933.977523 | 967.492399 | 1932.993507 | 967.000391 | G | 275.171382 | 138.089329 | 258.144833 | 129.576054 | | | 3 |
| 14 | 2022.041186 | 1011.524231 | 2005.014637 | 1003.010956 | 2004.030621 | 1002.518948 | A | 218.149918 | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 15 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.8 | 2167.139435 | 0.001501 | LTIGEGQQHHLGGAK |

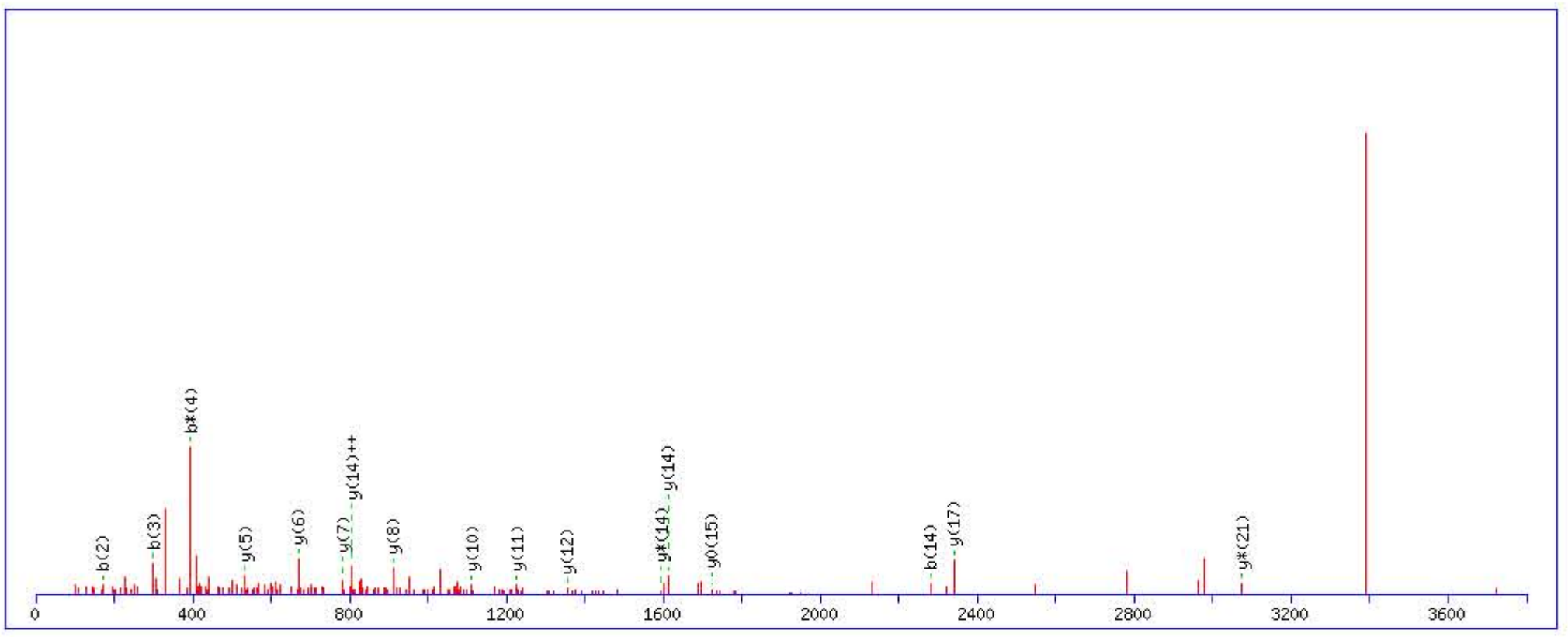
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VAQLEAQCQEPCKDTVQIHDITGK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

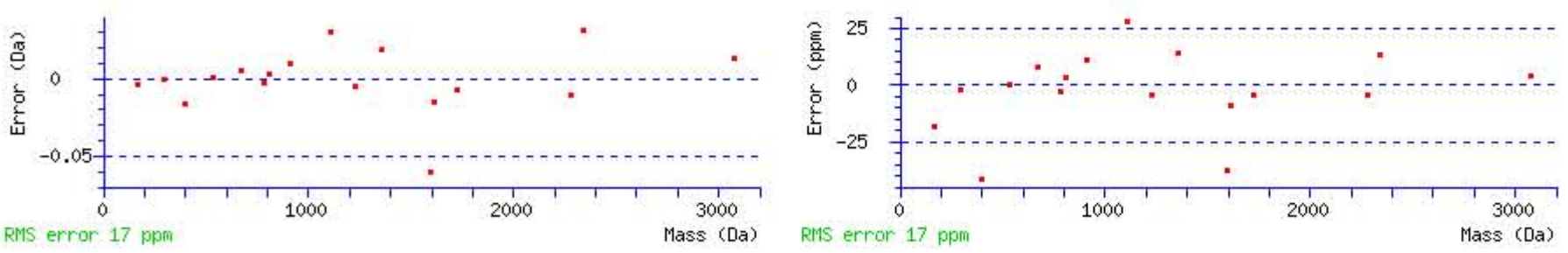
Match to Query 64876: 3389.708016 from(848.434280,4+) rtinseconds(2041) index(50592)
Title: Locus:1.1.1.1948.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3389.660416
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 0.00049
**Matches :** 17/260 fragment ions using 25 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 24 |
| 2 | 171.112804 | 86.060040 | | | | | A | 3291.599277 | 1646.303276 | 3274.572728 | 1637.790002 | 3273.588712 | 1637.297994 | 23 |
| 3 | 299.171382 | 150.089329 | 282.144833 | 141.576055 | | | Q | 3220.562163 | 1610.784719 | 3203.535614 | 1602.271445 | 3202.551598 | 1601.779437 | 22 |
| 4 | 412.255446 | 206.631361 | 395.228897 | 198.118087 | | | L | 3092.503585 | 1546.755430 | 3075.477036 | 1538.242156 | 3074.493020 | 1537.750148 | 21 |
| 5 | 541.298039 | 271.152658 | 524.271490 | 262.639383 | 523.287474 | 262.147375 | E | 2979.419521 | 1490.213398 | 2962.392972 | 1481.700124 | 2961.408956 | 1481.208116 | 20 |
| 6 | 612.335153 | 306.671215 | 595.308604 | 298.157940 | 594.324588 | 297.665932 | A | 2850.376928 | 1425.692102 | 2833.350379 | 1417.178827 | 2832.366363 | 1416.686819 | 19 |
| 7 | 1051.560479 | 526.283878 | 1034.533930 | 517.770603 | 1033.549914 | 517.278595 | Q | 2779.339814 | 1390.173545 | 2762.313265 | 1381.660270 | 2761.329249 | 1381.168262 | 18 |
| 8 | 1211.591128 | 606.299202 | 1194.564579 | 597.785928 | 1193.580563 | 597.293920 | C | *2340.114488* | 1170.560882 | 2323.087939 | 1162.047607 | 2322.103923 | 1161.555599 | 17 |
| 9 | 1650.816454 | 825.911865 | 1633.789905 | 817.398591 | 1632.805889 | 816.906583 | Q | 2180.083839 | 1090.545557 | 2163.057290 | 1082.032283 | 2162.073274 | 1081.540275 | 16 |
| 10 | 1779.859047 | 890.433162 | 1762.832498 | 881.919887 | 1761.848482 | 881.427879 | E | 1740.858513 | 870.932894 | 1723.831964 | 862.419620 | 1722.847948 | 861.927612 | 15 |
| 11 | 1876.911811 | 938.959544 | 1859.885262 | 930.446269 | 1858.901246 | 929.954261 | P | *1611.815920* | 806.411598 | 1594.789371 | 797.898323 | 1593.805355 | 797.406315 | 14 |
| 12 | 2036.942460 | 1018.974868 | 2019.915911 | 1010.461594 | 2018.931895 | 1009.969586 | C | 1514.763156 | 757.885216 | 1497.736607 | 749.371941 | 1496.752591 | 748.879933 | 13 |
| 13 | 2165.037423 | 1083.022350 | 2148.010874 | 1074.509075 | 2147.026858 | 1074.017067 | K | *1354.732507* | 677.869891 | 1337.705958 | 669.356617 | 1336.721942 | 668.864609 | 12 |
| 14 | 2280.064366 | 1140.535821 | 2263.037817 | 1132.022546 | 2262.053801 | 1131.530538 | D | *1226.637544* | 613.822410 | 1209.610995 | 605.309135 | 1208.626979 | 604.817127 | 11 |
| 15 | 2381.112045 | 1191.059660 | 2364.085496 | 1182.546386 | 2363.101480 | 1182.054378 | T | *1111.610601* | 556.308938 | 1094.584052 | 547.795664 | 1093.600036 | 547.303656 | 10 |
| 16 | 2480.180459 | 1240.593867 | 2463.153910 | 1232.080593 | 2462.169894 | 1231.588585 | V | 1010.562922 | 505.785099 | 993.536373 | 497.271824 | 992.552357 | 496.779816 | 9 |
| 17 | 2608.239037 | 1304.623156 | 2591.212488 | 1296.109882 | 2590.228472 | 1295.617874 | Q | *911.494508* | 456.250892 | 894.467959 | 447.737618 | 893.483943 | 447.245610 | 8 |
| 18 | 2721.323101 | 1361.165188 | 2704.296552 | 1352.651914 | 2703.312536 | 1352.159906 | I | *783.435930* | 392.221603 | 766.409381 | 383.708328 | 765.425365 | 383.216320 | 7 |
| 19 | 2858.382013 | 1429.694644 | 2841.355464 | 1421.181370 | 2840.371448 | 1420.689362 | H | *670.351866* | 335.679571 | 653.325317 | 327.166296 | 652.341301 | 326.674288 | 6 |
| 20 | 2973.408956 | 1487.208116 | 2956.382407 | 1478.694841 | 2955.398391 | 1478.202833 | D | *533.292954* | 267.150115 | 516.266405 | 258.636840 | 515.282389 | 258.144832 | 5 |
| 21 | 3086.493020 | 1543.750148 | 3069.466471 | 1535.236873 | 3068.482455 | 1534.744865 | I | 418.266011 | 209.636643 | 401.239462 | 201.123369 | 400.255446 | 200.631361 | 4 |
| 22 | 3187.540699 | 1594.273987 | 3170.514150 | 1585.760713 | 3169.530134 | 1585.268705 | T | 305.181947 | 153.094611 | 288.155398 | 144.581337 | 287.171382 | 144.089329 | 3 |
| 23 | 3244.562163 | 1622.784719 | 3227.535614 | 1614.271445 | 3226.551598 | 1613.779437 | G | 204.134268 | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 24 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 47.7 | 3389.660416 | 0.047600 | VAQLEAQCQEPCKDTVQIHDITGK |
| 38.4 | 3389.660416 | 0.047600 | VAQLEAQCQEPCKDTVQIHDITGK |
| 28.3 | 3389.660416 | 0.047600 | VAQLEAQCQEPCKDTVQIHDITGK |
| 5.2 | 3389.660416 | 0.047600 | VAQLEAQCQEPCKDTVQIHDITGK |
| 0.8 | 3389.660416 | 0.047600 | VAQLEAQCQEPCKDTVQIHDITGK |

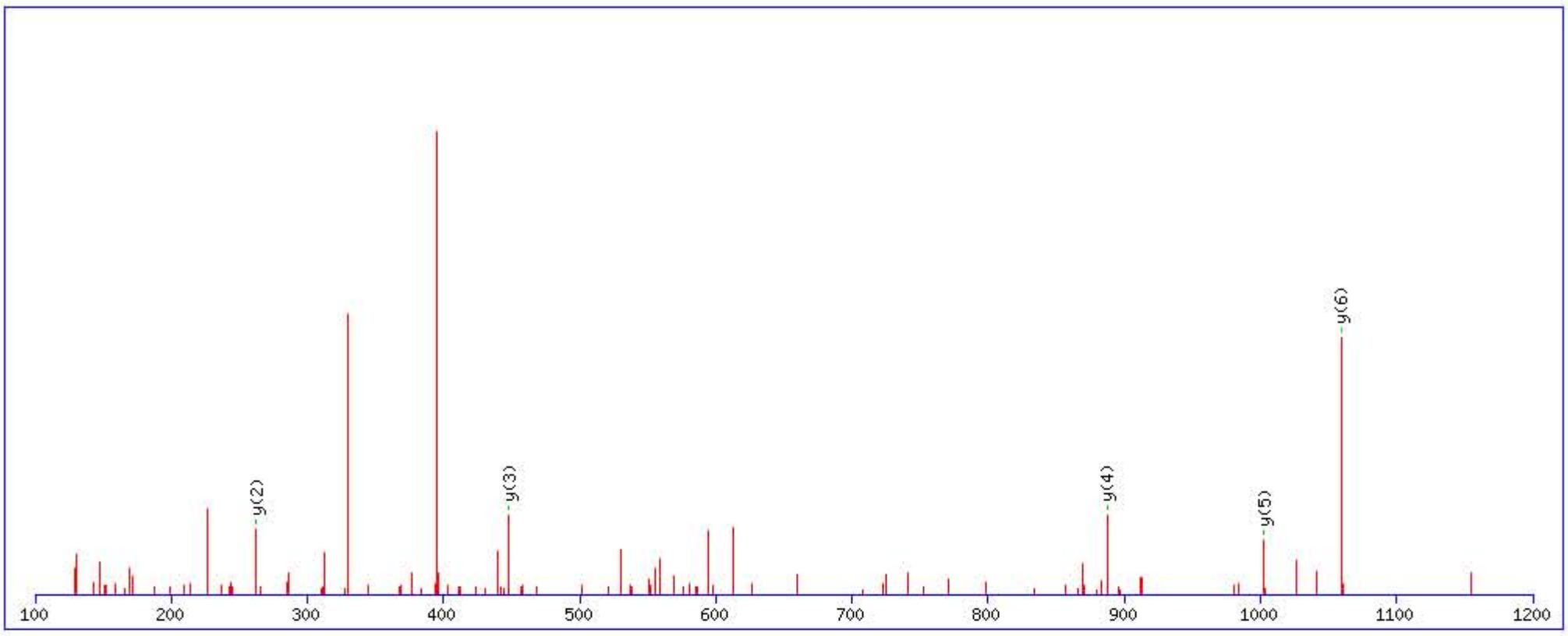
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IGDQWDK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

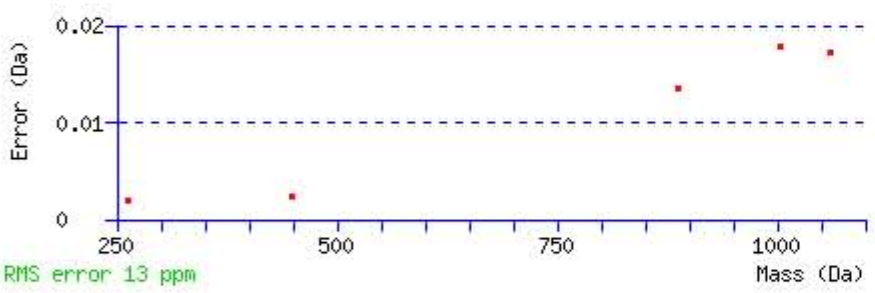
Match to Query 19627: 1171.575968 from(586.795260,2+) rtinseconds(1828) index(33080)
Title: Locus:1.1.1.745.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

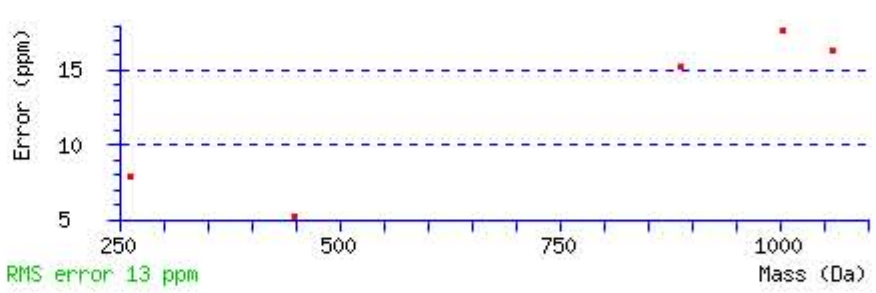
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1171.569580
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 28 **Expect:** 0.015
**Matches :** 5/60 fragment ions using 11 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 7 |
| 2 | 171.112804 | 86.060040 | | | | | G | *1059.492793* | 530.250035 | 1042.466244 | 521.736760 | 1041.482228 | 521.244752 | 6 |
| 3 | 286.139747 | 143.573512 | | | 268.129182 | 134.568229 | D | *1002.471329* | 501.739303 | 985.444780 | 493.226028 | 984.460764 | 492.734020 | 5 |
| 4 | 725.365073 | 363.186175 | 708.338524 | 354.672900 | 707.354508 | 354.180892 | Q | *887.444386* | 444.225831 | 870.417837 | 435.712557 | 869.433821 | 435.220549 | 4 |
| 5 | 911.444386 | 456.225831 | 894.417837 | 447.712557 | 893.433821 | 447.220549 | W | *448.219060* | 224.613168 | 431.192511 | 216.099894 | 430.208495 | 215.607886 | 3 |
| 6 | 1026.471329 | 513.739303 | 1009.444780 | 505.226028 | 1008.460764 | 504.734020 | D | *262.139747* | 131.573512 | 245.113198 | 123.060237 | 244.129182 | 122.568229 | 2 |
| 7 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 28.3 | 1171.569580 | 0.006388 | IGDQWDK |
| 8.3 | 1171.583328 | -0.007360 | GEVGDPGQKGTK |
| 6.0 | 1171.590714 | -0.014746 | GEVQVSDK |
| 5.4 | 1171.576096 | -0.000128 | LYFSDATLDK |
| 4.3 | 1171.572067 | 0.003901 | LGSGPDGAEEIK |
| 3.5 | 1171.569565 | 0.006403 | LGPEWSQPMK |
| 3.4 | 1171.590683 | -0.014715 | ELCADNPILK |
| 2.8 | 1171.590668 | -0.014700 | EKAEQEK |
| 2.8 | 1171.590668 | -0.014700 | EKAQEEK |
| 2.5 | 1171.559021 | 0.016947 | SQLHCRMPK |

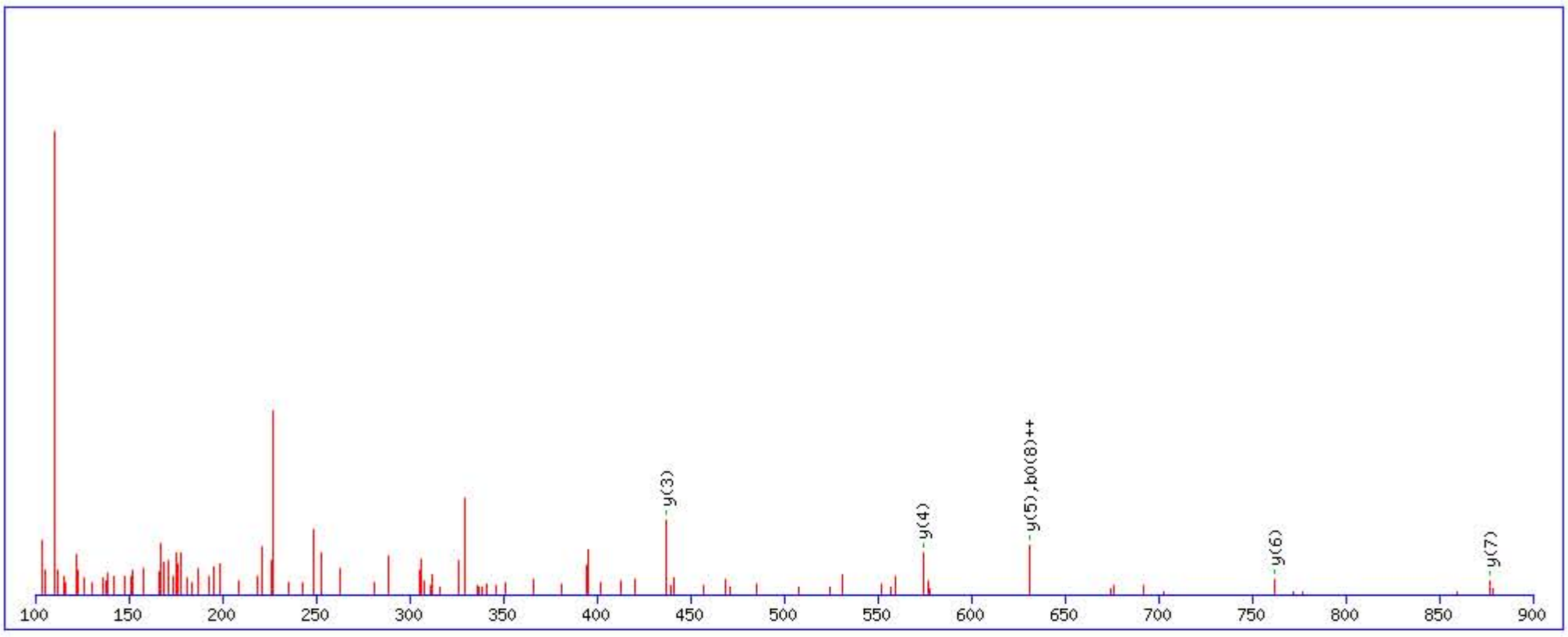
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QHDMGHMMR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

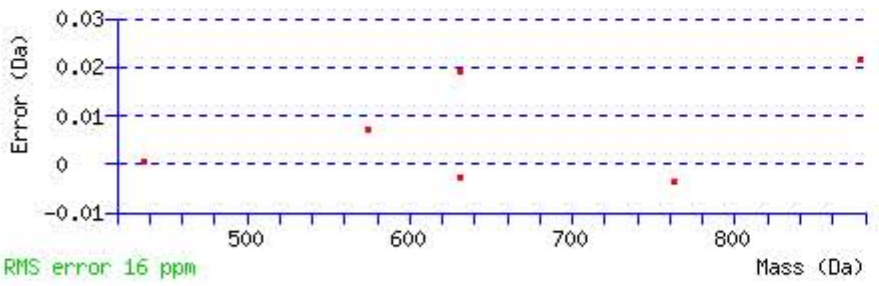
Match to Query 29671: 1452.617056 from(364.161540,4+) rtinseconds(1429) index(30593)
Title: Locus:1.1.1.606.2 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

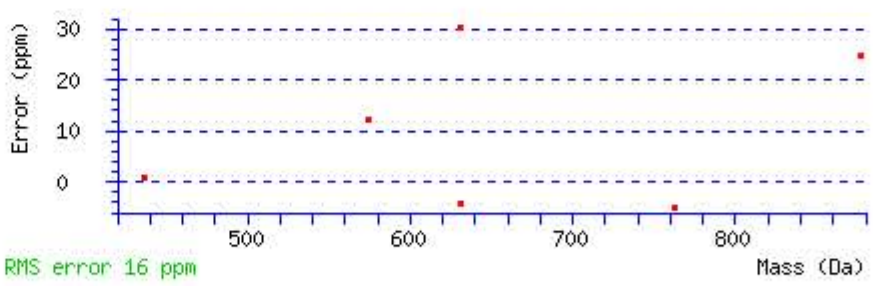
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1452.624680
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q1 : Biotin:Thermo-21345 (Q)
**Ions Score:** 26 **Expect:** 0.0092
**Matches :** 6/80 fragment ions using 8 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 9 |
| 2 | 577.291514 | 289.149395 | 560.264965 | 280.636121 | | | H | 1014.406638 | 507.706957 | 997.380089 | 499.193682 | 996.396073 | 498.701674 | 8 |
| 3 | 692.318457 | 346.662867 | 675.291908 | 338.149592 | 674.307892 | 337.657584 | D | *877.347726* | 439.177501 | 860.321177 | 430.664226 | 859.337161 | 430.172218 | 7 |
| 4 | 823.358942 | 412.183109 | 806.332393 | 403.669834 | 805.348377 | 403.177826 | M | *762.320783* | 381.664030 | 745.294234 | 373.150755 | | | 6 |
| 5 | 880.380406 | 440.693841 | 863.353857 | 432.180567 | 862.369841 | 431.688559 | G | *631.280298* | 316.143787 | 614.253749 | 307.630513 | | | 5 |
| 6 | 1017.439318 | 509.223297 | 1000.412769 | 500.710022 | 999.428753 | 500.218014 | H | *574.258834* | 287.633055 | 557.232285 | 279.119780 | | | 4 |
| 7 | 1148.479803 | 574.743540 | 1131.453254 | 566.230265 | 1130.469238 | 565.738257 | M | *437.199922* | 219.103599 | 420.173373 | 210.590324 | | | 3 |
| 8 | 1279.520288 | 640.263782 | 1262.493739 | 631.750508 | 1261.509723 | 631.258499 | M | 306.159437 | 153.583356 | 289.132888 | 145.070082 | | | 2 |
| 9 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 26.4 | 1452.624680 | -0.007624 | QHDMGHMMR |

**Mascot:** http://www.matrixscience.com/

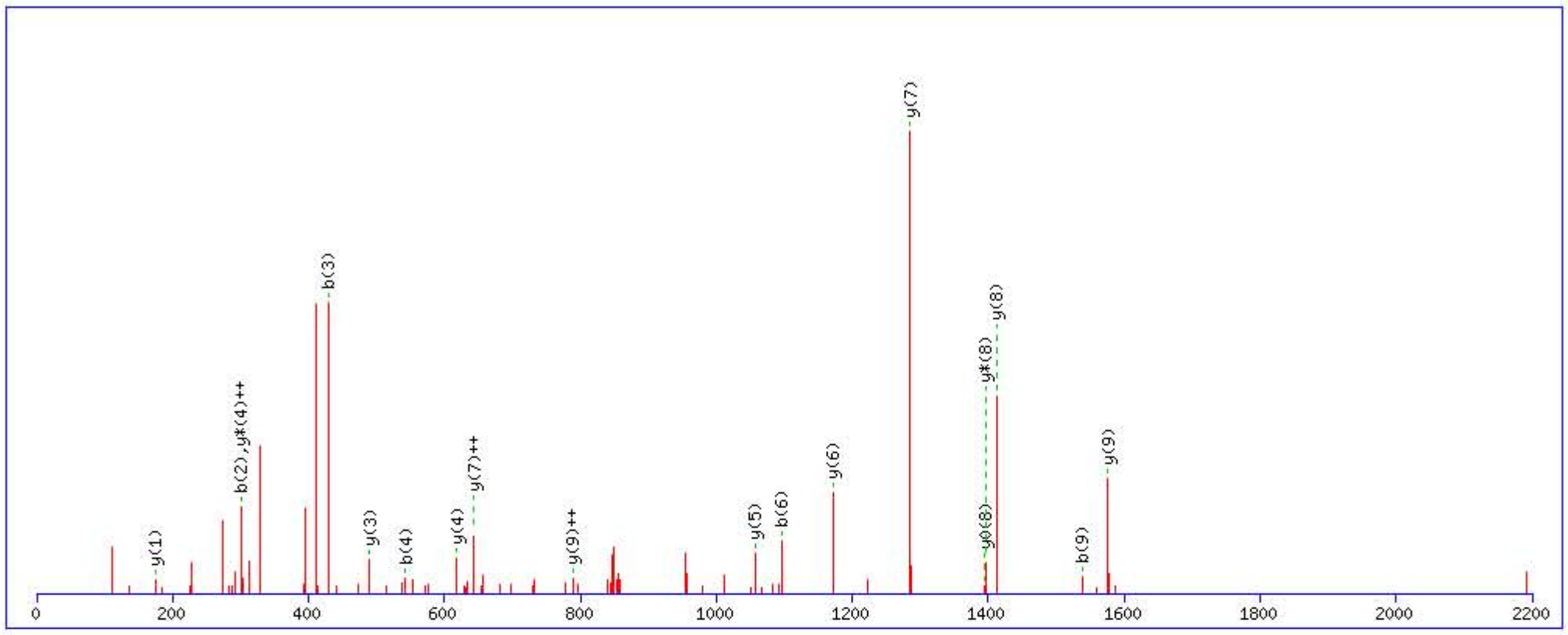
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HYQINQQWER**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

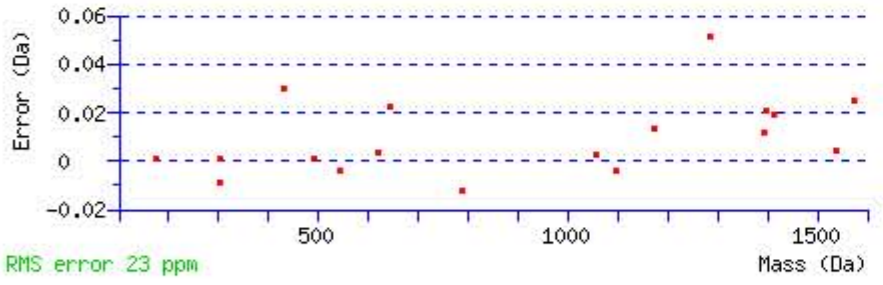
Match to Query 38230: 1711.849368 from(856.931960,2+) rtinseconds(1774) index(32766)
Title: Locus:1.1.1.726.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

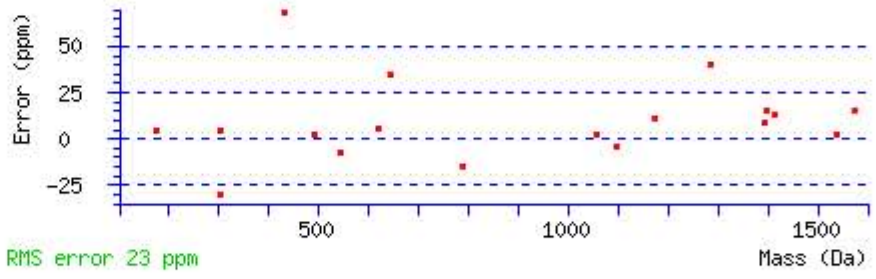
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1711.825272
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.00053
**Matches :** 18/86 fragment ions using 41 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 10 |
| 2 | **301.129517** | 151.068397 | | | | | Y | *1575.773660* | 788.390468 | 1558.747111 | 779.877194 | 1557.763095 | 779.385186 | 9 |
| 3 | **429.188095** | 215.097686 | 412.161546 | 206.584411 | | | Q | *1412.710331* | 706.858804 | 1395.683782 | 698.345529 | 1394.699766 | 697.853521 | 8 |
| 4 | **542.272159** | 271.639718 | 525.245610 | 263.126443 | | | I | *1284.651753* | 642.829514 | 1267.625204 | 634.316240 | 1266.641188 | 633.824232 | 7 |
| 5 | 656.315086 | 328.661181 | 639.288537 | 320.147907 | | | N | *1171.567689* | 586.287483 | 1154.541140 | 577.774208 | 1153.557124 | 577.282200 | 6 |
| 6 | **1095.540412** | 548.273844 | 1078.513863 | 539.760570 | | | Q | *1057.524762* | 529.266019 | 1040.498213 | 520.752745 | 1039.514197 | 520.260737 | 5 |
| 7 | 1223.598990 | 612.303133 | 1206.572441 | 603.789859 | | | Q | *618.299436* | 309.653356 | 601.272887 | 301.140082 | 600.288871 | 300.648074 | 4 |
| 8 | 1409.678303 | 705.342790 | 1392.651754 | 696.829515 | | | W | *490.240858* | 245.624067 | 473.214309 | 237.110792 | 472.230293 | 236.618784 | 3 |
| 9 | **1538.720896** | 769.864086 | 1521.694347 | 761.350812 | 1520.710331 | 760.858804 | E | 304.161545 | 152.584410 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 10 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

### All matches to this query

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 37.8 | 1711.825272 | 0.024096 | HYQINQQWER |
| 28.5 | 1711.825272 | 0.024096 | HYQINQQWER |
| 9.1 | 1711.825272 | 0.024096 | HYQINQQWER |
| 2.7 | 1711.871368 | -0.022000 | AQTQEGAGARAGAQAVAR |
| 0.1 | 1711.856293 | -0.006925 | LLQGQEKDGEER |

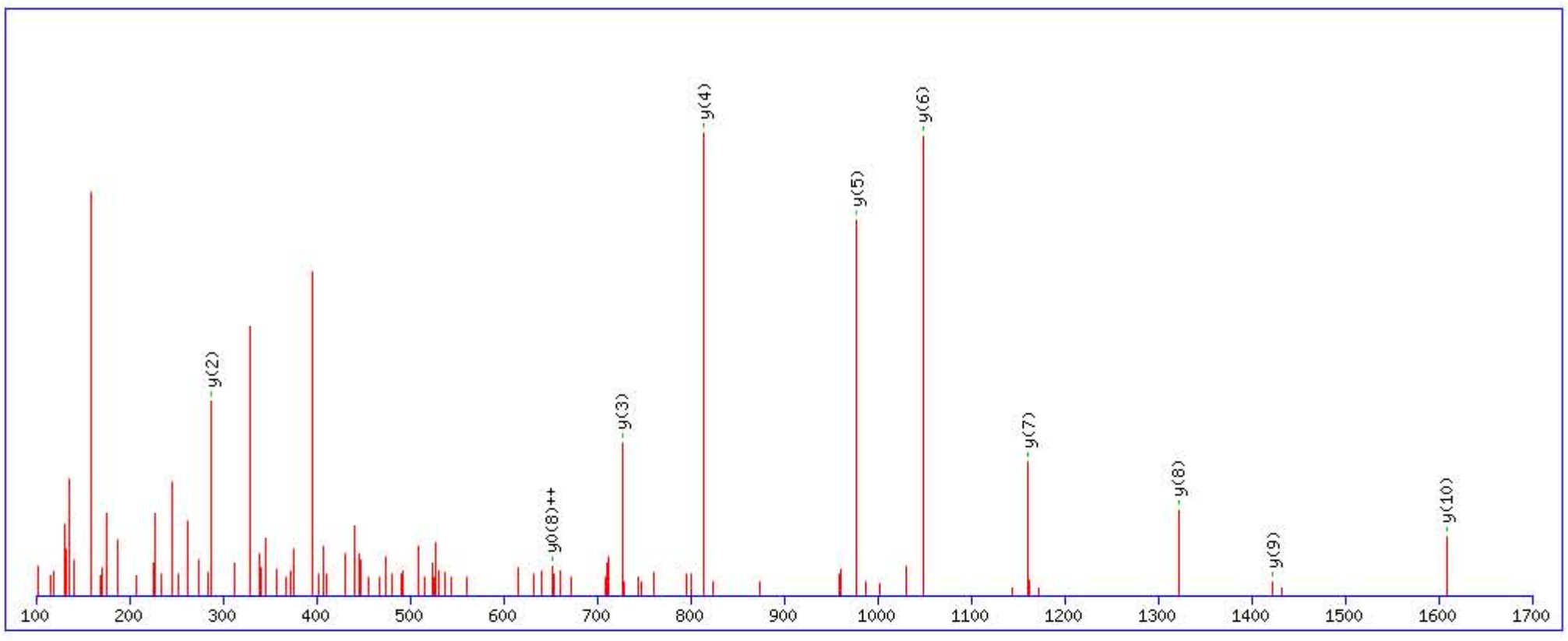
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GEWTCIAYSQLR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

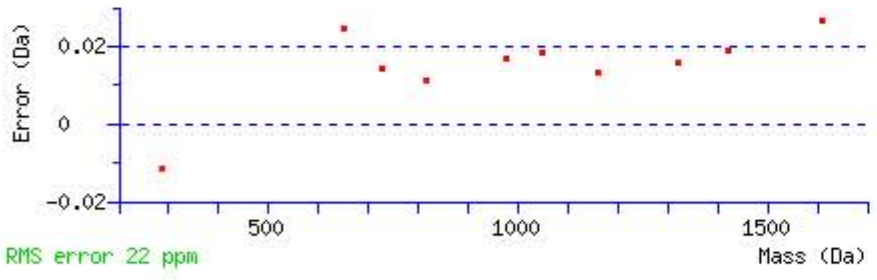
Match to Query 40139: 1793.879082 from(598.966970,3+) rtinseconds(2364) index(36382)
Title: Locus:1.1.1.932.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

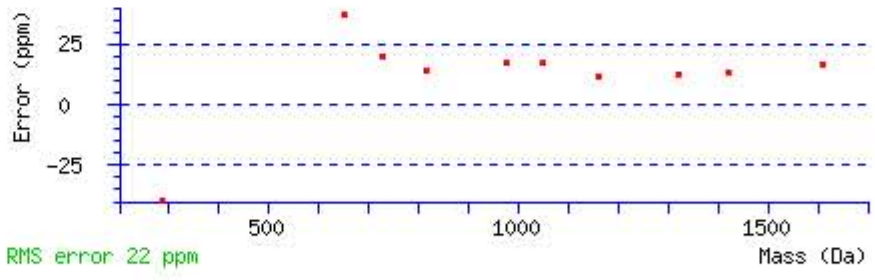
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1793.859283
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q10** : Biotin:Thermo-21345 (Q)
**Ions Score:** 72 **Expect:** 4.7e-007
**Matches** : 10/106 fragment ions using 14 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 12 |
| 2 | 187.071333 | 94.039305 | | | 169.060768 | 85.034022 | E | 1737.845111 | 869.426194 | 1720.818562 | 860.912919 | 1719.834546 | 860.420911 | 11 |
| 3 | 373.150646 | 187.078961 | | | 355.140081 | 178.073679 | W | *1608.802518* | 804.904897 | 1591.775969 | 796.391623 | 1590.791953 | 795.899614 | 10 |
| 4 | 474.198325 | 237.602801 | | | 456.187760 | 228.597518 | T | *1422.723205* | 711.865241 | 1405.696656 | 703.351966 | 1404.712640 | 702.859958 | 9 |
| 5 | 634.228974 | 317.618125 | | | 616.218409 | 308.612843 | C | *1321.675526* | 661.341401 | 1304.648977 | 652.828127 | 1303.664961 | 652.336119 | 8 |
| 6 | 747.313038 | 374.160157 | | | 729.302473 | 365.154875 | I | *1161.644877* | 581.326077 | 1144.618328 | 572.812802 | 1143.634312 | 572.320794 | 7 |
| 7 | 818.350152 | 409.678714 | | | 800.339587 | 400.673432 | A | *1048.560813* | 524.784044 | 1031.534264 | 516.270770 | 1030.550248 | 515.778762 | 6 |
| 8 | 981.413481 | 491.210379 | | | 963.402916 | 482.205096 | Y | *977.523699* | 489.265488 | 960.497150 | 480.752213 | 959.513134 | 480.260205 | 5 |
| 9 | 1068.445509 | 534.726393 | | | 1050.434944 | 525.721110 | S | *814.460370* | 407.733823 | 797.433821 | 399.220549 | 796.449805 | 398.728541 | 4 |
| 10 | 1507.670835 | 754.339056 | 1490.644286 | 745.825781 | 1489.660270 | 745.333773 | Q | *727.428342* | 364.217809 | 710.401793 | 355.704534 | | | 3 |
| 11 | 1620.754899 | 810.881088 | 1603.728350 | 802.367813 | 1602.744334 | 801.875805 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 12 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 71.6 | 1793.859283 | 0.019799 | GEWTCIAYSQLR |
| 3.9 | 1793.865158 | 0.013924 | ACLECELTSKDVTLR |
| 2.5 | 1793.873016 | 0.006066 | DQKLFVSESRMPDSR |
| 0.7 | 1793.873016 | 0.006066 | TCTADSKATAPAYKPGR |

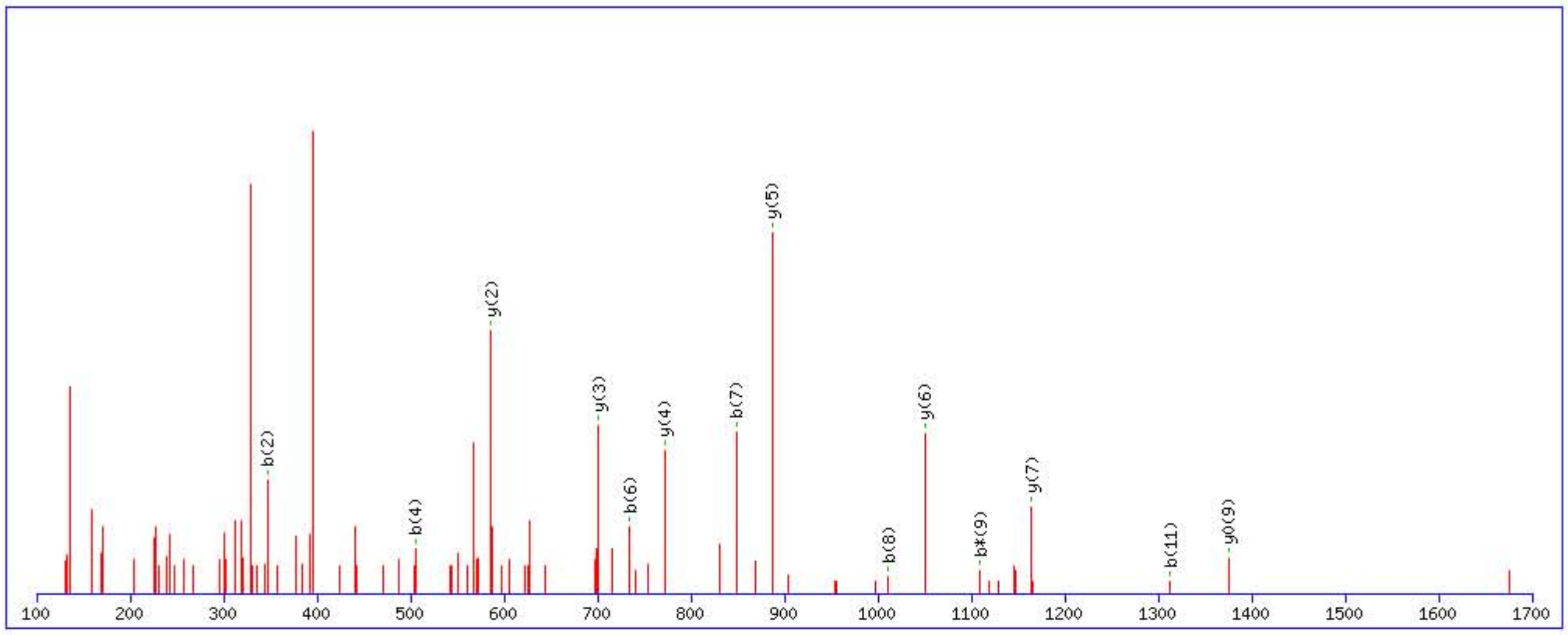
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **WCGTTQNYDADQK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

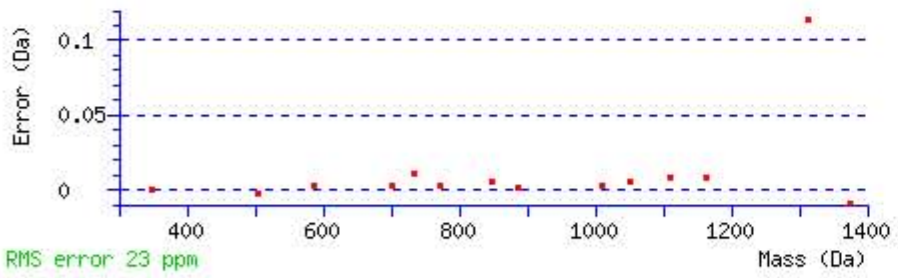
Match to Query 42045: 1896.821472 from(633.281100,3+) rtinseconds(1690) index(32220)
Title: Locus:1.1.1.697.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

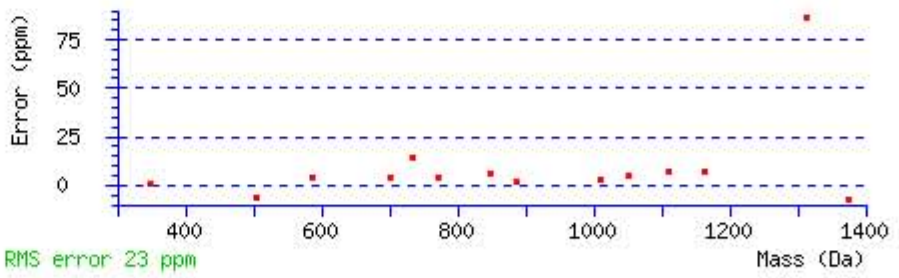
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1896.813477
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 35 **Expect:** 0.0014
**Matches :** 14/124 fragment ions using 25 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 187.086589 | 94.046932 | | | | | W | | | | | | | 13 |
| 2 | *347.117238* | 174.062257 | | | | | C | 1711.741435 | 856.374356 | 1694.714886 | 847.861081 | 1693.730870 | 847.369073 | 12 |
| 3 | 404.138702 | 202.572989 | | | | | G | 1551.710786 | 776.359031 | 1534.684237 | 767.845757 | 1533.700221 | 767.353749 | 11 |
| 4 | *505.186381* | 253.096828 | | | 487.175816 | 244.091546 | T | 1494.689322 | 747.848299 | 1477.662773 | 739.335025 | 1476.678757 | 738.843017 | 10 |
| 5 | 606.234060 | 303.620668 | | | 588.223495 | 294.615386 | T | 1393.641643 | 697.324460 | 1376.615094 | 688.811185 | 1375.631078 | 688.319177 | 9 |
| 6 | *734.292638* | 367.649957 | 717.266089 | 359.136683 | 716.282073 | 358.644675 | Q | 1292.593964 | 646.800620 | 1275.567415 | 638.287346 | 1274.583399 | 637.795338 | 8 |
| 7 | *848.335565* | 424.671421 | 831.309016 | 416.158146 | 830.325000 | 415.666138 | N | *1164.535386* | 582.771331 | 1147.508837 | 574.258057 | 1146.524821 | 573.766049 | 7 |
| 8 | *1011.398894* | 506.203085 | 994.372345 | 497.689810 | 993.388329 | 497.197802 | Y | *1050.492459* | 525.749868 | 1033.465910 | 517.236593 | 1032.481894 | 516.744585 | 6 |
| 9 | 1126.425837 | 563.716557 | 1109.399288 | 555.203282 | 1108.415272 | 554.711274 | D | *887.429130* | 444.218203 | 870.402581 | 435.704929 | 869.418565 | 435.212921 | 5 |
| 10 | 1197.462951 | 599.235114 | 1180.436402 | 590.721839 | 1179.452386 | 590.229831 | A | *772.402187* | 386.704732 | 755.375638 | 378.191457 | 754.391622 | 377.699449 | 4 |
| 11 | *1312.489894* | 656.748585 | 1295.463345 | 648.235311 | 1294.479329 | 647.743303 | D | *701.365073* | 351.186175 | 684.338524 | 342.672900 | 683.354508 | 342.180892 | 3 |
| 12 | 1751.715220 | 876.361248 | 1734.688671 | 867.847974 | 1733.704655 | 867.355966 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 13 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 35.3 | 1896.813477 | 0.007995 | WCGTTQNYDADQK |

**Mascot:** http://www.matrixscience.com/

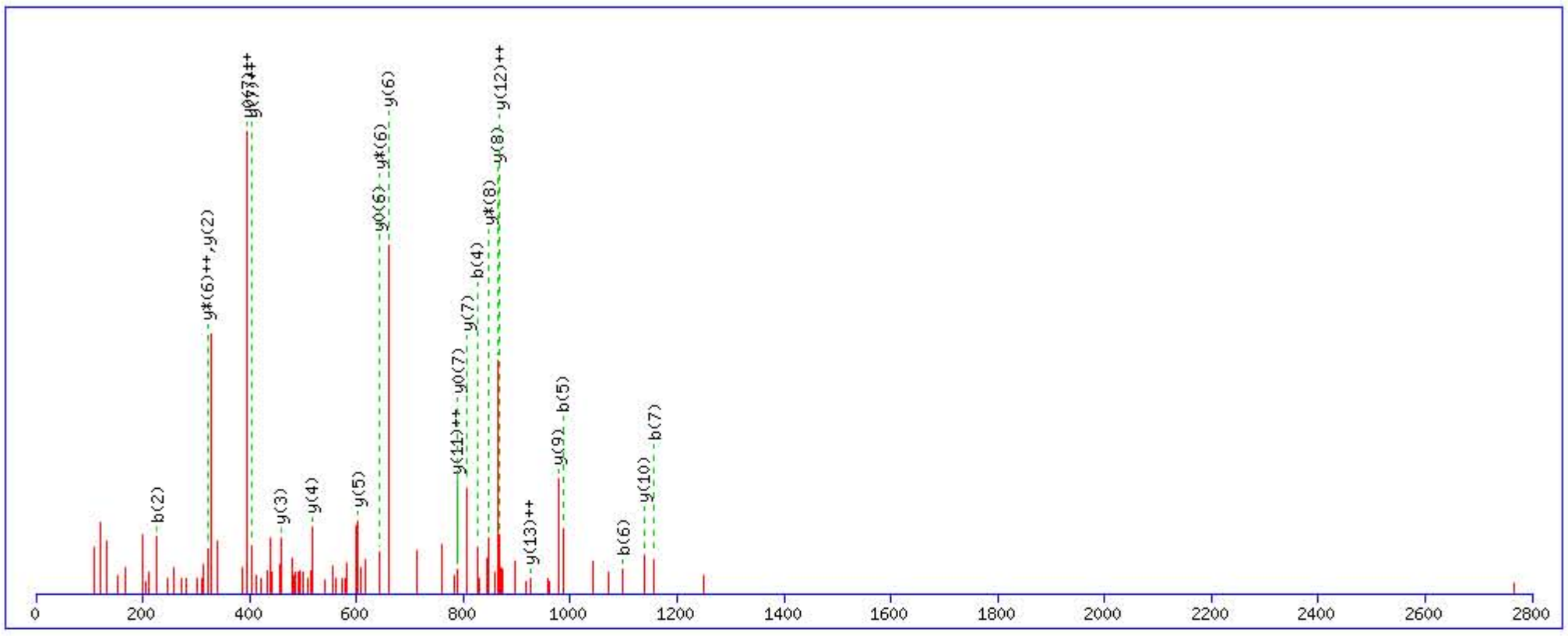
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LLCQCLGFGSGHFR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

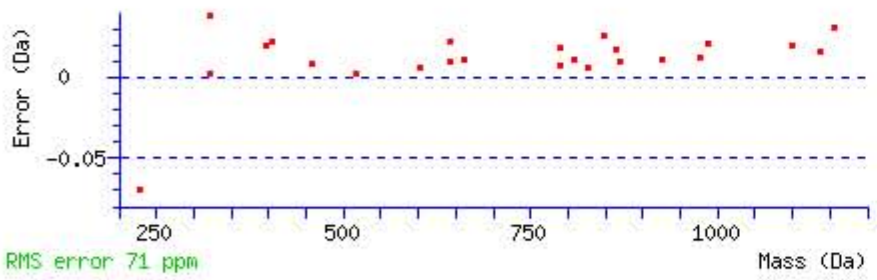
Match to Query 43363: 1961.967492 from(654.996440,3+) rtinseconds(2182) index(35378)
Title: Locus:1.1.1.868.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

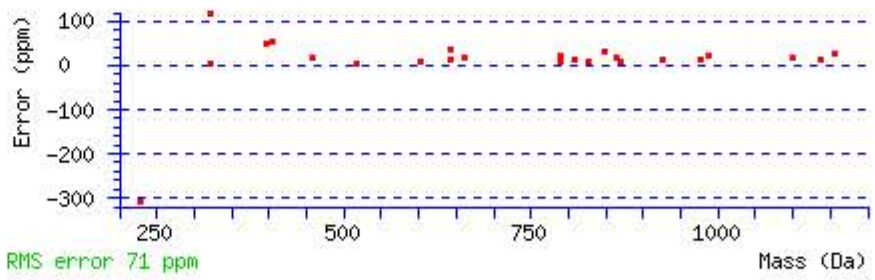
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1961.942673
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 41 **Expect:** 0.0022
**Matches :** 24/124 fragment ions using 51 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 14 |
| 2 | **227.175404** | 114.091340 | | | | | L | 1849.865864 | 925.436570 | 1832.839315 | 916.923296 | 1831.855299 | 916.431288 | 13 |
| 3 | 387.206053 | 194.106664 | | | | | C | 1736.781800 | 868.894538 | 1719.755251 | 860.381264 | 1718.771235 | 859.889255 | 12 |
| 4 | **826.431379** | 413.719328 | 809.404830 | 405.206053 | | | Q | 1576.751151 | 788.879213 | 1559.724602 | 780.365939 | 1558.740586 | 779.873931 | 11 |
| 5 | **986.462028** | 493.734652 | 969.435479 | 485.221378 | | | C | *1137.525825* | 569.266550 | 1120.499276 | 560.753276 | 1119.515260 | 560.261268 | 10 |
| 6 | **1099.546092** | 550.276684 | 1082.519543 | 541.763410 | | | L | *977.495176* | 489.251226 | 960.468627 | 480.737952 | 959.484611 | 480.245944 | 9 |
| 7 | **1156.567556** | 578.787416 | 1139.541007 | 570.274142 | | | G | *864.411112* | 432.709194 | 847.384563 | 424.195920 | 846.400547 | 423.703912 | 8 |
| 8 | 1303.635970 | 652.321623 | 1286.609421 | 643.808349 | | | F | *807.389648* | 404.198462 | 790.363099 | 395.685188 | 789.379083 | 395.193180 | 7 |
| 9 | 1360.657434 | 680.832355 | 1343.630885 | 672.319081 | | | G | *660.321234* | 330.664255 | 643.294685 | 322.150981 | 642.310669 | 321.658973 | 6 |
| 10 | 1447.689462 | 724.348369 | 1430.662913 | 715.835095 | 1429.678897 | 715.343087 | S | *603.299770* | 302.153523 | 586.273221 | 293.640249 | 585.289205 | 293.148241 | 5 |
| 11 | 1504.710926 | 752.859101 | 1487.684377 | 744.345827 | 1486.700361 | 743.853818 | G | *516.267742* | 258.637509 | 499.241193 | 250.124235 | | | 4 |
| 12 | 1641.769838 | 821.388557 | 1624.743289 | 812.875283 | 1623.759273 | 812.383274 | H | *459.246278* | 230.126777 | 442.219729 | 221.613502 | | | 3 |
| 13 | 1788.838252 | 894.922764 | 1771.811703 | 886.409490 | 1770.827687 | 885.917482 | F | *322.187366* | 161.597321 | 305.160817 | 153.084047 | | | 2 |
| 14 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 40.7 | 1961.942673 | 0.024819 | LLCQCLGFGSGHFR |

**Mascot:** http://www.matrixscience.com/

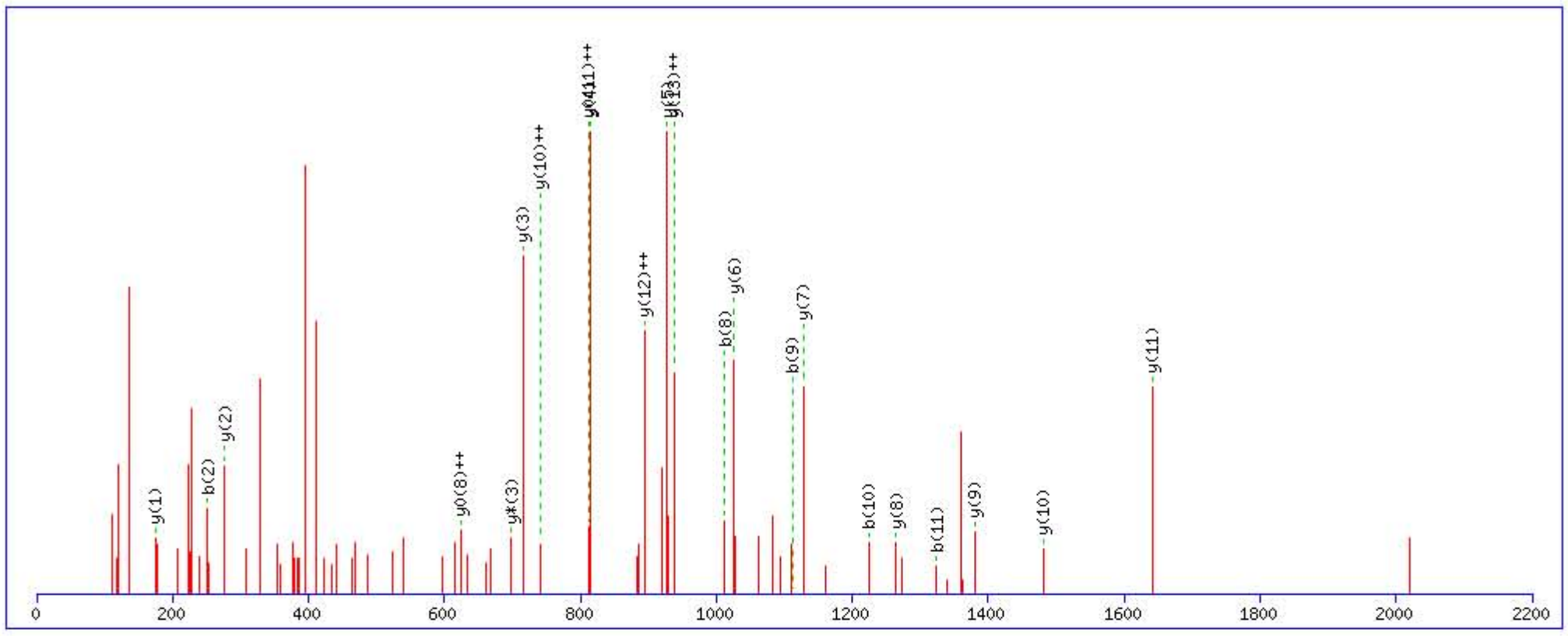
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YSFCTDHTVLVQTR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

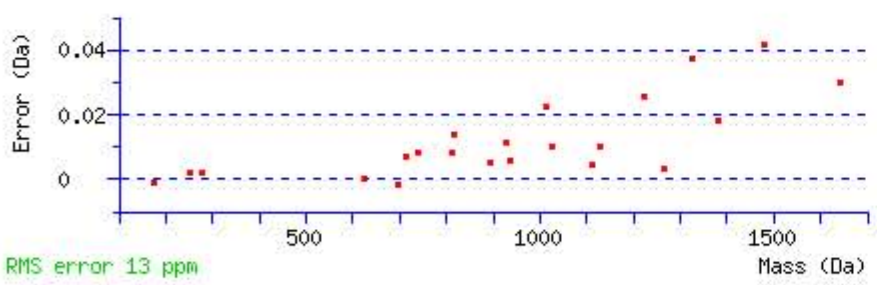
Match to Query 45400: 2036.995482 from(680.005770,3+) rtinseconds(2023) index(34416)
Title: Locus:1.1.1.813.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

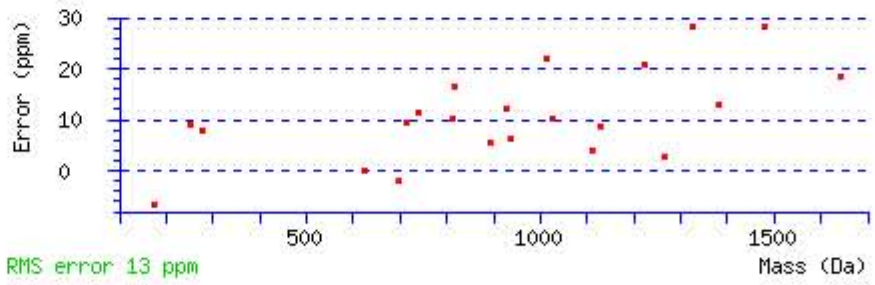
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2036.981232
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 54 **Expect:** 8.5e-005
**Matches :** 22/130 fragment ions using 52 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 14 |
| 2 | **251.102633** | 126.054954 | | | 233.092068 | 117.049672 | S | 1874.925153 | 937.966215 | 1857.898604 | 929.452940 | 1856.914588 | 928.960932 | 13 |
| 3 | 398.171047 | 199.589161 | | | 380.160482 | 190.583879 | F | 1787.893125 | 894.450201 | 1770.866576 | 885.936926 | 1769.882560 | 885.444918 | 12 |
| 4 | 558.201696 | 279.604486 | | | 540.191131 | 270.599204 | C | *1640.824711* | 820.915994 | 1623.798162 | 812.402719 | 1622.814146 | 811.910711 | 11 |
| 5 | 659.249375 | 330.128326 | | | 641.238810 | 321.123043 | T | *1480.794062* | 740.900669 | 1463.767513 | 732.387395 | 1462.783497 | 731.895387 | 10 |
| 6 | 774.276318 | 387.641797 | | | 756.265753 | 378.636515 | D | *1379.746383* | 690.376830 | 1362.719834 | 681.863555 | 1361.735818 | 681.371547 | 9 |
| 7 | 911.335230 | 456.171253 | | | 893.324665 | 447.165971 | H | *1264.719440* | 632.863358 | 1247.692891 | 624.350084 | 1246.708875 | 623.858076 | 8 |
| 8 | **1012.382909** | 506.695093 | | | 994.372344 | 497.689810 | T | *1127.660528* | 564.333902 | 1110.633979 | 555.820628 | 1109.649963 | 555.328620 | 7 |
| 9 | **1111.451323** | 556.229300 | | | 1093.440758 | 547.224017 | V | *1026.612849* | 513.810063 | 1009.586300 | 505.296788 | 1008.602284 | 504.804780 | 6 |
| 10 | **1224.535387** | 612.771331 | | | 1206.524822 | 603.766049 | L | *927.544435* | 464.275856 | 910.517886 | 455.762581 | 909.533870 | 455.270573 | 5 |
| 11 | **1323.603801** | 662.305539 | | | 1305.593236 | 653.300256 | V | *814.460371* | 407.733824 | 797.433822 | 399.220549 | 796.449806 | 398.728541 | 4 |
| 12 | 1762.829127 | 881.918202 | 1745.802578 | 873.404927 | 1744.818562 | 872.912919 | Q | *715.391957* | 358.199617 | 698.365408 | 349.686342 | 697.381392 | 349.194334 | 3 |
| 13 | 1863.876806 | 932.442041 | 1846.850257 | 923.928767 | 1845.866241 | 923.436759 | T | *276.166631* | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 14 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 54.2 | 2036.981232 | 0.014250 | YSFCTDHTVLVQTR |

**Mascot:** http://www.matrixscience.com/

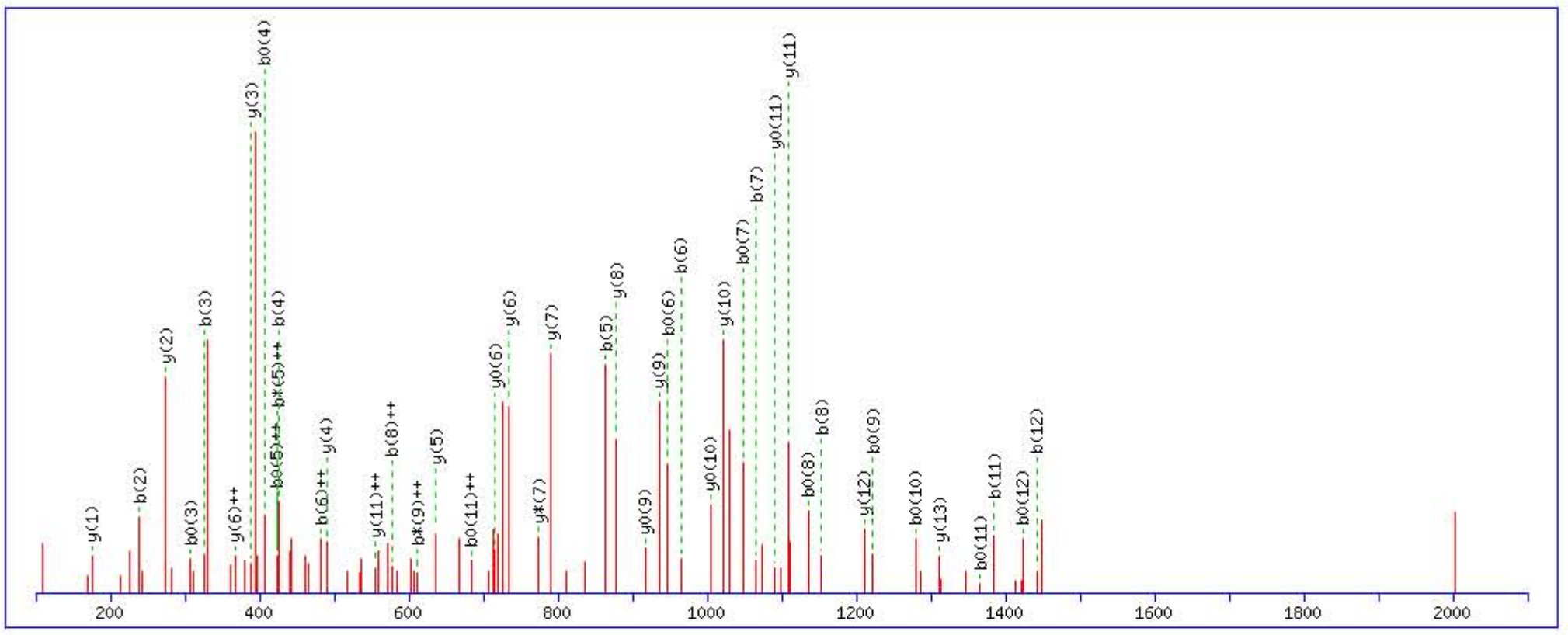
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HTSVQTTSSGSGPFTDVR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

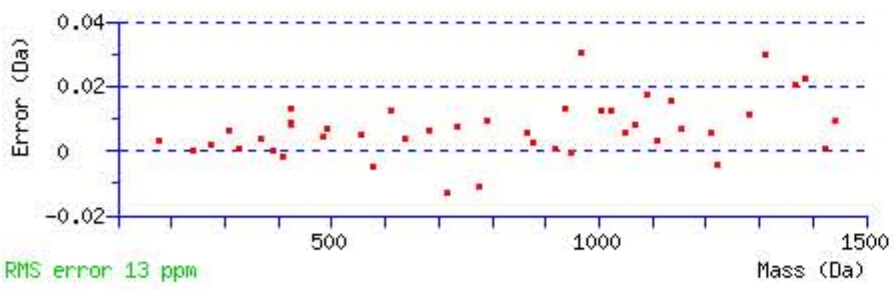
Match to Query 47972: 2174.057082 from(725.692970,3+) rtinseconds(1695) index(48223)
Title: Locus:1.1.1.1828.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

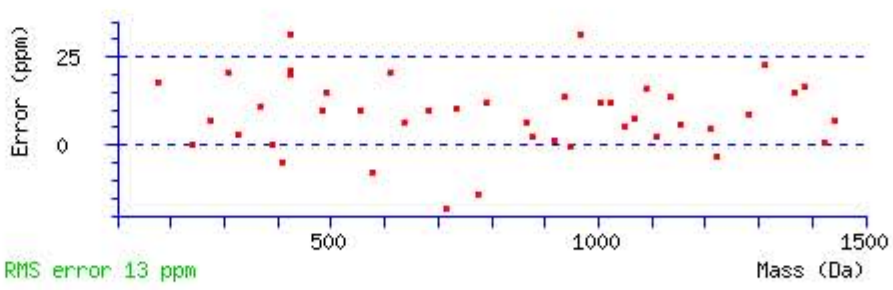
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2174.042664
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 70 **Expect:** 5.9e-007
**Matches :** 44/190 fragment ions using 85 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 18 |
| 2 | *239.113867* | 120.060571 | | | 221.103302 | 111.055289 | T | 2037.990983 | 1019.499130 | 2020.964434 | 1010.985855 | 2019.980418 | 1010.493847 | 17 |
| 3 | *326.145895* | 163.576585 | | | 308.135330 | 154.571303 | S | 1936.943304 | 968.975290 | 1919.916755 | 960.462016 | 1918.932739 | 959.970008 | 16 |
| 4 | *425.214309* | 213.110792 | | | 407.203744 | 204.105510 | V | 1849.911276 | 925.459276 | 1832.884727 | 916.946002 | 1831.900711 | 916.453994 | 15 |
| 5 | *864.439635* | 432.723456 | 847.413086 | 424.210181 | 846.429070 | 423.718173 | Q | 1750.842862 | 875.925069 | 1733.816313 | 867.411795 | 1732.832297 | 866.919787 | 14 |
| 6 | *965.487314* | **483.247295** | 948.460765 | 474.734021 | 947.476749 | 474.242013 | T | *1311.617536* | 656.312406 | 1294.590987 | 647.799132 | 1293.606971 | 647.307124 | 13 |
| 7 | *1066.534993* | 533.771135 | 1049.508444 | 525.257860 | 1048.524428 | 524.765852 | T | *1210.569857* | 605.788567 | 1193.543308 | 597.275292 | 1192.559292 | 596.783284 | 12 |
| 8 | *1153.567021* | **577.287149** | 1136.540472 | 568.773874 | 1135.556456 | 568.281866 | S | *1109.522178* | 555.264727 | 1092.495629 | 546.751453 | 1091.511613 | 546.259445 | 11 |
| 9 | 1240.599049 | 620.803163 | 1223.572500 | 612.289888 | 1222.588484 | 611.797880 | S | *1022.490150* | 511.748713 | 1005.463601 | 503.235439 | 1004.479585 | 502.743431 | 10 |
| 10 | 1297.620513 | 649.313895 | 1280.593964 | 640.800620 | 1279.609948 | 640.308612 | G | *935.458122* | 468.232699 | 918.431573 | 459.719425 | 917.447557 | 459.227417 | 9 |
| 11 | *1384.652541* | 692.829909 | 1367.625992 | 684.316634 | 1366.641976 | 683.824626 | S | *878.436658* | 439.721967 | 861.410109 | 431.208693 | 860.426093 | 430.716685 | 8 |
| 12 | *1441.674005* | 721.340641 | 1424.647456 | 712.827366 | 1423.663440 | 712.335358 | G | *791.404630* | 396.205953 | 774.378081 | 387.692679 | 773.394065 | 387.200671 | 7 |
| 13 | 1538.726769 | 769.867023 | 1521.700220 | 761.353748 | 1520.716204 | 760.861740 | P | *734.383166* | 367.695221 | 717.356617 | 359.181947 | 716.372601 | 358.689939 | 6 |
| 14 | 1685.795183 | 843.401230 | 1668.768634 | 834.887955 | 1667.784618 | 834.395947 | F | *637.330402* | 319.168839 | 620.303853 | 310.655565 | 619.319837 | 310.163557 | 5 |
| 15 | 1786.842862 | 893.925069 | 1769.816313 | 885.411795 | 1768.832297 | 884.919787 | T | *490.261988* | 245.634632 | 473.235439 | 237.121358 | 472.251423 | 236.629350 | 4 |
| 16 | 1901.869805 | 951.438541 | 1884.843256 | 942.925266 | 1883.859240 | 942.433258 | D | *389.214309* | 195.110793 | 372.187760 | 186.597518 | 371.203744 | 186.105510 | 3 |
| 17 | 2000.938219 | 1000.972748 | 1983.911670 | 992.459473 | 1982.927654 | 991.967465 | V | *274.187366* | 137.597321 | 257.160817 | 129.084047 | | | 2 |
| 18 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 69.9 | 2174.042664 | 0.014418 | HTSVQTTSSGSGPFTDVR |
| 3.4 | 2174.034729 | 0.022353 | QNKAEGLGMVTEEGSGEK |

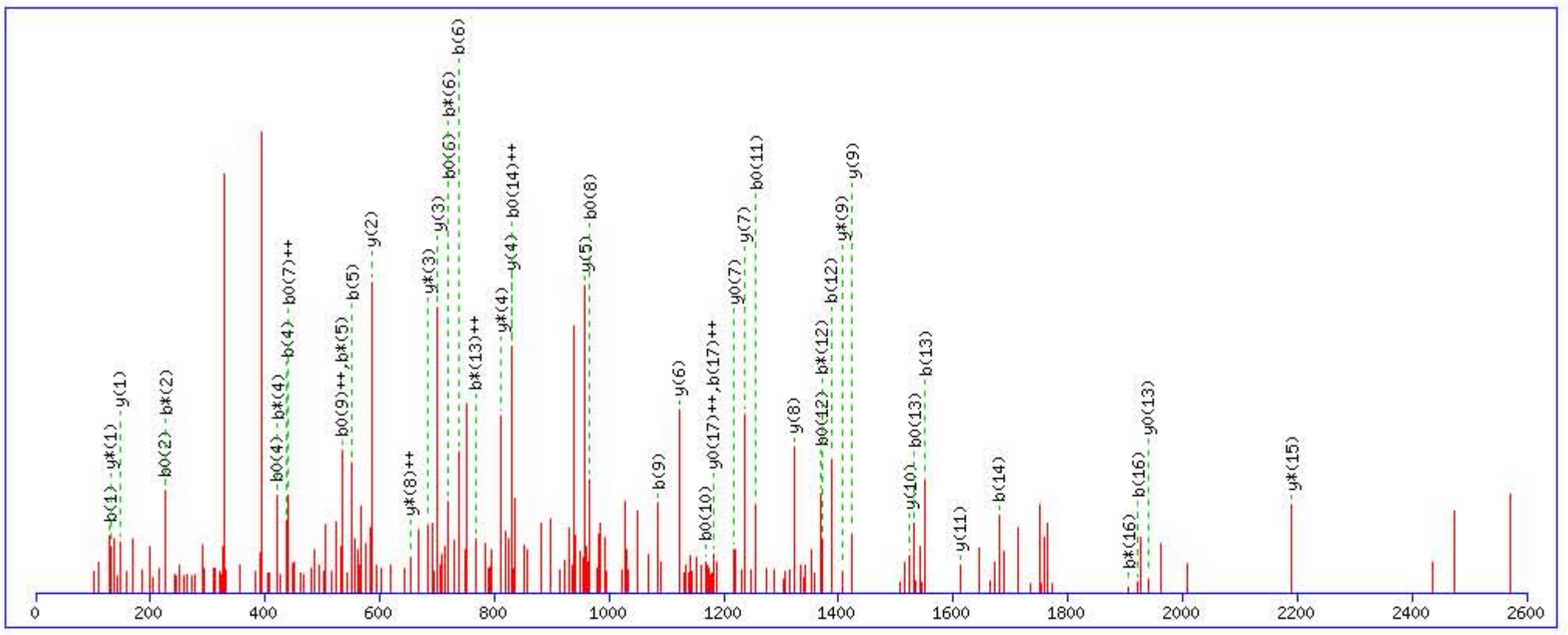
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QDGHLWCSTTSNYEQDQK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

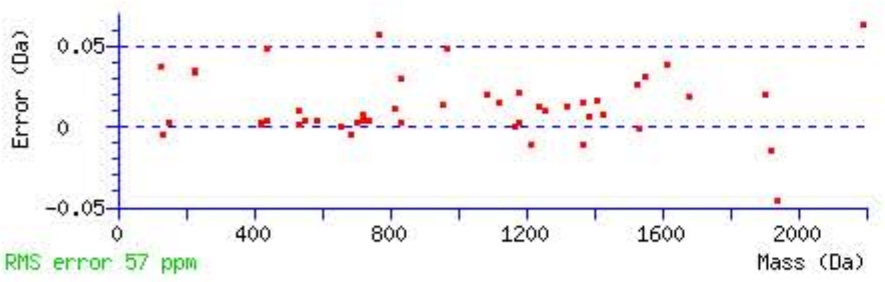
Match to Query 54484: 2507.111412 from(836.711080,3+) rtinseconds(1777) index(32792)
Title: Locus:1.1.1.727.26 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

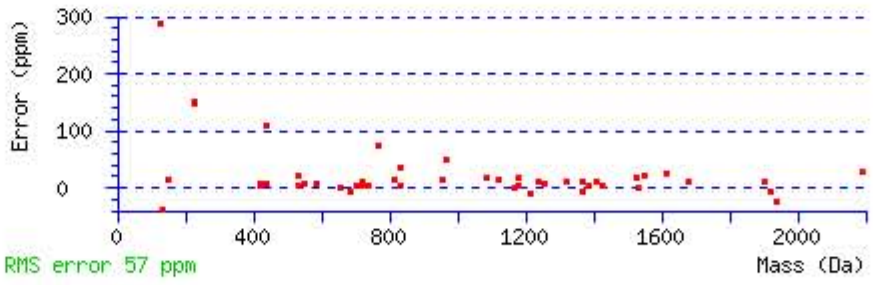
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2507.084564
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q17** : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 3.2e-005
**Matches** : 48/198 fragment ions using 91 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *129.065854* | 65.036565 | 112.039305 | 56.523291 | | | Q | | | | | | | 18 |
| 2 | 244.092797 | 122.550037 | 227.066248 | 114.036762 | 226.082232 | 113.544754 | D | 2380.033259 | 1190.520267 | 2363.006710 | 1182.006993 | 2362.022694 | 1181.514985 | 17 |
| 3 | 301.114261 | 151.060768 | 284.087712 | 142.547494 | 283.103696 | 142.055486 | G | 2265.006316 | 1133.006796 | 2247.979767 | 1124.493521 | 2246.995751 | 1124.001513 | 16 |
| 4 | *438.173173* | 219.590224 | 421.146624 | 211.076950 | 420.162608 | 210.584942 | H | 2207.984852 | 1104.496064 | 2190.958303 | 1095.982789 | 2189.974287 | 1095.490781 | 15 |
| 5 | *551.257237* | 276.132257 | 534.230688 | 267.618982 | 533.246672 | 267.126974 | L | 2070.925940 | 1035.966608 | 2053.899391 | 1027.453333 | 2052.915375 | 1026.961325 | 14 |
| 6 | *737.336550* | 369.171913 | 720.310001 | 360.658639 | 719.325985 | 360.166631 | W | 1957.841876 | 979.424576 | 1940.815327 | 970.911302 | 1939.831311 | 970.419294 | 13 |
| 7 | 897.367199 | 449.187238 | 880.340650 | 440.673963 | 879.356634 | 440.181955 | C | 1771.762563 | 886.384920 | 1754.736014 | 877.871645 | 1753.751998 | 877.379637 | 12 |
| 8 | 984.399227 | 492.703252 | 967.372678 | 484.189977 | 966.388662 | 483.697969 | S | *1611.731914* | 806.369595 | 1594.705365 | 797.856321 | 1593.721349 | 797.364313 | 11 |
| 9 | *1085.446906* | 543.227091 | 1068.420357 | 534.713817 | 1067.436341 | 534.221808 | T | *1524.699886* | 762.853581 | 1507.673337 | 754.340307 | 1506.689321 | 753.848299 | 10 |
| 10 | 1186.494585 | 593.750930 | 1169.468036 | 585.237656 | 1168.484020 | 584.745648 | T | *1423.652207* | 712.329742 | 1406.625658 | 703.816467 | 1405.641642 | 703.324459 | 9 |
| 11 | 1273.526613 | 637.266945 | 1256.500064 | 628.753670 | 1255.516048 | 628.261662 | S | *1322.604528* | 661.805902 | 1305.577979 | 653.292628 | 1304.593963 | 652.800620 | 8 |
| 12 | *1387.569540* | 694.288408 | 1370.542991 | 685.775134 | 1369.558975 | 685.283125 | N | *1235.572500* | 618.289888 | 1218.545951 | 609.776614 | 1217.561935 | 609.284606 | 7 |
| 13 | *1550.632869* | 775.820073 | 1533.606320 | 767.306798 | 1532.622304 | 766.814790 | Y | *1121.529573* | 561.268425 | 1104.503024 | 552.755150 | 1103.519008 | 552.263142 | 6 |
| 14 | *1679.675462* | 840.341369 | 1662.648913 | 831.828095 | 1661.664897 | 831.336086 | E | *958.466244* | 479.736760 | 941.439695 | 471.223486 | 940.455679 | 470.731478 | 5 |
| 15 | 1807.734040 | 904.370658 | 1790.707491 | 895.857384 | 1789.723475 | 895.365376 | Q | *829.423651* | 415.215464 | 812.397102 | 406.702189 | 811.413086 | 406.210181 | 4 |
| 16 | *1922.760983* | 961.884130 | 1905.734434 | 953.370855 | 1904.750418 | 952.878847 | D | *701.365073* | 351.186175 | 684.338524 | 342.672900 | 683.354508 | 342.180892 | 3 |
| 17 | 2361.986309 | 1181.496792 | 2344.959760 | 1172.983518 | 2343.975744 | 1172.491510 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 18 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 53.2 | 2507.084564 | 0.026848 | QDGHLWCSTTSNYEQDQK |
| 38.7 | 2507.084564 | 0.026848 | QDGHLWCSTTSNYEQDQK |

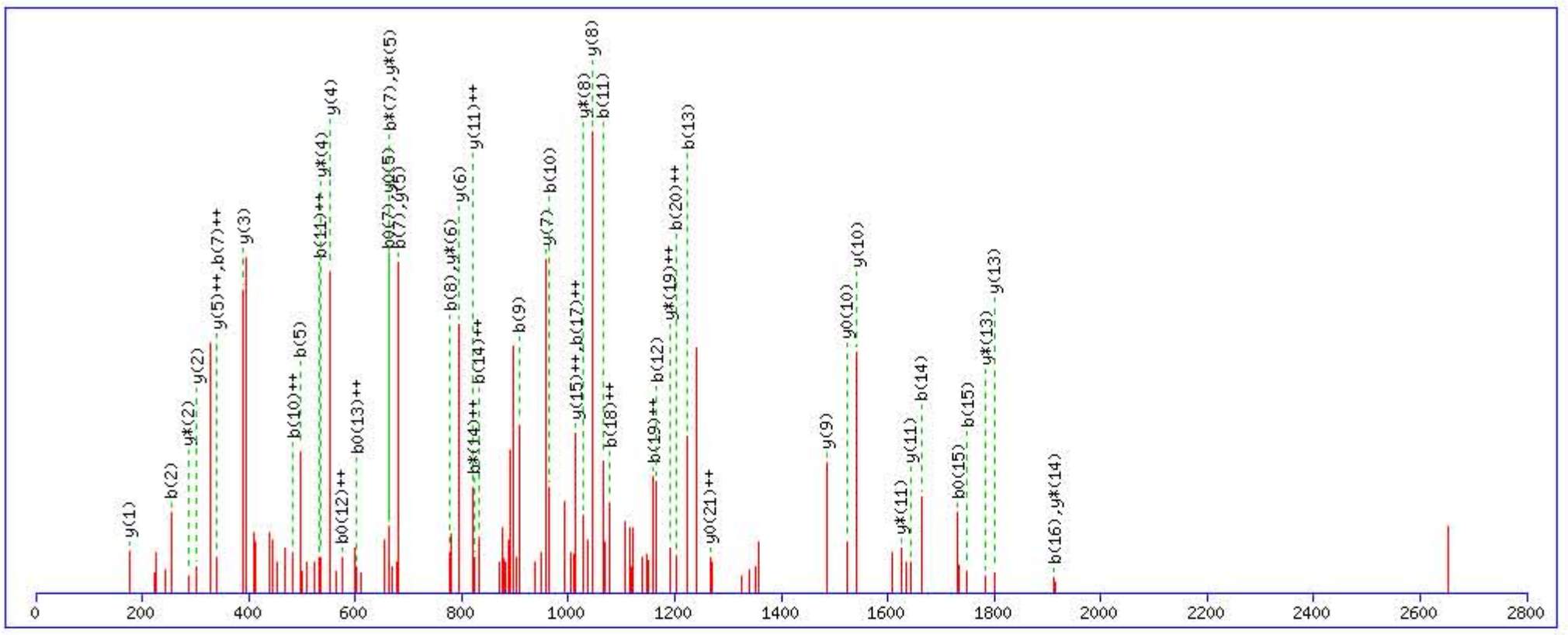
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **RPGGEPSPEGTTGQSYNQYSQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

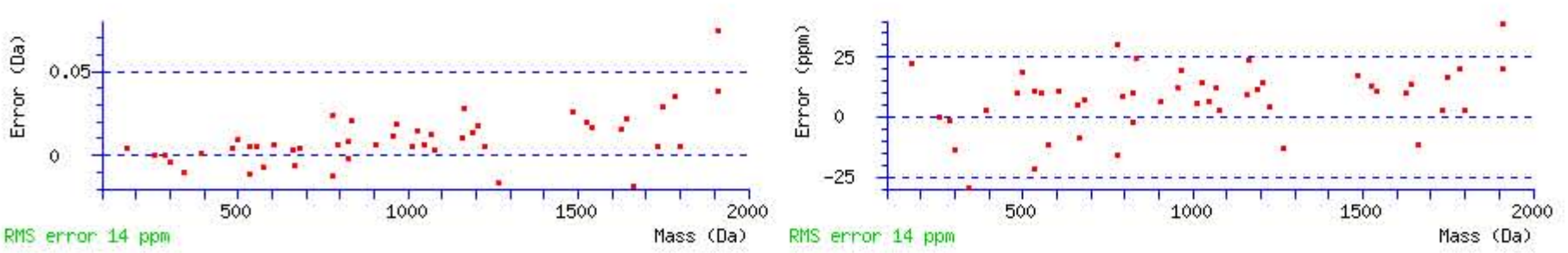
Match to Query 56391: 2706.278172 from(903.100000,3+) rtinseconds(1540) index(31319)
Title: Locus:1.1.1.644.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2706.245621
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q14** : Biotin:Thermo-21345 (Q)
**Ions Score:** 68 **Expect:** 3e-006
**Matches** : 54/240 fragment ions using 85 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 157.108387 | 79.057831 | 140.081838 | 70.544557 | | | R | | | | | | | 22 |
| 2 | *254.161151* | 127.584213 | 237.134602 | 119.070939 | | | P | 2551.151795 | 1276.079535 | 2534.125246 | 1267.566261 | 2533.141230 | 1267.074253 | 21 |
| 3 | 311.182615 | 156.094945 | 294.156066 | 147.581671 | | | G | 2454.099031 | 1227.553153 | 2437.072482 | 1219.039879 | 2436.088466 | 1218.547871 | 20 |
| 4 | 368.204079 | 184.605677 | 351.177530 | 176.092403 | | | G | 2397.077567 | 1199.042421 | 2380.051018 | 1190.529147 | 2379.067002 | 1190.037139 | 19 |
| 5 | *497.246672* | 249.126974 | 480.220123 | 240.613700 | 479.236107 | 240.121692 | E | 2340.056103 | 1170.531689 | 2323.029554 | 1162.018415 | 2322.045538 | 1161.526407 | 18 |
| 6 | 594.299436 | 297.653356 | 577.272887 | 289.140082 | 576.288871 | 288.648074 | P | 2211.013510 | 1106.010393 | 2193.986961 | 1097.497118 | 2193.002945 | 1097.005110 | 17 |
| 7 | *681.331464* | **341.169370** | 664.304915 | 332.656095 | 663.320899 | 332.164087 | S | 2113.960746 | 1057.484011 | 2096.934197 | 1048.970736 | 2095.950181 | 1048.478728 | 16 |
| 8 | *778.384228* | 389.695752 | 761.357679 | 381.182478 | 760.373663 | 380.690470 | P | 2026.928718 | 1013.967997 | 2009.902169 | 1005.454723 | 2008.918153 | 1004.962715 | 15 |
| 9 | *907.426821* | 454.217049 | 890.400272 | 445.703774 | 889.416256 | 445.211766 | E | 1929.875954 | 965.441615 | 1912.849405 | 956.928341 | 1911.865389 | 956.436333 | 14 |
| 10 | *964.448285* | **482.727781** | 947.421736 | 474.214506 | 946.437720 | 473.722498 | G | *1800.833361* | 900.920319 | 1783.806812 | 892.407044 | 1782.822796 | 891.915036 | 13 |
| 11 | *1065.495964* | **533.251620** | 1048.469415 | 524.738346 | 1047.485399 | 524.246337 | T | 1743.811897 | 872.409587 | 1726.785348 | 863.896312 | 1725.801332 | 863.404304 | 12 |
| 12 | *1166.543643* | 583.775460 | 1149.517094 | 575.262185 | 1148.533078 | 574.770177 | T | *1642.764218* | 821.885747 | 1625.737669 | 813.372473 | 1624.753653 | 812.880465 | 11 |
| 13 | *1223.565107* | 612.286191 | 1206.538558 | 603.772917 | 1205.554542 | 603.280909 | G | *1541.716539* | 771.361908 | 1524.689990 | 762.848633 | 1523.705974 | 762.356625 | 10 |
| 14 | *1662.790433* | **831.898854** | 1645.763884 | 823.385580 | 1644.779868 | 822.893572 | Q | *1484.695075* | 742.851176 | 1467.668526 | 734.337901 | 1466.684510 | 733.845893 | 9 |
| 15 | *1749.822461* | 875.414869 | 1732.795912 | 866.901594 | 1731.811896 | 866.409586 | S | *1045.469749* | 523.238513 | 1028.443200 | 514.725238 | 1027.459184 | 514.233230 | 8 |
| 16 | *1912.885790* | 956.946533 | 1895.859241 | 948.433259 | 1894.875225 | 947.941251 | Y | *958.437721* | 479.722499 | 941.411172 | 471.209224 | 940.427156 | 470.717216 | 7 |
| 17 | 2026.928717 | **1013.967997** | 2009.902168 | 1005.454722 | 2008.918152 | 1004.962714 | N | *795.374392* | 398.190834 | 778.347843 | 389.677560 | 777.363827 | 389.185552 | 6 |
| 18 | 2154.987295 | **1077.997285** | 2137.960746 | 1069.484011 | 2136.976730 | 1068.992003 | Q | *681.331465* | 341.169371 | 664.304916 | 332.656096 | 663.320900 | 332.164088 | 5 |
| 19 | 2318.050624 | **1159.528950** | 2301.024075 | 1151.015675 | 2300.040059 | 1150.523667 | Y | *553.272887* | 277.140082 | 536.246338 | 268.626807 | 535.262322 | 268.134799 | 4 |
| 20 | 2405.082652 | **1203.044964** | 2388.056103 | 1194.531689 | 2387.072087 | 1194.039681 | S | *390.209558* | 195.608417 | 373.183009 | 187.095143 | 372.198993 | 186.603135 | 3 |
| 21 | 2533.141230 | **1267.074253** | 2516.114681 | 1258.560978 | 2515.130665 | 1258.068971 | Q | *303.177530* | 152.092403 | 286.150981 | 143.579129 | | | 2 |
| 22 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 67.9 | 2706.245621 | 0.032551 | RPGGEPSPEGTTGQSYNQYSQR |
| 55.2 | 2706.245621 | 0.032551 | RPGGEPSPEGTTGQSYNQYSQR |
| 31.0 | 2706.245621 | 0.032551 | RPGGEPSPEGTTGQSYNQYSQR |

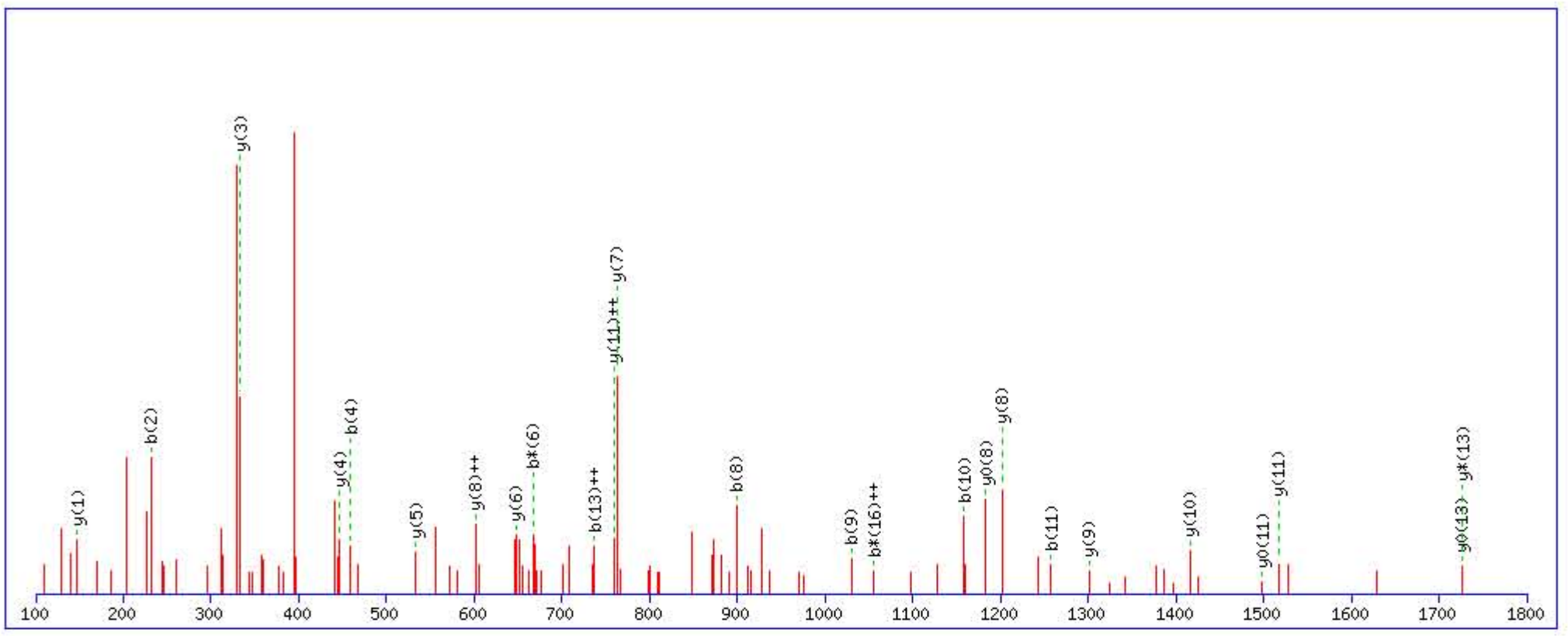
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TEIDKPSQMQVTDVQDNSISVK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

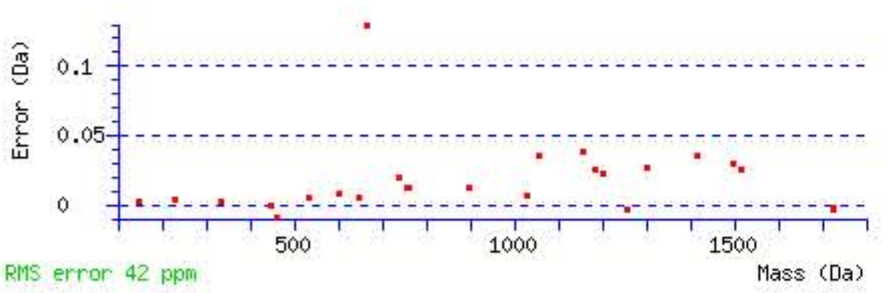
Match to Query 57231: 2772.391696 from(694.105200,4+) rtinseconds(1964) index(34012)
Title: Locus:1.1.1.792.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

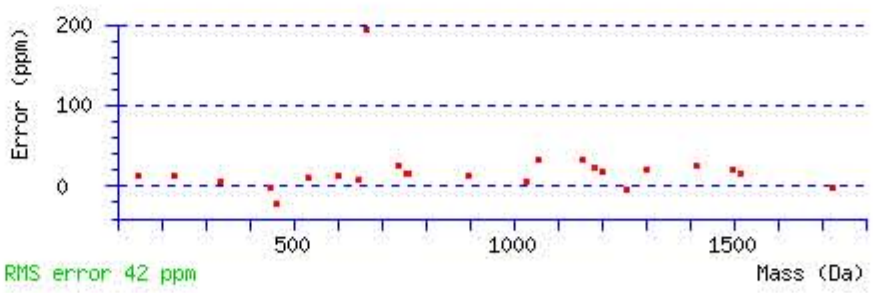
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2772.367386
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q15 : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 0.00013
**Matches :** 25/240 fragment ions using 48 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 22 |
| 2 | *231.097548* | 116.052412 | | | 213.086983 | 107.047130 | E | 2672.326980 | 1336.667128 | 2655.300431 | 1328.153854 | 2654.316415 | 1327.661846 | 21 |
| 3 | 344.181612 | 172.594444 | | | 326.171047 | 163.589162 | I | 2543.284387 | 1272.145832 | 2526.257838 | 1263.632557 | 2525.273822 | 1263.140549 | 20 |
| 4 | *459.208555* | 230.107916 | | | 441.197990 | 221.102633 | D | 2430.200323 | 1215.603799 | 2413.173774 | 1207.090525 | 2412.189758 | 1206.598517 | 19 |
| 5 | 587.303518 | 294.155397 | 570.276969 | 285.642123 | 569.292953 | 285.150115 | K | 2315.173380 | 1158.090328 | 2298.146831 | 1149.577053 | 2297.162815 | 1149.085046 | 18 |
| 6 | 684.356282 | 342.681779 | *667.329733* | 334.168505 | 666.345717 | 333.676497 | P | 2187.078417 | 1094.042847 | 2170.051868 | 1085.529572 | 2169.067852 | 1085.037564 | 17 |
| 7 | 771.388310 | 386.197793 | 754.361761 | 377.684519 | 753.377745 | 377.192511 | S | 2090.025653 | 1045.516465 | 2072.999104 | 1037.003190 | 2072.015088 | 1036.511182 | 16 |
| 8 | *899.446888* | 450.227082 | 882.420339 | 441.713808 | 881.436323 | 441.221800 | Q | 2002.993625 | 1002.000451 | 1985.967076 | 993.487176 | 1984.983060 | 992.995168 | 15 |
| 9 | *1030.487373* | 515.747325 | 1013.460824 | 507.234050 | 1012.476808 | 506.742042 | M | 1874.935047 | 937.971162 | 1857.908498 | 929.457887 | 1856.924482 | 928.965879 | 14 |
| 10 | *1158.545951* | 579.776614 | 1141.519402 | 571.263339 | 1140.535386 | 570.771331 | Q | 1743.894562 | 872.450919 | *1726.868013* | 863.937645 | *1725.883997* | 863.445637 | 13 |
| 11 | *1257.614365* | 629.310821 | 1240.587816 | 620.797546 | 1239.603800 | 620.305538 | V | 1615.835984 | 808.421630 | 1598.809435 | 799.908356 | 1597.825419 | 799.416348 | 12 |
| 12 | 1358.662044 | 679.834660 | 1341.635495 | 671.321386 | 1340.651479 | 670.829378 | T | *1516.767570* | *758.887423* | 1499.741021 | 750.374149 | *1498.757005* | 749.882141 | 11 |
| 13 | 1473.688987 | *737.348132* | 1456.662438 | 728.834857 | 1455.678422 | 728.342849 | D | *1415.719891* | 708.363584 | 1398.693342 | 699.850309 | 1397.709326 | 699.358301 | 10 |
| 14 | 1572.757401 | 786.882339 | 1555.730852 | 778.369064 | 1554.746836 | 777.877056 | V | *1300.692948* | 650.850112 | 1283.666399 | 642.336838 | 1282.682383 | 641.844830 | 9 |
| 15 | 2011.982727 | 1006.495002 | 1994.956178 | 997.981727 | 1993.972162 | 997.489719 | Q | *1201.624534* | *601.315905* | 1184.597985 | 592.802631 | *1183.613969* | 592.310623 | 8 |
| 16 | 2127.009670 | 1064.008473 | 2109.983121 | *1055.495199* | 2108.999105 | 1055.003191 | D | *762.399208* | 381.703242 | 745.372659 | 373.189968 | 744.388643 | 372.697960 | 7 |
| 17 | 2241.052597 | 1121.029937 | 2224.026048 | 1112.516662 | 2223.042032 | 1112.024654 | N | *647.372265* | 324.189771 | 630.345716 | 315.676496 | 629.361700 | 315.184488 | 6 |
| 18 | 2328.084625 | 1164.545951 | 2311.058076 | 1156.032676 | 2310.074060 | 1155.540668 | S | *533.329338* | 267.168307 | 516.302789 | 258.655033 | 515.318773 | 258.163025 | 5 |
| 19 | 2441.168689 | 1221.087983 | 2424.142140 | 1212.574708 | 2423.158124 | 1212.082700 | I | *446.297310* | 223.652293 | 429.270761 | 215.139019 | 428.286745 | 214.647011 | 4 |
| 20 | 2528.200717 | 1264.603997 | 2511.174168 | 1256.090722 | 2510.190152 | 1255.598714 | S | *333.213246* | 167.110261 | 316.186697 | 158.596986 | 315.202681 | 158.104978 | 3 |
| 21 | 2627.269131 | 1314.138204 | 2610.242582 | 1305.624929 | 2609.258566 | 1305.132921 | V | 246.181218 | 123.594247 | 229.154669 | 115.080972 | | | 2 |
| 22 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 53.2 | 2772.367386 | 0.024310 | TEIDKPSQMQVTDVQDNSISVK |
| 13.7 | 2772.367386 | 0.024310 | TEIDKPSQMQVTDVQDNSISVK |
| 7.0 | 2772.367386 | 0.024310 | TEIDKPSQMQVTDVQDNSISVK |

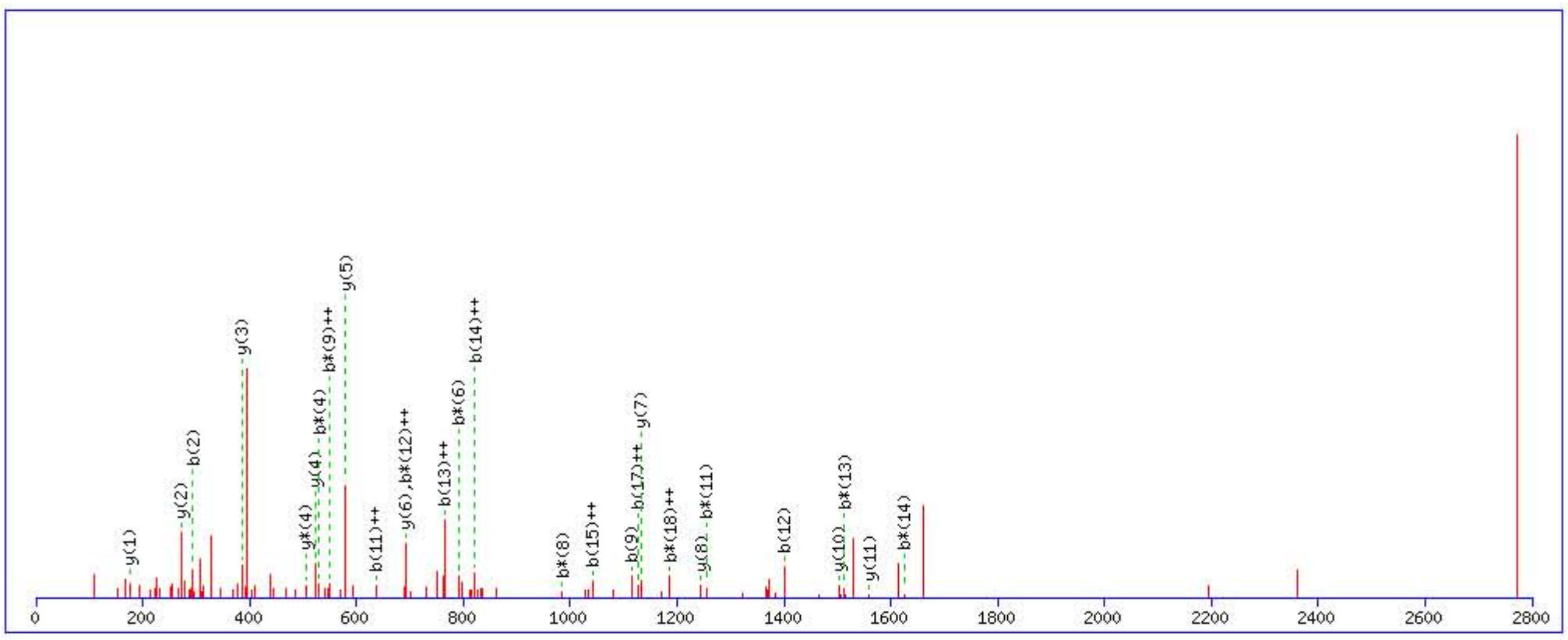
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HRPRPYPPNVGEEIQIGHIPR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

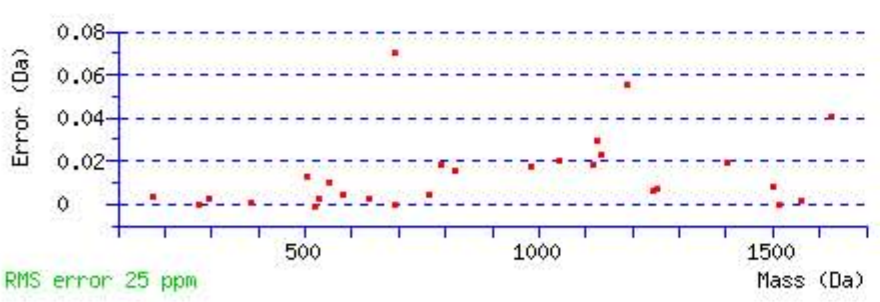
Match to Query 57234: 2772.500296 from(694.132350,4+) rtinseconds(1771) index(32740)
Title: Locus:1.1.1.725.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

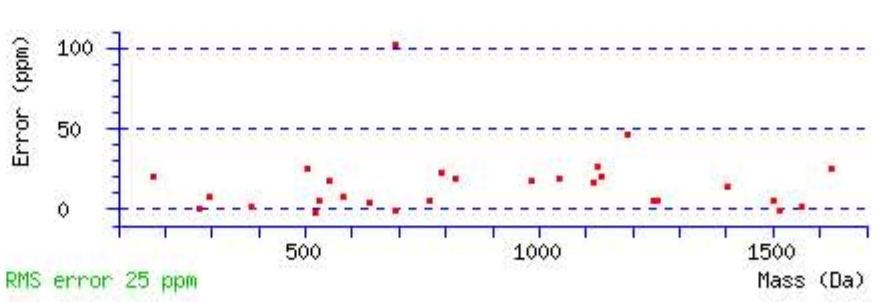
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2772.475815
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q15** : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.0025
**Matches** : 28/200 fragment ions using 60 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 21 |
| 2 | **294.167299** | 147.587288 | 277.140750 | 139.074013 | | | R | 2636.424208 | 1318.715742 | 2619.397659 | 1310.202467 | 2618.413643 | 1309.710459 | 20 |
| 3 | 391.220063 | 196.113670 | 374.193514 | 187.600395 | | | P | 2480.323097 | 1240.665186 | 2463.296548 | 1232.151912 | 2462.312532 | 1231.659904 | 19 |
| 4 | 547.321174 | 274.164225 | 530.294625 | 265.650951 | | | R | 2383.270333 | 1192.138804 | 2366.243784 | 1183.625530 | 2365.259768 | 1183.133522 | 18 |
| 5 | 644.373938 | 322.690607 | 627.347389 | 314.177333 | | | P | 2227.169222 | 1114.088249 | 2210.142673 | 1105.574974 | 2209.158657 | 1105.082966 | 17 |
| 6 | 807.437267 | 404.222272 | 790.410718 | 395.708997 | | | Y | 2130.116458 | 1065.561867 | 2113.089909 | 1057.048592 | 2112.105893 | 1056.556584 | 16 |
| 7 | 904.490031 | 452.748654 | 887.463482 | 444.235379 | | | P | 1967.053129 | 984.030203 | 1950.026580 | 975.516928 | 1949.042564 | 975.024920 | 15 |
| 8 | 1001.542795 | 501.275036 | 984.516246 | 492.761761 | | | P | 1870.000365 | 935.503821 | 1852.973816 | 926.990546 | 1851.989800 | 926.498538 | 14 |
| 9 | **1115.585722** | 558.296499 | 1098.559173 | 549.783225 | | | N | 1772.947601 | 886.977439 | 1755.921052 | 878.464164 | 1754.937036 | 877.972156 | 13 |
| 10 | 1214.654136 | 607.830706 | 1197.627587 | 599.317432 | | | V | 1658.904674 | 829.955975 | 1641.878125 | 821.442701 | 1640.894109 | 820.950693 | 12 |
| 11 | 1271.675600 | **636.341438** | 1254.649051 | 627.828164 | | | G | *1559.836260* | 780.421768 | 1542.809711 | 771.908494 | 1541.825695 | 771.416486 | 11 |
| 12 | **1400.718193** | 700.862735 | 1383.691644 | 692.349460 | 1382.707628 | 691.857452 | E | *1502.814796* | 751.911036 | 1485.788247 | 743.397762 | 1484.804231 | 742.905754 | 10 |
| 13 | 1529.760786 | **765.384031** | 1512.734237 | 756.870757 | 1511.750221 | 756.378749 | E | 1373.772203 | 687.389740 | 1356.745654 | 678.876465 | 1355.761638 | 678.384457 | 9 |
| 14 | 1642.844850 | **821.926063** | 1625.818301 | 813.412789 | 1624.834285 | 812.920781 | I | *1244.729610* | 622.868443 | 1227.703061 | 614.355169 | | | 8 |
| 15 | 2082.070176 | **1041.538726** | 2065.043627 | 1033.025451 | 2064.059611 | 1032.533444 | Q | *1131.645546* | 566.326411 | 1114.618997 | 557.813137 | | | 7 |
| 16 | 2195.154240 | 1098.080758 | 2178.127691 | 1089.567484 | 2177.143675 | 1089.075476 | I | *692.420220* | 346.713748 | 675.393671 | 338.200474 | | | 6 |
| 17 | 2252.175704 | **1126.591490** | 2235.149155 | 1118.078215 | 2234.165139 | 1117.586208 | G | *579.336156* | 290.171716 | 562.309607 | 281.658442 | | | 5 |
| 18 | 2389.234616 | 1195.120946 | 2372.208067 | 1186.607671 | 2371.224051 | 1186.115664 | H | *522.314692* | 261.660984 | 505.288143 | 253.147710 | | | 4 |
| 19 | 2502.318680 | 1251.662978 | 2485.292131 | 1243.149704 | 2484.308115 | 1242.657696 | I | *385.255780* | 193.131528 | 368.229231 | 184.618254 | | | 3 |
| 20 | 2599.371444 | 1300.189360 | 2582.344895 | 1291.676086 | 2581.360879 | 1291.184078 | P | *272.171716* | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 21 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.0 | 2772.475815 | 0.024481 | HRPRPYPPNVGEEIQIGHIPR |

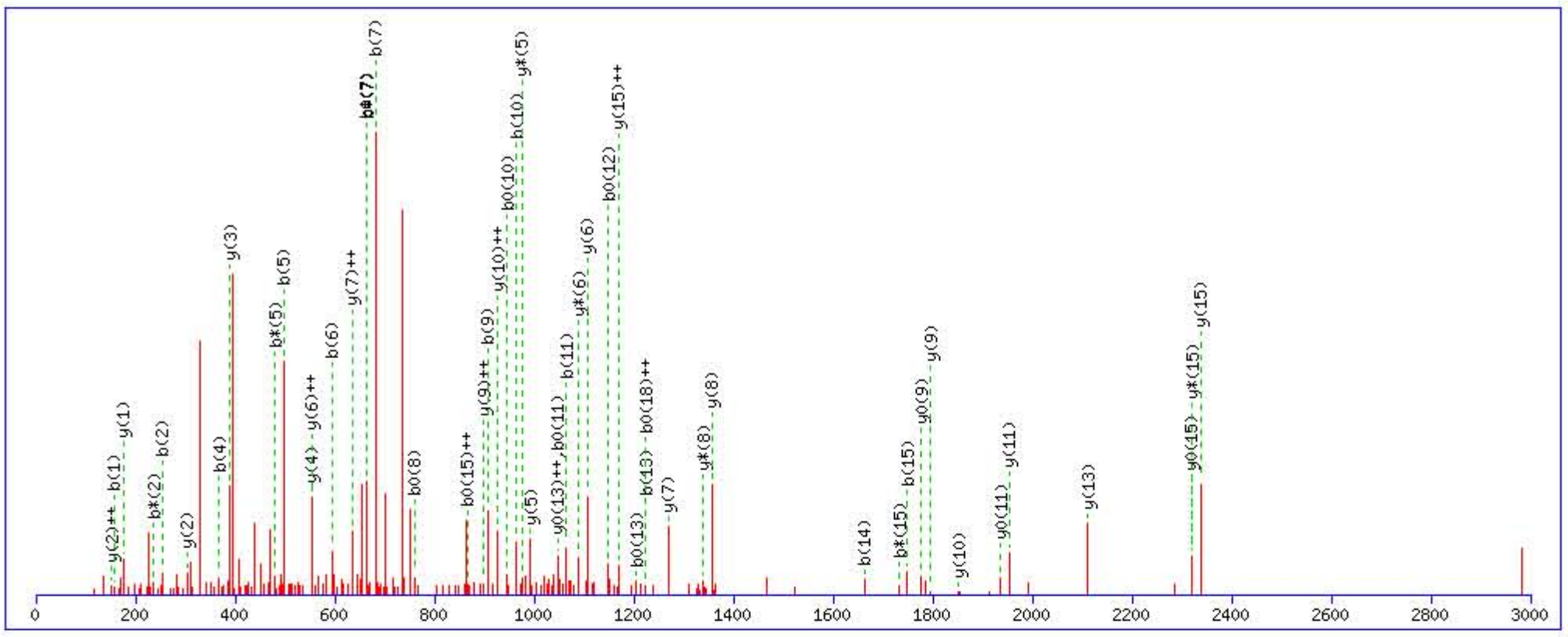
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **RPGGEPSPEGTTGQSYNQYSQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

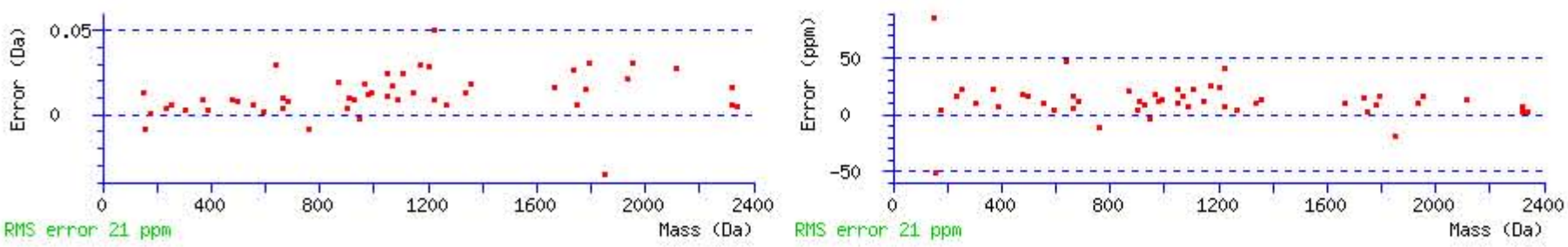
Match to Query 60239: 3017.446776 from(755.368970,4+) rtinseconds(1820) index(33046)
Title: Locus:1.1.1.742.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3017.412369
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q14 : Biotin:Thermo-21345 (Q)
Q18 : Biotin:Thermo-21345 (Q)
**Ions Score:** 61 **Expect:** 1.6e-005
**Matches :** 51/240 fragment ions using 114 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *157.108387* | 79.057831 | 140.081838 | 70.544557 | | | R | | | | | | | 22 |
| 2 | *254.161151* | 127.584213 | 237.134602 | 119.070939 | | | P | 2862.318543 | 1431.662909 | 2845.291994 | 1423.149635 | 2844.307978 | 1422.657627 | 21 |
| 3 | 311.182615 | 156.094945 | 294.156066 | 147.581671 | | | G | 2765.265779 | 1383.136527 | 2748.239230 | 1374.623253 | 2747.255214 | 1374.131245 | 20 |
| 4 | *368.204079* | 184.605677 | 351.177530 | 176.092403 | | | G | 2708.244315 | 1354.625795 | 2691.217766 | 1346.112521 | 2690.233750 | 1345.620513 | 19 |
| 5 | *497.246672* | 249.126974 | 480.220123 | 240.613700 | 479.236107 | 240.121692 | E | 2651.222851 | 1326.115063 | 2634.196302 | 1317.601789 | 2633.212286 | 1317.109781 | 18 |
| 6 | *594.299436* | 297.653356 | 577.272887 | 289.140082 | 576.288871 | 288.648074 | P | 2522.180258 | 1261.593767 | 2505.153709 | 1253.080492 | 2504.169693 | 1252.588484 | 17 |
| 7 | *681.331464* | 341.169370 | 664.304915 | 332.656095 | 663.320899 | 332.164087 | S | 2425.127494 | 1213.067385 | 2408.100945 | 1204.554110 | 2407.116929 | 1204.062102 | 16 |
| 8 | 778.384228 | 389.695752 | 761.357679 | 381.182478 | 760.373663 | 380.690470 | P | *2338.095466* | 1169.551371 | 2321.068917 | 1161.038096 | 2320.084901 | 1160.546088 | 15 |
| 9 | *907.426821* | 454.217049 | 890.400272 | 445.703774 | 889.416256 | 445.211766 | E | 2241.042702 | 1121.024989 | 2224.016153 | 1112.511714 | 2223.032137 | 1112.019706 | 14 |
| 10 | *964.448285* | 482.727781 | 947.421736 | 474.214506 | 946.437720 | 473.722498 | G | *2112.000109* | 1056.503692 | 2094.973560 | 1047.990418 | 2093.989544 | 1047.498410 | 13 |
| 11 | *1065.495964* | 533.251620 | 1048.469415 | 524.738346 | 1047.485399 | 524.246337 | T | 2054.978645 | 1027.992960 | 2037.952096 | 1019.479686 | 2036.968080 | 1018.987678 | 12 |
| 12 | 1166.543643 | 583.775460 | 1149.517094 | 575.262185 | 1148.533078 | 574.770177 | T | *1953.930966* | 977.469121 | 1936.904417 | 968.955847 | 1935.920401 | 968.463839 | 11 |
| 13 | *1223.565107* | 612.286191 | 1206.538558 | 603.772917 | 1205.554542 | 603.280909 | G | *1852.883287* | 926.945282 | 1835.856738 | 918.432007 | 1834.872722 | 917.939999 | 10 |
| 14 | *1662.790433* | 831.898854 | 1645.763884 | 823.385580 | 1644.779868 | 822.893572 | Q | *1795.861823* | 898.434550 | 1778.835274 | 889.921275 | 1777.851258 | 889.429267 | 9 |
| 15 | *1749.822461* | 875.414869 | 1732.795912 | 866.901594 | 1731.811896 | 866.409586 | S | *1356.636497* | 678.821887 | 1339.609948 | 670.308612 | 1338.625932 | 669.816604 | 8 |
| 16 | 1912.885790 | 956.946533 | 1895.859241 | 948.433259 | 1894.875225 | 947.941251 | Y | *1269.604469* | 635.305873 | 1252.577920 | 626.792598 | 1251.593904 | 626.300590 | 7 |
| 17 | 2026.928717 | 1013.967997 | 2009.902168 | 1005.454722 | 2008.918152 | 1004.962714 | N | *1106.541140* | 553.774208 | 1089.514591 | 545.260934 | 1088.530575 | 544.768926 | 6 |
| 18 | 2466.154043 | 1233.580659 | 2449.127494 | 1225.067385 | 2448.143478 | 1224.575377 | Q | *992.498213* | 496.752745 | 975.471664 | 488.239470 | 974.487648 | 487.747462 | 5 |
| 19 | 2629.217372 | 1315.112324 | 2612.190823 | 1306.599049 | 2611.206807 | 1306.107041 | Y | *553.272887* | 277.140082 | 536.246338 | 268.626807 | 535.262322 | 268.134799 | 4 |
| 20 | 2716.249400 | 1358.628338 | 2699.222851 | 1350.115063 | 2698.238835 | 1349.623056 | S | *390.209558* | 195.608417 | 373.183009 | 187.095143 | 372.198993 | 186.603135 | 3 |
| 21 | 2844.307978 | 1422.657627 | 2827.281429 | 1414.144353 | 2826.297413 | 1413.652345 | Q | *303.177530* | 152.092403 | 286.150981 | 143.579129 | | | 2 |
| 22 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 61.5 | 3017.412369 | 0.034407 | RPGGEPSPEGTTGQSYNQYSQR |
| 59.6 | 3017.412369 | 0.034407 | RPGGEPSPEGTTGQSYNQYSQR |
| 26.9 | 3017.412369 | 0.034407 | RPGGEPSPEGTTGQSYNQYSQR |

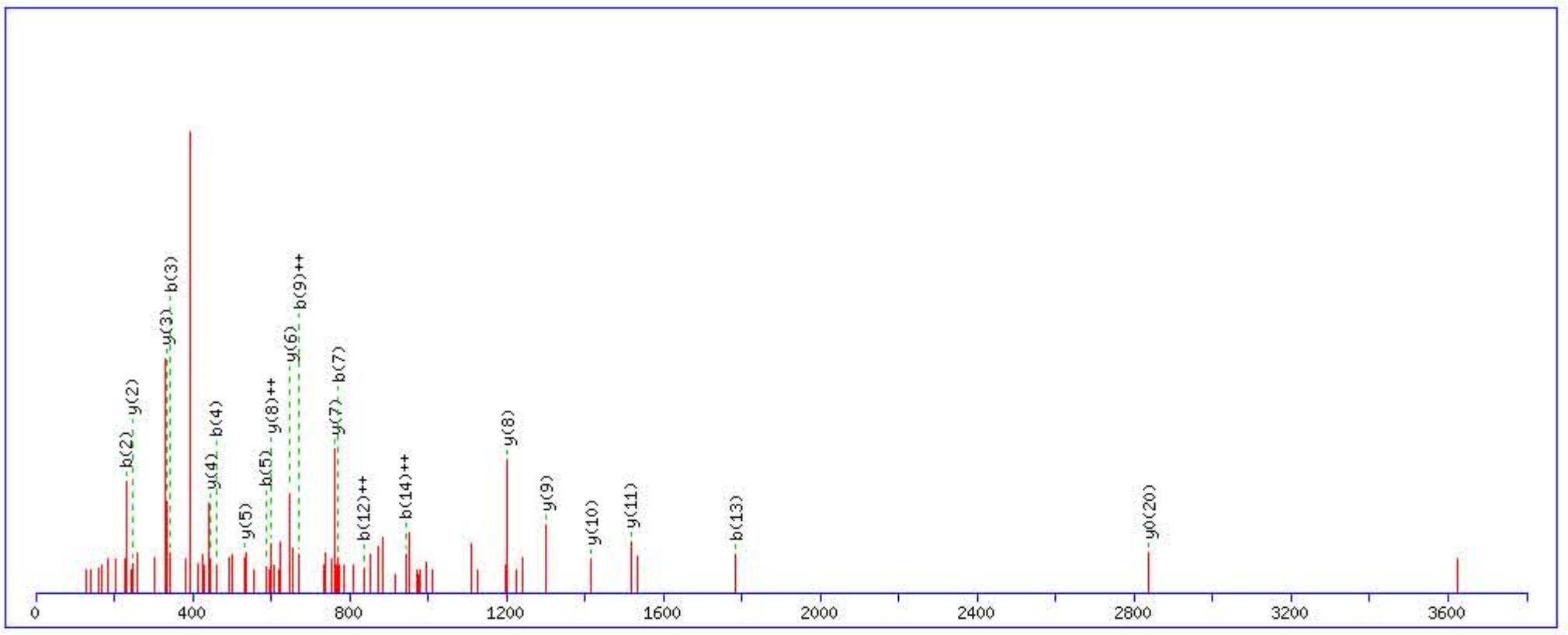
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TEIDKPSQMQVTDVQDNSISVK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

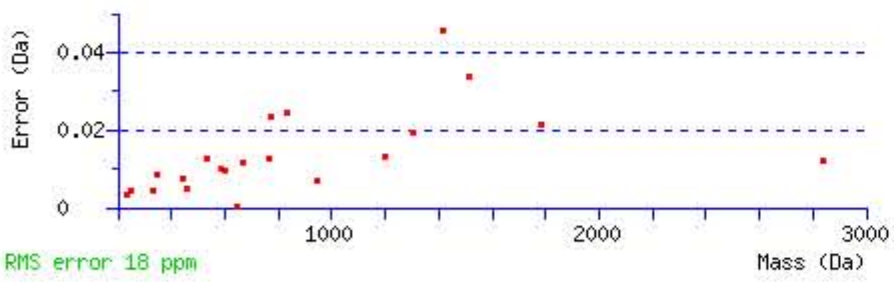
Match to Query 60759: 3083.578536 from(771.901910,4+) rtinseconds(2170) index(35288)
Title: Locus:1.1.1.864.21 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

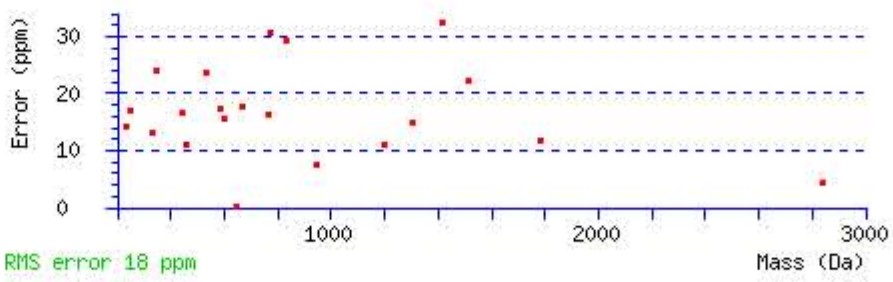
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3083.534134
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
Q15 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.016
**Matches :** 21/240 fragment ions using 63 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 22 |
| 2 | *231.097548* | 116.052412 | | | 213.086983 | 107.047130 | E | 2983.493728 | 1492.250502 | 2966.467179 | 1483.737228 | 2965.483163 | 1483.245220 | 21 |
| 3 | *344.181612* | 172.594444 | | | 326.171047 | 163.589162 | I | 2854.451135 | 1427.729206 | 2837.424586 | 1419.215931 | 2836.440570 | 1418.723923 | 20 |
| 4 | *459.208555* | 230.107916 | | | 441.197990 | 221.102633 | D | 2741.367071 | 1371.187174 | 2724.340522 | 1362.673899 | 2723.356506 | 1362.181891 | 19 |
| 5 | *587.303518* | 294.155397 | 570.276969 | 285.642123 | 569.292953 | 285.150115 | K | 2626.340128 | 1313.673702 | 2609.313579 | 1305.160428 | 2608.329563 | 1304.668420 | 18 |
| 6 | 684.356282 | 342.681779 | 667.329733 | 334.168505 | 666.345717 | 333.676497 | P | 2498.245165 | 1249.626220 | 2481.218616 | 1241.112946 | 2480.234600 | 1240.620938 | 17 |
| 7 | *771.388310* | 386.197793 | 754.361761 | 377.684519 | 753.377745 | 377.192511 | S | 2401.192401 | 1201.099838 | 2384.165852 | 1192.586564 | 2383.181836 | 1192.094556 | 16 |
| 8 | 1210.613636 | 605.810456 | 1193.587087 | 597.297182 | 1192.603071 | 596.805174 | Q | 2314.160373 | 1157.583825 | 2297.133824 | 1149.070550 | 2296.149808 | 1148.578542 | 15 |
| 9 | 1341.654121 | 671.330699 | 1324.627572 | 662.817424 | 1323.643556 | 662.325416 | M | 1874.935047 | 937.971162 | 1857.908498 | 929.457887 | 1856.924482 | 928.965879 | 14 |
| 10 | 1469.712699 | 735.359988 | 1452.686150 | 726.846713 | 1451.702134 | 726.354705 | Q | 1743.894562 | 872.450919 | 1726.868013 | 863.937645 | 1725.883997 | 863.445637 | 13 |
| 11 | 1568.781113 | 784.894195 | 1551.754564 | 776.380920 | 1550.770548 | 775.888912 | V | 1615.835984 | 808.421630 | 1598.809435 | 799.908356 | 1597.825419 | 799.416348 | 12 |
| 12 | 1669.828792 | 835.418034 | 1652.802243 | 826.904760 | 1651.818227 | 826.412752 | T | *1516.767570* | 758.887423 | 1499.741021 | 750.374149 | 1498.757005 | 749.882141 | 11 |
| 13 | *1784.855735* | 892.931506 | 1767.829186 | 884.418231 | 1766.845170 | 883.926223 | D | *1415.719891* | 708.363584 | 1398.693342 | 699.850309 | 1397.709326 | 699.358301 | 10 |
| 14 | 1883.924149 | 942.465713 | 1866.897600 | 933.952438 | 1865.913584 | 933.460430 | V | *1300.692948* | 650.850112 | 1283.666399 | 642.336838 | 1282.682383 | 641.844830 | 9 |
| 15 | 2323.149475 | 1162.078376 | 2306.122926 | 1153.565101 | 2305.138910 | 1153.073093 | Q | *1201.624534* | 601.315905 | 1184.597985 | 592.802631 | 1183.613969 | 592.310623 | 8 |
| 16 | 2438.176418 | 1219.591847 | 2421.149869 | 1211.078573 | 2420.165853 | 1210.586565 | D | *762.399208* | 381.703242 | 745.372659 | 373.189968 | 744.388643 | 372.697960 | 7 |
| 17 | 2552.219345 | 1276.613311 | 2535.192796 | 1268.100036 | 2534.208780 | 1267.608028 | N | *647.372265* | 324.189771 | 630.345716 | 315.676496 | 629.361700 | 315.184488 | 6 |
| 18 | 2639.251373 | 1320.129325 | 2622.224824 | 1311.616050 | 2621.240808 | 1311.124042 | S | *533.329338* | 267.168307 | 516.302789 | 258.655033 | 515.318773 | 258.163025 | 5 |
| 19 | 2752.335437 | 1376.671357 | 2735.308888 | 1368.158082 | 2734.324872 | 1367.666074 | I | *446.297310* | 223.652293 | 429.270761 | 215.139019 | 428.286745 | 214.647011 | 4 |
| 20 | 2839.367465 | 1420.187371 | 2822.340916 | 1411.674096 | 2821.356900 | 1411.182088 | S | *333.213246* | 167.110261 | 316.186697 | 158.596986 | 315.202681 | 158.104978 | 3 |
| 21 | 2938.435879 | 1469.721578 | 2921.409330 | 1461.208303 | 2920.425314 | 1460.716295 | V | *246.181218* | 123.594247 | 229.154669 | 115.080972 | | | 2 |
| 22 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 32.1 | 3083.534134 | 0.044402 | TEIDKPSQMQVTDVQDNSISVK |
| 30.8 | 3083.534134 | 0.044402 | TEIDKPSQMQVTDVQDNSISVK |
| 7.4 | 3083.534134 | 0.044402 | TEIDKPSQMQVTDVQDNSISVK |

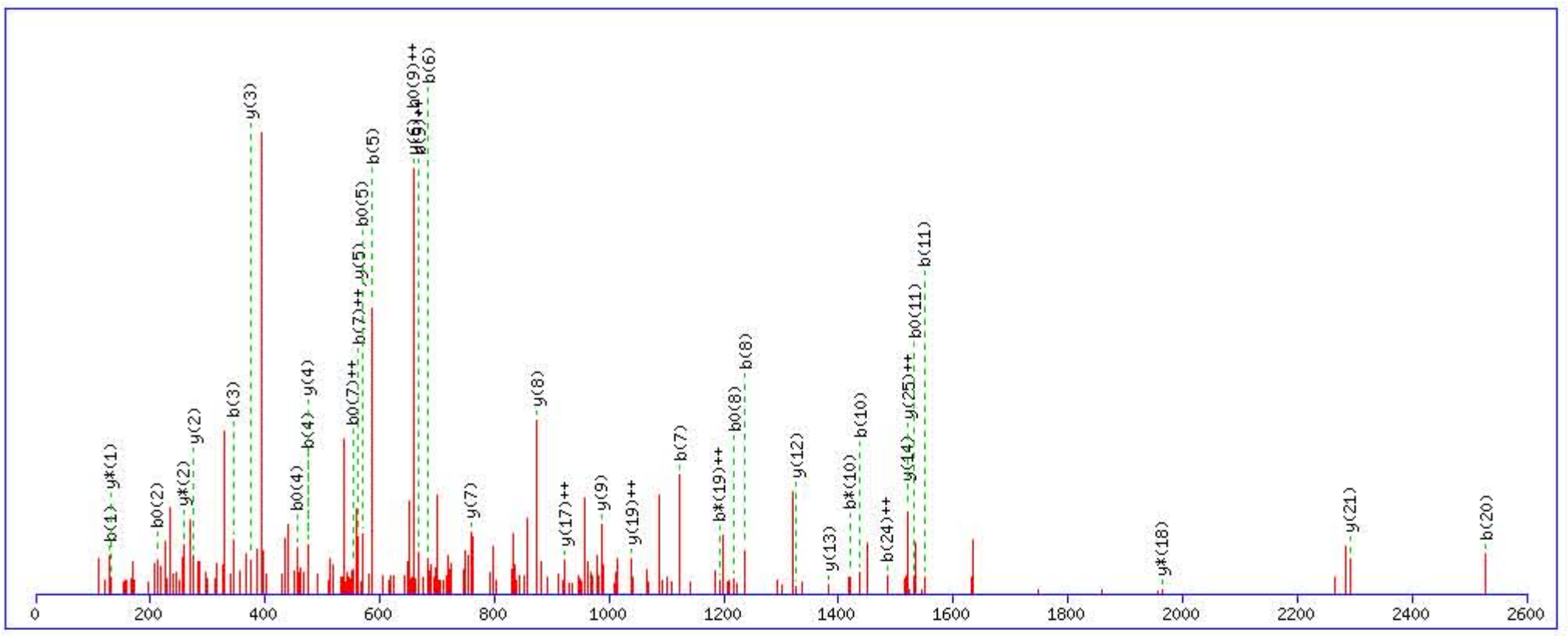
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KTDELPQLVTLPHPNLHGPEILDVPSTVQK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

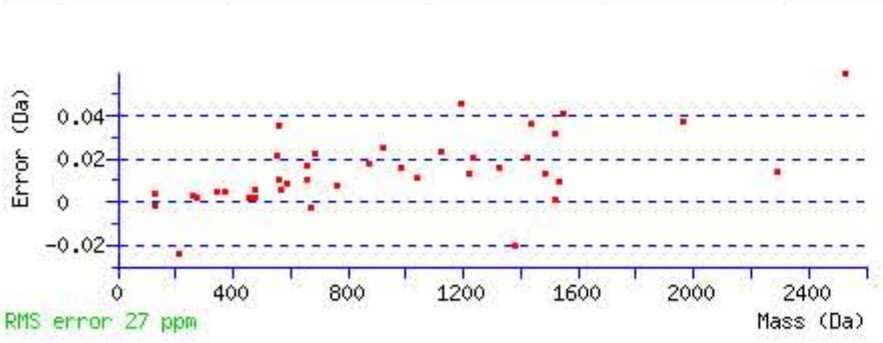
Match to Query 66809: 3626.007820 from(726.208840,5+) rtinseconds(2471) index(36881)
Title: Locus:1.1.1.969.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

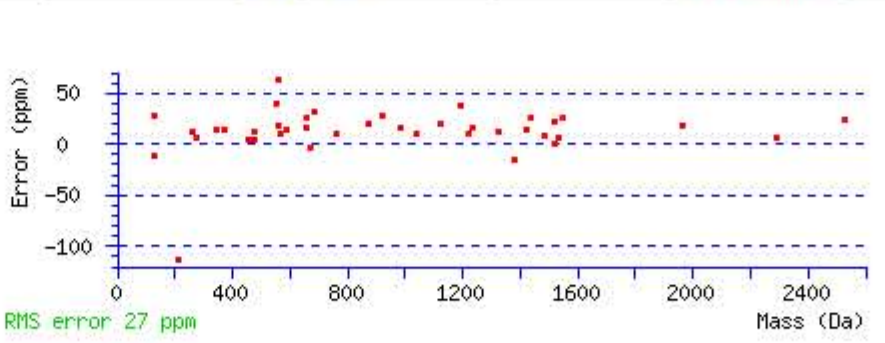
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3625.954193
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 40 **Expect:** 0.0004
**Matches :** 40/340 fragment ions using 123 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *129.102239* | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 30 |
| 2 | 230.149918 | 115.578597 | 213.123369 | 107.065323 | 212.139353 | 106.573315 | T | 3498.866506 | 1749.936891 | 3481.839957 | 1741.423616 | 3480.855941 | 1740.931608 | 29 |
| 3 | *345.176861* | 173.092069 | 328.150312 | 164.578794 | 327.166296 | 164.086786 | D | 3397.818827 | 1699.413051 | 3380.792278 | 1690.899777 | 3379.808262 | 1690.407769 | 28 |
| 4 | *474.219454* | 237.613365 | 457.192905 | 229.100091 | 456.208889 | 228.608083 | E | 3282.791884 | 1641.899580 | 3265.765335 | 1633.386305 | 3264.781319 | 1632.894297 | 27 |
| 5 | *587.303518* | 294.155397 | 570.276969 | 285.642123 | 569.292953 | 285.150115 | L | 3153.749291 | 1577.378283 | 3136.722742 | 1568.865009 | 3135.738726 | 1568.373001 | 26 |
| 6 | *684.356282* | 342.681779 | 667.329733 | 334.168505 | 666.345717 | 333.676497 | P | 3040.665227 | 1520.836251 | 3023.638678 | 1512.322977 | 3022.654662 | 1511.830969 | 25 |
| 7 | *1123.581608* | **562.294442** | 1106.555059 | 553.781168 | 1105.571043 | 553.289160 | Q | 2943.612463 | 1472.309869 | 2926.585914 | 1463.796595 | 2925.601898 | 1463.304587 | 24 |
| 8 | *1236.665672* | 618.836474 | 1219.639123 | 610.323200 | 1218.655107 | 609.831192 | L | 2504.387137 | 1252.697206 | 2487.360588 | 1244.183932 | 2486.376572 | 1243.691924 | 23 |
| 9 | 1335.734086 | **668.370681** | 1318.707537 | 659.857407 | 1317.723521 | 659.365399 | V | 2391.303073 | 1196.155174 | 2374.276524 | 1187.641900 | 2373.292508 | 1187.149892 | 22 |
| 10 | *1436.781765* | 718.894521 | 1419.755216 | 710.381246 | 1418.771200 | 709.889238 | T | *2292.234659* | 1146.620967 | 2275.208110 | 1138.107693 | 2274.224094 | 1137.615685 | 21 |
| 11 | *1549.865829* | 775.436553 | 1532.839280 | 766.923278 | 1531.855264 | 766.431270 | L | 2191.186980 | 1096.097128 | 2174.160431 | 1087.583853 | 2173.176415 | 1087.091845 | 20 |
| 12 | 1646.918593 | 823.962935 | 1629.892044 | 815.449660 | 1628.908028 | 814.957652 | P | 2078.102916 | 1039.555096 | 2061.076367 | 1031.041821 | 2060.092351 | 1030.549813 | 19 |
| 13 | 1783.977505 | 892.492391 | 1766.950956 | 883.979116 | 1765.966940 | 883.487108 | H | 1981.050152 | 991.028714 | 1964.023603 | 982.515440 | 1963.039587 | 982.023432 | 18 |
| 14 | 1881.030269 | 941.018773 | 1864.003720 | 932.505498 | 1863.019704 | 932.013490 | P | 1843.991240 | 922.499258 | 1826.964691 | 913.985984 | 1825.980675 | 913.493976 | 17 |
| 15 | 1995.073196 | 998.040236 | 1978.046647 | 989.526962 | 1977.062631 | 989.034954 | N | 1746.938476 | 873.972876 | 1729.911927 | 865.459602 | 1728.927911 | 864.967594 | 16 |
| 16 | 2108.157260 | 1054.582268 | 2091.130711 | 1046.068993 | 2090.146695 | 1045.576985 | L | 1632.895549 | 816.951413 | 1615.869000 | 808.438138 | 1614.884984 | 807.946130 | 15 |
| 17 | 2245.216172 | 1123.111724 | 2228.189623 | 1114.598449 | 2227.205607 | 1114.106441 | H | *1519.811485* | 760.409381 | 1502.784936 | 751.896106 | 1501.800920 | 751.404098 | 14 |
| 18 | 2302.237636 | 1151.622456 | 2285.211087 | 1143.109181 | 2284.227071 | 1142.617173 | G | *1382.752573* | 691.879925 | 1365.726024 | 683.366650 | 1364.742008 | 682.874642 | 13 |
| 19 | 2399.290400 | 1200.148838 | 2382.263851 | 1191.635563 | 2381.279835 | 1191.143555 | P | *1325.731109* | 663.369193 | 1308.704560 | 654.855918 | 1307.720544 | 654.363910 | 12 |
| 20 | *2528.332993* | 1264.670134 | 2511.306444 | 1256.156860 | 2510.322428 | 1255.664852 | E | 1228.678345 | 614.842811 | 1211.651796 | 606.329536 | 1210.667780 | 605.837528 | 11 |
| 21 | 2641.417057 | 1321.212167 | 2624.390508 | 1312.698892 | 2623.406492 | 1312.206884 | I | 1099.635752 | 550.321514 | 1082.609203 | 541.808240 | 1081.625187 | 541.316231 | 10 |
| 22 | 2754.501121 | 1377.754199 | 2737.474572 | 1369.240924 | 2736.490556 | 1368.748916 | L | *986.551688* | 493.779482 | 969.525139 | 485.266207 | 968.541123 | 484.774199 | 9 |
| 23 | 2869.528064 | 1435.267670 | 2852.501515 | 1426.754395 | 2851.517499 | 1426.262387 | D | *873.467624* | 437.237450 | 856.441075 | 428.724175 | 855.457059 | 428.232167 | 8 |
| 24 | 2968.596478 | **1484.801877** | 2951.569929 | 1476.288602 | 2950.585913 | 1475.796594 | V | *758.440681* | 379.723978 | 741.414132 | 371.210704 | 740.430116 | 370.718696 | 7 |
| 25 | 3065.649242 | 1533.328259 | 3048.622693 | 1524.814984 | 3047.638677 | 1524.322976 | P | *659.372267* | 330.189772 | 642.345718 | 321.676497 | 641.361702 | 321.184489 | 6 |
| 26 | 3152.681270 | 1576.844273 | 3135.654721 | 1568.330998 | 3134.670705 | 1567.838990 | S | *562.319503* | 281.663389 | 545.292954 | 273.150115 | 544.308938 | 272.658107 | 5 |
| 27 | 3253.728949 | 1627.368112 | 3236.702400 | 1618.854838 | 3235.718384 | 1618.362830 | T | *475.287475* | 238.147375 | 458.260926 | 229.634101 | 457.276910 | 229.142093 | 4 |
| 28 | 3352.797363 | 1676.902319 | 3335.770814 | 1668.389045 | 3334.786798 | 1667.897037 | V | *374.239796* | 187.623536 | 357.213247 | 179.110261 | | | 3 |
| 29 | 3480.855941 | 1740.931608 | 3463.829392 | 1732.418334 | 3462.845376 | 1731.926326 | Q | *275.171382* | 138.089329 | 258.144833 | 129.576055 | | | 2 |
| 30 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 40.3 | 3625.954193 | 0.053627 | KTDELPQLVTLPHPNLHGPEILDVPSTVQK |

**Mascot:** http://www.matrixscience.com/

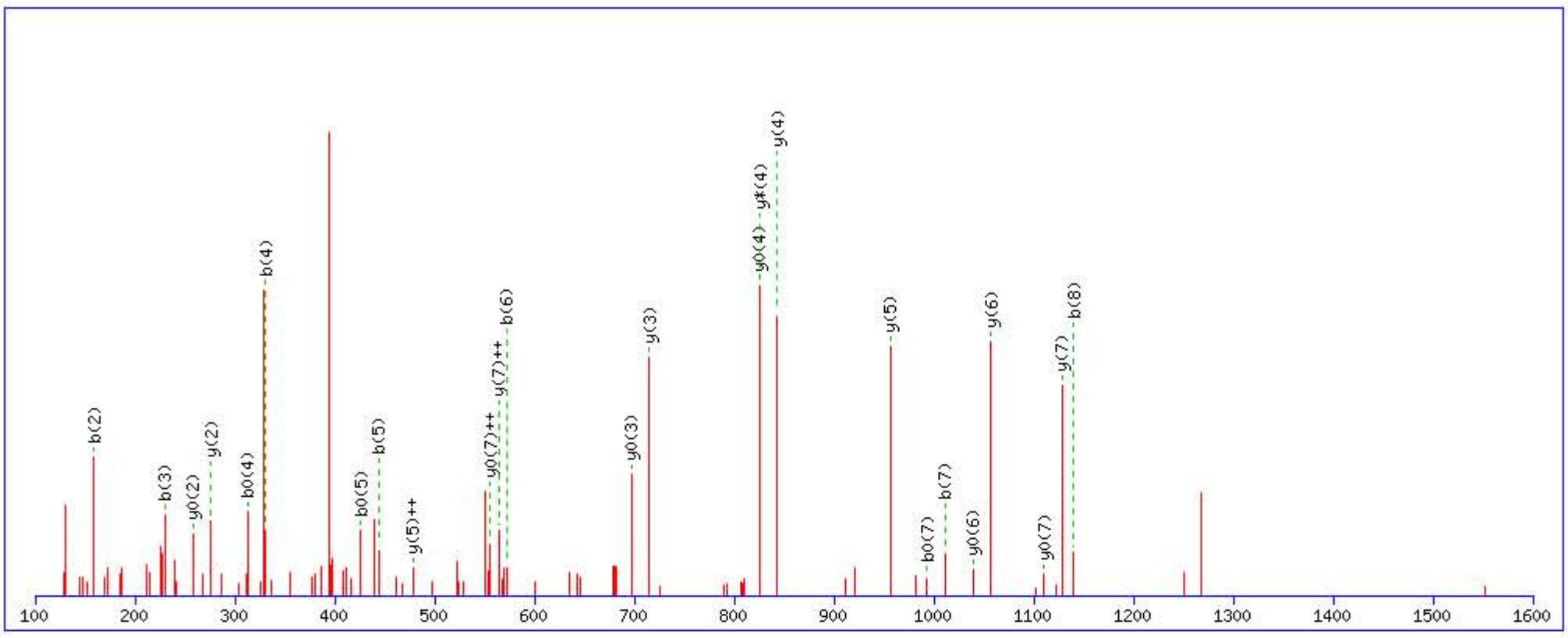
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SAATLQQEK**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

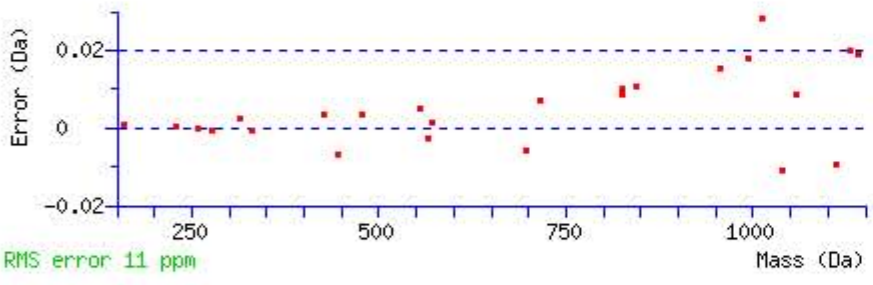
Match to Query 23030: 1285.678528 from(643.846540,2+) rtinseconds(1510) index(47025)
Title: Locus:1.1.1.1763.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

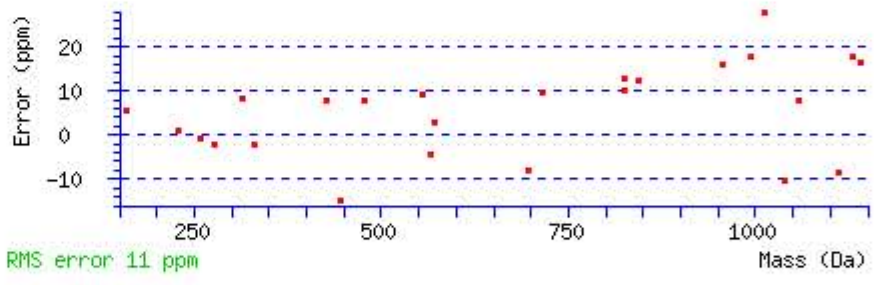
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1285.669998
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.00043
**Matches :** 25/84 fragment ions using 42 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 9 |
| 2 | *159.076418* | 80.041847 | | | 141.065853 | 71.036564 | A | 1199.645272 | 600.326274 | 1182.618723 | 591.813000 | 1181.634707 | 591.320991 | 8 |
| 3 | *230.113532* | 115.560404 | | | 212.102967 | 106.555121 | A | **1128.608158** | 564.807717 | 1111.581609 | 556.294443 | 1110.597593 | 555.802435 | 7 |
| 4 | *331.161211* | 166.084243 | | | 313.150646 | 157.078961 | T | **1057.571044** | 529.289160 | 1040.544495 | 520.775886 | 1039.560479 | 520.283878 | 6 |
| 5 | *444.245275* | 222.626275 | | | 426.234710 | 213.620993 | L | **956.523365** | 478.765321 | 939.496816 | 470.252046 | 938.512800 | 469.760038 | 5 |
| 6 | *572.303853* | 286.655565 | 555.277304 | 278.142290 | 554.293288 | 277.650282 | Q | **843.439301** | 422.223289 | 826.412752 | 413.710014 | 825.428736 | 413.218006 | 4 |
| 7 | *1011.529179* | 506.268228 | 994.502630 | 497.754953 | 993.518614 | 497.262945 | Q | **715.380723** | 358.194000 | 698.354174 | 349.680725 | 697.370158 | 349.188717 | 3 |
| 8 | *1140.571772* | 570.789524 | 1123.545223 | 562.276250 | 1122.561207 | 561.784242 | E | **276.155397** | 138.581336 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 9 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 43.8 | 1285.669998 | 0.008530 | SAATLQQEK |
| 31.2 | 1285.669998 | 0.008530 | SAATLQQEK |
| 7.4 | 1285.688614 | -0.010086 | SMANQLLAK |
| 6.9 | 1285.669998 | 0.008530 | ASLDQGKEK |
| 5.5 | 1285.670013 | 0.008515 | QLQETQTK |
| 3.5 | 1285.688614 | -0.010086 | QKEIQAMK |
| 2.9 | 1285.671326 | 0.007202 | MRRLANTAPAW |
| 2.1 | 1285.662598 | 0.015930 | EARSDQVKPEK |
| 1.6 | 1285.670013 | 0.008515 | QLQETQTK |
| 1.6 | 1285.669998 | 0.008530 | KQEESVQK |

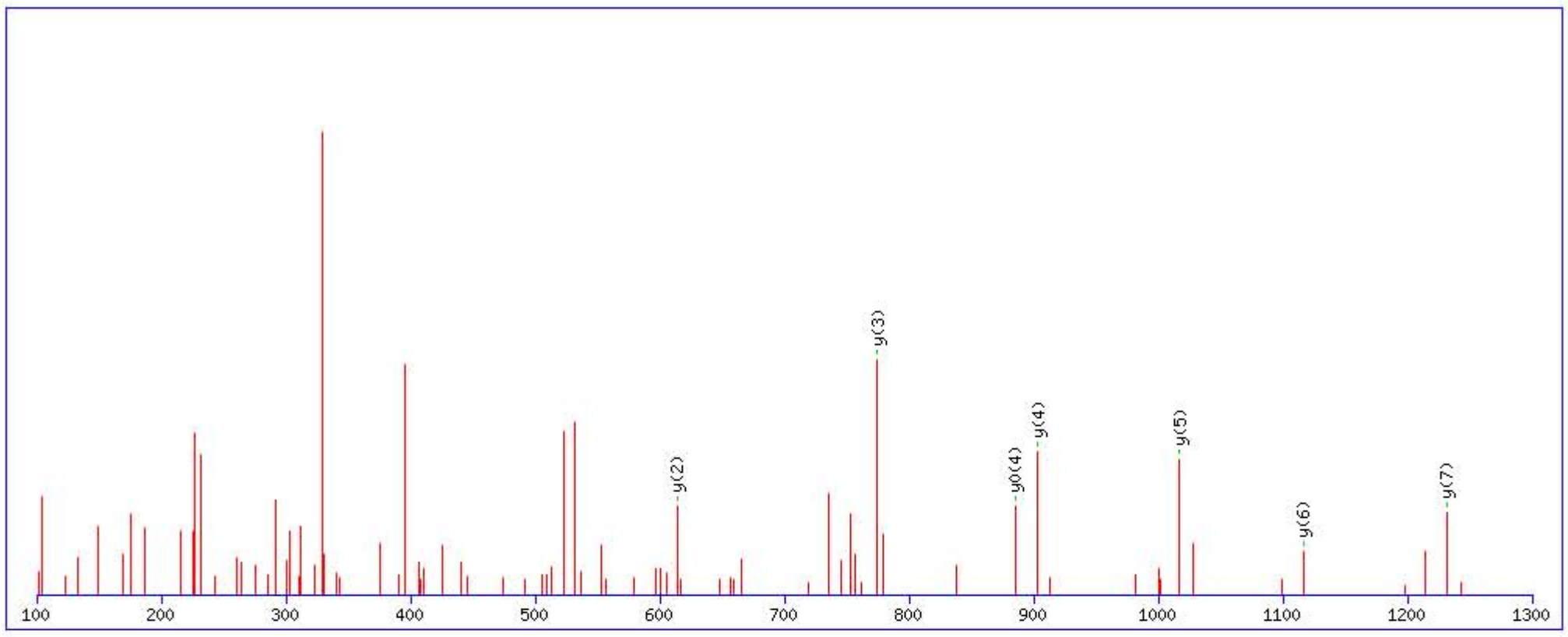
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MCVDVNECQR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

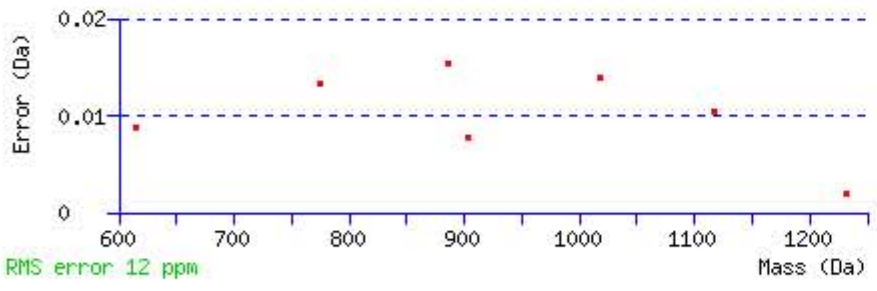
Match to Query 35494: 1620.690342 from(541.237390,3+) rtinseconds(1724) index(48434)
Title: Locus:1.1.1.1838.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

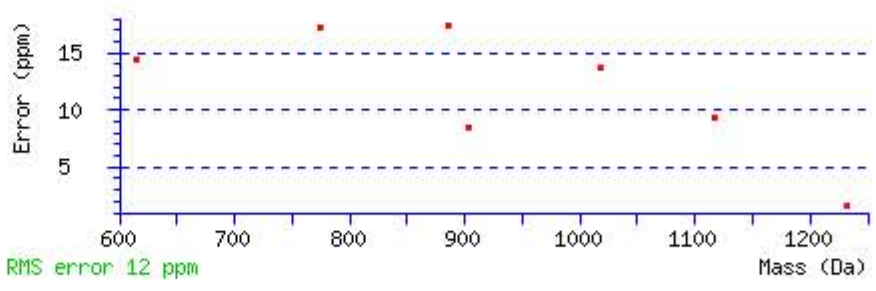
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1620.688080
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 34 **Expect:** 0.0017
**Matches :** 7/86 fragment ions using 12 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.047761 | 66.527518 | | | | | M | | | | | | | 10 |
| 2 | 292.078410 | 146.542843 | | | | | C | 1490.654867 | 745.831072 | 1473.628318 | 737.317797 | 1472.644302 | 736.825789 | 9 |
| 3 | 391.146824 | 196.077050 | | | | | V | 1330.624218 | 665.815747 | 1313.597669 | 657.302473 | 1312.613653 | 656.810464 | 8 |
| 4 | 506.173767 | 253.590522 | | | 488.163202 | 244.585239 | D | *1231.555804* | 616.281540 | 1214.529255 | 607.768265 | 1213.545239 | 607.276257 | 7 |
| 5 | 605.242181 | 303.124729 | | | 587.231616 | 294.119446 | V | *1116.528861* | 558.768069 | 1099.502312 | 550.254794 | 1098.518296 | 549.762786 | 6 |
| 6 | 719.285108 | 360.146192 | 702.258559 | 351.632918 | 701.274543 | 351.140910 | N | *1017.460447* | 509.233861 | 1000.433898 | 500.720587 | 999.449882 | 500.228579 | 5 |
| 7 | 848.327701 | 424.667489 | 831.301152 | 416.154214 | 830.317136 | 415.662206 | E | *903.417520* | 452.212398 | 886.390971 | 443.699123 | 885.406955 | 443.207115 | 4 |
| 8 | 1008.358350 | 504.682813 | 991.331801 | 496.169539 | 990.347785 | 495.677531 | C | *774.374927* | 387.691102 | 757.348378 | 379.177827 | | | 3 |
| 9 | 1447.583676 | 724.295476 | 1430.557127 | 715.782202 | 1429.573111 | 715.290193 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162502 | | | 2 |
| 10 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 34.2 | 1620.688080 | 0.002262 | MCVDVNECQR |

**Mascot:** http://www.matrixscience.com/

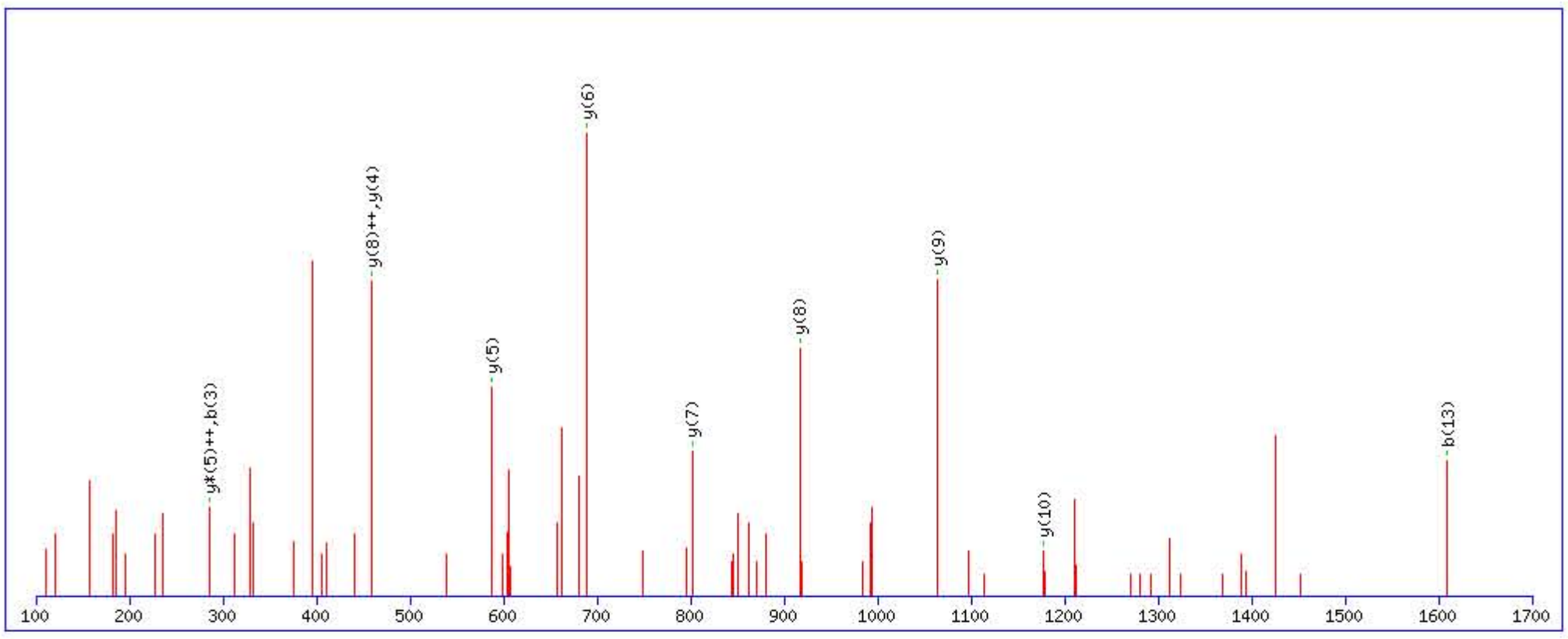
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AITPPHPASQANIIFDITEGNLR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

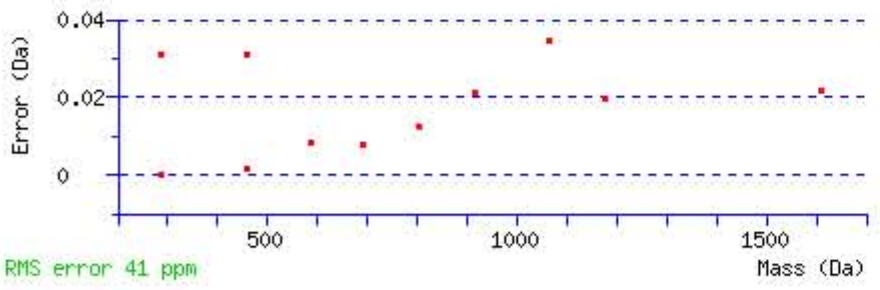
Match to Query 57343: 2785.491696 from(697.380200,4+) rtinseconds(2710) index(54778)
Title: Locus:1.1.1.2180.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

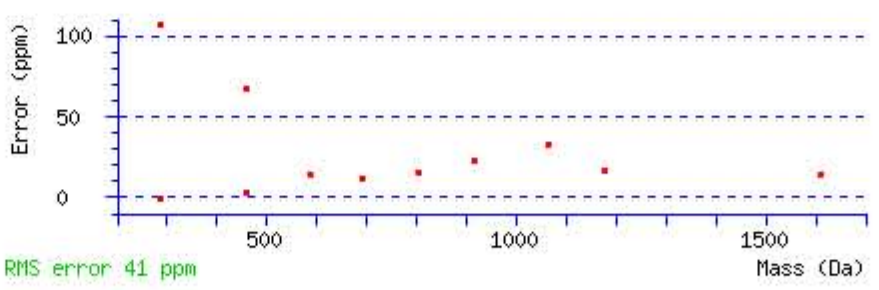
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2785.458496
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q10** : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.003
**Matches** : 11/234 fragment ions using 15 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 23 |
| 2 | 185.128454 | 93.067865 | | | | | I | 2715.428684 | 1358.217980 | 2698.402135 | 1349.704705 | 2697.418119 | 1349.212697 | 22 |
| 3 | **286.176133** | 143.591704 | | | 268.165568 | 134.586422 | T | 2602.344620 | 1301.675948 | 2585.318071 | 1293.162673 | 2584.334055 | 1292.670665 | 21 |
| 4 | 383.228897 | 192.118087 | | | 365.218332 | 183.112804 | P | 2501.296941 | 1251.152108 | 2484.270392 | 1242.638834 | 2483.286376 | 1242.146826 | 20 |
| 5 | 480.281661 | 240.644469 | | | 462.271096 | 231.639186 | P | 2404.244177 | 1202.625726 | 2387.217628 | 1194.112452 | 2386.233612 | 1193.620444 | 19 |
| 6 | 617.340573 | 309.173925 | | | 599.330008 | 300.168642 | H | 2307.191413 | 1154.099344 | 2290.164864 | 1145.586070 | 2289.180848 | 1145.094062 | 18 |
| 7 | 714.393337 | 357.700307 | | | 696.382772 | 348.695024 | P | 2170.132501 | 1085.569888 | 2153.105952 | 1077.056614 | 2152.121936 | 1076.564606 | 17 |
| 8 | 785.430451 | 393.218864 | | | 767.419886 | 384.213581 | A | 2073.079737 | 1037.043506 | 2056.053188 | 1028.530232 | 2055.069172 | 1028.038224 | 16 |
| 9 | 872.462479 | 436.734878 | | | 854.451914 | 427.729595 | S | 2002.042623 | 1001.524950 | 1985.016074 | 993.011675 | 1984.032058 | 992.519667 | 15 |
| 10 | 1311.687805 | 656.347541 | 1294.661256 | 647.834266 | 1293.677240 | 647.342258 | Q | 1915.010595 | 958.008936 | 1897.984046 | 949.495661 | 1897.000030 | 949.003653 | 14 |
| 11 | 1382.724919 | 691.866098 | 1365.698370 | 683.352823 | 1364.714354 | 682.860815 | A | 1475.785269 | 738.396273 | 1458.758720 | 729.882998 | 1457.774704 | 729.390990 | 13 |
| 12 | 1496.767846 | 748.887561 | 1479.741297 | 740.374287 | 1478.757281 | 739.882278 | N | 1404.748155 | 702.877716 | 1387.721606 | 694.364441 | 1386.737590 | 693.872433 | 12 |
| 13 | **1609.851910** | 805.429593 | 1592.825361 | 796.916318 | 1591.841345 | 796.424310 | I | 1290.705228 | 645.856252 | 1273.678679 | 637.342978 | 1272.694663 | 636.850970 | 11 |
| 14 | 1722.935974 | 861.971625 | 1705.909425 | 853.458350 | 1704.925409 | 852.966342 | I | *1177.621164* | 589.314220 | 1160.594615 | 580.800946 | 1159.610599 | 580.308938 | 10 |
| 15 | 1870.004388 | 935.505832 | 1852.977839 | 926.992557 | 1851.993823 | 926.500549 | F | *1064.537100* | 532.772188 | 1047.510551 | 524.258914 | 1046.526535 | 523.766906 | 9 |
| 16 | 1985.031331 | 993.019303 | 1968.004782 | 984.506029 | 1967.020766 | 984.014021 | D | *917.468686* | 459.237981 | 900.442137 | 450.724707 | 899.458121 | 450.232699 | 8 |
| 17 | 2098.115395 | 1049.561335 | 2081.088846 | 1041.048061 | 2080.104830 | 1040.556053 | I | *802.441743* | 401.724510 | 785.415194 | 393.211235 | 784.431178 | 392.719227 | 7 |
| 18 | 2199.163074 | 1100.085175 | 2182.136525 | 1091.571900 | 2181.152509 | 1091.079892 | T | *689.357679* | 345.182478 | 672.331130 | 336.669203 | 671.347114 | 336.177195 | 6 |
| 19 | 2328.205667 | 1164.606471 | 2311.179118 | 1156.093197 | 2310.195102 | 1155.601189 | E | *588.310000* | 294.658638 | 571.283451 | 286.145364 | 570.299435 | 285.653356 | 5 |
| 20 | 2385.227131 | 1193.117203 | 2368.200582 | 1184.603929 | 2367.216566 | 1184.111921 | G | *459.267407* | 230.137341 | 442.240858 | 221.624067 | | | 4 |
| 21 | 2499.270058 | 1250.138667 | 2482.243509 | 1241.625392 | 2481.259493 | 1241.133384 | N | 402.245943 | 201.626610 | 385.219394 | 193.113335 | | | 3 |
| 22 | 2612.354122 | 1306.680699 | 2595.327573 | 1298.167424 | 2594.343557 | 1297.675416 | L | 288.203016 | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 23 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.0 | 2785.458496 | 0.033200 | AITPPHPASQANIIFDITEGNLR |

**Mascot:** http://www.matrixscience.com/

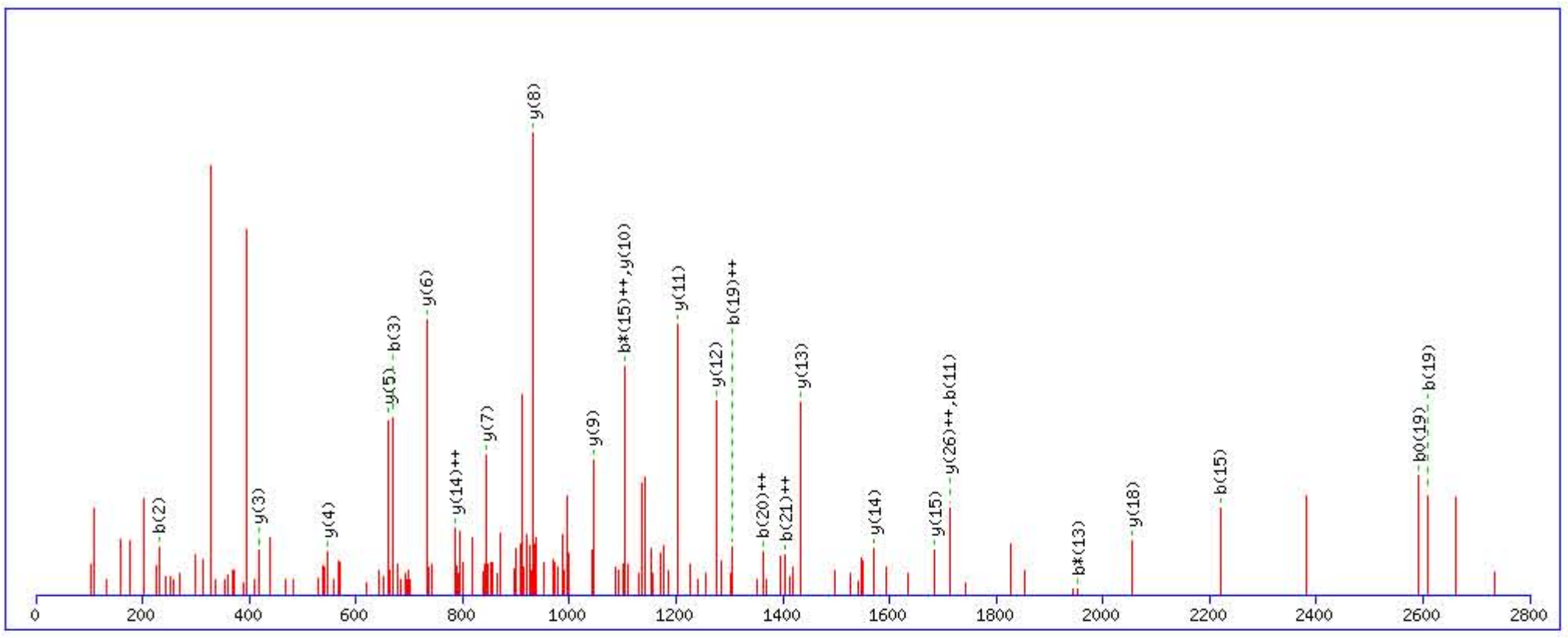
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

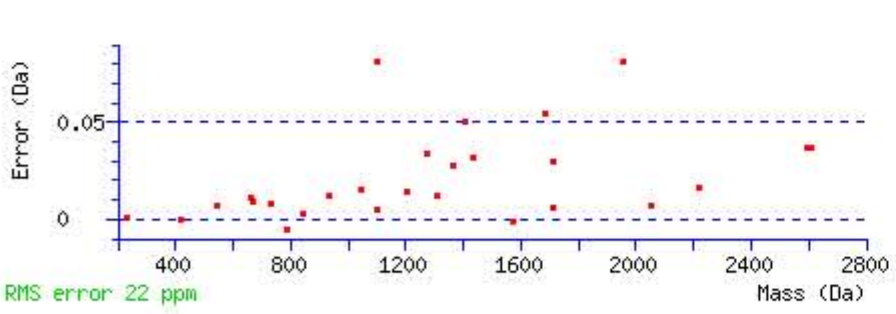
Match to Query 66976: 3653.666016 from(914.423780,4+) rtinseconds(1990) index(34228)
Title: Locus:1.1.1.801.24 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

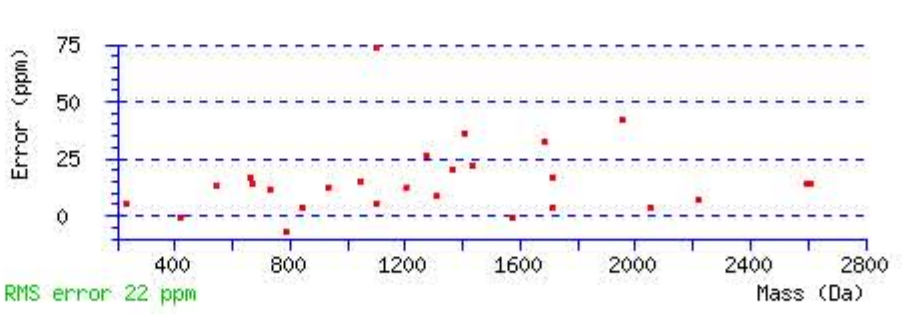
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3653.615311
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 76 **Expect:** 3.1e-007
**Matches :** 27/312 fragment ions using 45 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.047761 | 66.527518 | | | | | M | | | | | | | 28 |
| 2 | **231.116175** | 116.061725 | | | | | V | 3523.582122 | 1762.294699 | 3506.555573 | 1753.781424 | 3505.571557 | 1753.289416 | 27 |
| 3 | **670.341501** | 335.674389 | 653.314952 | 327.161114 | | | Q | 3424.513708 | 1712.760492 | 3407.487159 | 1704.247217 | 3406.503143 | 1703.755209 | 26 |
| 4 | 799.384094 | 400.195685 | 782.357545 | 391.682411 | 781.373529 | 391.190403 | E | 2985.288382 | 1493.147829 | 2968.261833 | 1484.634554 | 2967.277817 | 1484.142546 | 25 |
| 5 | 927.442672 | 464.224974 | 910.416123 | 455.711700 | 909.432107 | 455.219692 | Q | 2856.245789 | 1428.626532 | 2839.219240 | 1420.113258 | 2838.235224 | 1419.621250 | 24 |
| 6 | 1087.473321 | 544.240299 | 1070.446772 | 535.727024 | 1069.462756 | 535.235016 | C | 2728.187211 | 1364.597243 | 2711.160662 | 1356.083969 | 2710.176646 | 1355.591961 | 23 |
| 7 | 1247.503970 | 624.255623 | 1230.477421 | 615.742349 | 1229.493405 | 615.250341 | C | 2568.156562 | 1284.581919 | 2551.130013 | 1276.068644 | 2550.145997 | 1275.576636 | 22 |
| 8 | 1384.562882 | 692.785079 | 1367.536333 | 684.271805 | 1366.552317 | 683.779797 | H | 2408.125913 | 1204.566594 | 2391.099364 | 1196.053320 | 2390.115348 | 1195.561312 | 21 |
| 9 | 1471.594910 | 736.301093 | 1454.568361 | 727.787819 | 1453.584345 | 727.295811 | S | 2271.067001 | 1136.037138 | 2254.040452 | 1127.523864 | 2253.056436 | 1127.031856 | 20 |
| 10 | 1599.653488 | 800.330382 | 1582.626939 | 791.817108 | 1581.642923 | 791.325100 | Q | 2184.034973 | 1092.521124 | 2167.008424 | 1084.007850 | 2166.024408 | 1083.515842 | 19 |
| 11 | **1712.737552** | 856.872414 | 1695.711003 | 848.359140 | 1694.726987 | 847.867132 | L | *2055.976395* | 1028.491835 | 2038.949846 | 1019.978561 | 2037.965830 | 1019.486553 | 18 |
| 12 | 1841.780145 | 921.393711 | 1824.753596 | 912.880436 | 1823.769580 | 912.388428 | E | 1942.892331 | 971.949804 | 1925.865782 | 963.436529 | 1924.881766 | 962.944521 | 17 |
| 13 | 1970.822738 | 985.915007 | 1953.796189 | 977.401733 | 1952.812173 | 976.909725 | E | 1813.849738 | 907.428507 | 1796.823189 | 898.915233 | 1795.839173 | 898.423225 | 16 |
| 14 | 2083.906802 | 1042.457039 | 2066.880253 | 1033.943764 | 2065.896237 | 1033.451756 | L | *1684.807145* | 842.907211 | 1667.780596 | 834.393936 | 1666.796580 | 833.901928 | 15 |
| 15 | **2220.965714** | 1110.986495 | 2203.939165 | 1102.473220 | 2202.955149 | 1101.981212 | H | *1571.723081* | 786.365179 | 1554.696532 | 777.851904 | 1553.712516 | 777.359896 | 14 |
| 16 | 2380.996363 | 1191.001819 | 2363.969814 | 1182.488545 | 2362.985798 | 1181.996537 | C | *1434.664169* | 717.835723 | 1417.637620 | 709.322448 | 1416.653604 | 708.830440 | 13 |
| 17 | 2452.033477 | 1226.520376 | 2435.006928 | 1218.007102 | 2434.022912 | 1217.515094 | A | *1274.633520* | 637.820398 | 1257.606971 | 629.307124 | 1256.622955 | 628.815116 | 12 |
| 18 | 2553.081156 | 1277.044216 | 2536.054607 | 1268.530941 | 2535.070591 | 1268.038933 | T | *1203.596406* | 602.301841 | 1186.569857 | 593.788567 | 1185.585841 | 593.296559 | 11 |
| 19 | **2610.102620** | **1305.554948** | 2593.076071 | 1297.041673 | 2592.092055 | 1296.549665 | G | *1102.548727* | 551.778002 | 1085.522178 | 543.264727 | 1084.538162 | 542.772719 | 10 |
| 20 | 2723.186684 | **1362.096980** | 2706.160135 | 1353.583705 | 2705.176119 | 1353.091697 | I | *1045.527263* | 523.267270 | 1028.500714 | 514.753995 | 1027.516698 | 514.261987 | 9 |
| 21 | 2810.218712 | **1405.612994** | 2793.192163 | 1397.099719 | 2792.208147 | 1396.607711 | S | *932.443199* | 466.725238 | 915.416650 | 458.211963 | 914.432634 | 457.719955 | 8 |
| 22 | 2923.302776 | 1462.155026 | 2906.276227 | 1453.641751 | 2905.292211 | 1453.149743 | L | *845.411171* | 423.209224 | 828.384622 | 414.695949 | 827.400606 | 414.203941 | 7 |
| 23 | 2994.339890 | 1497.673583 | 2977.313341 | 1489.160308 | 2976.329325 | 1488.668301 | A | *732.327107* | 366.667192 | 715.300558 | 358.153917 | 714.316542 | 357.661909 | 6 |
| 24 | 3108.382817 | 1554.695047 | 3091.356268 | 1546.181772 | 3090.372252 | 1545.689764 | N | *661.289993* | 331.148635 | 644.263444 | 322.635360 | 643.279428 | 322.143352 | 5 |
| 25 | 3237.425410 | 1619.216343 | 3220.398861 | 1610.703069 | 3219.414845 | 1610.211061 | E | *547.247066* | 274.127171 | 530.220517 | 265.613897 | 529.236501 | 265.121889 | 4 |
| 26 | 3365.483988 | 1683.245632 | 3348.457439 | 1674.732358 | 3347.473423 | 1674.240350 | Q | *418.204473* | 209.605874 | 401.177924 | 201.092600 | 400.193908 | 200.600592 | 3 |
| 27 | 3480.510931 | 1740.759104 | 3463.484382 | 1732.245829 | 3462.500366 | 1731.753821 | D | 290.145895 | 145.576585 | 273.119346 | 137.063311 | 272.135330 | 136.571303 | 2 |
| 28 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 75.8 | 3653.615311 | 0.050705 | MVQEQCCHSQLEELHCATGISLANEQDR |
| 75.7 | 3653.615311 | 0.050705 | MVQEQCCHSQLEELHCATGISLANEQDR |
| 73.5 | 3653.615311 | 0.050705 | MVQEQCCHSQLEELHCATGISLANEQDR |

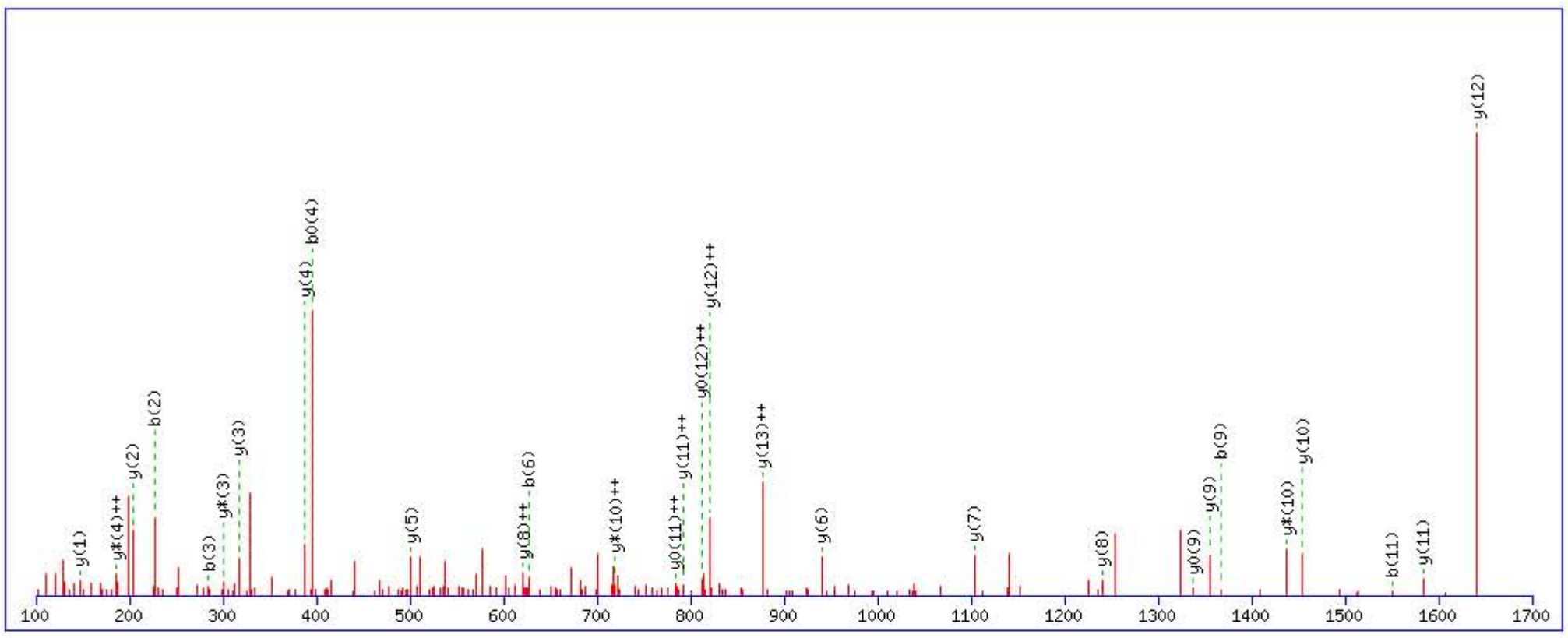
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LLGEVDHYQLALGK**
Found in **FCN3_HUMAN**, Ficolin-3 OS=Homo sapiens GN=FCN3 PE=1 SV=2

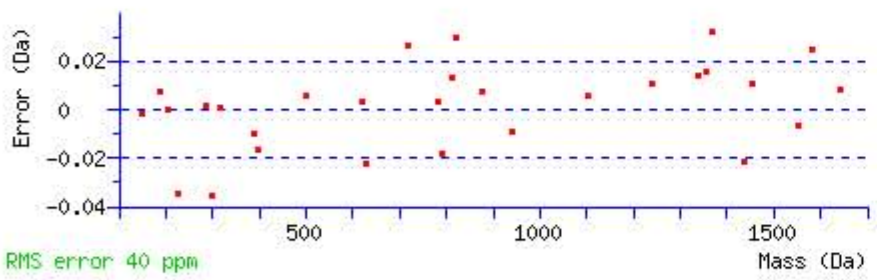
Match to Query 41620: 1866.012612 from(623.011480,3+) rtinseconds(2203) index(6769)
Title: Locus:1.1.1.2044.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

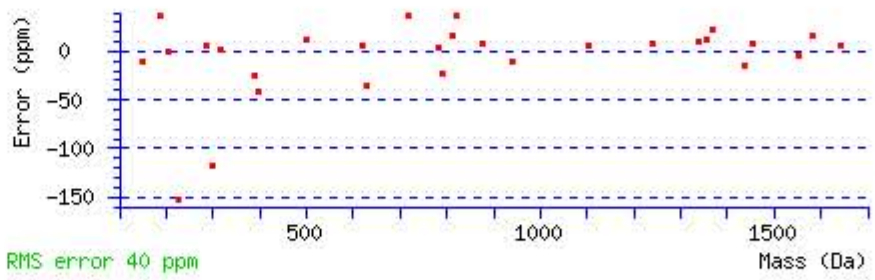
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1866.007324
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 51 **Expect:** 0.00017
**Matches :** 29/118 fragment ions using 84 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 14 |
| 2 | 227.175404 | 114.091340 | | | | | L | 1753.930555 | 877.468916 | 1736.904006 | 868.955641 | 1735.919990 | 868.463633 | 13 |
| 3 | 284.196868 | 142.602072 | | | | | G | *1640.846491* | 820.926884 | 1623.819942 | 812.413609 | 1622.835926 | 811.921601 | 12 |
| 4 | 413.239461 | 207.123369 | | | 395.228896 | 198.118086 | E | *1583.825027* | 792.416152 | 1566.798478 | 783.902877 | 1565.814462 | 783.410869 | 11 |
| 5 | 512.307875 | 256.657576 | | | 494.297310 | 247.652293 | V | *1454.782434* | 727.894855 | 1437.755885 | 719.381581 | 1436.771869 | 718.889572 | 10 |
| 6 | 627.334818 | 314.171047 | | | 609.324253 | 305.165765 | D | *1355.714020* | 678.360648 | 1338.687471 | 669.847374 | 1337.703455 | 669.355366 | 9 |
| 7 | 764.393730 | 382.700503 | | | 746.383165 | 373.695221 | H | *1240.687077* | 620.847177 | 1223.660528 | 612.333902 | | | 8 |
| 8 | 927.457059 | 464.232168 | | | 909.446494 | 455.226885 | Y | *1103.628165* | 552.317721 | 1086.601616 | 543.804446 | | | 7 |
| 9 | 1366.682385 | 683.844831 | 1349.655836 | 675.331556 | 1348.671820 | 674.839548 | Q | *940.564836* | 470.786056 | 923.538287 | 462.272782 | | | 6 |
| 10 | 1479.766449 | 740.386863 | 1462.739900 | 731.873588 | 1461.755884 | 731.381580 | L | *501.339510* | 251.173393 | 484.312961 | 242.660118 | | | 5 |
| 11 | 1550.803563 | 775.905420 | 1533.777014 | 767.392145 | 1532.792998 | 766.900137 | A | *388.255446* | 194.631361 | 371.228897 | 186.118086 | | | 4 |
| 12 | 1663.887627 | 832.447452 | 1646.861078 | 823.934177 | 1645.877062 | 823.442169 | L | *317.218332* | 159.112804 | 300.191783 | 150.599529 | | | 3 |
| 13 | 1720.909091 | 860.958184 | 1703.882542 | 852.444909 | 1702.898526 | 851.952901 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 14 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 50.6 | 1866.007324 | 0.005288 | LLGEVDHYQLALGK |

**Mascot:** http://www.matrixscience.com/

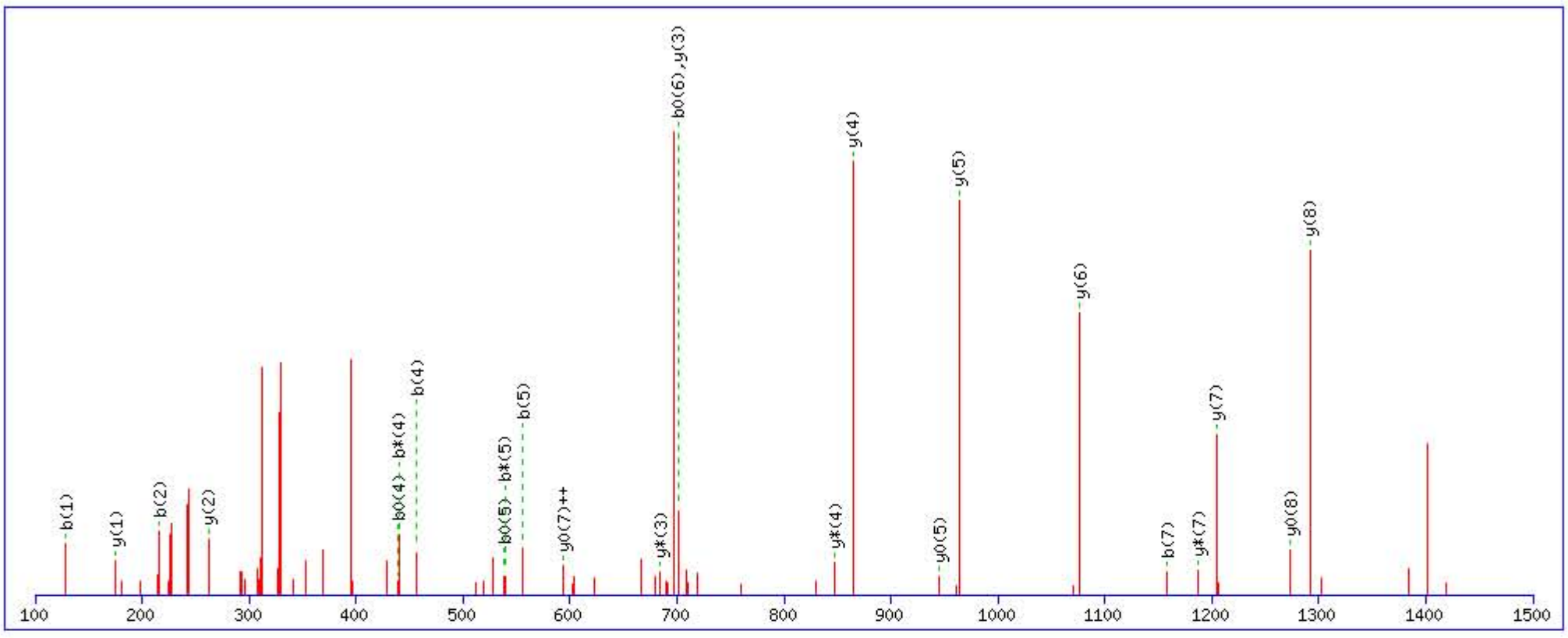
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KSQLVYQSR**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

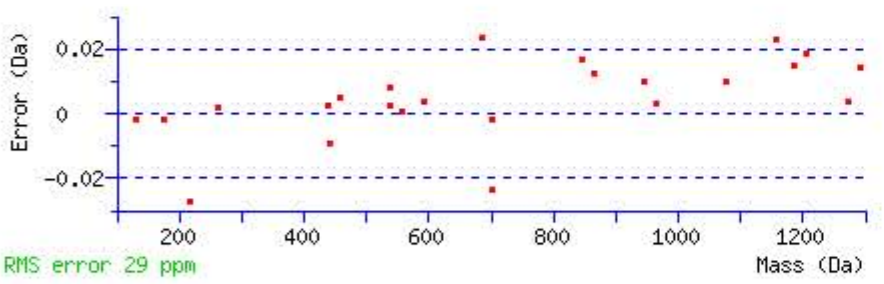
Match to Query 28344: 1418.782988 from(710.398770,2+) rtinseconds(1512) index(47044)
Title: Locus:1.1.1.1764.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

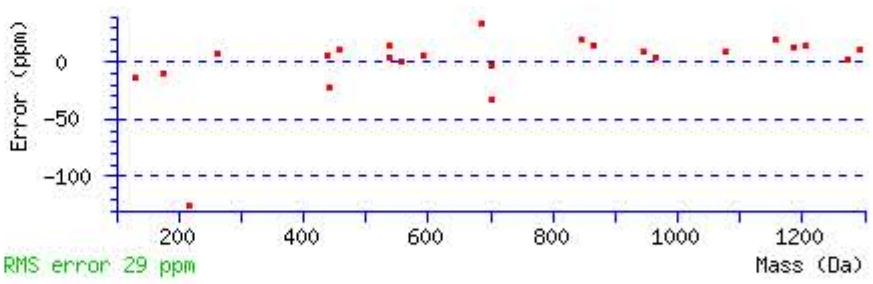
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1418.770386
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 40 **Expect:** 0.0013
**Matches :** 24/92 fragment ions using 52 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.102239 | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 9 |
| 2 | 216.134267 | 108.570771 | 199.107718 | 100.057497 | 198.123702 | 99.565489 | S | *1291.682719* | 646.344998 | 1274.656170 | 637.831723 | 1273.672154 | 637.339715 | 8 |
| 3 | 344.192845 | 172.600060 | 327.166296 | 164.086786 | 326.182280 | 163.594778 | Q | *1204.650691* | 602.828984 | 1187.624142 | 594.315709 | 1186.640126 | 593.823701 | 7 |
| 4 | 457.276909 | 229.142092 | 440.250360 | 220.628818 | 439.266344 | 220.136810 | L | *1076.592113* | 538.799695 | 1059.565564 | 530.286420 | 1058.581548 | 529.794412 | 6 |
| 5 | 556.345323 | 278.676300 | 539.318774 | 270.163025 | 538.334758 | 269.671017 | V | *963.508049* | 482.257663 | 946.481500 | 473.744388 | 945.497484 | 473.252380 | 5 |
| 6 | 719.408652 | 360.207964 | 702.382103 | 351.694690 | 701.398087 | 351.202682 | Y | *864.439635* | 432.723456 | 847.413086 | 424.210181 | 846.429070 | 423.718173 | 4 |
| 7 | 1158.633978 | 579.820627 | 1141.607429 | 571.307353 | 1140.623413 | 570.815345 | Q | *701.376306* | 351.191791 | 684.349757 | 342.678517 | 683.365741 | 342.186509 | 3 |
| 8 | 1245.666006 | 623.336641 | 1228.639457 | 614.823367 | 1227.655441 | 614.331359 | S | *262.150980* | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 9 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 40.1 | 1418.770386 | 0.012602 | KSQLVYQSR |
| 9.1 | 1418.780273 | 0.002715 | TNQLMETLKTIK |
| 7.3 | 1418.788147 | -0.005159 | QSQVDRLYVALK |
| 5.0 | 1418.763000 | 0.019988 | IKGEQGAPGLQGHK |
| 4.6 | 1418.799362 | -0.016374 | QLRIPEPPNLSR |
| 4.6 | 1418.776886 | 0.006102 | EKAKALEDLAGFK |
| 3.1 | 1418.770386 | 0.012602 | KSQLVYQSR |

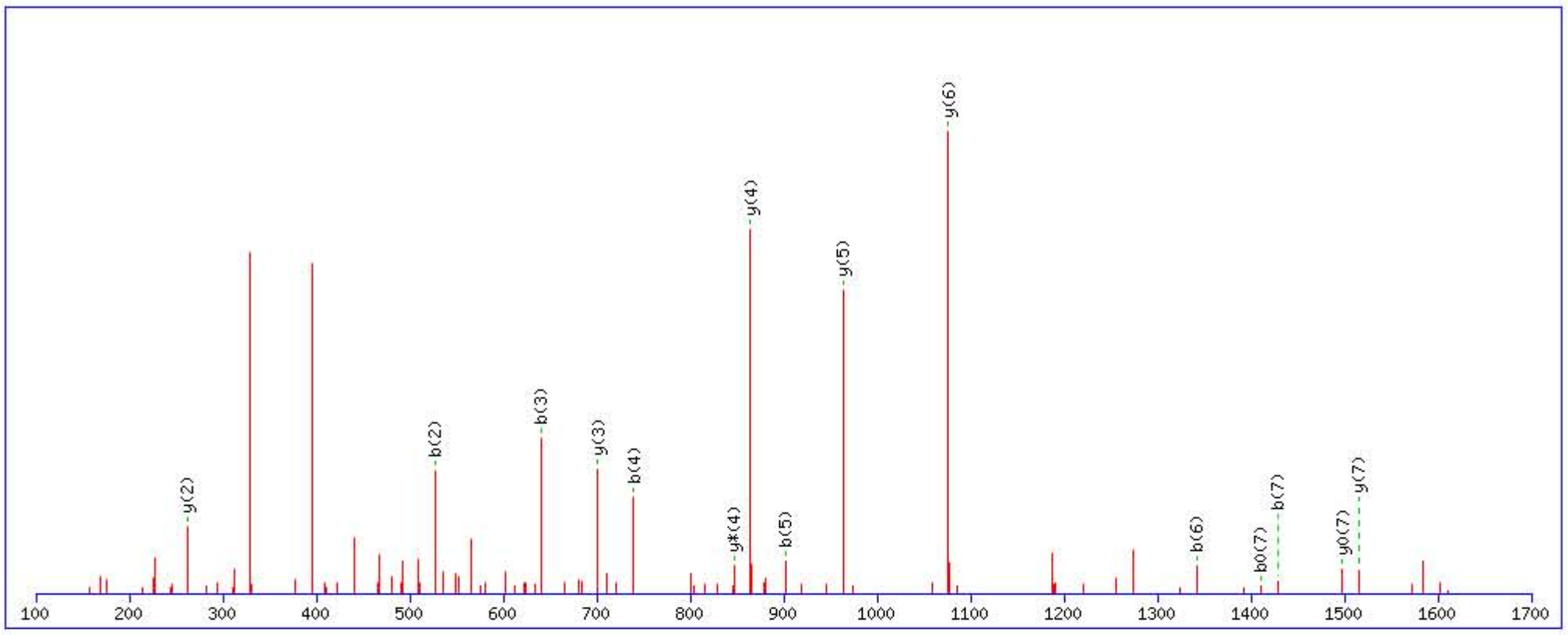
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SQLVYQSR**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

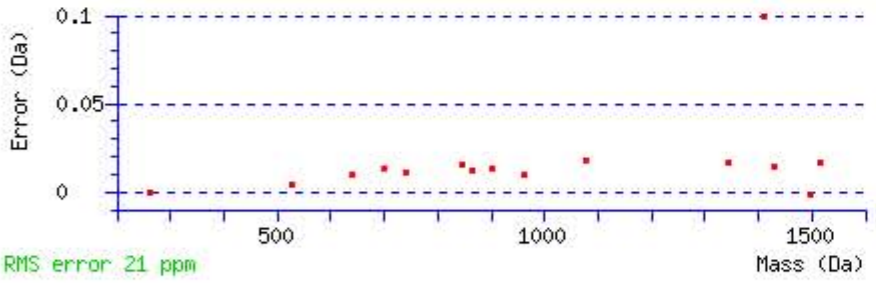
Match to Query 34755: 1601.862168 from(801.938360,2+) rtinseconds(2067) index(50766)
Title: Locus:1.1.1.1957.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

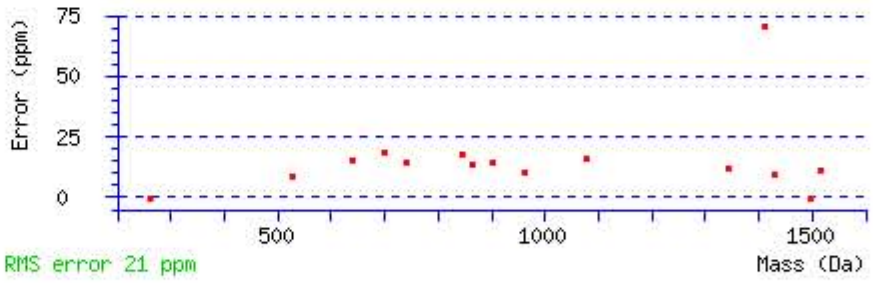
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1601.842178
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0042
**Matches :** 15/80 fragment ions using 30 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 8 |
| 2 | *527.264630* | 264.135953 | 510.238081 | 255.622679 | 509.254065 | 255.130671 | Q | *1515.817439* | 758.412358 | 1498.790890 | 749.899083 | 1497.806874 | 749.407075 | 7 |
| 3 | *640.348694* | 320.677985 | 623.322145 | 312.164711 | 622.338129 | 311.672703 | L | *1076.592113* | 538.799695 | 1059.565564 | 530.286420 | 1058.581548 | 529.794412 | 6 |
| 4 | *739.417108* | 370.212192 | 722.390559 | 361.698917 | 721.406543 | 361.206909 | V | *963.508049* | 482.257663 | 946.481500 | 473.744388 | 945.497484 | 473.252380 | 5 |
| 5 | *902.480437* | 451.743856 | 885.453888 | 443.230582 | 884.469872 | 442.738574 | Y | *864.439635* | 432.723456 | 847.413086 | 424.210181 | 846.429070 | 423.718173 | 4 |
| 6 | *1341.705763* | 671.356520 | 1324.679214 | 662.843245 | 1323.695198 | 662.351237 | Q | *701.376306* | 351.191791 | 684.349757 | 342.678517 | 683.365741 | 342.186509 | 3 |
| 7 | *1428.737791* | 714.872534 | 1411.711242 | 706.359259 | 1410.727226 | 705.867251 | S | *262.150980* | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 8 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.1 | 1601.842178 | 0.019990 | SQLVYQSR |
| 7.4 | 1601.846024 | 0.016144 | RFVLSCSLLSHQR |
| 2.0 | 1601.852051 | 0.010117 | SQISELNLLMK |
| 1.8 | 1601.841995 | 0.020173 | RPGTMTLQDGRKSR |
| 1.5 | 1601.855881 | 0.006287 | ELQRLQQAETMKK |

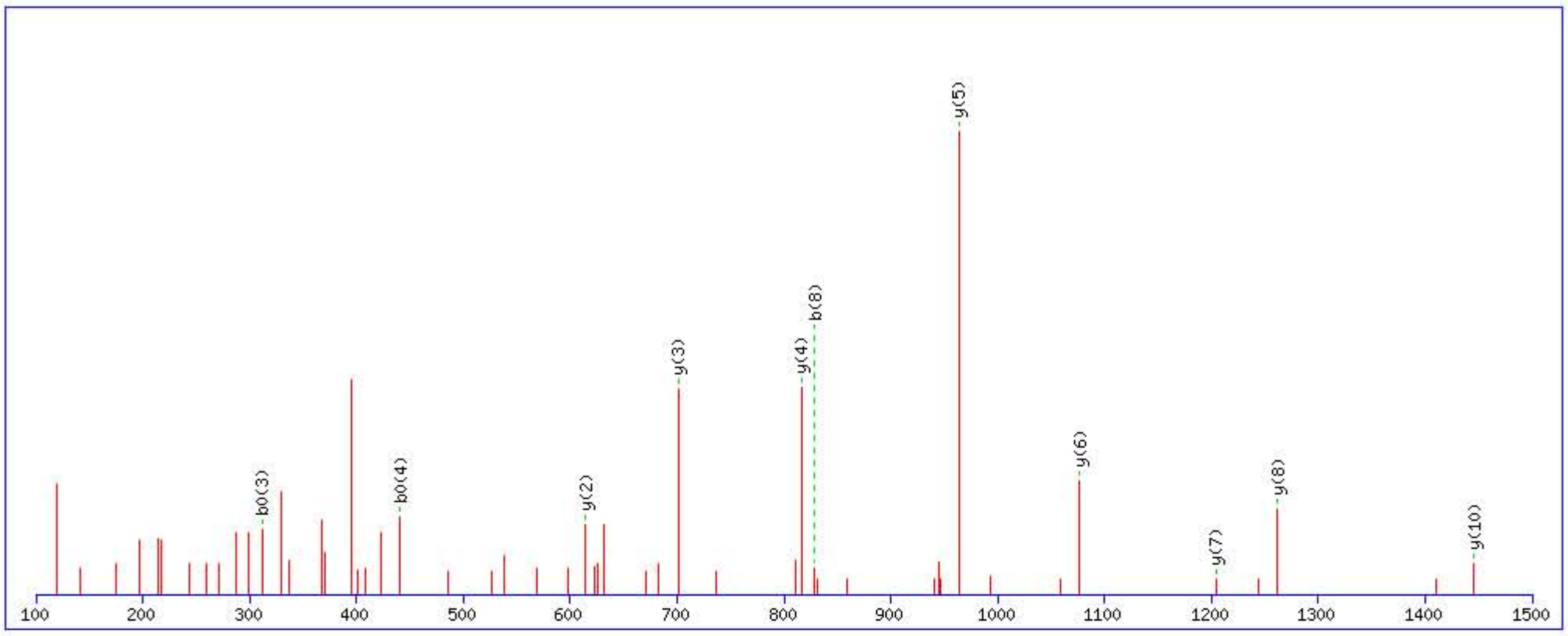
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ELSEALGQIFDSQR**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

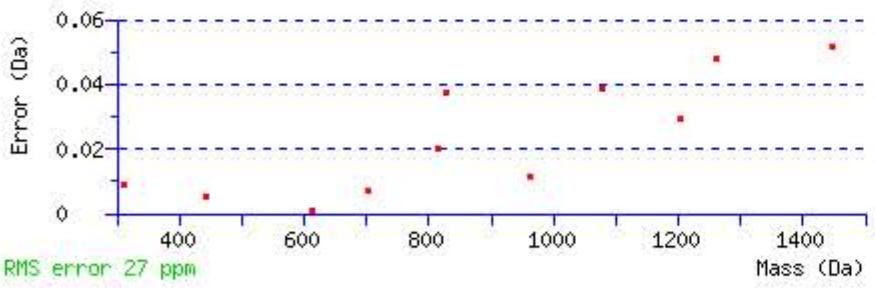
Match to Query 42158: 1902.972462 from(635.331430,3+) rtinseconds(2690) index(54611)
Title: Locus:1.1.1.2173.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

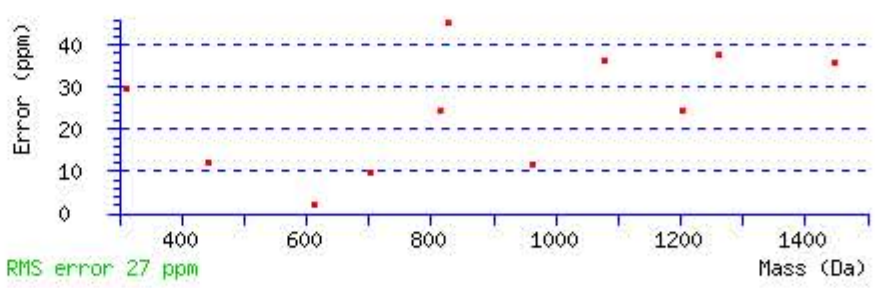
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1902.950928
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 64 **Expect:** 1.4e-006
**Matches :** 11/138 fragment ions using 14 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 14 |
| 2 | 243.133933 | 122.070605 | | | 225.123368 | 113.065322 | L | 1774.915632 | 887.961454 | 1757.889083 | 879.448180 | 1756.905067 | 878.956172 | 13 |
| 3 | 330.165961 | 165.586618 | | | 312.155396 | 156.581336 | S | 1661.831568 | 831.419422 | 1644.805019 | 822.906148 | 1643.821003 | 822.414140 | 12 |
| 4 | 459.208554 | 230.107915 | | | 441.197989 | 221.102633 | E | 1574.799540 | 787.903408 | 1557.772991 | 779.390134 | 1556.788975 | 778.898126 | 11 |
| 5 | 530.245668 | 265.626472 | | | 512.235103 | 256.621190 | A | *1445.756947* | 723.382112 | 1428.730398 | 714.868837 | 1427.746382 | 714.376829 | 10 |
| 6 | 643.329732 | 322.168504 | | | 625.319167 | 313.163222 | L | 1374.719833 | 687.863555 | 1357.693284 | 679.350280 | 1356.709268 | 678.858272 | 9 |
| 7 | 700.351196 | 350.679236 | | | 682.340631 | 341.673954 | G | *1261.635769* | 631.321523 | 1244.609220 | 622.808248 | 1243.625204 | 622.316240 | 8 |
| 8 | **828.409774** | 414.708525 | 811.383225 | 406.195251 | 810.399209 | 405.703243 | Q | *1204.614305* | 602.810791 | 1187.587756 | 594.297516 | 1186.603740 | 593.805508 | 7 |
| 9 | 941.493838 | 471.250557 | 924.467289 | 462.737283 | 923.483273 | 462.245275 | I | *1076.555727* | 538.781502 | 1059.529178 | 530.268227 | 1058.545162 | 529.776219 | 6 |
| 10 | 1088.562252 | 544.784764 | 1071.535703 | 536.271490 | 1070.551687 | 535.779482 | F | *963.471663* | 482.239470 | 946.445114 | 473.726195 | 945.461098 | 473.234187 | 5 |
| 11 | 1203.589195 | 602.298236 | 1186.562646 | 593.784961 | 1185.578630 | 593.292953 | D | *816.403249* | 408.705263 | 799.376700 | 400.191988 | 798.392684 | 399.699980 | 4 |
| 12 | 1290.621223 | 645.814250 | 1273.594674 | 637.300975 | 1272.610658 | 636.808967 | S | *701.376306* | 351.191791 | 684.349757 | 342.678517 | 683.365741 | 342.186509 | 3 |
| 13 | 1729.846549 | 865.426913 | 1712.820000 | 856.913638 | 1711.835984 | 856.421630 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 14 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 63.8 | 1902.950928 | 0.021534 | ELSEALGQIFDSQR |
| 1.3 | 1902.947739 | 0.024723 | MKEQLREMENLR |

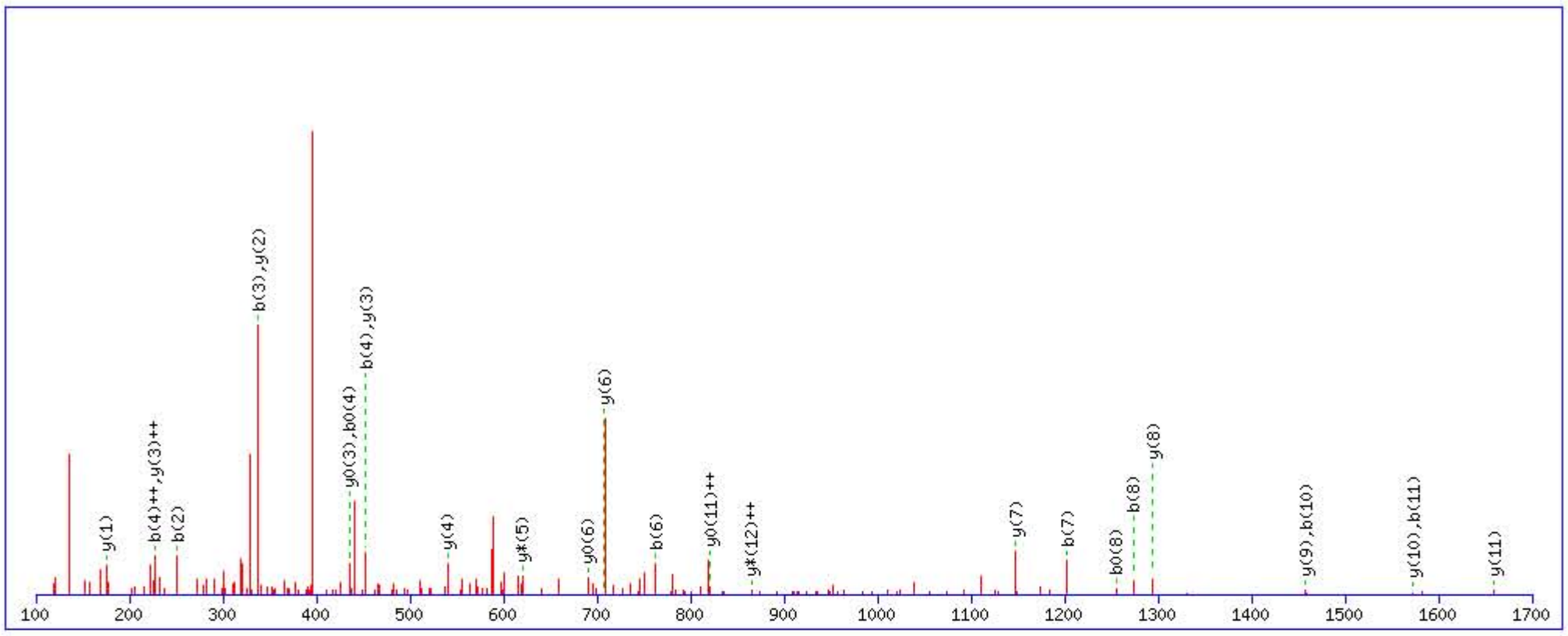
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YSSDYFQAPSDYR**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

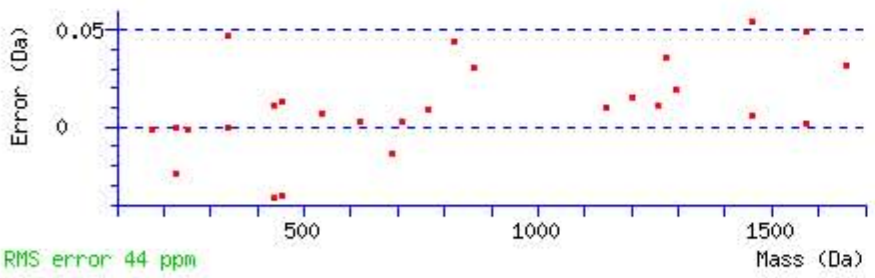
Match to Query 42285: 1908.849462 from(637.290430,3+) rtinseconds(2090) index(50915)
Title: Locus:1.1.1.1965.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

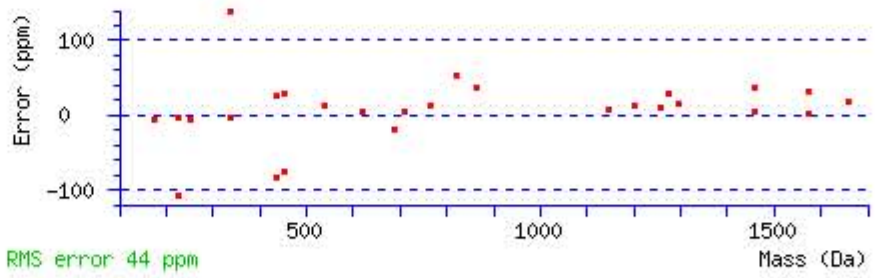
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1908.835236
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 51 **Expect:** 5.7e-005
**Matches :** 27/126 fragment ions using 42 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 13 |
| 2 | **251.102633** | 126.054954 | | | 233.092068 | 117.049672 | S | 1746.779198 | 873.893237 | 1729.752649 | 865.379963 | 1728.768633 | 864.887955 | 12 |
| 3 | **338.134661** | 169.570968 | | | 320.124096 | 160.565686 | S | *1659.747170* | 830.377223 | 1642.720621 | 821.863949 | 1641.736605 | 821.371941 | 11 |
| 4 | **453.161604** | 227.084440 | | | 435.151039 | 218.079158 | D | *1572.715142* | 786.861209 | 1555.688593 | 778.347935 | 1554.704577 | 777.855927 | 10 |
| 5 | 616.224933 | 308.616105 | | | 598.214368 | 299.610822 | Y | *1457.688199* | 729.347738 | 1440.661650 | 720.834463 | 1439.677634 | 720.342455 | 9 |
| 6 | **763.293347** | 382.150312 | | | 745.282782 | 373.145029 | F | *1294.624870* | 647.816073 | 1277.598321 | 639.302799 | 1276.614305 | 638.810791 | 8 |
| 7 | **1202.518673** | 601.762975 | 1185.492124 | 593.249700 | 1184.508108 | 592.757692 | Q | *1147.556456* | 574.281866 | 1130.529907 | 565.768592 | 1129.545891 | 565.276584 | 7 |
| 8 | **1273.555787** | 637.281532 | 1256.529238 | 628.768257 | 1255.545222 | 628.276249 | A | *708.331130* | 354.669203 | 691.304581 | 346.155929 | 690.320565 | 345.663921 | 6 |
| 9 | 1370.608551 | 685.807914 | 1353.582002 | 677.294639 | 1352.597986 | 676.802631 | P | 637.294016 | 319.150646 | 620.267467 | 310.637372 | 619.283451 | 310.145364 | 5 |
| 10 | **1457.640579** | 729.323928 | 1440.614030 | 720.810653 | 1439.630014 | 720.318645 | S | *540.241252* | 270.624264 | 523.214703 | 262.110990 | 522.230687 | 261.618982 | 4 |
| 11 | **1572.667522** | 786.837399 | 1555.640973 | 778.324125 | 1554.656957 | 777.832117 | D | *453.209224* | 227.108250 | 436.182675 | 218.594976 | 435.198659 | 218.102968 | 3 |
| 12 | 1735.730851 | 868.369064 | 1718.704302 | 859.855789 | 1717.720286 | 859.363781 | Y | *338.182281* | 169.594778 | 321.155732 | 161.081504 | | | 2 |
| 13 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 51.1 | 1908.835236 | 0.014226 | YSSDYFQAPSDYR |

**Mascot:** http://www.matrixscience.com/

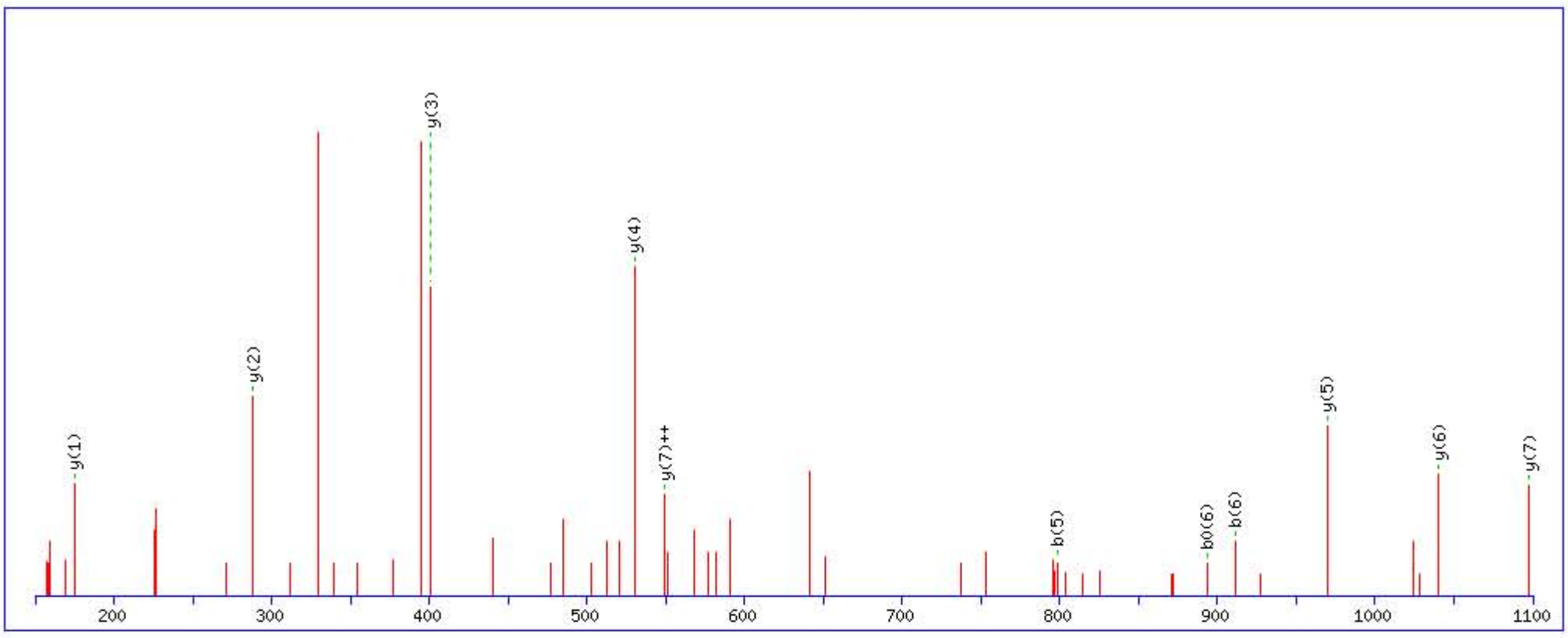
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TGAQELLR**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

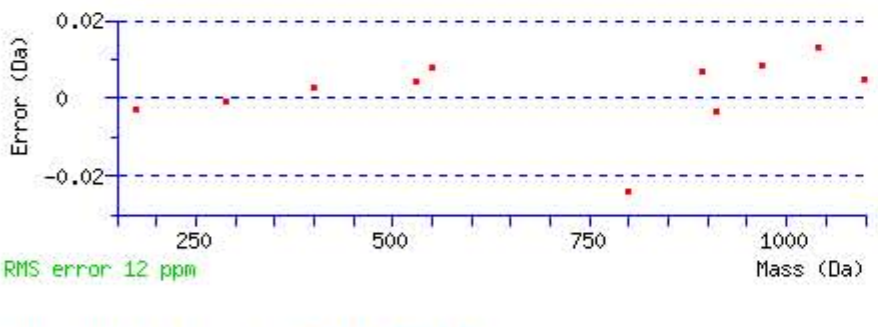
Match to Query 20501: 1197.658968 from(599.836760,2+) rtinseconds(1896) index(4916)
Title: Locus:1.1.1.1937.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

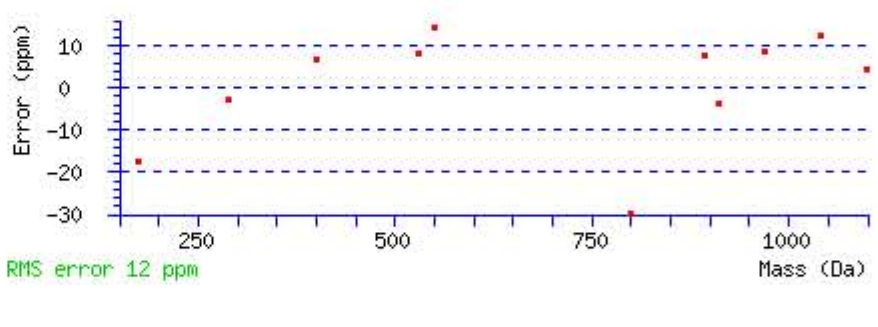
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1197.653961
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 49 **Expect:** 0.00031
**Matches :** 11/72 fragment ions using 19 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 8 |
| 2 | 159.076419 | 80.041847 | | | 141.065854 | 71.036565 | G | *1097.613577* | 549.310427 | 1080.587028 | 540.797152 | 1079.603012 | 540.305144 | 7 |
| 3 | 230.113533 | 115.560404 | | | 212.102968 | 106.555122 | A | *1040.592113* | 520.799695 | 1023.565564 | 512.286420 | 1022.581548 | 511.794412 | 6 |
| 4 | 669.338859 | 335.173068 | 652.312310 | 326.659793 | 651.328294 | 326.167785 | Q | *969.554999* | 485.281138 | 952.528450 | 476.767863 | 951.544434 | 476.275855 | 5 |
| 5 | **798.381452** | 399.694364 | 781.354903 | 391.181090 | 780.370887 | 390.689082 | E | *530.329673* | 265.668475 | 513.303124 | 257.155200 | 512.319108 | 256.663192 | 4 |
| 6 | **911.465516** | 456.236396 | 894.438967 | 447.723122 | 893.454951 | 447.231114 | L | *401.287080* | 201.147178 | 384.260531 | 192.633903 | | | 3 |
| 7 | 1024.549580 | 512.778428 | 1007.523031 | 504.265153 | 1006.539015 | 503.773145 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.8 | 1197.653961 | 0.005007 | TGAQELLR |
| 23.9 | 1197.653961 | 0.005007 | QTQEILR |
| 16.4 | 1197.653961 | 0.005007 | QTQEILR |
| 15.6 | 1197.646545 | 0.012423 | RSPQEAEILR |
| 15.1 | 1197.653961 | 0.005007 | TQQLLER |
| 13.4 | 1197.669220 | -0.010252 | TLWAQLR |
| 13.2 | 1197.653961 | 0.005007 | QTEQLLR |
| 11.2 | 1197.653961 | 0.005007 | QTEQLLR |
| 11.0 | 1197.669220 | -0.010252 | WTLQAIR |
| 9.8 | 1197.669220 | -0.010252 | QWTALIR |

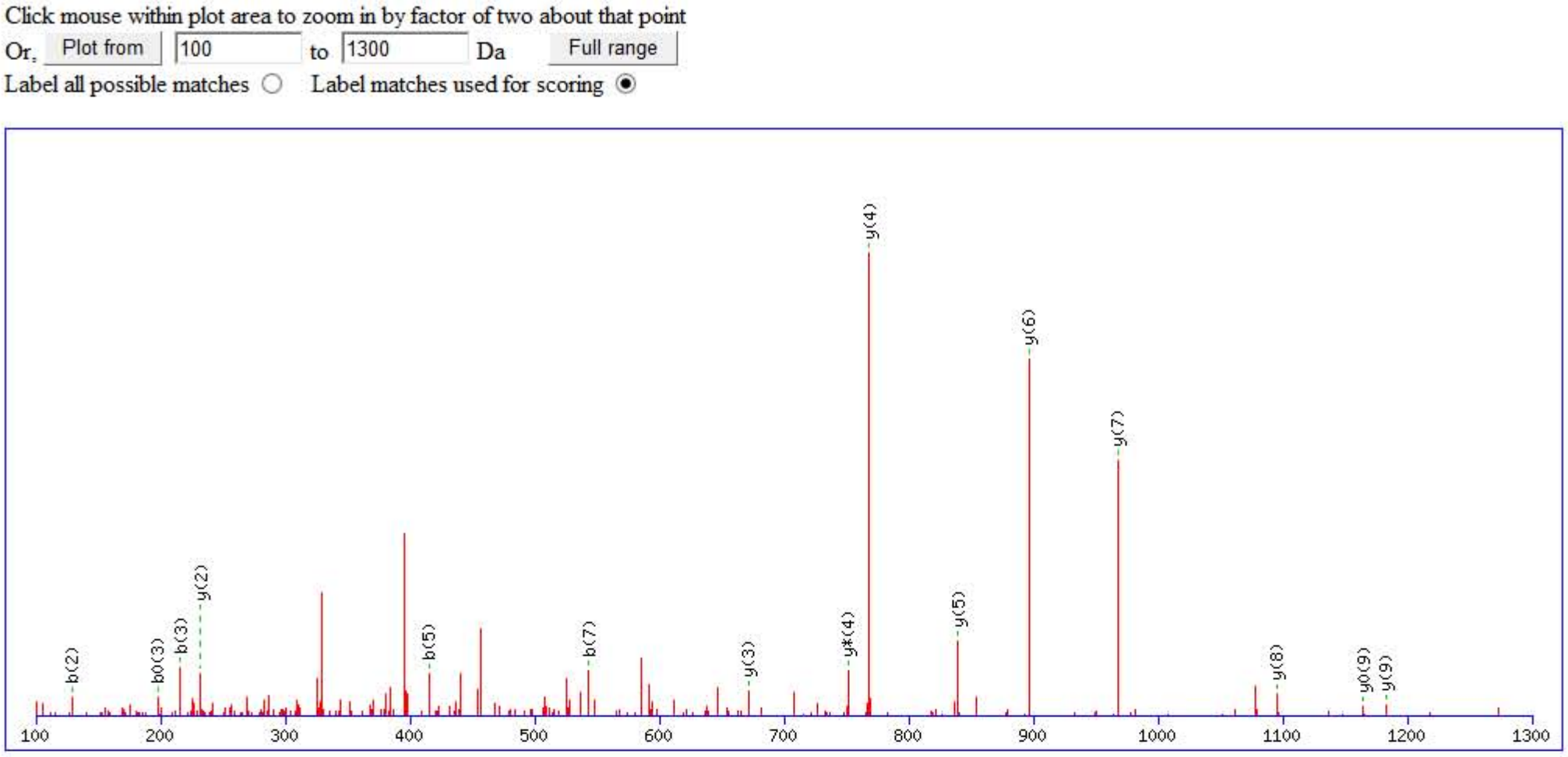
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GASQAGAPQGR**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

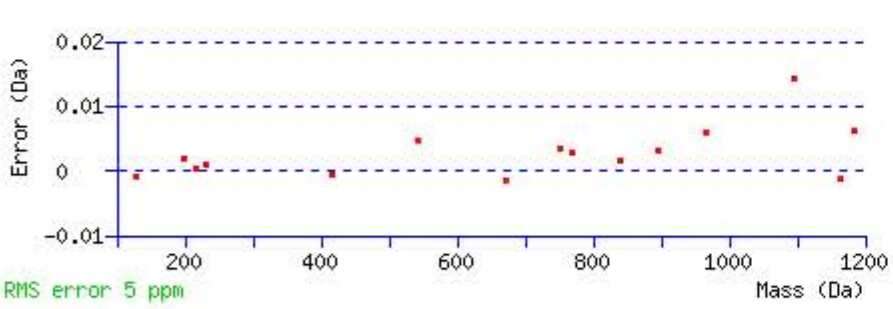
Match to Query 23488: 1309.659868 from(655.837210,2+) rtinseconds(1249) index(1079)
Title: Locus:1.1.1.1711.23 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

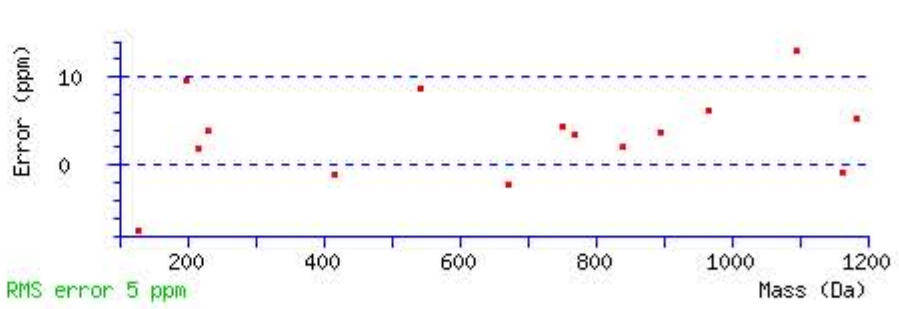
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1309.656097
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 62 **Expect:** 8.8e-006
**Matches :** 15/94 fragment ions using 24 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 11 |
| 2 | 129.065854 | 65.036565 | | | | | A | 1253.641918 | 627.324597 | 1236.615369 | 618.811323 | 1235.631353 | 618.319315 | 10 |
| 3 | 216.097882 | 108.552579 | | | 198.087317 | 99.547296 | S | *1182.604804* | 591.806040 | 1165.578255 | 583.292765 | 1164.594239 | 582.800757 | 9 |
| 4 | 344.156460 | 172.581868 | 327.129911 | 164.068593 | 326.145895 | 163.576585 | Q | *1095.572776* | 548.290026 | 1078.546227 | 539.776752 | | | 8 |
| 5 | 415.193574 | 208.100425 | 398.167025 | 199.587150 | 397.183009 | 199.095142 | A | *967.514198* | 484.260737 | 950.487649 | 475.747462 | | | 7 |
| 6 | 472.215038 | 236.611157 | 455.188489 | 228.097882 | 454.204473 | 227.605874 | G | *896.477084* | 448.742180 | 879.450535 | 440.228906 | | | 6 |
| 7 | 543.252152 | 272.129714 | 526.225603 | 263.616440 | 525.241587 | 263.124432 | A | *839.455620* | 420.231448 | 822.429071 | 411.718173 | | | 5 |
| 8 | 640.304916 | 320.656096 | 623.278367 | 312.142822 | 622.294351 | 311.650814 | P | *768.418506* | 384.712891 | 751.391957 | 376.199616 | | | 4 |
| 9 | 1079.530242 | 540.268759 | 1062.503693 | 531.755485 | 1061.519677 | 531.263477 | Q | *671.365742* | 336.186509 | 654.339193 | 327.673234 | | | 3 |
| 10 | 1136.551706 | 568.779491 | 1119.525157 | 560.266217 | 1118.541141 | 559.774208 | G | *232.140416* | 116.573846 | 215.113867 | 108.060571 | | | 2 |
| 11 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 61.6 | 1309.656097 | 0.003771 | GASQAGAPQGR |
| 19.4 | 1309.656097 | 0.003771 | GASQAGAPQGR |
| 7.2 | 1309.648682 | 0.011186 | KSTHRNPEDAR |
| 0.0 | 1309.654739 | 0.005129 | LTESNSAMVKSK |

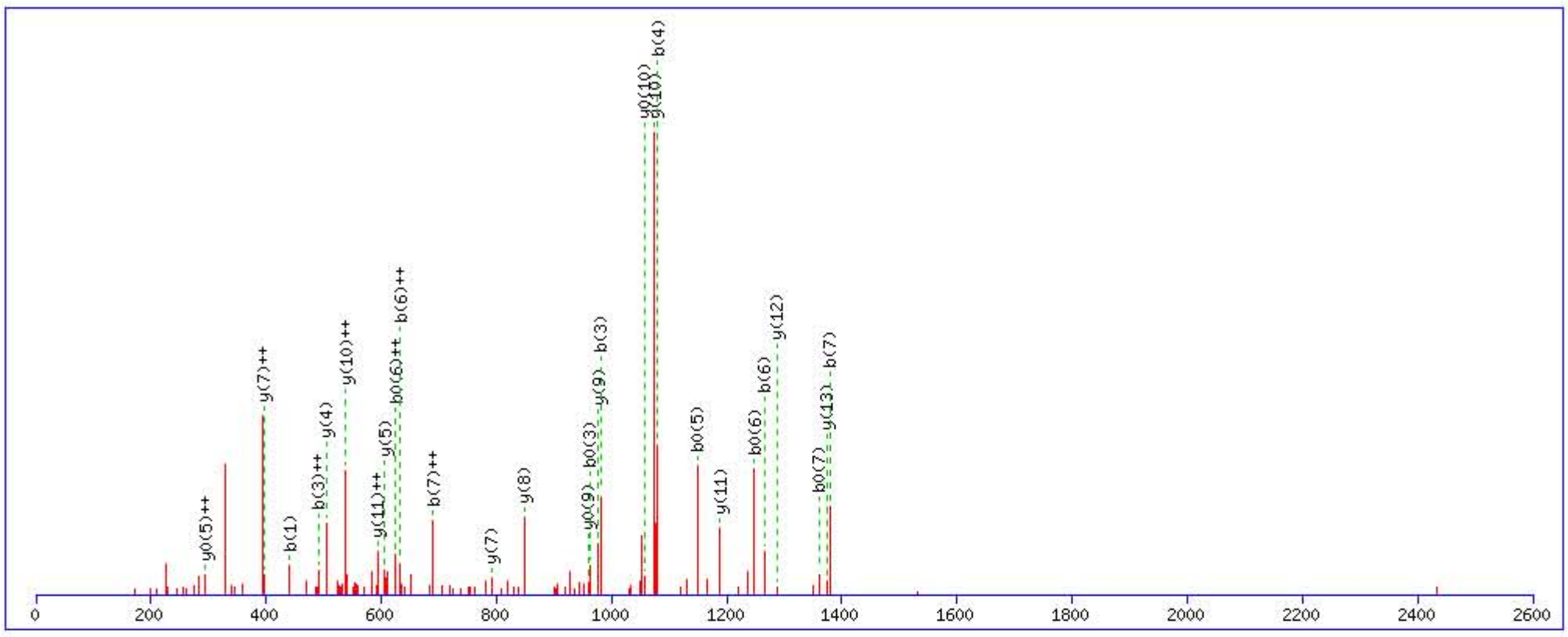
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QTQVSVLPEGGETPLFK**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

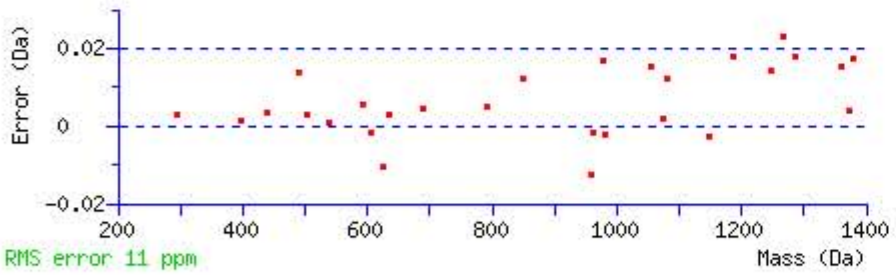
Match to Query 53014: 2451.312012 from(818.111280,3+) rtinseconds(2608) index(8836)
Title: Locus:1.1.1.2185.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

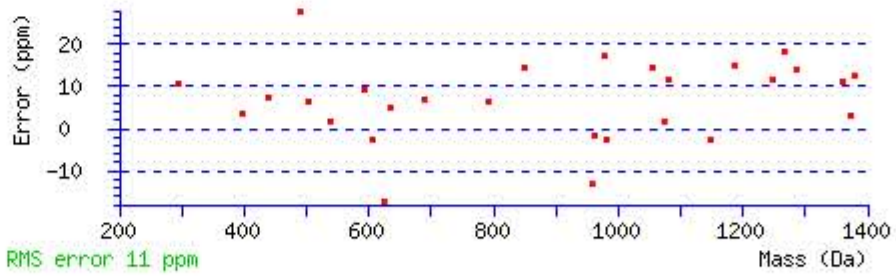
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2451.290588
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Q3** : Biotin:Thermo-21345 (Q)
**Ions Score:** 50 **Expect:** 0.00017
**Matches** : 29/182 fragment ions using 52 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **440.232602** | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 17 |
| 2 | 541.280281 | 271.143779 | 524.253732 | 262.630504 | 523.269716 | 262.138496 | T | 2013.072528 | 1007.039902 | 1996.045979 | 998.526628 | 1995.061963 | 998.034620 | 16 |
| 3 | **980.505607** | **490.756442** | 963.479058 | 482.243167 | 962.495042 | 481.751159 | Q | 1912.024849 | 956.516063 | 1894.998300 | 948.002788 | 1894.014284 | 947.510780 | 15 |
| 4 | **1079.574021** | 540.290649 | 1062.547472 | 531.777374 | 1061.563456 | 531.285366 | V | 1472.799523 | 736.903400 | 1455.772974 | 728.390125 | 1454.788958 | 727.898117 | 14 |
| 5 | 1166.606049 | 583.806663 | 1149.579500 | 575.293388 | 1148.595484 | 574.801380 | S | *1373.731109* | 687.369193 | 1356.704560 | 678.855918 | 1355.720544 | 678.363910 | 13 |
| 6 | **1265.674463** | **633.340870** | 1248.647914 | 624.827595 | 1247.663898 | 624.335587 | V | *1286.699081* | 643.853179 | 1269.672532 | 635.339904 | 1268.688516 | 634.847896 | 12 |
| 7 | **1378.758527** | **689.882902** | 1361.731978 | 681.369627 | 1360.747962 | 680.877619 | L | *1187.630667* | 594.318971 | 1170.604118 | 585.805697 | 1169.620102 | 585.313689 | 11 |
| 8 | 1475.811291 | 738.409284 | 1458.784742 | 729.896009 | 1457.800726 | 729.404001 | P | *1074.546603* | 537.776940 | 1057.520054 | 529.263665 | 1056.536038 | 528.771657 | 10 |
| 9 | 1604.853884 | 802.930580 | 1587.827335 | 794.417306 | 1586.843319 | 793.925298 | E | *977.493839* | 489.250558 | 960.467290 | 480.737283 | 959.483274 | 480.245275 | 9 |
| 10 | 1661.875348 | 831.441312 | 1644.848799 | 822.928038 | 1643.864783 | 822.436030 | G | *848.451246* | 424.729261 | 831.424697 | 416.215986 | 830.440681 | 415.723978 | 8 |
| 11 | 1718.896812 | 859.952044 | 1701.870263 | 851.438770 | 1700.886247 | 850.946762 | G | *791.429782* | 396.218529 | 774.403233 | 387.705254 | 773.419217 | 387.213246 | 7 |
| 12 | 1847.939405 | 924.473341 | 1830.912856 | 915.960066 | 1829.928840 | 915.468058 | E | 734.408318 | 367.707797 | 717.381769 | 359.194523 | 716.397753 | 358.702515 | 6 |
| 13 | 1948.987084 | 974.997180 | 1931.960535 | 966.483906 | 1930.976519 | 965.991898 | T | *605.365725* | 303.186500 | 588.339176 | 294.673226 | 587.355160 | 294.181218 | 5 |
| 14 | 2046.039848 | 1023.523562 | 2029.013299 | 1015.010288 | 2028.029283 | 1014.518280 | P | *504.318046* | 252.662661 | 487.291497 | 244.149386 | | | 4 |
| 15 | 2159.123912 | 1080.065594 | 2142.097363 | 1071.552319 | 2141.113347 | 1071.060311 | L | 407.265282 | 204.136279 | 390.238733 | 195.623004 | | | 3 |
| 16 | 2306.192326 | 1153.599801 | 2289.165777 | 1145.086526 | 2288.181761 | 1144.594518 | F | *294.181218* | 147.594247 | 277.154669 | 139.080972 | | | 2 |
| 17 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 50.4 | 2451.290588 | 0.021424 | QTQVSVLPEGGETPLFK |
| 9.7 | 2451.277130 | 0.034882 | GFPSDTQLLDLRRNHFPSVPR |
| 1.7 | 2451.330780 | -0.018768 | RQFQSQLADLQQLPDILK |
| 1.7 | 2451.330780 | -0.018768 | RQFQSQLADLQQLPDILK |

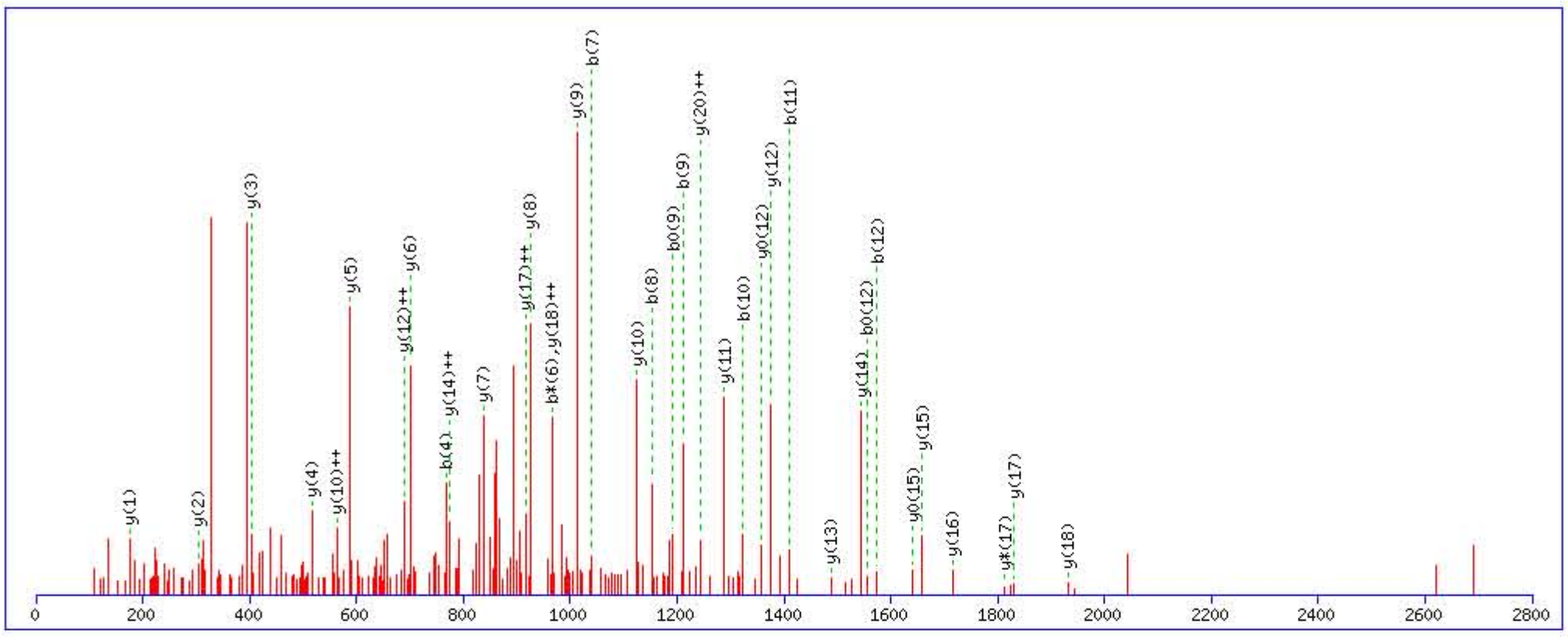
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DPDQTDGLGLSYLSSHIANVER**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

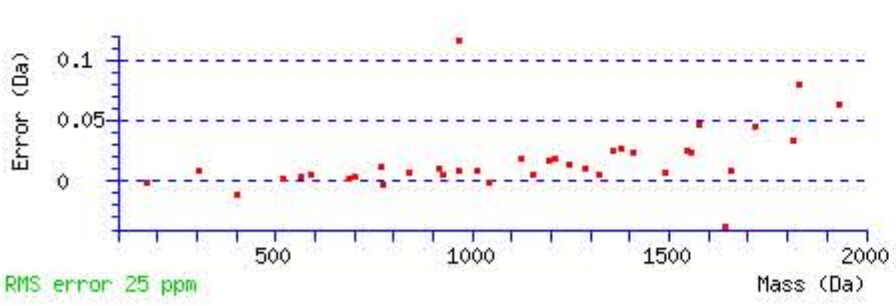
Match to Query 56330: 2697.340152 from(900.120660,3+) rtinseconds(2565) index(8607)
Title: Locus:1.1.1.2170.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

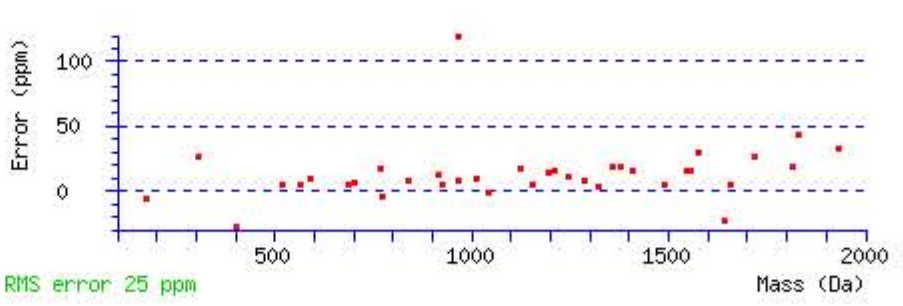
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2697.306824
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 134 **Expect:** 1.3e-012
**Matches :** 37/244 fragment ions using 57 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 22 |
| 2 | 213.086983 | 107.047129 | | | 195.076418 | 98.041847 | P | 2583.287164 | 1292.147220 | 2566.260615 | 1283.633945 | 2565.276599 | 1283.141937 | 21 |
| 3 | 328.113926 | 164.560601 | | | 310.103361 | 155.555319 | D | 2486.234400 | 1243.620838 | 2469.207851 | 1235.107563 | 2468.223835 | 1234.615555 | 20 |
| 4 | **767.339252** | 384.173264 | 750.312703 | 375.659989 | 749.328687 | 375.167982 | Q | 2371.207457 | 1186.107366 | 2354.180908 | 1177.594092 | 2353.196892 | 1177.102084 | 19 |
| 5 | 868.386931 | 434.697104 | 851.360382 | 426.183829 | 850.376366 | 425.691821 | T | *1931.982131* | 966.494704 | 1914.955582 | 957.981429 | 1913.971566 | 957.489421 | 18 |
| 6 | 983.413874 | 492.210575 | 966.387325 | 483.697300 | 965.403309 | 483.205292 | D | *1830.934452* | 915.970864 | 1813.907903 | 907.457590 | 1812.923887 | 906.965581 | 17 |
| 7 | **1040.435338** | 520.721307 | 1023.408789 | 512.208032 | 1022.424773 | 511.716025 | G | *1715.907509* | 858.457392 | 1698.880960 | 849.944118 | 1697.896944 | 849.452110 | 16 |
| 8 | **1153.519402** | 577.263339 | 1136.492853 | 568.750065 | 1135.508837 | 568.258056 | L | *1658.886045* | 829.946661 | 1641.859496 | 821.433386 | 1640.875480 | 820.941378 | 15 |
| 9 | **1210.540866** | 605.774071 | 1193.514317 | 597.260796 | 1192.530301 | 596.768788 | G | *1545.801981* | 773.404629 | 1528.775432 | 764.891354 | 1527.791416 | 764.399346 | 14 |
| 10 | **1323.624930** | 662.316103 | 1306.598381 | 653.802828 | 1305.614365 | 653.310820 | L | *1488.780517* | 744.893897 | 1471.753968 | 736.380622 | 1470.769952 | 735.888614 | 13 |
| 11 | **1410.656958** | 705.832117 | 1393.630409 | 697.318842 | 1392.646393 | 696.826834 | S | *1375.696453* | 688.351865 | 1358.669904 | 679.838590 | 1357.685888 | 679.346582 | 12 |
| 12 | **1573.720287** | 787.363781 | 1556.693738 | 778.850507 | 1555.709722 | 778.358499 | Y | *1288.664425* | 644.835851 | 1271.637876 | 636.322576 | 1270.653860 | 635.830568 | 11 |
| 13 | 1686.804351 | 843.905813 | 1669.777802 | 835.392539 | 1668.793786 | 834.900531 | L | *1125.601096* | 563.304186 | 1108.574547 | 554.790912 | 1107.590531 | 554.298904 | 10 |
| 14 | 1773.836379 | 887.421827 | 1756.809830 | 878.908553 | 1755.825814 | 878.416545 | S | *1012.517032* | 506.762154 | 995.490483 | 498.248880 | 994.506467 | 497.756872 | 9 |
| 15 | 1860.868407 | 930.937841 | 1843.841858 | 922.424567 | 1842.857842 | 921.932559 | S | *925.485004* | 463.246140 | 908.458455 | 454.732866 | 907.474439 | 454.240858 | 8 |
| 16 | 1997.927319 | 999.467297 | 1980.900770 | 990.954023 | 1979.916754 | 990.462015 | H | *838.452976* | 419.730126 | 821.426427 | 411.216852 | 820.442411 | 410.724844 | 7 |
| 17 | 2111.011383 | 1056.009329 | 2093.984834 | 1047.496055 | 2093.000818 | 1047.004047 | I | *701.394064* | 351.200670 | 684.367515 | 342.687396 | 683.383499 | 342.195388 | 6 |
| 18 | 2182.048497 | 1091.527886 | 2165.021948 | 1083.014612 | 2164.037932 | 1082.522604 | A | *588.310000* | 294.658638 | 571.283451 | 286.145364 | 570.299435 | 285.653356 | 5 |
| 19 | 2296.091424 | 1148.549350 | 2279.064875 | 1140.036075 | 2278.080859 | 1139.544067 | N | *517.272886* | 259.140081 | 500.246337 | 250.626806 | 499.262321 | 250.134798 | 4 |
| 20 | 2395.159838 | 1198.083557 | 2378.133289 | 1189.570282 | 2377.149273 | 1189.078274 | V | *403.229959* | 202.118617 | 386.203410 | 193.605343 | 385.219394 | 193.113335 | 3 |
| 21 | 2524.202431 | 1262.604853 | 2507.175882 | 1254.091579 | 2506.191866 | 1253.599571 | E | *304.161545* | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 22 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 133.7 | 2697.306824 | 0.033328 | DPDQTDGLGLSYLSSHIANVER |

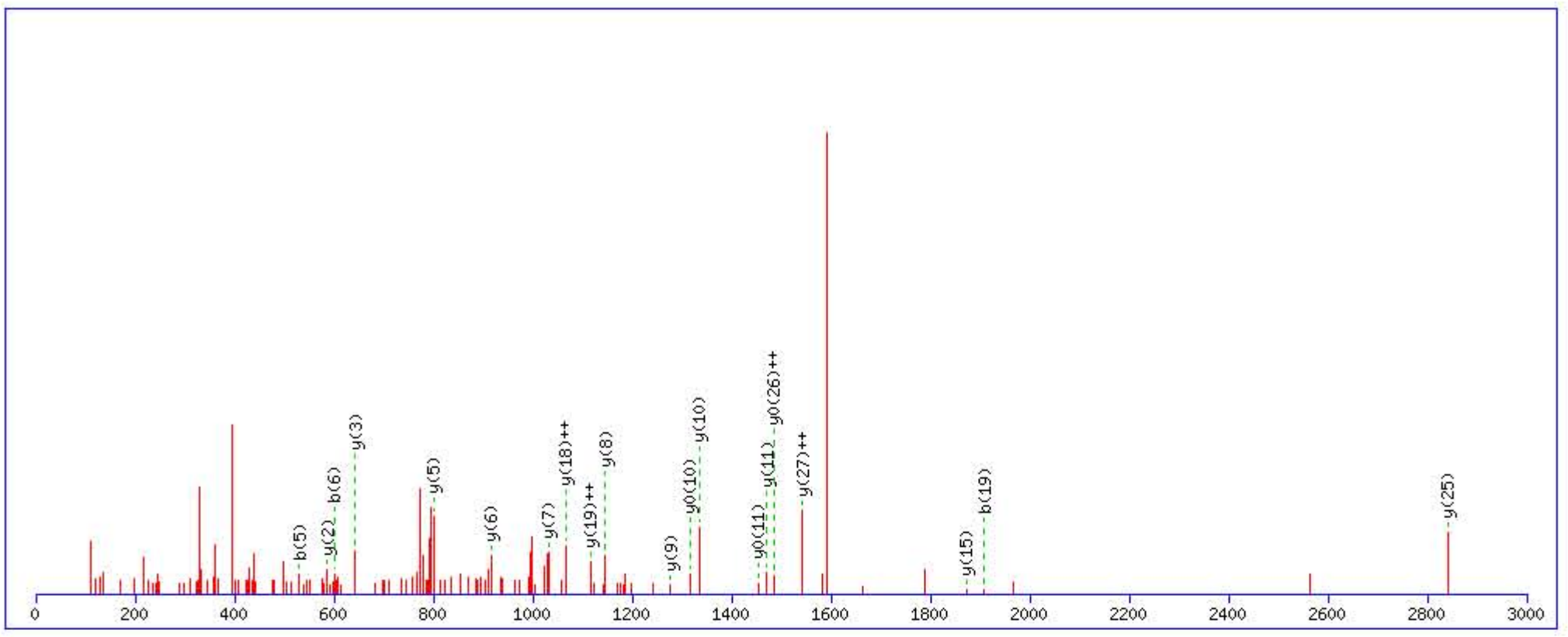
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VPFDAATLHTSTAMAAQHGMDDDGTGQK**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

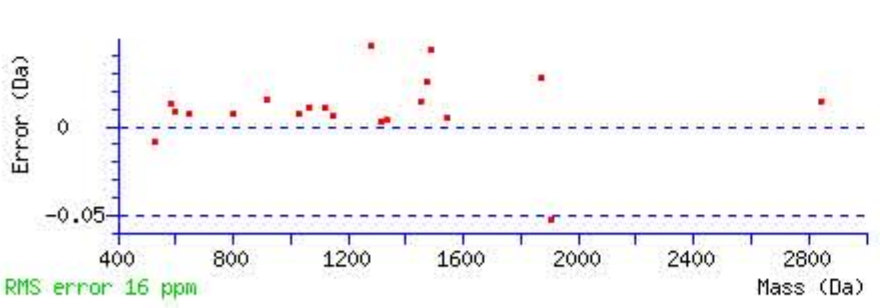
Match to Query 61546: 3183.465256 from(796.873590,4+) rtinseconds(1968) index(5482)
Title: Locus:1.1.1.1962.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

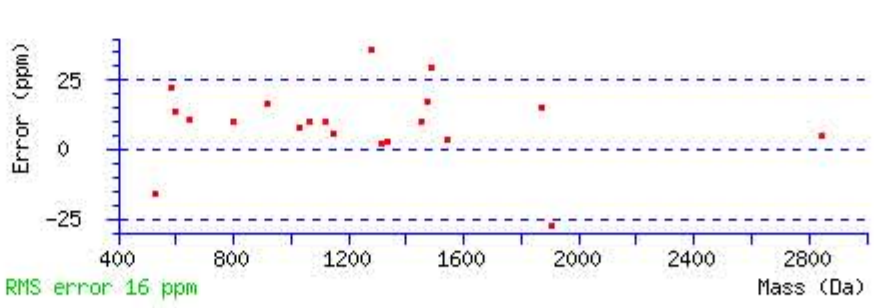
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3183.442383
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q27 : Biotin:Thermo-21345 (Q)
**Ions Score:** 41 **Expect:** 0.001
**Matches :** 20/280 fragment ions using 50 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 28 |
| 2 | 197.128454 | 99.067865 | | | | | P | 3085.381222 | 1543.194249 | 3068.354673 | 1534.680974 | 3067.370657 | 1534.188966 | 27 |
| 3 | 344.196868 | 172.602072 | | | | | F | 2988.328458 | 1494.667867 | 2971.301909 | 1486.154592 | 2970.317893 | 1485.662584 | 26 |
| 4 | 459.223811 | 230.115543 | | | 441.213246 | 221.110261 | D | *2841.260044* | 1421.133660 | 2824.233495 | 1412.620385 | 2823.249479 | 1412.128377 | 25 |
| 5 | 530.260925 | 265.634101 | | | 512.250360 | 256.628818 | A | 2726.233101 | 1363.620188 | 2709.206552 | 1355.106914 | 2708.222536 | 1354.614906 | 24 |
| 6 | 601.298039 | 301.152658 | | | 583.287474 | 292.147375 | A | 2655.195987 | 1328.101631 | 2638.169438 | 1319.588357 | 2637.185422 | 1319.096349 | 23 |
| 7 | 702.345718 | 351.676497 | | | 684.335153 | 342.671215 | T | 2584.158873 | 1292.583074 | 2567.132324 | 1284.069800 | 2566.148308 | 1283.577792 | 22 |
| 8 | 815.429782 | 408.218529 | | | 797.419217 | 399.213247 | L | 2483.111194 | 1242.059235 | 2466.084645 | 1233.545960 | 2465.100629 | 1233.053952 | 21 |
| 9 | 952.488694 | 476.747985 | | | 934.478129 | 467.742703 | H | 2370.027130 | 1185.517203 | 2353.000581 | 1177.003928 | 2352.016565 | 1176.511920 | 20 |
| 10 | 1053.536373 | 527.271824 | | | 1035.525808 | 518.266542 | T | 2232.968218 | 1116.987747 | 2215.941669 | 1108.474472 | 2214.957653 | 1107.982464 | 19 |
| 11 | 1140.568401 | 570.787839 | | | 1122.557836 | 561.782556 | S | 2131.920539 | 1066.463907 | 2114.893990 | 1057.950633 | 2113.909974 | 1057.458625 | 18 |
| 12 | 1241.616080 | 621.311678 | | | 1223.605515 | 612.306396 | T | 2044.888511 | 1022.947893 | 2027.861962 | 1014.434619 | 2026.877946 | 1013.942611 | 17 |
| 13 | 1312.653194 | 656.830235 | | | 1294.642629 | 647.824952 | A | 1943.840832 | 972.424054 | 1926.814283 | 963.910779 | 1925.830267 | 963.418771 | 16 |
| 14 | 1443.693679 | 722.350478 | | | 1425.683114 | 713.345195 | M | *1872.803718* | 936.905497 | 1855.777169 | 928.392222 | 1854.793153 | 927.900214 | 15 |
| 15 | 1514.730793 | 757.869035 | | | 1496.720228 | 748.863752 | A | 1741.763233 | 871.385254 | 1724.736684 | 862.871980 | 1723.752668 | 862.379972 | 14 |
| 16 | 1585.767907 | 793.387591 | | | 1567.757342 | 784.382309 | A | 1670.726119 | 835.866697 | 1653.699570 | 827.353423 | 1652.715554 | 826.861415 | 13 |
| 17 | 1713.826485 | 857.416880 | 1696.799936 | 848.903606 | 1695.815920 | 848.411598 | Q | 1599.689005 | 800.348140 | 1582.662456 | 791.834866 | 1581.678440 | 791.342858 | 12 |
| 18 | 1850.885397 | 925.946336 | 1833.858848 | 917.433062 | 1832.874832 | 916.941054 | H | *1471.630427* | 736.318851 | 1454.603878 | 727.805577 | 1453.619862 | 727.313569 | 11 |
| 19 | 1907.906861 | 954.457068 | 1890.880312 | 945.943794 | 1889.896296 | 945.451786 | G | *1334.571515* | 667.789395 | 1317.544966 | 659.276121 | 1316.560950 | 658.784113 | 10 |
| 20 | 2038.947346 | 1019.977311 | 2021.920797 | 1011.464036 | 2020.936781 | 1010.972028 | M | *1277.550051* | 639.278663 | 1260.523502 | 630.765389 | 1259.539486 | 630.273381 | 9 |
| 21 | 2153.974289 | 1077.490782 | 2136.947740 | 1068.977508 | 2135.963724 | 1068.485500 | D | *1146.509566* | 573.758421 | 1129.483017 | 565.245146 | 1128.499001 | 564.753138 | 8 |
| 22 | 2269.001232 | 1135.004254 | 2251.974683 | 1126.490979 | 2250.990667 | 1125.998971 | D | *1031.482623* | 516.244949 | 1014.456074 | 507.731675 | 1013.472058 | 507.239667 | 7 |
| 23 | 2384.028175 | 1192.517725 | 2367.001626 | 1184.004451 | 2366.017610 | 1183.512443 | D | *916.455680* | 458.731478 | 899.429131 | 450.218203 | 898.445115 | 449.726195 | 6 |
| 24 | 2441.049639 | 1221.028457 | 2424.023090 | 1212.515183 | 2423.039074 | 1212.023175 | G | *801.428737* | 401.218007 | 784.402188 | 392.704732 | 783.418172 | 392.212724 | 5 |
| 25 | 2542.097318 | 1271.552297 | 2525.070769 | 1263.039022 | 2524.086753 | 1262.547014 | T | 744.407273 | 372.707275 | 727.380724 | 364.194000 | 726.396708 | 363.701992 | 4 |
| 26 | 2599.118782 | 1300.063029 | 2582.092233 | 1291.549754 | 2581.108217 | 1291.057746 | G | *643.359594* | 322.183435 | 626.333045 | 313.670161 | | | 3 |
| 27 | 3038.344108 | 1519.675692 | 3021.317559 | 1511.162417 | 3020.333543 | 1510.670409 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 28 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 41.2 | 3183.442383 | 0.022873 | VPFDAATLHTSTAMAAQHGMDDDGTGQK |
| 9.6 | 3183.442383 | 0.022873 | VPFDAATLHTSTAMAAQHGMDDDGTGQK |

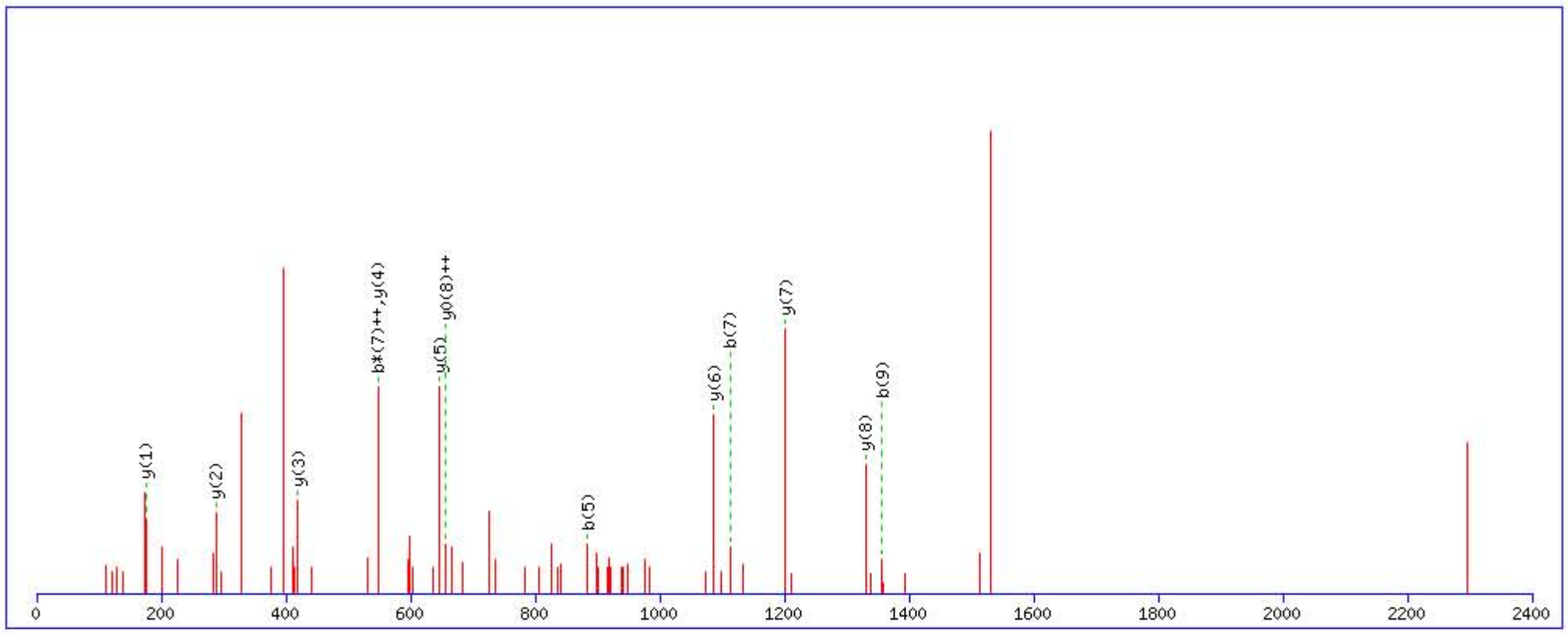
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SLEDQVEMLR**
Found in **GLU2B_HUMAN**, Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2

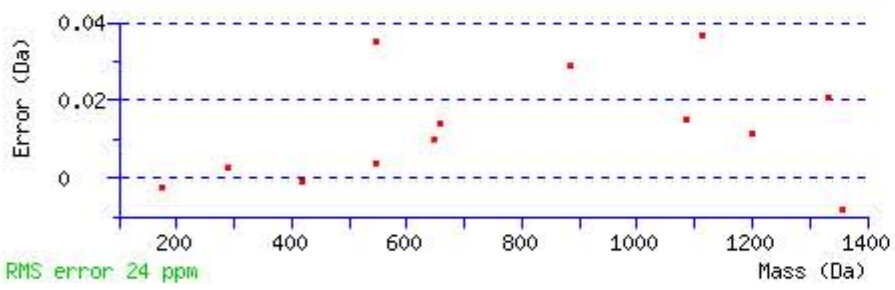
Match to Query 32031: 1529.780108 from(765.897330,2+) rtinseconds(2367) index(52662)
Title: Locus:1.1.1.2061.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

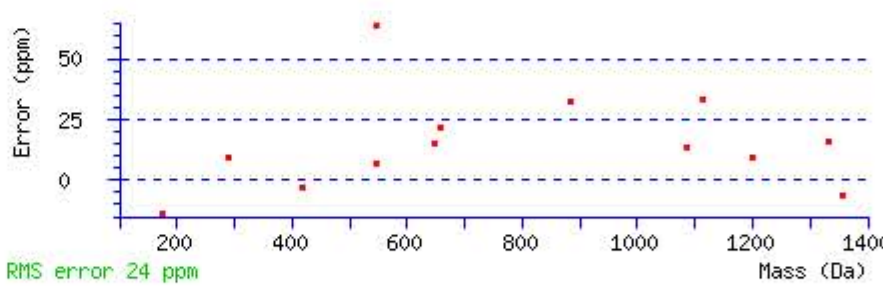
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1529.758163
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 47 **Expect:** 0.00033
**Matches :** 13/94 fragment ions using 26 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 10 |
| 2 | 201.123368 | 101.065322 | | | 183.112803 | 92.060039 | L | 1443.733434 | 722.370355 | 1426.706885 | 713.857080 | 1425.722869 | 713.365072 | 9 |
| 3 | 330.165961 | 165.586618 | | | 312.155396 | 156.581336 | E | *1330.649370* | 665.828323 | 1313.622821 | 657.315048 | 1312.638805 | 656.823040 | 8 |
| 4 | 445.192904 | 223.100090 | | | 427.182339 | 214.094808 | D | *1201.606777* | 601.307026 | 1184.580228 | 592.793752 | 1183.596212 | 592.301744 | 7 |
| 5 | **884.418230** | 442.712753 | 867.391681 | 434.199479 | 866.407665 | 433.707471 | Q | *1086.579834* | 543.793555 | 1069.553285 | 535.280281 | 1068.569269 | 534.788272 | 6 |
| 6 | 983.486644 | 492.246960 | 966.460095 | 483.733686 | 965.476079 | 483.241678 | V | *647.354508* | 324.180892 | 630.327959 | 315.667617 | 629.343943 | 315.175609 | 5 |
| 7 | **1112.529237** | 556.768257 | 1095.502688 | 548.254982 | 1094.518672 | 547.762974 | E | *548.286094* | 274.646685 | 531.259545 | 266.133410 | 530.275529 | 265.641402 | 4 |
| 8 | 1243.569722 | 622.288499 | 1226.543173 | 613.775225 | 1225.559157 | 613.283216 | M | *419.243501* | 210.125388 | 402.216952 | 201.612114 | | | 3 |
| 9 | **1356.653786** | 678.830531 | 1339.627237 | 670.317256 | 1338.643221 | 669.825248 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 10 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 47.0 | 1529.758163 | 0.021945 | SLEDQVEMLR |
| 9.4 | 1529.798386 | -0.018278 | SSLMPLRNDVDKR |
| 3.3 | 1529.780640 | -0.000532 | ATMVSQPSARR |
| 3.1 | 1529.798355 | -0.018247 | AEDLRREMIELR |
| 1.3 | 1529.787827 | -0.007719 | LSAFVDVGLYQYR |
| 0.9 | 1529.784637 | -0.004529 | FINSKCAKYMLR |
| 0.7 | 1529.772568 | 0.007540 | LSEDDTTHFKLPK |

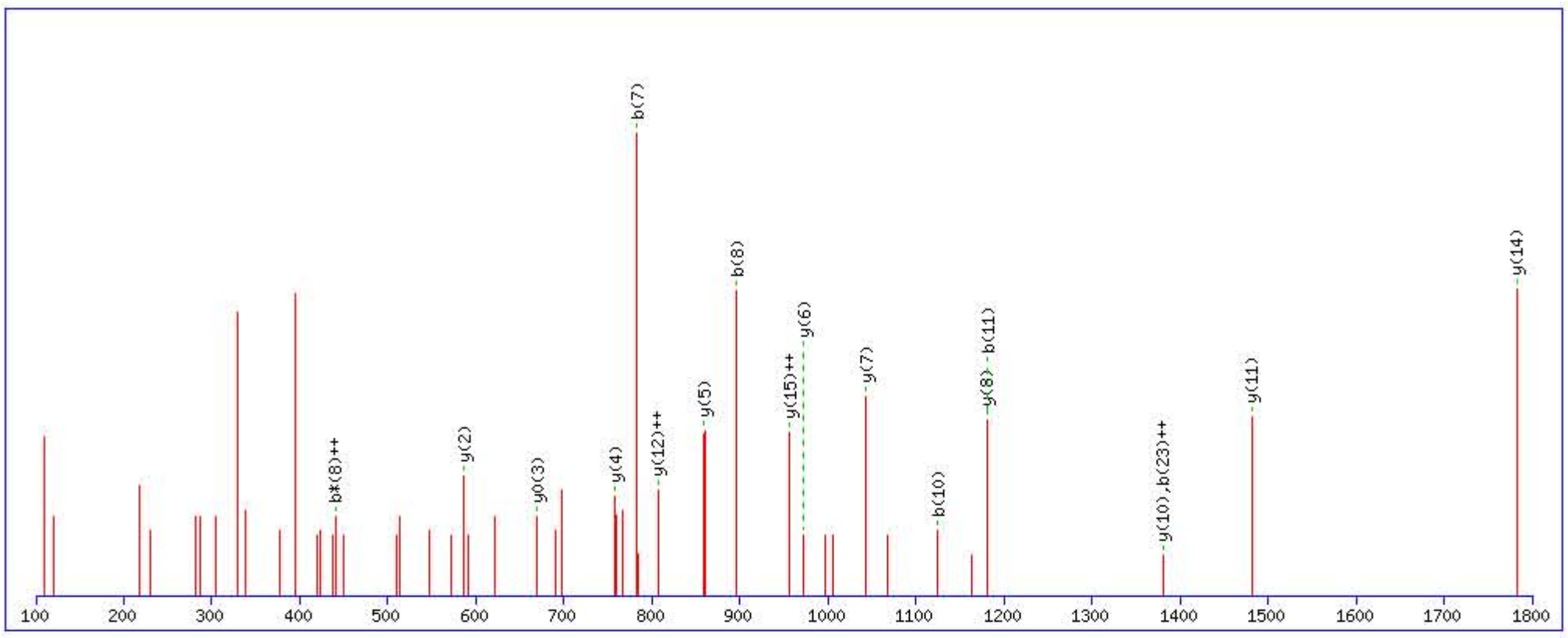
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VIHDNFGIVEGLMTTVHAITATQK**
Found in **G3P_HUMAN**, Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3

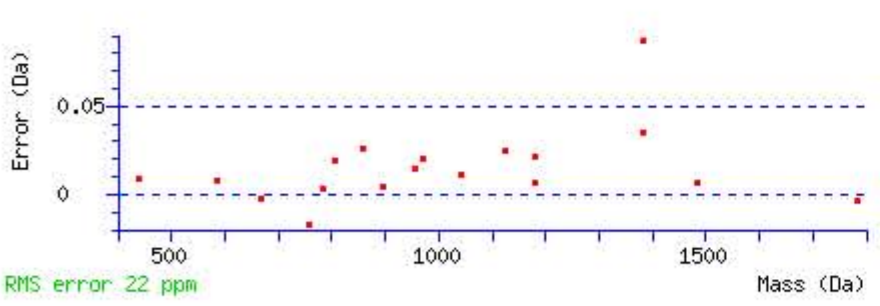
Match to Query 59134: 2905.559936 from(727.397260,4+) rtinseconds(3114) index(57835)
Title: Locus:1.1.1.2317.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

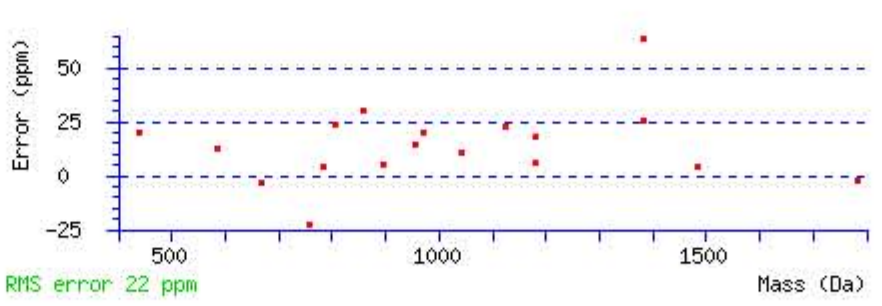
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2905.519424
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q23 : Biotin:Thermo-21345 (Q)
**Ions Score:** 40 **Expect:** 0.0015
**Matches :** 18/258 fragment ions using 34 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 24 |
| 2 | 213.159754 | 107.083515 | | | | | I | 2807.458272 | 1404.232774 | 2790.431723 | 1395.719499 | 2789.447707 | 1395.227491 | 23 |
| 3 | 350.218666 | 175.612971 | | | | | H | 2694.374208 | 1347.690742 | 2677.347659 | 1339.177467 | 2676.363643 | 1338.685459 | 22 |
| 4 | 465.245609 | 233.126443 | | | 447.235044 | 224.121160 | D | 2557.315296 | 1279.161286 | 2540.288747 | 1270.648011 | 2539.304731 | 1270.156003 | 21 |
| 5 | 579.288536 | 290.147906 | 562.261987 | 281.634632 | 561.277971 | 281.142624 | N | 2442.288353 | 1221.647814 | 2425.261804 | 1213.134540 | 2424.277788 | 1212.642532 | 20 |
| 6 | 726.356950 | 363.682113 | 709.330401 | 355.168838 | 708.346385 | 354.676830 | F | 2328.245426 | 1164.626351 | 2311.218877 | 1156.113076 | 2310.234861 | 1155.621068 | 19 |
| 7 | **783.378414** | 392.192845 | 766.351865 | 383.679571 | 765.367849 | 383.187563 | G | 2181.177012 | 1091.092144 | 2164.150463 | 1082.578869 | 2163.166447 | 1082.086861 | 18 |
| 8 | **896.462478** | 448.734877 | 879.435929 | 440.221603 | 878.451913 | 439.729595 | I | 2124.155548 | 1062.581412 | 2107.128999 | 1054.068137 | 2106.144983 | 1053.576129 | 17 |
| 9 | 995.530892 | 498.269084 | 978.504343 | 489.755810 | 977.520327 | 489.263802 | V | 2011.071484 | 1006.039380 | 1994.044935 | 997.526105 | 1993.060919 | 997.034097 | 16 |
| 10 | **1124.573485** | 562.790381 | 1107.546936 | 554.277106 | 1106.562920 | 553.785098 | E | 1912.003070 | 956.505173 | 1894.976521 | 947.991899 | 1893.992505 | 947.499890 | 15 |
| 11 | **1181.594949** | 591.301113 | 1164.568400 | 582.787838 | 1163.584384 | 582.295830 | G | *1782.960477* | 891.983876 | 1765.933928 | 883.470602 | 1764.949912 | 882.978594 | 14 |
| 12 | 1294.679013 | 647.843144 | 1277.652464 | 639.329870 | 1276.668448 | 638.837862 | L | 1725.939013 | 863.473144 | 1708.912464 | 854.959870 | 1707.928448 | 854.467862 | 13 |
| 13 | 1425.719498 | 713.363387 | 1408.692949 | 704.850113 | 1407.708933 | 704.358104 | M | 1612.854949 | 806.931113 | 1595.828400 | 798.417838 | 1594.844384 | 797.925830 | 12 |
| 14 | 1526.767177 | 763.887227 | 1509.740628 | 755.373952 | 1508.756612 | 754.881944 | T | *1481.814464* | 741.410870 | 1464.787915 | 732.897596 | 1463.803899 | 732.405588 | 11 |
| 15 | 1627.814856 | 814.411066 | 1610.788307 | 805.897792 | 1609.804291 | 805.405783 | T | *1380.766785* | 690.887031 | 1363.740236 | 682.373756 | 1362.756220 | 681.881748 | 10 |
| 16 | 1726.883270 | 863.945273 | 1709.856721 | 855.431999 | 1708.872705 | 854.939991 | V | 1279.719106 | 640.363191 | 1262.692557 | 631.849917 | 1261.708541 | 631.357909 | 9 |
| 17 | 1863.942182 | 932.474729 | 1846.915633 | 923.961455 | 1845.931617 | 923.469447 | H | *1180.650692* | 590.828984 | 1163.624143 | 582.315710 | 1162.640127 | 581.823701 | 8 |
| 18 | 1934.979296 | 967.993286 | 1917.952747 | 959.480012 | 1916.968731 | 958.988003 | A | *1043.591780* | 522.299528 | 1026.565231 | 513.786254 | 1025.581215 | 513.294245 | 7 |
| 19 | 2048.063360 | 1024.535318 | 2031.036811 | 1016.022044 | 2030.052795 | 1015.530036 | I | *972.554666* | 486.780971 | 955.528117 | 478.267697 | 954.544101 | 477.775689 | 6 |
| 20 | 2149.111039 | 1075.059157 | 2132.084490 | 1066.545883 | 2131.100474 | 1066.053875 | T | *859.470602* | 430.238939 | 842.444053 | 421.725665 | 841.460037 | 421.233657 | 5 |
| 21 | 2220.148153 | 1110.577714 | 2203.121604 | 1102.064440 | 2202.137588 | 1101.572432 | A | *758.422923* | 379.715100 | 741.396374 | 371.201825 | 740.412358 | 370.709817 | 4 |
| 22 | 2321.195832 | 1161.101554 | 2304.169283 | 1152.588279 | 2303.185267 | 1152.096271 | T | 687.385809 | 344.196543 | 670.359260 | 335.683268 | 669.375244 | 335.191260 | 3 |
| 23 | 2760.421158 | 1380.714217 | 2743.394609 | 1372.200942 | 2742.410593 | 1371.708934 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 24 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 40.4 | 2905.519424 | 0.040512 | VIHDNFGIVEGLMTTVHAITATQK |

**Mascot:** http://www.matrixscience.com/

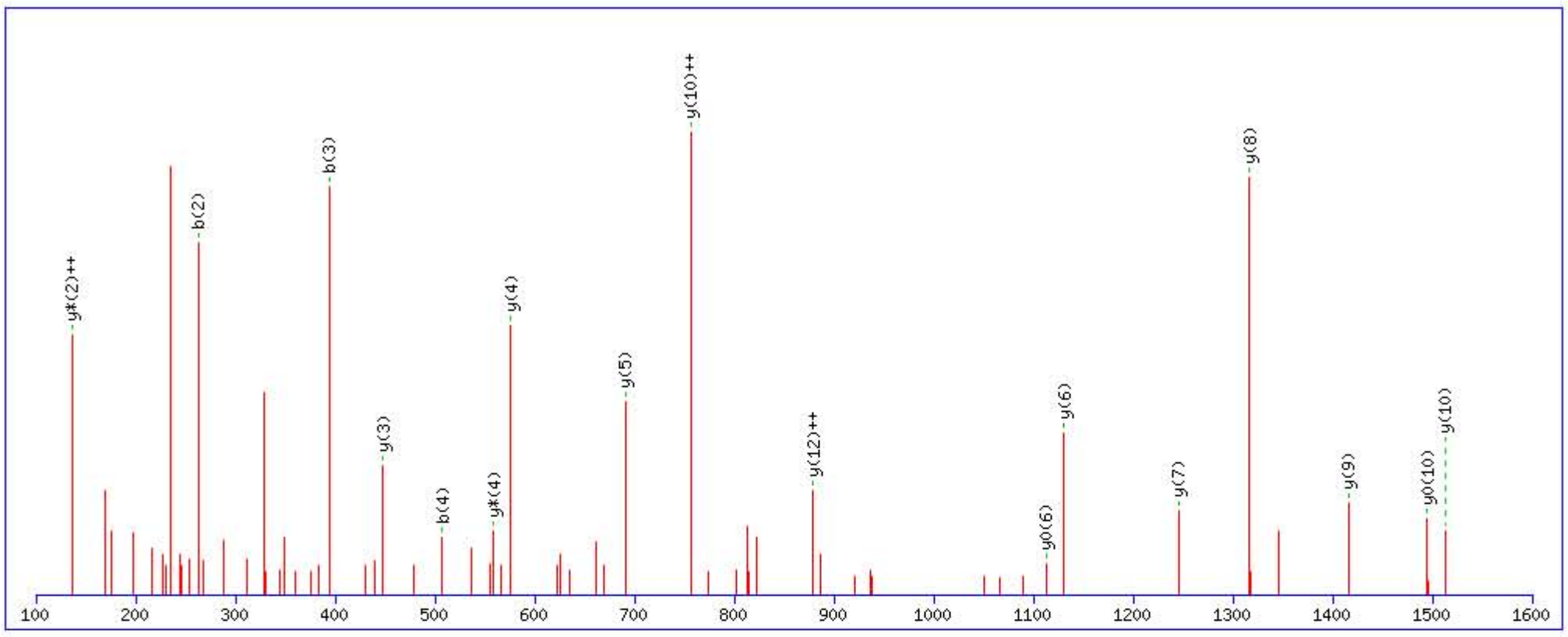
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YVMLPVADQDQCIR**
Found in **HPT_HUMAN**, Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1

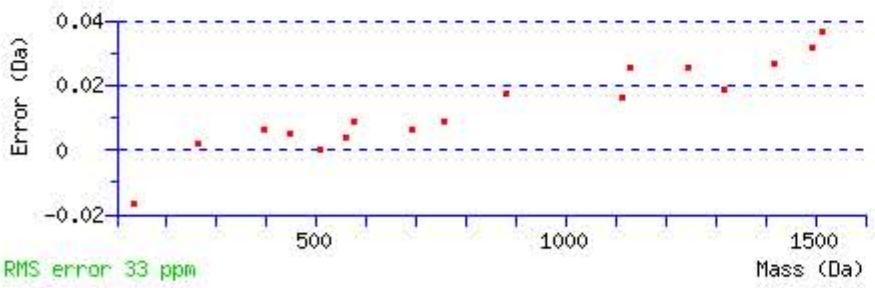
Match to Query 45031: 2017.998192 from(673.673340,3+) rtinseconds(2311) index(22075)
Title: Locus:1.1.1.3187.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

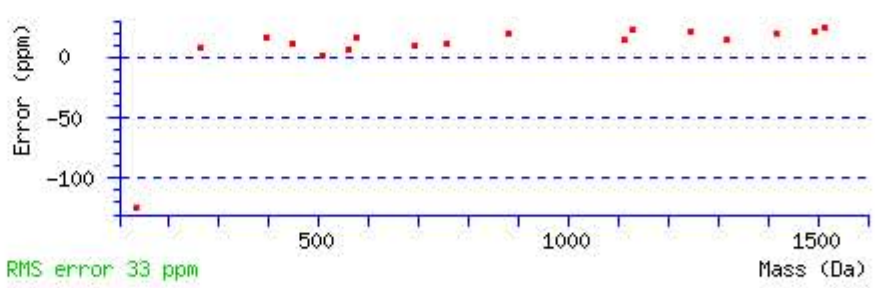
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2017.978760
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 50 **Expect:** 0.00024
**Matches :** 17/118 fragment ions using 26 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 14 |
| 2 | **263.139019** | 132.073148 | | | | | V | 1855.922710 | 928.464993 | 1838.896161 | 919.951719 | 1837.912145 | 919.459711 | 13 |
| 3 | **394.179504** | 197.593390 | | | | | M | 1756.854296 | 878.930786 | 1739.827747 | 870.417512 | 1738.843731 | 869.925504 | 12 |
| 4 | **507.263568** | 254.135422 | | | | | L | 1625.813811 | 813.410544 | 1608.787262 | 804.897269 | 1607.803246 | 804.405261 | 11 |
| 5 | 604.316332 | 302.661804 | | | | | P | *1512.729747* | 756.868512 | 1495.703198 | 748.355237 | 1494.719182 | 747.863229 | 10 |
| 6 | 703.384746 | 352.196011 | | | | | V | *1415.676983* | 708.342130 | 1398.650434 | 699.828855 | 1397.666418 | 699.336847 | 9 |
| 7 | 774.421860 | 387.714568 | | | | | A | *1316.608569* | 658.807923 | 1299.582020 | 650.294648 | 1298.598004 | 649.802640 | 8 |
| 8 | 889.448803 | 445.228040 | | | 871.438238 | 436.222757 | D | *1245.571455* | 623.289366 | 1228.544906 | 614.776091 | 1227.560890 | 614.284083 | 7 |
| 9 | 1328.674129 | 664.840703 | 1311.647580 | 656.327428 | 1310.663564 | 655.835420 | Q | *1130.544512* | 565.775894 | 1113.517963 | 557.262620 | 1112.533947 | 556.770612 | 6 |
| 10 | 1443.701072 | 722.354174 | 1426.674523 | 713.840900 | 1425.690507 | 713.348892 | D | *691.319186* | 346.163231 | 674.292637 | 337.649957 | 673.308621 | 337.157949 | 5 |
| 11 | 1571.759650 | 786.383463 | 1554.733101 | 777.870189 | 1553.749085 | 777.378181 | Q | *576.292243* | 288.649760 | 559.265694 | 280.136485 | | | 4 |
| 12 | 1731.790299 | 866.398788 | 1714.763750 | 857.885513 | 1713.779734 | 857.393505 | C | *448.233665* | 224.620470 | 431.207116 | 216.107196 | | | 3 |
| 13 | 1844.874363 | 922.940820 | 1827.847814 | 914.427545 | 1826.863798 | 913.935537 | I | 288.203016 | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 14 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 50.2 | 2017.978760 | 0.019432 | YVMLPVADQDQCIR |
| 38.0 | 2017.978760 | 0.019432 | YVMLPVADQDQCIR |

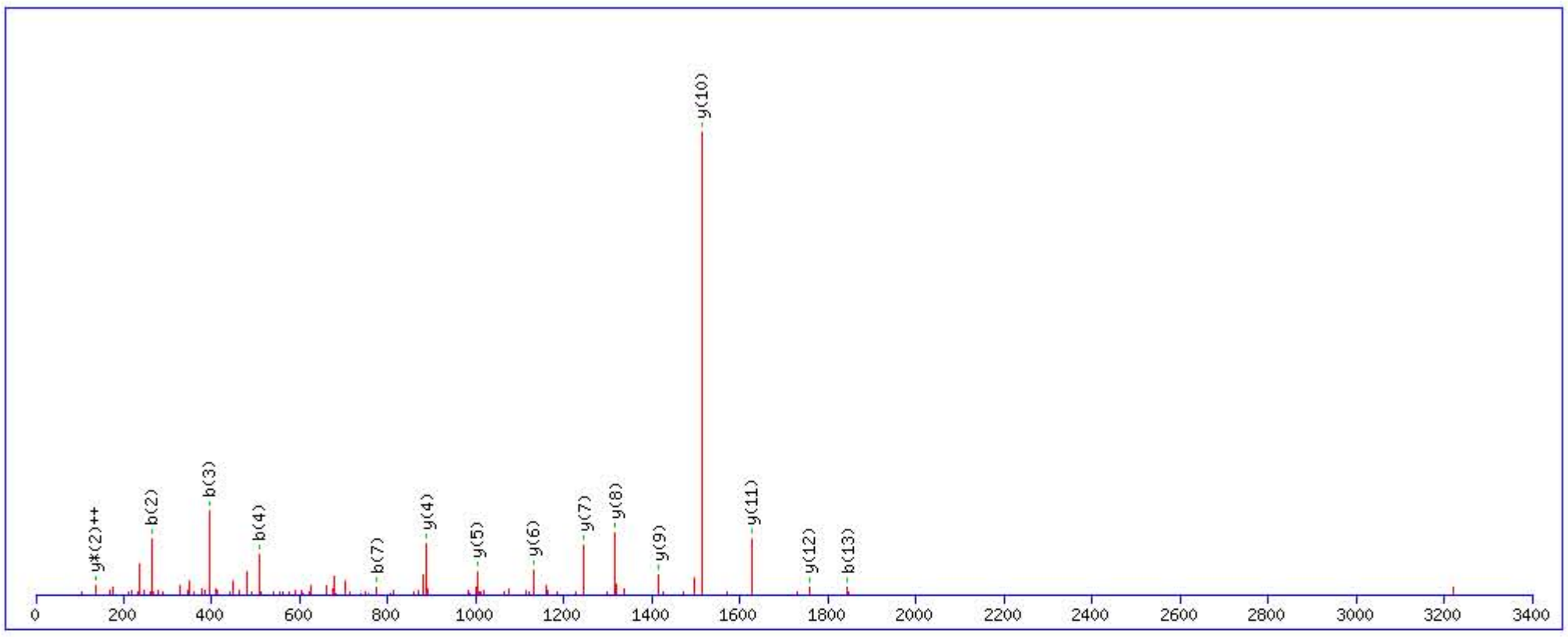
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YVMLPVADQDQCIR**
Found in **HPT_HUMAN**, Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1

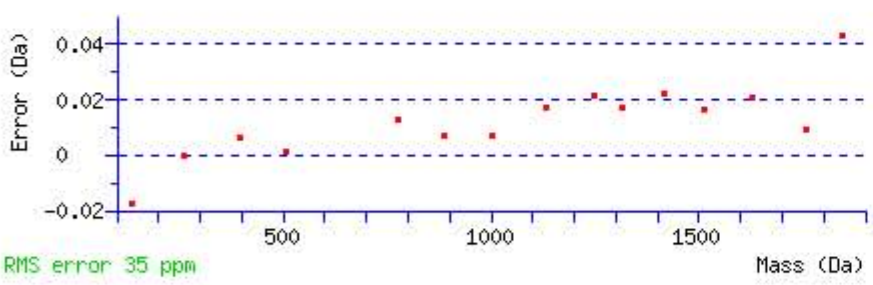
Match to Query 45033: 2018.003128 from(1010.008840,2+) rtinseconds(2290) index(7262)
Title: Locus:1.1.1.2074.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

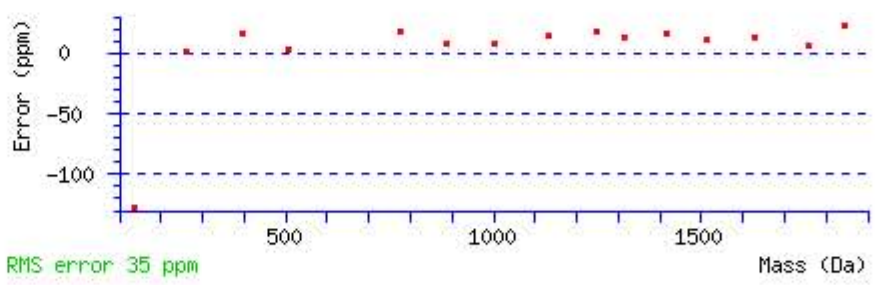
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2017.978760
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 77 **Expect:** 7.4e-008
**Matches :** 15/118 fragment ions using 18 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 14 |
| 2 | **263.139019** | 132.073148 | | | | | V | 1855.922710 | 928.464993 | 1838.896161 | 919.951719 | 1837.912145 | 919.459711 | 13 |
| 3 | **394.179504** | 197.593390 | | | | | M | *1756.854296* | 878.930786 | 1739.827747 | 870.417512 | 1738.843731 | 869.925504 | 12 |
| 4 | **507.263568** | 254.135422 | | | | | L | *1625.813811* | 813.410544 | 1608.787262 | 804.897269 | 1607.803246 | 804.405261 | 11 |
| 5 | 604.316332 | 302.661804 | | | | | P | *1512.729747* | 756.868512 | 1495.703198 | 748.355237 | 1494.719182 | 747.863229 | 10 |
| 6 | 703.384746 | 352.196011 | | | | | V | *1415.676983* | 708.342130 | 1398.650434 | 699.828855 | 1397.666418 | 699.336847 | 9 |
| 7 | **774.421860** | 387.714568 | | | | | A | *1316.608569* | 658.807923 | 1299.582020 | 650.294648 | 1298.598004 | 649.802640 | 8 |
| 8 | 889.448803 | 445.228040 | | | 871.438238 | 436.222757 | D | *1245.571455* | 623.289366 | 1228.544906 | 614.776091 | 1227.560890 | 614.284083 | 7 |
| 9 | 1017.507381 | 509.257329 | 1000.480832 | 500.744054 | 999.496816 | 500.252046 | Q | *1130.544512* | 565.775894 | 1113.517963 | 557.262620 | 1112.533947 | 556.770612 | 6 |
| 10 | 1132.534324 | 566.770800 | 1115.507775 | 558.257526 | 1114.523759 | 557.765517 | D | *1002.485934* | 501.746605 | 985.459385 | 493.233331 | 984.475369 | 492.741323 | 5 |
| 11 | 1571.759650 | 786.383463 | 1554.733101 | 777.870189 | 1553.749085 | 777.378181 | Q | *887.458991* | 444.233134 | 870.432442 | 435.719859 | | | 4 |
| 12 | 1731.790299 | 866.398788 | 1714.763750 | 857.885513 | 1713.779734 | 857.393505 | C | 448.233665 | 224.620470 | 431.207116 | 216.107196 | | | 3 |
| 13 | **1844.874363** | 922.940820 | 1827.847814 | 914.427545 | 1826.863798 | 913.935537 | I | 288.203016 | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 14 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 76.6 | 2017.978760 | 0.024368 | YVMLPVADQDQCIR |
| 49.4 | 2017.978760 | 0.024368 | YVMLPVADQDQCIR |
| 0.5 | 2017.977875 | 0.025253 | ITLTDLFENAYGSSMKGR |
| 0.1 | 2017.977875 | 0.025253 | ETIYPHLLCSTSVQENK |

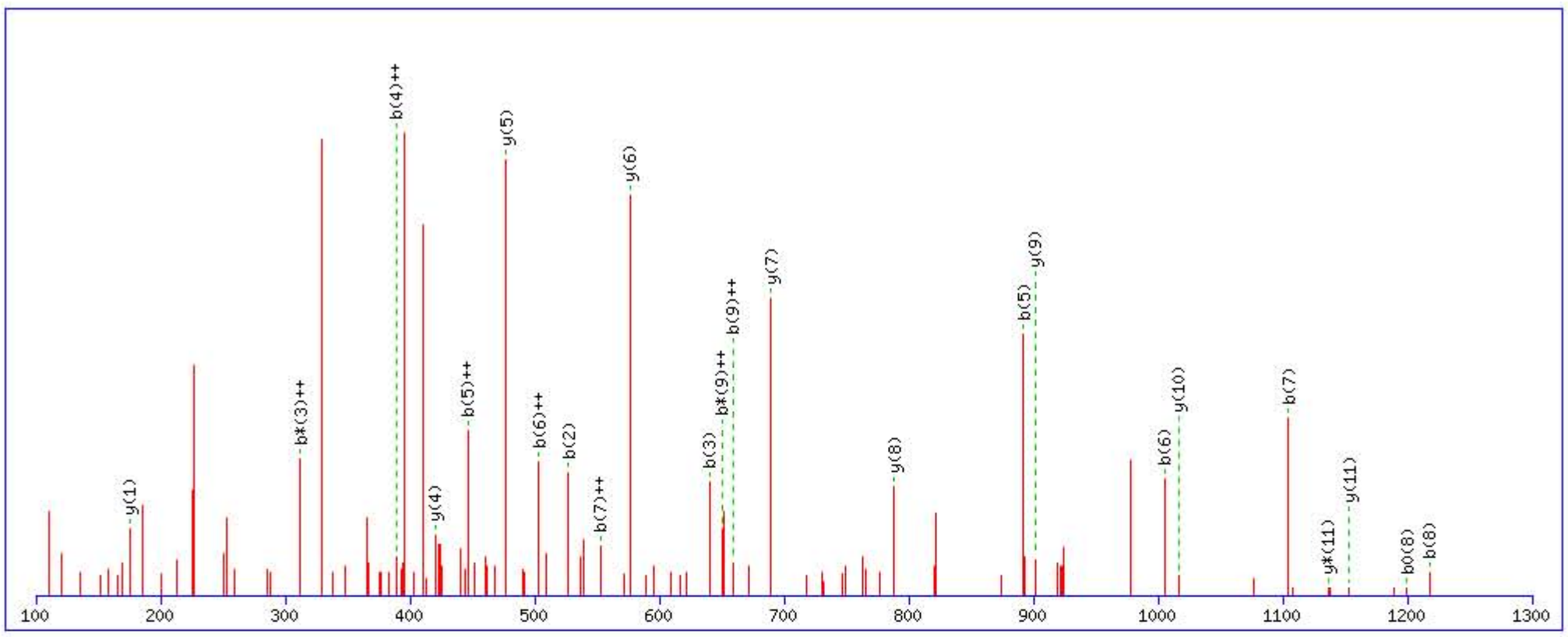
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SQIHDIVLVGGSTR**
Found in **HSP7C_HUMAN**, Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1

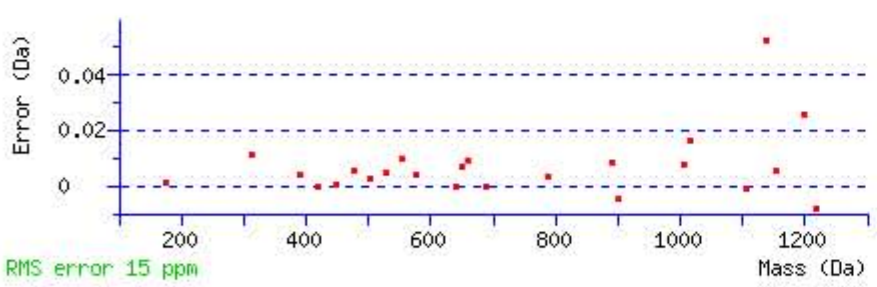
Match to Query 40109: 1791.982152 from(598.334660,3+) rtinseconds(1983) index(20142)
Title: Locus:1.1.1.3073.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

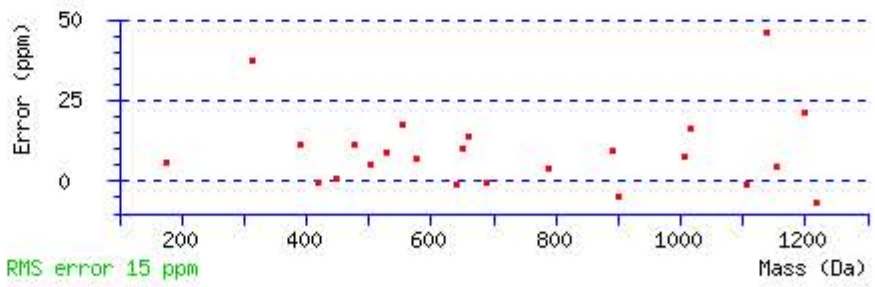
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1791.966553
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.003
**Matches :** 24/152 fragment ions using 56 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 14 |
| 2 | 527.264630 | 264.135953 | 510.238081 | 255.622679 | 509.254065 | 255.130671 | Q | 1705.941788 | 853.474532 | 1688.915239 | 844.961257 | 1687.931223 | 844.469249 | 13 |
| 3 | 640.348694 | 320.677985 | 623.322145 | 312.164711 | 622.338129 | 311.672703 | I | 1266.716462 | 633.861869 | 1249.689913 | 625.348595 | 1248.705897 | 624.856587 | 12 |
| 4 | 777.407606 | 389.207441 | 760.381057 | 380.694166 | 759.397041 | 380.202159 | H | 1153.632398 | 577.319837 | 1136.605849 | 568.806563 | 1135.621833 | 568.314554 | 11 |
| 5 | 892.434549 | 446.720913 | 875.408000 | 438.207638 | 874.423984 | 437.715630 | D | 1016.573486 | 508.790381 | 999.546937 | 500.277107 | 998.562921 | 499.785099 | 10 |
| 6 | 1005.518613 | 503.262945 | 988.492064 | 494.749670 | 987.508048 | 494.257662 | I | 901.546543 | 451.276910 | 884.519994 | 442.763635 | 883.535978 | 442.271627 | 9 |
| 7 | 1104.587027 | 552.797152 | 1087.560478 | 544.283877 | 1086.576462 | 543.791869 | V | 788.462479 | 394.734878 | 771.435930 | 386.221603 | 770.451914 | 385.729595 | 8 |
| 8 | 1217.671091 | 609.339183 | 1200.644542 | 600.825909 | 1199.660526 | 600.333901 | L | 689.394065 | 345.200671 | 672.367516 | 336.687396 | 671.383500 | 336.195388 | 7 |
| 9 | 1316.739505 | 658.873391 | 1299.712956 | 650.360116 | 1298.728940 | 649.868108 | V | 576.310001 | 288.658639 | 559.283452 | 280.145364 | 558.299436 | 279.653356 | 6 |
| 10 | 1373.760969 | 687.384122 | 1356.734420 | 678.870848 | 1355.750404 | 678.378840 | G | 477.241587 | 239.124431 | 460.215038 | 230.611157 | 459.231022 | 230.119149 | 5 |
| 11 | 1430.782433 | 715.894854 | 1413.755884 | 707.381580 | 1412.771868 | 706.889572 | G | 420.220123 | 210.613699 | 403.193574 | 202.100425 | 402.209558 | 201.608417 | 4 |
| 12 | 1517.814461 | 759.410868 | 1500.787912 | 750.897594 | 1499.803896 | 750.405586 | S | 363.198659 | 182.102968 | 346.172110 | 173.589693 | 345.188094 | 173.097685 | 3 |
| 13 | 1618.862140 | 809.934708 | 1601.835591 | 801.421434 | 1600.851575 | 800.929425 | T | 276.166631 | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 14 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 37.9 | 1791.966553 | 0.015599 | SQIHDIVLVGGSTR |

**Mascot:** http://www.matrixscience.com/

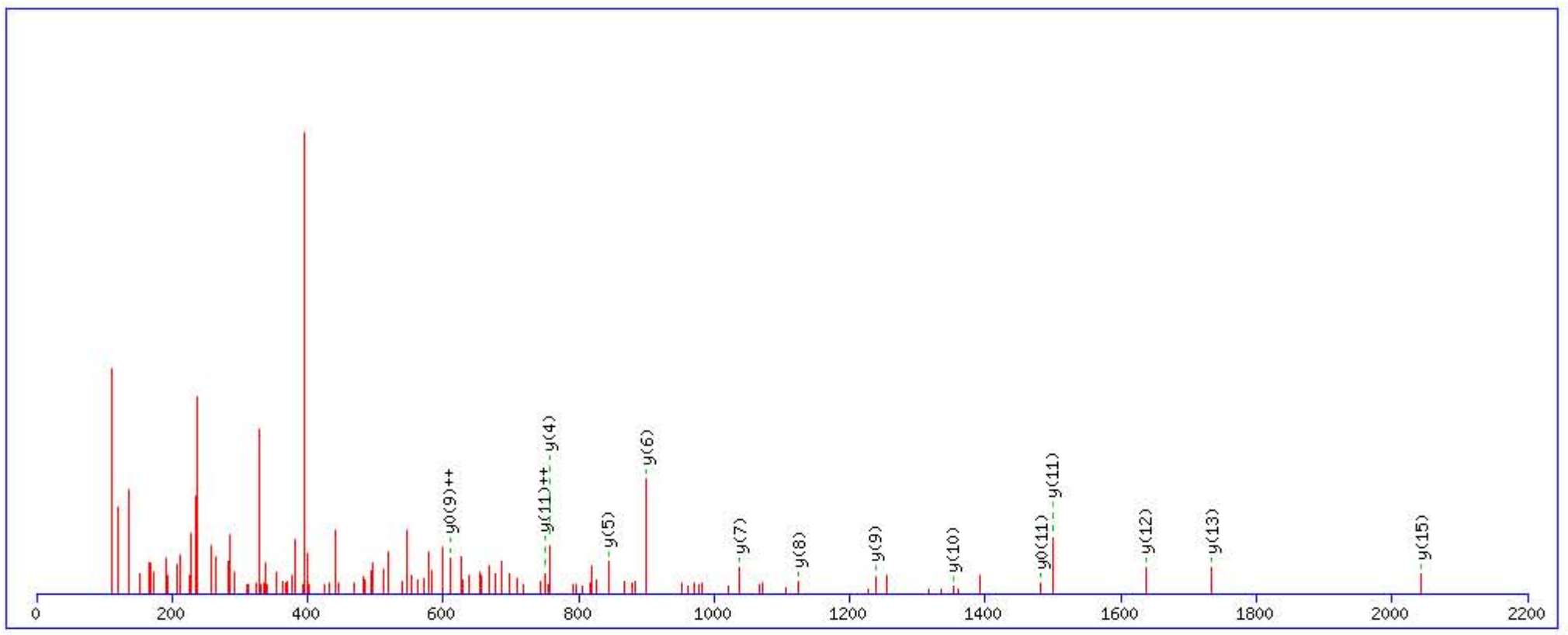
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TYFPHFDLSHGSAQVK**
Found in **HBA_HUMAN**, Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2

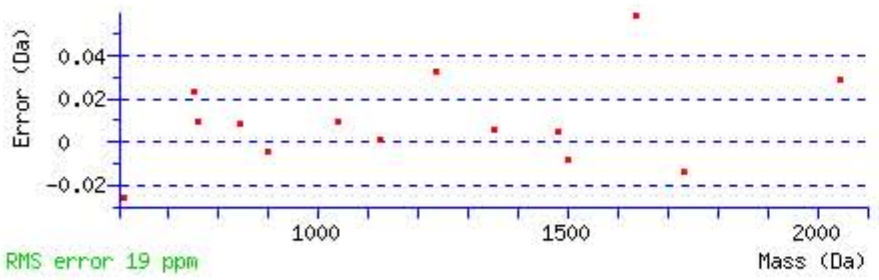
Match to Query 47302: 2144.056136 from(537.021310,4+) rtinseconds(2070) index(6048)
Title: Locus:1.1.1.1998.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

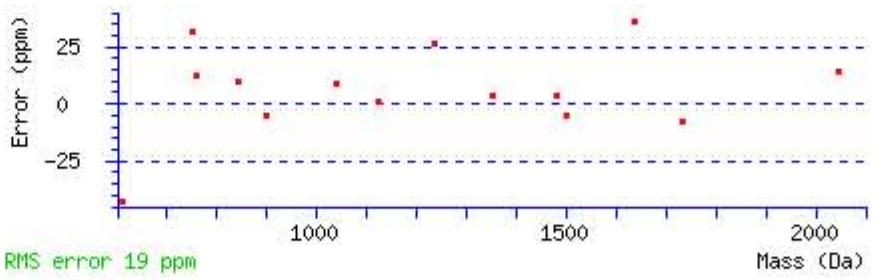
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2144.051346
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q14** : Biotin:Thermo-21345 (Q)
**Ions Score:** 56 **Expect:** 6.8e-005
**Matches :** 14/146 fragment ions using 30 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 16 |
| 2 | 265.118284 | 133.062780 | | | 247.107719 | 124.057498 | Y | *2044.010930* | 1022.509103 | 2026.984381 | 1013.995829 | 2026.000365 | 1013.503821 | 15 |
| 3 | 412.186698 | 206.596987 | | | 394.176133 | 197.591705 | F | 1880.947601 | 940.977438 | 1863.921052 | 932.464164 | 1862.937036 | 931.972156 | 14 |
| 4 | 509.239462 | 255.123369 | | | 491.228897 | 246.118087 | P | *1733.879187* | 867.443231 | 1716.852638 | 858.929957 | 1715.868622 | 858.437949 | 13 |
| 5 | 646.298374 | 323.652825 | | | 628.287809 | 314.647543 | H | *1636.826423* | 818.916849 | 1619.799874 | 810.403575 | 1618.815858 | 809.911567 | 12 |
| 6 | 793.366788 | 397.187032 | | | 775.356223 | 388.181750 | F | *1499.767511* | 750.387393 | 1482.740962 | 741.874119 | 1481.756946 | 741.382111 | 11 |
| 7 | 908.393731 | 454.700504 | | | 890.383166 | 445.695221 | D | *1352.699097* | 676.853186 | 1335.672548 | 668.339912 | 1334.688532 | 667.847904 | 10 |
| 8 | 1021.477795 | 511.242536 | | | 1003.467230 | 502.237253 | L | *1237.672154* | 619.339715 | 1220.645605 | 610.826441 | 1219.661589 | 610.334433 | 9 |
| 9 | 1108.509823 | 554.758550 | | | 1090.499258 | 545.753267 | S | *1124.588090* | 562.797683 | 1107.561541 | 554.284409 | 1106.577525 | 553.792400 | 8 |
| 10 | 1245.568735 | 623.288006 | | | 1227.558170 | 614.282723 | H | *1037.556062* | 519.281669 | 1020.529513 | 510.768394 | 1019.545497 | 510.276386 | 7 |
| 11 | 1302.590199 | 651.798738 | | | 1284.579634 | 642.793455 | G | *900.497150* | 450.752213 | 883.470601 | 442.238938 | 882.486585 | 441.746930 | 6 |
| 12 | 1389.622227 | 695.314752 | | | 1371.611662 | 686.309469 | S | *843.475686* | 422.241481 | 826.449137 | 413.728207 | 825.465121 | 413.236199 | 5 |
| 13 | 1460.659341 | 730.833309 | | | 1442.648776 | 721.828026 | A | *756.443658* | 378.725467 | 739.417109 | 370.212192 | | | 4 |
| 14 | 1899.884667 | 950.445972 | 1882.858118 | 941.932697 | 1881.874102 | 941.440689 | Q | 685.406544 | 343.206910 | 668.379995 | 334.693635 | | | 3 |
| 15 | 1998.953081 | 999.980179 | 1981.926532 | 991.466904 | 1980.942516 | 990.974896 | V | 246.181218 | 123.594247 | 229.154669 | 115.080972 | | | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 55.6 | 2144.051346 | 0.004790 | TYFPHFDLSHGSAQVK |

**Mascot:** http://www.matrixscience.com/

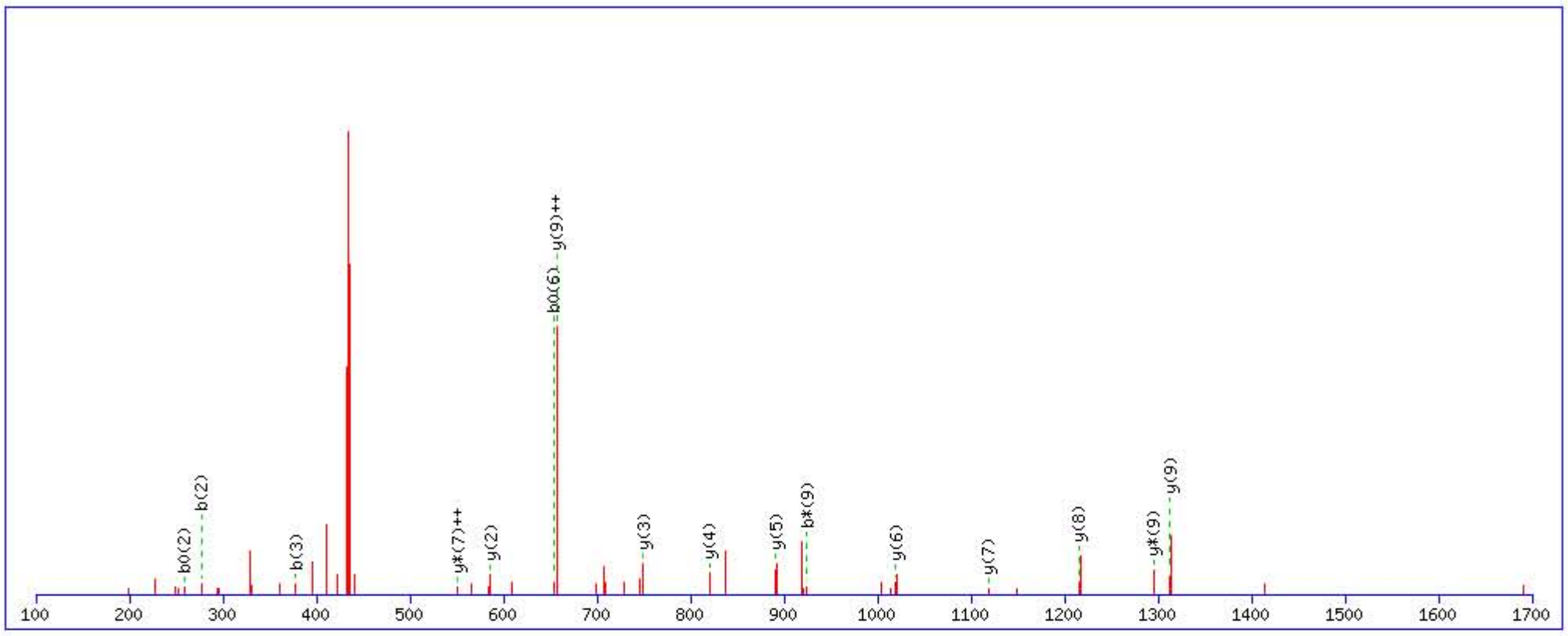
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EFTPPVQAAYQK**
Found in **HBB_HUMAN**, Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2

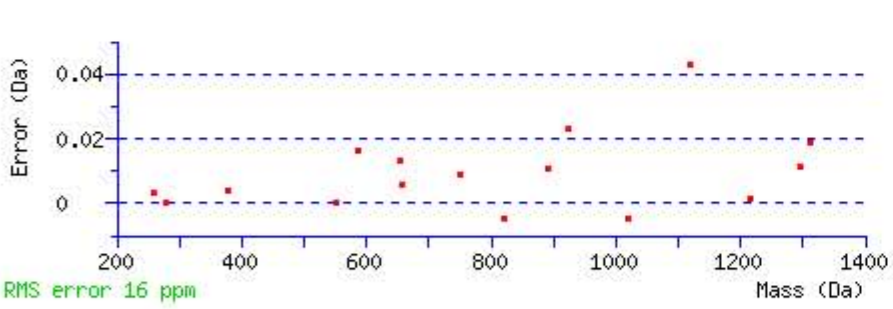
Match to Query 37725: 1688.877228 from(845.445890,2+) rtinseconds(1999) index(5620)
Title: Locus:1.1.1.1973.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

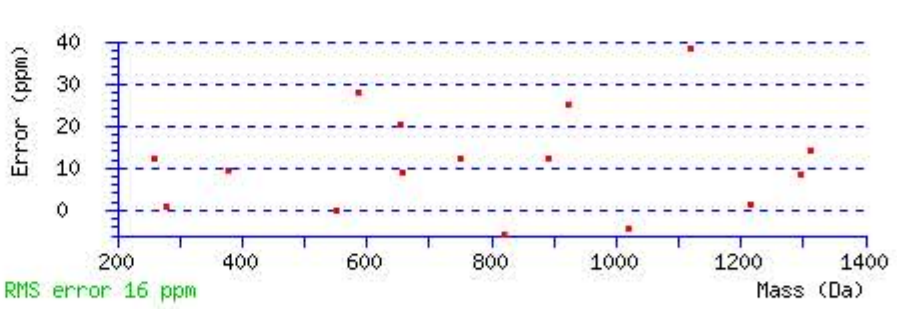
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1688.859604
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 26 **Expect:** 0.031
**Matches :** 16/102 fragment ions using 44 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 12 |
| 2 | 277.118283 | 139.062779 | | | 259.107718 | 130.057497 | F | 1560.824300 | 780.915788 | 1543.797751 | 772.402514 | 1542.813735 | 771.910506 | 11 |
| 3 | 378.165962 | 189.586619 | | | 360.155397 | 180.581336 | T | 1413.755886 | 707.381581 | 1396.729337 | 698.868307 | 1395.745321 | 698.376299 | 10 |
| 4 | 475.218726 | 238.113001 | | | 457.208161 | 229.107719 | P | *1312.708207* | 656.857742 | 1295.681658 | 648.344467 | | | 9 |
| 5 | 572.271490 | 286.639383 | | | 554.260925 | 277.634101 | P | *1215.655443* | 608.331360 | 1198.628894 | 599.818085 | | | 8 |
| 6 | 671.339904 | 336.173590 | | | 653.329339 | 327.168308 | V | *1118.602679* | 559.804978 | 1101.576130 | 551.291703 | | | 7 |
| 7 | 799.398482 | 400.202879 | 782.371933 | 391.689605 | 781.387917 | 391.197597 | Q | *1019.534265* | 510.270771 | 1002.507716 | 501.757496 | | | 6 |
| 8 | 870.435596 | 435.721436 | 853.409047 | 427.208162 | 852.425031 | 426.716154 | A | *891.475687* | 446.241482 | 874.449138 | 437.728207 | | | 5 |
| 9 | 941.472710 | 471.239993 | 924.446161 | 462.726719 | 923.462145 | 462.234711 | A | *820.438573* | 410.722925 | 803.412024 | 402.209650 | | | 4 |
| 10 | 1104.536039 | 552.771658 | 1087.509490 | 544.258383 | 1086.525474 | 543.766375 | Y | *749.401459* | 375.204368 | 732.374910 | 366.691093 | | | 3 |
| 11 | 1543.761365 | 772.384321 | 1526.734816 | 763.871046 | 1525.750800 | 763.379038 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 12 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.8 | 1688.859604 | 0.017624 | EFTPPVQAAYQK |
| 9.2 | 1688.885437 | -0.008209 | MKTPFGKAAAGQR |
| 2.1 | 1688.891983 | -0.014755 | KFTCQGPVDVNILAK |
| 1.6 | 1688.878036 | -0.000808 | GRDLAPRVSYTPAMR |

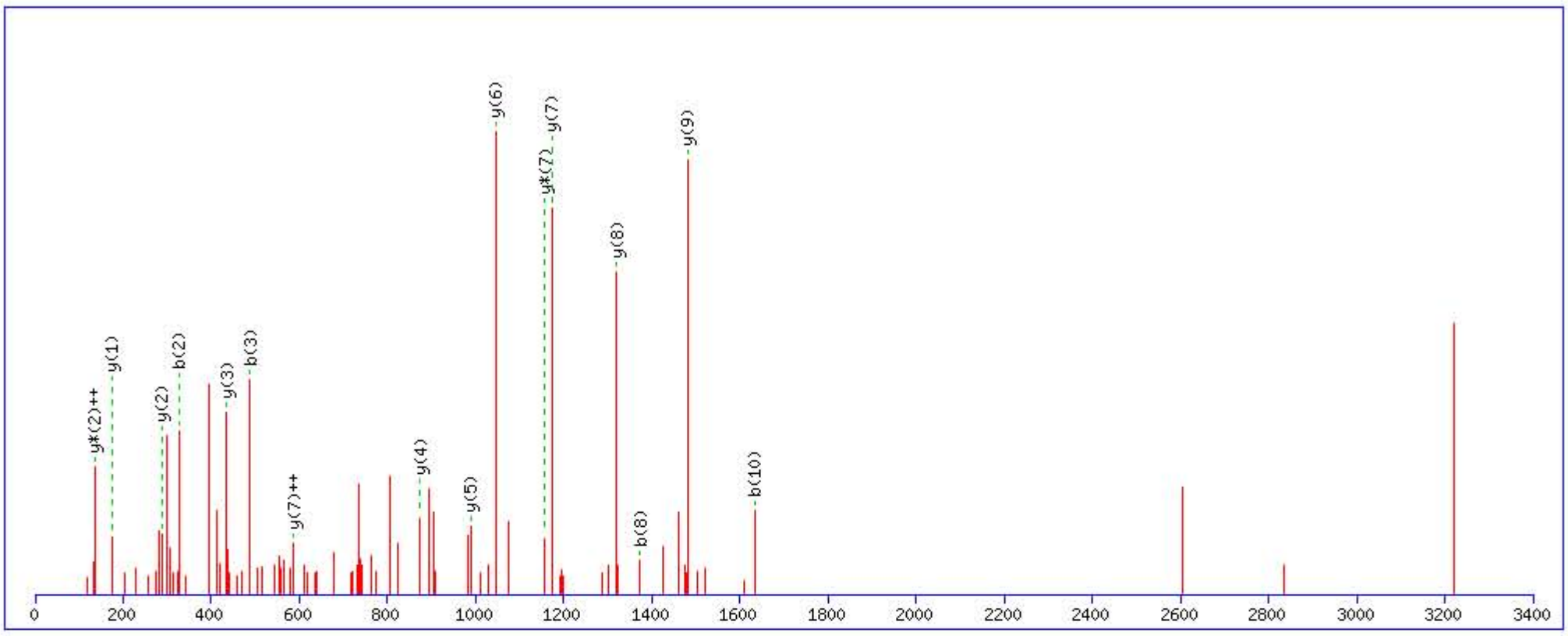
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YYCFQGNQFLR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

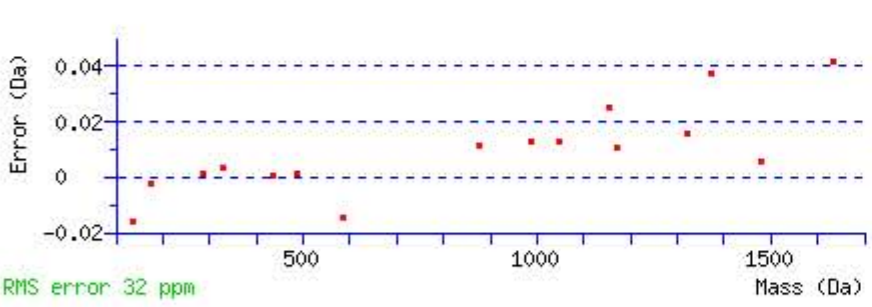
Match to Query 40356: 1805.854908 from(903.934730,2+) rtinseconds(2296) index(68143)
Title: Locus:1.1.1.2074.16 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

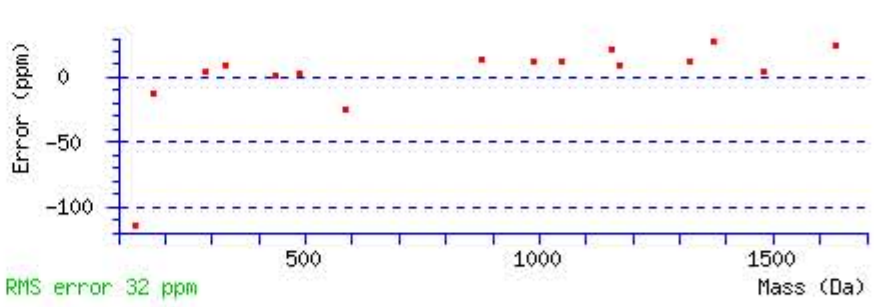
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1805.838165
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.0016
**Matches :** 16/72 fragment ions using 43 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | Y | | | | | 11 |
| 2 | **327.133934** | 164.070605 | | | Y | 1643.782117 | 822.394697 | 1626.755568 | 813.881422 | 10 |
| 3 | **487.164583** | 244.085930 | | | C | *1480.718788* | 740.863032 | 1463.692239 | 732.349758 | 9 |
| 4 | 634.232997 | 317.620137 | | | F | *1320.688139* | 660.847708 | 1303.661590 | 652.334433 | 8 |
| 5 | 762.291575 | 381.649426 | 745.265026 | 373.136151 | Q | *1173.619725* | 587.313501 | 1156.593176 | 578.800226 | 7 |
| 6 | 819.313039 | 410.160158 | 802.286490 | 401.646883 | G | *1045.561147* | 523.284212 | 1028.534598 | 514.770937 | 6 |
| 7 | 933.355966 | 467.181621 | 916.329417 | 458.668347 | N | *988.539683* | 494.773480 | 971.513134 | 486.260205 | 5 |
| 8 | **1372.581292** | 686.794284 | 1355.554743 | 678.281010 | Q | *874.496756* | 437.752016 | 857.470207 | 429.238742 | 4 |
| 9 | 1519.649706 | 760.328491 | 1502.623157 | 751.815217 | F | *435.271430* | 218.139353 | 418.244881 | 209.626078 | 3 |
| 10 | **1632.733770** | 816.870523 | 1615.707221 | 808.357249 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | 2 |
| 11 | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.2 | 1805.838165 | 0.016743 | YYCFQGNQFLR |
| 29.9 | 1805.838165 | 0.016743 | YYCFQGNQFLR |
| 7.9 | 1805.873886 | -0.018978 | QMFQERSSR |
| 5.2 | 1805.845383 | 0.009525 | WGTRGGFNGQMER |
| 1.8 | 1805.844055 | 0.010853 | LLQAPFTDCGDGPMLR |

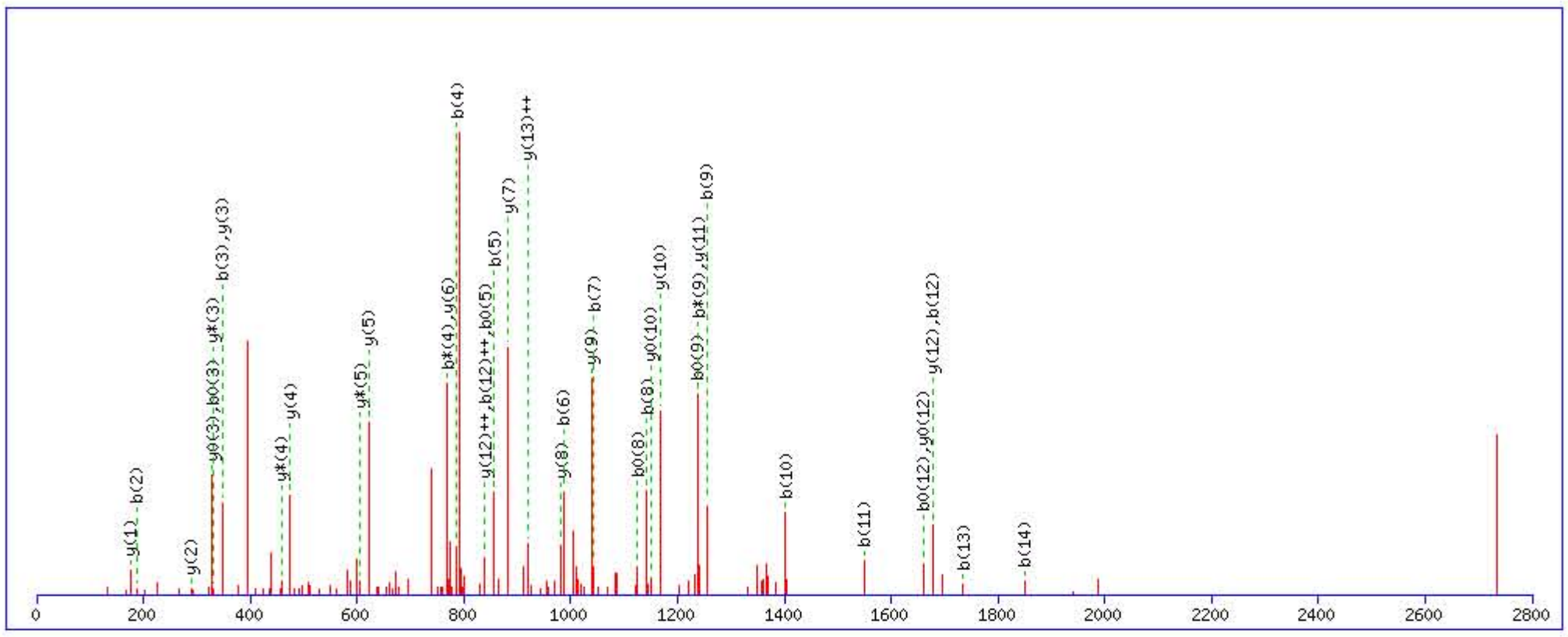
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GECQAEGVLFFQGDR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

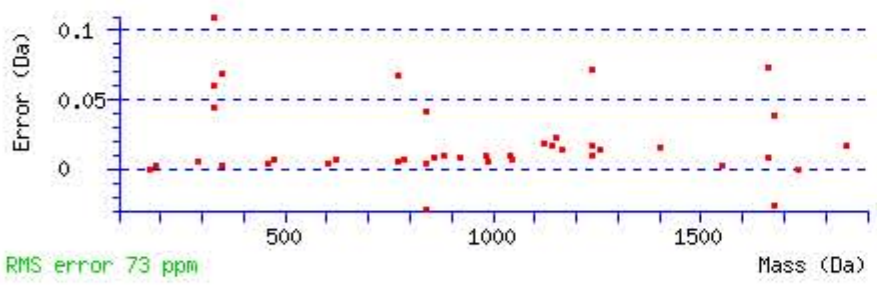
Match to Query 45111: 2022.956488 from(1012.485520,2+) rtinseconds(2413) index(68802)
Title: Locus:1.1.1.2115.10 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

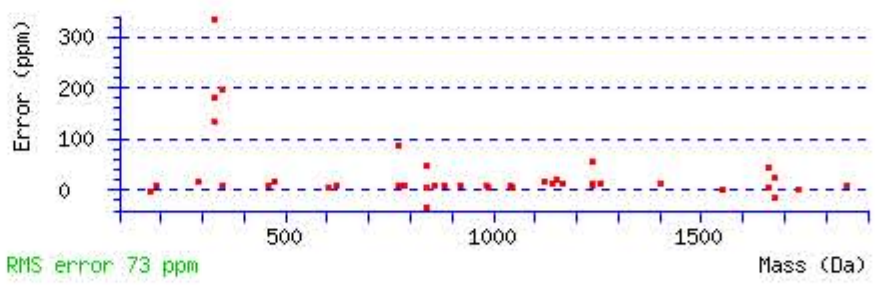
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2022.929184
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 70 **Expect:** 1.6e-006
**Matches** : 41/158 fragment ions using 75 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 15 |
| 2 | *187.071333* | 94.039305 | | | 169.060768 | 85.034022 | E | 1966.914982 | 983.961129 | 1949.888433 | 975.447855 | 1948.904417 | 974.955847 | 14 |
| 3 | *347.101982* | 174.054629 | | | 329.091417 | 165.049347 | C | 1837.872389 | 919.439833 | 1820.845840 | 910.926558 | 1819.861824 | 910.434550 | 13 |
| 4 | *786.327308* | 393.667292 | 769.300759 | 385.154018 | 768.316743 | 384.662010 | Q | **1677.841740** | 839.424508 | 1660.815191 | 830.911234 | 1659.831175 | 830.419226 | 12 |
| 5 | *857.364422* | 429.185849 | 840.337873 | 420.672575 | 839.353857 | 420.180567 | A | **1238.616414** | 619.811845 | 1221.589865 | 611.298571 | 1220.605849 | 610.806563 | 11 |
| 6 | *986.407015* | 493.707146 | 969.380466 | 485.193871 | 968.396450 | 484.701863 | E | **1167.579300** | 584.293288 | 1150.552751 | 575.780014 | 1149.568735 | 575.288006 | 10 |
| 7 | *1043.428479* | 522.217878 | 1026.401930 | 513.704603 | 1025.417914 | 513.212595 | G | **1038.536707** | 519.771992 | 1021.510158 | 511.258717 | 1020.526142 | 510.766709 | 9 |
| 8 | *1142.496893* | 571.752085 | 1125.470344 | 563.238810 | 1124.486328 | 562.746802 | V | **981.515243** | 491.261260 | 964.488694 | 482.747985 | 963.504678 | 482.255977 | 8 |
| 9 | *1255.580957* | 628.294117 | 1238.554408 | 619.780842 | 1237.570392 | 619.288834 | L | **882.446829** | 441.727053 | 865.420280 | 433.213778 | 864.436264 | 432.721770 | 7 |
| 10 | *1402.649371* | 701.828324 | 1385.622822 | 693.315049 | 1384.638806 | 692.823041 | F | **769.362765** | 385.185021 | 752.336216 | 376.671746 | 751.352200 | 376.179738 | 6 |
| 11 | *1549.717785* | 775.362531 | 1532.691236 | 766.849256 | 1531.707220 | 766.357248 | F | **622.294351** | 311.650814 | 605.267802 | 303.137539 | 604.283786 | 302.645531 | 5 |
| 12 | *1677.776363* | 839.391820 | 1660.749814 | 830.878545 | 1659.765798 | 830.386537 | Q | **475.225937** | 238.116606 | 458.199388 | 229.603332 | 457.215372 | 229.111324 | 4 |
| 13 | *1734.797827* | 867.902552 | 1717.771278 | 859.389277 | 1716.787262 | 858.897269 | G | **347.167359** | 174.087317 | 330.140810 | 165.574043 | 329.156794 | 165.082035 | 3 |
| 14 | *1849.824770* | 925.416023 | 1832.798221 | 916.902749 | 1831.814205 | 916.410741 | D | **290.145895** | 145.576585 | 273.119346 | 137.063311 | 272.135330 | 136.571303 | 2 |
| 15 | | | | | | | R | **175.118952** | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 70.5 | 2022.929184 | 0.027304 | GECQAEGVLFFQGDR |
| 15.9 | 2022.929184 | 0.027304 | GECQAEGVLFFQGDR |
| 9.2 | 2022.950317 | 0.006171 | NMSFVNDLTVTQDGR |
| 5.5 | 2022.980133 | -0.023645 | QHMEQKEQTAR |
| 4.9 | 2022.980133 | -0.023645 | QHMEQKEQTAR |
| 1.3 | 2022.986664 | -0.030176 | QQGQEEQVQEAK |
| 1.0 | 2022.986664 | -0.030176 | QQGQEEQVQEAK |
| 0.9 | 2022.961548 | -0.005060 | VMQVSPDGQHLASGDR |

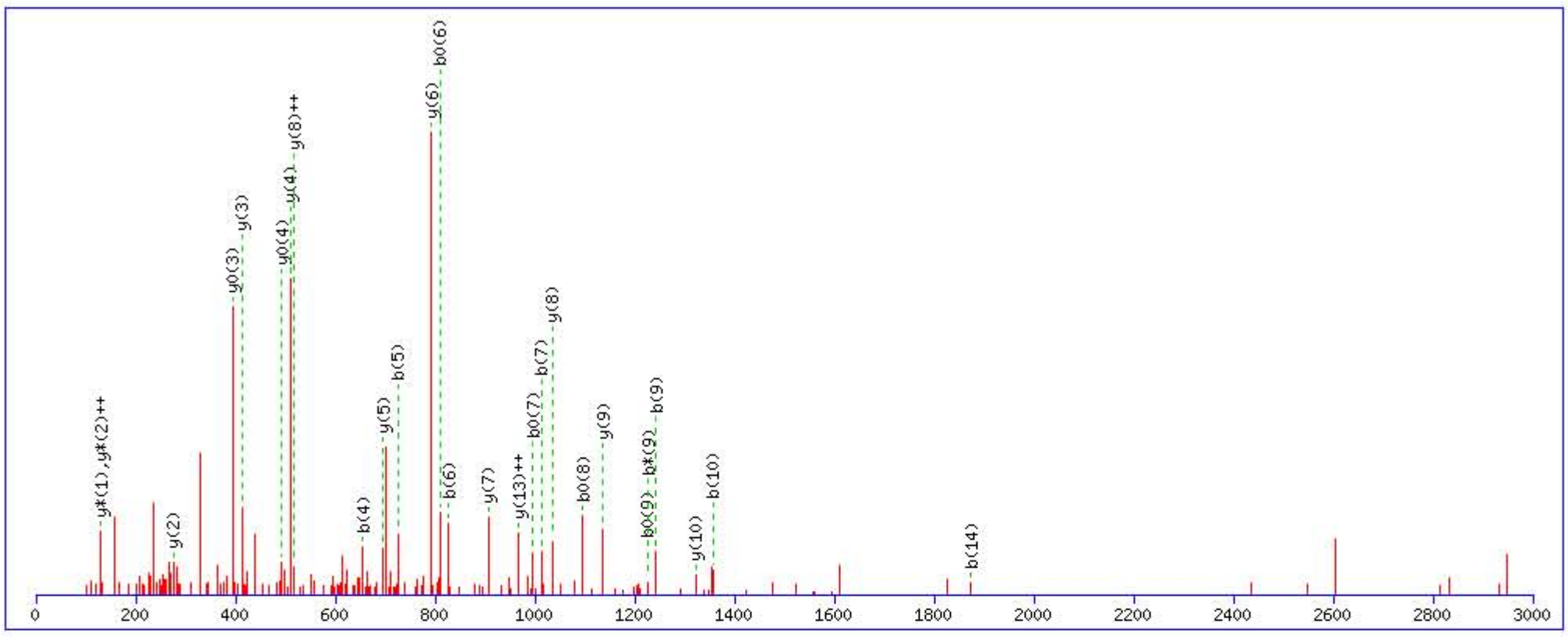
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SGAQATWTELPWPHEK**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

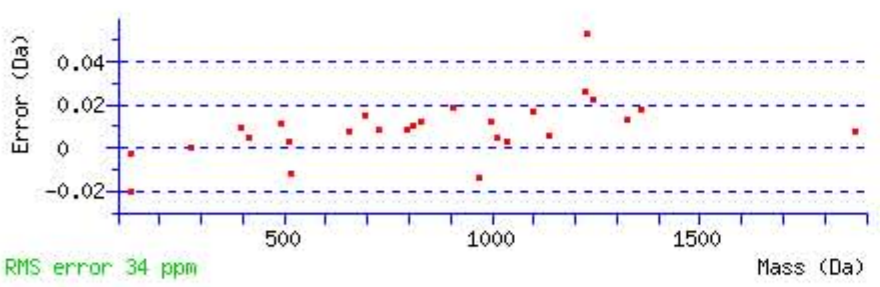
Match to Query 47366: 2148.065082 from(717.028970,3+) rtinseconds(2315) index(68245)
Title: Locus:1.1.1.2081.7 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

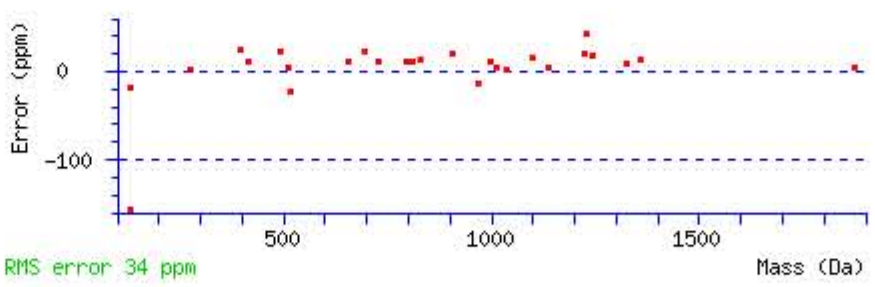
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2148.046234
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 47 **Expect:** 4.7e-005
**Matches :** 27/172 fragment ions using 48 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 16 |
| 2 | 145.060768 | 73.034022 | | | 127.050203 | 64.028740 | G | 2062.021496 | 1031.514386 | 2044.994947 | 1023.001111 | 2044.010931 | 1022.509103 | 15 |
| 3 | 216.097882 | 108.552579 | | | 198.087317 | 99.547296 | A | 2005.000032 | 1003.003654 | 1987.973483 | 994.490380 | 1986.989467 | 993.998372 | 14 |
| 4 | *655.323208* | 328.165242 | 638.296659 | 319.651968 | 637.312643 | 319.159960 | Q | 1933.962918 | 967.485097 | 1916.936369 | 958.971823 | 1915.952353 | 958.479815 | 13 |
| 5 | *726.360322* | 363.683799 | 709.333773 | 355.170525 | 708.349757 | 354.678517 | A | 1494.737592 | 747.872434 | 1477.711043 | 739.359160 | 1476.727027 | 738.867152 | 12 |
| 6 | *827.408001* | 414.207639 | 810.381452 | 405.694364 | 809.397436 | 405.202356 | T | 1423.700478 | 712.353877 | 1406.673929 | 703.840603 | 1405.689913 | 703.348595 | 11 |
| 7 | *1013.487314* | 507.247295 | 996.460765 | 498.734020 | 995.476749 | 498.242012 | W | *1322.652799* | 661.830038 | 1305.626250 | 653.316763 | 1304.642234 | 652.824755 | 10 |
| 8 | 1114.534993 | 557.771135 | 1097.508444 | 549.257860 | 1096.524428 | 548.765852 | T | *1136.573486* | 568.790381 | 1119.546937 | 560.277107 | 1118.562921 | 559.785099 | 9 |
| 9 | *1243.577586* | 622.292431 | 1226.551037 | 613.779157 | 1225.567021 | 613.287149 | E | *1035.525807* | 518.266542 | 1018.499258 | 509.753267 | 1017.515242 | 509.261259 | 8 |
| 10 | *1356.661650* | 678.834463 | 1339.635101 | 670.321189 | 1338.651085 | 669.829181 | L | *906.483214* | 453.745245 | 889.456665 | 445.231971 | 888.472649 | 444.739963 | 7 |
| 11 | 1453.714414 | 727.360845 | 1436.687865 | 718.847571 | 1435.703849 | 718.355563 | P | *793.399150* | 397.203213 | 776.372601 | 388.689939 | 775.388585 | 388.197931 | 6 |
| 12 | 1639.793727 | 820.400502 | 1622.767178 | 811.887227 | 1621.783162 | 811.395219 | W | *696.346386* | 348.676831 | 679.319837 | 340.163557 | 678.335821 | 339.671549 | 5 |
| 13 | 1736.846491 | 868.926884 | 1719.819942 | 860.413609 | 1718.835926 | 859.921601 | P | *510.267073* | 255.637175 | 493.240524 | 247.123900 | 492.256508 | 246.631892 | 4 |
| 14 | *1873.905403* | 937.456340 | 1856.878854 | 928.943065 | 1855.894838 | 928.451057 | H | *413.214309* | 207.110793 | 396.187760 | 198.597518 | 395.203744 | 198.105510 | 3 |
| 15 | 2002.947996 | 1001.977636 | 1985.921447 | 993.464362 | 1984.937431 | 992.972354 | E | *276.155397* | 138.581337 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 46.8 | 2148.046234 | 0.018848 | SGAQATWTELPWPHEK |
| 0.7 | 2148.073898 | -0.008816 | FVETSPSGLDPNASVYQPLK |

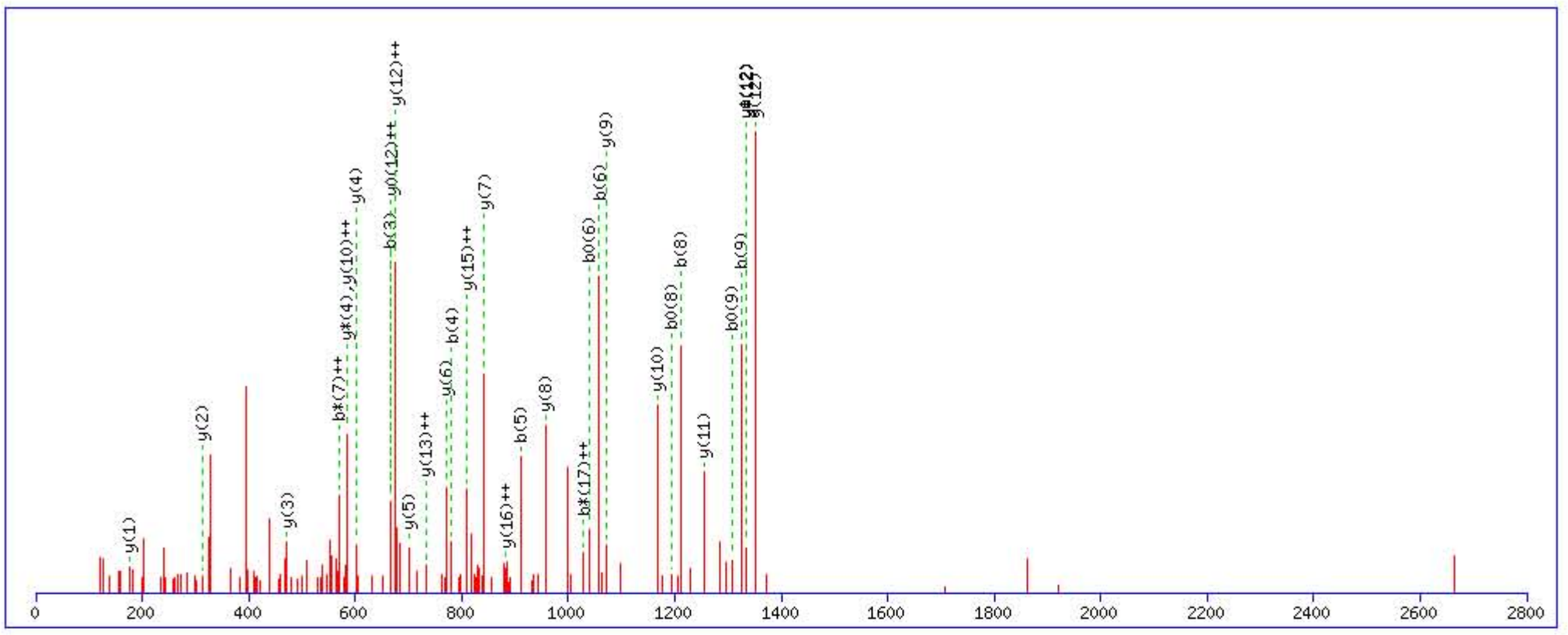
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LLQDEFPGIPSPLDAAVECHR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

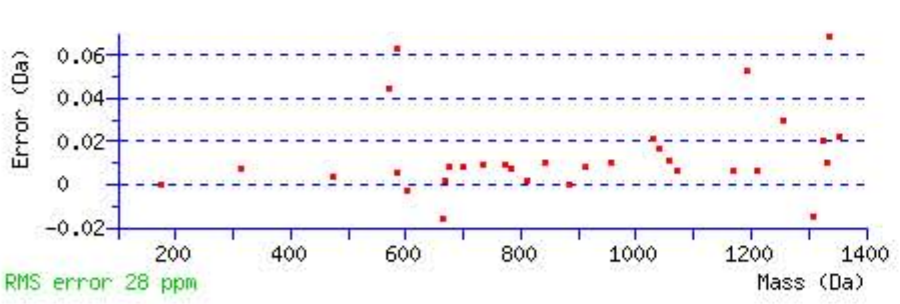
Match to Query 56140: 2674.354722 from(892.458850,3+) rtinseconds(2663) index(9042)
Title: Locus:1.1.1.2204.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

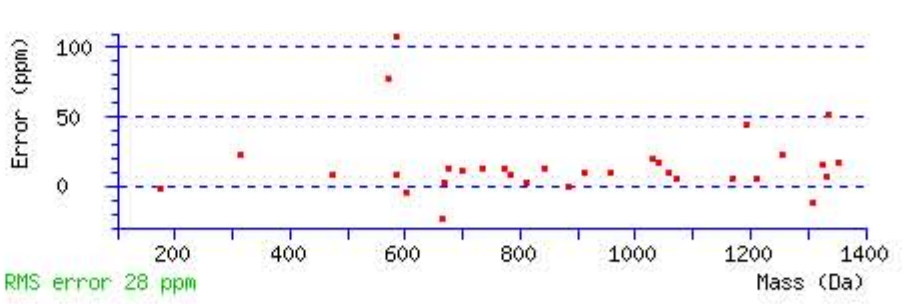
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2674.324722
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 0.00042
**Matches :** 32/224 fragment ions using 81 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 21 |
| 2 | 227.175404 | 114.091340 | | | | | L | 2562.247943 | 1281.627609 | 2545.221394 | 1273.114335 | 2544.237378 | 1272.622327 | 20 |
| 3 | *666.400730* | 333.704003 | 649.374181 | 325.190729 | | | Q | 2449.163879 | 1225.085577 | 2432.137330 | 1216.572303 | 2431.153314 | 1216.080295 | 19 |
| 4 | *781.427673* | 391.217475 | 764.401124 | 382.704200 | 763.417108 | 382.212192 | D | 2009.938553 | 1005.472914 | 1992.912004 | 996.959640 | 1991.927988 | 996.467632 | 18 |
| 5 | *910.470266* | 455.738771 | 893.443717 | 447.225497 | 892.459701 | 446.733489 | E | 1894.911610 | 947.959443 | 1877.885061 | 939.446169 | 1876.901045 | 938.954160 | 17 |
| 6 | *1057.538680* | 529.272978 | 1040.512131 | 520.759704 | 1039.528115 | 520.267696 | F | 1765.869017 | 883.438146 | 1748.842468 | 874.924872 | 1747.858452 | 874.432864 | 16 |
| 7 | 1154.591444 | 577.799360 | 1137.564895 | 569.286086 | 1136.580879 | 568.794078 | P | 1618.800603 | 809.903939 | 1601.774054 | 801.390665 | 1600.790038 | 800.898657 | 15 |
| 8 | *1211.612908* | 606.310092 | 1194.586359 | 597.796818 | 1193.602343 | 597.304810 | G | 1521.747839 | 761.377557 | 1504.721290 | 752.864283 | 1503.737274 | 752.372275 | 14 |
| 9 | *1324.696972* | 662.852124 | 1307.670423 | 654.338850 | 1306.686407 | 653.846841 | I | 1464.726375 | 732.866825 | 1447.699826 | 724.353551 | 1446.715810 | 723.861543 | 13 |
| 10 | 1421.749736 | 711.378506 | 1404.723187 | 702.865232 | 1403.739171 | 702.373223 | P | *1351.642311* | 676.324793 | 1334.615762 | 667.811519 | 1333.631746 | 667.319511 | 12 |
| 11 | 1508.781764 | 754.894520 | 1491.755215 | 746.381246 | 1490.771199 | 745.889238 | S | *1254.589547* | 627.798411 | 1237.562998 | 619.285137 | 1236.578982 | 618.793129 | 11 |
| 12 | 1605.834528 | 803.420902 | 1588.807979 | 794.907628 | 1587.823963 | 794.415620 | P | *1167.557519* | 584.282397 | 1150.530970 | 575.769123 | 1149.546954 | 575.277115 | 10 |
| 13 | 1718.918592 | 859.962934 | 1701.892043 | 851.449660 | 1700.908027 | 850.957652 | L | *1070.504755* | 535.756015 | 1053.478206 | 527.242741 | 1052.494190 | 526.750733 | 9 |
| 14 | 1833.945535 | 917.476406 | 1816.918986 | 908.963131 | 1815.934970 | 908.471123 | D | *957.420691* | 479.213983 | 940.394142 | 470.700709 | 939.410126 | 470.208701 | 8 |
| 15 | 1904.982649 | 952.994963 | 1887.956100 | 944.481688 | 1886.972084 | 943.989680 | A | *842.393748* | 421.700512 | 825.367199 | 413.187237 | 824.383183 | 412.695229 | 7 |
| 16 | 1976.019763 | 988.513520 | 1958.993214 | 980.000245 | 1958.009198 | 979.508237 | A | *771.356634* | 386.181955 | 754.330085 | 377.668680 | 753.346069 | 377.176672 | 6 |
| 17 | 2075.088177 | 1038.047726 | 2058.061628 | 1029.534452 | 2057.077612 | 1029.042444 | V | *700.319520* | 350.663398 | 683.292971 | 342.150123 | 682.308955 | 341.658115 | 5 |
| 18 | 2204.130770 | 1102.569023 | 2187.104221 | 1094.055748 | 2186.120205 | 1093.563740 | E | *601.251106* | 301.129191 | 584.224557 | 292.615916 | 583.240541 | 292.123908 | 4 |
| 19 | 2364.161419 | 1182.584347 | 2347.134870 | 1174.071073 | 2346.150854 | 1173.579065 | C | *472.208513* | 236.607894 | 455.181964 | 228.094620 | | | 3 |
| 20 | 2501.220331 | 1251.113803 | 2484.193782 | 1242.600529 | 2483.209766 | 1242.108521 | H | *312.177864* | 156.592570 | 295.151315 | 148.079295 | | | 2 |
| 21 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.4 | 2674.324722 | 0.030000 | LLQDEFPGIPSPLDAAVECHR |

**Mascot:** http://www.matrixscience.com/

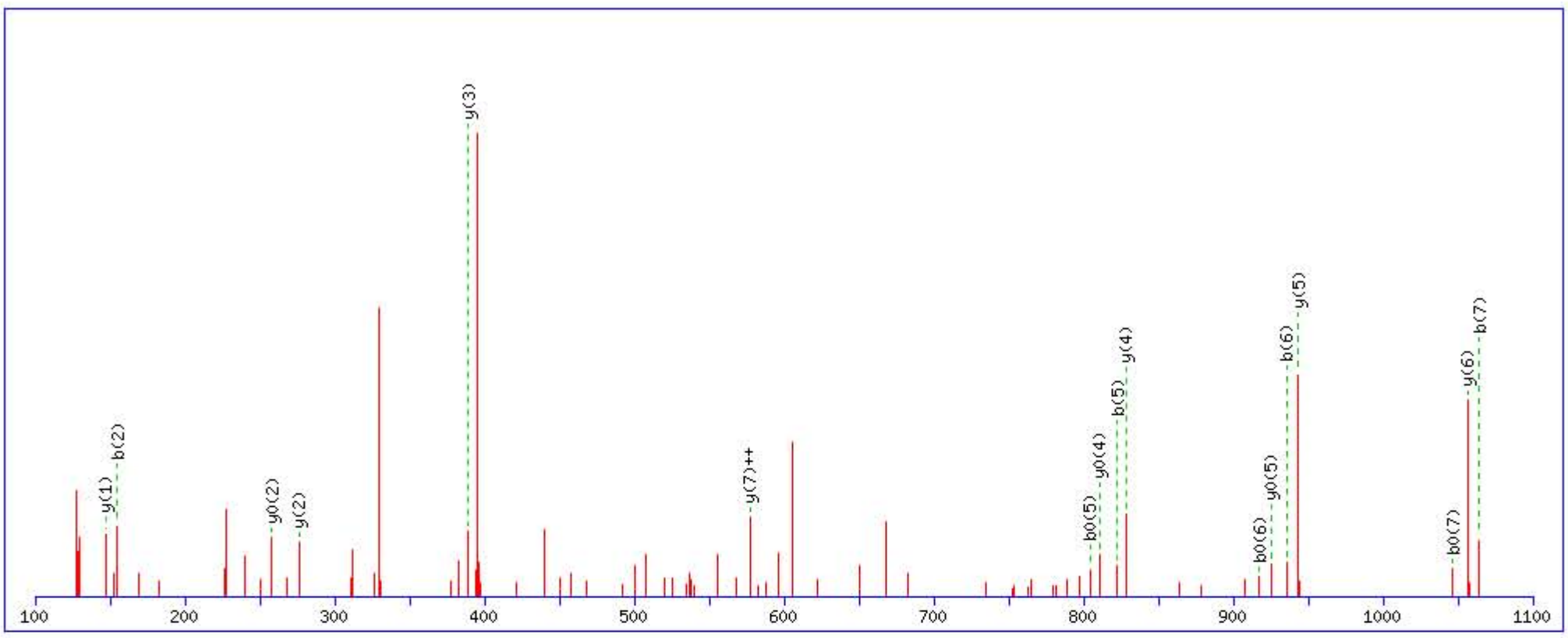
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GPLDQLEK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

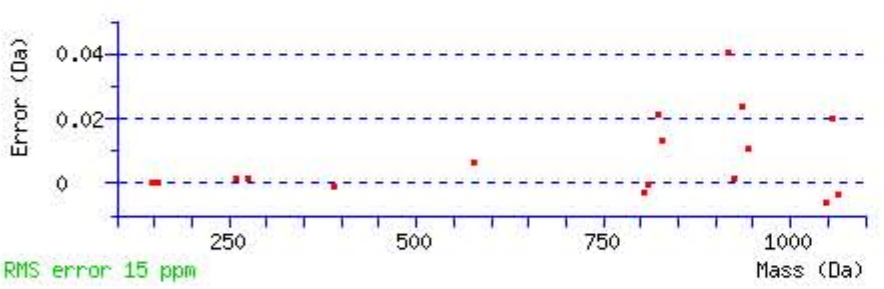
Match to Query 20769: 1209.652948 from(605.833750,2+) rtinseconds(2092) index(34814)
Title: Locus:1.1.1.837.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

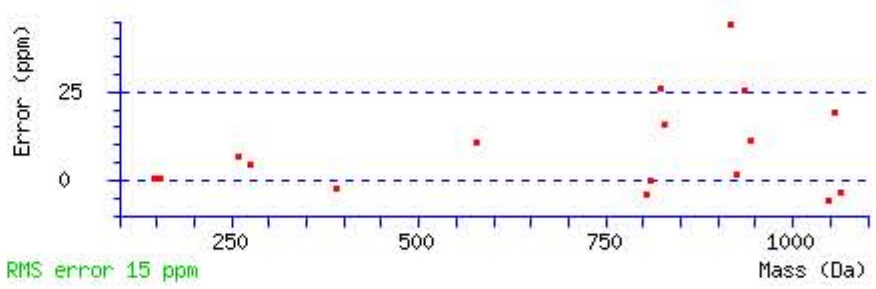
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1209.642731
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0055
**Matches :** 17/68 fragment ions using 30 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 8 |
| 2 | **155.081504** | 78.044390 | | | | | P | 1153.628558 | 577.317917 | 1136.602009 | 568.804643 | 1135.617993 | 568.312635 | 7 |
| 3 | 268.165568 | 134.586422 | | | | | L | *1056.575794* | 528.791535 | 1039.549245 | 520.278261 | 1038.565229 | 519.786253 | 6 |
| 4 | 383.192511 | 192.099894 | | | 365.181946 | 183.094611 | D | *943.491730* | 472.249503 | 926.465181 | 463.736228 | 925.481165 | 463.244220 | 5 |
| 5 | **822.417837** | 411.712557 | 805.391288 | 403.199282 | 804.407272 | 402.707274 | Q | *828.464787* | 414.736032 | 811.438238 | 406.222757 | 810.454222 | 405.730749 | 4 |
| 6 | **935.501901** | 468.254589 | 918.475352 | 459.741314 | 917.491336 | 459.249306 | L | *389.239461* | 195.123368 | 372.212912 | 186.610094 | 371.228896 | 186.118086 | 3 |
| 7 | **1064.544494** | 532.775885 | 1047.517945 | 524.262611 | 1046.533929 | 523.770603 | E | *276.155397* | 138.581336 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 8 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 32.9 | 1209.642731 | 0.010217 | GPLDQLEK |
| 8.4 | 1209.646545 | 0.006403 | EHNRLATELK |
| 5.3 | 1209.661835 | -0.008887 | QQLHKGPQFK |
| 4.5 | 1209.639343 | 0.013605 | AFAKGFLAEEK |
| 4.5 | 1209.664505 | -0.011557 | LLGEYEVIFK |
| 2.8 | 1209.665192 | -0.012244 | GQGKPREK |
| 2.7 | 1209.635300 | 0.017648 | ANHKIEELEK |
| 2.1 | 1209.653976 | -0.001028 | GPDGLKGQK |

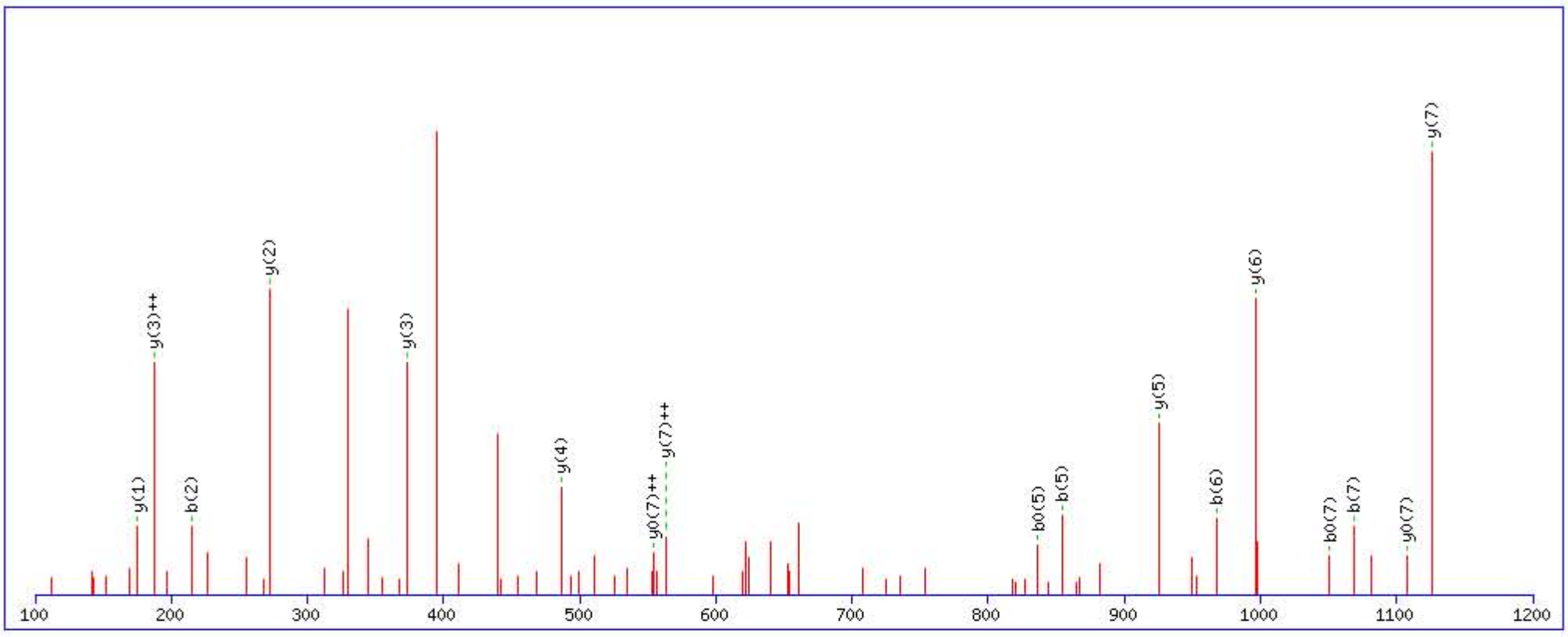
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TLEAQLTPR**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

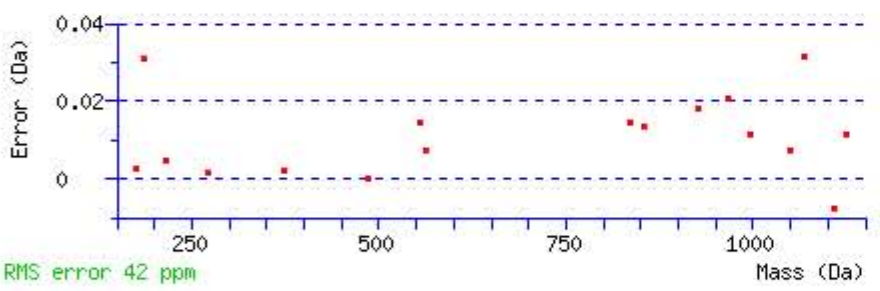
Match to Query 24070: 1338.742968 from(670.378760,2+) rtinseconds(1957) index(33958)
Title: Locus:1.1.1.790.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

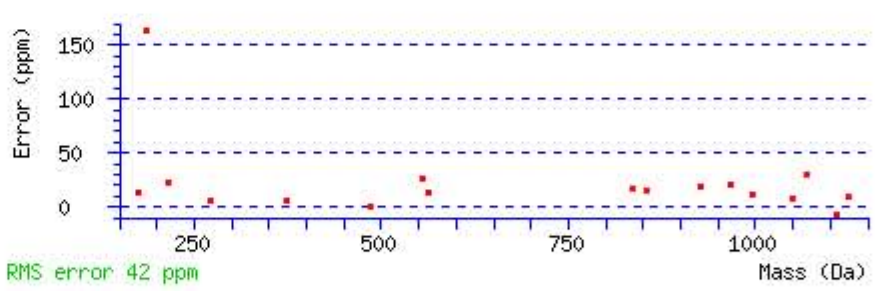
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1338.732941
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 41 **Expect:** 0.0015
**Matches :** 17/84 fragment ions using 32 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 9 |
| 2 | 215.139019 | 108.073147 | | | 197.128454 | 99.067865 | L | 1238.692556 | 619.849916 | 1221.666007 | 611.336642 | 1220.681991 | 610.844633 | 8 |
| 3 | 344.181612 | 172.594444 | | | 326.171047 | 163.589162 | E | *1125.608492* | 563.307884 | 1108.581943 | 554.794610 | 1107.597927 | 554.302602 | 7 |
| 4 | 415.218726 | 208.113001 | | | 397.208161 | 199.107719 | A | *996.565899* | 498.786588 | 979.539350 | 490.273313 | 978.555334 | 489.781305 | 6 |
| 5 | 854.444052 | 427.725664 | 837.417503 | 419.212390 | 836.433487 | 418.720382 | Q | *925.528785* | 463.268031 | 908.502236 | 454.754756 | 907.518220 | 454.262748 | 5 |
| 6 | 967.528116 | 484.267696 | 950.501567 | 475.754422 | 949.517551 | 475.262414 | L | *486.303459* | 243.655367 | 469.276910 | 235.142093 | 468.292894 | 234.650085 | 4 |
| 7 | 1068.575795 | 534.791536 | 1051.549246 | 526.278261 | 1050.565230 | 525.786253 | T | *373.219395* | 187.113335 | 356.192846 | 178.600061 | 355.208830 | 178.108053 | 3 |
| 8 | 1165.628559 | 583.317918 | 1148.602010 | 574.804643 | 1147.617994 | 574.312635 | P | *272.171716* | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 9 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 40.8 | 1338.732941 | 0.010027 | TLEAQLTPR |
| 10.2 | 1338.732956 | 0.010012 | VDLQSLPTR |
| 4.8 | 1338.761932 | -0.018964 | LTVLREDQIPR |
| 4.5 | 1338.725555 | 0.017413 | VDTVAAEHLTRK |
| 3.1 | 1338.725555 | 0.017413 | RSPTVEPSTLPR |
| 1.3 | 1338.744171 | -0.001203 | MKEALHQIVVR |
| 0.7 | 1338.740829 | 0.002139 | GPAGPPGLLGPPGPR |

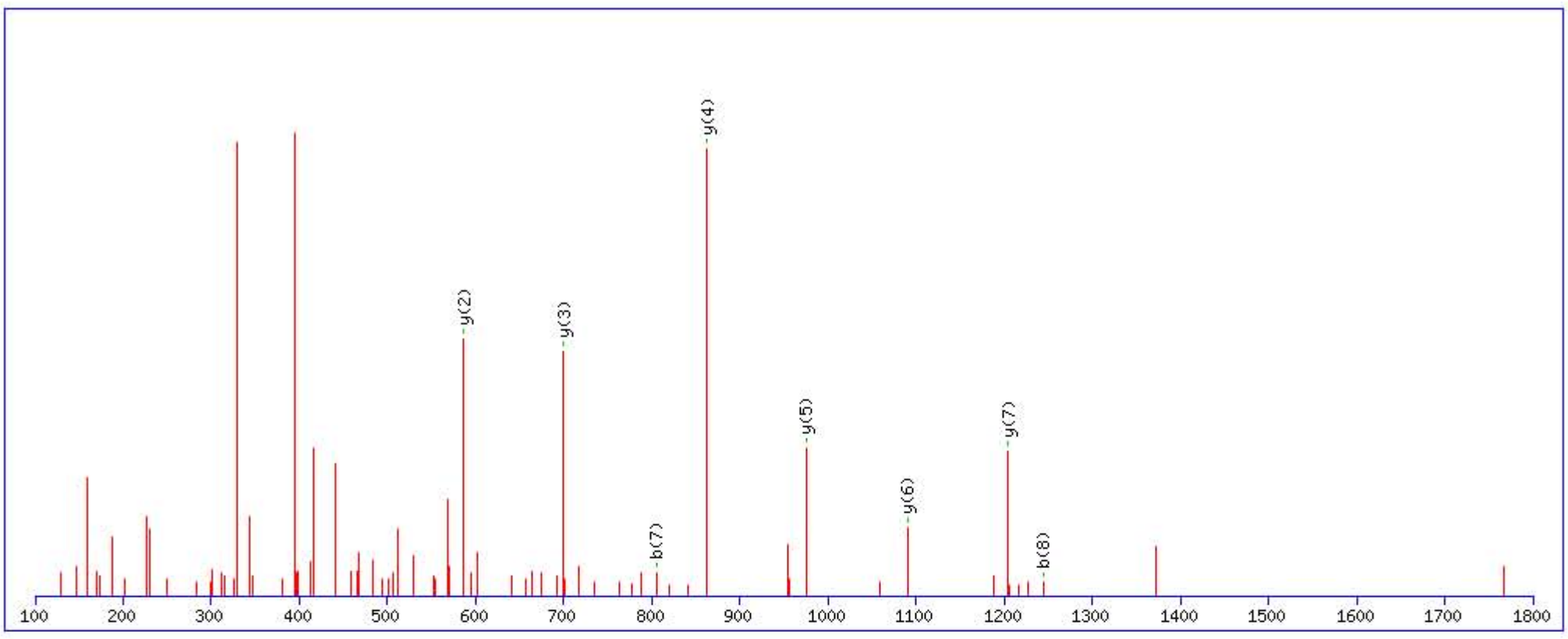
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SVNDLYIQK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

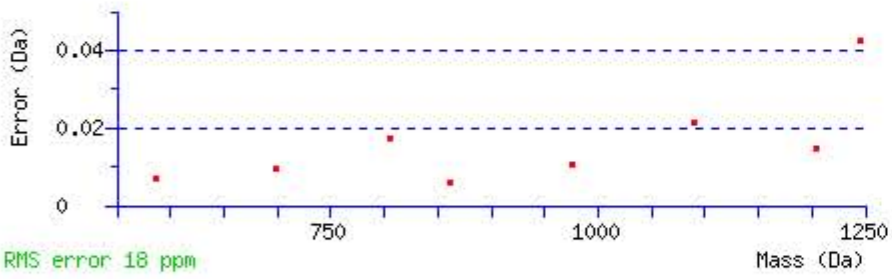
Match to Query 26910: 1389.744968 from(695.879760,2+) rtinseconds(1960) index(33985)
Title: Locus:1.1.1.791.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

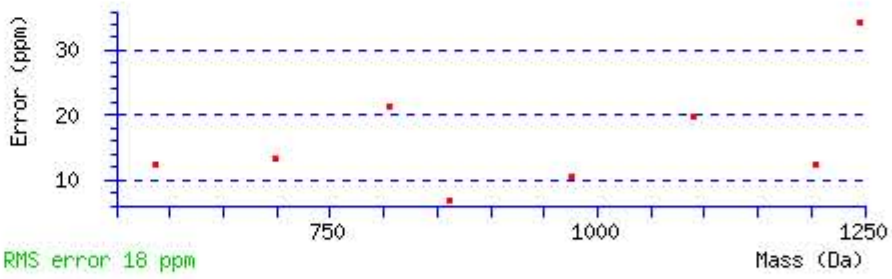
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1389.732605
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 42 **Expect:** 0.0004
**Matches :** 8/82 fragment ions using 13 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 9 |
| 2 | 187.107718 | 94.057497 | | | 169.097153 | 85.052214 | V | 1303.707871 | 652.357573 | 1286.681322 | 643.844299 | 1285.697306 | 643.352291 | 8 |
| 3 | 301.150645 | 151.078960 | 284.124096 | 142.565686 | 283.140080 | 142.073678 | N | *1204.639457* | 602.823367 | 1187.612908 | 594.310092 | 1186.628892 | 593.818084 | 7 |
| 4 | 416.177588 | 208.592432 | 399.151039 | 200.079158 | 398.167023 | 199.587150 | D | *1090.596530* | 545.801903 | 1073.569981 | 537.288629 | 1072.585965 | 536.796621 | 6 |
| 5 | 529.261652 | 265.134464 | 512.235103 | 256.621190 | 511.251087 | 256.129182 | L | *975.569587* | 488.288432 | 958.543038 | 479.775157 | | | 5 |
| 6 | 692.324981 | 346.666129 | 675.298432 | 338.152854 | 674.314416 | 337.660846 | Y | *862.485523* | 431.746400 | 845.458974 | 423.233125 | | | 4 |
| 7 | **805.409045** | 403.208161 | 788.382496 | 394.694886 | 787.398480 | 394.202878 | I | *699.422194* | 350.214735 | 682.395645 | 341.701461 | | | 3 |
| 8 | **1244.634371** | 622.820823 | 1227.607822 | 614.307549 | 1226.623806 | 613.815541 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159428 | | | 2 |
| 9 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 42.1 | 1389.732605 | 0.012363 | SVNDLYIQK |
| 5.5 | 1389.735107 | 0.009861 | ATGDIKVTESEIK |
| 4.3 | 1389.746307 | -0.001339 | SEKATSLQAKAEK |
| 4.3 | 1389.746323 | -0.001355 | TAKATLEQDSAKK |
| 3.7 | 1389.728577 | 0.016391 | NMLTESLVALQR |
| 3.3 | 1389.751236 | -0.006268 | QTLALMFQK |
| 2.6 | 1389.732605 | 0.012363 | KDVEINGMFIPK |
| 1.0 | 1389.761612 | -0.016644 | SGVGNIFVKNLDK |

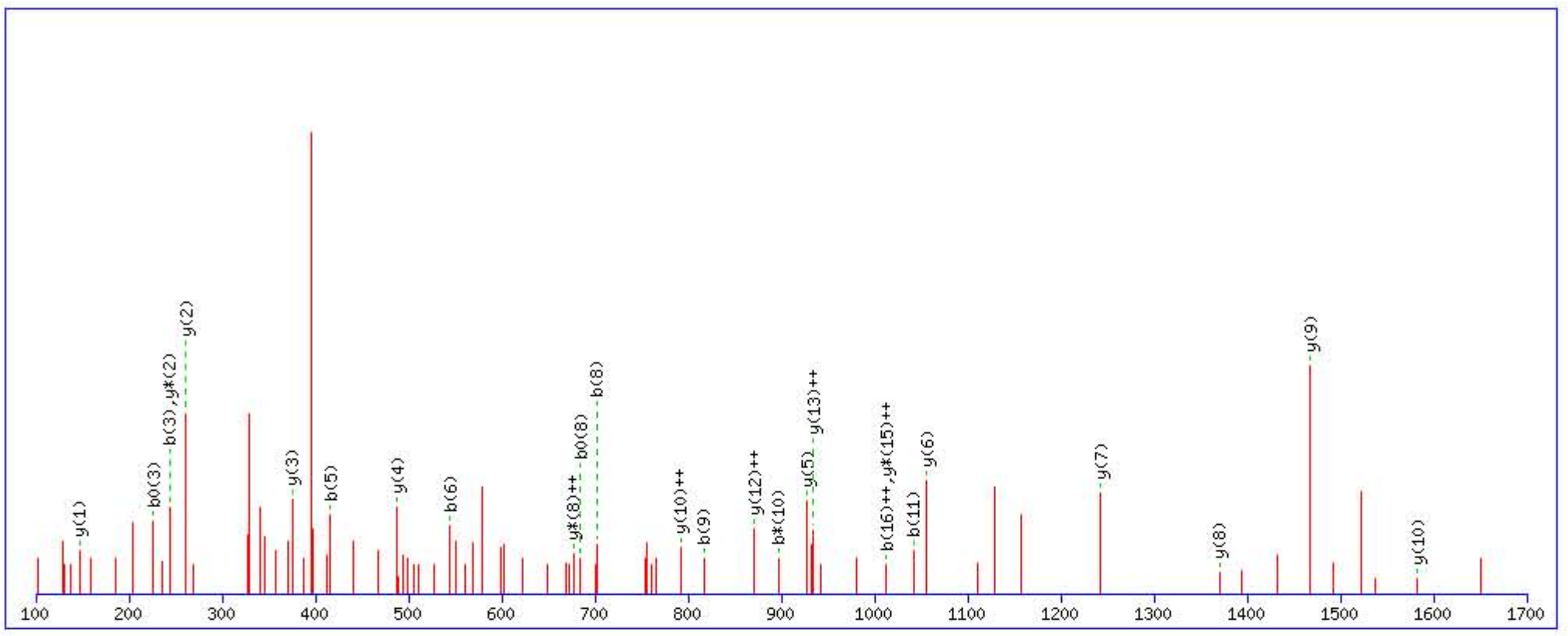
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

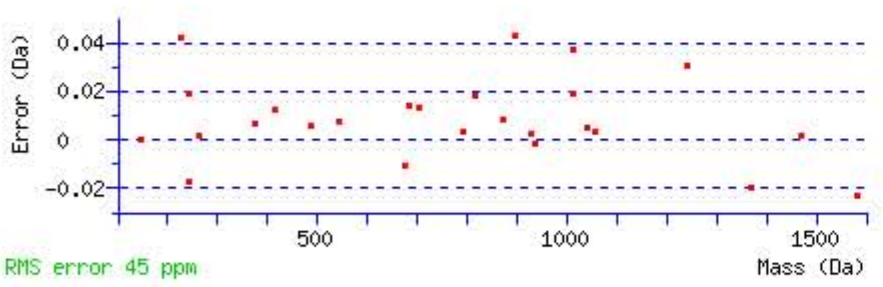
Match to Query 50211: 2283.077682 from(762.033170,3+) rtinseconds(1941) index(33814)
Title: Locus:1.1.1.784.21 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

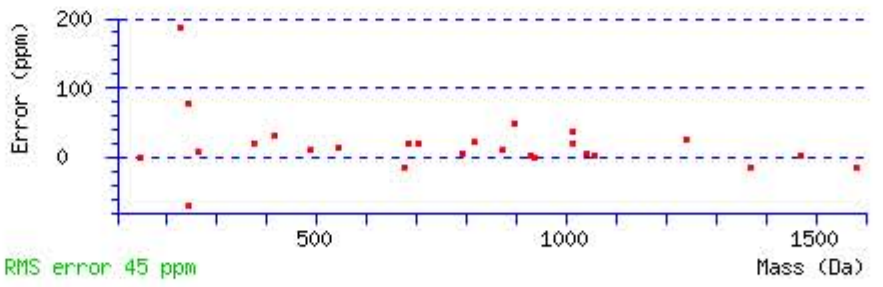
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2283.058975
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q14 : Biotin:Thermo-21345 (Q)
**Ions Score:** 55 **Expect:** 5.9e-005
**Matches :** 26/180 fragment ions using 43 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 18 |
| 2 | 115.050204 | 58.028740 | | | | | G | 2227.044809 | 1114.026042 | 2210.018260 | 1105.512768 | 2209.034244 | 1105.020760 | 17 |
| 3 | *244.092797* | 122.550037 | | | 226.082232 | 113.544754 | E | 2170.023345 | 1085.515310 | 2152.996796 | 1077.002036 | 2152.012780 | 1076.510028 | 16 |
| 4 | 345.140476 | 173.073876 | | | 327.129911 | 164.068594 | T | 2040.980752 | 1020.994014 | 2023.954203 | 1012.480740 | 2022.970187 | 1011.988732 | 15 |
| 5 | *416.177590* | 208.592433 | | | 398.167025 | 199.587151 | A | 1939.933073 | 970.470175 | 1922.906524 | 961.956900 | 1921.922508 | 961.464892 | 14 |
| 6 | *544.236168* | 272.621722 | 527.209619 | 264.108448 | 526.225603 | 263.616440 | Q | 1868.895959 | 934.951618 | 1851.869410 | 926.438343 | 1850.885394 | 925.946335 | 13 |
| 7 | 631.268196 | 316.137736 | 614.241647 | 307.624462 | 613.257631 | 307.132454 | S | 1740.837381 | 870.922329 | 1723.810832 | 862.409054 | 1722.826816 | 861.917046 | 12 |
| 8 | *702.305310* | 351.656293 | 685.278761 | 343.143019 | 684.294745 | 342.651011 | A | 1653.805353 | 827.406315 | 1636.778804 | 818.893040 | 1635.794788 | 818.401032 | 11 |
| 9 | *817.332253* | 409.169765 | 800.305704 | 400.656490 | 799.321688 | 400.164482 | D | *1582.768239* | 791.887758 | 1565.741690 | 783.374483 | 1564.757674 | 782.882475 | 10 |
| 10 | 914.385017 | 457.696147 | 897.358468 | 449.182872 | 896.374452 | 448.690864 | P | *1467.741296* | 734.374286 | 1450.714747 | 725.861012 | 1449.730731 | 725.369004 | 9 |
| 11 | *1042.443595* | 521.725436 | 1025.417046 | 513.212161 | 1024.433030 | 512.720153 | Q | *1370.688532* | 685.847904 | 1353.661983 | 677.334630 | 1352.677967 | 676.842622 | 8 |
| 12 | 1228.522908 | 614.765092 | 1211.496359 | 606.251818 | 1210.512343 | 605.759809 | W | *1242.629954* | 621.818615 | 1225.603405 | 613.305341 | 1224.619389 | 612.813333 | 7 |
| 13 | 1357.565501 | 679.286388 | 1340.538952 | 670.773114 | 1339.554936 | 670.281106 | E | *1056.550641* | 528.778959 | 1039.524092 | 520.265684 | 1038.540076 | 519.773676 | 6 |
| 14 | 1796.790827 | 898.899052 | 1779.764278 | 890.385777 | 1778.780262 | 889.893769 | Q | *927.508048* | 464.257662 | 910.481499 | 455.744388 | | | 5 |
| 15 | 1909.874891 | 955.441083 | 1892.848342 | 946.927809 | 1891.864326 | 946.435801 | L | *488.282722* | 244.644999 | 471.256173 | 236.131725 | | | 4 |
| 16 | 2023.917818 | 1012.462547 | 2006.891269 | 1003.949273 | 2005.907253 | 1003.457265 | N | *375.198658* | 188.102967 | 358.172109 | 179.589693 | | | 3 |
| 17 | 2137.960745 | 1069.484010 | 2120.934196 | 1060.970736 | 2119.950180 | 1060.478728 | N | *261.155731* | 131.081504 | 244.129182 | 122.568229 | | | 2 |
| 18 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 54.6 | 2283.058975 | 0.018707 | GGETAQSADPQWEQLNNK |
| 30.6 | 2283.058975 | 0.018707 | GGETAQSADPQWEQLNNK |
| 6.0 | 2283.058975 | 0.018707 | GGETAQSADPQWEQLNNK |

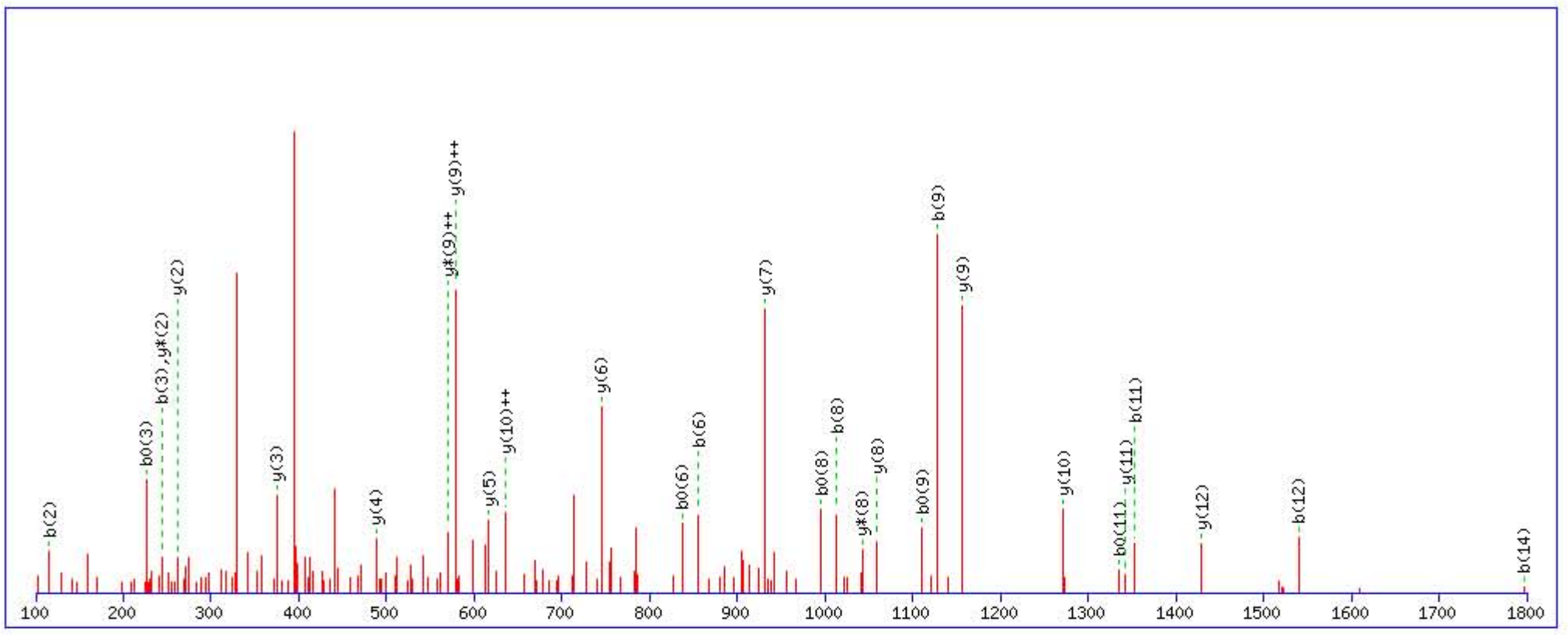
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

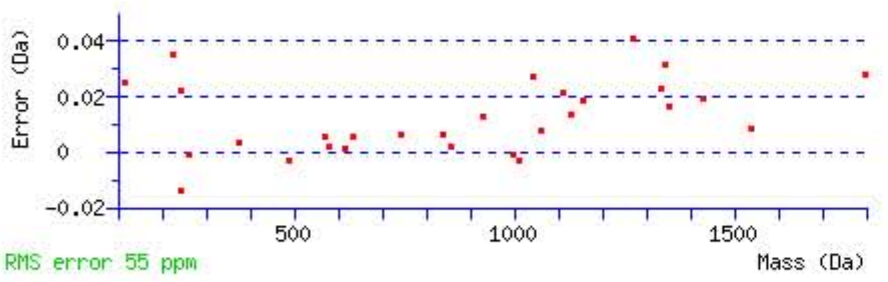
Match to Query 50213: 2283.087342 from(762.036390,3+) rtinseconds(1912) index(33568)
Title: Locus:1.1.1.774.25 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

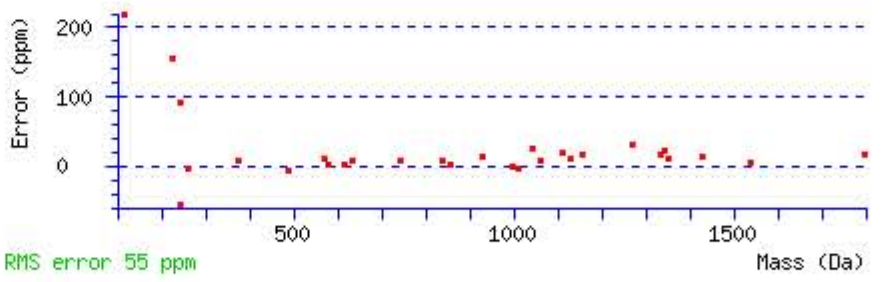
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2283.058975
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 69 **Expect:** 3.8e-007
**Matches :** 29/180 fragment ions using 44 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 18 |
| 2 | *115.050204* | 58.028740 | | | | | G | 2227.044809 | 1114.026042 | 2210.018260 | 1105.512768 | 2209.034244 | 1105.020760 | 17 |
| 3 | *244.092797* | 122.550037 | | | 226.082232 | 113.544754 | E | 2170.023345 | 1085.515310 | 2152.996796 | 1077.002036 | 2152.012780 | 1076.510028 | 16 |
| 4 | 345.140476 | 173.073876 | | | 327.129911 | 164.068594 | T | 2040.980752 | 1020.994014 | 2023.954203 | 1012.480740 | 2022.970187 | 1011.988732 | 15 |
| 5 | 416.177590 | 208.592433 | | | 398.167025 | 199.587151 | A | 1939.933073 | 970.470175 | 1922.906524 | 961.956900 | 1921.922508 | 961.464892 | 14 |
| 6 | *855.402916* | 428.205096 | 838.376367 | 419.691822 | 837.392351 | 419.199814 | Q | 1868.895959 | 934.951618 | 1851.869410 | 926.438343 | 1850.885394 | 925.946335 | 13 |
| 7 | 942.434944 | 471.721110 | 925.408395 | 463.207836 | 924.424379 | 462.715828 | S | *1429.670633* | 715.338955 | 1412.644084 | 706.825680 | 1411.660068 | 706.333672 | 12 |
| 8 | *1013.472058* | 507.239667 | 996.445509 | 498.726393 | 995.461493 | 498.234385 | A | *1342.638605* | 671.822941 | 1325.612056 | 663.309666 | 1324.628040 | 662.817658 | 11 |
| 9 | *1128.499001* | 564.753139 | 1111.472452 | 556.239864 | 1110.488436 | 555.747856 | D | *1271.601491* | 636.304384 | 1254.574942 | 627.791109 | 1253.590926 | 627.299101 | 10 |
| 10 | 1225.551765 | 613.279521 | 1208.525216 | 604.766246 | 1207.541200 | 604.274238 | P | *1156.574548* | 578.790912 | 1139.547999 | 570.277638 | 1138.563983 | 569.785630 | 9 |
| 11 | *1353.610343* | 677.308810 | 1336.583794 | 668.795535 | 1335.599778 | 668.303527 | Q | *1059.521784* | 530.264530 | 1042.495235 | 521.751256 | 1041.511219 | 521.259248 | 8 |
| 12 | *1539.689656* | 770.348466 | 1522.663107 | 761.835192 | 1521.679091 | 761.343184 | W | *931.463206* | 466.235241 | 914.436657 | 457.721967 | 913.452641 | 457.229959 | 7 |
| 13 | 1668.732249 | 834.869762 | 1651.705700 | 826.356488 | 1650.721684 | 825.864480 | E | *745.383893* | 373.195585 | 728.357344 | 364.682310 | 727.373328 | 364.190302 | 6 |
| 14 | *1796.790827* | 898.899052 | 1779.764278 | 890.385777 | 1778.780262 | 889.893769 | Q | *616.341300* | 308.674288 | 599.314751 | 300.161014 | | | 5 |
| 15 | 1909.874891 | 955.441083 | 1892.848342 | 946.927809 | 1891.864326 | 946.435801 | L | *488.282722* | 244.644999 | 471.256173 | 236.131725 | | | 4 |
| 16 | 2023.917818 | 1012.462547 | 2006.891269 | 1003.949273 | 2005.907253 | 1003.457265 | N | *375.198658* | 188.102967 | 358.172109 | 179.589693 | | | 3 |
| 17 | 2137.960745 | 1069.484010 | 2120.934196 | 1060.970736 | 2119.950180 | 1060.478728 | N | *261.155731* | 131.081504 | 244.129182 | 122.568229 | | | 2 |
| 18 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

### All matches to this query

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 69.4 | 2283.058975 | 0.028367 | GGETAQSADPQWEQLNNK |
| 15.1 | 2283.058975 | 0.028367 | GGETAQSADPQWEQLNNK |
| 0.9 | 2283.080109 | 0.007233 | RGVEKMVDPGEEQPTQENPK |
| 0.3 | 2283.058975 | 0.028367 | GGETAQSADPQWEQLNNK |

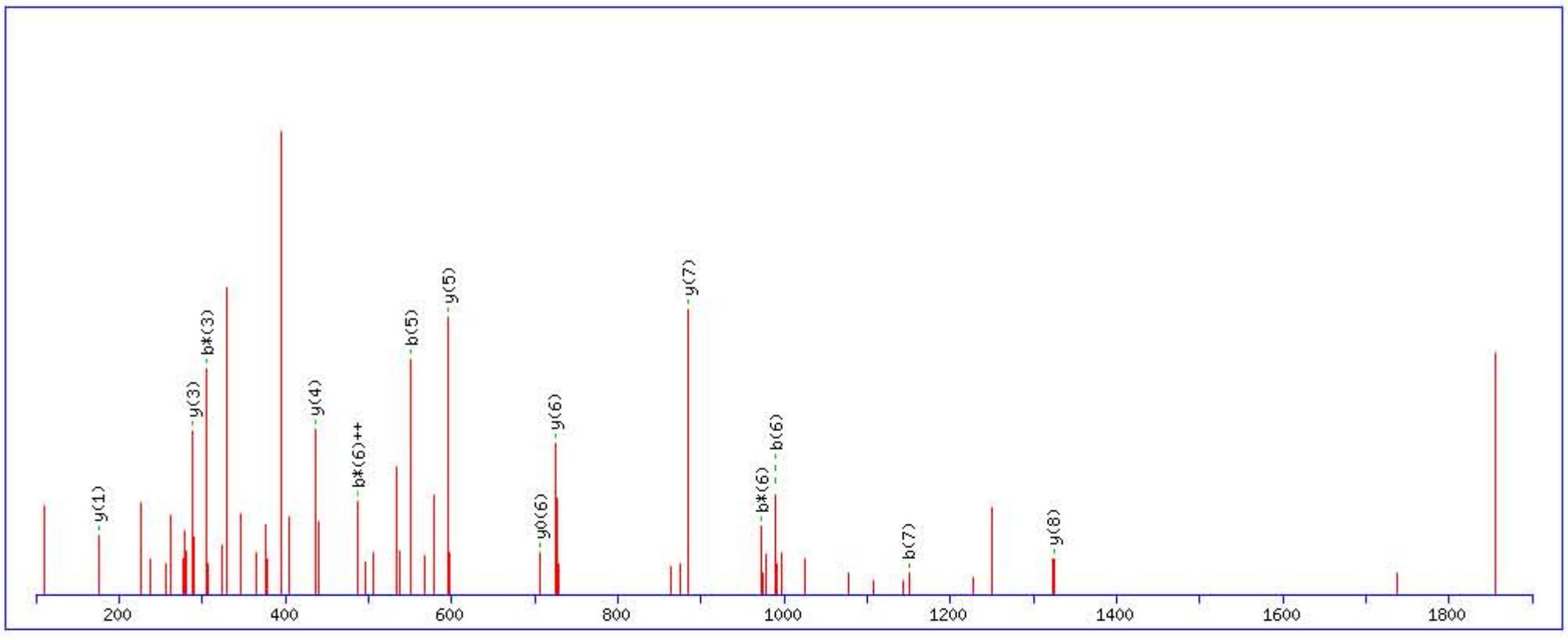
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QGHVEQCECFGGR**
Found in **HGFA_HUMAN**, Hepatocyte growth factor activator OS=Homo sapiens GN=HGFAC PE=1 SV=1

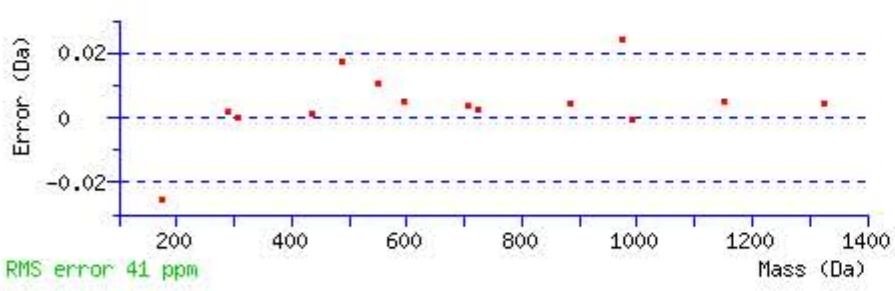
Match to Query 41763: 1873.814262 from(625.612030,3+) rtinseconds(1540) index(47213)
Title: Locus:1.1.1.1774.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

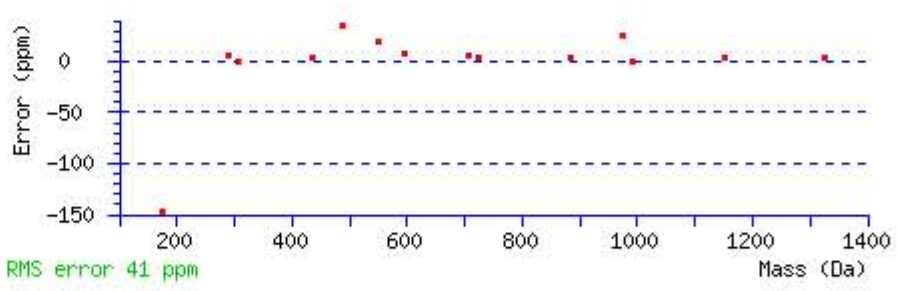
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1873.802216
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 37 **Expect:** 0.00037
**Matches :** 14/126 fragment ions using 27 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.065854 | 65.036565 | 112.039305 | 56.523291 | | | Q | | | | | | | 13 |
| 2 | 186.087318 | 93.547297 | 169.060769 | 85.034023 | | | G | 1746.750894 | 873.879085 | 1729.724345 | 865.365811 | 1728.740329 | 864.873803 | 12 |
| 3 | 323.146230 | 162.076753 | 306.119681 | 153.563479 | | | H | 1689.729430 | 845.368353 | 1672.702881 | 836.855079 | 1671.718865 | 836.363071 | 11 |
| 4 | 422.214644 | 211.610960 | 405.188095 | 203.097686 | | | V | 1552.670518 | 776.838897 | 1535.643969 | 768.325623 | 1534.659953 | 767.833615 | 10 |
| 5 | **551.257237** | 276.132257 | 534.230688 | 267.618982 | 533.246672 | 267.126974 | E | 1453.602104 | 727.304690 | 1436.575555 | 718.791416 | 1435.591539 | 718.299408 | 9 |
| 6 | **990.482563** | 495.744920 | 973.456014 | 487.231645 | 972.471998 | 486.739637 | Q | *1324.559511* | 662.783394 | 1307.532962 | 654.270119 | 1306.548946 | 653.778111 | 8 |
| 7 | **1150.513212** | 575.760244 | 1133.486663 | 567.246970 | 1132.502647 | 566.754962 | C | *885.334185* | 443.170731 | 868.307636 | 434.657456 | 867.323620 | 434.165448 | 7 |
| 8 | 1279.555805 | 640.281541 | 1262.529256 | 631.768266 | 1261.545240 | 631.276258 | E | *725.303536* | 363.155406 | 708.276987 | 354.642132 | 707.292971 | 354.150124 | 6 |
| 9 | 1439.586454 | 720.296865 | 1422.559905 | 711.783591 | 1421.575889 | 711.291583 | C | *596.260943* | 298.634110 | 579.234394 | 290.120835 | | | 5 |
| 10 | 1586.654868 | 793.831072 | 1569.628319 | 785.317798 | 1568.644303 | 784.825790 | F | *436.230294* | 218.618785 | 419.203745 | 210.105510 | | | 4 |
| 11 | 1643.676332 | 822.341804 | 1626.649783 | 813.828530 | 1625.665767 | 813.336522 | G | *289.161880* | 145.084578 | 272.135331 | 136.571303 | | | 3 |
| 12 | 1700.697796 | 850.852536 | 1683.671247 | 842.339262 | 1682.687231 | 841.847254 | G | 232.140416 | 116.573846 | 215.113867 | 108.060571 | | | 2 |
| 13 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

### All matches to this query

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 36.8 | 1873.802216 | 0.012046 | QGHVEQCECFGGR |
| 32.2 | 1873.802216 | 0.012046 | QGHVEQCECFGGR |
| 0.1 | 1873.841080 | -0.026818 | MDTTMEADLGATGHRPR |
| 0.1 | 1873.841080 | -0.026818 | MDTTMEADLGATGHRPR |

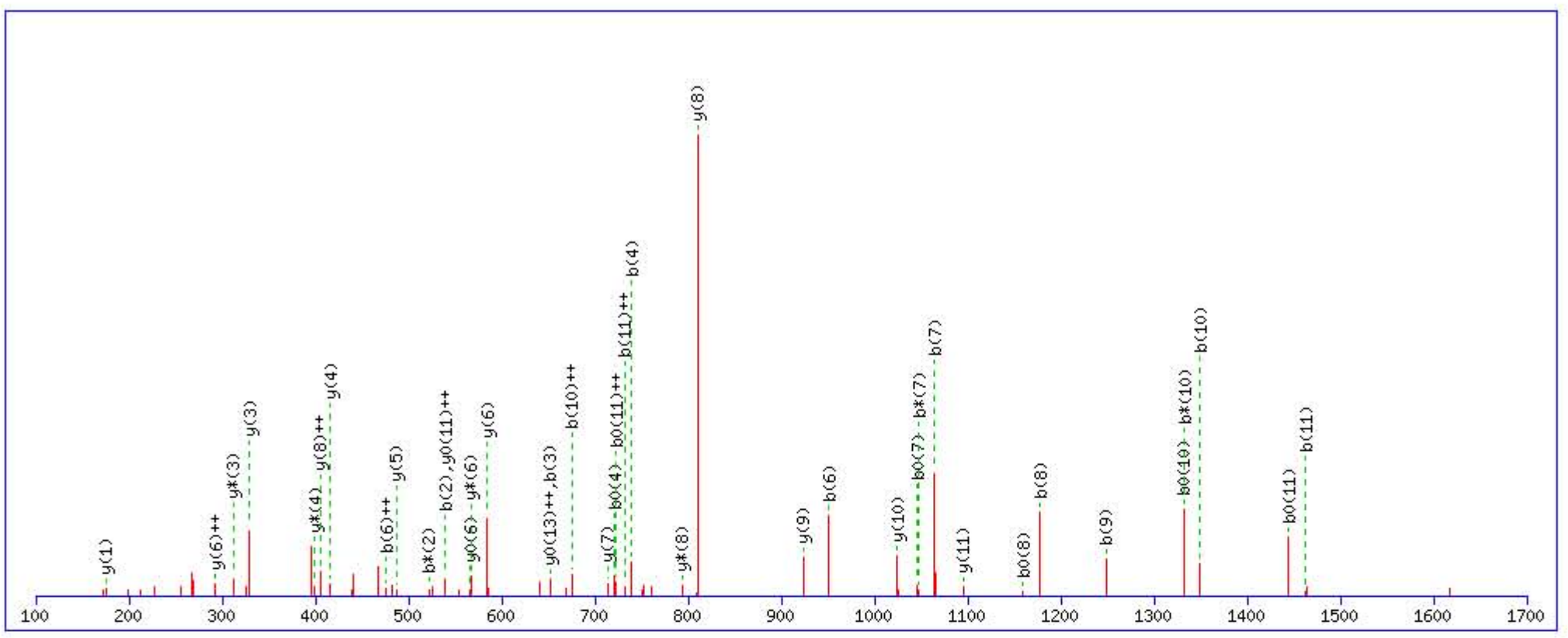
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VQLSPDLLATLPEPASPGR**
Found in **HGFA_HUMAN**, Hepatocyte growth factor activator OS=Homo sapiens GN=HGFAC PE=1 SV=1

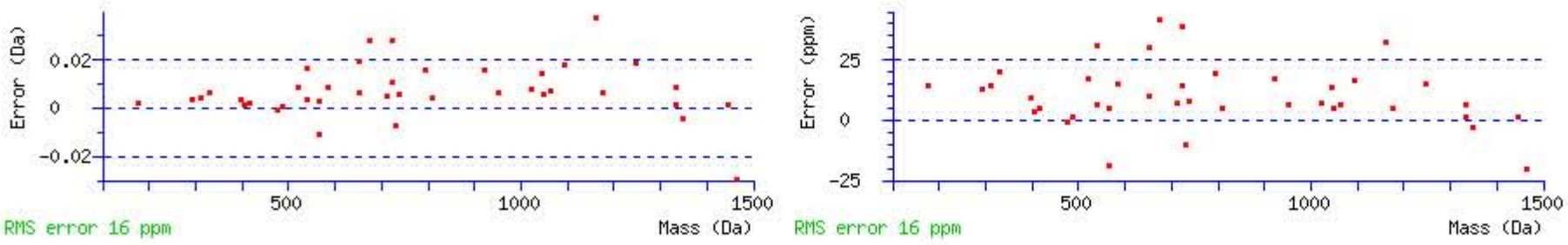
Match to Query 49941: 2271.249342 from(758.090390,3+) rtinseconds(2682) index(9175)
Title: Locus:1.1.1.2211.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2271.229675
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 70 **Expect:** 4.5e-007
**Matches :** 40/202 fragment ions using 64 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 19 |
| 2 | *539.301016* | 270.154146 | 522.274467 | 261.640872 | | | Q | 2173.168553 | 1087.087914 | 2156.142004 | 1078.574640 | 2155.157988 | 1078.082632 | 18 |
| 3 | *652.385080* | 326.696178 | 635.358531 | 318.182904 | | | L | 1733.943227 | 867.475252 | 1716.916678 | 858.961977 | 1715.932662 | 858.469969 | 17 |
| 4 | *739.417108* | 370.212192 | 722.390559 | 361.698918 | 721.406543 | 361.206910 | S | 1620.859163 | 810.933219 | 1603.832614 | 802.419945 | 1602.848598 | 801.927937 | 16 |
| 5 | 836.469872 | 418.738574 | 819.443323 | 410.225300 | 818.459307 | 409.733292 | P | 1533.827135 | 767.417206 | 1516.800586 | 758.903931 | 1515.816570 | 758.411923 | 15 |
| 6 | *951.496815* | *476.252046* | 934.470266 | 467.738771 | 933.486250 | 467.246763 | D | 1436.774371 | 718.890824 | 1419.747822 | 710.377549 | 1418.763806 | 709.885541 | 14 |
| 7 | *1064.580879* | 532.794078 | 1047.554330 | 524.280803 | 1046.570314 | 523.788795 | L | 1321.747428 | 661.377352 | 1304.720879 | 652.864078 | 1303.736863 | 652.372069 | 13 |
| 8 | *1177.664943* | 589.336110 | 1160.638394 | 580.822835 | 1159.654378 | 580.330827 | L | 1208.663364 | 604.835320 | 1191.636815 | 596.322046 | 1190.652799 | 595.830038 | 12 |
| 9 | *1248.702057* | 624.854667 | 1231.675508 | 616.341392 | 1230.691492 | 615.849384 | A | *1095.579300* | 548.293288 | 1078.552751 | 539.780014 | 1077.568735 | 539.288006 | 11 |
| 10 | *1349.749736* | *675.378506* | 1332.723187 | 666.865232 | 1331.739171 | 666.373223 | T | *1024.542186* | 512.774731 | 1007.515637 | 504.261456 | 1006.531621 | 503.769448 | 10 |
| 11 | *1462.833800* | *731.920538* | 1445.807251 | 723.407264 | 1444.823235 | 722.915255 | L | *923.494507* | 462.250892 | 906.467958 | 453.737617 | 905.483942 | 453.245609 | 9 |
| 12 | 1559.886564 | 780.446920 | 1542.860015 | 771.933646 | 1541.875999 | 771.441637 | P | *810.410443* | 405.708860 | 793.383894 | 397.195585 | 792.399878 | 396.703577 | 8 |
| 13 | 1688.929157 | 844.968216 | 1671.902608 | 836.454942 | 1670.918592 | 835.962934 | E | *713.357679* | 357.182478 | 696.331130 | 348.669203 | 695.347114 | 348.177195 | 7 |
| 14 | 1785.981921 | 893.494598 | 1768.955372 | 884.981324 | 1767.971356 | 884.489316 | P | *584.315086* | 292.661181 | 567.288537 | 284.147907 | 566.304521 | 283.655899 | 6 |
| 15 | 1857.019035 | 929.013155 | 1839.992486 | 920.499881 | 1839.008470 | 920.007873 | A | *487.262322* | 244.134799 | 470.235773 | 235.621525 | 469.251757 | 235.129517 | 5 |
| 16 | 1944.051063 | 972.529169 | 1927.024514 | 964.015895 | 1926.040498 | 963.523887 | S | *416.225208* | 208.616242 | 399.198659 | 200.102968 | 398.214643 | 199.610960 | 4 |
| 17 | 2041.103827 | 1021.055552 | 2024.077278 | 1012.542277 | 2023.093262 | 1012.050269 | P | *329.193180* | 165.100228 | 312.166631 | 156.586954 | | | 3 |
| 18 | 2098.125291 | 1049.566283 | 2081.098742 | 1041.053009 | 2080.114726 | 1040.561001 | G | 232.140416 | 116.573846 | 215.113867 | 108.060572 | | | 2 |
| 19 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 69.8 | 2271.229675 | 0.019667 | VQLSPDLLATLPEPASPGR |
| 1.9 | 2271.226303 | 0.023039 | IAKSDPPTLLTPSKWSVEFR |
| 0.3 | 2271.277283 | -0.027941 | IIQGDIIASNGLLHILDR |

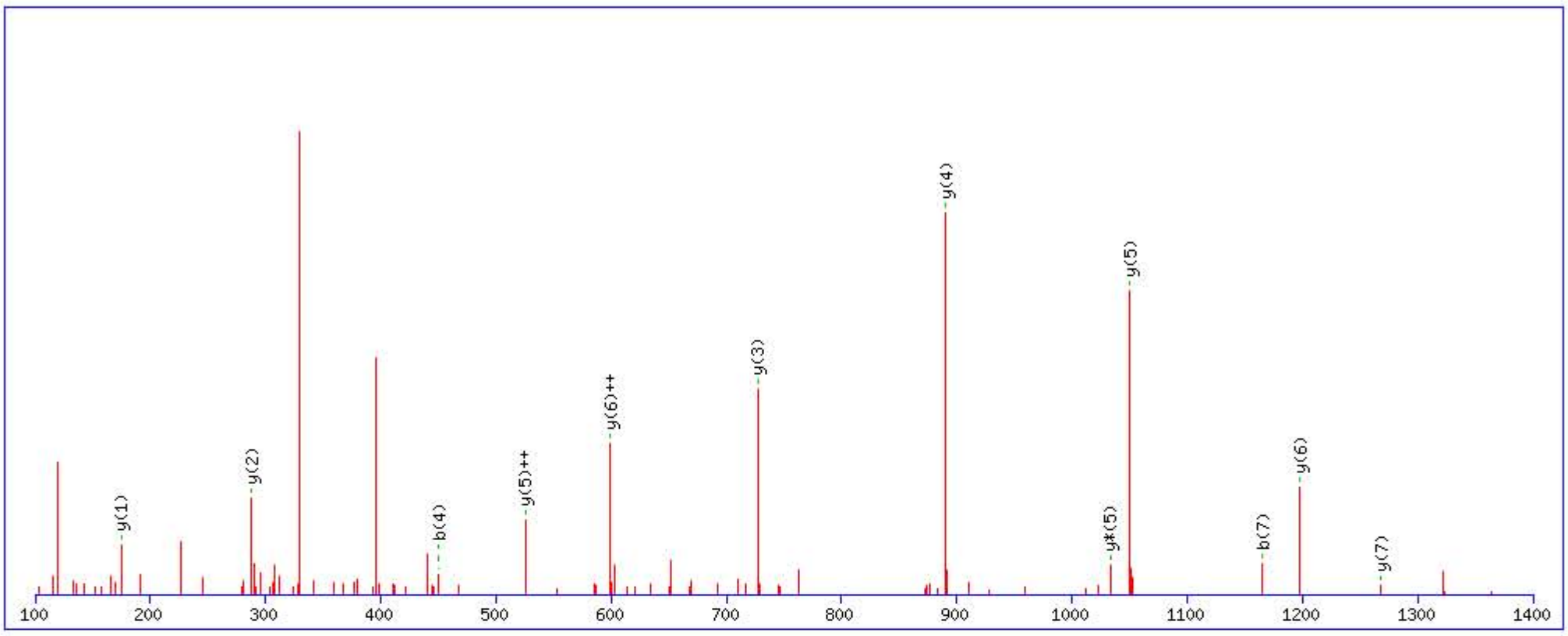
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AAFCYQIR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

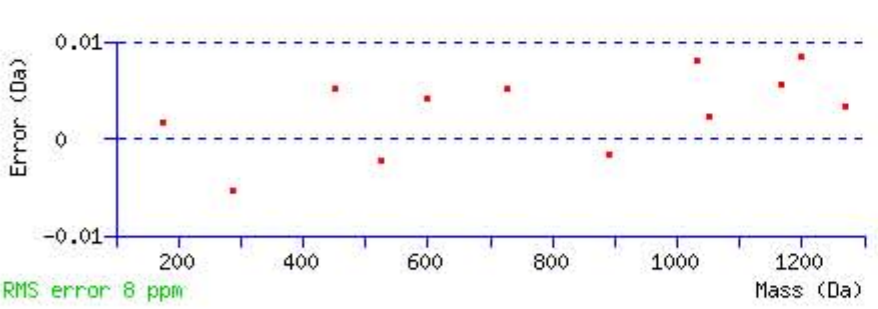
Match to Query 24058: 1338.665088 from(670.339820,2+) rtinseconds(2010) index(66474)
Title: Locus:1.1.1.1975.7 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

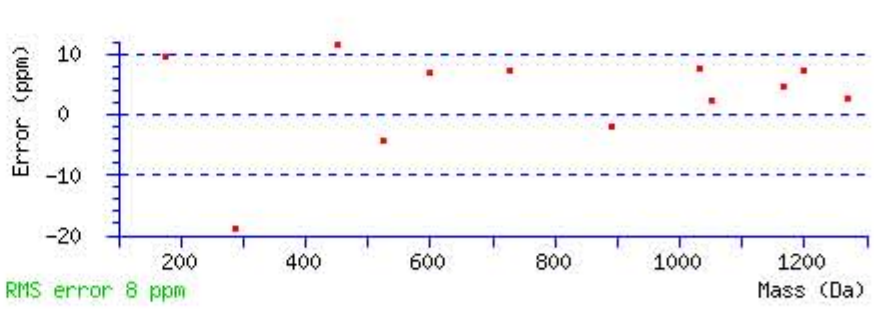
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1338.657669
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 41 **Expect:** 0.0007
**Matches :** 12/46 fragment ions using 25 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | A | | | | | 8 |
| 2 | 143.081504 | 72.044390 | | | A | *1268.627848* | 634.817562 | 1251.601299 | 626.304288 | 7 |
| 3 | 290.149918 | 145.578597 | | | F | *1197.590734* | 599.299005 | 1180.564185 | 590.785731 | 6 |
| 4 | **450.180567** | 225.593922 | | | C | *1050.522320* | 525.764798 | 1033.495771 | 517.251524 | 5 |
| 5 | 613.243896 | 307.125586 | | | Y | *890.491671* | 445.749474 | 873.465122 | 437.236199 | 4 |
| 6 | 1052.469222 | 526.738249 | 1035.442673 | 518.224975 | Q | *727.428342* | 364.217809 | 710.401793 | 355.704534 | 3 |
| 7 | **1165.553286** | 583.280281 | 1148.526737 | 574.767007 | I | *288.203016* | 144.605146 | 271.176467 | 136.091871 | 2 |
| 8 | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 40.7 | 1338.657669 | 0.007419 | AAFCYQIR |
| 7.1 | 1338.657669 | 0.007419 | AAFLQYCR |

**Mascot:** http://www.matrixscience.com/

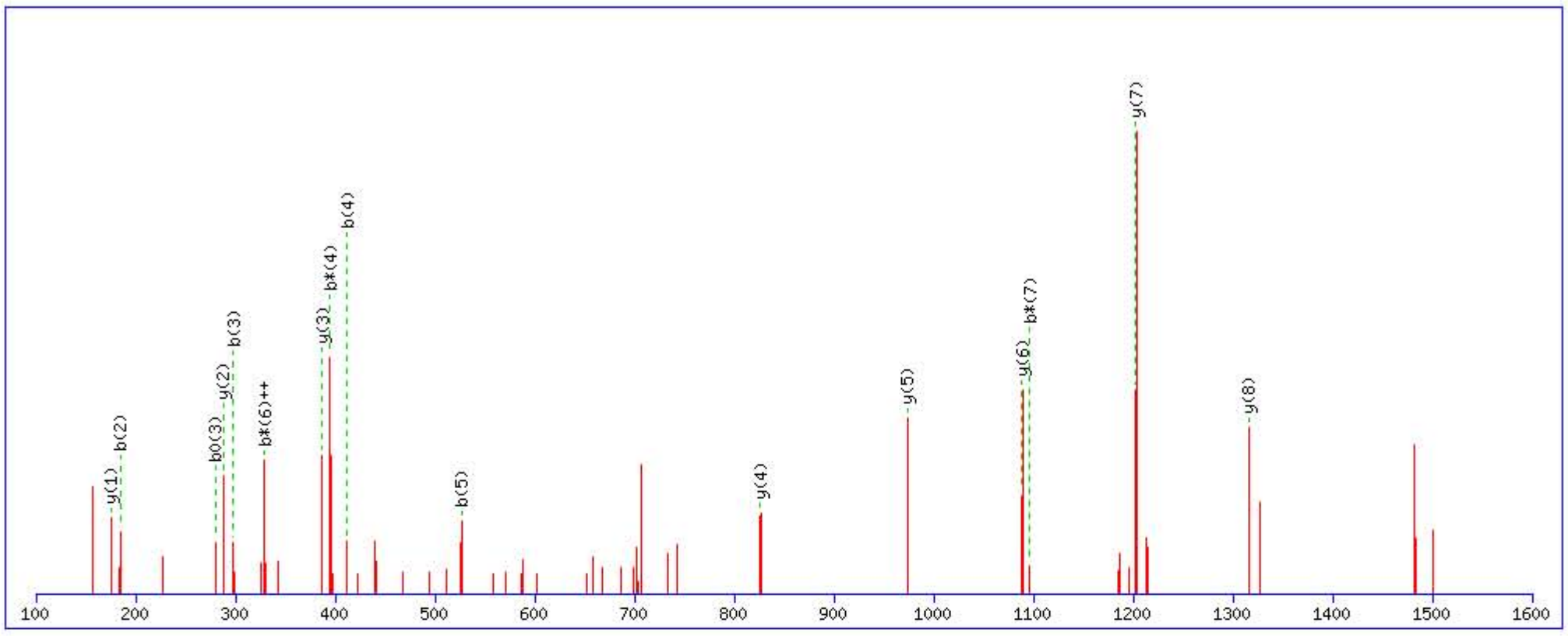
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SPLNDFQVLR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

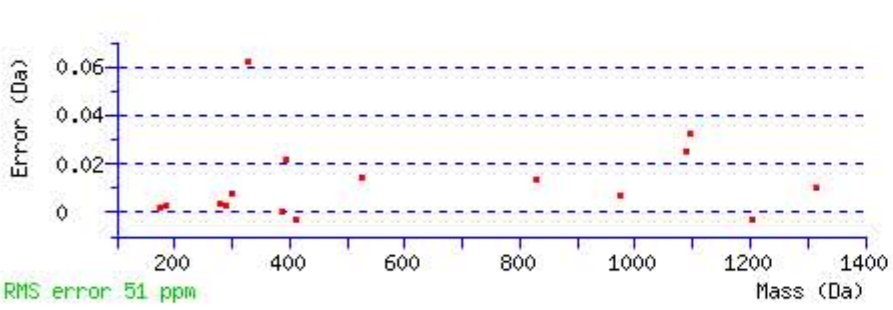
Match to Query 31006: 1498.808088 from(750.411320,2+) rtinseconds(2367) index(68554)
Title: Locus:1.1.1.2099.17 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

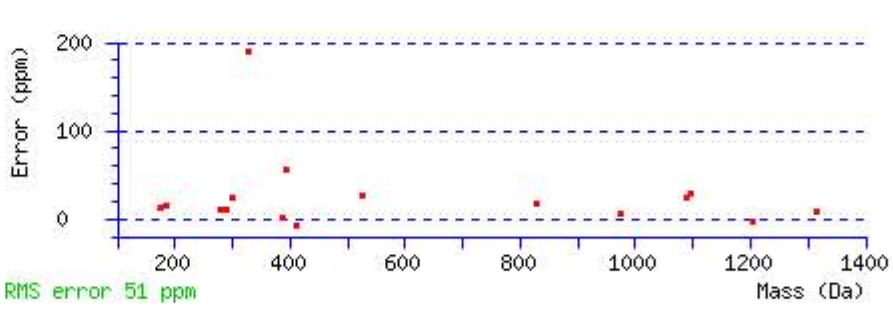
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1498.796616
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 36 **Expect:** 0.0045
**Matches :** 16/92 fragment ions using 41 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 10 |
| 2 | 185.092068 | 93.049672 | | | 167.081503 | 84.044389 | P | 1412.771868 | 706.889572 | 1395.745319 | 698.376298 | 1394.761303 | 697.884290 | 9 |
| 3 | 298.176132 | 149.591704 | | | 280.165567 | 140.586422 | L | 1315.719104 | 658.363190 | 1298.692555 | 649.849916 | 1297.708539 | 649.357908 | 8 |
| 4 | 412.219059 | 206.613168 | 395.192510 | 198.099893 | 394.208494 | 197.607885 | N | 1202.635040 | 601.821158 | 1185.608491 | 593.307884 | 1184.624475 | 592.815876 | 7 |
| 5 | 527.246002 | 264.126639 | 510.219453 | 255.613365 | 509.235437 | 255.121357 | D | 1088.592113 | 544.799695 | 1071.565564 | 536.286420 | 1070.581548 | 535.794412 | 6 |
| 6 | 674.314416 | 337.660846 | 657.287867 | 329.147572 | 656.303851 | 328.655564 | F | 973.565170 | 487.286223 | 956.538621 | 478.772949 | | | 5 |
| 7 | 1113.539742 | 557.273509 | 1096.513193 | 548.760235 | 1095.529177 | 548.268227 | Q | 826.496756 | 413.752016 | 809.470207 | 405.238742 | | | 4 |
| 8 | 1212.608156 | 606.807716 | 1195.581607 | 598.294442 | 1194.597591 | 597.802434 | V | 387.271430 | 194.139353 | 370.244881 | 185.626078 | | | 3 |
| 9 | 1325.692220 | 663.349748 | 1308.665671 | 654.836474 | 1307.681655 | 654.344466 | L | 288.203016 | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 10 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 36.4 | 1498.796616 | 0.011472 | SPLNDFQVLR |
| 10.8 | 1498.799103 | 0.008985 | ALLNLPGTQTSGEAK |
| 2.6 | 1498.792572 | 0.015516 | ALNITSLQMHSLR |
| 1.9 | 1498.799973 | 0.008115 | ALLDQLMGTAR |

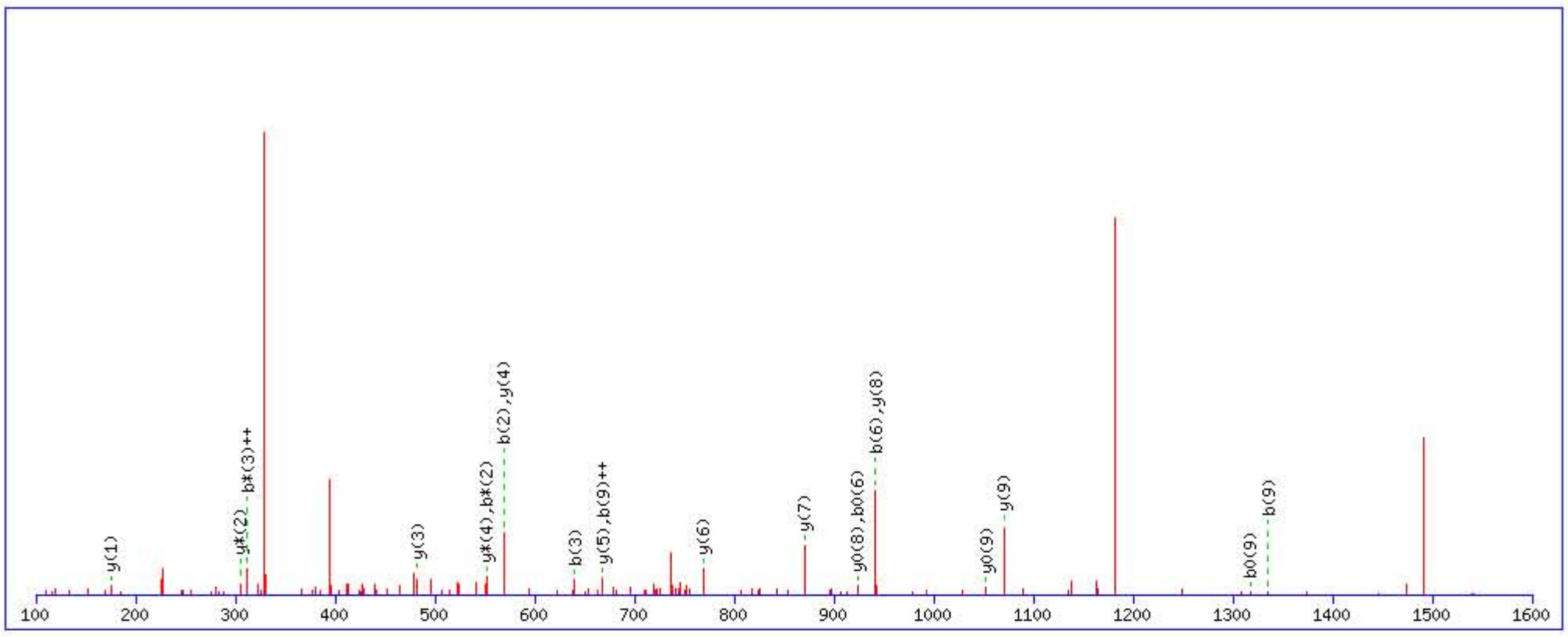
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QEATTVSCFR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

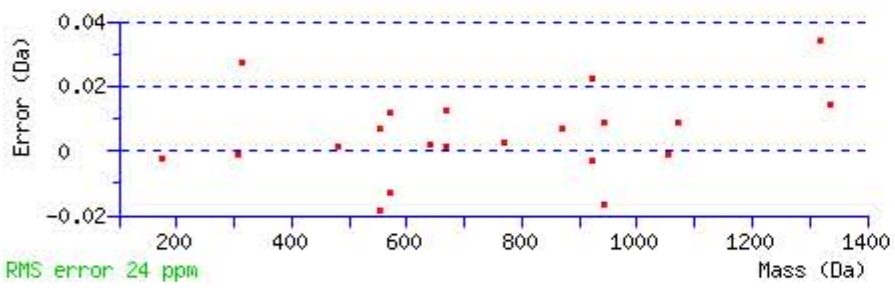
Match to Query 31440: 1508.716668 from(755.365610,2+) rtinseconds(1744) index(64846)
Title: Locus:1.1.1.1882.12 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

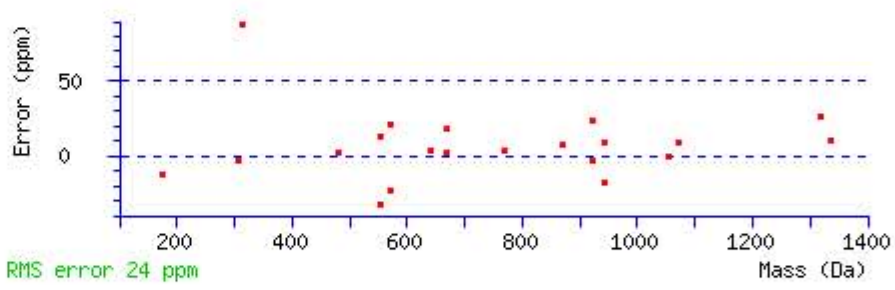
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1508.711578
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 40 **Expect:** 0.0018
**Matches :** 21/100 fragment ions using 41 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 10 |
| 2 | **569.275195** | 285.141236 | 552.248646 | 276.627961 | 551.264630 | 276.135953 | E | *1070.493522* | 535.750399 | 1053.466973 | 527.237125 | 1052.482957 | 526.745117 | 9 |
| 3 | **640.312309** | 320.659793 | 623.285760 | 312.146518 | 622.301744 | 311.654510 | A | *941.450929* | 471.229103 | 924.424380 | 462.715828 | 923.440364 | 462.223820 | 8 |
| 4 | 741.359988 | 371.183632 | 724.333439 | 362.670358 | 723.349423 | 362.178350 | T | *870.413815* | 435.710546 | 853.387266 | 427.197271 | 852.403250 | 426.705263 | 7 |
| 5 | 842.407667 | 421.707472 | 825.381118 | 413.194197 | 824.397102 | 412.702189 | T | *769.366136* | 385.186706 | 752.339587 | 376.673432 | 751.355571 | 376.181424 | 6 |
| 6 | **941.476081** | 471.241679 | 924.449532 | 462.728404 | 923.465516 | 462.236396 | V | *668.318457* | 334.662867 | 651.291908 | 326.149592 | 650.307892 | 325.657584 | 5 |
| 7 | 1028.508109 | 514.757693 | 1011.481560 | 506.244418 | 1010.497544 | 505.752410 | S | *569.250043* | 285.128660 | 552.223494 | 276.615385 | 551.239478 | 276.123377 | 4 |
| 8 | 1188.538758 | 594.773017 | 1171.512209 | 586.259743 | 1170.528193 | 585.767735 | C | *482.218015* | 241.612646 | 465.191466 | 233.099371 | | | 3 |
| 9 | **1335.607172** | 668.307224 | 1318.580623 | 659.793950 | 1317.596607 | 659.301942 | F | 322.187366 | 161.597321 | 305.160817 | 153.084047 | | | 2 |
| 10 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

### All matches to this query

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 39.5 | 1508.711578 | 0.005090 | QEATTVSCFR |
| 12.8 | 1508.711380 | 0.005288 | RTASGGRTEQGMSR |
| 8.3 | 1508.708191 | 0.008477 | EYGSMYTVHLGPR |
| 7.0 | 1508.726624 | -0.009956 | RDGQLQRMNYGR |
| 5.4 | 1508.733154 | -0.016486 | APGSRLSSGGTNYSR |
| 2.6 | 1508.703461 | 0.013207 | LKSFTYEYEDSK |
| 2.5 | 1508.715378 | 0.001290 | QRGHEAEESR |
| 2.2 | 1508.736710 | -0.020042 | LKSSQMEQFT |
| 1.9 | 1508.710648 | 0.006020 | DEEAAEKKFEASR |
| 1.4 | 1508.711548 | 0.005120 | QMSKYPSGER |

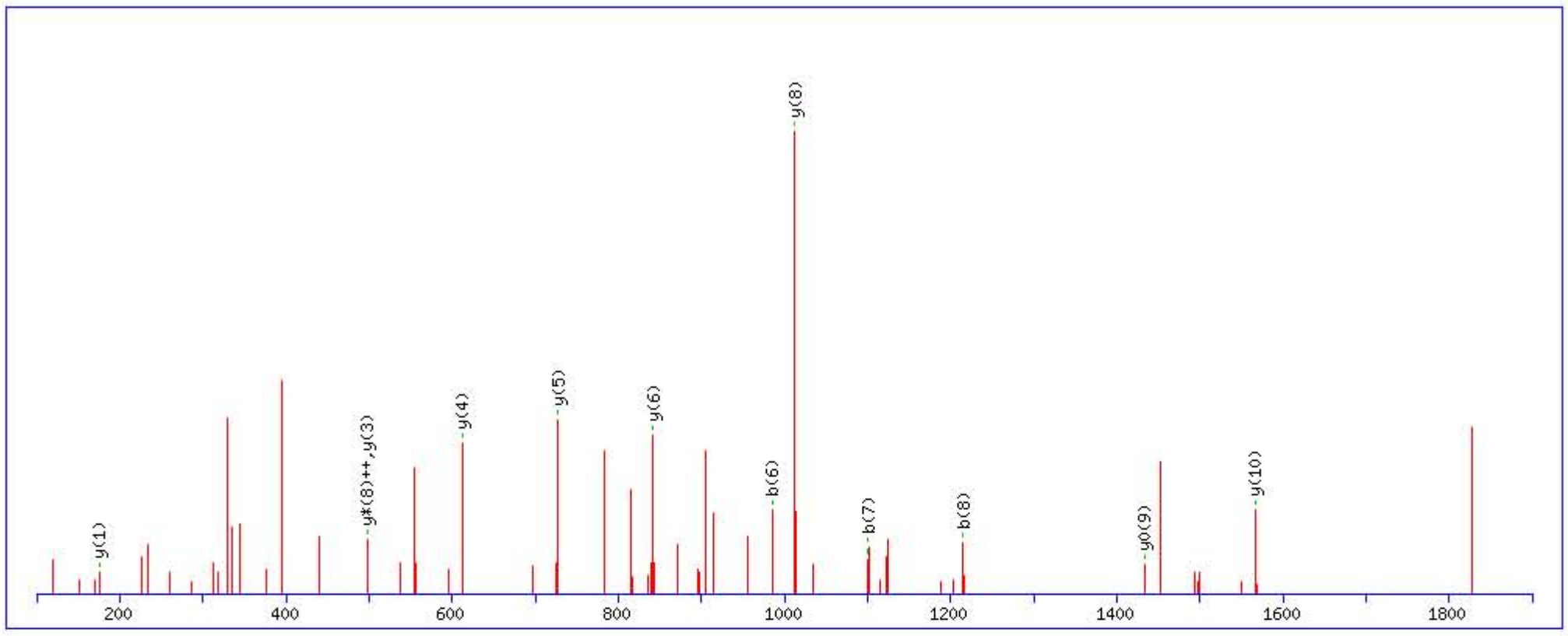
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FLDQGLDDNYCR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

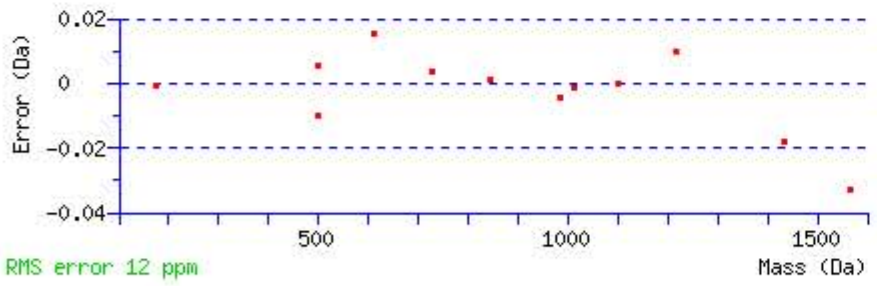
Match to Query 40804: 1825.830088 from(913.922320,2+) rtinseconds(2159) index(67402)
Title: Locus:1.1.1.2026.25 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

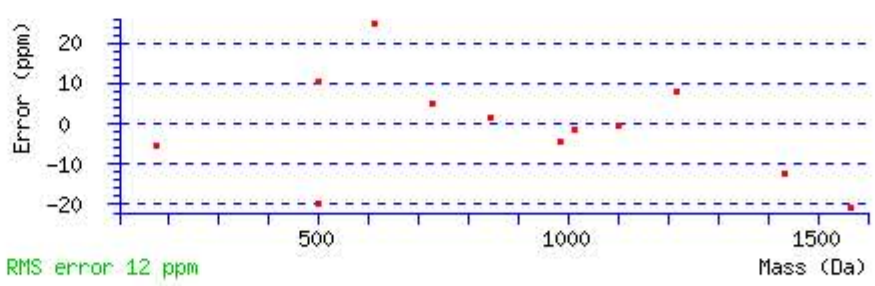
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1825.812744
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0051
**Matches :** 12/114 fragment ions using 25 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 12 |
| 2 | 261.159754 | 131.083515 | | | | | L | 1679.751604 | 840.379440 | 1662.725055 | 831.866166 | 1661.741039 | 831.374158 | 11 |
| 3 | 376.186697 | 188.596986 | | | 358.176132 | 179.591704 | D | *1566.667540* | 783.837408 | 1549.640991 | 775.324134 | 1548.656975 | 774.832126 | 10 |
| 4 | 815.412023 | 408.209650 | 798.385474 | 399.696375 | 797.401458 | 399.204367 | Q | 1451.640597 | 726.323937 | 1434.614048 | 717.810662 | 1433.630032 | 717.318654 | 9 |
| 5 | 872.433487 | 436.720382 | 855.406938 | 428.207107 | 854.422922 | 427.715099 | G | *1012.415271* | 506.711274 | 995.388722 | 498.197999 | 994.404706 | 497.705991 | 8 |
| 6 | **985.517551** | 493.262414 | 968.491002 | 484.749139 | 967.506986 | 484.257131 | L | 955.393807 | 478.200542 | 938.367258 | 469.687267 | 937.383242 | 469.195259 | 7 |
| 7 | **1100.544494** | 550.775885 | 1083.517945 | 542.262611 | 1082.533929 | 541.770603 | D | *842.309743* | 421.658510 | 825.283194 | 413.145235 | 824.299178 | 412.653227 | 6 |
| 8 | **1215.571437** | 608.289357 | 1198.544888 | 599.776082 | 1197.560872 | 599.284074 | D | *727.282800* | 364.145038 | 710.256251 | 355.631764 | 709.272235 | 355.139756 | 5 |
| 9 | 1329.614364 | 665.310820 | 1312.587815 | 656.797546 | 1311.603799 | 656.305538 | N | *612.255857* | 306.631567 | 595.229308 | 298.118292 | | | 4 |
| 10 | 1492.677693 | 746.842485 | 1475.651144 | 738.329210 | 1474.667128 | 737.837202 | Y | *498.212930* | 249.610103 | 481.186381 | 241.096829 | | | 3 |
| 11 | 1652.708342 | 826.857809 | 1635.681793 | 818.344535 | 1634.697777 | 817.852527 | C | 335.149601 | 168.078438 | 318.123052 | 159.565164 | | | 2 |
| 12 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.0 | 1825.812744 | 0.017344 | FLDQGLDDNYCR |

**Mascot:** http://www.matrixscience.com/

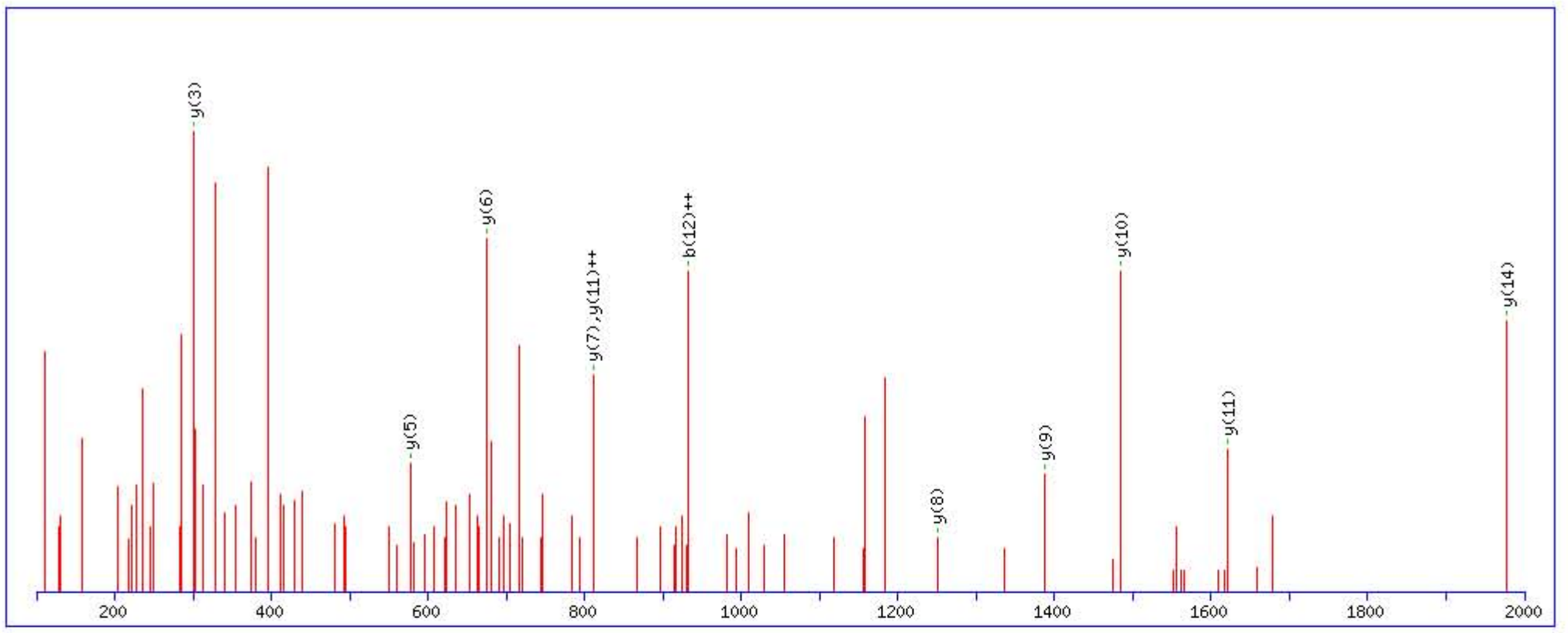
# MATRIX SCIENCE Mascot Search Results

## Peptide View

MS/MS Fragmentation of **WDLQHPHQHPFEPGK**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

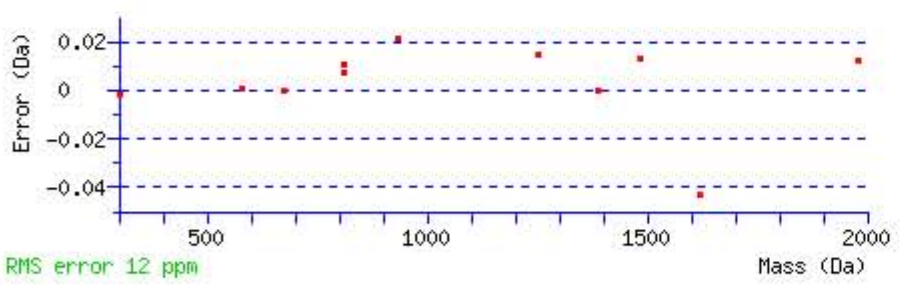
Match to Query 47659: 2163.054132 from(722.025320,3+) rtinseconds(1726) index(64730)
Title: Locus:1.1.1.1876.14 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

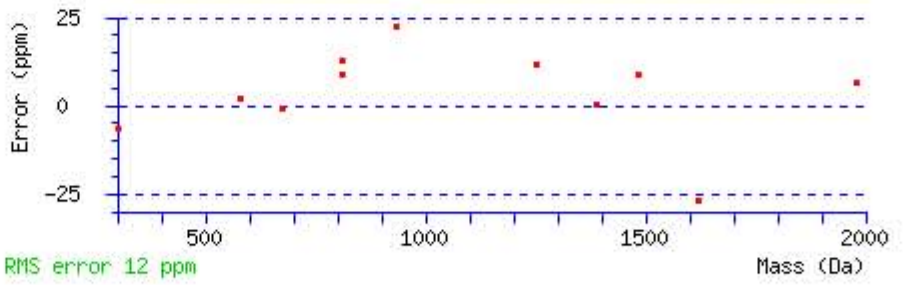
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2163.047256
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 0.00011
**Matches :** 11/154 fragment ions using 17 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 187.086589 | 94.046932 | | | | | W | | | | | | | 15 |
| 2 | 302.113532 | 151.560404 | | | 284.102967 | 142.555122 | D | *1977.975214* | 989.491245 | 1960.948665 | 980.977971 | 1959.964649 | 980.485963 | 14 |
| 3 | 415.197596 | 208.102436 | | | 397.187031 | 199.097154 | L | 1862.948271 | 931.977774 | 1845.921722 | 923.464499 | 1844.937706 | 922.972491 | 13 |
| 4 | 543.256174 | 272.131725 | 526.229625 | 263.618451 | 525.245609 | 263.126443 | Q | 1749.864207 | 875.435741 | 1732.837658 | 866.922467 | 1731.853642 | 866.430459 | 12 |
| 5 | 680.315086 | 340.661181 | 663.288537 | 332.147907 | 662.304521 | 331.655899 | H | *1621.805629* | 811.406453 | 1604.779080 | 802.893178 | 1603.795064 | 802.401170 | 11 |
| 6 | 777.367850 | 389.187563 | 760.341301 | 380.674289 | 759.357285 | 380.182281 | P | *1484.746717* | 742.876997 | 1467.720168 | 734.363722 | 1466.736152 | 733.871714 | 10 |
| 7 | 914.426762 | 457.717019 | 897.400213 | 449.203745 | 896.416197 | 448.711737 | H | *1387.693953* | 694.350615 | 1370.667404 | 685.837340 | 1369.683388 | 685.345332 | 9 |
| 8 | 1353.652088 | 677.329682 | 1336.625539 | 668.816408 | 1335.641523 | 668.324400 | Q | *1250.635041* | 625.821159 | 1233.608492 | 617.307884 | 1232.624476 | 616.815876 | 8 |
| 9 | 1490.711000 | 745.859138 | 1473.684451 | 737.345864 | 1472.700435 | 736.853856 | H | *811.409715* | 406.208496 | 794.383166 | 397.695221 | 793.399150 | 397.203213 | 7 |
| 10 | 1587.763764 | 794.385520 | 1570.737215 | 785.872246 | 1569.753199 | 785.380238 | P | *674.350803* | 337.679040 | 657.324254 | 329.165765 | 656.340238 | 328.673757 | 6 |
| 11 | 1734.832178 | 867.919727 | 1717.805629 | 859.406453 | 1716.821613 | 858.914445 | F | *577.298039* | 289.152658 | 560.271490 | 280.639383 | 559.287474 | 280.147375 | 5 |
| 12 | 1863.874771 | 932.441024 | 1846.848222 | 923.927749 | 1845.864206 | 923.435741 | E | 430.229625 | 215.618450 | 413.203076 | 207.105176 | 412.219060 | 206.613168 | 4 |
| 13 | 1960.927535 | 980.967406 | 1943.900986 | 972.454131 | 1942.916970 | 971.962123 | P | *301.187032* | 151.097154 | 284.160483 | 142.583879 | | | 3 |
| 14 | 2017.948999 | 1009.478138 | 2000.922450 | 1000.964863 | 1999.938434 | 1000.472855 | G | 204.134268 | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 15 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 53.5 | 2163.047256 | 0.006876 | WDLQHPHQHPFEPGK |
| 11.6 | 2163.047256 | 0.006876 | WDLQHPHQHPFEPGK |

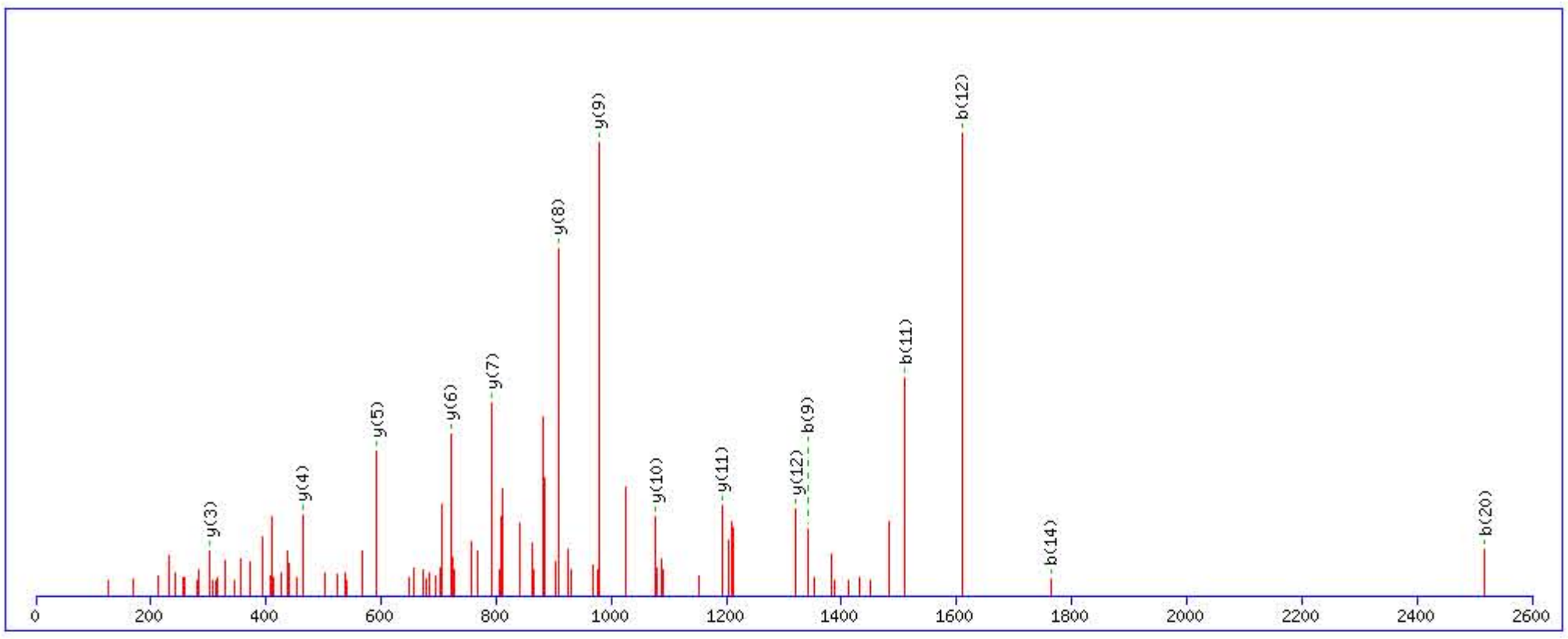
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GTELQHLLHAVVPGPWQEDVADAEECAGR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

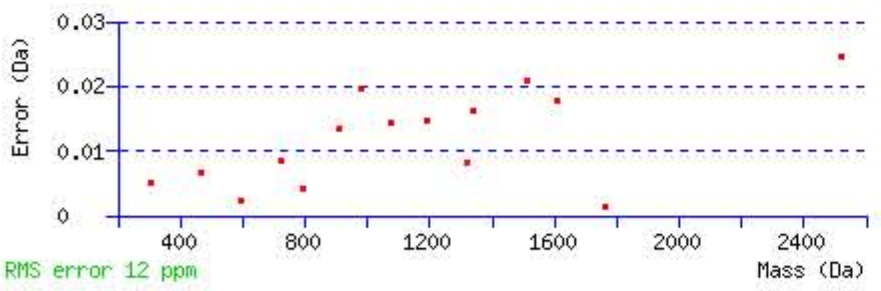
Match to Query 65765: 3494.715656 from(874.686190,4+) rtinseconds(2818) index(71509)
Title: Locus:1.1.1.2255.16 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

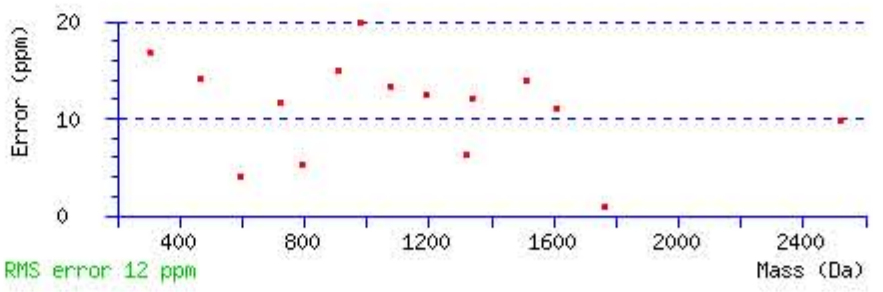
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3494.671112
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 82 **Expect:** 1.5e-007
**Matches :** 15/318 fragment ions using 17 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 29 |
| 2 | 159.076419 | 80.041847 | | | 141.065854 | 71.036565 | T | 3438.656925 | 1719.832100 | 3421.630376 | 1711.318826 | 3420.646360 | 1710.826818 | 28 |
| 3 | 288.119012 | 144.563144 | | | 270.108447 | 135.557862 | E | 3337.609246 | 1669.308261 | 3320.582697 | 1660.794986 | 3319.598681 | 1660.302978 | 27 |
| 4 | 401.203076 | 201.105176 | | | 383.192511 | 192.099894 | L | 3208.566653 | 1604.786964 | 3191.540104 | 1596.273690 | 3190.556088 | 1595.781682 | 26 |
| 5 | 840.428402 | 420.717839 | 823.401853 | 412.204565 | 822.417837 | 411.712557 | Q | 3095.482589 | 1548.244932 | 3078.456040 | 1539.731658 | 3077.472024 | 1539.239650 | 25 |
| 6 | 977.487314 | 489.247295 | 960.460765 | 480.734021 | 959.476749 | 480.242013 | H | 2656.257263 | 1328.632269 | 2639.230714 | 1320.118995 | 2638.246698 | 1319.626987 | 24 |
| 7 | 1090.571378 | 545.789327 | 1073.544829 | 537.276053 | 1072.560813 | 536.784045 | L | 2519.198351 | 1260.102813 | 2502.171802 | 1251.589539 | 2501.187786 | 1251.097531 | 23 |
| 8 | 1203.655442 | 602.331359 | 1186.628893 | 593.818085 | 1185.644877 | 593.326077 | L | 2406.114287 | 1203.560781 | 2389.087738 | 1195.047507 | 2388.103722 | 1194.555499 | 22 |
| 9 | *1340.714354* | 670.860815 | 1323.687805 | 662.347541 | 1322.703789 | 661.855532 | H | 2293.030223 | 1147.018749 | 2276.003674 | 1138.505475 | 2275.019658 | 1138.013467 | 21 |
| 10 | 1411.751468 | 706.379372 | 1394.724919 | 697.866098 | 1393.740903 | 697.374089 | A | 2155.971311 | 1078.489293 | 2138.944762 | 1069.976019 | 2137.960746 | 1069.484011 | 20 |
| 11 | *1510.819882* | 755.913579 | 1493.793333 | 747.400305 | 1492.809317 | 746.908297 | V | 2084.934197 | 1042.970736 | 2067.907648 | 1034.457462 | 2066.923632 | 1033.965454 | 19 |
| 12 | *1609.888296* | 805.447786 | 1592.861747 | 796.934512 | 1591.877731 | 796.442504 | V | 1985.865783 | 993.436530 | 1968.839234 | 984.923255 | 1967.855218 | 984.431247 | 18 |
| 13 | 1706.941060 | 853.974168 | 1689.914511 | 845.460894 | 1688.930495 | 844.968886 | P | 1886.797369 | 943.902323 | 1869.770820 | 935.389048 | 1868.786804 | 934.897040 | 17 |
| 14 | *1763.962524* | 882.484900 | 1746.935975 | 873.971626 | 1745.951959 | 873.479618 | G | 1789.744605 | 895.375941 | 1772.718056 | 886.862666 | 1771.734040 | 886.370658 | 16 |
| 15 | 1861.015288 | 931.011282 | 1843.988739 | 922.498008 | 1843.004723 | 922.006000 | P | 1732.723141 | 866.865209 | 1715.696592 | 858.351934 | 1714.712576 | 857.859926 | 15 |
| 16 | 2047.094601 | 1024.050939 | 2030.068052 | 1015.537664 | 2029.084036 | 1015.045656 | W | 1635.670377 | 818.338827 | 1618.643828 | 809.825552 | 1617.659812 | 809.333544 | 14 |
| 17 | 2175.153179 | 1088.080227 | 2158.126630 | 1079.566953 | 2157.142614 | 1079.074945 | Q | 1449.591064 | 725.299170 | 1432.564515 | 716.785896 | 1431.580499 | 716.293888 | 13 |
| 18 | 2304.195772 | 1152.601524 | 2287.169223 | 1144.088249 | 2286.185207 | 1143.596241 | E | *1321.532486* | 661.269881 | 1304.505937 | 652.756607 | 1303.521921 | 652.264599 | 12 |
| 19 | 2419.222715 | 1210.114995 | 2402.196166 | 1201.601721 | 2401.212150 | 1201.109713 | D | *1192.489893* | 596.748585 | 1175.463344 | 588.235310 | 1174.479328 | 587.743302 | 11 |
| 20 | *2518.291129* | 1259.649202 | 2501.264580 | 1251.135928 | 2500.280564 | 1250.643920 | V | *1077.462950* | 539.235113 | 1060.436401 | 530.721839 | 1059.452385 | 530.229831 | 10 |
| 21 | 2589.328243 | 1295.167759 | 2572.301694 | 1286.654485 | 2571.317678 | 1286.162477 | A | *978.394536* | 489.700906 | 961.367987 | 481.187632 | 960.383971 | 480.695624 | 9 |
| 22 | 2704.355186 | 1352.681231 | 2687.328637 | 1344.167956 | 2686.344621 | 1343.675948 | D | *907.357422* | 454.182349 | 890.330873 | 445.669075 | 889.346857 | 445.177067 | 8 |
| 23 | 2775.392300 | 1388.199788 | 2758.365751 | 1379.686513 | 2757.381735 | 1379.194505 | A | *792.330479* | 396.668878 | 775.303930 | 388.155603 | 774.319914 | 387.663595 | 7 |
| 24 | 2904.434893 | 1452.721085 | 2887.408344 | 1444.207810 | 2886.424328 | 1443.715802 | E | *721.293365* | 361.150321 | 704.266816 | 352.637046 | 703.282800 | 352.145038 | 6 |
| 25 | 3033.477486 | 1517.242381 | 3016.450937 | 1508.729106 | 3015.466921 | 1508.237099 | E | *592.250772* | 296.629024 | 575.224223 | 288.115750 | 574.240207 | 287.623742 | 5 |
| 26 | 3193.508135 | 1597.257705 | 3176.481586 | 1588.744431 | 3175.497570 | 1588.252423 | C | *463.208179* | 232.107727 | 446.181630 | 223.594453 | | | 4 |
| 27 | 3264.545249 | 1632.776263 | 3247.518700 | 1624.262988 | 3246.534684 | 1623.770980 | A | *303.177530* | 152.092403 | 286.150981 | 143.579129 | | | 3 |
| 28 | 3321.566713 | 1661.286995 | 3304.540164 | 1652.773720 | 3303.556148 | 1652.281712 | G | 232.140416 | 116.573846 | 215.113867 | 108.060571 | | | 2 |
| 29 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 82.0 | 3494.671112 | 0.044544 | GTELQHLLHAVVPGPWQEDVADAEECAGR |
| 57.9 | 3494.671112 | 0.044544 | GTELQHLLHAVVPGPWQEDVADAEECAGR |

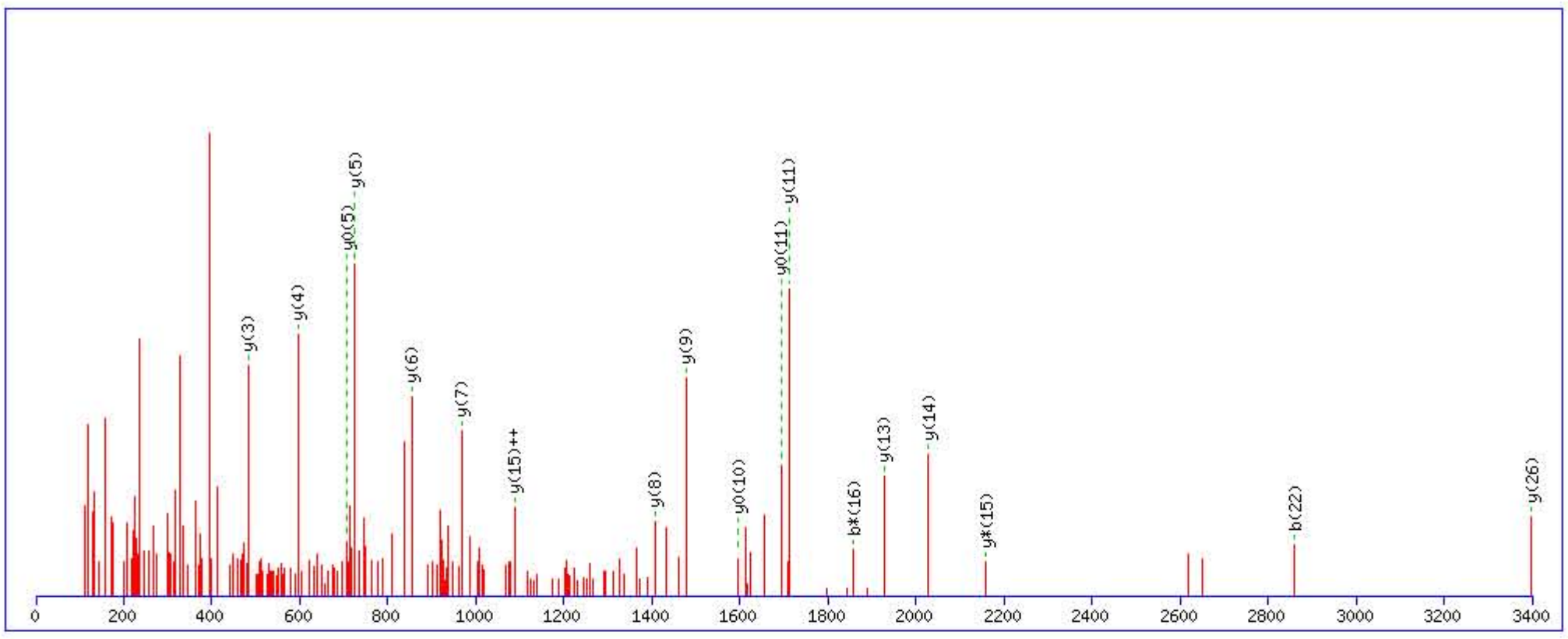
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **WSAETPHKPQFTFTSEPHAQLEENFCR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

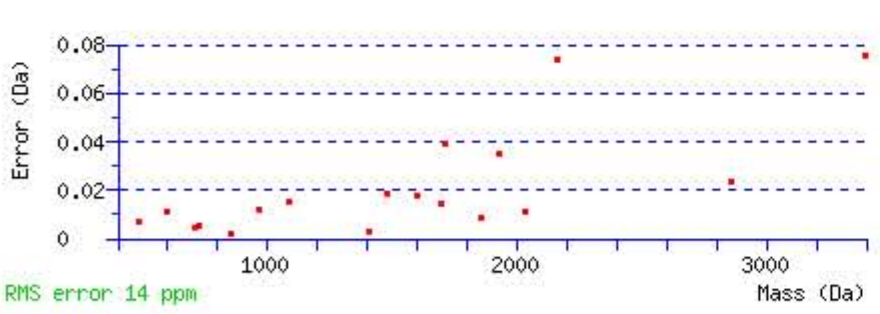
Match to Query 66620: 3584.687770 from(717.944830,5+) rtinseconds(2014) index(66496)
Title: Locus:1.1.1.1976.11 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

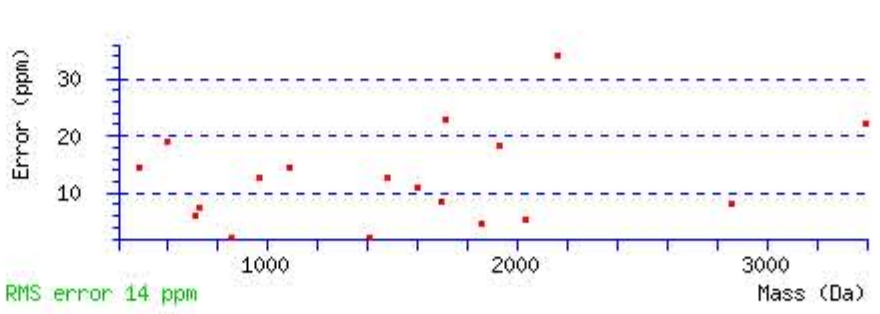
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3584.660538
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q20 : Biotin:Thermo-21345 (Q)
**Ions Score:** 64 **Expect:** 7.3e-006
**Matches :** 18/288 fragment ions using 24 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 187.086589 | 94.046932 | | | | | W | | | | | | | 27 |
| 2 | 274.118617 | 137.562947 | | | 256.108052 | 128.557664 | S | *3399.588510* | 1700.297893 | 3382.561961 | 1691.784618 | 3381.577945 | 1691.292610 | 26 |
| 3 | 345.155731 | 173.081504 | | | 327.145166 | 164.076221 | A | 3312.556482 | 1656.781879 | 3295.529933 | 1648.268605 | 3294.545917 | 1647.776597 | 25 |
| 4 | 474.198324 | 237.602800 | | | 456.187759 | 228.597518 | E | 3241.519368 | 1621.263322 | 3224.492819 | 1612.750047 | 3223.508803 | 1612.258040 | 24 |
| 5 | 575.246003 | 288.126640 | | | 557.235438 | 279.121357 | T | 3112.476775 | 1556.742026 | 3095.450226 | 1548.228751 | 3094.466210 | 1547.736743 | 23 |
| 6 | 672.298767 | 336.653022 | | | 654.288202 | 327.647739 | P | 3011.429096 | 1506.218186 | 2994.402547 | 1497.704912 | 2993.418531 | 1497.212904 | 22 |
| 7 | 809.357679 | 405.182478 | | | 791.347114 | 396.177195 | H | 2914.376332 | 1457.691804 | 2897.349783 | 1449.178530 | 2896.365767 | 1448.686522 | 21 |
| 8 | 937.452642 | 469.229959 | 920.426093 | 460.716685 | 919.442077 | 460.224677 | K | 2777.317420 | 1389.162348 | 2760.290871 | 1380.649074 | 2759.306855 | 1380.157066 | 20 |
| 9 | 1034.505406 | 517.756341 | 1017.478857 | 509.243067 | 1016.494841 | 508.751059 | P | 2649.222457 | 1325.114867 | 2632.195908 | 1316.601592 | 2631.211892 | 1316.109584 | 19 |
| 10 | 1162.563984 | 581.785630 | 1145.537435 | 573.272356 | 1144.553419 | 572.780348 | Q | 2552.169693 | 1276.588485 | 2535.143144 | 1268.075210 | 2534.159128 | 1267.583202 | 18 |
| 11 | 1309.632398 | 655.319837 | 1292.605849 | 646.806563 | 1291.621833 | 646.314555 | F | 2424.111115 | 1212.559196 | 2407.084566 | 1204.045921 | 2406.100550 | 1203.553913 | 17 |
| 12 | 1410.680077 | 705.843677 | 1393.653528 | 697.330402 | 1392.669512 | 696.838394 | T | 2277.042701 | 1139.024988 | 2260.016152 | 1130.511714 | 2259.032136 | 1130.019706 | 16 |
| 13 | 1557.748491 | 779.377884 | 1540.721942 | 770.864609 | 1539.737926 | 770.372601 | F | 2175.995022 | 1088.501149 | 2158.968473 | 1079.987874 | 2157.984457 | 1079.495866 | 15 |
| 14 | 1658.796170 | 829.901723 | 1641.769621 | 821.388449 | 1640.785605 | 820.896441 | T | *2028.926608* | 1014.966942 | 2011.900059 | 1006.453668 | 2010.916043 | 1005.961660 | 14 |
| 15 | 1745.828198 | 873.417737 | 1728.801649 | 864.904463 | 1727.817633 | 864.412455 | S | *1927.878929* | 964.443103 | 1910.852380 | 955.929828 | 1909.868364 | 955.437820 | 13 |
| 16 | 1874.870791 | 937.939034 | 1857.844242 | 929.425759 | 1856.860226 | 928.933751 | E | 1840.846901 | 920.927089 | 1823.820352 | 912.413814 | 1822.836336 | 911.921806 | 12 |
| 17 | 1971.923555 | 986.465416 | 1954.897006 | 977.952141 | 1953.912990 | 977.460133 | P | *1711.804308* | 856.405792 | 1694.777759 | 847.892518 | 1693.793743 | 847.400510 | 11 |
| 18 | 2108.982467 | 1054.994872 | 2091.955918 | 1046.481597 | 2090.971902 | 1045.989589 | H | 1614.751544 | 807.879410 | 1597.724995 | 799.366136 | 1596.740979 | 798.874128 | 10 |
| 19 | 2180.019581 | 1090.513429 | 2162.993032 | 1082.000154 | 2162.009016 | 1081.508146 | A | *1477.692632* | 739.349954 | 1460.666083 | 730.836680 | 1459.682067 | 730.344672 | 9 |
| 20 | 2619.244907 | 1310.126092 | 2602.218358 | 1301.612817 | 2601.234342 | 1301.120809 | Q | *1406.655518* | 703.831397 | 1389.628969 | 695.318123 | 1388.644953 | 694.826115 | 8 |
| 21 | 2732.328971 | 1366.668124 | 2715.302422 | 1358.154849 | 2714.318406 | 1357.662841 | L | *967.430192* | 484.218734 | 950.403643 | 475.705460 | 949.419627 | 475.213452 | 7 |
| 22 | 2861.371564 | 1431.189420 | 2844.345015 | 1422.676146 | 2843.360999 | 1422.184138 | E | *854.346128* | 427.676702 | 837.319579 | 419.163427 | 836.335563 | 418.671419 | 6 |
| 23 | 2990.414157 | 1495.710717 | 2973.387608 | 1487.197442 | 2972.403592 | 1486.705434 | E | *725.303535* | 363.155405 | 708.276986 | 354.642131 | 707.292970 | 354.150123 | 5 |
| 24 | 3104.457084 | 1552.732180 | 3087.430535 | 1544.218906 | 3086.446519 | 1543.726898 | N | *596.260942* | 298.634109 | 579.234393 | 290.120834 | | | 4 |
| 25 | 3251.525498 | 1626.266387 | 3234.498949 | 1617.753113 | 3233.514933 | 1617.261105 | F | *482.218015* | 241.612645 | 465.191466 | 233.099371 | | | 3 |
| 26 | 3411.556147 | 1706.281712 | 3394.529598 | 1697.768437 | 3393.545582 | 1697.276429 | C | 335.149601 | 168.078438 | 318.123052 | 159.565164 | | | 2 |
| 27 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 63.6 | 3584.660538 | 0.027232 | WSAETPHKPQFTFTSEPHAQLEENFCR |
| 8.1 | 3584.660538 | 0.027232 | WSAETPHKPQFTFTSEPHAQLEENFCR |

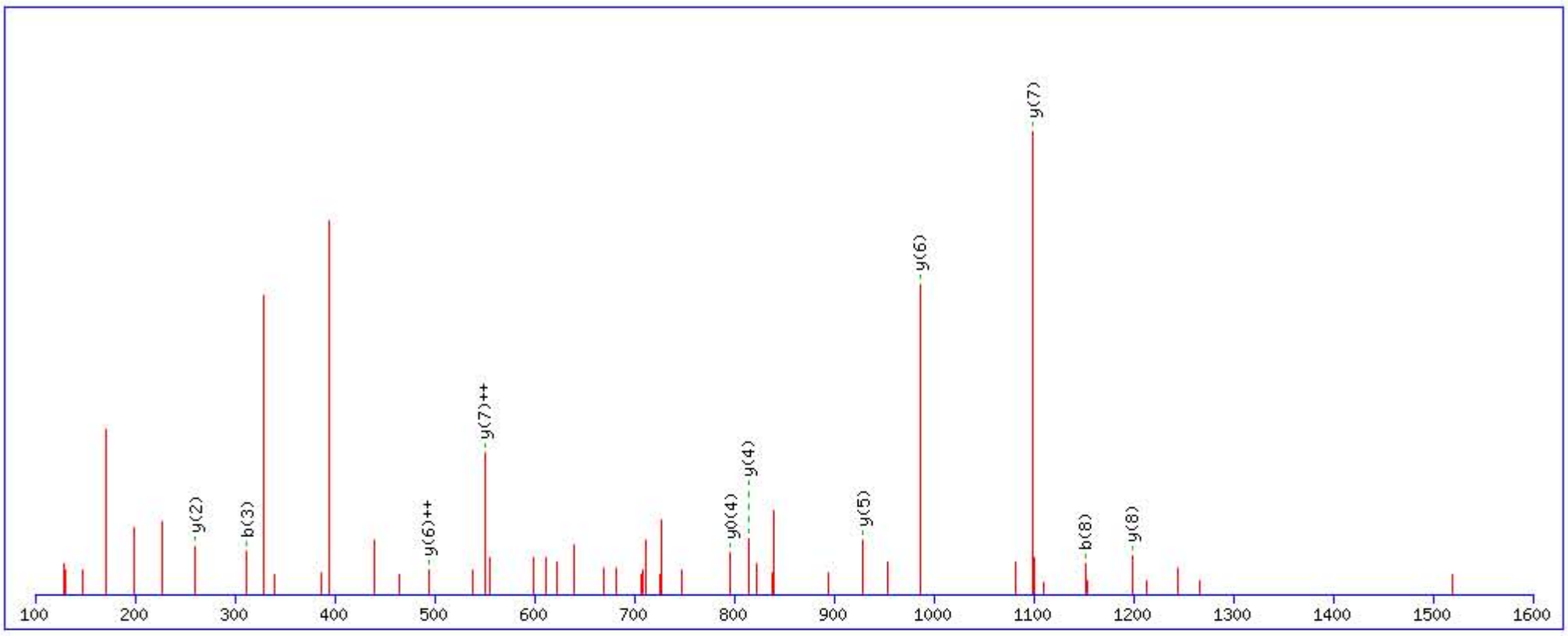
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VVLGDQDLK**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

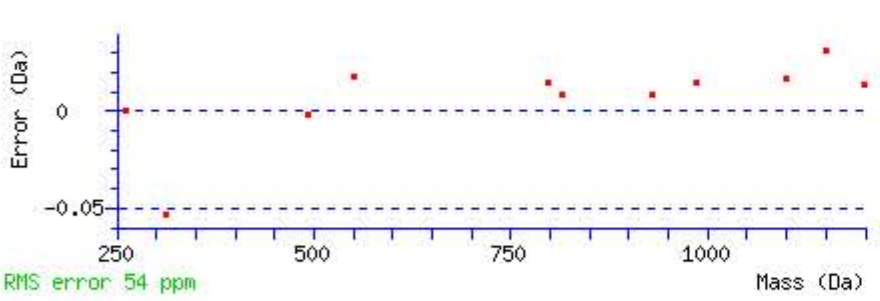
Match to Query 23261: 1296.721428 from(649.367990,2+) rtinseconds(1975) index(50200)
Title: Locus:1.1.1.1925.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

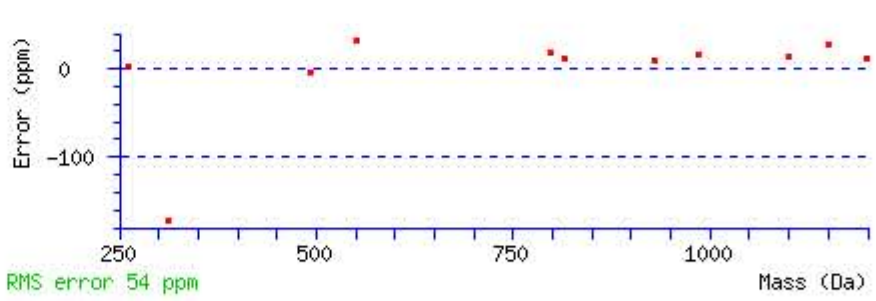
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1296.711166
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q6** : Biotin:Thermo-21345 (Q)
**Ions Score:** 30 **Expect:** 0.0053
**Matches** : 11/74 fragment ions using 24 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 9 |
| 2 | 199.144104 | 100.075690 | | | | | V | *1198.650022* | 599.828649 | 1181.623473 | 591.315374 | 1180.639457 | 590.823366 | 8 |
| 3 | **312.228168** | 156.617722 | | | | | L | *1099.581608* | 550.294442 | 1082.555059 | 541.781168 | 1081.571043 | 541.289159 | 7 |
| 4 | 369.249632 | 185.128454 | | | | | G | *986.497544* | 493.752410 | 969.470995 | 485.239135 | 968.486979 | 484.747127 | 6 |
| 5 | 484.276575 | 242.641925 | | | 466.266010 | 233.636643 | D | *929.476080* | 465.241678 | 912.449531 | 456.728403 | 911.465515 | 456.236395 | 5 |
| 6 | 923.501901 | 462.254589 | 906.475352 | 453.741314 | 905.491336 | 453.249306 | Q | *814.449137* | 407.728206 | 797.422588 | 399.214932 | 796.438572 | 398.722924 | 4 |
| 7 | 1038.528844 | 519.768060 | 1021.502295 | 511.254785 | 1020.518279 | 510.762777 | D | 375.223811 | 188.115543 | 358.197262 | 179.602269 | 357.213246 | 179.110261 | 3 |
| 8 | **1151.612908** | 576.310092 | 1134.586359 | 567.796817 | 1133.602343 | 567.304809 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 9 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 29.6 | 1296.711166 | 0.010262 | VVLGDQDLK |
| 5.0 | 1296.719025 | 0.002403 | VVSIHQDPKFK |
| 0.5 | 1296.704636 | 0.016792 | VVAVSPQMR |

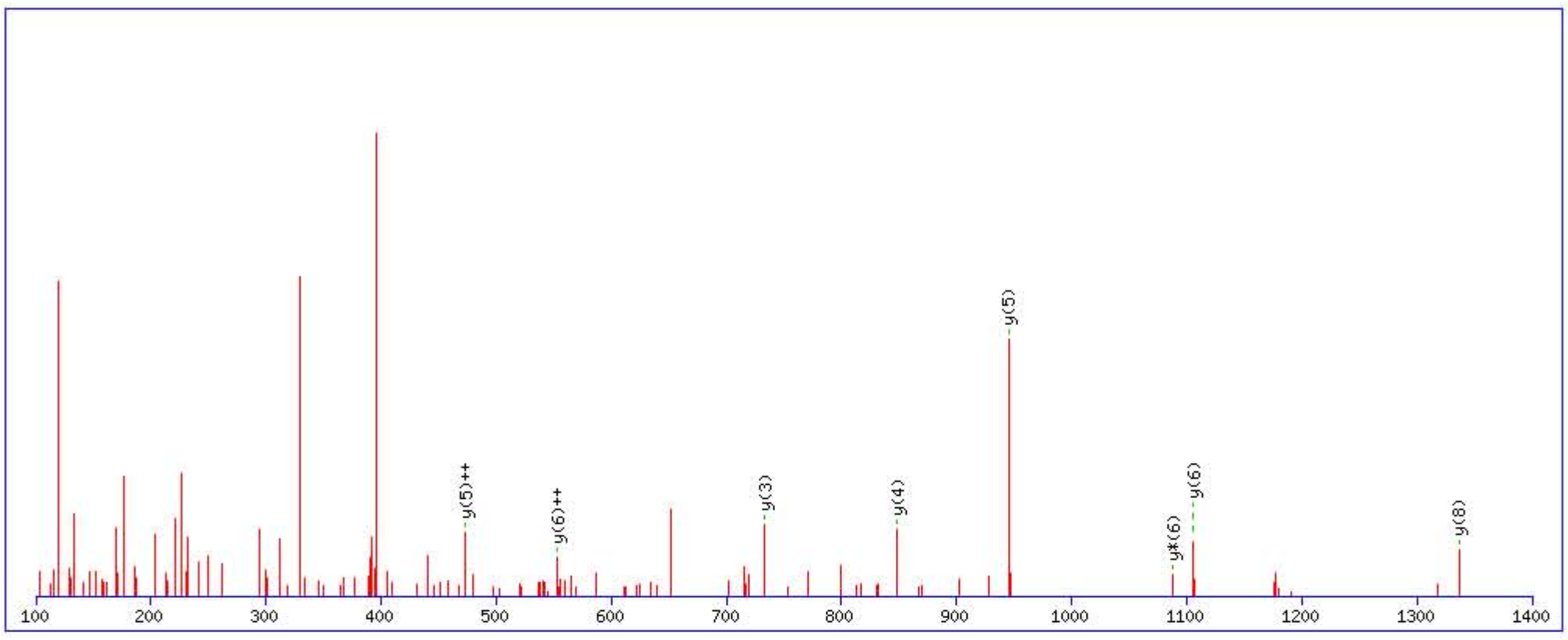
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FTCACPDQFK**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

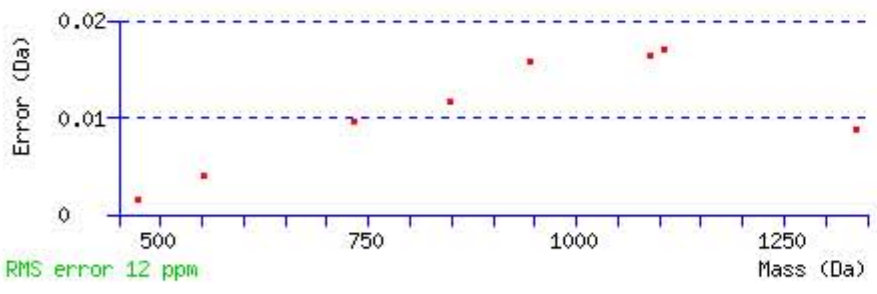
Match to Query 33915: 1583.698782 from(528.906870,3+) rtinseconds(1887) index(49456)
Title: Locus:1.1.1.1895.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

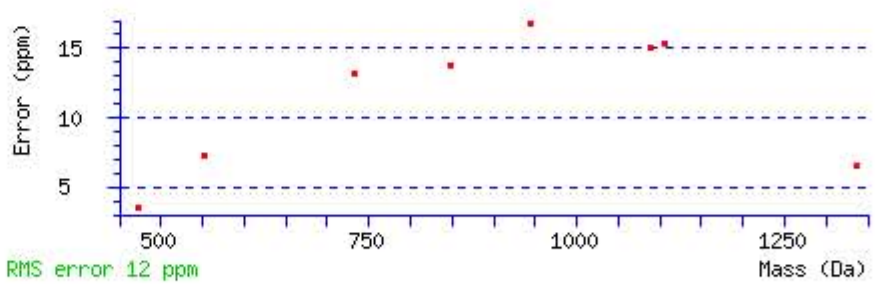
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1583.693497
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 27 **Expect:** 0.014
**Matches :** 8/86 fragment ions using 12 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 10 |
| 2 | 249.123369 | 125.065322 | | | 231.112804 | 116.060040 | T | 1437.632342 | 719.319809 | 1420.605793 | 710.806535 | 1419.621777 | 710.314527 | 9 |
| 3 | 409.154018 | 205.080647 | | | 391.143453 | 196.075365 | C | *1336.584663* | 668.795970 | 1319.558114 | 660.282695 | 1318.574098 | 659.790687 | 8 |
| 4 | 480.191132 | 240.599204 | | | 462.180567 | 231.593921 | A | 1176.554014 | 588.780645 | 1159.527465 | 580.267371 | 1158.543449 | 579.775363 | 7 |
| 5 | 640.221781 | 320.614529 | | | 622.211216 | 311.609246 | C | *1105.516900* | 553.262088 | 1088.490351 | 544.748814 | 1087.506335 | 544.256806 | 6 |
| 6 | 737.274545 | 369.140911 | | | 719.263980 | 360.135628 | P | *945.486251* | 473.246764 | 928.459702 | 464.733489 | 927.475686 | 464.241481 | 5 |
| 7 | 852.301488 | 426.654382 | | | 834.290923 | 417.649100 | D | *848.433487* | 424.720382 | 831.406938 | 416.207107 | 830.422922 | 415.715099 | 4 |
| 8 | 1291.526814 | 646.267045 | 1274.500265 | 637.753771 | 1273.516249 | 637.261763 | Q | *733.406544* | 367.206910 | 716.379995 | 358.693636 | | | 3 |
| 9 | 1438.595228 | 719.801252 | 1421.568679 | 711.287978 | 1420.584663 | 710.795970 | F | 294.181218 | 147.594247 | 277.154669 | 139.080973 | | | 2 |
| 10 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 26.9 | 1583.693497 | 0.005285 | FTCACPDQFK |

**Mascot:** http://www.matrixscience.com/

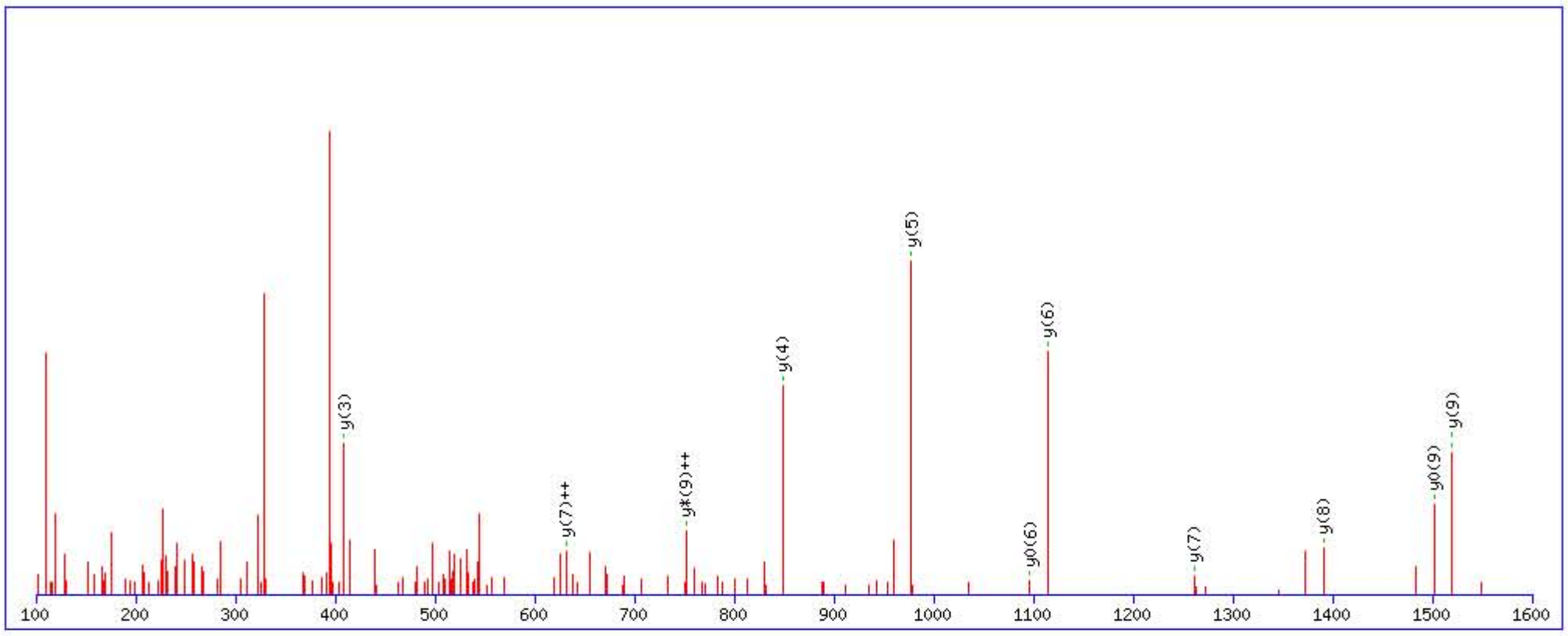
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KEEFHEQSFR**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

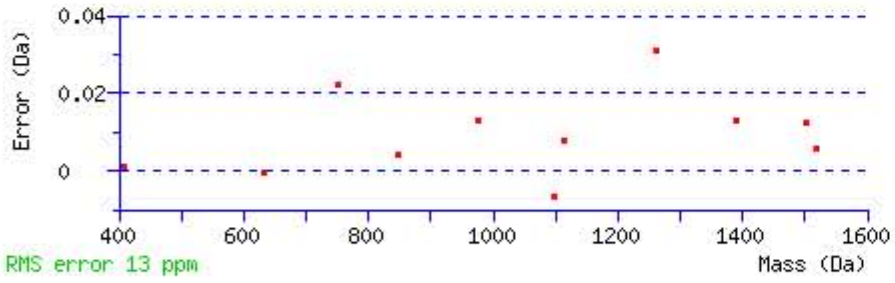
Match to Query 36784: 1646.793852 from(549.938560,3+) rtinseconds(1529) index(47148)
Title: Locus:1.1.1.1770.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

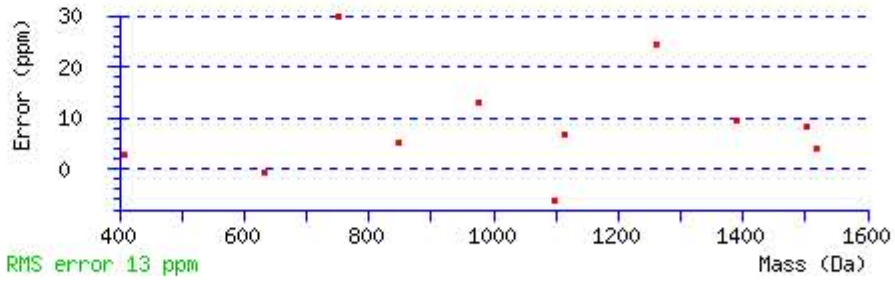
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1646.787491
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 0.00012
**Matches :** 11/102 fragment ions using 15 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.102239 | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 10 |
| 2 | 258.144832 | 129.576054 | 241.118283 | 121.062780 | 240.134267 | 120.570772 | E | *1519.699825* | 760.353551 | 1502.673276 | 751.840276 | 1501.689260 | 751.348268 | 9 |
| 3 | 387.187425 | 194.097351 | 370.160876 | 185.584076 | 369.176860 | 185.092068 | E | *1390.657232* | 695.832254 | 1373.630683 | 687.318980 | 1372.646667 | 686.826972 | 8 |
| 4 | 534.255839 | 267.631558 | 517.229290 | 259.118283 | 516.245274 | 258.626275 | F | *1261.614639* | 631.310958 | 1244.588090 | 622.797683 | 1243.604074 | 622.305675 | 7 |
| 5 | 671.314751 | 336.161014 | 654.288202 | 327.647739 | 653.304186 | 327.155731 | H | *1114.546225* | 557.776751 | 1097.519676 | 549.263476 | 1096.535660 | 548.771468 | 6 |
| 6 | 800.357344 | 400.682310 | 783.330795 | 392.169036 | 782.346779 | 391.677028 | E | *977.487313* | 489.247295 | 960.460764 | 480.734020 | 959.476748 | 480.242012 | 5 |
| 7 | 1239.582670 | 620.294973 | 1222.556121 | 611.781699 | 1221.572105 | 611.289691 | Q | *848.444720* | 424.725998 | 831.418171 | 416.212724 | 830.434155 | 415.720716 | 4 |
| 8 | 1326.614698 | 663.810987 | 1309.588149 | 655.297713 | 1308.604133 | 654.805705 | S | *409.219394* | 205.113335 | 392.192845 | 196.600061 | 391.208829 | 196.108053 | 3 |
| 9 | 1473.683112 | 737.345194 | 1456.656563 | 728.831920 | 1455.672547 | 728.339912 | F | 322.187366 | 161.597321 | 305.160817 | 153.084047 | | | 2 |
| 10 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 47.8 | 1646.787491 | 0.006361 | KEEFHEQSFR |
| 6.0 | 1646.818497 | -0.024645 | QLDDAKEGEMALLSK |
| 4.5 | 1646.812469 | -0.018617 | QEERLGRGGLDDFR |

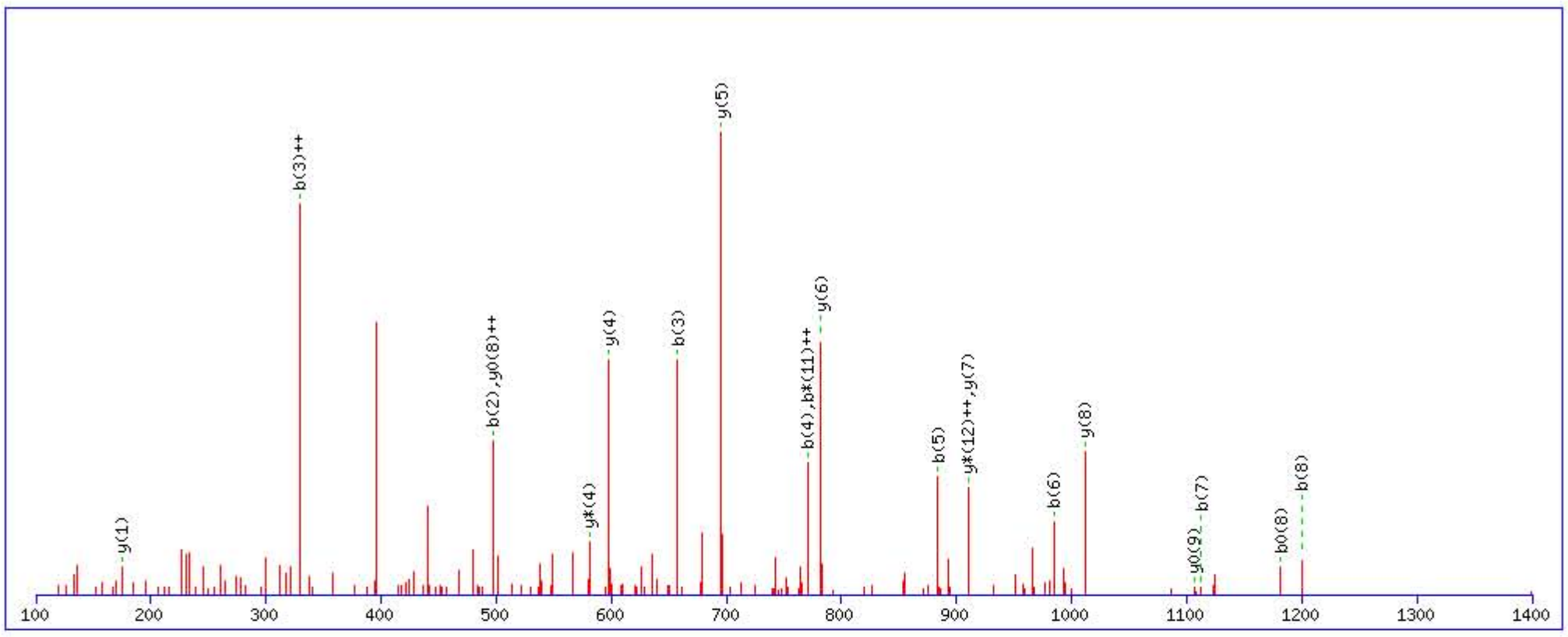
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GQCLITQSPPYYR**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

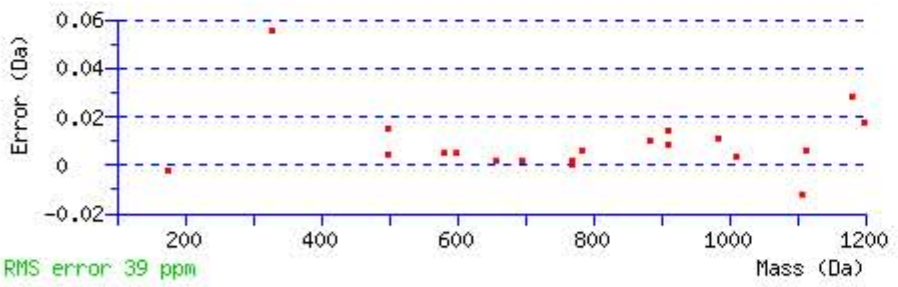
Match to Query 41995: 1892.941872 from(631.987900,3+) rtinseconds(2087) index(50888)
Title: Locus:1.1.1.1964.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

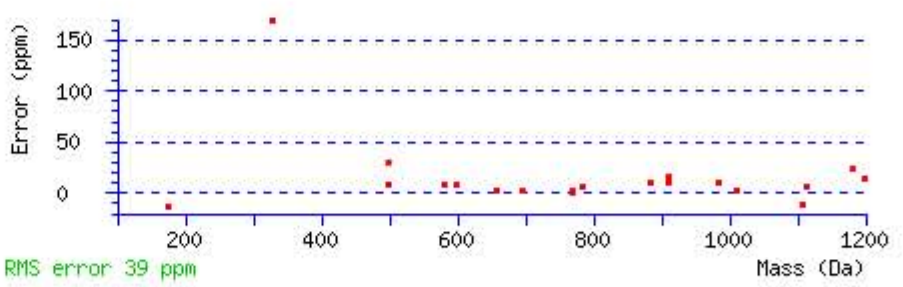
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1892.927704
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 52 **Expect:** 0.00015
**Matches :** 20/122 fragment ions using 23 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 13 |
| 2 | *497.254066* | 249.130671 | 480.227517 | 240.617397 | | | Q | 1836.913526 | 918.960401 | 1819.886977 | 910.447127 | 1818.902961 | 909.955119 | 12 |
| 3 | *657.284715* | 329.145996 | 640.258166 | 320.632721 | | | C | 1397.688200 | 699.347738 | 1380.661651 | 690.834464 | 1379.677635 | 690.342456 | 11 |
| 4 | *770.368779* | 385.688028 | 753.342230 | 377.174753 | | | L | 1237.657551 | 619.332414 | 1220.631002 | 610.819139 | 1219.646986 | 610.327131 | 10 |
| 5 | *883.452843* | 442.230060 | 866.426294 | 433.716785 | | | I | 1124.573487 | 562.790382 | 1107.546938 | 554.277107 | 1106.562922 | 553.785099 | 9 |
| 6 | *984.500522* | 492.753899 | 967.473973 | 484.240625 | 966.489957 | 483.748617 | T | *1011.489423* | 506.248350 | 994.462874 | 497.735075 | 993.478858 | 497.243067 | 8 |
| 7 | *1112.559100* | 556.783188 | 1095.532551 | 548.269914 | 1094.548535 | 547.777906 | Q | *910.441744* | 455.724510 | 893.415195 | 447.211236 | 892.431179 | 446.719228 | 7 |
| 8 | *1199.591128* | 600.299202 | 1182.564579 | 591.785928 | 1181.580563 | 591.293920 | S | *782.383166* | 391.695221 | 765.356617 | 383.181947 | 764.372601 | 382.689939 | 6 |
| 9 | 1296.643892 | 648.825584 | 1279.617343 | 640.312310 | 1278.633327 | 639.820302 | P | *695.351138* | 348.179207 | 678.324589 | 339.665933 | | | 5 |
| 10 | 1393.696656 | 697.351966 | 1376.670107 | 688.838692 | 1375.686091 | 688.346684 | P | *598.298374* | 299.652825 | 581.271825 | 291.139551 | | | 4 |
| 11 | 1556.759985 | 778.883631 | 1539.733436 | 770.370356 | 1538.749420 | 769.878348 | Y | 501.245610 | 251.126443 | 484.219061 | 242.613169 | | | 3 |
| 12 | 1719.823314 | 860.415295 | 1702.796765 | 851.902021 | 1701.812749 | 851.410013 | Y | 338.182281 | 169.594778 | 321.155732 | 161.081504 | | | 2 |
| 13 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 51.8 | 1892.927704 | 0.014168 | GQCLITQSPPYYR |
| 12.4 | 1892.927704 | 0.014168 | GQCLITQSPPYYR |

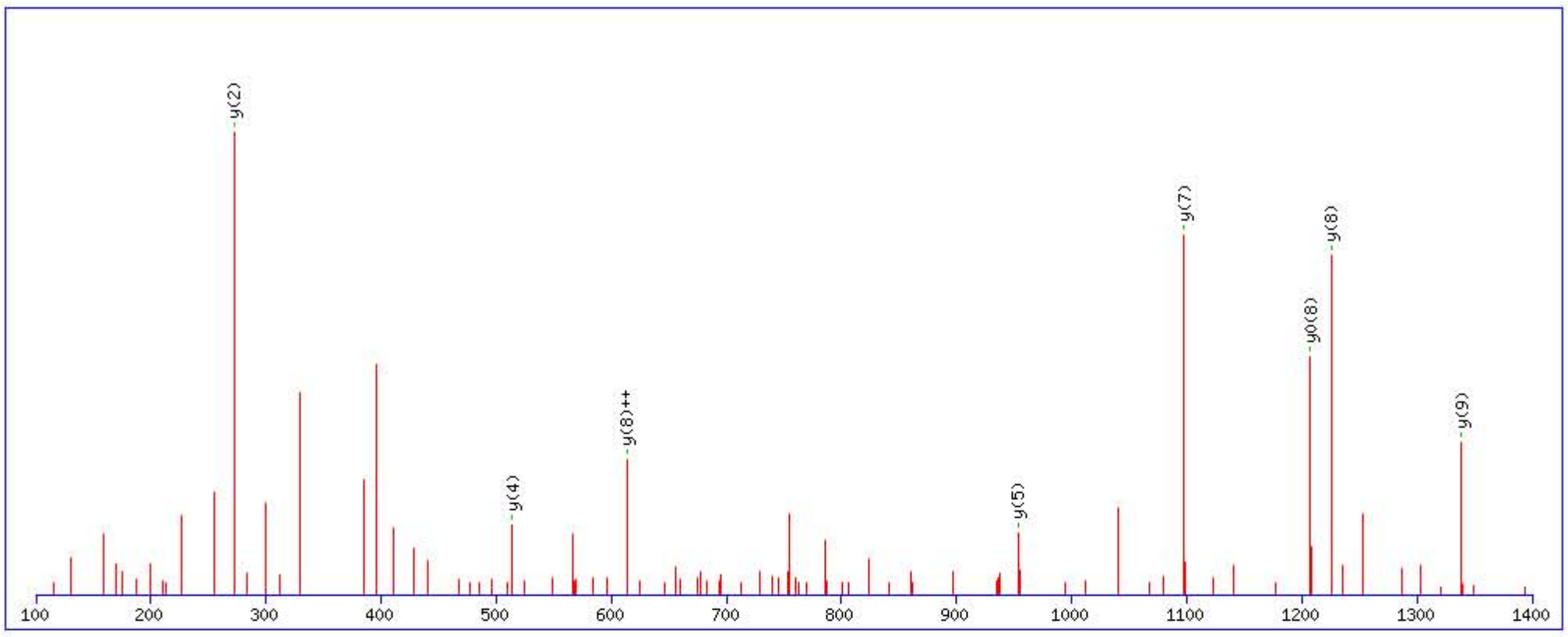
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **WLQGSQELPR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

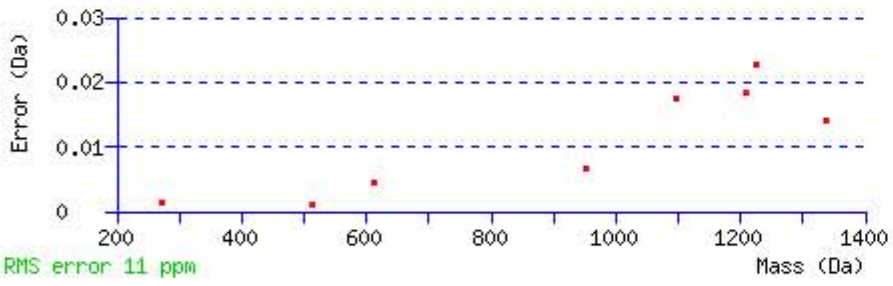
Match to Query 31932: 1523.804548 from(762.909550,2+) rtinseconds(2070) index(34688)
Title: Locus:1.1.1.829.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

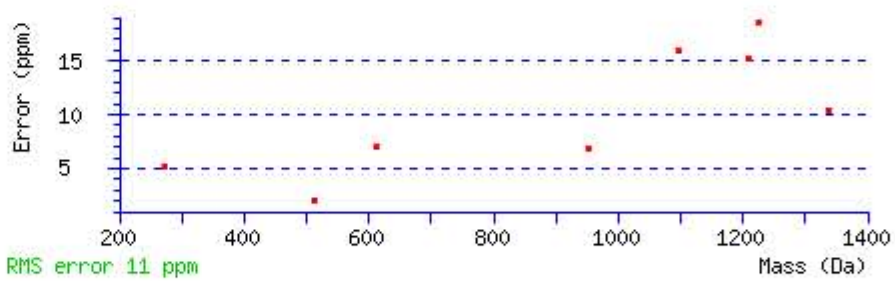
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1523.791855
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 42 **Expect:** 0.0015
**Matches :** 8/90 fragment ions using 13 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 187.086589 | 94.046932 | | | | | W | | | | | | | 10 |
| 2 | 300.170653 | 150.588965 | | | | | L | *1338.719833* | 669.863554 | 1321.693284 | 661.350280 | 1320.709268 | 660.858272 | 9 |
| 3 | 428.229231 | 214.618254 | 411.202682 | 206.104979 | | | Q | *1225.635769* | 613.321522 | 1208.609220 | 604.808248 | *1207.625204* | 604.316240 | 8 |
| 4 | 485.250695 | 243.128986 | 468.224146 | 234.615711 | | | G | *1097.577191* | 549.292233 | 1080.550642 | 540.778959 | 1079.566626 | 540.286951 | 7 |
| 5 | 572.282723 | 286.645000 | 555.256174 | 278.131725 | 554.272158 | 277.639717 | S | 1040.555727 | 520.781501 | 1023.529178 | 512.268227 | 1022.545162 | 511.776219 | 6 |
| 6 | 1011.508049 | 506.257663 | 994.481500 | 497.744388 | 993.497484 | 497.252380 | Q | *953.523699* | 477.265487 | 936.497150 | 468.752213 | 935.513134 | 468.260205 | 5 |
| 7 | 1140.550642 | 570.778959 | 1123.524093 | 562.265685 | 1122.540077 | 561.773676 | E | *514.298373* | 257.652824 | 497.271824 | 249.139550 | 496.287808 | 248.647542 | 4 |
| 8 | 1253.634706 | 627.320991 | 1236.608157 | 618.807716 | 1235.624141 | 618.315708 | L | 385.255780 | 193.131528 | 368.229231 | 184.618253 | | | 3 |
| 9 | 1350.687470 | 675.847373 | 1333.660921 | 667.334098 | 1332.676905 | 666.842090 | P | *272.171716* | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 10 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 42.2 | 1523.791855 | 0.012693 | WLQGSQELPR |
| 26.5 | 1523.791855 | 0.012693 | WLQGSQELPR |
| 21.8 | 1523.816833 | -0.012285 | KGLGEGVPSSQRGPR |
| 6.9 | 1523.824219 | -0.019671 | SVQIRTEAGPR |
| 5.0 | 1523.812988 | -0.008440 | EGQGIKTDIPR |
| 4.4 | 1523.813644 | -0.009096 | WIPTSNPLPQPFK |
| 0.9 | 1523.784470 | 0.020078 | SVLENHHISSVFR |
| 0.2 | 1523.801743 | 0.002805 | ASLDMKLIFLDSR |

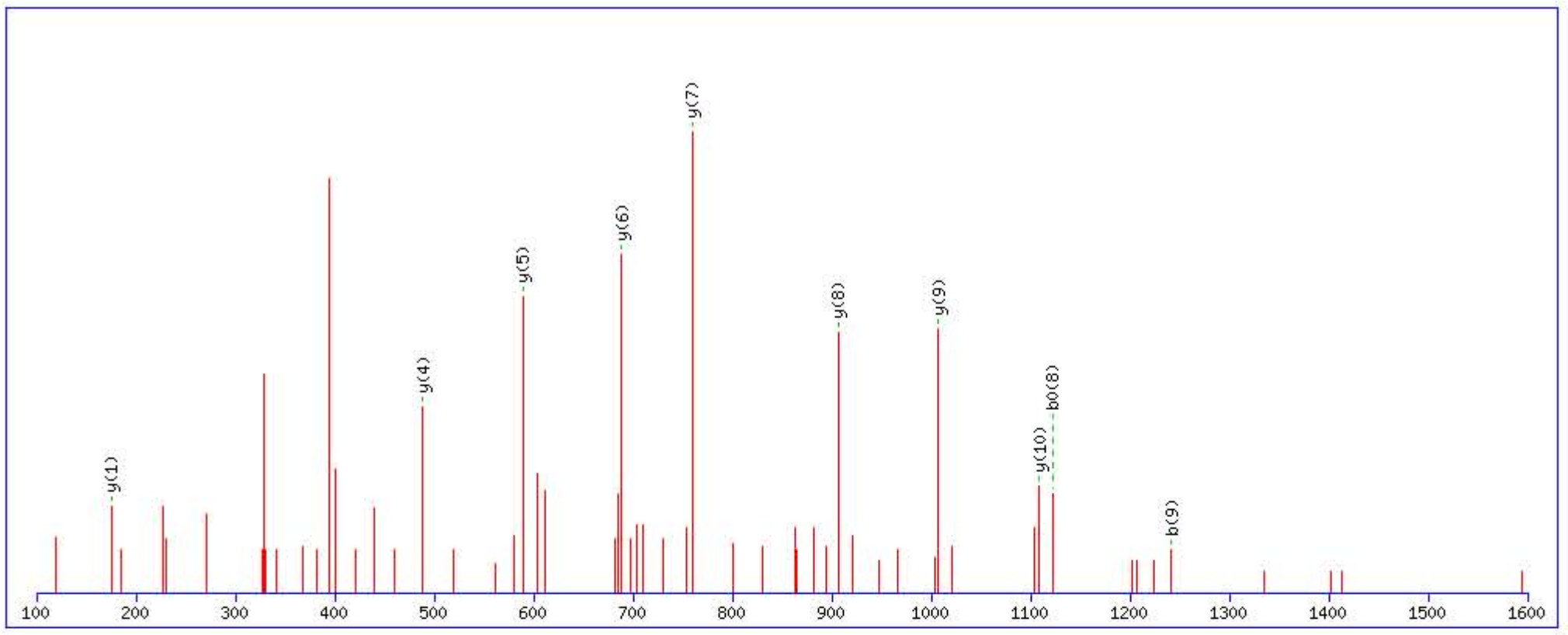
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QEPSQGTTTFAVTSILR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

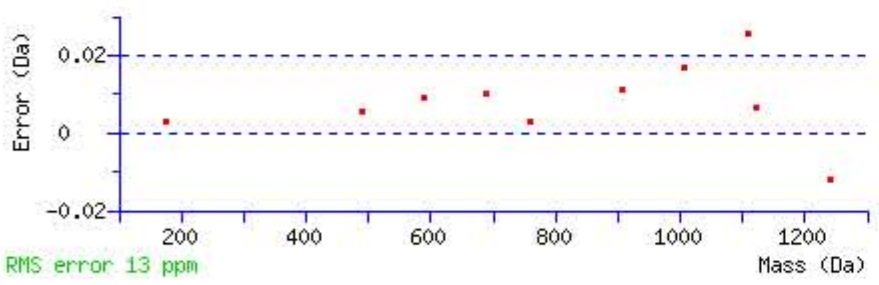
Match to Query 47325: 2146.129302 from(716.383710,3+) rtinseconds(2492) index(8262)
Title: Locus:1.1.1.2145.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

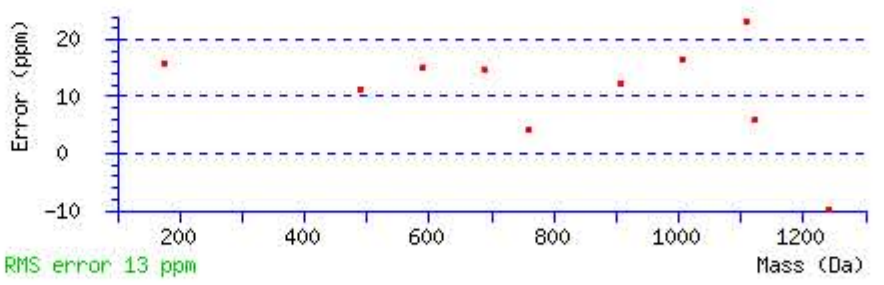
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2146.109253
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 1.5e-005
**Matches :** 10/184 fragment ions using 14 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.065854 | 65.036565 | 112.039305 | 56.523291 | | | Q | | | | | | | 17 |
| 2 | 258.108447 | 129.557862 | 241.081898 | 121.044587 | 240.097882 | 120.552579 | E | 2019.057941 | 1010.032609 | 2002.031392 | 1001.519334 | 2001.047376 | 1001.027326 | 16 |
| 3 | 355.161211 | 178.084244 | 338.134662 | 169.570969 | 337.150646 | 169.078961 | P | 1890.015348 | 945.511312 | 1872.988799 | 936.998038 | 1872.004783 | 936.506030 | 15 |
| 4 | 442.193239 | 221.600258 | 425.166690 | 213.086983 | 424.182674 | 212.594975 | S | 1792.962584 | 896.984930 | 1775.936035 | 888.471656 | 1774.952019 | 887.979648 | 14 |
| 5 | 881.418565 | 441.212921 | 864.392016 | 432.699646 | 863.408000 | 432.207638 | Q | 1705.930556 | 853.468916 | 1688.904007 | 844.955642 | 1687.919991 | 844.463634 | 13 |
| 6 | 938.440029 | 469.723653 | 921.413480 | 461.210378 | 920.429464 | 460.718370 | G | 1266.705230 | 633.856253 | 1249.678681 | 625.342979 | 1248.694665 | 624.850971 | 12 |
| 7 | 1039.487708 | 520.247492 | 1022.461159 | 511.734218 | 1021.477143 | 511.242210 | T | 1209.683766 | 605.345521 | 1192.657217 | 596.832247 | 1191.673201 | 596.340239 | 11 |
| 8 | 1140.535387 | 570.771332 | 1123.508838 | 562.258057 | 1122.524822 | 561.766049 | T | *1108.636087* | 554.821682 | 1091.609538 | 546.308407 | 1090.625522 | 545.816399 | 10 |
| 9 | **1241.583066** | 621.295171 | 1224.556517 | 612.781897 | 1223.572501 | 612.289889 | T | *1007.588408* | 504.297842 | 990.561859 | 495.784568 | 989.577843 | 495.292560 | 9 |
| 10 | 1388.651480 | 694.829378 | 1371.624931 | 686.316104 | 1370.640915 | 685.824096 | F | *906.540729* | 453.774003 | 889.514180 | 445.260728 | 888.530164 | 444.768720 | 8 |
| 11 | 1459.688594 | 730.347935 | 1442.662045 | 721.834661 | 1441.678029 | 721.342653 | A | *759.472315* | 380.239796 | 742.445766 | 371.726521 | 741.461750 | 371.234513 | 7 |
| 12 | 1558.757008 | 779.882142 | 1541.730459 | 771.368868 | 1540.746443 | 770.876860 | V | *688.435201* | 344.721239 | 671.408652 | 336.207964 | 670.424636 | 335.715956 | 6 |
| 13 | 1659.804687 | 830.405982 | 1642.778138 | 821.892707 | 1641.794122 | 821.400699 | T | *589.366787* | 295.187032 | 572.340238 | 286.673757 | 571.356222 | 286.181749 | 5 |
| 14 | 1746.836715 | 873.921996 | 1729.810166 | 865.408721 | 1728.826150 | 864.916713 | S | *488.319108* | 244.663192 | 471.292559 | 236.149918 | 470.308543 | 235.657910 | 4 |
| 15 | 1859.920779 | 930.464028 | 1842.894230 | 921.950753 | 1841.910214 | 921.458745 | I | 401.287080 | 201.147178 | 384.260531 | 192.633903 | | | 3 |
| 16 | 1973.004843 | 987.006060 | 1955.978294 | 978.492785 | 1954.994278 | 978.000777 | L | 288.203016 | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 17 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 57.5 | 2146.109253 | 0.020049 | QEPSQGTTTFAVTSILR |
| 57.5 | 2146.109253 | 0.020049 | QEPSQGTTTFAVTSILR |
| 5.7 | 2146.125351 | 0.003951 | LQKMGPFQPMNIFLR |
| 3.6 | 2146.121124 | 0.008178 | DPFAHLPKSTFVLDEFKR |
| 1.1 | 2146.142929 | -0.013627 | TKRPAPARPTMPPPQVSGSR |
| 0.1 | 2146.131683 | -0.002381 | FCLGLLSNVNRNAAVELTR |

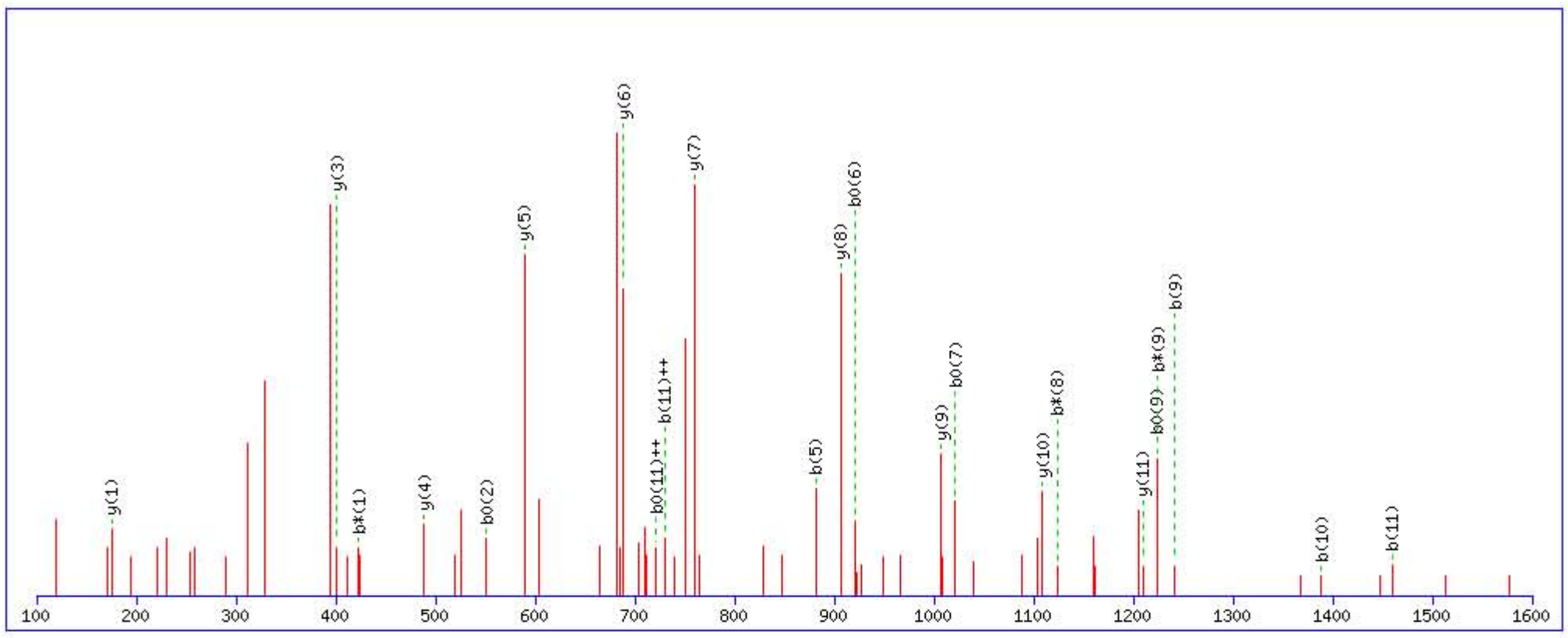
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QEPSQGTTTFAVTSILR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

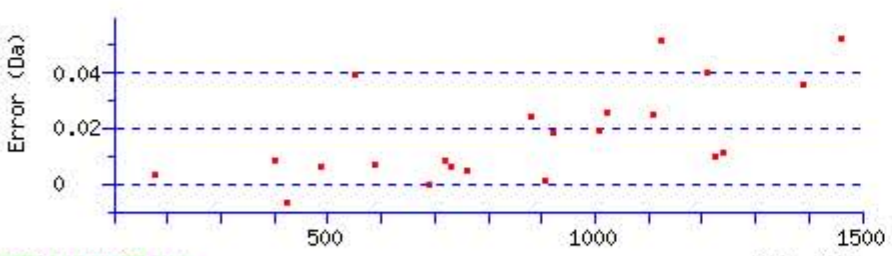
Match to Query 47326: 2146.136562 from(716.386130,3+) rtinseconds(2507) index(23201)
Title: Locus:1.1.1.3255.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

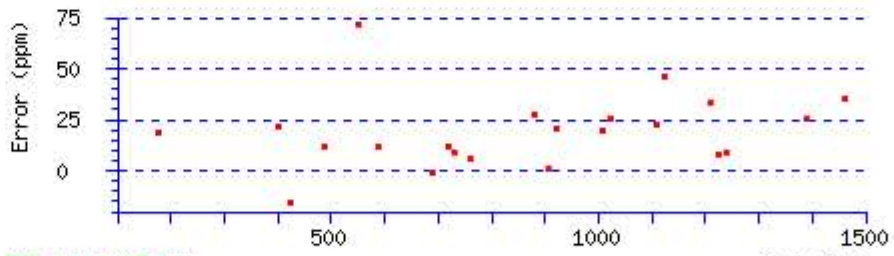
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2146.109253
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 43 **Expect:** 0.00043
**Matches :** 23/184 fragment ions using 52 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 17 |
| 2 | 569.275195 | 285.141236 | 552.248646 | 276.627961 | 551.264630 | 276.135953 | E | 1707.891193 | 854.449235 | 1690.864644 | 845.935960 | 1689.880628 | 845.443952 | 16 |
| 3 | 666.327959 | 333.667618 | 649.301410 | 325.154343 | 648.317394 | 324.662335 | P | 1578.848600 | 789.927938 | 1561.822051 | 781.414664 | 1560.838035 | 780.922656 | 15 |
| 4 | 753.359987 | 377.183632 | 736.333438 | 368.670357 | 735.349422 | 368.178349 | S | 1481.795836 | 741.401556 | 1464.769287 | 732.888282 | 1463.785271 | 732.396274 | 14 |
| 5 | **881.418565** | 441.212921 | 864.392016 | 432.699646 | 863.408000 | 432.207638 | Q | 1394.763808 | 697.885542 | 1377.737259 | 689.372268 | 1376.753243 | 688.880260 | 13 |
| 6 | 938.440029 | 469.723653 | 921.413480 | 461.210378 | 920.429464 | 460.718370 | G | 1266.705230 | 633.856253 | 1249.678681 | 625.342979 | 1248.694665 | 624.850971 | 12 |
| 7 | 1039.487708 | 520.247492 | 1022.461159 | 511.734218 | 1021.477143 | 511.242210 | T | *1209.683766* | 605.345521 | 1192.657217 | 596.832247 | 1191.673201 | 596.340239 | 11 |
| 8 | 1140.535387 | 570.771332 | 1123.508838 | 562.258057 | 1122.524822 | 561.766049 | T | *1108.636087* | 554.821682 | 1091.609538 | 546.308407 | 1090.625522 | 545.816399 | 10 |
| 9 | **1241.583066** | 621.295171 | 1224.556517 | 612.781897 | 1223.572501 | 612.289889 | T | *1007.588408* | 504.297842 | 990.561859 | 495.784568 | 989.577843 | 495.292560 | 9 |
| 10 | **1388.651480** | 694.829378 | 1371.624931 | 686.316104 | 1370.640915 | 685.824096 | F | *906.540729* | 453.774003 | 889.514180 | 445.260728 | 888.530164 | 444.768720 | 8 |
| 11 | **1459.688594** | 730.347935 | 1442.662045 | 721.834661 | 1441.678029 | 721.342653 | A | *759.472315* | 380.239796 | 742.445766 | 371.726521 | 741.461750 | 371.234513 | 7 |
| 12 | 1558.757008 | 779.882142 | 1541.730459 | 771.368868 | 1540.746443 | 770.876860 | V | *688.435201* | 344.721239 | 671.408652 | 336.207964 | 670.424636 | 335.715956 | 6 |
| 13 | 1659.804687 | 830.405982 | 1642.778138 | 821.892707 | 1641.794122 | 821.400699 | T | *589.366787* | 295.187032 | 572.340238 | 286.673757 | 571.356222 | 286.181749 | 5 |
| 14 | 1746.836715 | 873.921996 | 1729.810166 | 865.408721 | 1728.826150 | 864.916713 | S | *488.319108* | 244.663192 | 471.292559 | 236.149918 | 470.308543 | 235.657910 | 4 |
| 15 | 1859.920779 | 930.464028 | 1842.894230 | 921.950753 | 1841.910214 | 921.458745 | I | *401.287080* | 201.147178 | 384.260531 | 192.633903 | | | 3 |
| 16 | 1973.004843 | 987.006060 | 1955.978294 | 978.492785 | 1954.994278 | 978.000777 | L | 288.203016 | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 17 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 42.9 | 2146.109253 | 0.027309 | QEPSQGTTTFAVTSILR |
| 42.9 | 2146.109253 | 0.027309 | QEPSQGTTTFAVTSILR |
| 6.7 | 2146.142929 | -0.006367 | TKRPAPARPTMPPPQVSGSR |
| 2.3 | 2146.164688 | -0.028126 | VQEDIILLRELHVNHYR |

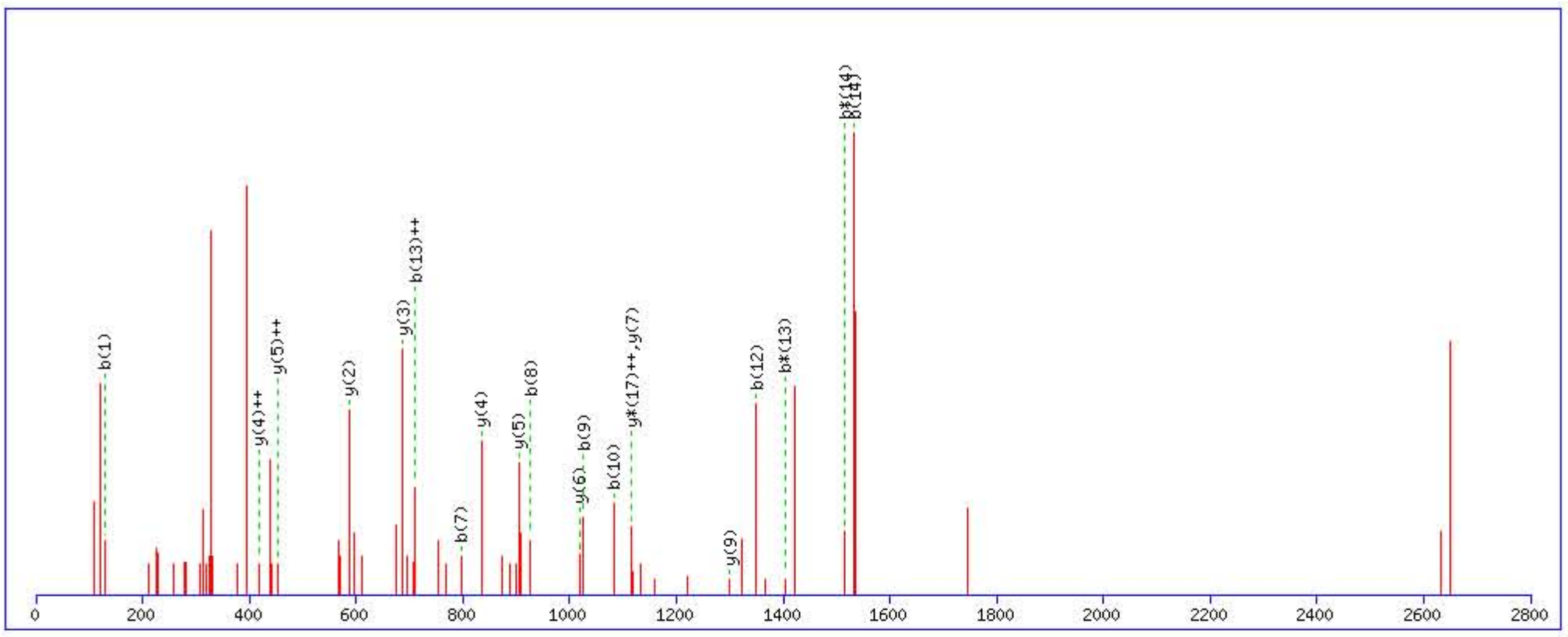
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KGDTFSCMVGHEALPLAFTQK**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

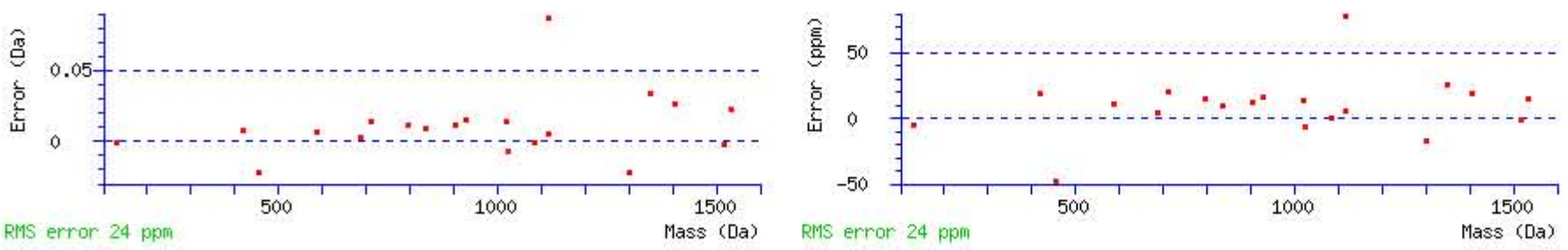
Match to Query 55880: 2647.317016 from(662.836530,4+) rtinseconds(2361) index(68505)
Title: Locus:1.1.1.2097.18 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2647.296082
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q20 : Biotin:Thermo-21345 (Q)
**Ions Score:** 28 **Expect:** 0.0028
**Matches :** 20/232 fragment ions using 52 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *129.102239* | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 21 |
| 2 | 186.123703 | 93.565489 | 169.097154 | 85.052215 | | | G | 2520.208388 | 1260.607832 | 2503.181839 | 1252.094557 | 2502.197823 | 1251.602549 | 20 |
| 3 | 301.150646 | 151.078961 | 284.124097 | 142.565687 | 283.140081 | 142.073679 | D | 2463.186924 | 1232.097100 | 2446.160375 | 1223.583825 | 2445.176359 | 1223.091817 | 19 |
| 4 | 402.198325 | 201.602801 | 385.171776 | 193.089526 | 384.187760 | 192.597518 | T | 2348.159981 | 1174.583628 | 2331.133432 | 1166.070354 | 2330.149416 | 1165.578346 | 18 |
| 5 | 549.266739 | 275.137008 | 532.240190 | 266.623733 | 531.256174 | 266.131725 | F | 2247.112302 | 1124.059789 | 2230.085753 | 1115.546514 | 2229.101737 | 1115.054506 | 17 |
| 6 | 636.298767 | 318.653022 | 619.272218 | 310.139747 | 618.288202 | 309.647739 | S | 2100.043888 | 1050.525582 | 2083.017339 | 1042.012307 | 2082.033323 | 1041.520299 | 16 |
| 7 | *796.329416* | 398.668346 | 779.302867 | 390.155072 | 778.318851 | 389.663064 | C | 2013.011860 | 1007.009568 | 1995.985311 | 998.496294 | 1995.001295 | 998.004286 | 15 |
| 8 | *927.369901* | 464.188589 | 910.343352 | 455.675314 | 909.359336 | 455.183306 | M | 1852.981211 | 926.994244 | 1835.954662 | 918.480969 | 1834.970646 | 917.988961 | 14 |
| 9 | *1026.438315* | 513.722796 | 1009.411766 | 505.209521 | 1008.427750 | 504.717513 | V | 1721.940726 | 861.474001 | 1704.914177 | 852.960727 | 1703.930161 | 852.468719 | 13 |
| 10 | *1083.459779* | 542.233528 | 1066.433230 | 533.720253 | 1065.449214 | 533.228245 | G | 1622.872312 | 811.939794 | 1605.845763 | 803.426520 | 1604.861747 | 802.934512 | 12 |
| 11 | 1220.518691 | 610.762984 | 1203.492142 | 602.249709 | 1202.508126 | 601.757701 | H | 1565.850848 | 783.429062 | 1548.824299 | 774.915788 | 1547.840283 | 774.423780 | 11 |
| 12 | *1349.561284* | 675.284280 | 1332.534735 | 666.771006 | 1331.550719 | 666.278998 | E | 1428.791936 | 714.899606 | 1411.765387 | 706.386332 | 1410.781371 | 705.894324 | 10 |
| 13 | 1420.598398 | 710.802837 | 1403.571849 | 702.289563 | 1402.587833 | 701.797555 | A | *1299.749343* | 650.378310 | 1282.722794 | 641.865035 | 1281.738778 | 641.373027 | 9 |
| 14 | *1533.682462* | 767.344869 | 1516.655913 | 758.831595 | 1515.671897 | 758.339587 | L | 1228.712229 | 614.859753 | 1211.685680 | 606.346478 | 1210.701664 | 605.854470 | 8 |
| 15 | 1630.735226 | 815.871251 | 1613.708677 | 807.357977 | 1612.724661 | 806.865969 | P | *1115.628165* | 558.317721 | 1098.601616 | 549.804446 | 1097.617600 | 549.312438 | 7 |
| 16 | 1743.819290 | 872.413283 | 1726.792741 | 863.900009 | 1725.808725 | 863.408000 | L | *1018.575401* | 509.791339 | 1001.548852 | 501.278064 | 1000.564836 | 500.786056 | 6 |
| 17 | 1814.856404 | 907.931840 | 1797.829855 | 899.418566 | 1796.845839 | 898.926557 | A | *905.491337* | 453.249307 | 888.464788 | 444.736032 | 887.480772 | 444.244024 | 5 |
| 18 | 1961.924818 | 981.466047 | 1944.898269 | 972.952773 | 1943.914253 | 972.460764 | F | *834.454223* | 417.730750 | 817.427674 | 409.217475 | 816.443658 | 408.725467 | 4 |
| 19 | 2062.972497 | 1031.989886 | 2045.945948 | 1023.476612 | 2044.961932 | 1022.984604 | T | *687.385809* | 344.196543 | 670.359260 | 335.683268 | 669.375244 | 335.191260 | 3 |
| 20 | 2502.197823 | 1251.602549 | 2485.171274 | 1243.089275 | 2484.187258 | 1242.597267 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 21 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 28.4 | 2647.296082 | 0.020934 | KGDTFSCMVGHEALPLAFTQK |
| 1.0 | 2647.279907 | 0.037109 | QMLRAADDFLEDLPLEETGAIER |
| 0.1 | 2647.281662 | 0.035354 | AAVLACQACCMLAIFLSMLVSYR |

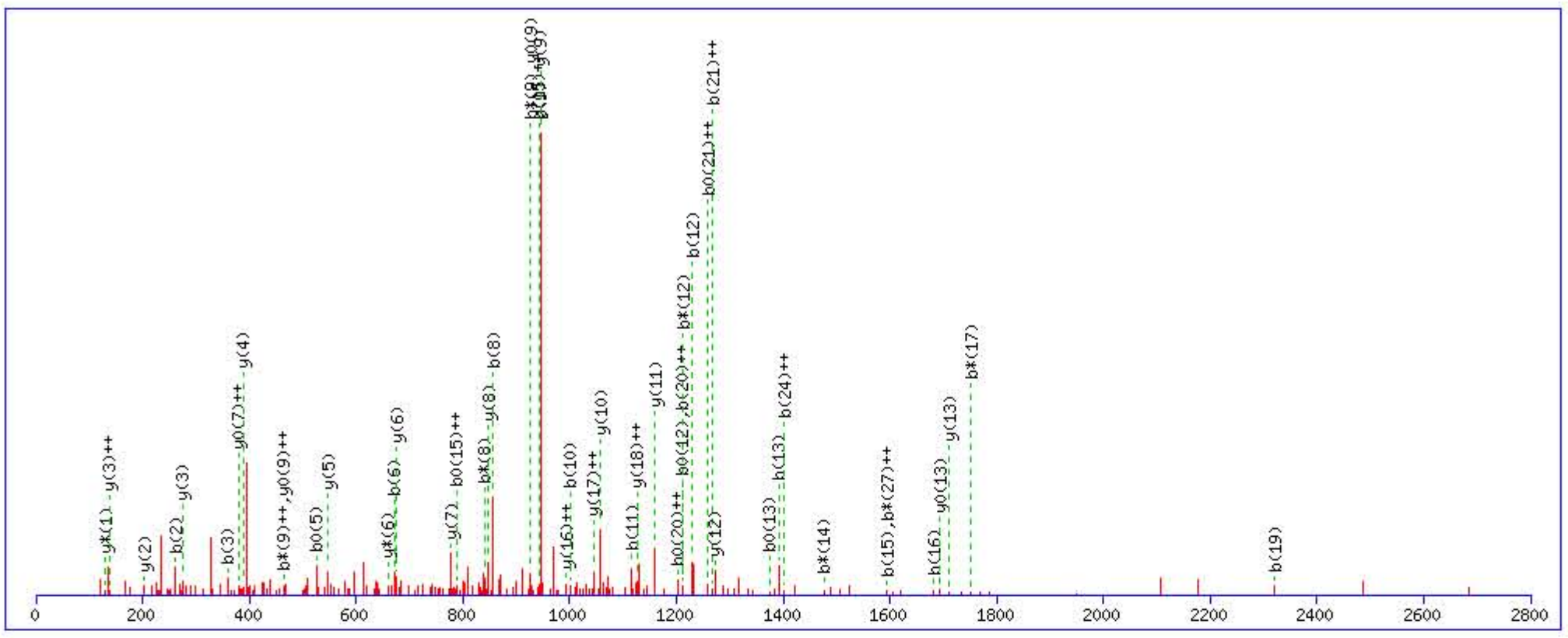
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NFPPSQDASGDLYTTSSQLTLPATQCLAGK**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

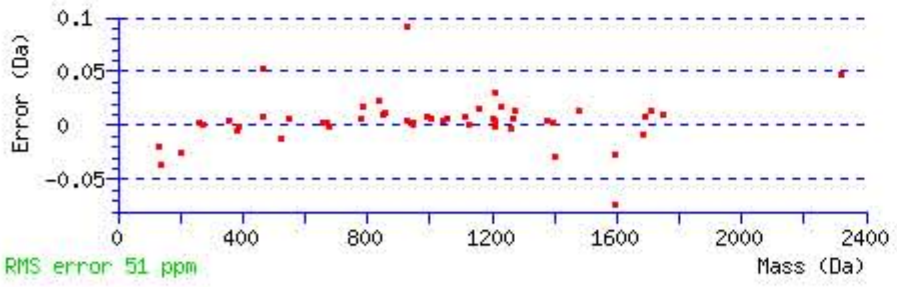
Match to Query 65579: 3478.711096 from(870.685050,4+) rtinseconds(2579) index(8646)
Title: Locus:1.1.1.2175.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

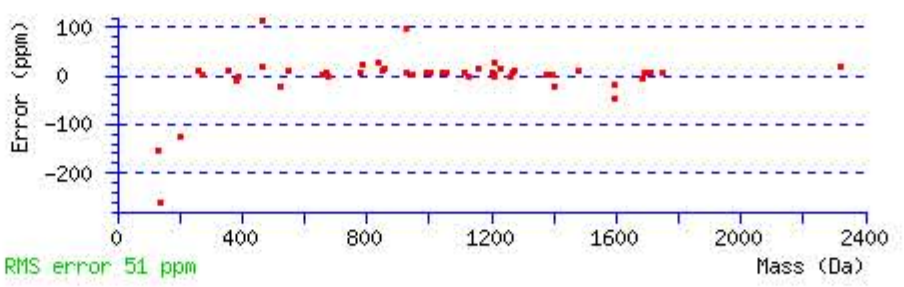
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3478.674866
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q18 : Biotin:Thermo-21345 (Q)
**Ions Score:** 50 **Expect:** 0.00028
**Matches :** 51/328 fragment ions using 148 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 30 |
| 2 | *262.118617* | 131.562946 | 245.092068 | 123.049672 | | | F | 3365.639210 | 1683.323243 | 3348.612661 | 1674.809968 | 3347.628645 | 1674.317960 | 29 |
| 3 | *359.171381* | 180.089328 | 342.144832 | 171.576054 | | | P | 3218.570796 | 1609.789036 | 3201.544247 | 1601.275761 | 3200.560231 | 1600.783753 | 28 |
| 4 | 456.224145 | 228.615710 | 439.197596 | 220.102436 | | | P | 3121.518032 | 1561.262654 | 3104.491483 | 1552.749379 | 3103.507467 | 1552.257371 | 27 |
| 5 | 543.256173 | 272.131725 | 526.229624 | 263.618450 | 525.245608 | 263.126442 | S | 3024.465268 | 1512.736272 | 3007.438719 | 1504.222997 | 3006.454703 | 1503.730989 | 26 |
| 6 | *671.314751* | 336.161014 | 654.288202 | 327.647739 | 653.304186 | 327.155731 | Q | 2937.433240 | 1469.220258 | 2920.406691 | 1460.706983 | 2919.422675 | 1460.214975 | 25 |
| 7 | 786.341694 | 393.674485 | 769.315145 | 385.161210 | 768.331129 | 384.669202 | D | 2809.374662 | 1405.190969 | 2792.348113 | 1396.677694 | 2791.364097 | 1396.185686 | 24 |
| 8 | *857.378808* | 429.193042 | 840.352259 | 420.679767 | 839.368243 | 420.187759 | A | 2694.347719 | 1347.677497 | 2677.321170 | 1339.164223 | 2676.337154 | 1338.672215 | 23 |
| 9 | *944.410836* | 472.709056 | 927.384287 | 464.195781 | 926.400271 | 463.703773 | S | 2623.310605 | 1312.158941 | 2606.284056 | 1303.645666 | 2605.300040 | 1303.153658 | 22 |
| 10 | *1001.432300* | 501.219788 | 984.405751 | 492.706513 | 983.421735 | 492.214505 | G | 2536.278577 | 1268.642926 | 2519.252028 | 1260.129652 | 2518.268012 | 1259.637644 | 21 |
| 11 | *1116.459243* | 558.733260 | 1099.432694 | 550.219985 | 1098.448678 | 549.727977 | D | 2479.257113 | 1240.132195 | 2462.230564 | 1231.618920 | 2461.246548 | 1231.126912 | 20 |
| 12 | *1229.543307* | 615.275291 | 1212.516758 | 606.762017 | 1211.532742 | 606.270009 | L | 2364.230170 | 1182.618723 | 2347.203621 | 1174.105448 | 2346.219605 | 1173.613440 | 19 |
| 13 | *1392.606636* | 696.806956 | 1375.580087 | 688.293682 | 1374.596071 | 687.801673 | Y | 2251.146106 | 1126.076691 | 2234.119557 | 1117.563416 | 2233.135541 | 1117.071408 | 18 |
| 14 | 1493.654315 | 747.330796 | 1476.627766 | 738.817521 | 1475.643750 | 738.325513 | T | 2088.082777 | 1044.545026 | 2071.056228 | 1036.031752 | 2070.072212 | 1035.539744 | 17 |
| 15 | *1594.701994* | 797.854635 | 1577.675445 | 789.341361 | 1576.691429 | 788.849353 | T | 1987.035098 | 994.021187 | 1970.008549 | 985.507913 | 1969.024533 | 985.015905 | 16 |
| 16 | *1681.734022* | 841.370649 | 1664.707473 | 832.857375 | 1663.723457 | 832.365367 | S | 1885.987419 | 943.497348 | 1868.960870 | 934.984073 | 1867.976854 | 934.492065 | 15 |
| 17 | 1768.766050 | 884.886663 | 1751.739501 | 876.373389 | 1750.755485 | 875.881381 | S | 1798.955391 | 899.981334 | 1781.928842 | 891.468059 | 1780.944826 | 890.976051 | 14 |
| 18 | 2207.991376 | 1104.499326 | 2190.964827 | 1095.986051 | 2189.980811 | 1095.494043 | Q | *1711.923363* | 856.465320 | 1694.896814 | 847.952045 | 1693.912798 | 847.460037 | 13 |
| 19 | *2321.075440* | 1161.041358 | 2304.048891 | 1152.528083 | 2303.064875 | 1152.036075 | L | *1272.698037* | 636.852657 | 1255.671488 | 628.339382 | 1254.687472 | 627.847374 | 12 |
| 20 | 2422.123119 | **1211.565197** | 2405.096570 | 1203.051923 | 2404.112554 | 1202.559915 | T | *1159.613973* | 580.310625 | 1142.587424 | 571.797350 | 1141.603408 | 571.305342 | 11 |
| 21 | 2535.207183 | **1268.107229** | 2518.180634 | 1259.593955 | 2517.196618 | 1259.101947 | L | *1058.566294* | 529.786785 | 1041.539745 | 521.273511 | 1040.555729 | 520.781503 | 10 |
| 22 | 2632.259947 | 1316.633611 | 2615.233398 | 1308.120337 | 2614.249382 | 1307.628329 | P | *945.482230* | 473.244753 | 928.455681 | 464.731479 | 927.471665 | 464.239471 | 9 |
| 23 | 2703.297061 | 1352.152169 | 2686.270512 | 1343.638894 | 2685.286496 | 1343.146886 | A | *848.429466* | 424.718371 | 831.402917 | 416.205097 | 830.418901 | 415.713089 | 8 |
| 24 | 2804.344740 | **1402.676008** | 2787.318191 | 1394.162733 | 2786.334175 | 1393.670725 | T | *777.392352* | 389.199814 | 760.365803 | 380.686540 | 759.381787 | 380.194532 | 7 |
| 25 | 2932.403318 | 1466.705297 | 2915.376769 | 1458.192022 | 2914.392753 | 1457.700015 | Q | *676.344673* | 338.675975 | 659.318124 | 330.162700 | | | 6 |
| 26 | 3092.433967 | 1546.720621 | 3075.407418 | 1538.207347 | 3074.423402 | 1537.715339 | C | *548.286095* | 274.646686 | 531.259546 | 266.133411 | | | 5 |
| 27 | 3205.518031 | 1603.262653 | 3188.491482 | 1594.749379 | 3187.507466 | 1594.257371 | L | *388.255446* | 194.631361 | 371.228897 | 186.118087 | | | 4 |
| 28 | 3276.555145 | 1638.781211 | 3259.528596 | 1630.267936 | 3258.544580 | 1629.775928 | A | *275.171382* | 138.089329 | 258.144833 | 129.576055 | | | 3 |
| 29 | 3333.576609 | 1667.291943 | 3316.550060 | 1658.778668 | 3315.566044 | 1658.286660 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 30 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 49.7 | 3478.674866 | 0.036230 | NFPPSQDASGDLYTTSSQLTLPATQCLAGK |
| 17.1 | 3478.674866 | 0.036230 | NFPPSQDASGDLYTTSSQLTLPATQCLAGK |
| 12.4 | 3478.674866 | 0.036230 | NFPPSQDASGDLYTTSSQLTLPATQCLAGK |

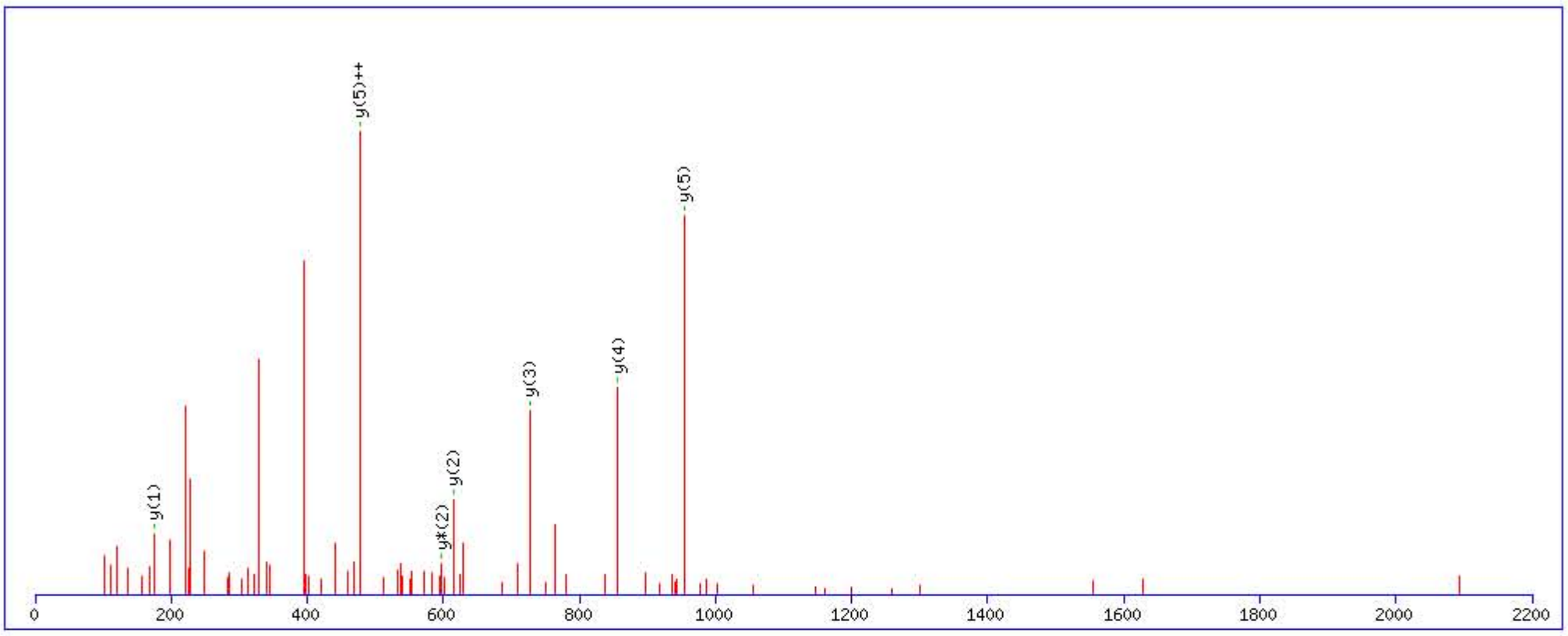
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TFPEIQR**
Found in **IGHD_HUMAN**, Ig delta chain C region OS=Homo sapiens GN=IGHD PE=1 SV=2

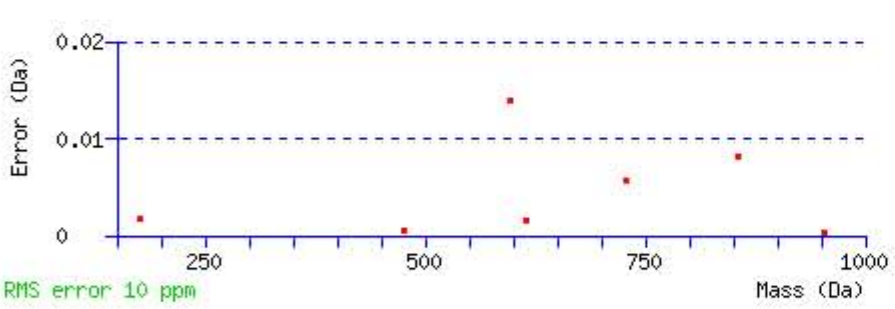
Match to Query 20564: 1200.633508 from(601.324030,2+) rtinseconds(1951) index(5389)
Title: Locus:1.1.1.1956.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

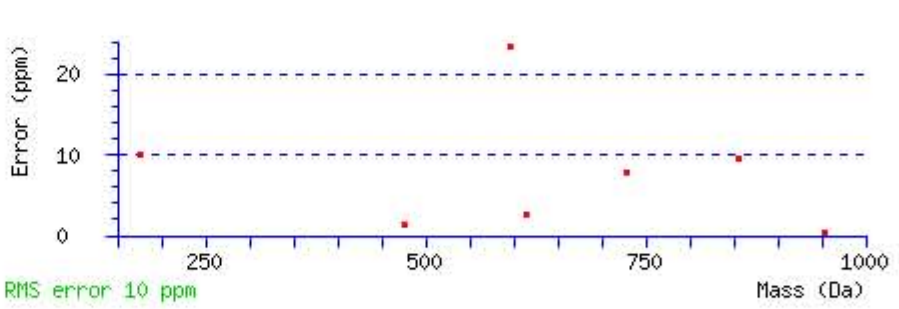
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1200.632507
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 34 **Expect:** 0.0018
**Matches :** 7/56 fragment ions using 11 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 7 |
| 2 | 249.123369 | 125.065322 | | | 231.112804 | 116.060040 | F | 1100.592113 | 550.799695 | 1083.565564 | 542.286420 | 1082.581548 | 541.794412 | 6 |
| 3 | 346.176133 | 173.591704 | | | 328.165568 | 164.586422 | P | *953.523699* | 477.265488 | 936.497150 | 468.752213 | 935.513134 | 468.260205 | 5 |
| 4 | 475.218726 | 238.113001 | | | 457.208161 | 229.107719 | E | *856.470935* | 428.739106 | 839.444386 | 420.225831 | 838.460370 | 419.733823 | 4 |
| 5 | 588.302790 | 294.655033 | | | 570.292225 | 285.649751 | I | *727.428342* | 364.217809 | 710.401793 | 355.704535 | | | 3 |
| 6 | 1027.528116 | 514.267696 | 1010.501567 | 505.754422 | 1009.517551 | 505.262414 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 7 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.8 | 1200.632507 | 0.001001 | TFPEIQR |
| 4.4 | 1200.628464 | 0.005044 | LLQLQEMGNR |
| 1.7 | 1200.650269 | -0.016761 | ETDKPPFVIR |

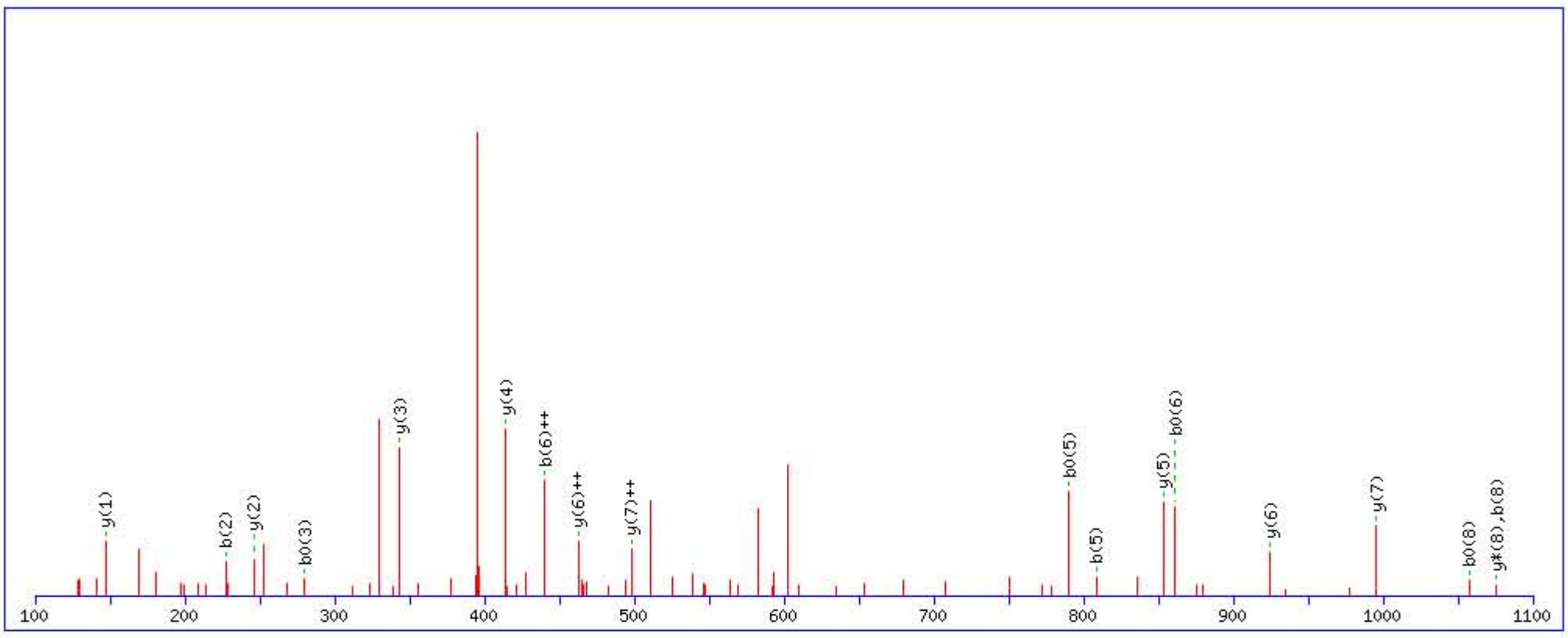
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EPAAQAPVK**
Found in **IGHD_HUMAN**, Ig delta chain C region OS=Homo sapiens GN=IGHD PE=1 SV=2

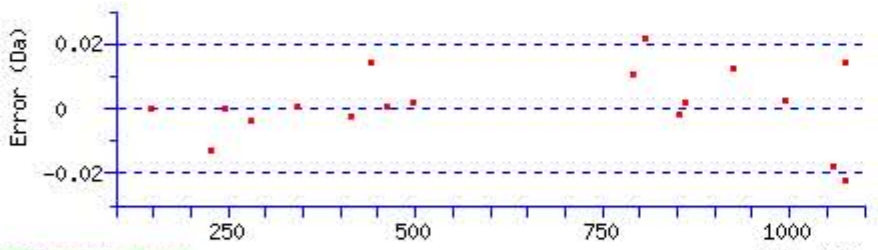
Match to Query 20992: 1220.659248 from(611.336900,2+) rtinseconds(1426) index(63003)
Title: Locus:1.1.1.1771.21 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

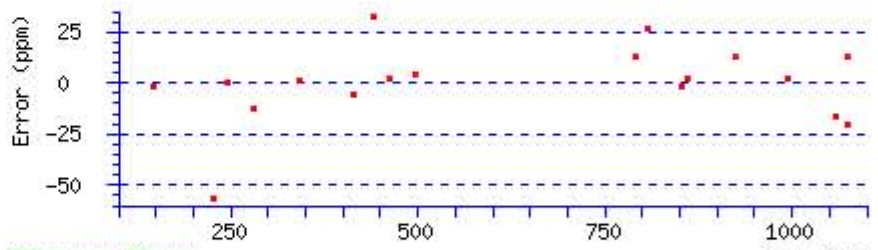
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1220.658707
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.0028
**Matches :** 18/72 fragment ions using 37 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | 9 |
| 2 | **227.102633** | 114.054954 | | | 209.092068 | 105.049672 | P | 1092.623414 | 546.815345 | 1075.596865 | 538.302071 | 8 |
| 3 | 298.139747 | 149.573512 | | | 280.129182 | 140.568229 | A | ***995.570650*** | 498.288963 | 978.544101 | 489.775689 | 7 |
| 4 | 369.176861 | 185.092068 | | | 351.166296 | 176.086786 | A | ***924.533536*** | 462.770406 | 907.506987 | 454.257132 | 6 |
| 5 | **808.402187** | 404.704732 | 791.375638 | 396.191457 | 790.391622 | 395.699449 | Q | ***853.496422*** | 427.251849 | 836.469873 | 418.738575 | 5 |
| 6 | 879.439301 | 440.223289 | 862.412752 | 431.710014 | 861.428736 | 431.218006 | A | ***414.271096*** | 207.639186 | 397.244547 | 199.125911 | 4 |
| 7 | 976.492065 | 488.749671 | 959.465516 | 480.236396 | 958.481500 | 479.744388 | P | ***343.233982*** | 172.120629 | 326.207433 | 163.607354 | 3 |
| 8 | **1075.560479** | 538.283878 | 1058.533930 | 529.770603 | 1057.549914 | 529.278595 | V | ***246.181218*** | 123.594247 | 229.154669 | 115.080972 | 2 |
| 9 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.1 | 1220.658707 | 0.000541 | EPAAQAPVK |
| 11.3 | 1220.658722 | 0.000526 | EQNVPVPK |
| 11.1 | 1220.676468 | -0.017220 | AEPPPSKPTVAK |
| 4.3 | 1220.658722 | 0.000526 | QPNLPDVK |
| 3.6 | 1220.654678 | 0.004570 | SVRMLSGSKEK |
| 3.5 | 1220.644806 | 0.014442 | GGHVQREK |
| 2.8 | 1220.676468 | -0.017220 | EKAATVFNTLK |
| 2.5 | 1220.669952 | -0.010704 | QTGKKPFKCK |
| 1.7 | 1220.647476 | 0.011772 | LEMYVLNPVK |
| 1.7 | 1220.658722 | 0.000526 | NLQDPVPK |

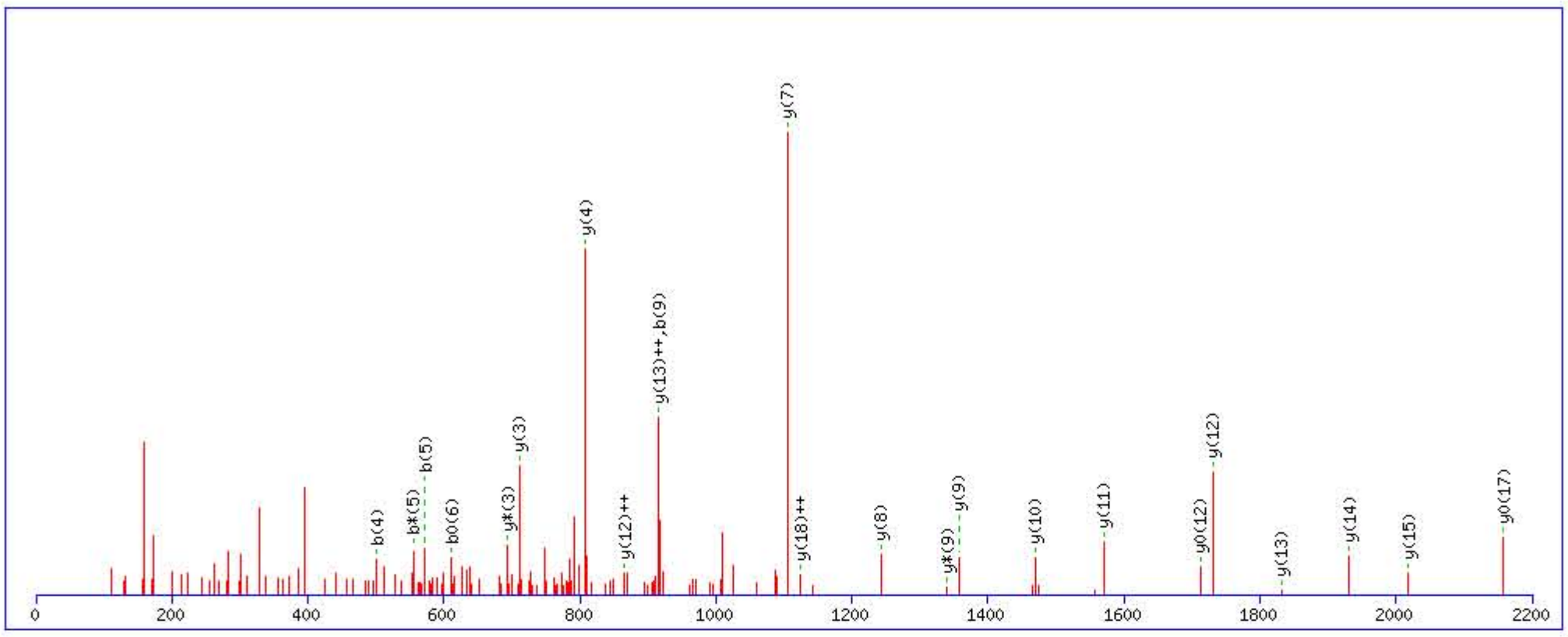
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SLWNAGTSVTCTLNHPSLPPQR**
Found in **IGHD_HUMAN**, Ig delta chain C region OS=Homo sapiens GN=IGHD PE=1 SV=2

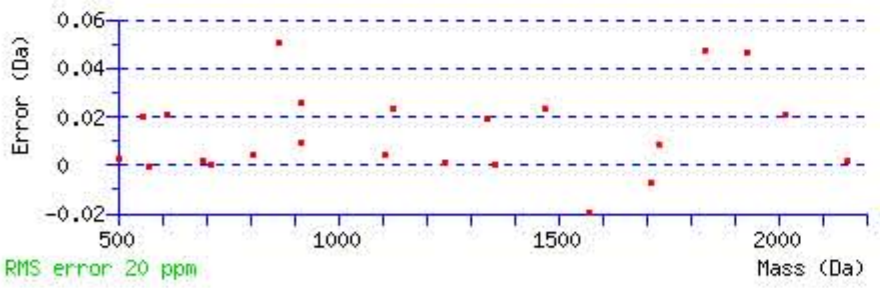
Match to Query 56903: 2746.384696 from(687.603450,4+) rtinseconds(2237) index(7006)
Title: Locus:1.1.1.2056.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

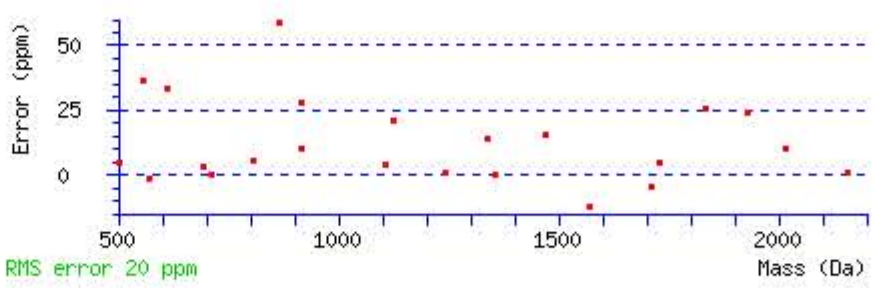
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2746.368332
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q21 : Biotin:Thermo-21345 (Q)
**Ions Score:** 64 **Expect:** 1.2e-005
**Matches :** 23/236 fragment ions using 37 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 22 |
| 2 | 201.123368 | 101.065322 | | | 183.112803 | 92.060039 | L | 2660.343575 | 1330.675425 | 2643.317026 | 1322.162151 | 2642.333010 | 1321.670143 | 21 |
| 3 | 387.202681 | 194.104978 | | | 369.192116 | 185.099696 | W | 2547.259511 | 1274.133393 | 2530.232962 | 1265.620119 | 2529.248946 | 1265.128111 | 20 |
| 4 | **501.245608** | 251.126442 | 484.219059 | 242.613168 | 483.235043 | 242.121160 | N | 2361.180198 | 1181.093737 | 2344.153649 | 1172.580462 | 2343.169633 | 1172.088454 | 19 |
| 5 | **572.282722** | 286.644999 | 555.256173 | 278.131725 | 554.272157 | 277.639717 | A | 2247.137271 | 1124.072273 | 2230.110722 | 1115.558999 | 2229.126706 | 1115.066991 | 18 |
| 6 | 629.304186 | 315.155731 | 612.277637 | 306.642457 | 611.293621 | 306.150449 | G | 2176.100157 | 1088.553716 | 2159.073608 | 1080.040442 | 2158.089592 | 1079.548434 | 17 |
| 7 | 730.351865 | 365.679571 | 713.325316 | 357.166296 | 712.341300 | 356.674288 | T | 2119.078693 | 1060.042984 | 2102.052144 | 1051.529710 | 2101.068128 | 1051.037702 | 16 |
| 8 | 817.383893 | 409.195585 | 800.357344 | 400.682310 | 799.373328 | 400.190302 | S | *2018.031014* | 1009.519145 | 2001.004465 | 1001.005871 | 2000.020449 | 1000.513863 | 15 |
| 9 | **916.452307** | 458.729792 | 899.425758 | 450.216517 | 898.441742 | 449.724509 | V | *1930.998986* | 966.003131 | 1913.972437 | 957.489857 | 1912.988421 | 956.997849 | 14 |
| 10 | 1017.499986 | 509.253631 | 1000.473437 | 500.740357 | 999.489421 | 500.248349 | T | *1831.930572* | 916.468924 | 1814.904023 | 907.955650 | 1813.920007 | 907.463642 | 13 |
| 11 | 1177.530635 | 589.268956 | 1160.504086 | 580.755681 | 1159.520070 | 580.263673 | C | *1730.882893* | 865.945085 | 1713.856344 | 857.431810 | 1712.872328 | 856.939802 | 12 |
| 12 | 1278.578314 | 639.792795 | 1261.551765 | 631.279521 | 1260.567749 | 630.787513 | T | *1570.852244* | 785.929760 | 1553.825695 | 777.416486 | 1552.841679 | 776.924478 | 11 |
| 13 | 1391.662378 | 696.334827 | 1374.635829 | 687.821553 | 1373.651813 | 687.329545 | L | *1469.804565* | 735.405921 | 1452.778016 | 726.892646 | 1451.794000 | 726.400638 | 10 |
| 14 | 1505.705305 | 753.356291 | 1488.678756 | 744.843016 | 1487.694740 | 744.351008 | N | *1356.720501* | 678.863889 | 1339.693952 | 670.350614 | 1338.709936 | 669.858606 | 9 |
| 15 | 1642.764217 | 821.885746 | 1625.737668 | 813.372472 | 1624.753652 | 812.880464 | H | *1242.677574* | 621.842425 | 1225.651025 | 613.329151 | 1224.667009 | 612.837143 | 8 |
| 16 | 1739.816981 | 870.412128 | 1722.790432 | 861.898854 | 1721.806416 | 861.406846 | P | *1105.618662* | 553.312969 | 1088.592113 | 544.799695 | 1087.608097 | 544.307687 | 7 |
| 17 | 1826.849009 | 913.928143 | 1809.822460 | 905.414868 | 1808.838444 | 904.922860 | S | 1008.565898 | 504.786587 | 991.539349 | 496.273313 | 990.555333 | 495.781305 | 6 |
| 18 | 1939.933073 | 970.470174 | 1922.906524 | 961.956900 | 1921.922508 | 961.464892 | L | 921.533870 | 461.270573 | 904.507321 | 452.757299 | | | 5 |
| 19 | 2036.985837 | 1018.996557 | 2019.959288 | 1010.483282 | 2018.975272 | 1009.991274 | P | *808.449806* | 404.728541 | 791.423257 | 396.215267 | | | 4 |
| 20 | 2134.038601 | 1067.522938 | 2117.012052 | 1059.009664 | 2116.028036 | 1058.517656 | P | *711.397042* | 356.202159 | 694.370493 | 347.688885 | | | 3 |
| 21 | 2573.263927 | 1287.135601 | 2556.237378 | 1278.622327 | 2555.253362 | 1278.130319 | Q | 614.344278 | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 22 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 63.8 | 2746.368332 | 0.016364 | SLWNAGTSVTCTLNHPSLPPQR |

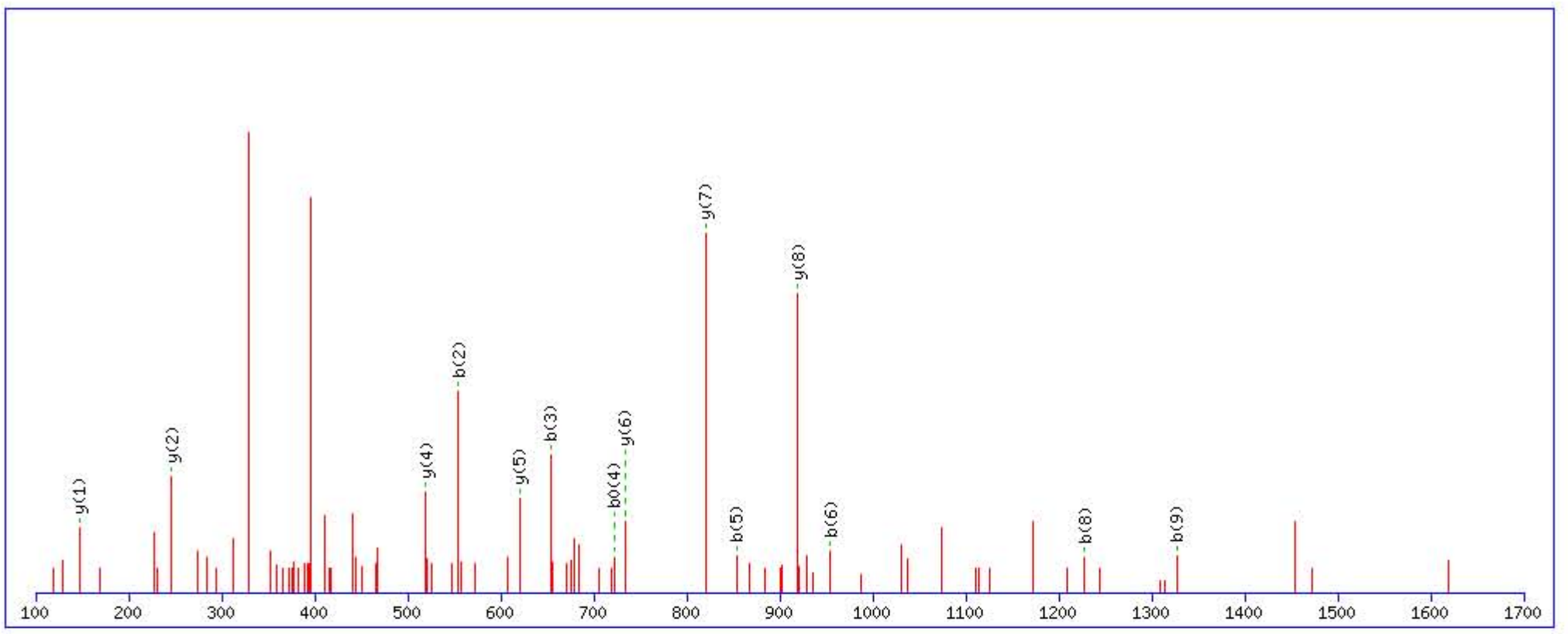
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NQVSLTCLVK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

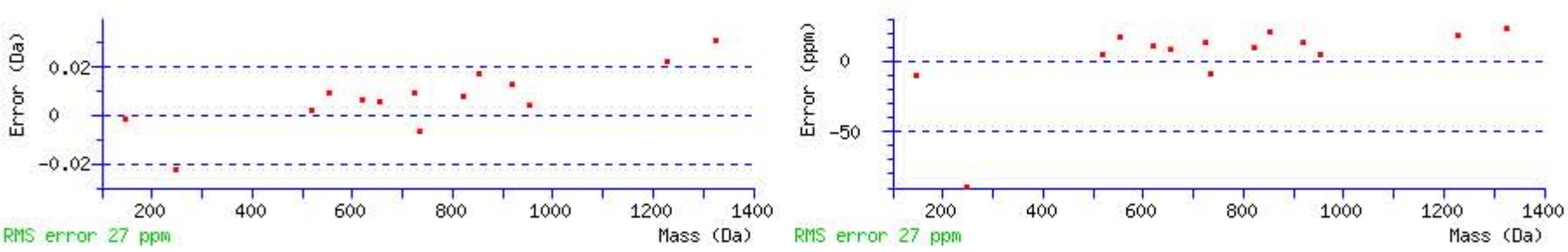
Match to Query 30278: 1471.795568 from(736.905060,2+) rtinseconds(2229) index(6944)
Title: Locus:1.1.1.2053.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1471.789093
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0026
**Matches :** 14/94 fragment ions using 27 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 10 |
| 2 | **554.275529** | 277.641403 | 537.248980 | 269.128128 | | | Q | 1358.753442 | 679.880359 | 1341.726893 | 671.367085 | 1340.742877 | 670.875076 | 9 |
| 3 | **653.343943** | 327.175610 | 636.317394 | 318.662335 | | | V | ***919.528116*** | 460.267696 | 902.501567 | 451.754421 | 901.517551 | 451.262413 | 8 |
| 4 | 740.375971 | 370.691623 | 723.349422 | 362.178349 | 722.365406 | 361.686341 | S | ***820.459702*** | 410.733489 | 803.433153 | 402.220215 | 802.449137 | 401.728207 | 7 |
| 5 | **853.460035** | 427.233656 | 836.433486 | 418.720381 | 835.449470 | 418.228373 | L | ***733.427674*** | 367.217475 | 716.401125 | 358.704201 | 715.417109 | 358.212193 | 6 |
| 6 | **954.507714** | 477.757495 | 937.481165 | 469.244220 | 936.497149 | 468.752212 | T | ***620.343610*** | 310.675443 | 603.317061 | 302.162169 | 602.333045 | 301.670161 | 5 |
| 7 | 1114.538363 | 557.772819 | 1097.511814 | 549.259545 | 1096.527798 | 548.767537 | C | ***519.295931*** | 260.151604 | 502.269382 | 251.638329 | | | 4 |
| 8 | **1227.622427** | 614.314851 | 1210.595878 | 605.801577 | 1209.611862 | 605.309569 | L | 359.265282 | 180.136279 | 342.238733 | 171.623004 | | | 3 |
| 9 | **1326.690841** | 663.849058 | 1309.664292 | 655.335784 | 1308.680276 | 654.843776 | V | ***246.181218*** | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 10 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 39.5 | 1471.789093 | 0.006475 | NQVSLTCLVK |
| 12.6 | 1471.778305 | 0.017263 | WNVSRPSLLADSK |
| 7.5 | 1471.777847 | 0.017721 | QLDMELVSVK |
| 4.9 | 1471.797592 | -0.002024 | KYFWDRAFLVK |
| 3.0 | 1471.806793 | -0.011225 | AAALLAKQAEMEVK |
| 3.0 | 1471.796951 | -0.001383 | QRAAQFDVVK |
| 1.6 | 1471.814713 | -0.019145 | RQVIVGTWGESLK |

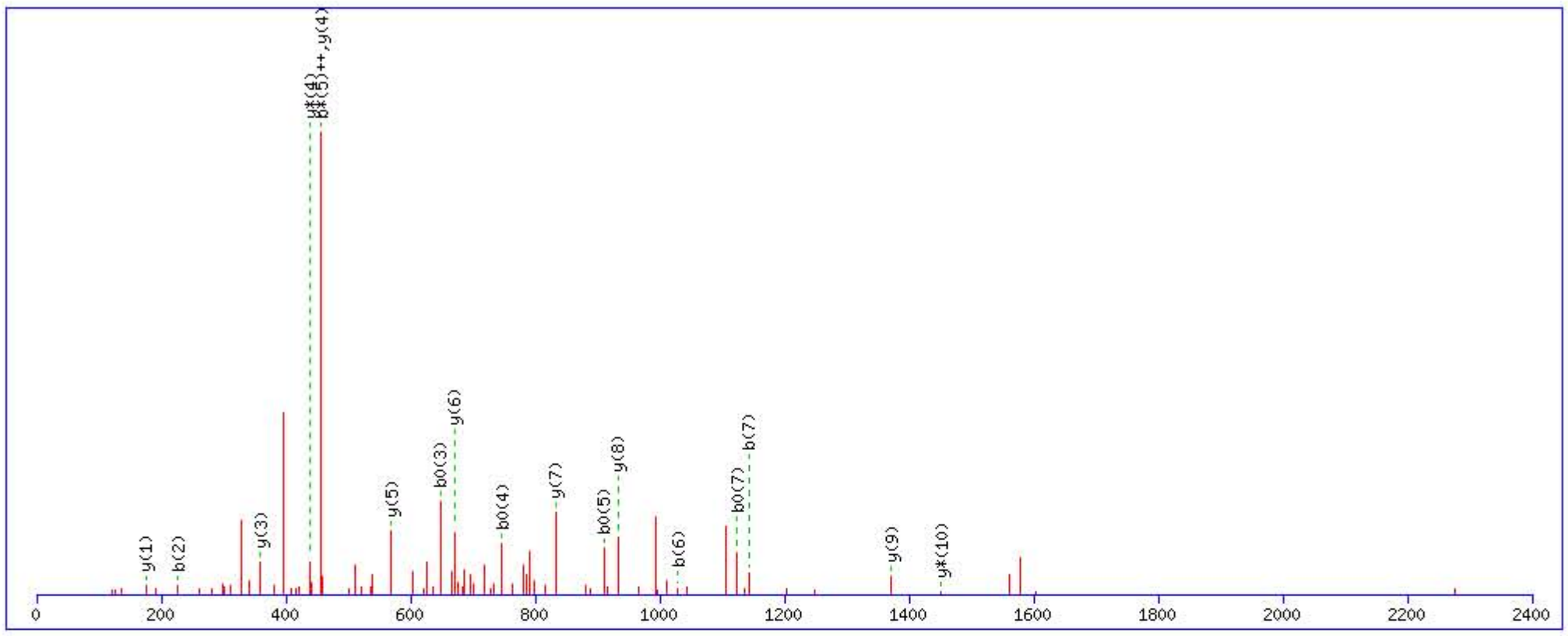
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EPQVYTLPPSR**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

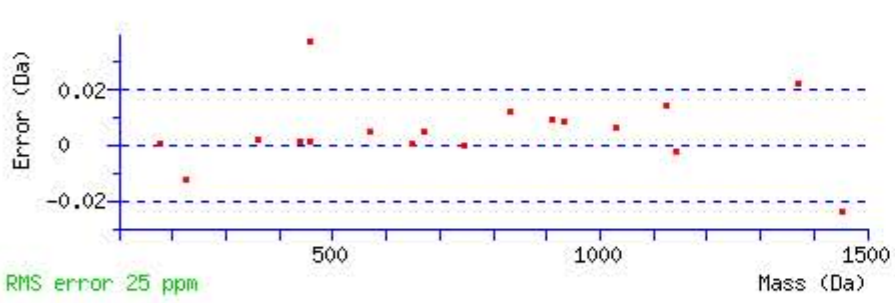
Match to Query 34615: 1596.841748 from(799.428150,2+) rtinseconds(1923) index(65896)
Title: Locus:1.1.1.1944.26 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

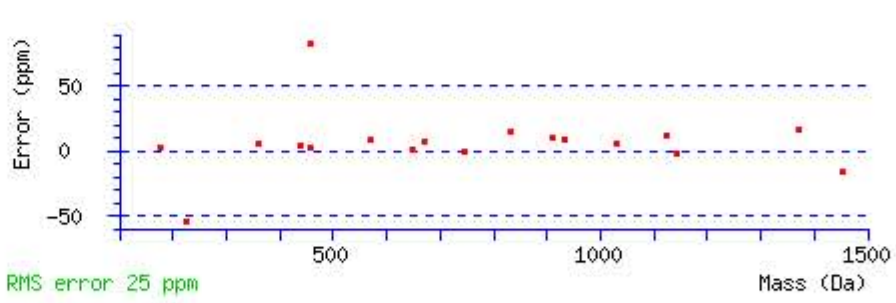
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1596.833389
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.00031
**Matches :** 18/114 fragment ions using 38 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 11 |
| 2 | **227.102633** | 114.054954 | | | 209.092068 | 105.049672 | P | 1468.798084 | 734.902680 | 1451.771535 | 726.389406 | 1450.787519 | 725.897398 | 10 |
| 3 | 666.327959 | 333.667618 | 649.301410 | 325.154343 | 648.317394 | 324.662335 | Q | ***1371.745320*** | 686.376298 | 1354.718771 | 677.863024 | 1353.734755 | 677.371016 | 9 |
| 4 | 765.396373 | 383.201825 | 748.369824 | 374.688550 | 747.385808 | 374.196542 | V | ***932.519994*** | 466.763635 | 915.493445 | 458.250361 | 914.509429 | 457.758353 | 8 |
| 5 | 928.459702 | 464.733489 | 911.433153 | 456.220215 | 910.449137 | 455.728207 | Y | ***833.451580*** | 417.229428 | 816.425031 | 408.716154 | 815.441015 | 408.224146 | 7 |
| 6 | **1029.507381** | 515.257329 | 1012.480832 | 506.744054 | 1011.496816 | 506.252046 | T | ***670.388251*** | 335.697764 | 653.361702 | 327.184489 | 652.377686 | 326.692481 | 6 |
| 7 | **1142.591445** | 571.799361 | 1125.564896 | 563.286086 | 1124.580880 | 562.794078 | L | ***569.340572*** | 285.173924 | 552.314023 | 276.660650 | 551.330007 | 276.168642 | 5 |
| 8 | 1239.644209 | 620.325743 | 1222.617660 | 611.812468 | 1221.633644 | 611.320460 | P | ***456.256508*** | 228.631892 | 439.229959 | 220.118618 | 438.245943 | 219.626610 | 4 |
| 9 | 1336.696973 | 668.852125 | 1319.670424 | 660.338850 | 1318.686408 | 659.846842 | P | ***359.203744*** | 180.105510 | 342.177195 | 171.592236 | 341.193179 | 171.100228 | 3 |
| 10 | 1423.729001 | 712.368139 | 1406.702452 | 703.854864 | 1405.718436 | 703.362856 | S | 262.150980 | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 11 | | | | | | | R | ***175.118952*** | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.2 | 1596.833389 | 0.008359 | EPQVYTLPPSR |
| 7.3 | 1596.847122 | -0.005374 | ATPSSSPGTATALPALR |
| 5.4 | 1596.825974 | 0.015774 | KLSDLEAQWAPSPR |
| 1.7 | 1596.835876 | 0.005872 | TLHQGEESLLELTK |
| 0.5 | 1596.854507 | -0.012759 | EQLVTKDPASAK |

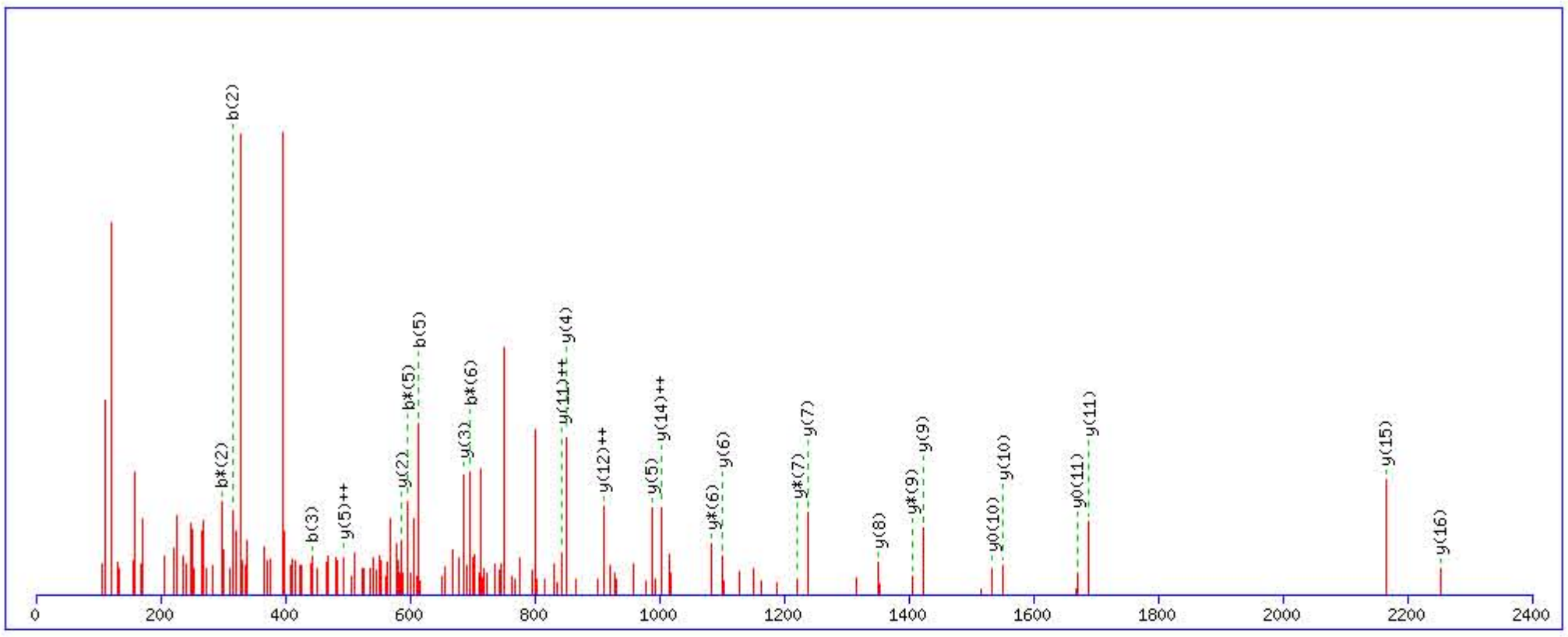
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **WQQGNVFSCSVMHEALHNHYTQK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

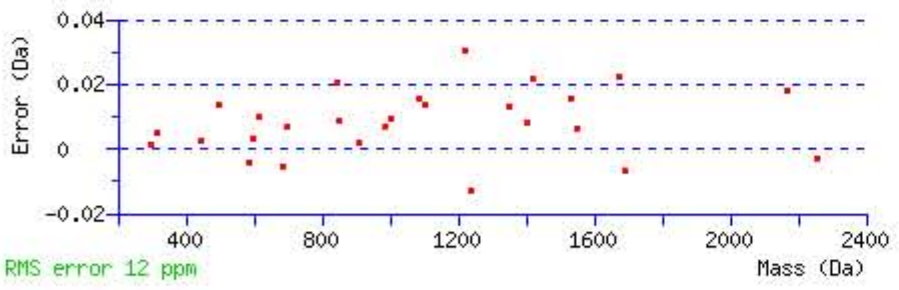
Match to Query 60915: 3111.440870 from(623.295450,5+) rtinseconds(2037) index(66628)
Title: Locus:1.1.1.1984.10 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

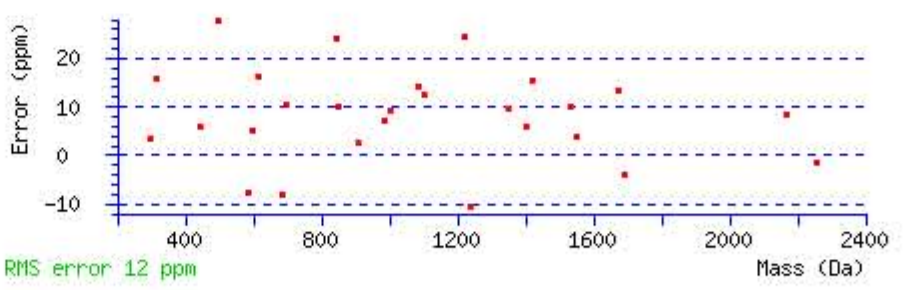
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3111.426590
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q22 : Biotin:Thermo-21345 (Q)
**Ions Score:** 60 **Expect:** 1.6e-005
**Matches :** 27/244 fragment ions using 48 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 187.086589 | 94.046932 | | | | | W | | | | | | | 23 |
| 2 | 315.145167 | 158.076222 | 298.118618 | 149.562947 | | | Q | 2926.354551 | 1463.680913 | 2909.328002 | 1455.167639 | 2908.343986 | 1454.675631 | 22 |
| 3 | 443.203745 | 222.105511 | 426.177196 | 213.592236 | | | Q | 2798.295973 | 1399.651624 | 2781.269424 | 1391.138350 | 2780.285408 | 1390.646342 | 21 |
| 4 | 500.225209 | 250.616243 | 483.198660 | 242.102968 | | | G | 2670.237395 | 1335.622335 | 2653.210846 | 1327.109061 | 2652.226830 | 1326.617053 | 20 |
| 5 | 614.268136 | 307.637706 | 597.241587 | 299.124432 | | | N | 2613.215931 | 1307.111603 | 2596.189382 | 1298.598329 | 2595.205366 | 1298.106321 | 19 |
| 6 | 713.336550 | 357.171913 | 696.310001 | 348.658639 | | | V | 2499.173004 | 1250.090140 | 2482.146455 | 1241.576865 | 2481.162439 | 1241.084857 | 18 |
| 7 | 860.404964 | 430.706120 | 843.378415 | 422.192845 | | | F | 2400.104590 | 1200.555933 | 2383.078041 | 1192.042658 | 2382.094025 | 1191.550650 | 17 |
| 8 | 947.436992 | 474.222134 | 930.410443 | 465.708859 | 929.426427 | 465.216851 | S | *2253.036176* | 1127.021726 | 2236.009627 | 1118.508451 | 2235.025611 | 1118.016443 | 16 |
| 9 | 1107.467641 | 554.237459 | 1090.441092 | 545.724184 | 1089.457076 | 545.232176 | C | *2166.004148* | 1083.505712 | 2148.977599 | 1074.992437 | 2147.993583 | 1074.500429 | 15 |
| 10 | 1194.499669 | 597.753473 | 1177.473120 | 589.240198 | 1176.489104 | 588.748190 | S | 2005.973499 | 1003.490388 | 1988.946950 | 994.977113 | 1987.962934 | 994.485105 | 14 |
| 11 | 1293.568083 | 647.287680 | 1276.541534 | 638.774405 | 1275.557518 | 638.282397 | V | 1918.941471 | 959.974373 | 1901.914922 | 951.461099 | 1900.930906 | 950.969091 | 13 |
| 12 | 1424.608568 | 712.807922 | 1407.582019 | 704.294648 | 1406.598003 | 703.802640 | M | 1819.873057 | 910.440166 | 1802.846508 | 901.926892 | 1801.862492 | 901.434884 | 12 |
| 13 | 1561.667480 | 781.337378 | 1544.640931 | 772.824104 | 1543.656915 | 772.332096 | H | *1688.832572* | 844.919924 | 1671.806023 | 836.406649 | 1670.822007 | 835.914641 | 11 |
| 14 | 1690.710073 | 845.858675 | 1673.683524 | 837.345400 | 1672.699508 | 836.853392 | E | *1551.773660* | 776.390468 | 1534.747111 | 767.877193 | 1533.763095 | 767.385185 | 10 |
| 15 | 1761.747187 | 881.377231 | 1744.720638 | 872.863957 | 1743.736622 | 872.371949 | A | *1422.731067* | 711.869171 | 1405.704518 | 703.355897 | 1404.720502 | 702.863889 | 9 |
| 16 | 1874.831251 | 937.919263 | 1857.804702 | 929.405989 | 1856.820686 | 928.913981 | L | *1351.693953* | 676.350615 | 1334.667404 | 667.837340 | 1333.683388 | 667.345332 | 8 |
| 17 | 2011.890163 | 1006.448719 | 1994.863614 | 997.935445 | 1993.879598 | 997.443437 | H | *1238.609889* | 619.808583 | 1221.583340 | 611.295308 | 1220.599324 | 610.803300 | 7 |
| 18 | 2125.933090 | 1063.470183 | 2108.906541 | 1054.956908 | 2107.922525 | 1054.464900 | N | *1101.550977* | 551.279127 | 1084.524428 | 542.765852 | 1083.540412 | 542.273844 | 6 |
| 19 | 2262.992002 | 1131.999639 | 2245.965453 | 1123.486364 | 2244.981437 | 1122.994356 | H | *987.508050* | 494.257663 | 970.481501 | 485.744389 | 969.497485 | 485.252381 | 5 |
| 20 | 2426.055331 | 1213.531303 | 2409.028782 | 1205.018029 | 2408.044766 | 1204.526021 | Y | *850.449138* | 425.728207 | 833.422589 | 417.214933 | 832.438573 | 416.722925 | 4 |
| 21 | 2527.103010 | 1264.055143 | 2510.076461 | 1255.541868 | 2509.092445 | 1255.049860 | T | *687.385809* | 344.196543 | 670.359260 | 335.683268 | 669.375244 | 335.191260 | 3 |
| 22 | 2966.328336 | 1483.667806 | 2949.301787 | 1475.154531 | 2948.317771 | 1474.662523 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 23 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 59.7 | 3111.426590 | 0.014280 | WQQGNVFSCSVMHEALHNHYTQK |

**Mascot:** http://www.matrixscience.com/

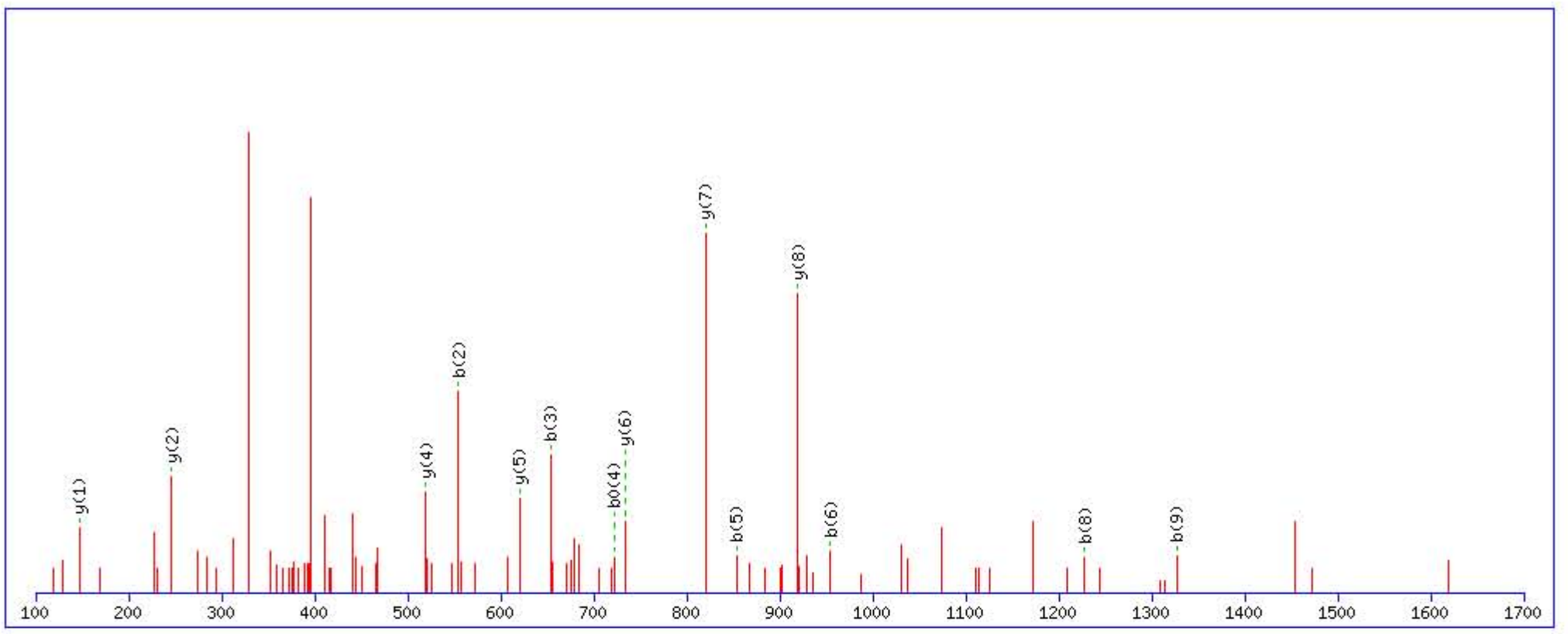
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NQVSLTCLVK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

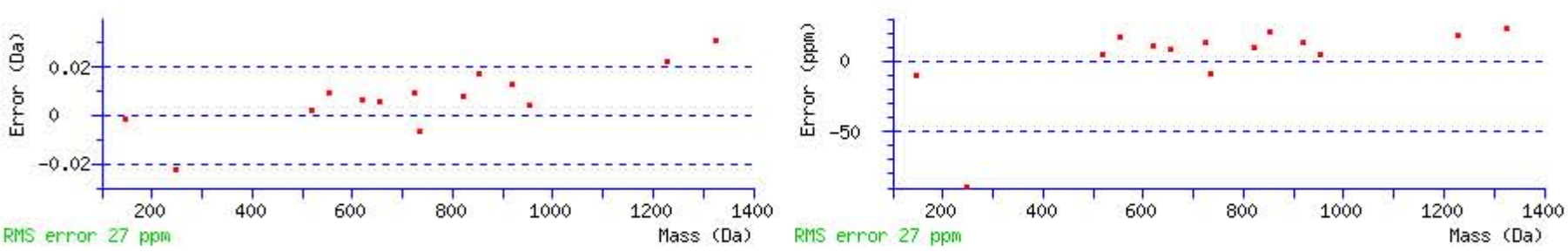
Match to Query 30278: 1471.795568 from(736.905060,2+) rtinseconds(2229) index(6944)
Title: Locus:1.1.1.2053.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1471.789093
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0026
**Matches :** 14/94 fragment ions using 27 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 10 |
| 2 | **554.275529** | 277.641403 | 537.248980 | 269.128128 | | | Q | 1358.753442 | 679.880359 | 1341.726893 | 671.367085 | 1340.742877 | 670.875076 | 9 |
| 3 | **653.343943** | 327.175610 | 636.317394 | 318.662335 | | | V | ***919.528116*** | 460.267696 | 902.501567 | 451.754421 | 901.517551 | 451.262413 | 8 |
| 4 | 740.375971 | 370.691623 | 723.349422 | 362.178349 | 722.365406 | 361.686341 | S | ***820.459702*** | 410.733489 | 803.433153 | 402.220215 | 802.449137 | 401.728207 | 7 |
| 5 | **853.460035** | 427.233656 | 836.433486 | 418.720381 | 835.449470 | 418.228373 | L | ***733.427674*** | 367.217475 | 716.401125 | 358.704201 | 715.417109 | 358.212193 | 6 |
| 6 | **954.507714** | 477.757495 | 937.481165 | 469.244220 | 936.497149 | 468.752212 | T | ***620.343610*** | 310.675443 | 603.317061 | 302.162169 | 602.333045 | 301.670161 | 5 |
| 7 | 1114.538363 | 557.772819 | 1097.511814 | 549.259545 | 1096.527798 | 548.767537 | C | ***519.295931*** | 260.151604 | 502.269382 | 251.638329 | | | 4 |
| 8 | **1227.622427** | 614.314851 | 1210.595878 | 605.801577 | 1209.611862 | 605.309569 | L | 359.265282 | 180.136279 | 342.238733 | 171.623004 | | | 3 |
| 9 | **1326.690841** | 663.849058 | 1309.664292 | 655.335784 | 1308.680276 | 654.843776 | V | ***246.181218*** | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 10 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 39.5 | 1471.789093 | 0.006475 | NQVSLTCLVK |
| 12.6 | 1471.778305 | 0.017263 | WNVSRPSLLADSK |
| 7.5 | 1471.777847 | 0.017721 | QLDMELVSVK |
| 4.9 | 1471.797592 | -0.002024 | KYFWDRAFLVK |
| 3.0 | 1471.806793 | -0.011225 | AAALLAKQAEMEVK |
| 3.0 | 1471.796951 | -0.001383 | QRAAQFDVVK |
| 1.6 | 1471.814713 | -0.019145 | RQVIVGTWGESLK |

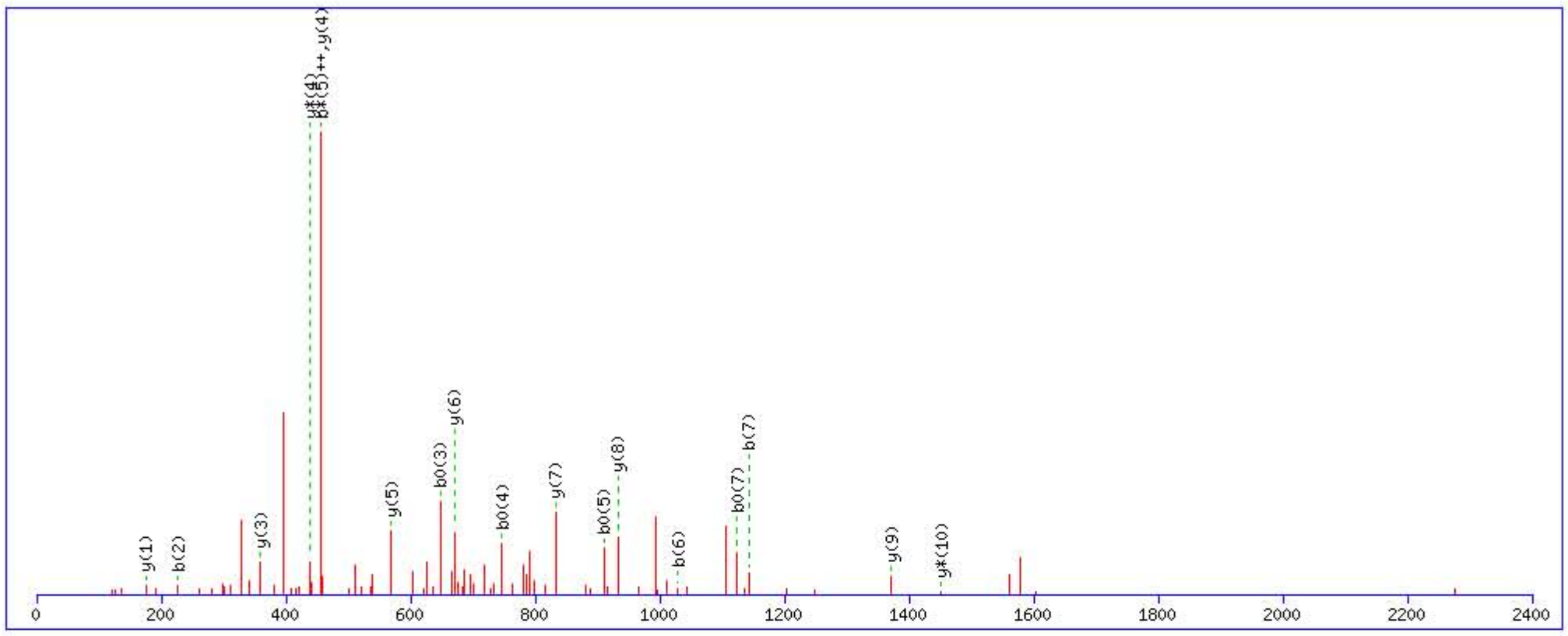
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EPQVYTLPPSR**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

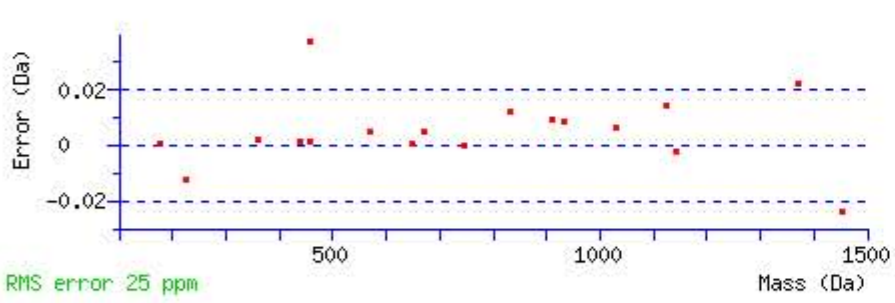
Match to Query 34615: 1596.841748 from(799.428150,2+) rtinseconds(1923) index(65896)
Title: Locus:1.1.1.1944.26 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

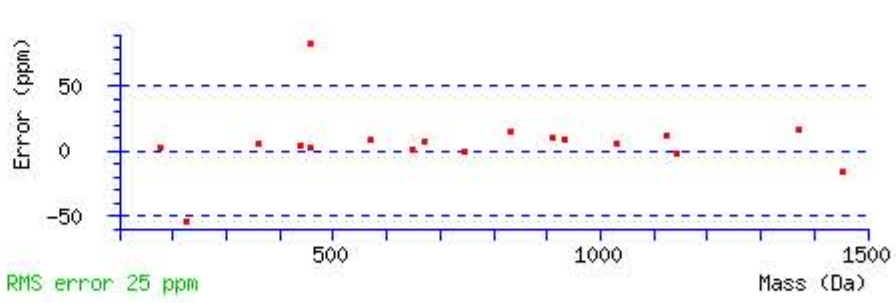
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1596.833389
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.00031
**Matches :** 18/114 fragment ions using 38 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 11 |
| 2 | **227.102633** | 114.054954 | | | 209.092068 | 105.049672 | P | 1468.798084 | 734.902680 | 1451.771535 | 726.389406 | 1450.787519 | 725.897398 | 10 |
| 3 | 666.327959 | 333.667618 | 649.301410 | 325.154343 | 648.317394 | 324.662335 | Q | ***1371.745320*** | 686.376298 | 1354.718771 | 677.863024 | 1353.734755 | 677.371016 | 9 |
| 4 | 765.396373 | 383.201825 | 748.369824 | 374.688550 | 747.385808 | 374.196542 | V | ***932.519994*** | 466.763635 | 915.493445 | 458.250361 | 914.509429 | 457.758353 | 8 |
| 5 | 928.459702 | 464.733489 | 911.433153 | 456.220215 | 910.449137 | 455.728207 | Y | ***833.451580*** | 417.229428 | 816.425031 | 408.716154 | 815.441015 | 408.224146 | 7 |
| 6 | **1029.507381** | 515.257329 | 1012.480832 | 506.744054 | 1011.496816 | 506.252046 | T | ***670.388251*** | 335.697764 | 653.361702 | 327.184489 | 652.377686 | 326.692481 | 6 |
| 7 | **1142.591445** | 571.799361 | 1125.564896 | 563.286086 | 1124.580880 | 562.794078 | L | ***569.340572*** | 285.173924 | 552.314023 | 276.660650 | 551.330007 | 276.168642 | 5 |
| 8 | 1239.644209 | 620.325743 | 1222.617660 | 611.812468 | 1221.633644 | 611.320460 | P | ***456.256508*** | 228.631892 | 439.229959 | 220.118618 | 438.245943 | 219.626610 | 4 |
| 9 | 1336.696973 | 668.852125 | 1319.670424 | 660.338850 | 1318.686408 | 659.846842 | P | ***359.203744*** | 180.105510 | 342.177195 | 171.592236 | 341.193179 | 171.100228 | 3 |
| 10 | 1423.729001 | 712.368139 | 1406.702452 | 703.854864 | 1405.718436 | 703.362856 | S | 262.150980 | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 11 | | | | | | | R | ***175.118952*** | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.2 | 1596.833389 | 0.008359 | EPQVYTLPPSR |
| 7.3 | 1596.847122 | -0.005374 | ATPSSSPGTATALPALR |
| 5.4 | 1596.825974 | 0.015774 | KLSDLEAQWAPSPR |
| 1.7 | 1596.835876 | 0.005872 | TLHQGEESLLELTK |
| 0.5 | 1596.854507 | -0.012759 | EQLVTKDPASAK |

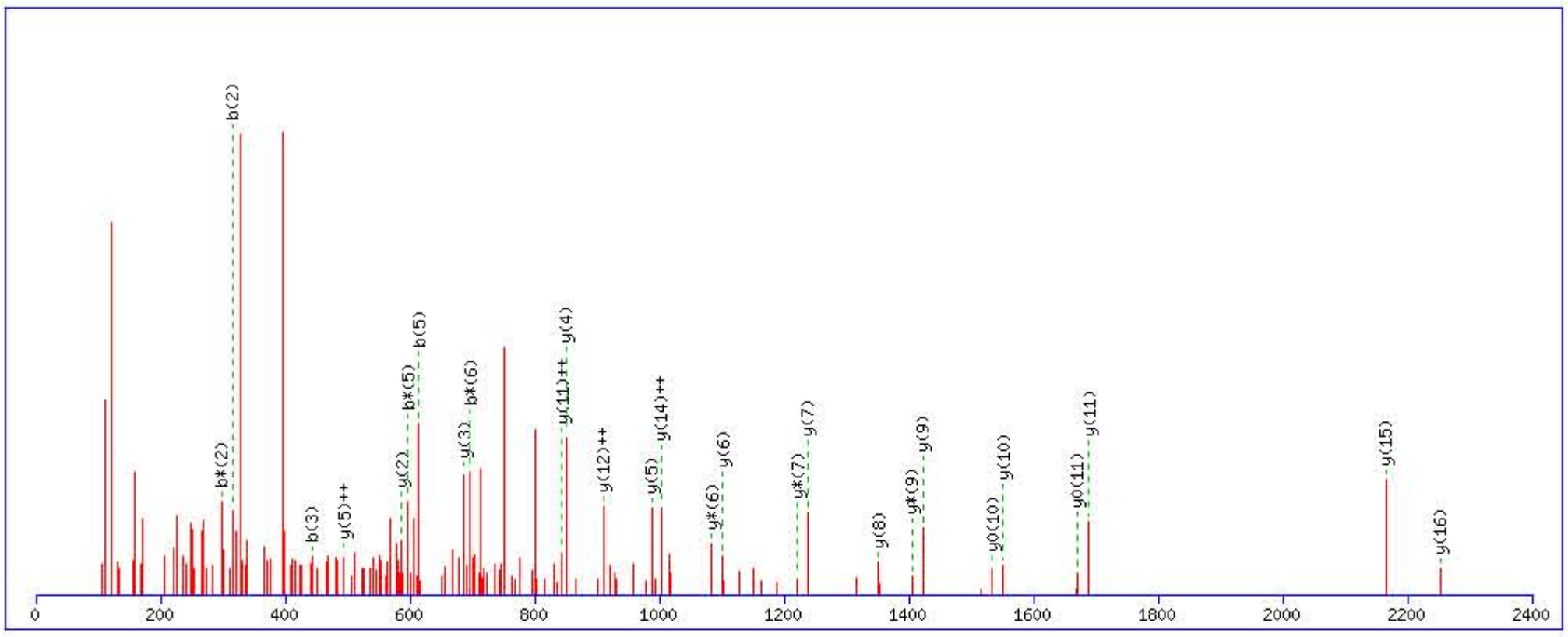
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **WQQGNVFSCSVMHEALHNHYTQK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

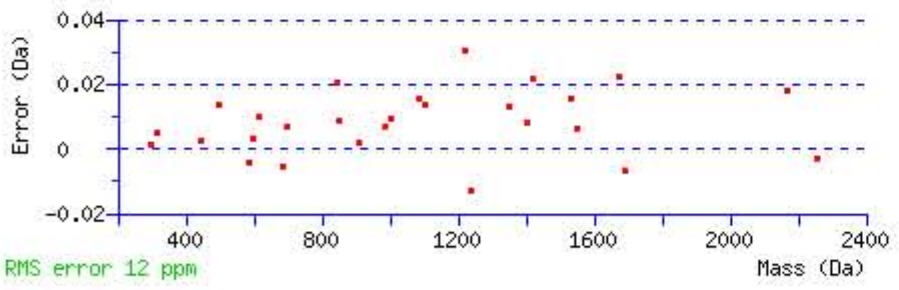
Match to Query 60915: 3111.440870 from(623.295450,5+) rtinseconds(2037) index(66628)
Title: Locus:1.1.1.1984.10 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

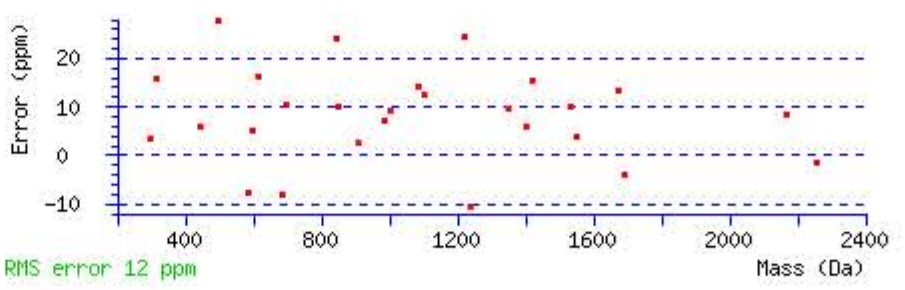
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3111.426590
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q22 : Biotin:Thermo-21345 (Q)
**Ions Score:** 60 **Expect:** 1.6e-005
**Matches :** 27/244 fragment ions using 48 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 187.086589 | 94.046932 | | | | | W | | | | | | | 23 |
| 2 | 315.145167 | 158.076222 | 298.118618 | 149.562947 | | | Q | 2926.354551 | 1463.680913 | 2909.328002 | 1455.167639 | 2908.343986 | 1454.675631 | 22 |
| 3 | 443.203745 | 222.105511 | 426.177196 | 213.592236 | | | Q | 2798.295973 | 1399.651624 | 2781.269424 | 1391.138350 | 2780.285408 | 1390.646342 | 21 |
| 4 | 500.225209 | 250.616243 | 483.198660 | 242.102968 | | | G | 2670.237395 | 1335.622335 | 2653.210846 | 1327.109061 | 2652.226830 | 1326.617053 | 20 |
| 5 | 614.268136 | 307.637706 | 597.241587 | 299.124432 | | | N | 2613.215931 | 1307.111603 | 2596.189382 | 1298.598329 | 2595.205366 | 1298.106321 | 19 |
| 6 | 713.336550 | 357.171913 | 696.310001 | 348.658639 | | | V | 2499.173004 | 1250.090140 | 2482.146455 | 1241.576865 | 2481.162439 | 1241.084857 | 18 |
| 7 | 860.404964 | 430.706120 | 843.378415 | 422.192845 | | | F | 2400.104590 | 1200.555933 | 2383.078041 | 1192.042658 | 2382.094025 | 1191.550650 | 17 |
| 8 | 947.436992 | 474.222134 | 930.410443 | 465.708859 | 929.426427 | 465.216851 | S | *2253.036176* | 1127.021726 | 2236.009627 | 1118.508451 | 2235.025611 | 1118.016443 | 16 |
| 9 | 1107.467641 | 554.237459 | 1090.441092 | 545.724184 | 1089.457076 | 545.232176 | C | *2166.004148* | 1083.505712 | 2148.977599 | 1074.992437 | 2147.993583 | 1074.500429 | 15 |
| 10 | 1194.499669 | 597.753473 | 1177.473120 | 589.240198 | 1176.489104 | 588.748190 | S | 2005.973499 | 1003.490388 | 1988.946950 | 994.977113 | 1987.962934 | 994.485105 | 14 |
| 11 | 1293.568083 | 647.287680 | 1276.541534 | 638.774405 | 1275.557518 | 638.282397 | V | 1918.941471 | 959.974373 | 1901.914922 | 951.461099 | 1900.930906 | 950.969091 | 13 |
| 12 | 1424.608568 | 712.807922 | 1407.582019 | 704.294648 | 1406.598003 | 703.802640 | M | 1819.873057 | 910.440166 | 1802.846508 | 901.926892 | 1801.862492 | 901.434884 | 12 |
| 13 | 1561.667480 | 781.337378 | 1544.640931 | 772.824104 | 1543.656915 | 772.332096 | H | *1688.832572* | 844.919924 | 1671.806023 | 836.406649 | 1670.822007 | 835.914641 | 11 |
| 14 | 1690.710073 | 845.858675 | 1673.683524 | 837.345400 | 1672.699508 | 836.853392 | E | *1551.773660* | 776.390468 | 1534.747111 | 767.877193 | 1533.763095 | 767.385185 | 10 |
| 15 | 1761.747187 | 881.377231 | 1744.720638 | 872.863957 | 1743.736622 | 872.371949 | A | *1422.731067* | 711.869171 | 1405.704518 | 703.355897 | 1404.720502 | 702.863889 | 9 |
| 16 | 1874.831251 | 937.919263 | 1857.804702 | 929.405989 | 1856.820686 | 928.913981 | L | *1351.693953* | 676.350615 | 1334.667404 | 667.837340 | 1333.683388 | 667.345332 | 8 |
| 17 | 2011.890163 | 1006.448719 | 1994.863614 | 997.935445 | 1993.879598 | 997.443437 | H | *1238.609889* | 619.808583 | 1221.583340 | 611.295308 | 1220.599324 | 610.803300 | 7 |
| 18 | 2125.933090 | 1063.470183 | 2108.906541 | 1054.956908 | 2107.922525 | 1054.464900 | N | *1101.550977* | 551.279127 | 1084.524428 | 542.765852 | 1083.540412 | 542.273844 | 6 |
| 19 | 2262.992002 | 1131.999639 | 2245.965453 | 1123.486364 | 2244.981437 | 1122.994356 | H | *987.508050* | 494.257663 | 970.481501 | 485.744389 | 969.497485 | 485.252381 | 5 |
| 20 | 2426.055331 | 1213.531303 | 2409.028782 | 1205.018029 | 2408.044766 | 1204.526021 | Y | *850.449138* | 425.728207 | 833.422589 | 417.214933 | 832.438573 | 416.722925 | 4 |
| 21 | 2527.103010 | 1264.055143 | 2510.076461 | 1255.541868 | 2509.092445 | 1255.049860 | T | *687.385809* | 344.196543 | 670.359260 | 335.683268 | 669.375244 | 335.191260 | 3 |
| 22 | 2966.328336 | 1483.667806 | 2949.301787 | 1475.154531 | 2948.317771 | 1474.662523 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 23 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 59.7 | 3111.426590 | 0.014280 | WQQGNVFSCSVMHEALHNHYTQK |

**Mascot:** http://www.matrixscience.com/

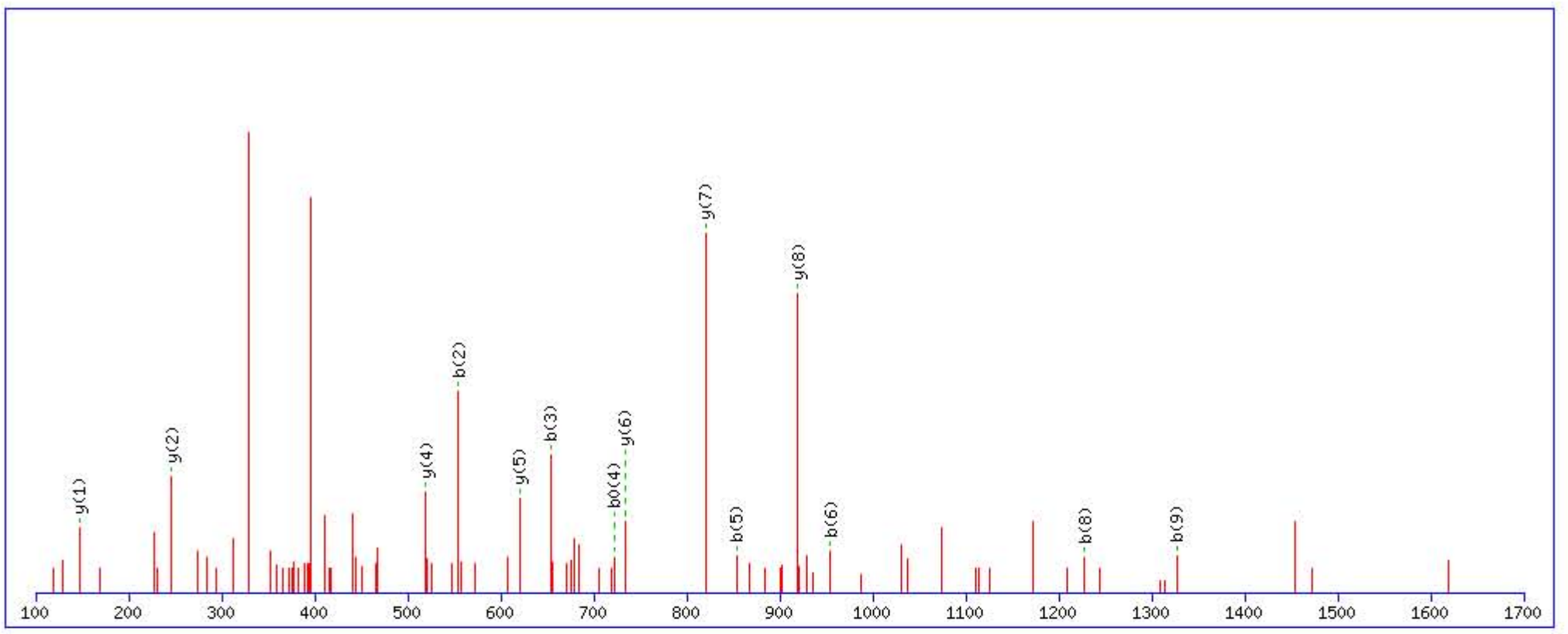
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NQVSLTCLVK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

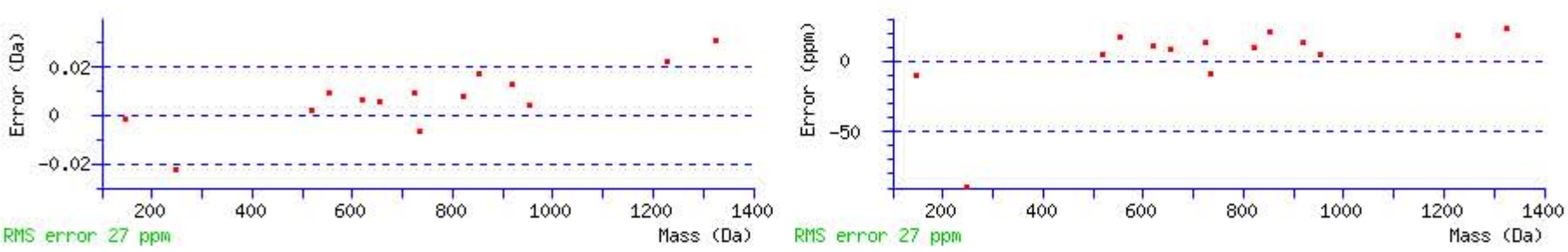
Match to Query 30278: 1471.795568 from(736.905060,2+) rtinseconds(2229) index(6944)
Title: Locus:1.1.1.2053.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1471.789093
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0026
**Matches :** 14/94 fragment ions using 27 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 10 |
| 2 | **554.275529** | 277.641403 | 537.248980 | 269.128128 | | | Q | 1358.753442 | 679.880359 | 1341.726893 | 671.367085 | 1340.742877 | 670.875076 | 9 |
| 3 | **653.343943** | 327.175610 | 636.317394 | 318.662335 | | | V | ***919.528116*** | 460.267696 | 902.501567 | 451.754421 | 901.517551 | 451.262413 | 8 |
| 4 | 740.375971 | 370.691623 | 723.349422 | 362.178349 | 722.365406 | 361.686341 | S | ***820.459702*** | 410.733489 | 803.433153 | 402.220215 | 802.449137 | 401.728207 | 7 |
| 5 | **853.460035** | 427.233656 | 836.433486 | 418.720381 | 835.449470 | 418.228373 | L | ***733.427674*** | 367.217475 | 716.401125 | 358.704201 | 715.417109 | 358.212193 | 6 |
| 6 | **954.507714** | 477.757495 | 937.481165 | 469.244220 | 936.497149 | 468.752212 | T | ***620.343610*** | 310.675443 | 603.317061 | 302.162169 | 602.333045 | 301.670161 | 5 |
| 7 | 1114.538363 | 557.772819 | 1097.511814 | 549.259545 | 1096.527798 | 548.767537 | C | ***519.295931*** | 260.151604 | 502.269382 | 251.638329 | | | 4 |
| 8 | **1227.622427** | 614.314851 | 1210.595878 | 605.801577 | 1209.611862 | 605.309569 | L | 359.265282 | 180.136279 | 342.238733 | 171.623004 | | | 3 |
| 9 | **1326.690841** | 663.849058 | 1309.664292 | 655.335784 | 1308.680276 | 654.843776 | V | ***246.181218*** | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 10 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 39.5 | 1471.789093 | 0.006475 | NQVSLTCLVK |
| 12.6 | 1471.778305 | 0.017263 | WNVSRPSLLADSK |
| 7.5 | 1471.777847 | 0.017721 | QLDMELVSVK |
| 4.9 | 1471.797592 | -0.002024 | KYFWDRAFLVK |
| 3.0 | 1471.806793 | -0.011225 | AAALLAKQAEMEVK |
| 3.0 | 1471.796951 | -0.001383 | QRAAQFDVVK |
| 1.6 | 1471.814713 | -0.019145 | RQVIVGTWGESLK |

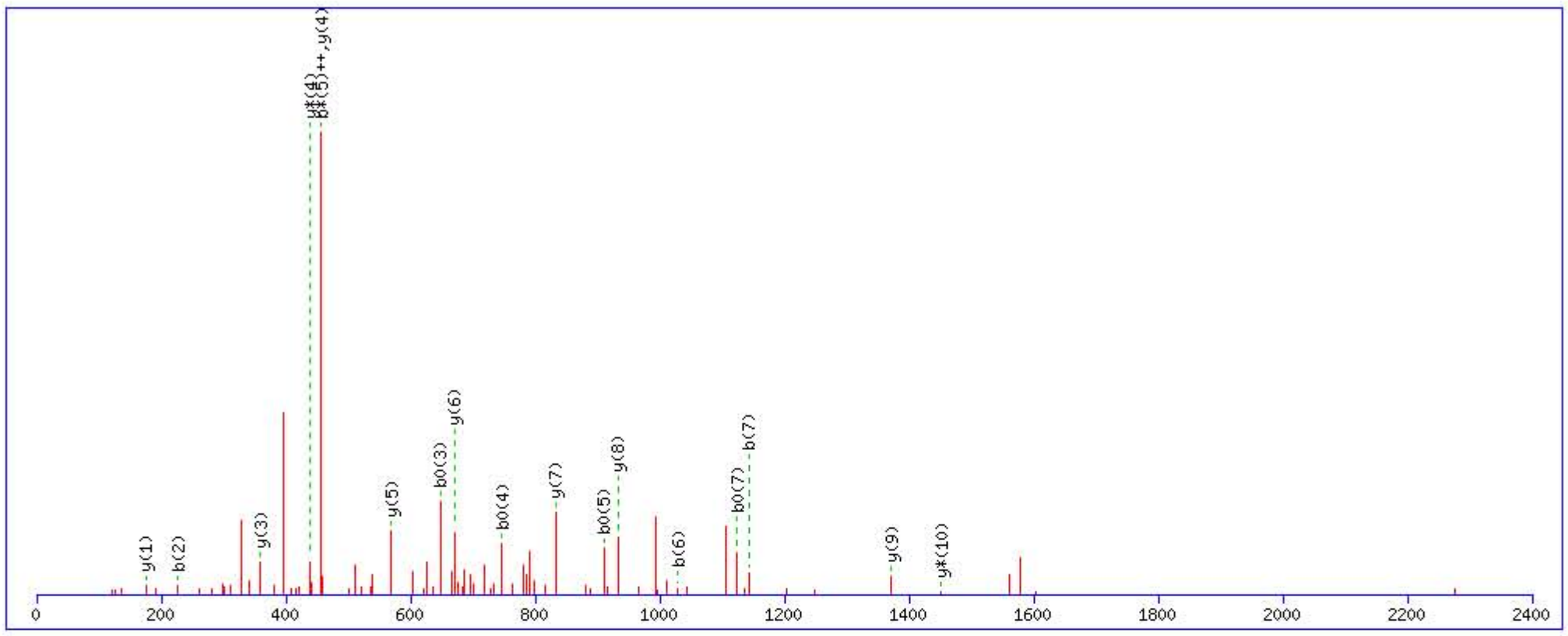
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EPQVYTLPPSR**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

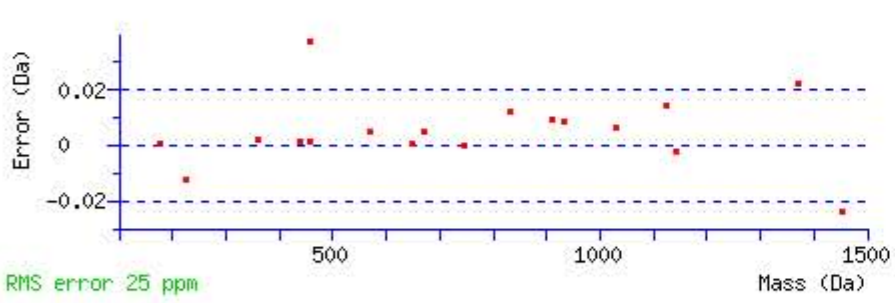
Match to Query 34615: 1596.841748 from(799.428150,2+) rtinseconds(1923) index(65896)
Title: Locus:1.1.1.1944.26 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

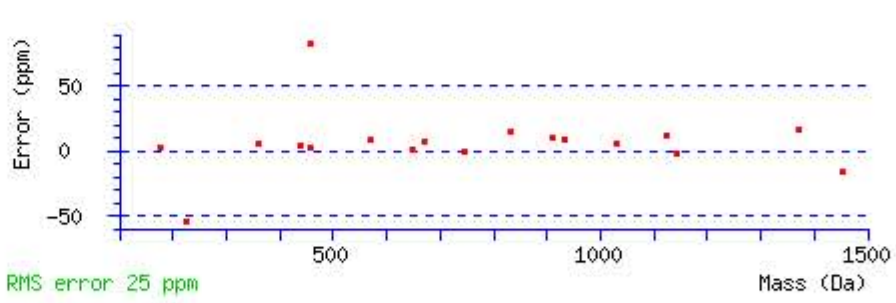
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1596.833389
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.00031
**Matches :** 18/114 fragment ions using 38 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 11 |
| 2 | **227.102633** | 114.054954 | | | 209.092068 | 105.049672 | P | 1468.798084 | 734.902680 | 1451.771535 | 726.389406 | 1450.787519 | 725.897398 | 10 |
| 3 | 666.327959 | 333.667618 | 649.301410 | 325.154343 | 648.317394 | 324.662335 | Q | ***1371.745320*** | 686.376298 | 1354.718771 | 677.863024 | 1353.734755 | 677.371016 | 9 |
| 4 | 765.396373 | 383.201825 | 748.369824 | 374.688550 | 747.385808 | 374.196542 | V | ***932.519994*** | 466.763635 | 915.493445 | 458.250361 | 914.509429 | 457.758353 | 8 |
| 5 | 928.459702 | 464.733489 | 911.433153 | 456.220215 | 910.449137 | 455.728207 | Y | ***833.451580*** | 417.229428 | 816.425031 | 408.716154 | 815.441015 | 408.224146 | 7 |
| 6 | **1029.507381** | 515.257329 | 1012.480832 | 506.744054 | 1011.496816 | 506.252046 | T | ***670.388251*** | 335.697764 | 653.361702 | 327.184489 | 652.377686 | 326.692481 | 6 |
| 7 | **1142.591445** | 571.799361 | 1125.564896 | 563.286086 | 1124.580880 | 562.794078 | L | ***569.340572*** | 285.173924 | 552.314023 | 276.660650 | 551.330007 | 276.168642 | 5 |
| 8 | 1239.644209 | 620.325743 | 1222.617660 | 611.812468 | 1221.633644 | 611.320460 | P | ***456.256508*** | 228.631892 | 439.229959 | 220.118618 | 438.245943 | 219.626610 | 4 |
| 9 | 1336.696973 | 668.852125 | 1319.670424 | 660.338850 | 1318.686408 | 659.846842 | P | ***359.203744*** | 180.105510 | 342.177195 | 171.592236 | 341.193179 | 171.100228 | 3 |
| 10 | 1423.729001 | 712.368139 | 1406.702452 | 703.854864 | 1405.718436 | 703.362856 | S | 262.150980 | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 11 | | | | | | | R | ***175.118952*** | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.2 | 1596.833389 | 0.008359 | EPQVYTLPPSR |
| 7.3 | 1596.847122 | -0.005374 | ATPSSSPGTATALPALR |
| 5.4 | 1596.825974 | 0.015774 | KLSDLEAQWAPSPR |
| 1.7 | 1596.835876 | 0.005872 | TLHQGEESLLELTK |
| 0.5 | 1596.854507 | -0.012759 | EQLVTKDPASAK |

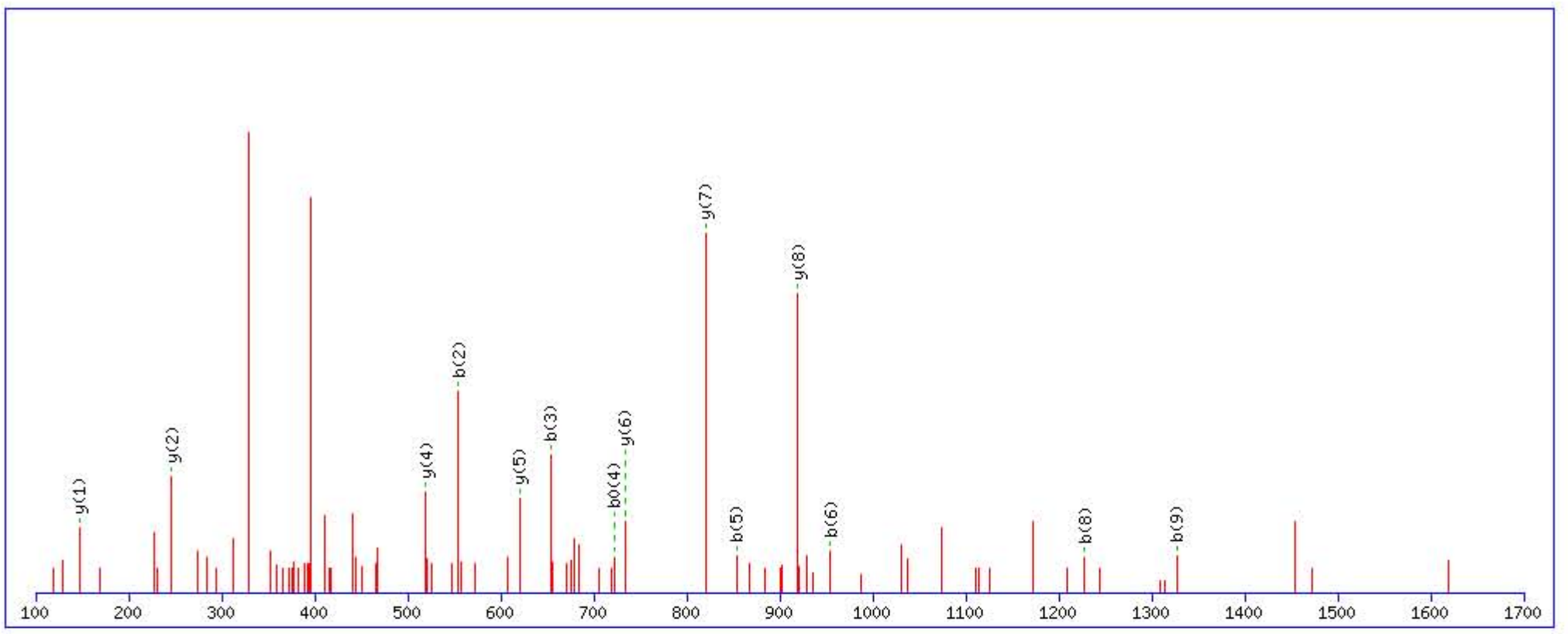
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NQVSLTCLVK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

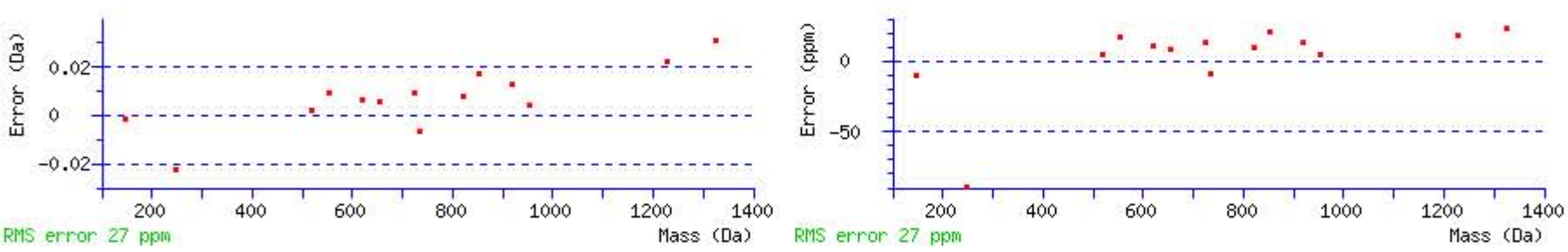
Match to Query 30278: 1471.795568 from(736.905060,2+) rtinseconds(2229) index(6944)
Title: Locus:1.1.1.2053.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1471.789093
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0026
**Matches :** 14/94 fragment ions using 27 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 10 |
| 2 | **554.275529** | 277.641403 | 537.248980 | 269.128128 | | | Q | 1358.753442 | 679.880359 | 1341.726893 | 671.367085 | 1340.742877 | 670.875076 | 9 |
| 3 | **653.343943** | 327.175610 | 636.317394 | 318.662335 | | | V | ***919.528116*** | 460.267696 | 902.501567 | 451.754421 | 901.517551 | 451.262413 | 8 |
| 4 | 740.375971 | 370.691623 | 723.349422 | 362.178349 | 722.365406 | 361.686341 | S | ***820.459702*** | 410.733489 | 803.433153 | 402.220215 | 802.449137 | 401.728207 | 7 |
| 5 | **853.460035** | 427.233656 | 836.433486 | 418.720381 | 835.449470 | 418.228373 | L | ***733.427674*** | 367.217475 | 716.401125 | 358.704201 | 715.417109 | 358.212193 | 6 |
| 6 | **954.507714** | 477.757495 | 937.481165 | 469.244220 | 936.497149 | 468.752212 | T | ***620.343610*** | 310.675443 | 603.317061 | 302.162169 | 602.333045 | 301.670161 | 5 |
| 7 | 1114.538363 | 557.772819 | 1097.511814 | 549.259545 | 1096.527798 | 548.767537 | C | ***519.295931*** | 260.151604 | 502.269382 | 251.638329 | | | 4 |
| 8 | **1227.622427** | 614.314851 | 1210.595878 | 605.801577 | 1209.611862 | 605.309569 | L | 359.265282 | 180.136279 | 342.238733 | 171.623004 | | | 3 |
| 9 | **1326.690841** | 663.849058 | 1309.664292 | 655.335784 | 1308.680276 | 654.843776 | V | ***246.181218*** | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 10 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 39.5 | 1471.789093 | 0.006475 | NQVSLTCLVK |
| 12.6 | 1471.778305 | 0.017263 | WNVSRPSLLADSK |
| 7.5 | 1471.777847 | 0.017721 | QLDMELVSVK |
| 4.9 | 1471.797592 | -0.002024 | KYFWDRAFLVK |
| 3.0 | 1471.806793 | -0.011225 | AAALLAKQAEMEVK |
| 3.0 | 1471.796951 | -0.001383 | QRAAQFDVVK |
| 1.6 | 1471.814713 | -0.019145 | RQVIVGTWGESLK |

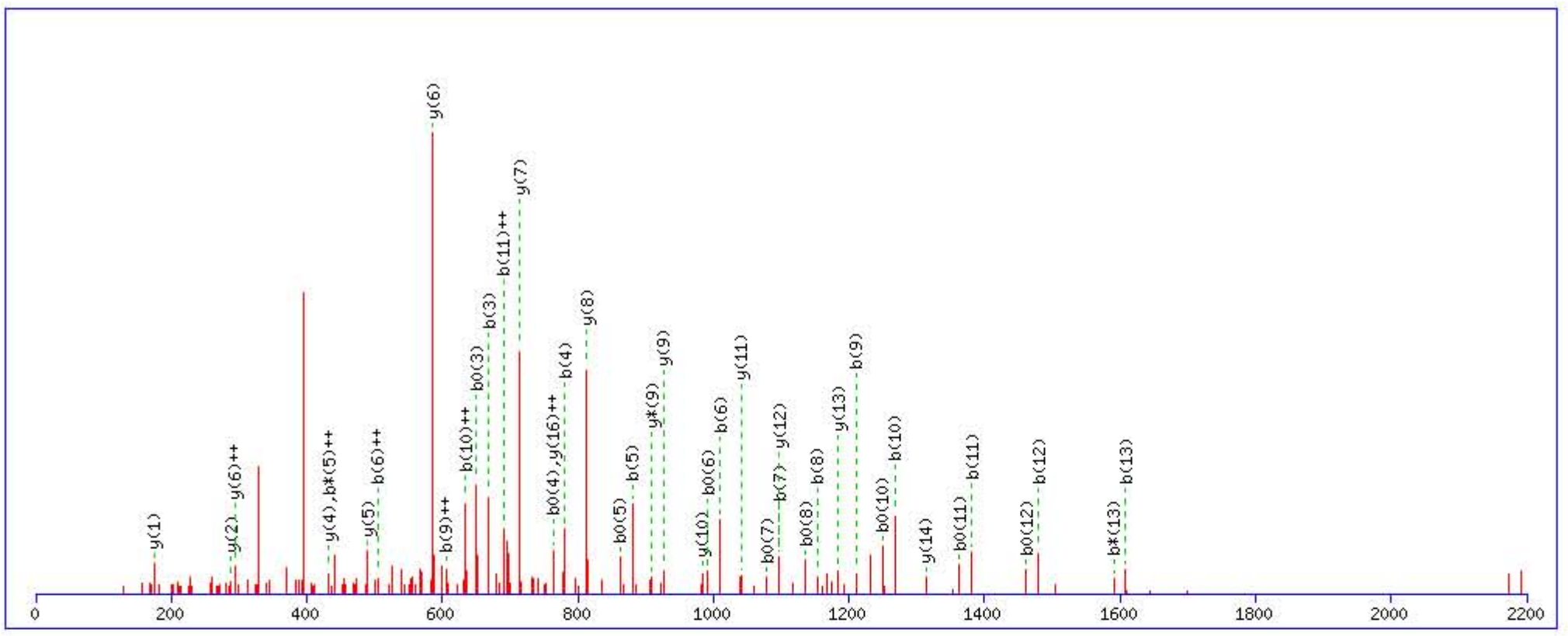
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVQPGGSLR**
Found in **HV305_HUMAN**, Ig heavy chain V-III region BRO OS=Homo sapiens PE=1 SV=1

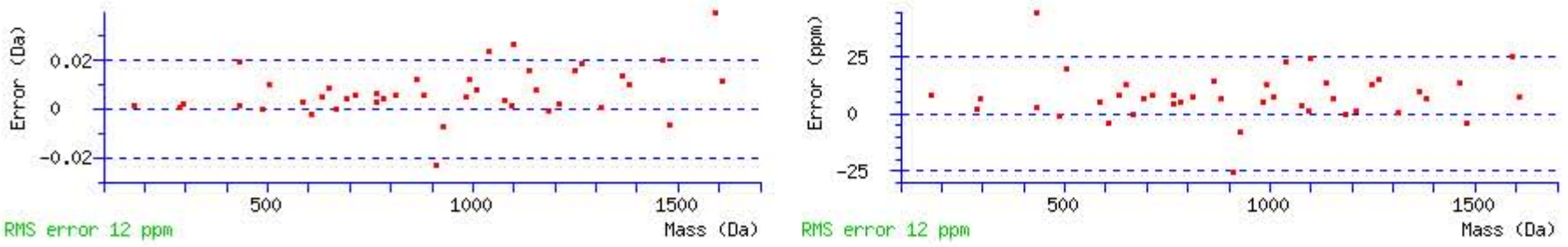
Match to Query 48333: 2192.179362 from(731.733730,3+) rtinseconds(2213) index(21553)
Title: Locus:1.1.1.3153.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2192.162354
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 75 **Expect:** 1.3e-007
**Matches :** 42/208 fragment ions using 74 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 19 |
| 2 | 229.118283 | 115.062780 | | | 211.107718 | 106.057497 | V | 2064.127023 | 1032.567149 | 2047.100474 | 1024.053875 | 2046.116458 | 1023.561867 | 18 |
| 3 | *668.343609* | 334.675443 | 651.317060 | 326.162168 | 650.333044 | 325.670160 | Q | 1965.058609 | 983.032942 | 1948.032060 | 974.519668 | 1947.048044 | 974.027660 | 17 |
| 4 | *781.427673* | 391.217475 | 764.401124 | 382.704200 | 763.417108 | 382.212192 | L | 1525.833283 | 763.420279 | 1508.806734 | 754.907005 | 1507.822718 | 754.414997 | 16 |
| 5 | *880.496087* | 440.751682 | 863.469538 | 432.238407 | 862.485522 | 431.746399 | V | 1412.749219 | 706.878248 | 1395.722670 | 698.364973 | 1394.738654 | 697.872965 | 15 |
| 6 | *1009.538680* | **505.272978** | 992.512131 | 496.759704 | 991.528115 | 496.267696 | E | *1313.680805* | 657.344041 | 1296.654256 | 648.830766 | 1295.670240 | 648.338758 | 14 |
| 7 | *1096.570708* | 548.788992 | 1079.544159 | 540.275718 | 1078.560143 | 539.783709 | S | *1184.638212* | 592.822744 | 1167.611663 | 584.309470 | 1166.627647 | 583.817462 | 13 |
| 8 | *1153.592172* | 577.299724 | 1136.565623 | 568.786450 | 1135.581607 | 568.294441 | G | *1097.606184* | 549.306730 | 1080.579635 | 540.793456 | 1079.595619 | 540.301447 | 12 |
| 9 | *1210.613636* | **605.810456** | 1193.587087 | 597.297181 | 1192.603071 | 596.805173 | G | *1040.584720* | 520.795998 | 1023.558171 | 512.282723 | 1022.574155 | 511.790716 | 11 |
| 10 | *1267.635100* | **634.321188** | 1250.608551 | 625.807913 | 1249.624535 | 625.315905 | G | *983.563256* | 492.285266 | 966.536707 | 483.771992 | 965.552691 | 483.279984 | 10 |
| 11 | *1380.719164* | **690.863220** | 1363.692615 | 682.349945 | 1362.708599 | 681.857937 | L | *926.541792* | 463.774534 | 909.515243 | 455.261260 | 908.531227 | 454.769252 | 9 |
| 12 | *1479.787578* | 740.397427 | 1462.761029 | 731.884152 | 1461.777013 | 731.392144 | V | *813.457728* | 407.232502 | 796.431179 | 398.719228 | 795.447163 | 398.227220 | 8 |
| 13 | *1607.846156* | 804.426716 | 1590.819607 | 795.913441 | 1589.835591 | 795.421433 | Q | *714.389314* | 357.698295 | 697.362765 | 349.185021 | 696.378749 | 348.693013 | 7 |
| 14 | 1704.898920 | 852.953098 | 1687.872371 | 844.439823 | 1686.888355 | 843.947815 | P | *586.330736* | 293.669006 | 569.304187 | 285.155732 | 568.320171 | 284.663724 | 6 |
| 15 | 1761.920384 | 881.463830 | 1744.893835 | 872.950555 | 1743.909819 | 872.458547 | G | *489.277972* | 245.142624 | 472.251423 | 236.629349 | 471.267407 | 236.137341 | 5 |
| 16 | 1818.941848 | 909.974562 | 1801.915299 | 901.461287 | 1800.931283 | 900.969279 | G | *432.256508* | 216.631892 | 415.229959 | 208.118618 | 414.245943 | 207.626610 | 4 |
| 17 | 1905.973876 | 953.490576 | 1888.947327 | 944.977301 | 1887.963311 | 944.485293 | S | 375.235044 | 188.121160 | 358.208495 | 179.607886 | 357.224479 | 179.115878 | 3 |
| 18 | 2019.057940 | 1010.032608 | 2002.031391 | 1001.519333 | 2001.047375 | 1001.027325 | L | *288.203016* | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 19 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 74.6 | 2192.162354 | 0.017008 | EVQLVESGGGLVQPGGSLR |
| 1.3 | 2192.196228 | -0.016866 | TVQTLWQQLVAQR |

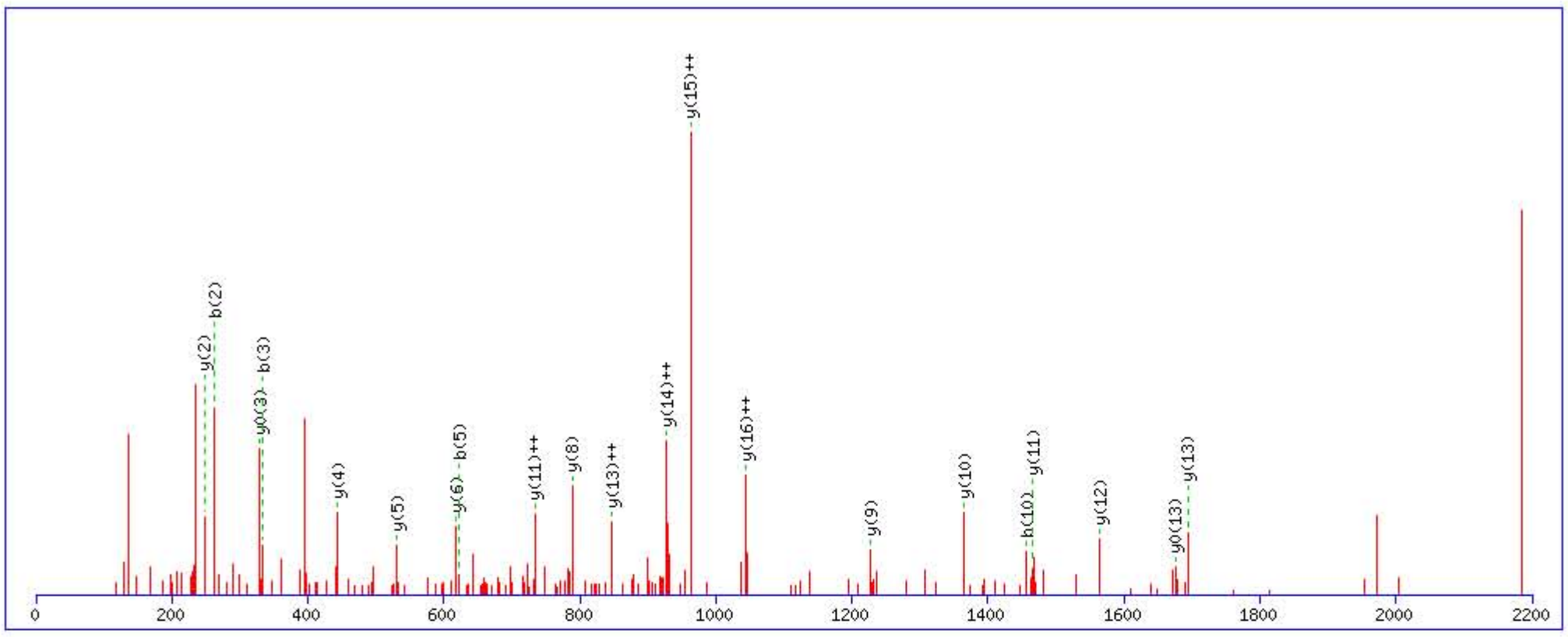
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VYACEVTHQGLSSPVTK**
Found in **IGKC_HUMAN**, Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1

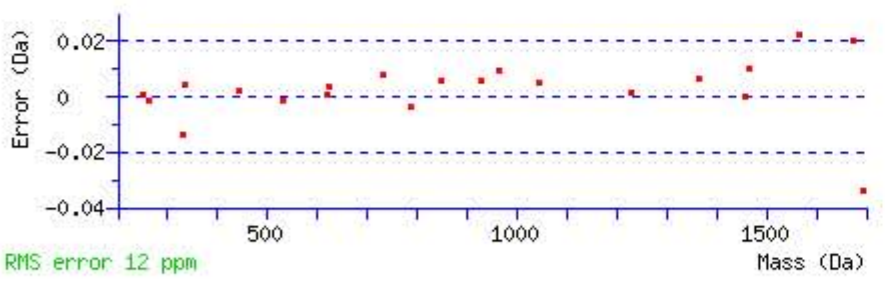
Match to Query 48222: 2186.083602 from(729.701810,3+) rtinseconds(1770) index(4211)
Title: Locus:1.1.1.1893.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

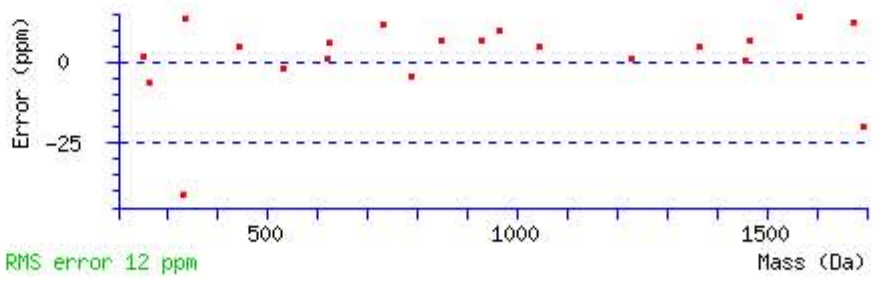
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2186.086411
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 41 **Expect:** 0.0024
**Matches :** 21/166 fragment ions using 53 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 17 |
| 2 | **263.139019** | 132.073148 | | | | | Y | 2088.025261 | 1044.516268 | 2070.998712 | 1036.002994 | 2070.014696 | 1035.510986 | 16 |
| 3 | **334.176133** | 167.591704 | | | | | A | 1924.961932 | 962.984604 | 1907.935383 | 954.471330 | 1906.951367 | 953.979322 | 15 |
| 4 | 494.206782 | 247.607029 | | | | | C | 1853.924818 | 927.466047 | 1836.898269 | 918.952773 | 1835.914253 | 918.460765 | 14 |
| 5 | **623.249375** | 312.128326 | | | 605.238810 | 303.123043 | E | *1693.894169* | 847.450723 | 1676.867620 | 838.937448 | 1675.883604 | 838.445440 | 13 |
| 6 | 722.317789 | 361.662533 | | | 704.307224 | 352.657250 | V | *1564.851576* | 782.929426 | 1547.825027 | 774.416152 | 1546.841011 | 773.924144 | 12 |
| 7 | 823.365468 | 412.186372 | | | 805.354903 | 403.181090 | T | *1465.783162* | 733.395219 | 1448.756613 | 724.881945 | 1447.772597 | 724.389937 | 11 |
| 8 | 960.424380 | 480.715828 | | | 942.413815 | 471.710546 | H | *1364.735483* | 682.871380 | 1347.708934 | 674.358105 | 1346.724918 | 673.866097 | 10 |
| 9 | 1399.649706 | 700.328491 | 1382.623157 | 691.815217 | 1381.639141 | 691.323208 | Q | *1227.676571* | 614.341924 | 1210.650022 | 605.828649 | 1209.666006 | 605.336641 | 9 |
| 10 | **1456.671170** | 728.839223 | 1439.644621 | 720.325948 | 1438.660605 | 719.833940 | G | *788.451245* | 394.729261 | 771.424696 | 386.215986 | 770.440680 | 385.723978 | 8 |
| 11 | 1569.755234 | 785.381255 | 1552.728685 | 776.867980 | 1551.744669 | 776.375972 | L | 731.429781 | 366.218529 | 714.403232 | 357.705254 | 713.419216 | 357.213246 | 7 |
| 12 | 1656.787262 | 828.897269 | 1639.760713 | 820.383994 | 1638.776697 | 819.891986 | S | *618.345717* | 309.676497 | 601.319168 | 301.163222 | 600.335152 | 300.671214 | 6 |
| 13 | 1743.819290 | 872.413283 | 1726.792741 | 863.900009 | 1725.808725 | 863.408000 | S | *531.313689* | 266.160483 | 514.287140 | 257.647208 | 513.303124 | 257.155200 | 5 |
| 14 | 1840.872054 | 920.939665 | 1823.845505 | 912.426391 | 1822.861489 | 911.934382 | P | *444.281661* | 222.644469 | 427.255112 | 214.131194 | 426.271096 | 213.639186 | 4 |
| 15 | 1939.940468 | 970.473872 | 1922.913919 | 961.960598 | 1921.929903 | 961.468590 | V | 347.228897 | 174.118087 | 330.202348 | 165.604812 | 329.218332 | 165.112804 | 3 |
| 16 | 2040.988147 | 1020.997712 | 2023.961598 | 1012.484437 | 2022.977582 | 1011.992429 | T | *248.160483* | 124.583880 | 231.133934 | 116.070605 | 230.149918 | 115.578597 | 2 |
| 17 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546766 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 40.5 | 2186.086411 | -0.002809 | VYACEVTHQGLSSPVTK |

**Mascot:** http://www.matrixscience.com/

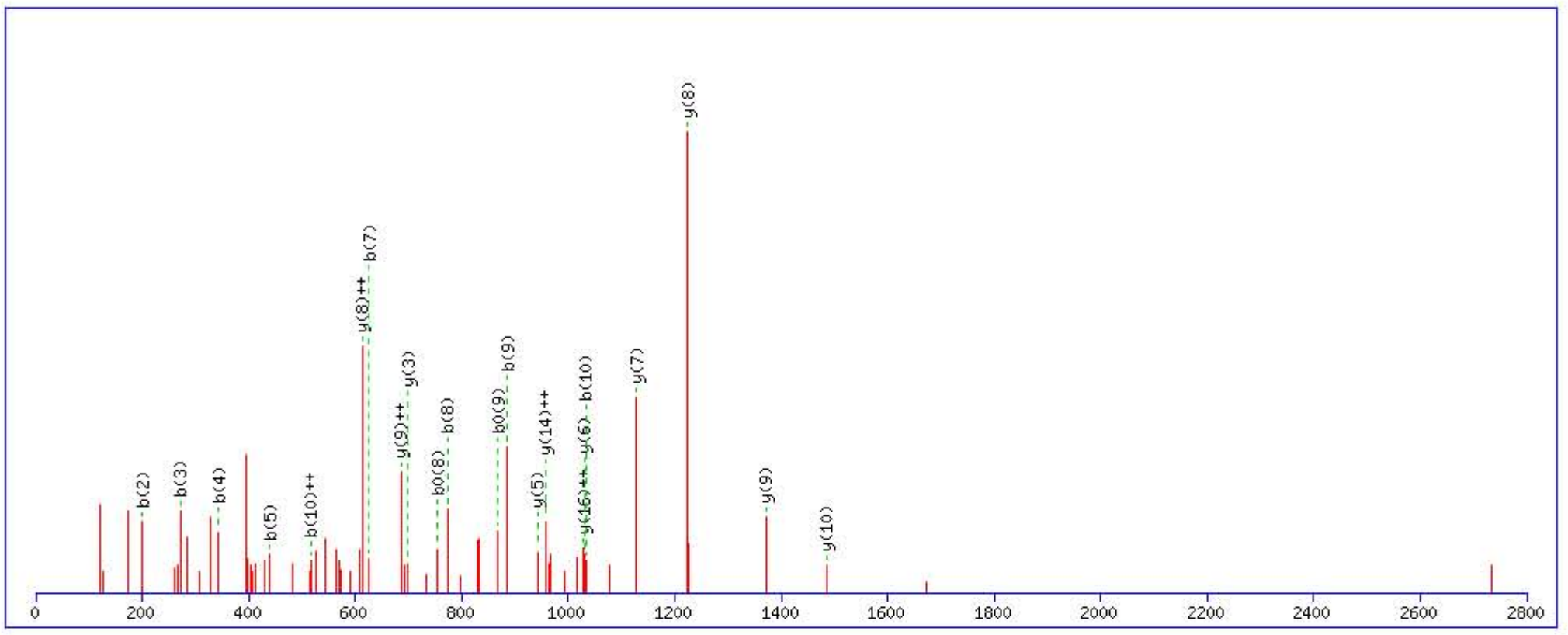
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TVAAPSVFIFPPSDEQLK**
Found in **IGKC_HUMAN**, Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1

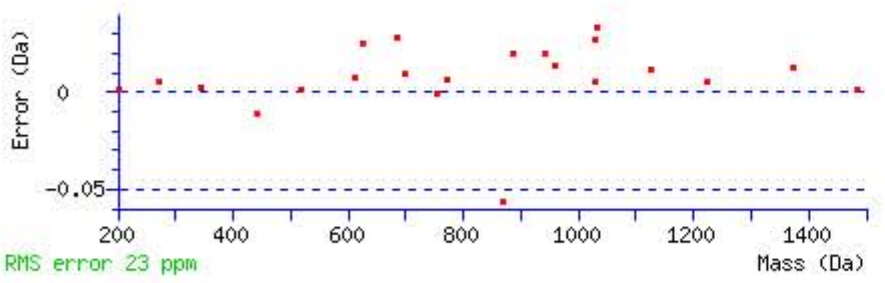
Match to Query 49580: 2256.207552 from(753.076460,3+) rtinseconds(2671) index(9093)
Title: Locus:1.1.1.2207.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

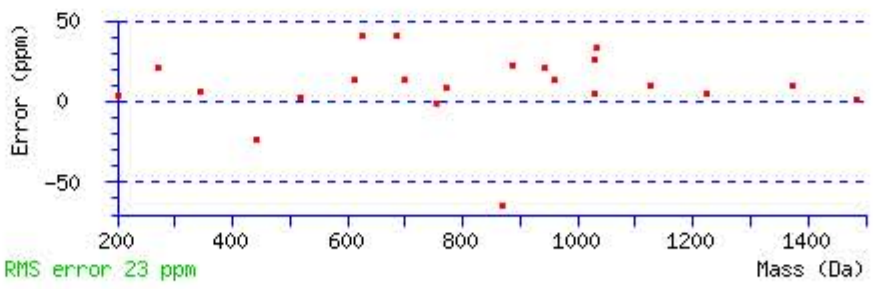
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2256.186432
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q16** : Biotin:Thermo-21345 (Q)
**Ions Score:** 52 **Expect:** 0.00012
**Matches :** 22/168 fragment ions using 37 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 18 |
| 2 | *201.123369* | 101.065322 | | | 183.112804 | 92.060040 | V | 2156.146026 | 1078.576651 | 2139.119477 | 1070.063377 | 2138.135461 | 1069.571369 | 17 |
| 3 | *272.160483* | 136.583879 | | | 254.149918 | 127.578597 | A | 2057.077612 | 1029.042444 | 2040.051063 | 1020.529170 | 2039.067047 | 1020.037162 | 16 |
| 4 | *343.197597* | 172.102437 | | | 325.187032 | 163.097154 | A | 1986.040498 | 993.523887 | 1969.013949 | 985.010613 | 1968.029933 | 984.518605 | 15 |
| 5 | *440.250361* | 220.628819 | | | 422.239796 | 211.623536 | P | 1915.003384 | 958.005330 | 1897.976835 | 949.492056 | 1896.992819 | 949.000048 | 14 |
| 6 | 527.282389 | 264.144833 | | | 509.271824 | 255.139550 | S | 1817.950620 | 909.478948 | 1800.924071 | 900.965674 | 1799.940055 | 900.473666 | 13 |
| 7 | *626.350803* | 313.679040 | | | 608.340238 | 304.673757 | V | 1730.918592 | 865.962934 | 1713.892043 | 857.449660 | 1712.908027 | 856.957652 | 12 |
| 8 | *773.419217* | 387.213247 | | | 755.408652 | 378.207964 | F | 1631.850178 | 816.428727 | 1614.823629 | 807.915453 | 1613.839613 | 807.423445 | 11 |
| 9 | *886.503281* | 443.755279 | | | 868.492716 | 434.749996 | I | *1484.781764* | 742.894520 | 1467.755215 | 734.381246 | 1466.771199 | 733.889238 | 10 |
| 10 | *1033.571695* | 517.289486 | | | 1015.561130 | 508.284203 | F | *1371.697700* | 686.352488 | 1354.671151 | 677.839214 | 1353.687135 | 677.347206 | 9 |
| 11 | 1130.624459 | 565.815868 | | | 1112.613894 | 556.810585 | P | *1224.629286* | 612.818281 | 1207.602737 | 604.305007 | 1206.618721 | 603.812999 | 8 |
| 12 | 1227.677223 | 614.342250 | | | 1209.666658 | 605.336967 | P | *1127.576522* | 564.291899 | 1110.549973 | 555.778625 | 1109.565957 | 555.286617 | 7 |
| 13 | 1314.709251 | 657.858264 | | | 1296.698686 | 648.852981 | S | *1030.523758* | 515.765517 | 1013.497209 | 507.252243 | 1012.513193 | 506.760235 | 6 |
| 14 | 1429.736194 | 715.371735 | | | 1411.725629 | 706.366453 | D | *943.491730* | 472.249503 | 926.465181 | 463.736229 | 925.481165 | 463.244221 | 5 |
| 15 | 1558.778787 | 779.893032 | | | 1540.768222 | 770.887749 | E | 828.464787 | 414.736032 | 811.438238 | 406.222757 | 810.454222 | 405.730749 | 4 |
| 16 | 1998.004113 | 999.505695 | 1980.977564 | 990.992420 | 1979.993548 | 990.500412 | Q | *699.422194* | 350.214735 | 682.395645 | 341.701461 | | | 3 |
| 17 | 2111.088177 | 1056.047727 | 2094.061628 | 1047.534452 | 2093.077612 | 1047.042444 | L | 260.196868 | 130.602072 | 243.170319 | 122.088798 | | | 2 |
| 18 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.5 | 2256.186432 | 0.021120 | TVAAPSVFIFPPSDEQLK |

**Mascot:** http://www.matrixscience.com/

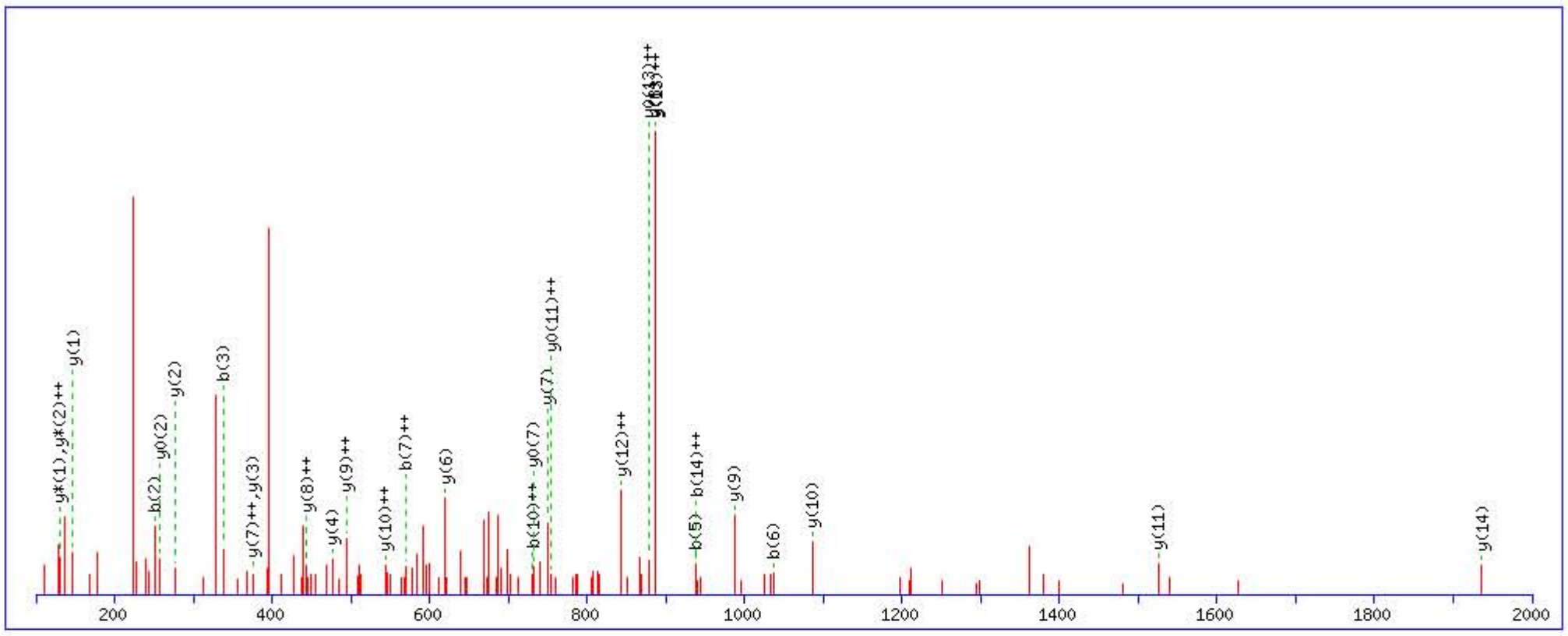
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SYSCQVTHEGSTVEK**
Found in **IGLL5_HUMAN**, Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2

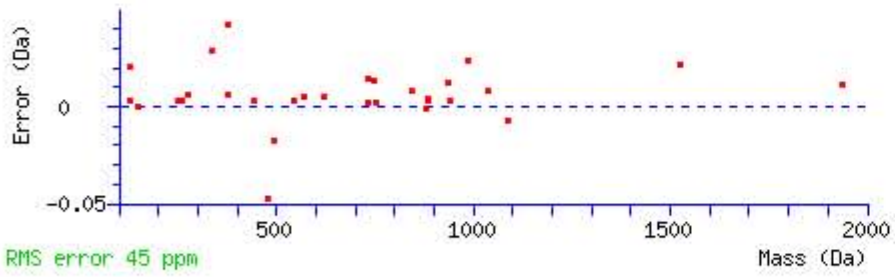
Match to Query 45088: 2021.920212 from(674.980680,3+) rtinseconds(1377) index(62628)
Title: Locus:1.1.1.1754.26 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

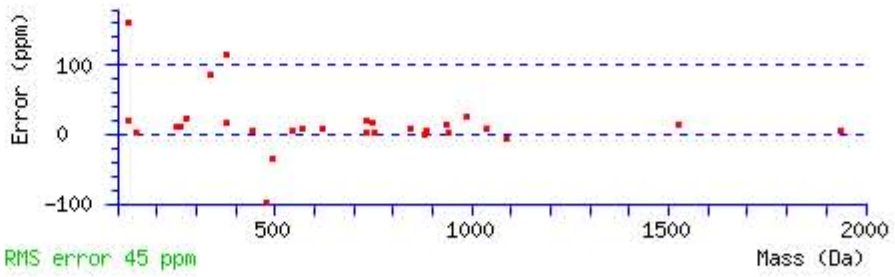
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2021.918671
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0015
**Matches :** 30/158 fragment ions using 80 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 15 |
| 2 | **251.102633** | 126.054954 | | | 233.092068 | 117.049672 | Y | *1935.893912* | 968.450594 | 1918.867363 | 959.937320 | 1917.883347 | 959.445312 | 14 |
| 3 | **338.134661** | 169.570968 | | | 320.124096 | 160.565686 | S | 1772.830583 | 886.918930 | 1755.804034 | 878.405655 | 1754.820018 | 877.913647 | 13 |
| 4 | 498.165310 | 249.586293 | | | 480.154745 | 240.581011 | C | 1685.798555 | 843.402916 | 1668.772006 | 834.889641 | 1667.787990 | 834.397633 | 12 |
| 5 | **937.390636** | 469.198956 | 920.364087 | 460.685682 | 919.380071 | 460.193674 | Q | *1525.767906* | 763.387591 | 1508.741357 | 754.874317 | 1507.757341 | 754.382309 | 11 |
| 6 | **1036.459050** | 518.733163 | 1019.432501 | 510.219889 | 1018.448485 | 509.727881 | V | *1086.542580* | 543.774928 | 1069.516031 | 535.261654 | 1068.532015 | 534.769646 | 10 |
| 7 | 1137.506729 | **569.257003** | 1120.480180 | 560.743728 | 1119.496164 | 560.251720 | T | *987.474166* | 494.240721 | 970.447617 | 485.727447 | 969.463601 | 485.235439 | 9 |
| 8 | 1274.565641 | 637.786459 | 1257.539092 | 629.273184 | 1256.555076 | 628.781176 | H | *886.426487* | 443.716882 | 869.399938 | 435.203607 | 868.415922 | 434.711599 | 8 |
| 9 | 1403.608234 | 702.307755 | 1386.581685 | 693.794481 | 1385.597669 | 693.302473 | E | *749.367575* | 375.187426 | 732.341026 | 366.674151 | 731.357010 | 366.182143 | 7 |
| 10 | 1460.629698 | **730.818487** | 1443.603149 | 722.305213 | 1442.619133 | 721.813204 | G | *620.324982* | 310.666129 | 603.298433 | 302.152855 | 602.314417 | 301.660847 | 6 |
| 11 | 1547.661726 | 774.334501 | 1530.635177 | 765.821227 | 1529.651161 | 765.329219 | S | 563.303518 | 282.155397 | 546.276969 | 273.642123 | 545.292953 | 273.150115 | 5 |
| 12 | 1648.709405 | 824.858341 | 1631.682856 | 816.345066 | 1630.698840 | 815.853058 | T | *476.271490* | 238.639383 | 459.244941 | 230.126109 | 458.260925 | 229.634101 | 4 |
| 13 | 1747.777819 | 874.392548 | 1730.751270 | 865.879273 | 1729.767254 | 865.387265 | V | *375.223811* | 188.115544 | 358.197262 | 179.602269 | 357.213246 | 179.110261 | 3 |
| 14 | 1876.820412 | **938.913844** | 1859.793863 | 930.400570 | 1858.809847 | 929.908562 | E | *276.155397* | 138.581337 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 15 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.7 | 2021.918671 | 0.001541 | SYSCQVTHEGSTVEK |

**Mascot:** http://www.matrixscience.com/

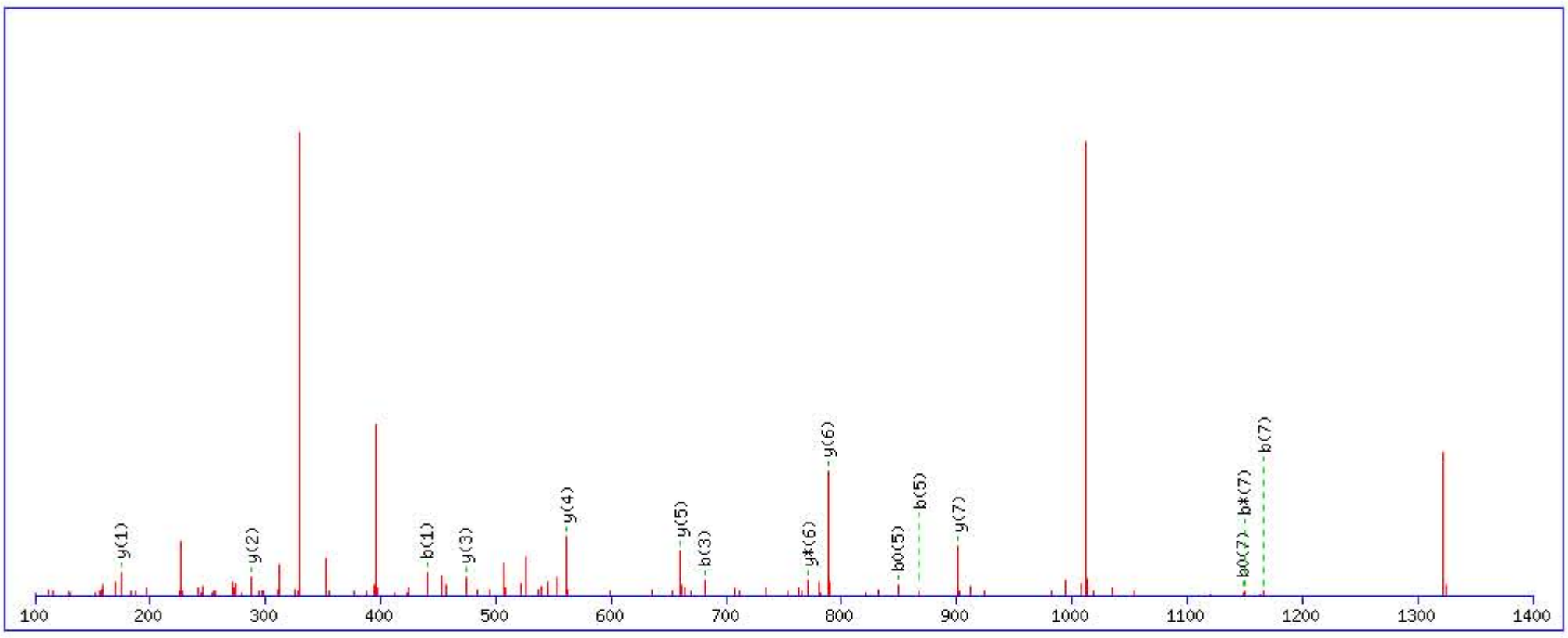
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QIQVSWLR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

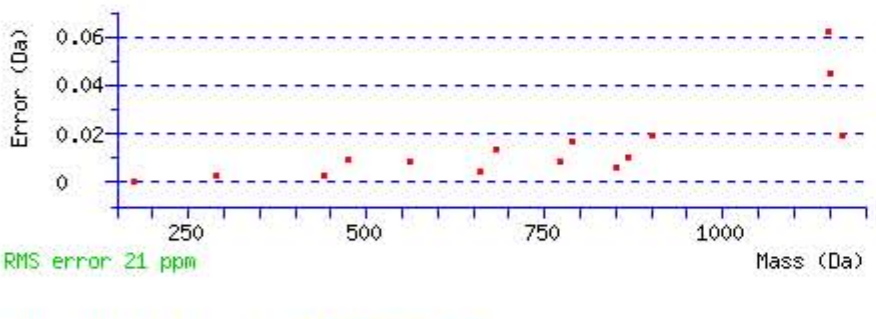
Match to Query 24109: 1339.762728 from(670.888640,2+) rtinseconds(2359) index(36346)
Title: Locus:1.1.1.930.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

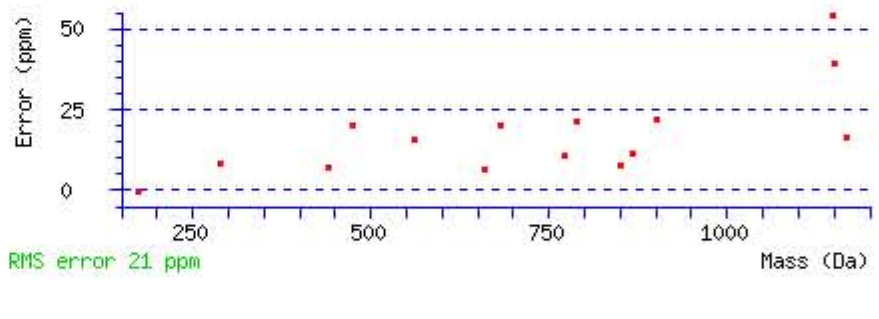
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1339.743454
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0093
**Matches** : 15/70 fragment ions using 35 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **440.232602** | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 8 |
| 2 | 553.316666 | 277.161971 | 536.290117 | 268.648697 | | | I | ***901.525413*** | 451.266344 | 884.498864 | 442.753070 | 883.514848 | 442.261062 | 7 |
| 3 | **681.375244** | 341.191260 | 664.348695 | 332.677986 | | | Q | ***788.441349*** | 394.724312 | 771.414800 | 386.211038 | 770.430784 | 385.719030 | 6 |
| 4 | 780.443658 | 390.725467 | 763.417109 | 382.212193 | | | V | ***660.382771*** | 330.695023 | 643.356222 | 322.181749 | 642.372206 | 321.689741 | 5 |
| 5 | **867.475686** | 434.241481 | 850.449137 | 425.728207 | 849.465121 | 425.236199 | S | ***561.314357*** | 281.160816 | 544.287808 | 272.647542 | 543.303792 | 272.155534 | 4 |
| 6 | 1053.554999 | 527.281138 | 1036.528450 | 518.767863 | 1035.544434 | 518.275855 | W | ***474.282329*** | 237.644802 | 457.255780 | 229.131528 | | | 3 |
| 7 | **1166.639063** | 583.823169 | 1149.612514 | 575.309895 | 1148.628498 | 574.817887 | L | ***288.203016*** | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 8 | | | | | | | R | ***175.118952*** | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 32.6 | 1339.743454 | 0.019274 | QIQVSWLR |
| 15.8 | 1339.765915 | -0.003187 | QRLRFGPR |
| 12.7 | 1339.743454 | 0.019274 | QIQVSWLR |
| 11.1 | 1339.753326 | 0.009402 | QLQISIAEK |
| 9.9 | 1339.764557 | -0.001829 | AKETIQALR |
| 7.5 | 1339.775787 | -0.013059 | QLRSIEKR |
| 7.5 | 1339.743439 | 0.019289 | QLSWLINR |
| 7.5 | 1339.743454 | 0.019274 | QLTWLVNR |
| 5.8 | 1339.764557 | -0.001829 | LQKEIDKR |
| 5.3 | 1339.745941 | 0.016787 | KAELEGVAVTAPR |

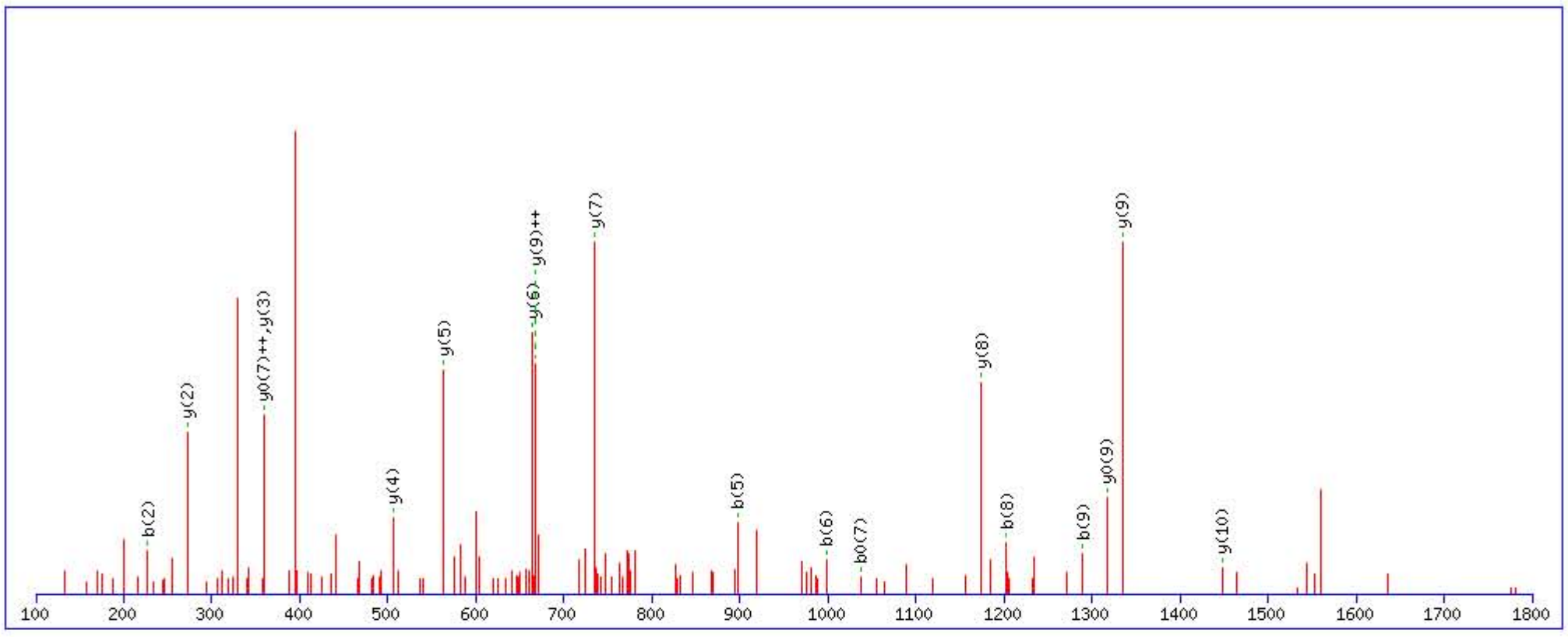
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LICQATGFSPR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

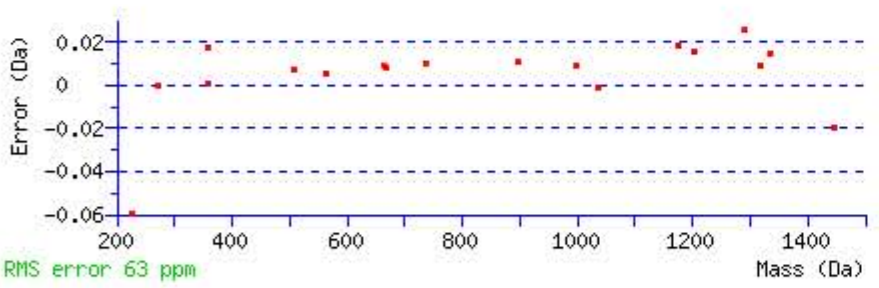
Match to Query 32763: 1559.813228 from(780.913890,2+) rtinseconds(1992) index(50341)
Title: Locus:1.1.1.1931.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

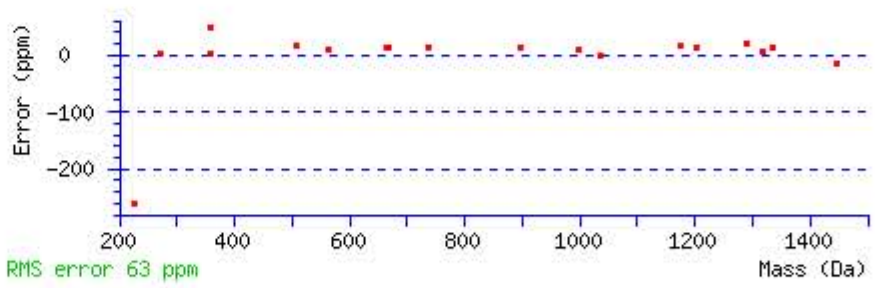
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1559.795242
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 2.1e-005
**Matches :** 18/100 fragment ions using 30 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 11 |
| 2 | 227.175404 | 114.091340 | | | | | I | *1447.718454* | 724.362865 | 1430.691905 | 715.849591 | 1429.707889 | 715.357583 | 10 |
| 3 | 387.206053 | 194.106664 | | | | | C | *1334.634390* | 667.820833 | 1317.607841 | 659.307559 | 1316.623825 | 658.815551 | 9 |
| 4 | 826.431379 | 413.719328 | 809.404830 | 405.206053 | | | Q | *1174.603741* | 587.805509 | 1157.577192 | 579.292234 | 1156.593176 | 578.800226 | 8 |
| 5 | 897.468493 | 449.237885 | 880.441944 | 440.724610 | | | A | *735.378415* | 368.192846 | 718.351866 | 359.679571 | 717.367850 | 359.187563 | 7 |
| 6 | 998.516172 | 499.761724 | 981.489623 | 491.248449 | 980.505607 | 490.756441 | T | *664.341301* | 332.674289 | 647.314752 | 324.161014 | 646.330736 | 323.669006 | 6 |
| 7 | 1055.537636 | 528.272456 | 1038.511087 | 519.759182 | 1037.527071 | 519.267174 | G | *563.293622* | 282.150449 | 546.267073 | 273.637175 | 545.283057 | 273.145167 | 5 |
| 8 | 1202.606050 | 601.806663 | 1185.579501 | 593.293389 | 1184.595485 | 592.801381 | F | *506.272158* | 253.639717 | 489.245609 | 245.126443 | 488.261593 | 244.634435 | 4 |
| 9 | 1289.638078 | 645.322677 | 1272.611529 | 636.809403 | 1271.627513 | 636.317395 | S | *359.203744* | 180.105510 | 342.177195 | 171.592236 | 341.193179 | 171.100228 | 3 |
| 10 | 1386.690842 | 693.849059 | 1369.664293 | 685.335785 | 1368.680277 | 684.843777 | P | *272.171716* | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 11 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.1 | 1559.795242 | 0.017986 | LICQATGFSPR |
| 8.2 | 1559.808960 | 0.004268 | LDRLSGLADQMVAR |
| 5.4 | 1559.820190 | -0.006962 | MTRSATQAAKQVPR |

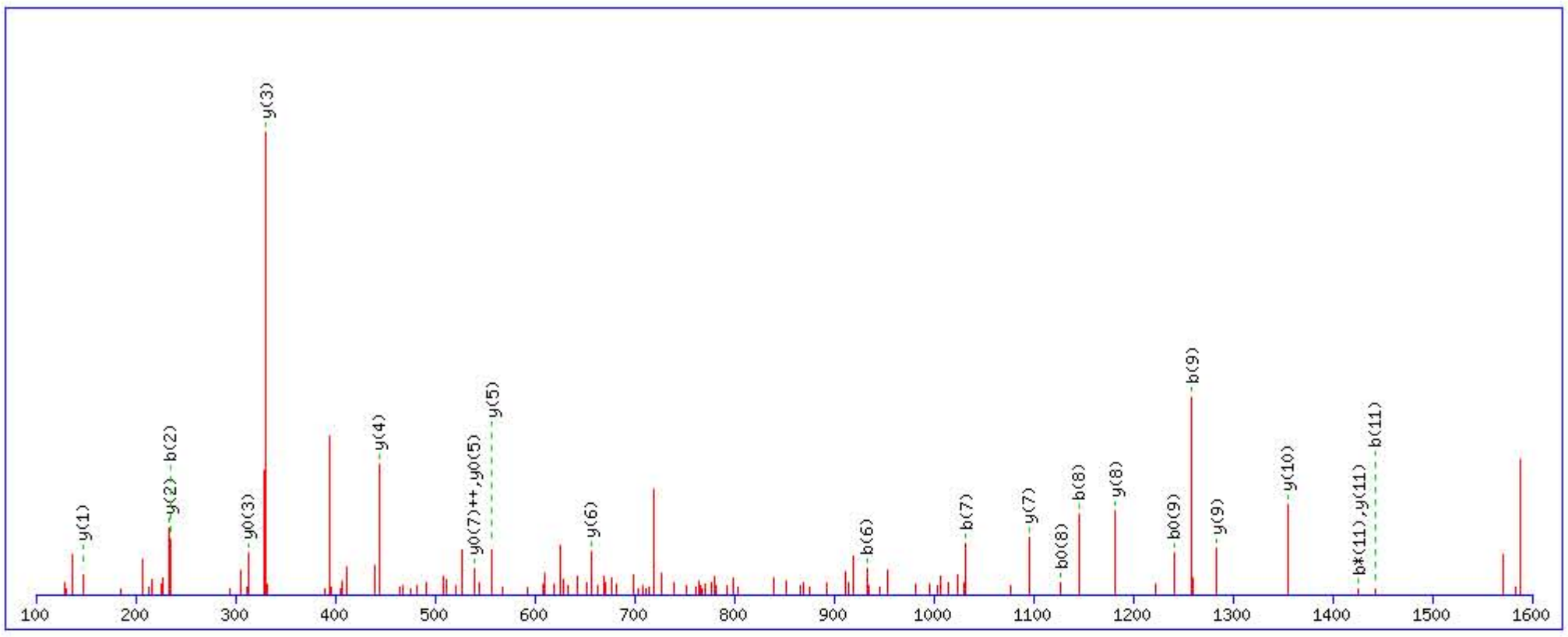
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YAATSQVLLPSK**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

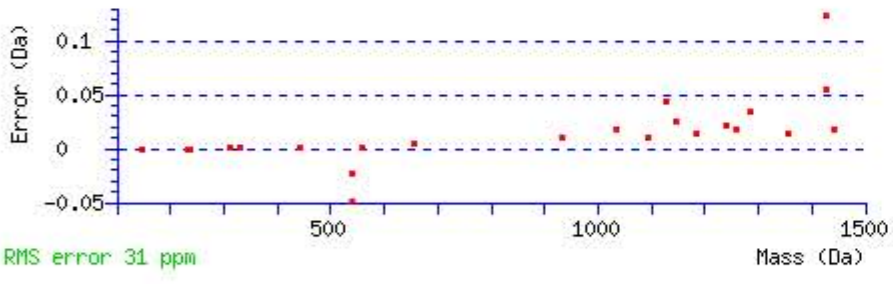
Match to Query 34094: 1587.885168 from(794.949860,2+) rtinseconds(2036) index(50559)
Title: Locus:1.1.1.1946.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

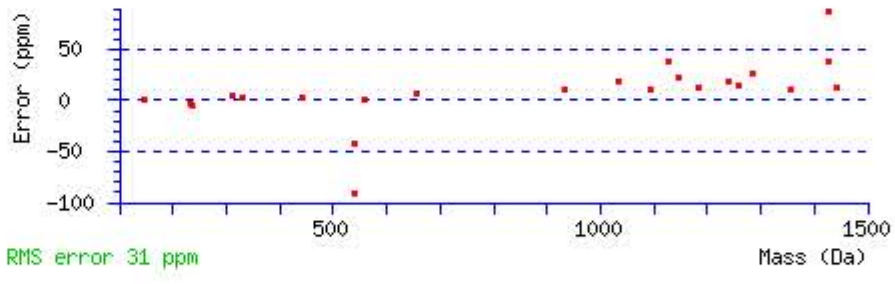
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1587.869431
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 74 **Expect:** 7.2e-007
**Matches :** 23/114 fragment ions using 41 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 12 |
| 2 | **235.107719** | 118.057498 | | | | | A | *1425.813399* | 713.410337 | 1408.786850 | 704.897063 | 1407.802834 | 704.405055 | 11 |
| 3 | 306.144833 | 153.576055 | | | | | A | *1354.776285* | 677.891780 | 1337.749736 | 669.378506 | 1336.765720 | 668.886498 | 10 |
| 4 | 407.192512 | 204.099894 | | | 389.181947 | 195.094612 | T | *1283.739171* | 642.373223 | 1266.712622 | 633.859949 | 1265.728606 | 633.367941 | 9 |
| 5 | 494.224540 | 247.615908 | | | 476.213975 | 238.610626 | S | *1182.691492* | 591.849384 | 1165.664943 | 583.336110 | 1164.680927 | 582.844101 | 8 |
| 6 | **933.449866** | 467.228571 | 916.423317 | 458.715297 | 915.439301 | 458.223289 | Q | *1095.659464* | 548.333370 | 1078.632915 | 539.820096 | 1077.648899 | 539.328088 | 7 |
| 7 | **1032.518280** | 516.762778 | 1015.491731 | 508.249504 | 1014.507715 | 507.757496 | V | *656.434138* | 328.720707 | 639.407589 | 320.207432 | 638.423573 | 319.715424 | 6 |
| 8 | **1145.602344** | 573.304810 | 1128.575795 | 564.791536 | 1127.591779 | 564.299527 | L | *557.365724* | 279.186500 | 540.339175 | 270.673226 | 539.355159 | 270.181218 | 5 |
| 9 | **1258.686408** | 629.846842 | 1241.659859 | 621.333567 | 1240.675843 | 620.841559 | L | *444.281660* | 222.644468 | 427.255111 | 214.131193 | 426.271095 | 213.639186 | 4 |
| 10 | 1355.739172 | 678.373224 | 1338.712623 | 669.859949 | 1337.728607 | 669.367941 | P | *331.197596* | 166.102436 | 314.171047 | 157.589162 | 313.187031 | 157.097154 | 3 |
| 11 | **1442.771200** | 721.889238 | 1425.744651 | 713.375964 | 1424.760635 | 712.883955 | S | *234.144832* | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 12 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 73.9 | 1587.869431 | 0.015737 | YAATSQVLLPSK |
| 8.7 | 1587.862045 | 0.023123 | VTGQNQEQFLLLAK |
| 8.0 | 1587.862030 | 0.023138 | EDAKLSFKHVSSLK |
| 6.0 | 1587.865402 | 0.019766 | ENGLRDILAVLTMK |
| 3.8 | 1587.891220 | -0.006052 | TIQTIVFLYSLYK |
| 2.2 | 1587.862045 | 0.023123 | SKDLTAADVVKQWK |
| 2.1 | 1587.870773 | 0.014395 | FSWMKLLAHKVGR |
| 2.0 | 1587.884018 | 0.001150 | TKTKMSAAQALK |
| 1.6 | 1587.880646 | 0.004522 | RIQAEYVSALK |
| 0.9 | 1587.890533 | -0.005365 | EPTTKAEMLKIISK |

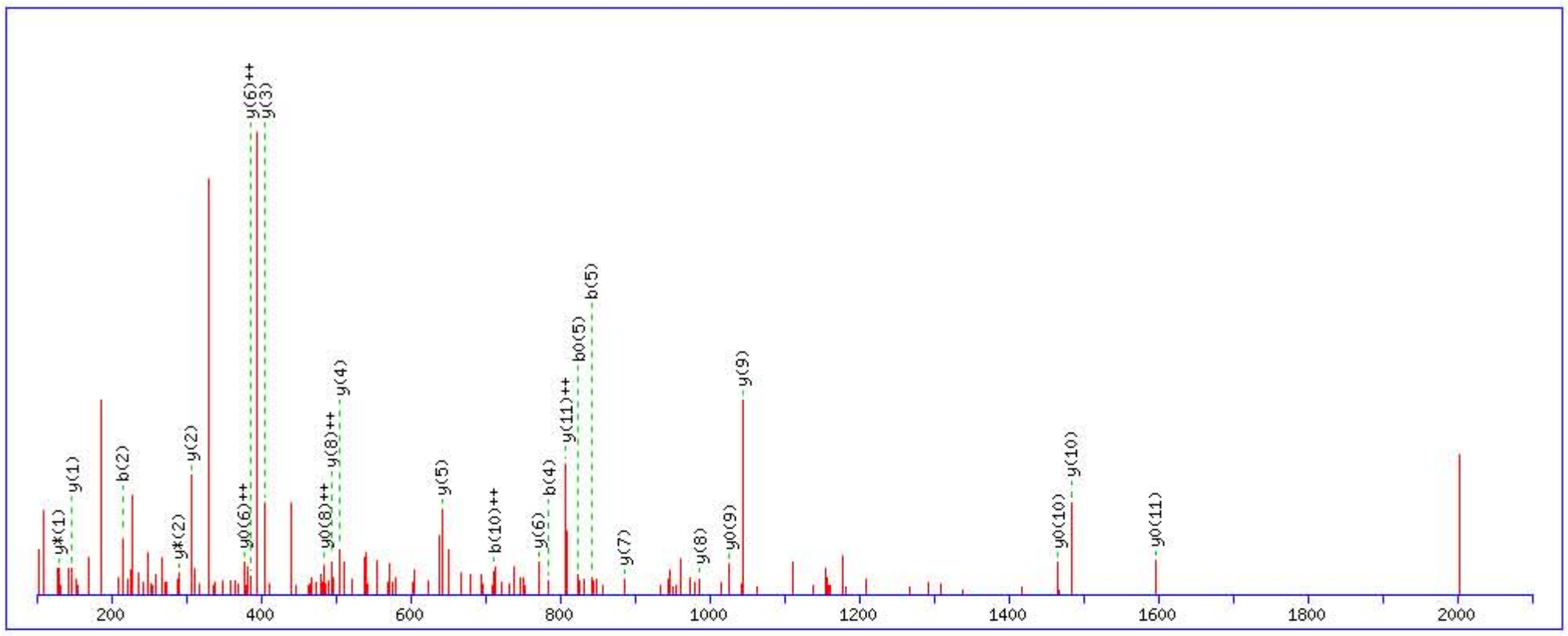
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DVMQGTDEHVVCK**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

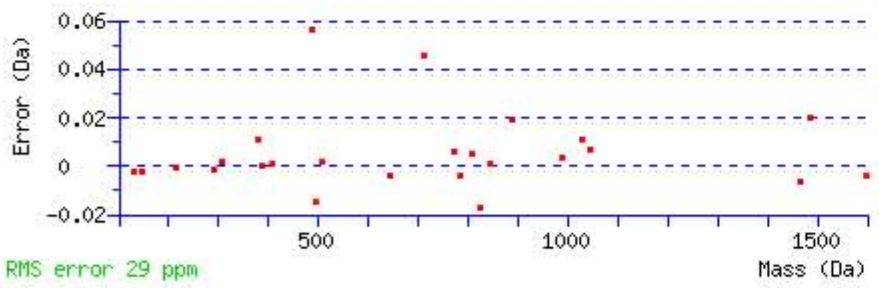
Match to Query 40852: 1827.840042 from(610.287290,3+) rtinseconds(1640) index(31997)
Title: Locus:1.1.1.679.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

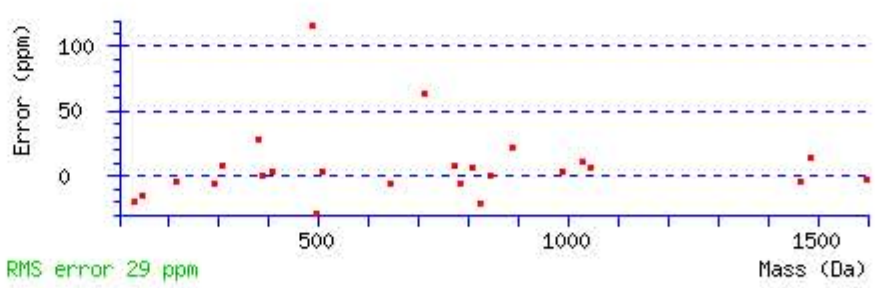
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1827.831787
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 26 **Expect:** 0.028
**Matches :** 25/128 fragment ions using 87 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 13 |
| 2 | **215.102633** | 108.054954 | | | 197.092068 | 99.049672 | V | 1713.812097 | 857.409687 | 1696.785548 | 848.896412 | 1695.801532 | 848.404404 | 12 |
| 3 | 346.143118 | 173.575197 | | | 328.132553 | 164.569915 | M | 1614.743683 | 807.875480 | 1597.717134 | 799.362205 | 1596.733118 | 798.870197 | 11 |
| 4 | **785.368444** | 393.187860 | 768.341895 | 384.674586 | 767.357879 | 384.182578 | Q | *1483.703198* | 742.355237 | 1466.676649 | 733.841963 | 1465.692633 | 733.349955 | 10 |
| 5 | **842.389908** | 421.698592 | 825.363359 | 413.185318 | 824.379343 | 412.693310 | G | *1044.477872* | 522.742574 | 1027.451323 | 514.229300 | 1026.467307 | 513.737292 | 9 |
| 6 | 943.437587 | 472.222432 | 926.411038 | 463.709157 | 925.427022 | 463.217149 | T | *987.456408* | 494.231842 | 970.429859 | 485.718568 | 969.445843 | 485.226560 | 8 |
| 7 | 1058.464530 | 529.735903 | 1041.437981 | 521.222629 | 1040.453965 | 520.730621 | D | *886.408729* | 443.708003 | 869.382180 | 435.194728 | 868.398164 | 434.702720 | 7 |
| 8 | 1187.507123 | 594.257200 | 1170.480574 | 585.743925 | 1169.496558 | 585.251917 | E | *771.381786* | 386.194531 | 754.355237 | 377.681257 | 753.371221 | 377.189249 | 6 |
| 9 | 1324.566035 | 662.786656 | 1307.539486 | 654.273381 | 1306.555470 | 653.781373 | H | *642.339193* | 321.673235 | 625.312644 | 313.159960 | | | 5 |
| 10 | 1423.634449 | 712.320863 | 1406.607900 | 703.807588 | 1405.623884 | 703.315580 | V | *505.280281* | 253.143779 | 488.253732 | 244.630504 | | | 4 |
| 11 | 1522.702863 | 761.855070 | 1505.676314 | 753.341795 | 1504.692298 | 752.849787 | V | *406.211867* | 203.609572 | 389.185318 | 195.096297 | | | 3 |
| 12 | 1682.733512 | 841.870394 | 1665.706963 | 833.357120 | 1664.722947 | 832.865112 | C | *307.143453* | 154.075365 | 290.116904 | 145.562090 | | | 2 |
| 13 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 26.4 | 1827.831787 | 0.008255 | DVMQGTDEHVVCK |

**Mascot:** http://www.matrixscience.com/

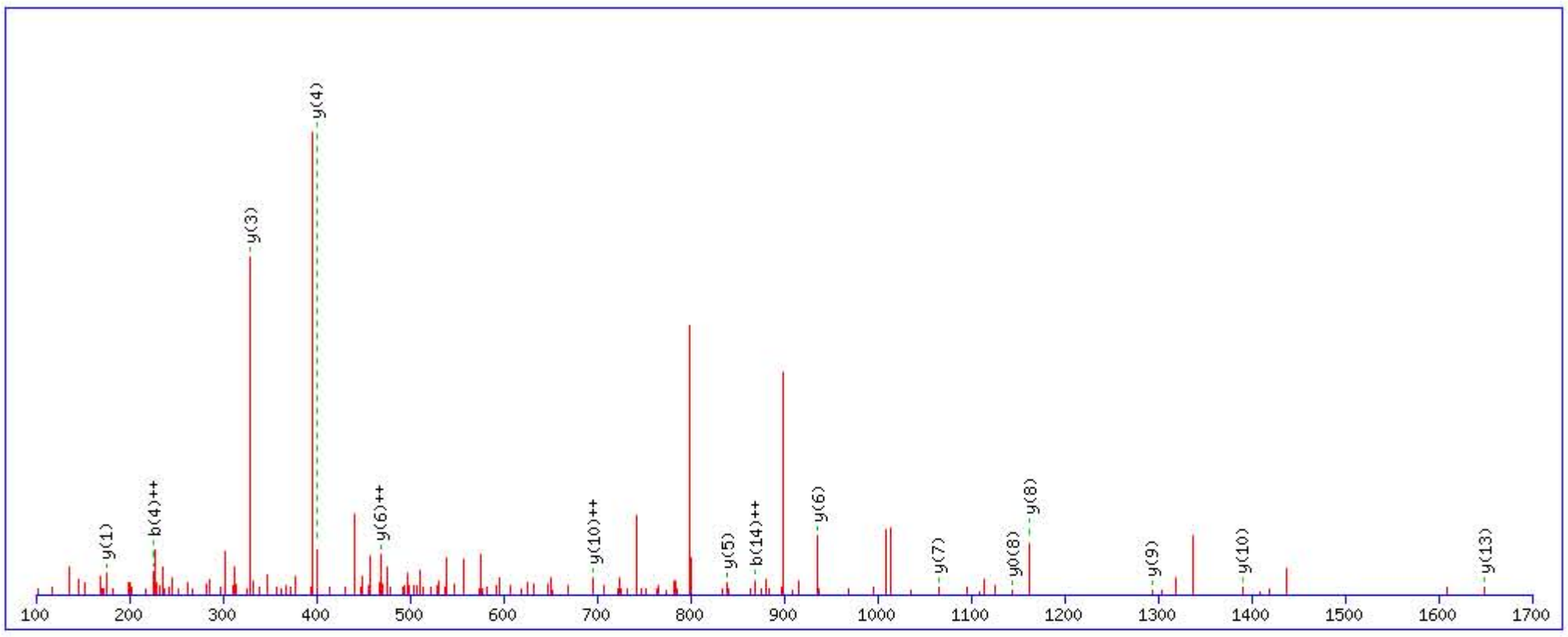
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YVTSAPMPEPQAPGR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

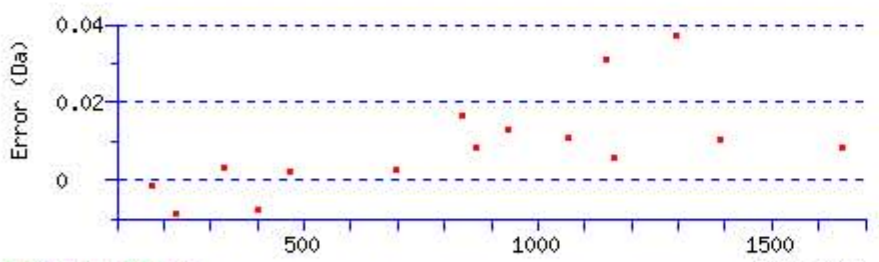
Match to Query 42356: 1910.947692 from(637.989840,3+) rtinseconds(1891) index(33386)
Title: Locus:1.1.1.767.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

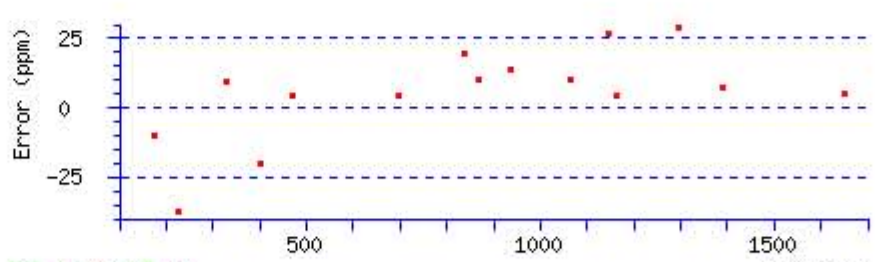
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1910.938263
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 30 **Expect:** 0.022
**Matches :** 15/132 fragment ions using 54 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 15 |
| 2 | 263.139019 | 132.073148 | | | | | V | 1748.882225 | 874.944750 | 1731.855676 | 866.431476 | 1730.871660 | 865.939468 | 14 |
| 3 | 364.186698 | 182.596987 | | | 346.176133 | 173.591705 | T | *1649.813811* | 825.410543 | 1632.787262 | 816.897269 | 1631.803246 | 816.405261 | 13 |
| 4 | 451.218726 | **226.113001** | | | 433.208161 | 217.107719 | S | 1548.766132 | 774.886704 | 1531.739583 | 766.373430 | 1530.755567 | 765.881421 | 12 |
| 5 | 522.255840 | 261.631558 | | | 504.245275 | 252.626276 | A | 1461.734104 | 731.370690 | 1444.707555 | 722.857416 | 1443.723539 | 722.365407 | 11 |
| 6 | 619.308604 | 310.157940 | | | 601.298039 | 301.152658 | P | *1390.696990* | 695.852133 | 1373.670441 | 687.338859 | 1372.686425 | 686.846850 | 10 |
| 7 | 750.349089 | 375.678183 | | | 732.338524 | 366.672900 | M | *1293.644226* | 647.325751 | 1276.617677 | 638.812477 | 1275.633661 | 638.320468 | 9 |
| 8 | 847.401853 | 424.204565 | | | 829.391288 | 415.199282 | P | *1162.603741* | 581.805508 | 1145.577192 | 573.292234 | 1144.593176 | 572.800226 | 8 |
| 9 | 976.444446 | 488.725861 | | | 958.433881 | 479.720579 | E | *1065.550977* | 533.279126 | 1048.524428 | 524.765852 | 1047.540412 | 524.273844 | 7 |
| 10 | 1073.497210 | 537.252243 | | | 1055.486645 | 528.246961 | P | *936.508384* | 468.757830 | 919.481835 | 460.244555 | | | 6 |
| 11 | 1512.722536 | 756.864906 | 1495.695987 | 748.351632 | 1494.711971 | 747.859624 | Q | *839.455620* | 420.231448 | 822.429071 | 411.718173 | | | 5 |
| 12 | 1583.759650 | 792.383463 | 1566.733101 | 783.870189 | 1565.749085 | 783.378180 | A | *400.230294* | 200.618785 | 383.203745 | 192.105510 | | | 4 |
| 13 | 1680.812414 | 840.909845 | 1663.785865 | 832.396571 | 1662.801849 | 831.904563 | P | *329.193180* | 165.100228 | 312.166631 | 156.586953 | | | 3 |
| 14 | 1737.833878 | **869.420577** | 1720.807329 | 860.907303 | 1719.823313 | 860.415294 | G | 232.140416 | 116.573846 | 215.113867 | 108.060571 | | | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 30.4 | 1910.938263 | 0.009429 | YVTSAPMPEPQAPGR |
| 22.5 | 1910.934265 | 0.013427 | SGSDEVQVGQQR |
| 21.1 | 1910.934265 | 0.013427 | SGSDEVQVGQQR |

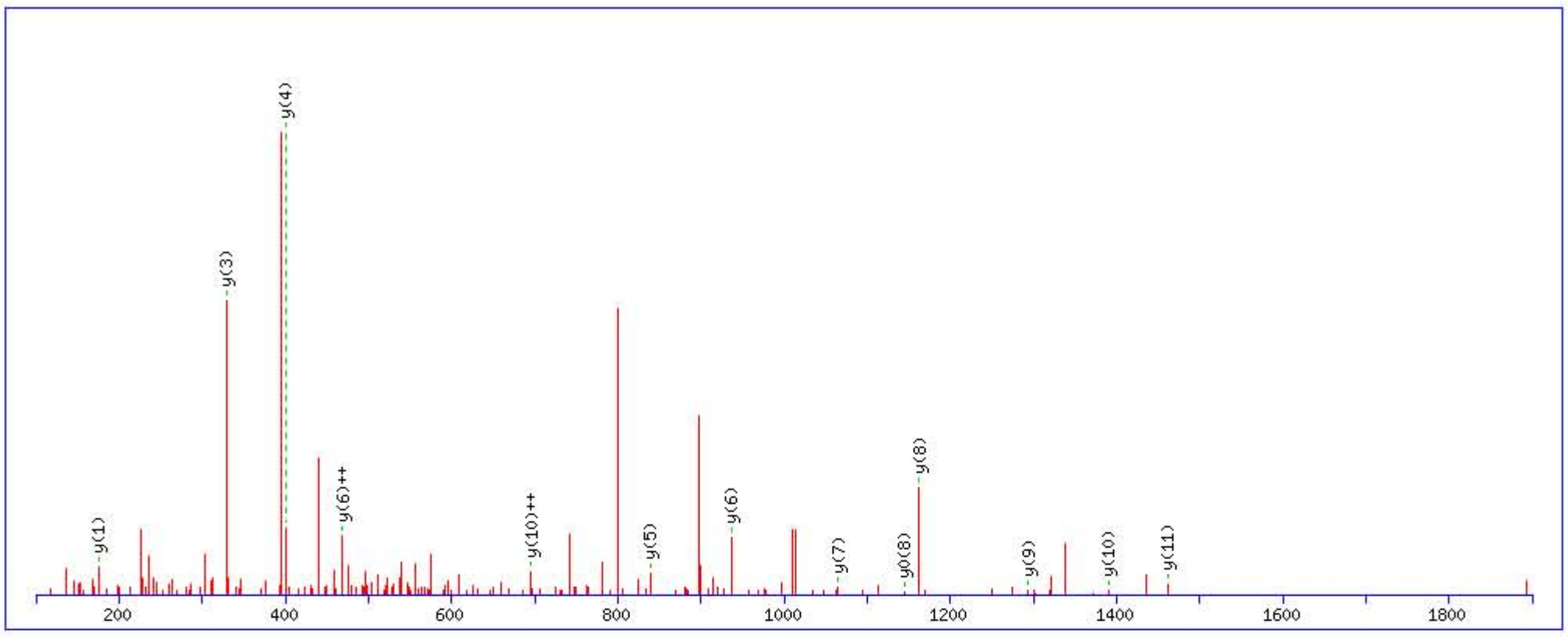
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YVTSAPMPEPQAPGR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

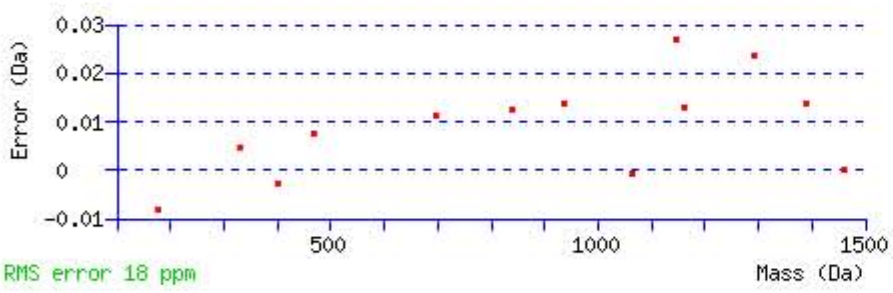
Match to Query 42357: 1910.947692 from(637.989840,3+) rtinseconds(1882) index(33320)
Title: Locus:1.1.1.764.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

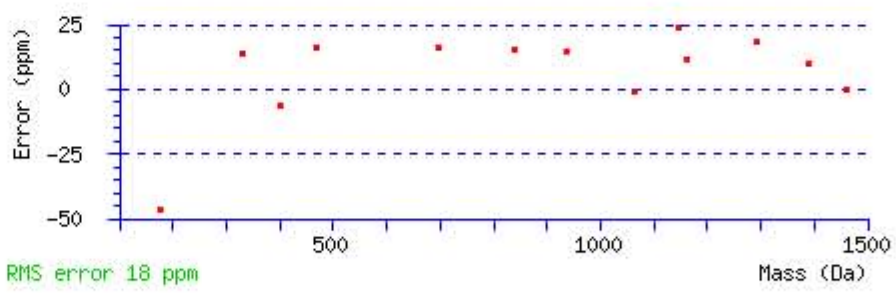
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1910.938263
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0031
**Matches** : 13/132 fragment ions using 42 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 15 |
| 2 | 263.139019 | 132.073148 | | | | | V | 1748.882225 | 874.944750 | 1731.855676 | 866.431476 | 1730.871660 | 865.939468 | 14 |
| 3 | 364.186698 | 182.596987 | | | 346.176133 | 173.591705 | T | 1649.813811 | 825.410543 | 1632.787262 | 816.897269 | 1631.803246 | 816.405261 | 13 |
| 4 | 451.218726 | 226.113001 | | | 433.208161 | 217.107719 | S | 1548.766132 | 774.886704 | 1531.739583 | 766.373430 | 1530.755567 | 765.881421 | 12 |
| 5 | 522.255840 | 261.631558 | | | 504.245275 | 252.626276 | A | *1461.734104* | 731.370690 | 1444.707555 | 722.857416 | 1443.723539 | 722.365407 | 11 |
| 6 | 619.308604 | 310.157940 | | | 601.298039 | 301.152658 | P | *1390.696990* | 695.852133 | 1373.670441 | 687.338859 | 1372.686425 | 686.846850 | 10 |
| 7 | 750.349089 | 375.678183 | | | 732.338524 | 366.672900 | M | *1293.644226* | 647.325751 | 1276.617677 | 638.812477 | 1275.633661 | 638.320468 | 9 |
| 8 | 847.401853 | 424.204565 | | | 829.391288 | 415.199282 | P | *1162.603741* | 581.805508 | 1145.577192 | 573.292234 | 1144.593176 | 572.800226 | 8 |
| 9 | 976.444446 | 488.725861 | | | 958.433881 | 479.720579 | E | *1065.550977* | 533.279126 | 1048.524428 | 524.765852 | 1047.540412 | 524.273844 | 7 |
| 10 | 1073.497210 | 537.252243 | | | 1055.486645 | 528.246961 | P | *936.508384* | 468.757830 | 919.481835 | 460.244555 | | | 6 |
| 11 | 1512.722536 | 756.864906 | 1495.695987 | 748.351632 | 1494.711971 | 747.859624 | Q | *839.455620* | 420.231448 | 822.429071 | 411.718173 | | | 5 |
| 12 | 1583.759650 | 792.383463 | 1566.733101 | 783.870189 | 1565.749085 | 783.378180 | A | *400.230294* | 200.618785 | 383.203745 | 192.105510 | | | 4 |
| 13 | 1680.812414 | 840.909845 | 1663.785865 | 832.396571 | 1662.801849 | 831.904563 | P | *329.193180* | 165.100228 | 312.166631 | 156.586953 | | | 3 |
| 14 | 1737.833878 | 869.420577 | 1720.807329 | 860.907303 | 1719.823313 | 860.415294 | G | 232.140416 | 116.573846 | 215.113867 | 108.060571 | | | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.9 | 1910.938263 | 0.009429 | YVTSAPMPEPQAPGR |
| 30.9 | 1910.934265 | 0.013427 | SGSDEVQVGQQR |
| 21.9 | 1910.934265 | 0.013427 | SGSDEVQVGQQR |
| 1.6 | 1910.971970 | -0.024278 | KAPMGTARFGHHMAVLR |

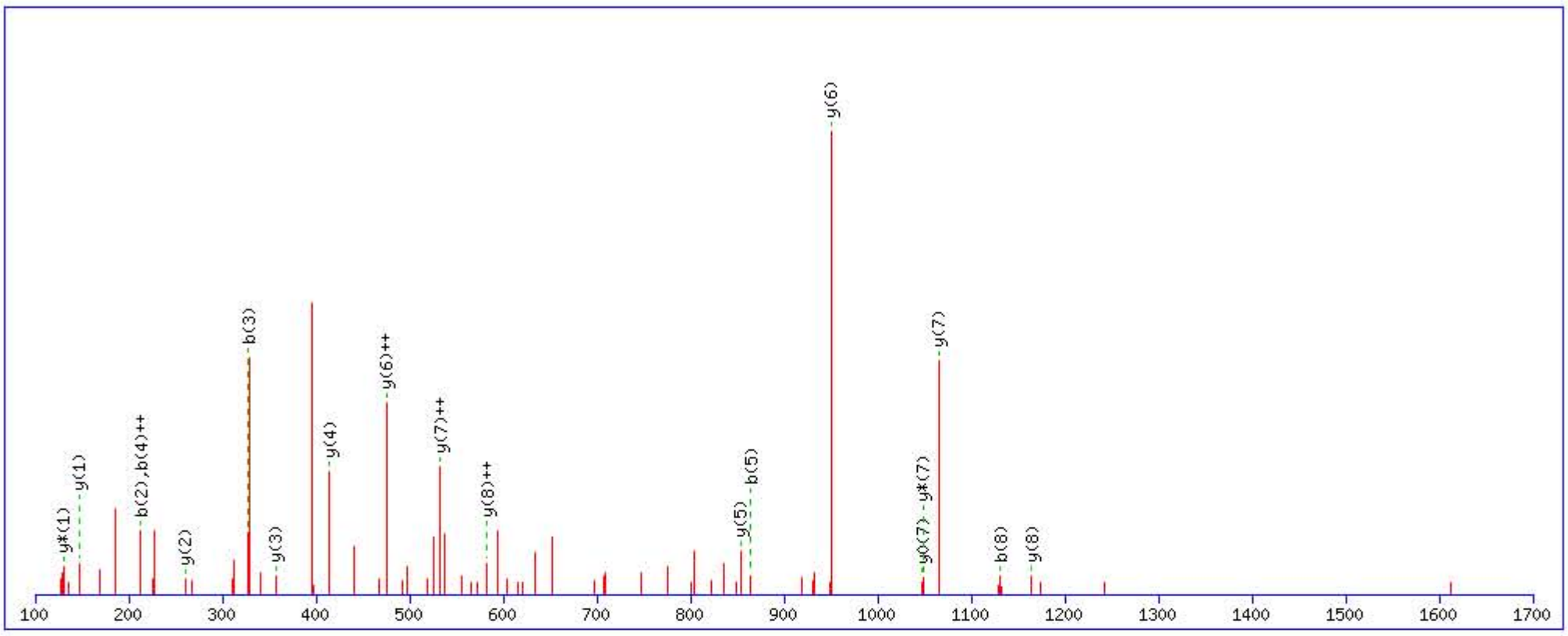
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LVDPQGPLK**
Found in **FCGBP_HUMAN**, IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3

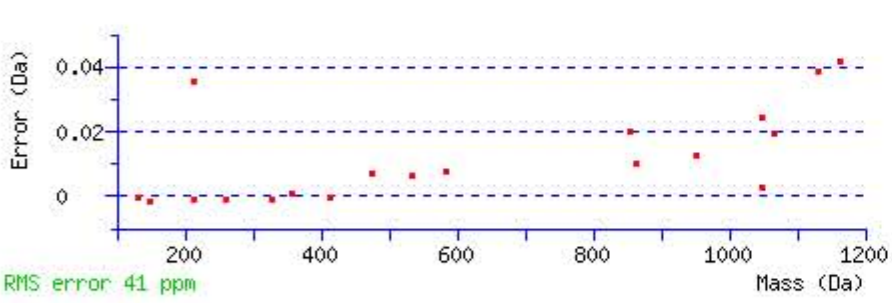
Match to Query 22640: 1276.730548 from(639.372550,2+) rtinseconds(1897) index(33434)
Title: Locus:1.1.1.769.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

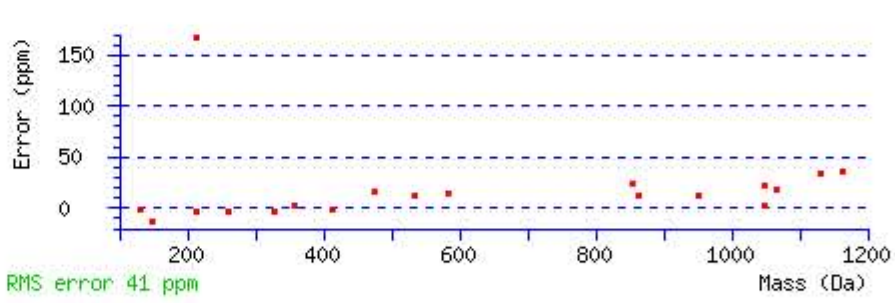
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1276.721329
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.0037
**Matches :** 19/72 fragment ions using 59 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 9 |
| 2 | **213.159754** | 107.083515 | | | | | V | *1164.644543* | 582.825910 | 1147.617994 | 574.312635 | 1146.633978 | 573.820627 | 8 |
| 3 | **328.186697** | 164.596986 | | | 310.176132 | 155.591704 | D | *1065.576129* | 533.291703 | 1048.549580 | 524.778428 | 1047.565564 | 524.286420 | 7 |
| 4 | 425.239461 | 213.123368 | | | 407.228896 | 204.118086 | P | *950.549186* | 475.778231 | 933.522637 | 467.264956 | | | 6 |
| 5 | **864.464787** | 432.736032 | 847.438238 | 424.222757 | 846.454222 | 423.730749 | Q | *853.496422* | 427.251849 | 836.469873 | 418.738575 | | | 5 |
| 6 | 921.486251 | 461.246764 | 904.459702 | 452.733489 | 903.475686 | 452.241481 | G | *414.271096* | 207.639186 | 397.244547 | 199.125911 | | | 4 |
| 7 | 1018.539015 | 509.773146 | 1001.512466 | 501.259871 | 1000.528450 | 500.767863 | P | *357.249632* | 179.128454 | 340.223083 | 170.615179 | | | 3 |
| 8 | **1131.623079** | 566.315178 | 1114.596530 | 557.801903 | 1113.612514 | 557.309895 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 9 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 30.6 | 1276.721329 | 0.009219 | LVDPQGPLK |
| 4.4 | 1276.725174 | 0.005374 | LVLGDQHQLVR |
| 2.7 | 1276.739075 | -0.008527 | AGTPSLVTYLKK |
| 2.5 | 1276.713913 | 0.016635 | VIDAKFETKAR |
| 0.8 | 1276.732529 | -0.001981 | EKALLQHK |

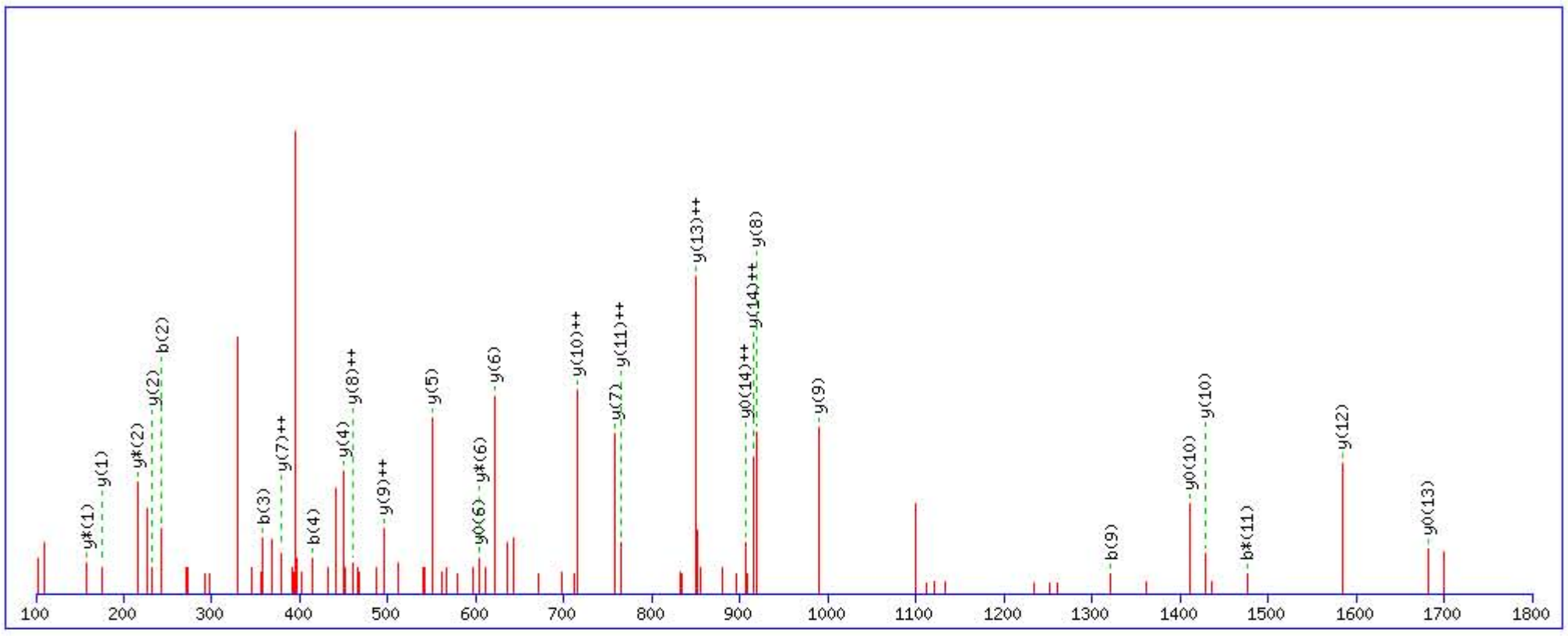
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LEDGVQACHATGCGR**
Found in **FCGBP_HUMAN**, IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3

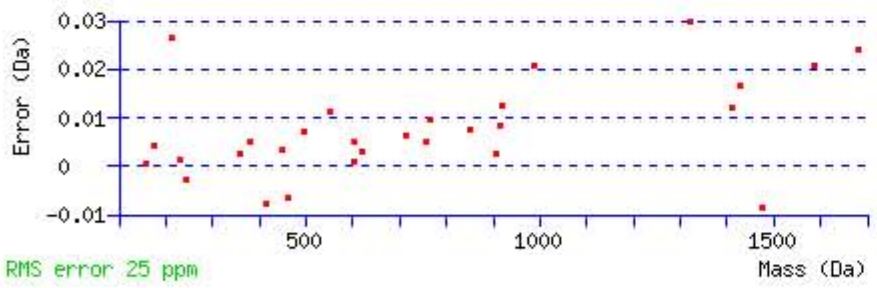
Match to Query 42939: 1940.881602 from(647.967810,3+) rtinseconds(1445) index(30661)
Title: Locus:1.1.1.611.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

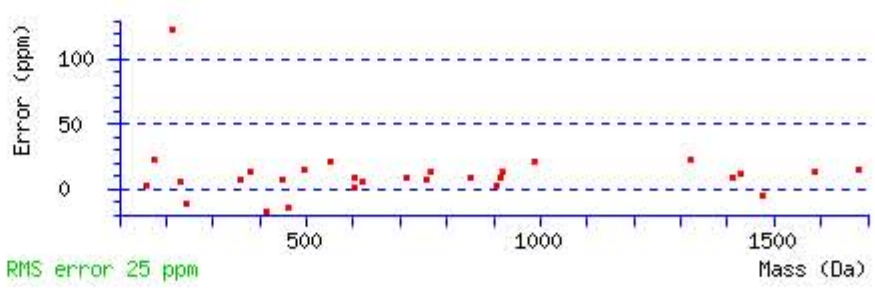
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1940.865540
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 52 **Expect:** 5.5e-005
**Matches** : 29/148 fragment ions using 60 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 15 |
| 2 | **243.133933** | 122.070605 | | | 225.123368 | 113.065322 | E | 1828.788737 | 914.898006 | 1811.762188 | 906.384732 | 1810.778172 | 905.892724 | 14 |
| 3 | **358.160876** | 179.584076 | | | 340.150311 | 170.578794 | D | 1699.746144 | 850.376710 | 1682.719595 | 841.863435 | 1681.735579 | 841.371427 | 13 |
| 4 | **415.182340** | 208.094808 | | | 397.171775 | 199.089526 | G | *1584.719201* | 792.863238 | 1567.692652 | 784.349964 | 1566.708636 | 783.857956 | 12 |
| 5 | 514.250754 | 257.629015 | | | 496.240189 | 248.623733 | V | 1527.697737 | 764.352506 | 1510.671188 | 755.839232 | 1509.687172 | 755.347224 | 11 |
| 6 | 953.476080 | 477.241678 | 936.449531 | 468.728404 | 935.465515 | 468.236396 | Q | *1428.629323* | 714.818299 | 1411.602774 | 706.305025 | 1410.618758 | 705.813017 | 10 |
| 7 | 1024.513194 | 512.760235 | 1007.486645 | 504.246960 | 1006.502629 | 503.754952 | A | *989.403997* | 495.205636 | 972.377448 | 486.692362 | 971.393432 | 486.200354 | 9 |
| 8 | 1184.543843 | 592.775559 | 1167.517294 | 584.262285 | 1166.533278 | 583.770277 | C | *918.366883* | 459.687079 | 901.340334 | 451.173805 | 900.356318 | 450.681797 | 8 |
| 9 | **1321.602755** | 661.305015 | 1304.576206 | 652.791741 | 1303.592190 | 652.299733 | H | *758.336234* | 379.671755 | 741.309685 | 371.158480 | 740.325669 | 370.666472 | 7 |
| 10 | 1392.639869 | 696.823572 | 1375.613320 | 688.310298 | 1374.629304 | 687.818290 | A | *621.277322* | 311.142299 | 604.250773 | 302.629024 | 603.266757 | 302.137016 | 6 |
| 11 | 1493.687548 | 747.347412 | 1476.660999 | 738.834138 | 1475.676983 | 738.342129 | T | *550.240208* | 275.623742 | 533.213659 | 267.110467 | 532.229643 | 266.618459 | 5 |
| 12 | 1550.709012 | 775.858144 | 1533.682463 | 767.344869 | 1532.698447 | 766.852861 | G | *449.192529* | 225.099902 | 432.165980 | 216.586628 | | | 4 |
| 13 | 1710.739661 | 855.873468 | 1693.713112 | 847.360194 | 1692.729096 | 846.868186 | C | 392.171065 | 196.589170 | 375.144516 | 188.075896 | | | 3 |
| 14 | 1767.761125 | 884.384200 | 1750.734576 | 875.870926 | 1749.750560 | 875.378918 | G | *232.140416* | 116.573846 | 215.113867 | 108.060571 | | | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.1 | 1940.865540 | 0.016062 | LEDGVQACHATGCGR |

**Mascot:** http://www.matrixscience.com/

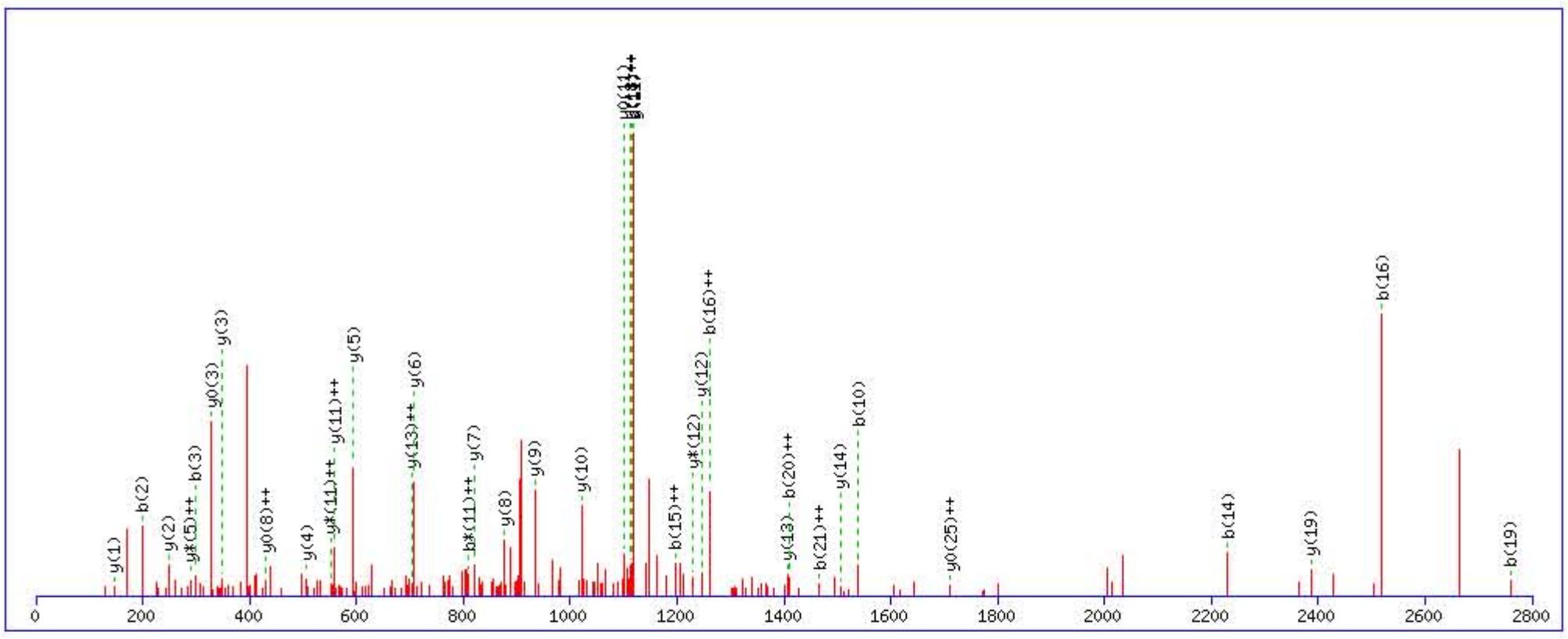
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VVVCQEHSCKPGQVCQPSGGILSCVTK**
Found in **FCGBP_HUMAN**, IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3

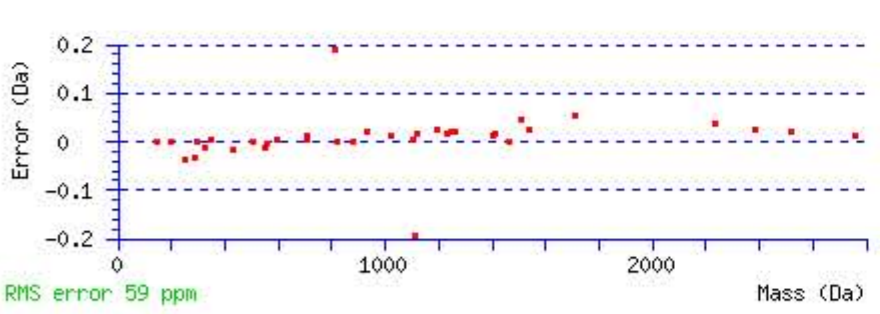
Match to Query 66866: 3635.807736 from(909.959210,4+) rtinseconds(2001) index(34298)
Title: Locus:1.1.1.805.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

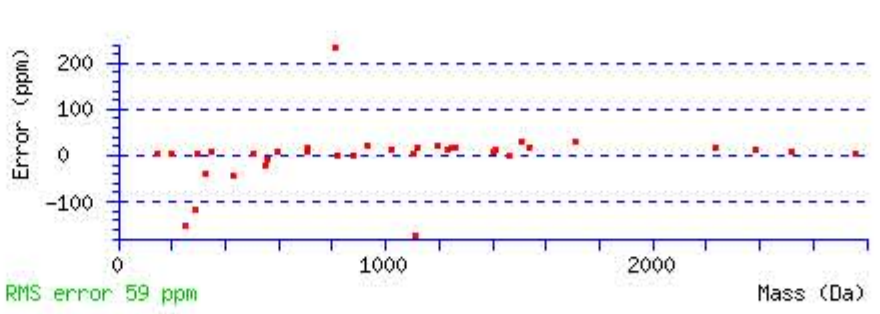
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3635.757751
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 46 **Expect:** 0.00054
**Matches :** 37/292 fragment ions using 105 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 27 |
| 2 | **199.144104** | 100.075690 | | | | | V | 3537.696565 | 1769.351920 | 3520.670016 | 1760.838646 | 3519.686000 | 1760.346638 | 26 |
| 3 | **298.212518** | 149.609897 | | | | | V | 3438.628151 | 1719.817713 | 3421.601602 | 1711.304439 | 3420.617586 | 1710.812431 | 25 |
| 4 | 458.243167 | 229.625222 | | | | | C | 3339.559737 | 1670.283506 | 3322.533188 | 1661.770232 | 3321.549172 | 1661.278224 | 24 |
| 5 | 897.468493 | 449.237885 | 880.441944 | 440.724610 | | | Q | 3179.529088 | 1590.268182 | 3162.502539 | 1581.754907 | 3161.518523 | 1581.262899 | 23 |
| 6 | 1026.511086 | 513.759181 | 1009.484537 | 505.245907 | 1008.500521 | 504.753899 | E | 2740.303762 | 1370.655519 | 2723.277213 | 1362.142244 | 2722.293197 | 1361.650236 | 22 |
| 7 | 1163.569998 | 582.288637 | 1146.543449 | 573.775363 | 1145.559433 | 573.283355 | H | 2611.261169 | 1306.134222 | 2594.234620 | 1297.620948 | 2593.250604 | 1297.128940 | 21 |
| 8 | 1250.602026 | 625.804651 | 1233.575477 | 617.291377 | 1232.591461 | 616.799369 | S | 2474.202257 | 1237.604766 | 2457.175708 | 1229.091492 | 2456.191692 | 1228.599484 | 20 |
| 9 | 1410.632675 | 705.819976 | 1393.606126 | 697.306701 | 1392.622110 | 696.814693 | C | *2387.170229* | 1194.088752 | 2370.143680 | 1185.575478 | 2369.159664 | 1185.083470 | 19 |
| 10 | **1538.727638** | 769.867457 | 1521.701089 | 761.354183 | 1520.717073 | 760.862175 | K | 2227.139580 | 1114.073428 | 2210.113031 | 1105.560153 | 2209.129015 | 1105.068145 | 18 |
| 11 | 1635.780402 | 818.393839 | 1618.753853 | 809.880565 | 1617.769837 | 809.388557 | P | 2099.044617 | 1050.025946 | 2082.018068 | 1041.512672 | 2081.034052 | 1041.020664 | 17 |
| 12 | 1692.801866 | 846.904571 | 1675.775317 | 838.391297 | 1674.791301 | 837.899289 | G | 2001.991853 | 1001.499564 | 1984.965304 | 992.986290 | 1983.981288 | 992.494282 | 16 |
| 13 | 2132.027192 | 1066.517234 | 2115.000643 | 1058.003959 | 2114.016627 | 1057.511951 | Q | 1944.970389 | 972.988832 | 1927.943840 | 964.475558 | 1926.959824 | 963.983550 | 15 |
| 14 | **2231.095606** | **1116.051441** | 2214.069057 | 1107.538166 | 2213.085041 | 1107.046158 | V | *1505.745063* | 753.376169 | 1488.718514 | 744.862895 | 1487.734498 | 744.370887 | 14 |
| 15 | 2391.126255 | **1196.066765** | 2374.099706 | 1187.553491 | 2373.115690 | 1187.061483 | C | *1406.676649* | 703.841962 | 1389.650100 | 695.328688 | 1388.666084 | 694.836680 | 13 |
| 16 | **2519.184833** | **1260.096054** | 2502.158284 | 1251.582780 | 2501.174268 | 1251.090772 | Q | *1246.646000* | 623.826638 | 1229.619451 | 615.313364 | 1228.635435 | 614.821355 | 12 |
| 17 | 2616.237597 | 1308.622436 | 2599.211048 | 1300.109162 | 2598.227032 | 1299.617154 | P | *1118.587422* | 559.797349 | 1101.560873 | 551.284074 | 1100.576857 | 550.792066 | 11 |
| 18 | 2703.269625 | 1352.138450 | 2686.243076 | 1343.625176 | 2685.259060 | 1343.133168 | S | *1021.534658* | 511.270967 | 1004.508109 | 502.757692 | 1003.524093 | 502.265684 | 10 |
| 19 | **2760.291089** | 1380.649182 | 2743.264540 | 1372.135908 | 2742.280524 | 1371.643900 | G | *934.502630* | 467.754953 | 917.476081 | 459.241678 | 916.492065 | 458.749670 | 9 |
| 20 | 2817.312553 | **1409.159914** | 2800.286004 | 1400.646640 | 2799.301988 | 1400.154632 | G | *877.481166* | 439.244221 | 860.454617 | 430.730946 | 859.470601 | 430.238938 | 8 |
| 21 | 2930.396617 | **1465.701946** | 2913.370068 | 1457.188672 | 2912.386052 | 1456.696664 | I | *820.459702* | 410.733489 | 803.433153 | 402.220214 | 802.449137 | 401.728206 | 7 |
| 22 | 3043.480681 | 1522.243978 | 3026.454132 | 1513.730704 | 3025.470116 | 1513.238696 | L | *707.375638* | 354.191457 | 690.349089 | 345.678182 | 689.365073 | 345.186174 | 6 |
| 23 | 3130.512709 | 1565.759993 | 3113.486160 | 1557.246718 | 3112.502144 | 1556.754710 | S | *594.291574* | 297.649425 | 577.265025 | 289.136150 | 576.281009 | 288.644142 | 5 |
| 24 | 3290.543358 | 1645.775317 | 3273.516809 | 1637.262042 | 3272.532793 | 1636.770034 | C | *507.259546* | 254.133411 | 490.232997 | 245.620136 | 489.248981 | 245.128128 | 4 |
| 25 | 3389.611772 | 1695.309524 | 3372.585223 | 1686.796249 | 3371.601207 | 1686.304241 | V | *347.228897* | 174.118086 | 330.202348 | 165.604812 | 329.218332 | 165.112804 | 3 |
| 26 | 3490.659451 | 1745.833363 | 3473.632902 | 1737.320089 | 3472.648886 | 1736.828081 | T | *248.160483* | 124.583879 | 231.133934 | 116.070605 | 230.149918 | 115.578597 | 2 |
| 27 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 46.5 | 3635.757751 | 0.049985 | VVVCQEHSCKPGQVCQPSGGILSCVTK |
| 28.5 | 3635.757751 | 0.049985 | VVVCQEHSCKPGQVCQPSGGILSCVTK |
| 19.4 | 3635.757751 | 0.049985 | VVVCQEHSCKPGQVCQPSGGILSCVTK |

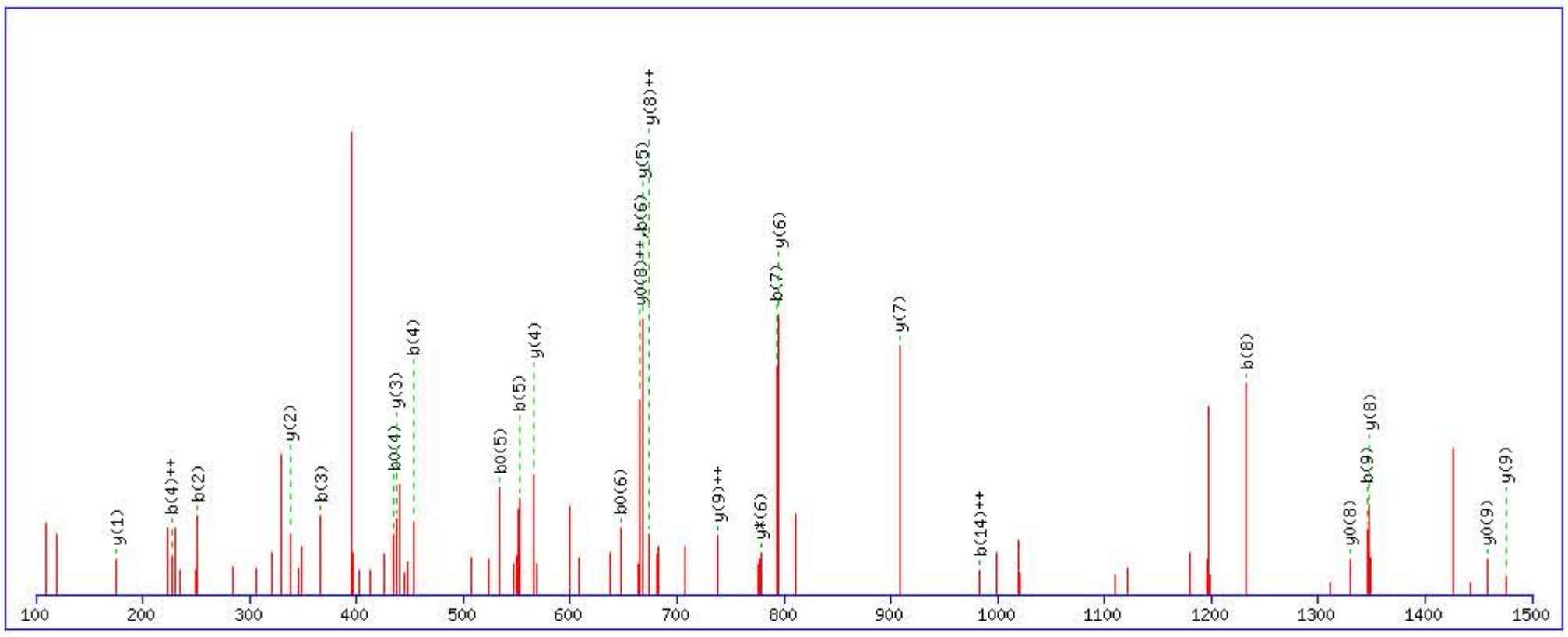
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HLDSVLQQLQTEVYR**
Found in **IBP6_HUMAN**, Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1

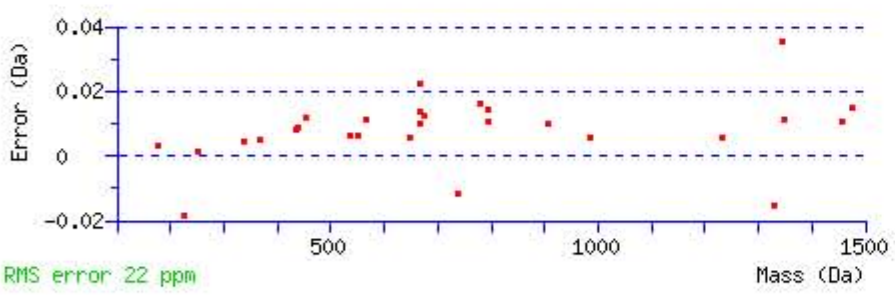
Match to Query 47255: 2139.136032 from(714.052620,3+) rtinseconds(2580) index(69703)
Title: Locus:1.1.1.2174.8 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

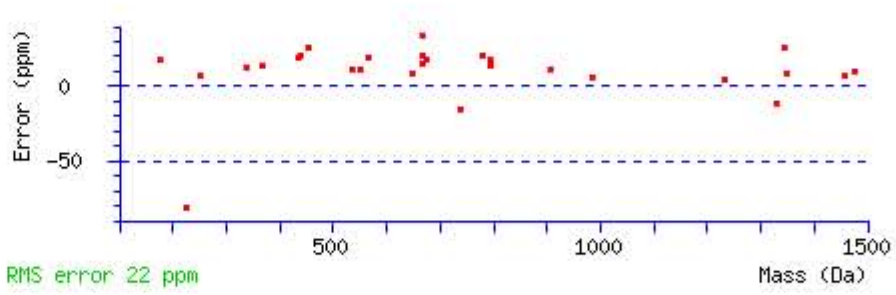
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2139.114655
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 3.6e-006
**Matches :** 28/146 fragment ions using 47 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 15 |
| 2 | *251.150252* | 126.078764 | | | | | L | 2003.063026 | 1002.035151 | 1986.036477 | 993.521877 | 1985.052461 | 993.029869 | 14 |
| 3 | *366.177195* | 183.592235 | | | 348.166630 | 174.586953 | D | 1889.978962 | 945.493119 | 1872.952413 | 936.979845 | 1871.968397 | 936.487836 | 13 |
| 4 | *453.209223* | 227.108250 | | | 435.198658 | 218.102967 | S | 1774.952019 | 887.979648 | 1757.925470 | 879.466373 | 1756.941454 | 878.974365 | 12 |
| 5 | *552.277637* | 276.642457 | | | 534.267072 | 267.637174 | V | 1687.919991 | 844.463634 | 1670.893442 | 835.950359 | 1669.909426 | 835.458351 | 11 |
| 6 | *665.361701* | 333.184489 | | | 647.351136 | 324.179206 | L | 1588.851577 | 794.929427 | 1571.825028 | 786.416152 | 1570.841012 | 785.924144 | 10 |
| 7 | *793.420279* | 397.213778 | 776.393730 | 388.700503 | 775.409714 | 388.208495 | Q | *1475.767513* | 738.387395 | 1458.740964 | 729.874120 | 1457.756948 | 729.382112 | 9 |
| 8 | *1232.645605* | 616.826440 | 1215.619056 | 608.313166 | 1214.635040 | 607.821158 | Q | *1347.708935* | 674.358105 | 1330.682386 | 665.844831 | 1329.698370 | 665.352823 | 8 |
| 9 | *1345.729669* | 673.368472 | 1328.703120 | 664.855198 | 1327.719104 | 664.363190 | L | *908.483609* | 454.745443 | 891.457060 | 446.232168 | 890.473044 | 445.740160 | 7 |
| 10 | 1473.788247 | 737.397761 | 1456.761698 | 728.884487 | 1455.777682 | 728.392479 | Q | *795.399545* | 398.203411 | 778.372996 | 389.690136 | 777.388980 | 389.198128 | 6 |
| 11 | 1574.835926 | 787.921601 | 1557.809377 | 779.408326 | 1556.825361 | 778.916318 | T | *667.340967* | 334.174122 | 650.314418 | 325.660847 | 649.330402 | 325.168839 | 5 |
| 12 | 1703.878519 | 852.442897 | 1686.851970 | 843.929623 | 1685.867954 | 843.437615 | E | *566.293288* | 283.650282 | 549.266739 | 275.137008 | 548.282723 | 274.645000 | 4 |
| 13 | 1802.946933 | 901.977104 | 1785.920384 | 893.463830 | 1784.936368 | 892.971822 | V | *437.250695* | 219.128986 | 420.224146 | 210.615711 | | | 3 |
| 14 | 1966.010262 | **983.508769** | 1948.983713 | 974.995494 | 1947.999697 | 974.503486 | Y | *338.182281* | 169.594779 | 321.155732 | 161.081504 | | | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 59.1 | 2139.114655 | 0.021377 | HLDSVLQQLQTEVYR |
| 43.9 | 2139.114655 | 0.021377 | HLDSVLQQLQTEVYR |
| 33.6 | 2139.114655 | 0.021377 | HLDSVLQQLQTEVYR |
| 1.0 | 2139.122025 | 0.014007 | FNVETMAQLLNIPPNK |

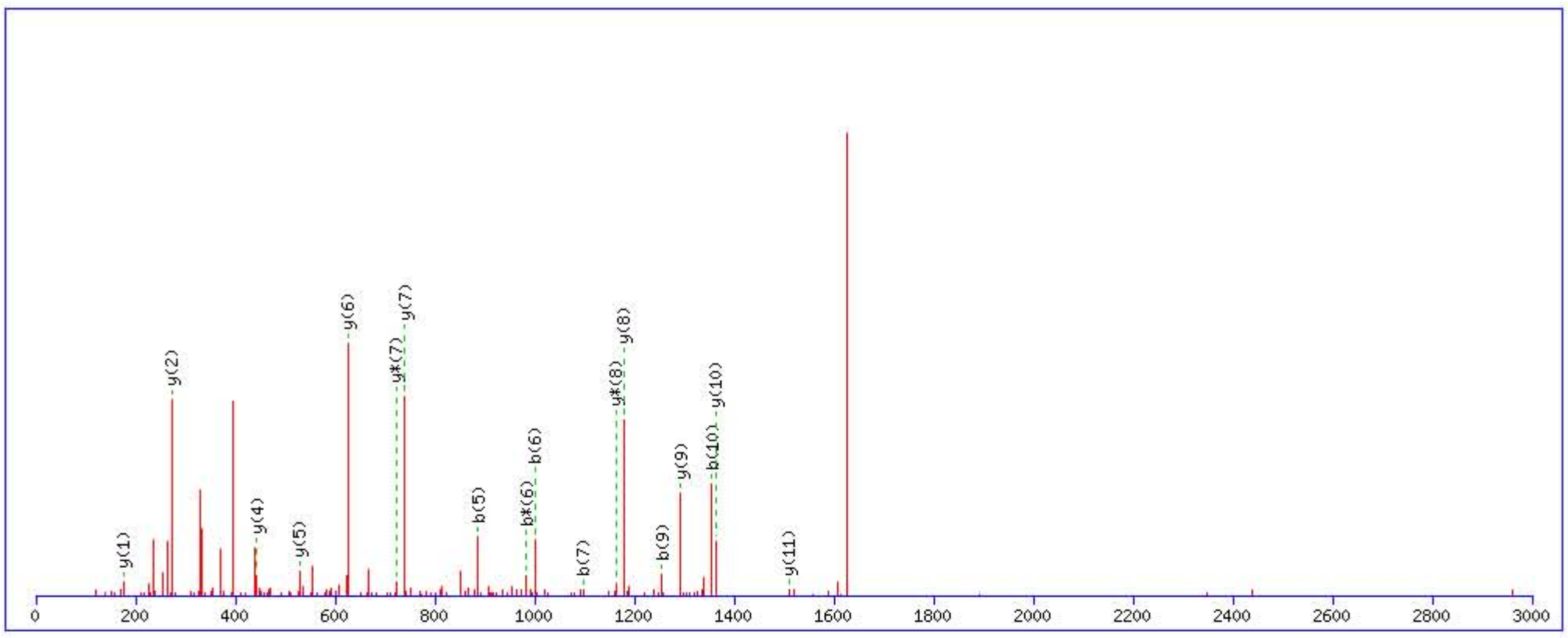
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DFALQNPSAVPR**
Found in **ALS_HUMAN**, Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

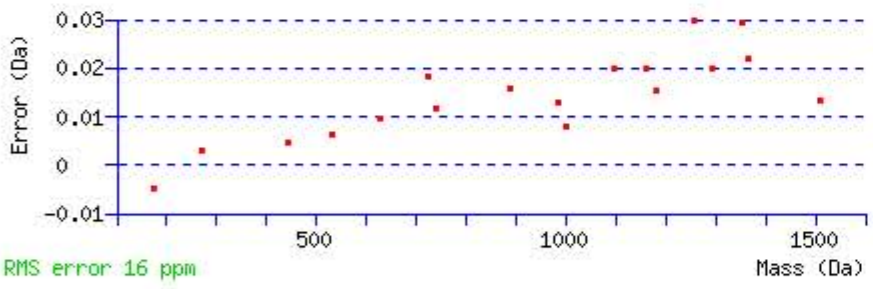
Match to Query 35734: 1624.860088 from(813.437320,2+) rtinseconds(2179) index(35361)
Title: Locus:1.1.1.867.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

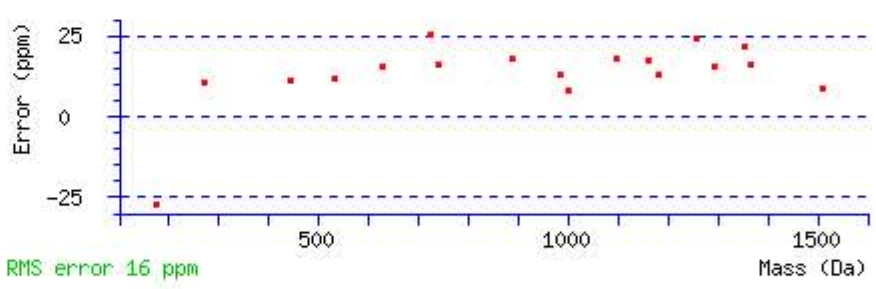
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1624.839539
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 79 **Expect:** 3.2e-007
**Matches :** 18/116 fragment ions using 29 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 12 |
| 2 | 263.102633 | 132.054954 | | | 245.092068 | 123.049672 | F | *1510.819881* | 755.913579 | 1493.793332 | 747.400304 | 1492.809316 | 746.908296 | 11 |
| 3 | 334.139747 | 167.573512 | | | 316.129182 | 158.568229 | A | *1363.751467* | 682.379372 | 1346.724918 | 673.866097 | 1345.740902 | 673.374089 | 10 |
| 4 | 447.223811 | 224.115544 | | | 429.213246 | 215.110261 | L | *1292.714353* | 646.860815 | 1275.687804 | 638.347540 | 1274.703788 | 637.855532 | 9 |
| 5 | **886.449137** | 443.728207 | 869.422588 | 435.214932 | 868.438572 | 434.722924 | Q | *1179.630289* | 590.318783 | 1162.603740 | 581.805508 | 1161.619724 | 581.313500 | 8 |
| 6 | **1000.492064** | 500.749670 | 983.465515 | 492.236396 | 982.481499 | 491.744388 | N | *740.404963* | 370.706120 | 723.378414 | 362.192845 | 722.394398 | 361.700837 | 7 |
| 7 | **1097.544828** | 549.276052 | 1080.518279 | 540.762778 | 1079.534263 | 540.270770 | P | *626.362036* | 313.684656 | 609.335487 | 305.171382 | 608.351471 | 304.679374 | 6 |
| 8 | 1184.576856 | 592.792066 | 1167.550307 | 584.278792 | 1166.566291 | 583.786784 | S | *529.309272* | 265.158274 | 512.282723 | 256.645000 | 511.298707 | 256.152992 | 5 |
| 9 | **1255.613970** | 628.310623 | 1238.587421 | 619.797349 | 1237.603405 | 619.305341 | A | *442.277244* | 221.642260 | 425.250695 | 213.128986 | | | 4 |
| 10 | **1354.682384** | 677.844830 | 1337.655835 | 669.331556 | 1336.671819 | 668.839548 | V | 371.240130 | 186.123703 | 354.213581 | 177.610429 | | | 3 |
| 11 | 1451.735148 | 726.371212 | 1434.708599 | 717.857938 | 1433.724583 | 717.365930 | P | *272.171716* | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 12 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 78.9 | 1624.839539 | 0.020549 | DFALQNPSAVPR |
| 18.8 | 1624.860672 | -0.000584 | VGDCVIIENPLIQR |
| 12.1 | 1624.853271 | 0.006817 | ASDPVRTGSEGLALPR |
| 7.7 | 1624.864471 | -0.004383 | RELRSQETPEKPR |
| 6.6 | 1624.871887 | -0.011799 | RTSSEQAVALPR |
| 3.2 | 1624.875916 | -0.015828 | QWLEATIQLGR |
| 1.5 | 1624.854813 | 0.005275 | QWVAAGGHITFK |
| 1.2 | 1624.839554 | 0.020534 | DRNFLFVGVMTAQK |
| 0.7 | 1624.850296 | 0.009792 | QQLQMEVK |

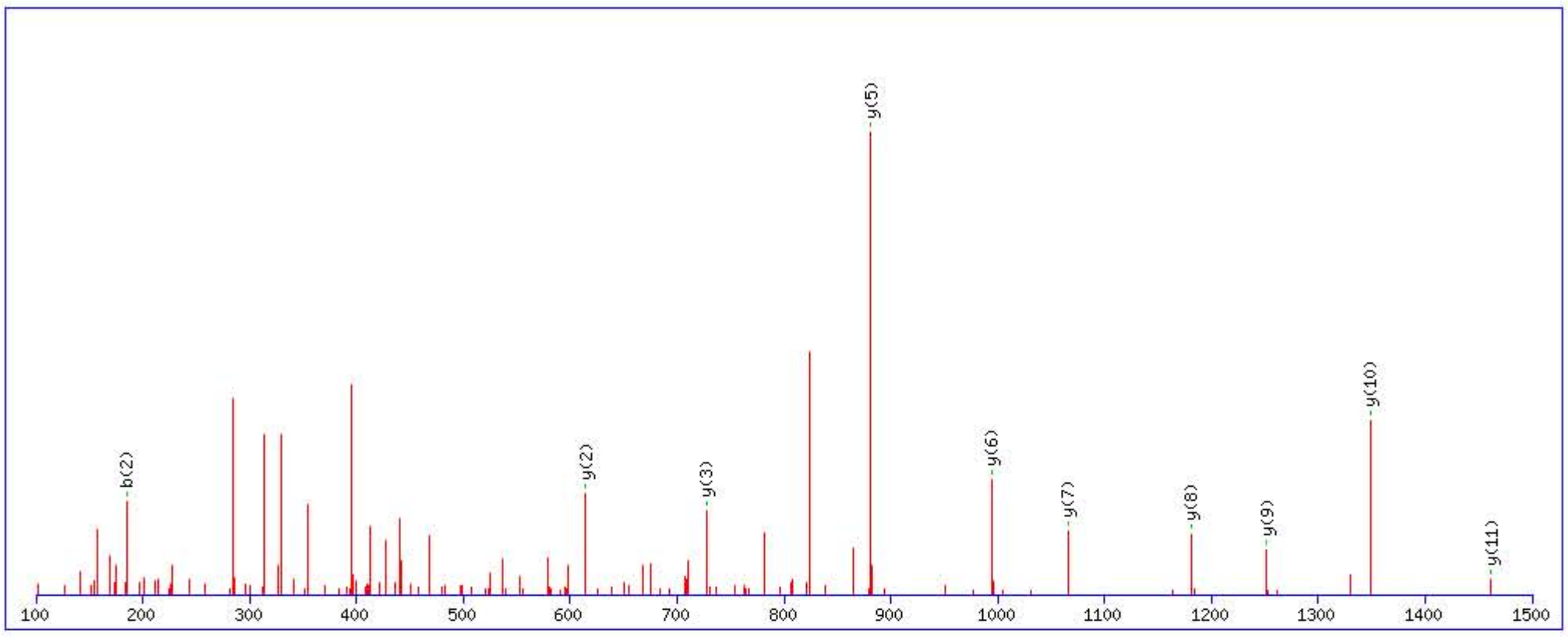
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LAELPADALGPLQR**
Found in **ALS_HUMAN**, Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

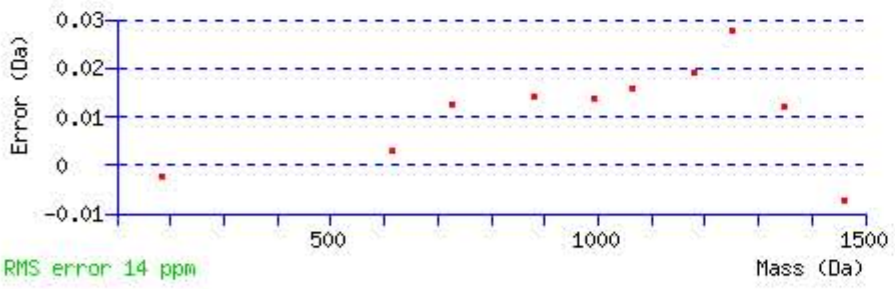
Match to Query 39764: 1773.998472 from(592.340100,3+) rtinseconds(2466) index(22911)
Title: Locus:1.1.1.3241.2 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

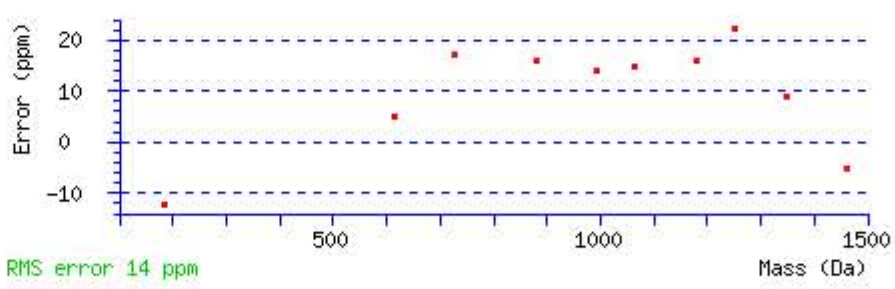
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1773.981094
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 73 **Expect:** 3.1e-007
**Matches :** 10/114 fragment ions using 14 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 14 |
| 2 | **185.128454** | 93.067865 | | | | | A | 1661.904340 | 831.455808 | 1644.877791 | 822.942534 | 1643.893775 | 822.450526 | 13 |
| 3 | 314.171047 | 157.589161 | | | 296.160482 | 148.583879 | E | 1590.867226 | 795.937251 | 1573.840677 | 787.423977 | 1572.856661 | 786.931969 | 12 |
| 4 | 427.255111 | 214.131193 | | | 409.244546 | 205.125911 | L | *1461.824633* | 731.415955 | 1444.798084 | 722.902680 | 1443.814068 | 722.410672 | 11 |
| 5 | 524.307875 | 262.657576 | | | 506.297310 | 253.652293 | P | *1348.740569* | 674.873922 | 1331.714020 | 666.360648 | 1330.730004 | 665.868640 | 10 |
| 6 | 595.344989 | 298.176133 | | | 577.334424 | 289.170850 | A | *1251.687805* | 626.347540 | 1234.661256 | 617.834266 | 1233.677240 | 617.342258 | 9 |
| 7 | 710.371932 | 355.689604 | | | 692.361367 | 346.684322 | D | *1180.650691* | 590.828984 | 1163.624142 | 582.315709 | 1162.640126 | 581.823701 | 8 |
| 8 | 781.409046 | 391.208161 | | | 763.398481 | 382.202879 | A | *1065.623748* | 533.315512 | 1048.597199 | 524.802238 | | | 7 |
| 9 | 894.493110 | 447.750193 | | | 876.482545 | 438.744911 | L | *994.586634* | 497.796955 | 977.560085 | 489.283681 | | | 6 |
| 10 | 951.514574 | 476.260925 | | | 933.504009 | 467.255643 | G | *881.502570* | 441.254923 | 864.476021 | 432.741649 | | | 5 |
| 11 | 1048.567338 | 524.787307 | | | 1030.556773 | 515.782025 | P | 824.481106 | 412.744191 | 807.454557 | 404.230916 | | | 4 |
| 12 | 1161.651402 | 581.329339 | | | 1143.640837 | 572.324056 | L | *727.428342* | 364.217809 | 710.401793 | 355.704534 | | | 3 |
| 13 | 1600.876728 | 800.942002 | 1583.850179 | 792.428728 | 1582.866163 | 791.936719 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 14 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 72.5 | 1773.981094 | 0.017378 | LAELPADALGPLQR |
| 3.0 | 1774.014099 | -0.015627 | LLLQEALWPEGKLHK |

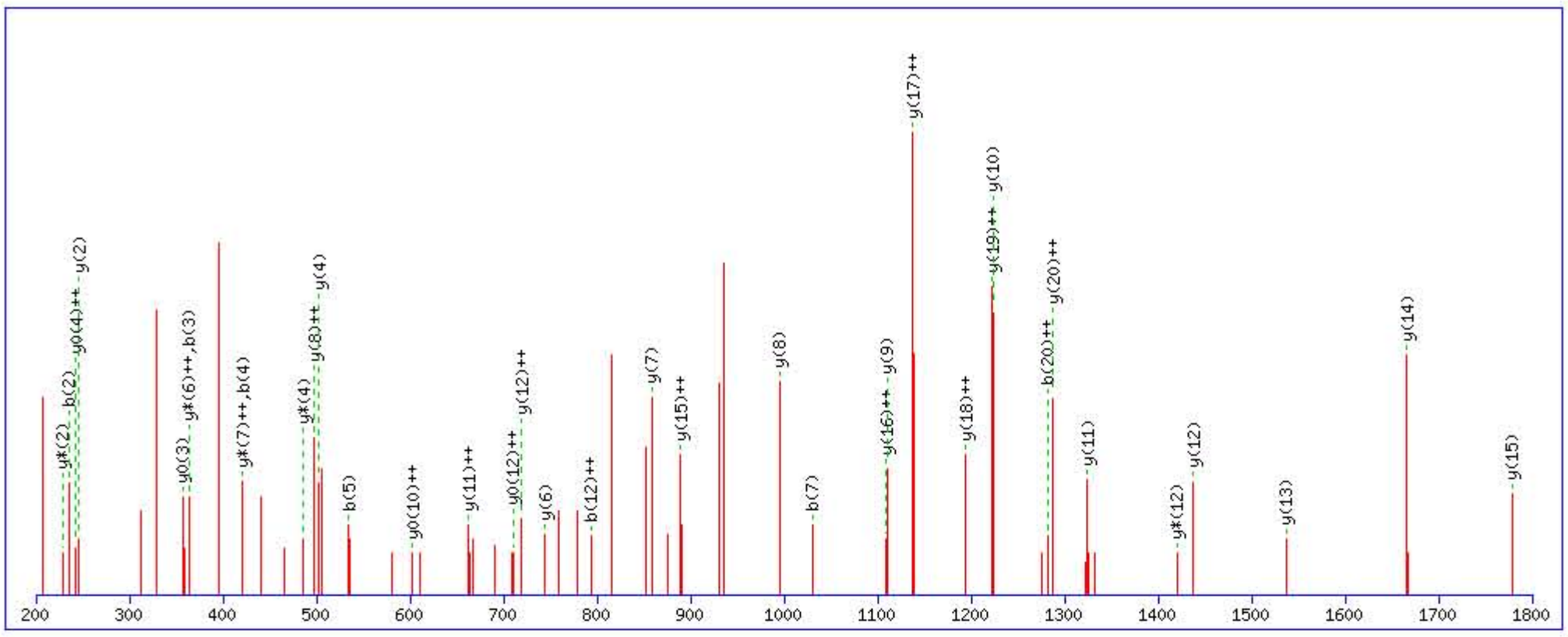
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SFEGLGQLEVLTLDHNQLQEVK**
Found in **ALS_HUMAN**, Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

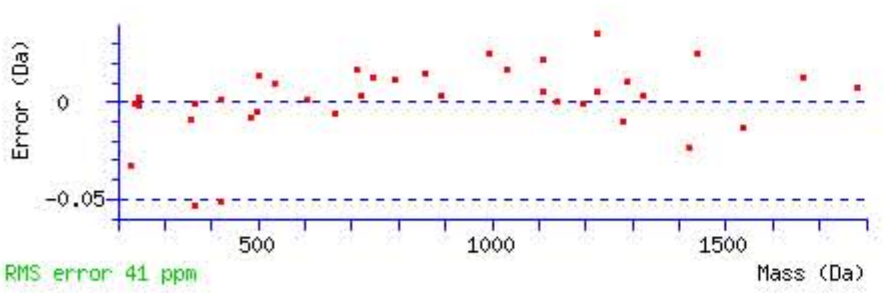
Match to Query 57684: 2807.477142 from(936.832990,3+) rtinseconds(2709) index(9409)
Title: Locus:1.1.1.2220.24 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

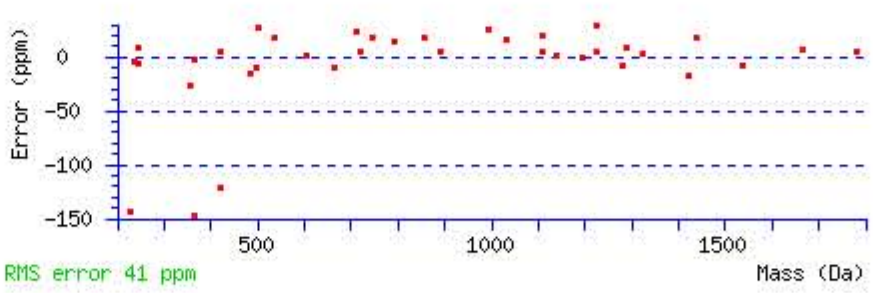
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2807.452759
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 65 **Expect:** 6.8e-006
**Matches :** 37/236 fragment ions using 69 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 22 |
| 2 | **235.107718** | 118.057497 | | | 217.097153 | 109.052214 | F | 2721.428016 | 1361.217646 | 2704.401467 | 1352.704371 | 2703.417451 | 1352.212363 | 21 |
| 3 | **364.150311** | 182.578793 | | | 346.139746 | 173.573511 | E | 2574.359602 | 1287.683439 | 2557.333053 | 1279.170164 | 2556.349037 | 1278.678156 | 20 |
| 4 | **421.171775** | 211.089525 | | | 403.161210 | 202.084243 | G | 2445.317009 | 1223.162142 | 2428.290460 | 1214.648868 | 2427.306444 | 1214.156860 | 19 |
| 5 | **534.255839** | 267.631558 | | | 516.245274 | 258.626275 | L | 2388.295545 | 1194.651410 | 2371.268996 | 1186.138136 | 2370.284980 | 1185.646128 | 18 |
| 6 | 591.277303 | 296.142290 | | | 573.266738 | 287.137007 | G | 2275.211481 | 1138.109378 | 2258.184932 | 1129.596104 | 2257.200916 | 1129.104096 | 17 |
| 7 | **1030.502629** | 515.754953 | 1013.476080 | 507.241678 | 1012.492064 | 506.749670 | Q | 2218.190017 | 1109.598646 | 2201.163468 | 1101.085372 | 2200.179452 | 1100.593364 | 16 |
| 8 | 1143.586693 | 572.296985 | 1126.560144 | 563.783710 | 1125.576128 | 563.291702 | L | *1778.964691* | 889.985984 | 1761.938142 | 881.472709 | 1760.954126 | 880.980701 | 15 |
| 9 | 1272.629286 | 636.818281 | 1255.602737 | 628.305007 | 1254.618721 | 627.812999 | E | *1665.880627* | 833.443952 | 1648.854078 | 824.930677 | 1647.870062 | 824.438669 | 14 |
| 10 | 1371.697700 | 686.352488 | 1354.671151 | 677.839214 | 1353.687135 | 677.347206 | V | *1536.838034* | 768.922655 | 1519.811485 | 760.409381 | 1518.827469 | 759.917373 | 13 |
| 11 | 1484.781764 | 742.894520 | 1467.755215 | 734.381246 | 1466.771199 | 733.889238 | L | *1437.769620* | 719.388448 | 1420.743071 | 710.875174 | 1419.759055 | 710.383166 | 12 |
| 12 | 1585.829443 | **793.418360** | 1568.802894 | 784.905085 | 1567.818878 | 784.413077 | T | *1324.685556* | 662.846416 | 1307.659007 | 654.333142 | 1306.674991 | 653.841134 | 11 |
| 13 | 1698.913507 | 849.960392 | 1681.886958 | 841.447117 | 1680.902942 | 840.955109 | L | *1223.637877* | 612.322577 | 1206.611328 | 603.809302 | 1205.627312 | 603.317294 | 10 |
| 14 | 1813.940450 | 907.473863 | 1796.913901 | 898.960589 | 1795.929885 | 898.468581 | D | *1110.553813* | 555.780545 | 1093.527264 | 547.267270 | 1092.543248 | 546.775262 | 9 |
| 15 | 1950.999362 | 976.003319 | 1933.972813 | 967.490045 | 1932.988797 | 966.998037 | H | *995.526870* | 498.267073 | 978.500321 | 489.753799 | 977.516305 | 489.261791 | 8 |
| 16 | 2065.042289 | 1033.024782 | 2048.015740 | 1024.511508 | 2047.031724 | 1024.019500 | N | *858.467958* | 429.737617 | 841.441409 | 421.224343 | 840.457393 | 420.732335 | 7 |
| 17 | 2193.100867 | 1097.054072 | 2176.074318 | 1088.540797 | 2175.090302 | 1088.048789 | Q | *744.425031* | 372.716154 | 727.398482 | 364.202879 | 726.414466 | 363.710871 | 6 |
| 18 | 2306.184931 | 1153.596104 | 2289.158382 | 1145.082829 | 2288.174366 | 1144.590821 | L | 616.366453 | 308.686865 | 599.339904 | 300.173590 | 598.355888 | 299.681582 | 5 |
| 19 | 2434.243509 | 1217.625393 | 2417.216960 | 1209.112118 | 2416.232944 | 1208.620110 | Q | *503.282389* | 252.144833 | 486.255840 | 243.631558 | 485.271824 | 243.139550 | 4 |
| 20 | 2563.286102 | **1282.146689** | 2546.259553 | 1273.633415 | 2545.275537 | 1273.141407 | E | 375.223811 | 188.115543 | 358.197262 | 179.602269 | 357.213246 | 179.110261 | 3 |
| 21 | 2662.354516 | 1331.680896 | 2645.327967 | 1323.167622 | 2644.343951 | 1322.675614 | V | *246.181218* | 123.594247 | 229.154669 | 115.080972 | | | 2 |
| 22 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 65.2 | 2807.452759 | 0.024383 | SFEGLGQLEVLTLDHNQLQEVK |
| 4.5 | 2807.452759 | 0.024383 | SFEGLGQLEVLTLDHNQLQEVK |
| 0.7 | 2807.452759 | 0.024383 | SFEGLGQLEVLTLDHNQLQEVK |

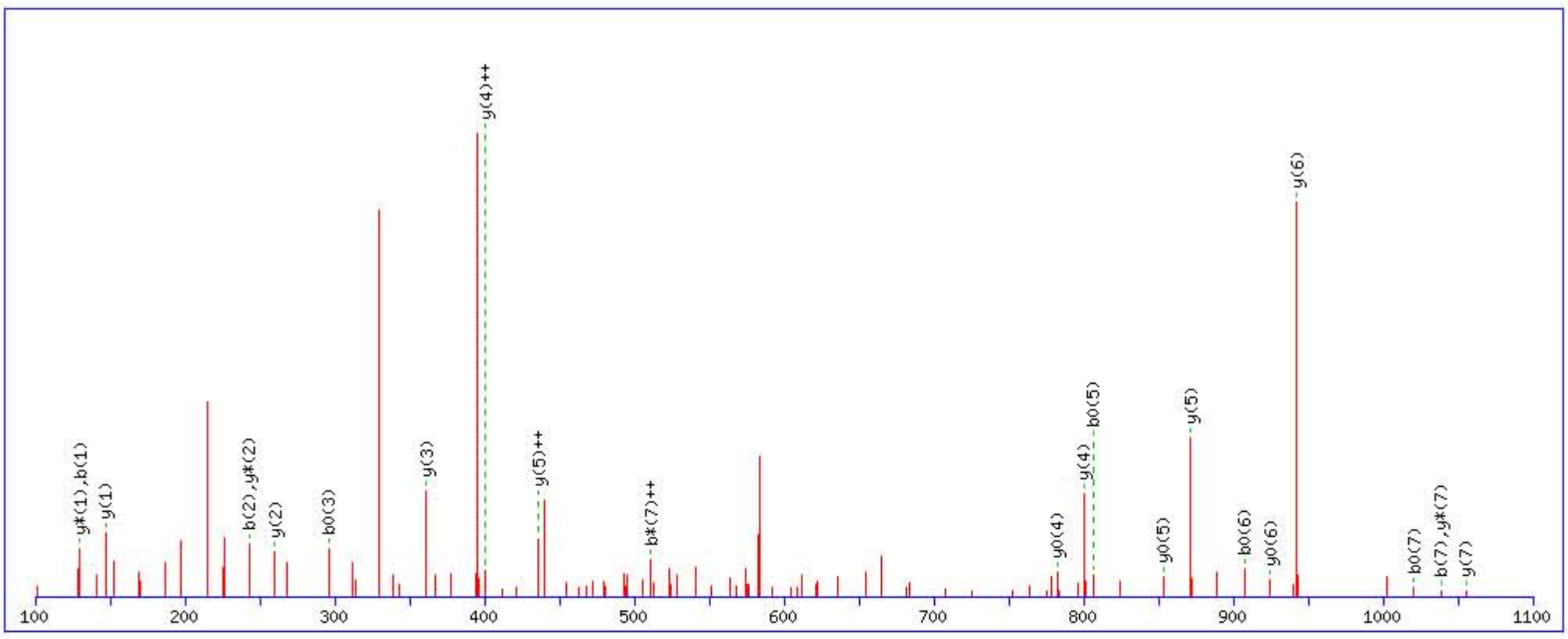
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ELAAQTIK**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

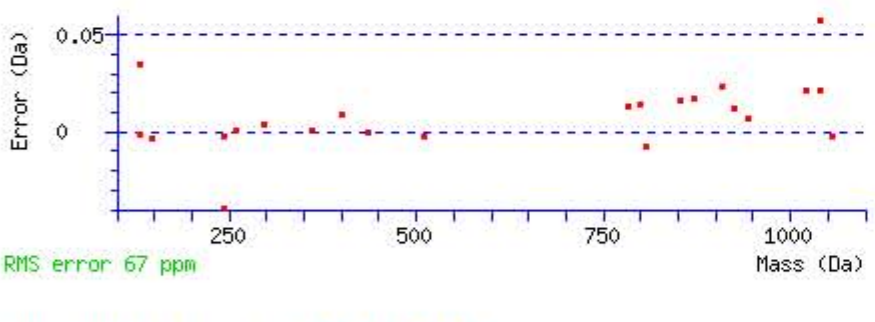
Match to Query 20131: 1183.669448 from(592.842000,2+) rtinseconds(1741) index(48562)
Title: Locus:1.1.1.1844.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

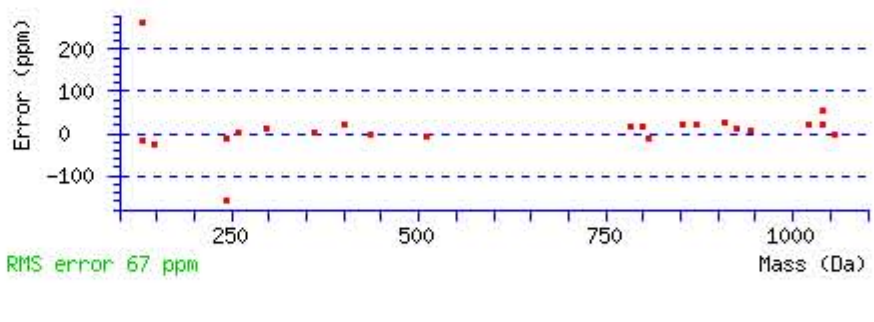
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1183.663452
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.015
**Matches :** 23/72 fragment ions using 49 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **130.049869** | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 8 |
| 2 | **243.133933** | 122.070605 | | | 225.123368 | 113.065322 | L | ***1055.628165*** | 528.317720 | 1038.601616 | 519.804446 | 1037.617600 | 519.312438 | 7 |
| 3 | 314.171047 | 157.589161 | | | 296.160482 | 148.583879 | A | ***942.544101*** | 471.775689 | 925.517552 | 463.262414 | 924.533536 | 462.770406 | 6 |
| 4 | 385.208161 | 193.107718 | | | 367.197596 | 184.102436 | A | ***871.506987*** | 436.257132 | 854.480438 | 427.743857 | 853.496422 | 427.251849 | 5 |
| 5 | 824.433487 | 412.720382 | 807.406938 | 404.207107 | 806.422922 | 403.715099 | Q | ***800.469873*** | 400.738575 | 783.443324 | 392.225300 | 782.459308 | 391.733292 | 4 |
| 6 | 925.481166 | 463.244221 | 908.454617 | 454.730947 | 907.470601 | 454.238939 | T | ***361.244547*** | 181.125911 | 344.217998 | 172.612637 | 343.233982 | 172.120629 | 3 |
| 7 | **1038.565230** | 519.786253 | 1021.538681 | 511.272978 | 1020.554665 | 510.780970 | I | ***260.196868*** | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 8 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.3 | 1183.663452 | 0.005996 | ELAAQTIK |
| 27.1 | 1183.663452 | 0.005996 | ELAAQITK |
| 8.0 | 1183.681198 | -0.011750 | LEALLEAAGIGK |
| 6.3 | 1183.660080 | 0.009368 | AIEAVAISPWK |
| 6.3 | 1183.667282 | 0.002166 | GKQASEPALRK |
| 5.5 | 1183.667297 | 0.002151 | EPTGRVEIRK |
| 5.0 | 1183.663452 | 0.005996 | LEQAATLK |
| 3.9 | 1183.667282 | 0.002166 | ELQRLQAAQK |
| 3.9 | 1183.674683 | -0.005235 | ELRQLSK |
| 3.3 | 1183.667282 | 0.002166 | QLLRALEEGR |

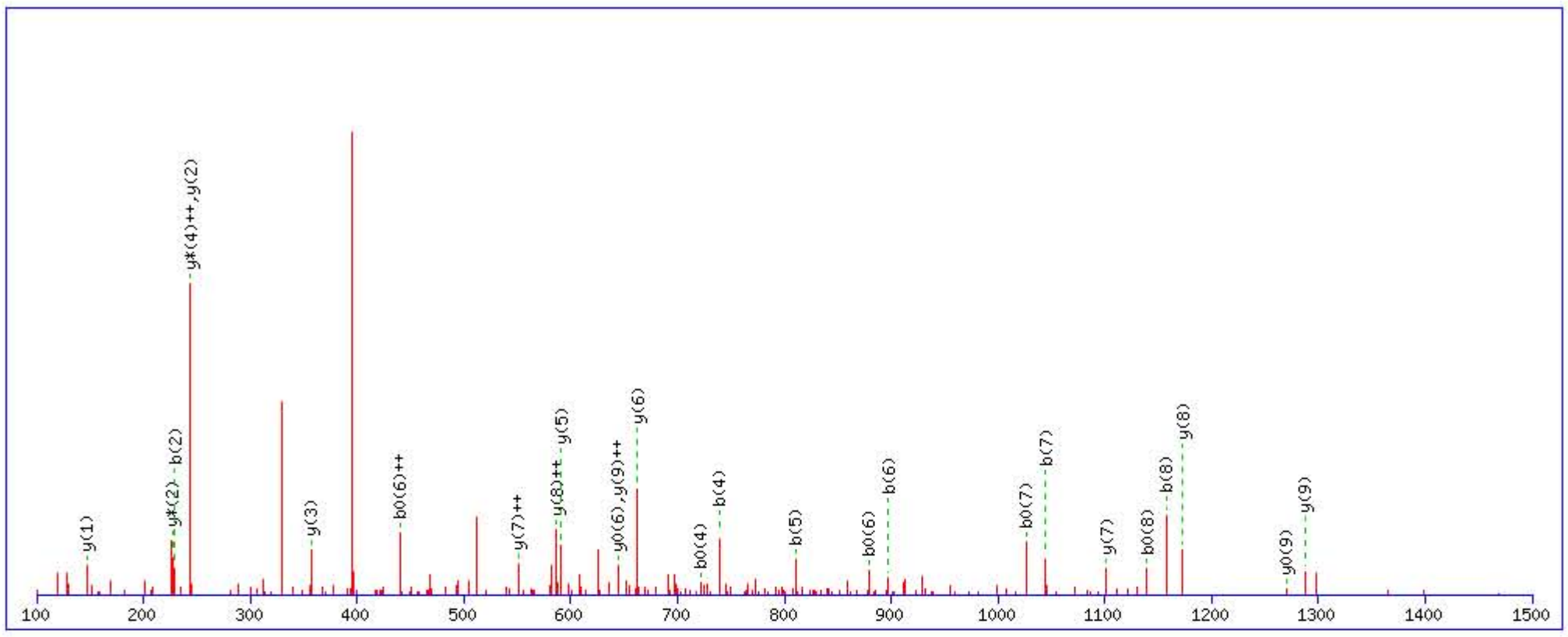
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LDAQASFLPK**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

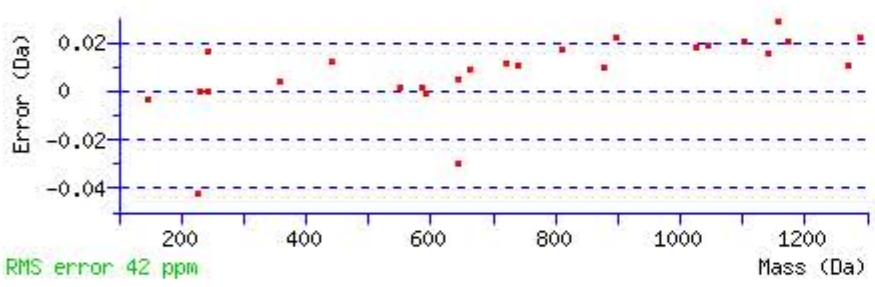
Match to Query 27298: 1399.770668 from(700.892610,2+) rtinseconds(2217) index(51780)
Title: Locus:1.1.1.2009.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

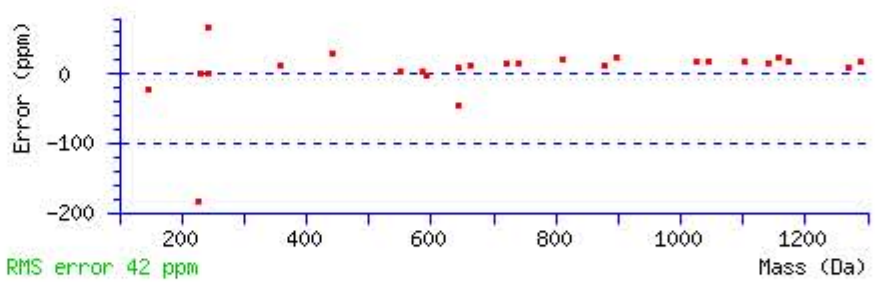
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1399.753342
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 42 **Expect:** 0.00041
**Matches :** 26/92 fragment ions using 49 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 10 |
| 2 | **229.118283** | 115.062779 | | | 211.107718 | 106.057497 | D | *1287.676571* | 644.341924 | 1270.650022 | 635.828649 | 1269.666006 | 635.336641 | 9 |
| 3 | 300.155397 | 150.581336 | | | 282.144832 | 141.576054 | A | *1172.649628* | 586.828452 | 1155.623079 | 578.315178 | 1154.639063 | 577.823169 | 8 |
| 4 | **739.380723** | 370.194000 | 722.354174 | 361.680725 | 721.370158 | 361.188717 | Q | *1101.612514* | 551.309895 | 1084.585965 | 542.796621 | 1083.601949 | 542.304612 | 7 |
| 5 | **810.417837** | 405.712557 | 793.391288 | 397.199282 | 792.407272 | 396.707274 | A | *662.387188* | 331.697232 | 645.360639 | 323.183957 | 644.376623 | 322.691949 | 6 |
| 6 | **897.449865** | 449.228570 | 880.423316 | 440.715296 | 879.439300 | 440.223288 | S | *591.350074* | 296.178675 | 574.323525 | 287.665400 | 573.339509 | 287.173392 | 5 |
| 7 | **1044.518279** | 522.762777 | 1027.491730 | 514.249503 | 1026.507714 | 513.757495 | F | 504.318046 | 252.662661 | 487.291497 | 244.149386 | | | 4 |
| 8 | **1157.602343** | 579.304809 | 1140.575794 | 570.791535 | 1139.591778 | 570.299527 | L | *357.249632* | 179.128454 | 340.223083 | 170.615179 | | | 3 |
| 9 | 1254.655107 | 627.831191 | 1237.628558 | 619.317917 | 1236.644542 | 618.825909 | P | *244.165568* | 122.586422 | 227.139019 | 114.073148 | | | 2 |
| 10 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 41.8 | 1399.753342 | 0.017326 | LDAQASFLPK |
| 5.3 | 1399.753342 | 0.017326 | LLDFAASQPK |
| 5.3 | 1399.755859 | 0.014809 | LSTPDTLTQISPK |
| 4.7 | 1399.755814 | 0.014854 | KTELGPLKEEEK |
| 3.6 | 1399.767059 | 0.003609 | EKAVTDEKPKQK |
| 2.2 | 1399.771973 | -0.001305 | IWQGMLTIK |
| 2.2 | 1399.756714 | 0.013954 | LSQVPMSALK |
| 2.1 | 1399.771103 | -0.000435 | QKEPSVLFEVPK |
| 1.7 | 1399.785660 | -0.014992 | LNENIKNAMLIK |
| 0.3 | 1399.772430 | -0.001762 | QHAFKQAFAKPK |

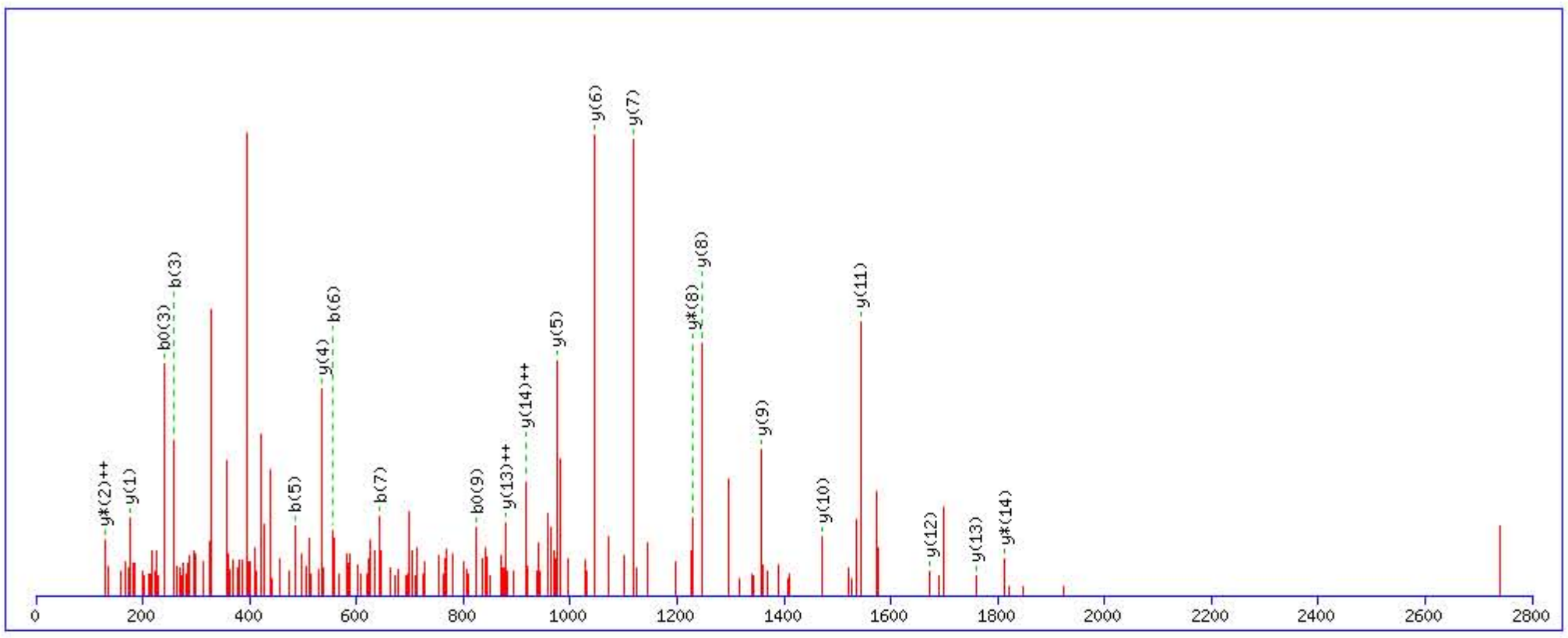
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GSLVQASEANLQAAQDFVR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

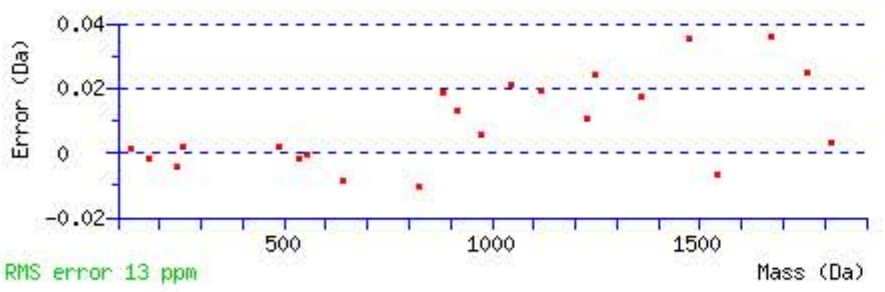
Match to Query 50766: 2314.198782 from(772.406870,3+) rtinseconds(2640) index(54213)
Title: Locus:1.1.1.2156.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

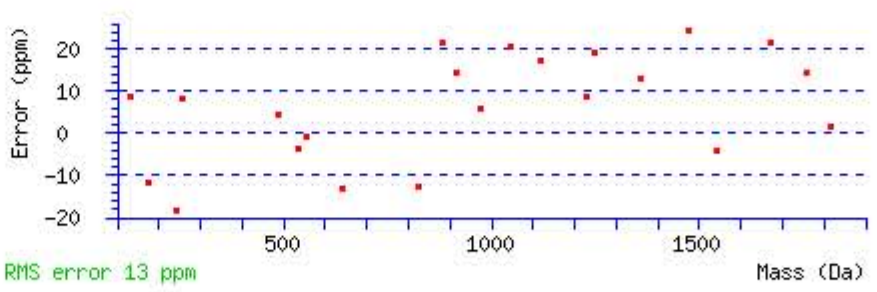
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2314.173950
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q15 : Biotin:Thermo-21345 (Q)
**Ions Score:** 69 **Expect:** 3.2e-006
**Matches :** 22/200 fragment ions using 36 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 19 |
| 2 | 145.060768 | 73.034022 | | | 127.050203 | 64.028740 | S | 2258.159779 | 1129.583527 | 2241.133230 | 1121.070253 | 2240.149214 | 1120.578245 | 18 |
| 3 | **258.144832** | 129.576054 | | | 240.134267 | 120.570772 | L | 2171.127751 | 1086.067513 | 2154.101202 | 1077.554239 | 2153.117186 | 1077.062231 | 17 |
| 4 | 357.213246 | 179.110261 | | | 339.202681 | 170.104979 | V | 2058.043687 | 1029.525481 | 2041.017138 | 1021.012207 | 2040.033122 | 1020.520199 | 16 |
| 5 | **485.271824** | 243.139550 | 468.245275 | 234.626276 | 467.261259 | 234.134268 | Q | 1958.975273 | 979.991275 | 1941.948724 | 971.478000 | 1940.964708 | 970.985992 | 15 |
| 6 | **556.308938** | 278.658107 | 539.282389 | 270.144833 | 538.298373 | 269.652825 | A | 1830.916695 | 915.961986 | 1813.890146 | 907.448711 | 1812.906130 | 906.956703 | 14 |
| 7 | **643.340966** | 322.174121 | 626.314417 | 313.660847 | 625.330401 | 313.168839 | S | *1759.879581* | 880.443429 | 1742.853032 | 871.930154 | 1741.869016 | 871.438146 | 13 |
| 8 | 772.383559 | 386.695418 | 755.357010 | 378.182143 | 754.372994 | 377.690135 | E | *1672.847553* | 836.927415 | 1655.821004 | 828.414140 | 1654.836988 | 827.922132 | 12 |
| 9 | 843.420673 | 422.213975 | 826.394124 | 413.700700 | 825.410108 | 413.208692 | A | *1543.804960* | 772.406118 | 1526.778411 | 763.892844 | 1525.794395 | 763.400836 | 11 |
| 10 | 957.463600 | 479.235438 | 940.437051 | 470.722164 | 939.453035 | 470.230156 | N | *1472.767846* | 736.887561 | 1455.741297 | 728.374287 | 1454.757281 | 727.882279 | 10 |
| 11 | 1070.547664 | 535.777470 | 1053.521115 | 527.264196 | 1052.537099 | 526.772187 | L | *1358.724919* | 679.866098 | 1341.698370 | 671.352823 | 1340.714354 | 670.860815 | 9 |
| 12 | 1198.606242 | 599.806759 | 1181.579693 | 591.293485 | 1180.595677 | 590.801477 | Q | *1245.640855* | 623.324066 | 1228.614306 | 614.810791 | 1227.630290 | 614.318783 | 8 |
| 13 | 1269.643356 | 635.325316 | 1252.616807 | 626.812042 | 1251.632791 | 626.320034 | A | *1117.582277* | 559.294777 | 1100.555728 | 550.781502 | 1099.571712 | 550.289494 | 7 |
| 14 | 1340.680470 | 670.843873 | 1323.653921 | 662.330599 | 1322.669905 | 661.838591 | A | *1046.545163* | 523.776220 | 1029.518614 | 515.262945 | 1028.534598 | 514.770937 | 6 |
| 15 | 1779.905796 | 890.456536 | 1762.879247 | 881.943262 | 1761.895231 | 881.451254 | Q | *975.508049* | 488.257663 | 958.481500 | 479.744388 | 957.497484 | 479.252380 | 5 |
| 16 | 1894.932739 | 947.970008 | 1877.906190 | 939.456733 | 1876.922174 | 938.964725 | D | *536.282723* | 268.645000 | 519.256174 | 260.131725 | 518.272158 | 259.639717 | 4 |
| 17 | 2042.001153 | 1021.504215 | 2024.974604 | 1012.990940 | 2023.990588 | 1012.498932 | F | 421.255780 | 211.131528 | 404.229231 | 202.618253 | | | 3 |
| 18 | 2141.069567 | 1071.038421 | 2124.043018 | 1062.525147 | 2123.059002 | 1062.033139 | V | 274.187366 | 137.597321 | 257.160817 | 129.084046 | | | 2 |
| 19 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 69.4 | 2314.173950 | 0.024832 | GSLVQASEANLQAAQDFVR |
| 37.0 | 2314.173950 | 0.024832 | GSLVQASEANLQAAQDFVR |

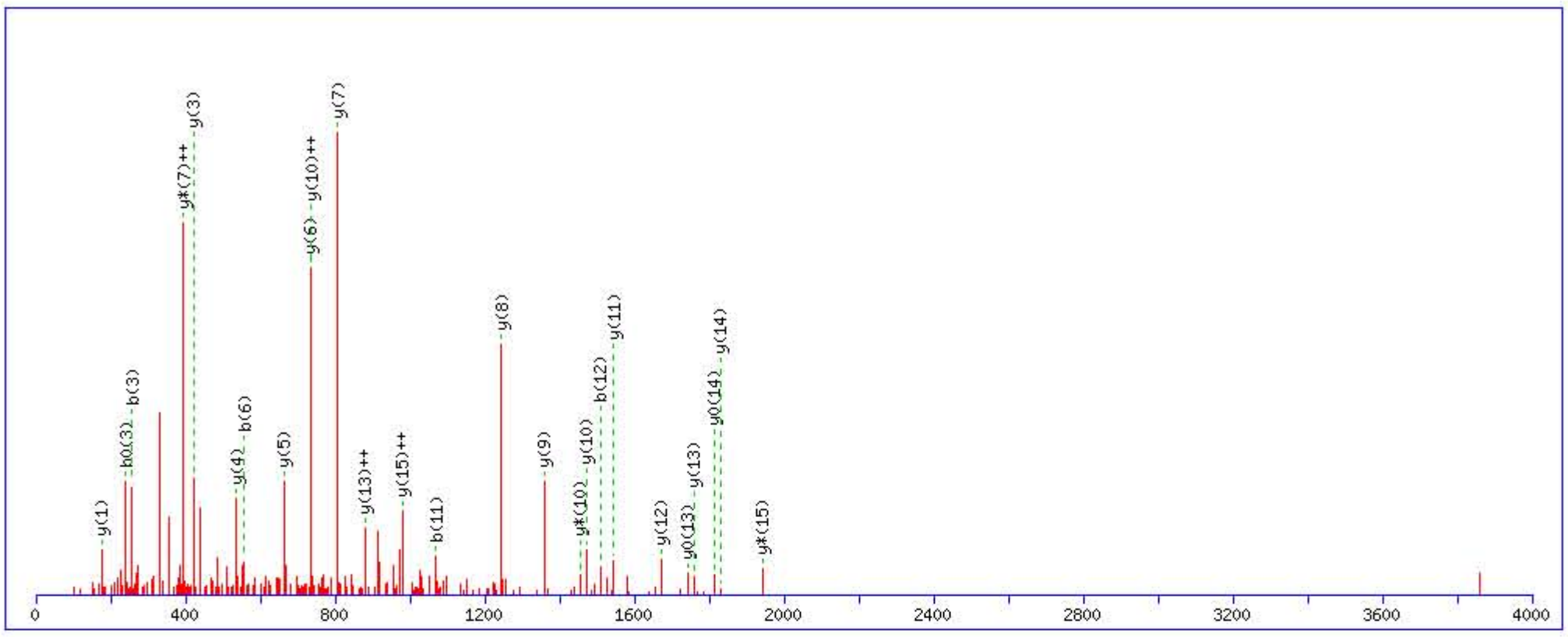
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GSLVQASEANLQAAQDFVR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

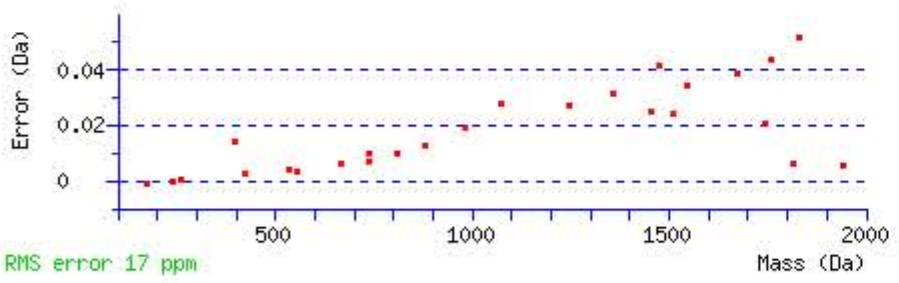
Match to Query 50767: 2314.206372 from(772.409400,3+) rtinseconds(2533) index(53557)
Title: Locus:1.1.1.2119.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

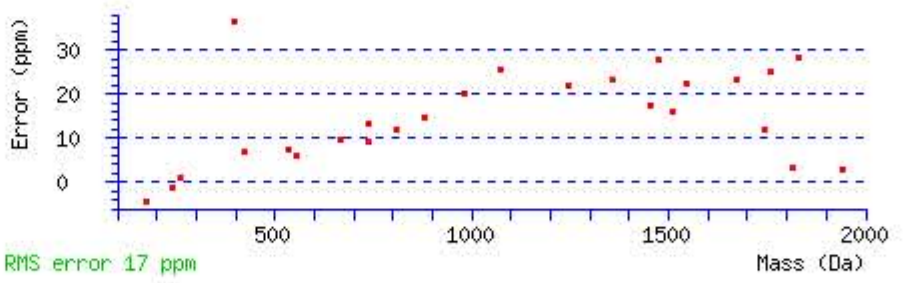
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2314.173950
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 101 **Expect:** 1.3e-009
**Matches :** 26/200 fragment ions using 37 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 19 |
| 2 | 145.060768 | 73.034022 | | | 127.050203 | 64.028740 | S | 2258.159779 | 1129.583527 | 2241.133230 | 1121.070253 | 2240.149214 | 1120.578245 | 18 |
| 3 | **258.144832** | 129.576054 | | | 240.134267 | 120.570772 | L | 2171.127751 | 1086.067513 | 2154.101202 | 1077.554239 | 2153.117186 | 1077.062231 | 17 |
| 4 | 357.213246 | 179.110261 | | | 339.202681 | 170.104979 | V | 2058.043687 | 1029.525481 | 2041.017138 | 1021.012207 | 2040.033122 | 1020.520199 | 16 |
| 5 | 485.271824 | 243.139550 | 468.245275 | 234.626276 | 467.261259 | 234.134268 | Q | 1958.975273 | 979.991275 | 1941.948724 | 971.478000 | 1940.964708 | 970.985992 | 15 |
| 6 | **556.308938** | 278.658107 | 539.282389 | 270.144833 | 538.298373 | 269.652825 | A | *1830.916695* | 915.961986 | 1813.890146 | 907.448711 | 1812.906130 | 906.956703 | 14 |
| 7 | 643.340966 | 322.174121 | 626.314417 | 313.660847 | 625.330401 | 313.168839 | S | *1759.879581* | 880.443429 | 1742.853032 | 871.930154 | 1741.869016 | 871.438146 | 13 |
| 8 | 772.383559 | 386.695418 | 755.357010 | 378.182143 | 754.372994 | 377.690135 | E | *1672.847553* | 836.927415 | 1655.821004 | 828.414140 | 1654.836988 | 827.922132 | 12 |
| 9 | 843.420673 | 422.213975 | 826.394124 | 413.700700 | 825.410108 | 413.208692 | A | *1543.804960* | 772.406118 | 1526.778411 | 763.892844 | 1525.794395 | 763.400836 | 11 |
| 10 | 957.463600 | 479.235438 | 940.437051 | 470.722164 | 939.453035 | 470.230156 | N | *1472.767846* | 736.887561 | 1455.741297 | 728.374287 | 1454.757281 | 727.882279 | 10 |
| 11 | **1070.547664** | 535.777470 | 1053.521115 | 527.264196 | 1052.537099 | 526.772187 | L | *1358.724919* | 679.866098 | 1341.698370 | 671.352823 | 1340.714354 | 670.860815 | 9 |
| 12 | **1509.772990** | 755.390133 | 1492.746441 | 746.876859 | 1491.762425 | 746.384851 | Q | *1245.640855* | 623.324066 | 1228.614306 | 614.810791 | 1227.630290 | 614.318783 | 8 |
| 13 | 1580.810104 | 790.908690 | 1563.783555 | 782.395416 | 1562.799539 | 781.903408 | A | *806.415529* | 403.711403 | 789.388980 | 395.198128 | 788.404964 | 394.706120 | 7 |
| 14 | 1651.847218 | 826.427247 | 1634.820669 | 817.913973 | 1633.836653 | 817.421965 | A | *735.378415* | 368.192846 | 718.351866 | 359.679571 | 717.367850 | 359.187563 | 6 |
| 15 | 1779.905796 | 890.456536 | 1762.879247 | 881.943262 | 1761.895231 | 881.451254 | Q | *664.341301* | 332.674289 | 647.314752 | 324.161014 | 646.330736 | 323.669006 | 5 |
| 16 | 1894.932739 | 947.970008 | 1877.906190 | 939.456733 | 1876.922174 | 938.964725 | D | *536.282723* | 268.645000 | 519.256174 | 260.131725 | 518.272158 | 259.639717 | 4 |
| 17 | 2042.001153 | 1021.504215 | 2024.974604 | 1012.990940 | 2023.990588 | 1012.498932 | F | *421.255780* | 211.131528 | 404.229231 | 202.618253 | | | 3 |
| 18 | 2141.069567 | 1071.038421 | 2124.043018 | 1062.525147 | 2123.059002 | 1062.033139 | V | 274.187366 | 137.597321 | 257.160817 | 129.084046 | | | 2 |
| 19 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 100.5 | 2314.173950 | 0.032422 | GSLVQASEANLQAAQDFVR |
| 54.8 | 2314.173950 | 0.032422 | GSLVQASEANLQAAQDFVR |
| 23.7 | 2314.173950 | 0.032422 | GSLVQASEANLQAAQDFVR |
| 5.7 | 2314.240173 | -0.033801 | IMERIQEVAAQSGFIRR |
| 3.6 | 2314.178635 | 0.027737 | NKDRPAMQLYQPGARSR |

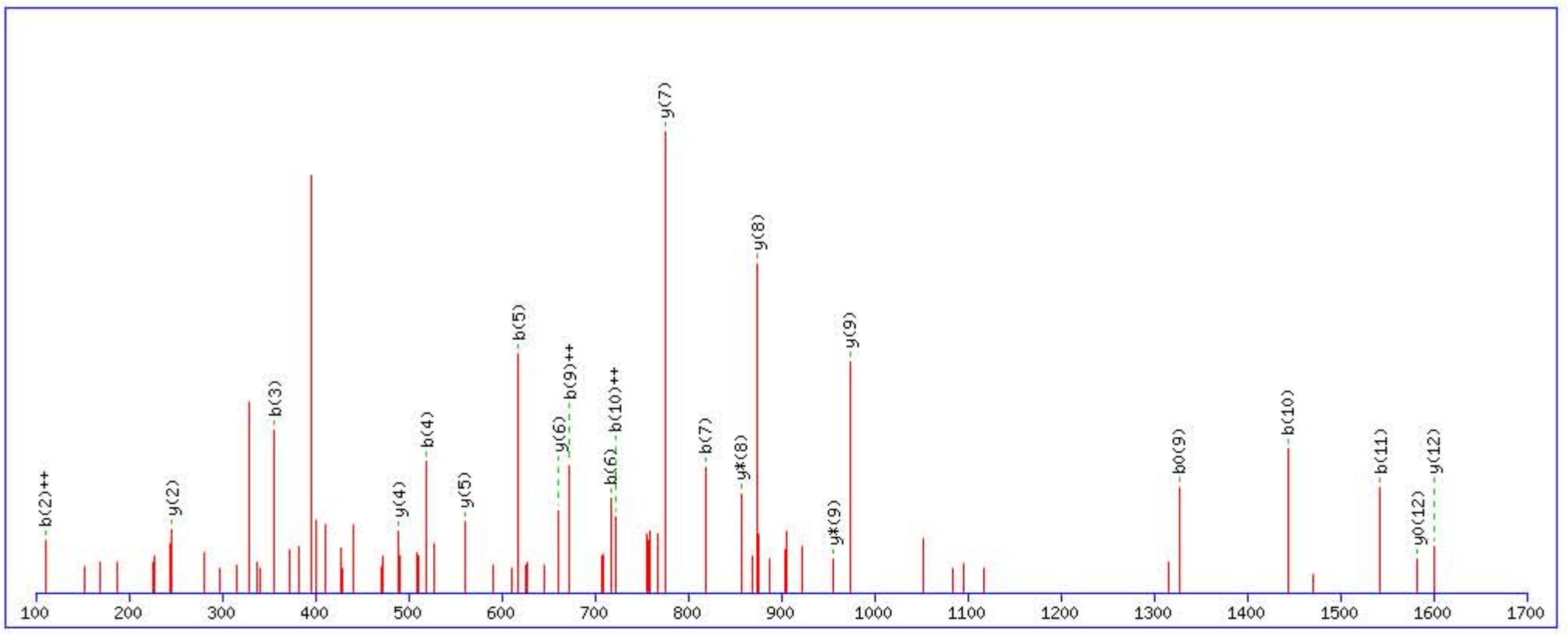
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FAHYVVTSQVVNTANEAR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

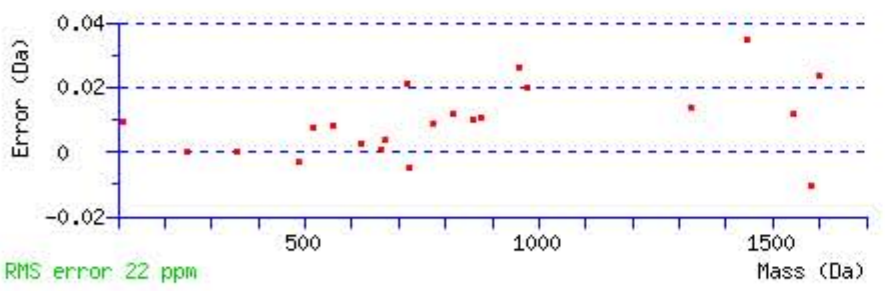
Match to Query 50794: 2316.193932 from(773.071920,3+) rtinseconds(1950) index(49990)
Title: Locus:1.1.1.1916.23 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

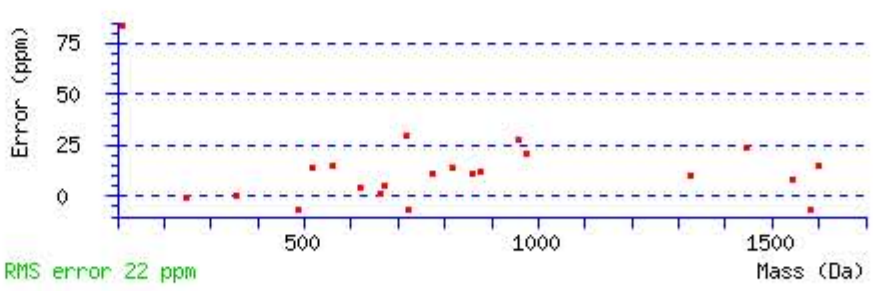
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2316.168488
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 0.00015
**Matches :** 22/172 fragment ions using 38 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 18 |
| 2 | 219.112804 | **110.060040** | | | | | A | 2170.107350 | 1085.557313 | 2153.080801 | 1077.044038 | 2152.096785 | 1076.552030 | 17 |
| 3 | *356.171716* | 178.589496 | | | | | H | 2099.070236 | 1050.038756 | 2082.043687 | 1041.525481 | 2081.059671 | 1041.033473 | 16 |
| 4 | *519.235045* | 260.121161 | | | | | Y | 1962.011324 | 981.509300 | 1944.984775 | 972.996026 | 1944.000759 | 972.504018 | 15 |
| 5 | *618.303459* | 309.655368 | | | | | V | 1798.947995 | 899.977636 | 1781.921446 | 891.464361 | 1780.937430 | 890.972353 | 14 |
| 6 | *717.371873* | 359.189575 | | | | | V | 1699.879581 | 850.443429 | 1682.853032 | 841.930154 | 1681.869016 | 841.438146 | 13 |
| 7 | *818.419552* | 409.713414 | | | 800.408987 | 400.708132 | T | *1600.811167* | 800.909222 | 1583.784618 | 792.395947 | 1582.800602 | 791.903939 | 12 |
| 8 | 905.451580 | 453.229428 | | | 887.441015 | 444.224146 | S | 1499.763488 | 750.385382 | 1482.736939 | 741.872108 | 1481.752923 | 741.380100 | 11 |
| 9 | 1344.676906 | **672.842091** | 1327.650357 | 664.328817 | 1326.666341 | 663.836808 | Q | 1412.731460 | 706.869368 | 1395.704911 | 698.356094 | 1394.720895 | 697.864086 | 10 |
| 10 | *1443.745320* | *722.376298* | 1426.718771 | 713.863024 | 1425.734755 | 713.371016 | V | *973.506134* | 487.256705 | 956.479585 | 478.743431 | 955.495569 | 478.251423 | 9 |
| 11 | *1542.813734* | 771.910505 | 1525.787185 | 763.397231 | 1524.803169 | 762.905223 | V | *874.437720* | 437.722498 | 857.411171 | 429.209224 | 856.427155 | 428.717216 | 8 |
| 12 | 1656.856661 | 828.931969 | 1639.830112 | 820.418694 | 1638.846096 | 819.926686 | N | *775.369306* | 388.188291 | 758.342757 | 379.675017 | 757.358741 | 379.183009 | 7 |
| 13 | 1757.904340 | 879.455808 | 1740.877791 | 870.942534 | 1739.893775 | 870.450526 | T | *661.326379* | 331.166828 | 644.299830 | 322.653553 | 643.315814 | 322.161545 | 6 |
| 14 | 1828.941454 | 914.974365 | 1811.914905 | 906.461091 | 1810.930889 | 905.969083 | A | *560.278700* | 280.642988 | 543.252151 | 272.129714 | 542.268135 | 271.637706 | 5 |
| 15 | 1942.984381 | 971.995829 | 1925.957832 | 963.482554 | 1924.973816 | 962.990546 | N | *489.241586* | 245.124431 | 472.215037 | 236.611157 | 471.231021 | 236.119149 | 4 |
| 16 | 2072.026974 | 1036.517125 | 2055.000425 | 1028.003850 | 2054.016409 | 1027.511842 | E | 375.198659 | 188.102968 | 358.172110 | 179.589693 | 357.188094 | 179.097685 | 3 |
| 17 | 2143.064088 | 1072.035682 | 2126.037539 | 1063.522407 | 2125.053523 | 1063.030399 | A | *246.156066* | 123.581671 | 229.129517 | 115.068397 | | | 2 |
| 18 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.5 | 2316.168488 | 0.025444 | FAHYVVTSQVVNTANEAR |

**Mascot:** http://www.matrixscience.com/

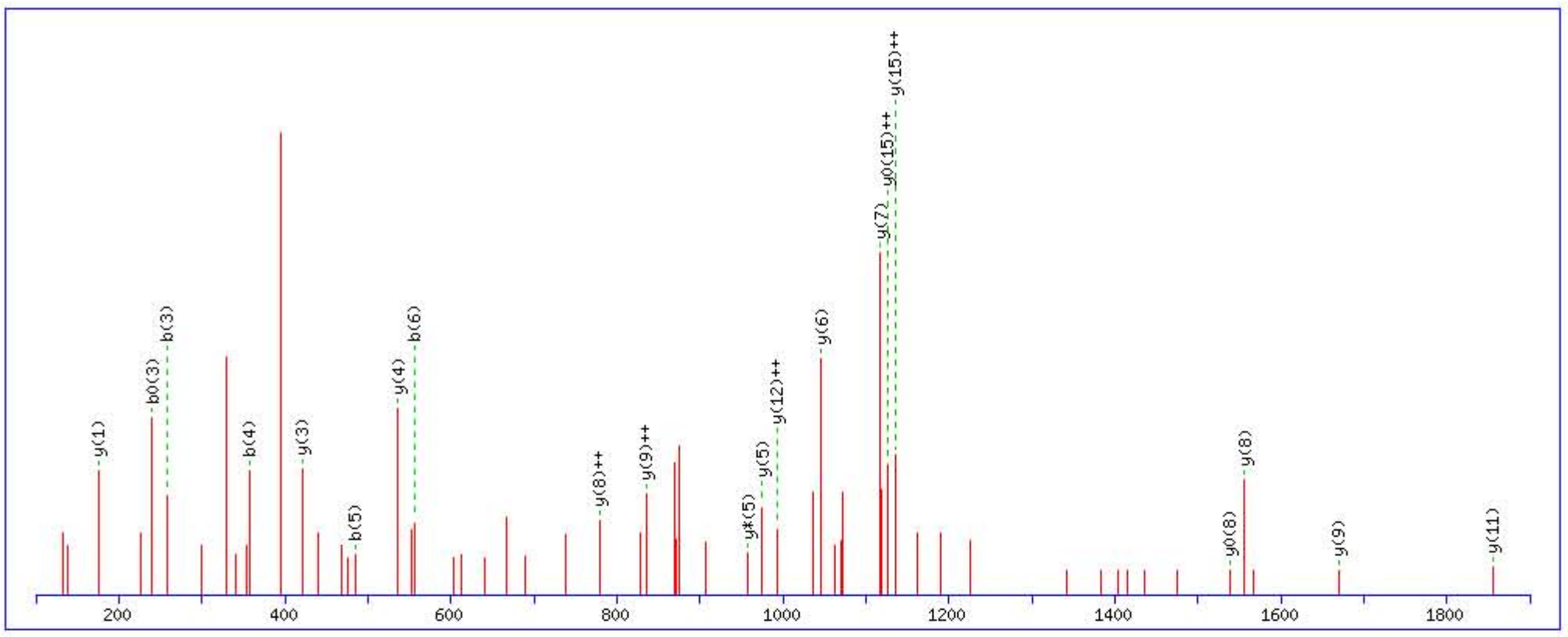
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GSLVQASEANLQAAQDFVR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

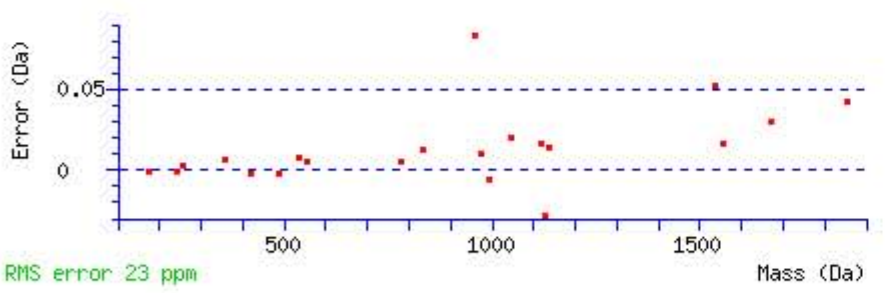
Match to Query 55730: 2625.379302 from(876.133710,3+) rtinseconds(2732) index(54964)
Title: Locus:1.1.1.2187.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

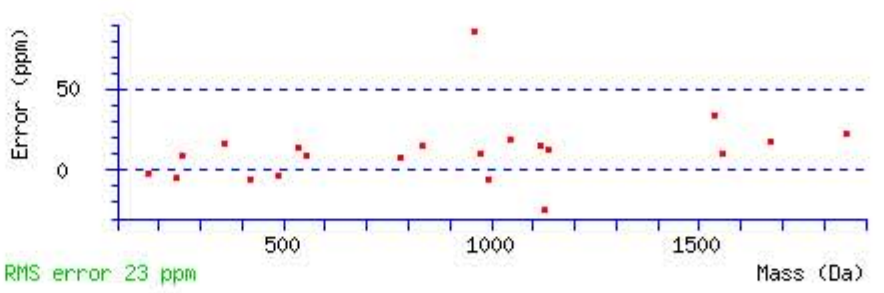
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2625.340698
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
Q15 : Biotin:Thermo-21345 (Q)
**Ions Score:** 41 **Expect:** 0.0019
**Matches :** 21/200 fragment ions using 43 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 19 |
| 2 | 145.060768 | 73.034022 | | | 127.050203 | 64.028740 | S | 2569.326527 | 1285.166901 | 2552.299978 | 1276.653627 | 2551.315962 | 1276.161619 | 18 |
| 3 | *258.144832* | 129.576054 | | | 240.134267 | 120.570772 | L | 2482.294499 | 1241.650887 | 2465.267950 | 1233.137613 | 2464.283934 | 1232.645605 | 17 |
| 4 | *357.213246* | 179.110261 | | | 339.202681 | 170.104979 | V | 2369.210435 | 1185.108855 | 2352.183886 | 1176.595581 | 2351.199870 | 1176.103573 | 16 |
| 5 | *485.271824* | 243.139550 | 468.245275 | 234.626276 | 467.261259 | 234.134268 | Q | 2270.142021 | 1135.574648 | 2253.115472 | 1127.061374 | 2252.131456 | 1126.569366 | 15 |
| 6 | *556.308938* | 278.658107 | 539.282389 | 270.144833 | 538.298373 | 269.652825 | A | 2142.083443 | 1071.545359 | 2125.056894 | 1063.032085 | 2124.072878 | 1062.540077 | 14 |
| 7 | 643.340966 | 322.174121 | 626.314417 | 313.660847 | 625.330401 | 313.168839 | S | 2071.046329 | 1036.026802 | 2054.019780 | 1027.513528 | 2053.035764 | 1027.021520 | 13 |
| 8 | 772.383559 | 386.695418 | 755.357010 | 378.182143 | 754.372994 | 377.690135 | E | 1984.014301 | 992.510788 | 1966.987752 | 983.997514 | 1966.003736 | 983.505506 | 12 |
| 9 | 843.420673 | 422.213975 | 826.394124 | 413.700700 | 825.410108 | 413.208692 | A | *1854.971708* | 927.989492 | 1837.945159 | 919.476217 | 1836.961143 | 918.984209 | 11 |
| 10 | 957.463600 | 479.235438 | 940.437051 | 470.722164 | 939.453035 | 470.230156 | N | 1783.934594 | 892.470935 | 1766.908045 | 883.957660 | 1765.924029 | 883.465652 | 10 |
| 11 | 1070.547664 | 535.777470 | 1053.521115 | 527.264196 | 1052.537099 | 526.772187 | L | *1669.891667* | 835.449471 | 1652.865118 | 826.936197 | 1651.881102 | 826.444189 | 9 |
| 12 | 1509.772990 | 755.390133 | 1492.746441 | 746.876859 | 1491.762425 | 746.384851 | Q | *1556.807603* | 778.907440 | 1539.781054 | 770.394165 | 1538.797038 | 769.902157 | 8 |
| 13 | 1580.810104 | 790.908690 | 1563.783555 | 782.395416 | 1562.799539 | 781.903408 | A | *1117.582277* | 559.294776 | 1100.555728 | 550.781502 | 1099.571712 | 550.289494 | 7 |
| 14 | 1651.847218 | 826.427247 | 1634.820669 | 817.913973 | 1633.836653 | 817.421965 | A | *1046.545163* | 523.776219 | 1029.518614 | 515.262945 | 1028.534598 | 514.770937 | 6 |
| 15 | 2091.072544 | 1046.039910 | 2074.045995 | 1037.526635 | 2073.061979 | 1037.034627 | Q | *975.508049* | 488.257662 | 958.481500 | 479.744388 | 957.497484 | 479.252380 | 5 |
| 16 | 2206.099487 | 1103.553381 | 2189.072938 | 1095.040107 | 2188.088922 | 1094.548099 | D | *536.282723* | 268.644999 | 519.256174 | 260.131725 | 518.272158 | 259.639717 | 4 |
| 17 | 2353.167901 | 1177.087588 | 2336.141352 | 1168.574314 | 2335.157336 | 1168.082306 | F | *421.255780* | 211.131528 | 404.229231 | 202.618253 | | | 3 |
| 18 | 2452.236315 | 1226.621795 | 2435.209766 | 1218.108521 | 2434.225750 | 1217.616513 | V | 274.187366 | 137.597321 | 257.160817 | 129.084046 | | | 2 |
| 19 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 41.0 | 2625.340698 | 0.038604 | GSLVQASEANLQAAQDFVR |
| 11.2 | 2625.340698 | 0.038604 | GSLVQASEANLQAAQDFVR |

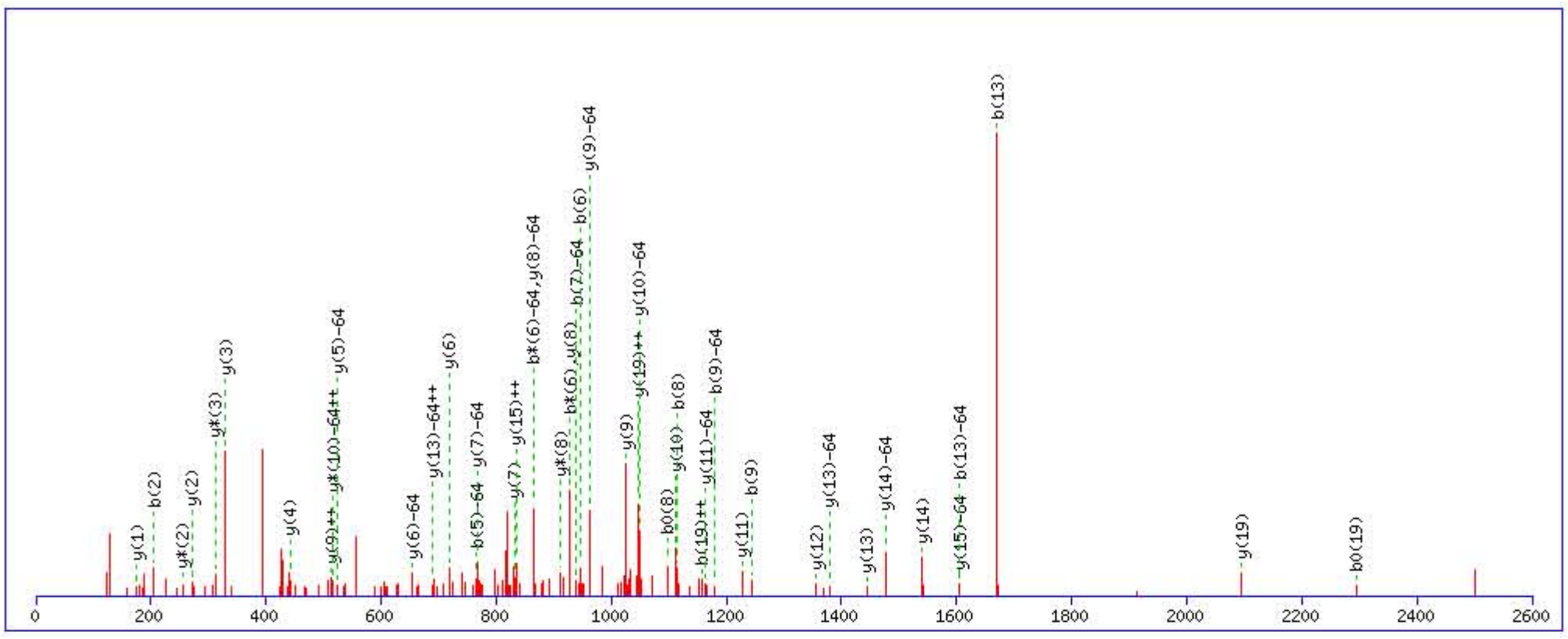
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GMADQDGLKPTIDKPSEDSPPLEMLGPR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

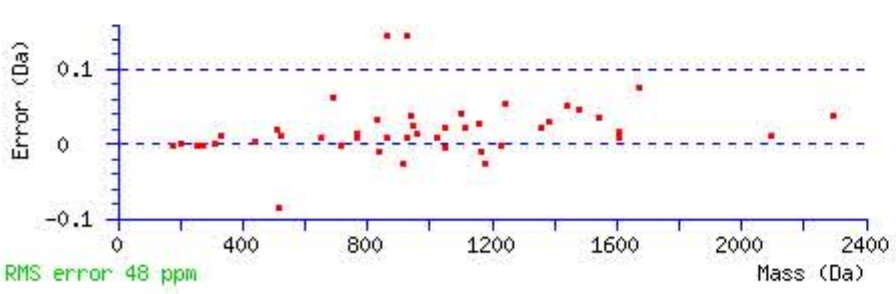
Match to Query 64454: 3336.644816 from(835.168480,4+) rtinseconds(1976) index(50210)
Title: Locus:1.1.1.1925.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

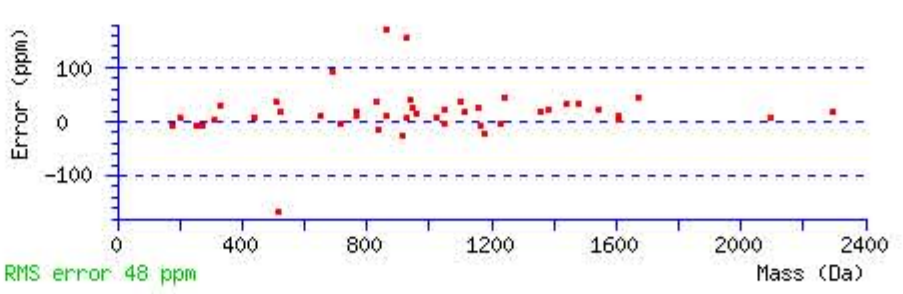
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3336.603989
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
M2 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q5 : Biotin:Thermo-21345 (Q)
M24 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
**Ions Score:** 55 **Expect:** 9e-005
**Matches :** 46/582 fragment ions using 94 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 28 |
| 2 | **205.064140** | 103.035708 | | | | | M | 3280.589815 | 1640.798546 | 3263.563266 | 1632.285271 | 3262.579250 | 1631.793263 | 27 |
| 3 | 276.101254 | 138.554265 | | | | | A | 3133.554415 | 1567.280845 | 3116.527866 | 1558.767571 | 3115.543850 | 1558.275563 | 26 |
| 4 | 391.128197 | 196.067737 | | | 373.117632 | 187.062454 | D | 3062.517301 | 1531.762289 | 3045.490752 | 1523.249014 | 3044.506736 | 1522.757006 | 25 |
| 5 | 830.353523 | 415.680400 | 813.326974 | 407.167125 | 812.342958 | 406.675117 | Q | 2947.490358 | 1474.248817 | 2930.463809 | 1465.735542 | 2929.479793 | 1465.243534 | 24 |
| 6 | **945.380466** | 473.193871 | 928.353917 | 464.680597 | 927.369901 | 464.188589 | D | 2508.265032 | 1254.636154 | 2491.238483 | 1246.122880 | 2490.254467 | 1245.630872 | 23 |
| 7 | 1002.401930 | 501.704603 | 985.375381 | 493.191329 | 984.391365 | 492.699321 | G | 2393.238089 | 1197.122682 | 2376.211540 | 1188.609408 | 2375.227524 | 1188.117400 | 22 |
| 8 | **1115.485994** | 558.246635 | 1098.459445 | 549.733361 | 1097.475429 | 549.241353 | L | 2336.216625 | 1168.611950 | 2319.190076 | 1160.098676 | 2318.206060 | 1159.606668 | 21 |
| 9 | **1243.580957** | 622.294117 | 1226.554408 | 613.780842 | 1225.570392 | 613.288834 | K | 2223.132561 | 1112.069918 | 2206.106012 | 1103.556644 | 2205.121996 | 1103.064636 | 20 |
| 10 | 1340.633721 | 670.820499 | 1323.607172 | 662.307224 | 1322.623156 | 661.815216 | P | *2095.037598* | 1048.022437 | 2078.011049 | 1039.509163 | 2077.027033 | 1039.017155 | 19 |
| 11 | 1441.681400 | 721.344338 | 1424.654851 | 712.831064 | 1423.670835 | 712.339056 | T | 1997.984834 | 999.496055 | 1980.958285 | 990.982781 | 1979.974269 | 990.490773 | 18 |
| 12 | 1554.765464 | 777.886370 | 1537.738915 | 769.373096 | 1536.754899 | 768.881088 | I | 1896.937155 | 948.972216 | 1879.910606 | 940.458941 | 1878.926590 | 939.966933 | 17 |
| 13 | **1669.792407** | 835.399842 | 1652.765858 | 826.886567 | 1651.781842 | 826.394559 | D | 1783.853091 | 892.430184 | 1766.826542 | 883.916909 | 1765.842526 | 883.424901 | 16 |
| 14 | 1797.887370 | 899.447323 | 1780.860821 | 890.934049 | 1779.876805 | 890.442041 | K | 1668.826148 | 834.916712 | 1651.799599 | 826.403438 | 1650.815583 | 825.911430 | 15 |
| 15 | 1894.940134 | 947.973705 | 1877.913585 | 939.460431 | 1876.929569 | 938.968423 | P | *1540.731185* | 770.869231 | 1523.704636 | 762.355956 | 1522.720620 | 761.863948 | 14 |
| 16 | 1981.972162 | 991.489719 | 1964.945613 | 982.976445 | 1963.961597 | 982.484437 | S | *1443.678421* | 722.342849 | 1426.651872 | 713.829574 | 1425.667856 | 713.337566 | 13 |
| 17 | 2111.014755 | 1056.011016 | 2093.988206 | 1047.497741 | 2093.004190 | 1047.005733 | E | *1356.646393* | 678.826835 | 1339.619844 | 670.313560 | 1338.635828 | 669.821552 | 12 |
| 18 | 2226.041698 | 1113.524487 | 2209.015149 | 1105.011212 | 2208.031133 | 1104.519204 | D | *1227.603800* | 614.305538 | 1210.577251 | 605.792264 | 1209.593235 | 605.300256 | 11 |
| 19 | 2313.073726 | 1157.040501 | 2296.047177 | 1148.527226 | 2295.063161 | 1148.035218 | S | *1112.576857* | 556.792067 | 1095.550308 | 548.278792 | 1094.566292 | 547.786784 | 10 |
| 20 | 2410.126490 | 1205.566883 | 2393.099941 | 1197.053608 | 2392.115925 | 1196.561600 | P | *1025.544829* | 513.276053 | 1008.518280 | 504.762778 | 1007.534264 | 504.270770 | 9 |
| 21 | 2507.179254 | 1254.093265 | 2490.152705 | 1245.579990 | 2489.168689 | 1245.087983 | P | *928.492065* | 464.749671 | 911.465516 | 456.236396 | 910.481500 | 455.744388 | 8 |
| 22 | 2620.263318 | 1310.635297 | 2603.236769 | 1302.122023 | 2602.252753 | 1301.630015 | L | *831.439301* | 416.223289 | 814.412752 | 407.710014 | 813.428736 | 407.218006 | 7 |
| 23 | 2749.305911 | 1375.156594 | 2732.279362 | 1366.643319 | 2731.295346 | 1366.151311 | E | *718.355237* | 359.681257 | 701.328688 | 351.167982 | 700.344672 | 350.675974 | 6 |
| 24 | 2896.341311 | 1448.674294 | 2879.314762 | 1440.161019 | 2878.330746 | 1439.669011 | M | 589.312644 | 295.159960 | 572.286095 | 286.646686 | | | 5 |
| 25 | 3009.425375 | 1505.216326 | 2992.398826 | 1496.703051 | 2991.414810 | 1496.211043 | L | *442.277244* | 221.642260 | 425.250695 | 213.128986 | | | 4 |
| 26 | 3066.446839 | 1533.727058 | 3049.420290 | 1525.213783 | 3048.436274 | 1524.721775 | G | *329.193180* | 165.100228 | 312.166631 | 156.586953 | | | 3 |
| 27 | 3163.499603 | 1582.253440 | 3146.473054 | 1573.740165 | 3145.489038 | 1573.248157 | P | *272.171716* | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 28 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 54.7 | 3336.603989 | 0.040827 | GMADQDGLKPTIDKPSEDSPPLEMLGPR |

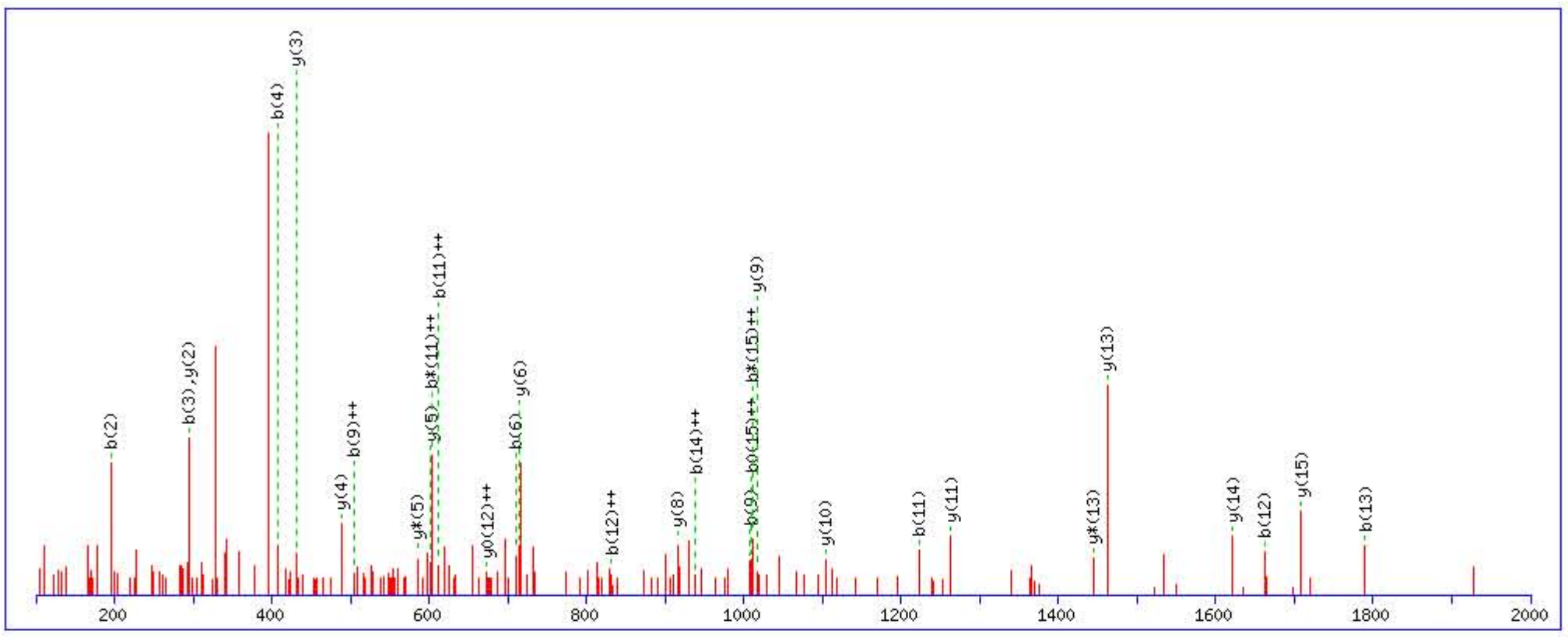
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GHVLFRPTVSQQQSCPTCSTSLLNGHFK**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

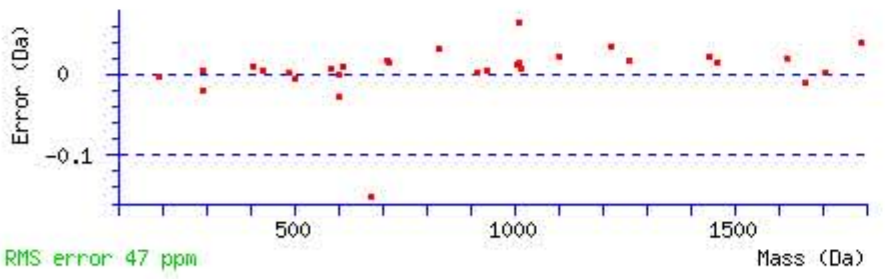
Match to Query 65792: 3496.739170 from(700.355110,5+) rtinseconds(1960) index(50079)
Title: Locus:1.1.1.1920.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

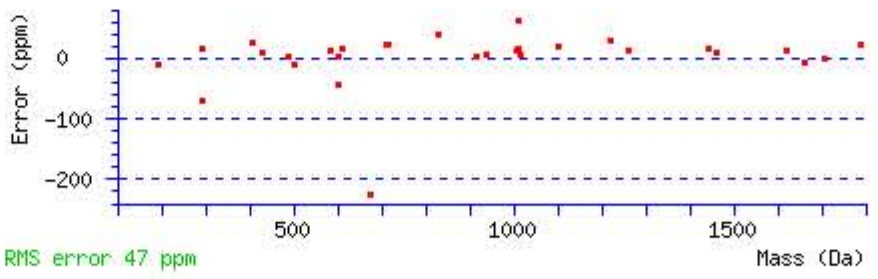
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3496.716660
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.0017
**Matches :** 30/286 fragment ions using 100 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 28 |
| 2 | *195.087652* | 98.047464 | | | | | H | 3440.702435 | 1720.854855 | 3423.675886 | 1712.341581 | 3422.691870 | 1711.849573 | 27 |
| 3 | *294.156066* | 147.581671 | | | | | V | 3303.643523 | 1652.325399 | 3286.616974 | 1643.812125 | 3285.632958 | 1643.320117 | 26 |
| 4 | *407.240130* | 204.123703 | | | | | L | 3204.575109 | 1602.791192 | 3187.548560 | 1594.277918 | 3186.564544 | 1593.785910 | 25 |
| 5 | 554.308544 | 277.657910 | | | | | F | 3091.491045 | 1546.249160 | 3074.464496 | 1537.735886 | 3073.480480 | 1537.243878 | 24 |
| 6 | *710.409655* | 355.708466 | 693.383106 | 347.195191 | | | R | 2944.422631 | 1472.714953 | 2927.396082 | 1464.201679 | 2926.412066 | 1463.709671 | 23 |
| 7 | 807.462419 | 404.234848 | 790.435870 | 395.721573 | | | P | 2788.321520 | 1394.664398 | 2771.294971 | 1386.151123 | 2770.310955 | 1385.659115 | 22 |
| 8 | 908.510098 | 454.758687 | 891.483549 | 446.245413 | 890.499533 | 445.753405 | T | 2691.268756 | 1346.138016 | 2674.242207 | 1337.624741 | 2673.258191 | 1337.132733 | 21 |
| 9 | *1007.578512* | **504.292894** | 990.551963 | 495.779620 | 989.567947 | 495.287612 | V | 2590.221077 | 1295.614176 | 2573.194528 | 1287.100902 | 2572.210512 | 1286.608894 | 20 |
| 10 | 1094.610540 | 547.808908 | 1077.583991 | 539.295634 | 1076.599975 | 538.803626 | S | 2491.152663 | 1246.079969 | 2474.126114 | 1237.566695 | 2473.142098 | 1237.074687 | 19 |
| 11 | *1222.669118* | **611.838197** | 1205.642569 | 603.324923 | 1204.658553 | 602.832915 | Q | 2404.120635 | 1202.563955 | 2387.094086 | 1194.050681 | 2386.110070 | 1193.558673 | 18 |
| 12 | *1661.894444* | **831.450860** | 1644.867895 | 822.937586 | 1643.883879 | 822.445578 | Q | 2276.062057 | 1138.534666 | 2259.035508 | 1130.021392 | 2258.051492 | 1129.529384 | 17 |
| 13 | *1789.953022* | 895.480149 | 1772.926473 | 886.966875 | 1771.942457 | 886.474867 | Q | 1836.836731 | 918.922003 | 1819.810182 | 910.408729 | 1818.826166 | 909.916721 | 16 |
| 14 | 1876.985050 | **938.996163** | 1859.958501 | 930.482889 | 1858.974485 | 929.990881 | S | *1708.778153* | 854.892714 | 1691.751604 | 846.379440 | 1690.767588 | 845.887432 | 15 |
| 15 | 2037.015699 | 1019.011488 | 2019.989150 | 1010.498213 | 2019.005134 | 1010.006205 | C | *1621.746125* | 811.376700 | 1604.719576 | 802.863426 | 1603.735560 | 802.371418 | 14 |
| 16 | 2134.068463 | 1067.537869 | 2117.041914 | 1059.024595 | 2116.057898 | 1058.532587 | P | *1461.715476* | 731.361376 | 1444.688927 | 722.848101 | 1443.704911 | 722.356093 | 13 |
| 17 | 2235.116142 | 1118.061709 | 2218.089593 | 1109.548434 | 2217.105577 | 1109.056426 | T | 1364.662712 | 682.834994 | 1347.636163 | 674.321719 | 1346.652147 | 673.829711 | 12 |
| 18 | 2395.146791 | 1198.077033 | 2378.120242 | 1189.563759 | 2377.136226 | 1189.071751 | C | *1263.615033* | 632.311154 | 1246.588484 | 623.797880 | 1245.604468 | 623.305872 | 11 |
| 19 | 2482.178819 | 1241.593047 | 2465.152270 | 1233.079773 | 2464.168254 | 1232.587765 | S | *1103.584384* | 552.295830 | 1086.557835 | 543.782556 | 1085.573819 | 543.290548 | 10 |
| 20 | 2583.226498 | 1292.116887 | 2566.199949 | 1283.603612 | 2565.215933 | 1283.111604 | T | *1016.552356* | 508.779816 | 999.525807 | 500.266541 | 998.541791 | 499.774533 | 9 |
| 21 | 2670.258526 | 1335.632901 | 2653.231977 | 1327.119626 | 2652.247961 | 1326.627618 | S | *915.504677* | 458.255977 | 898.478128 | 449.742702 | 897.494112 | 449.250694 | 8 |
| 22 | 2783.342590 | 1392.174933 | 2766.316041 | 1383.661658 | 2765.332025 | 1383.169650 | L | 828.472649 | 414.739963 | 811.446100 | 406.226688 | | | 7 |
| 23 | 2896.426654 | 1448.716965 | 2879.400105 | 1440.203690 | 2878.416089 | 1439.711682 | L | *715.388585* | 358.197930 | 698.362036 | 349.684656 | | | 6 |
| 24 | 3010.469581 | 1505.738428 | 2993.443032 | 1497.225154 | 2992.459016 | 1496.733146 | N | *602.304521* | 301.655898 | 585.277972 | 293.142624 | | | 5 |
| 25 | 3067.491045 | 1534.249160 | 3050.464496 | 1525.735886 | 3049.480480 | 1525.243878 | G | *488.261594* | 244.634435 | 471.235045 | 236.121160 | | | 4 |
| 26 | 3204.549957 | 1602.778616 | 3187.523408 | 1594.265342 | 3186.539392 | 1593.773334 | H | *431.240130* | 216.123703 | 414.213581 | 207.610428 | | | 3 |
| 27 | 3351.618371 | 1676.312823 | 3334.591822 | 1667.799549 | 3333.607806 | 1667.307541 | F | *294.181218* | 147.594247 | 277.154669 | 139.080972 | | | 2 |
| 28 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.7 | 3496.716660 | 0.022510 | GHVLFRPTVSQQQSCPTCSTSLLNGHFK |
| 29.2 | 3496.716660 | 0.022510 | GHVLFRPTVSQQQSCPTCSTSLLNGHFK |
| 26.1 | 3496.716660 | 0.022510 | GHVLFRPTVSQQQSCPTCSTSLLNGHFK |
| 2.2 | 3496.723343 | 0.015827 | NPFLDFLQKGLMISLSTDDPMQFHFTK |

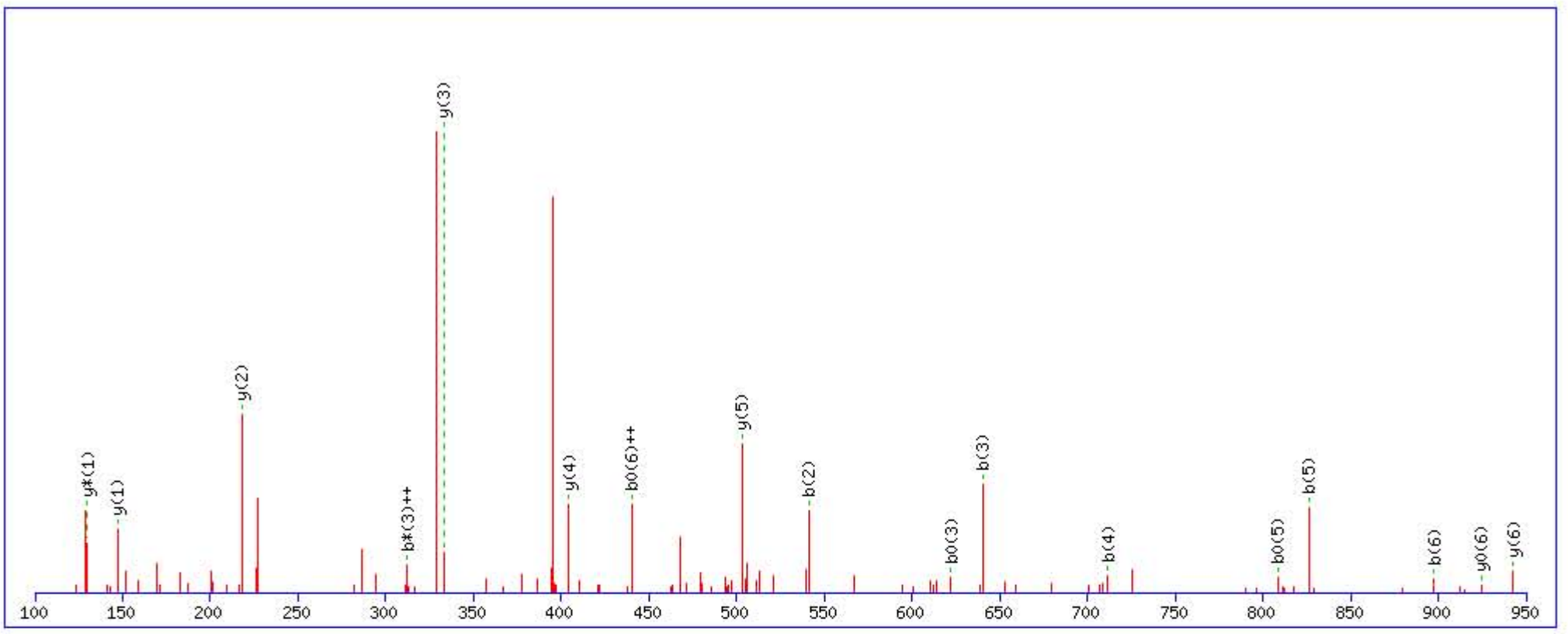
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TQVADAK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

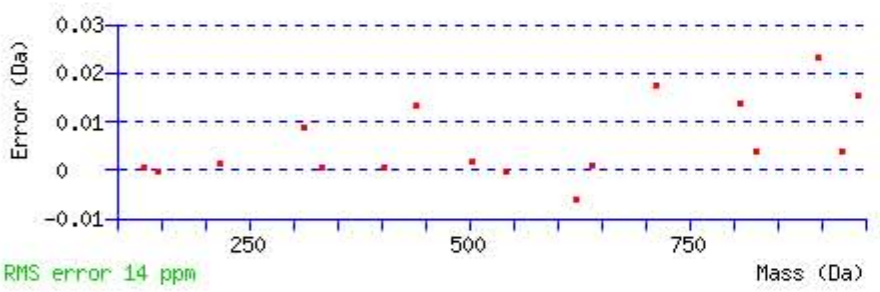
Match to Query 14978: 1042.550808 from(522.282680,2+) rtinseconds(1303) index(45747)
Title: Locus:1.1.1.1691.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

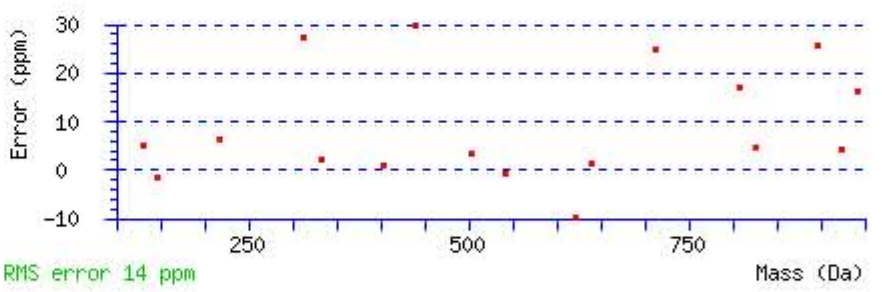
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1042.548111
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.021
**Matches :** 17/66 fragment ions using 34 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 7 |
| 2 | **541.280281** | 271.143779 | 524.253732 | 262.630504 | 523.269716 | 262.138496 | Q | ***942.507715*** | 471.757496 | 925.481166 | 463.244221 | 924.497150 | 462.752213 | 6 |
| 3 | **640.348695** | 320.677986 | 623.322146 | 312.164711 | 622.338130 | 311.672703 | V | ***503.282389*** | 252.144832 | 486.255840 | 243.631558 | 485.271824 | 243.139550 | 5 |
| 4 | **711.385809** | 356.196543 | 694.359260 | 347.683268 | 693.375244 | 347.191260 | A | ***404.213975*** | 202.610625 | 387.187426 | 194.097351 | 386.203410 | 193.605343 | 4 |
| 5 | **826.412752** | 413.710014 | 809.386203 | 405.196739 | 808.402187 | 404.704731 | D | ***333.176861*** | 167.092068 | 316.150312 | 158.578794 | 315.166296 | 158.086786 | 3 |
| 6 | **897.449866** | 449.228571 | 880.423317 | 440.715296 | 879.439301 | 440.223288 | A | ***218.149918*** | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 7 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 30.9 | 1042.548111 | 0.002697 | TQVADAK |
| 13.9 | 1042.540726 | 0.010082 | KPVSEVGDGR |
| 11.2 | 1042.548096 | 0.002712 | SLQADAK |
| 6.2 | 1042.548080 | 0.002728 | KEQEAK |
| 6.2 | 1042.548080 | 0.002728 | KQEEAK |
| 5.8 | 1042.548080 | 0.002728 | KAEEQK |
| 4.2 | 1042.548096 | 0.002712 | QEAGLSK |
| 4.2 | 1042.565857 | -0.015049 | QALEGLGDLK |
| 3.0 | 1042.544724 | 0.006084 | ETFYRISK |
| 2.8 | 1042.563354 | -0.012546 | SLQAWK |

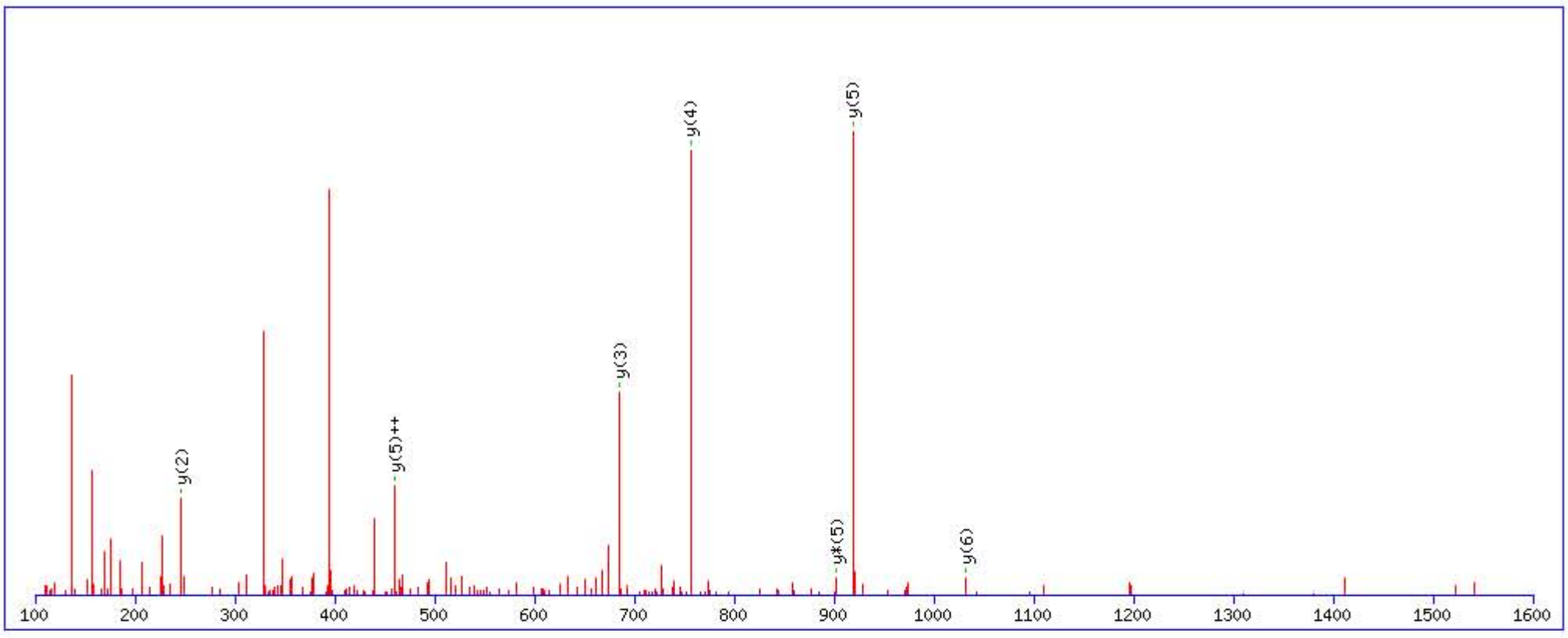
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ALYAQAR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

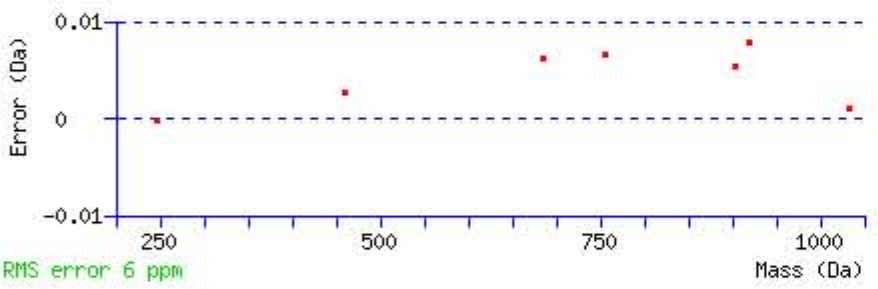
Match to Query 16271: 1102.598448 from(552.306500,2+) rtinseconds(1649) index(47979)
Title: Locus:1.1.1.1812.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

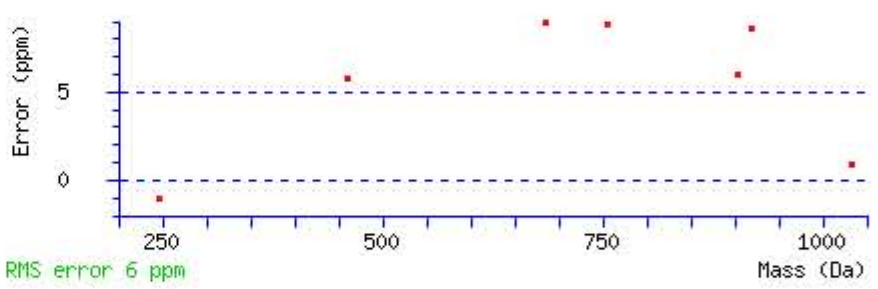
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1102.595703
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 37 **Expect:** 0.0035
**Matches :** 7/40 fragment ions using 10 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | A | | | | | 7 |
| 2 | 185.128454 | 93.067865 | | | L | *1032.565899* | 516.786588 | 1015.539350 | 508.273313 | 6 |
| 3 | 348.191783 | 174.599529 | | | Y | *919.481835* | 460.244556 | 902.455286 | 451.731281 | 5 |
| 4 | 419.228897 | 210.118087 | | | A | *756.418506* | 378.712891 | 739.391957 | 370.199617 | 4 |
| 5 | 858.454223 | 429.730750 | 841.427674 | 421.217475 | Q | *685.381392* | 343.194334 | 668.354843 | 334.681060 | 3 |
| 6 | 929.491337 | 465.249307 | 912.464788 | 456.736032 | A | *246.156066* | 123.581671 | 229.129517 | 115.068397 | 2 |
| 7 | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549840 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 37.4 | 1102.595703 | 0.002745 | ALYAQAR |
| 10.5 | 1102.602234 | -0.003786 | AIELGYNPVK |
| 3.7 | 1102.613495 | -0.015047 | ALTQGPLTFR |
| 3.5 | 1102.598221 | 0.000227 | LAGSLATDLSR |
| 2.2 | 1102.602249 | -0.003801 | KEGFDPAIVK |
| 1.6 | 1102.591675 | 0.006773 | AKQAKMAPSR |
| 1.6 | 1102.584305 | 0.014143 | QSSQRGLTAR |
| 1.1 | 1102.588333 | 0.010115 | SPYGLTPRGR |
| 0.4 | 1102.598221 | 0.000227 | DDLKATLTAR |
| 0.0 | 1102.613464 | -0.015016 | AIPEKYGAVR |

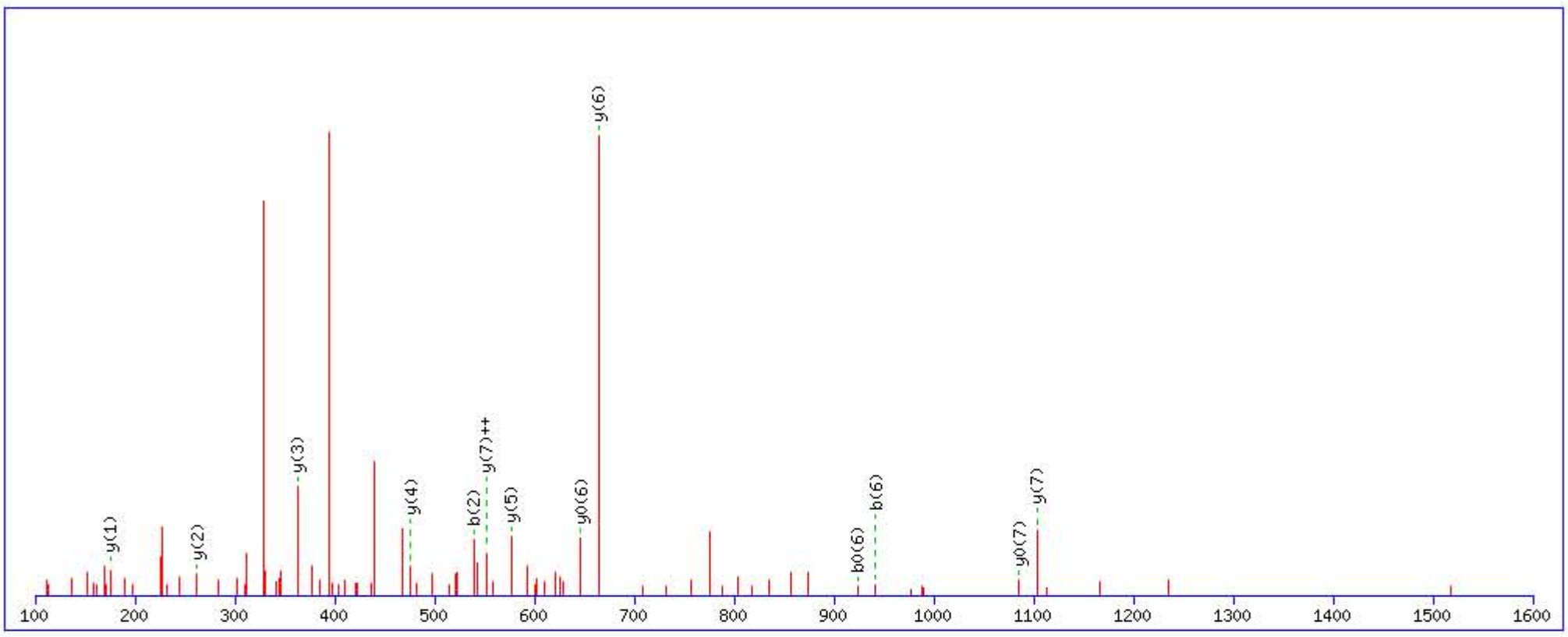
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VQSTITSR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

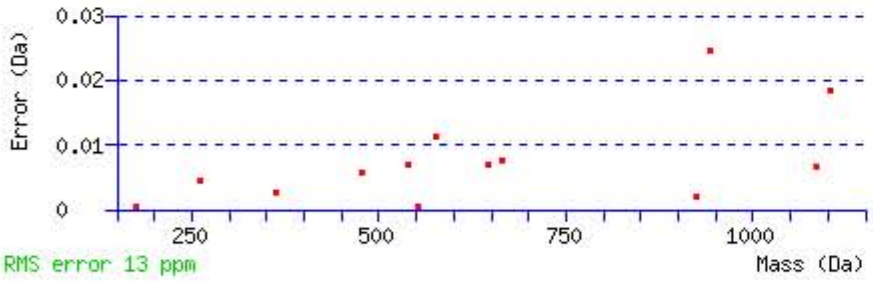
Match to Query 20583: 1201.654888 from(601.834720,2+) rtinseconds(1506) index(47009)
Title: Locus:1.1.1.1762.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

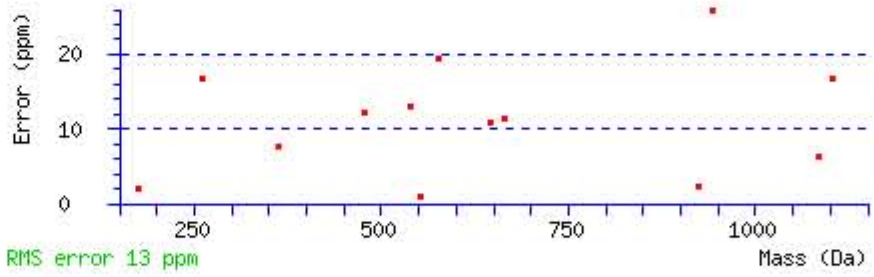
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1201.648895
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 35 **Expect:** 0.00065
**Matches :** 13/76 fragment ions using 31 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 8 |
| 2 | **539.301016** | 270.154146 | 522.274467 | 261.640872 | | | Q | *1103.587756* | 552.297516 | 1086.561207 | 543.784242 | 1085.577191 | 543.292234 | 7 |
| 3 | 626.333044 | 313.670160 | 609.306495 | 305.156886 | 608.322479 | 304.664878 | S | *664.362430* | 332.684853 | 647.335881 | 324.171579 | 646.351865 | 323.679571 | 6 |
| 4 | 727.380723 | 364.194000 | 710.354174 | 355.680725 | 709.370158 | 355.188717 | T | *577.330402* | 289.168839 | 560.303853 | 280.655565 | 559.319837 | 280.163557 | 5 |
| 5 | 840.464787 | 420.736032 | 823.438238 | 412.222757 | 822.454222 | 411.730749 | I | *476.282723* | 238.645000 | 459.256174 | 230.131725 | 458.272158 | 229.639717 | 4 |
| 6 | **941.512466** | 471.259871 | 924.485917 | 462.746597 | 923.501901 | 462.254589 | T | *363.198659* | 182.102968 | 346.172110 | 173.589693 | 345.188094 | 173.097685 | 3 |
| 7 | 1028.544494 | 514.775885 | 1011.517945 | 506.262611 | 1010.533929 | 505.770603 | S | *262.150980* | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 34.9 | 1201.648895 | 0.005993 | VQSTITSR |
| 0.8 | 1201.660767 | -0.005879 | VWKPQLFER |
| 0.2 | 1201.638992 | 0.015896 | VQPPSHAR |
| 0.0 | 1201.641495 | 0.013393 | NLTNVLGTQSR |

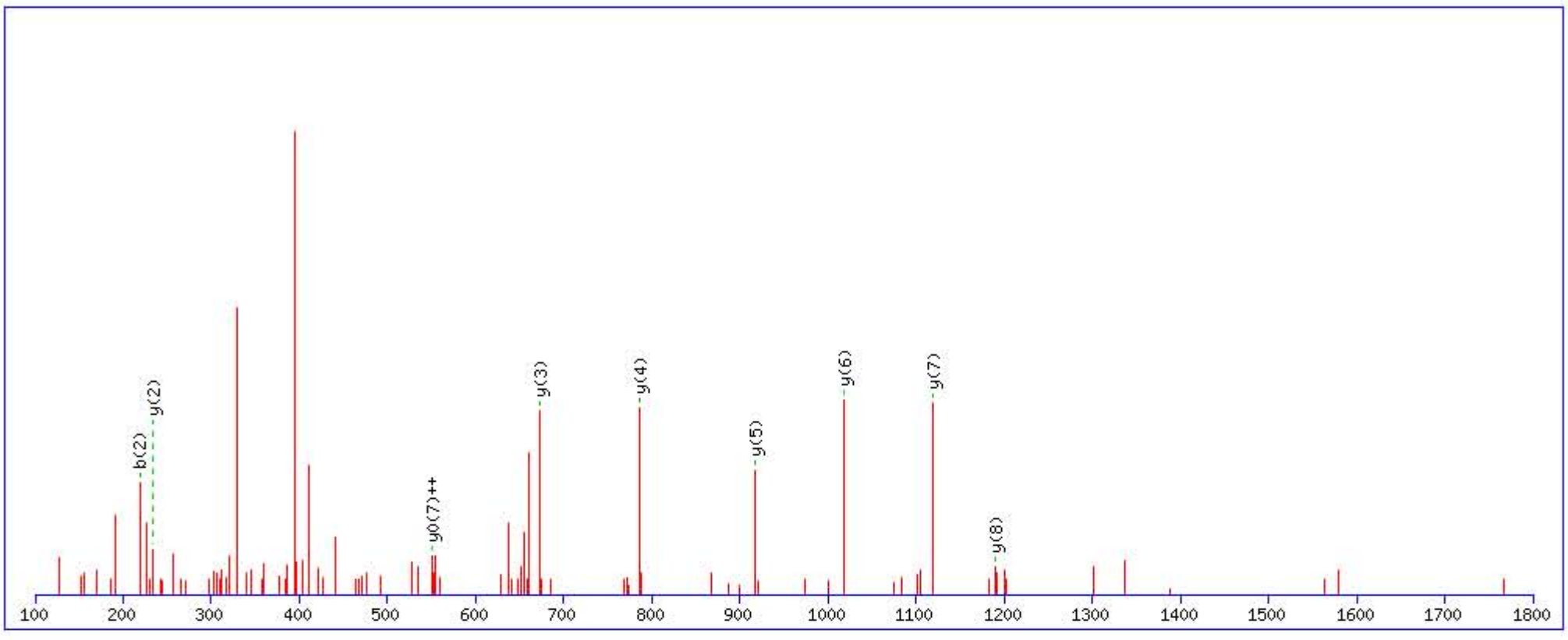
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MATTMIQSK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

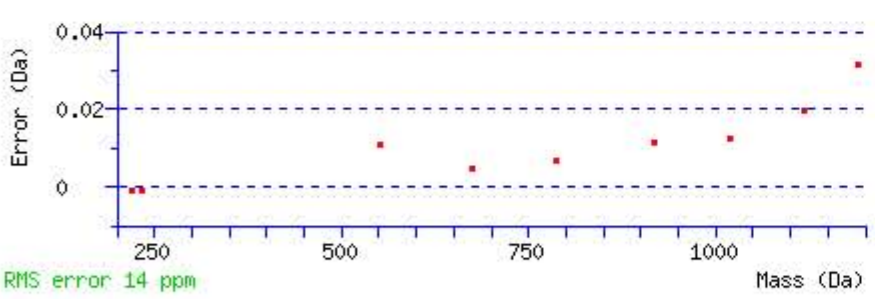
Match to Query 24038: 1336.662008 from(669.338280,2+) rtinseconds(1604) index(47668)
Title: Locus:1.1.1.1796.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

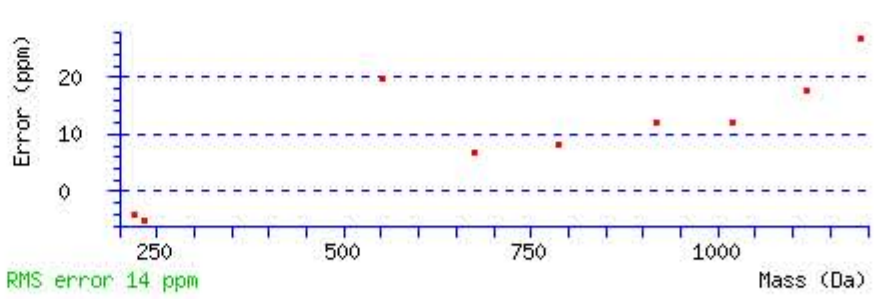
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1336.655289
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
M1 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 60 **Expect:** 8.7e-006
**Matches :** 9/110 fragment ions using 12 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.042676 | 74.524976 | | | | | M | | | | | | | 9 |
| 2 | 219.079790 | 110.043533 | | | | | A | *1190.627179* | 595.817228 | 1173.600630 | 587.303953 | 1172.616614 | 586.811945 | 8 |
| 3 | 320.127469 | 160.567372 | | | 302.116904 | 151.562090 | T | *1119.590065* | 560.298671 | 1102.563516 | 551.785396 | 1101.579500 | 551.293388 | 7 |
| 4 | 421.175148 | 211.091212 | | | 403.164583 | 202.085929 | T | *1018.542386* | 509.774831 | 1001.515837 | 501.261557 | 1000.531821 | 500.769549 | 6 |
| 5 | 552.215633 | 276.611455 | | | 534.205068 | 267.606172 | M | *917.494707* | 459.250992 | 900.468158 | 450.737717 | 899.484142 | 450.245709 | 5 |
| 6 | 665.299697 | 333.153487 | | | 647.289132 | 324.148204 | I | *786.454222* | 393.730749 | 769.427673 | 385.217475 | 768.443657 | 384.725467 | 4 |
| 7 | 1104.525023 | 552.766149 | 1087.498474 | 544.252875 | 1086.514458 | 543.760867 | Q | *673.370158* | 337.188717 | 656.343609 | 328.675443 | 655.359593 | 328.183435 | 3 |
| 8 | 1191.557051 | 596.282164 | 1174.530502 | 587.768889 | 1173.546486 | 587.276881 | S | *234.144832* | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 9 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 60.2 | 1336.655289 | 0.006719 | MATTMIQSK |
| 6.2 | 1336.662277 | -0.000269 | FADTQKDKEQK |

**Mascot:** http://www.matrixscience.com/

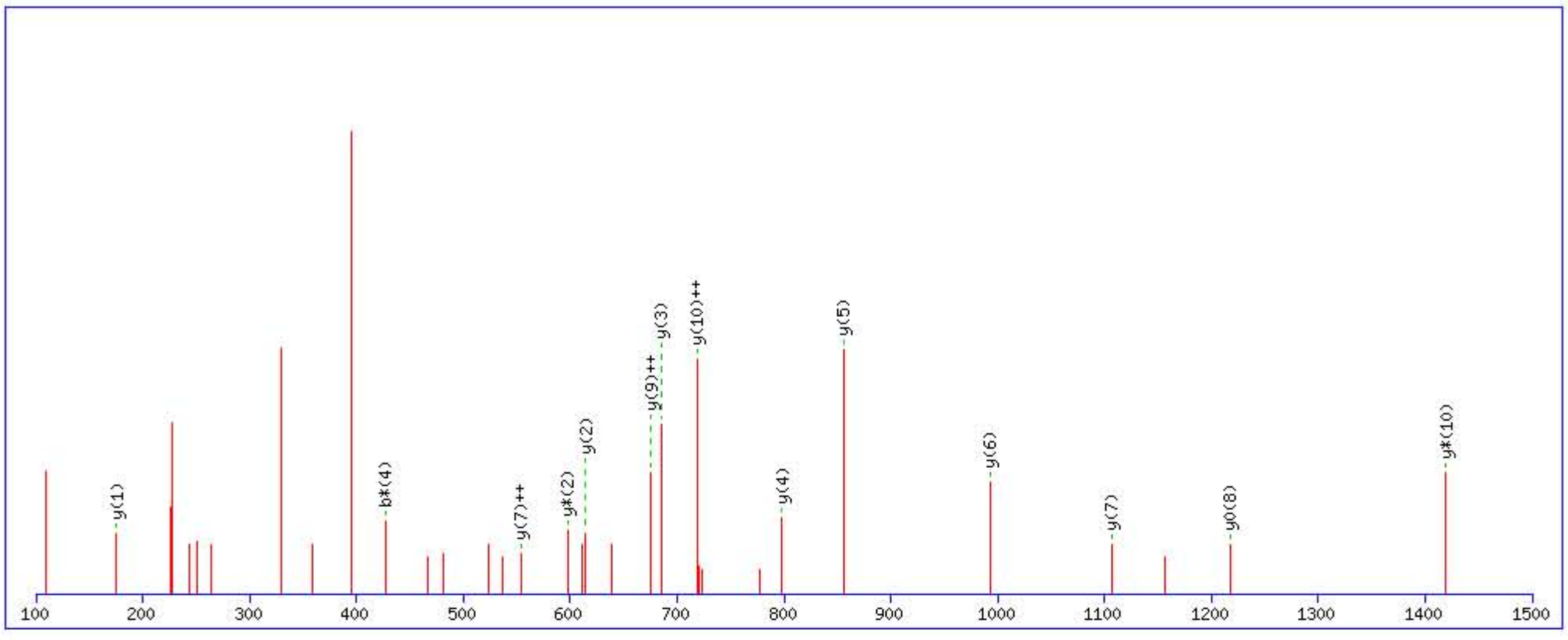
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LSNENHGIAQR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

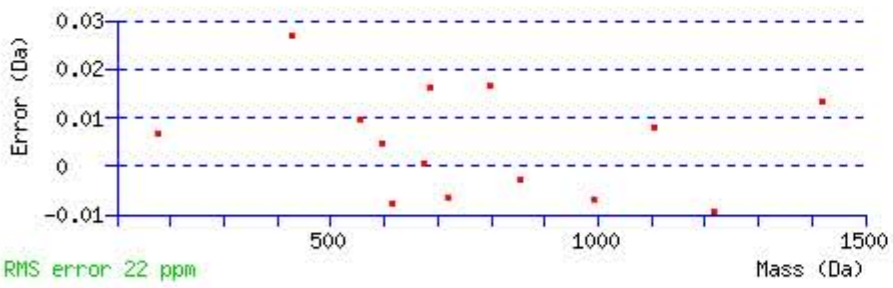
Match to Query 32461: 1548.778002 from(517.266610,3+) rtinseconds(1363) index(15946)
Title: Locus:1.1.1.2857.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

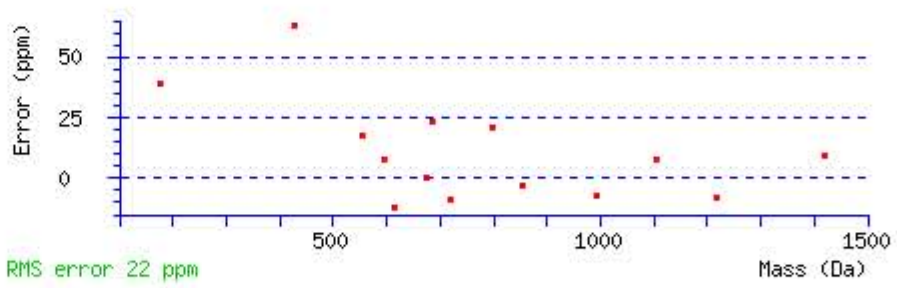
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1548.783066
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.0007
**Matches :** 14/100 fragment ions using 26 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 11 |
| 2 | 201.123368 | 101.065322 | | | 183.112803 | 92.060039 | S | 1436.706307 | 718.856792 | 1419.679758 | 710.343517 | 1418.695742 | 709.851509 | 10 |
| 3 | 315.166295 | 158.086785 | 298.139746 | 149.573511 | 297.155730 | 149.081503 | N | 1349.674279 | 675.340778 | 1332.647730 | 666.827503 | 1331.663714 | 666.335495 | 9 |
| 4 | 444.208888 | 222.608082 | 427.182339 | 214.094808 | 426.198323 | 213.602800 | E | 1235.631352 | 618.319314 | 1218.604803 | 609.806040 | 1217.620787 | 609.314032 | 8 |
| 5 | 558.251815 | 279.629546 | 541.225266 | 271.116271 | 540.241250 | 270.624263 | N | *1106.588759* | 553.798018 | 1089.562210 | 545.284743 | | | 7 |
| 6 | 695.310727 | 348.159002 | 678.284178 | 339.645727 | 677.300162 | 339.153719 | H | *992.545832* | 496.776554 | 975.519283 | 488.263280 | | | 6 |
| 7 | 752.332191 | 376.669734 | 735.305642 | 368.156459 | 734.321626 | 367.664451 | G | *855.486920* | 428.247098 | 838.460371 | 419.733824 | | | 5 |
| 8 | 865.416255 | 433.211766 | 848.389706 | 424.698491 | 847.405690 | 424.206483 | I | *798.465456* | 399.736366 | 781.438907 | 391.223092 | | | 4 |
| 9 | 936.453369 | 468.730323 | 919.426820 | 460.217048 | 918.442804 | 459.725040 | A | *685.381392* | 343.194334 | 668.354843 | 334.681060 | | | 3 |
| 10 | 1375.678695 | 688.342986 | 1358.652146 | 679.829711 | 1357.668130 | 679.337703 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 37.8 | 1548.783066 | -0.005064 | LSNENHGIAQR |
| 3.9 | 1548.798340 | -0.020338 | LSALRCGHLFGYR |
| 0.8 | 1548.800827 | -0.022825 | LPKNEPQNATGAPGR |

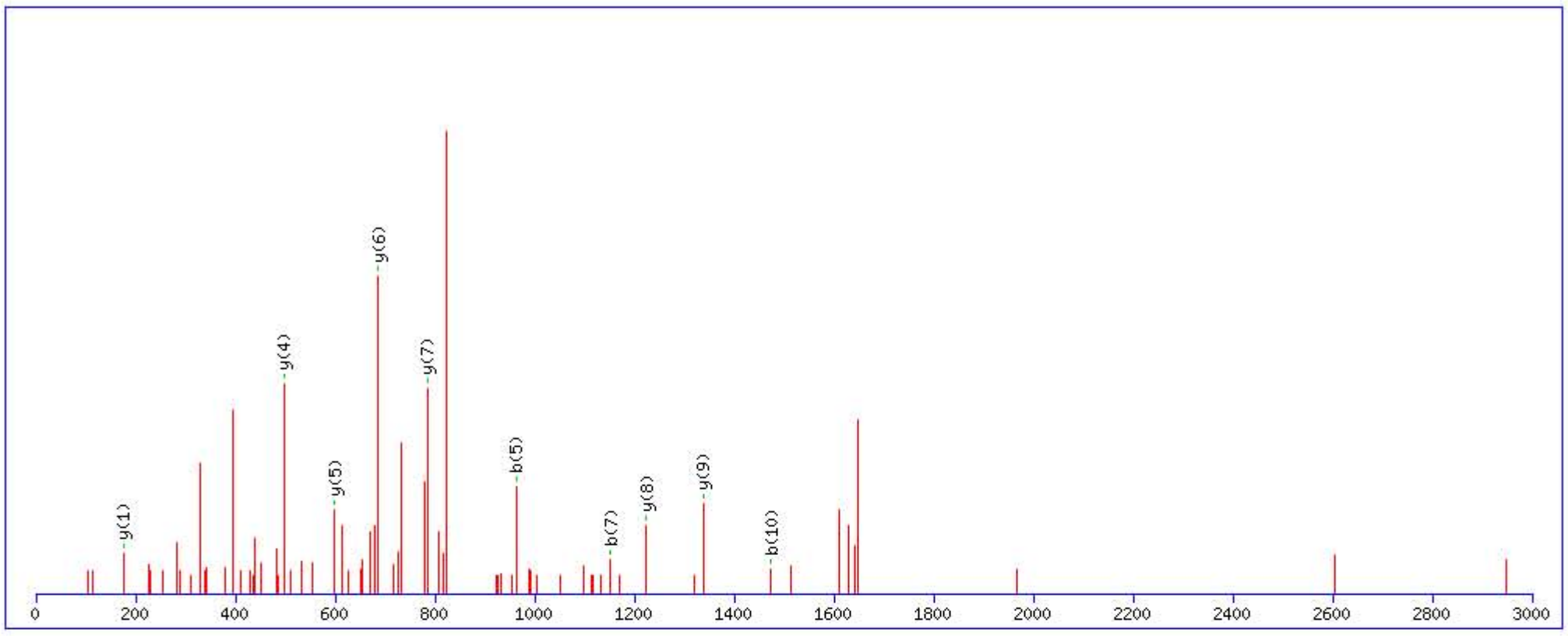
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FYNQVSTPLLR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

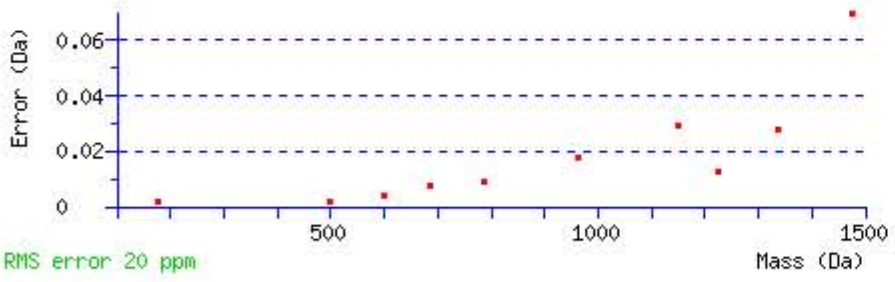
Match to Query 36818: 1647.902228 from(824.958390,2+) rtinseconds(2300) index(52281)
Title: Locus:1.1.1.2038.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

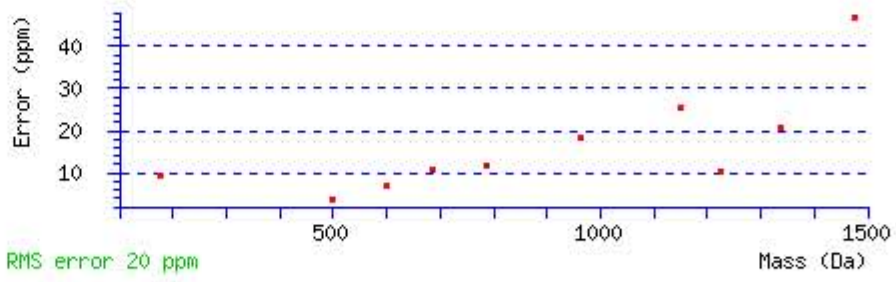
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1647.880676
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.00051
**Matches :** 10/98 fragment ions using 16 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 11 |
| 2 | 311.139019 | 156.073148 | | | | | Y | 1501.819547 | 751.413411 | 1484.792998 | 742.900137 | 1483.808982 | 742.408129 | 10 |
| 3 | 425.181946 | 213.094611 | 408.155397 | 204.581337 | | | N | *1338.756218* | 669.881747 | 1321.729669 | 661.368472 | 1320.745653 | 660.876464 | 9 |
| 4 | 864.407272 | 432.707274 | 847.380723 | 424.194000 | | | Q | *1224.713291* | 612.860283 | 1207.686742 | 604.347009 | 1206.702726 | 603.855001 | 8 |
| 5 | **963.475686** | 482.241481 | 946.449137 | 473.728207 | | | V | *785.487965* | 393.247620 | 768.461416 | 384.734346 | 767.477400 | 384.242338 | 7 |
| 6 | 1050.507714 | 525.757495 | 1033.481165 | 517.244221 | 1032.497149 | 516.752213 | S | *686.419551* | 343.713414 | 669.393002 | 335.200139 | 668.408986 | 334.708131 | 6 |
| 7 | **1151.555393** | 576.281335 | 1134.528844 | 567.768060 | 1133.544828 | 567.276052 | T | *599.387523* | 300.197399 | 582.360974 | 291.684125 | 581.376958 | 291.192117 | 5 |
| 8 | 1248.608157 | 624.807717 | 1231.581608 | 616.294442 | 1230.597592 | 615.802434 | P | *498.339844* | 249.673560 | 481.313295 | 241.160285 | | | 4 |
| 9 | 1361.692221 | 681.349749 | 1344.665672 | 672.836474 | 1343.681656 | 672.344466 | L | 401.287080 | 201.147178 | 384.260531 | 192.633903 | | | 3 |
| 10 | **1474.776285** | 737.891780 | 1457.749736 | 729.378506 | 1456.765720 | 728.886498 | L | 288.203016 | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.3 | 1647.880676 | 0.021552 | FYNQVSTPLLR |

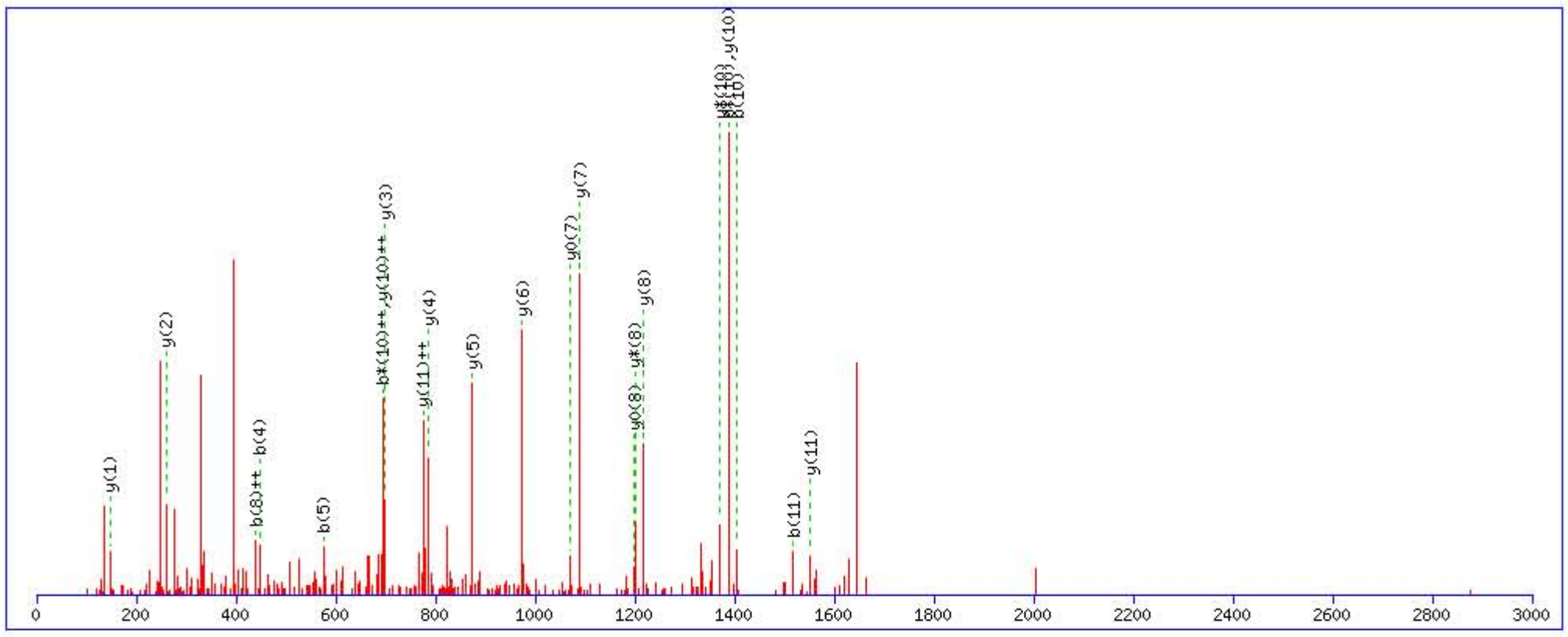
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IYGNQDTSSQLK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

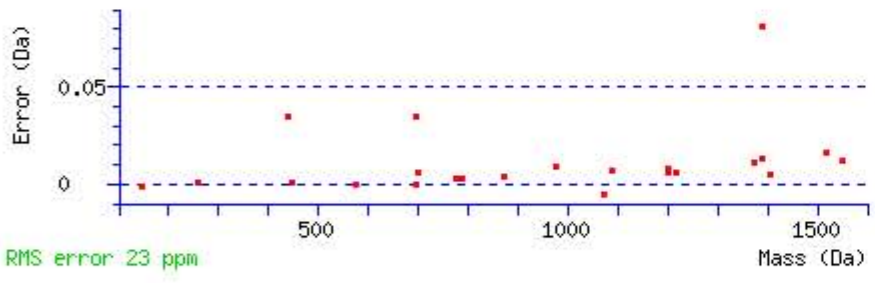
Match to Query 37175: 1663.839408 from(832.926980,2+) rtinseconds(1648) index(47971)
Title: Locus:1.1.1.1811.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

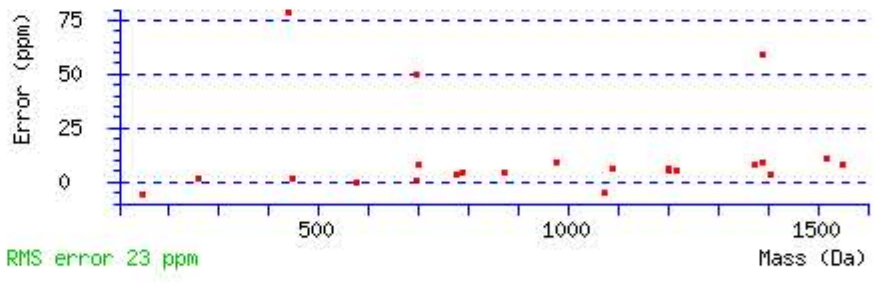
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1663.823944
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 79 **Expect:** 2.9e-007
**Matches :** 23/110 fragment ions using 32 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 12 |
| 2 | 277.154669 | 139.080973 | | | | | Y | *1551.747170* | 776.377223 | 1534.720621 | 767.863948 | 1533.736605 | 767.371940 | 11 |
| 3 | 334.176133 | 167.591704 | | | | | G | *1388.683841* | 694.845558 | 1371.657292 | 686.332284 | 1370.673276 | 685.840276 | 10 |
| 4 | **448.219060** | 224.613168 | 431.192511 | 216.099894 | | | N | 1331.662377 | 666.334826 | 1314.635828 | 657.821552 | 1313.651812 | 657.329544 | 9 |
| 5 | **576.277638** | 288.642457 | 559.251089 | 280.129183 | | | Q | *1217.619450* | 609.313363 | 1200.592901 | 600.800088 | 1199.608885 | 600.308080 | 8 |
| 6 | 691.304581 | 346.155929 | 674.278032 | 337.642654 | 673.294016 | 337.150646 | D | *1089.560872* | 545.284074 | 1072.534323 | 536.770799 | 1071.550307 | 536.278791 | 7 |
| 7 | 792.352260 | 396.679768 | 775.325711 | 388.166494 | 774.341695 | 387.674486 | T | *974.533929* | 487.770602 | 957.507380 | 479.257328 | 956.523364 | 478.765320 | 6 |
| 8 | 879.384288 | 440.195782 | 862.357739 | 431.682507 | 861.373723 | 431.190499 | S | *873.486250* | 437.246763 | 856.459701 | 428.733488 | 855.475685 | 428.241480 | 5 |
| 9 | 966.416316 | 483.711796 | 949.389767 | 475.198521 | 948.405751 | 474.706513 | S | *786.454222* | 393.730749 | 769.427673 | 385.217474 | 768.443657 | 384.725466 | 4 |
| 10 | **1405.641642** | 703.324459 | 1388.615093 | 694.811184 | 1387.631077 | 694.319176 | Q | *699.422194* | 350.214735 | 682.395645 | 341.701460 | | | 3 |
| 11 | **1518.725706** | 759.866491 | 1501.699157 | 751.353216 | 1500.715141 | 750.861208 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 12 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 79.4 | 1663.823944 | 0.015464 | IYGNQDTSSQLK |
| 30.9 | 1663.823944 | 0.015464 | IYGNQDTSSQLK |
| 11.2 | 1663.863663 | -0.024255 | EAQKEMQKIMTSLK |
| 6.7 | 1663.861191 | -0.021783 | LMHQEQLK |
| 4.2 | 1663.827957 | 0.011451 | EEAFLHVAVDMYLK |
| 4.2 | 1663.821442 | 0.017966 | LYGCFLRVYMQSK |
| 3.7 | 1663.850433 | -0.011025 | HQIQSWQGELK |
| 1.7 | 1663.845078 | -0.005670 | LMSGVENSGKVDISTK |
| 0.7 | 1663.860306 | -0.020898 | QETKYSNKDIK |
| 0.7 | 1663.831345 | 0.008063 | QLTDCISEFLK |

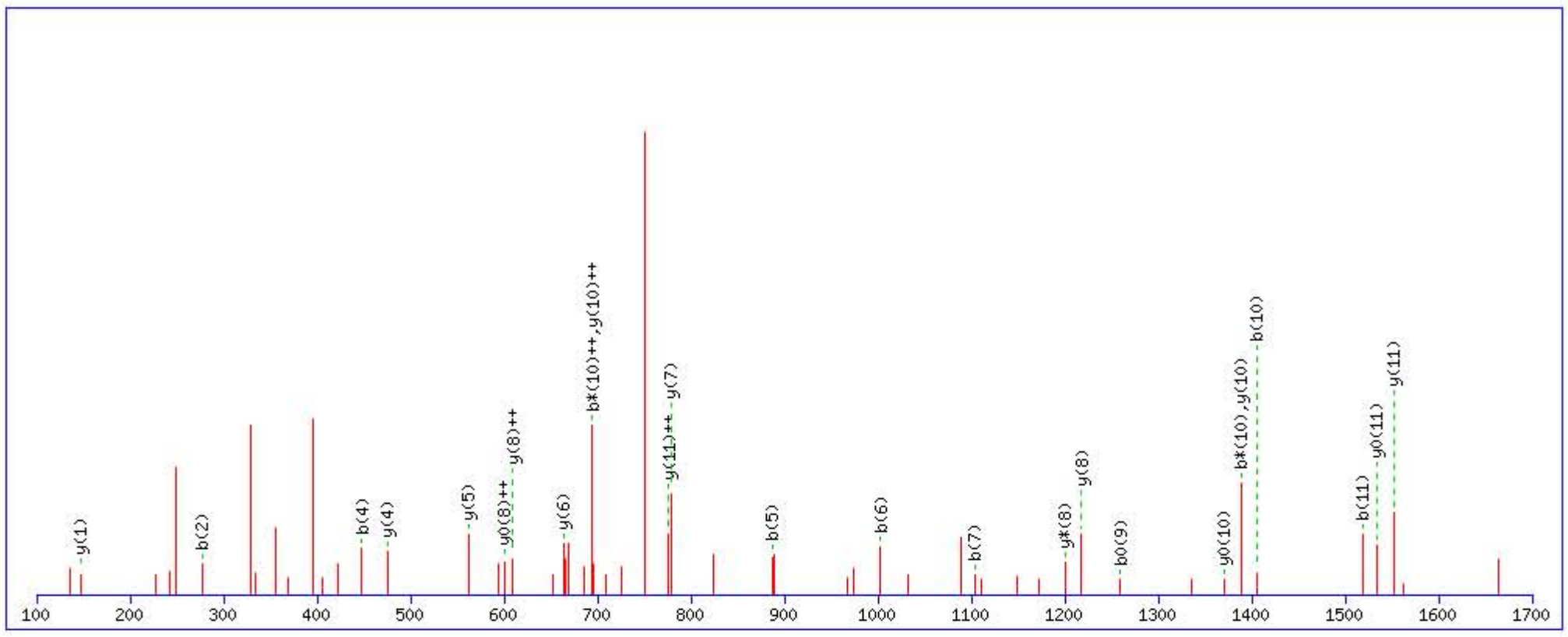
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IYGNQDTSSQLK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

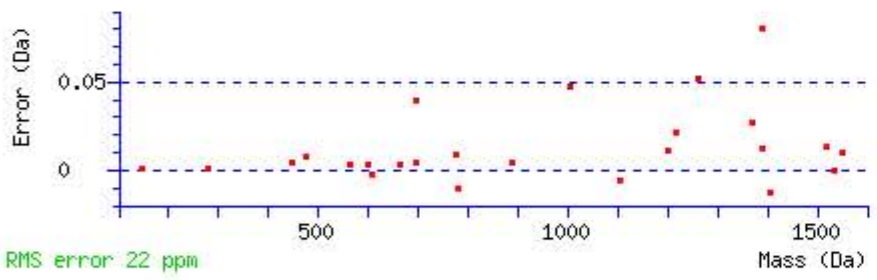
Match to Query 37176: 1663.839568 from(832.927060,2+) rtinseconds(1639) index(47925)
Title: Locus:1.1.1.1808.25 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

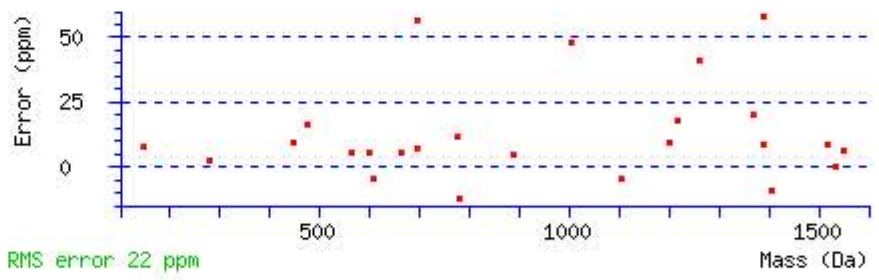
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1663.823944
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.00036
**Matches :** 25/110 fragment ions using 40 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 12 |
| 2 | *277.154669* | 139.080973 | | | | | Y | *1551.747170* | 776.377223 | 1534.720621 | 767.863949 | 1533.736605 | 767.371941 | 11 |
| 3 | 334.176133 | 167.591704 | | | | | G | *1388.683841* | 694.845559 | 1371.657292 | 686.332284 | 1370.673276 | 685.840276 | 10 |
| 4 | *448.219060* | 224.613168 | 431.192511 | 216.099894 | | | N | 1331.662377 | 666.334827 | 1314.635828 | 657.821552 | 1313.651812 | 657.329544 | 9 |
| 5 | *887.444386* | 444.225831 | 870.417837 | 435.712557 | | | Q | *1217.619450* | 609.313363 | 1200.592901 | 600.800089 | 1199.608885 | 600.308081 | 8 |
| 6 | *1002.471329* | 501.739303 | 985.444780 | 493.226028 | 984.460764 | 492.734020 | D | *778.394124* | 389.700700 | 761.367575 | 381.187426 | 760.383559 | 380.695418 | 7 |
| 7 | *1103.519008* | 552.263142 | 1086.492459 | 543.749868 | 1085.508443 | 543.257860 | T | *663.367181* | 332.187229 | 646.340632 | 323.673954 | 645.356616 | 323.181946 | 6 |
| 8 | 1190.551036 | 595.779156 | 1173.524487 | 587.265882 | 1172.540471 | 586.773874 | S | *562.319502* | 281.663389 | 545.292953 | 273.150115 | 544.308937 | 272.658107 | 5 |
| 9 | 1277.583064 | 639.295170 | 1260.556515 | 630.781896 | 1259.572499 | 630.289888 | S | *475.287474* | 238.147375 | 458.260925 | 229.634101 | 457.276909 | 229.142093 | 4 |
| 10 | *1405.641642* | 703.324459 | 1388.615093 | 694.811185 | 1387.631077 | 694.319177 | Q | 388.255446 | 194.631361 | 371.228897 | 186.118087 | | | 3 |
| 11 | *1518.725706* | 759.866491 | 1501.699157 | 751.353217 | 1500.715141 | 750.861209 | L | 260.196868 | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 12 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.2 | 1663.823944 | 0.015624 | IYGNQDTSSQLK |
| 21.0 | 1663.823944 | 0.015624 | IYGNQDTSSQLK |
| 8.0 | 1663.863663 | -0.024095 | EAQKEMQKIMTSLK |
| 6.0 | 1663.860321 | -0.020753 | ISSQMWLQLSQSLK |
| 3.4 | 1663.821442 | 0.018126 | LYGCFLRVYMQSK |
| 1.3 | 1663.823944 | 0.015624 | MATGANATPLDFPSKK |
| 1.3 | 1663.856934 | -0.017366 | LKSYENQKPPFDAK |

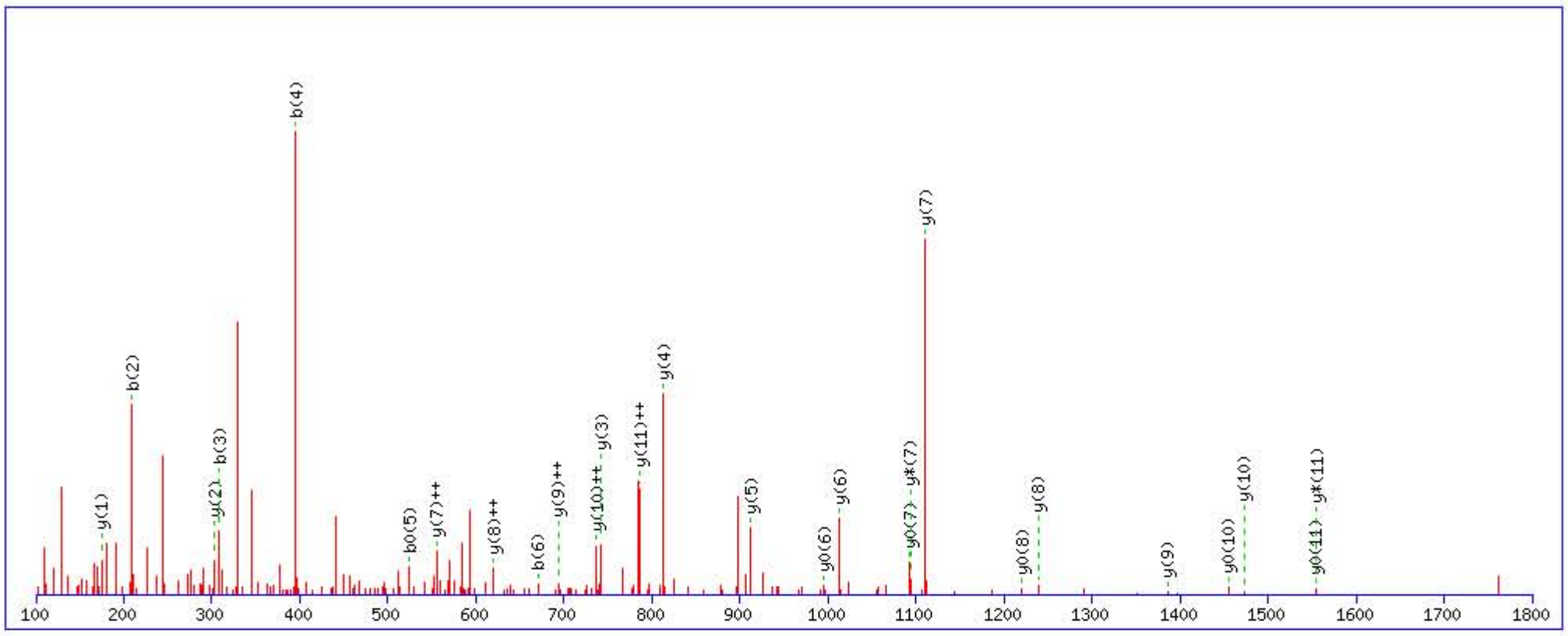
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AHVSFKPTVAQQR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

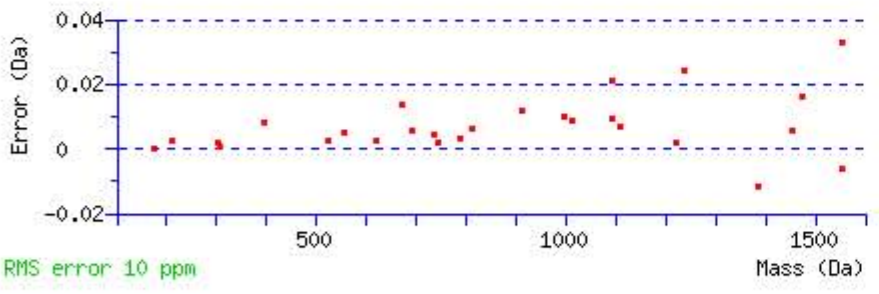
Match to Query 39830: 1778.970432 from(593.997420,3+) rtinseconds(1538) index(47200)
Title: Locus:1.1.1.1773.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

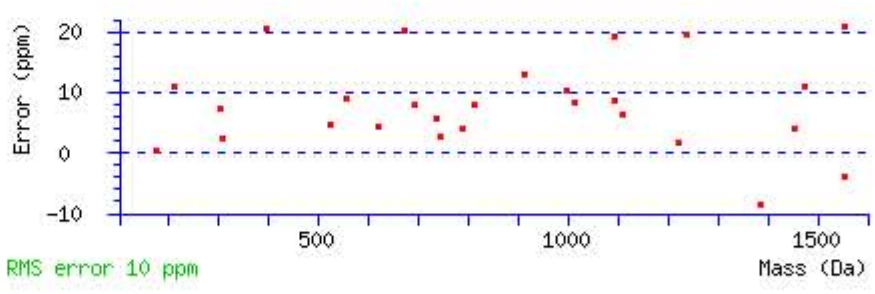
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1778.961395
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q11 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.00024
**Matches :** 27/118 fragment ions using 66 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 13 |
| 2 | **209.103302** | 105.055289 | | | | | H | 1708.931558 | 854.969417 | 1691.905009 | 846.456143 | 1690.920993 | 845.964135 | 12 |
| 3 | **308.171716** | 154.589496 | | | | | V | 1571.872646 | 786.439961 | 1554.846097 | 777.926687 | 1553.862081 | 777.434679 | 11 |
| 4 | **395.203744** | 198.105510 | | | 377.193179 | 189.100227 | S | *1472.804232* | 736.905754 | 1455.777683 | 728.392480 | 1454.793667 | 727.900472 | 10 |
| 5 | 542.272158 | 271.639717 | | | 524.261593 | 262.634435 | F | *1385.772204* | 693.389740 | 1368.745655 | 684.876466 | 1367.761639 | 684.384458 | 9 |
| 6 | **670.367121** | 335.687199 | 653.340572 | 327.173924 | 652.356556 | 326.681916 | K | *1238.703790* | 619.855533 | 1221.677241 | 611.342259 | 1220.693225 | 610.850251 | 8 |
| 7 | 767.419885 | 384.213581 | 750.393336 | 375.700306 | 749.409320 | 375.208298 | P | *1110.608827* | 555.808052 | 1093.582278 | 547.294777 | 1092.598262 | 546.802769 | 7 |
| 8 | 868.467564 | 434.737420 | 851.441015 | 426.224146 | 850.456999 | 425.732138 | T | *1013.556063* | 507.281670 | 996.529514 | 498.768395 | 995.545498 | 498.276387 | 6 |
| 9 | 967.535978 | 484.271627 | 950.509429 | 475.758353 | 949.525413 | 475.266345 | V | *912.508384* | 456.757830 | 895.481835 | 448.244556 | | | 5 |
| 10 | 1038.573092 | 519.790184 | 1021.546543 | 511.276910 | 1020.562527 | 510.784902 | A | *813.439970* | 407.223623 | 796.413421 | 398.710349 | | | 4 |
| 11 | 1477.798418 | 739.402847 | 1460.771869 | 730.889573 | 1459.787853 | 730.397565 | Q | *742.402856* | 371.705066 | 725.376307 | 363.191792 | | | 3 |
| 12 | 1605.856996 | 803.432136 | 1588.830447 | 794.918862 | 1587.846431 | 794.426854 | Q | *303.177530* | 152.092403 | 286.150981 | 143.579129 | | | 2 |
| 13 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 43.8 | 1778.961395 | 0.009037 | AHVSFKPTVAQQR |
| 37.1 | 1778.961395 | 0.009037 | AHVSFKPTVAQQR |
| 5.2 | 1778.982498 | -0.012066 | SRDAKLVLLNMPGPPR |

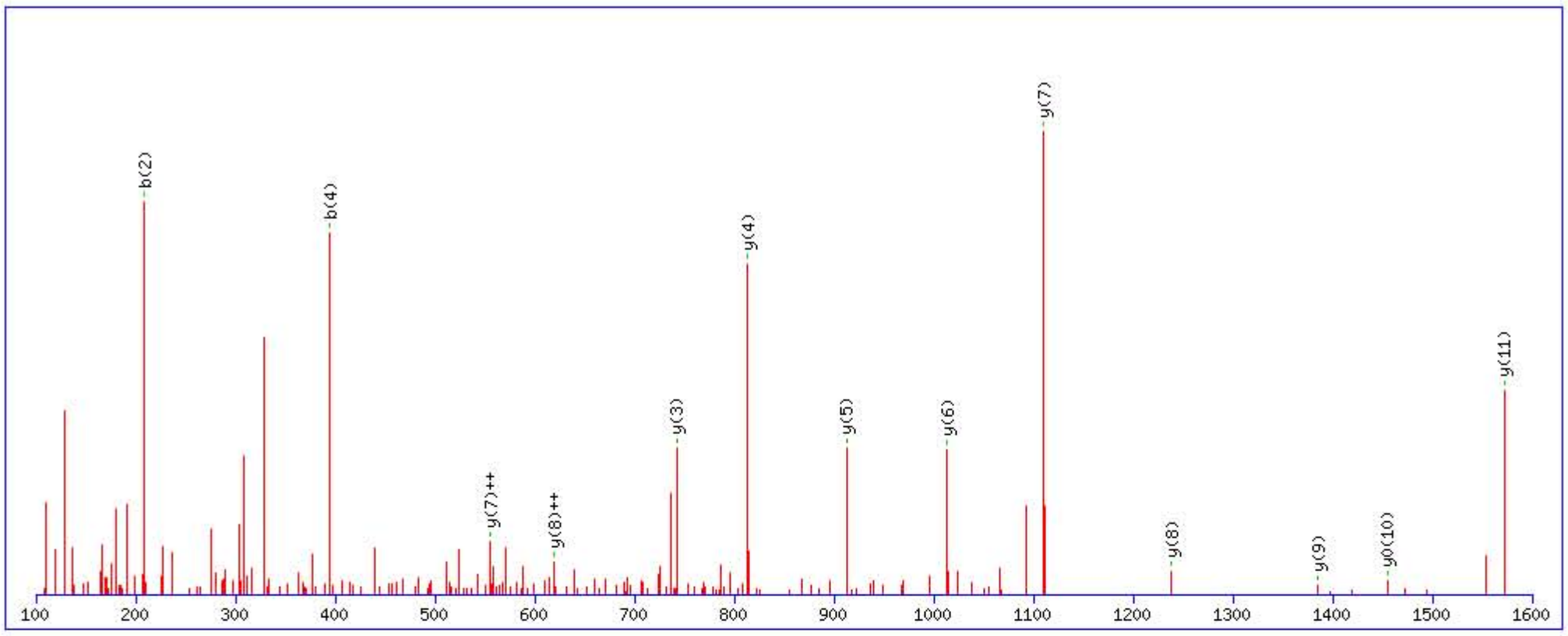
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AHVSFKPTVAQQR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

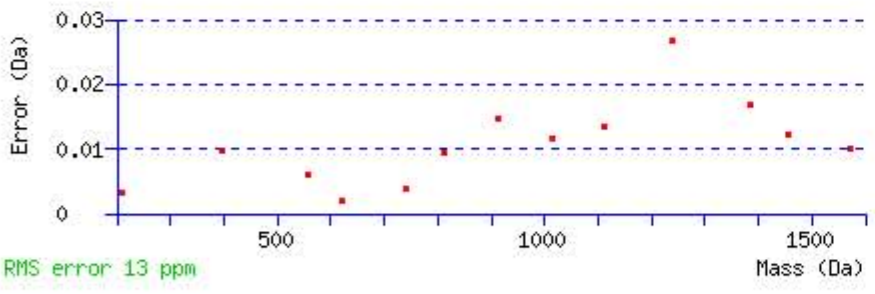
Match to Query 39831: 1778.970852 from(593.997560,3+) rtinseconds(1515) index(47060)
Title: Locus:1.1.1.1765.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

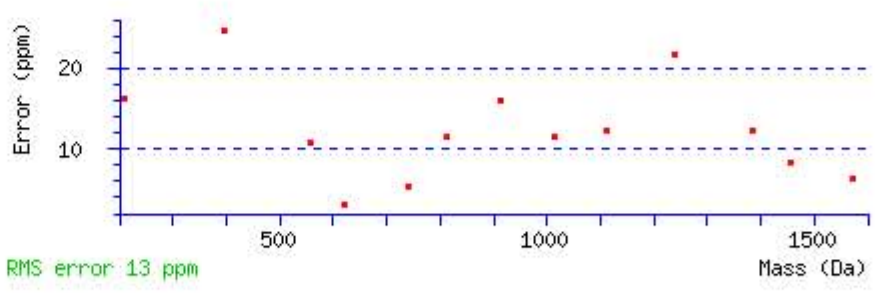
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1778.961395
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 69 **Expect:** 3.8e-007
**Matches :** 13/118 fragment ions using 15 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 13 |
| 2 | **209.103302** | 105.055289 | | | | | H | 1708.931558 | 854.969417 | 1691.905009 | 846.456143 | 1690.920993 | 845.964135 | 12 |
| 3 | 308.171716 | 154.589496 | | | | | V | *1571.872646* | 786.439961 | 1554.846097 | 777.926687 | 1553.862081 | 777.434679 | 11 |
| 4 | **395.203744** | 198.105510 | | | 377.193179 | 189.100227 | S | 1472.804232 | 736.905754 | 1455.777683 | 728.392480 | 1454.793667 | 727.900472 | 10 |
| 5 | 542.272158 | 271.639717 | | | 524.261593 | 262.634435 | F | *1385.772204* | 693.389740 | 1368.745655 | 684.876466 | 1367.761639 | 684.384458 | 9 |
| 6 | 670.367121 | 335.687199 | 653.340572 | 327.173924 | 652.356556 | 326.681916 | K | *1238.703790* | 619.855533 | 1221.677241 | 611.342259 | 1220.693225 | 610.850251 | 8 |
| 7 | 767.419885 | 384.213581 | 750.393336 | 375.700306 | 749.409320 | 375.208298 | P | *1110.608827* | 555.808052 | 1093.582278 | 547.294777 | 1092.598262 | 546.802769 | 7 |
| 8 | 868.467564 | 434.737420 | 851.441015 | 426.224146 | 850.456999 | 425.732138 | T | *1013.556063* | 507.281670 | 996.529514 | 498.768395 | 995.545498 | 498.276387 | 6 |
| 9 | 967.535978 | 484.271627 | 950.509429 | 475.758353 | 949.525413 | 475.266345 | V | *912.508384* | 456.757830 | 895.481835 | 448.244556 | | | 5 |
| 10 | 1038.573092 | 519.790184 | 1021.546543 | 511.276910 | 1020.562527 | 510.784902 | A | *813.439970* | 407.223623 | 796.413421 | 398.710349 | | | 4 |
| 11 | 1166.631670 | 583.819473 | 1149.605121 | 575.306199 | 1148.621105 | 574.814191 | Q | *742.402856* | 371.705066 | 725.376307 | 363.191792 | | | 3 |
| 12 | 1605.856996 | 803.432136 | 1588.830447 | 794.918862 | 1587.846431 | 794.426854 | Q | 614.344278 | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 13 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 69.2 | 1778.961395 | 0.009457 | AHVSFKPTVAQQR |
| 69.2 | 1778.961395 | 0.009457 | AHVSFKPTVAQQR |
| 0.7 | 1778.990372 | -0.019520 | HAEGRVEPIHAVVLPR |

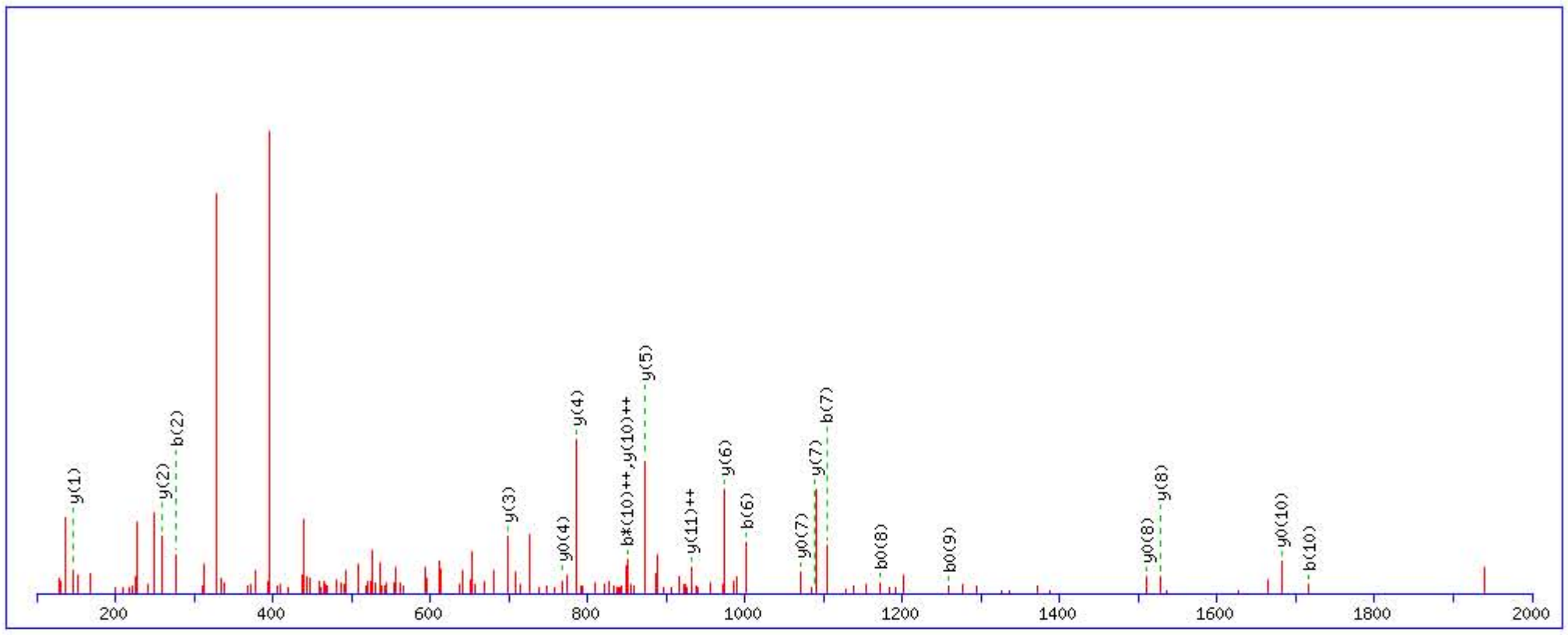
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IYGNQDTSSQLK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

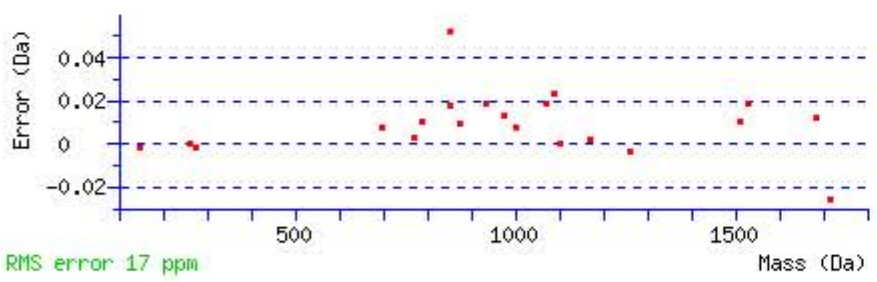
Match to Query 43672: 1975.009032 from(659.343620,3+) rtinseconds(1989) index(50324)
Title: Locus:1.1.1.1930.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

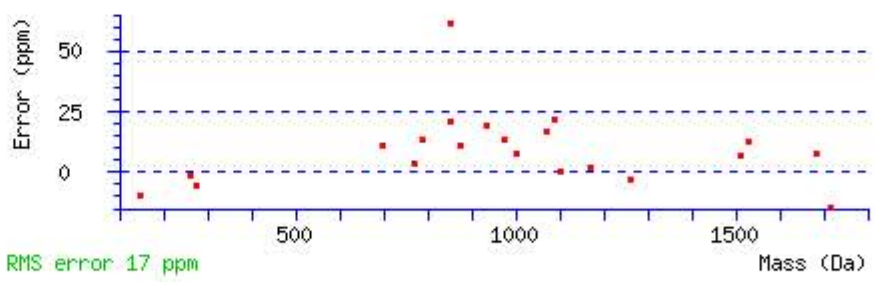
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1974.990692
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.0026
**Matches :** 21/110 fragment ions using 47 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 12 |
| 2 | 277.154669 | 139.080973 | | | | | Y | 1862.913918 | 931.960597 | 1845.887369 | 923.447323 | 1844.903353 | 922.955315 | 11 |
| 3 | 334.176133 | 167.591704 | | | | | G | 1699.850589 | 850.428933 | 1682.824040 | 841.915658 | 1681.840024 | 841.423650 | 10 |
| 4 | 448.219060 | 224.613168 | 431.192511 | 216.099894 | | | N | 1642.829125 | 821.918201 | 1625.802576 | 813.404926 | 1624.818560 | 812.912918 | 9 |
| 5 | 887.444386 | 444.225831 | 870.417837 | 435.712557 | | | Q | *1528.786198* | 764.896737 | 1511.759649 | 756.383463 | 1510.775633 | 755.891455 | 8 |
| 6 | 1002.471329 | 501.739303 | 985.444780 | 493.226028 | 984.460764 | 492.734020 | D | *1089.560872* | 545.284074 | 1072.534323 | 536.770800 | 1071.550307 | 536.278792 | 7 |
| 7 | 1103.519008 | 552.263142 | 1086.492459 | 543.749868 | 1085.508443 | 543.257860 | T | *974.533929* | 487.770603 | 957.507380 | 479.257328 | 956.523364 | 478.765320 | 6 |
| 8 | 1190.551036 | 595.779156 | 1173.524487 | 587.265882 | 1172.540471 | 586.773874 | S | *873.486250* | 437.246763 | 856.459701 | 428.733489 | 855.475685 | 428.241481 | 5 |
| 9 | 1277.583064 | 639.295170 | 1260.556515 | 630.781896 | 1259.572499 | 630.289888 | S | *786.454222* | 393.730749 | 769.427673 | 385.217475 | 768.443657 | 384.725467 | 4 |
| 10 | 1716.808390 | 858.907833 | 1699.781841 | 850.394559 | 1698.797825 | 849.902551 | Q | *699.422194* | 350.214735 | 682.395645 | 341.701461 | | | 3 |
| 11 | 1829.892454 | 915.449865 | 1812.865905 | 906.936591 | 1811.881889 | 906.444583 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 12 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 30.6 | 1974.990692 | 0.018340 | IYGNQDTSSQLK |
| 2.9 | 1975.027069 | -0.018037 | ISSQMWLQLSQSLK |
| 0.9 | 1975.031128 | -0.022096 | VCFGDFPTMPKLIPPLK |
| 0.8 | 1975.030411 | -0.021379 | EAQKEMQKIMTSLK |

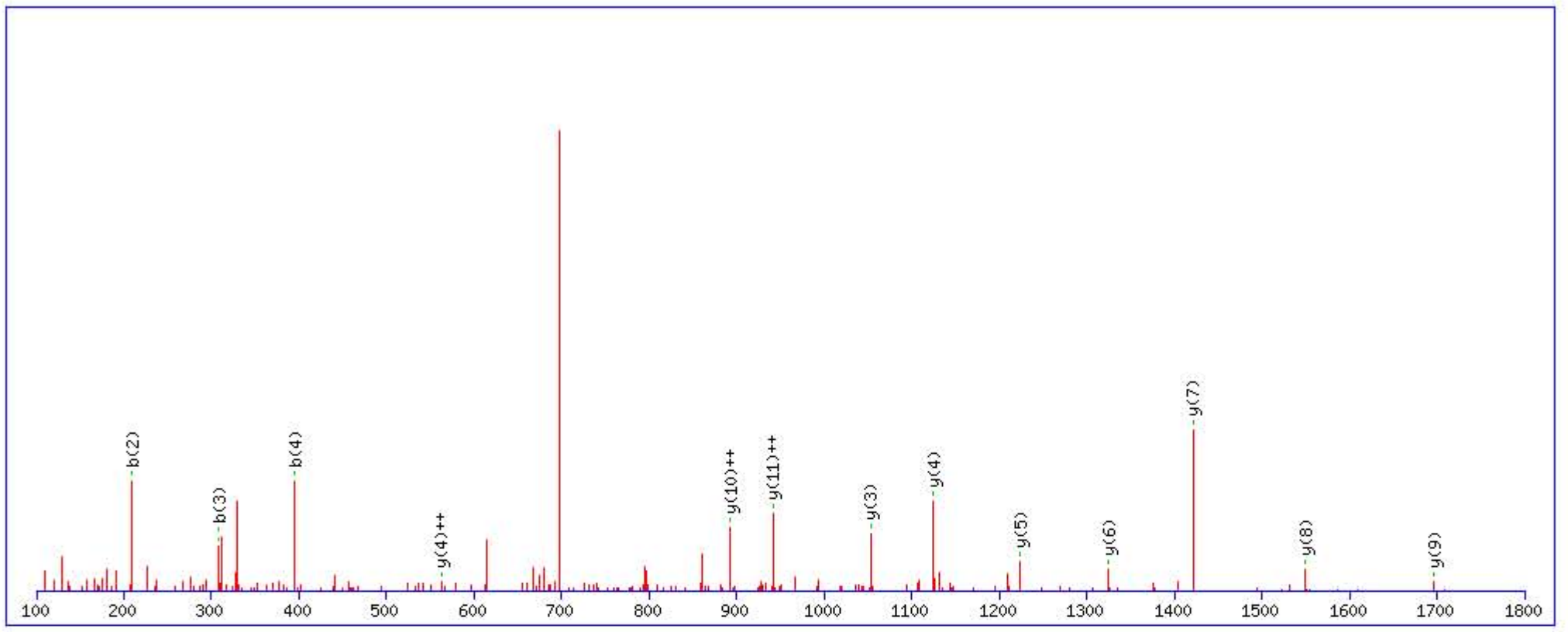
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AHVSFKPTVAQQR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

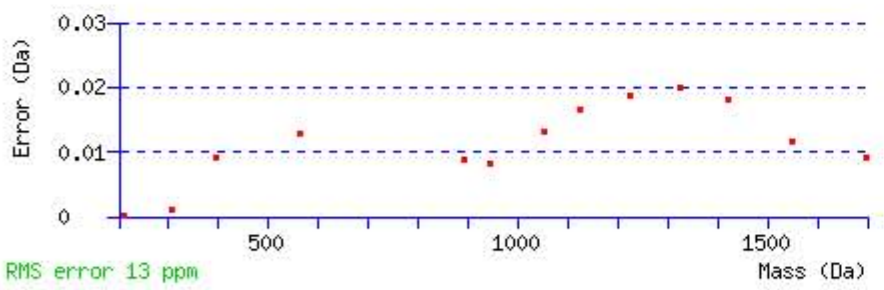
Match to Query 46440: 2090.146332 from(697.722720,3+) rtinseconds(1775) index(48823)
Title: Locus:1.1.1.1856.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

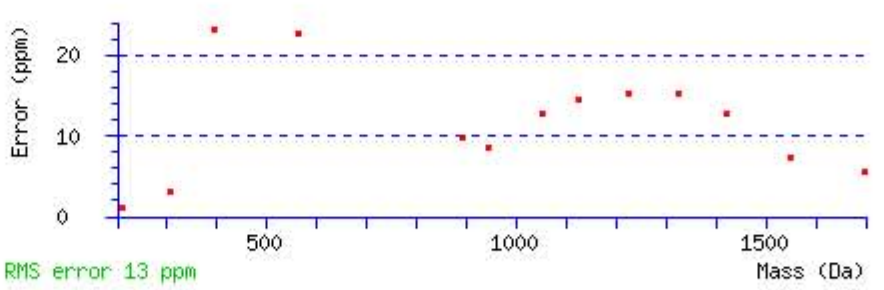
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2090.128143
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Q12** : Biotin:Thermo-21345 (Q)
**Ions Score:** 51 **Expect:** 0.00013
**Matches :** 13/118 fragment ions using 16 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 13 |
| 2 | **209.103302** | 105.055289 | | | | | H | 2020.098306 | 1010.552791 | 2003.071757 | 1002.039517 | 2002.087741 | 1001.547509 | 12 |
| 3 | **308.171716** | 154.589496 | | | | | V | 1883.039394 | 942.023335 | 1866.012845 | 933.510061 | 1865.028829 | 933.018053 | 11 |
| 4 | **395.203744** | 198.105510 | | | 377.193179 | 189.100227 | S | 1783.970980 | 892.489128 | 1766.944431 | 883.975854 | 1765.960415 | 883.483846 | 10 |
| 5 | 542.272158 | 271.639717 | | | 524.261593 | 262.634435 | F | *1696.938952* | 848.973114 | 1679.912403 | 840.459840 | 1678.928387 | 839.967832 | 9 |
| 6 | 670.367121 | 335.687199 | 653.340572 | 327.173924 | 652.356556 | 326.681916 | K | *1549.870538* | 775.438907 | 1532.843989 | 766.925633 | 1531.859973 | 766.433625 | 8 |
| 7 | 767.419885 | 384.213581 | 750.393336 | 375.700306 | 749.409320 | 375.208298 | P | *1421.775575* | 711.391426 | 1404.749026 | 702.878151 | 1403.765010 | 702.386143 | 7 |
| 8 | 868.467564 | 434.737420 | 851.441015 | 426.224146 | 850.456999 | 425.732138 | T | *1324.722811* | 662.865044 | 1307.696262 | 654.351769 | 1306.712246 | 653.859761 | 6 |
| 9 | 967.535978 | 484.271627 | 950.509429 | 475.758353 | 949.525413 | 475.266345 | V | *1223.675132* | 612.341204 | 1206.648583 | 603.827930 | | | 5 |
| 10 | 1038.573092 | 519.790184 | 1021.546543 | 511.276910 | 1020.562527 | 510.784902 | A | *1124.606718* | 562.806997 | 1107.580169 | 554.293723 | | | 4 |
| 11 | 1477.798418 | 739.402847 | 1460.771869 | 730.889573 | 1459.787853 | 730.397565 | Q | *1053.569604* | 527.288440 | 1036.543055 | 518.775166 | | | 3 |
| 12 | 1917.023744 | 959.015510 | 1899.997195 | 950.502236 | 1899.013179 | 950.010228 | Q | 614.344278 | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 13 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 51.0 | 2090.128143 | 0.018189 | AHVSFKPTVAQQR |

**Mascot:** http://www.matrixscience.com/

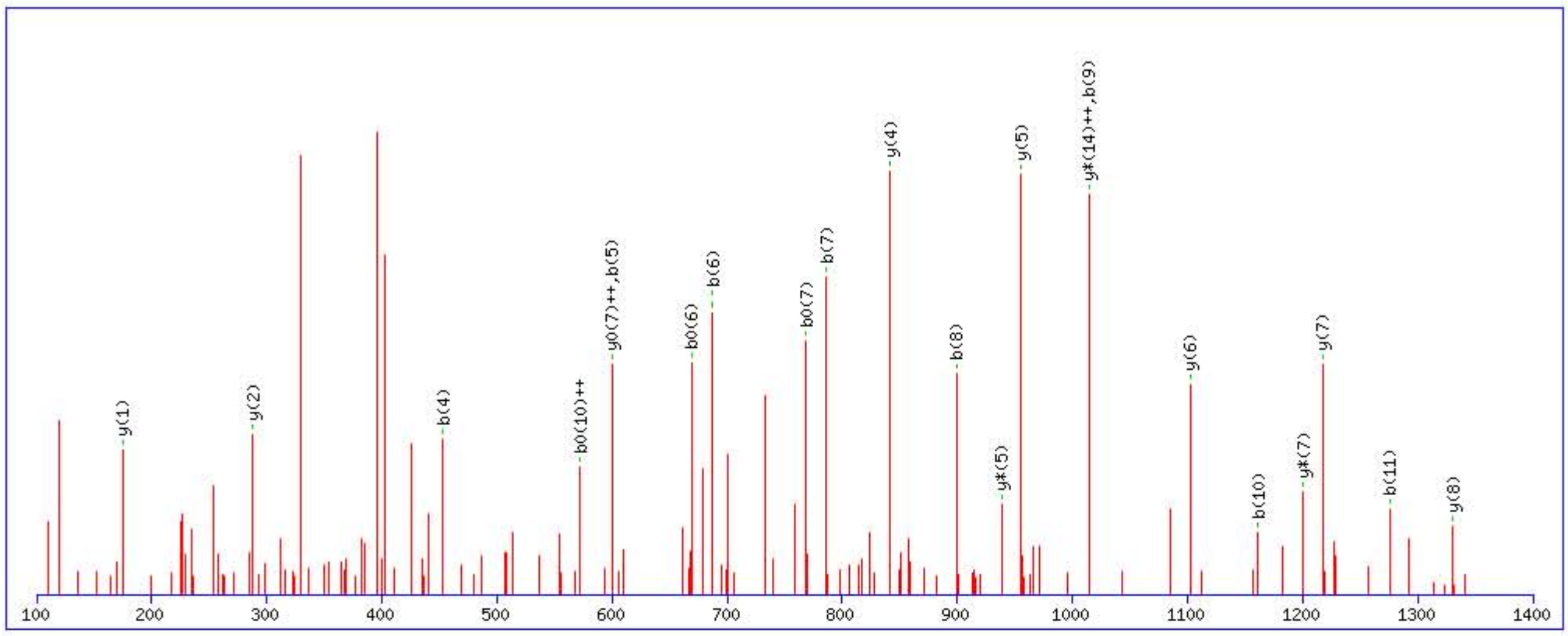
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AEDHFSVIDFNQNIR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

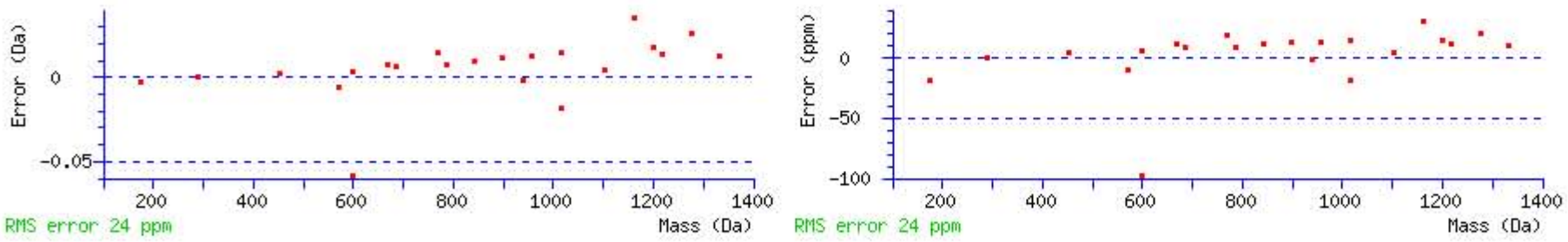
Match to Query 46829: 2115.043932 from(706.021920,3+) rtinseconds(2271) index(52141)
Title: Locus:1.1.1.2028.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2115.020752
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q12** : Biotin:Thermo-21345 (Q)
**Ions Score:** 63 **Expect:** 5.6e-006
**Matches** : 22/134 fragment ions using 26 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 15 |
| 2 | 201.086983 | 101.047130 | | | 183.076418 | 92.041847 | E | 2044.990921 | 1022.999099 | 2027.964372 | 1014.485824 | 2026.980356 | 1013.993816 | 14 |
| 3 | 316.113926 | 158.560601 | | | 298.103361 | 149.555319 | D | 1915.948328 | 958.477802 | 1898.921779 | 949.964528 | 1897.937763 | 949.472519 | 13 |
| 4 | *453.172838* | 227.090057 | | | 435.162273 | 218.084775 | H | 1800.921385 | 900.964331 | 1783.894836 | 892.451056 | 1782.910820 | 891.959048 | 12 |
| 5 | *600.241252* | 300.624264 | | | 582.230687 | 291.618982 | F | 1663.862473 | 832.434874 | 1646.835924 | 823.921600 | 1645.851908 | 823.429592 | 11 |
| 6 | *687.273280* | 344.140278 | | | 669.262715 | 335.134996 | S | 1516.794059 | 758.900668 | 1499.767510 | 750.387393 | 1498.783494 | 749.895385 | 10 |
| 7 | *786.341694* | 393.674485 | | | 768.331129 | 384.669202 | V | 1429.762031 | 715.384654 | 1412.735482 | 706.871379 | 1411.751466 | 706.379371 | 9 |
| 8 | *899.425758* | 450.216517 | | | 881.415193 | 441.211234 | I | *1330.693617* | 665.850447 | 1313.667068 | 657.337172 | 1312.683052 | 656.845164 | 8 |
| 9 | *1014.452701* | 507.729988 | | | 996.442136 | 498.724706 | D | *1217.609553* | 609.308415 | 1200.583004 | 600.795140 | 1199.598988 | 600.303132 | 7 |
| 10 | *1161.521115* | 581.264196 | | | 1143.510550 | 572.258913 | F | *1102.582610* | 551.794943 | 1085.556061 | 543.281669 | | | 6 |
| 11 | *1275.564042* | 638.285659 | 1258.537493 | 629.772385 | 1257.553477 | 629.280376 | N | *955.514196* | 478.260736 | 938.487647 | 469.747462 | | | 5 |
| 12 | 1714.789368 | 857.898322 | 1697.762819 | 849.385048 | 1696.778803 | 848.893039 | Q | *841.471269* | 421.239273 | 824.444720 | 412.725998 | | | 4 |
| 13 | 1828.832295 | 914.919785 | 1811.805746 | 906.406511 | 1810.821730 | 905.914503 | N | 402.245943 | 201.626610 | 385.219394 | 193.113335 | | | 3 |
| 14 | 1941.916359 | 971.461817 | 1924.889810 | 962.948543 | 1923.905794 | 962.456535 | I | *288.203016* | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 63.0 | 2115.020752 | 0.023180 | AEDHFSVIDFNQNIR |
| 7.0 | 2115.033981 | 0.009951 | ESADRQVLMQEEEIK |

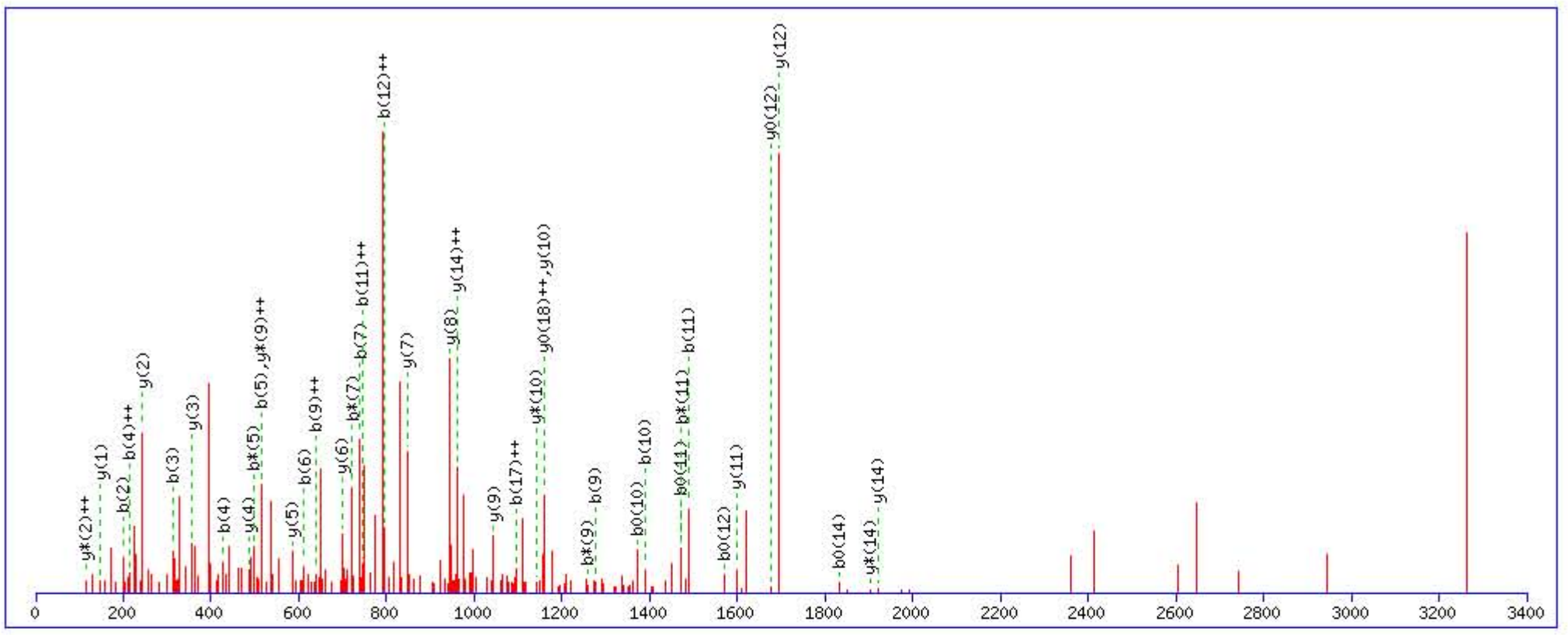
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VVNNSPQPQNVVFDVQIPK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

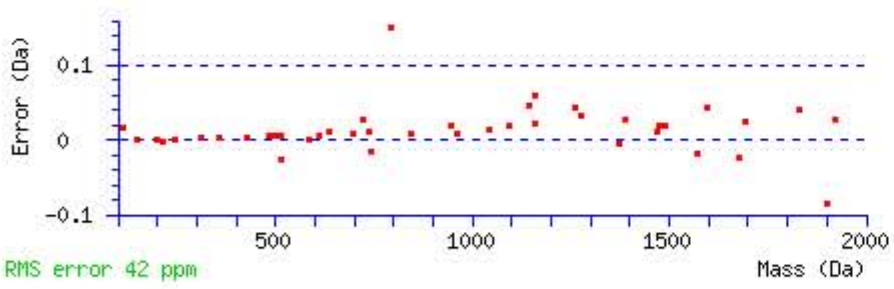
Match to Query 52690: 2432.323452 from(811.781760,3+) rtinseconds(2459) index(53146)
Title: Locus:1.1.1.2093.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

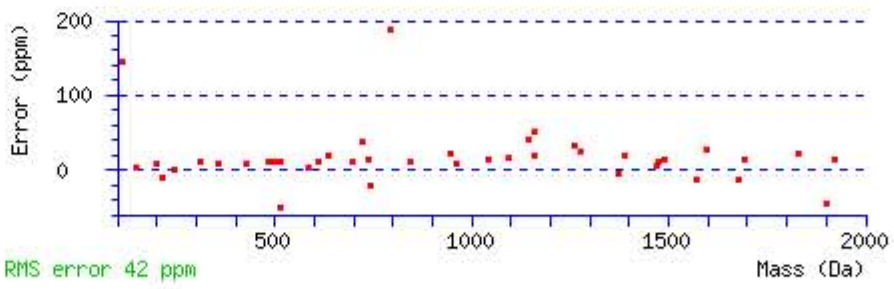
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2432.288620
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 0.00023
**Matches :** 42/194 fragment ions using 114 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 19 |
| 2 | *199.144104* | 100.075690 | | | | | V | 2334.227464 | 1167.617370 | 2317.200915 | 1159.104095 | 2316.216899 | 1158.612087 | 18 |
| 3 | *313.187031* | 157.097153 | 296.160482 | 148.583879 | | | N | 2235.159050 | 1118.083163 | 2218.132501 | 1109.569888 | 2217.148485 | 1109.077880 | 17 |
| 4 | *427.229958* | **214.118617** | 410.203409 | 205.605343 | | | N | 2121.116123 | 1061.061699 | 2104.089574 | 1052.548425 | 2103.105558 | 1052.056417 | 16 |
| 5 | *514.261986* | 257.634631 | *497.235437* | 249.121357 | 496.251421 | 248.629349 | S | 2007.073196 | 1004.040236 | 1990.046647 | 995.526962 | 1989.062631 | 995.034954 | 15 |
| 6 | *611.314750* | 306.161013 | 594.288201 | 297.647739 | 593.304185 | 297.155731 | P | *1920.041168* | 960.524222 | 1903.014619 | 952.010948 | 1902.030603 | 951.518940 | 14 |
| 7 | *739.373328* | 370.190302 | *722.346779* | 361.677028 | 721.362763 | 361.185020 | Q | 1822.988404 | 911.997840 | 1805.961855 | 903.484566 | 1804.977839 | 902.992558 | 13 |
| 8 | 836.426092 | 418.716684 | 819.399543 | 410.203410 | 818.415527 | 409.711402 | P | *1694.929826* | 847.968551 | 1677.903277 | 839.455277 | *1676.919261* | 838.963269 | 12 |
| 9 | *1275.651418* | **638.329347** | *1258.624869* | 629.816073 | 1257.640853 | 629.324065 | Q | *1597.877062* | 799.442169 | 1580.850513 | 790.928895 | 1579.866497 | 790.436887 | 11 |
| 10 | *1389.694345* | 695.350811 | 1372.667796 | 686.837536 | *1371.683780* | 686.345528 | N | *1158.651736* | 579.829506 | *1141.625187* | 571.316232 | 1140.641171 | 570.824224 | 10 |
| 11 | *1488.762759* | **744.885018** | *1471.736210* | 736.371743 | *1470.752194* | 735.879735 | V | *1044.608809* | 522.808043 | 1027.582260 | *514.294768* | 1026.598244 | 513.802760 | 9 |
| 12 | 1587.831173 | **794.419225** | 1570.804624 | 785.905950 | *1569.820608* | 785.413942 | V | *945.540395* | 473.273836 | 928.513846 | 464.760561 | 927.529830 | 464.268553 | 8 |
| 13 | 1734.899587 | 867.953432 | 1717.873038 | 859.440157 | 1716.889022 | 858.948149 | F | *846.471981* | 423.739629 | 829.445432 | 415.226354 | 828.461416 | 414.734346 | 7 |
| 14 | 1849.926530 | 925.466903 | 1832.899981 | 916.953629 | *1831.915965* | 916.461621 | D | *699.403567* | 350.205422 | 682.377018 | 341.692147 | 681.393002 | 341.200139 | 6 |
| 15 | 1948.994944 | 975.001110 | 1931.968395 | 966.487836 | 1930.984379 | 965.995828 | V | *584.376624* | 292.691950 | 567.350075 | 284.178676 | | | 5 |
| 16 | 2077.053522 | 1039.030399 | 2060.026973 | 1030.517124 | 2059.042957 | 1030.025117 | Q | *485.308210* | 243.157743 | 468.281661 | 234.644469 | | | 4 |
| 17 | 2190.137586 | **1095.572431** | 2173.111037 | 1087.059157 | 2172.127021 | 1086.567149 | I | *357.249632* | 179.128454 | 340.223083 | 170.615180 | | | 3 |
| 18 | 2287.190350 | 1144.098813 | 2270.163801 | 1135.585539 | 2269.179785 | 1135.093531 | P | *244.165568* | 122.586422 | 227.139019 | *114.073148* | | | 2 |
| 19 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.4 | 2432.288620 | 0.034832 | VVNNSPQPQNVVFDVQIPK |
| 31.2 | 2432.288620 | 0.034832 | VVNNSPQPQNVVFDVQIPK |
| 16.7 | 2432.288620 | 0.034832 | VVNNSPQPQNVVFDVQIPK |

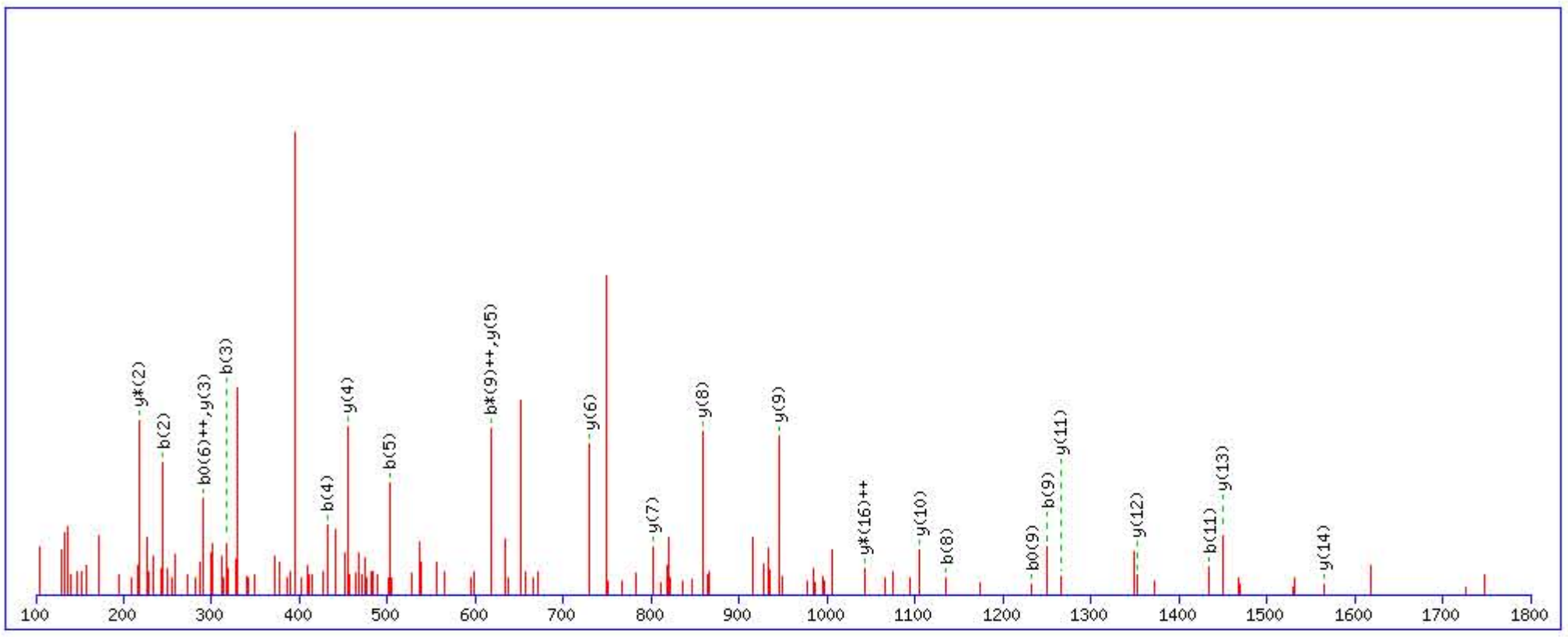
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **MLADAPPQDPSCCSGALYYGSK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

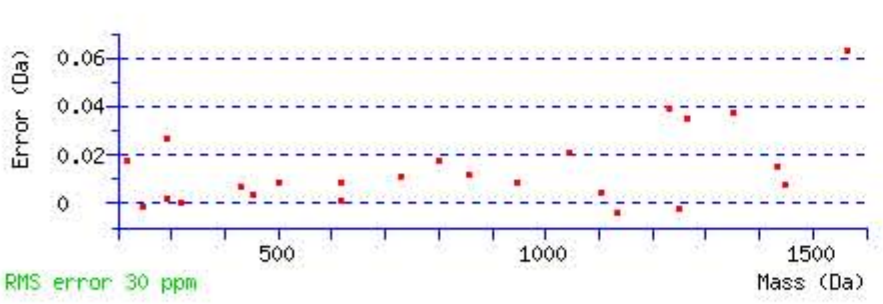
Match to Query 56340: 2698.215496 from(675.561150,4+) rtinseconds(2101) index(50985)
Title: Locus:1.1.1.1969.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

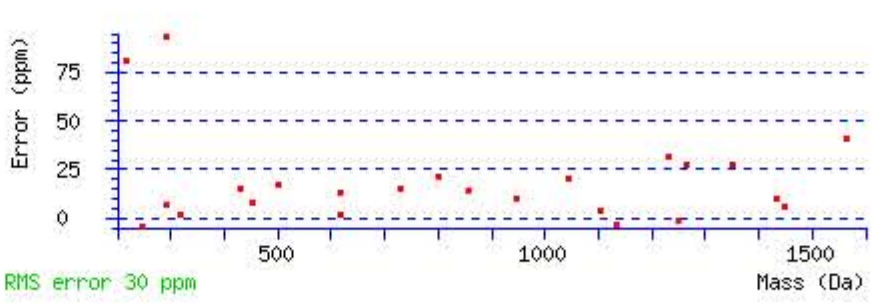
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2698.189941
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 60 **Expect:** 9.8e-006
**Matches :** 24/230 fragment ions using 48 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.047761 | 66.527518 | | | | | M | | | | | | | 22 |
| 2 | *245.131825* | 123.069550 | | | | | L | 2568.156746 | 1284.582011 | 2551.130197 | 1276.068736 | 2550.146181 | 1275.576728 | 21 |
| 3 | *316.168939* | 158.588107 | | | | | A | 2455.072682 | 1228.039979 | 2438.046133 | 1219.526704 | 2437.062117 | 1219.034696 | 20 |
| 4 | *431.195882* | 216.101579 | | | 413.185317 | 207.096296 | D | 2384.035568 | 1192.521422 | 2367.009019 | 1184.008148 | 2366.025003 | 1183.516140 | 19 |
| 5 | *502.232996* | 251.620136 | | | 484.222431 | 242.614854 | A | 2269.008625 | 1135.007950 | 2251.982076 | 1126.494676 | 2250.998060 | 1126.002668 | 18 |
| 6 | 599.285760 | 300.146518 | | | 581.275195 | 291.141236 | P | 2197.971511 | 1099.489394 | 2180.944962 | 1090.976119 | 2179.960946 | 1090.484111 | 17 |
| 7 | 696.338524 | 348.672900 | | | 678.327959 | 339.667618 | P | 2100.918747 | 1050.963012 | 2083.892198 | 1042.449737 | 2082.908182 | 1041.957729 | 16 |
| 8 | *1135.563850* | 568.285563 | 1118.537301 | 559.772289 | 1117.553285 | 559.280281 | Q | 2003.865983 | 1002.436630 | 1986.839434 | 993.923355 | 1985.855418 | 993.431347 | 15 |
| 9 | *1250.590793* | 625.799035 | 1233.564244 | 617.285760 | 1232.580228 | 616.793752 | D | *1564.640657* | 782.823967 | 1547.614108 | 774.310692 | 1546.630092 | 773.818684 | 14 |
| 10 | 1347.643557 | 674.325417 | 1330.617008 | 665.812142 | 1329.632992 | 665.320134 | P | *1449.613714* | 725.310495 | 1432.587165 | 716.797221 | 1431.603149 | 716.305213 | 13 |
| 11 | *1434.675585* | 717.841431 | 1417.649036 | 709.328156 | 1416.665020 | 708.836148 | S | *1352.560950* | 676.784113 | 1335.534401 | 668.270839 | 1334.550385 | 667.778831 | 12 |
| 12 | 1594.706234 | 797.856755 | 1577.679685 | 789.343481 | 1576.695669 | 788.851473 | C | *1265.528922* | 633.268099 | 1248.502373 | 624.754825 | 1247.518357 | 624.262817 | 11 |
| 13 | 1754.736883 | 877.872080 | 1737.710334 | 869.358805 | 1736.726318 | 868.866797 | C | *1105.498273* | 553.252775 | 1088.471724 | 544.739500 | 1087.487708 | 544.247492 | 10 |
| 14 | 1841.768911 | 921.388094 | 1824.742362 | 912.874819 | 1823.758346 | 912.382811 | S | *945.467624* | 473.237450 | 928.441075 | 464.724176 | 927.457059 | 464.232168 | 9 |
| 15 | 1898.790375 | 949.898826 | 1881.763826 | 941.385551 | 1880.779810 | 940.893543 | G | *858.435596* | 429.721436 | 841.409047 | 421.208162 | 840.425031 | 420.716154 | 8 |
| 16 | 1969.827489 | 985.417383 | 1952.800940 | 976.904108 | 1951.816924 | 976.412100 | A | *801.414132* | 401.210704 | 784.387583 | 392.697430 | 783.403567 | 392.205422 | 7 |
| 17 | 2082.911553 | 1041.959415 | 2065.885004 | 1033.446140 | 2064.900988 | 1032.954132 | L | *730.377018* | 365.692147 | 713.350469 | 357.178873 | 712.366453 | 356.686865 | 6 |
| 18 | 2245.974882 | 1123.491079 | 2228.948333 | 1114.977805 | 2227.964317 | 1114.485797 | Y | *617.292954* | 309.150115 | 600.266405 | 300.636841 | 599.282389 | 300.144833 | 5 |
| 19 | 2409.038211 | 1205.022744 | 2392.011662 | 1196.509469 | 2391.027646 | 1196.017461 | Y | *454.229625* | 227.618451 | 437.203076 | 219.105176 | 436.219060 | 218.613168 | 4 |
| 20 | 2466.059675 | 1233.533476 | 2449.033126 | 1225.020201 | 2448.049110 | 1224.528193 | G | *291.166296* | 146.086786 | 274.139747 | 137.573512 | 273.155731 | 137.081504 | 3 |
| 21 | 2553.091703 | 1277.049490 | 2536.065154 | 1268.536215 | 2535.081138 | 1268.044207 | S | 234.144832 | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 22 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 59.7 | 2698.189941 | 0.025555 | MLADAPPQDPSCCSGALYYGSK |

**Mascot:** http://www.matrixscience.com/

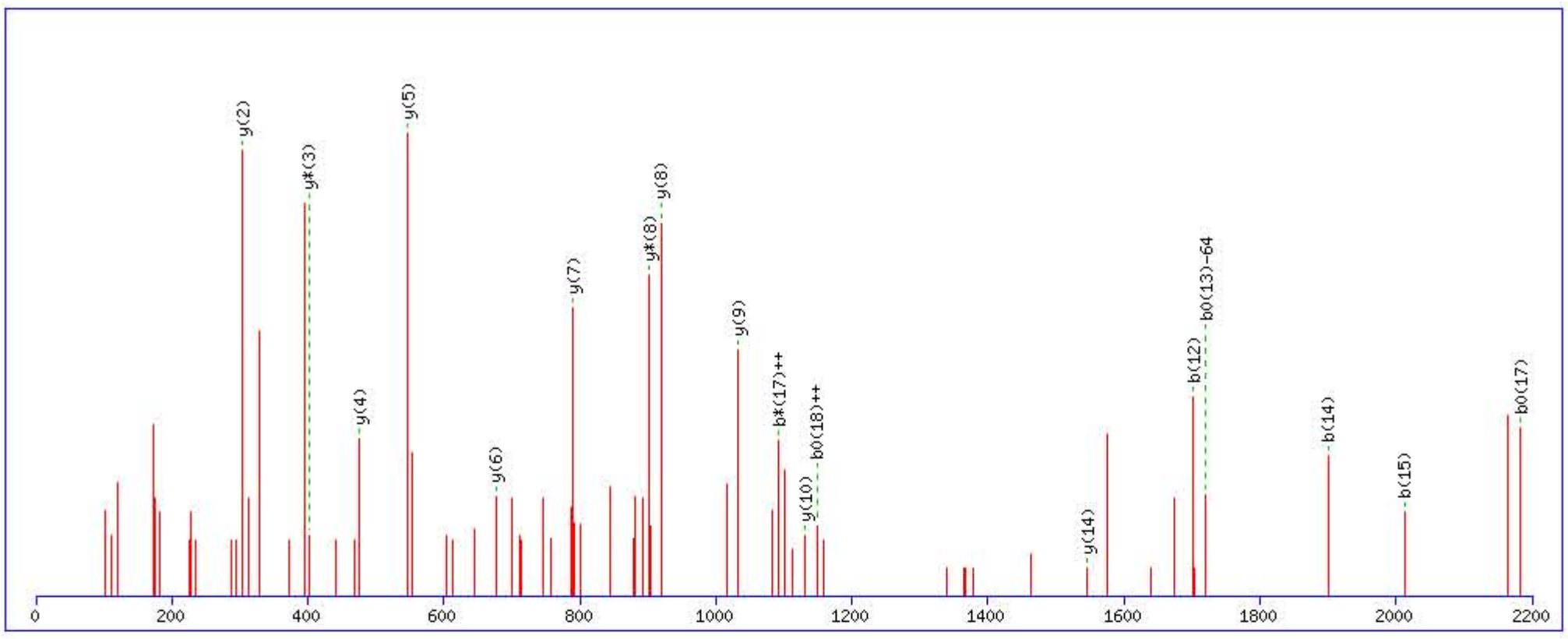
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SILQMSLDHHIVTPLTSLVIENEAGDER**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

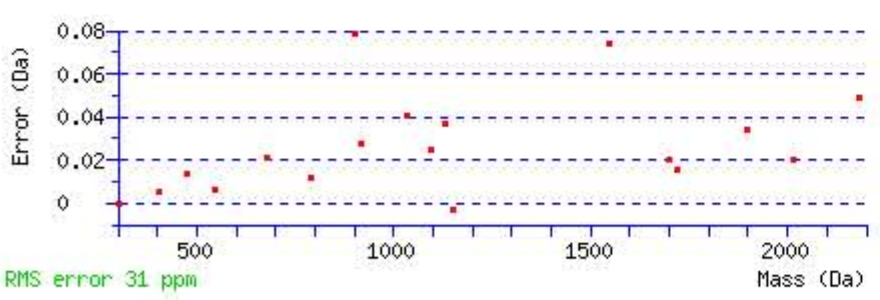
Match to Query 65343: 3443.787320 from(689.764740,5+) rtinseconds(2657) index(54337)
Title: Locus:1.1.1.2162.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

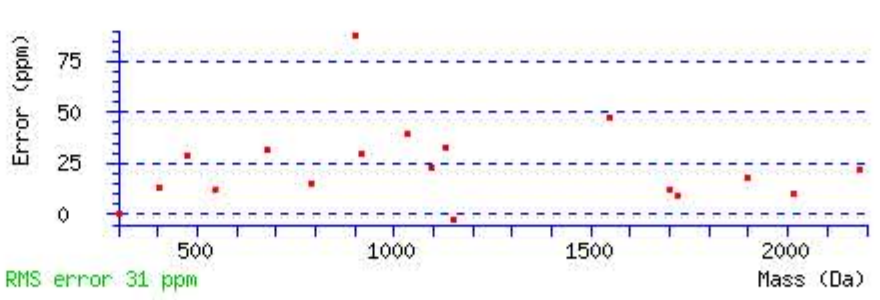
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3443.742859
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
M5 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
**Ions Score:** 36 **Expect:** 0.0062
**Matches :** 18/478 fragment ions using 35 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 28 |
| 2 | 201.123368 | 101.065322 | | | 183.112803 | 92.060039 | I | 3357.718126 | 1679.362701 | 3340.691577 | 1670.849426 | 3339.707561 | 1670.357418 | 27 |
| 3 | 314.207432 | 157.607354 | | | 296.196867 | 148.602071 | L | 3244.634062 | 1622.820669 | 3227.607513 | 1614.307394 | 3226.623497 | 1613.815386 | 26 |
| 4 | 753.432758 | 377.220017 | 736.406209 | 368.706743 | 735.422193 | 368.214735 | Q | 3131.549998 | 1566.278637 | 3114.523449 | 1557.765362 | 3113.539433 | 1557.273354 | 25 |
| 5 | 900.468158 | 450.737717 | 883.441609 | 442.224443 | 882.457593 | 441.732435 | M | 2692.324672 | 1346.665974 | 2675.298123 | 1338.152699 | 2674.314107 | 1337.660691 | 24 |
| 6 | 987.500186 | 494.253731 | 970.473637 | 485.740456 | 969.489621 | 485.248448 | S | 2545.289272 | 1273.148274 | 2528.262723 | 1264.634999 | 2527.278707 | 1264.142991 | 23 |
| 7 | 1100.584250 | 550.795763 | 1083.557701 | 542.282489 | 1082.573685 | 541.790480 | L | 2458.257244 | 1229.632260 | 2441.230695 | 1221.118985 | 2440.246679 | 1220.626977 | 22 |
| 8 | 1215.611193 | 608.309235 | 1198.584644 | 599.795960 | 1197.600628 | 599.303952 | D | 2345.173180 | 1173.090228 | 2328.146631 | 1164.576953 | 2327.162615 | 1164.084945 | 21 |
| 9 | 1352.670105 | 676.838690 | 1335.643556 | 668.325416 | 1334.659540 | 667.833408 | H | 2230.146237 | 1115.576756 | 2213.119688 | 1107.063482 | 2212.135672 | 1106.571474 | 20 |
| 10 | 1489.729017 | 745.368146 | 1472.702468 | 736.854872 | 1471.718452 | 736.362864 | H | 2093.087325 | 1047.047300 | 2076.060776 | 1038.534026 | 2075.076760 | 1038.042018 | 19 |
| 11 | 1602.813081 | 801.910178 | 1585.786532 | 793.396904 | 1584.802516 | 792.904896 | I | 1956.028413 | 978.517845 | 1939.001864 | 970.004570 | 1938.017848 | 969.512562 | 18 |
| 12 | **1701.881495** | 851.444385 | 1684.854946 | 842.931111 | 1683.870930 | 842.439103 | V | 1842.944349 | 921.975813 | 1825.917800 | 913.462538 | 1824.933784 | 912.970530 | 17 |
| 13 | 1802.929174 | 901.968225 | 1785.902625 | 893.454951 | 1784.918609 | 892.962942 | T | 1743.875935 | 872.441606 | 1726.849386 | 863.928331 | 1725.865370 | 863.436323 | 16 |
| 14 | **1899.981938** | 950.494607 | 1882.955389 | 941.981333 | 1881.971373 | 941.489324 | P | 1642.828256 | 821.917766 | 1625.801707 | 813.404492 | 1624.817691 | 812.912484 | 15 |
| 15 | **2013.066002** | 1007.036639 | 1996.039453 | 998.523364 | 1995.055437 | 998.031356 | L | *1545.775492* | 773.391384 | 1528.748943 | 764.878110 | 1527.764927 | 764.386102 | 14 |
| 16 | 2114.113681 | 1057.560478 | 2097.087132 | 1049.047204 | 2096.103116 | 1048.555196 | T | 1432.691428 | 716.849352 | 1415.664879 | 708.336078 | 1414.680863 | 707.844070 | 13 |
| 17 | 2201.145709 | 1101.076492 | 2184.119160 | 1092.563218 | 2183.135144 | 1092.071210 | S | 1331.643749 | 666.325513 | 1314.617200 | 657.812238 | 1313.633184 | 657.320230 | 12 |
| 18 | 2314.229773 | 1157.618524 | 2297.203224 | 1149.105250 | 2296.219208 | 1148.613242 | L | 1244.611721 | 622.809499 | 1227.585172 | 614.296224 | 1226.601156 | 613.804216 | 11 |
| 19 | 2413.298187 | 1207.152731 | 2396.271638 | 1198.639457 | 2395.287622 | 1198.147449 | V | *1131.527657* | 566.267467 | 1114.501108 | 557.754192 | 1113.517092 | 557.262184 | 10 |
| 20 | 2526.382251 | 1263.694763 | 2509.355702 | 1255.181489 | 2508.371686 | 1254.689481 | I | *1032.459243* | 516.733260 | 1015.432694 | 508.219985 | 1014.448678 | 507.727977 | 9 |
| 21 | 2655.424844 | 1328.216060 | 2638.398295 | 1319.702785 | 2637.414279 | 1319.210777 | E | *919.375179* | 460.191228 | 902.348630 | 451.677953 | 901.364614 | 451.185945 | 8 |
| 22 | 2769.467771 | 1385.237523 | 2752.441222 | 1376.724249 | 2751.457206 | 1376.232241 | N | *790.332586* | 395.669931 | 773.306037 | 387.156657 | 772.322021 | 386.664649 | 7 |
| 23 | 2898.510364 | 1449.758820 | 2881.483815 | 1441.245545 | 2880.499799 | 1440.753537 | E | *676.289659* | 338.648468 | 659.263110 | 330.135193 | 658.279094 | 329.643185 | 6 |
| 24 | 2969.547478 | 1485.277377 | 2952.520929 | 1476.764102 | 2951.536913 | 1476.272094 | A | *547.247066* | 274.127171 | 530.220517 | 265.613897 | 529.236501 | 265.121889 | 5 |
| 25 | 3026.568942 | 1513.788109 | 3009.542393 | 1505.274834 | 3008.558377 | 1504.782826 | G | *476.209952* | 238.608614 | 459.183403 | 230.095339 | 458.199387 | 229.603331 | 4 |
| 26 | 3141.595885 | 1571.301580 | 3124.569336 | 1562.788306 | 3123.585320 | 1562.296298 | D | 419.188488 | 210.097882 | 402.161939 | 201.584607 | 401.177923 | 201.092599 | 3 |
| 27 | 3270.638478 | 1635.822877 | 3253.611929 | 1627.309602 | 3252.627913 | 1626.817594 | E | *304.161545* | 152.584411 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 28 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 35.9 | 3443.742859 | 0.044461 | SILQMSLDHHIVTPLTSLVIENEAGDER |

**Mascot:** http://www.matrixscience.com/

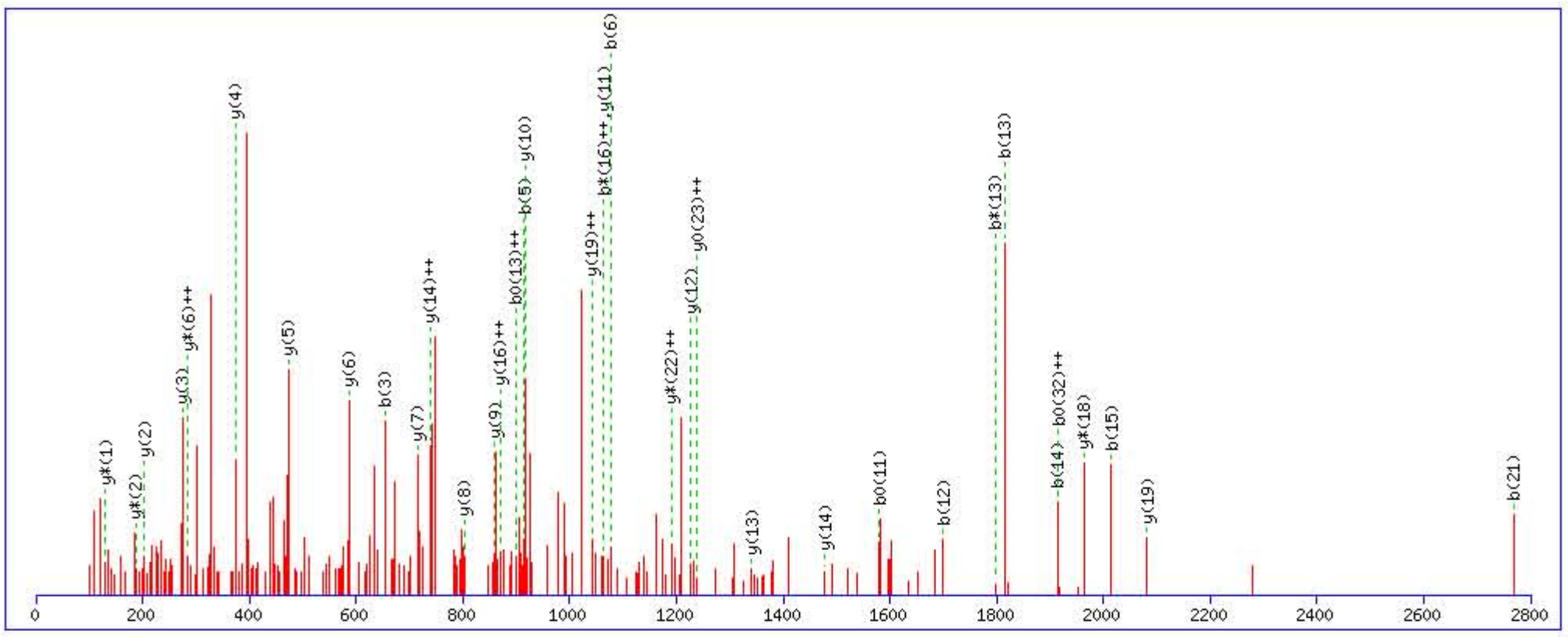
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

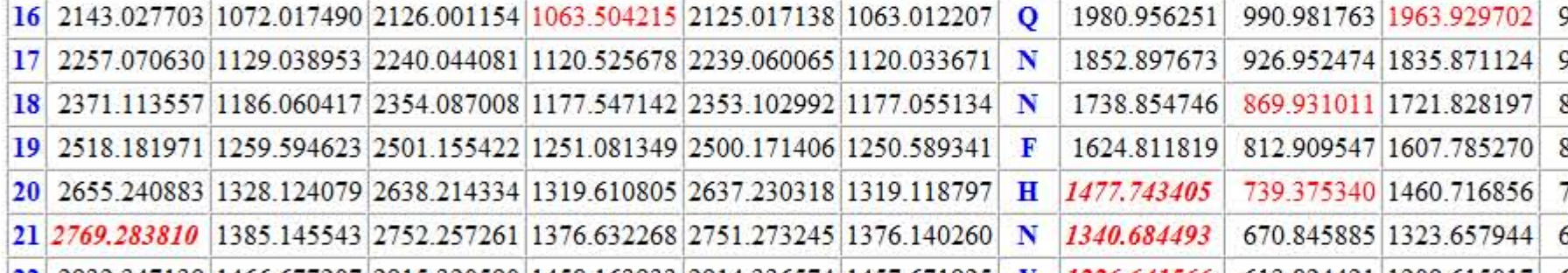
Match to Query 68599: 3993.962520 from(799.799780,5+) rtinseconds(2384) index(52772)
Title: Locus:1.1.1.2067.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3993.910858
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 26 **Expect:** 0.065
**Matches :** 36/356 fragment ions using 142 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 33 |
| 2 | 214.118617 | 107.562947 | 197.092068 | 99.049672 | | | V | 3880.875173 | 1940.941224 | 3863.848624 | 1932.427950 | 3862.864608 | 1931.935942 | 32 |
| 3 | *653.343943* | 327.175610 | 636.317394 | 318.662335 | | | Q | 3781.806759 | 1891.407017 | 3764.780210 | 1882.893743 | 3763.796194 | 1882.401735 | 31 |
| 4 | 800.412357 | 400.709817 | 783.385808 | 392.196542 | | | F | 3342.581433 | 1671.794354 | 3325.554884 | 1663.281080 | 3324.570868 | 1662.789072 | 30 |
| 5 | *914.455284* | 457.731280 | 897.428735 | 449.218006 | | | N | 3195.513019 | 1598.260147 | 3178.486470 | 1589.746873 | 3177.502454 | 1589.254865 | 29 |
| 6 | *1077.518613* | 539.262945 | 1060.492064 | 530.749670 | | | Y | 3081.470092 | 1541.238684 | 3064.443543 | 1532.725409 | 3063.459527 | 1532.233401 | 28 |
| 7 | 1174.571377 | 587.789327 | 1157.544828 | 579.276052 | | | P | 2918.406763 | 1459.707019 | 2901.380214 | 1451.193745 | 2900.396198 | 1450.701737 | 27 |
| 8 | 1311.630289 | 656.318783 | 1294.603740 | 647.805508 | | | H | 2821.353999 | 1411.180637 | 2804.327450 | 1402.667363 | 2803.343434 | 1402.175355 | 26 |
| 9 | 1412.677968 | 706.842622 | 1395.651419 | 698.329348 | 1394.667403 | 697.837339 | T | 2684.295087 | 1342.651181 | 2667.268538 | 1334.137907 | 2666.284522 | 1333.645899 | 25 |
| 10 | 1499.709996 | 750.358636 | 1482.683447 | 741.845362 | 1481.699431 | 741.353354 | S | 2583.247408 | 1292.127342 | 2566.220859 | 1283.614067 | 2565.236843 | 1283.122059 | 24 |
| 11 | 1598.778410 | 799.892843 | 1581.751861 | 791.379569 | 1580.767845 | 790.887561 | V | 2496.215380 | 1248.611328 | 2479.188831 | 1240.098053 | 2478.204815 | 1239.606045 | 23 |
| 12 | *1699.826089* | 850.416683 | 1682.799540 | 841.903408 | 1681.815524 | 841.411400 | T | 2397.146966 | 1199.077121 | 2380.120417 | 1190.563846 | 2379.136401 | 1190.071838 | 22 |
| 13 | *1814.853032* | 907.930154 | 1797.826483 | 899.416880 | 1796.842467 | 898.924872 | D | 2296.099287 | 1148.553281 | 2279.072738 | 1140.040007 | 2278.088722 | 1139.547999 | 21 |
| 14 | *1913.921446* | 957.464361 | 1896.894897 | 948.951087 | 1895.910881 | 948.459079 | V | 2181.072344 | 1091.039810 | 2164.045795 | 1082.526535 | 2163.061779 | 1082.034527 | 20 |
| 15 | *2014.969125* | 1007.988201 | 1997.942576 | 999.474926 | 1996.958560 | 998.982918 | T | *2082.003930* | 1041.505603 | 2064.977381 | 1032.992328 | 2063.993365 | 1032.500320 | 19 |
| 16 | 2143.027703 | 1072.017490 | 2126.001154 | 1063.504215 | 2125.017138 | 1063.012207 | Q | 1980.956251 | 990.981763 | 1963.929702 | 982.468489 | 1962.945686 | 981.976481 | 18 |
| 17 | 2257.070630 | 1129.038953 | 2240.044081 | 1120.525678 | 2239.060065 | 1120.033671 | N | 1852.897673 | 926.952474 | 1835.871124 | 918.439200 | 1834.887108 | 917.947192 | 17 |
| 18 | 2371.113557 | 1186.060417 | 2354.087008 | 1177.547142 | 2353.102992 | 1177.055134 | N | 1738.854746 | 869.931011 | 1721.828197 | 861.417736 | 1720.844181 | 860.925728 | 16 |
| 19 | 2518.181971 | 1259.594623 | 2501.155422 | 1251.081349 | 2500.171406 | 1250.589341 | F | 1624.811819 | 812.909547 | 1607.785270 | 804.396273 | 1606.801254 | 803.904265 | 15 |
| 20 | 2655.240883 | 1328.124079 | 2638.214334 | 1319.610805 | 2637.230318 | 1319.118797 | H | *1477.743405* | 739.375340 | 1460.716856 | 730.862066 | 1459.732840 | 730.370058 | 14 |
| 21 | *2769.283810* | 1385.145543 | 2752.257261 | 1376.632268 | 2751.273245 | 1376.140260 | N | *1340.684493* | 670.845885 | 1323.657944 | 662.332610 | 1322.673928 | 661.840602 | 13 |
| 22 | 2932.347139 | 1466.677207 | 2915.320590 | 1458.163933 | 2914.336574 | 1457.671925 | Y | *1226.641566* | 613.824421 | 1209.615017 | 605.311147 | 1208.631001 | 604.819139 | 12 |
| 23 | 3079.415553 | 1540.211414 | 3062.389004 | 1531.698140 | 3061.404988 | 1531.206132 | F | *1063.578237* | 532.292757 | 1046.551688 | 523.779482 | 1045.567672 | 523.287474 | 11 |
| 24 | 3136.437017 | 1568.722146 | 3119.410468 | 1560.208872 | 3118.426452 | 1559.716864 | G | *916.509823* | 458.758550 | 899.483274 | 450.245275 | 898.499258 | 449.753267 | 10 |
| 25 | 3193.458481 | 1597.232878 | 3176.431932 | 1588.719604 | 3175.447916 | 1588.227596 | G | *859.488359* | 430.247818 | 842.461810 | 421.734543 | 841.477794 | 421.242535 | 9 |
| 26 | 3280.490509 | 1640.748892 | 3263.463960 | 1632.235618 | 3262.479944 | 1631.743610 | S | *802.466895* | 401.737086 | 785.440346 | 393.223811 | 784.456330 | 392.731803 | 8 |
| 27 | 3409.533102 | 1705.270189 | 3392.506553 | 1696.756914 | 3391.522537 | 1696.264906 | E | *715.434867* | 358.221072 | 698.408318 | 349.707797 | 697.424302 | 349.215789 | 7 |
| 28 | 3522.617166 | 1761.812221 | 3505.590617 | 1753.298946 | 3504.606601 | 1752.806938 | I | *586.392274* | 293.699775 | 569.365725 | 285.186501 | | | 6 |
| 29 | 3621.685580 | 1811.346428 | 3604.659031 | 1802.833153 | 3603.675015 | 1802.341145 | V | *473.308210* | 237.157743 | 456.281661 | 228.644468 | | | 5 |
| 30 | 3720.753994 | 1860.880635 | 3703.727445 | 1852.367360 | 3702.743429 | 1851.875352 | V | *374.239796* | 187.623536 | 357.213247 | 179.110261 | | | 4 |
| 31 | 3791.791108 | 1896.399192 | 3774.764559 | 1887.885917 | 3773.780543 | 1887.393909 | A | *275.171382* | 138.089329 | 258.144833 | 129.576055 | | | 3 |
| 32 | 3848.812572 | 1924.909924 | 3831.786023 | 1916.396649 | 3830.802007 | 1915.904641 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 33 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.6 | 3993.910858 | 0.051662 | NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK |
| 3.9 | 3993.910858 | 0.051662 | NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK |

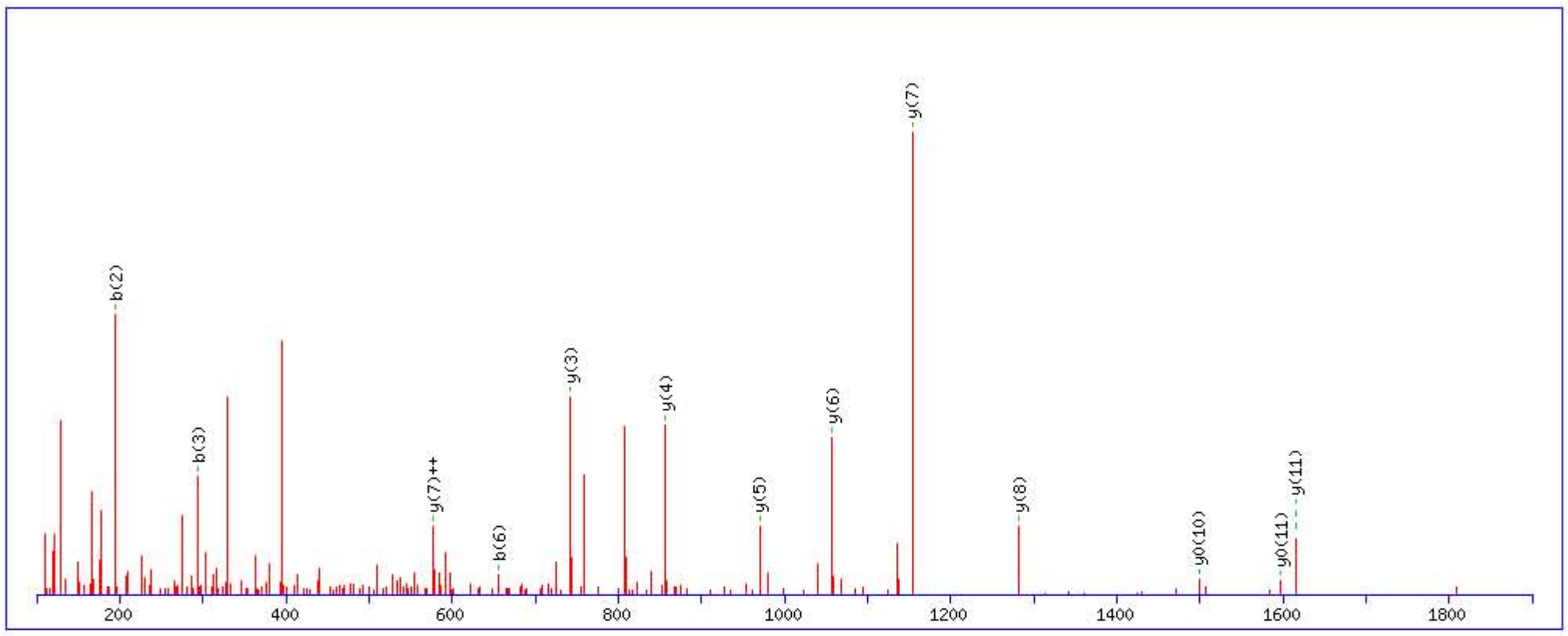
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GHVSFKPSLDQQR**
Found in **ITIH3_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

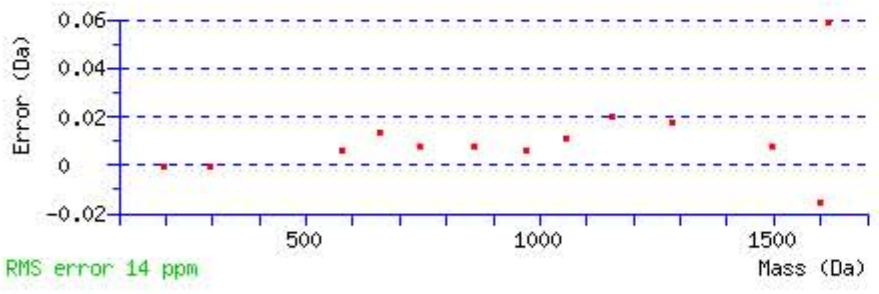
Match to Query 40463: 1808.943612 from(603.988480,3+) rtinseconds(1623) index(47808)
Title: Locus:1.1.1.1803.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

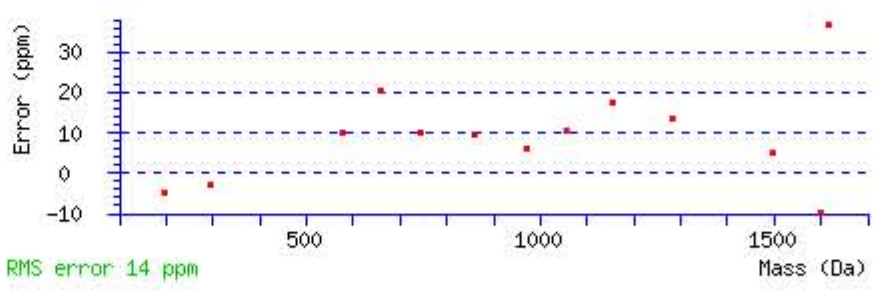
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1808.935577
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 50 **Expect:** 2e-005
**Matches :** 13/122 fragment ions using 16 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 13 |
| 2 | 195.087652 | 98.047464 | | | | | H | 1752.921386 | 876.964331 | 1735.894837 | 868.451057 | 1734.910821 | 867.959049 | 12 |
| 3 | 294.156066 | 147.581671 | | | | | V | *1615.862474* | 808.434875 | 1598.835925 | 799.921601 | 1597.851909 | 799.429593 | 11 |
| 4 | 381.188094 | 191.097685 | | | 363.177529 | 182.092403 | S | 1516.794060 | 758.900668 | 1499.767511 | 750.387394 | 1498.783495 | 749.895386 | 10 |
| 5 | 528.256508 | 264.631892 | | | 510.245943 | 255.626610 | F | 1429.762032 | 715.384654 | 1412.735483 | 706.871380 | 1411.751467 | 706.379372 | 9 |
| 6 | 656.351471 | 328.679374 | 639.324922 | 320.166099 | 638.340906 | 319.674091 | K | *1282.693618* | 641.850447 | 1265.667069 | 633.337173 | 1264.683053 | 632.845165 | 8 |
| 7 | 753.404235 | 377.205756 | 736.377686 | 368.692481 | 735.393670 | 368.200473 | P | *1154.598655* | 577.802966 | 1137.572106 | 569.289691 | 1136.588090 | 568.797683 | 7 |
| 8 | 840.436263 | 420.721770 | 823.409714 | 412.208495 | 822.425698 | 411.716487 | S | *1057.545891* | 529.276584 | 1040.519342 | 520.763309 | 1039.535326 | 520.271301 | 6 |
| 9 | 953.520327 | 477.263802 | 936.493778 | 468.750527 | 935.509762 | 468.258519 | L | *970.513863* | 485.760570 | 953.487314 | 477.247295 | 952.503298 | 476.755287 | 5 |
| 10 | 1068.547270 | 534.777273 | 1051.520721 | 526.263999 | 1050.536705 | 525.771991 | D | *857.429799* | 429.218538 | 840.403250 | 420.705263 | 839.419234 | 420.213255 | 4 |
| 11 | 1196.605848 | 598.806562 | 1179.579299 | 590.293288 | 1178.595283 | 589.801279 | Q | *742.402856* | 371.705066 | 725.376307 | 363.191792 | | | 3 |
| 12 | 1635.831174 | 818.419225 | 1618.804625 | 809.905951 | 1617.820609 | 809.413943 | Q | 614.344278 | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 13 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 50.3 | 1808.935577 | 0.008035 | GHVSFKPSLDQQR |
| 50.3 | 1808.935577 | 0.008035 | GHVSFKPSLDQQR |
| 0.3 | 1808.946793 | -0.003181 | IFRQNSDLVNHR |

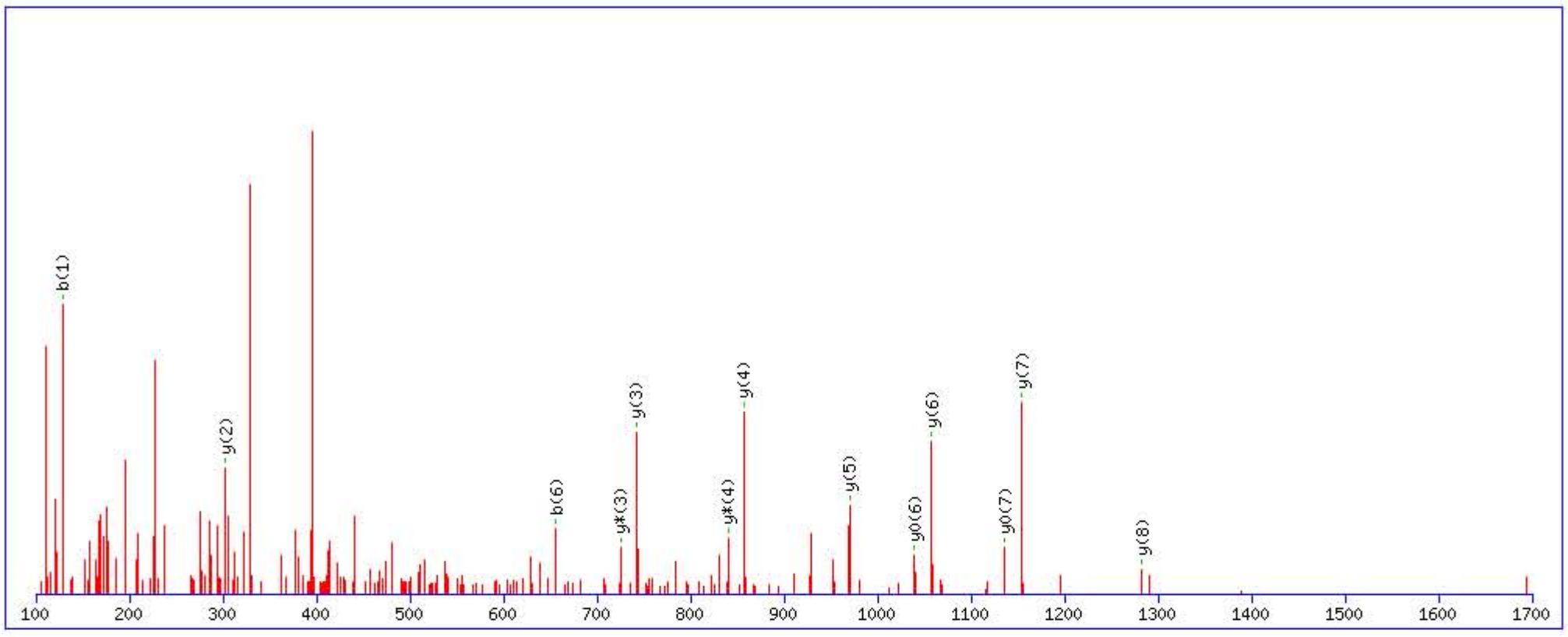
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KGHVSFKPSLDQQR**
Found in **ITIH3_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

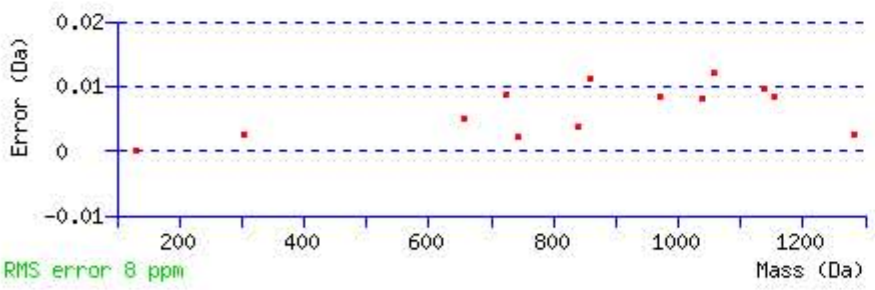
Match to Query 42896: 1937.035056 from(485.266040,4+) rtinseconds(1497) index(46944)
Title: Locus:1.1.1.1759.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

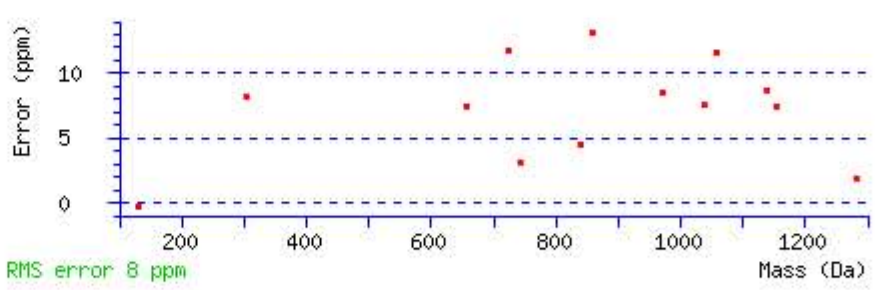
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1937.030533
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.015
**Matches :** 13/142 fragment ions using 26 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.102239 | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 14 |
| 2 | 186.123703 | 93.565489 | 169.097154 | 85.052215 | | | G | 1809.942850 | 905.475063 | 1792.916301 | 896.961789 | 1791.932285 | 896.469781 | 13 |
| 3 | 323.182615 | 162.094945 | 306.156066 | 153.581671 | | | H | 1752.921386 | 876.964331 | 1735.894837 | 868.451057 | 1734.910821 | 867.959049 | 12 |
| 4 | 422.251029 | 211.629153 | 405.224480 | 203.115878 | | | V | 1615.862474 | 808.434875 | 1598.835925 | 799.921601 | 1597.851909 | 799.429593 | 11 |
| 5 | 509.283057 | 255.145167 | 492.256508 | 246.631892 | 491.272492 | 246.139884 | S | 1516.794060 | 758.900668 | 1499.767511 | 750.387394 | 1498.783495 | 749.895386 | 10 |
| 6 | 656.351471 | 328.679374 | 639.324922 | 320.166099 | 638.340906 | 319.674091 | F | 1429.762032 | 715.384654 | 1412.735483 | 706.871380 | 1411.751467 | 706.379372 | 9 |
| 7 | 784.446434 | 392.726855 | 767.419885 | 384.213581 | 766.435869 | 383.721573 | K | *1282.693618* | 641.850447 | 1265.667069 | 633.337173 | 1264.683053 | 632.845165 | 8 |
| 8 | 881.499198 | 441.253237 | 864.472649 | 432.739963 | 863.488633 | 432.247955 | P | *1154.598655* | 577.802966 | 1137.572106 | 569.289691 | 1136.588090 | 568.797683 | 7 |
| 9 | 968.531226 | 484.769251 | 951.504677 | 476.255977 | 950.520661 | 475.763969 | S | *1057.545891* | 529.276584 | 1040.519342 | 520.763309 | 1039.535326 | 520.271301 | 6 |
| 10 | 1081.615290 | 541.311283 | 1064.588741 | 532.798009 | 1063.604725 | 532.306000 | L | *970.513863* | 485.760570 | 953.487314 | 477.247295 | 952.503298 | 476.755287 | 5 |
| 11 | 1196.642233 | 598.824755 | 1179.615684 | 590.311480 | 1178.631668 | 589.819472 | D | *857.429799* | 429.218538 | 840.403250 | 420.705263 | 839.419234 | 420.213255 | 4 |
| 12 | 1635.867559 | 818.437418 | 1618.841010 | 809.924143 | 1617.856994 | 809.432135 | Q | *742.402856* | 371.705066 | 725.376307 | 363.191792 | | | 3 |
| 13 | 1763.926137 | 882.466707 | 1746.899588 | 873.953432 | 1745.915572 | 873.461424 | Q | *303.177530* | 152.092403 | 286.150981 | 143.579129 | | | 2 |
| 14 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.7 | 1937.030533 | 0.004523 | KGHVSFKPSLDQQR |
| 30.6 | 1937.030533 | 0.004523 | KGHVSFKPSLDQQR |

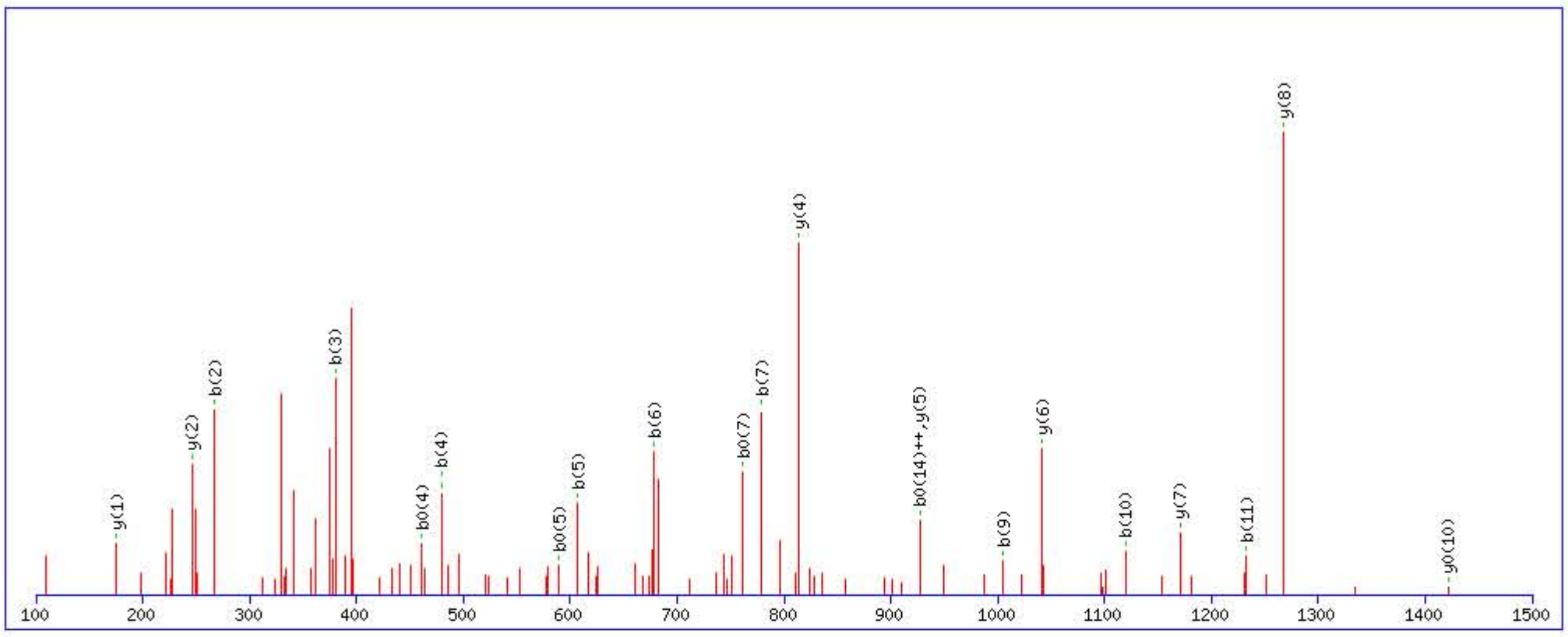
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EHLVQATPENLQEAR**
Found in **ITIH3_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

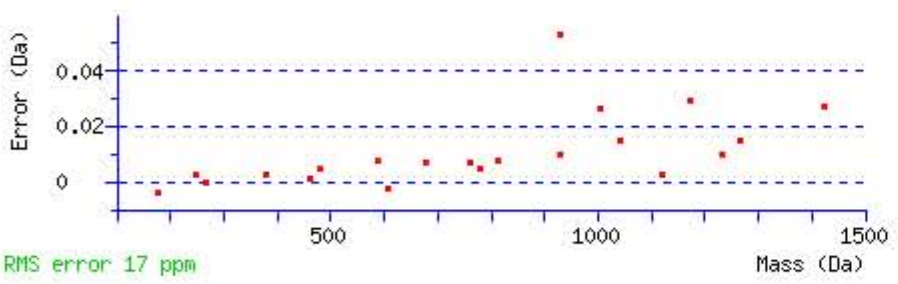
Match to Query 45615: 2045.052612 from(682.691480,3+) rtinseconds(1756) index(48675)
Title: Locus:1.1.1.1849.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

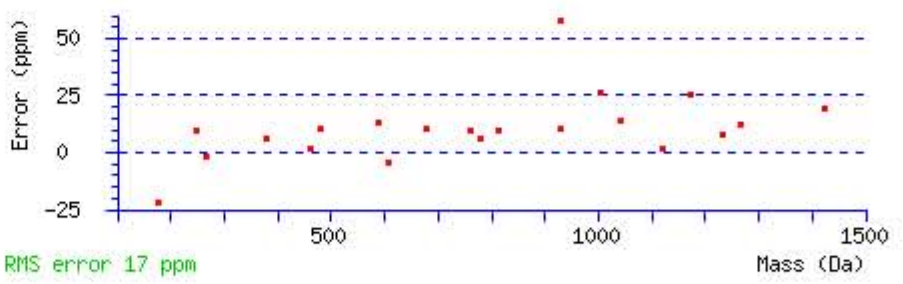
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2045.036377
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 77 **Expect:** 2e-007
**Matches :** 21/156 fragment ions using 26 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 15 |
| 2 | *267.108781* | 134.058028 | | | 249.098216 | 125.052746 | H | 1917.001094 | 959.004185 | 1899.974545 | 950.490911 | 1898.990529 | 949.998903 | 14 |
| 3 | *380.192845* | 190.600060 | | | 362.182280 | 181.594778 | L | 1779.942182 | 890.474729 | 1762.915633 | 881.961455 | 1761.931617 | 881.469447 | 13 |
| 4 | *479.261259* | 240.134267 | | | 461.250694 | 231.128985 | V | 1666.858118 | 833.932697 | 1649.831569 | 825.419423 | 1648.847553 | 824.927415 | 12 |
| 5 | *607.319837* | 304.163557 | 590.293288 | 295.650282 | 589.309272 | 295.158274 | Q | 1567.789704 | 784.398490 | 1550.763155 | 775.885216 | 1549.779139 | 775.393208 | 11 |
| 6 | *678.356951* | 339.682114 | 661.330402 | 331.168839 | 660.346386 | 330.676831 | A | 1439.731126 | 720.369201 | 1422.704577 | 711.855927 | 1421.720561 | 711.363919 | 10 |
| 7 | *779.404630* | 390.205953 | 762.378081 | 381.692679 | 761.394065 | 381.200671 | T | 1368.694012 | 684.850644 | 1351.667463 | 676.337370 | 1350.683447 | 675.845362 | 9 |
| 8 | 876.457394 | 438.732335 | 859.430845 | 430.219061 | 858.446829 | 429.727053 | P | *1267.646333* | 634.326805 | 1250.619784 | 625.813530 | 1249.635768 | 625.321522 | 8 |
| 9 | *1005.499987* | 503.253632 | 988.473438 | 494.740357 | 987.489422 | 494.248349 | E | *1170.593569* | 585.800423 | 1153.567020 | 577.287148 | 1152.583004 | 576.795140 | 7 |
| 10 | *1119.542914* | 560.275095 | 1102.516365 | 551.761821 | 1101.532349 | 551.269813 | N | *1041.550976* | 521.279126 | 1024.524427 | 512.765852 | 1023.540411 | 512.273844 | 6 |
| 11 | *1232.626978* | 616.817127 | 1215.600429 | 608.303853 | 1214.616413 | 607.811845 | L | *927.508049* | 464.257663 | 910.481500 | 455.744388 | 909.497484 | 455.252380 | 5 |
| 12 | 1671.852304 | 836.429790 | 1654.825755 | 827.916516 | 1653.841739 | 827.424508 | Q | *814.423985* | 407.715631 | 797.397436 | 399.202356 | 796.413420 | 398.710348 | 4 |
| 13 | 1800.894897 | 900.951087 | 1783.868348 | 892.437812 | 1782.884332 | 891.945804 | E | 375.198659 | 188.102968 | 358.172110 | 179.589693 | 357.188094 | 179.097685 | 3 |
| 14 | 1871.932011 | 936.469644 | 1854.905462 | 927.956369 | 1853.921446 | 927.464361 | A | *246.156066* | 123.581671 | 229.129517 | 115.068396 | | | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 76.5 | 2045.036377 | 0.016235 | EHLVQATPENLQEAR |
| 4.8 | 2045.022446 | 0.030166 | EHNENMLRNILPSHVAR |
| 2.7 | 2045.036377 | 0.016235 | EHLVQATPENLQEAR |
| 0.9 | 2045.040421 | 0.012191 | QIEFNFPSQAITSPR |

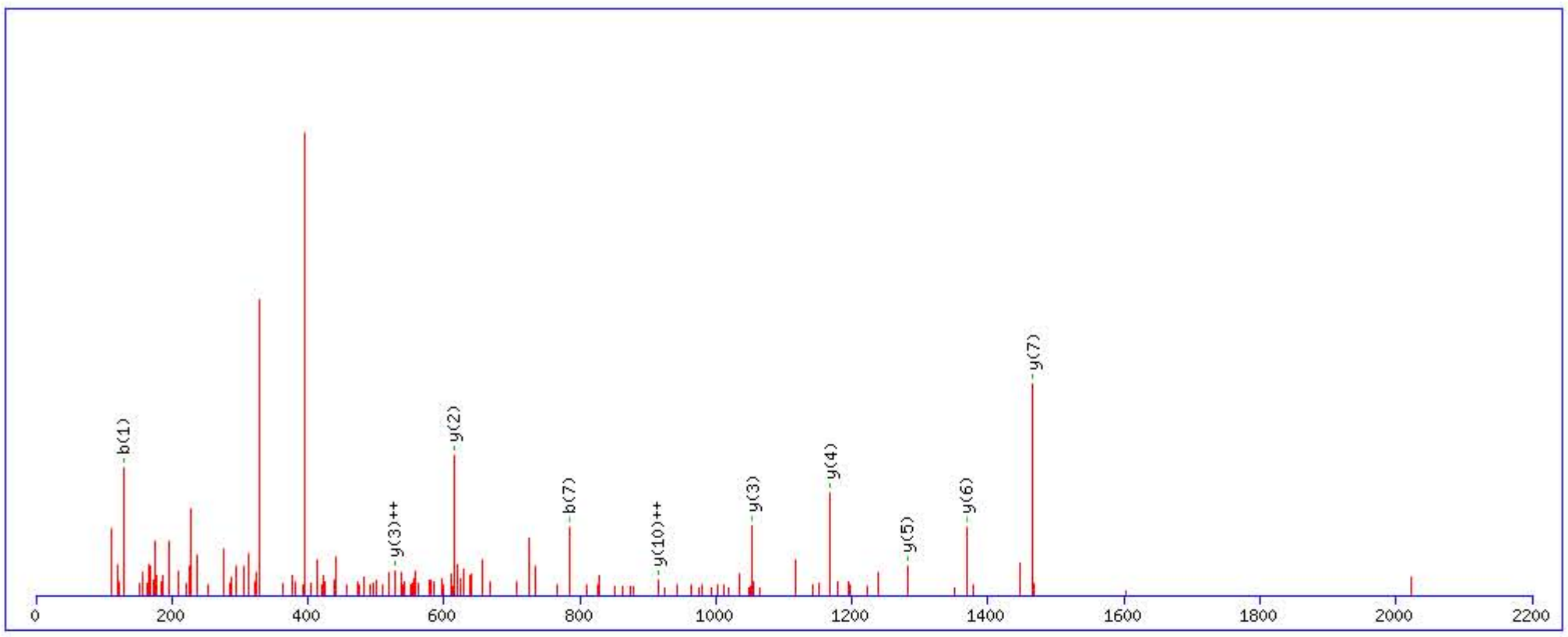
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KGHVSFKPSLDQQR**
Found in **ITIH3_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

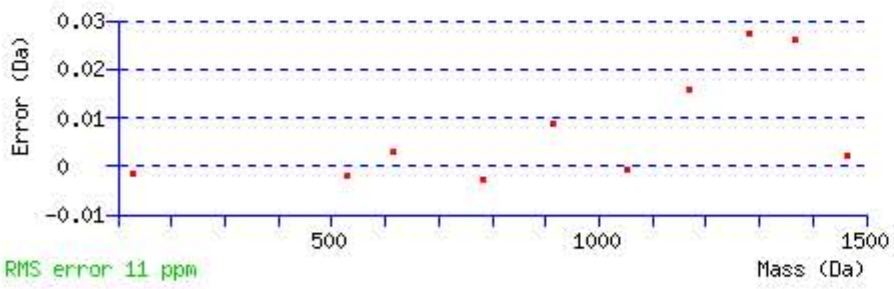
Match to Query 49411: 2248.203496 from(563.058150,4+) rtinseconds(1715) index(48372)
Title: Locus:1.1.1.1835.4 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

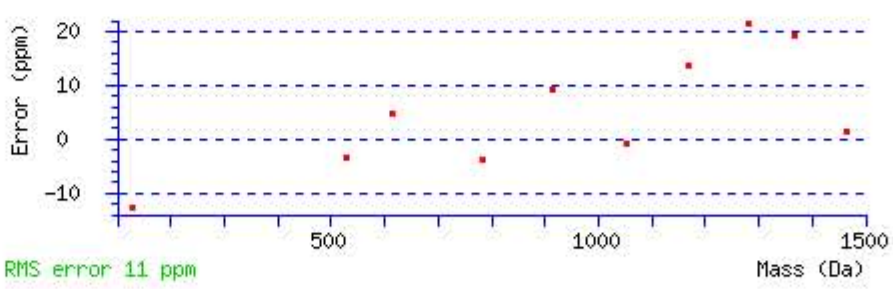
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2248.197281
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.0027
**Matches** : 10/142 fragment ions using 16 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.102239 | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 14 |
| 2 | 186.123703 | 93.565489 | 169.097154 | 85.052215 | | | G | 2121.109598 | 1061.058437 | 2104.083049 | 1052.545162 | 2103.099033 | 1052.053154 | 13 |
| 3 | 323.182615 | 162.094945 | 306.156066 | 153.581671 | | | H | 2064.088134 | 1032.547705 | 2047.061585 | 1024.034430 | 2046.077569 | 1023.542422 | 12 |
| 4 | 422.251029 | 211.629153 | 405.224480 | 203.115878 | | | V | 1927.029222 | 964.018249 | 1910.002673 | 955.504975 | 1909.018657 | 955.012967 | 11 |
| 5 | 509.283057 | 255.145167 | 492.256508 | 246.631892 | 491.272492 | 246.139884 | S | 1827.960808 | 914.484042 | 1810.934259 | 905.970768 | 1809.950243 | 905.478760 | 10 |
| 6 | 656.351471 | 328.679374 | 639.324922 | 320.166099 | 638.340906 | 319.674091 | F | 1740.928780 | 870.968028 | 1723.902231 | 862.454754 | 1722.918215 | 861.962746 | 9 |
| 7 | 784.446434 | 392.726855 | 767.419885 | 384.213581 | 766.435869 | 383.721573 | K | 1593.860366 | 797.433821 | 1576.833817 | 788.920547 | 1575.849801 | 788.428539 | 8 |
| 8 | 881.499198 | 441.253237 | 864.472649 | 432.739963 | 863.488633 | 432.247955 | P | *1465.765403* | 733.386340 | 1448.738854 | 724.873065 | 1447.754838 | 724.381057 | 7 |
| 9 | 968.531226 | 484.769251 | 951.504677 | 476.255977 | 950.520661 | 475.763969 | S | *1368.712639* | 684.859958 | 1351.686090 | 676.346683 | 1350.702074 | 675.854675 | 6 |
| 10 | 1081.615290 | 541.311283 | 1064.588741 | 532.798009 | 1063.604725 | 532.306000 | L | *1281.680611* | 641.343944 | 1264.654062 | 632.830669 | 1263.670046 | 632.338661 | 5 |
| 11 | 1196.642233 | 598.824755 | 1179.615684 | 590.311480 | 1178.631668 | 589.819472 | D | *1168.596547* | 584.801912 | 1151.569998 | 576.288637 | 1150.585982 | 575.796629 | 4 |
| 12 | 1635.867559 | 818.437418 | 1618.841010 | 809.924143 | 1617.856994 | 809.432135 | Q | *1053.569604* | 527.288440 | 1036.543055 | 518.775166 | | | 3 |
| 13 | 2075.092885 | 1038.050080 | 2058.066336 | 1029.536806 | 2057.082320 | 1029.044798 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 14 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 30.6 | 2248.197281 | 0.006215 | KGHVSFKPSLDQQR |
| 3.3 | 2248.174805 | 0.028691 | QSKETPVGWQELPK |

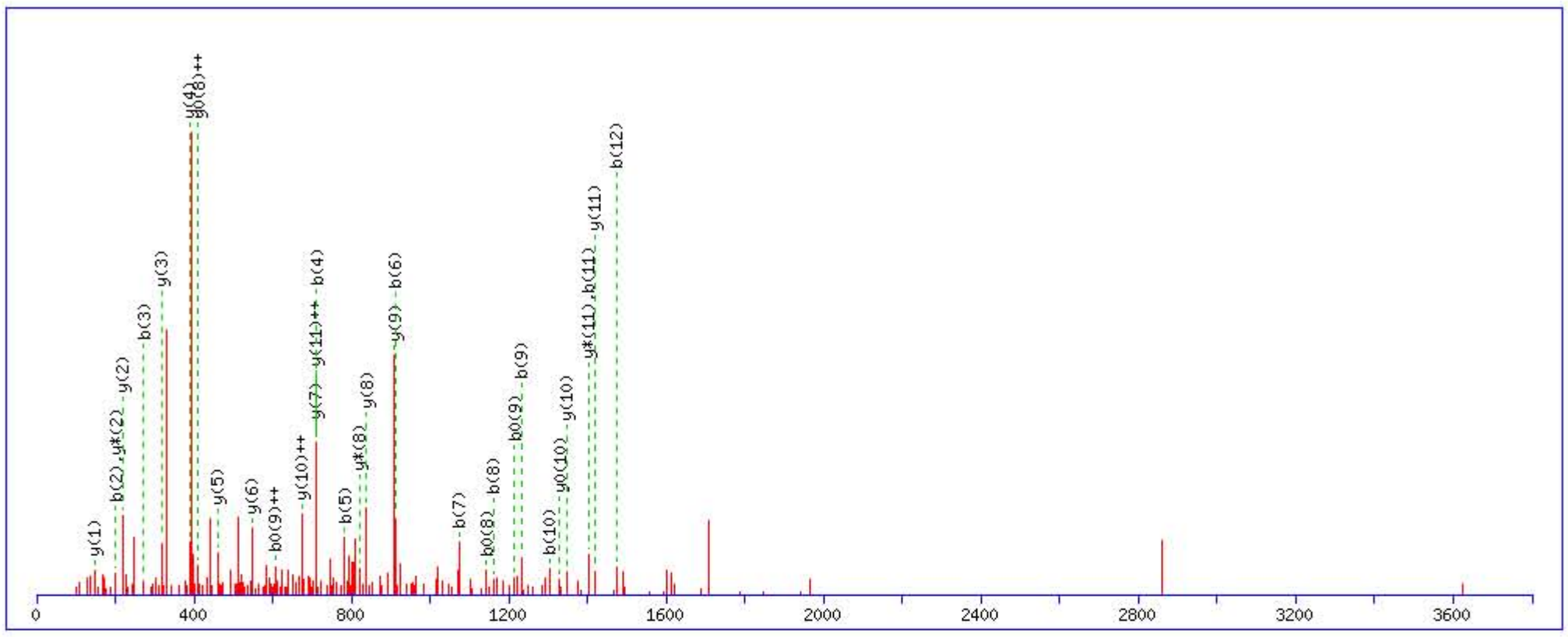
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AEAQAQYSAAVAK**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

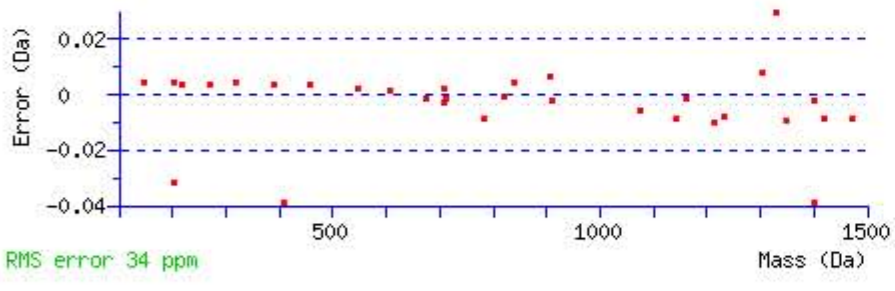
Match to Query 35413: 1617.817888 from(809.916220,2+) rtinseconds(1588) index(17524)
Title: Locus:1.1.1.2935.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

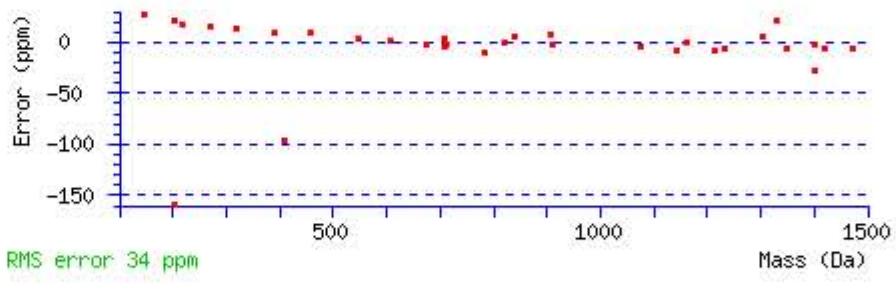
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1617.818436
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 65 **Expect:** 6.2e-006
**Matches :** 32/126 fragment ions using 61 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 13 |
| 2 | *201.086983* | 101.047130 | | | 183.076418 | 92.041847 | E | 1547.788642 | 774.397959 | 1530.762093 | 765.884685 | 1529.778077 | 765.392677 | 12 |
| 3 | *272.124097* | 136.565687 | | | 254.113532 | 127.560404 | A | **1418.746049** | 709.876663 | 1401.719500 | 701.363388 | 1400.735484 | 700.871380 | 11 |
| 4 | *711.349423* | 356.178350 | 694.322874 | 347.665075 | 693.338858 | 347.173067 | Q | **1347.708935** | 674.358106 | 1330.682386 | 665.844831 | 1329.698370 | 665.352823 | 10 |
| 5 | *782.386537* | 391.696907 | 765.359988 | 383.183632 | 764.375972 | 382.691624 | A | **908.483609** | 454.745443 | 891.457060 | 446.232168 | 890.473044 | 445.740160 | 9 |
| 6 | *910.445115* | 455.726196 | 893.418566 | 447.212921 | 892.434550 | 446.720913 | Q | **837.446495** | 419.226886 | 820.419946 | 410.713611 | 819.435930 | 410.221603 | 8 |
| 7 | *1073.508444* | 537.257860 | 1056.481895 | 528.744586 | 1055.497879 | 528.252578 | Y | **709.387917** | 355.197597 | 692.361368 | 346.684322 | 691.377352 | 346.192314 | 7 |
| 8 | *1160.540472* | 580.773874 | 1143.513923 | 572.260600 | 1142.529907 | 571.768592 | S | **546.324588** | 273.665932 | 529.298039 | 265.152658 | 528.314023 | 264.660650 | 6 |
| 9 | *1231.577586* | 616.292431 | 1214.551037 | 607.779157 | 1213.567021 | 607.287149 | A | **459.292560** | 230.149918 | 442.266011 | 221.636643 | | | 5 |
| 10 | *1302.614700* | 651.810988 | 1285.588151 | 643.297714 | 1284.604135 | 642.805706 | A | **388.255446** | 194.631361 | 371.228897 | 186.118087 | | | 4 |
| 11 | *1401.683114* | 701.345195 | 1384.656565 | 692.831921 | 1383.672549 | 692.339913 | V | **317.218332** | 159.112804 | 300.191783 | 150.599530 | | | 3 |
| 12 | *1472.720228* | 736.863752 | 1455.693679 | 728.350478 | 1454.709663 | 727.858470 | A | **218.149918** | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 13 | | | | | | | K | **147.112804** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 65.2 | 1617.818436 | -0.000548 | AEAQAQYSAAVAK |
| 48.8 | 1617.818436 | -0.000548 | AEAQAQYSAAVAK |
| 9.1 | 1617.800690 | 0.017198 | EAAQAIFPSMAR |
| 4.4 | 1617.803162 | 0.014726 | EATEINMKNEALQK |
| 4.0 | 1617.823639 | -0.005751 | GLHSWQKAAHGDRR |
| 2.4 | 1617.823166 | -0.005278 | QLRLHNDMHK |
| 0.3 | 1617.807236 | 0.010652 | LSGKCFSLVESTYK |
| 0.0 | 1617.796677 | 0.021211 | GAISSEAVCKPLCAR |

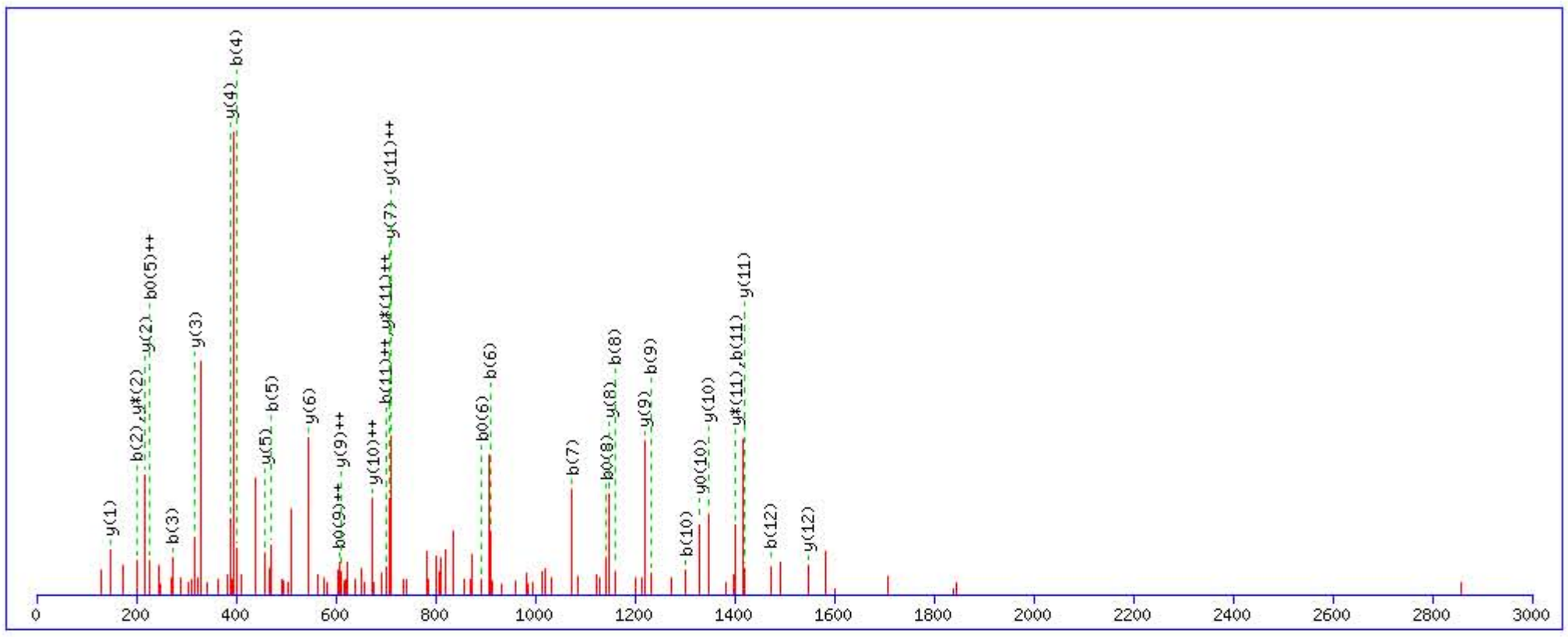
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AEAQAQYSAAVAK**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

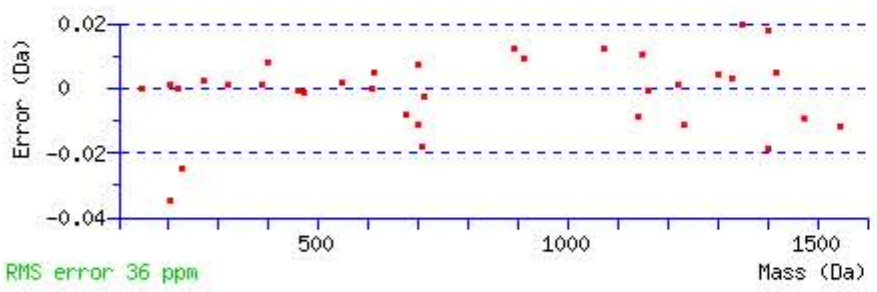
Match to Query 35417: 1617.825588 from(809.920070,2+) rtinseconds(1573) index(3140)
Title: Locus:1.1.1.1824.21 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

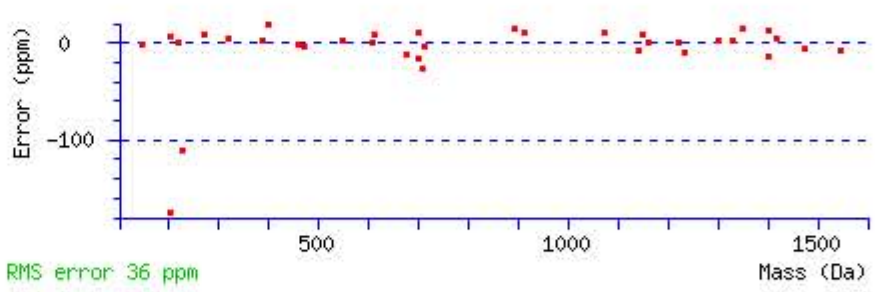
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1617.818436
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q6** : Biotin:Thermo-21345 (Q)
**Ions Score:** 76 **Expect:** 3.4e-007
**Matches :** 35/126 fragment ions using 67 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 13 |
| 2 | 201.086983 | 101.047130 | | | 183.076418 | 92.041847 | E | *1547.788642* | 774.397959 | 1530.762093 | 765.884685 | 1529.778077 | 765.392677 | 12 |
| 3 | 272.124097 | 136.565687 | | | 254.113532 | 127.560404 | A | *1418.746049* | 709.876663 | 1401.719500 | 701.363388 | 1400.735484 | 700.871380 | 11 |
| 4 | 400.182675 | 200.594976 | 383.156126 | 192.081701 | 382.172110 | 191.589693 | Q | *1347.708935* | 674.358106 | 1330.682386 | 665.844831 | 1329.698370 | 665.352823 | 10 |
| 5 | 471.219789 | 236.113533 | 454.193240 | 227.600258 | 453.209224 | 227.108250 | A | *1219.650357* | 610.328817 | 1202.623808 | 601.815542 | 1201.639792 | 601.323534 | 9 |
| 6 | 910.445115 | 455.726196 | 893.418566 | 447.212921 | 892.434550 | 446.720913 | Q | *1148.613243* | 574.810260 | 1131.586694 | 566.296985 | 1130.602678 | 565.804977 | 8 |
| 7 | 1073.508444 | 537.257860 | 1056.481895 | 528.744586 | 1055.497879 | 528.252578 | Y | *709.387917* | 355.197597 | 692.361368 | 346.684322 | 691.377352 | 346.192314 | 7 |
| 8 | 1160.540472 | 580.773874 | 1143.513923 | 572.260600 | 1142.529907 | 571.768592 | S | *546.324588* | 273.665932 | 529.298039 | 265.152658 | 528.314023 | 264.660650 | 6 |
| 9 | 1231.577586 | 616.292431 | 1214.551037 | 607.779157 | 1213.567021 | 607.287149 | A | *459.292560* | 230.149918 | 442.266011 | 221.636643 | | | 5 |
| 10 | 1302.614700 | 651.810988 | 1285.588151 | 643.297714 | 1284.604135 | 642.805706 | A | *388.255446* | 194.631361 | 371.228897 | 186.118087 | | | 4 |
| 11 | 1401.683114 | 701.345195 | 1384.656565 | 692.831921 | 1383.672549 | 692.339913 | V | *317.218332* | 159.112804 | 300.191783 | 150.599530 | | | 3 |
| 12 | 1472.720228 | 736.863752 | 1455.693679 | 728.350478 | 1454.709663 | 727.858470 | A | *218.149918* | 109.578597 | 201.123369 | 101.065322 | | | 2 |
| 13 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 76.2 | 1617.818436 | 0.007152 | AEAQAQYSAAVAK |
| 74.8 | 1617.818436 | 0.007152 | AEAQAQYSAAVAK |
| 6.8 | 1617.803162 | 0.022426 | EATEINMKNEALQK |
| 3.4 | 1617.823639 | 0.001949 | GLHSWQKAAHGDRR |
| 3.2 | 1617.848358 | -0.022770 | QCVFISKVVVHMR |
| 1.4 | 1617.818451 | 0.007137 | KKMFDLETNEHVK |
| 0.7 | 1617.843613 | -0.018025 | SLMESPFPAPGKTIK |

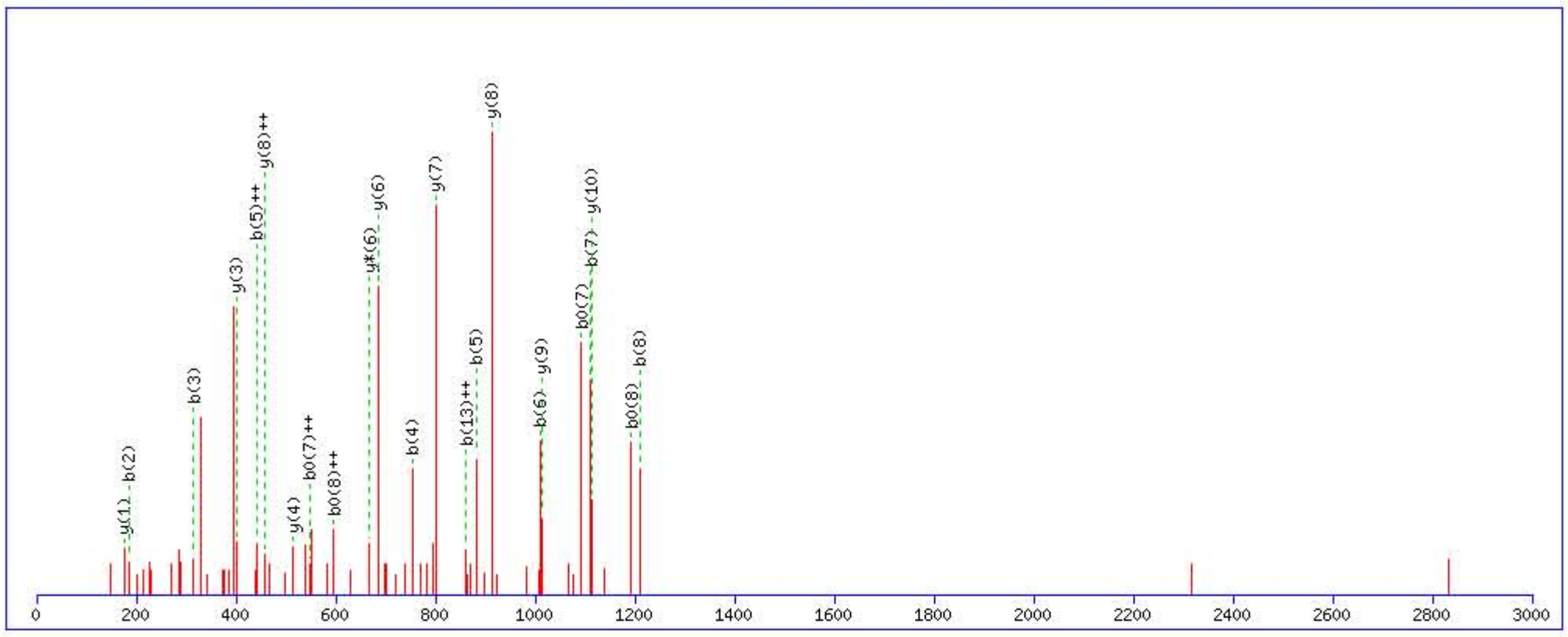
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SPEQQETVLDGNLIIR**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

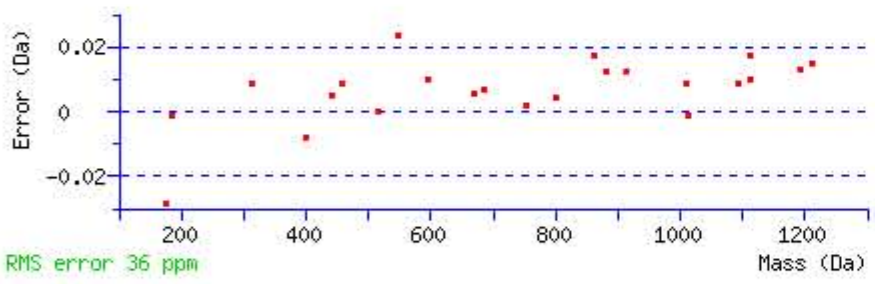
Match to Query 46958: 2122.123542 from(708.381790,3+) rtinseconds(2360) index(7623)
Title: Locus:1.1.1.2099.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

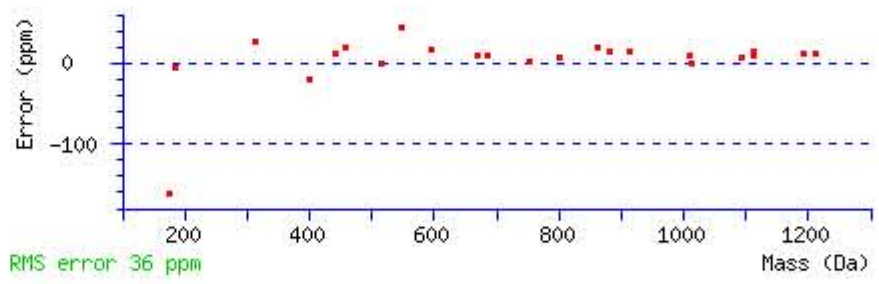
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2122.109222
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 64 **Expect:** 9.7e-006
**Matches :** 23/162 fragment ions using 32 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 16 |
| 2 | *185.092068* | 93.049672 | | | 167.081503 | 84.044389 | P | 2036.084489 | 1018.545882 | 2019.057940 | 1010.032608 | 2018.073924 | 1009.540600 | 15 |
| 3 | *314.134661* | 157.570968 | | | 296.124096 | 148.565686 | E | 1939.031725 | 970.019500 | 1922.005176 | 961.506226 | 1921.021160 | 961.014218 | 14 |
| 4 | *753.359987* | 377.183632 | 736.333438 | 368.670357 | 735.349422 | 368.178349 | Q | 1809.989132 | 905.498204 | 1792.962583 | 896.984929 | 1791.978567 | 896.492921 | 13 |
| 5 | *881.418565* | **441.212921** | 864.392016 | 432.699646 | 863.408000 | 432.207638 | Q | 1370.763806 | 685.885541 | 1353.737257 | 677.372266 | 1352.753241 | 676.880258 | 12 |
| 6 | *1010.461158* | 505.734217 | 993.434609 | 497.220943 | 992.450593 | 496.728935 | E | 1242.705228 | 621.856252 | 1225.678679 | 613.342977 | 1224.694663 | 612.850969 | 11 |
| 7 | *1111.508837* | 556.258057 | 1094.482288 | 547.744782 | 1093.498272 | 547.252774 | T | *1113.662635* | 557.334955 | 1096.636086 | 548.821681 | 1095.652070 | 548.329673 | 10 |
| 8 | *1210.577251* | 605.792264 | 1193.550702 | 597.278989 | 1192.566686 | 596.786981 | V | *1012.614956* | 506.811116 | 995.588407 | 498.297841 | 994.604391 | 497.805833 | 9 |
| 9 | 1323.661315 | 662.334296 | 1306.634766 | 653.821021 | 1305.650750 | 653.329013 | L | *913.546542* | 457.276909 | 896.519993 | 448.763634 | 895.535977 | 448.271626 | 8 |
| 10 | 1438.688258 | 719.847767 | 1421.661709 | 711.334493 | 1420.677693 | 710.842485 | D | *800.462478* | 400.734877 | 783.435929 | 392.221602 | 782.451913 | 391.729594 | 7 |
| 11 | 1495.709722 | 748.358499 | 1478.683173 | 739.845225 | 1477.699157 | 739.353217 | G | *685.435535* | 343.221405 | 668.408986 | 334.708131 | | | 6 |
| 12 | 1609.752649 | 805.379963 | 1592.726100 | 796.866688 | 1591.742084 | 796.374680 | N | 628.414071 | 314.710673 | 611.387522 | 306.197399 | | | 5 |
| 13 | 1722.836713 | **861.921994** | 1705.810164 | 853.408720 | 1704.826148 | 852.916712 | L | *514.371144* | 257.689210 | 497.344595 | 249.175935 | | | 4 |
| 14 | 1835.920777 | 918.464026 | 1818.894228 | 909.950752 | 1817.910212 | 909.458744 | I | *401.287080* | 201.147178 | 384.260531 | 192.633903 | | | 3 |
| 15 | 1949.004841 | 975.006058 | 1931.978292 | 966.492784 | 1930.994276 | 966.000776 | I | 288.203016 | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 16 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 64.0 | 2122.109222 | 0.014320 | SPEQQETVLDGNLIIR |
| 54.7 | 2122.109222 | 0.014320 | SPEQQETVLDGNLIIR |
| 12.2 | 2122.100189 | 0.023353 | MIAPQRWIDAQR |
| 5.1 | 2122.139053 | -0.015511 | RRVYDALNVLMAMNIISK |
| 3.0 | 2122.149612 | -0.026070 | LPALRLMNATITEELFFK |
| 2.0 | 2122.143112 | -0.019570 | LYQFLLGLLTRGDMR |
| 1.8 | 2122.135025 | -0.011483 | EPTPFIIEWIPDILPQSK |
| 1.3 | 2122.117081 | 0.006461 | SFEISPNRVQISLVQYSR |
| 0.6 | 2122.100204 | 0.023338 | QQGQCLLLWQAR |
| 0.6 | 2122.100204 | 0.023338 | QQGQCLLLWQAR |

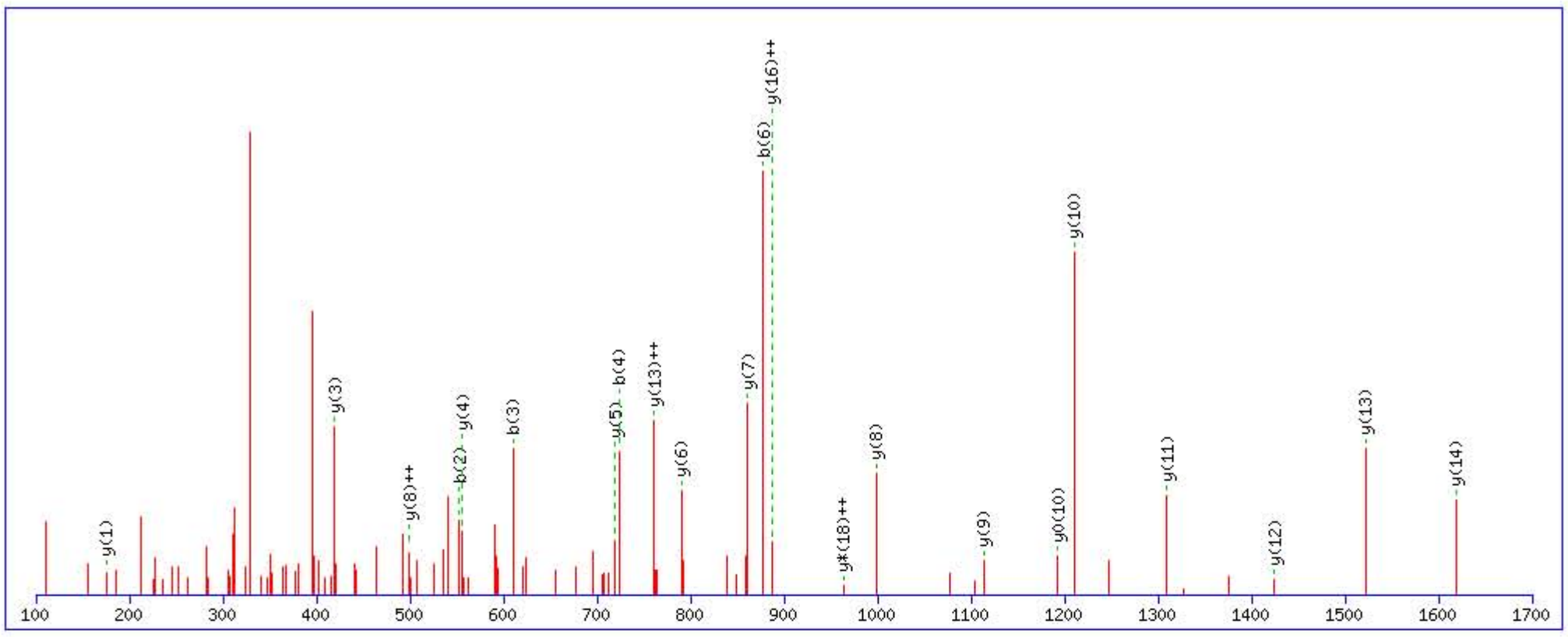
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QLGLPGPPDVPDHAAYHPFR**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

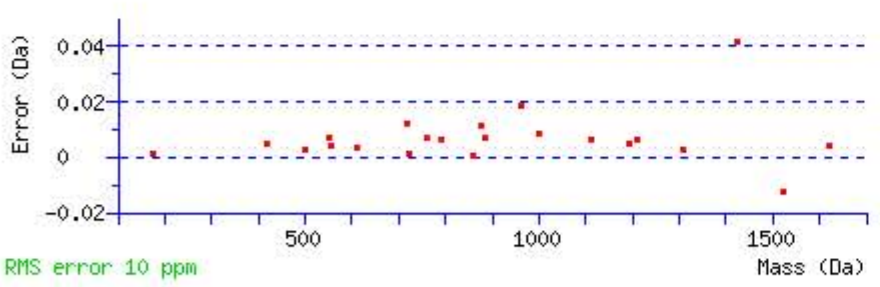
Match to Query 54242: 2494.267896 from(624.574250,4+) rtinseconds(2165) index(6568)
Title: Locus:1.1.1.2031.4 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

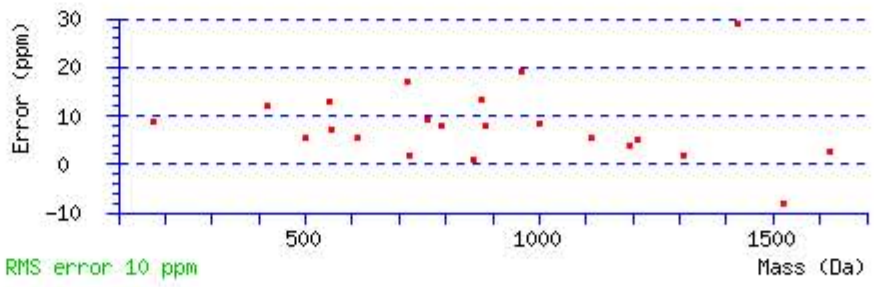
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2494.257980
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q1 : Biotin:Thermo-21345 (Q)
**Ions Score:** 74 **Expect:** 1.1e-006
**Matches :** 22/196 fragment ions using 46 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 20 |
| 2 | 553.316666 | 277.161971 | 536.290117 | 268.648697 | | | L | 2056.039923 | 1028.523599 | 2039.013374 | 1020.010325 | 2038.029358 | 1019.518317 | 19 |
| 3 | 610.338130 | 305.672703 | 593.311581 | 297.159429 | | | G | 1942.955859 | 971.981568 | 1925.929310 | 963.468293 | 1924.945294 | 962.976285 | 18 |
| 4 | 723.422194 | 362.214735 | 706.395645 | 353.701461 | | | L | 1885.934395 | 943.470836 | 1868.907846 | 934.957561 | 1867.923830 | 934.465553 | 17 |
| 5 | 820.474958 | 410.741117 | 803.448409 | 402.227843 | | | P | 1772.850331 | 886.928804 | 1755.823782 | 878.415529 | 1754.839766 | 877.923521 | 16 |
| 6 | 877.496422 | 439.251849 | 860.469873 | 430.738575 | | | G | 1675.797567 | 838.402422 | 1658.771018 | 829.889147 | 1657.787002 | 829.397139 | 15 |
| 7 | 974.549186 | 487.778231 | 957.522637 | 479.264957 | | | P | *1618.776103* | 809.891690 | 1601.749554 | 801.378415 | 1600.765538 | 800.886407 | 14 |
| 8 | 1071.601950 | 536.304613 | 1054.575401 | 527.791339 | | | P | *1521.723339* | 761.365308 | 1504.696790 | 752.852033 | 1503.712774 | 752.360025 | 13 |
| 9 | 1186.628893 | 593.818085 | 1169.602344 | 585.304810 | 1168.618328 | 584.812802 | D | *1424.670575* | 712.838926 | 1407.644026 | 704.325651 | 1406.660010 | 703.833643 | 12 |
| 10 | 1285.697307 | 643.352292 | 1268.670758 | 634.839017 | 1267.686742 | 634.347009 | V | *1309.643632* | 655.325454 | 1292.617083 | 646.812180 | 1291.633067 | 646.320172 | 11 |
| 11 | 1382.750071 | 691.878674 | 1365.723522 | 683.365399 | 1364.739506 | 682.873391 | P | *1210.575218* | 605.791247 | 1193.548669 | 597.277973 | 1192.564653 | 596.785964 | 10 |
| 12 | 1497.777014 | 749.392145 | 1480.750465 | 740.878871 | 1479.766449 | 740.386863 | D | *1113.522454* | 557.264865 | 1096.495905 | 548.751591 | 1095.511889 | 548.259582 | 9 |
| 13 | 1634.835926 | 817.921601 | 1617.809377 | 809.408327 | 1616.825361 | 808.916319 | H | *998.495511* | 499.751393 | 981.468962 | 491.238119 | | | 8 |
| 14 | 1705.873040 | 853.440158 | 1688.846491 | 844.926884 | 1687.862475 | 844.434876 | A | *861.436599* | 431.221937 | 844.410050 | 422.708663 | | | 7 |
| 15 | 1776.910154 | 888.958715 | 1759.883605 | 880.445441 | 1758.899589 | 879.953433 | A | *790.399485* | 395.703380 | 773.372936 | 387.190106 | | | 6 |
| 16 | 1939.973483 | 970.490380 | 1922.946934 | 961.977105 | 1921.962918 | 961.485097 | Y | *719.362371* | 360.184823 | 702.335822 | 351.671549 | | | 5 |
| 17 | 2077.032395 | 1039.019836 | 2060.005846 | 1030.506561 | 2059.021830 | 1030.014553 | H | *556.299042* | 278.653159 | 539.272493 | 270.139884 | | | 4 |
| 18 | 2174.085159 | 1087.546218 | 2157.058610 | 1079.032943 | 2156.074594 | 1078.540935 | P | *419.240130* | 210.123703 | 402.213581 | 201.610428 | | | 3 |
| 19 | 2321.153573 | 1161.080424 | 2304.127024 | 1152.567150 | 2303.143008 | 1152.075142 | F | 322.187366 | 161.597321 | 305.160817 | 153.084046 | | | 2 |
| 20 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 74.1 | 2494.257980 | 0.009916 | QLGLPGPPDVPDHAAYHPFR |

**Mascot:** http://www.matrixscience.com/

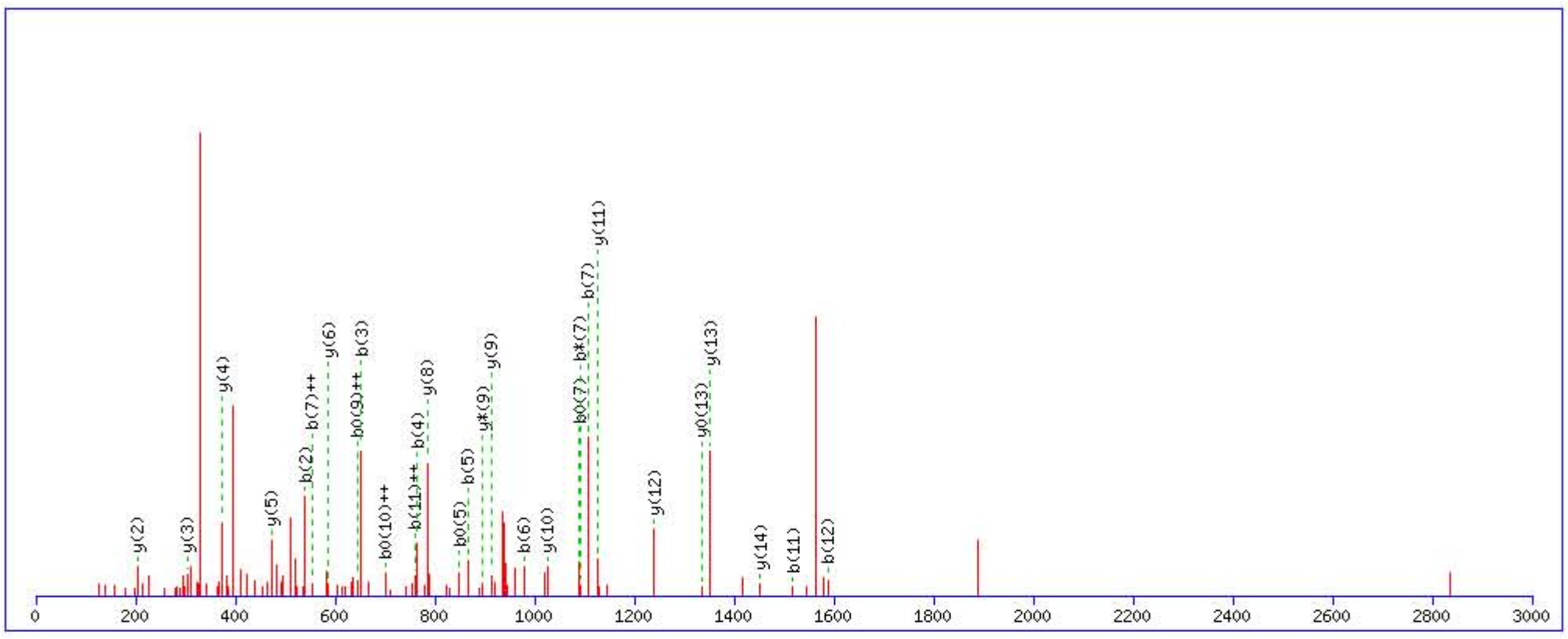
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QVILTLQPTLVAVGK**
Found in **ICAM2_HUMAN**, Intercellular adhesion molecule 2 OS=Homo sapiens GN=ICAM2 PE=1 SV=2

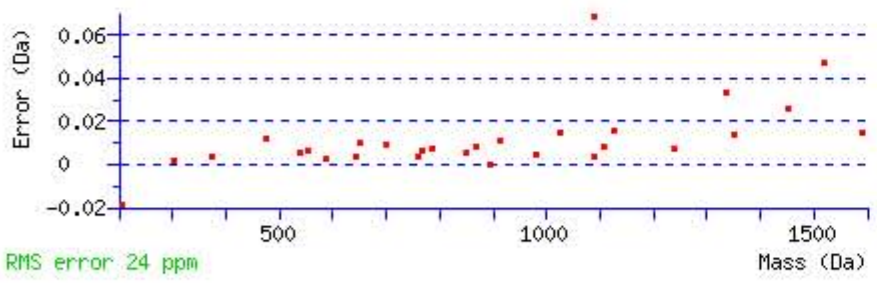
Match to Query 41962: 1890.147488 from(946.081020,2+) rtinseconds(2651) index(9005)
Title: Locus:1.1.1.2200.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

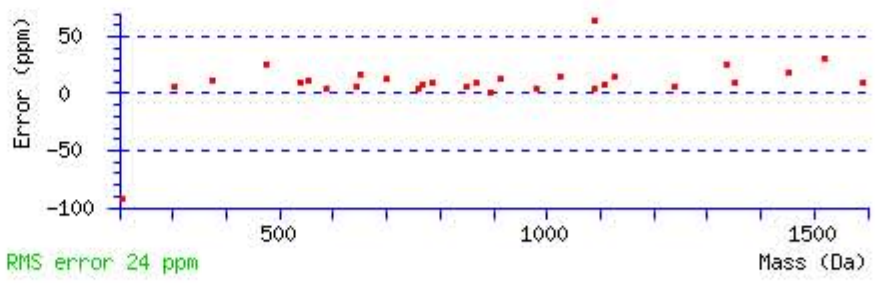
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1890.137634
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 66 **Expect:** 1.4e-006
**Matches** : 29/148 fragment ions using 63 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 15 |
| 2 | **539.301016** | 270.154146 | 522.274467 | 261.640872 | | | V | *1451.919580* | 726.463428 | 1434.893031 | 717.950154 | 1433.909015 | 717.458146 | 14 |
| 3 | **652.385080** | 326.696178 | 635.358531 | 318.182904 | | | I | *1352.851166* | 676.929221 | 1335.824617 | 668.415947 | 1334.840601 | 667.923939 | 13 |
| 4 | **765.469144** | 383.238210 | 748.442595 | 374.724936 | | | L | *1239.767102* | 620.387189 | 1222.740553 | 611.873915 | 1221.756537 | 611.381907 | 12 |
| 5 | **866.516823** | 433.762050 | 849.490274 | 425.248775 | 848.506258 | 424.756767 | T | *1126.683038* | 563.845157 | 1109.656489 | 555.331883 | 1108.672473 | 554.839874 | 11 |
| 6 | **979.600887** | 490.304082 | 962.574338 | 481.790807 | 961.590322 | 481.298799 | L | *1025.635359* | 513.321318 | 1008.608810 | 504.808043 | 1007.624794 | 504.316035 | 10 |
| 7 | **1107.659465** | **554.333371** | 1090.632916 | 545.820096 | 1089.648900 | 545.328088 | Q | *912.551295* | 456.779286 | 895.524746 | 448.266011 | 894.540730 | 447.774003 | 9 |
| 8 | 1204.712229 | 602.859753 | 1187.685680 | 594.346478 | 1186.701664 | 593.854470 | P | *784.492717* | 392.749997 | 767.466168 | 384.236722 | 766.482152 | 383.744714 | 8 |
| 9 | 1305.759908 | 653.383592 | 1288.733359 | 644.870318 | 1287.749343 | 644.378310 | T | 687.439953 | 344.223615 | 670.413404 | 335.710340 | 669.429388 | 335.218332 | 7 |
| 10 | 1418.843972 | 709.925624 | 1401.817423 | 701.412350 | 1400.833407 | 700.920341 | L | *586.392274* | 293.699775 | 569.365725 | 285.186501 | | | 6 |
| 11 | **1517.912386** | **759.459831** | 1500.885837 | 750.946557 | 1499.901821 | 750.454548 | V | *473.308210* | 237.157743 | 456.281661 | 228.644469 | | | 5 |
| 12 | **1588.949500** | 794.978388 | 1571.922951 | 786.465114 | 1570.938935 | 785.973105 | A | *374.239796* | 187.623536 | 357.213247 | 179.110261 | | | 4 |
| 13 | 1688.017914 | 844.512595 | 1670.991365 | 835.999321 | 1670.007349 | 835.507313 | V | *303.202682* | 152.104979 | 286.176133 | 143.591704 | | | 3 |
| 14 | 1745.039378 | 873.023327 | 1728.012829 | 864.510053 | 1727.028813 | 864.018044 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 15 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 65.9 | 1890.137634 | 0.009854 | QVILTLQPTLVAVGK |
| 9.1 | 1890.137634 | 0.009854 | QVILTLQPTLVAVGK |

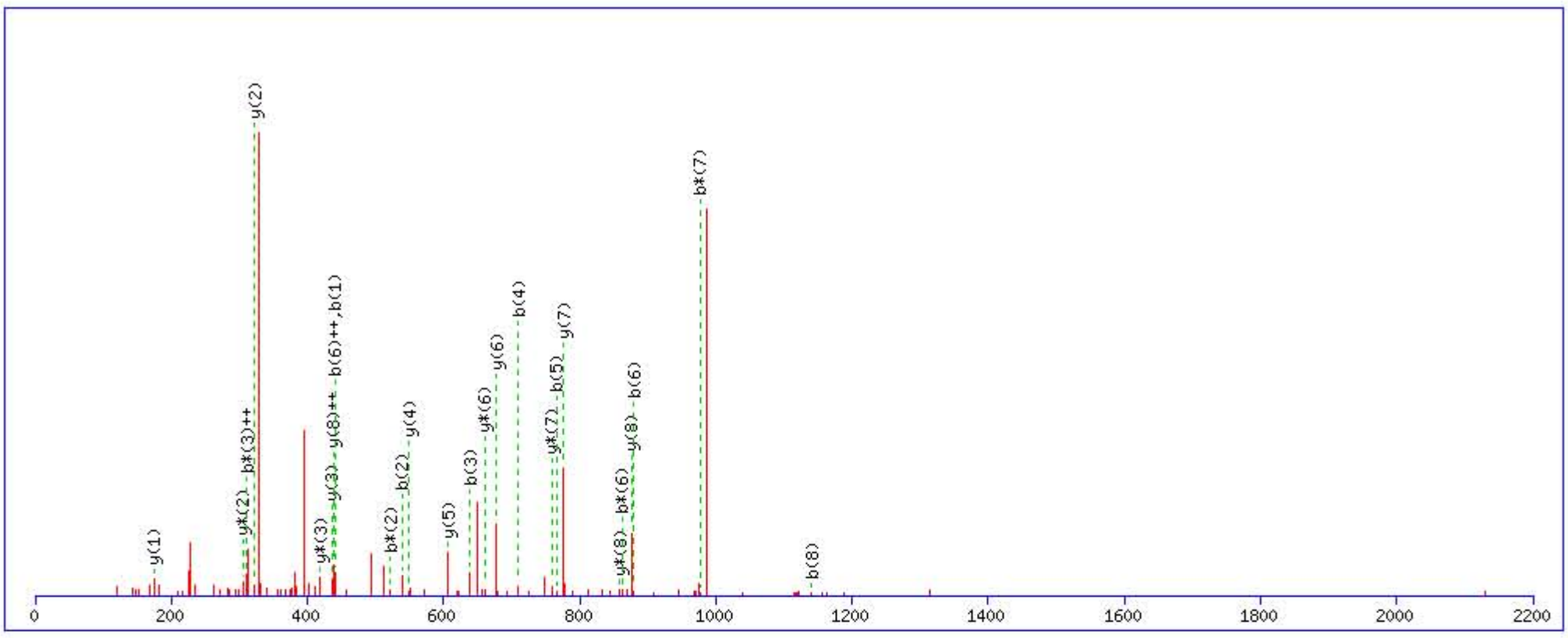
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QVVAGLNFR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

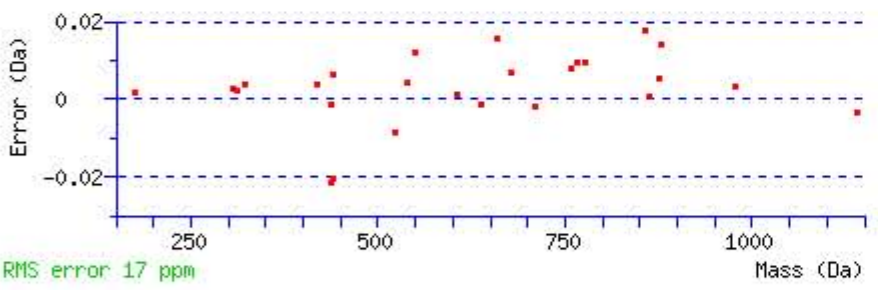
Match to Query 23570: 1313.740828 from(657.877690,2+) rtinseconds(2208) index(21529)
Title: Locus:1.1.1.3151.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

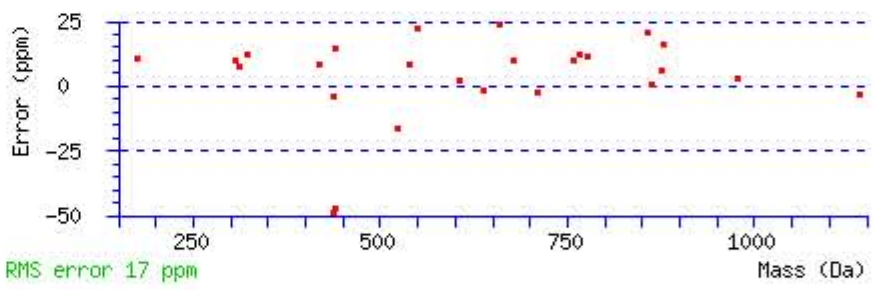
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1313.727814
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 25 **Expect:** 0.031
**Matches :** 26/64 fragment ions using 79 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | Q | | | | | 9 |
| 2 | 539.301016 | 270.154146 | 522.274467 | 261.640872 | V | 875.509763 | 438.258520 | 858.483214 | 429.745245 | 8 |
| 3 | 638.369430 | 319.688353 | 621.342881 | 311.175078 | V | 776.441349 | 388.724313 | 759.414800 | 380.211038 | 7 |
| 4 | 709.406544 | 355.206910 | 692.379995 | 346.693635 | A | 677.372935 | 339.190106 | 660.346386 | 330.676831 | 6 |
| 5 | 766.428008 | 383.717642 | 749.401459 | 375.204367 | G | 606.335821 | 303.671549 | 589.309272 | 295.158274 | 5 |
| 6 | 879.512072 | 440.259674 | 862.485523 | 431.746400 | L | 549.314357 | 275.160817 | 532.287808 | 266.647542 | 4 |
| 7 | 993.554999 | 497.281138 | 976.528450 | 488.767863 | N | 436.230293 | 218.618784 | 419.203744 | 210.105510 | 3 |
| 8 | 1140.623413 | 570.815345 | 1123.596864 | 562.302070 | F | 322.187366 | 161.597321 | 305.160817 | 153.084047 | 2 |
| 9 | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.2 | 1313.727814 | 0.013014 | QVVAGLNFR |
| 8.6 | 1313.756805 | -0.015977 | KTVTHQFAVKR |
| 8.4 | 1313.723755 | 0.017073 | SSVKHRLAAMSK |
| 7.5 | 1313.730301 | 0.010527 | LSQTLQVQLER |
| 7.5 | 1313.723755 | 0.017073 | SLKMLPERGQR |
| 5.3 | 1313.731644 | 0.009184 | GEPPPPVRRPGR |
| 3.0 | 1313.748947 | -0.008119 | VLVQSVCIQIR |
| 2.7 | 1313.730286 | 0.010542 | AKEDVLQKEVR |
| 2.7 | 1313.745575 | -0.004747 | GSLALQPFLVGGR |
| 2.7 | 1313.727798 | 0.013030 | KSLSVWQR |

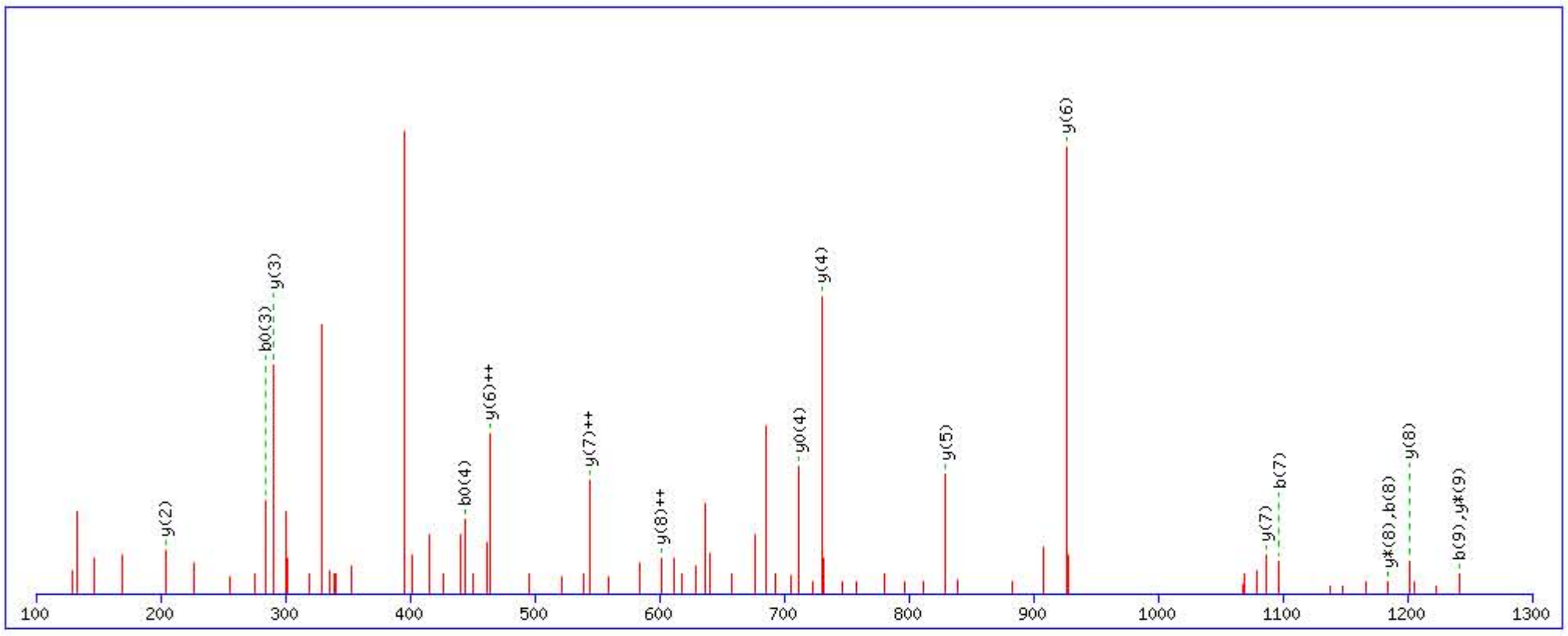
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EGDCPVQSGK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

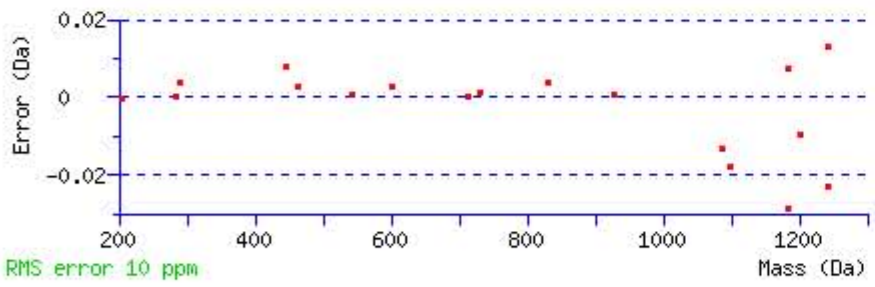
Match to Query 26677: 1386.627968 from(694.321260,2+) rtinseconds(1376) index(16053)
Title: Locus:1.1.1.2861.25 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

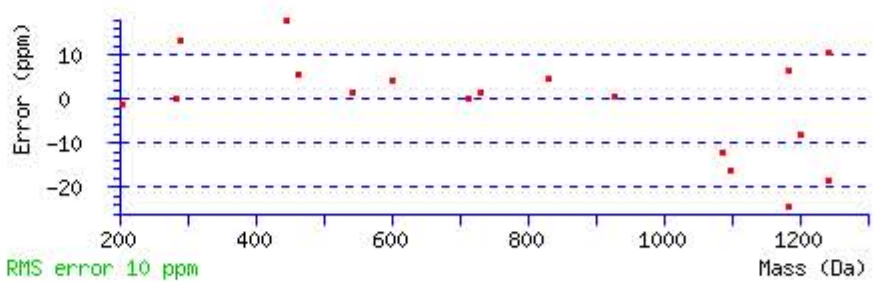
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1386.627182
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 57 **Expect:** 1.4e-005
**Matches** : 18/92 fragment ions using 21 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 10 |
| 2 | 187.071333 | 94.039305 | | | 169.060768 | 85.034022 | G | 1258.591856 | 629.799566 | 1241.565307 | 621.286292 | 1240.581291 | 620.794284 | 9 |
| 3 | 302.098276 | 151.552776 | | | 284.087711 | 142.547494 | D | *1201.570392* | 601.288834 | 1184.543843 | 592.775560 | 1183.559827 | 592.283552 | 8 |
| 4 | 462.128925 | 231.568101 | | | 444.118360 | 222.562818 | C | *1086.543449* | 543.775363 | 1069.516900 | 535.262088 | 1068.532884 | 534.770080 | 7 |
| 5 | 559.181689 | 280.094483 | | | 541.171124 | 271.089200 | P | *926.512800* | 463.760038 | 909.486251 | 455.246764 | 908.502235 | 454.754756 | 6 |
| 6 | 658.250103 | 329.628690 | | | 640.239538 | 320.623407 | V | *829.460036* | 415.233656 | 812.433487 | 406.720382 | 811.449471 | 406.228374 | 5 |
| 7 | 1097.475429 | 549.241353 | 1080.448880 | 540.728078 | 1079.464864 | 540.236070 | Q | *730.391622* | 365.699449 | 713.365073 | 357.186175 | 712.381057 | 356.694167 | 4 |
| 8 | 1184.507457 | 592.757367 | 1167.480908 | 584.244092 | 1166.496892 | 583.752084 | S | *291.166296* | 146.086786 | 274.139747 | 137.573512 | 273.155731 | 137.081504 | 3 |
| 9 | 1241.528921 | 621.268099 | 1224.502372 | 612.754824 | 1223.518356 | 612.262816 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 10 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 57.1 | 1386.627182 | 0.000786 | EGDCPVQSGK |
| 7.1 | 1386.619766 | 0.008202 | QMQQQEHDSLK |

**Mascot:** http://www.matrixscience.com/

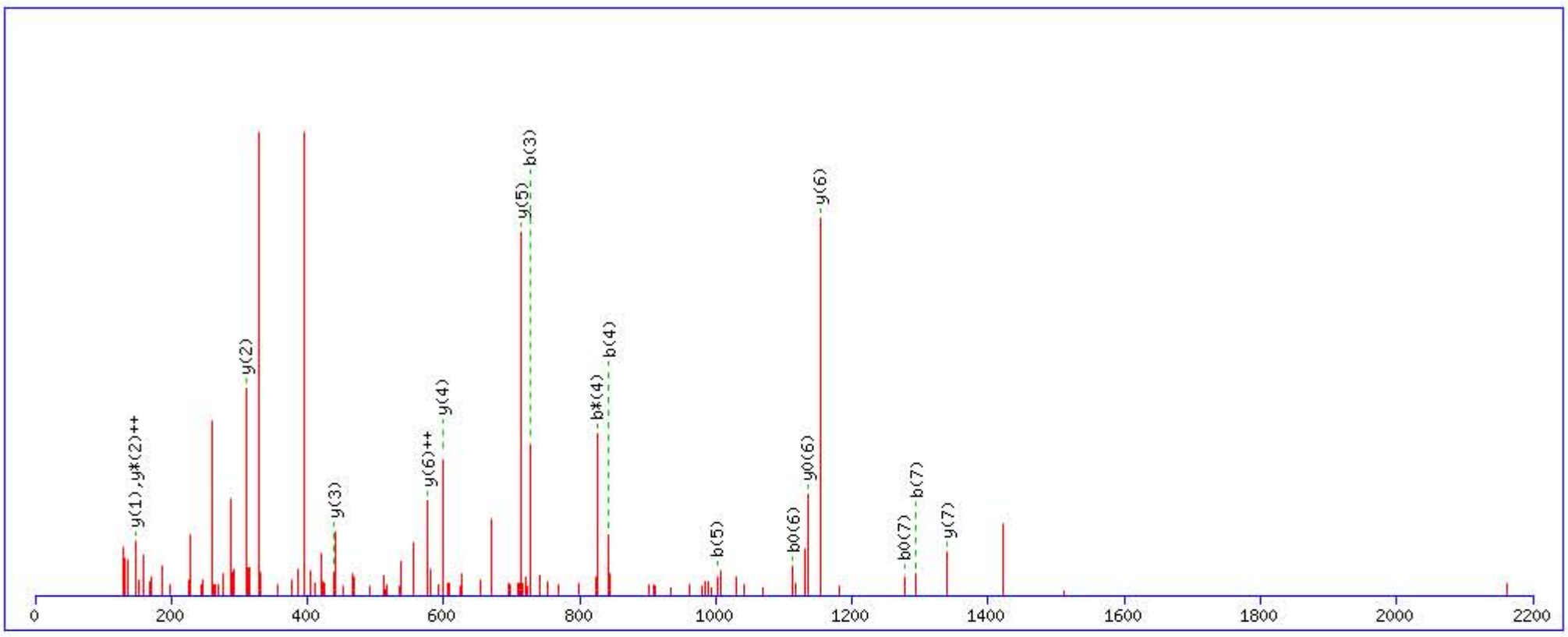
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TWQDCEYK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

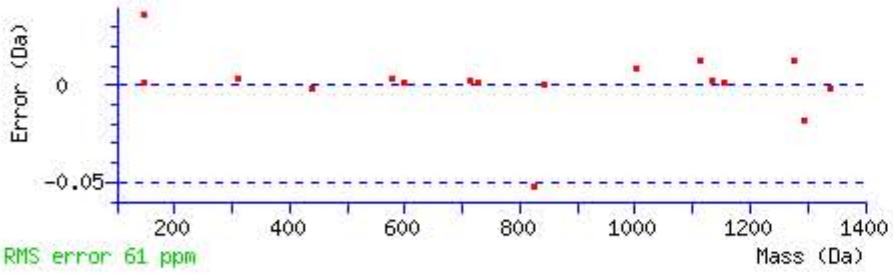
Match to Query 29331: 1439.626308 from(720.820430,2+) rtinseconds(1751) index(18577)
Title: Locus:1.1.1.2992.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

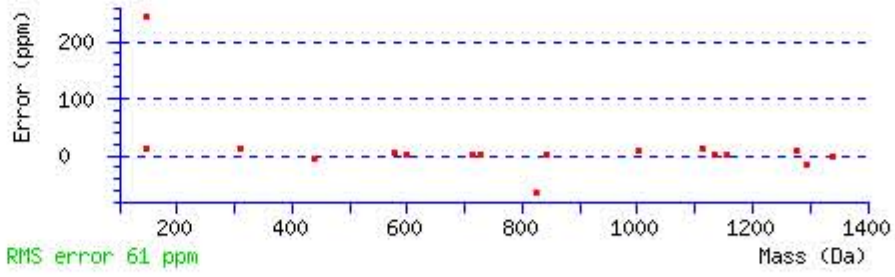
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1439.621353
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.00017
**Matches :** 17/76 fragment ions using 26 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 8 |
| 2 | 288.134268 | 144.570772 | | | 270.123703 | 135.565490 | W | *1339.580957* | 670.294117 | 1322.554408 | 661.780842 | 1321.570392 | 661.288834 | 7 |
| 3 | **727.359594** | 364.183435 | 710.333045 | 355.670161 | 709.349029 | 355.178153 | Q | *1153.501644* | 577.254460 | 1136.475095 | 568.741186 | 1135.491079 | 568.249178 | 6 |
| 4 | **842.386537** | 421.696907 | 825.359988 | 413.183632 | 824.375972 | 412.691624 | D | *714.276318* | 357.641797 | 697.249769 | 349.128523 | 696.265753 | 348.636515 | 5 |
| 5 | **1002.417186** | 501.712231 | 985.390637 | 493.198957 | 984.406621 | 492.706949 | C | *599.249375* | 300.128326 | 582.222826 | 291.615051 | 581.238810 | 291.123043 | 4 |
| 6 | 1131.459779 | 566.233528 | 1114.433230 | 557.720253 | 1113.449214 | 557.228245 | E | *439.218726* | 220.113001 | 422.192177 | 211.599727 | 421.208161 | 211.107719 | 3 |
| 7 | **1294.523108** | 647.765192 | 1277.496559 | 639.251918 | 1276.512543 | 638.759910 | Y | *310.176133* | 155.591705 | 293.149584 | 147.078430 | | | 2 |
| 8 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 44.3 | 1439.621353 | 0.004955 | TWQDCEYK |

**Mascot:** http://www.matrixscience.com/

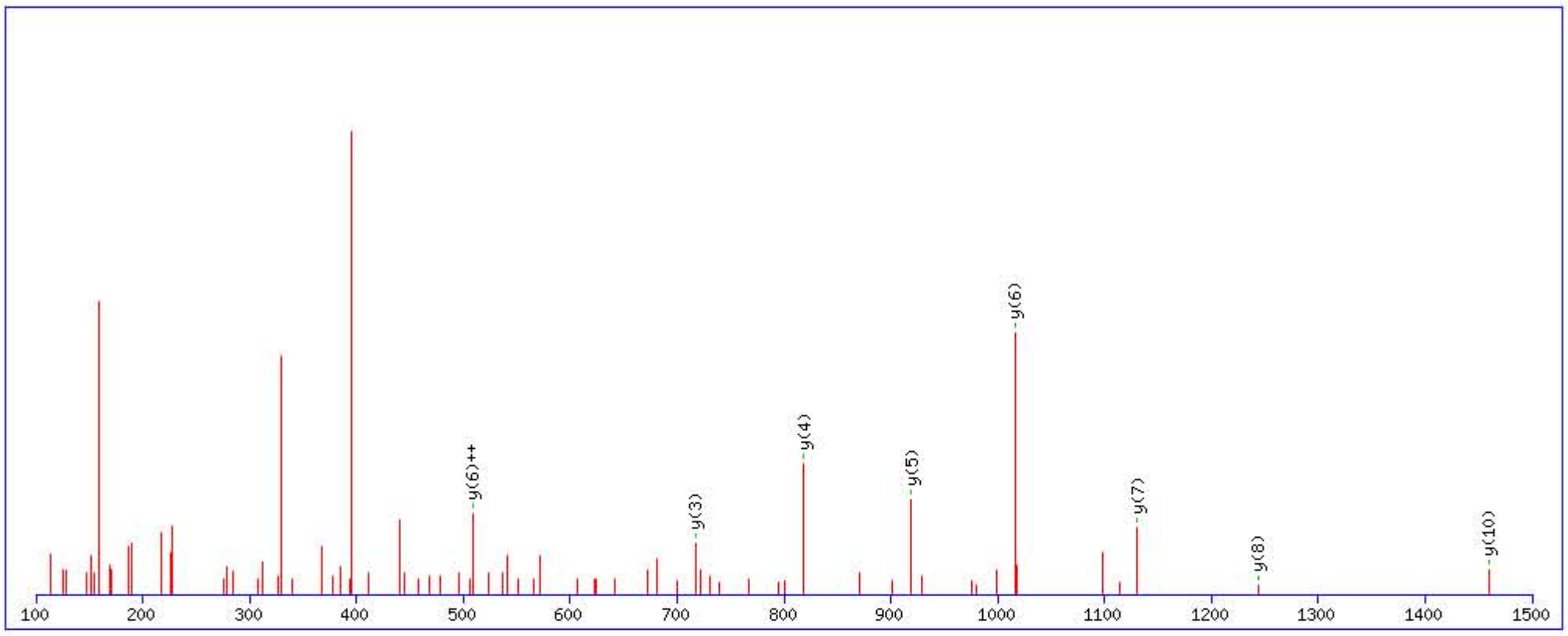
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SVSEINPTTQMK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

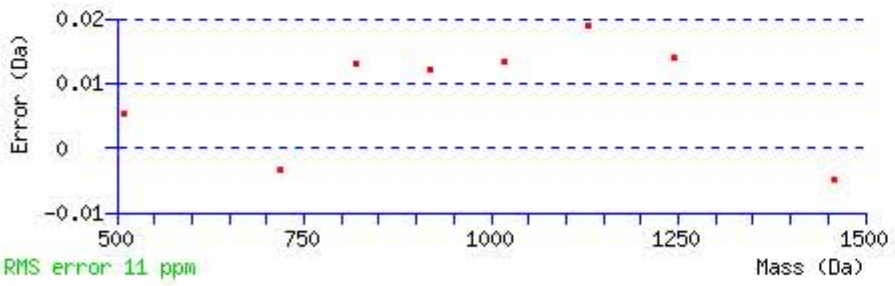
Match to Query 36752: 1644.826002 from(549.282610,3+) rtinseconds(1853) index(33186)
Title: Locus:1.1.1.754.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

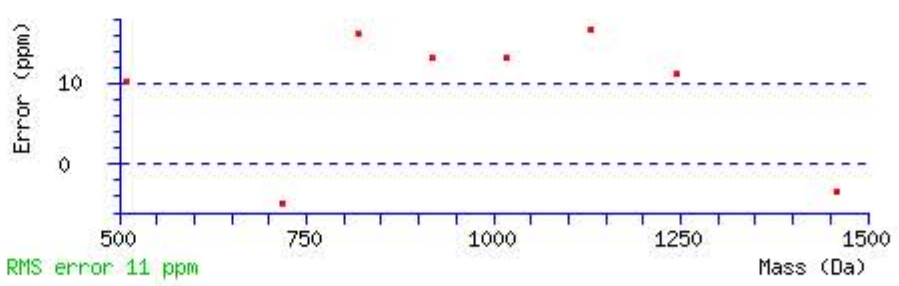
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1644.821503
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.00071
**Matches :** 8/116 fragment ions using 13 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 12 |
| 2 | 187.107718 | 94.057497 | | | 169.097153 | 85.052214 | V | 1558.796763 | 779.902020 | 1541.770214 | 771.388745 | 1540.786198 | 770.896737 | 11 |
| 3 | 274.139746 | 137.573511 | | | 256.129181 | 128.568229 | S | *1459.728349* | 730.367813 | 1442.701800 | 721.854538 | 1441.717784 | 721.362530 | 10 |
| 4 | 403.182339 | 202.094808 | | | 385.171774 | 193.089525 | E | 1372.696321 | 686.851799 | 1355.669772 | 678.338524 | 1354.685756 | 677.846516 | 9 |
| 5 | 516.266403 | 258.636840 | | | 498.255838 | 249.631557 | I | *1243.653728* | 622.330502 | 1226.627179 | 613.817228 | 1225.643163 | 613.325220 | 8 |
| 6 | 630.309330 | 315.658303 | 613.282781 | 307.145029 | 612.298765 | 306.653021 | N | *1130.569664* | 565.788470 | 1113.543115 | 557.275196 | 1112.559099 | 556.783188 | 7 |
| 7 | 727.362094 | 364.184685 | 710.335545 | 355.671411 | 709.351529 | 355.179403 | P | *1016.526737* | 508.767007 | 999.500188 | 500.253732 | 998.516172 | 499.761724 | 6 |
| 8 | 828.409773 | 414.708525 | 811.383224 | 406.195250 | 810.399208 | 405.703242 | T | *919.473973* | 460.240625 | 902.447424 | 451.727350 | 901.463408 | 451.235342 | 5 |
| 9 | 929.457452 | 465.232364 | 912.430903 | 456.719090 | 911.446887 | 456.227082 | T | *818.426294* | 409.716785 | 801.399745 | 401.203511 | 800.415729 | 400.711503 | 4 |
| 10 | 1368.682778 | 684.845027 | 1351.656229 | 676.331753 | 1350.672213 | 675.839745 | Q | *717.378615* | 359.192946 | 700.352066 | 350.679671 | | | 3 |
| 11 | 1499.723263 | 750.365270 | 1482.696714 | 741.851995 | 1481.712698 | 741.359987 | M | 278.153289 | 139.580282 | 261.126740 | 131.067008 | | | 2 |
| 12 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.4 | 1644.821503 | 0.004499 | SVSEINPTTQMK |

**Mascot:** http://www.matrixscience.com/

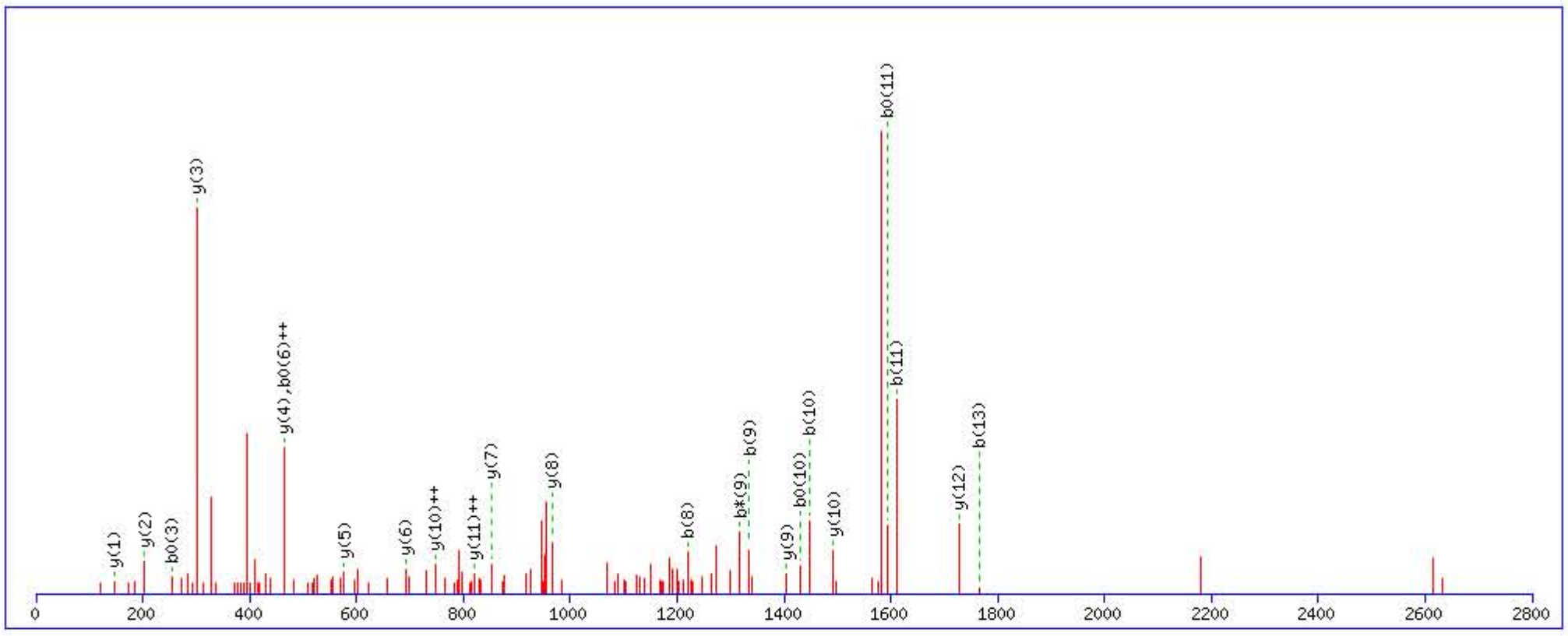
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IASFSQNCDIYPGK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

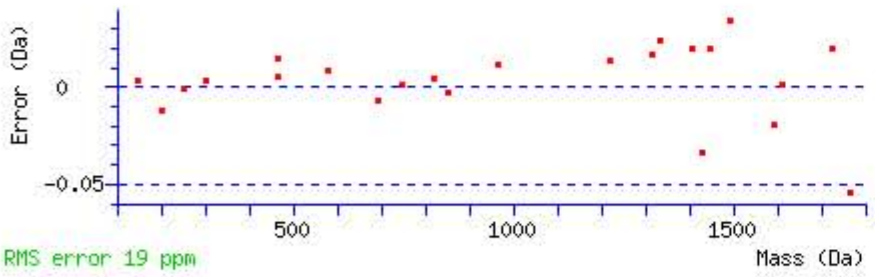
Match to Query 42338: 1909.928328 from(955.971440,2+) rtinseconds(2054) index(20559)
Title: Locus:1.1.1.3097.21 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

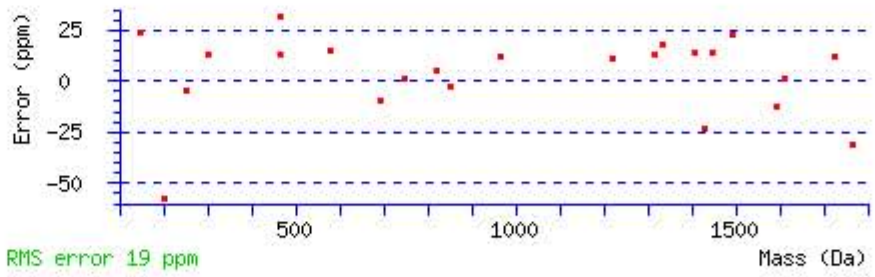
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1909.906631
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 61 **Expect:** 2.8e-006
**Matches :** 23/132 fragment ions using 47 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 14 |
| 2 | 185.128454 | 93.067865 | | | | | A | 1797.829854 | 899.418565 | 1780.803305 | 890.905291 | 1779.819289 | 890.413283 | 13 |
| 3 | 272.160482 | 136.583879 | | | 254.149917 | 127.578596 | S | *1726.792740* | 863.900008 | 1709.766191 | 855.386734 | 1708.782175 | 854.894726 | 12 |
| 4 | 419.228896 | 210.118086 | | | 401.218331 | 201.112803 | F | 1639.760712 | 820.383994 | 1622.734163 | 811.870720 | 1621.750147 | 811.378712 | 11 |
| 5 | 506.260924 | 253.634100 | | | 488.250359 | 244.628817 | S | *1492.692298* | 746.849787 | 1475.665749 | 738.336513 | 1474.681733 | 737.844505 | 10 |
| 6 | 945.486250 | 473.246763 | 928.459701 | 464.733488 | 927.475685 | 464.241480 | Q | *1405.660270* | 703.333773 | 1388.633721 | 694.820499 | 1387.649705 | 694.328491 | 9 |
| 7 | 1059.529177 | 530.268226 | 1042.502628 | 521.754952 | 1041.518612 | 521.262944 | N | *966.434944* | 483.721110 | 949.408395 | 475.207836 | 948.424379 | 474.715828 | 8 |
| 8 | **1219.559826** | 610.283551 | 1202.533277 | 601.770277 | 1201.549261 | 601.278268 | C | *852.392017* | 426.699647 | 835.365468 | 418.186372 | 834.381452 | 417.694364 | 7 |
| 9 | **1334.586769** | 667.797023 | 1317.560220 | 659.283748 | 1316.576204 | 658.791740 | D | *692.361368* | 346.684322 | 675.334819 | 338.171048 | 674.350803 | 337.679040 | 6 |
| 10 | **1447.670833** | 724.339054 | 1430.644284 | 715.825780 | 1429.660268 | 715.333772 | I | *577.334425* | 289.170851 | 560.307876 | 280.657576 | | | 5 |
| 11 | **1610.734162** | 805.870719 | 1593.707613 | 797.357445 | 1592.723597 | 796.865436 | Y | *464.250361* | 232.628818 | 447.223812 | 224.115544 | | | 4 |
| 12 | 1707.786926 | 854.397101 | 1690.760377 | 845.883827 | 1689.776361 | 845.391819 | P | *301.187032* | 151.097154 | 284.160483 | 142.583879 | | | 3 |
| 13 | **1764.808390** | 882.907833 | 1747.781841 | 874.394559 | 1746.797825 | 873.902550 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 14 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 60.6 | 1909.906631 | 0.021697 | IASFSQNCDIYPGK |
| 1.5 | 1909.905975 | 0.022353 | KRMTSQDCLETSK |

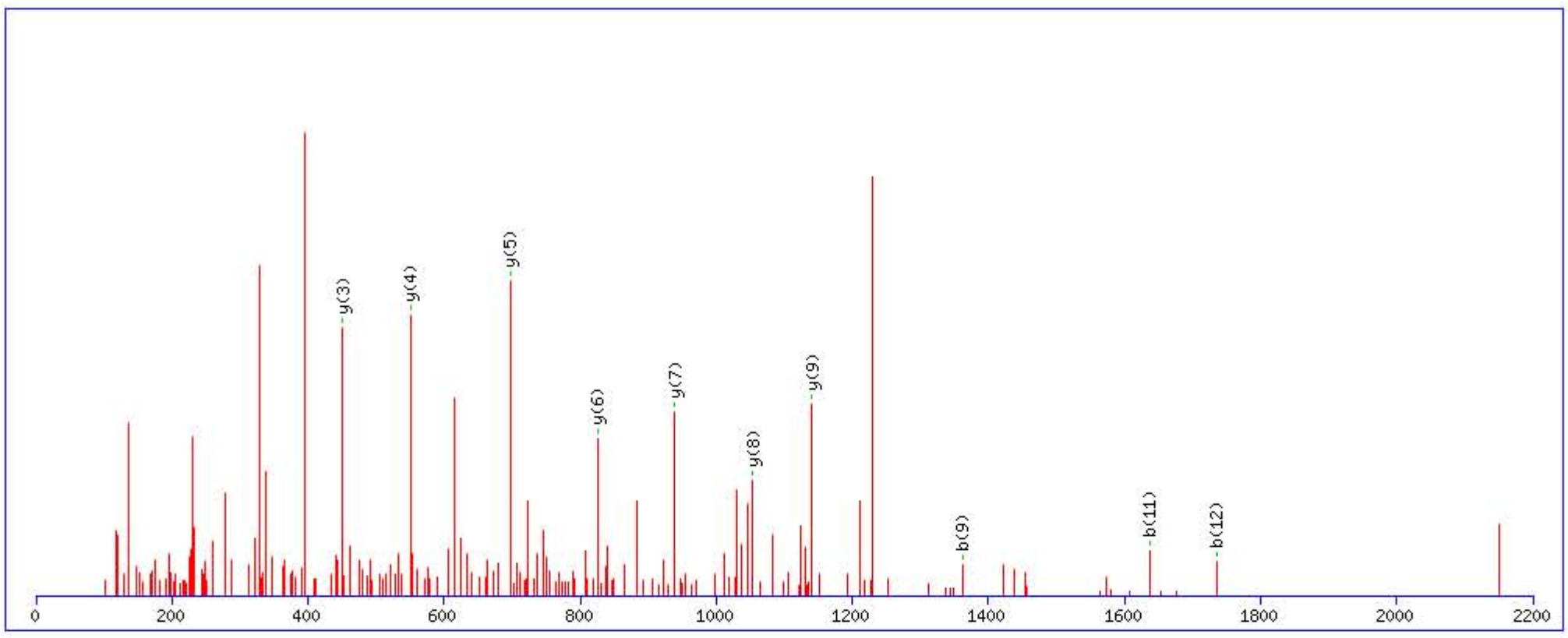
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YNSQNQSNNQFVLYR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

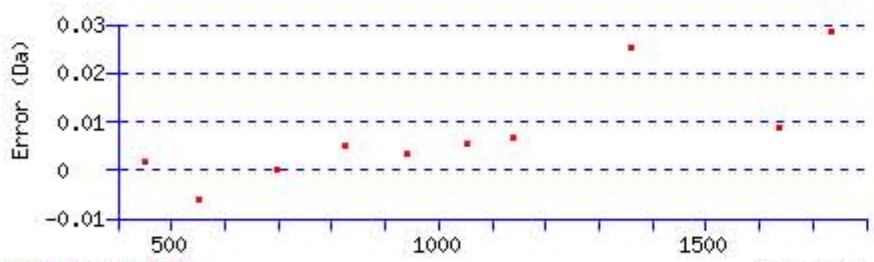
Match to Query 48190: 2185.054452 from(729.358760,3+) rtinseconds(2030) index(20408)
Title: Locus:1.1.1.3089.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

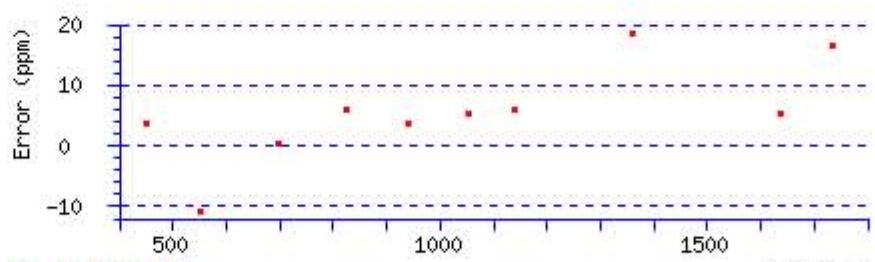
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2185.037445
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.0031
**Matches :** 10/146 fragment ions using 18 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 15 |
| 2 | 278.113532 | 139.560404 | 261.086983 | 131.047130 | | | N | 2022.981419 | 1011.994348 | 2005.954870 | 1003.481073 | 2004.970854 | 1002.989065 | 14 |
| 3 | 365.145560 | 183.076418 | 348.119011 | 174.563144 | 347.134995 | 174.071136 | S | 1908.938492 | 954.972884 | 1891.911943 | 946.459610 | 1890.927927 | 945.967602 | 13 |
| 4 | 493.204138 | 247.105707 | 476.177589 | 238.592433 | 475.193573 | 238.100425 | Q | 1821.906464 | 911.456870 | 1804.879915 | 902.943596 | 1803.895899 | 902.451588 | 12 |
| 5 | 607.247065 | 304.127171 | 590.220516 | 295.613896 | 589.236500 | 295.121888 | N | 1693.847886 | 847.427581 | 1676.821337 | 838.914307 | 1675.837321 | 838.422299 | 11 |
| 6 | 1046.472391 | 523.739834 | 1029.445842 | 515.226559 | 1028.461826 | 514.734551 | Q | 1579.804959 | 790.406118 | 1562.778410 | 781.892843 | 1561.794394 | 781.400835 | 10 |
| 7 | 1133.504419 | 567.255848 | 1116.477870 | 558.742573 | 1115.493854 | 558.250565 | S | *1140.579633* | 570.793455 | 1123.553084 | 562.280180 | 1122.569068 | 561.788172 | 9 |
| 8 | 1247.547346 | 624.277311 | 1230.520797 | 615.764037 | 1229.536781 | 615.272029 | N | *1053.547605* | 527.277441 | 1036.521056 | 518.764166 | | | 8 |
| 9 | **1361.590273** | 681.298775 | 1344.563724 | 672.785500 | 1343.579708 | 672.293492 | N | *939.504678* | 470.255977 | 922.478129 | 461.742703 | | | 7 |
| 10 | 1489.648851 | 745.328064 | 1472.622302 | 736.814789 | 1471.638286 | 736.322781 | Q | *825.461751* | 413.234514 | 808.435202 | 404.721239 | | | 6 |
| 11 | **1636.717265** | 818.862271 | 1619.690716 | 810.348996 | 1618.706700 | 809.856988 | F | *697.403173* | 349.205225 | 680.376624 | 340.691950 | | | 5 |
| 12 | **1735.785679** | 868.396478 | 1718.759130 | 859.883203 | 1717.775114 | 859.391195 | V | *550.334759* | 275.671018 | 533.308210 | 267.157743 | | | 4 |
| 13 | 1848.869743 | 924.938510 | 1831.843194 | 916.425235 | 1830.859178 | 915.933227 | L | *451.266345* | 226.136811 | 434.239796 | 217.623536 | | | 3 |
| 14 | 2011.933072 | 1006.470174 | 1994.906523 | 997.956900 | 1993.922507 | 997.464892 | Y | 338.182281 | 169.594779 | 321.155732 | 161.081504 | | | 2 |
| 15 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.2 | 2185.037445 | 0.017007 | YNSQNQSNNQFVLYR |
| 38.2 | 2185.037445 | 0.017007 | YNSQNQSNNQFVLYR |
| 4.2 | 2185.037445 | 0.017007 | YNSQNQSNNQFVLYR |

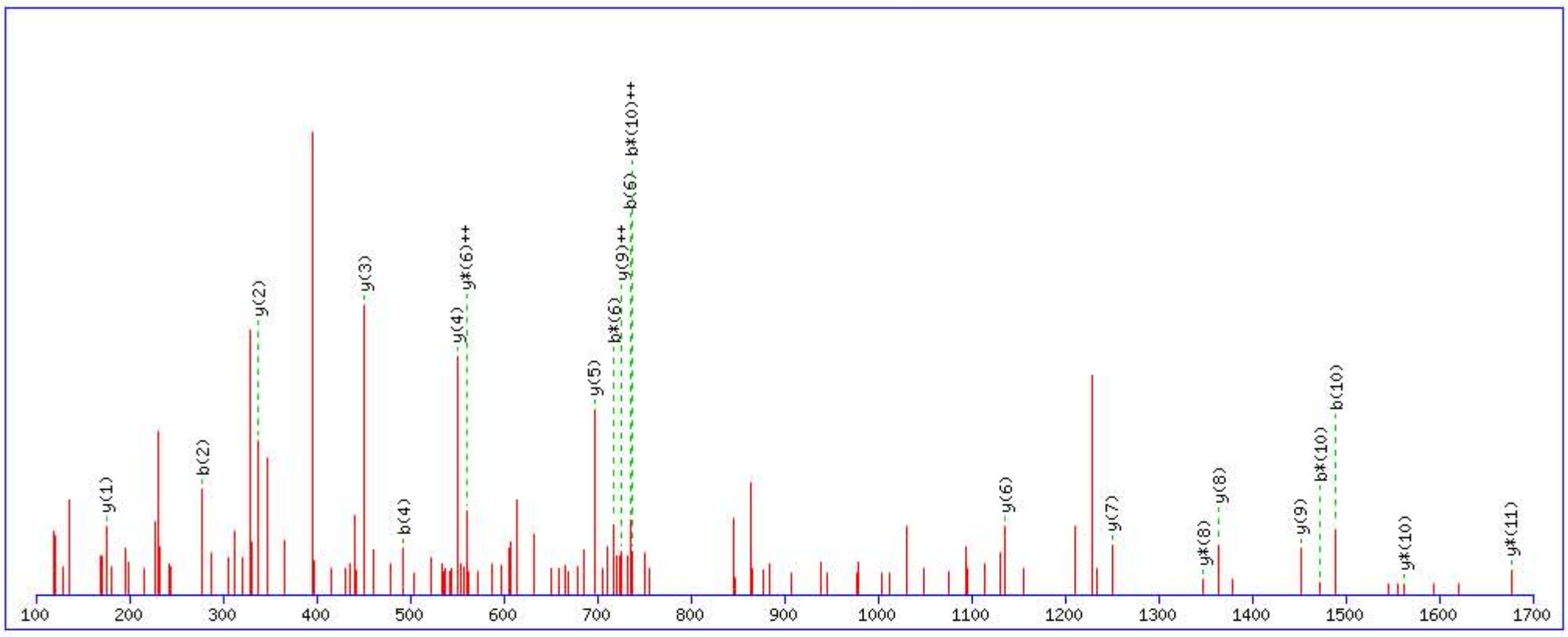
# MATRIX SCIENCE Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YNSQNQSNNQFVLYR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

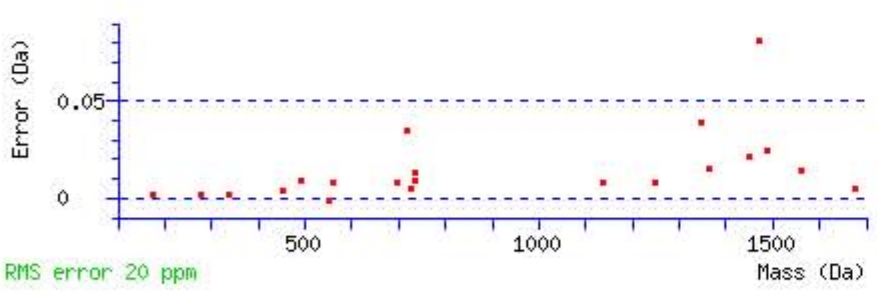
Match to Query 48192: 2185.056162 from(729.359330,3+) rtinseconds(2107) index(20885)
Title: Locus:1.1.1.3116.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

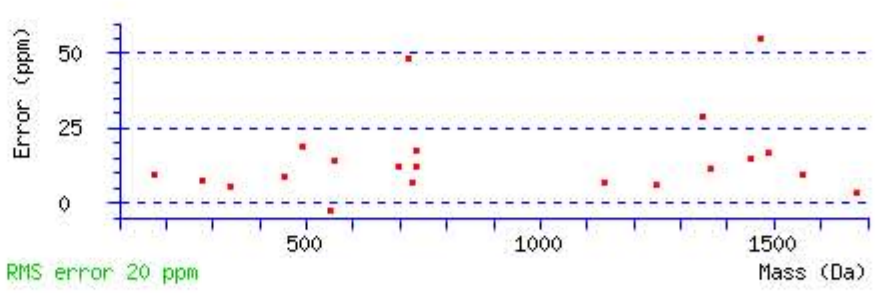
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2185.037445
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 35 **Expect:** 0.0065
**Matches :** 21/146 fragment ions using 47 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 15 |
| 2 | **278.113532** | 139.560404 | 261.086983 | 131.047130 | | | N | 2022.981419 | 1011.994348 | 2005.954870 | 1003.481073 | 2004.970854 | 1002.989065 | 14 |
| 3 | 365.145560 | 183.076418 | 348.119011 | 174.563144 | 347.134995 | 174.071136 | S | 1908.938492 | 954.972884 | 1891.911943 | 946.459610 | 1890.927927 | 945.967602 | 13 |
| 4 | **493.204138** | 247.105707 | 476.177589 | 238.592433 | 475.193573 | 238.100425 | Q | 1821.906464 | 911.456870 | 1804.879915 | 902.943596 | 1803.895899 | 902.451588 | 12 |
| 5 | 607.247065 | 304.127171 | 590.220516 | 295.613896 | 589.236500 | 295.121888 | N | 1693.847886 | 847.427581 | 1676.821337 | 838.914307 | 1675.837321 | 838.422299 | 11 |
| 6 | **735.305643** | 368.156460 | 718.279094 | 359.643185 | 717.295078 | 359.151177 | Q | 1579.804959 | 790.406118 | 1562.778410 | 781.892843 | 1561.794394 | 781.400835 | 10 |
| 7 | 822.337671 | 411.672474 | 805.311122 | 403.159199 | 804.327106 | 402.667191 | S | *1451.746381* | 726.376829 | 1434.719832 | 717.863554 | 1433.735816 | 717.371546 | 9 |
| 8 | 936.380598 | 468.693937 | 919.354049 | 460.180662 | 918.370033 | 459.688654 | N | *1364.714353* | 682.860815 | 1347.687804 | 674.347540 | | | 8 |
| 9 | 1050.423525 | 525.715400 | 1033.396976 | 517.202126 | 1032.412960 | 516.710118 | N | *1250.671426* | 625.839351 | 1233.644877 | 617.326077 | | | 7 |
| 10 | **1489.648851** | 745.328064 | 1472.622302 | 736.814789 | 1471.638286 | 736.322781 | Q | *1136.628499* | 568.817888 | 1119.601950 | 560.304613 | | | 6 |
| 11 | 1636.717265 | 818.862271 | 1619.690716 | 810.348996 | 1618.706700 | 809.856988 | F | *697.403173* | 349.205225 | 680.376624 | 340.691950 | | | 5 |
| 12 | 1735.785679 | 868.396478 | 1718.759130 | 859.883203 | 1717.775114 | 859.391195 | V | *550.334759* | 275.671018 | 533.308210 | 267.157743 | | | 4 |
| 13 | 1848.869743 | 924.938510 | 1831.843194 | 916.425235 | 1830.859178 | 915.933227 | L | *451.266345* | 226.136811 | 434.239796 | 217.623536 | | | 3 |
| 14 | 2011.933072 | 1006.470174 | 1994.906523 | 997.956900 | 1993.922507 | 997.464892 | Y | *338.182281* | 169.594779 | 321.155732 | 161.081504 | | | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 35.0 | 2185.037445 | 0.018717 | YNSQNQSNNQFVLYR |
| 12.3 | 2185.037445 | 0.018717 | YNSQNQSNNQFVLYR |
| 8.8 | 2185.037445 | 0.018717 | YNSQNQSNNQFVLYR |

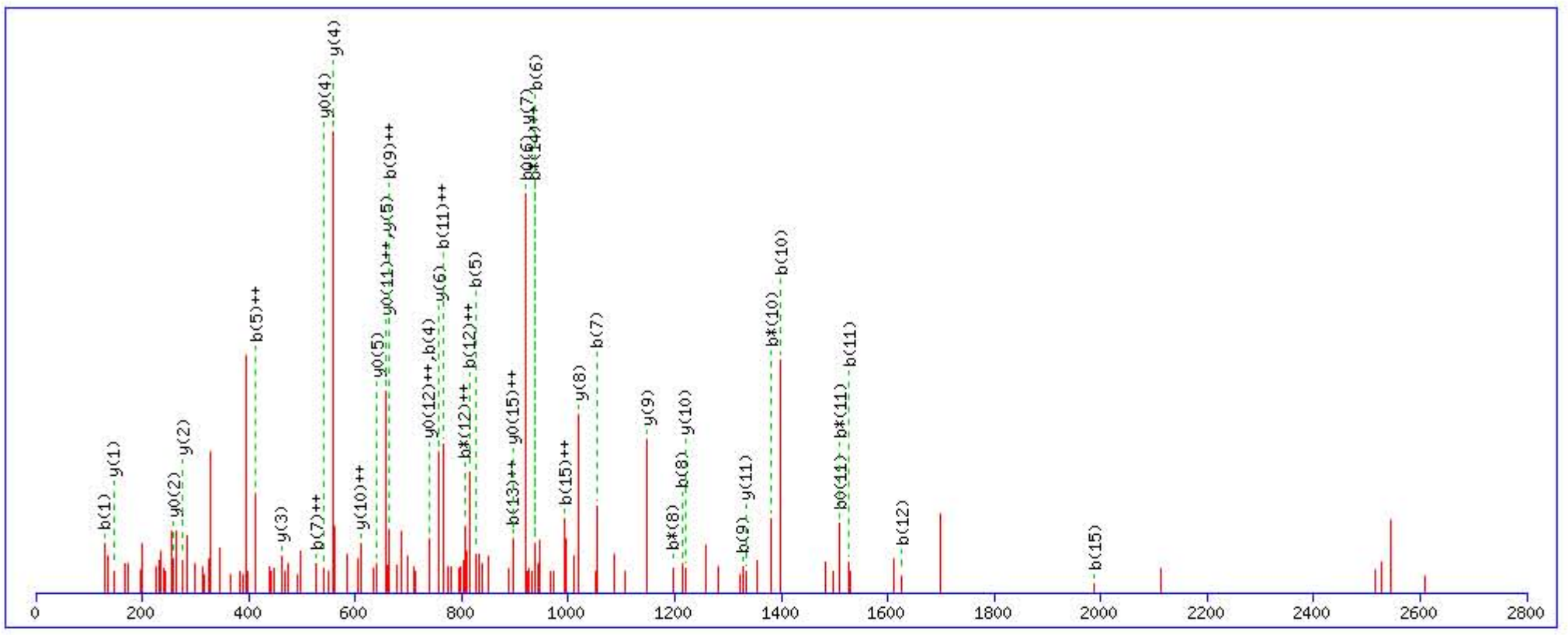
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KLGQSLDCNAEVYVVPWEK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

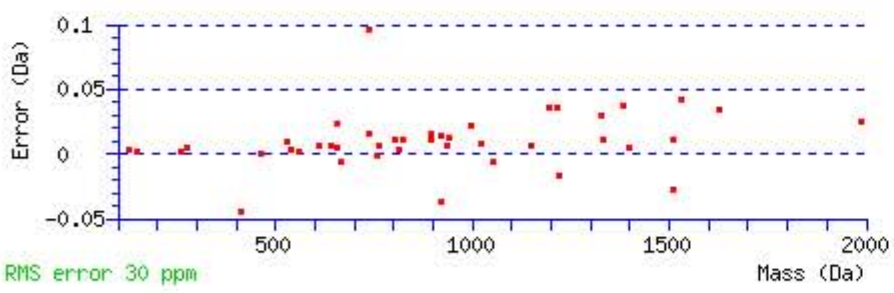
Match to Query 54955: 2545.307172 from(849.443000,3+) rtinseconds(2341) index(22265)
Title: Locus:1.1.1.3197.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

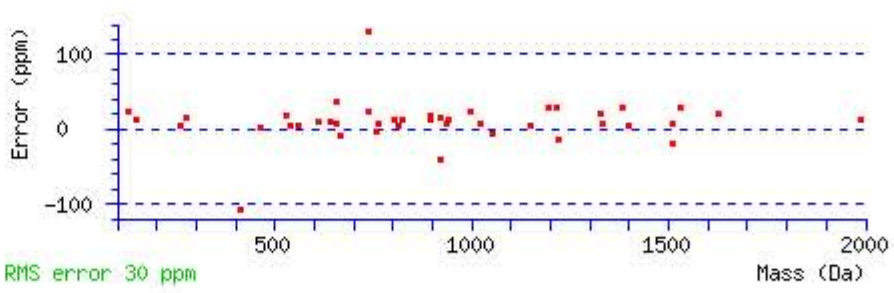
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2545.270889
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.0011
**Matches :** 43/206 fragment ions using 111 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *129.102239* | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 19 |
| 2 | 242.186303 | 121.596790 | 225.159754 | 113.083515 | | | L | 2418.183217 | 1209.595246 | 2401.156668 | 1201.081972 | 2400.172652 | 1200.589964 | 18 |
| 3 | 299.207767 | 150.107521 | 282.181218 | 141.594247 | | | G | 2305.099153 | 1153.053214 | 2288.072604 | 1144.539940 | 2287.088588 | 1144.047932 | 17 |
| 4 | *738.433093* | 369.720185 | 721.406544 | 361.206910 | | | Q | 2248.077689 | 1124.542482 | 2231.051140 | 1116.029208 | 2230.067124 | 1115.537200 | 16 |
| 5 | *825.465121* | **413.236199** | 808.438572 | 404.722924 | 807.454556 | 404.230916 | S | 1808.852363 | 904.929820 | 1791.825814 | 896.416545 | 1790.841798 | 895.924537 | 15 |
| 6 | *938.549185* | 469.778231 | 921.522636 | 461.264956 | 920.538620 | 460.772948 | L | 1721.820335 | 861.413806 | 1704.793786 | 852.900531 | 1703.809770 | 852.408523 | 14 |
| 7 | *1053.576128* | **527.291702** | 1036.549579 | 518.778428 | 1035.565563 | 518.286420 | D | 1608.736271 | 804.871774 | 1591.709722 | 796.358499 | 1590.725706 | 795.866491 | 13 |
| 8 | *1213.606777* | 607.307027 | 1196.580228 | 598.793752 | 1195.596212 | 598.301744 | C | 1493.709328 | 747.358302 | 1476.682779 | 738.845028 | 1475.698763 | 738.353020 | 12 |
| 9 | *1327.649704* | **664.328490** | 1310.623155 | 655.815216 | 1309.639139 | 655.323208 | N | *1333.678679* | 667.342978 | 1316.652130 | 658.829703 | 1315.668114 | 658.337695 | 11 |
| 10 | *1398.686818* | 699.847047 | 1381.660269 | 691.333773 | 1380.676253 | 690.841765 | A | *1219.635752* | 610.321514 | 1202.609203 | 601.808240 | 1201.625187 | 601.316232 | 10 |
| 11 | *1527.729411* | **764.368344** | 1510.702862 | 755.855069 | 1509.718846 | 755.363061 | E | *1148.598638* | 574.802957 | 1131.572089 | 566.289683 | 1130.588073 | 565.797675 | 9 |
| 12 | *1626.797825* | **813.902551** | 1609.771276 | 805.389276 | 1608.787260 | 804.897268 | V | *1019.556045* | 510.281661 | 1002.529496 | 501.768386 | 1001.545480 | 501.276378 | 8 |
| 13 | 1789.861154 | **895.434215** | 1772.834605 | 886.920941 | 1771.850589 | 886.428933 | Y | *920.487631* | 460.747454 | 903.461082 | 452.234179 | 902.477066 | 451.742171 | 7 |
| 14 | 1888.929568 | 944.968422 | 1871.903019 | 936.455148 | 1870.919003 | 935.963140 | V | *757.424302* | 379.215789 | 740.397753 | 370.702515 | 739.413737 | 370.210507 | 6 |
| 15 | *1987.997982* | **994.502629** | 1970.971433 | 985.989355 | 1969.987417 | 985.497347 | V | *658.355888* | 329.681582 | 641.329339 | 321.168308 | 640.345323 | 320.676300 | 5 |
| 16 | 2085.050746 | 1043.029011 | 2068.024197 | 1034.515736 | 2067.040181 | 1034.023728 | P | *559.287474* | 280.147375 | 542.260925 | 271.634101 | 541.276909 | 271.142093 | 4 |
| 17 | 2271.130059 | 1136.068667 | 2254.103510 | 1127.555393 | 2253.119494 | 1127.063385 | W | *462.234710* | 231.620993 | 445.208161 | 223.107719 | 444.224145 | 222.615711 | 3 |
| 18 | 2400.172652 | 1200.589964 | 2383.146103 | 1192.076689 | 2382.162087 | 1191.584682 | E | *276.155397* | 138.581337 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 19 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 44.0 | 2545.270889 | 0.036283 | KLGQSLDCNAEVYVVPWEK |

**Mascot:** http://www.matrixscience.com/

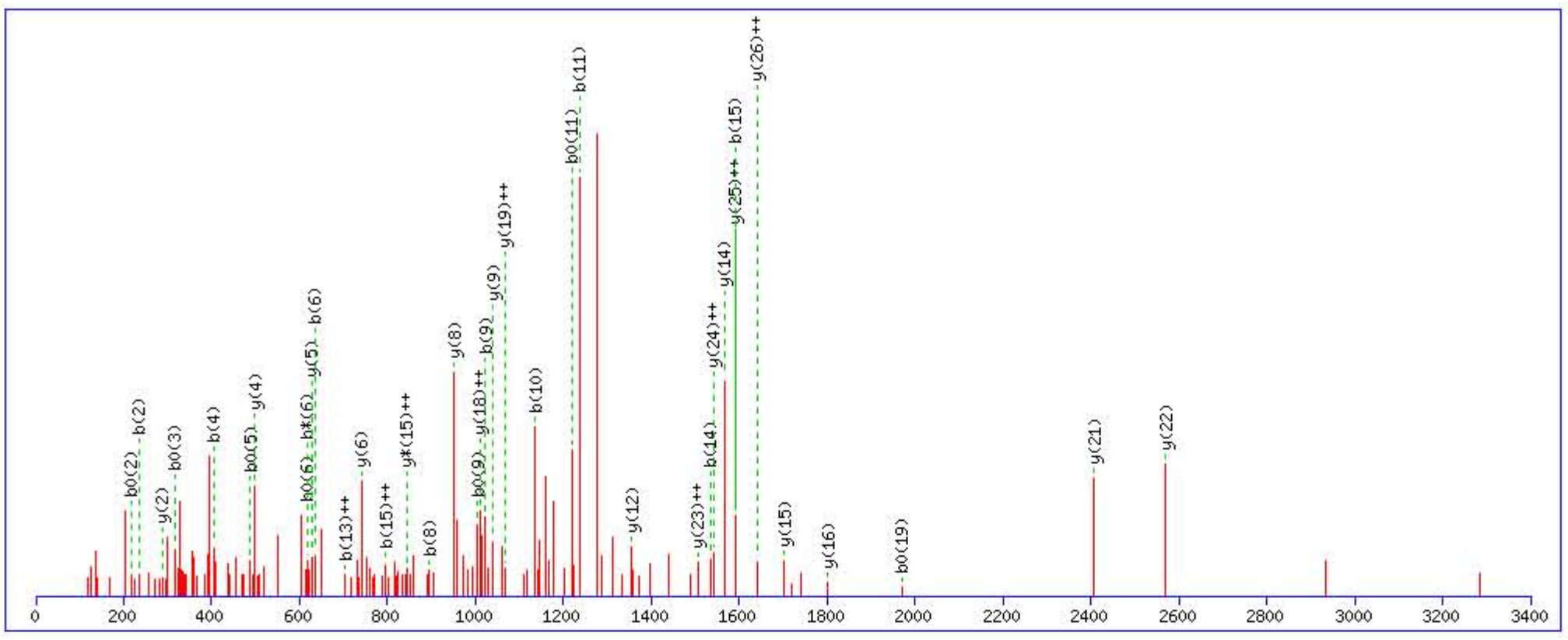
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

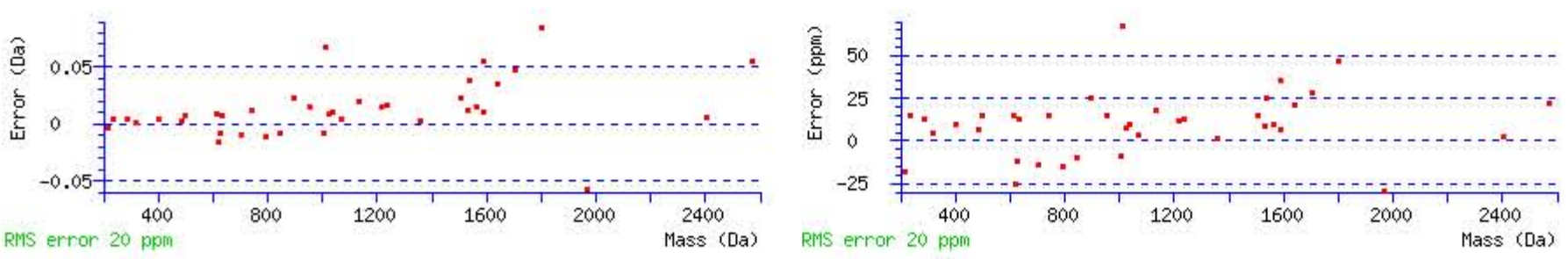
Match to Query 74066: 5066.523820 from(1014.312040,5+) rtinseconds(2663) index(9043)
Title: Locus:1.1.1.2204.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 5066.465057
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q21 : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 9e-005
**Matches :** 38/484 fragment ions using 85 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 43 |
| 2 | *235.107718* | 118.057497 | | | 217.097153 | 109.052214 | S | 4920.403881 | 2460.705578 | 4903.377332 | 2452.192304 | 4902.393316 | 2451.700296 | 42 |
| 3 | 334.176132 | 167.591704 | | | 316.165567 | 158.586422 | V | 4833.371853 | 2417.189565 | 4816.345304 | 2408.676290 | 4815.361288 | 2408.184282 | 41 |
| 4 | *405.213246* | 203.110261 | | | 387.202681 | 194.104978 | A | 4734.303439 | 2367.655357 | 4717.276890 | 2359.142083 | 4716.292874 | 2358.650075 | 40 |
| 5 | 506.260925 | 253.634100 | | | 488.250360 | 244.628818 | T | 4663.266325 | 2332.136800 | 4646.239776 | 2323.623526 | 4645.255760 | 2323.131518 | 39 |
| 6 | *634.319503* | 317.663390 | 617.292954 | 309.150115 | 616.308938 | 308.658107 | Q | 4562.218646 | 2281.612961 | 4545.192097 | 2273.099686 | 4544.208081 | 2272.607679 | 38 |
| 7 | 735.367182 | 368.187229 | 718.340633 | 359.673955 | 717.356617 | 359.181947 | T | 4434.160068 | 2217.583672 | 4417.133519 | 2209.070397 | 4416.149503 | 2208.578390 | 37 |
| 8 | *895.397831* | 448.202554 | 878.371282 | 439.689279 | 877.387266 | 439.197271 | C | 4333.112389 | 2167.059833 | 4316.085840 | 2158.546558 | 4315.101824 | 2158.054550 | 36 |
| 9 | *1023.456409* | 512.231843 | 1006.429860 | 503.718568 | 1005.445844 | 503.226560 | Q | 4173.081740 | 2087.044508 | 4156.055191 | 2078.531233 | 4155.071175 | 2078.039226 | 35 |
| 10 | *1136.540473* | 568.773875 | 1119.513924 | 560.260600 | 1118.529908 | 559.768592 | I | 4045.023162 | 2023.015219 | 4027.996613 | 2014.501944 | 4027.012597 | 2014.009936 | 34 |
| 11 | *1237.588152* | 619.297714 | 1220.561603 | 610.784440 | 1219.577587 | 610.292432 | T | 3931.939098 | 1966.473187 | 3914.912549 | 1957.959912 | 3913.928533 | 1957.467904 | 33 |
| 12 | 1334.640916 | 667.824096 | 1317.614367 | 659.310822 | 1316.630351 | 658.818814 | P | 3830.891419 | 1915.949347 | 3813.864870 | 1907.436073 | 3812.880854 | 1906.944065 | 32 |
| 13 | 1405.678030 | **703.342653** | 1388.651481 | 694.829379 | 1387.667465 | 694.337371 | A | 3733.838655 | 1867.422965 | 3716.812106 | 1858.909691 | 3715.828090 | 1858.417683 | 31 |
| 14 | *1534.720623* | 767.863949 | 1517.694074 | 759.350675 | 1516.710058 | 758.858667 | E | 3662.801541 | 1831.904408 | 3645.774992 | 1823.391134 | 3644.790976 | 1822.899126 | 30 |
| 15 | *1591.742087* | **796.374681** | 1574.715538 | 787.861407 | 1573.731522 | 787.369399 | G | 3533.758948 | 1767.383112 | 3516.732399 | 1758.869837 | 3515.748383 | 1758.377829 | 29 |
| 16 | 1688.794851 | 844.901063 | 1671.768302 | 836.387789 | 1670.784286 | 835.895781 | P | 3476.737484 | 1738.872380 | 3459.710935 | 1730.359105 | 3458.726919 | 1729.867097 | 28 |
| 17 | 1787.863265 | 894.435271 | 1770.836716 | 885.921996 | 1769.852700 | 885.429988 | V | 3379.684720 | 1690.345998 | 3362.658171 | 1681.832723 | 3361.674155 | 1681.340715 | 27 |
| 18 | 1886.931679 | 943.969478 | 1869.905130 | 935.456203 | 1868.921114 | 934.964195 | V | 3280.616306 | 1640.811791 | 3263.589757 | 1632.298516 | 3262.605741 | 1631.806508 | 26 |
| 19 | 1987.979358 | 994.493317 | 1970.952809 | 985.980043 | 1969.968793 | 985.488035 | T | 3181.547892 | 1591.277584 | 3164.521343 | 1582.764309 | 3163.537327 | 1582.272301 | 25 |
| 20 | 2059.016472 | 1030.011874 | 2041.989923 | 1021.498600 | 2041.005907 | 1021.006591 | A | 3080.500213 | 1540.753744 | 3063.473664 | 1532.240470 | 3062.489648 | 1531.748462 | 24 |
| 21 | 2498.241798 | 1249.624537 | 2481.215249 | 1241.111262 | 2480.231233 | 1240.619254 | Q | 3009.463099 | 1505.235187 | 2992.436550 | 1496.721913 | 2991.452534 | 1496.229905 | 23 |
| 22 | 2661.305127 | 1331.156202 | 2644.278578 | 1322.642927 | 2643.294562 | 1322.150919 | Y | *2570.237773* | 1285.622524 | 2553.211224 | 1277.109250 | 2552.227208 | 1276.617242 | 22 |
| 23 | 2776.332070 | 1388.669673 | 2759.305521 | 1380.156398 | 2758.321505 | 1379.664390 | D | *2407.174444* | 1204.090860 | 2390.147895 | 1195.577585 | 2389.163879 | 1195.085577 | 21 |
| 24 | 2936.362719 | 1468.684997 | 2919.336170 | 1460.171723 | 2918.352154 | 1459.679715 | C | 2292.147501 | 1146.577388 | 2275.120952 | 1138.064114 | 2274.136936 | 1137.572106 | 20 |
| 25 | 3049.446783 | 1525.227029 | 3032.420234 | 1516.713755 | 3031.436218 | 1516.221747 | L | 2132.116852 | 1066.562064 | 2115.090303 | 1058.048789 | 2114.106287 | 1057.556781 | 19 |
| 26 | 3106.468247 | 1553.737761 | 3089.441698 | 1545.224487 | 3088.457682 | 1544.732479 | G | 2019.032788 | 1010.020032 | 2002.006239 | 1001.506757 | 2001.022223 | 1001.014749 | 18 |
| 27 | 3266.498896 | 1633.753086 | 3249.472347 | 1625.239811 | 3248.488331 | 1624.747803 | C | 1962.011324 | 981.509300 | 1944.984775 | 972.996025 | 1944.000759 | 972.504017 | 17 |
| 28 | 3365.567310 | 1683.287293 | 3348.540761 | 1674.774018 | 3347.556745 | 1674.282010 | V | *1801.980675* | 901.493975 | 1784.954126 | 892.980701 | 1783.970110 | 892.488693 | 16 |
| 29 | 3502.626222 | 1751.816749 | 3485.599673 | 1743.303474 | 3484.615657 | 1742.811466 | H | *1702.912261* | 851.959768 | 1685.885712 | 843.446494 | 1684.901696 | 842.954486 | 15 |
| 30 | 3599.678986 | 1800.343131 | 3582.652437 | 1791.829856 | 3581.668421 | 1791.337848 | P | *1565.853349* | 783.430312 | 1548.826800 | 774.917038 | 1547.842784 | 774.425030 | 14 |
| 31 | 3712.763050 | 1856.885163 | 3695.736501 | 1848.371888 | 3694.752485 | 1847.879880 | I | 1468.800585 | 734.903930 | 1451.774036 | 726.390656 | 1450.790020 | 725.898648 | 13 |
| 32 | 3799.795078 | 1900.401177 | 3782.768529 | 1891.887902 | 3781.784513 | 1891.395894 | S | *1355.716521* | 678.361898 | 1338.689972 | 669.848624 | 1337.705956 | 669.356616 | 12 |
| 33 | 3900.842757 | 1950.925016 | 3883.816208 | 1942.411742 | 3882.832192 | 1941.919734 | T | 1268.684493 | 634.845884 | 1251.657944 | 626.332610 | 1250.673928 | 625.840602 | 11 |
| 34 | 4028.901335 | 2014.954305 | 4011.874786 | 2006.441031 | 4010.890770 | 2005.949023 | Q | 1167.636814 | 584.322045 | 1150.610265 | 575.808770 | 1149.626249 | 575.316762 | 10 |
| 35 | 4115.933363 | 2058.470320 | 4098.906814 | 2049.957045 | 4097.922798 | 2049.465037 | S | *1039.578236* | 520.292756 | 1022.551687 | 511.779481 | 1021.567671 | 511.287473 | 9 |
| 36 | 4212.986127 | 2106.996702 | 4195.959578 | 2098.483427 | 4194.975562 | 2097.991419 | P | *952.546208* | 476.776742 | 935.519659 | 468.263467 | 934.535643 | 467.771459 | 8 |
| 37 | 4328.013070 | 2164.510173 | 4310.986521 | 2155.996899 | 4310.002505 | 2155.504891 | D | 855.493444 | 428.250360 | 838.466895 | 419.737085 | 837.482879 | 419.245077 | 7 |
| 38 | 4441.097134 | 2221.052205 | 4424.070585 | 2212.538930 | 4423.086569 | 2212.046923 | L | *740.466501* | 370.736888 | 723.439952 | 362.223614 | 722.455936 | 361.731606 | 6 |
| 39 | 4570.139727 | 2285.573502 | 4553.113178 | 2277.060227 | 4552.129162 | 2276.568219 | E | *627.382437* | 314.194856 | 610.355888 | 305.681582 | 609.371872 | 305.189574 | 5 |
| 40 | 4667.192491 | 2334.099884 | 4650.165942 | 2325.586609 | 4649.181926 | 2325.094601 | P | *498.339844* | 249.673560 | 481.313295 | 241.160285 | | | 4 |
| 41 | 4780.276555 | 2390.641915 | 4763.250006 | 2382.128641 | 4762.265990 | 2381.636633 | I | 401.287080 | 201.147178 | 384.260531 | 192.633903 | | | 3 |
| 42 | 4893.360619 | 2447.183947 | 4876.334070 | 2438.670673 | 4875.350054 | 2438.178665 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 43 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 53.4 | 5066.465057 | 0.058763 | FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR |
| 23.7 | 5066.465057 | 0.058763 | FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR |
| 22.0 | 5066.465057 | 0.058763 | FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR |
| 17.5 | 5066.465057 | 0.058763 | FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR |

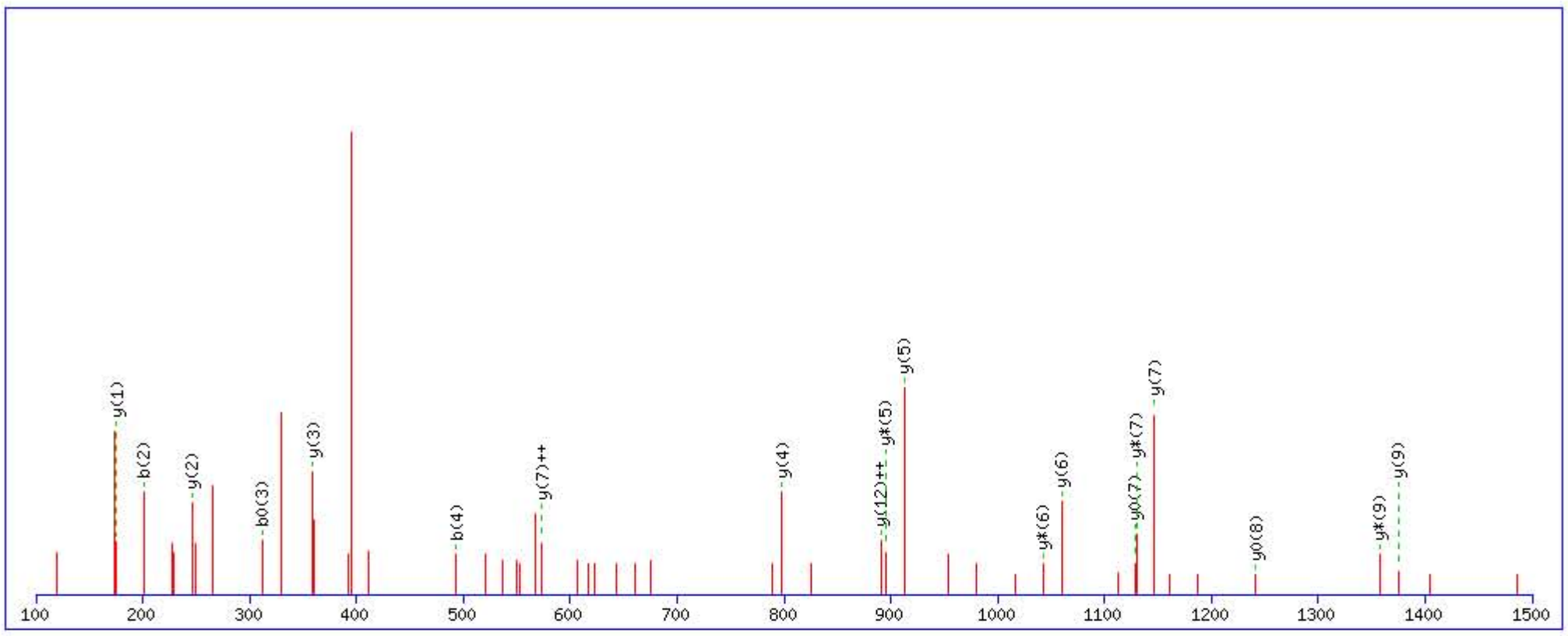
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SLEYLDLSFNQIAR**
Found in **LUM_HUMAN**, Lumican OS=Homo sapiens GN=LUM PE=1 SV=2

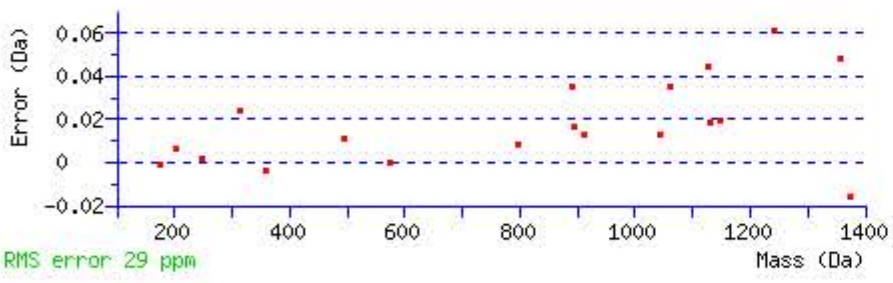
Match to Query 43731: 1979.043492 from(660.688440,3+) rtinseconds(2755) index(55154)
Title: Locus:1.1.1.2195.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

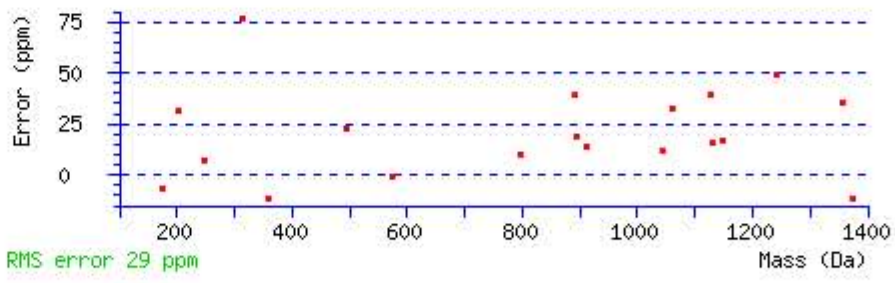
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1979.018600
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 40 **Expect:** 0.0018
**Matches :** 19/126 fragment ions using 36 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 14 |
| 2 | **201.123368** | 101.065322 | | | 183.112803 | 92.060039 | L | 1892.993882 | 947.000579 | 1875.967333 | 938.487305 | 1874.983317 | 937.995296 | 13 |
| 3 | 330.165961 | 165.586618 | | | 312.155396 | 156.581336 | E | 1779.909818 | 890.458547 | 1762.883269 | 881.945273 | 1761.899253 | 881.453265 | 12 |
| 4 | **493.229290** | 247.118283 | | | 475.218725 | 238.113001 | Y | 1650.867225 | 825.937251 | 1633.840676 | 817.423976 | 1632.856660 | 816.931968 | 11 |
| 5 | 606.313354 | 303.660315 | | | 588.302789 | 294.655033 | L | 1487.803896 | 744.405586 | 1470.777347 | 735.892312 | 1469.793331 | 735.400304 | 10 |
| 6 | 721.340297 | 361.173787 | | | 703.329732 | 352.168504 | D | *1374.719832* | 687.863554 | 1357.693283 | 679.350280 | 1356.709267 | 678.858272 | 9 |
| 7 | 834.424361 | 417.715819 | | | 816.413796 | 408.710536 | L | 1259.692889 | 630.350083 | 1242.666340 | 621.836808 | 1241.682324 | 621.344800 | 8 |
| 8 | 921.456389 | 461.231833 | | | 903.445824 | 452.226550 | S | *1146.608825* | 573.808051 | 1129.582276 | 565.294776 | 1128.598260 | 564.802768 | 7 |
| 9 | 1068.524803 | 534.766040 | | | 1050.514238 | 525.760757 | F | *1059.576797* | 530.292037 | 1042.550248 | 521.778762 | | | 6 |
| 10 | 1182.567730 | 591.787503 | 1165.541181 | 583.274229 | 1164.557165 | 582.782220 | N | *912.508383* | 456.757830 | 895.481834 | 448.244555 | | | 5 |
| 11 | 1621.793056 | 811.400166 | 1604.766507 | 802.886892 | 1603.782491 | 802.394884 | Q | *798.465456* | 399.736366 | 781.438907 | 391.223092 | | | 4 |
| 12 | 1734.877120 | 867.942198 | 1717.850571 | 859.428924 | 1716.866555 | 858.936916 | I | *359.240130* | 180.123703 | 342.213581 | 171.610428 | | | 3 |
| 13 | 1805.914234 | 903.460755 | 1788.887685 | 894.947481 | 1787.903669 | 894.455473 | A | *246.156066* | 123.581671 | 229.129517 | 115.068396 | | | 2 |
| 14 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 39.7 | 1979.018600 | 0.024892 | SLEYLDLSFNQIAR |
| 10.1 | 1979.058838 | -0.015346 | EPAPVPTQTFQNPAKKAR |
| 2.9 | 1979.025787 | 0.017705 | HQNLQEKLAEEMLGLAR |

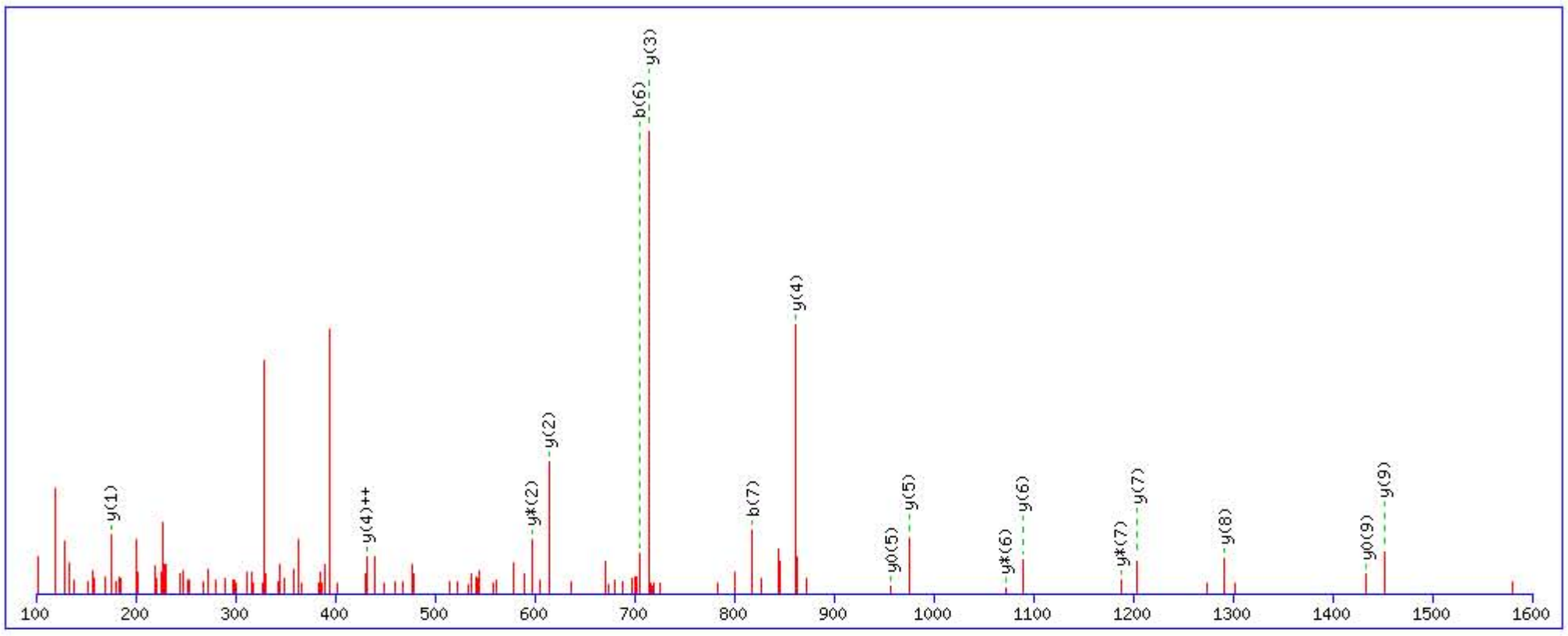
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VECSDNLFTQR**
Found in **MASP1_HUMAN**, Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3

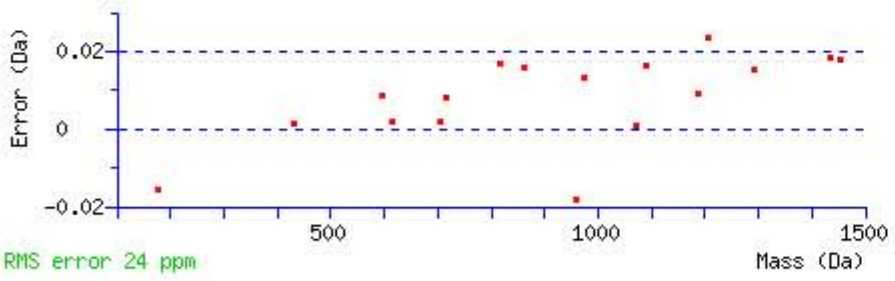
Match to Query 37509: 1678.786902 from(560.602910,3+) rtinseconds(2095) index(50940)
Title: Locus:1.1.1.1967.3 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

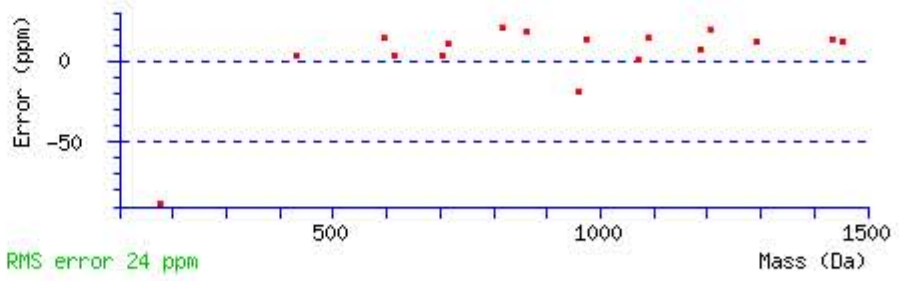
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1678.780716
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q10** : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 1.8e-005
**Matches :** 17/104 fragment ions using 27 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 11 |
| 2 | 229.118283 | 115.062780 | | | 211.107718 | 106.057497 | E | 1580.719575 | 790.863426 | 1563.693026 | 782.350151 | 1562.709010 | 781.858143 | 10 |
| 3 | 389.148932 | 195.078104 | | | 371.138367 | 186.072822 | C | *1451.676982* | 726.342129 | 1434.650433 | 717.828855 | 1433.666417 | 717.336847 | 9 |
| 4 | 476.180960 | 238.594118 | | | 458.170395 | 229.588835 | S | *1291.646333* | 646.326805 | 1274.619784 | 637.813530 | 1273.635768 | 637.321522 | 8 |
| 5 | 591.207903 | 296.107590 | | | 573.197338 | 287.102307 | D | *1204.614305* | 602.810791 | 1187.587756 | 594.297516 | 1186.603740 | 593.805508 | 7 |
| 6 | **705.250830** | 353.129053 | 688.224281 | 344.615778 | 687.240265 | 344.123770 | N | *1089.587362* | 545.297319 | 1072.560813 | 536.784045 | 1071.576797 | 536.292037 | 6 |
| 7 | **818.334894** | 409.671085 | 801.308345 | 401.157810 | 800.324329 | 400.665802 | L | *975.544435* | 488.275856 | 958.517886 | 479.762581 | 957.533870 | 479.270573 | 5 |
| 8 | 965.403308 | 483.205292 | 948.376759 | 474.692017 | 947.392743 | 474.200009 | F | *862.460371* | 431.733824 | 845.433822 | 423.220549 | 844.449806 | 422.728541 | 4 |
| 9 | 1066.450987 | 533.729131 | 1049.424438 | 525.215857 | 1048.440422 | 524.723849 | T | *715.391957* | 358.199617 | 698.365408 | 349.686342 | 697.381392 | 349.194334 | 3 |
| 10 | 1505.676313 | 753.341795 | 1488.649764 | 744.828520 | 1487.665748 | 744.336512 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.9 | 1678.780716 | 0.006186 | VECSDNLFTQR |

**Mascot:** http://www.matrixscience.com/

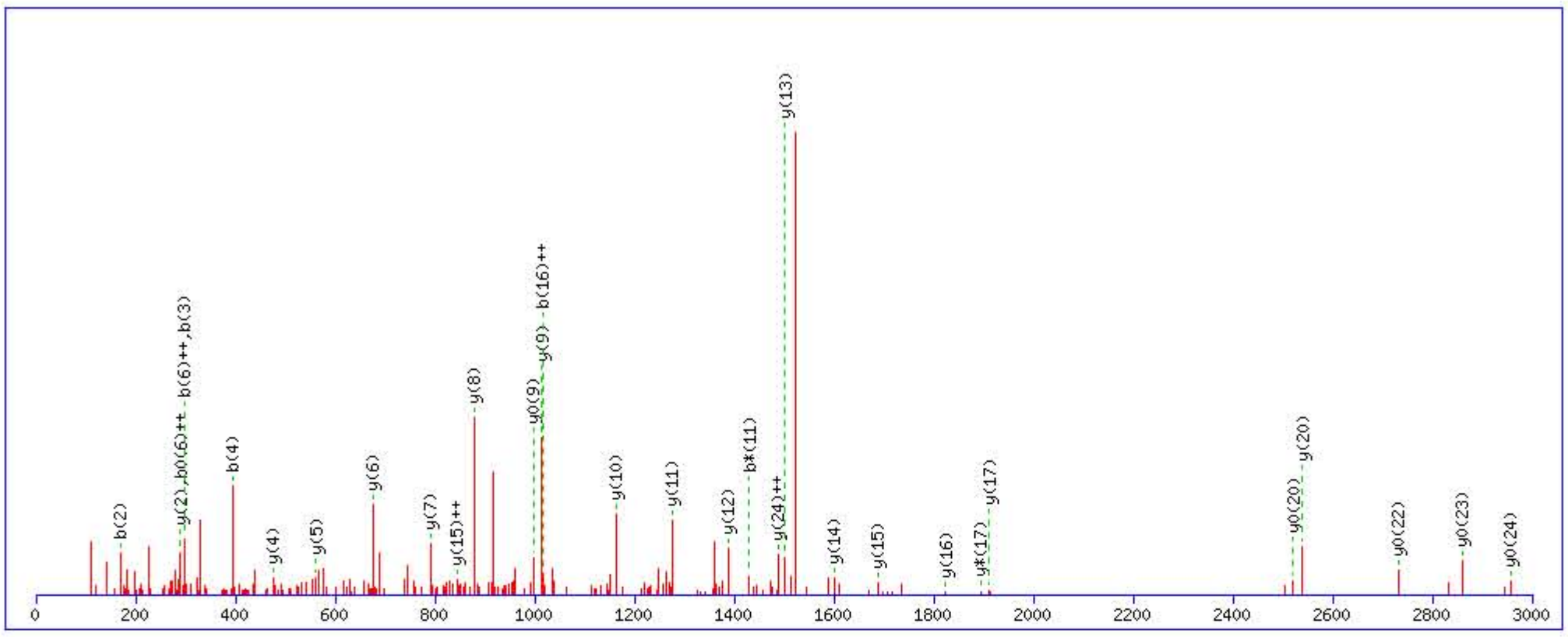
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **APEPISTQSHSVLILFHSDNSGENR**
Found in **MASP1_HUMAN**, Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3

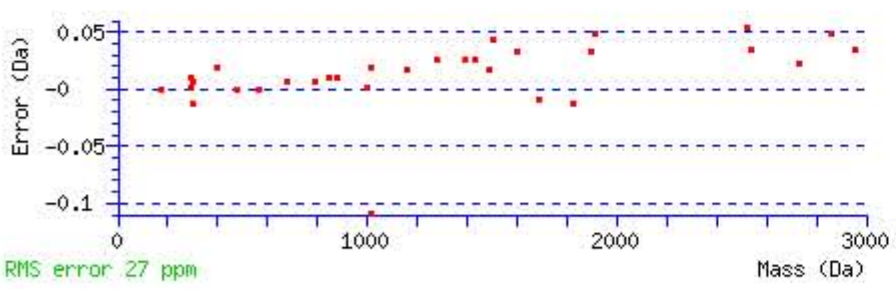
Match to Query 60489: 3045.543256 from(762.393090,4+) rtinseconds(2252) index(52026)
Title: Locus:1.1.1.2021.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

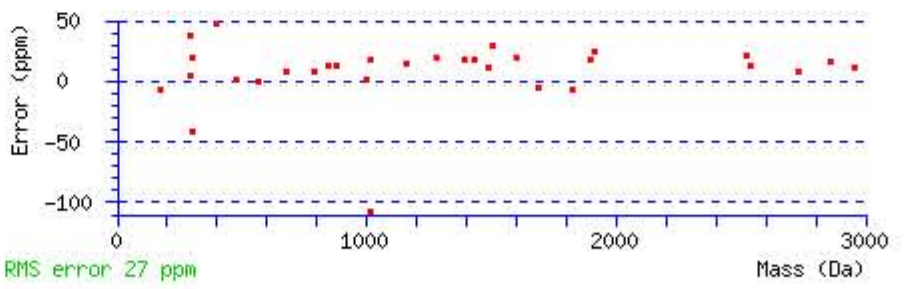
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3045.497803
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 86 **Expect:** 6.7e-008
**Matches :** 31/266 fragment ions using 64 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 25 |
| 2 | **169.097154** | 85.052215 | | | | | P | 2975.467980 | 1488.237628 | 2958.441431 | 1479.724353 | 2957.457415 | 1479.232345 | 24 |
| 3 | **298.139747** | 149.573512 | | | 280.129182 | 140.568229 | E | 2878.415216 | 1439.711246 | 2861.388667 | 1431.197971 | 2860.404651 | 1430.705963 | 23 |
| 4 | **395.192511** | 198.099894 | | | 377.181946 | 189.094611 | P | 2749.372623 | 1375.189949 | 2732.346074 | 1366.676675 | 2731.362058 | 1366.184667 | 22 |
| 5 | 508.276575 | 254.641926 | | | 490.266010 | 245.636643 | I | 2652.319859 | 1326.663567 | 2635.293310 | 1318.150293 | 2634.309294 | 1317.658285 | 21 |
| 6 | 595.308603 | **298.157940** | | | 577.298038 | 289.152657 | S | *2539.235795* | 1270.121535 | 2522.209246 | 1261.608261 | 2521.225230 | 1261.116253 | 20 |
| 7 | 696.356282 | 348.681779 | | | 678.345717 | 339.676497 | T | 2452.203767 | 1226.605521 | 2435.177218 | 1218.092247 | 2434.193202 | 1217.600239 | 19 |
| 8 | 1135.581608 | 568.294442 | 1118.555059 | 559.781168 | 1117.571043 | 559.289160 | Q | 2351.156088 | 1176.081682 | 2334.129539 | 1167.568407 | 2333.145523 | 1167.076399 | 18 |
| 9 | 1222.613636 | 611.810456 | 1205.587087 | 603.297182 | 1204.603071 | 602.805174 | S | *1911.930762* | 956.469019 | 1894.904213 | 947.955745 | 1893.920197 | 947.463737 | 17 |
| 10 | 1359.672548 | 680.339912 | 1342.645999 | 671.826638 | 1341.661983 | 671.334630 | H | *1824.898734* | 912.953005 | 1807.872185 | 904.439731 | 1806.888169 | 903.947723 | 16 |
| 11 | 1446.704576 | 723.855926 | 1429.678027 | 715.342652 | 1428.694011 | 714.850644 | S | *1687.839822* | 844.423549 | 1670.813273 | 835.910275 | 1669.829257 | 835.418267 | 15 |
| 12 | 1545.772990 | 773.390133 | 1528.746441 | 764.876859 | 1527.762425 | 764.384851 | V | *1600.807794* | 800.907535 | 1583.781245 | 792.394261 | 1582.797229 | 791.902253 | 14 |
| 13 | 1658.857054 | 829.932165 | 1641.830505 | 821.418891 | 1640.846489 | 820.926883 | L | *1501.739380* | 751.373328 | 1484.712831 | 742.860054 | 1483.728815 | 742.368045 | 13 |
| 14 | 1771.941118 | 886.474197 | 1754.914569 | 877.960923 | 1753.930553 | 877.468915 | I | *1388.655316* | 694.831296 | 1371.628767 | 686.318022 | 1370.644751 | 685.826014 | 12 |
| 15 | 1885.025182 | 943.016229 | 1867.998633 | 934.502955 | 1867.014617 | 934.010947 | L | *1275.571252* | 638.289264 | 1258.544703 | 629.775990 | 1257.560687 | 629.283982 | 11 |
| 16 | 2032.093596 | **1016.550436** | 2015.067047 | 1008.037162 | 2014.083031 | 1007.545154 | F | *1162.487188* | 581.747232 | 1145.460639 | 573.233958 | 1144.476623 | 572.741950 | 10 |
| 17 | 2169.152508 | 1085.079892 | 2152.125959 | 1076.566617 | 2151.141943 | 1076.074610 | H | *1015.418774* | 508.213025 | 998.392225 | 499.699751 | 997.408209 | 499.207743 | 9 |
| 18 | 2256.184536 | 1128.595906 | 2239.157987 | 1120.082631 | 2238.173971 | 1119.590624 | S | *878.359862* | 439.683569 | 861.333313 | 431.170295 | 860.349297 | 430.678287 | 8 |
| 19 | 2371.211479 | 1186.109377 | 2354.184930 | 1177.596103 | 2353.200914 | 1177.104095 | D | *791.327834* | 396.167555 | 774.301285 | 387.654280 | 773.317269 | 387.162272 | 7 |
| 20 | 2485.254406 | 1243.130841 | 2468.227857 | 1234.617566 | 2467.243841 | 1234.125558 | N | *676.300891* | 338.654084 | 659.274342 | 330.140809 | 658.290326 | 329.648801 | 6 |
| 21 | 2572.286434 | 1286.646855 | 2555.259885 | 1278.133580 | 2554.275869 | 1277.641572 | S | *562.257964* | 281.632620 | 545.231415 | 273.119346 | 544.247399 | 272.627338 | 5 |
| 22 | 2629.307898 | 1315.157587 | 2612.281349 | 1306.644312 | 2611.297333 | 1306.152304 | G | *475.225936* | 238.116606 | 458.199387 | 229.603331 | 457.215371 | 229.111323 | 4 |
| 23 | 2758.350491 | 1379.678884 | 2741.323942 | 1371.165609 | 2740.339926 | 1370.673601 | E | 418.204472 | 209.605874 | 401.177923 | 201.092600 | 400.193907 | 200.600592 | 3 |
| 24 | 2872.393418 | 1436.700347 | 2855.366869 | 1428.187072 | 2854.382853 | 1427.695064 | N | *289.161879* | 145.084577 | 272.135330 | 136.571303 | | | 2 |
| 25 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 86.1 | 3045.497803 | 0.045453 | APEPISTQSHSVLILFHSDNSGENR |

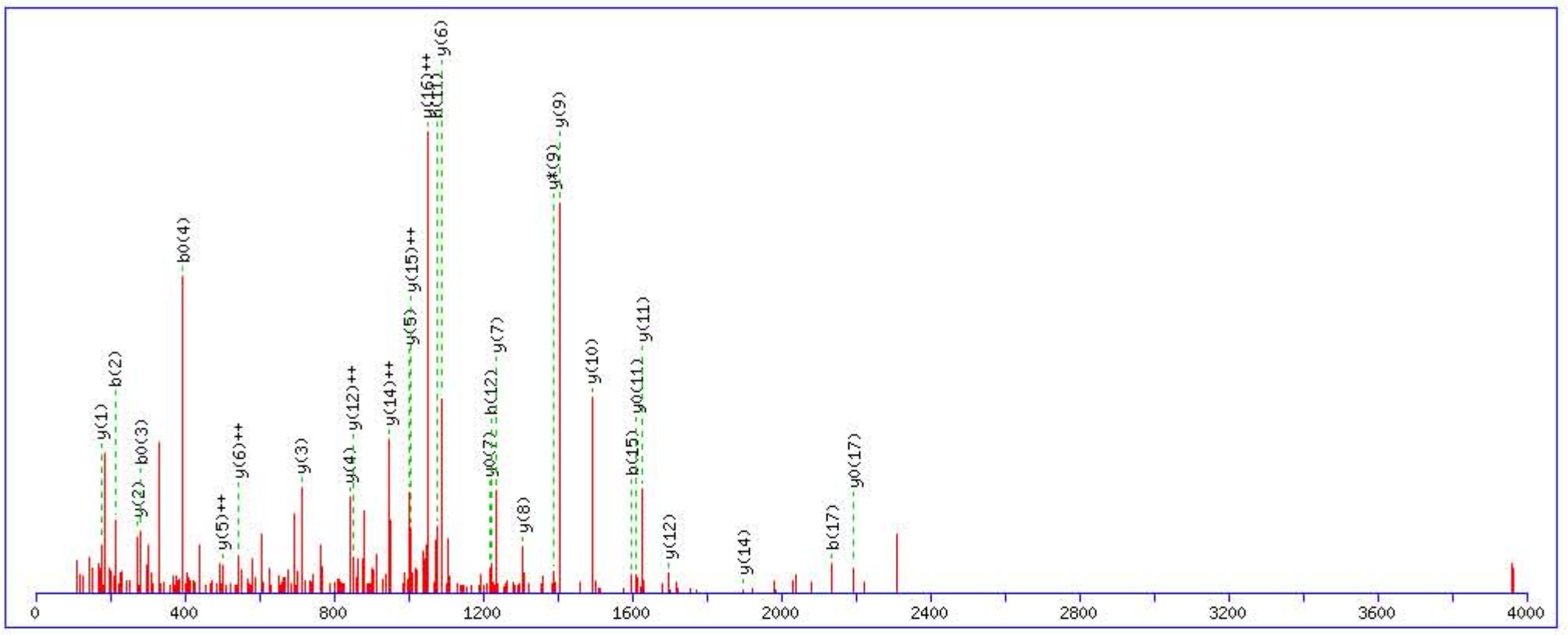
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VLSIAQAHSPAFSCEQVR**
Found in **CD14_HUMAN**, Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2

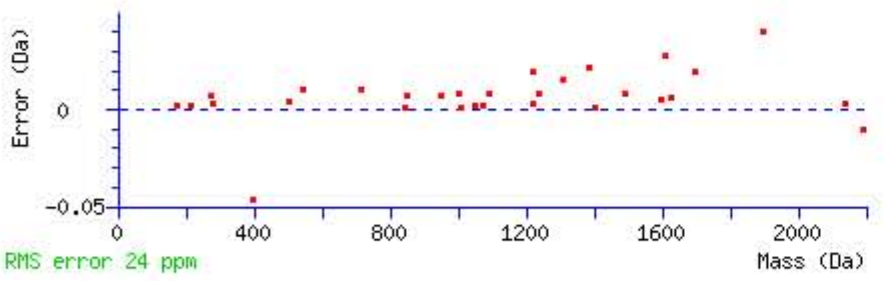
Match to Query 50707: 2310.175092 from(771.065640,3+) rtinseconds(1967) index(20059)
Title: Locus:1.1.1.3067.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

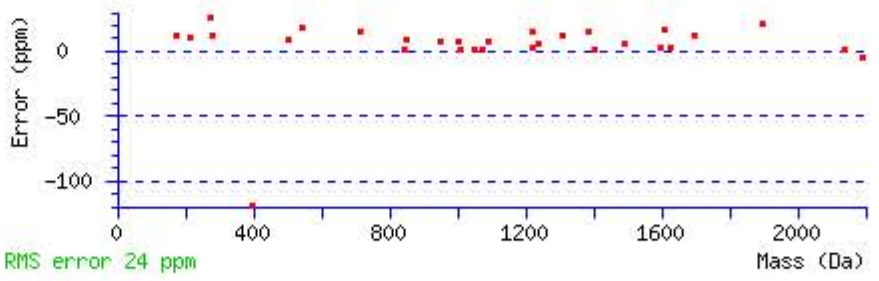
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2310.161285
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q16** : Biotin:Thermo-21345 (Q)
**Ions Score:** 55 **Expect:** 8.3e-005
**Matches :** 30/184 fragment ions using 79 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 18 |
| 2 | **213.159754** | 107.083515 | | | | | L | 2212.100156 | 1106.553716 | 2195.073607 | 1098.040441 | 2194.089591 | 1097.548433 | 17 |
| 3 | 300.191782 | 150.599529 | | | 282.181217 | 141.594247 | S | 2099.016092 | 1050.011684 | 2081.989543 | 1041.498409 | 2081.005527 | 1041.006401 | 16 |
| 4 | 413.275846 | 207.141561 | | | 395.265281 | 198.136279 | I | 2011.984064 | 1006.495670 | 1994.957515 | 997.982396 | 1993.973499 | 997.490388 | 15 |
| 5 | 484.312960 | 242.660118 | | | 466.302395 | 233.654836 | A | *1898.900000* | 949.953638 | 1881.873451 | 941.440364 | 1880.889435 | 940.948356 | 14 |
| 6 | 612.371538 | 306.689407 | 595.344989 | 298.176133 | 594.360973 | 297.684125 | Q | 1827.862886 | 914.435081 | 1810.836337 | 905.921807 | 1809.852321 | 905.429799 | 13 |
| 7 | 683.408652 | 342.207964 | 666.382103 | 333.694690 | 665.398087 | 333.202682 | A | *1699.804308* | 850.405792 | 1682.777759 | 841.892518 | 1681.793743 | 841.400510 | 12 |
| 8 | 820.467564 | 410.737420 | 803.441015 | 402.224146 | 802.456999 | 401.732138 | H | *1628.767194* | 814.887235 | 1611.740645 | 806.373961 | 1610.756629 | 805.881953 | 11 |
| 9 | 907.499592 | 454.253434 | 890.473043 | 445.740160 | 889.489027 | 445.248152 | S | *1491.708282* | 746.357779 | 1474.681733 | 737.844505 | 1473.697717 | 737.352497 | 10 |
| 10 | 1004.552356 | 502.779816 | 987.525807 | 494.266542 | 986.541791 | 493.774534 | P | *1404.676254* | 702.841765 | 1387.649705 | 694.328491 | 1386.665689 | 693.836483 | 9 |
| 11 | **1075.589470** | 538.298373 | 1058.562921 | 529.785099 | 1057.578905 | 529.293091 | A | *1307.623490* | 654.315383 | 1290.596941 | 645.802109 | 1289.612925 | 645.310101 | 8 |
| 12 | **1222.657884** | 611.832580 | 1205.631335 | 603.319306 | 1204.647319 | 602.827298 | F | *1236.586376* | 618.796826 | 1219.559827 | 610.283552 | 1218.575811 | 609.791544 | 7 |
| 13 | 1309.689912 | 655.348594 | 1292.663363 | 646.835320 | 1291.679347 | 646.343312 | S | *1089.517962* | 545.262619 | 1072.491413 | 536.749345 | 1071.507397 | 536.257337 | 6 |
| 14 | 1469.720561 | 735.363919 | 1452.694012 | 726.850644 | 1451.709996 | 726.358636 | C | *1002.485934* | 501.746605 | 985.459385 | 493.233331 | 984.475369 | 492.741323 | 5 |
| 15 | **1598.763154** | 799.885215 | 1581.736605 | 791.371941 | 1580.752589 | 790.879933 | E | *842.455285* | 421.731281 | 825.428736 | 413.218006 | 824.444720 | 412.725998 | 4 |
| 16 | 2037.988480 | 1019.497878 | 2020.961931 | 1010.984604 | 2019.977915 | 1010.492596 | Q | *713.412692* | 357.209984 | 696.386143 | 348.696710 | | | 3 |
| 17 | **2137.056894** | 1069.032085 | 2120.030345 | 1060.518811 | 2119.046329 | 1060.026803 | V | *274.187366* | 137.597321 | 257.160817 | 129.084046 | | | 2 |
| 18 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 55.3 | 2310.161285 | 0.013807 | VLSIAQAHSPAFSCEQVR |
| 3.8 | 2310.161285 | 0.013807 | VLSIAQAHSPAFSCEQVR |

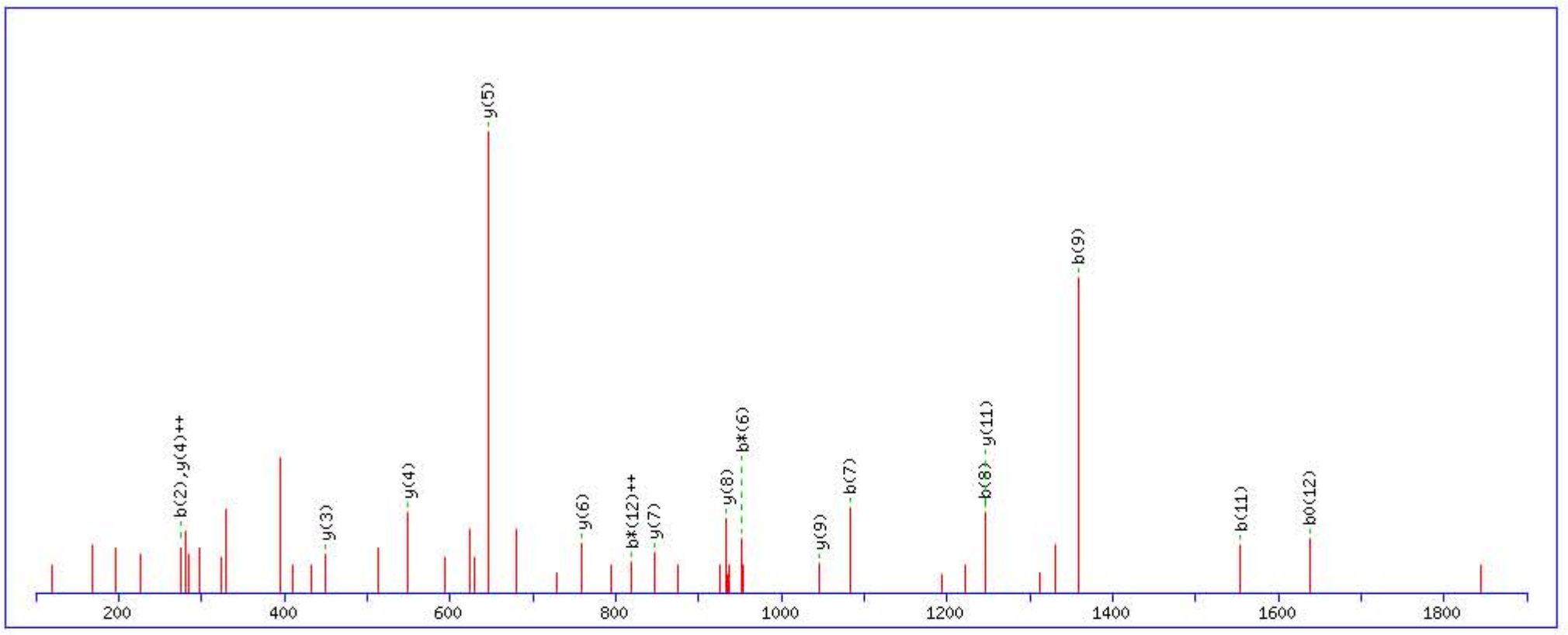
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HHGPQTLYLPVTLSSIPVFQR**
Found in **GANAB_HUMAN**, Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3

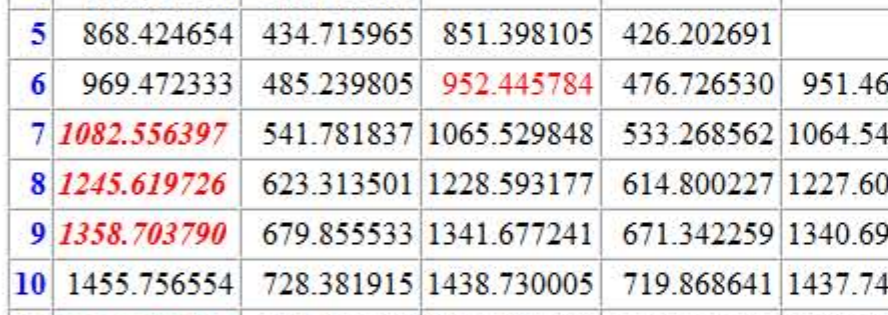
Match to Query 56360: 2700.491656 from(676.130190,4+) rtinseconds(2681) index(38166)
Title: Locus:1.1.1.1042.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

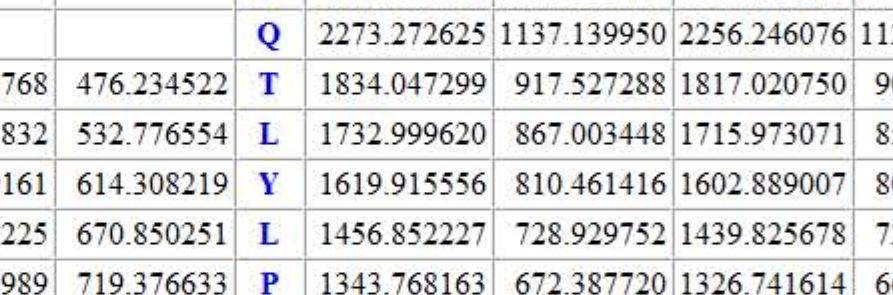
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2700.457413
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 51 **Expect:** 8.2e-005
**Matches :** 17/210 fragment ions using 28 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 21 |
| 2 | *275.125100* | 138.066188 | | | | | H | 2564.405765 | 1282.706520 | 2547.379216 | 1274.193246 | 2546.395200 | 1273.701238 | 20 |
| 3 | 332.146564 | 166.576920 | | | | | G | 2427.346853 | 1214.177064 | 2410.320304 | 1205.663790 | 2409.336288 | 1205.171782 | 19 |
| 4 | 429.199328 | 215.103302 | | | | | P | 2370.325389 | 1185.666332 | 2353.298840 | 1177.153058 | 2352.314824 | 1176.661050 | 18 |
| 5 | 868.424654 | 434.715965 | 851.398105 | 426.202691 | | | Q | 2273.272625 | 1137.139950 | 2256.246076 | 1128.626676 | 2255.262060 | 1128.134668 | 17 |
| 6 | 969.472333 | 485.239805 | 952.445784 | 476.726530 | 951.461768 | 476.234522 | T | 1834.047299 | 917.527288 | 1817.020750 | 909.014013 | 1816.036734 | 908.522005 | 16 |
| 7 | *1082.556397* | 541.781837 | 1065.529848 | 533.268562 | 1064.545832 | 532.776554 | L | 1732.999620 | 867.003448 | 1715.973071 | 858.490174 | 1714.989055 | 857.998166 | 15 |
| 8 | *1245.619726* | 623.313501 | 1228.593177 | 614.800227 | 1227.609161 | 614.308219 | Y | 1619.915556 | 810.461416 | 1602.889007 | 801.948142 | 1601.904991 | 801.456134 | 14 |
| 9 | *1358.703790* | 679.855533 | 1341.677241 | 671.342259 | 1340.693225 | 670.850251 | L | 1456.852227 | 728.929752 | 1439.825678 | 720.416477 | 1438.841662 | 719.924469 | 13 |
| 10 | 1455.756554 | 728.381915 | 1438.730005 | 719.868641 | 1437.745989 | 719.376633 | P | 1343.768163 | 672.387720 | 1326.741614 | 663.874445 | 1325.757598 | 663.382437 | 12 |
| 11 | *1554.824968* | 777.916122 | 1537.798419 | 769.402848 | 1536.814403 | 768.910840 | V | *1246.715399* | 623.861338 | 1229.688850 | 615.348063 | 1228.704834 | 614.856055 | 11 |
| 12 | 1655.872647 | 828.439962 | 1638.846098 | 819.926687 | 1637.862082 | 819.434679 | T | 1147.646985 | 574.327131 | 1130.620436 | 565.813856 | 1129.636420 | 565.321848 | 10 |
| 13 | 1768.956711 | 884.981994 | 1751.930162 | 876.468719 | 1750.946146 | 875.976711 | L | *1046.599306* | 523.803291 | 1029.572757 | 515.290017 | 1028.588741 | 514.798009 | 9 |
| 14 | 1855.988739 | 928.498008 | 1838.962190 | 919.984733 | 1837.978174 | 919.492725 | S | *933.515242* | 467.261259 | 916.488693 | 458.747985 | 915.504677 | 458.255977 | 8 |
| 15 | 1943.020767 | 972.014022 | 1925.994218 | 963.500747 | 1925.010202 | 963.008739 | S | *846.483214* | 423.745245 | 829.456665 | 415.231971 | 828.472649 | 414.739963 | 7 |
| 16 | 2056.104831 | 1028.556054 | 2039.078282 | 1020.042779 | 2038.094266 | 1019.550771 | I | *759.451186* | 380.229231 | 742.424637 | 371.715957 | | | 6 |
| 17 | 2153.157595 | 1077.082436 | 2136.131046 | 1068.569161 | 2135.147030 | 1068.077153 | P | *646.367122* | 323.687199 | 629.340573 | 315.173924 | | | 5 |
| 18 | 2252.226009 | 1126.616642 | 2235.199460 | 1118.103368 | 2234.215444 | 1117.611360 | V | *549.314358* | 275.160817 | 532.287809 | 266.647542 | | | 4 |
| 19 | 2399.294423 | 1200.150849 | 2382.267874 | 1191.637575 | 2381.283858 | 1191.145567 | F | *450.245944* | 225.626610 | 433.219395 | 217.113335 | | | 3 |
| 20 | 2527.353001 | 1264.180138 | 2510.326452 | 1255.666864 | 2509.342436 | 1255.174856 | Q | 303.177530 | 152.092403 | 286.150981 | 143.579129 | | | 2 |
| 21 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 50.9 | 2700.457413 | 0.034243 | HHGPQTLYLPVTLSSIPVFQR |

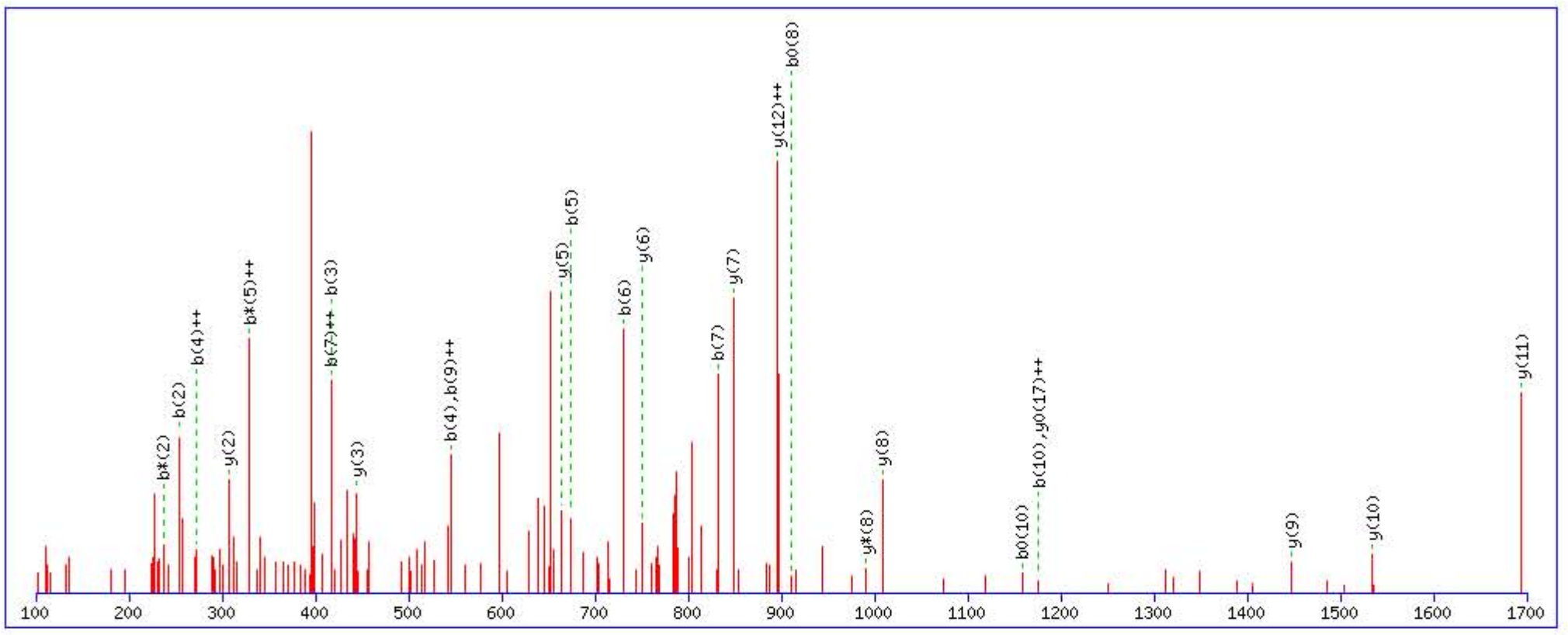
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **RPYQEGTPCSQCPSGYHCK**
Found in **PI16_HUMAN**, Peptidase inhibitor 16 OS=Homo sapiens GN=PI16 PE=1 SV=1

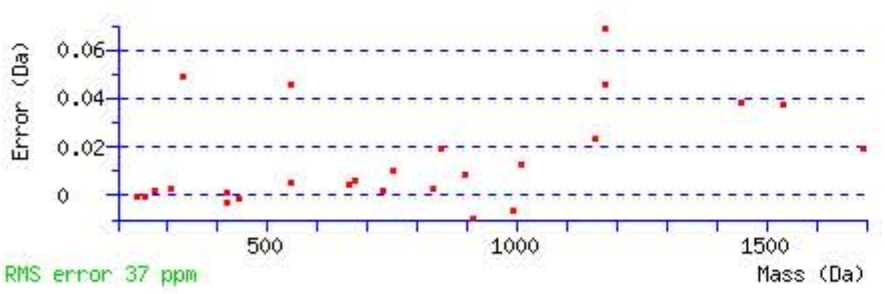
Match to Query 55686: 2622.136176 from(656.541320,4+) rtinseconds(1353) index(30150)
Title: Locus:1.1.1.579.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

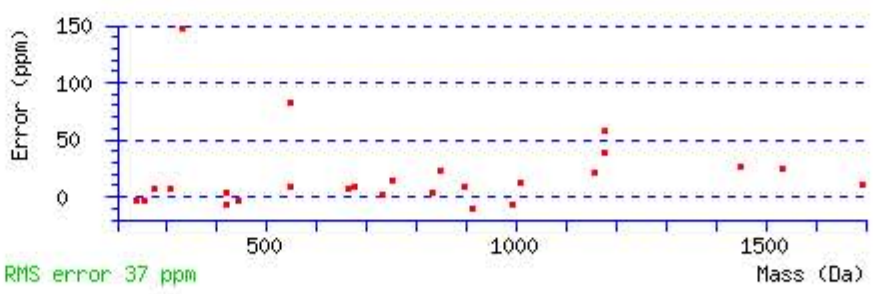
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2622.123611
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q11 : Biotin:Thermo-21345 (Q)
**Ions Score:** 37 **Expect:** 0.0011
**Matches :** 26/198 fragment ions using 62 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 157.108387 | 79.057831 | 140.081838 | 70.544557 | | | R | | | | | | | 19 |
| 2 | *254.161151* | 127.584213 | 237.134602 | 119.070939 | | | P | 2467.029773 | 1234.018524 | 2450.003224 | 1225.505250 | 2449.019208 | 1225.013242 | 18 |
| 3 | *417.224480* | 209.115878 | 400.197931 | 200.602604 | | | Y | 2369.977009 | 1185.492142 | 2352.950460 | 1176.978868 | 2351.966444 | 1176.486860 | 17 |
| 4 | *545.283058* | 273.145167 | 528.256509 | 264.631893 | | | Q | 2206.913680 | 1103.960478 | 2189.887131 | 1095.447203 | 2188.903115 | 1094.955195 | 16 |
| 5 | *674.325651* | 337.666464 | 657.299102 | 329.153189 | 656.315086 | 328.661181 | E | 2078.855102 | 1039.931189 | 2061.828553 | 1031.417914 | 2060.844537 | 1030.925906 | 15 |
| 6 | *731.347115* | 366.177196 | 714.320566 | 357.663921 | 713.336550 | 357.171913 | G | 1949.812509 | 975.409892 | 1932.785960 | 966.896618 | 1931.801944 | 966.404610 | 14 |
| 7 | *832.394794* | 416.701035 | 815.368245 | 408.187761 | 814.384229 | 407.695753 | T | 1892.791045 | 946.899160 | 1875.764496 | 938.385886 | 1874.780480 | 937.893878 | 13 |
| 8 | 929.447558 | 465.227417 | 912.421009 | 456.714143 | 911.436993 | 456.222135 | P | 1791.743366 | 896.375321 | 1774.716817 | 887.862047 | 1773.732801 | 887.370038 | 12 |
| 9 | 1089.478207 | 545.242742 | 1072.451658 | 536.729467 | 1071.467642 | 536.237459 | C | *1694.690602* | 847.848939 | 1677.664053 | 839.335665 | 1676.680037 | 838.843656 | 11 |
| 10 | *1176.510235* | 588.758756 | 1159.483686 | 580.245481 | 1158.499670 | 579.753473 | S | *1534.659953* | 767.833614 | 1517.633404 | 759.320340 | 1516.649388 | 758.828332 | 10 |
| 11 | 1615.735561 | 808.371419 | 1598.709012 | 799.858144 | 1597.724996 | 799.366136 | Q | *1447.627925* | 724.317600 | 1430.601376 | 715.804326 | 1429.617360 | 715.312318 | 9 |
| 12 | 1775.766210 | 888.386743 | 1758.739661 | 879.873469 | 1757.755645 | 879.381461 | C | *1008.402599* | 504.704937 | 991.376050 | 496.191663 | 990.392034 | 495.699655 | 8 |
| 13 | 1872.818974 | 936.913125 | 1855.792425 | 928.399851 | 1854.808409 | 927.907843 | P | *848.371950* | 424.689613 | 831.345401 | 416.176338 | 830.361385 | 415.684330 | 7 |
| 14 | 1959.851002 | 980.429139 | 1942.824453 | 971.915865 | 1941.840437 | 971.423857 | S | *751.319186* | 376.163231 | 734.292637 | 367.649956 | 733.308621 | 367.157948 | 6 |
| 15 | 2016.872466 | 1008.939871 | 1999.845917 | 1000.426597 | 1998.861901 | 999.934589 | G | *664.287158* | 332.647217 | 647.260609 | 324.133942 | | | 5 |
| 16 | 2179.935795 | 1090.471535 | 2162.909246 | 1081.958261 | 2161.925230 | 1081.466253 | Y | 607.265694 | 304.136485 | 590.239145 | 295.623210 | | | 4 |
| 17 | 2316.994707 | 1159.000991 | 2299.968158 | 1150.487717 | 2298.984142 | 1149.995709 | H | *444.202365* | 222.604820 | 427.175816 | 214.091546 | | | 3 |
| 18 | 2477.025356 | 1239.016316 | 2459.998807 | 1230.503041 | 2459.014791 | 1230.011033 | C | *307.143453* | 154.075364 | 290.116904 | 145.562090 | | | 2 |
| 19 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 36.5 | 2622.123611 | 0.012565 | RPYQEGTPCSQCPSGYHCK |

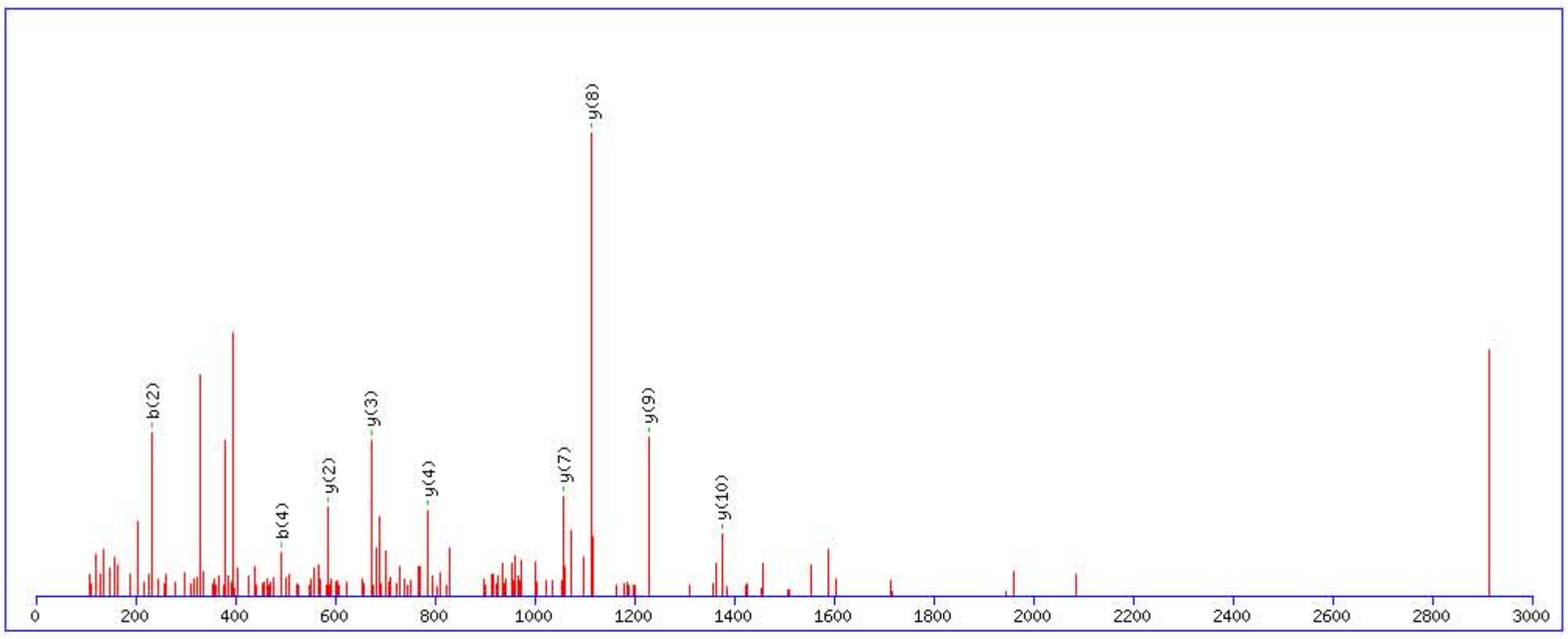
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TMFIGGSQLSQK**
Found in **PHLD_HUMAN**, Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

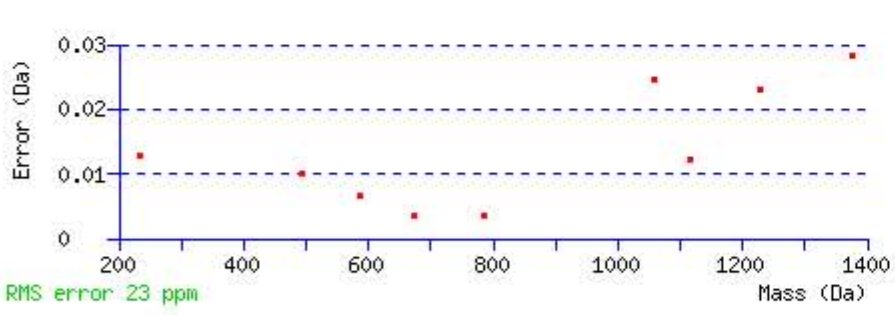
Match to Query 34893: 1606.828428 from(804.421490,2+) rtinseconds(2121) index(34978)
Title: Locus:1.1.1.847.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

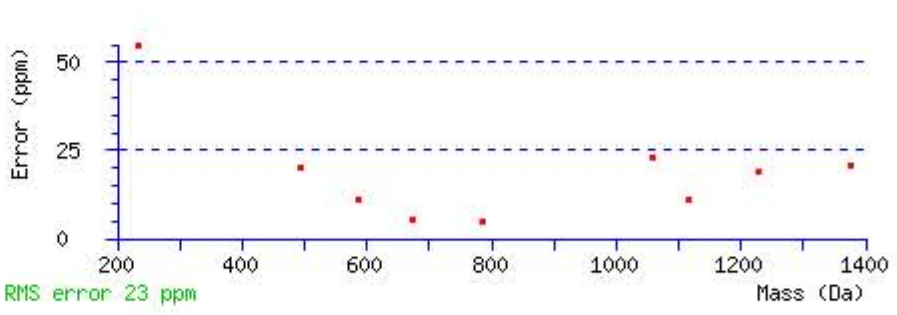
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1606.821121
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q11 : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 3.4e-005
**Matches :** 9/114 fragment ions using 15 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 12 |
| 2 | **233.095440** | 117.051358 | | | 215.084875 | 108.046076 | M | 1506.780719 | 753.893998 | 1489.754170 | 745.380723 | 1488.770154 | 744.888715 | 11 |
| 3 | 380.163854 | 190.585565 | | | 362.153289 | 181.580282 | F | *1375.740234* | 688.373755 | 1358.713685 | 679.860481 | 1357.729669 | 679.368473 | 10 |
| 4 | **493.247918** | 247.127597 | | | 475.237353 | 238.122314 | I | *1228.671820* | 614.839548 | 1211.645271 | 606.326274 | 1210.661255 | 605.834266 | 9 |
| 5 | 550.269382 | 275.638329 | | | 532.258817 | 266.633047 | G | *1115.587756* | 558.297516 | 1098.561207 | 549.784242 | 1097.577191 | 549.292234 | 8 |
| 6 | 607.290846 | 304.149061 | | | 589.280281 | 295.143779 | G | *1058.566292* | 529.786784 | 1041.539743 | 521.273510 | 1040.555727 | 520.781502 | 7 |
| 7 | 694.322874 | 347.665075 | | | 676.312309 | 338.659793 | S | 1001.544828 | 501.276052 | 984.518279 | 492.762778 | 983.534263 | 492.270770 | 6 |
| 8 | 822.381452 | 411.694364 | 805.354903 | 403.181090 | 804.370887 | 402.689082 | Q | 914.512800 | 457.760038 | 897.486251 | 449.246764 | 896.502235 | 448.754756 | 5 |
| 9 | 935.465516 | 468.236396 | 918.438967 | 459.723122 | 917.454951 | 459.231114 | L | *786.454222* | 393.730749 | 769.427673 | 385.217475 | 768.443657 | 384.725467 | 4 |
| 10 | 1022.497544 | 511.752410 | 1005.470995 | 503.239136 | 1004.486979 | 502.747128 | S | *673.370158* | 337.188717 | 656.343609 | 328.675443 | 655.359593 | 328.183435 | 3 |
| 11 | 1461.722870 | 731.365073 | 1444.696321 | 722.851799 | 1443.712305 | 722.359791 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 12 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.1 | 1606.821121 | 0.007307 | TMFIGGSQLSQK |
| 18.7 | 1606.821121 | 0.007307 | TMFIGGSQLSQK |
| 0.4 | 1606.809860 | 0.018568 | AIPEYMTISQK |

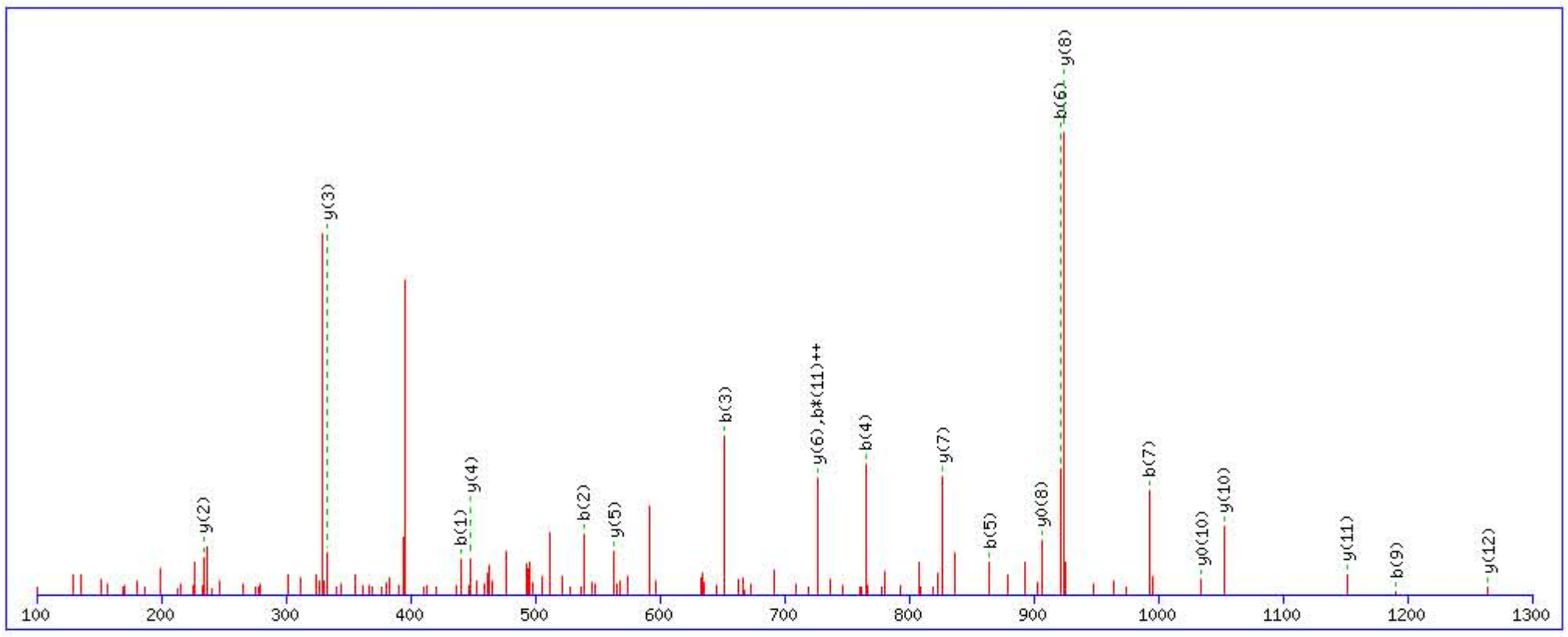
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QVLLVGAPTYDDVSK**
Found in **PHLD_HUMAN**, Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

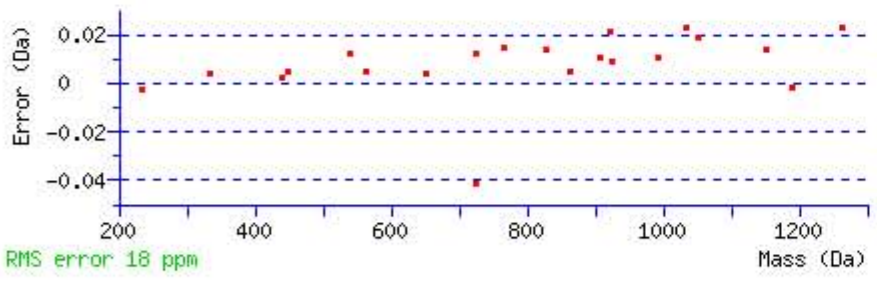
Match to Query 42443: 1915.030542 from(639.350790,3+) rtinseconds(2302) index(52288)
Title: Locus:1.1.1.2039.3 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

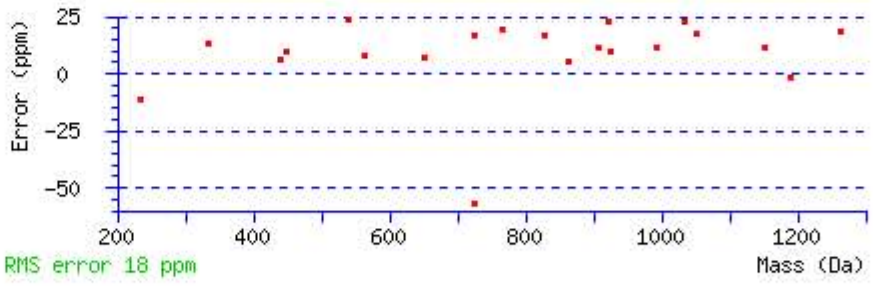
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1915.012497
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 61 **Expect:** 2.4e-006
**Matches :** 21/150 fragment ions using 41 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *440.232602* | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 15 |
| 2 | *539.301016* | 270.154146 | 522.274467 | 261.640872 | | | V | 1476.794438 | 738.900857 | 1459.767889 | 730.387583 | 1458.783873 | 729.895575 | 14 |
| 3 | *652.385080* | 326.696178 | 635.358531 | 318.182904 | | | L | 1377.726024 | 689.366650 | 1360.699475 | 680.853376 | 1359.715459 | 680.361368 | 13 |
| 4 | *765.469144* | 383.238210 | 748.442595 | 374.724936 | | | L | *1264.641960* | 632.824618 | 1247.615411 | 624.311344 | 1246.631395 | 623.819336 | 12 |
| 5 | *864.537558* | 432.772417 | 847.511009 | 424.259143 | | | V | *1151.557896* | 576.282586 | 1134.531347 | 567.769312 | 1133.547331 | 567.277304 | 11 |
| 6 | *921.559022* | 461.283149 | 904.532473 | 452.769875 | | | G | *1052.489482* | 526.748379 | 1035.462933 | 518.235105 | 1034.478917 | 517.743097 | 10 |
| 7 | *992.596136* | 496.801706 | 975.569587 | 488.288432 | | | A | 995.468018 | 498.237647 | 978.441469 | 489.724373 | 977.457453 | 489.232365 | 9 |
| 8 | 1089.648900 | 545.328088 | 1072.622351 | 536.814814 | | | P | *924.430904* | 462.719090 | 907.404355 | 454.205816 | 906.420339 | 453.713808 | 8 |
| 9 | *1190.696579* | 595.851927 | 1173.670030 | 587.338653 | 1172.686014 | 586.846645 | T | *827.378140* | 414.192708 | 810.351591 | 405.679434 | 809.367575 | 405.187426 | 7 |
| 10 | 1353.759908 | 677.383592 | 1336.733359 | 668.870318 | 1335.749343 | 668.378310 | Y | *726.330461* | 363.668869 | 709.303912 | 355.155594 | 708.319896 | 354.663586 | 6 |
| 11 | 1468.786851 | 734.897064 | 1451.760302 | 726.383789 | 1450.776286 | 725.891781 | D | *563.267132* | 282.137204 | 546.240583 | 273.623930 | 545.256567 | 273.131922 | 5 |
| 12 | 1583.813794 | 792.410535 | 1566.787245 | 783.897261 | 1565.803229 | 783.405253 | D | *448.240189* | 224.623733 | 431.213640 | 216.110458 | 430.229624 | 215.618450 | 4 |
| 13 | 1682.882208 | 841.944742 | 1665.855659 | 833.431468 | 1664.871643 | 832.939460 | V | *333.213246* | 167.110261 | 316.186697 | 158.596987 | 315.202681 | 158.104979 | 3 |
| 14 | 1769.914236 | 885.460756 | 1752.887687 | 876.947482 | 1751.903671 | 876.455474 | S | *234.144832* | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 15 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 60.5 | 1915.012497 | 0.018045 | QVLLVGAPTYDDVSK |
| 0.6 | 1915.048859 | -0.018317 | SSSSYTIFLCILAKVVK |
| 0.6 | 1915.027710 | 0.002832 | DYPIYLLKFKQCLSK |
| 0.6 | 1915.008438 | 0.022104 | VIQKNQEETTSISK |

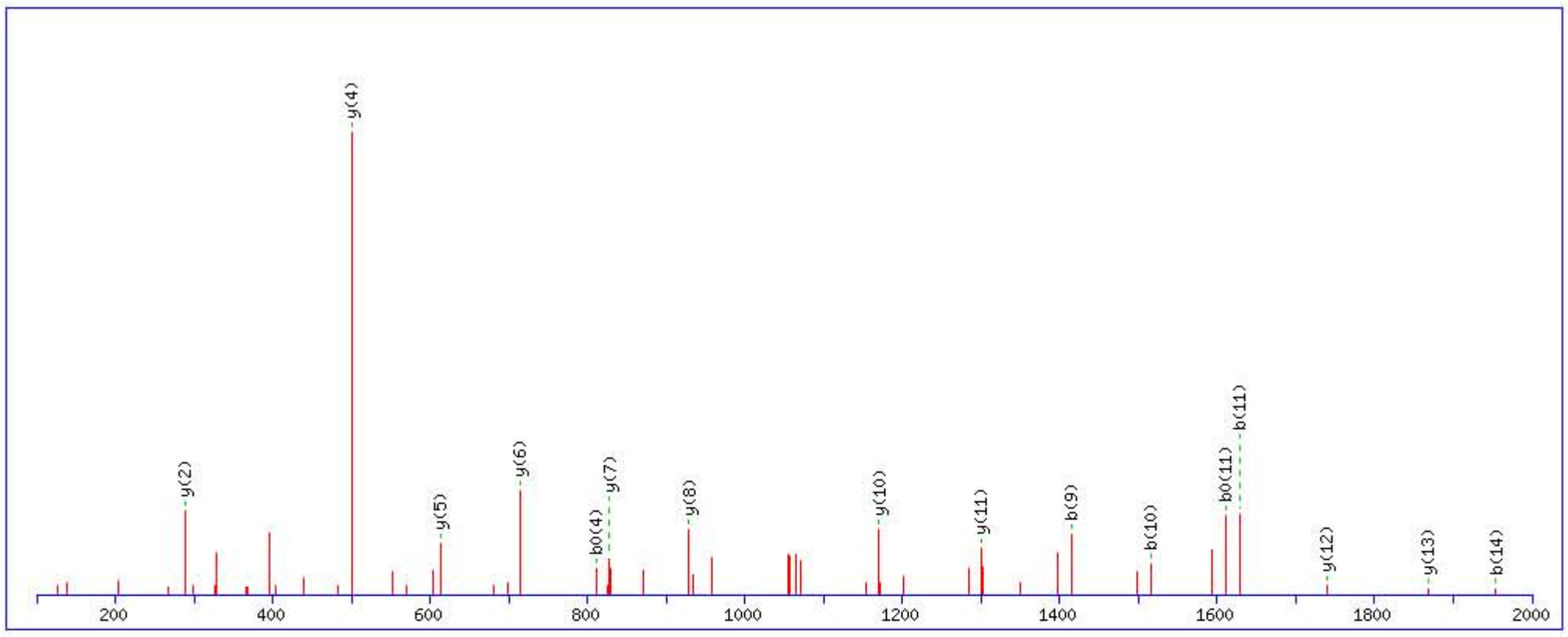
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FLEQELETITIPDLR**
Found in **PLTP_HUMAN**, Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=1 SV=1

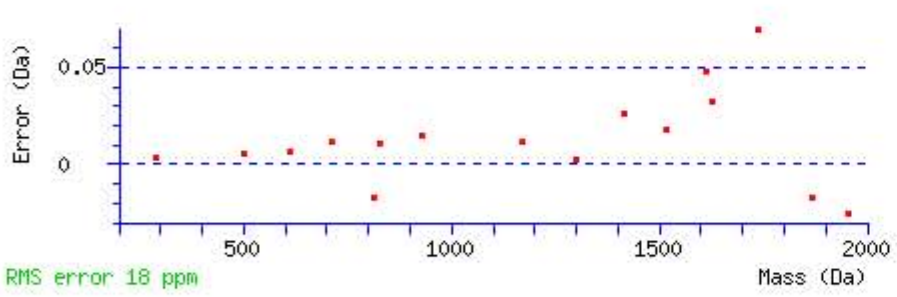
Match to Query 47051: 2127.157688 from(1064.586120,2+) rtinseconds(2894) index(39827)
Title: Locus:1.1.1.1114.24 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

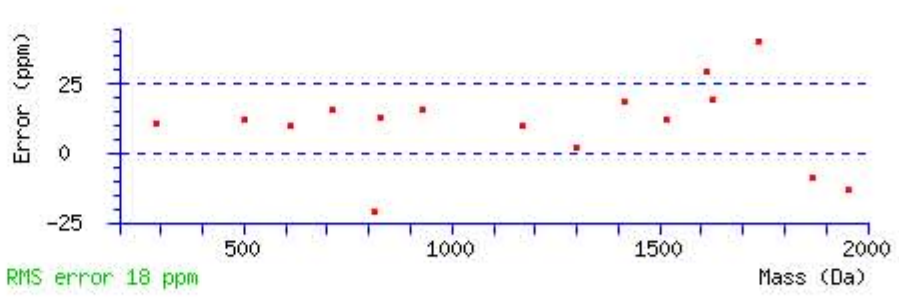
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2127.128555
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 87 **Expect:** 3.8e-008
**Matches :** 16/154 fragment ions using 19 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 15 |
| 2 | 261.159754 | 131.083515 | | | | | L | 1981.067442 | 991.037359 | 1964.040893 | 982.524084 | 1963.056877 | 982.032076 | 14 |
| 3 | 390.202347 | 195.604811 | | | 372.191782 | 186.599529 | E | *1867.983378* | 934.495327 | 1850.956829 | 925.982052 | 1849.972813 | 925.490044 | 13 |
| 4 | 829.427673 | 415.217475 | 812.401124 | 406.704200 | 811.417108 | 406.212192 | Q | *1738.940785* | 869.974030 | 1721.914236 | 861.460756 | 1720.930220 | 860.968748 | 12 |
| 5 | 958.470266 | 479.738771 | 941.443717 | 471.225497 | 940.459701 | 470.733489 | E | *1299.715459* | 650.361367 | 1282.688910 | 641.848093 | 1281.704894 | 641.356085 | 11 |
| 6 | 1071.554330 | 536.280803 | 1054.527781 | 527.767529 | 1053.543765 | 527.275520 | L | *1170.672866* | 585.840071 | 1153.646317 | 577.326796 | 1152.662301 | 576.834788 | 10 |
| 7 | 1200.596923 | 600.802099 | 1183.570374 | 592.288825 | 1182.586358 | 591.796817 | E | 1057.588802 | 529.298039 | 1040.562253 | 520.784764 | 1039.578237 | 520.292756 | 9 |
| 8 | 1301.644602 | 651.325939 | 1284.618053 | 642.812664 | 1283.634037 | 642.320656 | T | *928.546209* | 464.776742 | 911.519660 | 456.263468 | 910.535644 | 455.771460 | 8 |
| 9 | **1414.728666** | 707.867971 | 1397.702117 | 699.354696 | 1396.718101 | 698.862688 | I | *827.498530* | 414.252903 | 810.471981 | 405.739628 | 809.487965 | 405.247620 | 7 |
| 10 | **1515.776345** | 758.391810 | 1498.749796 | 749.878536 | 1497.765780 | 749.386528 | T | *714.414466* | 357.710871 | 697.387917 | 349.197596 | 696.403901 | 348.705588 | 6 |
| 11 | **1628.860409** | 814.933842 | 1611.833860 | 806.420568 | 1610.849844 | 805.928560 | I | *613.366787* | 307.187031 | 596.340238 | 298.673757 | 595.356222 | 298.181749 | 5 |
| 12 | 1725.913173 | 863.460224 | 1708.886624 | 854.946950 | 1707.902608 | 854.454942 | P | *500.282723* | 250.644999 | 483.256174 | 242.131725 | 482.272158 | 241.639717 | 4 |
| 13 | 1840.940116 | 920.973696 | 1823.913567 | 912.460421 | 1822.929551 | 911.968413 | D | 403.229959 | 202.118617 | 386.203410 | 193.605343 | 385.219394 | 193.113335 | 3 |
| 14 | **1954.024180** | 977.515728 | 1936.997631 | 969.002453 | 1936.013615 | 968.510445 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 15 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 86.9 | 2127.128555 | 0.029133 | FLEQELETITIPDLR |
| 14.6 | 2127.139816 | 0.017872 | QKSIFTSVPDTPDLLR |
| 11.8 | 2127.125870 | 0.031818 | SLPGYMTRHNNLDLVIIR |
| 8.8 | 2127.135727 | 0.021961 | EAADMLKALQGASQIIAEIR |
| 0.1 | 2127.136429 | 0.021259 | GAFELAYTGFVKLTEVLNR |

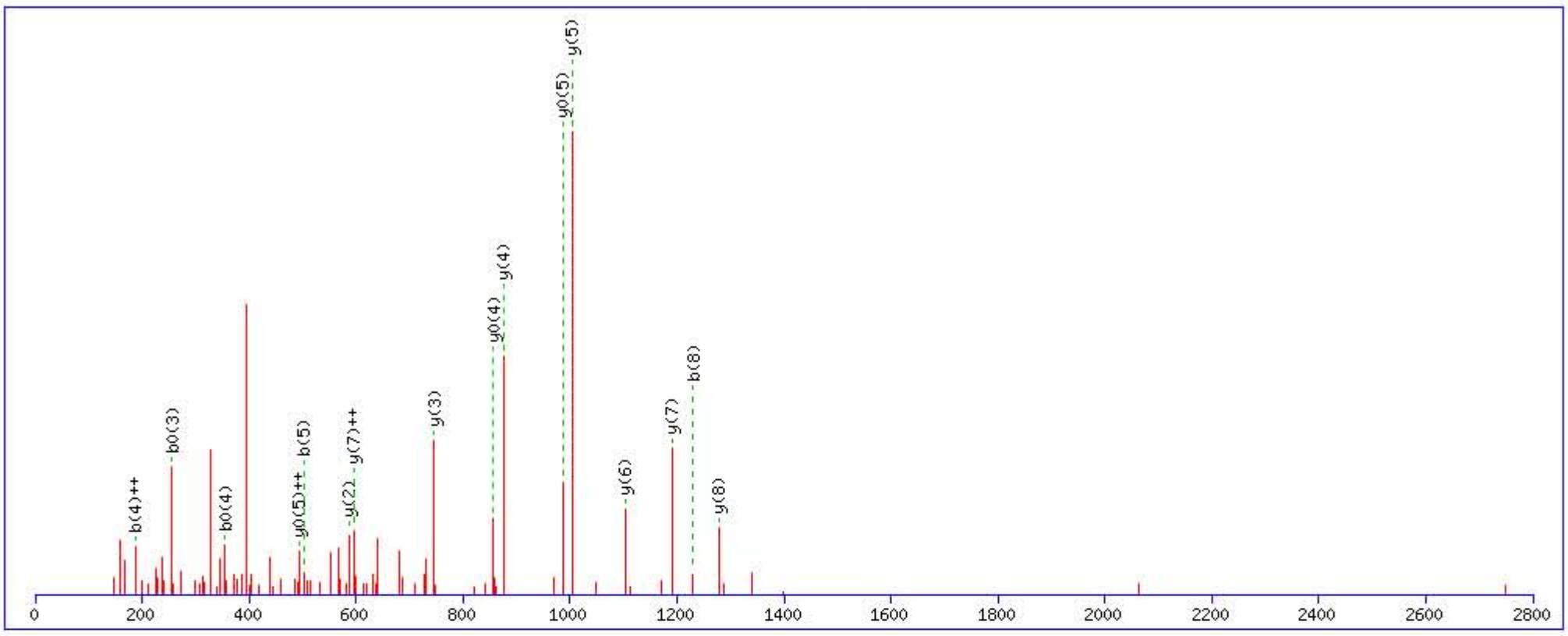
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VSSVEECQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

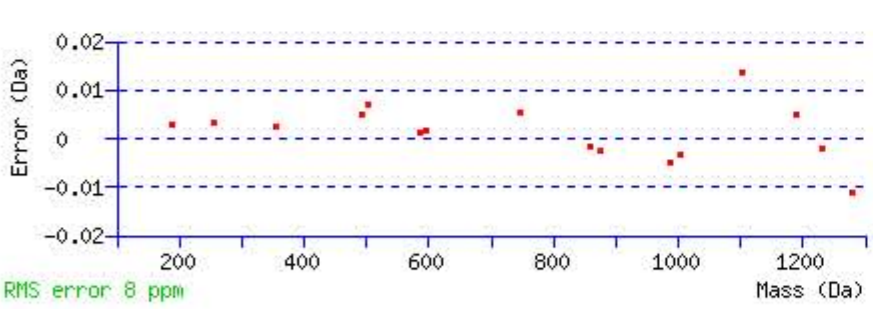
Match to Query 26410: 1375.648848 from(688.831700,2+) rtinseconds(1376) index(16052)
Title: Locus:1.1.1.2861.24 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

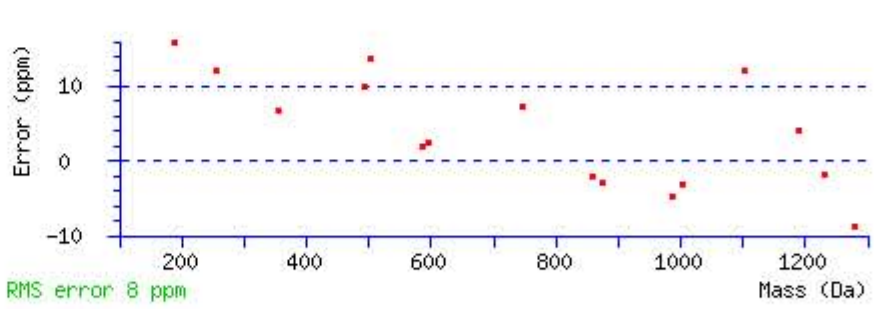
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1375.647568
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 51 **Expect:** 5e-005
**Matches :** 17/74 fragment ions using 24 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 9 |
| 2 | **187.107718** | 94.057497 | | | 169.097153 | 85.052214 | S | *1277.586435* | 639.296856 | 1260.559886 | 630.783581 | 1259.575870 | 630.291573 | 8 |
| 3 | 274.139746 | 137.573511 | | | 256.129181 | 128.568229 | S | *1190.554407* | 595.780842 | 1173.527858 | 587.267567 | 1172.543842 | 586.775559 | 7 |
| 4 | 373.208160 | 187.107718 | | | 355.197595 | 178.102436 | V | *1103.522379* | 552.264828 | 1086.495830 | 543.751553 | 1085.511814 | 543.259545 | 6 |
| 5 | **502.250753** | 251.629015 | | | 484.240188 | 242.623732 | E | *1004.453965* | 502.730621 | 987.427416 | 494.217346 | 986.443400 | 493.725338 | 5 |
| 6 | 631.293346 | 316.150311 | | | 613.282781 | 307.145029 | E | *875.411372* | 438.209324 | 858.384823 | 429.696050 | 857.400807 | 429.204042 | 4 |
| 7 | 791.323995 | 396.165636 | | | 773.313430 | 387.160353 | C | *746.368779* | 373.688028 | 729.342230 | 365.174753 | | | 3 |
| 8 | **1230.549321** | 615.778299 | 1213.522772 | 607.265024 | 1212.538756 | 606.773016 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 9 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 51.0 | 1375.647568 | 0.001280 | VSSVEECQK |
| 5.0 | 1375.662827 | -0.013979 | GFSIPECQK |
| 2.7 | 1375.665329 | -0.016481 | ADVSLPSMQGDLK |

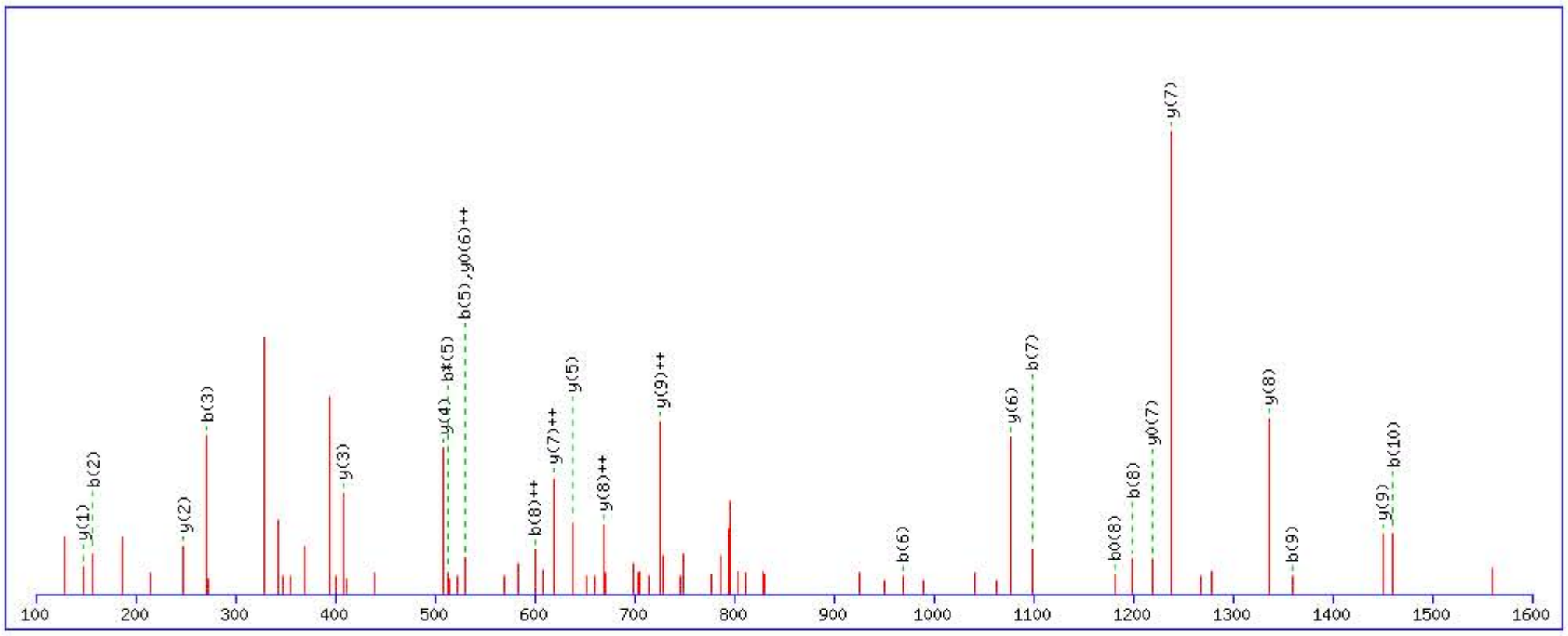
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GVNVCQETCTK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

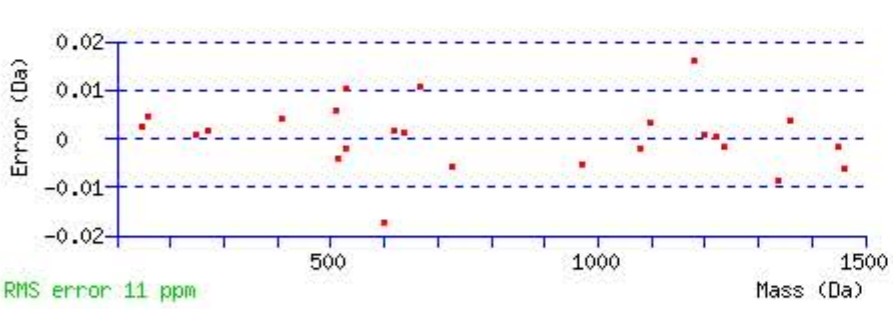
Match to Query 34869: 1605.737588 from(803.876070,2+) rtinseconds(1533) index(17150)
Title: Locus:1.1.1.2916.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

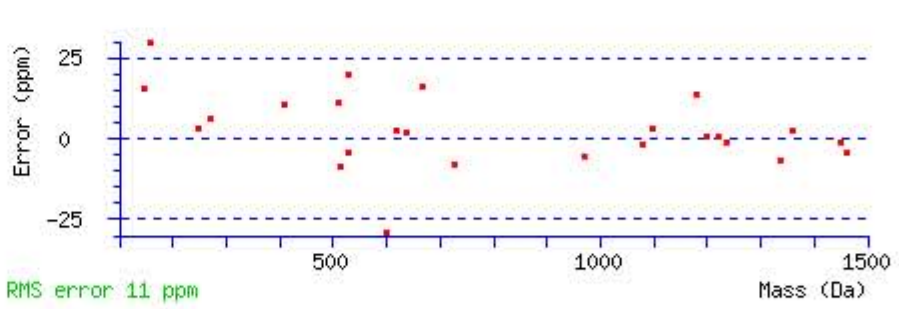
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1605.731339
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 51 **Expect:** 3.4e-005
**Matches :** 25/102 fragment ions using 47 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 11 |
| 2 | **157.097154** | 79.052215 | | | | | V | 1549.717134 | 775.362205 | 1532.690585 | 766.848931 | 1531.706569 | 766.356923 | 10 |
| 3 | **271.140081** | 136.073679 | 254.113532 | 127.560404 | | | N | *1450.648720* | 725.827998 | 1433.622171 | 717.314724 | 1432.638155 | 716.822716 | 9 |
| 4 | 370.208495 | 185.607886 | 353.181946 | 177.094611 | | | V | *1336.605793* | 668.806535 | 1319.579244 | 660.293260 | 1318.595228 | 659.801252 | 8 |
| 5 | **530.239144** | 265.623210 | 513.212595 | 257.109936 | | | C | *1237.537379* | 619.272328 | 1220.510830 | 610.759053 | 1219.526814 | 610.267045 | 7 |
| 6 | **969.464470** | 485.235873 | 952.437921 | 476.722599 | | | Q | *1077.506730* | 539.257003 | 1060.480181 | 530.743729 | 1059.496165 | 530.251721 | 6 |
| 7 | **1098.507063** | 549.757170 | 1081.480514 | 541.243895 | 1080.496498 | 540.751887 | E | *638.281404* | 319.644340 | 621.254855 | 311.131066 | 620.270839 | 310.639058 | 5 |
| 8 | **1199.554742** | 600.281009 | 1182.528193 | 591.767735 | 1181.544177 | 591.275727 | T | *509.238811* | 255.123044 | 492.212262 | 246.609769 | 491.228246 | 246.117761 | 4 |
| 9 | **1359.585391** | 680.296334 | 1342.558842 | 671.783059 | 1341.574826 | 671.291051 | C | *408.191132* | 204.599204 | 391.164583 | 196.085930 | 390.180567 | 195.593922 | 3 |
| 10 | **1460.633070** | 730.820173 | 1443.606521 | 722.306899 | 1442.622505 | 721.814891 | T | *248.160483* | 124.583879 | 231.133934 | 116.070605 | 230.149918 | 115.578597 | 2 |
| 11 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 51.2 | 1605.731339 | 0.006249 | GVNVCQETCTK |
| 3.4 | 1605.716507 | 0.021081 | RNEEAQDLSGGMQR |
| 3.0 | 1605.724121 | 0.013467 | MVFFLEDVMACTK |
| 1.5 | 1605.760269 | -0.022681 | AKEMQQQELAQMR |

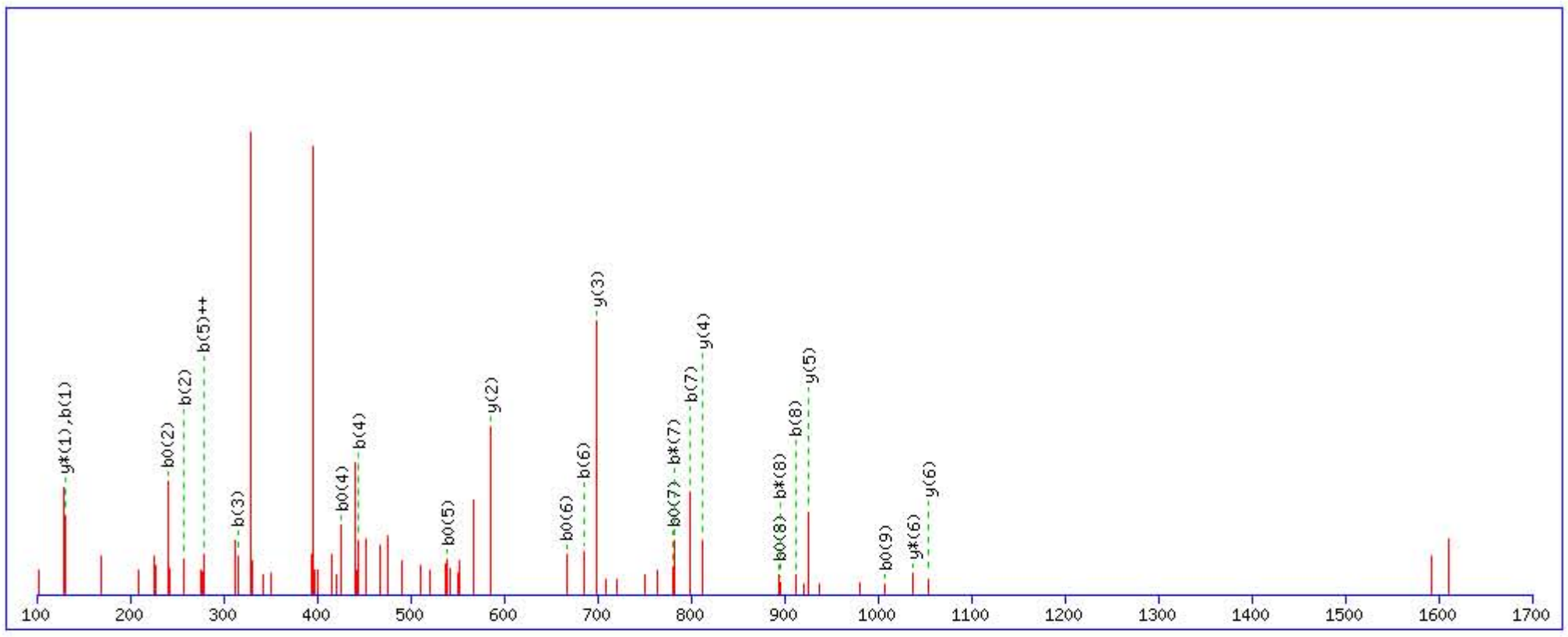
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EKGEIQNILQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

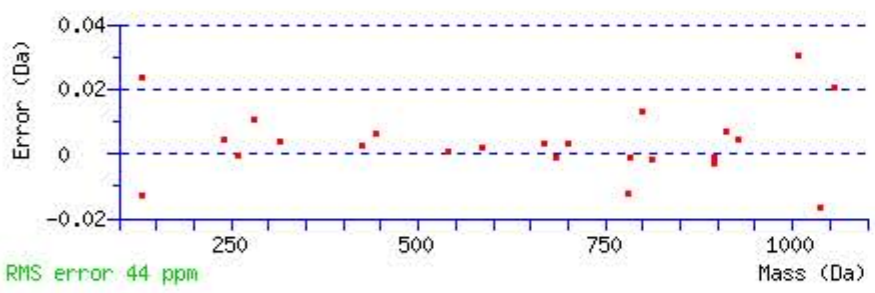
Match to Query 35028: 1609.889982 from(537.637270,3+) rtinseconds(1857) index(19236)
Title: Locus:1.1.1.3029.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

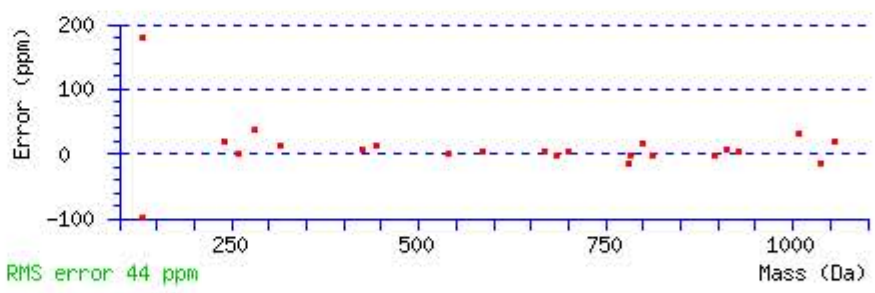
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1609.886124
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q10** : Biotin:Thermo-21345 (Q)
**Ions Score:** 34 **Expect:** 0.0074
**Matches :** 24/104 fragment ions using 44 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *130.049869* | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 11 |
| 2 | *258.144832* | 129.576054 | 241.118283 | 121.062780 | 240.134267 | 120.570772 | K | 1481.850847 | 741.429061 | 1464.824298 | 732.915787 | 1463.840282 | 732.423779 | 10 |
| 3 | *315.166296* | 158.086786 | 298.139747 | 149.573512 | 297.155731 | 149.081504 | G | 1353.755884 | 677.381580 | 1336.729335 | 668.868306 | 1335.745319 | 668.376297 | 9 |
| 4 | *444.208889* | 222.608082 | 427.182340 | 214.094808 | 426.198324 | 213.602800 | E | 1296.734420 | 648.870848 | 1279.707871 | 640.357574 | 1278.723855 | 639.865566 | 8 |
| 5 | 557.292953 | 279.150115 | 540.266404 | 270.636840 | 539.282388 | 270.144832 | I | 1167.691827 | 584.349552 | 1150.665278 | 575.836277 | | | 7 |
| 6 | *685.351531* | 343.179404 | 668.324982 | 334.666129 | 667.340966 | 334.174121 | Q | *1054.607763* | 527.807520 | 1037.581214 | 519.294245 | | | 6 |
| 7 | *799.394458* | 400.200867 | 782.367909 | 391.687592 | 781.383893 | 391.195585 | N | *926.549185* | 463.778231 | 909.522636 | 455.264956 | | | 5 |
| 8 | *912.478522* | 456.742899 | 895.451973 | 448.229625 | 894.467957 | 447.737617 | I | *812.506258* | 406.756767 | 795.479709 | 398.243493 | | | 4 |
| 9 | 1025.562586 | 513.284931 | 1008.536037 | 504.771657 | 1007.552021 | 504.279649 | L | *699.422194* | 350.214735 | 682.395645 | 341.701461 | | | 3 |
| 10 | 1464.787912 | 732.897594 | 1447.761363 | 724.384320 | 1446.777347 | 723.892312 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 11 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.8 | 1609.886124 | 0.003858 | EKGEIQNILQK |
| 10.5 | 1609.872192 | 0.017790 | QEAERALKQAR |
| 10.0 | 1609.908615 | -0.018633 | QLSQHAMKGVIRVK |
| 5.3 | 1609.878754 | 0.011228 | AGPLTVNTEAQQLLR |
| 4.8 | 1609.897400 | -0.007418 | TNLRIVDVGGQK |
| 4.1 | 1609.886154 | 0.003828 | KTVTAMDVVYALKR |
| 2.6 | 1609.872208 | 0.017774 | AGSLRAQLEAQR |
| 1.8 | 1609.879623 | 0.010359 | APGSLIKLQGCR |
| 1.7 | 1609.908630 | -0.018648 | CQGRTVPLAVLQLR |

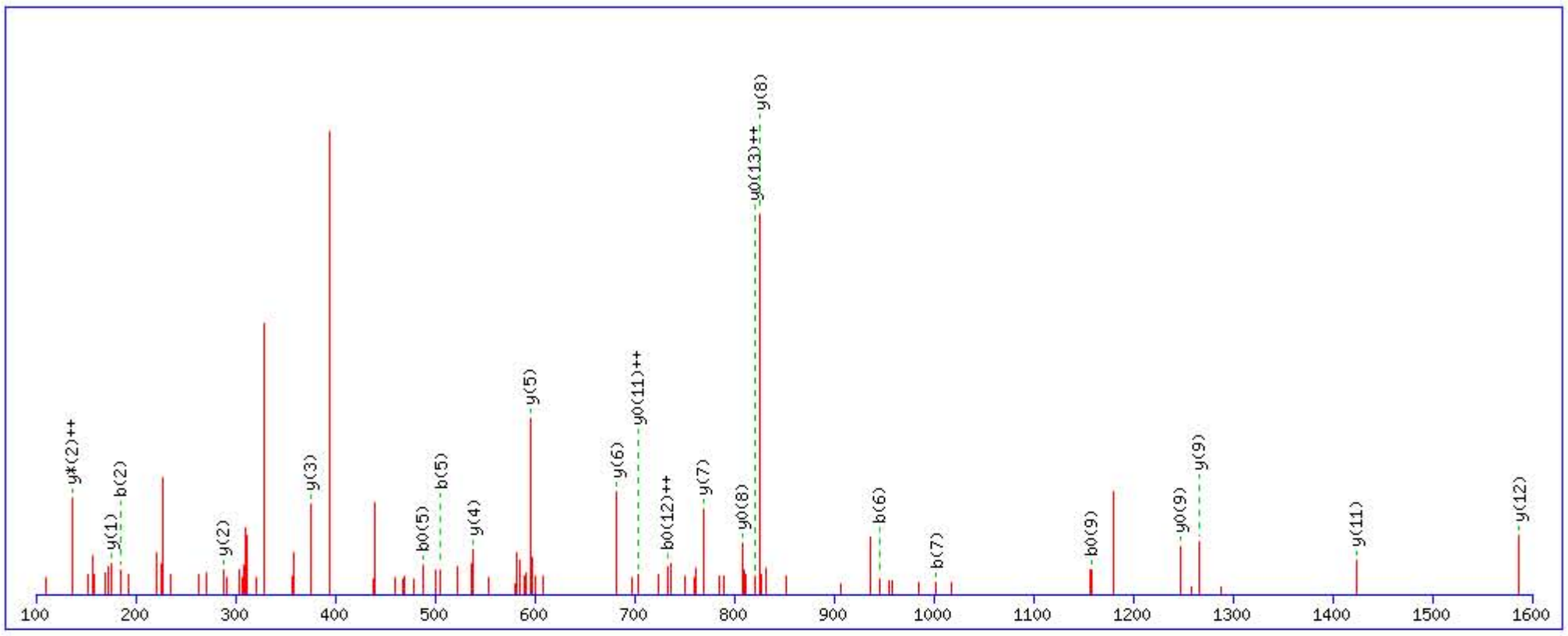
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IAYGTQGSSGYSLR**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

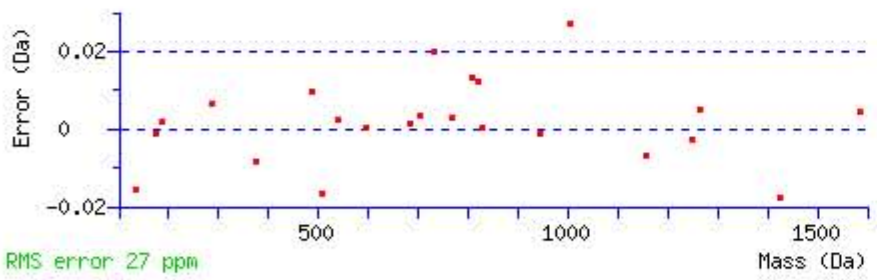
Match to Query 39611: 1769.883222 from(590.968350,3+) rtinseconds(1889) index(65608)
Title: Locus:1.1.1.1933.13 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

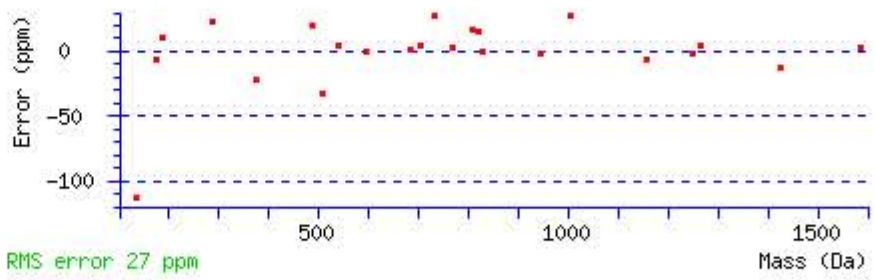
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1769.877045
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 4.6e-005
**Matches** : 23/134 fragment ions using 53 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 14 |
| 2 | **185.128454** | 93.067865 | | | | | A | 1657.800269 | 829.403773 | 1640.773720 | 820.890498 | 1639.789704 | 820.398490 | 13 |
| 3 | 348.191783 | 174.599529 | | | | | Y | *1586.763155* | 793.885216 | 1569.736606 | 785.371941 | 1568.752590 | 784.879933 | 12 |
| 4 | 405.213247 | 203.110261 | | | | | G | *1423.699826* | 712.353551 | 1406.673277 | 703.840277 | 1405.689261 | 703.348269 | 11 |
| 5 | **506.260926** | 253.634101 | | | 488.250361 | 244.628818 | T | 1366.678362 | 683.842819 | 1349.651813 | 675.329545 | 1348.667797 | 674.837537 | 10 |
| 6 | **945.486252** | 473.246764 | 928.459703 | 464.733490 | 927.475687 | 464.241482 | Q | *1265.630683* | 633.318980 | 1248.604134 | 624.805705 | 1247.620118 | 624.313697 | 9 |
| 7 | **1002.507716** | 501.757496 | 985.481167 | 493.244222 | 984.497151 | 492.752214 | G | *826.405357* | 413.706317 | 809.378808 | 405.193042 | 808.394792 | 404.701034 | 8 |
| 8 | 1089.539744 | 545.273510 | 1072.513195 | 536.760236 | 1071.529179 | 536.268228 | S | *769.383893* | 385.195585 | 752.357344 | 376.682310 | 751.373328 | 376.190302 | 7 |
| 9 | 1176.571772 | 588.789524 | 1159.545223 | 580.276250 | 1158.561207 | 579.784242 | S | *682.351865* | 341.679571 | 665.325316 | 333.166296 | 664.341300 | 332.674288 | 6 |
| 10 | 1233.593236 | 617.300256 | 1216.566687 | 608.786982 | 1215.582671 | 608.294974 | G | *595.319837* | 298.163557 | 578.293288 | 289.650282 | 577.309272 | 289.158274 | 5 |
| 11 | 1396.656565 | 698.831921 | 1379.630016 | 690.318646 | 1378.646000 | 689.826638 | Y | *538.298373* | 269.652825 | 521.271824 | 261.139550 | 520.287808 | 260.647542 | 4 |
| 12 | 1483.688593 | 742.347935 | 1466.662044 | 733.834660 | 1465.678028 | 733.342652 | S | *375.235044* | 188.121160 | 358.208495 | 179.607885 | 357.224479 | 179.115877 | 3 |
| 13 | 1596.772657 | 798.889967 | 1579.746108 | 790.376692 | 1578.762092 | 789.884684 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 14 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 57.8 | 1769.877045 | 0.006177 | IAYGTQGSSGYSLR |

**Mascot:** http://www.matrixscience.com/

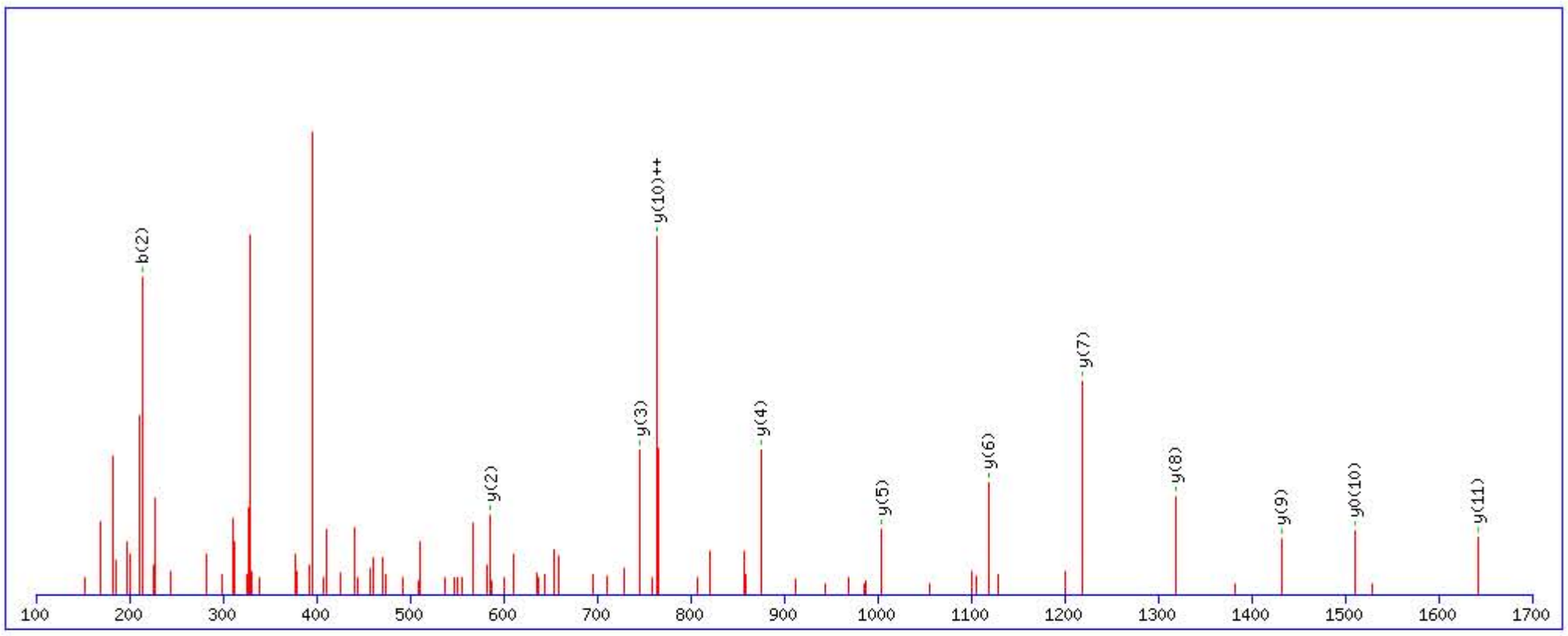
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VNIPLVTNEECQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

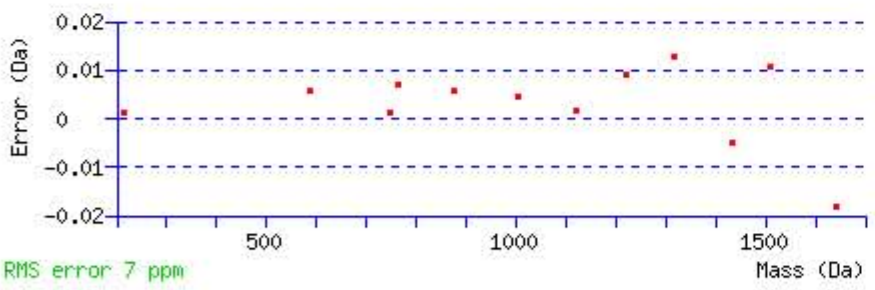
Match to Query 41441: 1853.948772 from(618.990200,3+) rtinseconds(2149) index(67316)
Title: Locus:1.1.1.2023.14 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

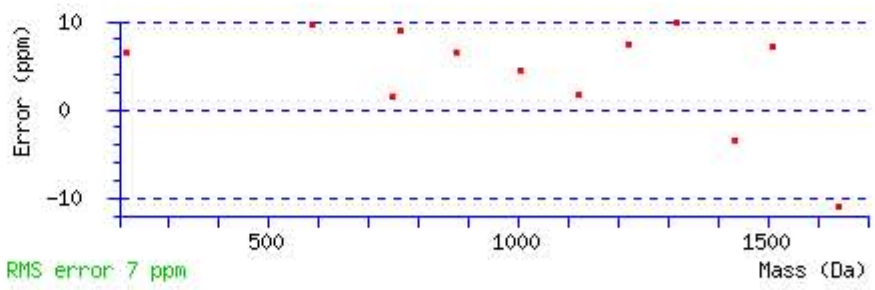
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1853.937927
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 68 **Expect:** 1.8e-006
**Matches :** 12/124 fragment ions using 15 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 13 |
| 2 | 214.118617 | 107.562947 | 197.092068 | 99.049672 | | | N | 1755.876804 | 878.442040 | 1738.850255 | 869.928766 | 1737.866239 | 869.436758 | 12 |
| 3 | 327.202681 | 164.104978 | 310.176132 | 155.591704 | | | I | *1641.833877* | 821.420577 | 1624.807328 | 812.907302 | 1623.823312 | 812.415294 | 11 |
| 4 | 424.255445 | 212.631360 | 407.228896 | 204.118086 | | | P | 1528.749813 | 764.878545 | 1511.723264 | 756.365270 | 1510.739248 | 755.873262 | 10 |
| 5 | 537.339509 | 269.173393 | 520.312960 | 260.660118 | | | L | *1431.697049* | 716.352163 | 1414.670500 | 707.838888 | 1413.686484 | 707.346880 | 9 |
| 6 | 636.407923 | 318.707600 | 619.381374 | 310.194325 | | | V | *1318.612985* | 659.810131 | 1301.586436 | 651.296856 | 1300.602420 | 650.804848 | 8 |
| 7 | 737.455602 | 369.231439 | 720.429053 | 360.718165 | 719.445037 | 360.226157 | T | *1219.544571* | 610.275924 | 1202.518022 | 601.762649 | 1201.534006 | 601.270641 | 7 |
| 8 | 851.498529 | 426.252903 | 834.471980 | 417.739628 | 833.487964 | 417.247620 | N | *1118.496892* | 559.752084 | 1101.470343 | 551.238810 | 1100.486327 | 550.746802 | 6 |
| 9 | 980.541122 | 490.774199 | 963.514573 | 482.260924 | 962.530557 | 481.768916 | E | *1004.453965* | 502.730621 | 987.427416 | 494.217346 | 986.443400 | 493.725338 | 5 |
| 10 | 1109.583715 | 555.295496 | 1092.557166 | 546.782221 | 1091.573150 | 546.290213 | E | *875.411372* | 438.209324 | 858.384823 | 429.696050 | 857.400807 | 429.204042 | 4 |
| 11 | 1269.614364 | 635.310820 | 1252.587815 | 626.797546 | 1251.603799 | 626.305538 | C | *746.368779* | 373.688028 | 729.342230 | 365.174753 | | | 3 |
| 12 | 1708.839690 | 854.923483 | 1691.813141 | 846.410209 | 1690.829125 | 845.918201 | Q | *586.338130* | 293.672703 | 569.311581 | 285.159429 | | | 2 |
| 13 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 67.9 | 1853.937927 | 0.010845 | VNIPLVTNEECQK |
| 6.8 | 1853.934341 | 0.014431 | RGLSNPNELQAAIDSNR |

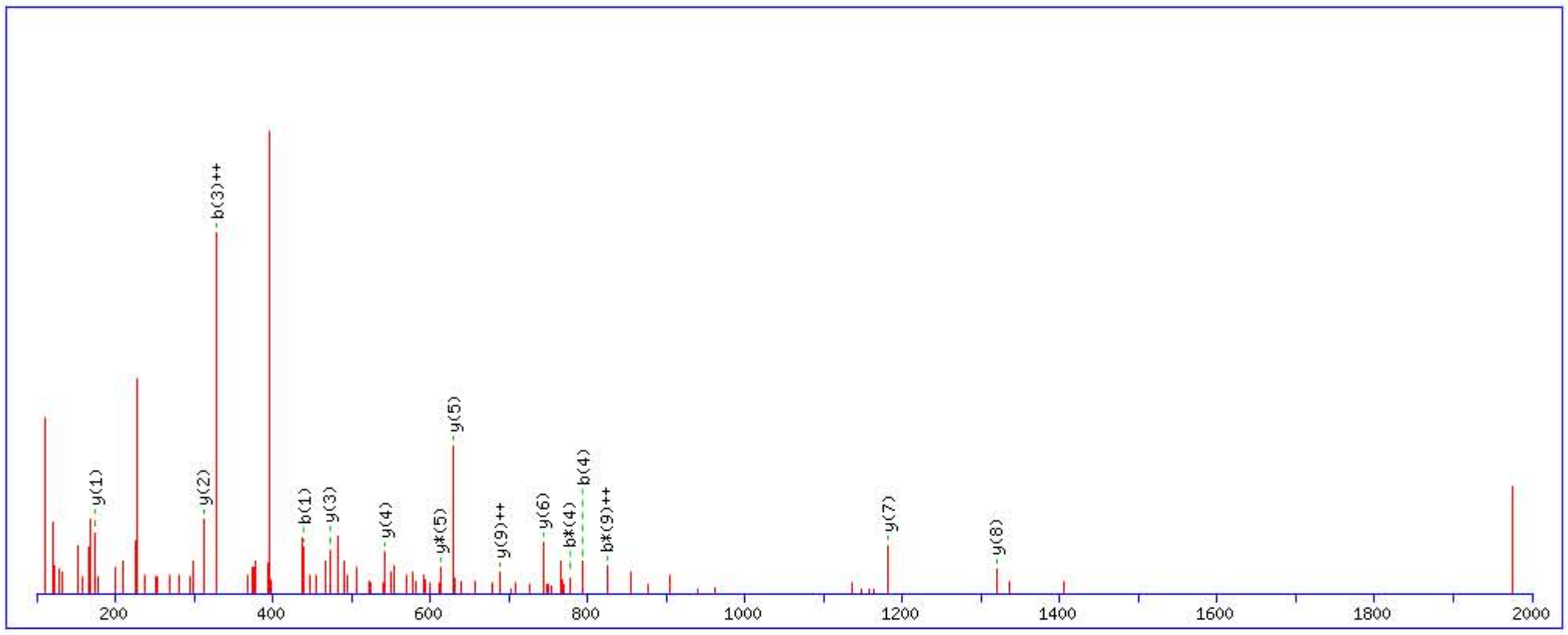
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QCGHQISACHR**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

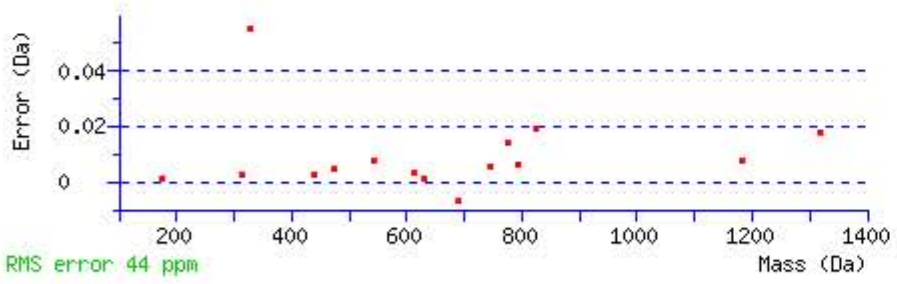
Match to Query 43665: 1974.915336 from(494.736110,4+) rtinseconds(1434) index(63039)
Title: Locus:1.1.1.1774.10 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

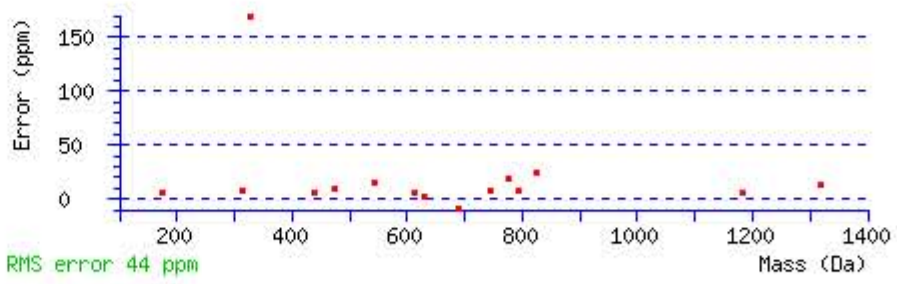
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1974.916122
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q1 : Biotin:Thermo-21345 (Q)
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 25 **Expect:** 0.04
**Matches :** 15/100 fragment ions using 41 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **440.232602** | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 11 |
| 2 | 600.263251 | 300.635264 | 583.236702 | 292.121989 | | | C | 1536.698070 | 768.852673 | 1519.671521 | 760.339399 | 1518.687505 | 759.847391 | 10 |
| 3 | 657.284715 | 329.145996 | 640.258166 | 320.632721 | | | G | 1376.667421 | 688.837349 | 1359.640872 | 680.324074 | 1358.656856 | 679.832066 | 9 |
| 4 | **794.343627** | 397.675452 | 777.317078 | 389.162177 | | | H | *1319.645957* | 660.326617 | 1302.619408 | 651.813342 | 1301.635392 | 651.321334 | 8 |
| 5 | 1233.568953 | 617.288115 | 1216.542404 | 608.774840 | | | Q | *1182.587045* | 591.797161 | 1165.560496 | 583.283886 | 1164.576480 | 582.791878 | 7 |
| 6 | 1346.653017 | 673.830147 | 1329.626468 | 665.316872 | | | I | *743.361719* | 372.184498 | 726.335170 | 363.671223 | 725.351154 | 363.179215 | 6 |
| 7 | 1433.685045 | 717.346161 | 1416.658496 | 708.832886 | 1415.674480 | 708.340878 | S | *630.277655* | 315.642466 | 613.251106 | 307.129191 | 612.267090 | 306.637183 | 5 |
| 8 | 1504.722159 | 752.864718 | 1487.695610 | 744.351443 | 1486.711594 | 743.859435 | A | *543.245627* | 272.126452 | 526.219078 | 263.613177 | | | 4 |
| 9 | 1664.752808 | 832.880042 | 1647.726259 | 824.366768 | 1646.742243 | 823.874760 | C | *472.208513* | 236.607894 | 455.181964 | 228.094620 | | | 3 |
| 10 | 1801.811720 | 901.409498 | 1784.785171 | 892.896224 | 1783.801155 | 892.404216 | H | *312.177864* | 156.592570 | 295.151315 | 148.079295 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 25.2 | 1974.916122 | -0.000786 | QCGHQISACHR |

**Mascot:** http://www.matrixscience.com/

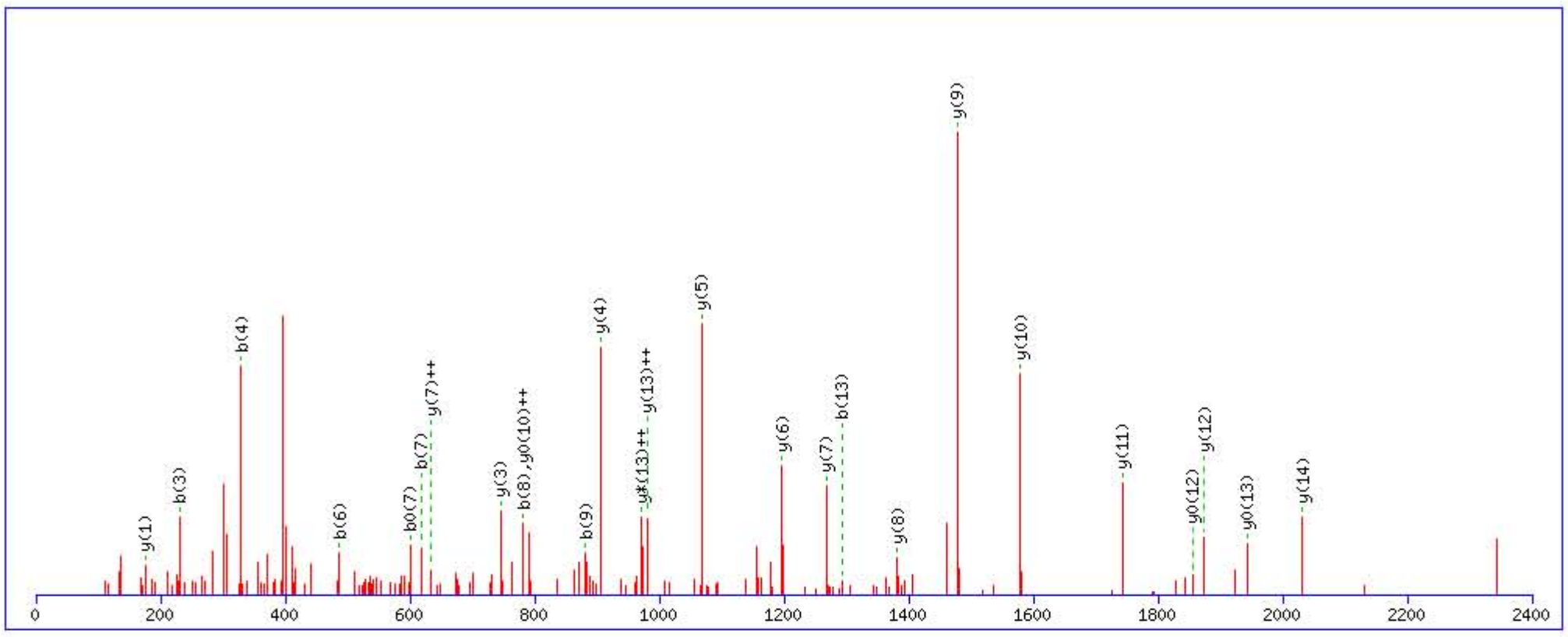
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GGDVASMYTPNAQYCQMR**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

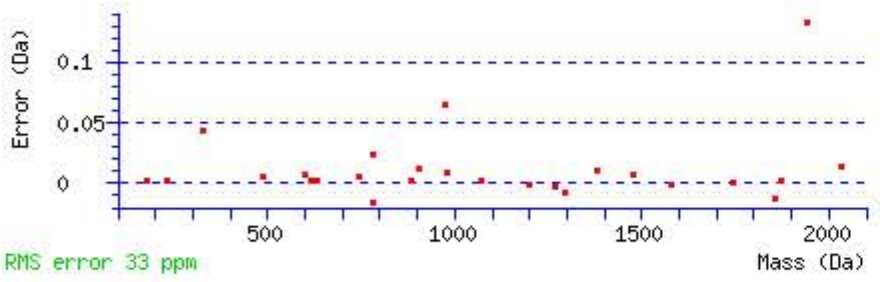
Match to Query 51445: 2359.046952 from(787.356260,3+) rtinseconds(2046) index(66688)
Title: Locus:1.1.1.1987.15 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

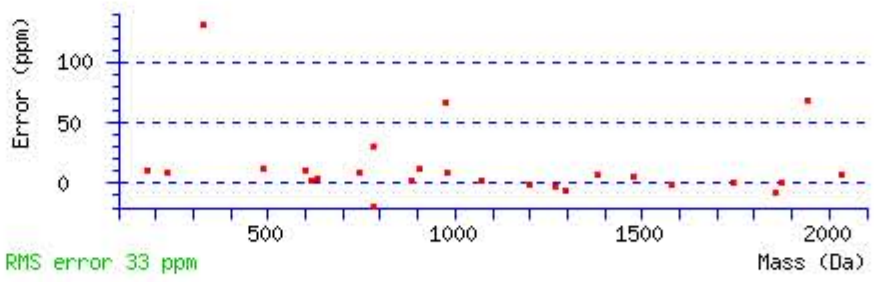
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2359.021759
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q16** : Biotin:Thermo-21345 (Q)
**Ions Score:** 83 **Expect:** 3.6e-008
**Matches** : 26/162 fragment ions using 39 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 18 |
| 2 | 115.050204 | 58.028740 | | | | | G | 2303.007580 | 1152.007428 | 2285.981031 | 1143.494153 | 2284.997015 | 1143.002145 | 17 |
| 3 | **230.077147** | 115.542211 | | | 212.066582 | 106.536929 | D | 2245.986116 | 1123.496696 | 2228.959567 | 1114.983421 | 2227.975551 | 1114.491413 | 16 |
| 4 | **329.145561** | 165.076418 | | | 311.134996 | 156.071136 | V | 2130.959173 | 1065.983224 | 2113.932624 | 1057.469950 | 2112.948608 | 1056.977942 | 15 |
| 5 | 400.182675 | 200.594975 | | | 382.172110 | 191.589693 | A | *2031.890759* | 1016.449018 | 2014.864210 | 1007.935743 | 2013.880194 | 1007.443735 | 14 |
| 6 | **487.214703** | 244.110989 | | | 469.204138 | 235.105707 | S | 1960.853645 | 980.930461 | 1943.827096 | 972.417186 | 1942.843080 | 971.925178 | 13 |
| 7 | **618.255188** | 309.631232 | | | 600.244623 | 300.625949 | M | *1873.821617* | 937.414447 | 1856.795068 | 928.901172 | 1855.811052 | 928.409164 | 12 |
| 8 | **781.318517** | 391.162896 | | | 763.307952 | 382.157614 | Y | *1742.781132* | 871.894204 | 1725.754583 | 863.380930 | 1724.770567 | 862.888922 | 11 |
| 9 | **882.366196** | 441.686736 | | | 864.355631 | 432.681453 | T | *1579.717803* | 790.362540 | 1562.691254 | 781.849265 | 1561.707238 | 781.357257 | 10 |
| 10 | 979.418960 | 490.213118 | | | 961.408395 | 481.207835 | P | *1478.670124* | 739.838700 | 1461.643575 | 731.325426 | | | 9 |
| 11 | 1093.461887 | 547.234581 | 1076.435338 | 538.721307 | 1075.451322 | 538.229299 | N | *1381.617360* | 691.312318 | 1364.590811 | 682.799044 | | | 8 |
| 12 | 1164.499001 | 582.753138 | 1147.472452 | 574.239864 | 1146.488436 | 573.747856 | A | *1267.574433* | 634.290855 | 1250.547884 | 625.777580 | | | 7 |
| 13 | **1292.557579** | 646.782428 | 1275.531030 | 638.269153 | 1274.547014 | 637.777145 | Q | *1196.537319* | 598.772298 | 1179.510770 | 590.259023 | | | 6 |
| 14 | 1455.620908 | 728.314092 | 1438.594359 | 719.800818 | 1437.610343 | 719.308810 | Y | *1068.478741* | 534.743009 | 1051.452192 | 526.229734 | | | 5 |
| 15 | 1615.651557 | 808.329417 | 1598.625008 | 799.816142 | 1597.640992 | 799.324134 | C | *905.415412* | 453.211344 | 888.388863 | 444.698070 | | | 4 |
| 16 | 2054.876883 | 1027.942079 | 2037.850334 | 1019.428805 | 2036.866318 | 1018.936797 | Q | *745.384763* | 373.196020 | 728.358214 | 364.682745 | | | 3 |
| 17 | 2185.917368 | 1093.462322 | 2168.890819 | 1084.949047 | 2167.906803 | 1084.457039 | M | 306.159437 | 153.583356 | 289.132888 | 145.070082 | | | 2 |
| 18 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

### All matches to this query

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 82.9 | 2359.021759 | 0.025193 | GGDVASMYTPNAQYCQMR |
| 45.5 | 2359.021759 | 0.025193 | GGDVASMYTPNAQYCQMR |
| 9.6 | 2359.079300 | -0.032348 | TPMSVLQQAGGSMMDGPGPR |
| 3.6 | 2359.079300 | -0.032348 | TPMSVLQQAGGSMMDGPGPR |

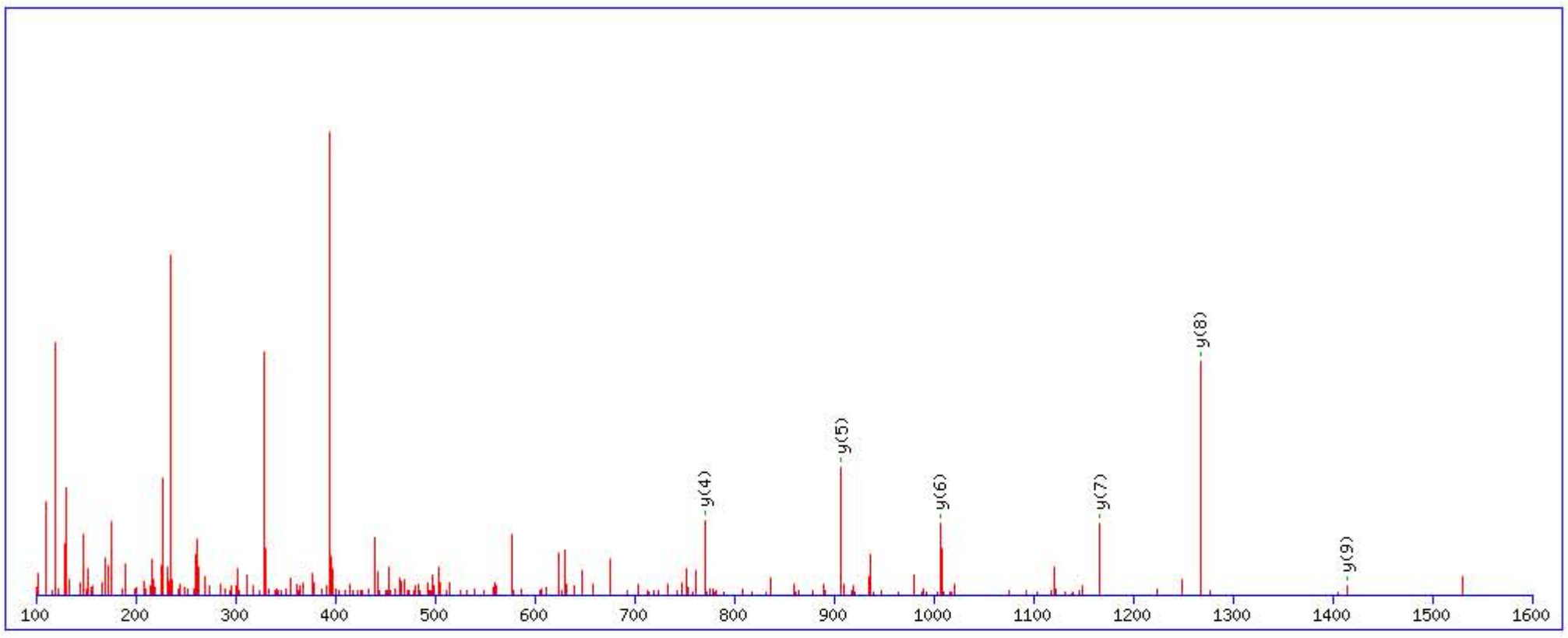
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DFTCVHQALK**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

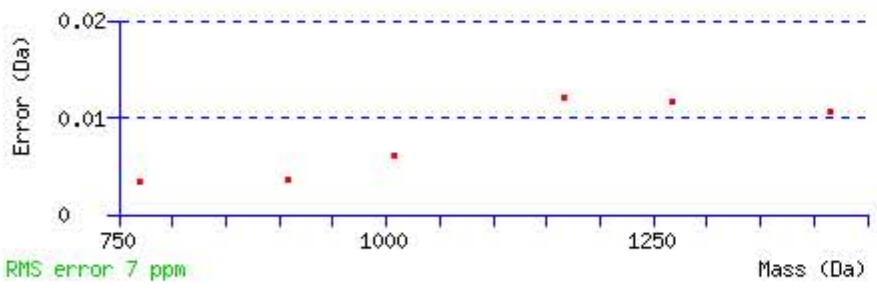
Match to Query 32006: 1528.757982 from(510.593270,3+) rtinseconds(1824) index(33062)
Title: Locus:1.1.1.744.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

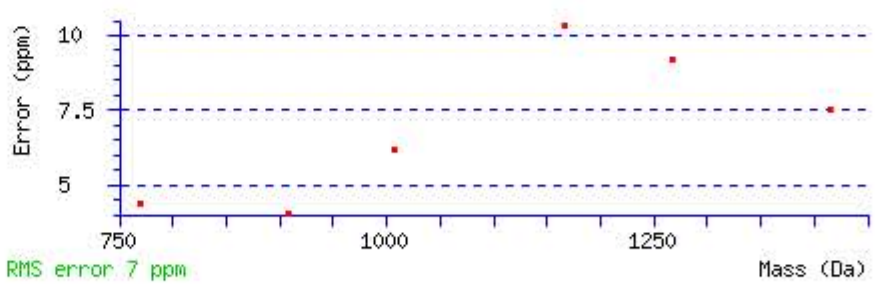
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1528.753052
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 29 **Expect:** 0.03
**Matches :** 6/82 fragment ions using 13 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 10 |
| 2 | 263.102633 | 132.054954 | | | 245.092068 | 123.049672 | F | *1414.733376* | 707.870326 | 1397.706827 | 699.357051 | 1396.722811 | 698.865043 | 9 |
| 3 | 364.150312 | 182.578794 | | | 346.139747 | 173.573512 | T | *1267.664962* | 634.336119 | 1250.638413 | 625.822844 | 1249.654397 | 625.330836 | 8 |
| 4 | 524.180961 | 262.594119 | | | 506.170396 | 253.588836 | C | *1166.617283* | 583.812279 | 1149.590734 | 575.299005 | | | 7 |
| 5 | 623.249375 | 312.128326 | | | 605.238810 | 303.123043 | V | *1006.586634* | 503.796955 | 989.560085 | 495.283680 | | | 6 |
| 6 | 760.308287 | 380.657782 | | | 742.297722 | 371.652499 | H | *907.518220* | 454.262748 | 890.491671 | 445.749473 | | | 5 |
| 7 | 1199.533613 | 600.270444 | 1182.507064 | 591.757170 | 1181.523048 | 591.265162 | Q | *770.459308* | 385.733292 | 753.432759 | 377.220017 | | | 4 |
| 8 | 1270.570727 | 635.789001 | 1253.544178 | 627.275727 | 1252.560162 | 626.783719 | A | 331.233982 | 166.120629 | 314.207433 | 157.607354 | | | 3 |
| 9 | 1383.654791 | 692.331033 | 1366.628242 | 683.817759 | 1365.644226 | 683.325751 | L | 260.196868 | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 10 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 28.8 | 1528.753052 | 0.004930 | DFTCVHQALK |

**Mascot:** http://www.matrixscience.com/

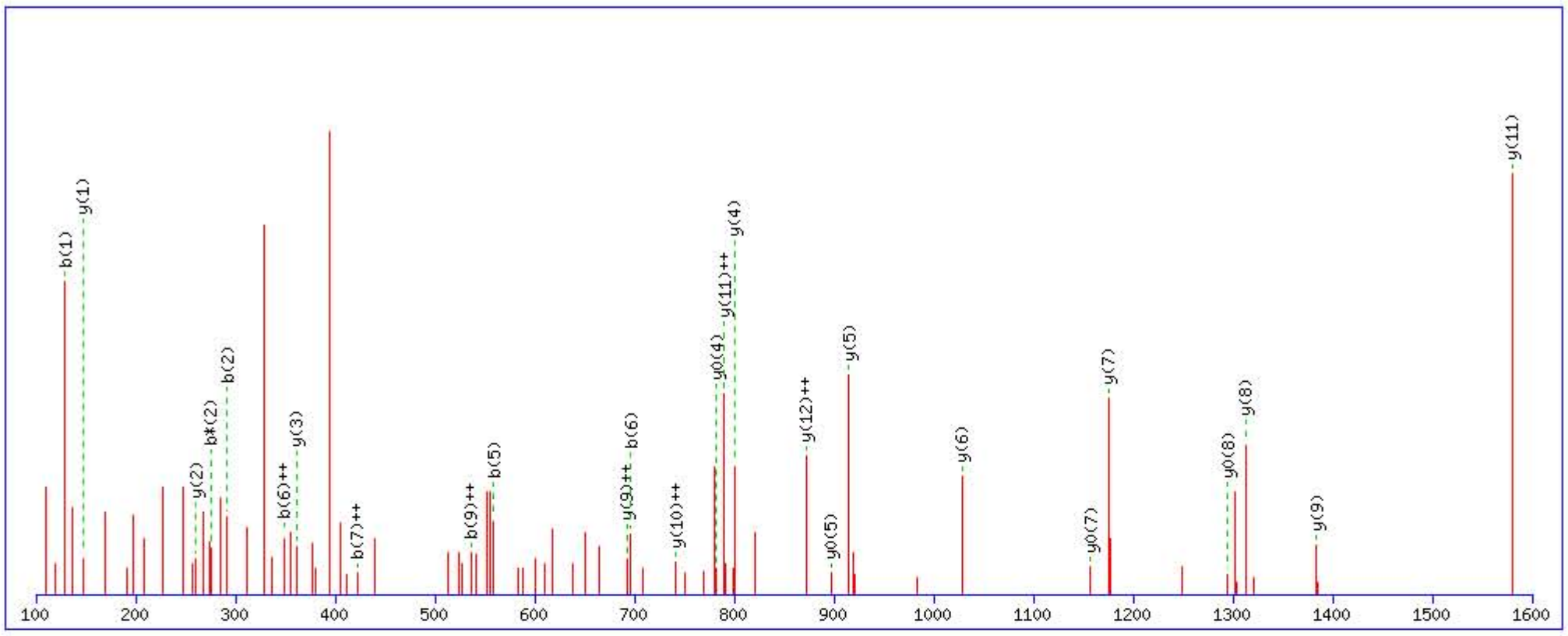
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KYPVAHFIDQTLK**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

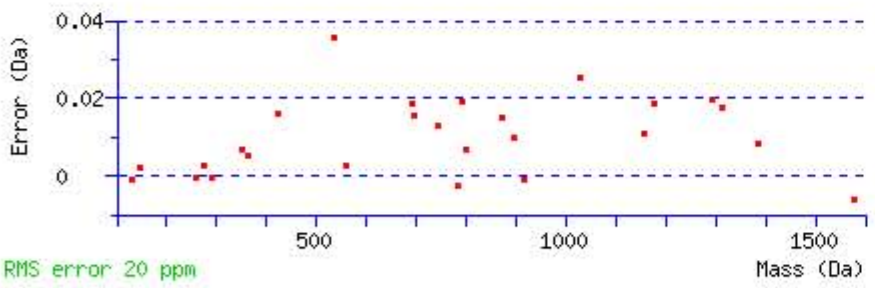
Match to Query 41684: 1870.033602 from(624.351810,3+) rtinseconds(2037) index(34499)
Title: Locus:1.1.1.818.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

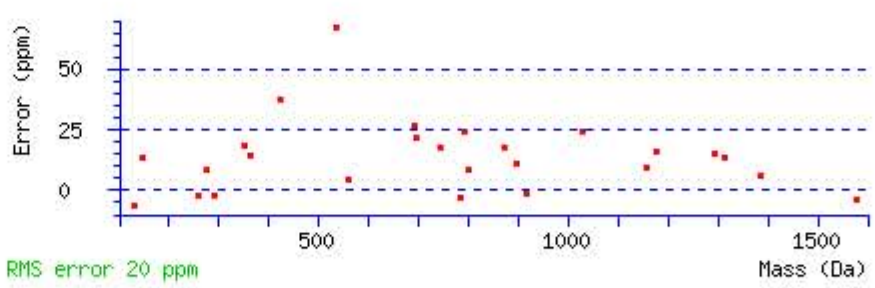
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1870.017502
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 36 **Expect:** 0.004
**Matches :** 26/124 fragment ions using 74 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.102239 | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 13 |
| 2 | 292.165568 | 146.586422 | 275.139019 | 138.073148 | | | Y | 1742.929827 | 871.968552 | 1725.903278 | 863.455277 | 1724.919262 | 862.963269 | 12 |
| 3 | 389.218332 | 195.112804 | 372.191783 | 186.599529 | | | P | *1579.866498* | 790.436887 | 1562.839949 | 781.923613 | 1561.855933 | 781.431605 | 11 |
| 4 | 488.286746 | 244.647011 | 471.260197 | 236.133737 | | | V | 1482.813734 | 741.910505 | 1465.787185 | 733.397231 | 1464.803169 | 732.905223 | 10 |
| 5 | 559.323860 | 280.165568 | 542.297311 | 271.652294 | | | A | *1383.745320* | 692.376298 | 1366.718771 | 683.863024 | 1365.734755 | 683.371016 | 9 |
| 6 | 696.382772 | 348.695024 | 679.356223 | 340.181750 | | | H | *1312.708206* | 656.857741 | 1295.681657 | 648.344467 | 1294.697641 | 647.852459 | 8 |
| 7 | 843.451186 | 422.229231 | 826.424637 | 413.715957 | | | F | *1175.649294* | 588.328285 | 1158.622745 | 579.815011 | 1157.638729 | 579.323003 | 7 |
| 8 | 956.535250 | 478.771263 | 939.508701 | 470.257989 | | | I | *1028.580880* | 514.794078 | 1011.554331 | 506.280804 | 1010.570315 | 505.788796 | 6 |
| 9 | 1071.562193 | 536.284735 | 1054.535644 | 527.771460 | 1053.551628 | 527.279452 | D | *915.496816* | 458.252046 | 898.470267 | 449.738772 | 897.486251 | 449.246764 | 5 |
| 10 | 1510.787519 | 755.897398 | 1493.760970 | 747.384123 | 1492.776954 | 746.892115 | Q | *800.469873* | 400.738575 | 783.443324 | 392.225300 | 782.459308 | 391.733292 | 4 |
| 11 | 1611.835198 | 806.421237 | 1594.808649 | 797.907963 | 1593.824633 | 797.415955 | T | *361.244547* | 181.125911 | 344.217998 | 172.612637 | 343.233982 | 172.120629 | 3 |
| 12 | 1724.919262 | 862.963269 | 1707.892713 | 854.449995 | 1706.908697 | 853.957987 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 13 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 36.2 | 1870.017502 | 0.016100 | KYPVAHFIDQTLK |

**Mascot:** http://www.matrixscience.com/

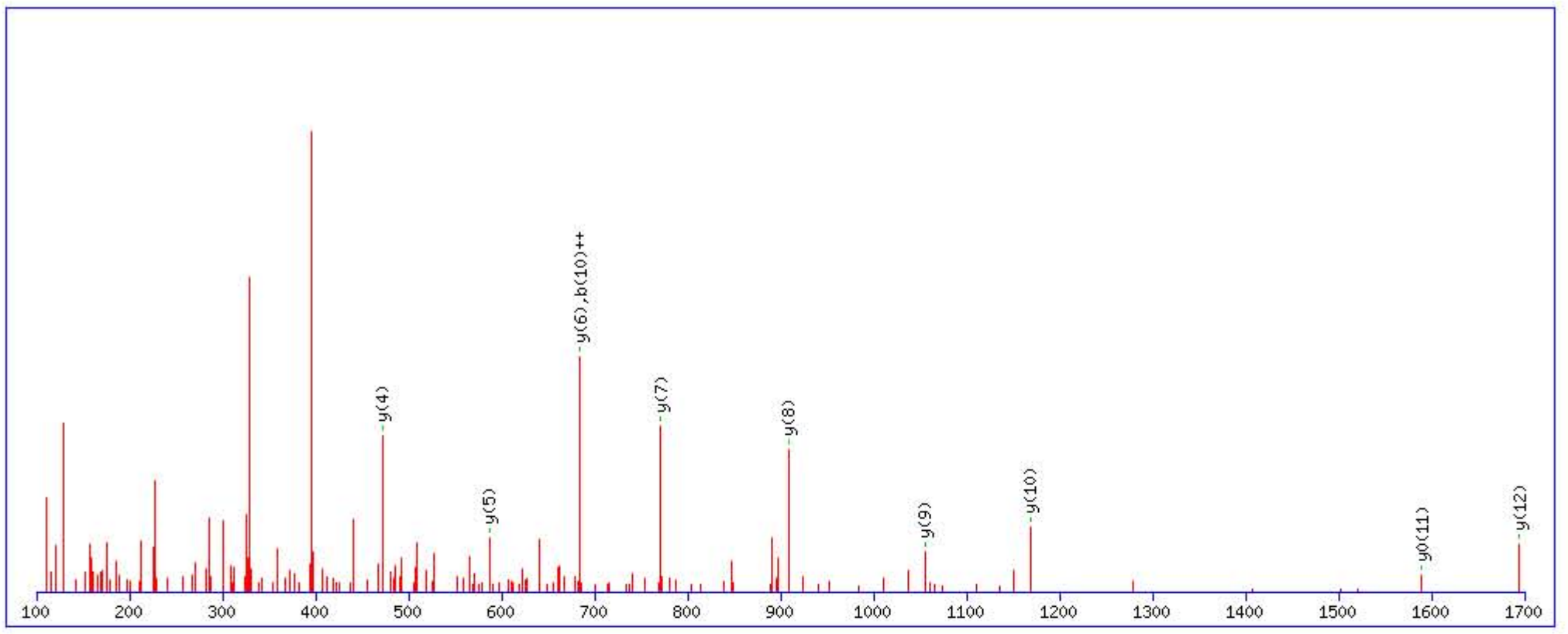
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GVTSVSQIFHSPDLAIR**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

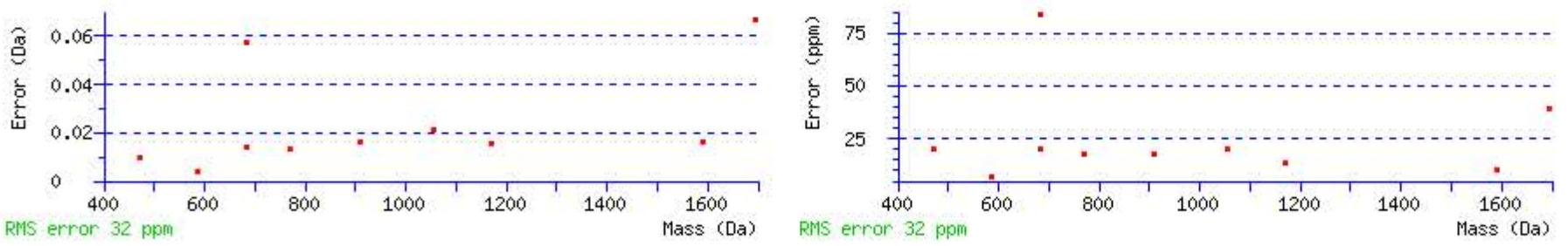
Match to Query 47221: 2137.154536 from(535.295910,4+) rtinseconds(2352) index(36300)
Title: Locus:1.1.1.928.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2137.135406
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 46 **Expect:** 0.00047
**Matches :** 10/168 fragment ions using 16 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 17 |
| 2 | 157.097154 | 79.052215 | | | | | V | 2081.121208 | 1041.064242 | 2064.094659 | 1032.550967 | 2063.110643 | 1032.058959 | 16 |
| 3 | 258.144833 | 129.576055 | | | 240.134268 | 120.570772 | T | 1982.052794 | 991.530035 | 1965.026245 | 983.016761 | 1964.042229 | 982.524753 | 15 |
| 4 | 345.176861 | 173.092068 | | | 327.166296 | 164.086786 | S | 1881.005115 | 941.006196 | 1863.978566 | 932.492921 | 1862.994550 | 932.000913 | 14 |
| 5 | 444.245275 | 222.626275 | | | 426.234710 | 213.620993 | V | 1793.973087 | 897.490182 | 1776.946538 | 888.976907 | 1775.962522 | 888.484899 | 13 |
| 6 | 531.277303 | 266.142290 | | | 513.266738 | 257.137007 | S | *1694.904673* | 847.955975 | 1677.878124 | 839.442700 | 1676.894108 | 838.950692 | 12 |
| 7 | 970.502629 | 485.754953 | 953.476080 | 477.241678 | 952.492064 | 476.749670 | Q | 1607.872645 | 804.439961 | 1590.846096 | 795.926686 | 1589.862080 | 795.434678 | 11 |
| 8 | 1083.586693 | 542.296985 | 1066.560144 | 533.783710 | 1065.576128 | 533.291702 | I | *1168.647319* | 584.827298 | 1151.620770 | 576.314023 | 1150.636754 | 575.822015 | 10 |
| 9 | 1230.655107 | 615.831192 | 1213.628558 | 607.317917 | 1212.644542 | 606.825909 | F | *1055.563255* | 528.285266 | 1038.536706 | 519.771991 | 1037.552690 | 519.279983 | 9 |
| 10 | 1367.714019 | 684.360648 | 1350.687470 | 675.847373 | 1349.703454 | 675.355365 | H | *908.494841* | 454.751059 | 891.468292 | 446.237784 | 890.484276 | 445.745776 | 8 |
| 11 | 1454.746047 | 727.876662 | 1437.719498 | 719.363387 | 1436.735482 | 718.871379 | S | *771.435929* | 386.221603 | 754.409380 | 377.708328 | 753.425364 | 377.216320 | 7 |
| 12 | 1551.798811 | 776.403044 | 1534.772262 | 767.889769 | 1533.788246 | 767.397761 | P | *684.403901* | 342.705589 | 667.377352 | 334.192314 | 666.393336 | 333.700306 | 6 |
| 13 | 1666.825754 | 833.916515 | 1649.799205 | 825.403241 | 1648.815189 | 824.911233 | D | *587.351137* | 294.179207 | 570.324588 | 285.665932 | 569.340572 | 285.173924 | 5 |
| 14 | 1779.909818 | 890.458547 | 1762.883269 | 881.945273 | 1761.899253 | 881.453265 | L | *472.324194* | 236.665735 | 455.297645 | 228.152460 | | | 4 |
| 15 | 1850.946932 | 925.977104 | 1833.920383 | 917.463830 | 1832.936367 | 916.971822 | A | 359.240130 | 180.123703 | 342.213581 | 171.610429 | | | 3 |
| 16 | 1964.030996 | 982.519136 | 1947.004447 | 974.005862 | 1946.020431 | 973.513853 | I | 288.203016 | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 17 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 46.2 | 2137.135406 | 0.019130 | GVTSVSQIFHSPDLAIR |

**Mascot:** http://www.matrixscience.com/

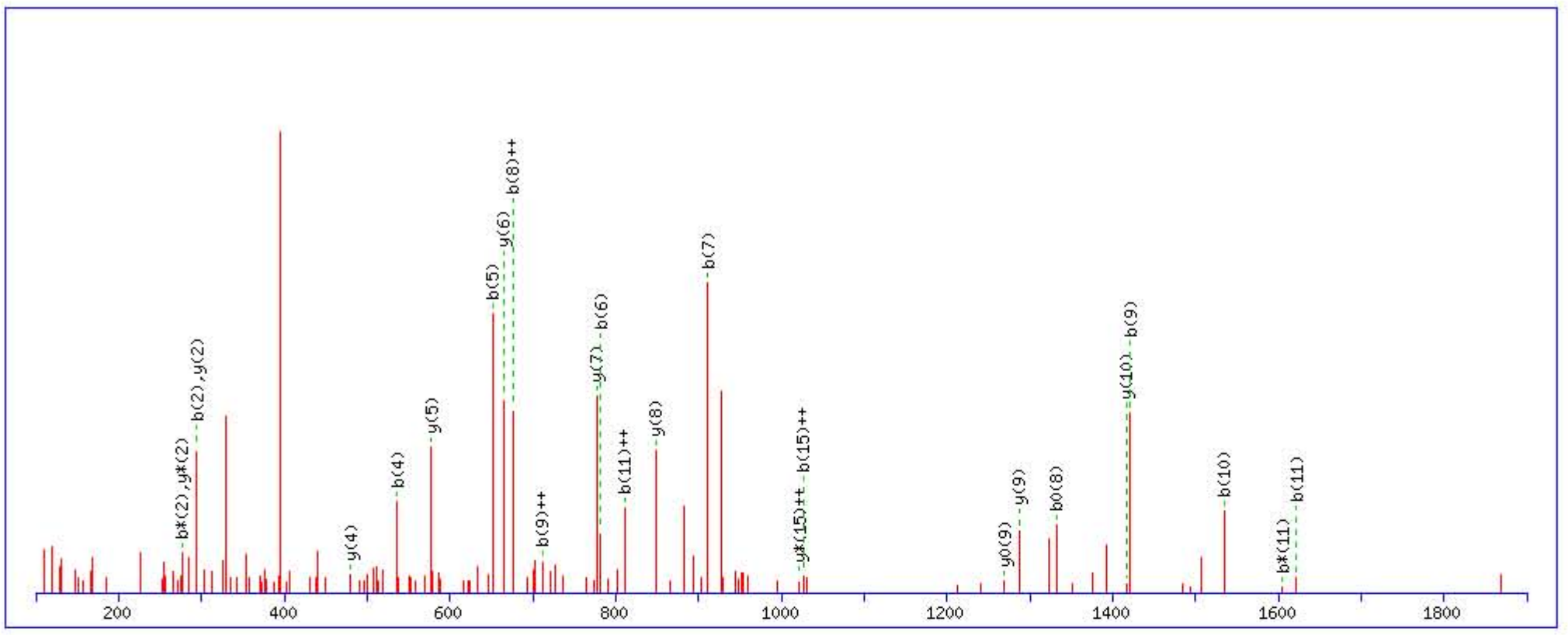
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HRLEDMEQALSPSVFK**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

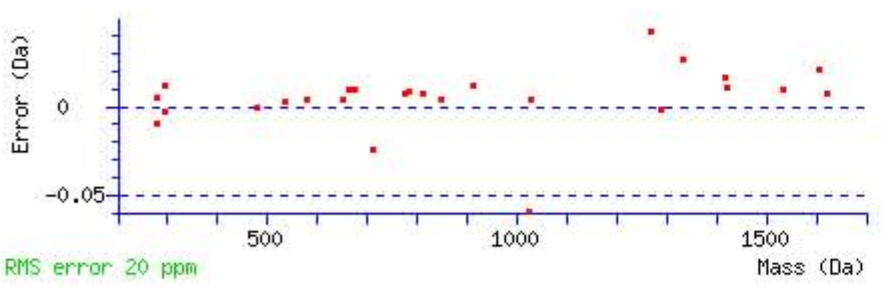
Match to Query 48411: 2197.130592 from(733.384140,3+) rtinseconds(2161) index(35219)
Title: Locus:1.1.1.861.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

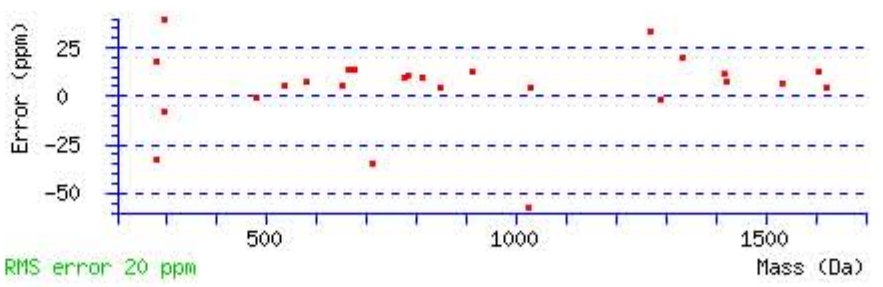
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2197.102356
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 7e-005
**Matches :** 26/166 fragment ions using 43 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 16 |
| 2 | ***294.167299*** | 147.587288 | 277.140750 | 139.074013 | | | R | 2061.050745 | 1031.029010 | 2044.024196 | 1022.515736 | 2043.040180 | 1022.023728 | 15 |
| 3 | 407.251363 | 204.129320 | 390.224814 | 195.616045 | | | L | 1904.949634 | 952.978455 | 1887.923085 | 944.465181 | 1886.939069 | 943.973173 | 14 |
| 4 | ***536.293956*** | 268.650616 | 519.267407 | 260.137342 | 518.283391 | 259.645334 | E | 1791.865570 | 896.436423 | 1774.839021 | 887.923149 | 1773.855005 | 887.431141 | 13 |
| 5 | ***651.320899*** | 326.164088 | 634.294350 | 317.650813 | 633.310334 | 317.158805 | D | 1662.822977 | 831.915127 | 1645.796428 | 823.401852 | 1644.812412 | 822.909844 | 12 |
| 6 | ***782.361384*** | 391.684330 | 765.334835 | 383.171056 | 764.350819 | 382.679048 | M | 1547.796034 | 774.401655 | 1530.769485 | 765.888381 | 1529.785469 | 765.396373 | 11 |
| 7 | ***911.403977*** | 456.205627 | 894.377428 | 447.692352 | 893.393412 | 447.200344 | E | ***1416.755549*** | 708.881413 | 1399.729000 | 700.368138 | 1398.744984 | 699.876130 | 10 |
| 8 | 1350.629303 | **675.818289** | 1333.602754 | 667.305015 | 1332.618738 | 666.813007 | Q | ***1287.712956*** | 644.360116 | 1270.686407 | 635.846842 | 1269.702391 | 635.354834 | 9 |
| 9 | ***1421.666417*** | **711.336846** | 1404.639868 | 702.823572 | 1403.655852 | 702.331564 | A | ***848.487630*** | 424.747453 | 831.461081 | 416.234179 | 830.477065 | 415.742171 | 8 |
| 10 | ***1534.750481*** | 767.878878 | 1517.723932 | 759.365604 | 1516.739916 | 758.873596 | L | ***777.450516*** | 389.228896 | 760.423967 | 380.715622 | 759.439951 | 380.223614 | 7 |
| 11 | ***1621.782509*** | **811.394892** | 1604.755960 | 802.881618 | 1603.771944 | 802.389610 | S | ***664.366452*** | 332.686864 | 647.339903 | 324.173590 | 646.355887 | 323.681582 | 6 |
| 12 | 1718.835273 | 859.921274 | 1701.808724 | 851.408000 | 1700.824708 | 850.915992 | P | ***577.334424*** | 289.170850 | 560.307875 | 280.657576 | 559.323859 | 280.165568 | 5 |
| 13 | 1805.867301 | 903.437289 | 1788.840752 | 894.924014 | 1787.856736 | 894.432006 | S | ***480.281660*** | 240.644468 | 463.255111 | 232.131194 | 462.271095 | 231.639186 | 4 |
| 14 | 1904.935715 | 952.971496 | 1887.909166 | 944.458221 | 1886.925150 | 943.966213 | V | 393.249632 | 197.128454 | 376.223083 | 188.615180 | | | 3 |
| 15 | 2052.004129 | **1026.505702** | 2034.977580 | 1017.992428 | 2033.993564 | 1017.500420 | F | ***294.181218*** | 147.594247 | 277.154669 | 139.080973 | | | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.3 | 2197.102356 | 0.028236 | HRLEDMEQALSPSVFK |
| 0.9 | 2197.113602 | 0.016990 | QRPQLSSDSPSAFR |

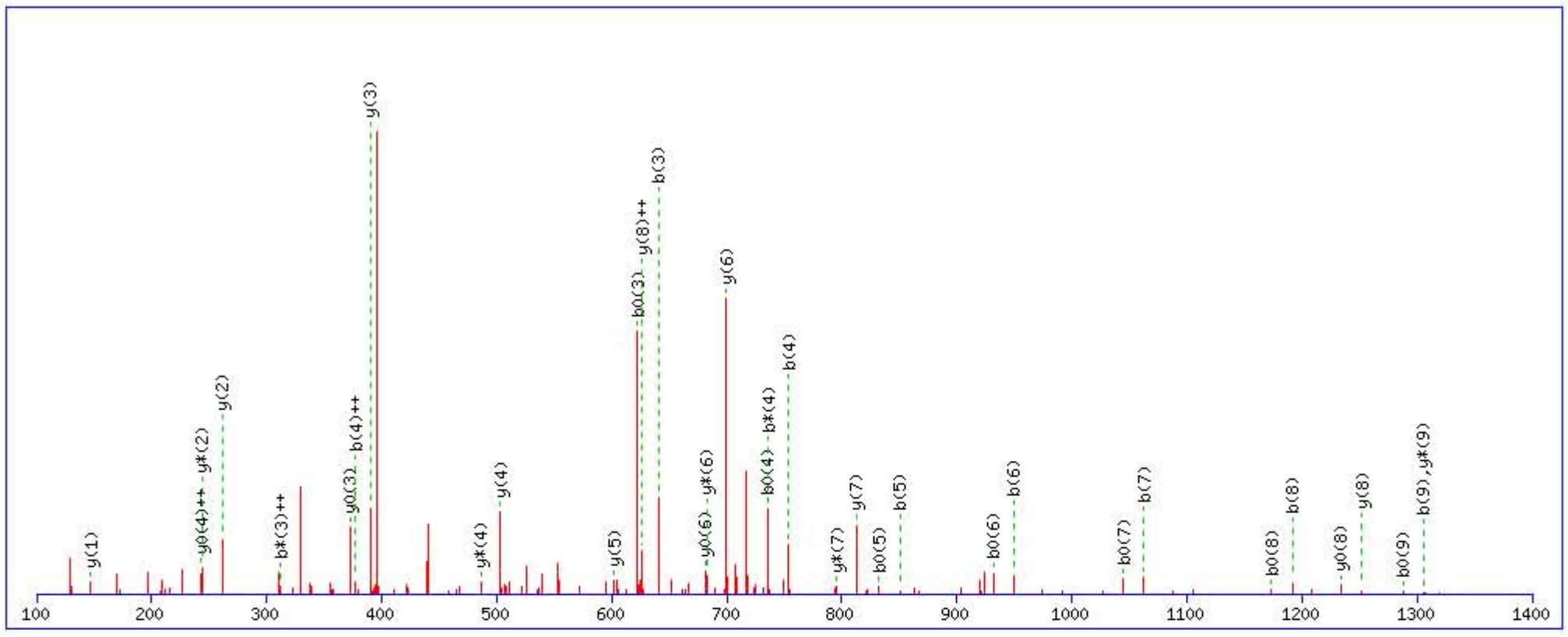
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EAQLPVIENK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

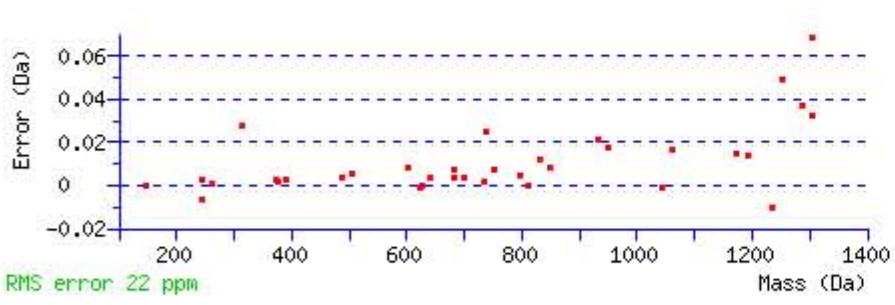
Match to Query 29663: 1450.794708 from(726.404630,2+) rtinseconds(1977) index(66323)
Title: Locus:1.1.1.1963.11 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

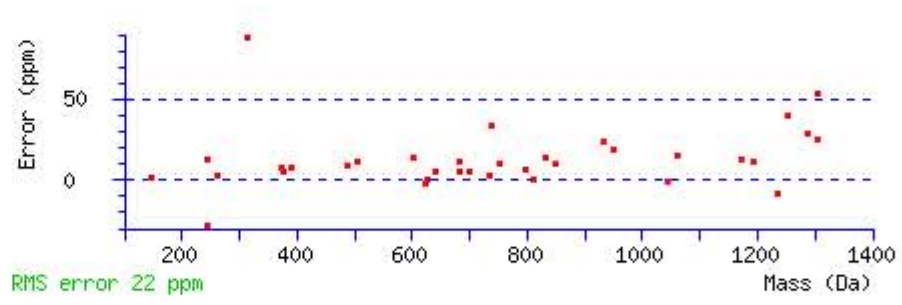
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1450.785355
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 34 **Expect:** 0.0016
**Matches :** 35/100 fragment ions using 74 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 10 |
| 2 | 201.086983 | 101.047130 | | | 183.076418 | 92.041847 | A | 1322.750070 | 661.878673 | 1305.723521 | 653.365398 | 1304.739505 | 652.873390 | 9 |
| 3 | **640.312309** | 320.659793 | 623.285760 | 312.146518 | 622.301744 | 311.654510 | Q | ***1251.712956*** | 626.360116 | 1234.686407 | 617.846841 | 1233.702391 | 617.354833 | 8 |
| 4 | **753.396373** | 377.201825 | 736.369824 | 368.688550 | 735.385808 | 368.196542 | L | ***812.487630*** | 406.747453 | 795.461081 | 398.234178 | 794.477065 | 397.742170 | 7 |
| 5 | **850.449137** | 425.728207 | 833.422588 | 417.214932 | 832.438572 | 416.722924 | P | ***699.403566*** | 350.205421 | 682.377017 | 341.692146 | 681.393001 | 341.200138 | 6 |
| 6 | **949.517551** | 475.262414 | 932.491002 | 466.749139 | 931.506986 | 466.257131 | V | ***602.350802*** | 301.679039 | 585.324253 | 293.165764 | 584.340237 | 292.673756 | 5 |
| 7 | **1062.601615** | 531.804446 | 1045.575066 | 523.291171 | 1044.591050 | 522.799163 | I | ***503.282388*** | 252.144832 | 486.255839 | 243.631557 | 485.271823 | 243.139549 | 4 |
| 8 | **1191.644208** | 596.325742 | 1174.617659 | 587.812468 | 1173.633643 | 587.320459 | E | ***390.198324*** | 195.602800 | 373.171775 | 187.089525 | 372.187759 | 186.597517 | 3 |
| 9 | **1305.687135** | 653.347205 | 1288.660586 | 644.833931 | 1287.676570 | 644.341923 | N | ***261.155731*** | 131.081503 | 244.129182 | 122.568229 | | | 2 |
| 10 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.6 | 1450.785355 | 0.009353 | EAQLPVIENK |
| 3.8 | 1450.807816 | -0.013108 | KKMITNNPHLQK |
| 2.9 | 1450.790527 | 0.004181 | QNIWRHNRLSK |
| 2.7 | 1450.803986 | -0.009278 | QLAEQIK |

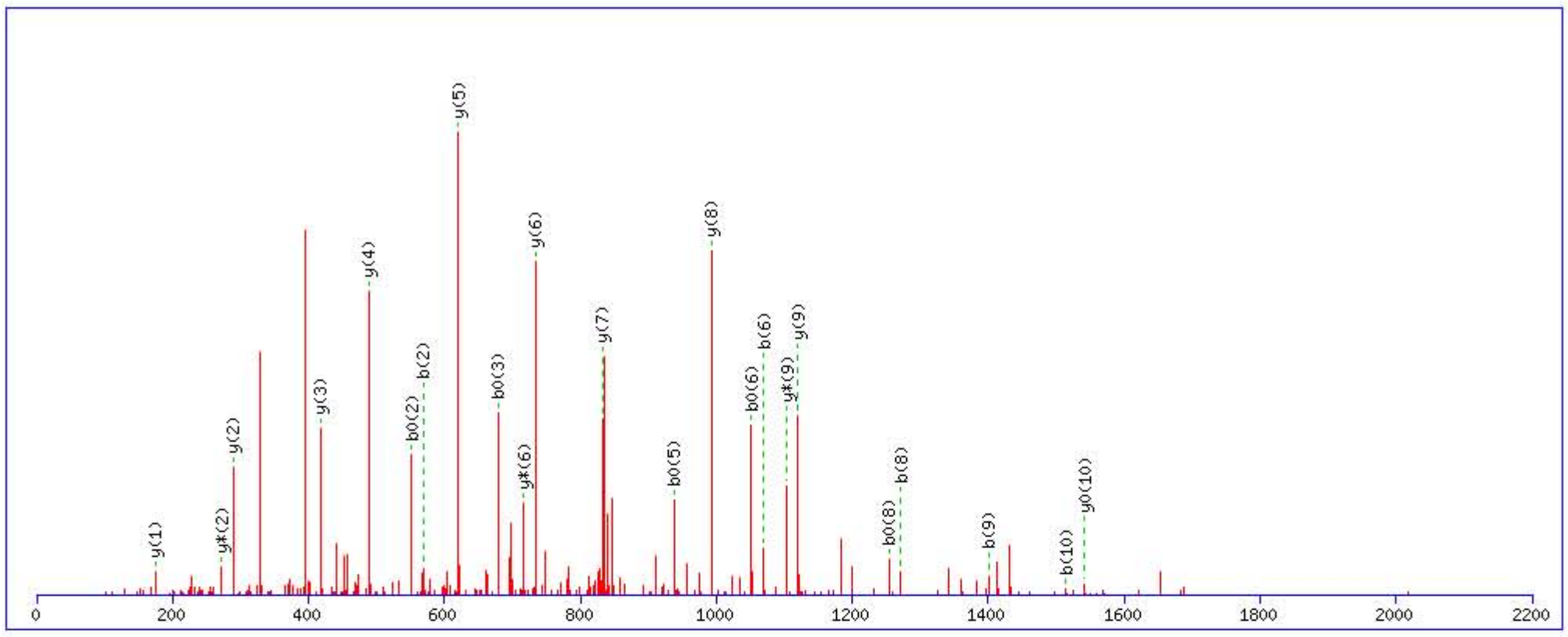
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EQQCVIMAENR**
Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

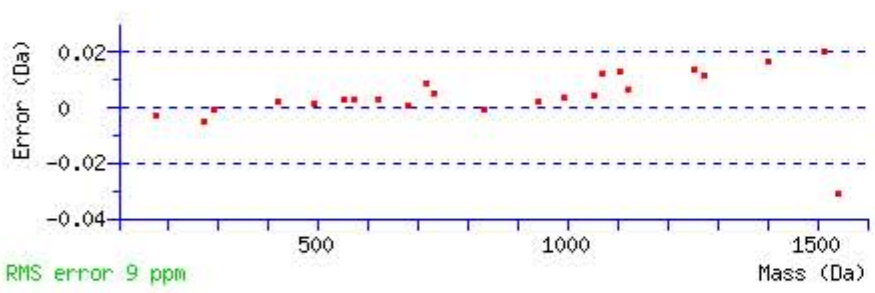
Match to Query 37702: 1687.793408 from(844.903980,2+) rtinseconds(1782) index(65083)
Title: Locus:1.1.1.1895.11 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

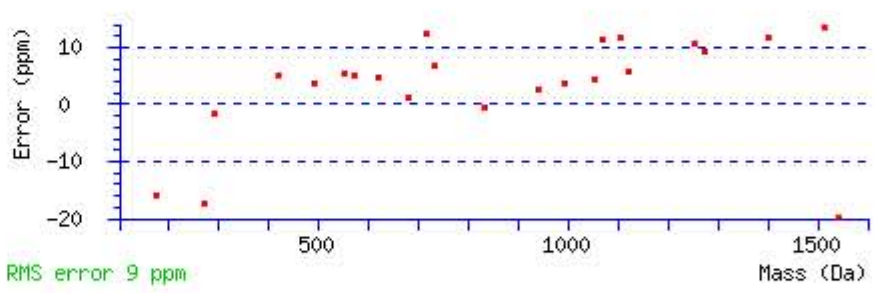
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1687.784393
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 71 **Expect:** 7.6e-007
**Matches :** 23/114 fragment ions using 32 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 11 |
| 2 | **569.275195** | 285.141236 | 552.248646 | 276.627961 | 551.264630 | 276.135953 | Q | 1559.749102 | 780.378189 | 1542.722553 | 771.864915 | 1541.738537 | 771.372907 | 10 |
| 3 | 697.333773 | 349.170525 | 680.307224 | 340.657250 | 679.323208 | 340.165242 | Q | ***1120.523776*** | 560.765526 | 1103.497227 | 552.252252 | 1102.513211 | 551.760244 | 9 |
| 4 | 857.364422 | 429.185849 | 840.337873 | 420.672575 | 839.353857 | 420.180567 | C | ***992.465198*** | 496.736237 | 975.438649 | 488.222963 | 974.454633 | 487.730955 | 8 |
| 5 | 956.432836 | 478.720056 | 939.406287 | 470.206782 | 938.422271 | 469.714774 | V | ***832.434549*** | 416.720913 | 815.408000 | 408.207638 | 814.423984 | 407.715630 | 7 |
| 6 | **1069.516900** | 535.262088 | 1052.490351 | 526.748814 | 1051.506335 | 526.256806 | I | ***733.366135*** | 367.186706 | 716.339586 | 358.673431 | 715.355570 | 358.181423 | 6 |
| 7 | 1200.557385 | 600.782331 | 1183.530836 | 592.269056 | 1182.546820 | 591.777048 | M | ***620.282071*** | 310.644674 | 603.255522 | 302.131399 | 602.271506 | 301.639391 | 5 |
| 8 | **1271.594499** | 636.300888 | 1254.567950 | 627.787613 | 1253.583934 | 627.295605 | A | ***489.241586*** | 245.124431 | 472.215037 | 236.611156 | 471.231021 | 236.119148 | 4 |
| 9 | **1400.637092** | 700.822184 | 1383.610543 | 692.308910 | 1382.626527 | 691.816902 | E | ***418.204472*** | 209.605874 | 401.177923 | 201.092600 | 400.193907 | 200.600592 | 3 |
| 10 | **1514.680019** | 757.843648 | 1497.653470 | 749.330373 | 1496.669454 | 748.838365 | N | ***289.161879*** | 145.084577 | 272.135330 | 136.571303 | | | 2 |
| 11 | | | | | | | R | ***175.118952*** | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 71.0 | 1687.784393 | 0.009015 | EQQCVIMAENR |
| 66.0 | 1687.784393 | 0.009015 | EQQCVIMAENR |
| 5.4 | 1687.781006 | 0.012402 | ELMAWNQAENR |
| 4.4 | 1687.784882 | 0.008526 | APPPSSESRPPCHGGR |
| 4.1 | 1687.813370 | -0.019962 | MKQSPALAPEERCR |
| 3.3 | 1687.809998 | -0.016590 | NMTAQNYTYAIRSR |
| 3.2 | 1687.773193 | 0.020215 | FGAVCTCMEKATGLK |
| 2.9 | 1687.776093 | 0.017315 | QQEEAQAAAAAASAESR |
| 0.1 | 1687.817383 | -0.023975 | EQKEKYMEHR |

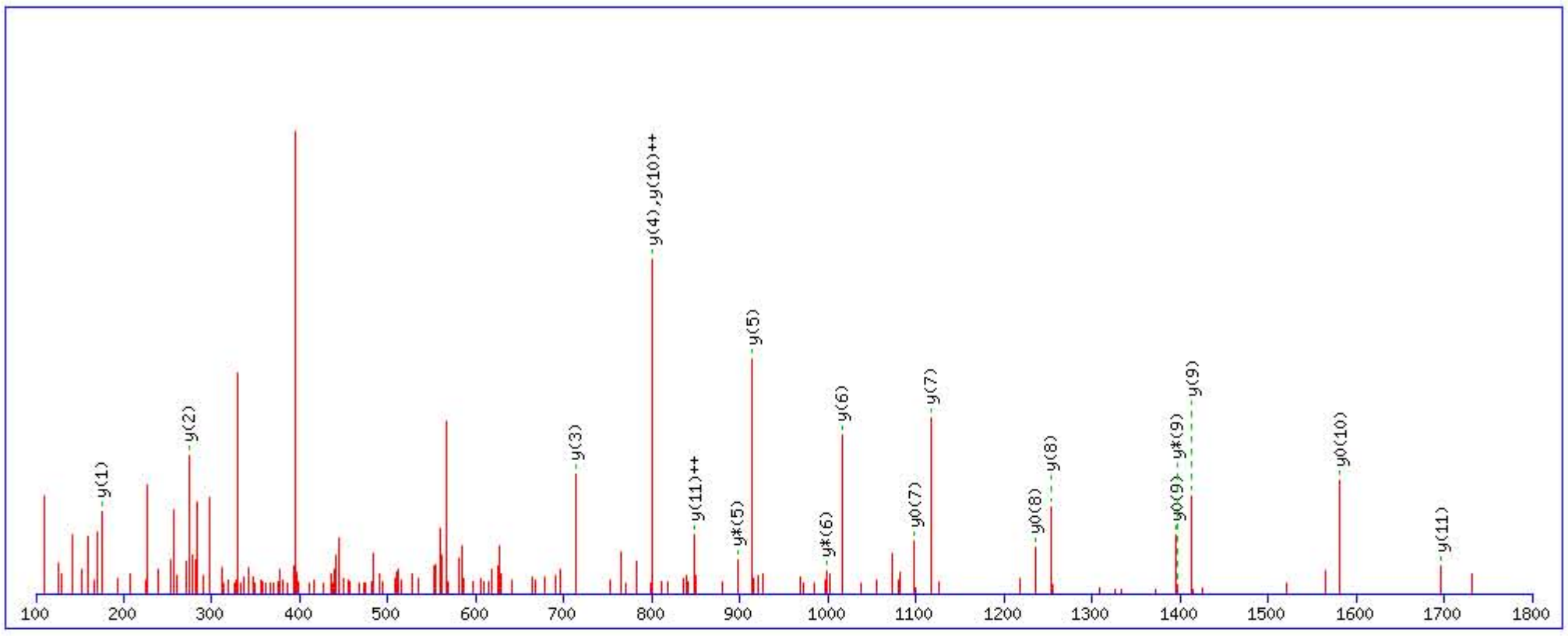
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **APWCHTTNSQVR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

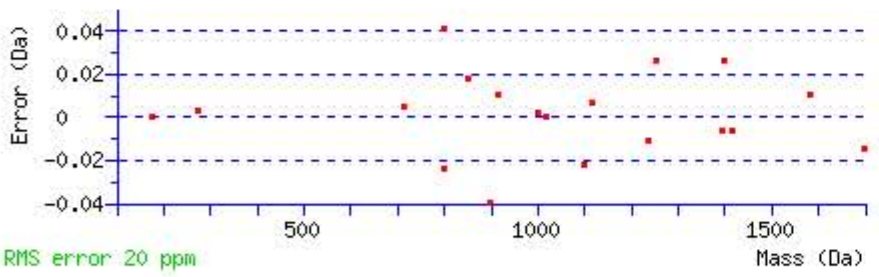
Match to Query 39497: 1766.835372 from(589.952400,3+) rtinseconds(1509) index(2695)
Title: Locus:1.1.1.1802.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

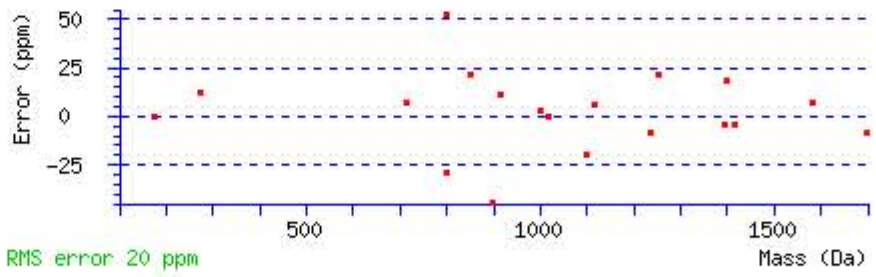
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1766.834488
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 65 **Expect:** 5.2e-006
**Matches :** 19/102 fragment ions using 32 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 12 |
| 2 | 169.097154 | 85.052215 | | | | | P | *1696.804643* | 848.905960 | 1679.778094 | 840.392685 | 1678.794078 | 839.900677 | 11 |
| 3 | 355.176467 | 178.091872 | | | | | W | 1599.751879 | 800.379578 | 1582.725330 | 791.866303 | 1581.741314 | 791.374295 | 10 |
| 4 | 515.207116 | 258.107196 | | | | | C | *1413.672566* | 707.339921 | 1396.646017 | 698.826647 | 1395.662001 | 698.334639 | 9 |
| 5 | 652.266028 | 326.636652 | | | | | H | *1253.641917* | 627.324597 | 1236.615368 | 618.811322 | 1235.631352 | 618.319314 | 8 |
| 6 | 753.313707 | 377.160492 | | | 735.303142 | 368.155209 | T | *1116.583005* | 558.795141 | 1099.556456 | 550.281866 | 1098.572440 | 549.789858 | 7 |
| 7 | 854.361386 | 427.684331 | | | 836.350821 | 418.679049 | T | *1015.535326* | 508.271301 | 998.508777 | 499.758027 | 997.524761 | 499.266019 | 6 |
| 8 | 968.404313 | 484.705795 | 951.377764 | 476.192520 | 950.393748 | 475.700512 | N | *914.487647* | 457.747462 | 897.461098 | 449.234187 | 896.477082 | 448.742179 | 5 |
| 9 | 1055.436341 | 528.221809 | 1038.409792 | 519.708534 | 1037.425776 | 519.216526 | S | *800.444720* | 400.725998 | 783.418171 | 392.212724 | 782.434155 | 391.720716 | 4 |
| 10 | 1494.661667 | 747.834472 | 1477.635118 | 739.321197 | 1476.651102 | 738.829189 | Q | *713.412692* | 357.209984 | 696.386143 | 348.696710 | | | 3 |
| 11 | 1593.730081 | 797.368679 | 1576.703532 | 788.855404 | 1575.719516 | 788.363396 | V | *274.187366* | 137.597321 | 257.160817 | 129.084047 | | | 2 |
| 12 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 64.8 | 1766.834488 | 0.000884 | APWCHTTNSQVR |

**Mascot:** http://www.matrixscience.com/

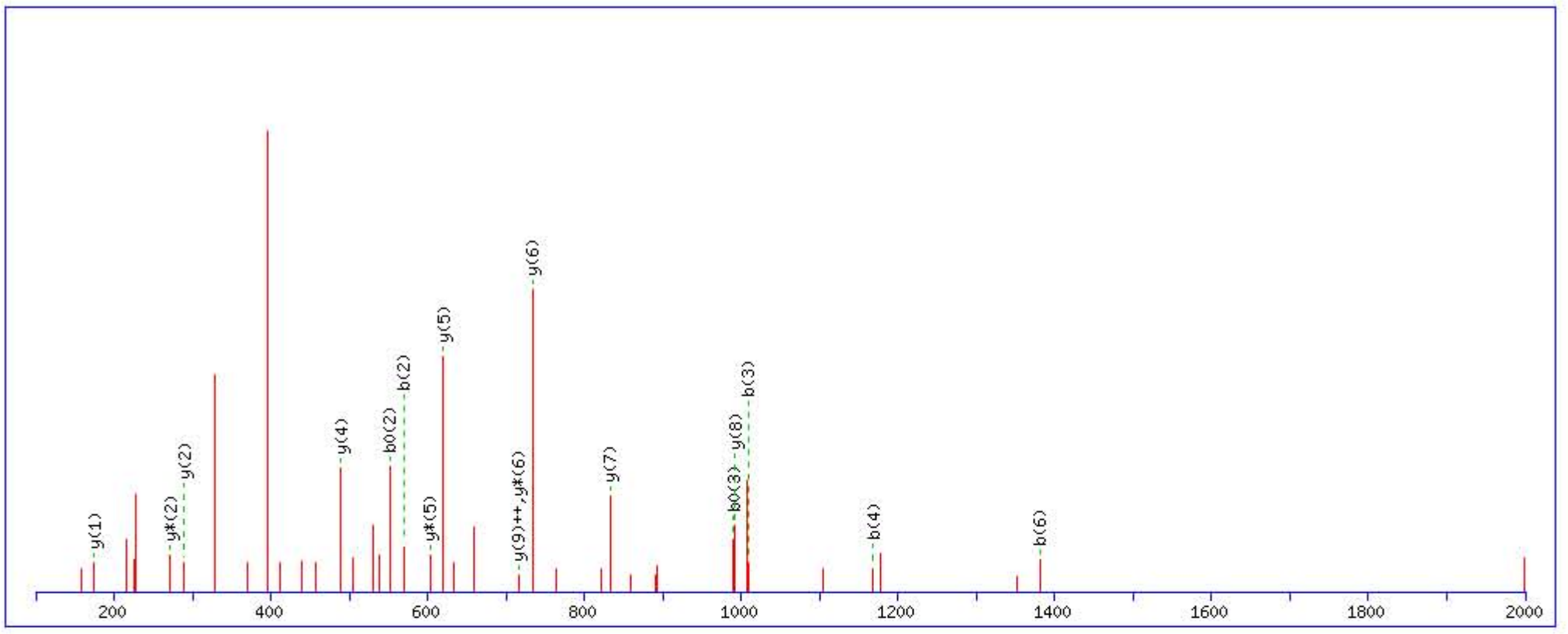
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EQQCVIMAENR**
Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

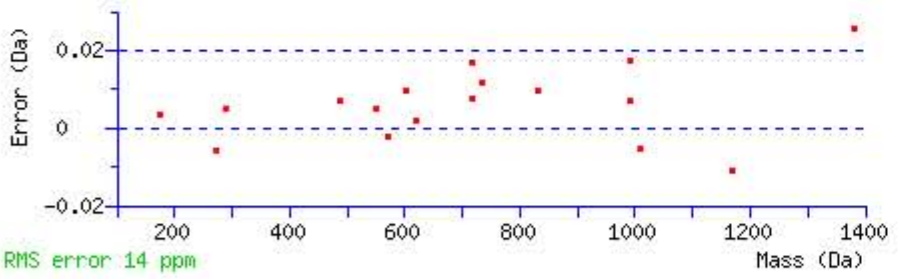
Match to Query 44106: 1998.963642 from(667.328490,3+) rtinseconds(2126) index(67159)
Title: Locus:1.1.1.2015.16 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

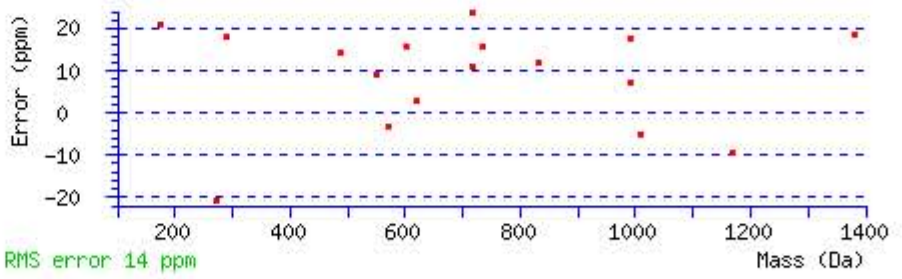
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1998.951141
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 27 **Expect:** 0.039
**Matches :** 17/114 fragment ions using 36 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 11 |
| 2 | **569.275195** | 285.141236 | 552.248646 | 276.627961 | 551.264630 | 276.135953 | Q | 1870.915850 | 935.961563 | 1853.889301 | 927.448288 | 1852.905285 | 926.956280 | 10 |
| 3 | **1008.500521** | 504.753899 | 991.473972 | 496.240624 | 990.489956 | 495.748616 | Q | 1431.690524 | 716.348900 | 1414.663975 | 707.835625 | 1413.679959 | 707.343617 | 9 |
| 4 | **1168.531170** | 584.769223 | 1151.504621 | 576.255949 | 1150.520605 | 575.763940 | C | *992.465198* | 496.736237 | 975.438649 | 488.222962 | 974.454633 | 487.730954 | 8 |
| 5 | 1267.599584 | 634.303430 | 1250.573035 | 625.790156 | 1249.589019 | 625.298148 | V | *832.434549* | 416.720912 | 815.408000 | 408.207638 | 814.423984 | 407.715630 | 7 |
| 6 | **1380.683648** | 690.845462 | 1363.657099 | 682.332188 | 1362.673083 | 681.840179 | I | *733.366135* | 367.186705 | 716.339586 | 358.673431 | 715.355570 | 358.181423 | 6 |
| 7 | 1511.724133 | 756.365704 | 1494.697584 | 747.852430 | 1493.713568 | 747.360422 | M | *620.282071* | 310.644673 | 603.255522 | 302.131399 | 602.271506 | 301.639391 | 5 |
| 8 | 1582.761247 | 791.884261 | 1565.734698 | 783.370987 | 1564.750682 | 782.878979 | A | *489.241586* | 245.124431 | 472.215037 | 236.611156 | 471.231021 | 236.119148 | 4 |
| 9 | 1711.803840 | 856.405558 | 1694.777291 | 847.892283 | 1693.793275 | 847.400275 | E | 418.204472 | 209.605874 | 401.177923 | 201.092599 | 400.193907 | 200.600591 | 3 |
| 10 | 1825.846767 | 913.427021 | 1808.820218 | 904.913747 | 1807.836202 | 904.421739 | N | *289.161879* | 145.084577 | 272.135330 | 136.571303 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 27.3 | 1998.951141 | 0.012501 | EQQCVIMAENR |

**Mascot:** http://www.matrixscience.com/

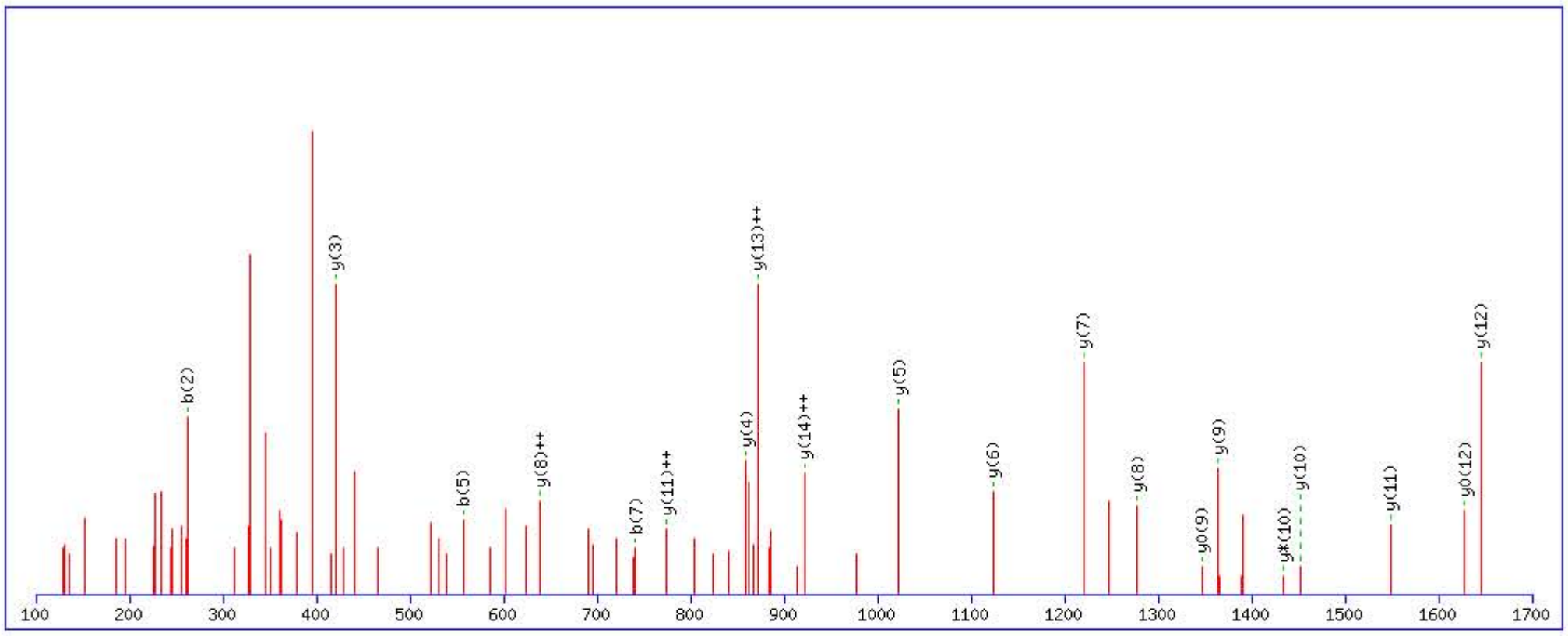
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **CTTPPPSSGPTYQCLK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

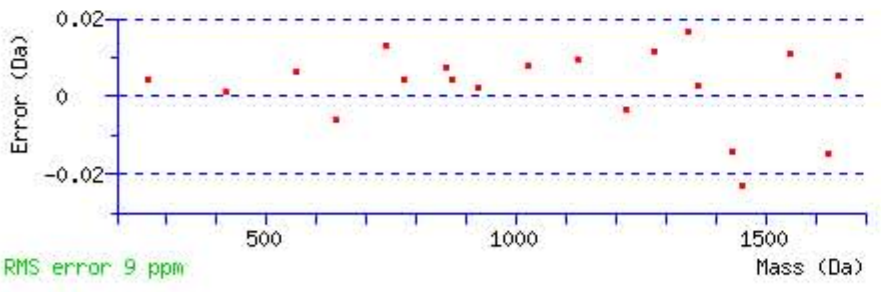
Match to Query 46698: 2103.985452 from(702.335760,3+) rtinseconds(1729) index(64746)
Title: Locus:1.1.1.1877.12 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

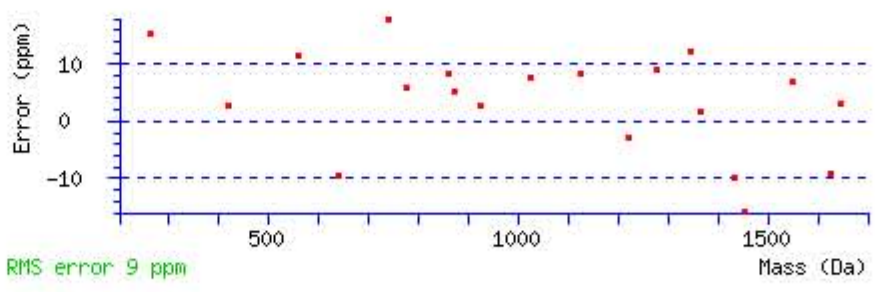
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2103.979172
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 8.5e-005
**Matches :** 20/144 fragment ions using 40 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 161.037925 | 81.022600 | | | | | C | | | | | | | 16 |
| 2 | **262.085604** | 131.546440 | | | 244.075039 | 122.541158 | T | 1944.955785 | 972.981531 | 1927.929236 | 964.468256 | 1926.945220 | 963.976248 | 15 |
| 3 | 363.133283 | 182.070280 | | | 345.122718 | 173.064997 | T | 1843.908106 | 922.457691 | 1826.881557 | 913.944417 | 1825.897541 | 913.452409 | 14 |
| 4 | 460.186047 | 230.596661 | | | 442.175482 | 221.591379 | P | 1742.860427 | 871.933852 | 1725.833878 | 863.420577 | 1724.849862 | 862.928569 | 13 |
| 5 | **557.238811** | 279.123044 | | | 539.228246 | 270.117761 | P | *1645.807663* | 823.407470 | 1628.781114 | 814.894195 | 1627.797098 | 814.402187 | 12 |
| 6 | 654.291575 | 327.649426 | | | 636.281010 | 318.644143 | P | *1548.754899* | 774.881088 | 1531.728350 | 766.367813 | 1530.744334 | 765.875805 | 11 |
| 7 | **741.323603** | 371.165440 | | | 723.313038 | 362.160157 | S | *1451.702135* | 726.354706 | 1434.675586 | 717.841431 | 1433.691570 | 717.349423 | 10 |
| 8 | 828.355631 | 414.681454 | | | 810.345066 | 405.676171 | S | *1364.670107* | 682.838692 | 1347.643558 | 674.325417 | 1346.659542 | 673.833409 | 9 |
| 9 | 885.377095 | 443.192186 | | | 867.366530 | 434.186903 | G | *1277.638079* | 639.322678 | 1260.611530 | 630.809403 | 1259.627514 | 630.317395 | 8 |
| 10 | 982.429859 | 491.718568 | | | 964.419294 | 482.713285 | P | *1220.616615* | 610.811946 | 1203.590066 | 602.298671 | 1202.606050 | 601.806663 | 7 |
| 11 | 1083.477538 | 542.242407 | | | 1065.466973 | 533.237125 | T | *1123.563851* | 562.285564 | 1106.537302 | 553.772289 | 1105.553286 | 553.280281 | 6 |
| 12 | 1246.540867 | 623.774072 | | | 1228.530302 | 614.768789 | Y | *1022.516172* | 511.761724 | 1005.489623 | 503.248450 | | | 5 |
| 13 | 1685.766193 | 843.386735 | 1668.739644 | 834.873460 | 1667.755628 | 834.381452 | Q | *859.452843* | 430.230060 | 842.426294 | 421.716785 | | | 4 |
| 14 | 1845.796842 | 923.402059 | 1828.770293 | 914.888785 | 1827.786277 | 914.396777 | C | *420.227517* | 210.617396 | 403.200968 | 202.104122 | | | 3 |
| 15 | 1958.880906 | 979.944091 | 1941.854357 | 971.430817 | 1940.870341 | 970.938809 | L | 260.196868 | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 16 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 53.0 | 2103.979172 | 0.006280 | CTTPPPSSGPTYQCLK |

**Mascot:** http://www.matrixscience.com/

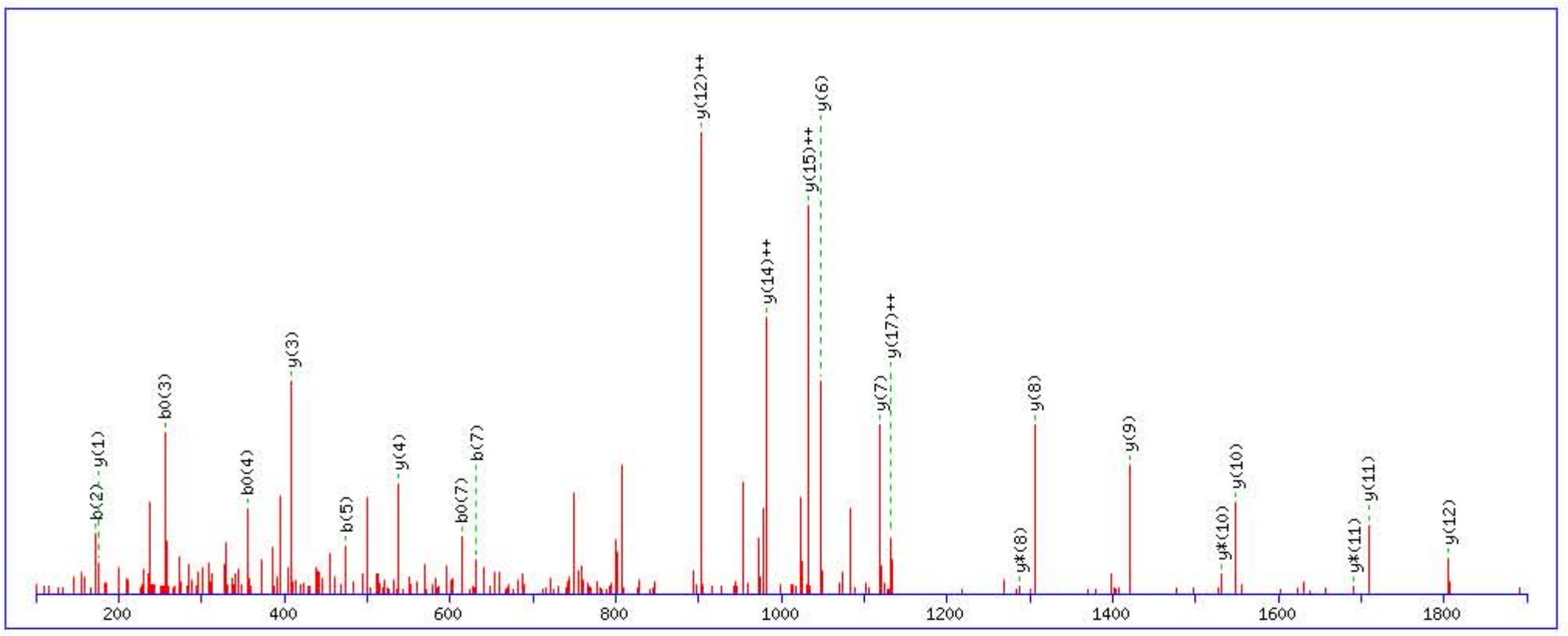
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ATTVTGTPCQDWAAQEPHR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

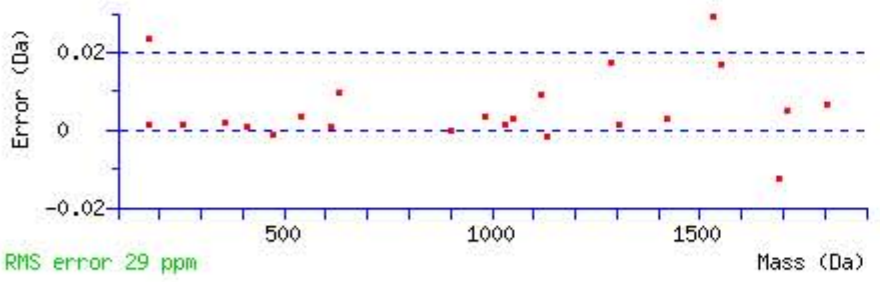
Match to Query 52747: 2436.146322 from(813.056050,3+) rtinseconds(1827) index(65280)
Title: Locus:1.1.1.1911.11 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

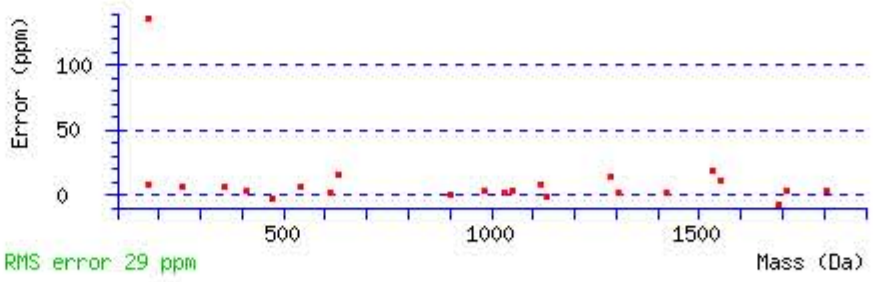
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2436.131470
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q15 : Biotin:Thermo-21345 (Q)
**Ions Score:** 61 **Expect:** 1.3e-005
**Matches :** 23/190 fragment ions using 36 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 19 |
| 2 | **173.092069** | 87.049672 | | | 155.081504 | 78.044390 | T | 2366.101616 | 1183.554446 | 2349.075067 | 1175.041171 | 2348.091051 | 1174.549163 | 18 |
| 3 | 274.139748 | 137.573512 | | | 256.129183 | 128.568230 | T | 2265.053937 | 1133.030606 | 2248.027388 | 1124.517332 | 2247.043372 | 1124.025324 | 17 |
| 4 | 373.208162 | 187.107719 | | | 355.197597 | 178.102437 | V | 2164.006258 | 1082.506767 | 2146.979709 | 1073.993492 | 2145.995693 | 1073.501484 | 16 |
| 5 | **474.255841** | 237.631559 | | | 456.245276 | 228.626276 | T | 2064.937844 | 1032.972560 | 2047.911295 | 1024.459285 | 2046.927279 | 1023.967277 | 15 |
| 6 | 531.277305 | 266.142291 | | | 513.266740 | 257.137008 | G | 1963.890165 | 982.448721 | 1946.863616 | 973.935446 | 1945.879600 | 973.443438 | 14 |
| 7 | **632.324984** | 316.666130 | | | 614.314419 | 307.660848 | T | 1906.868701 | 953.937989 | 1889.842152 | 945.424714 | 1888.858136 | 944.932706 | 13 |
| 8 | 729.377748 | 365.192512 | | | 711.367183 | 356.187230 | P | *1805.821022* | 903.414149 | 1788.794473 | 894.900875 | 1787.810457 | 894.408867 | 12 |
| 9 | 889.408397 | 445.207837 | | | 871.397832 | 436.202554 | C | *1708.768258* | 854.887767 | 1691.741709 | 846.374493 | 1690.757693 | 845.882485 | 11 |
| 10 | 1017.466975 | 509.237126 | 1000.440426 | 500.723851 | 999.456410 | 500.231843 | Q | *1548.737609* | 774.872443 | 1531.711060 | 766.359168 | 1530.727044 | 765.867160 | 10 |
| 11 | 1132.493918 | 566.750597 | 1115.467369 | 558.237323 | 1114.483353 | 557.745315 | D | *1420.679031* | 710.843154 | 1403.652482 | 702.329879 | 1402.668466 | 701.837871 | 9 |
| 12 | 1318.573231 | 659.790254 | 1301.546682 | 651.276979 | 1300.562666 | 650.784971 | W | *1305.652088* | 653.329682 | 1288.625539 | 644.816408 | 1287.641523 | 644.324400 | 8 |
| 13 | 1389.610345 | 695.308811 | 1372.583796 | 686.795536 | 1371.599780 | 686.303528 | A | *1119.572775* | 560.290026 | 1102.546226 | 551.776751 | 1101.562210 | 551.284743 | 7 |
| 14 | 1460.647459 | 730.827368 | 1443.620910 | 722.314093 | 1442.636894 | 721.822085 | A | *1048.535661* | 524.771469 | 1031.509112 | 516.258194 | 1030.525096 | 515.766186 | 6 |
| 15 | 1899.872785 | 950.440031 | 1882.846236 | 941.926756 | 1881.862220 | 941.434748 | Q | 977.498547 | 489.252912 | 960.471998 | 480.739637 | 959.487982 | 480.247629 | 5 |
| 16 | 2028.915378 | 1014.961327 | 2011.888829 | 1006.448053 | 2010.904813 | 1005.956045 | E | *538.273221* | 269.640249 | 521.246672 | 261.126974 | 520.262656 | 260.634966 | 4 |
| 17 | 2125.968142 | 1063.487709 | 2108.941593 | 1054.974434 | 2107.957577 | 1054.482427 | P | *409.230628* | 205.118952 | 392.204079 | 196.605677 | | | 3 |
| 18 | 2263.027054 | 1132.017165 | 2246.000505 | 1123.503890 | 2245.016489 | 1123.011883 | H | 312.177864 | 156.592570 | 295.151315 | 148.079295 | | | 2 |
| 19 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 61.1 | 2436.131470 | 0.014852 | ATTVTGTPCQDWAAQEPHR |
| 25.8 | 2436.131470 | 0.014852 | ATTVTGTPCQDWAAQEPHR |

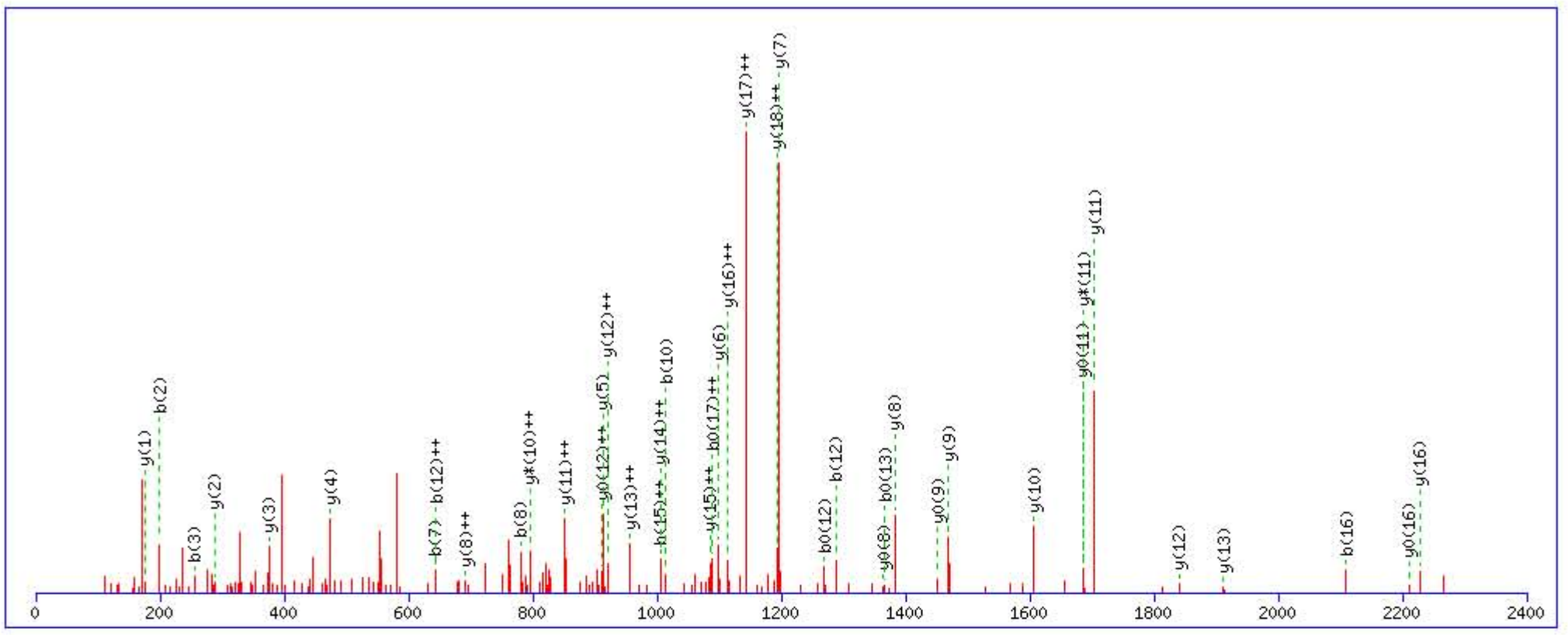
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VVGGCVAHPHSWPWQVSLR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

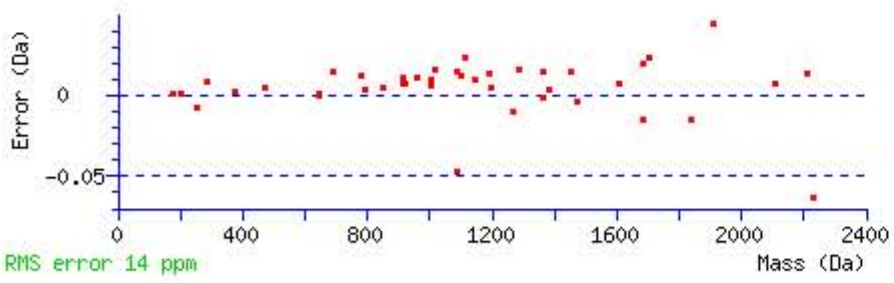
Match to Query 53789: 2482.274382 from(828.432070,3+) rtinseconds(2201) index(67629)
Title: Locus:1.1.1.2041.10 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

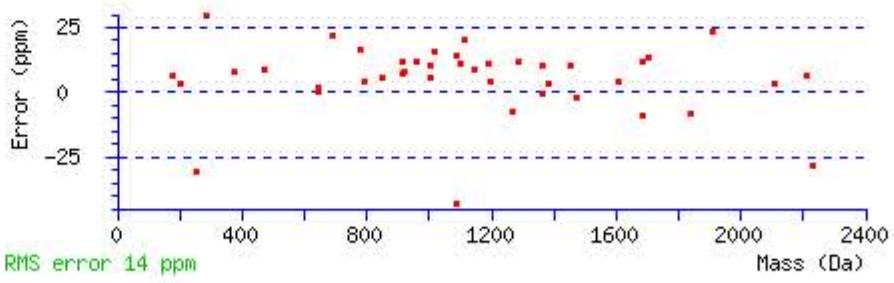
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2482.251480
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q15 : Biotin:Thermo-21345 (Q)
**Ions Score:** 62 **Expect:** 1.8e-005
**Matches :** 42/164 fragment ions using 101 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 19 |
| 2 | **199.144104** | 100.075690 | | | | | V | 2384.190309 | 1192.598792 | 2367.163760 | 1184.085518 | 2366.179744 | 1183.593510 | 18 |
| 3 | **256.165568** | 128.586422 | | | | | G | 2285.121895 | 1143.064585 | 2268.095346 | 1134.551311 | 2267.111330 | 1134.059303 | 17 |
| 4 | 313.187032 | 157.097154 | | | | | G | *2228.100431* | 1114.553853 | 2211.073882 | 1106.040579 | 2210.089866 | 1105.548571 | 16 |
| 5 | 473.217681 | 237.112479 | | | | | C | 2171.078967 | 1086.043121 | 2154.052418 | 1077.529847 | 2153.068402 | 1077.037839 | 15 |
| 6 | 572.286095 | 286.646686 | | | | | V | 2011.048318 | 1006.027797 | 1994.021769 | 997.514523 | 1993.037753 | 997.022515 | 14 |
| 7 | **643.323209** | 322.165243 | | | | | A | *1911.979904* | 956.493590 | 1894.953355 | 947.980316 | 1893.969339 | 947.488308 | 13 |
| 8 | **780.382121** | 390.694699 | | | | | H | *1840.942790* | 920.975033 | 1823.916241 | 912.461759 | 1822.932225 | 911.969751 | 12 |
| 9 | 877.434885 | 439.221081 | | | | | P | *1703.883878* | 852.445577 | 1686.857329 | 843.932303 | 1685.873313 | 843.440295 | 11 |
| 10 | **1014.493797** | 507.750537 | | | | | H | *1606.831114* | 803.919195 | 1589.804565 | 795.405921 | 1588.820549 | 794.913913 | 10 |
| 11 | 1101.525825 | 551.266550 | | | 1083.515260 | 542.261268 | S | *1469.772202* | 735.389739 | 1452.745653 | 726.876465 | 1451.761637 | 726.384457 | 9 |
| 12 | **1287.605138** | **644.306207** | | | 1269.594573 | 635.300924 | W | *1382.740174* | 691.873725 | 1365.713625 | 683.360451 | 1364.729609 | 682.868443 | 8 |
| 13 | 1384.657902 | 692.832589 | | | 1366.647337 | 683.827306 | P | *1196.660861* | 598.834069 | 1179.634312 | 590.320794 | 1178.650296 | 589.828786 | 7 |
| 14 | 1570.737215 | 785.872245 | | | 1552.726650 | 776.866963 | W | *1099.608097* | 550.307687 | 1082.581548 | 541.794412 | 1081.597532 | 541.302404 | 6 |
| 15 | 2009.962541 | **1005.484909** | 1992.935992 | 996.971634 | 1991.951976 | 996.479626 | Q | *913.528784* | 457.268030 | 896.502235 | 448.754756 | 895.518219 | 448.262748 | 5 |
| 16 | **2109.030955** | 1055.019115 | 2092.004406 | 1046.505841 | 2091.020390 | 1046.013833 | V | *474.303458* | 237.655367 | 457.276909 | 229.142092 | 456.292893 | 228.650084 | 4 |
| 17 | 2196.062983 | 1098.535129 | 2179.036434 | 1090.021855 | 2178.052418 | 1089.529847 | S | *375.235044* | 188.121160 | 358.208495 | 179.607886 | 357.224479 | 179.115878 | 3 |
| 18 | 2309.147047 | 1155.077161 | 2292.120498 | 1146.563887 | 2291.136482 | 1146.071879 | L | *288.203016* | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 19 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 62.3 | 2482.251480 | 0.022902 | VVGGCVAHPHSWPWQVSLR |

**Mascot:** http://www.matrixscience.com/

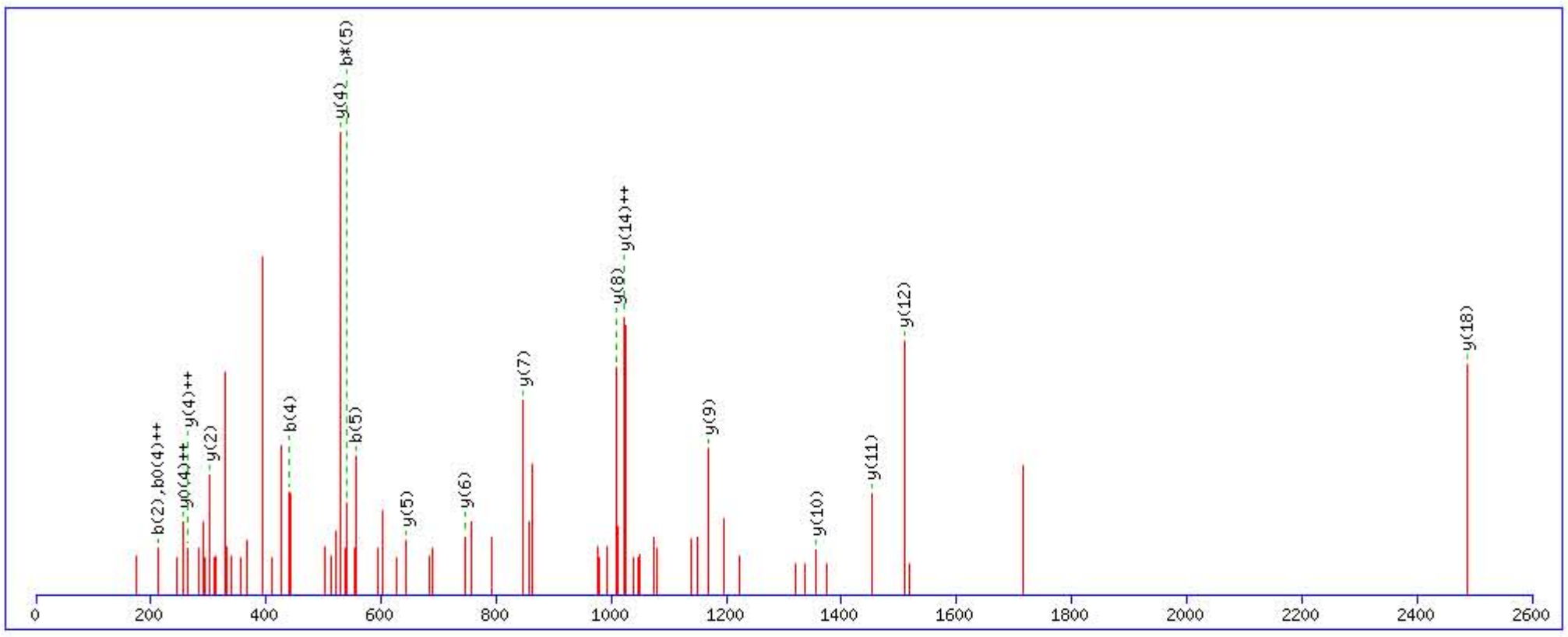
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NPDNDPQGPWCYTTDPEKR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

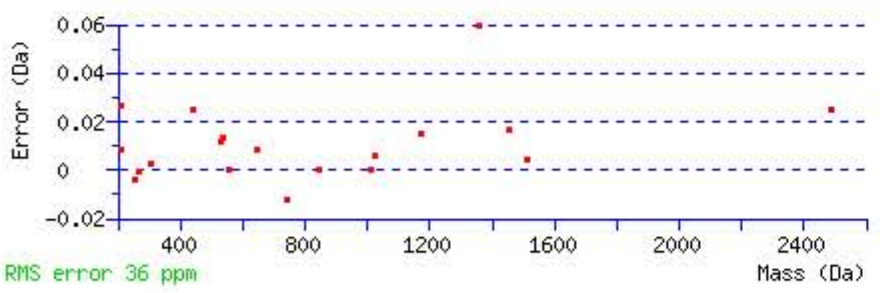
Match to Query 55507: 2600.161812 from(867.727880,3+) rtinseconds(1946) index(66095)
Title: Locus:1.1.1.1952.25 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

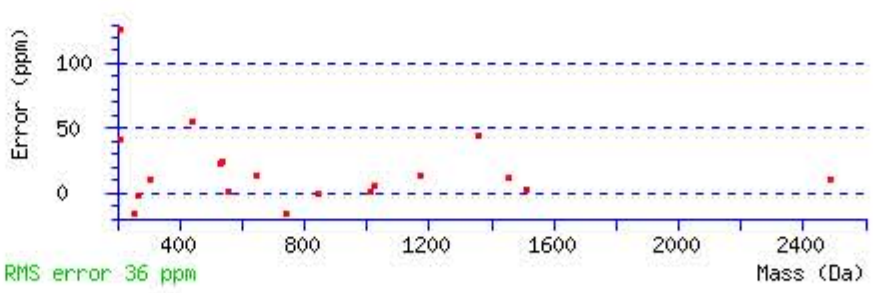
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2600.142410
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 57 **Expect:** 1.8e-005
**Matches :** 19/208 fragment ions using 37 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 19 |
| 2 | **212.102967** | 106.555121 | 195.076418 | 98.041847 | | | P | *2487.106759* | 1244.057017 | 2470.080210 | 1235.543743 | 2469.096194 | 1235.051735 | 18 |
| 3 | 327.129910 | 164.068593 | 310.103361 | 155.555319 | 309.119345 | 155.063311 | D | 2390.053995 | 1195.530635 | 2373.027446 | 1187.017361 | 2372.043430 | 1186.525353 | 17 |
| 4 | **441.172837** | 221.090057 | 424.146288 | 212.576782 | 423.162272 | 212.084774 | N | 2275.027052 | 1138.017164 | 2258.000503 | 1129.503889 | 2257.016487 | 1129.011881 | 16 |
| 5 | **556.199780** | 278.603528 | 539.173231 | 270.090254 | 538.189215 | 269.598246 | D | 2160.984125 | 1080.995700 | 2143.957576 | 1072.482426 | 2142.973560 | 1071.990418 | 15 |
| 6 | 653.252544 | 327.129910 | 636.225995 | 318.616636 | 635.241979 | 318.124628 | P | 2045.957182 | 1023.482229 | 2028.930633 | 1014.968955 | 2027.946617 | 1014.476946 | 14 |
| 7 | 1092.477870 | 546.742573 | 1075.451321 | 538.229299 | 1074.467305 | 537.737290 | Q | 1948.904418 | 974.955847 | 1931.877869 | 966.442572 | 1930.893853 | 965.950564 | 13 |
| 8 | 1149.499334 | 575.253305 | 1132.472785 | 566.740030 | 1131.488769 | 566.248022 | G | *1509.679092* | 755.343184 | 1492.652543 | 746.829910 | 1491.668527 | 746.337902 | 12 |
| 9 | 1246.552098 | 623.779687 | 1229.525549 | 615.266413 | 1228.541533 | 614.774404 | P | *1452.657628* | 726.832452 | 1435.631079 | 718.319178 | 1434.647063 | 717.827170 | 11 |
| 10 | 1432.631411 | 716.819343 | 1415.604862 | 708.306069 | 1414.620846 | 707.814061 | W | *1355.604864* | 678.306070 | 1338.578315 | 669.792796 | 1337.594299 | 669.300788 | 10 |
| 11 | 1592.662060 | 796.834668 | 1575.635511 | 788.321394 | 1574.651495 | 787.829385 | C | *1169.525551* | 585.266414 | 1152.499002 | 576.753139 | 1151.514986 | 576.261131 | 9 |
| 12 | 1755.725389 | 878.366333 | 1738.698840 | 869.853058 | 1737.714824 | 869.361050 | Y | *1009.494902* | 505.251089 | 992.468353 | 496.737815 | 991.484337 | 496.245807 | 8 |
| 13 | 1856.773068 | 928.890172 | 1839.746519 | 920.376898 | 1838.762503 | 919.884889 | T | *846.431573* | 423.719425 | 829.405024 | 415.206150 | 828.421008 | 414.714142 | 7 |
| 14 | 1957.820747 | 979.414012 | 1940.794198 | 970.900737 | 1939.810182 | 970.408729 | T | *745.383894* | 373.195585 | 728.357345 | 364.682311 | 727.373329 | 364.190303 | 6 |
| 15 | 2072.847690 | 1036.927483 | 2055.821141 | 1028.414208 | 2054.837125 | 1027.922200 | D | *644.336215* | 322.671746 | 627.309666 | 314.158471 | 626.325650 | 313.666463 | 5 |
| 16 | 2169.900454 | 1085.453865 | 2152.873905 | 1076.940590 | 2151.889889 | 1076.448582 | P | *529.309272* | 265.158274 | 512.282723 | 256.645000 | 511.298707 | 256.152992 | 4 |
| 17 | 2298.943047 | 1149.975161 | 2281.916498 | 1141.461887 | 2280.932482 | 1140.969879 | E | 432.256508 | 216.631892 | 415.229959 | 208.118618 | 414.245943 | 207.626610 | 3 |
| 18 | 2427.038010 | 1214.022643 | 2410.011461 | 1205.509368 | 2409.027445 | 1205.017360 | K | *303.213915* | 152.110595 | 286.187366 | 143.597321 | | | 2 |
| 19 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 56.6 | 2600.142410 | 0.019402 | NPDNDPQGPWCYTTDPEKR |

**Mascot:** http://www.matrixscience.com/

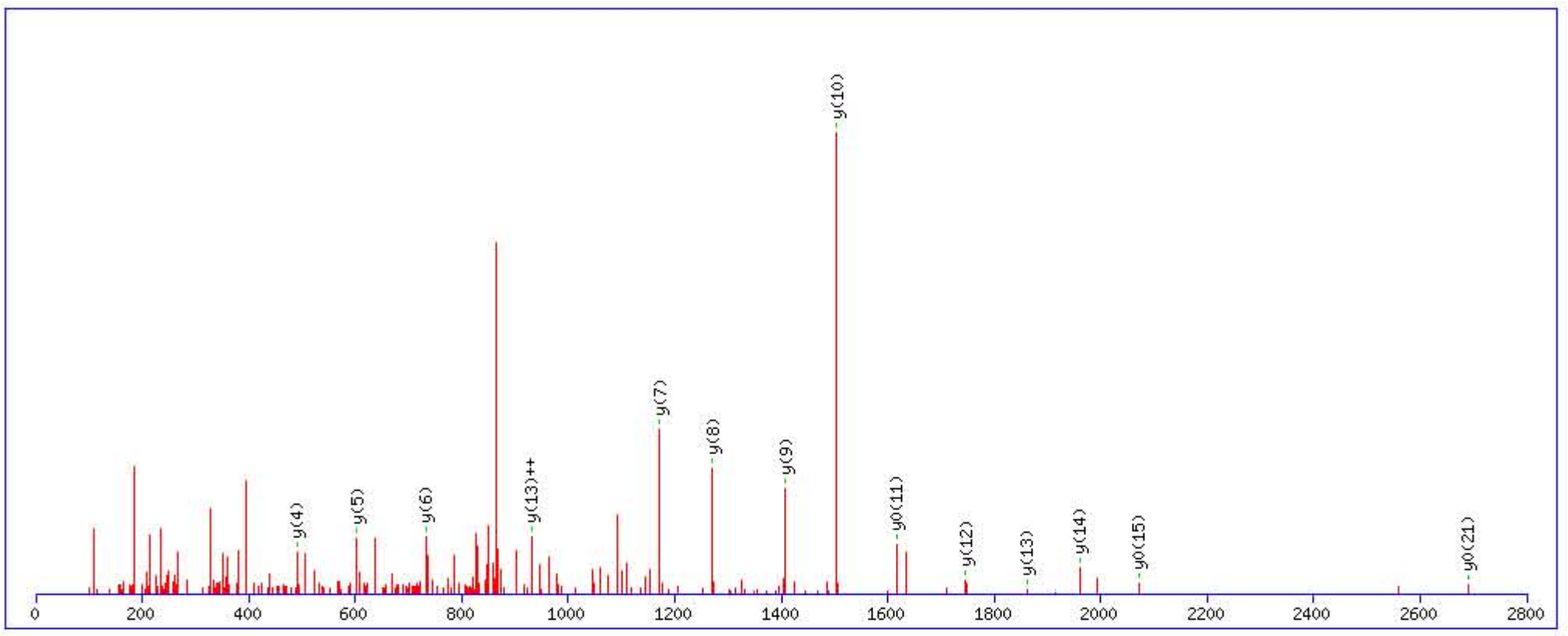
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

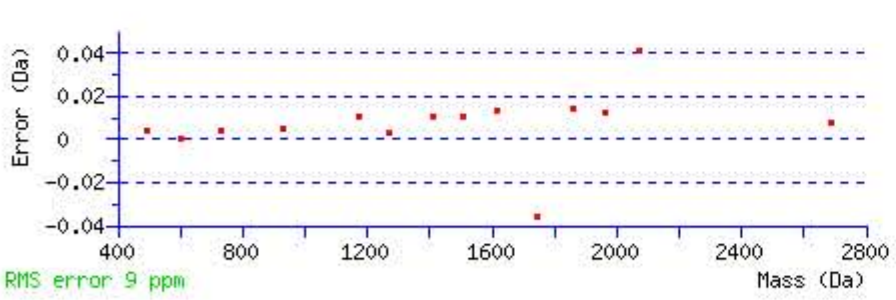
Match to Query 57673: 2806.495776 from(702.631220,4+) rtinseconds(2043) index(66669)
Title: Locus:1.1.1.1986.12 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

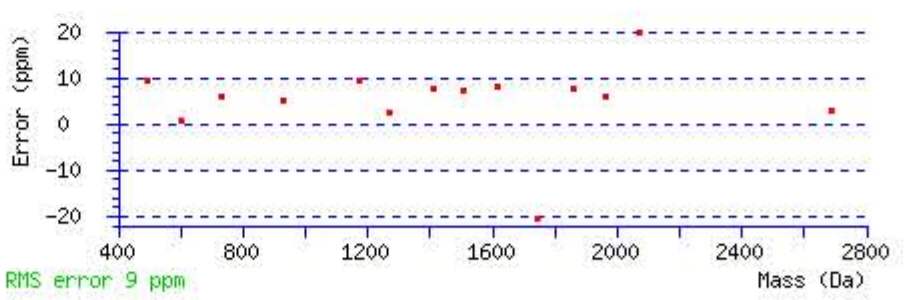
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2806.479965
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q16 : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 2.7e-005
**Matches :** 14/224 fragment ions using 22 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 22 |
| 2 | 213.159754 | 107.083515 | | | | | I | 2708.418847 | 1354.713061 | 2691.392298 | 1346.199787 | 2690.408282 | 1345.707779 | 21 |
| 3 | 326.243818 | 163.625547 | | | | | L | 2595.334783 | 1298.171029 | 2578.308234 | 1289.657755 | 2577.324218 | 1289.165747 | 20 |
| 4 | 383.265282 | 192.136279 | | | | | G | 2482.250719 | 1241.628997 | 2465.224170 | 1233.115723 | 2464.240154 | 1232.623715 | 19 |
| 5 | 454.302396 | 227.654836 | | | | | A | 2425.229255 | 1213.118265 | 2408.202706 | 1204.604991 | 2407.218690 | 1204.112983 | 18 |
| 6 | 591.361308 | 296.184292 | | | | | H | 2354.192141 | 1177.599708 | 2337.165592 | 1169.086434 | 2336.181576 | 1168.594426 | 17 |
| 7 | 719.419886 | 360.213581 | 702.393337 | 351.700307 | | | Q | 2217.133229 | 1109.070252 | 2200.106680 | 1100.556978 | 2199.122664 | 1100.064970 | 16 |
| 8 | 848.462479 | 424.734878 | 831.435930 | 416.221603 | 830.451914 | 415.729595 | E | 2089.074651 | 1045.040963 | 2072.048102 | 1036.527689 | 2071.064086 | 1036.035681 | 15 |
| 9 | 947.530893 | 474.269085 | 930.504344 | 465.755810 | 929.520328 | 465.263802 | V | *1960.032058* | 980.519667 | 1943.005509 | 972.006393 | 1942.021493 | 971.514385 | 14 |
| 10 | 1061.573820 | 531.290548 | 1044.547271 | 522.777274 | 1043.563255 | 522.285266 | N | *1860.963644* | 930.985460 | 1843.937095 | 922.472186 | 1842.953079 | 921.980178 | 13 |
| 11 | 1174.657884 | 587.832580 | 1157.631335 | 579.319306 | 1156.647319 | 578.827297 | L | *1746.920717* | 873.963997 | 1729.894168 | 865.450722 | 1728.910152 | 864.958714 | 12 |
| 12 | 1303.700477 | 652.353877 | 1286.673928 | 643.840602 | 1285.689912 | 643.348594 | E | 1633.836653 | 817.421965 | 1616.810104 | 808.908690 | 1615.826088 | 808.416682 | 11 |
| 13 | 1400.753241 | 700.880259 | 1383.726692 | 692.366984 | 1382.742676 | 691.874976 | P | *1504.794060* | 752.900668 | 1487.767511 | 744.387394 | 1486.783495 | 743.895386 | 10 |
| 14 | 1537.812153 | 769.409715 | 1520.785604 | 760.896440 | 1519.801588 | 760.404432 | H | *1407.741296* | 704.374286 | 1390.714747 | 695.861012 | 1389.730731 | 695.369004 | 9 |
| 15 | 1636.880567 | 818.943922 | 1619.854018 | 810.430647 | 1618.870002 | 809.938639 | V | *1270.682384* | 635.844830 | 1253.655835 | 627.331556 | 1252.671819 | 626.839548 | 8 |
| 16 | 2076.105893 | 1038.556584 | 2059.079344 | 1030.043310 | 2058.095328 | 1029.551302 | Q | *1171.613970* | 586.310623 | 1154.587421 | 577.797349 | 1153.603405 | 577.305341 | 7 |
| 17 | 2205.148486 | 1103.077881 | 2188.121937 | 1094.564606 | 2187.137921 | 1094.072598 | E | *732.388644* | 366.697960 | 715.362095 | 358.184686 | 714.378079 | 357.692678 | 6 |
| 18 | 2318.232550 | 1159.619913 | 2301.206001 | 1151.106638 | 2300.221985 | 1150.614631 | I | *603.346051* | 302.176664 | 586.319502 | 293.663389 | 585.335486 | 293.171381 | 5 |
| 19 | 2447.275143 | 1224.141210 | 2430.248594 | 1215.627935 | 2429.264578 | 1215.135927 | E | *490.261987* | 245.634631 | 473.235438 | 237.121357 | 472.251422 | 236.629349 | 4 |
| 20 | 2546.343557 | 1273.675417 | 2529.317008 | 1265.162142 | 2528.332992 | 1264.670134 | V | 361.219394 | 181.113335 | 344.192845 | 172.600060 | 343.208829 | 172.108052 | 3 |
| 21 | 2633.375585 | 1317.191431 | 2616.349036 | 1308.678156 | 2615.365020 | 1308.186148 | S | 262.150980 | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 22 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.6 | 2806.479965 | 0.015811 | VILGAHQEVNLEPHVQEIEVSR |

**Mascot:** http://www.matrixscience.com/

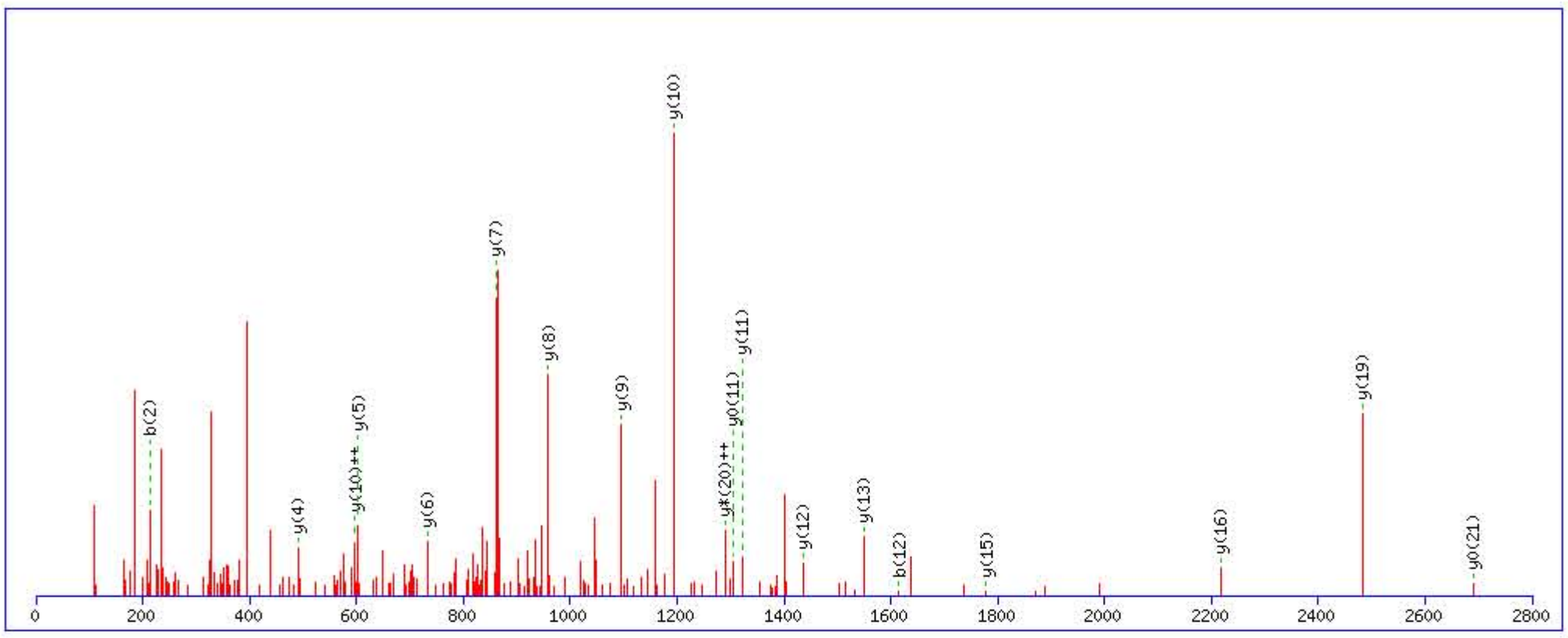
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

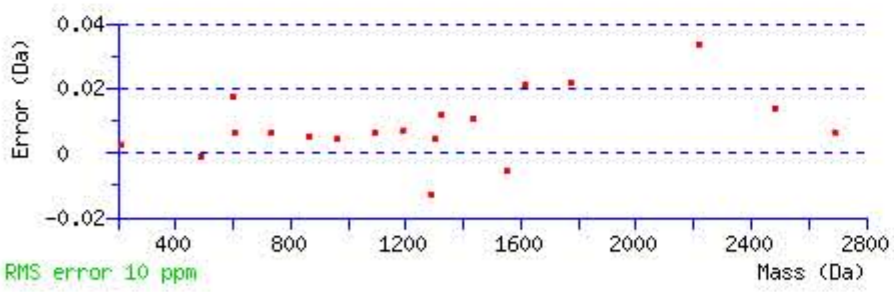
Match to Query 57675: 2806.496136 from(702.631310,4+) rtinseconds(2091) index(66945)
Title: Locus:1.1.1.2003.14 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

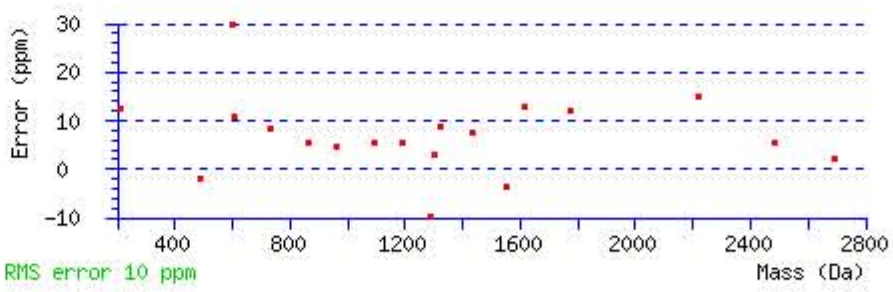
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2806.479965
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 66 **Expect:** 4.6e-006
**Matches :** 19/224 fragment ions using 40 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 22 |
| 2 | **213.159754** | 107.083515 | | | | | I | 2708.418847 | 1354.713061 | 2691.392298 | 1346.199787 | 2690.408282 | 1345.707779 | 21 |
| 3 | 326.243818 | 163.625547 | | | | | L | 2595.334783 | 1298.171029 | 2578.308234 | 1289.657755 | 2577.324218 | 1289.165747 | 20 |
| 4 | 383.265282 | 192.136279 | | | | | G | *2482.250719* | 1241.628997 | 2465.224170 | 1233.115723 | 2464.240154 | 1232.623715 | 19 |
| 5 | 454.302396 | 227.654836 | | | | | A | 2425.229255 | 1213.118265 | 2408.202706 | 1204.604991 | 2407.218690 | 1204.112983 | 18 |
| 6 | 591.361308 | 296.184292 | | | | | H | 2354.192141 | 1177.599708 | 2337.165592 | 1169.086434 | 2336.181576 | 1168.594426 | 17 |
| 7 | 1030.586634 | 515.796955 | 1013.560085 | 507.283681 | | | Q | *2217.133229* | 1109.070252 | 2200.106680 | 1100.556978 | 2199.122664 | 1100.064970 | 16 |
| 8 | 1159.629227 | 580.318252 | 1142.602678 | 571.804977 | 1141.618662 | 571.312969 | E | *1777.907903* | 889.457590 | 1760.881354 | 880.944315 | 1759.897338 | 880.452307 | 15 |
| 9 | 1258.697641 | 629.852459 | 1241.671092 | 621.339184 | 1240.687076 | 620.847176 | V | 1648.865310 | 824.936293 | 1631.838761 | 816.423019 | 1630.854745 | 815.931011 | 14 |
| 10 | 1372.740568 | 686.873922 | 1355.714019 | 678.360648 | 1354.730003 | 677.868640 | N | *1549.796896* | 775.402086 | 1532.770347 | 766.888812 | 1531.786331 | 766.396804 | 13 |
| 11 | 1485.824632 | 743.415954 | 1468.798083 | 734.902680 | 1467.814067 | 734.410672 | L | *1435.753969* | 718.380623 | 1418.727420 | 709.867348 | 1417.743404 | 709.375340 | 12 |
| 12 | **1614.867225** | 807.937251 | 1597.840676 | 799.423976 | 1596.856660 | 798.931968 | E | *1322.669905* | 661.838591 | 1305.643356 | 653.325316 | 1304.659340 | 652.833308 | 11 |
| 13 | 1711.919989 | 856.463633 | 1694.893440 | 847.950358 | 1693.909424 | 847.458350 | P | *1193.627312* | 597.317294 | 1176.600763 | 588.804020 | 1175.616747 | 588.312012 | 10 |
| 14 | 1848.978901 | 924.993089 | 1831.952352 | 916.479814 | 1830.968336 | 915.987806 | H | *1096.574548* | 548.790912 | 1079.547999 | 540.277638 | 1078.563983 | 539.785630 | 9 |
| 15 | 1948.047315 | 974.527296 | 1931.020766 | 966.014021 | 1930.036750 | 965.522013 | V | *959.515636* | 480.261456 | 942.489087 | 471.748182 | 941.505071 | 471.256174 | 8 |
| 16 | 2076.105893 | 1038.556584 | 2059.079344 | 1030.043310 | 2058.095328 | 1029.551302 | Q | *860.447222* | 430.727249 | 843.420673 | 422.213975 | 842.436657 | 421.721967 | 7 |
| 17 | 2205.148486 | 1103.077881 | 2188.121937 | 1094.564606 | 2187.137921 | 1094.072598 | E | *732.388644* | 366.697960 | 715.362095 | 358.184686 | 714.378079 | 357.692678 | 6 |
| 18 | 2318.232550 | 1159.619913 | 2301.206001 | 1151.106638 | 2300.221985 | 1150.614631 | I | *603.346051* | 302.176664 | 586.319502 | 293.663389 | 585.335486 | 293.171381 | 5 |
| 19 | 2447.275143 | 1224.141210 | 2430.248594 | 1215.627935 | 2429.264578 | 1215.135927 | E | *490.261987* | 245.634631 | 473.235438 | 237.121357 | 472.251422 | 236.629349 | 4 |
| 20 | 2546.343557 | 1273.675417 | 2529.317008 | 1265.162142 | 2528.332992 | 1264.670134 | V | 361.219394 | 181.113335 | 344.192845 | 172.600060 | 343.208829 | 172.108052 | 3 |
| 21 | 2633.375585 | 1317.191431 | 2616.349036 | 1308.678156 | 2615.365020 | 1308.186148 | S | 262.150980 | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 22 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 66.3 | 2806.479965 | 0.016171 | VILGAHQEVNLEPHVQEIEVSR |
| 11.4 | 2806.479965 | 0.016171 | VILGAHQEVNLEPHVQEIEVSR |

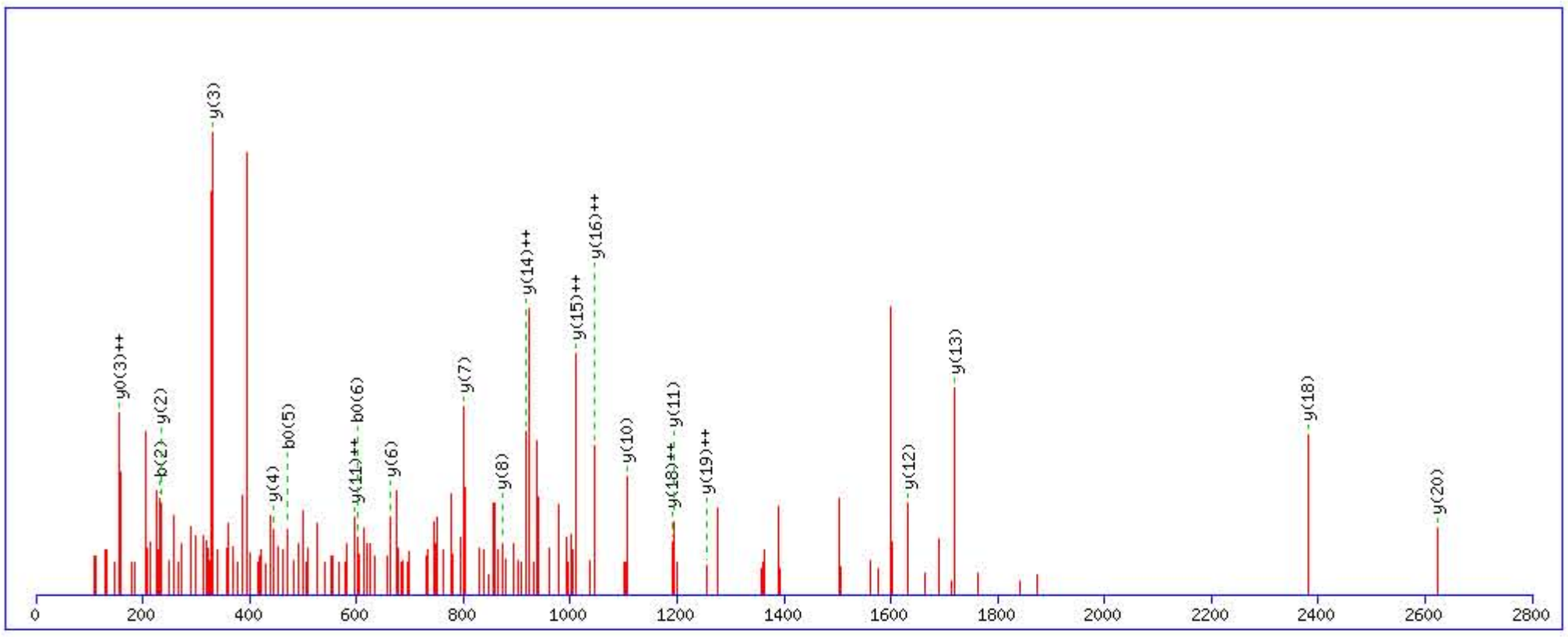
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TMSGLECQAWDSQSPHAHGYIPSK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

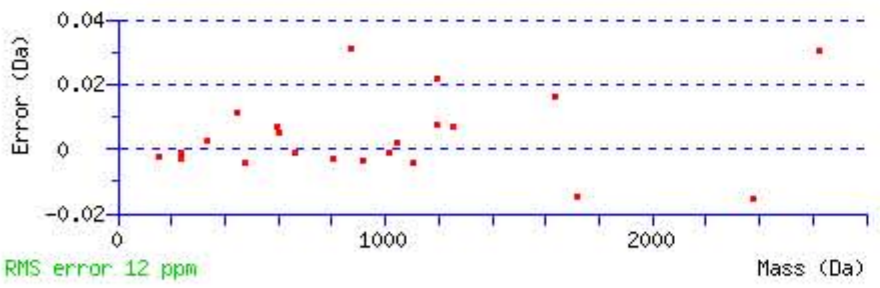
Match to Query 60084: 2997.375376 from(750.351120,4+) rtinseconds(1963) index(66237)
Title: Locus:1.1.1.1958.23 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

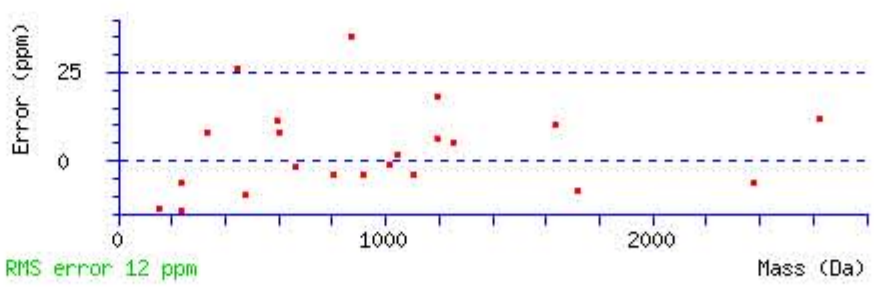
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2997.357162
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0058
**Matches :** 22/260 fragment ions using 66 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 24 |
| 2 | 233.095440 | 117.051358 | | | 215.084875 | 108.046076 | M | 2897.316768 | 1449.162022 | 2880.290219 | 1440.648748 | 2879.306203 | 1440.156740 | 23 |
| 3 | 320.127468 | 160.567372 | | | 302.116903 | 151.562089 | S | 2766.276283 | 1383.641780 | 2749.249734 | 1375.128505 | 2748.265718 | 1374.636497 | 22 |
| 4 | 377.148932 | 189.078104 | | | 359.138367 | 180.072821 | G | 2679.244255 | 1340.125766 | 2662.217706 | 1331.612491 | 2661.233690 | 1331.120483 | 21 |
| 5 | 490.232996 | 245.620136 | | | 472.222431 | 236.614853 | L | *2622.222791* | 1311.615034 | 2605.196242 | 1303.101759 | 2604.212226 | 1302.609751 | 20 |
| 6 | 619.275589 | 310.141433 | | | 601.265024 | 301.136150 | E | 2509.138727 | 1255.073002 | 2492.112178 | 1246.559727 | 2491.128162 | 1246.067719 | 19 |
| 7 | 779.306238 | 390.156757 | | | 761.295673 | 381.151475 | C | *2380.096134* | 1190.551705 | 2363.069585 | 1182.038431 | 2362.085569 | 1181.546423 | 18 |
| 8 | 907.364816 | 454.186046 | 890.338267 | 445.672772 | 889.354251 | 445.180764 | Q | 2220.065485 | 1110.536381 | 2203.038936 | 1102.023106 | 2202.054920 | 1101.531098 | 17 |
| 9 | 978.401930 | 489.704603 | 961.375381 | 481.191329 | 960.391365 | 480.699321 | A | 2092.006907 | 1046.507092 | 2074.980358 | 1037.993817 | 2073.996342 | 1037.501809 | 16 |
| 10 | 1164.481243 | 582.744260 | 1147.454694 | 574.230985 | 1146.470678 | 573.738977 | W | 2020.969793 | 1010.988535 | 2003.943244 | 1002.475260 | 2002.959228 | 1001.983252 | 15 |
| 11 | 1279.508186 | 640.257731 | 1262.481637 | 631.744457 | 1261.497621 | 631.252449 | D | 1834.890480 | 917.948878 | 1817.863931 | 909.435604 | 1816.879915 | 908.943596 | 14 |
| 12 | 1366.540214 | 683.773745 | 1349.513665 | 675.260471 | 1348.529649 | 674.768463 | S | *1719.863537* | 860.435407 | 1702.836988 | 851.922132 | 1701.852972 | 851.430124 | 13 |
| 13 | 1805.765540 | 903.386408 | 1788.738991 | 894.873134 | 1787.754975 | 894.381126 | Q | *1632.831509* | 816.919393 | 1615.804960 | 808.406118 | 1614.820944 | 807.914110 | 12 |
| 14 | 1892.797568 | 946.902422 | 1875.771019 | 938.389148 | 1874.787003 | 937.897140 | S | *1193.606183* | 597.306730 | 1176.579634 | 588.793455 | 1175.595618 | 588.301447 | 11 |
| 15 | 1989.850332 | 995.428804 | 1972.823783 | 986.915530 | 1971.839767 | 986.423522 | P | *1106.574155* | 553.790716 | 1089.547606 | 545.277441 | 1088.563590 | 544.785433 | 10 |
| 16 | 2126.909244 | 1063.958260 | 2109.882695 | 1055.444986 | 2108.898679 | 1054.952978 | H | 1009.521391 | 505.264334 | 992.494842 | 496.751059 | 991.510826 | 496.259051 | 9 |
| 17 | 2197.946358 | 1099.476817 | 2180.919809 | 1090.963543 | 2179.935793 | 1090.471535 | A | *872.462479* | 436.734878 | 855.435930 | 428.221603 | 854.451914 | 427.729595 | 8 |
| 18 | 2335.005270 | 1168.006273 | 2317.978721 | 1159.492999 | 2316.994705 | 1159.000991 | H | *801.425365* | 401.216321 | 784.398816 | 392.703046 | 783.414800 | 392.211038 | 7 |
| 19 | 2392.026734 | 1196.517005 | 2375.000185 | 1188.003731 | 2374.016169 | 1187.511723 | G | *664.366453* | 332.686865 | 647.339904 | 324.173590 | 646.355888 | 323.681582 | 6 |
| 20 | 2555.090063 | 1278.048670 | 2538.063514 | 1269.535395 | 2537.079498 | 1269.043387 | Y | 607.344989 | 304.176133 | 590.318440 | 295.662858 | 589.334424 | 295.170850 | 5 |
| 21 | 2668.174127 | 1334.590702 | 2651.147578 | 1326.077427 | 2650.163562 | 1325.585419 | I | *444.281660* | 222.644468 | 427.255111 | 214.131194 | 426.271095 | 213.639186 | 4 |
| 22 | 2765.226891 | 1383.117084 | 2748.200342 | 1374.603809 | 2747.216326 | 1374.111801 | P | *331.197596* | 166.102436 | 314.171047 | 157.589162 | 313.187031 | 157.097154 | 3 |
| 23 | 2852.258919 | 1426.633098 | 2835.232370 | 1418.119823 | 2834.248354 | 1417.627815 | S | *234.144832* | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 24 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.5 | 2997.357162 | 0.018214 | TMSGLECQAWDSQSPHAHGYIPSK |
| 16.9 | 2997.357162 | 0.018214 | TMSGLECQAWDSQSPHAHGYIPSK |

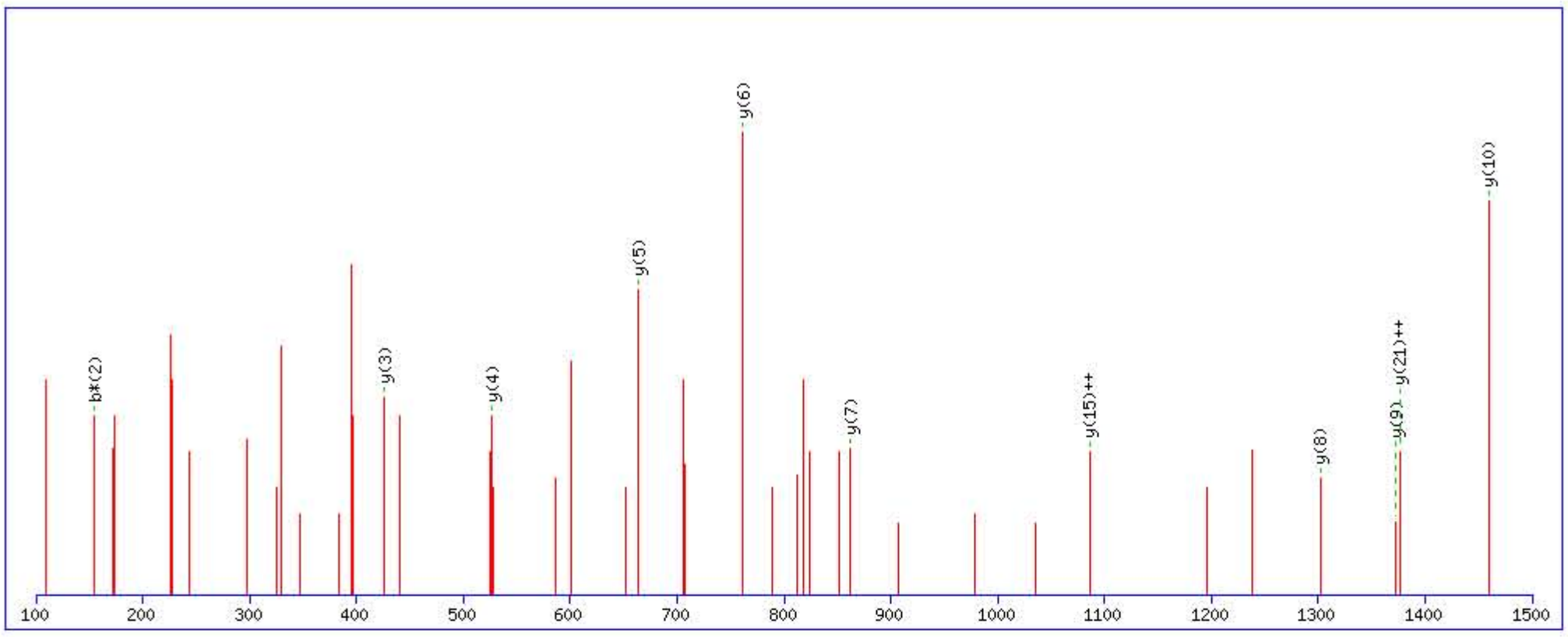
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

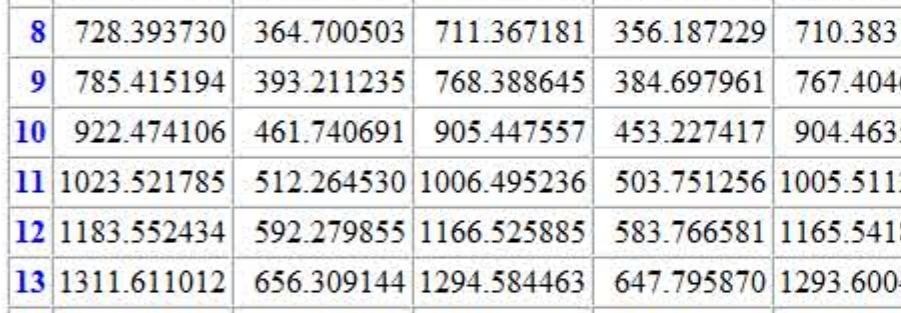
Match to Query 60818: 3092.456970 from(619.498670,5+) rtinseconds(1380) index(62652)
Title: Locus:1.1.1.1755.25 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

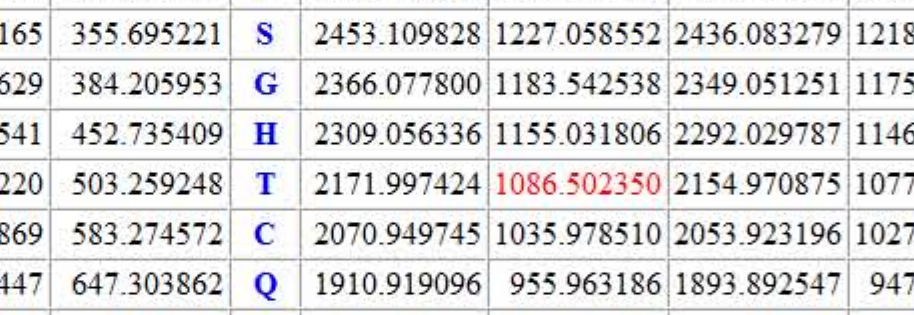
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3092.457016
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q18 : Biotin:Thermo-21345 (Q)
**Ions Score:** 29 **Expect:** 0.022
**Matches :** 11/270 fragment ions using 25 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 25 |
| 2 | 172.071667 | 86.539471 | 155.045118 | 78.026197 | | | N | 3036.442790 | 1518.725033 | 3019.416241 | 1510.211758 | 3018.432225 | 1509.719750 | 24 |
| 3 | 271.140081 | 136.073679 | 254.113532 | 127.560404 | | | V | 2922.399863 | 1461.703569 | 2905.373314 | 1453.190295 | 2904.389298 | 1452.698287 | 23 |
| 4 | 342.177195 | 171.592236 | 325.150646 | 163.078961 | | | A | 2823.331449 | 1412.169362 | 2806.304900 | 1403.656088 | 2805.320884 | 1403.164080 | 22 |
| 5 | 441.245609 | 221.126443 | 424.219060 | 212.613168 | | | V | 2752.294335 | 1376.650805 | 2735.267786 | 1368.137531 | 2734.283770 | 1367.645523 | 21 |
| 6 | 542.293288 | 271.650282 | 525.266739 | 263.137008 | 524.282723 | 262.645000 | T | 2653.225921 | 1327.116598 | 2636.199372 | 1318.603324 | 2635.215356 | 1318.111316 | 20 |
| 7 | 641.361702 | 321.184489 | 624.335153 | 312.671215 | 623.351137 | 312.179207 | V | 2552.178242 | 1276.592759 | 2535.151693 | 1268.079484 | 2534.167677 | 1267.587476 | 19 |
| 8 | 728.393730 | 364.700503 | 711.367181 | 356.187229 | 710.383165 | 355.695221 | S | 2453.109828 | 1227.058552 | 2436.083279 | 1218.545277 | 2435.099263 | 1218.053269 | 18 |
| 9 | 785.415194 | 393.211235 | 768.388645 | 384.697961 | 767.404629 | 384.205953 | G | 2366.077800 | 1183.542538 | 2349.051251 | 1175.029263 | 2348.067235 | 1174.537255 | 17 |
| 10 | 922.474106 | 461.740691 | 905.447557 | 453.227417 | 904.463541 | 452.735409 | H | 2309.056336 | 1155.031806 | 2292.029787 | 1146.518531 | 2291.045771 | 1146.026523 | 16 |
| 11 | 1023.521785 | 512.264530 | 1006.495236 | 503.751256 | 1005.511220 | 503.259248 | T | 2171.997424 | 1086.502350 | 2154.970875 | 1077.989075 | 2153.986859 | 1077.497067 | 15 |
| 12 | 1183.552434 | 592.279855 | 1166.525885 | 583.766581 | 1165.541869 | 583.274572 | C | 2070.949745 | 1035.978510 | 2053.923196 | 1027.465236 | 2052.939180 | 1026.973228 | 14 |
| 13 | 1311.611012 | 656.309144 | 1294.584463 | 647.795870 | 1293.600447 | 647.303862 | Q | 1910.919096 | 955.963186 | 1893.892547 | 947.449911 | 1892.908531 | 946.957903 | 13 |
| 14 | 1448.669924 | 724.838600 | 1431.643375 | 716.325326 | 1430.659359 | 715.833318 | H | 1782.860518 | 891.933897 | 1765.833969 | 883.420622 | 1764.849953 | 882.928614 | 12 |
| 15 | 1634.749237 | 817.878257 | 1617.722688 | 809.364982 | 1616.738672 | 808.872974 | W | 1645.801606 | 823.404441 | 1628.775057 | 814.891166 | 1627.791041 | 814.399158 | 11 |
| 16 | 1721.781265 | 861.394271 | 1704.754716 | 852.880996 | 1703.770700 | 852.388988 | S | *1459.722293* | 730.364784 | 1442.695744 | 721.851510 | 1441.711728 | 721.359502 | 10 |
| 17 | 1792.818379 | 896.912828 | 1775.791830 | 888.399553 | 1774.807814 | 887.907545 | A | *1372.690265* | 686.848770 | 1355.663716 | 678.335496 | 1354.679700 | 677.843488 | 9 |
| 18 | 2232.043705 | 1116.525490 | 2215.017156 | 1108.012216 | 2214.033140 | 1107.520208 | Q | *1301.653151* | 651.330213 | 1284.626602 | 642.816939 | 1283.642586 | 642.324931 | 8 |
| 19 | 2333.091384 | 1167.049330 | 2316.064835 | 1158.536055 | 2315.080819 | 1158.044047 | T | *862.427825* | 431.717550 | 845.401276 | 423.204276 | 844.417260 | 422.712268 | 7 |
| 20 | 2430.144148 | 1215.575712 | 2413.117599 | 1207.062437 | 2412.133583 | 1206.570429 | P | *761.380146* | 381.193711 | 744.353597 | 372.680436 | 743.369581 | 372.188428 | 6 |
| 21 | 2567.203060 | 1284.105168 | 2550.176511 | 1275.591893 | 2549.192495 | 1275.099885 | H | *664.327382* | 332.667329 | 647.300833 | 324.154054 | 646.316817 | 323.662046 | 5 |
| 22 | 2668.250739 | 1334.629007 | 2651.224190 | 1326.115733 | 2650.240174 | 1325.623725 | T | *527.268470* | 264.137873 | 510.241921 | 255.624598 | 509.257905 | 255.132590 | 4 |
| 23 | 2805.309651 | 1403.158463 | 2788.283102 | 1394.645189 | 2787.299086 | 1394.153181 | H | *426.220791* | 213.614033 | 409.194242 | 205.100759 | | | 3 |
| 24 | 2919.352578 | 1460.179927 | 2902.326029 | 1451.666652 | 2901.342013 | 1451.174644 | N | 289.161879 | 145.084577 | 272.135330 | 136.571303 | | | 2 |
| 25 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 29.2 | 3092.457016 | -0.000046 | GNVAVTVSGHTCQHWSAQTPHTHNR |
| 6.6 | 3092.457016 | -0.000046 | GNVAVTVSGHTCQHWSAQTPHTHNR |

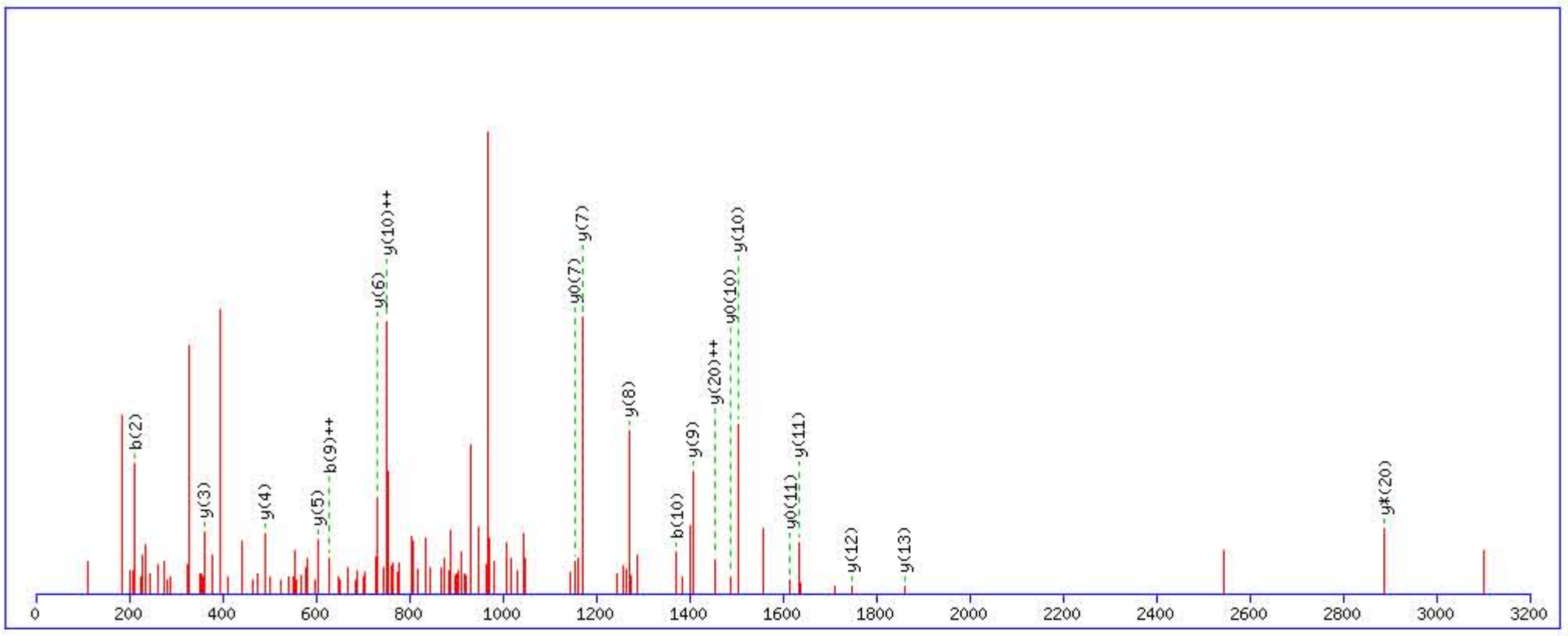
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

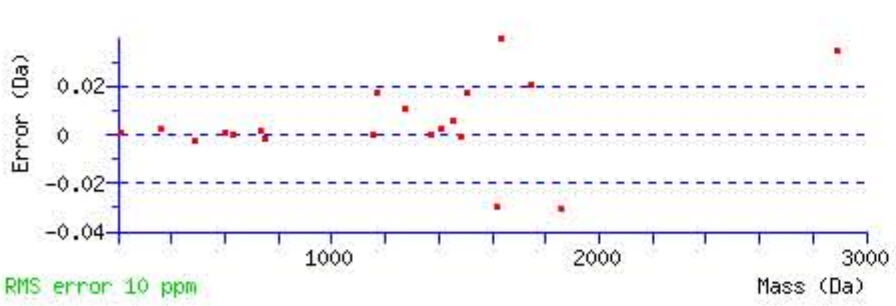
Match to Query 60947: 3117.671016 from(780.425030,4+) rtinseconds(2221) index(67736)
Title: Locus:1.1.1.2048.22 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

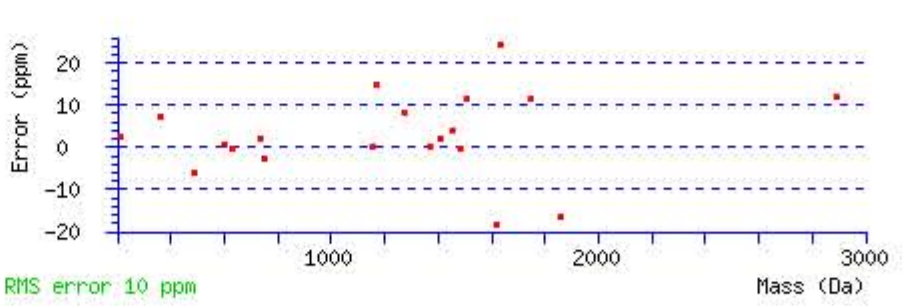
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3117.646713
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
Q16 : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.0025
**Matches :** 20/224 fragment ions using 53 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 22 |
| 2 | 213.159754 | 107.083515 | | | | | I | 3019.585595 | 1510.296435 | 3002.559046 | 1501.783161 | 3001.575030 | 1501.291153 | 21 |
| 3 | 326.243818 | 163.625547 | | | | | L | 2906.501531 | 1453.754403 | 2889.474982 | 1445.241129 | 2888.490966 | 1444.749121 | 20 |
| 4 | 383.265282 | 192.136279 | | | | | G | 2793.417467 | 1397.212371 | 2776.390918 | 1388.699097 | 2775.406902 | 1388.207089 | 19 |
| 5 | 454.302396 | 227.654836 | | | | | A | 2736.396003 | 1368.701639 | 2719.369454 | 1360.188365 | 2718.385438 | 1359.696357 | 18 |
| 6 | 591.361308 | 296.184292 | | | | | H | 2665.358889 | 1333.183082 | 2648.332340 | 1324.669808 | 2647.348324 | 1324.177800 | 17 |
| 7 | 1030.586634 | 515.796955 | 1013.560085 | 507.283681 | | | Q | 2528.299977 | 1264.653627 | 2511.273428 | 1256.140352 | 2510.289412 | 1255.648344 | 16 |
| 8 | 1159.629227 | 580.318252 | 1142.602678 | 571.804977 | 1141.618662 | 571.312969 | E | 2089.074651 | 1045.040963 | 2072.048102 | 1036.527689 | 2071.064086 | 1036.035681 | 15 |
| 9 | 1258.697641 | 629.852459 | 1241.671092 | 621.339184 | 1240.687076 | 620.847176 | V | 1960.032058 | 980.519667 | 1943.005509 | 972.006393 | 1942.021493 | 971.514385 | 14 |
| 10 | 1372.740568 | 686.873922 | 1355.714019 | 678.360648 | 1354.730003 | 677.868640 | N | *1860.963644* | 930.985460 | 1843.937095 | 922.472186 | 1842.953079 | 921.980178 | 13 |
| 11 | 1485.824632 | 743.415954 | 1468.798083 | 734.902680 | 1467.814067 | 734.410672 | L | *1746.920717* | 873.963997 | 1729.894168 | 865.450722 | 1728.910152 | 864.958714 | 12 |
| 12 | 1614.867225 | 807.937251 | 1597.840676 | 799.423976 | 1596.856660 | 798.931968 | E | *1633.836653* | 817.421965 | 1616.810104 | 808.908690 | 1615.826088 | 808.416682 | 11 |
| 13 | 1711.919989 | 856.463633 | 1694.893440 | 847.950358 | 1693.909424 | 847.458350 | P | *1504.794060* | 752.900668 | 1487.767511 | 744.387394 | 1486.783495 | 743.895386 | 10 |
| 14 | 1848.978901 | 924.993089 | 1831.952352 | 916.479814 | 1830.968336 | 915.987806 | H | *1407.741296* | 704.374286 | 1390.714747 | 695.861012 | 1389.730731 | 695.369004 | 9 |
| 15 | 1948.047315 | 974.527296 | 1931.020766 | 966.014021 | 1930.036750 | 965.522013 | V | *1270.682384* | 635.844830 | 1253.655835 | 627.331556 | 1252.671819 | 626.839548 | 8 |
| 16 | 2387.272641 | 1194.139958 | 2370.246092 | 1185.626684 | 2369.262076 | 1185.134676 | Q | *1171.613970* | 586.310623 | 1154.587421 | 577.797349 | 1153.603405 | 577.305341 | 7 |
| 17 | 2516.315234 | 1258.661255 | 2499.288685 | 1250.147980 | 2498.304669 | 1249.655973 | E | *732.388644* | 366.697960 | 715.362095 | 358.184686 | 714.378079 | 357.692678 | 6 |
| 18 | 2629.399298 | 1315.203287 | 2612.372749 | 1306.690013 | 2611.388733 | 1306.198005 | I | *603.346051* | 302.176664 | 586.319502 | 293.663389 | 585.335486 | 293.171381 | 5 |
| 19 | 2758.441891 | 1379.724584 | 2741.415342 | 1371.211309 | 2740.431326 | 1370.719301 | E | *490.261987* | 245.634631 | 473.235438 | 237.121357 | 472.251422 | 236.629349 | 4 |
| 20 | 2857.510305 | 1429.258791 | 2840.483756 | 1420.745516 | 2839.499740 | 1420.253508 | V | *361.219394* | 181.113335 | 344.192845 | 172.600060 | 343.208829 | 172.108052 | 3 |
| 21 | 2944.542333 | 1472.774805 | 2927.515784 | 1464.261530 | 2926.531768 | 1463.769522 | S | 262.150980 | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 22 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 37.7 | 3117.646713 | 0.024303 | VILGAHQEVNLEPHVQEIEVSR |

**Mascot:** http://www.matrixscience.com/

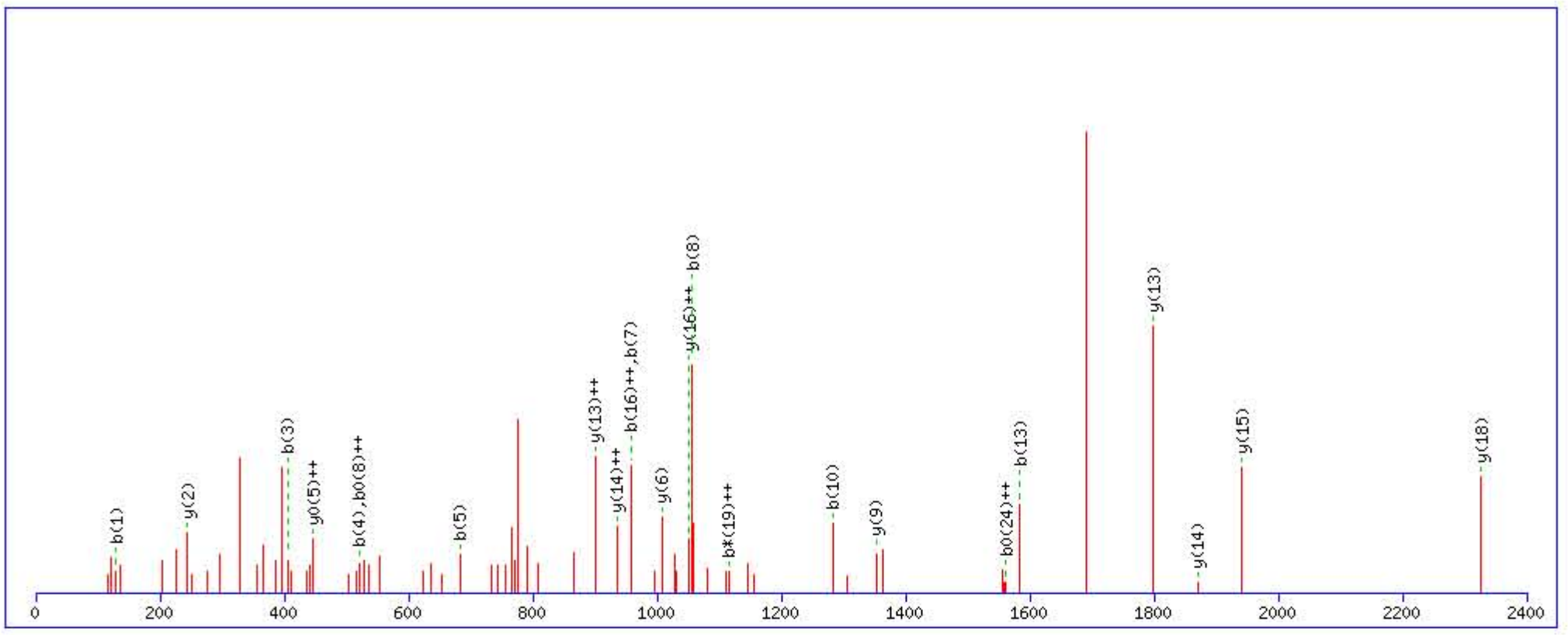
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KLYDYCDVPQCAAPSFDCGKPQVEPK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

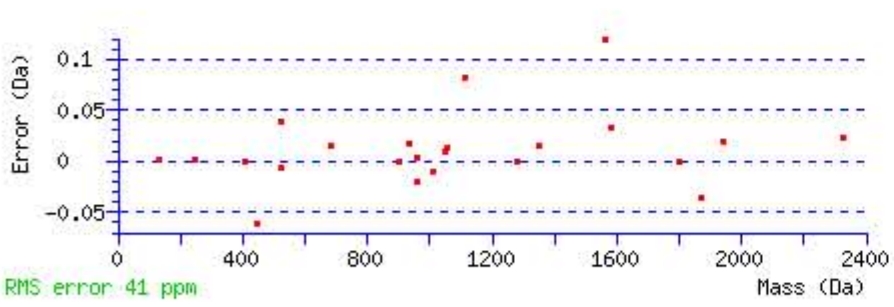
Match to Query 64791: 3382.570776 from(846.649970,4+) rtinseconds(1920) index(65869)
Title: Locus:1.1.1.1943.24 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

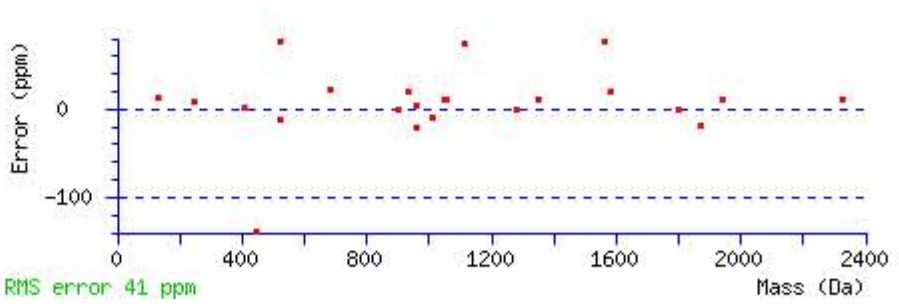
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3382.549469
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q22 : Biotin:Thermo-21345 (Q)
**Ions Score:** 29 **Expect:** 0.018
**Matches :** 23/290 fragment ions using 57 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *129.102239* | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 26 |
| 2 | 242.186303 | 121.596790 | 225.159754 | 113.083515 | | | L | 3255.461780 | 1628.234528 | 3238.435231 | 1619.721253 | 3237.451215 | 1619.229245 | 25 |
| 3 | *405.249632* | 203.128454 | 388.223083 | 194.615180 | | | Y | 3142.377716 | 1571.692496 | 3125.351167 | 1563.179221 | 3124.367151 | 1562.687213 | 24 |
| 4 | *520.276575* | 260.641926 | 503.250026 | 252.128651 | 502.266010 | 251.636643 | D | 2979.314387 | 1490.160831 | 2962.287838 | 1481.647557 | 2961.303822 | 1481.155549 | 23 |
| 5 | *683.339904* | 342.173590 | 666.313355 | 333.660316 | 665.329339 | 333.168308 | Y | 2864.287444 | 1432.647360 | 2847.260895 | 1424.134085 | 2846.276879 | 1423.642077 | 22 |
| 6 | 843.370553 | 422.188915 | 826.344004 | 413.675640 | 825.359988 | 413.183632 | C | 2701.224115 | 1351.115695 | 2684.197566 | 1342.602421 | 2683.213550 | 1342.110413 | 21 |
| 7 | *958.397496* | 479.702386 | 941.370947 | 471.189112 | 940.386931 | 470.697104 | D | 2541.193466 | 1271.100371 | 2524.166917 | 1262.587096 | 2523.182901 | 1262.095089 | 20 |
| 8 | *1057.465910* | 529.236593 | 1040.439361 | 520.723319 | 1039.455345 | 520.231311 | V | 2426.166523 | 1213.586899 | 2409.139974 | 1205.073625 | 2408.155958 | 1204.581617 | 19 |
| 9 | 1154.518674 | 577.762975 | 1137.492125 | 569.249701 | 1136.508109 | 568.757693 | P | *2327.098109* | 1164.052692 | 2310.071560 | 1155.539418 | 2309.087544 | 1155.047410 | 18 |
| 10 | *1282.577252* | 641.792264 | 1265.550703 | 633.278990 | 1264.566687 | 632.786982 | Q | 2230.045345 | 1115.526310 | 2213.018796 | 1107.013036 | 2212.034780 | 1106.521028 | 17 |
| 11 | 1442.607901 | 721.807589 | 1425.581352 | 713.294314 | 1424.597336 | 712.802306 | C | 2101.986767 | 1051.497021 | 2084.960218 | 1042.983747 | 2083.976202 | 1042.491739 | 16 |
| 12 | 1513.645015 | 757.326146 | 1496.618466 | 748.812871 | 1495.634450 | 748.320863 | A | *1941.956118* | 971.481697 | 1924.929569 | 962.968423 | 1923.945553 | 962.476415 | 15 |
| 13 | *1584.682129* | 792.844703 | 1567.655580 | 784.331428 | 1566.671564 | 783.839420 | A | *1870.919004* | 935.963140 | 1853.892455 | 927.449866 | 1852.908439 | 926.957858 | 14 |
| 14 | 1681.734893 | 841.371085 | 1664.708344 | 832.857810 | 1663.724328 | 832.365802 | P | *1799.881890* | 900.444583 | 1782.855341 | 891.931309 | 1781.871325 | 891.439301 | 13 |
| 15 | 1768.766921 | 884.887099 | 1751.740372 | 876.373824 | 1750.756356 | 875.881816 | S | 1702.829126 | 851.918201 | 1685.802577 | 843.404927 | 1684.818561 | 842.912919 | 12 |
| 16 | 1915.835335 | 958.421306 | 1898.808786 | 949.908031 | 1897.824770 | 949.416023 | F | 1615.797098 | 808.402187 | 1598.770549 | 799.888913 | 1597.786533 | 799.396905 | 11 |
| 17 | 2030.862278 | 1015.934777 | 2013.835729 | 1007.421503 | 2012.851713 | 1006.929495 | D | 1468.728684 | 734.867980 | 1451.702135 | 726.354706 | 1450.718119 | 725.862698 | 10 |
| 18 | 2190.892927 | 1095.950102 | 2173.866378 | 1087.436827 | 2172.882362 | 1086.944819 | C | *1353.701741* | 677.354509 | 1336.675192 | 668.841234 | 1335.691176 | 668.349226 | 9 |
| 19 | 2247.914391 | 1124.460834 | 2230.887842 | 1115.947559 | 2229.903826 | 1115.455551 | G | 1193.671092 | 597.339184 | 1176.644543 | 588.825910 | 1175.660527 | 588.333902 | 8 |
| 20 | 2376.009354 | 1188.508315 | 2358.982805 | 1179.995041 | 2357.998789 | 1179.503033 | K | 1136.649628 | 568.828452 | 1119.623079 | 560.315178 | 1118.639063 | 559.823170 | 7 |
| 21 | 2473.062118 | 1237.034697 | 2456.035569 | 1228.521423 | 2455.051553 | 1228.029415 | P | *1008.554665* | 504.780971 | 991.528116 | 496.267696 | 990.544100 | 495.775688 | 6 |
| 22 | 2912.287444 | 1456.647360 | 2895.260895 | 1448.134086 | 2894.276879 | 1447.642078 | Q | 911.501901 | 456.254589 | 894.475352 | 447.741314 | 893.491336 | 447.249306 | 5 |
| 23 | 3011.355858 | 1506.181567 | 2994.329309 | 1497.668293 | 2993.345293 | 1497.176285 | V | 472.276575 | 236.641925 | 455.250026 | 228.128651 | 454.266010 | 227.636643 | 4 |
| 24 | 3140.398451 | 1570.702864 | 3123.371902 | 1562.189589 | 3122.387886 | 1561.697581 | E | 373.208161 | 187.107719 | 356.181612 | 178.594444 | 355.197596 | 178.102436 | 3 |
| 25 | 3237.451215 | 1619.229246 | 3220.424666 | 1610.715971 | 3219.440650 | 1610.223963 | P | *244.165568* | 122.586422 | 227.139019 | 114.073148 | | | 2 |
| 26 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 28.8 | 3382.549469 | 0.021307 | KLYDYCDVPQCAAPSFDCGKPQVEPK |

**Mascot:** http://www.matrixscience.com/

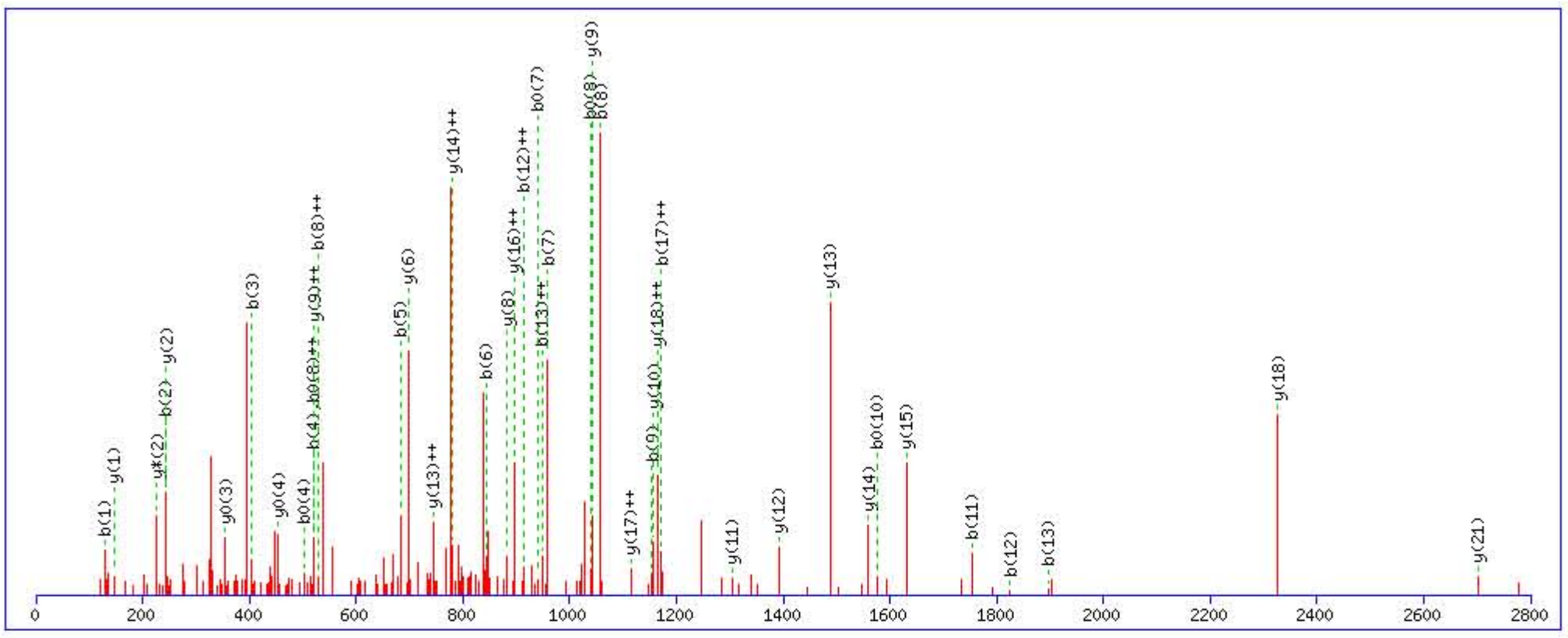
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KLYDYCDVPQCAAPSFDCGKPQVEPK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

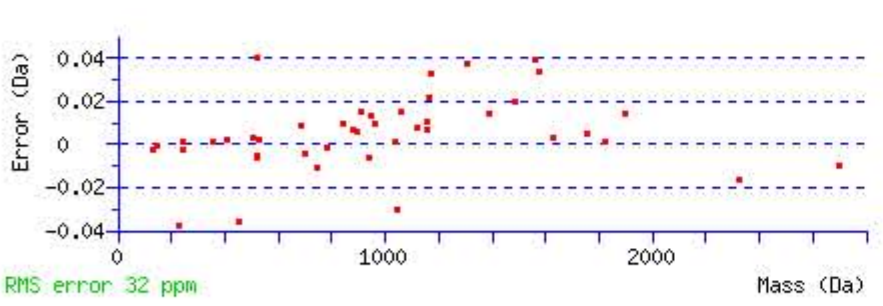
Match to Query 64792: 3382.575176 from(846.651070,4+) rtinseconds(1972) index(5503)
Title: Locus:1.1.1.1963.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

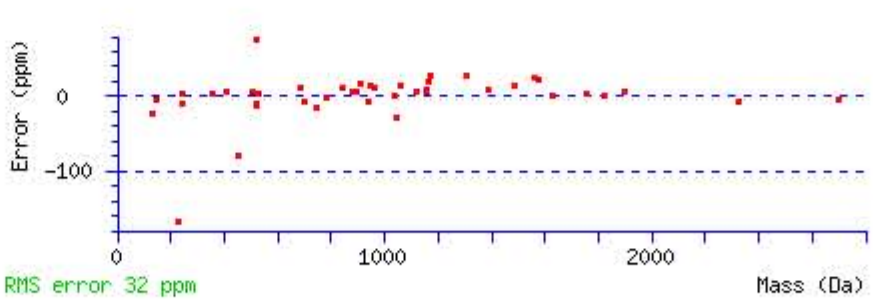
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3382.549469
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 60 **Expect:** 1.6e-005
**Matches :** 43/290 fragment ions using 103 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *129.102239* | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 26 |
| 2 | *242.186303* | 121.596790 | 225.159754 | 113.083515 | | | L | 3255.461780 | 1628.234528 | 3238.435231 | 1619.721253 | 3237.451215 | 1619.229245 | 25 |
| 3 | *405.249632* | 203.128454 | 388.223083 | 194.615180 | | | Y | 3142.377716 | 1571.692496 | 3125.351167 | 1563.179221 | 3124.367151 | 1562.687213 | 24 |
| 4 | *520.276575* | 260.641926 | 503.250026 | 252.128651 | 502.266010 | 251.636643 | D | 2979.314387 | 1490.160831 | 2962.287838 | 1481.647557 | 2961.303822 | 1481.155549 | 23 |
| 5 | *683.339904* | 342.173590 | 666.313355 | 333.660316 | 665.329339 | 333.168308 | Y | 2864.287444 | 1432.647360 | 2847.260895 | 1424.134085 | 2846.276879 | 1423.642077 | 22 |
| 6 | *843.370553* | 422.188915 | 826.344004 | 413.675640 | 825.359988 | 413.183632 | C | *2701.224115* | 1351.115695 | 2684.197566 | 1342.602421 | 2683.213550 | 1342.110413 | 21 |
| 7 | *958.397496* | 479.702386 | 941.370947 | 471.189112 | 940.386931 | 470.697104 | D | 2541.193466 | 1271.100371 | 2524.166917 | 1262.587096 | 2523.182901 | 1262.095088 | 20 |
| 8 | *1057.465910* | **529.236593** | 1040.439361 | 520.723319 | 1039.455345 | 520.231311 | V | 2426.166523 | 1213.586899 | 2409.139974 | 1205.073625 | 2408.155958 | 1204.581617 | 19 |
| 9 | *1154.518674* | 577.762975 | 1137.492125 | 569.249701 | 1136.508109 | 568.757693 | P | *2327.098109* | 1164.052692 | 2310.071560 | 1155.539418 | 2309.087544 | 1155.047410 | 18 |
| 10 | 1593.744000 | 797.375638 | 1576.717451 | 788.862364 | 1575.733435 | 788.370356 | Q | 2230.045345 | 1115.526310 | 2213.018796 | 1107.013036 | 2212.034780 | 1106.521028 | 17 |
| 11 | *1753.774649* | 877.390963 | 1736.748100 | 868.877688 | 1735.764084 | 868.385680 | C | 1790.820019 | 895.913647 | 1773.793470 | 887.400373 | 1772.809454 | 886.908365 | 16 |
| 12 | *1824.811763* | **912.909520** | 1807.785214 | 904.396245 | 1806.801198 | 903.904237 | A | *1630.789370* | 815.898323 | 1613.762821 | 807.385048 | 1612.778805 | 806.893040 | 15 |
| 13 | *1895.848877* | **948.428077** | 1878.822328 | 939.914802 | 1877.838312 | 939.422794 | A | *1559.752256* | 780.379766 | 1542.725707 | 771.866491 | 1541.741691 | 771.374483 | 14 |
| 14 | 1992.901641 | 996.954459 | 1975.875092 | 988.441184 | 1974.891076 | 987.949176 | P | *1488.715142* | 744.861209 | 1471.688593 | 736.347934 | 1470.704577 | 735.855926 | 13 |
| 15 | 2079.933669 | 1040.470472 | 2062.907120 | 1031.957198 | 2061.923104 | 1031.465190 | S | *1391.662378* | 696.334827 | 1374.635829 | 687.821552 | 1373.651813 | 687.329544 | 12 |
| 16 | 2227.002083 | 1114.004679 | 2209.975534 | 1105.491405 | 2208.991518 | 1104.999397 | F | *1304.630350* | 652.818813 | 1287.603801 | 644.305538 | 1286.619785 | 643.813530 | 11 |
| 17 | 2342.029026 | **1171.518151** | 2325.002477 | 1163.004876 | 2324.018461 | 1162.512868 | D | *1157.561936* | 579.284606 | 1140.535387 | 570.771331 | 1139.551371 | 570.279323 | 10 |
| 18 | 2502.059675 | 1251.533475 | 2485.033126 | 1243.020201 | 2484.049110 | 1242.528193 | C | *1042.534993* | 521.771135 | 1025.508444 | 513.257860 | 1024.524428 | 512.765852 | 9 |
| 19 | 2559.081139 | 1280.044207 | 2542.054590 | 1271.530933 | 2541.070574 | 1271.038925 | G | *882.504344* | 441.755810 | 865.477795 | 433.242536 | 864.493779 | 432.750528 | 8 |
| 20 | 2687.176102 | 1344.091689 | 2670.149553 | 1335.578414 | 2669.165537 | 1335.086406 | K | 825.482880 | 413.245078 | 808.456331 | 404.731804 | 807.472315 | 404.239796 | 7 |
| 21 | 2784.228866 | 1392.618071 | 2767.202317 | 1384.104796 | 2766.218301 | 1383.612788 | P | *697.387917* | 349.197597 | 680.361368 | 340.684322 | 679.377352 | 340.192314 | 6 |
| 22 | 2912.287444 | 1456.647360 | 2895.260895 | 1448.134085 | 2894.276879 | 1447.642077 | Q | 600.335153 | 300.671215 | 583.308604 | 292.157940 | 582.324588 | 291.665932 | 5 |
| 23 | 3011.355858 | 1506.181567 | 2994.329309 | 1497.668292 | 2993.345293 | 1497.176284 | V | 472.276575 | 236.641925 | 455.250026 | 228.128651 | 454.266010 | 227.636643 | 4 |
| 24 | 3140.398451 | 1570.702863 | 3123.371902 | 1562.189589 | 3122.387886 | 1561.697581 | E | 373.208161 | 187.107719 | 356.181612 | 178.594444 | 355.197596 | 178.102436 | 3 |
| 25 | 3237.451215 | 1619.229245 | 3220.424666 | 1610.715971 | 3219.440650 | 1610.223963 | P | *244.165568* | 122.586422 | 227.139019 | 114.073148 | | | 2 |
| 26 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 59.6 | 3382.549469 | 0.025707 | KLYDYCDVPQCAAPSFDCGKPQVEPK |
| 8.5 | 3382.549469 | 0.025707 | KLYDYCDVPQCAAPSFDCGKPQVEPK |

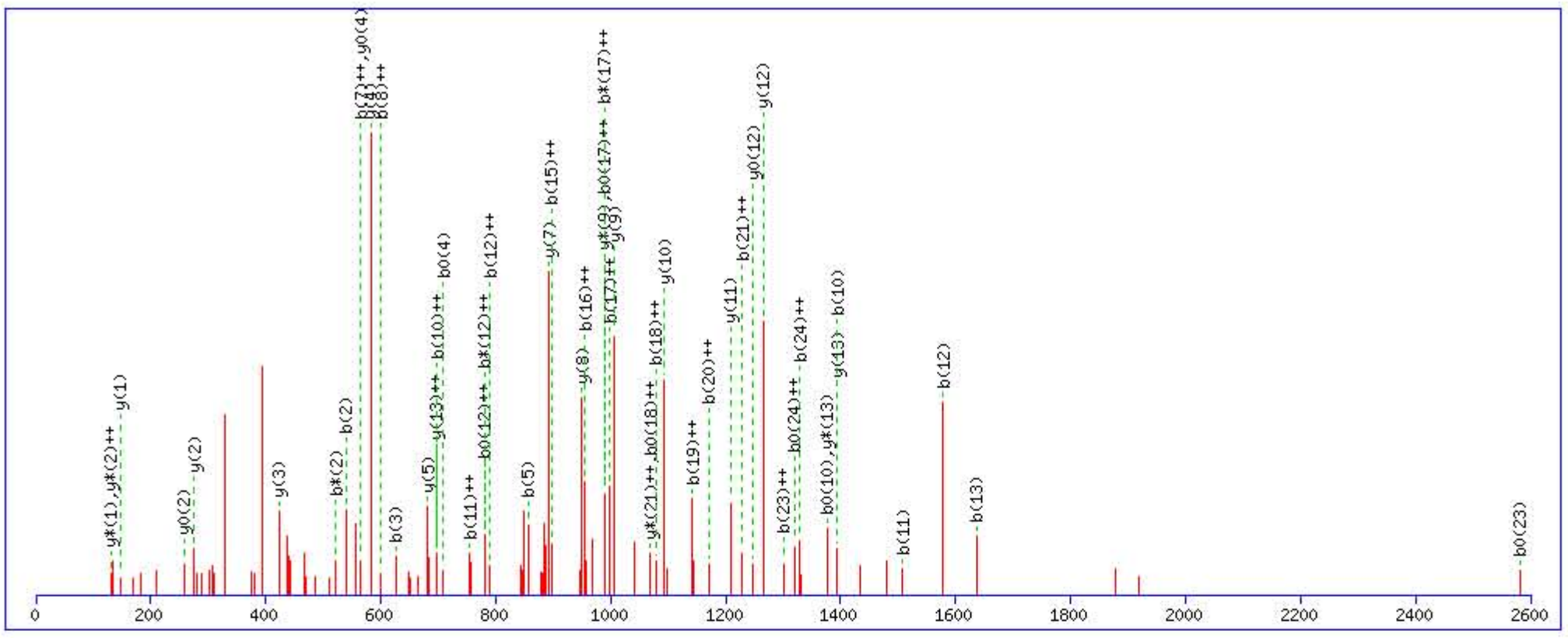
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

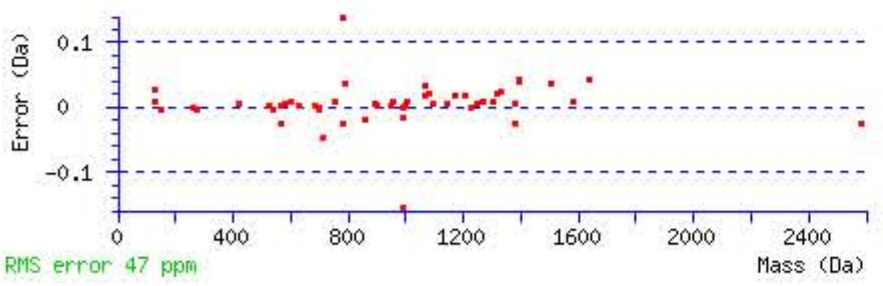
Match to Query 66147: 3547.615736 from(887.911210,4+) rtinseconds(2160) index(67416)
Title: Locus:1.1.1.2027.14 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

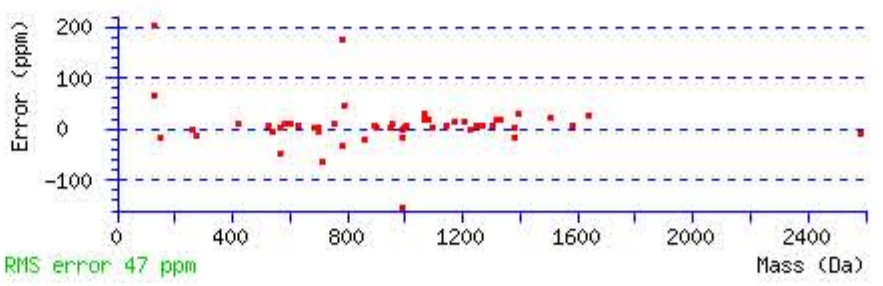
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3547.584061
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 83 **Expect:** 5.5e-008
**Matches :** 52/352 fragment ions using 83 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 31 |
| 2 | **539.301016** | 270.154146 | 522.274467 | 261.640872 | | | Q | 3449.522877 | 1725.265076 | 3432.496328 | 1716.751802 | 3431.512312 | 1716.259794 | 30 |
| 3 | **626.333044** | 313.670160 | 609.306495 | 305.156886 | 608.322479 | 304.664878 | S | 3010.297551 | 1505.652413 | 2993.271002 | 1497.139139 | 2992.286986 | 1496.647131 | 29 |
| 4 | 727.380723 | 364.194000 | 710.354174 | 355.680725 | 709.370158 | 355.188717 | T | 2923.265523 | 1462.136399 | 2906.238974 | 1453.623125 | 2905.254958 | 1453.131117 | 28 |
| 5 | **856.423316** | 428.715296 | 839.396767 | 420.202022 | 838.412751 | 419.710014 | E | 2822.217844 | 1411.612560 | 2805.191295 | 1403.099285 | 2804.207279 | 1402.607277 | 27 |
| 6 | 969.507380 | 485.257328 | 952.480831 | 476.744054 | 951.496815 | 476.252046 | L | 2693.175251 | 1347.091263 | 2676.148702 | 1338.577989 | 2675.164686 | 1338.085981 | 26 |
| 7 | 1129.538029 | ***565.272653*** | 1112.511480 | 556.759378 | 1111.527464 | 556.267370 | C | 2580.091187 | 1290.549231 | 2563.064638 | 1282.035957 | 2562.080622 | 1281.543949 | 25 |
| 8 | 1200.575143 | ***600.791210*** | 1183.548594 | 592.277935 | 1182.564578 | 591.785927 | A | 2420.060538 | 1210.533907 | 2403.033989 | 1202.020632 | 2402.049973 | 1201.528624 | 24 |
| 9 | 1257.596607 | 629.301942 | 1240.570058 | 620.788667 | 1239.586042 | 620.296659 | G | 2349.023424 | 1175.015350 | 2331.996875 | 1166.502075 | 2331.012859 | 1166.010067 | 23 |
| 10 | **1394.655519** | ***697.831397*** | 1377.628970 | 689.318123 | 1376.644954 | 688.826115 | H | 2292.001960 | 1146.504618 | 2274.975411 | 1137.991343 | 2273.991395 | 1137.499335 | 22 |
| 11 | **1507.739583** | ***754.373429*** | 1490.713034 | 745.860155 | 1489.729018 | 745.368147 | L | 2154.943048 | 1077.975162 | 2137.916499 | 1069.461887 | 2136.932483 | 1068.969879 | 21 |
| 12 | **1578.776697** | ***789.891986*** | 1561.750148 | 781.378712 | 1560.766132 | 780.886704 | A | 2041.858984 | 1021.433130 | 2024.832435 | 1012.919855 | 2023.848419 | 1012.427847 | 20 |
| 13 | **1635.798161** | 818.402718 | 1618.771612 | 809.889444 | 1617.787596 | 809.397436 | G | 1970.821870 | 985.914573 | 1953.795321 | 977.401298 | 1952.811305 | 976.909290 | 19 |
| 14 | 1692.819625 | 846.913450 | 1675.793076 | 838.400176 | 1674.809060 | 837.908168 | G | 1913.800406 | 957.403841 | 1896.773857 | 948.890566 | 1895.789841 | 948.398558 | 18 |
| 15 | 1793.867304 | ***897.437290*** | 1776.840755 | 888.924015 | 1775.856739 | 888.432007 | T | 1856.778942 | 928.893109 | 1839.752393 | 920.379835 | 1838.768377 | 919.887826 | 17 |
| 16 | 1908.894247 | ***954.950761*** | 1891.867698 | 946.437487 | 1890.883682 | 945.945479 | D | 1755.731263 | 878.369269 | 1738.704714 | 869.855995 | 1737.720698 | 869.363987 | 16 |
| 17 | 1995.926275 | ***998.466775*** | 1978.899726 | 989.953501 | 1977.915710 | 989.461493 | S | 1640.704320 | 820.855798 | 1623.677771 | 812.342523 | 1622.693755 | 811.850515 | 15 |
| 18 | 2155.956924 | ***1078.482100*** | 2138.930375 | 1069.968825 | 2137.946359 | 1069.476817 | C | 1553.672292 | 777.339784 | 1536.645743 | 768.826509 | 1535.661727 | 768.334501 | 14 |
| 19 | 2284.015502 | ***1142.511389*** | 2266.988953 | 1133.998114 | 2266.004937 | 1133.506106 | Q | ***1393.641643*** | 697.324459 | 1376.615094 | 688.811185 | 1375.631078 | 688.319177 | 13 |
| 20 | 2341.036966 | ***1171.022121*** | 2324.010417 | 1162.508846 | 2323.026401 | 1162.016838 | G | ***1265.583065*** | 633.295170 | 1248.556516 | 624.781896 | 1247.572500 | 624.289888 | 12 |
| 21 | 2456.063909 | ***1228.535592*** | 2439.037360 | 1220.022318 | 2438.053344 | 1219.530310 | D | ***1208.561601*** | 604.784438 | 1191.535052 | 596.271164 | 1190.551036 | 595.779156 | 11 |
| 22 | 2543.095937 | 1272.051606 | 2526.069388 | 1263.538332 | 2525.085372 | 1263.046324 | S | ***1093.534658*** | 547.270967 | 1076.508109 | 538.757692 | 1075.524093 | 538.265684 | 10 |
| 23 | 2600.117401 | ***1300.562338*** | 2583.090852 | 1292.049064 | 2582.106836 | 1291.557056 | G | ***1006.502630*** | 503.754953 | 989.476081 | 495.241678 | 988.492065 | 494.749670 | 9 |
| 24 | 2657.138865 | ***1329.073070*** | 2640.112316 | 1320.559796 | 2639.128300 | 1320.067788 | G | ***949.481166*** | 475.244221 | 932.454617 | 466.730946 | 931.470601 | 466.238938 | 8 |
| 25 | 2754.191629 | 1377.599452 | 2737.165080 | 1369.086178 | 2736.181064 | 1368.594170 | P | ***892.459702*** | 446.733489 | 875.433153 | 438.220214 | 874.449137 | 437.728206 | 7 |
| 26 | 2867.275693 | 1434.141484 | 2850.249144 | 1425.628210 | 2849.265128 | 1425.136202 | L | 795.406938 | 398.207107 | 778.380389 | 389.693832 | 777.396373 | 389.201824 | 6 |
| 27 | 2966.344107 | 1483.675691 | 2949.317558 | 1475.162417 | 2948.333542 | 1474.670409 | V | ***682.322874*** | 341.665075 | 665.296325 | 333.151800 | 664.312309 | 332.659792 | 5 |
| 28 | 3126.374756 | 1563.691016 | 3109.348207 | 1555.177741 | 3108.364191 | 1554.685733 | C | ***583.254460*** | 292.130868 | 566.227911 | 283.617593 | 565.243895 | 283.125585 | 4 |
| 29 | 3273.443170 | 1637.225223 | 3256.416621 | 1628.711948 | 3255.432605 | 1628.219940 | F | ***423.223811*** | 212.115543 | 406.197262 | 203.602269 | 405.213246 | 203.110261 | 3 |
| 30 | 3402.485763 | 1701.746519 | 3385.459214 | 1693.233245 | 3384.475198 | 1692.741237 | E | ***276.155397*** | 138.581337 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 31 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 82.8 | 3547.584061 | 0.031675 | VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK |
| 35.8 | 3547.584061 | 0.031675 | VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK |

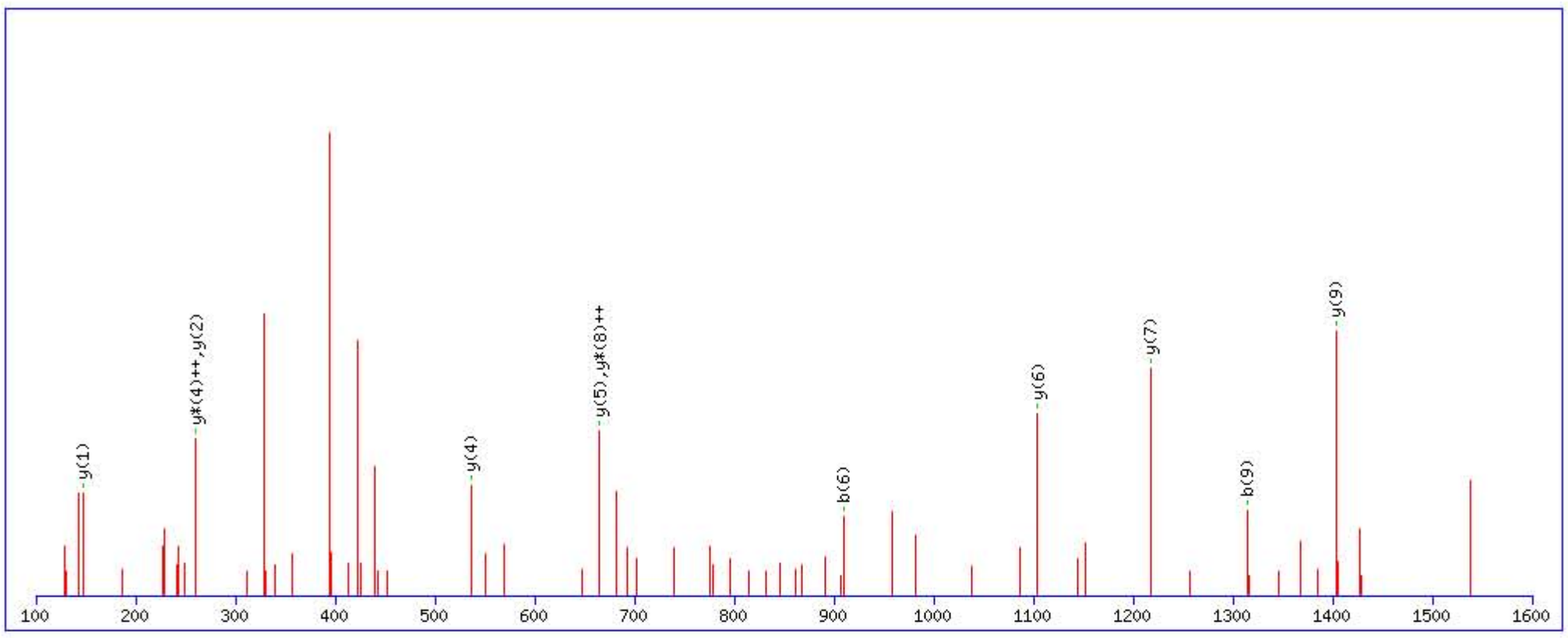
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GLGELQELYLK**
Found in **GP1BA_HUMAN**, Platelet glycoprotein Ib alpha chain OS=Homo sapiens GN=GP1BA PE=1 SV=1

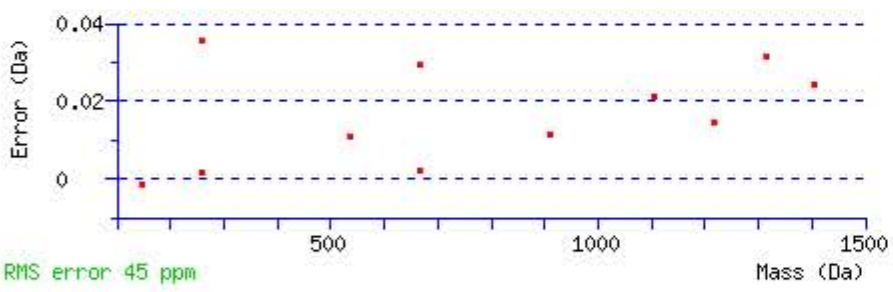
Match to Query 33318: 1572.881228 from(787.447890,2+) rtinseconds(2567) index(53696)
Title: Locus:1.1.1.2131.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

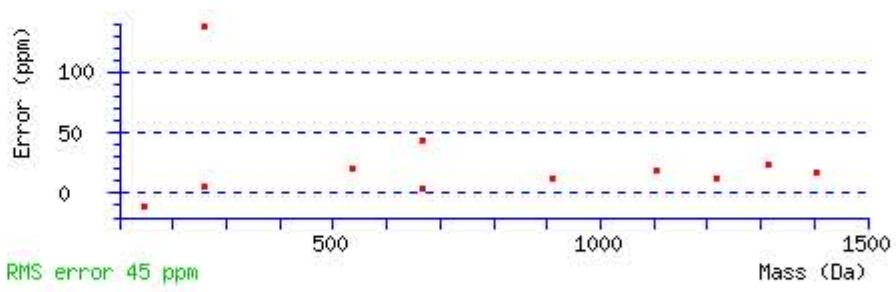
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1572.858521
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q6** : Biotin:Thermo-21345 (Q)
**Ions Score:** 51 **Expect:** 0.00012
**Matches :** 11/96 fragment ions using 14 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 11 |
| 2 | 171.112804 | 86.060040 | | | | | L | 1516.844365 | 758.925821 | 1499.817816 | 750.412546 | 1498.833800 | 749.920538 | 10 |
| 3 | 228.134268 | 114.570772 | | | | | G | *1403.760301* | 702.383789 | 1386.733752 | 693.870514 | 1385.749736 | 693.378506 | 9 |
| 4 | 357.176861 | 179.092068 | | | 339.166296 | 170.086786 | E | 1346.738837 | 673.873057 | 1329.712288 | 665.359782 | 1328.728272 | 664.867774 | 8 |
| 5 | 470.260925 | 235.634100 | | | 452.250360 | 226.628818 | L | *1217.696244* | 609.351760 | 1200.669695 | 600.838486 | 1199.685679 | 600.346477 | 7 |
| 6 | **909.486251** | 455.246764 | 892.459702 | 446.733489 | 891.475686 | 446.241481 | Q | *1104.612180* | 552.809728 | 1087.585631 | 544.296454 | 1086.601615 | 543.804446 | 6 |
| 7 | 1038.528844 | 519.768060 | 1021.502295 | 511.254786 | 1020.518279 | 510.762778 | E | *665.386854* | 333.197065 | 648.360305 | 324.683791 | 647.376289 | 324.191783 | 5 |
| 8 | 1151.612908 | 576.310092 | 1134.586359 | 567.796818 | 1133.602343 | 567.304810 | L | *536.344261* | 268.675769 | 519.317712 | 260.162494 | | | 4 |
| 9 | **1314.676237** | 657.841757 | 1297.649688 | 649.328482 | 1296.665672 | 648.836474 | Y | 423.260197 | 212.133736 | 406.233648 | 203.620462 | | | 3 |
| 10 | 1427.760301 | 714.383789 | 1410.733752 | 705.870514 | 1409.749736 | 705.378506 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 11 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 51.0 | 1572.858521 | 0.022707 | GLGELQELYLK |
| 9.2 | 1572.861923 | 0.019305 | QVLEVTSMVLK |
| 8.2 | 1572.897385 | -0.016157 | TKSIAEELELSILK |
| 4.4 | 1572.862350 | 0.018878 | QQLQAKNFELNLK |
| 3.7 | 1572.890884 | -0.009656 | LLNLTVRIDIMEK |
| 2.7 | 1572.890900 | -0.009672 | NISVLGQAGLLTMIK |
| 2.0 | 1572.887527 | -0.006299 | TLTFALRADDPLLK |
| 1.6 | 1572.869781 | 0.011447 | IQGPQPVPGEIK |
| 1.4 | 1572.887512 | -0.006284 | EFQALIKGGAALDLK |
| 1.0 | 1572.879654 | 0.001574 | GITMLEEIKVPSIK |

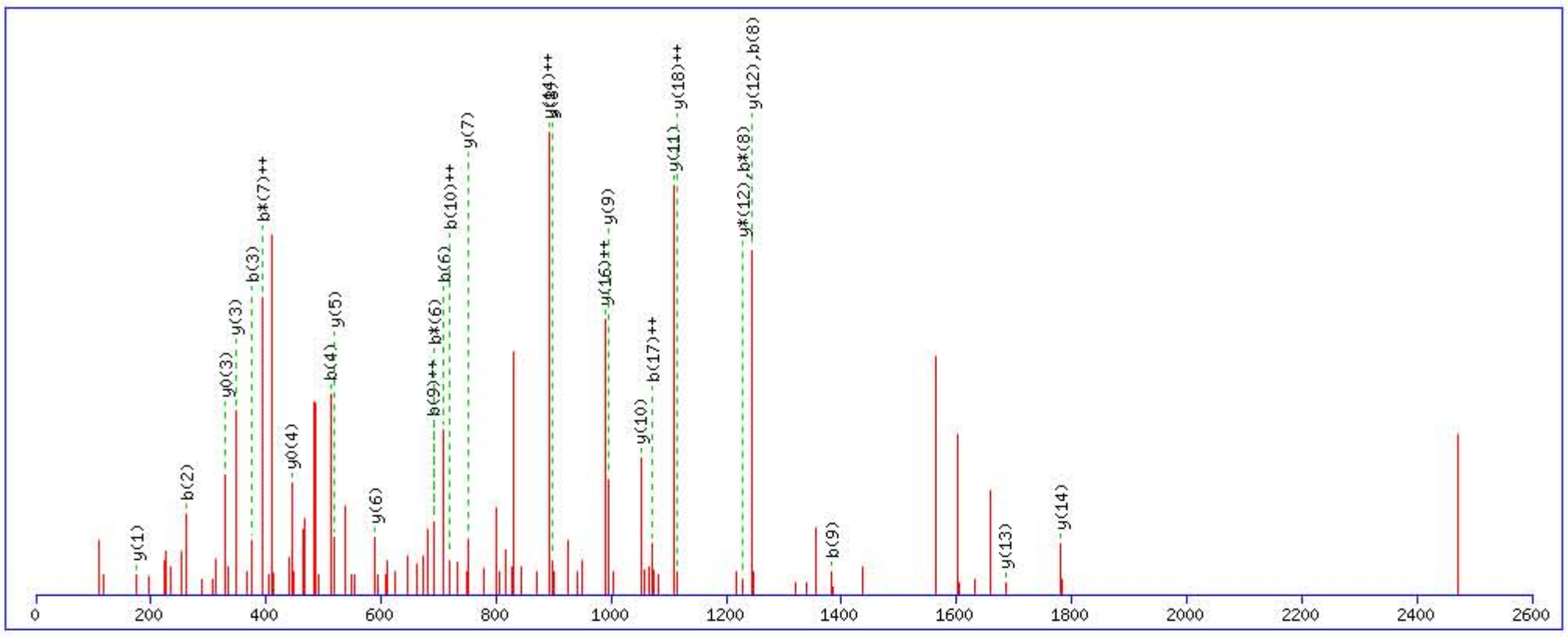
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TCNHPVPQHGGPFCAGDATR**
Found in **PROP_HUMAN**, Properdin OS=Homo sapiens GN=CFP PE=1 SV=2

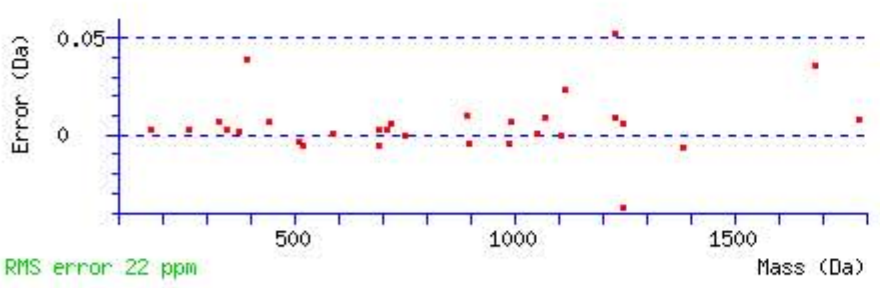
Match to Query 54008: 2489.124462 from(830.715430,3+) rtinseconds(1500) index(63490)
Title: Locus:1.1.1.1797.12 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

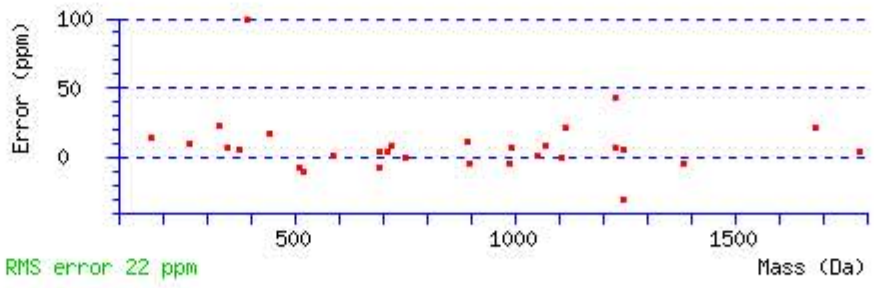
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2489.115128
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 0.00015
**Matches :** 30/222 fragment ions using 73 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 20 |
| 2 | **262.085604** | 131.546440 | | | 244.075039 | 122.541158 | C | 2389.074689 | 1195.040982 | 2372.048140 | 1186.527708 | 2371.064124 | 1186.035700 | 19 |
| 3 | **376.128531** | 188.567904 | 359.101982 | 180.054629 | 358.117966 | 179.562621 | N | 2229.044040 | 1115.025658 | 2212.017491 | 1106.512383 | 2211.033475 | 1106.020375 | 18 |
| 4 | **513.187443** | 257.097360 | 496.160894 | 248.584085 | 495.176878 | 248.092077 | H | 2115.001113 | 1058.004194 | 2097.974564 | 1049.490920 | 2096.990548 | 1048.998912 | 17 |
| 5 | 610.240207 | 305.623742 | 593.213658 | 297.110467 | 592.229642 | 296.618459 | P | 1977.942201 | 989.474739 | 1960.915652 | 980.961464 | 1959.931636 | 980.469456 | 16 |
| 6 | **709.308621** | 355.157949 | **692.282072** | 346.644674 | 691.298056 | 346.152666 | V | 1880.889437 | 940.948357 | 1863.862888 | 932.435082 | 1862.878872 | 931.943074 | 15 |
| 7 | 806.361385 | 403.684331 | 789.334836 | **395.171056** | 788.350820 | 394.679048 | P | *1781.821023* | 891.414150 | 1764.794474 | 882.900875 | 1763.810458 | 882.408867 | 14 |
| 8 | **1245.586711** | 623.296994 | **1228.560162** | 614.783719 | 1227.576146 | 614.291711 | Q | *1684.768259* | 842.887768 | 1667.741710 | 834.374493 | 1666.757694 | 833.882485 | 13 |
| 9 | **1382.645623** | **691.826450** | 1365.619074 | 683.313175 | 1364.635058 | 682.821167 | H | *1245.542933* | 623.275105 | **1228.516384** | 614.761830 | 1227.532368 | 614.269822 | 12 |
| 10 | 1439.667087 | **720.337182** | 1422.640538 | 711.823907 | 1421.656522 | 711.331899 | G | *1108.484021* | 554.745649 | 1091.457472 | 546.232374 | 1090.473456 | 545.740366 | 11 |
| 11 | 1496.688551 | 748.847914 | 1479.662002 | 740.334639 | 1478.677986 | 739.842631 | G | *1051.462557* | 526.234917 | 1034.436008 | 517.721642 | 1033.451992 | 517.229634 | 10 |
| 12 | 1593.741315 | 797.374296 | 1576.714766 | 788.861021 | 1575.730750 | 788.369013 | P | *994.441093* | 497.724185 | 977.414544 | 489.210910 | 976.430528 | 488.718902 | 9 |
| 13 | 1740.809729 | 870.908503 | 1723.783180 | 862.395228 | 1722.799164 | 861.903220 | F | *897.388329* | 449.197803 | 880.361780 | 440.684528 | 879.377764 | 440.192520 | 8 |
| 14 | 1900.840378 | 950.923827 | 1883.813829 | 942.410553 | 1882.829813 | 941.918545 | C | *750.319915* | 375.663596 | 733.293366 | 367.150321 | 732.309350 | 366.658313 | 7 |
| 15 | 1971.877492 | 986.442384 | 1954.850943 | 977.929110 | 1953.866927 | 977.437102 | A | *590.289266* | 295.648271 | 573.262717 | 287.134997 | 572.278701 | 286.642989 | 6 |
| 16 | 2028.898956 | 1014.953116 | 2011.872407 | 1006.439842 | 2010.888391 | 1005.947834 | G | *519.252152* | 260.129714 | 502.225603 | 251.616440 | 501.241587 | 251.124432 | 5 |
| 17 | 2143.925899 | **1072.466587** | 2126.899350 | 1063.953313 | 2125.915334 | 1063.461305 | D | 462.230688 | 231.618982 | 445.204139 | 223.105707 | **444.220123** | 222.613700 | 4 |
| 18 | 2214.963013 | 1107.985144 | 2197.936464 | 1099.471870 | 2196.952448 | 1098.979862 | A | *347.203745* | 174.105510 | 330.177196 | 165.592236 | **329.193180** | 165.100228 | 3 |
| 19 | 2316.010692 | 1158.508984 | 2298.984143 | 1149.995709 | 2298.000127 | 1149.503701 | T | 276.166631 | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 20 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 47.5 | 2489.115128 | 0.009334 | TCNHPVPQHGGPFCAGDATR |

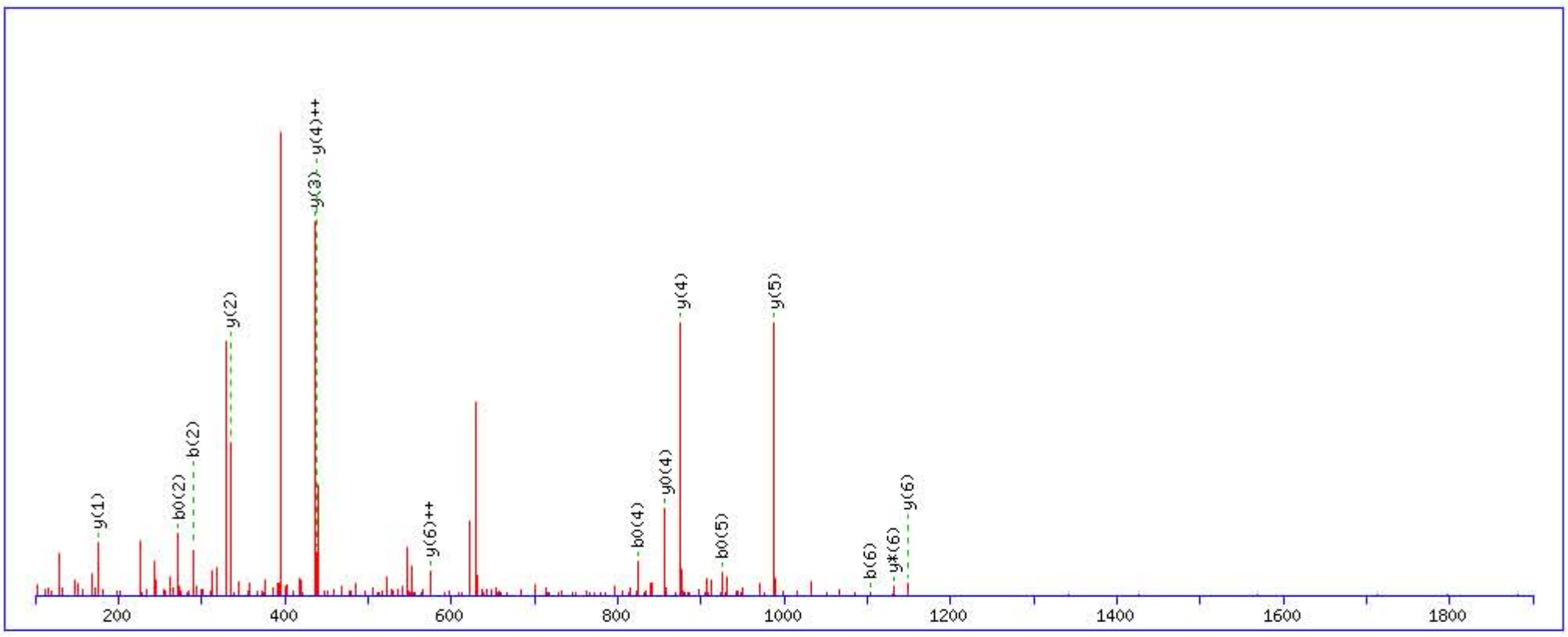
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ECLQTCR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

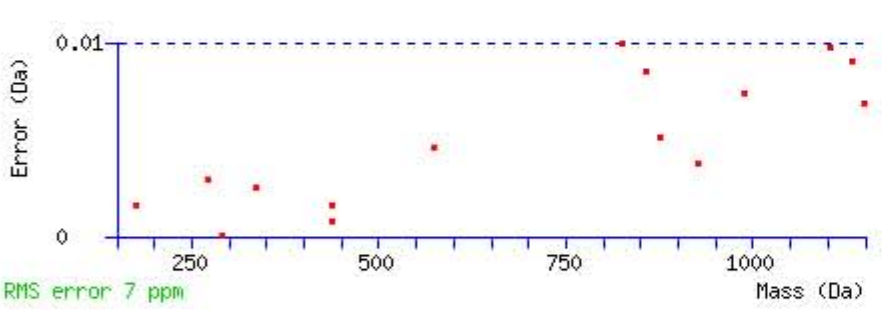
Match to Query 22624: 1276.577808 from(639.296180,2+) rtinseconds(1490) index(31008)
Title: Locus:1.1.1.627.16 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

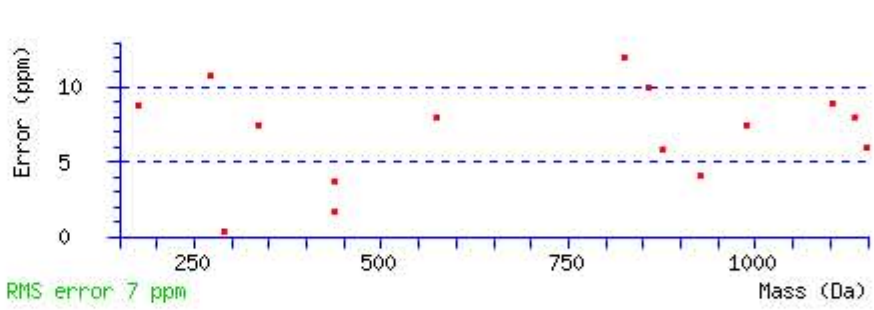
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1276.572632
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.005
**Matches :** 15/62 fragment ions using 33 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 7 |
| 2 | **290.080518** | 145.543897 | | | 272.069953 | 136.538615 | C | ***1148.537319*** | 574.772298 | 1131.510770 | 566.259023 | 1130.526754 | 565.767015 | 6 |
| 3 | 403.164582 | 202.085929 | | | 385.154017 | 193.080647 | L | ***988.506670*** | 494.756973 | 971.480121 | 486.243699 | 970.496105 | 485.751691 | 5 |
| 4 | 842.389908 | 421.698592 | 825.363359 | 413.185318 | 824.379343 | 412.693310 | Q | ***875.422606*** | 438.214941 | 858.396057 | 429.701667 | 857.412041 | 429.209659 | 4 |
| 5 | 943.437587 | 472.222432 | 926.411038 | 463.709157 | 925.427022 | 463.217149 | T | ***436.197280*** | 218.602278 | 419.170731 | 210.089003 | 418.186715 | 209.596995 | 3 |
| 6 | **1103.468236** | 552.237756 | 1086.441687 | 543.724482 | 1085.457671 | 543.232474 | C | ***335.149601*** | 168.078438 | 318.123052 | 159.565164 | | | 2 |
| 7 | | | | | | | R | ***175.118952*** | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 31.6 | 1276.572632 | 0.005176 | ECLQTCR |
| 9.8 | 1276.590393 | -0.012585 | TMHTSVMALDR |
| 7.9 | 1276.590378 | -0.012570 | MSPSMLTGNSPR |
| 7.3 | 1276.583862 | -0.006054 | KMSLSCHVCR |
| 6.3 | 1276.569275 | 0.008533 | MPMWAGGVGSPR |
| 6.0 | 1276.579605 | -0.001797 | EEQRSPFNDR |
| 5.5 | 1276.587006 | -0.009198 | EDGTWAPMRSK |
| 4.7 | 1276.560516 | 0.017292 | QQVPSEDSMEK |
| 4.5 | 1276.590393 | -0.012585 | TMHTSVMALDR |
| 3.4 | 1276.582977 | -0.005169 | EMQLGREDQR |

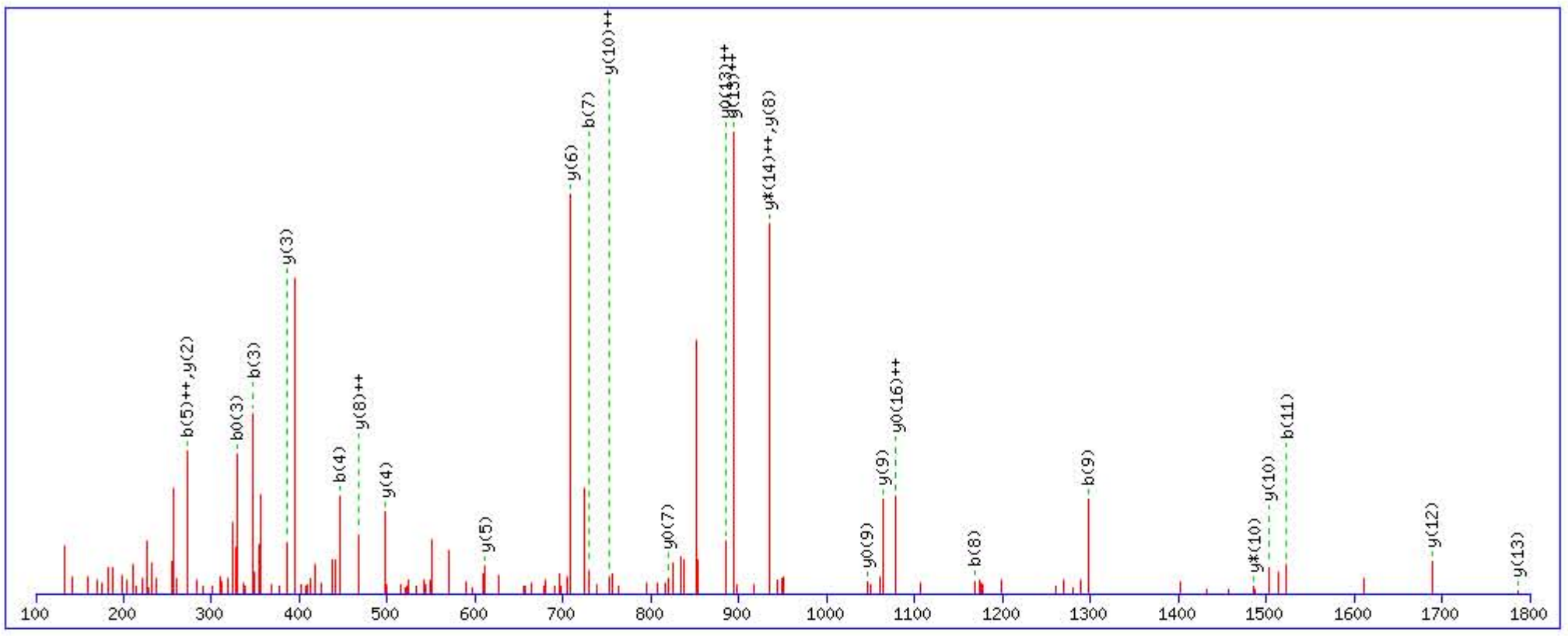
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GECVPGEQEPEPILIPR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

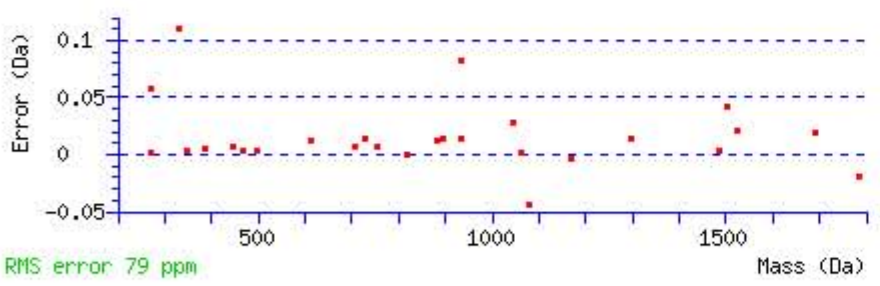
Match to Query 49134: 2230.126092 from(744.382640,3+) rtinseconds(2286) index(7238)
Title: Locus:1.1.1.2073.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

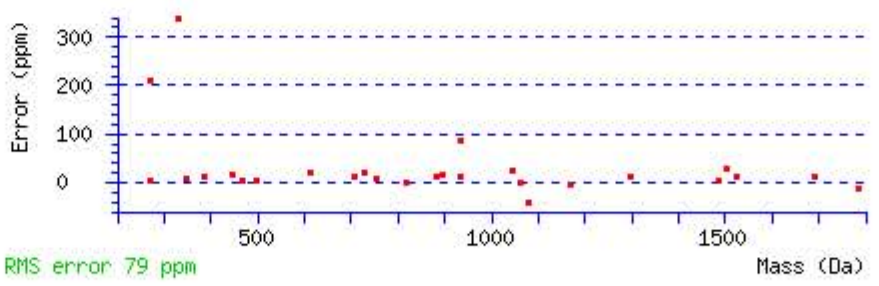
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2230.112595
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 42 **Expect:** 0.00013
**Matches :** 27/164 fragment ions using 57 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 17 |
| 2 | 187.071333 | 94.039305 | | | 169.060768 | 85.034022 | E | 2174.098425 | 1087.552850 | 2157.071876 | 1079.039576 | 2156.087860 | 1078.547568 | 16 |
| 3 | **347.101982** | 174.054629 | | | 329.091417 | 165.049347 | C | 2045.055832 | 1023.031554 | 2028.029283 | 1014.518279 | 2027.045267 | 1014.026271 | 15 |
| 4 | **446.170396** | 223.588836 | | | 428.159831 | 214.583554 | V | 1885.025183 | 943.016229 | 1867.998634 | 934.502955 | 1867.014618 | 934.010947 | 14 |
| 5 | 543.223160 | 272.115218 | | | 525.212595 | 263.109936 | P | *1785.956769* | 893.482022 | 1768.930220 | 884.968748 | 1767.946204 | 884.476740 | 13 |
| 6 | 600.244624 | 300.625950 | | | 582.234059 | 291.620668 | G | *1688.904005* | 844.955640 | 1671.877456 | 836.442366 | 1670.893440 | 835.950358 | 12 |
| 7 | **729.287217** | 365.147247 | | | 711.276652 | 356.141964 | E | 1631.882541 | 816.444908 | 1614.855992 | 807.931634 | 1613.871976 | 807.439626 | 11 |
| 8 | **1168.512543** | 584.759910 | 1151.485994 | 576.246635 | 1150.501978 | 575.754627 | Q | *1502.839948* | 751.923612 | 1485.813399 | 743.410337 | 1484.829383 | 742.918329 | 10 |
| 9 | **1297.555136** | 649.281206 | 1280.528587 | 640.767932 | 1279.544571 | 640.275924 | E | *1063.614622* | 532.310949 | 1046.588073 | 523.797674 | 1045.604057 | 523.305666 | 9 |
| 10 | 1394.607900 | 697.807588 | 1377.581351 | 689.294314 | 1376.597335 | 688.802306 | P | *934.572029* | 467.789652 | 917.545480 | 459.276378 | 916.561464 | 458.784370 | 8 |
| 11 | **1523.650493** | 762.328885 | 1506.623944 | 753.815610 | 1505.639928 | 753.323602 | E | 837.519265 | 419.263270 | 820.492716 | 410.749996 | 819.508700 | 410.257988 | 7 |
| 12 | 1620.703257 | 810.855267 | 1603.676708 | 802.341992 | 1602.692692 | 801.849984 | P | *708.476672* | 354.741974 | 691.450123 | 346.228699 | | | 6 |
| 13 | 1733.787321 | 867.397299 | 1716.760772 | 858.884024 | 1715.776756 | 858.392016 | I | *611.423908* | 306.215592 | 594.397359 | 297.702317 | | | 5 |
| 14 | 1846.871385 | 923.939331 | 1829.844836 | 915.426056 | 1828.860820 | 914.934048 | L | *498.339844* | 249.673560 | 481.313295 | 241.160285 | | | 4 |
| 15 | 1959.955449 | 980.481363 | 1942.928900 | 971.968088 | 1941.944884 | 971.476080 | I | *385.255780* | 193.131528 | 368.229231 | 184.618253 | | | 3 |
| 16 | 2057.008213 | 1029.007744 | 2039.981664 | 1020.494470 | 2038.997648 | 1020.002462 | P | *272.171716* | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 17 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 41.8 | 2230.112595 | 0.013497 | GECVPGEQEPEPILIPR |
| 0.4 | 2230.116409 | 0.009683 | ESQSPSSSASRQKNIWK |

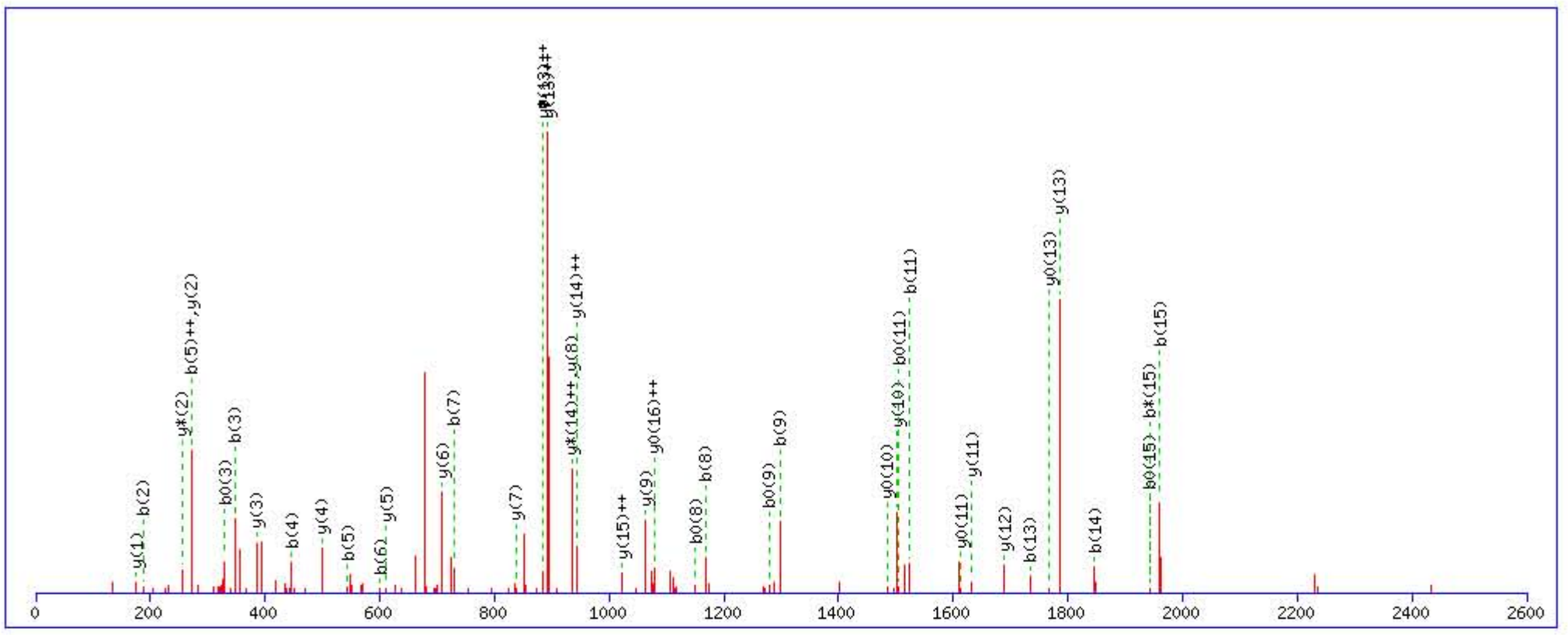
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GECVPGEQEPEPILIPR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

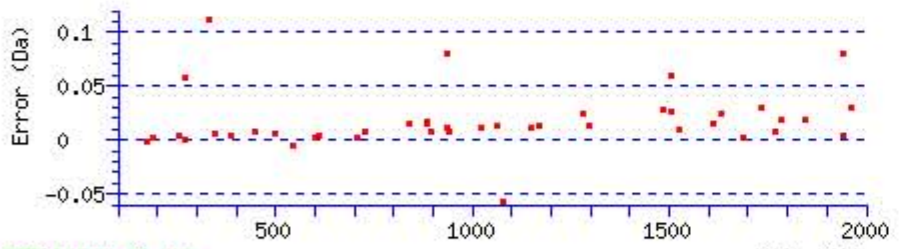
Match to Query 49136: 2230.143108 from(1116.078830,2+) rtinseconds(2286) index(7242)
Title: Locus:1.1.1.2073.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

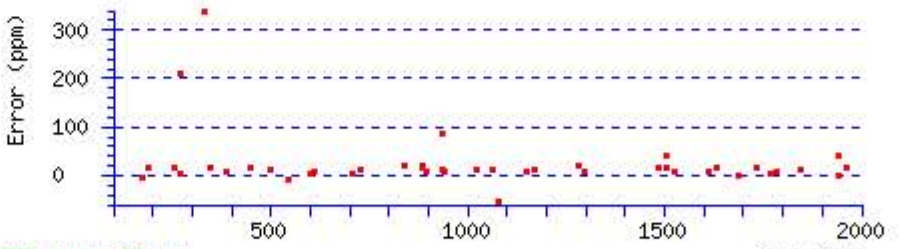
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2230.112595
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 55 **Expect:** 8.2e-005
**Matches :** 43/164 fragment ions using 105 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 17 |
| 2 | *187.071333* | 94.039305 | | | 169.060768 | 85.034022 | E | 2174.098425 | 1087.552850 | 2157.071876 | 1079.039576 | 2156.087860 | 1078.547568 | 16 |
| 3 | *347.101982* | 174.054629 | | | 329.091417 | 165.049347 | C | 2045.055832 | 1023.031554 | 2028.029283 | 1014.518279 | 2027.045267 | 1014.026271 | 15 |
| 4 | *446.170396* | 223.588836 | | | 428.159831 | 214.583554 | V | 1885.025183 | 943.016229 | 1867.998634 | 934.502955 | 1867.014618 | 934.010947 | 14 |
| 5 | *543.223160* | 272.115218 | | | 525.212595 | 263.109936 | P | *1785.956769* | 893.482022 | 1768.930220 | 884.968748 | 1767.946204 | 884.476740 | 13 |
| 6 | *600.244624* | 300.625950 | | | 582.234059 | 291.620668 | G | *1688.904005* | 844.955640 | 1671.877456 | 836.442366 | 1670.893440 | 835.950358 | 12 |
| 7 | *729.287217* | 365.147247 | | | 711.276652 | 356.141964 | E | *1631.882541* | 816.444908 | 1614.855992 | 807.931634 | 1613.871976 | 807.439626 | 11 |
| 8 | *1168.512543* | 584.759910 | 1151.485994 | 576.246635 | 1150.501978 | 575.754627 | Q | *1502.839948* | 751.923612 | 1485.813399 | 743.410337 | 1484.829383 | 742.918329 | 10 |
| 9 | *1297.555136* | 649.281206 | 1280.528587 | 640.767932 | 1279.544571 | 640.275924 | E | *1063.614622* | 532.310949 | 1046.588073 | 523.797674 | 1045.604057 | 523.305666 | 9 |
| 10 | 1394.607900 | 697.807588 | 1377.581351 | 689.294314 | 1376.597335 | 688.802306 | P | *934.572029* | 467.789652 | 917.545480 | 459.276378 | 916.561464 | 458.784370 | 8 |
| 11 | *1523.650493* | 762.328885 | 1506.623944 | 753.815610 | 1505.639928 | 753.323602 | E | *837.519265* | 419.263270 | 820.492716 | 410.749996 | 819.508700 | 410.257988 | 7 |
| 12 | 1620.703257 | 810.855267 | 1603.676708 | 802.341992 | 1602.692692 | 801.849984 | P | *708.476672* | 354.741974 | 691.450123 | 346.228699 | | | 6 |
| 13 | *1733.787321* | 867.397299 | 1716.760772 | 858.884024 | 1715.776756 | 858.392016 | I | *611.423908* | 306.215592 | 594.397359 | 297.702317 | | | 5 |
| 14 | *1846.871385* | 923.939331 | 1829.844836 | 915.426056 | 1828.860820 | 914.934048 | L | *498.339844* | 249.673560 | 481.313295 | 241.160285 | | | 4 |
| 15 | *1959.955449* | 980.481363 | 1942.928900 | 971.968088 | 1941.944884 | 971.476080 | I | *385.255780* | 193.131528 | 368.229231 | 184.618253 | | | 3 |
| 16 | 2057.008213 | 1029.007744 | 2039.981664 | 1020.494470 | 2038.997648 | 1020.002462 | P | *272.171716* | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 17 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 54.9 | 2230.112595 | 0.030513 | GECVPGEQEPEPILIPR |
| 10.7 | 2230.131714 | 0.011394 | SSTQFHVFESTRQLPR |
| 2.8 | 2230.122971 | 0.020137 | QFLGPEGNVDVELIDKSTNR |
| 1.5 | 2230.172104 | -0.028996 | RPPWQICSKFGALPFVAEK |

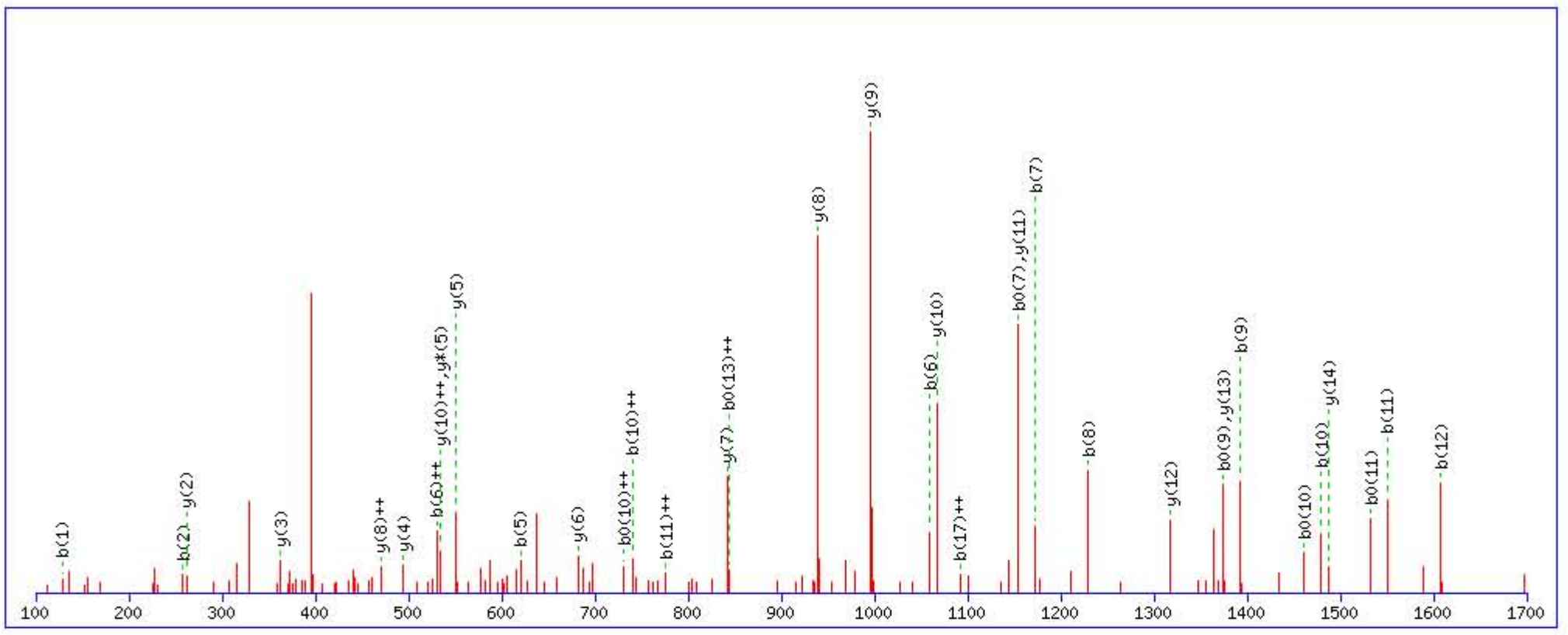
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KEDSCQLGYSAGPCMGMTSR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

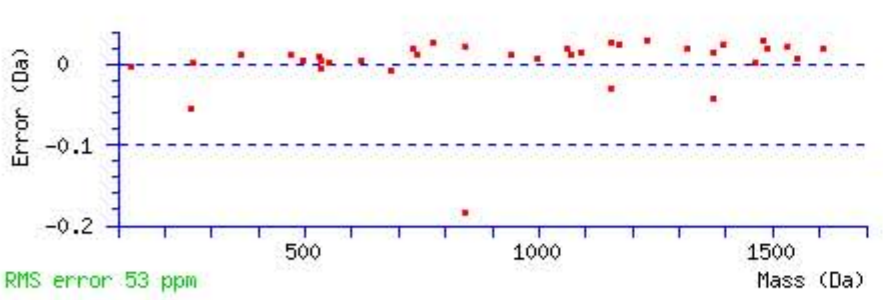
Match to Query 54951: 2545.125642 from(849.382490,3+) rtinseconds(1888) index(49468)
Title: Locus:1.1.1.1895.21 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

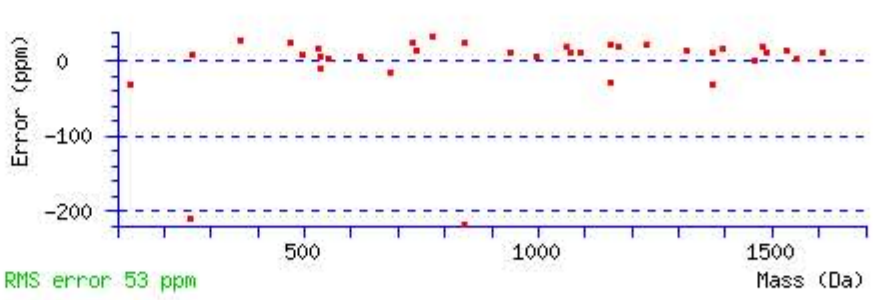
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2545.089188
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 105 **Expect:** 1.9e-010
**Matches :** 36/224 fragment ions using 45 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *129.102239* | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 20 |
| 2 | *258.144832* | 129.576054 | 241.118283 | 121.062780 | 240.134267 | 120.570772 | E | 2418.001508 | 1209.504392 | 2400.974959 | 1200.991117 | 2399.990943 | 1200.499109 | 19 |
| 3 | 373.171775 | 187.089526 | 356.145226 | 178.576251 | 355.161210 | 178.084243 | D | 2288.958915 | 1144.983095 | 2271.932366 | 1136.469821 | 2270.948350 | 1135.977813 | 18 |
| 4 | 460.203803 | 230.605540 | 443.177254 | 222.092265 | 442.193238 | 221.600257 | S | 2173.931972 | 1087.469624 | 2156.905423 | 1078.956349 | 2155.921407 | 1078.464341 | 17 |
| 5 | *620.234452* | 310.620864 | 603.207903 | 302.107590 | 602.223887 | 301.615582 | C | 2086.899944 | 1043.953610 | 2069.873395 | 1035.440335 | 2068.889379 | 1034.948327 | 16 |
| 6 | *1059.459778* | **530.233527** | 1042.433229 | 521.720253 | 1041.449213 | 521.228245 | Q | 1926.869295 | 963.938286 | 1909.842746 | 955.425011 | 1908.858730 | 954.933003 | 15 |
| 7 | *1172.543842* | 586.775559 | 1155.517293 | 578.262285 | 1154.533277 | 577.770277 | L | *1487.643969* | 744.325623 | 1470.617420 | 735.812348 | 1469.633404 | 735.320340 | 14 |
| 8 | *1229.565306* | 615.286291 | 1212.538757 | 606.773017 | 1211.554741 | 606.281008 | G | *1374.559905* | 687.783591 | 1357.533356 | 679.270316 | 1356.549340 | 678.778308 | 13 |
| 9 | *1392.628635* | 696.817956 | 1375.602086 | 688.304681 | 1374.618070 | 687.812673 | Y | *1317.538441* | 659.272859 | 1300.511892 | 650.759584 | 1299.527876 | 650.267576 | 12 |
| 10 | *1479.660663* | **740.333970** | 1462.634114 | 731.820695 | 1461.650098 | 731.328687 | S | *1154.475112* | 577.741194 | 1137.448563 | 569.227920 | 1136.464547 | 568.735912 | 11 |
| 11 | *1550.697777* | **775.852527** | 1533.671228 | 767.339252 | 1532.687212 | 766.847244 | A | *1067.443084* | 534.225180 | 1050.416535 | 525.711906 | 1049.432519 | 525.219898 | 10 |
| 12 | *1607.719241* | 804.363259 | 1590.692692 | 795.849984 | 1589.708676 | 795.357976 | G | *996.405970* | 498.706623 | 979.379421 | 490.193349 | 978.395405 | 489.701341 | 9 |
| 13 | 1704.772005 | 852.889641 | 1687.745456 | 844.376366 | 1686.761440 | 843.884358 | P | *939.384506* | 470.195891 | 922.357957 | 461.682617 | 921.373941 | 461.190609 | 8 |
| 14 | 1864.802654 | 932.904965 | 1847.776105 | 924.391691 | 1846.792089 | 923.899683 | C | *842.331742* | 421.669509 | 825.305193 | 413.156235 | 824.321177 | 412.664227 | 7 |
| 15 | 1995.843139 | 998.425208 | 1978.816590 | 989.911933 | 1977.832574 | 989.419925 | M | *682.301093* | 341.654185 | 665.274544 | 333.140910 | 664.290528 | 332.648902 | 6 |
| 16 | 2052.864603 | 1026.935939 | 2035.838054 | 1018.422665 | 2034.854038 | 1017.930657 | G | *551.260608* | 276.133942 | 534.234059 | 267.620668 | 533.250043 | 267.128660 | 5 |
| 17 | 2183.905088 | **1092.456182** | 2166.878539 | 1083.942907 | 2165.894523 | 1083.450899 | M | *494.239144* | 247.623210 | 477.212595 | 239.109935 | 476.228579 | 238.617927 | 4 |
| 18 | 2284.952767 | 1142.980021 | 2267.926218 | 1134.466747 | 2266.942202 | 1133.974739 | T | *363.198659* | 182.102967 | 346.172110 | 173.589693 | 345.188094 | 173.097685 | 3 |
| 19 | 2371.984795 | 1186.496035 | 2354.958246 | 1177.982761 | 2353.974230 | 1177.490753 | S | *262.150980* | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 20 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 105.0 | 2545.089188 | 0.036454 | KEDSCQLGYSAGPCMGMTSR |

**Mascot:** http://www.matrixscience.com/

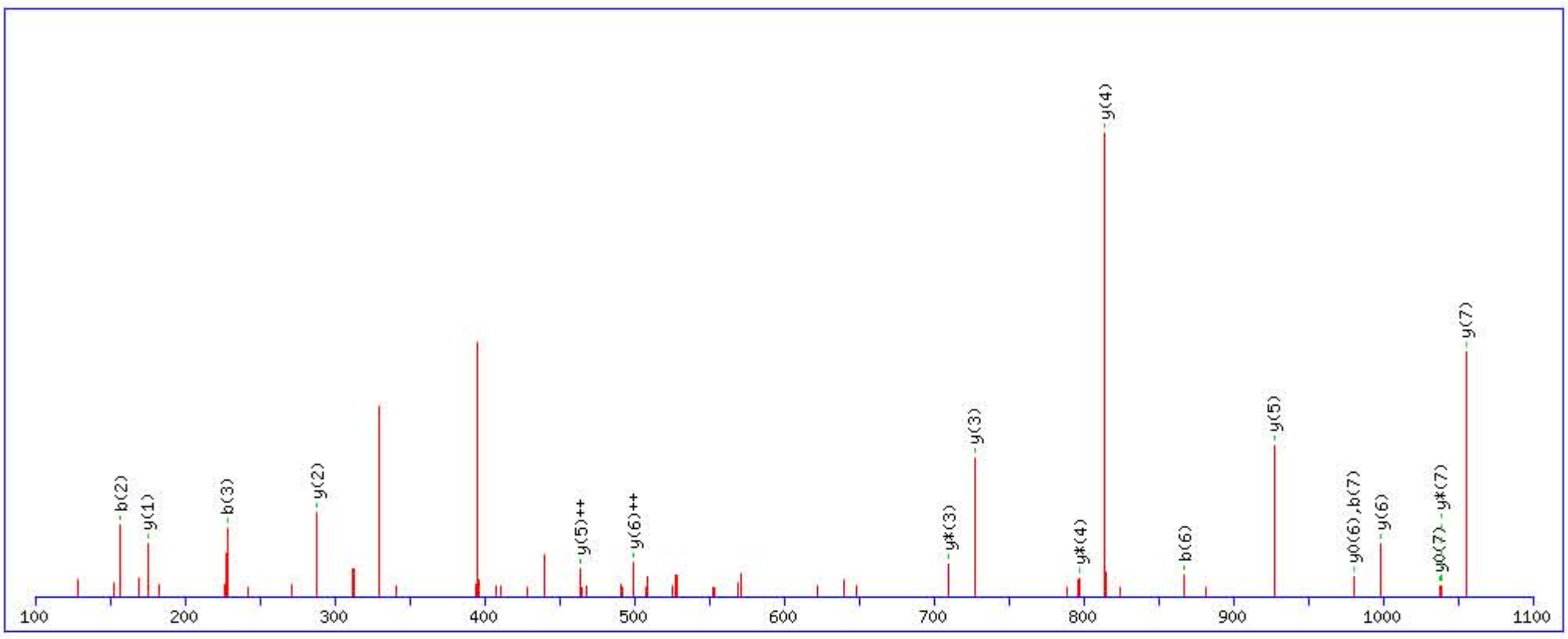
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VGALSQLR**
Found in **MENT_HUMAN**, Protein MENT OS=Homo sapiens GN=MENT PE=2 SV=1

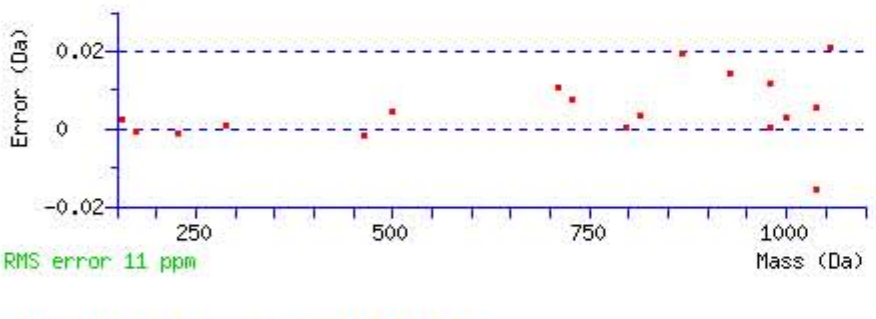
Match to Query 19078: 1153.669948 from(577.842250,2+) rtinseconds(1943) index(49932)
Title: Locus:1.1.1.1914.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

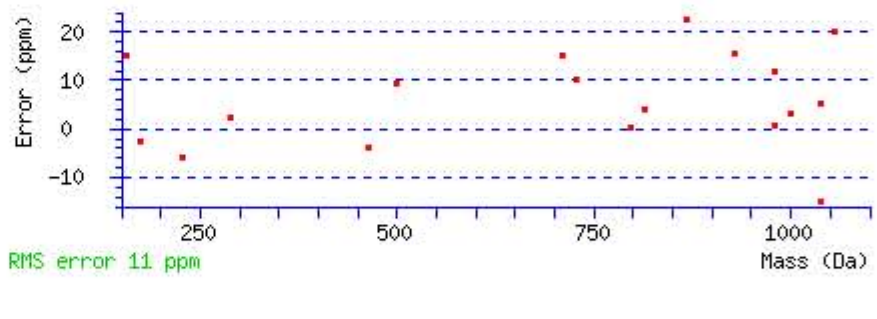
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1153.664139
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 0.00021
**Matches :** 18/60 fragment ions using 29 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 8 |
| 2 | **157.097154** | 79.052215 | | | | | G | *1055.603012* | 528.305144 | 1038.576463 | 519.791870 | 1037.592447 | 519.299862 | 7 |
| 3 | **228.134268** | 114.570772 | | | | | A | *998.581548* | 499.794412 | 981.554999 | 491.281138 | 980.570983 | 490.789130 | 6 |
| 4 | 341.218332 | 171.112804 | | | | | L | *927.544434* | 464.275855 | 910.517885 | 455.762581 | 909.533869 | 455.270573 | 5 |
| 5 | 428.250360 | 214.628818 | | | 410.239795 | 205.623535 | S | *814.460370* | 407.733823 | 797.433821 | 399.220549 | 796.449805 | 398.728541 | 4 |
| 6 | **867.475686** | 434.241481 | 850.449137 | 425.728207 | 849.465121 | 425.236199 | Q | *727.428342* | 364.217809 | 710.401793 | 355.704535 | | | 3 |
| 7 | **980.559750** | 490.783513 | 963.533201 | 482.270239 | 962.549185 | 481.778231 | L | *288.203016* | 144.605146 | 271.176467 | 136.091872 | | | 2 |
| 8 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.4 | 1153.664139 | 0.005809 | VGALSQLR |
| 22.6 | 1153.681870 | -0.011922 | RALENLLPTK |
| 15.6 | 1153.681885 | -0.011937 | VQEKTALPLR |
| 11.7 | 1153.675354 | -0.005406 | RALLSQR |
| 11.7 | 1153.675369 | -0.005421 | RALTVQR |
| 10.4 | 1153.664124 | 0.005824 | VKQEALR |
| 9.1 | 1153.675369 | -0.005421 | QTVRALR |
| 6.9 | 1153.681870 | -0.011922 | NLELNGLILR |
| 5.7 | 1153.664139 | 0.005809 | VTQINLR |
| 5.3 | 1153.656723 | 0.013225 | RPSADPGKKAK |

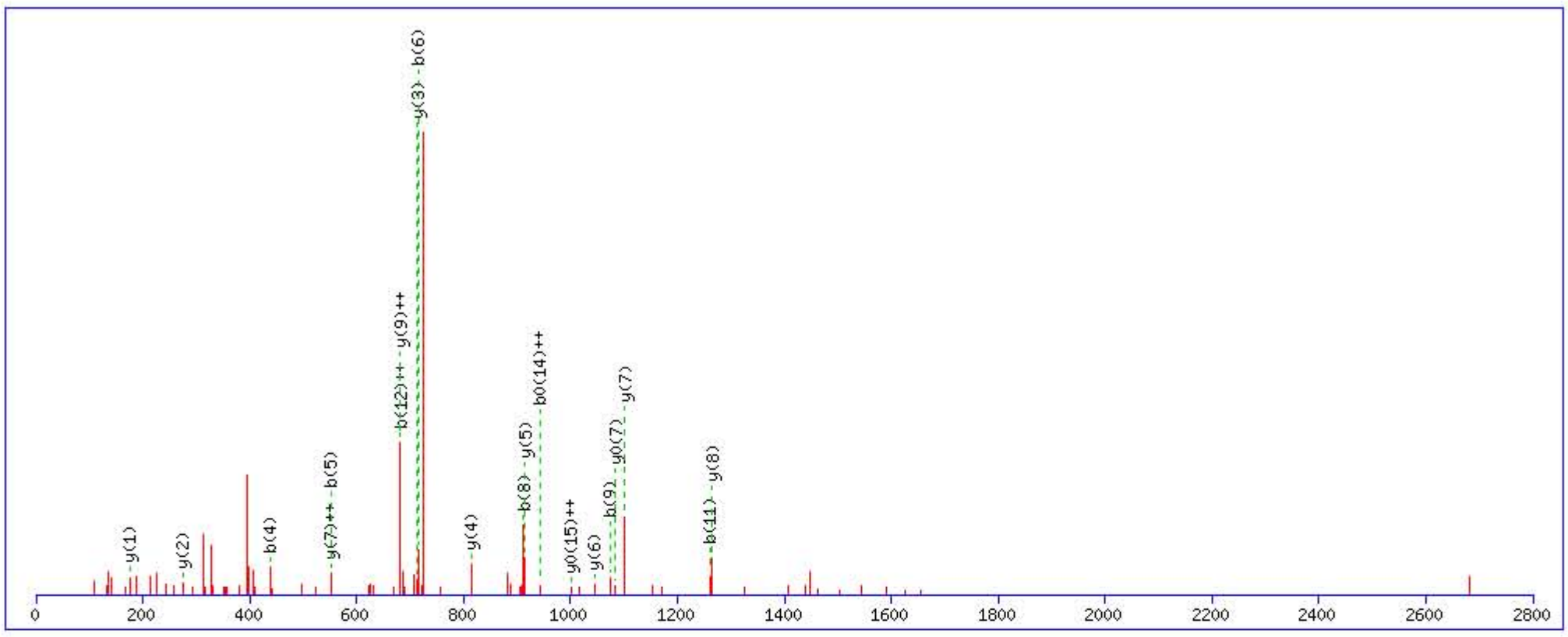
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **RPALNYPVYGETTQVR**
Found in **PRG4_HUMAN**, Proteoglycan 4 OS=Homo sapiens GN=PRG4 PE=1 SV=2

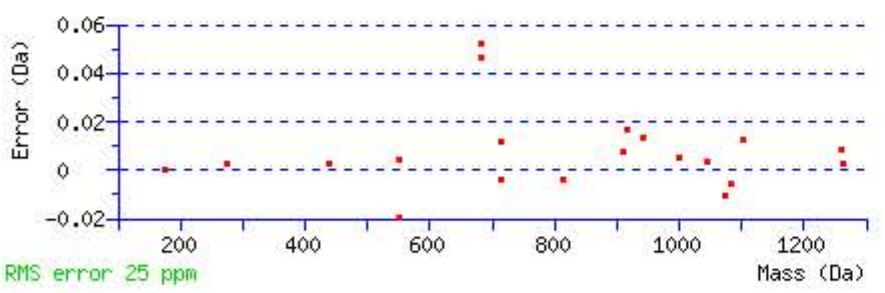
Match to Query 47980: 2174.141832 from(725.721220,3+) rtinseconds(1892) index(19534)
Title: Locus:1.1.1.3041.14 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

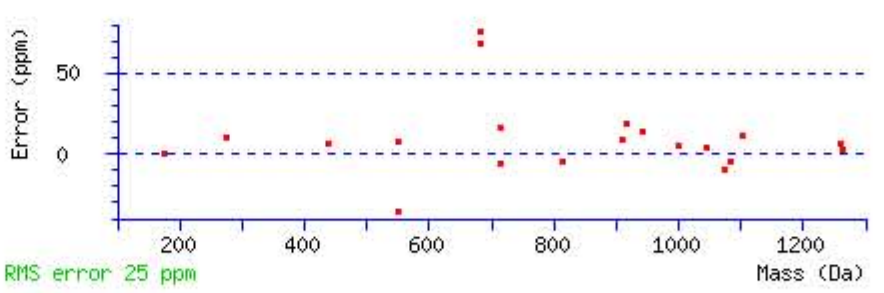
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2174.130630
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q14 : Biotin:Thermo-21345 (Q)
**Ions Score:** 29 **Expect:** 0.0019
**Matches :** 21/154 fragment ions using 53 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 157.108387 | 79.057831 | 140.081838 | 70.544557 | | | R | | | | | | | 16 |
| 2 | 254.161151 | 127.584213 | 237.134602 | 119.070939 | | | P | 2019.036812 | 1010.022044 | 2002.010263 | 1001.508770 | 2001.026247 | 1001.016762 | 15 |
| 3 | 325.198265 | 163.102770 | 308.171716 | 154.589496 | | | A | 1921.984048 | 961.495662 | 1904.957499 | 952.982388 | 1903.973483 | 952.490380 | 14 |
| 4 | *438.282329* | 219.644803 | 421.255780 | 211.131528 | | | L | 1850.946934 | 925.977105 | 1833.920385 | 917.463831 | 1832.936369 | 916.971823 | 13 |
| 5 | *552.325256* | 276.666266 | 535.298707 | 268.152992 | | | N | 1737.862870 | 869.435073 | 1720.836321 | 860.921799 | 1719.852305 | 860.429791 | 12 |
| 6 | *715.388585* | 358.197931 | 698.362036 | 349.684656 | | | Y | 1623.819943 | 812.413610 | 1606.793394 | 803.900335 | 1605.809378 | 803.408327 | 11 |
| 7 | 812.441349 | 406.724313 | 795.414800 | 398.211038 | | | P | 1460.756614 | 730.881945 | 1443.730065 | 722.368671 | 1442.746049 | 721.876663 | 10 |
| 8 | *911.509763* | 456.258520 | 894.483214 | 447.745245 | | | V | 1363.703850 | 682.355563 | 1346.677301 | 673.842289 | 1345.693285 | 673.350281 | 9 |
| 9 | *1074.573092* | 537.790184 | 1057.546543 | 529.276910 | | | Y | *1264.635436* | 632.821356 | 1247.608887 | 624.308082 | 1246.624871 | 623.816074 | 8 |
| 10 | 1131.594556 | 566.300916 | 1114.568007 | 557.787642 | | | G | *1101.572107* | 551.289692 | 1084.545558 | 542.776417 | 1083.561542 | 542.284409 | 7 |
| 11 | *1260.637149* | 630.822212 | 1243.610600 | 622.308938 | 1242.626584 | 621.816930 | E | *1044.550643* | 522.778960 | 1027.524094 | 514.265685 | 1026.540078 | 513.773677 | 6 |
| 12 | 1361.684828 | **681.346052** | 1344.658279 | 672.832778 | 1343.674263 | 672.340769 | T | *915.508050* | 458.257663 | 898.481501 | 449.744389 | 897.497485 | 449.252381 | 5 |
| 13 | 1462.732507 | 731.869891 | 1445.705958 | 723.356617 | 1444.721942 | 722.864609 | T | *814.460371* | 407.733824 | 797.433822 | 399.220549 | 796.449806 | 398.728541 | 4 |
| 14 | 1901.957833 | 951.482555 | 1884.931284 | 942.969280 | 1883.947268 | 942.477272 | Q | *713.412692* | 357.209984 | 696.386143 | 348.696710 | | | 3 |
| 15 | 2001.026247 | **1001.016762** | 1983.999698 | 992.503487 | 1983.015682 | 992.011479 | V | *274.187366* | 137.597321 | 257.160817 | 129.084047 | | | 2 |
| 16 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549840 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 29.0 | 2174.130630 | 0.011202 | RPALNYPVYGETTQVR |
| 0.0 | 2174.144363 | -0.002531 | RETSRLAWTNVASEVQVTK |

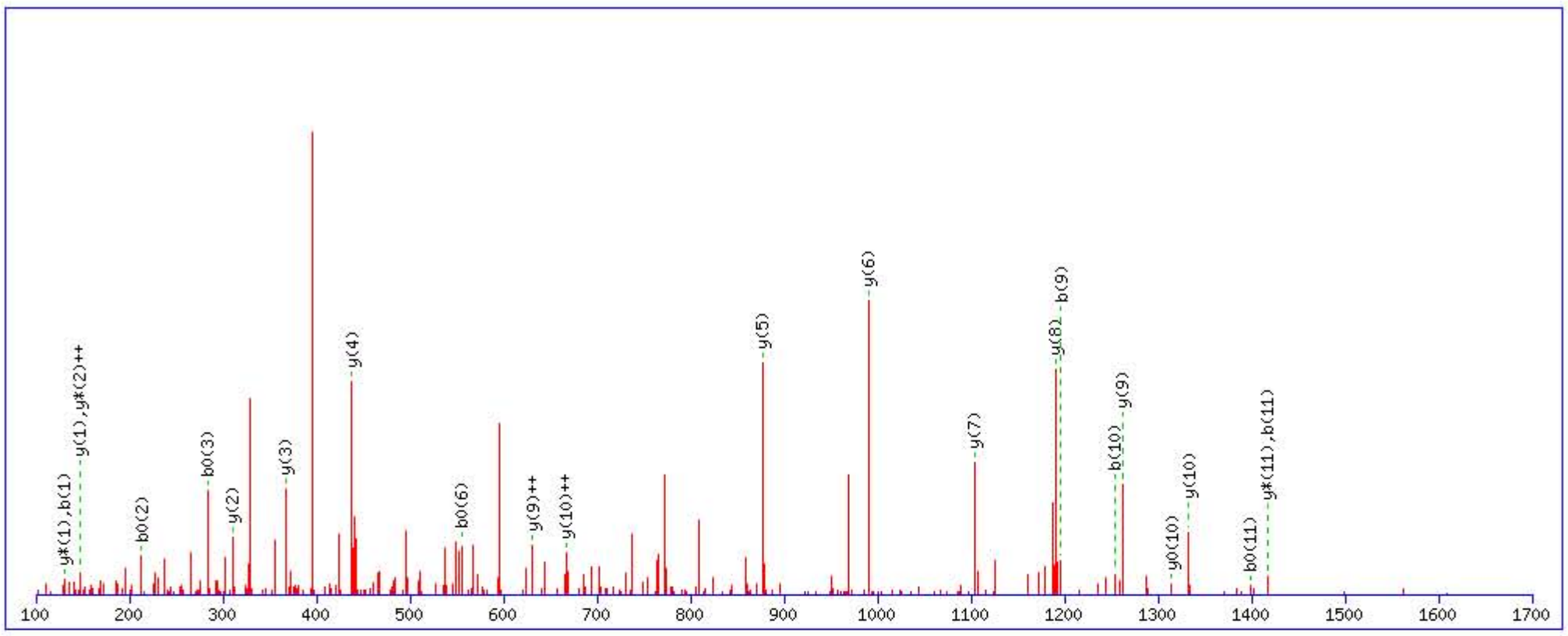
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ETAASLLQAGYK**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

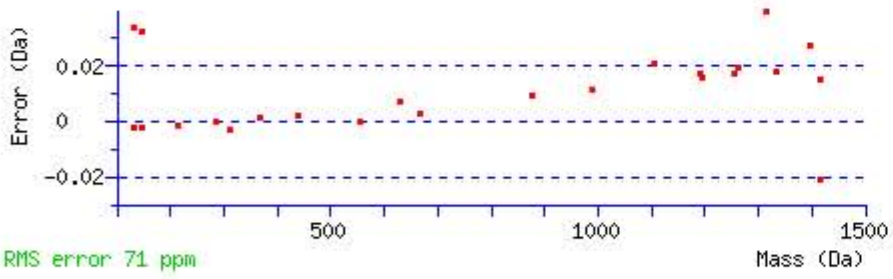
Match to Query 32844: 1561.838148 from(781.926350,2+) rtinseconds(2119) index(51137)
Title: Locus:1.1.1.1975.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

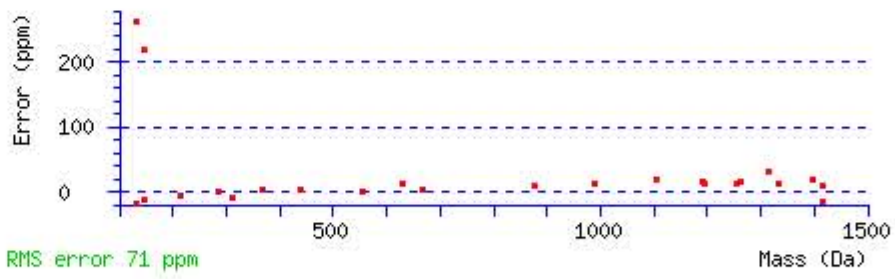
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1561.817383
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 47 **Expect:** 6.4e-005
**Matches :** 24/104 fragment ions using 57 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 12 |
| 2 | 231.097548 | 116.052412 | | | 213.086983 | 107.047130 | T | 1433.782100 | 717.394688 | 1416.755551 | 708.881414 | 1415.771535 | 708.389406 | 11 |
| 3 | 302.134662 | 151.570969 | | | 284.124097 | 142.565687 | A | *1332.734421* | 666.870848 | 1315.707872 | 658.357574 | 1314.723856 | 657.865566 | 10 |
| 4 | 373.171776 | 187.089526 | | | 355.161211 | 178.084243 | A | *1261.697307* | 631.352292 | 1244.670758 | 622.839017 | 1243.686742 | 622.347009 | 9 |
| 5 | 460.203804 | 230.605540 | | | 442.193239 | 221.600257 | S | *1190.660193* | 595.833734 | 1173.633644 | 587.320460 | 1172.649628 | 586.828452 | 8 |
| 6 | 573.287868 | 287.147572 | | | 555.277303 | 278.142290 | L | *1103.628165* | 552.317721 | 1086.601616 | 543.804446 | | | 7 |
| 7 | 686.371932 | 343.689604 | | | 668.361367 | 334.684322 | L | *990.544101* | 495.775689 | 973.517552 | 487.262414 | | | 6 |
| 8 | 1125.597258 | 563.302267 | 1108.570709 | 554.788993 | 1107.586693 | 554.296985 | Q | *877.460037* | 439.233657 | 860.433488 | 430.720382 | | | 5 |
| 9 | 1196.634372 | 598.820824 | 1179.607823 | 590.307550 | 1178.623807 | 589.815541 | A | *438.234711* | 219.620993 | 421.208162 | 211.107719 | | | 4 |
| 10 | 1253.655836 | 627.331556 | 1236.629287 | 618.818282 | 1235.645271 | 618.326273 | G | *367.197597* | 184.102436 | 350.171048 | 175.589162 | | | 3 |
| 11 | 1416.719165 | 708.863221 | 1399.692616 | 700.349946 | 1398.708600 | 699.857938 | Y | *310.176133* | 155.591705 | 293.149584 | 147.078430 | | | 2 |
| 12 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 47.0 | 1561.817383 | 0.020765 | ETAASLLQAGYK |
| 2.3 | 1561.817398 | 0.020750 | VLPEVLEKQCGYK |
| 2.1 | 1561.821243 | 0.016905 | TEKHPPVSPGRTEK |

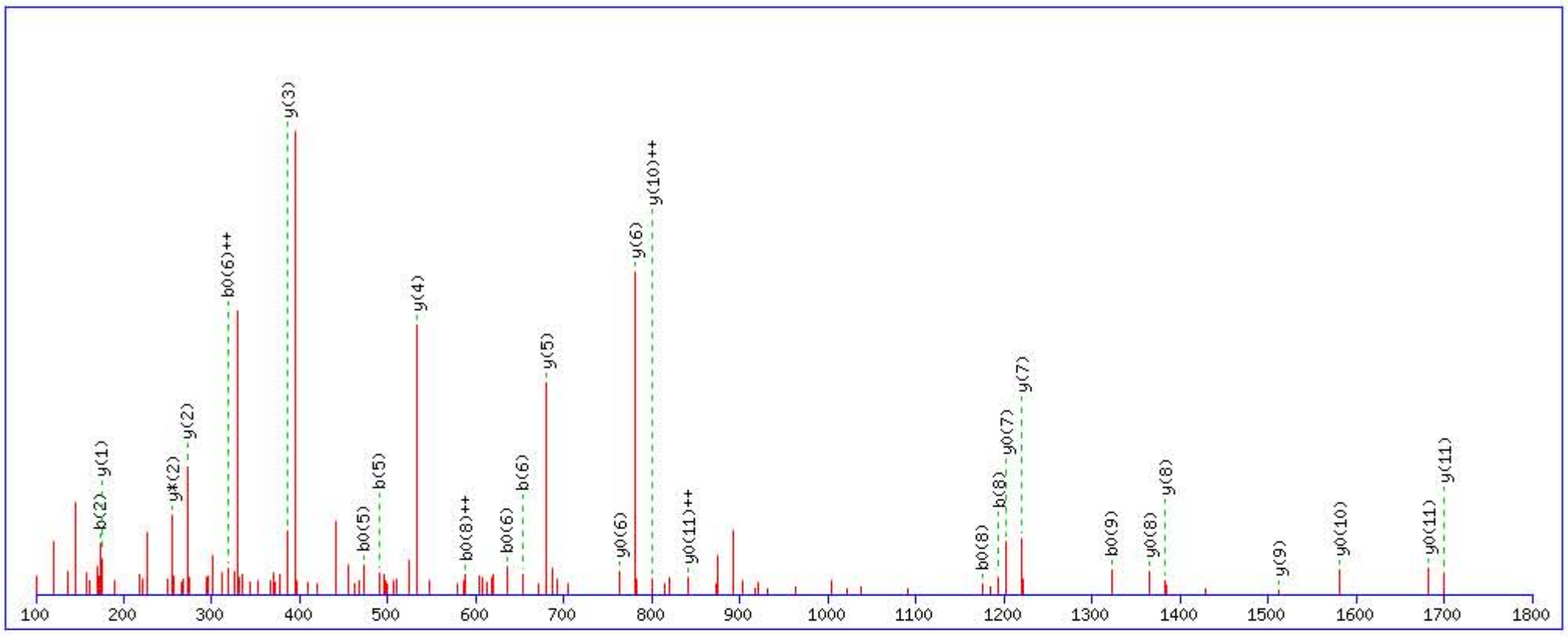
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TATSEYQTFFNPR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

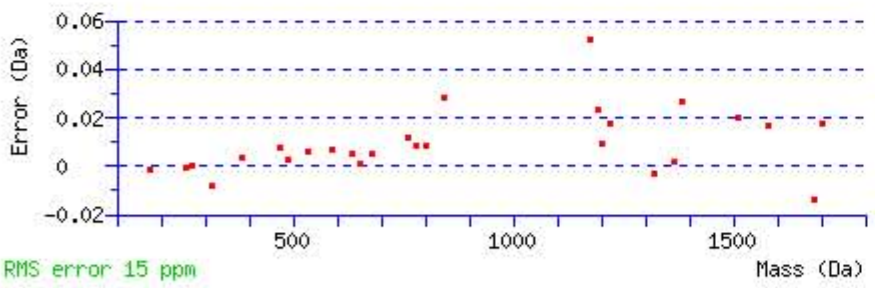
Match to Query 41727: 1871.904852 from(624.975560,3+) rtinseconds(2262) index(52086)
Title: Locus:1.1.1.2025.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

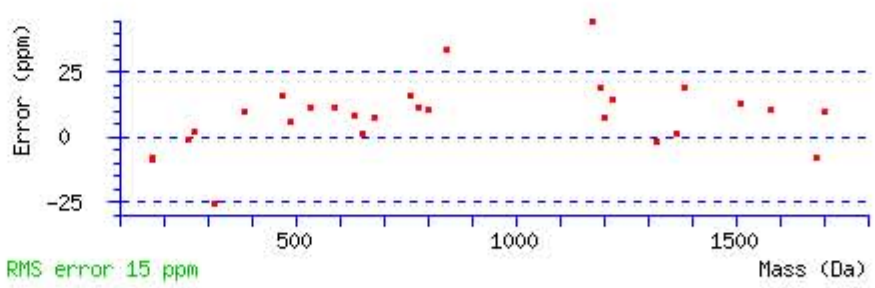
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1871.887619
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 51 **Expect:** 0.00017
**Matches :** 28/122 fragment ions using 55 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 102.054955 | 51.531116 | | | 84.044390 | 42.525833 | T | | | | | | | 13 |
| 2 | **173.092069** | 87.049672 | | | 155.081504 | 78.044390 | A | 1771.847219 | 886.427248 | 1754.820670 | 877.913973 | 1753.836654 | 877.421965 | 12 |
| 3 | 274.139748 | 137.573512 | | | 256.129183 | 128.568230 | T | *1700.810105* | 850.908691 | 1683.783556 | 842.395416 | 1682.799540 | 841.903408 | 11 |
| 4 | 361.171776 | 181.089526 | | | 343.161211 | 172.084243 | S | 1599.762426 | 800.384851 | 1582.735877 | 791.871577 | 1581.751861 | 791.379569 | 10 |
| 5 | **490.214369** | 245.610822 | | | 472.203804 | 236.605540 | E | *1512.730398* | 756.868837 | 1495.703849 | 748.355563 | 1494.719833 | 747.863555 | 9 |
| 6 | **653.277698** | 327.142487 | | | 635.267133 | 318.137205 | Y | *1383.687805* | 692.347541 | 1366.661256 | 683.834266 | 1365.677240 | 683.342258 | 8 |
| 7 | 1092.503024 | 546.755150 | 1075.476475 | 538.241876 | 1074.492459 | 537.749868 | Q | *1220.624476* | 610.815876 | 1203.597927 | 602.302602 | 1202.613911 | 601.810594 | 7 |
| 8 | **1193.550703** | 597.278990 | 1176.524154 | 588.765715 | 1175.540138 | 588.273707 | T | *781.399150* | 391.203213 | 764.372601 | 382.689939 | 763.388585 | 382.197931 | 6 |
| 9 | 1340.619117 | 670.813197 | 1323.592568 | 662.299922 | 1322.608552 | 661.807914 | F | *680.351471* | 340.679374 | 663.324922 | 332.166099 | | | 5 |
| 10 | 1487.687531 | 744.347404 | 1470.660982 | 735.834129 | 1469.676966 | 735.342121 | F | *533.283057* | 267.145167 | 516.256508 | 258.631892 | | | 4 |
| 11 | 1601.730458 | 801.368867 | 1584.703909 | 792.855593 | 1583.719893 | 792.363585 | N | *386.214643* | 193.610959 | 369.188094 | 185.097685 | | | 3 |
| 12 | 1698.783222 | 849.895249 | 1681.756673 | 841.381975 | 1680.772657 | 840.889967 | P | *272.171716* | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 13 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 51.0 | 1871.887619 | 0.017233 | TATSEYQTFFNPR |

**Mascot:** http://www.matrixscience.com/

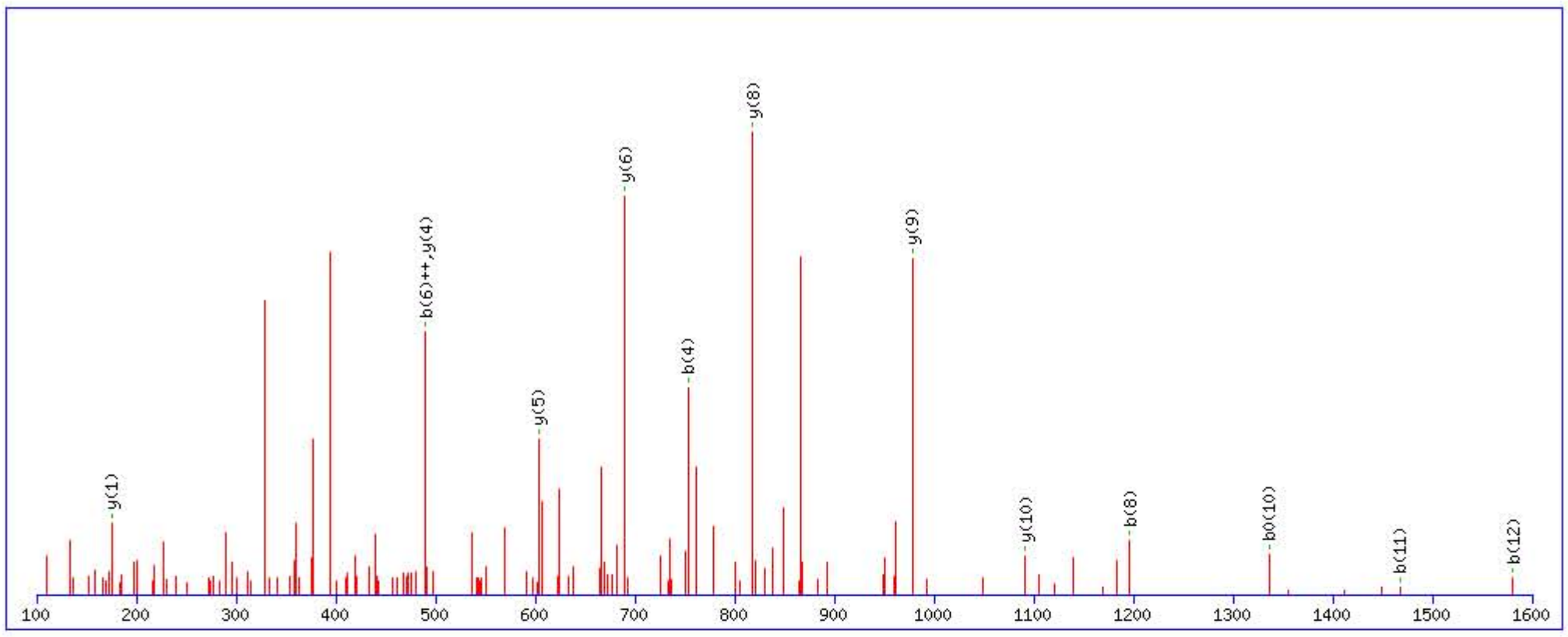
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SPQELLCGASLISDR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

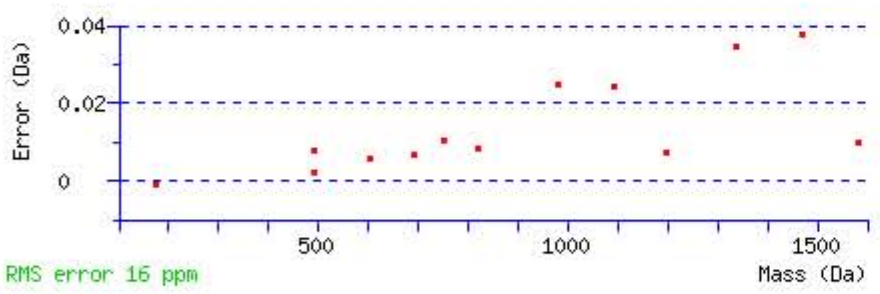
Match to Query 43223: 1956.003732 from(653.008520,3+) rtinseconds(2472) index(53195)
Title: Locus:1.1.1.2098.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

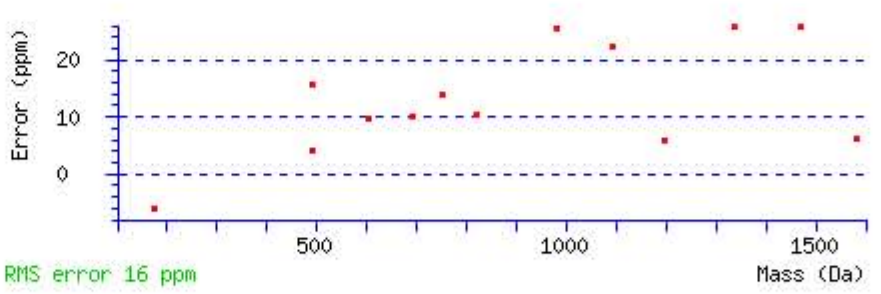
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1955.980850
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 60 **Expect:** 9.6e-006
**Matches :** 13/162 fragment ions using 14 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 15 |
| 2 | 185.092068 | 93.049672 | | | 167.081503 | 84.044389 | P | 1869.956117 | 935.481697 | 1852.929568 | 926.968422 | 1851.945552 | 926.476414 | 14 |
| 3 | 624.317394 | 312.662335 | 607.290845 | 304.149061 | 606.306829 | 303.657053 | Q | 1772.903353 | 886.955314 | 1755.876804 | 878.442040 | 1754.892788 | 877.950032 | 13 |
| 4 | *753.359987* | 377.183632 | 736.333438 | 368.670357 | 735.349422 | 368.178349 | E | 1333.678027 | 667.342652 | 1316.651478 | 658.829377 | 1315.667462 | 658.337369 | 12 |
| 5 | 866.444051 | 433.725664 | 849.417502 | 425.212389 | 848.433486 | 424.720381 | L | 1204.635434 | 602.821355 | 1187.608885 | 594.308081 | 1186.624869 | 593.816073 | 11 |
| 6 | 979.528115 | **490.267696** | 962.501566 | 481.754421 | 961.517550 | 481.262413 | L | *1091.551370* | 546.279323 | 1074.524821 | 537.766049 | 1073.540805 | 537.274040 | 10 |
| 7 | 1139.558764 | 570.283020 | 1122.532215 | 561.769746 | 1121.548199 | 561.277738 | C | *978.467306* | 489.737291 | 961.440757 | 481.224017 | 960.456741 | 480.732009 | 9 |
| 8 | *1196.580228* | 598.793752 | 1179.553679 | 590.280478 | 1178.569663 | 589.788470 | G | *818.436657* | 409.721967 | 801.410108 | 401.208692 | 800.426092 | 400.716684 | 8 |
| 9 | 1267.617342 | 634.312309 | 1250.590793 | 625.799035 | 1249.606777 | 625.307027 | A | 761.415193 | 381.211235 | 744.388644 | 372.697960 | 743.404628 | 372.205952 | 7 |
| 10 | 1354.649370 | 677.828323 | 1337.622821 | 669.315049 | 1336.638805 | 668.823041 | S | *690.378079* | 345.692678 | 673.351530 | 337.179403 | 672.367514 | 336.687395 | 6 |
| 11 | *1467.733434* | 734.370355 | 1450.706885 | 725.857081 | 1449.722869 | 725.365073 | L | *603.346051* | 302.176664 | 586.319502 | 293.663389 | 585.335486 | 293.171381 | 5 |
| 12 | *1580.817498* | 790.912387 | 1563.790949 | 782.399113 | 1562.806933 | 781.907104 | I | *490.261987* | 245.634631 | 473.235438 | 237.121357 | 472.251422 | 236.629349 | 4 |
| 13 | 1667.849526 | 834.428401 | 1650.822977 | 825.915127 | 1649.838961 | 825.423118 | S | 377.177923 | 189.092600 | 360.151374 | 180.579325 | 359.167358 | 180.087317 | 3 |
| 14 | 1782.876469 | 891.941873 | 1765.849920 | 883.428598 | 1764.865904 | 882.936590 | D | 290.145895 | 145.576585 | 273.119346 | 137.063311 | 272.135330 | 136.571303 | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 60.4 | 1955.980850 | 0.022882 | SPQELLCGASLISDR |
| 6.4 | 1956.025101 | -0.021369 | VYQVLAIMDFNSTRKR |
| 3.9 | 1955.989594 | 0.014138 | MKMVSQSFTQRFR |
| 1.3 | 1955.989594 | 0.014138 | MKMVSQSFTQRFR |
| 0.5 | 1955.975464 | 0.028268 | QHSLHSAQWFAGAFTLR |

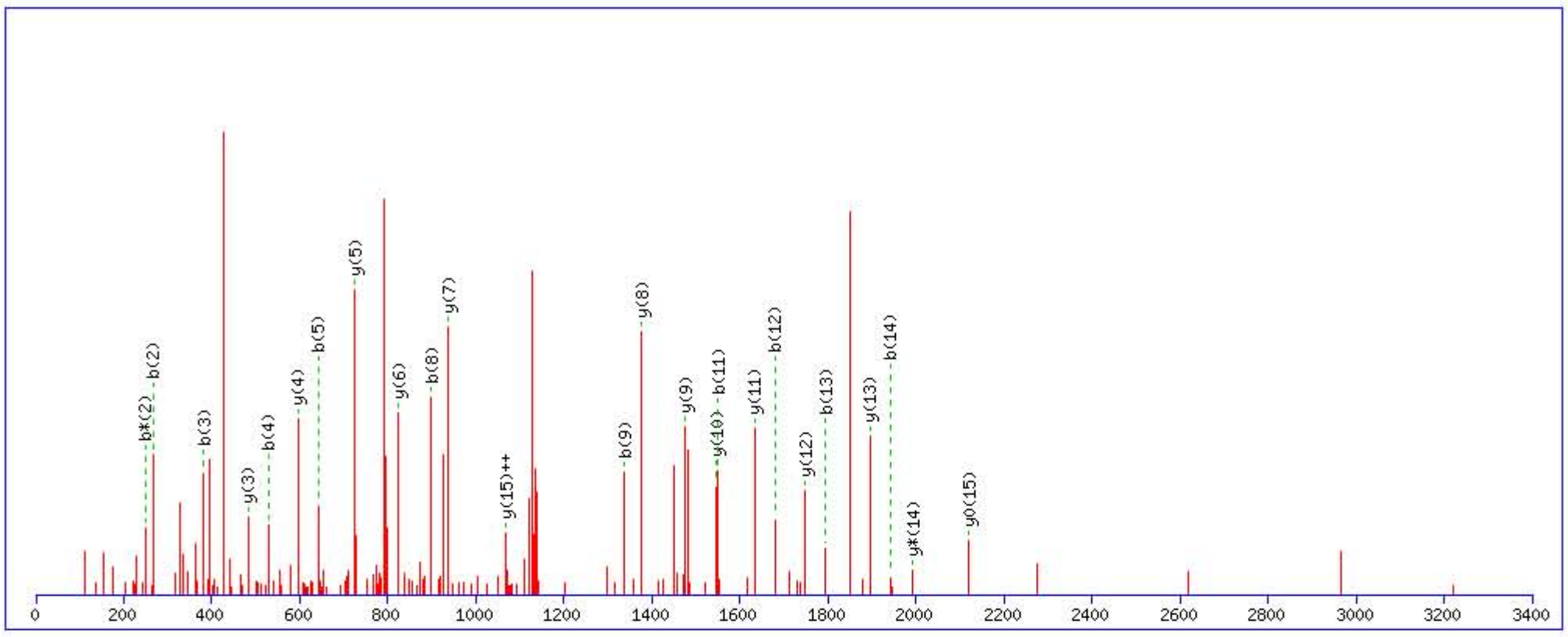
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HQDFNSAVQLVENFCR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

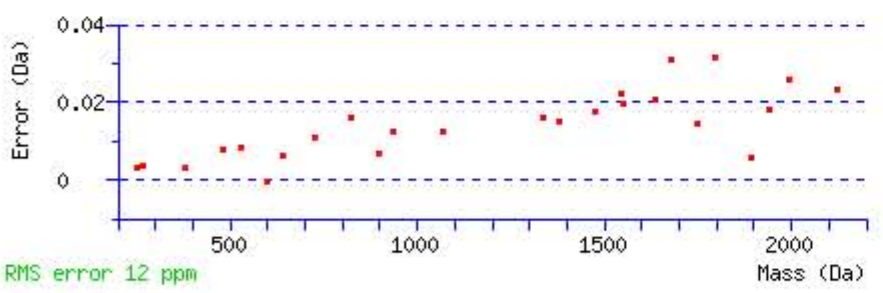
Match to Query 49959: 2274.082628 from(1138.048590,2+) rtinseconds(2448) index(68949)
Title: Locus:1.1.1.2127.11 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

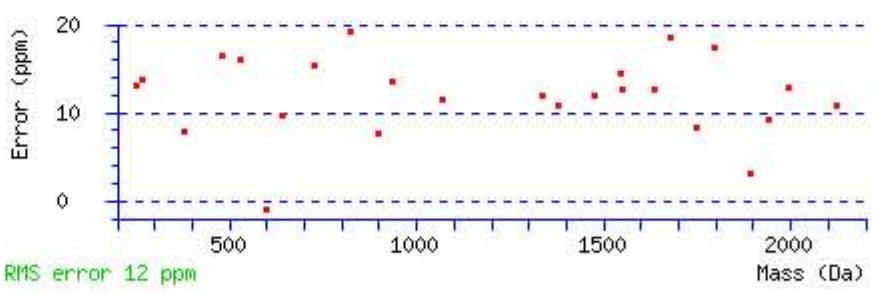
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2274.067398
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 82 **Expect:** 2.7e-007
**Matches :** 25/166 fragment ions using 38 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 16 |
| 2 | *266.124766* | 133.566021 | 249.098217 | 125.052746 | | | Q | 2138.015757 | 1069.511516 | 2120.989208 | 1060.998242 | 2120.005192 | 1060.506234 | 15 |
| 3 | *381.151709* | 191.079492 | 364.125160 | 182.566218 | 363.141144 | 182.074210 | D | 2009.957179 | 1005.482228 | 1992.930630 | 996.968953 | 1991.946614 | 996.476945 | 14 |
| 4 | *528.220123* | 264.613700 | 511.193574 | 256.100425 | 510.209558 | 255.608417 | F | *1894.930236* | 947.968756 | 1877.903687 | 939.455482 | 1876.919671 | 938.963474 | 13 |
| 5 | *642.263050* | 321.635163 | 625.236501 | 313.121889 | 624.252485 | 312.629881 | N | *1747.861822* | 874.434549 | 1730.835273 | 865.921275 | 1729.851257 | 865.429267 | 12 |
| 6 | 729.295078 | 365.151177 | 712.268529 | 356.637903 | 711.284513 | 356.145895 | S | *1633.818895* | 817.413086 | 1616.792346 | 808.899811 | 1615.808330 | 808.407803 | 11 |
| 7 | 800.332192 | 400.669734 | 783.305643 | 392.156459 | 782.321627 | 391.664451 | A | *1546.786867* | 773.897072 | 1529.760318 | 765.383797 | 1528.776302 | 764.891789 | 10 |
| 8 | *899.400606* | 450.203941 | 882.374057 | 441.690666 | 881.390041 | 441.198658 | V | *1475.749753* | 738.378515 | 1458.723204 | 729.865240 | 1457.739188 | 729.373232 | 9 |
| 9 | *1338.625932* | 669.816604 | 1321.599383 | 661.303330 | 1320.615367 | 660.811322 | Q | *1376.681339* | 688.844308 | 1359.654790 | 680.331033 | 1358.670774 | 679.839025 | 8 |
| 10 | 1451.709996 | 726.358636 | 1434.683447 | 717.845362 | 1433.699431 | 717.353354 | L | *937.456013* | 469.231645 | 920.429464 | 460.718370 | 919.445448 | 460.226362 | 7 |
| 11 | *1550.778410* | 775.892843 | 1533.751861 | 767.379569 | 1532.767845 | 766.887561 | V | *824.371949* | 412.689613 | 807.345400 | 404.176338 | 806.361384 | 403.684330 | 6 |
| 12 | *1679.821003* | 840.414140 | 1662.794454 | 831.900865 | 1661.810438 | 831.408857 | E | *725.303535* | 363.155406 | 708.276986 | 354.642131 | 707.292970 | 354.150123 | 5 |
| 13 | *1793.863930* | 897.435603 | 1776.837381 | 888.922329 | 1775.853365 | 888.430321 | N | *596.260942* | 298.634109 | 579.234393 | 290.120835 | | | 4 |
| 14 | *1940.932344* | 970.969810 | 1923.905795 | 962.456536 | 1922.921779 | 961.964528 | F | *482.218015* | 241.612646 | 465.191466 | 233.099371 | | | 3 |
| 15 | 2100.962993 | 1050.985135 | 2083.936444 | 1042.471860 | 2082.952428 | 1041.979852 | C | 335.149601 | 168.078438 | 318.123052 | 159.565164 | | | 2 |
| 16 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 81.8 | 2274.067398 | 0.015230 | HQDFNSAVQLVENFCR |
| 11.7 | 2274.067398 | 0.015230 | HQDFNSAVQLVENFCR |

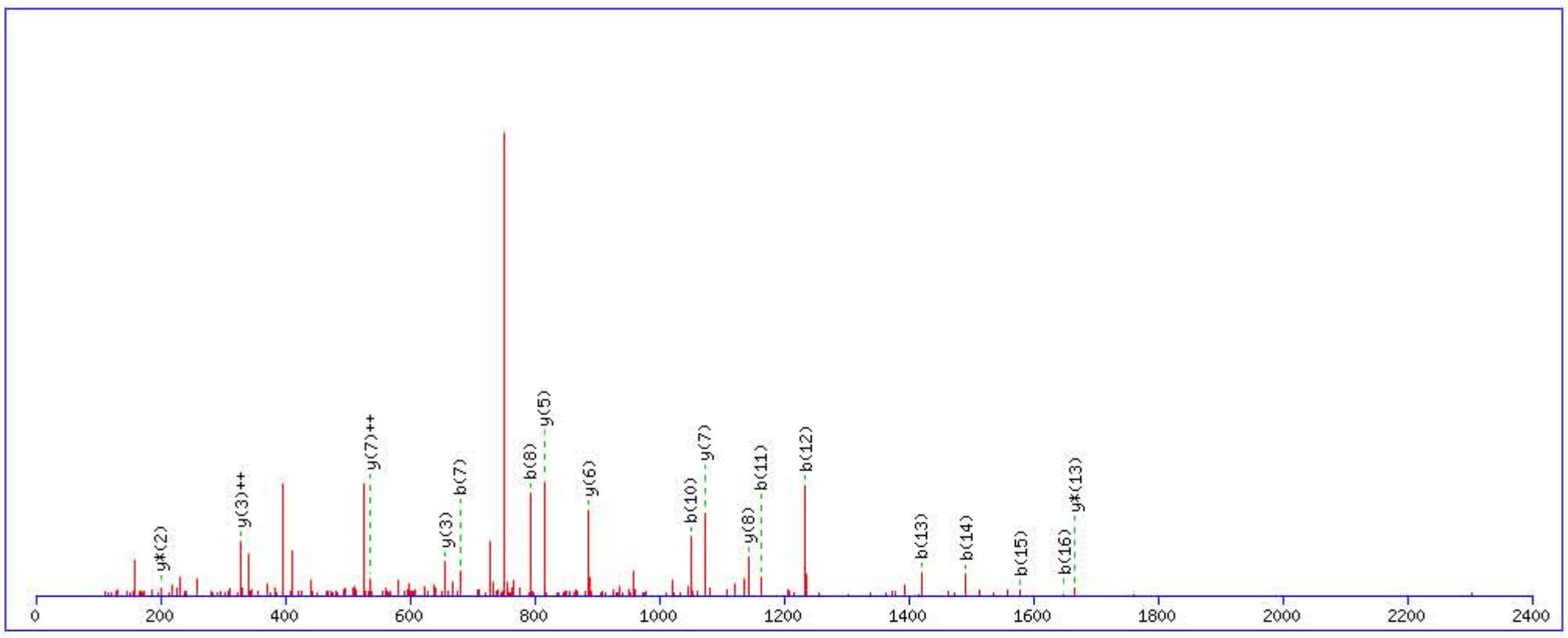
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LAVTTHGLPCLAWASAQAK**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

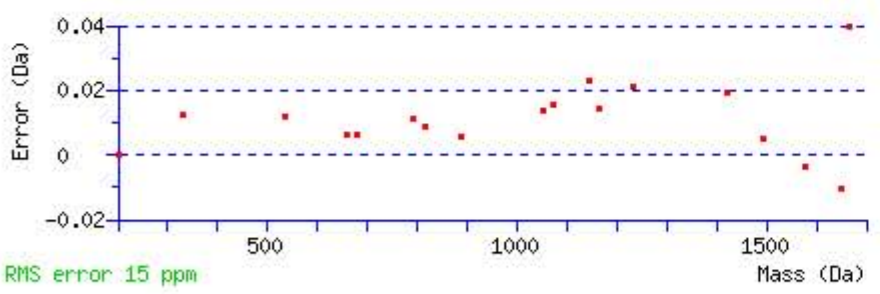
Match to Query 50628: 2305.240302 from(769.420710,3+) rtinseconds(2381) index(52753)
Title: Locus:1.1.1.2066.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

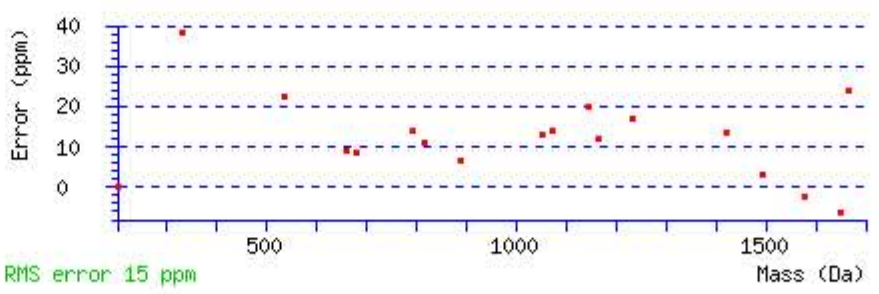
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2305.207504
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q17** : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.0006
**Matches** : 18/170 fragment ions using 34 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 19 |
| 2 | 185.128454 | 93.067865 | | | | | A | 2193.130730 | 1097.069003 | 2176.104181 | 1088.555728 | 2175.120165 | 1088.063720 | 18 |
| 3 | 284.196868 | 142.602072 | | | | | V | 2122.093616 | 1061.550446 | 2105.067067 | 1053.037171 | 2104.083051 | 1052.545163 | 17 |
| 4 | 385.244547 | 193.125912 | | | 367.233982 | 184.120629 | T | 2023.025202 | 1012.016239 | 2005.998653 | 1003.502965 | 2005.014637 | 1003.010957 | 16 |
| 5 | 486.292226 | 243.649751 | | | 468.281661 | 234.644469 | T | 1921.977523 | 961.492400 | 1904.950974 | 952.979125 | 1903.966958 | 952.487117 | 15 |
| 6 | 623.351138 | 312.179207 | | | 605.340573 | 303.173925 | H | 1820.929844 | 910.968560 | 1803.903295 | 902.455286 | 1802.919279 | 901.963278 | 14 |
| 7 | *680.372602* | 340.689939 | | | 662.362037 | 331.684657 | G | 1683.870932 | 842.439104 | 1666.844383 | 833.925830 | 1665.860367 | 833.433822 | 13 |
| 8 | *793.456666* | 397.231971 | | | 775.446101 | 388.226689 | L | 1626.849468 | 813.928372 | 1609.822919 | 805.415098 | 1608.838903 | 804.923090 | 12 |
| 9 | 890.509430 | 445.758353 | | | 872.498865 | 436.753071 | P | 1513.765404 | 757.386340 | 1496.738855 | 748.873066 | 1495.754839 | 748.381058 | 11 |
| 10 | *1050.540079* | 525.773678 | | | 1032.529514 | 516.768395 | C | 1416.712640 | 708.859958 | 1399.686091 | 700.346684 | 1398.702075 | 699.854675 | 10 |
| 11 | *1163.624143* | 582.315710 | | | 1145.613578 | 573.310427 | L | 1256.681991 | 628.844634 | 1239.655442 | 620.331359 | 1238.671426 | 619.839351 | 9 |
| 12 | *1234.661257* | 617.834267 | | | 1216.650692 | 608.828984 | A | **1143.597927** | 572.302602 | 1126.571378 | 563.789327 | 1125.587362 | 563.297319 | 8 |
| 13 | *1420.740570* | 710.873923 | | | 1402.730005 | 701.868640 | W | **1072.560813** | 536.784045 | 1055.534264 | 528.270770 | 1054.550248 | 527.778762 | 7 |
| 14 | *1491.777684* | 746.392480 | | | 1473.767119 | 737.387197 | A | **886.481500** | 443.744388 | 869.454951 | 435.231114 | 868.470935 | 434.739106 | 6 |
| 15 | *1578.809712* | 789.908494 | | | 1560.799147 | 780.903212 | S | **815.444386** | 408.225831 | 798.417837 | 399.712557 | 797.433821 | 399.220549 | 5 |
| 16 | *1649.846826* | 825.427051 | | | 1631.836261 | 816.421768 | A | 728.412358 | 364.709817 | 711.385809 | 356.196543 | | | 4 |
| 17 | 2089.072152 | 1045.039714 | 2072.045603 | 1036.526439 | 2071.061587 | 1036.034431 | Q | **657.375244** | 329.191260 | 640.348695 | 320.677986 | | | 3 |
| 18 | 2160.109266 | 1080.558271 | 2143.082717 | 1072.044996 | 2142.098701 | 1071.552988 | A | 218.149918 | 109.578597 | 201.123369 | 101.065323 | | | 2 |
| 19 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.3 | 2305.207504 | 0.032798 | LAVTTHGLPCLAWASAQAK |

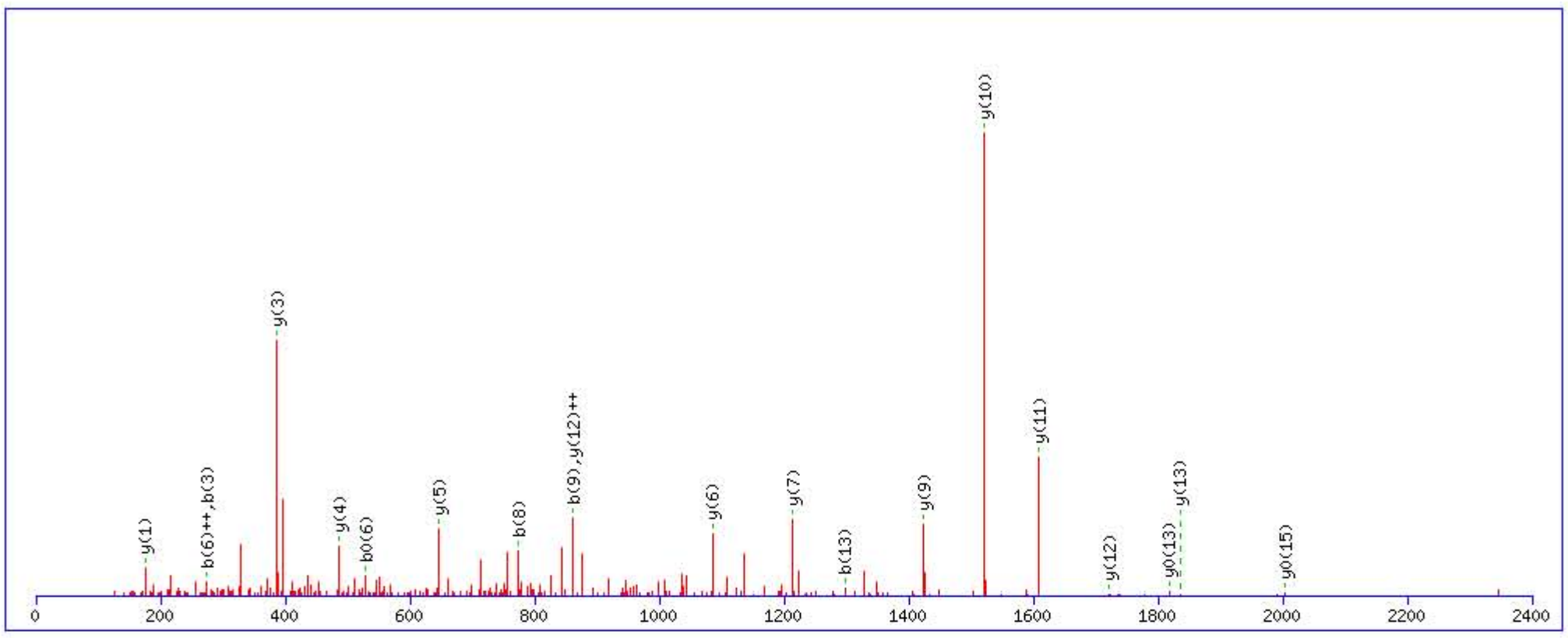
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SEGSSVNLSPPLEQCVPDR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

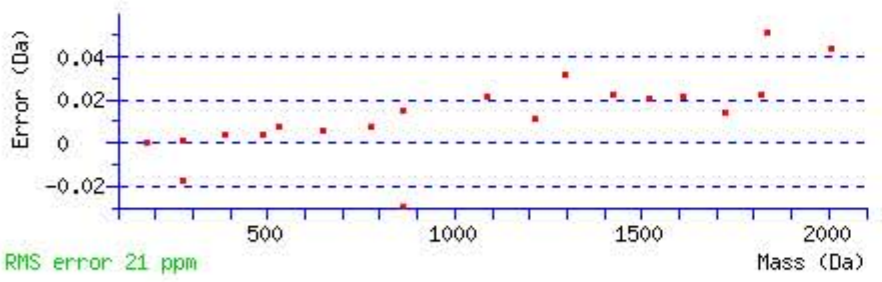
Match to Query 51654: 2381.170092 from(794.730640,3+) rtinseconds(2174) index(51564)
Title: Locus:1.1.1.1994.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

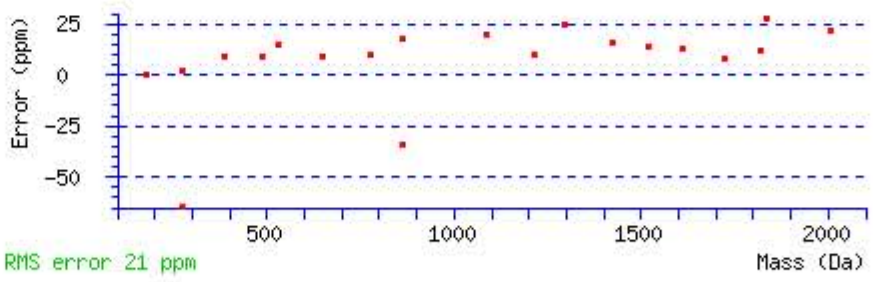
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2381.135529
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q14 : Biotin:Thermo-21345 (Q)
**Ions Score:** 100 **Expect:** 1.4e-009
**Matches :** 20/202 fragment ions using 20 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 19 |
| 2 | 217.081897 | 109.044586 | | | 199.071332 | 100.039304 | E | 2295.110779 | 1148.059027 | 2278.084230 | 1139.545753 | 2277.100214 | 1139.053745 | 18 |
| 3 | 274.103361 | 137.555319 | | | 256.092796 | 128.550036 | G | 2166.068186 | 1083.537731 | 2149.041637 | 1075.024456 | 2148.057621 | 1074.532448 | 17 |
| 4 | 361.135389 | 181.071332 | | | 343.124824 | 172.066050 | S | 2109.046722 | 1055.026999 | 2092.020173 | 1046.513724 | 2091.036157 | 1046.021716 | 16 |
| 5 | 448.167417 | 224.587346 | | | 430.156852 | 215.582064 | S | 2022.014694 | 1011.510985 | 2004.988145 | 1002.997711 | 2004.004129 | 1002.505703 | 15 |
| 6 | 547.235831 | 274.121554 | | | 529.225266 | 265.116271 | V | 1934.982666 | 967.994971 | 1917.956117 | 959.481697 | 1916.972101 | 958.989689 | 14 |
| 7 | 661.278758 | 331.143017 | 644.252209 | 322.629742 | 643.268193 | 322.137734 | N | *1835.914252* | 918.460764 | 1818.887703 | 909.947490 | 1817.903687 | 909.455482 | 13 |
| 8 | 774.362822 | 387.685049 | 757.336273 | 379.171774 | 756.352257 | 378.679766 | L | *1721.871325* | 861.439301 | 1704.844776 | 852.926026 | 1703.860760 | 852.434018 | 12 |
| 9 | 861.394850 | 431.201063 | 844.368301 | 422.687788 | 843.384285 | 422.195780 | S | *1608.787261* | 804.897269 | 1591.760712 | 796.383994 | 1590.776696 | 795.891986 | 11 |
| 10 | 958.447614 | 479.727445 | 941.421065 | 471.214170 | 940.437049 | 470.722162 | P | *1521.755233* | 761.381255 | 1504.728684 | 752.867980 | 1503.744668 | 752.375972 | 10 |
| 11 | 1055.500378 | 528.253827 | 1038.473829 | 519.740553 | 1037.489813 | 519.248544 | P | *1424.702469* | 712.854873 | 1407.675920 | 704.341598 | 1406.691904 | 703.849590 | 9 |
| 12 | 1168.584442 | 584.795859 | 1151.557893 | 576.282584 | 1150.573877 | 575.790576 | L | 1327.649705 | 664.328491 | 1310.623156 | 655.815216 | 1309.639140 | 655.323208 | 8 |
| 13 | 1297.627035 | 649.317155 | 1280.600486 | 640.803881 | 1279.616470 | 640.311873 | E | *1214.565641* | 607.786459 | 1197.539092 | 599.273184 | 1196.555076 | 598.781176 | 7 |
| 14 | 1736.852361 | 868.929819 | 1719.825812 | 860.416544 | 1718.841796 | 859.924536 | Q | *1085.523048* | 543.265162 | 1068.496499 | 534.751888 | 1067.512483 | 534.259880 | 6 |
| 15 | 1896.883010 | 948.945143 | 1879.856461 | 940.431869 | 1878.872445 | 939.939861 | C | *646.297722* | 323.652499 | 629.271173 | 315.139225 | 628.287157 | 314.647217 | 5 |
| 16 | 1995.951424 | 998.479350 | 1978.924875 | 989.966076 | 1977.940859 | 989.474068 | V | *486.267073* | 243.637174 | 469.240524 | 235.123900 | 468.256508 | 234.631892 | 4 |
| 17 | 2093.004188 | 1047.005732 | 2075.977639 | 1038.492457 | 2074.993623 | 1038.000449 | P | *387.198659* | 194.102967 | 370.172110 | 185.589693 | 369.188094 | 185.097685 | 3 |
| 18 | 2208.031131 | 1104.519203 | 2191.004582 | 1096.005929 | 2190.020566 | 1095.513921 | D | 290.145895 | 145.576585 | 273.119346 | 137.063311 | 272.135330 | 136.571303 | 2 |
| 19 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 100.4 | 2381.135529 | 0.034563 | SEGSSVNLSPPLEQCVPDR |
| 5.7 | 2381.201736 | -0.031644 | CIDSANLKVHQIEKEMR |
| 4.3 | 2381.168564 | 0.001528 | GNAVVGYLQCFDLEGESGLVVR |

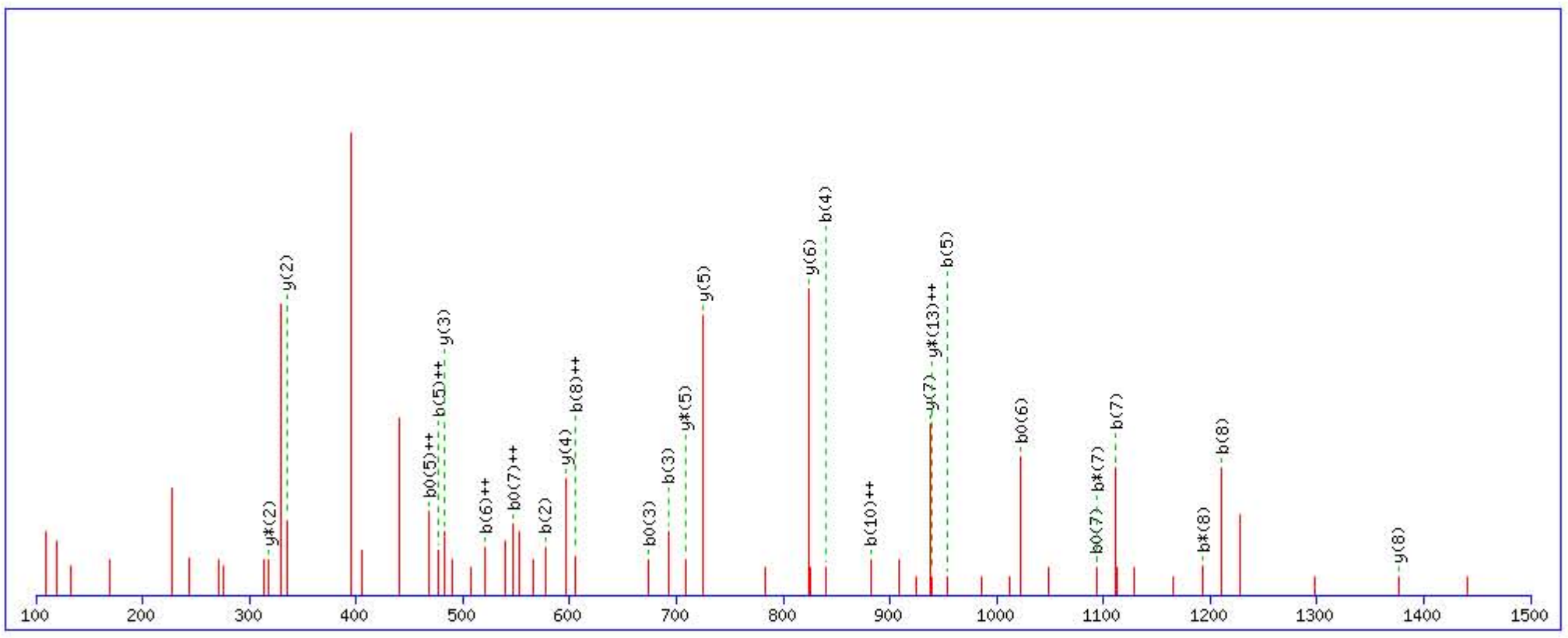
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HQDFNSAVQLVENFCR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

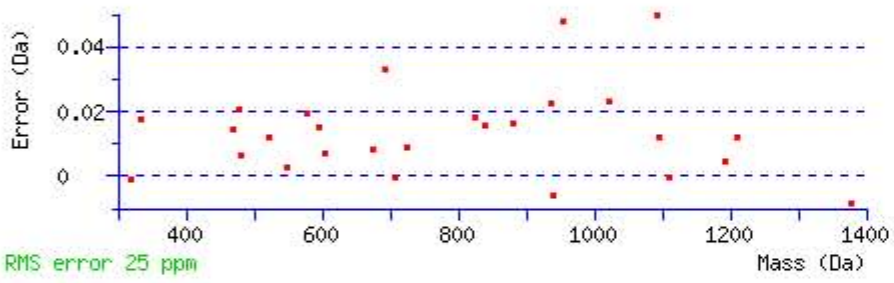
Match to Query 55349: 2585.264856 from(647.323490,4+) rtinseconds(2654) index(54311)
Title: Locus:1.1.1.2161.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

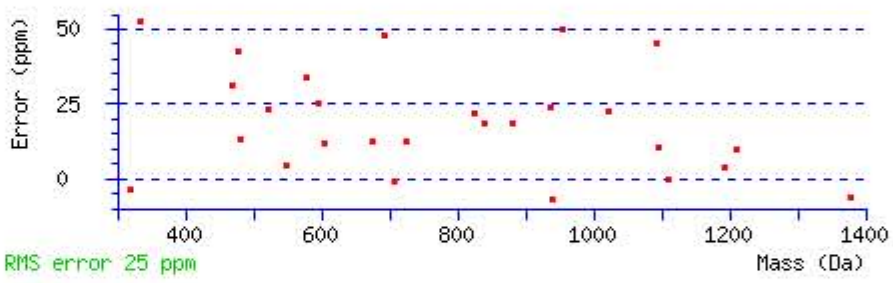
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2585.234146
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.013
**Matches :** 27/166 fragment ions using 57 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 16 |
| 2 | *577.291514* | 289.149395 | 560.264965 | 280.636121 | | | Q | 2449.182505 | 1225.094890 | 2432.155956 | 1216.581616 | 2431.171940 | 1216.089608 | 15 |
| 3 | *692.318457* | 346.662867 | 675.291908 | 338.149592 | 674.307892 | 337.657584 | D | 2009.957179 | 1005.482228 | 1992.930630 | 996.968953 | 1991.946614 | 996.476945 | 14 |
| 4 | *839.386871* | 420.197073 | 822.360322 | 411.683799 | 821.376306 | 411.191791 | F | 1894.930236 | 947.968756 | 1877.903687 | 939.455482 | 1876.919671 | 938.963473 | 13 |
| 5 | *953.429798* | 477.218537 | 936.403249 | 468.705262 | 935.419233 | 468.213254 | N | 1747.861822 | 874.434549 | 1730.835273 | 865.921275 | 1729.851257 | 865.429267 | 12 |
| 6 | 1040.461826 | 520.734551 | 1023.435277 | 512.221276 | 1022.451261 | 511.729268 | S | 1633.818895 | 817.413086 | 1616.792346 | 808.899811 | 1615.808330 | 808.407803 | 11 |
| 7 | *1111.498940* | 556.253108 | 1094.472391 | 547.739834 | 1093.488375 | 547.247825 | A | 1546.786867 | 773.897072 | 1529.760318 | 765.383797 | 1528.776302 | 764.891789 | 10 |
| 8 | *1210.567354* | 605.787315 | 1193.540805 | 597.274041 | 1192.556789 | 596.782033 | V | 1475.749753 | 738.378515 | 1458.723204 | 729.865240 | 1457.739188 | 729.373232 | 9 |
| 9 | 1649.792680 | 825.399978 | 1632.766131 | 816.886704 | 1631.782115 | 816.394696 | Q | *1376.681339* | 688.844308 | 1359.654790 | 680.331033 | 1358.670774 | 679.839025 | 8 |
| 10 | 1762.876744 | 881.942010 | 1745.850195 | 873.428736 | 1744.866179 | 872.936728 | L | *937.456013* | 469.231644 | 920.429464 | 460.718370 | 919.445448 | 460.226362 | 7 |
| 11 | 1861.945158 | 931.476217 | 1844.918609 | 922.962943 | 1843.934593 | 922.470935 | V | *824.371949* | 412.689612 | 807.345400 | 404.176338 | 806.361384 | 403.684330 | 6 |
| 12 | 1990.987751 | 995.997514 | 1973.961202 | 987.484239 | 1972.977186 | 986.992231 | E | *725.303535* | 363.155405 | 708.276986 | 354.642131 | 707.292970 | 354.150123 | 5 |
| 13 | 2105.030678 | 1053.018977 | 2088.004129 | 1044.505702 | 2087.020113 | 1044.013694 | N | *596.260942* | 298.634109 | 579.234393 | 290.120834 | | | 4 |
| 14 | 2252.099092 | 1126.553184 | 2235.072543 | 1118.039909 | 2234.088527 | 1117.547901 | F | *482.218015* | 241.612645 | 465.191466 | 233.099371 | | | 3 |
| 15 | 2412.129741 | 1206.568508 | 2395.103192 | 1198.055234 | 2394.119176 | 1197.563226 | C | *335.149601* | 168.078438 | 318.123052 | 159.565164 | | | 2 |
| 16 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.1 | 2585.234146 | 0.030710 | HQDFNSAVQLVENFCR |

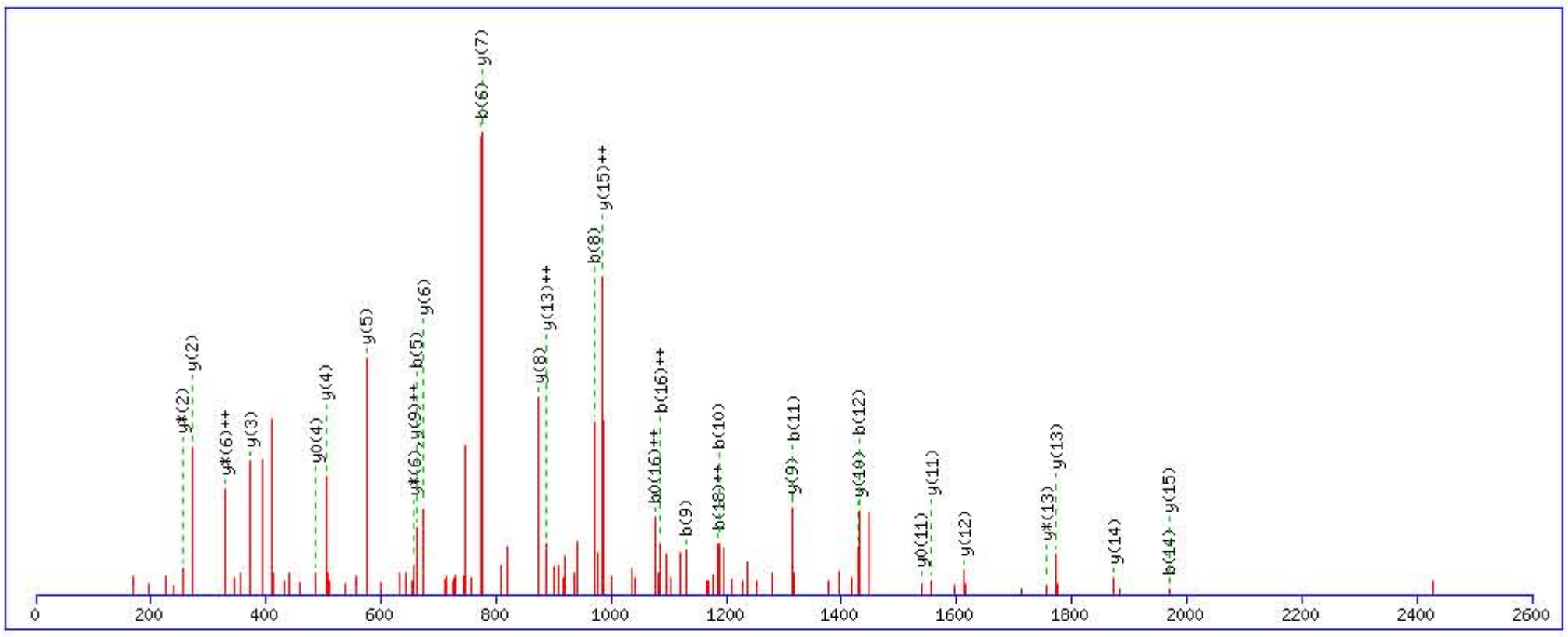
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **RQECSIPVCGQDQVTVAMTPR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

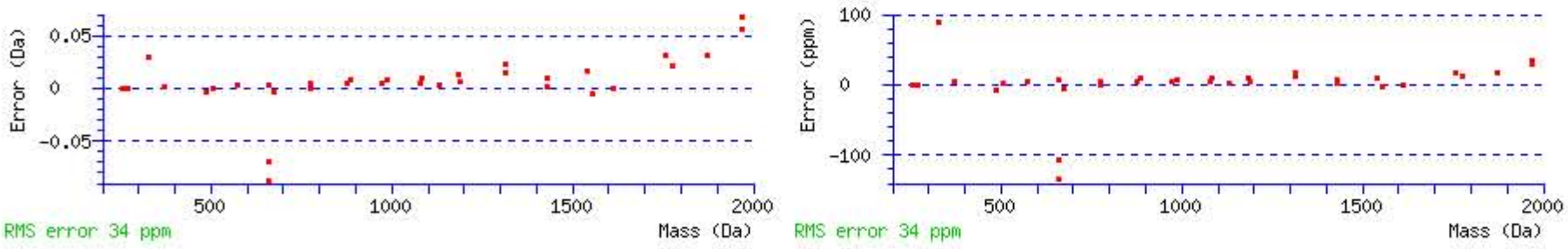
Match to Query 56846: 2742.332382 from(915.118070,3+) rtinseconds(1989) index(66365)
Title: Locus:1.1.1.1967.10 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2742.307404
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 91 **Expect:** 3.3e-009
**Matches :** 34/232 fragment ions using 53 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 157.108387 | 79.057831 | 140.081838 | 70.544557 | | | R | | | | | | | 21 |
| 2 | 285.166965 | 143.087121 | 268.140416 | 134.573846 | | | Q | 2587.213551 | 1294.110413 | 2570.187002 | 1285.597139 | 2569.202986 | 1285.105131 | 20 |
| 3 | 414.209558 | 207.608417 | 397.183009 | 199.095143 | 396.198993 | 198.603135 | E | 2459.154973 | 1230.081124 | 2442.128424 | 1221.567850 | 2441.144408 | 1221.075842 | 19 |
| 4 | 574.240207 | 287.623742 | 557.213658 | 279.110467 | 556.229642 | 278.618459 | C | 2330.112380 | 1165.559828 | 2313.085831 | 1157.046553 | 2312.101815 | 1156.554545 | 18 |
| 5 | **661.272235** | 331.139756 | 644.245686 | 322.626481 | 643.261670 | 322.134473 | S | 2170.081731 | 1085.544503 | 2153.055182 | 1077.031229 | 2152.071166 | 1076.539221 | 17 |
| 6 | **774.356299** | 387.681788 | 757.329750 | 379.168513 | 756.345734 | 378.676505 | I | 2083.049703 | 1042.028489 | 2066.023154 | 1033.515215 | 2065.039138 | 1033.023207 | 16 |
| 7 | 871.409063 | 436.208170 | 854.382514 | 427.694895 | 853.398498 | 427.202887 | P | *1969.965639* | 985.486458 | 1952.939090 | 976.973183 | 1951.955074 | 976.481175 | 15 |
| 8 | **970.477477** | 485.742377 | 953.450928 | 477.229102 | 952.466912 | 476.737094 | V | *1872.912875* | 936.960076 | 1855.886326 | 928.446801 | 1854.902310 | 927.954793 | 14 |
| 9 | **1130.508126** | 565.757701 | 1113.481577 | 557.244427 | 1112.497561 | 556.752418 | C | *1773.844461* | 887.425868 | 1756.817912 | 878.912594 | 1755.833896 | 878.420586 | 13 |
| 10 | **1187.529590** | 594.268433 | 1170.503041 | 585.755158 | 1169.519025 | 585.263150 | G | *1613.813812* | 807.410544 | 1596.787263 | 798.897270 | 1595.803247 | 798.405262 | 12 |
| 11 | **1315.588168** | 658.297722 | 1298.561619 | 649.784448 | 1297.577603 | 649.292440 | Q | *1556.792348* | 778.899812 | 1539.765799 | 770.386538 | 1538.781783 | 769.894530 | 11 |
| 12 | **1430.615111** | 715.811194 | 1413.588562 | 707.297919 | 1412.604546 | 706.805911 | D | *1428.733770* | 714.870523 | 1411.707221 | 706.357249 | 1410.723205 | 705.865241 | 10 |
| 13 | 1869.840437 | 935.423857 | 1852.813888 | 926.910582 | 1851.829872 | 926.418574 | Q | *1313.706827* | 657.357052 | 1296.680278 | 648.843777 | 1295.696262 | 648.351769 | 9 |
| 14 | **1968.908851** | 984.958064 | 1951.882302 | 976.444789 | 1950.898286 | 975.952781 | V | *874.481501* | 437.744389 | 857.454952 | 429.231114 | 856.470936 | 428.739106 | 8 |
| 15 | 2069.956530 | 1035.481903 | 2052.929981 | 1026.968628 | 2051.945965 | 1026.476620 | T | *775.413087* | 388.210181 | 758.386538 | 379.696907 | 757.402522 | 379.204899 | 7 |
| 16 | 2169.024944 | **1085.016110** | 2151.998395 | 1076.502835 | 2151.014379 | 1076.010827 | V | *674.365408* | 337.686342 | 657.338859 | 329.173067 | 656.354843 | 328.681059 | 6 |
| 17 | 2240.062058 | 1120.534667 | 2223.035509 | 1112.021392 | 2222.051493 | 1111.529384 | A | *575.296994* | 288.152135 | 558.270445 | 279.638861 | 557.286429 | 279.146853 | 5 |
| 18 | 2371.102543 | **1186.054909** | 2354.075994 | 1177.541635 | 2353.091978 | 1177.049627 | M | *504.259880* | 252.633578 | 487.233331 | 244.120303 | 486.249315 | 243.628295 | 4 |
| 19 | 2472.150222 | 1236.578749 | 2455.123673 | 1228.065474 | 2454.139657 | 1227.573466 | T | *373.219395* | 187.113335 | 356.192846 | 178.600061 | 355.208830 | 178.108053 | 3 |
| 20 | 2569.202986 | 1285.105131 | 2552.176437 | 1276.591856 | 2551.192421 | 1276.099848 | P | *272.171716* | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 21 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 90.6 | 2742.307404 | 0.024978 | RQECSIPVCGQDQVTVAMTPR |
| 64.9 | 2742.307404 | 0.024978 | RQECSIPVCGQDQVTVAMTPR |
| 13.1 | 2742.307404 | 0.024978 | RQECSIPVCGQDQVTVAMTPR |
| 0.1 | 2742.313873 | 0.018509 | MLPSGMASSSQLIPEESGAVGNNR |

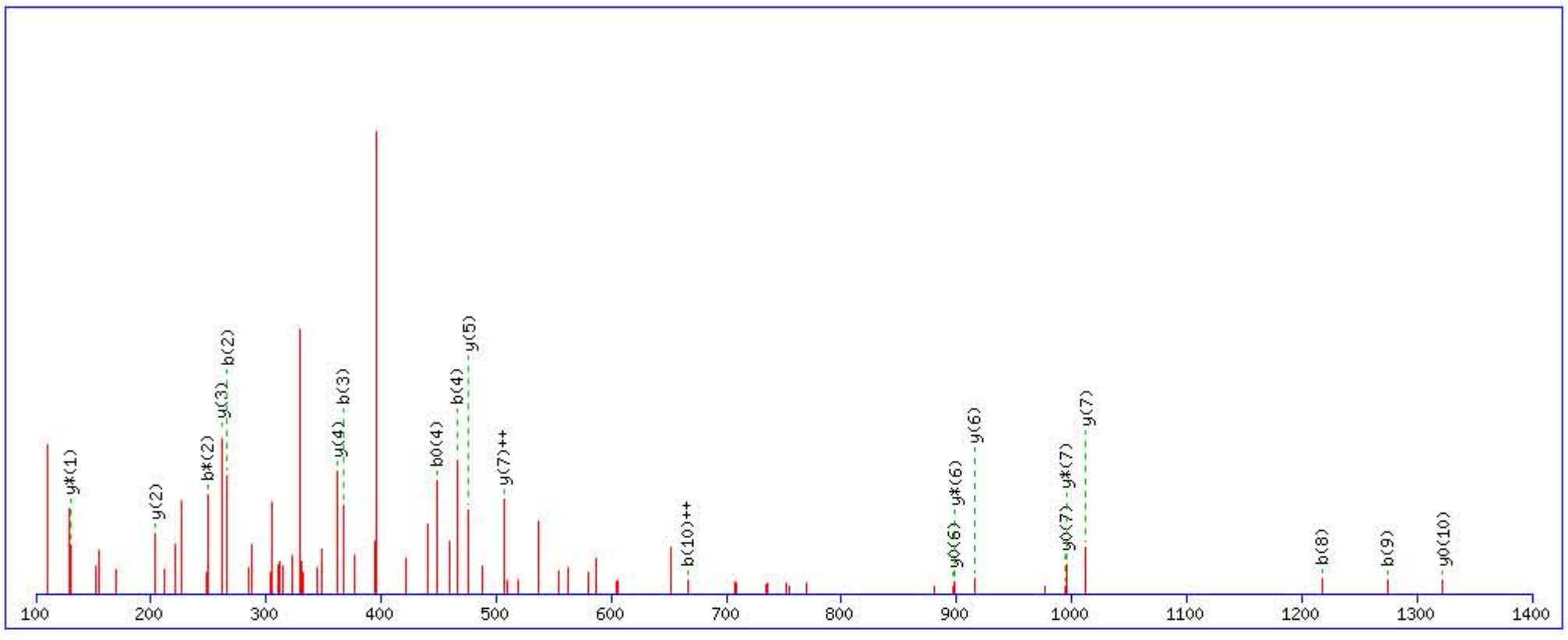
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HQTVPQNTGGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

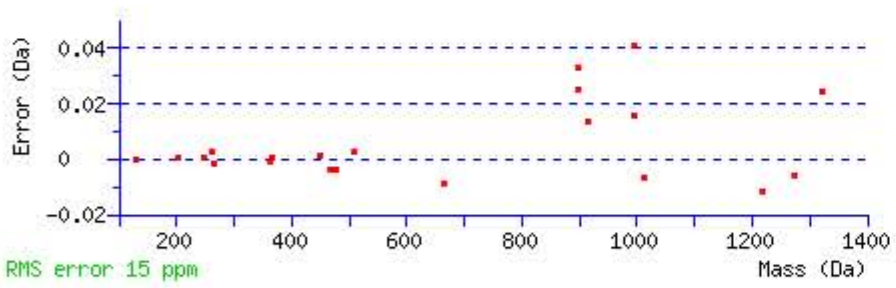
Match to Query 30419: 1476.749502 from(493.257110,3+) rtinseconds(1179) index(832)
Title: Locus:1.1.1.1687.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

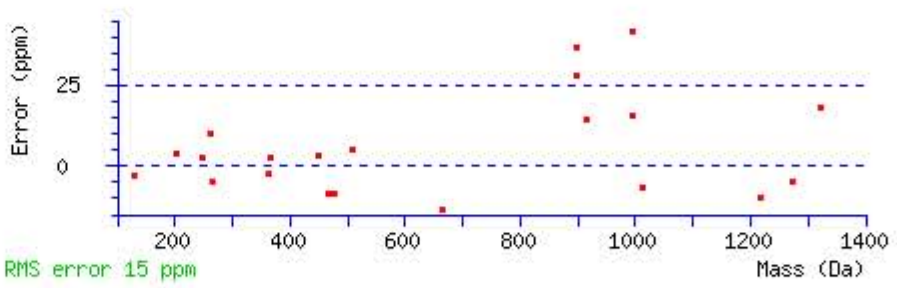
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1476.750748
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 28 **Expect:** 0.017
**Matches :** 21/108 fragment ions using 39 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 11 |
| 2 | *266.124766* | 133.566021 | 249.098217 | 125.052746 | | | Q | 1340.699099 | 670.853187 | 1323.672550 | 662.339913 | 1322.688534 | 661.847905 | 10 |
| 3 | *367.172445* | 184.089860 | 350.145896 | 175.576586 | 349.161880 | 175.084578 | T | 1212.640521 | 606.823899 | 1195.613972 | 598.310624 | 1194.629956 | 597.818616 | 9 |
| 4 | *466.240859* | 233.624068 | 449.214310 | 225.110793 | 448.230294 | 224.618785 | V | 1111.592842 | 556.300059 | 1094.566293 | 547.786784 | 1093.582277 | 547.294776 | 8 |
| 5 | 563.293623 | 282.150450 | 546.267074 | 273.637175 | 545.283058 | 273.145167 | P | *1012.524428* | 506.765852 | 995.497879 | 498.252577 | 994.513863 | 497.760569 | 7 |
| 6 | 1002.518949 | 501.763113 | 985.492400 | 493.249838 | 984.508384 | 492.757830 | Q | *915.471664* | 458.239470 | 898.445115 | 449.726195 | 897.461099 | 449.234187 | 6 |
| 7 | 1116.561876 | 558.784576 | 1099.535327 | 550.271302 | 1098.551311 | 549.779293 | N | *476.246338* | 238.626807 | 459.219789 | 230.113532 | 458.235773 | 229.621524 | 5 |
| 8 | *1217.609555* | 609.308416 | 1200.583006 | 600.795141 | 1199.598990 | 600.303133 | T | *362.203411* | 181.605343 | 345.176862 | 173.092069 | 344.192846 | 172.600061 | 4 |
| 9 | *1274.631019* | 637.819147 | 1257.604470 | 629.305873 | 1256.620454 | 628.813865 | G | *261.155732* | 131.081504 | 244.129183 | 122.568229 | | | 3 |
| 10 | 1331.652483 | 666.329879 | 1314.625934 | 657.816605 | 1313.641918 | 657.324597 | G | *204.134268* | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 11 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 28.4 | 1476.750748 | -0.001246 | HQTVPQNTGGK |
| 9.6 | 1476.736115 | 0.013387 | HQEALIGQSFYGK |
| 2.1 | 1476.750748 | -0.001246 | HQTVPQNTGGK |

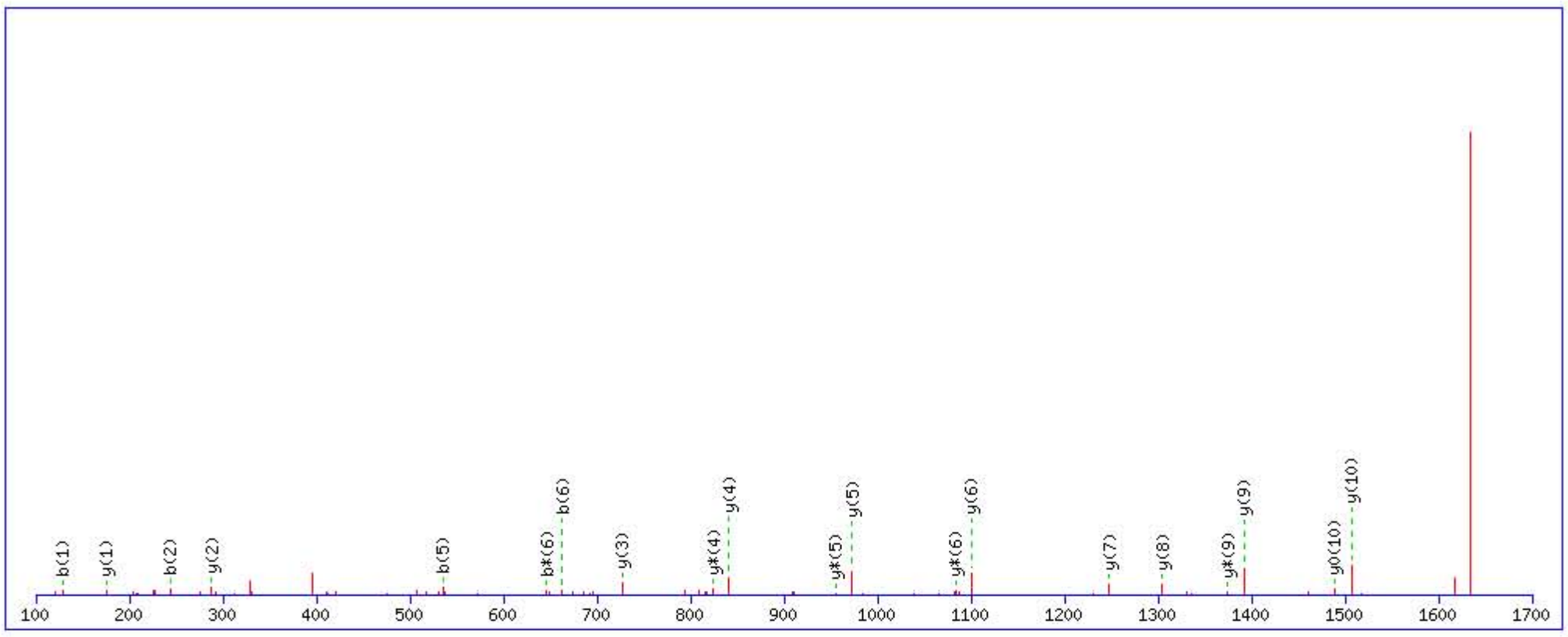
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KDSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

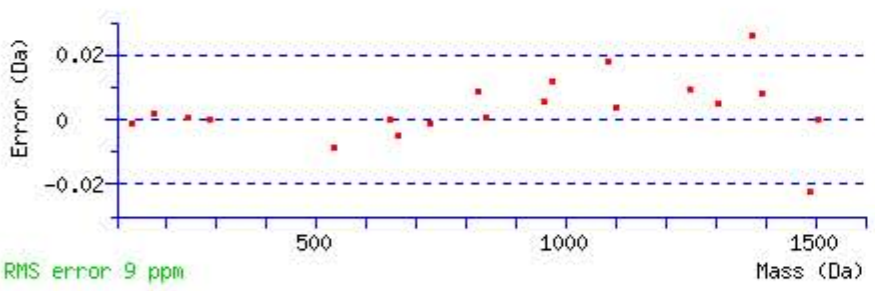
Match to Query 36470: 1633.814148 from(817.914350,2+) rtinseconds(1810) index(65218)
Title: Locus:1.1.1.1905.15 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

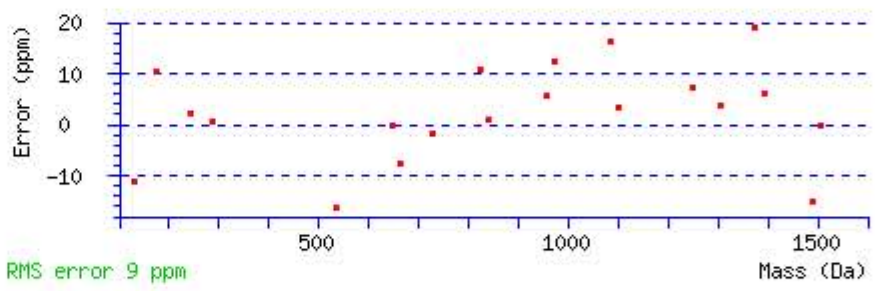
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1633.806854
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 90 **Expect:** 2.2e-008
**Matches :** 20/102 fragment ions using 27 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.102239 | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 11 |
| 2 | 244.129182 | 122.568229 | 227.102633 | 114.054955 | 226.118617 | 113.562947 | D | *1506.719181* | 753.863228 | 1489.692632 | 745.349954 | 1488.708616 | 744.857946 | 10 |
| 3 | 331.161210 | 166.084243 | 314.134661 | 157.570969 | 313.150645 | 157.078961 | S | *1391.692238* | 696.349757 | 1374.665689 | 687.836482 | 1373.681673 | 687.344474 | 9 |
| 4 | 388.182674 | 194.594975 | 371.156125 | 186.081701 | 370.172109 | 185.589693 | G | *1304.660210* | 652.833743 | 1287.633661 | 644.320468 | | | 8 |
| 5 | 535.251088 | 268.129182 | 518.224539 | 259.615908 | 517.240523 | 259.123900 | F | *1247.638746* | 624.323011 | 1230.612197 | 615.809736 | | | 7 |
| 6 | 663.309666 | 332.158471 | 646.283117 | 323.645197 | 645.299101 | 323.153189 | Q | *1100.570332* | 550.788804 | 1083.543783 | 542.275530 | | | 6 |
| 7 | 794.350151 | 397.678714 | 777.323602 | 389.165439 | 776.339586 | 388.673431 | M | *972.511754* | 486.759515 | 955.485205 | 478.246240 | | | 5 |
| 8 | 908.393078 | 454.700177 | 891.366529 | 446.186903 | 890.382513 | 445.694895 | N | *841.471269* | 421.239272 | 824.444720 | 412.725998 | | | 4 |
| 9 | 1347.618404 | 674.312840 | 1330.591855 | 665.799566 | 1329.607839 | 665.307558 | Q | *727.428342* | 364.217809 | 710.401793 | 355.704534 | | | 3 |
| 10 | 1460.702468 | 730.854872 | 1443.675919 | 722.341598 | 1442.691903 | 721.849589 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 90.1 | 1633.806854 | 0.007294 | KDSGFQMNQLR |
| 39.1 | 1633.806854 | 0.007294 | KDSGFQMNQLR |
| 15.1 | 1633.799454 | 0.014694 | DANSFKSRDQR |
| 13.2 | 1633.834518 | -0.020370 | KADIGVAMGIAGSDVSK |
| 12.3 | 1633.798096 | 0.016052 | QDQEKDNMIEKLK |
| 10.7 | 1633.795609 | 0.018539 | KFMEDEQQLR |
| 9.9 | 1633.832016 | -0.017868 | MSIFTPTNQIR |
| 7.9 | 1633.809998 | 0.004150 | KQYDSFTYRAEVK |
| 7.2 | 1633.822128 | -0.007980 | QFMKGQVSWGR |
| 7.1 | 1633.817184 | -0.003036 | HLHEGAKSASAEELR |

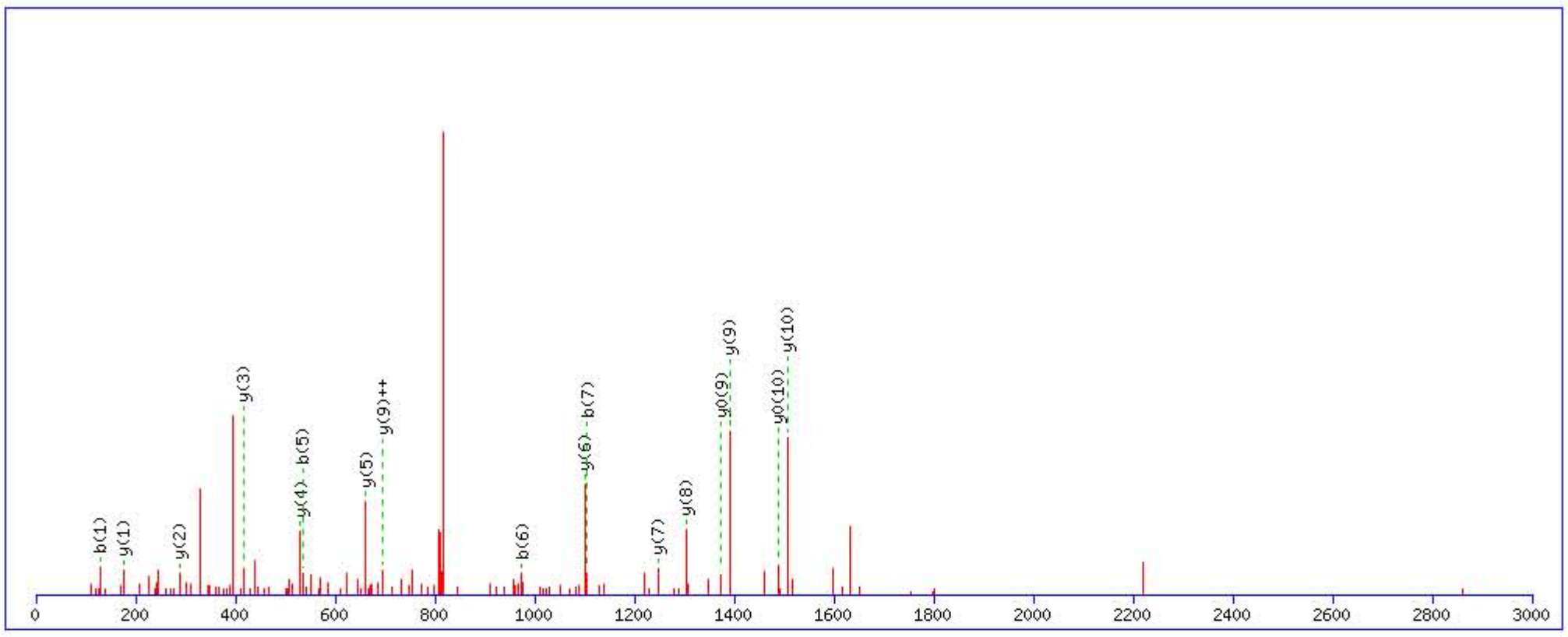
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KDSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

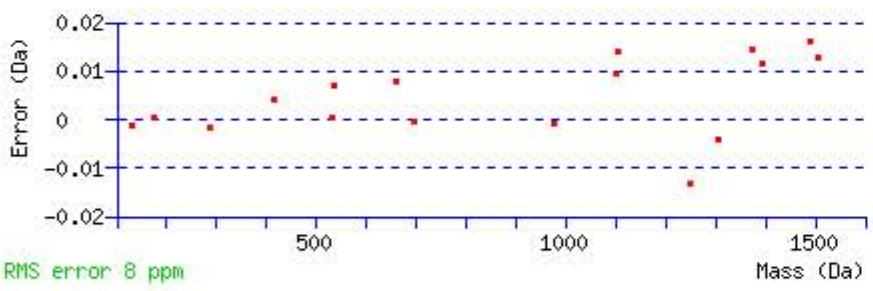
Match to Query 36471: 1633.814788 from(817.914670,2+) rtinseconds(1747) index(64864)
Title: Locus:1.1.1.1883.14 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

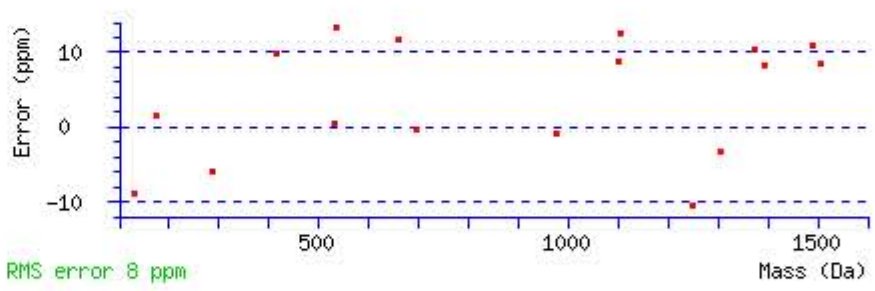
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1633.806854
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q6** : Biotin:Thermo-21345 (Q)
**Ions Score:** 71 **Expect:** 6.6e-007
**Matches :** 17/102 fragment ions using 31 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.102239 | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 11 |
| 2 | 244.129182 | 122.568229 | 227.102633 | 114.054955 | 226.118617 | 113.562947 | D | *1506.719181* | 753.863228 | 1489.692632 | 745.349954 | 1488.708616 | 744.857946 | 10 |
| 3 | 331.161210 | 166.084243 | 314.134661 | 157.570969 | 313.150645 | 157.078961 | S | *1391.692238* | 696.349757 | 1374.665689 | 687.836482 | 1373.681673 | 687.344474 | 9 |
| 4 | 388.182674 | 194.594975 | 371.156125 | 186.081701 | 370.172109 | 185.589693 | G | *1304.660210* | 652.833743 | 1287.633661 | 644.320468 | | | 8 |
| 5 | 535.251088 | 268.129182 | 518.224539 | 259.615908 | 517.240523 | 259.123900 | F | *1247.638746* | 624.323011 | 1230.612197 | 615.809736 | | | 7 |
| 6 | 974.476414 | 487.741845 | 957.449865 | 479.228571 | 956.465849 | 478.736563 | Q | *1100.570332* | 550.788804 | 1083.543783 | 542.275530 | | | 6 |
| 7 | 1105.516899 | 553.262088 | 1088.490350 | 544.748813 | 1087.506334 | 544.256805 | M | *661.345006* | 331.176141 | 644.318457 | 322.662866 | | | 5 |
| 8 | 1219.559826 | 610.283551 | 1202.533277 | 601.770277 | 1201.549261 | 601.278268 | N | *530.304521* | 265.655899 | 513.277972 | 257.142624 | | | 4 |
| 9 | 1347.618404 | 674.312840 | 1330.591855 | 665.799566 | 1329.607839 | 665.307558 | Q | *416.261594* | 208.634435 | 399.235045 | 200.121160 | | | 3 |
| 10 | 1460.702468 | 730.854872 | 1443.675919 | 722.341598 | 1442.691903 | 721.849589 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 71.0 | 1633.806854 | 0.007934 | KDSGFQMNQLR |
| 30.9 | 1633.806854 | 0.007934 | KDSGFQMNQLR |
| 4.8 | 1633.798096 | 0.016692 | QDQEKDNMIEKLK |
| 4.3 | 1633.824615 | -0.009827 | AGGAFLMAGQVAEQLR |
| 3.1 | 1633.835129 | -0.020341 | YSLSPSKSYKYSPK |
| 2.9 | 1633.803482 | 0.011306 | QLFERDWSSR |
| 2.7 | 1633.795609 | 0.019179 | KFMEDEQQLR |
| 2.3 | 1633.809998 | 0.004790 | KQYDSFTYRAEVK |
| 2.2 | 1633.832443 | -0.017655 | NRYINILAYDHSR |
| 1.5 | 1633.805954 | 0.008834 | LFREENDINESIR |

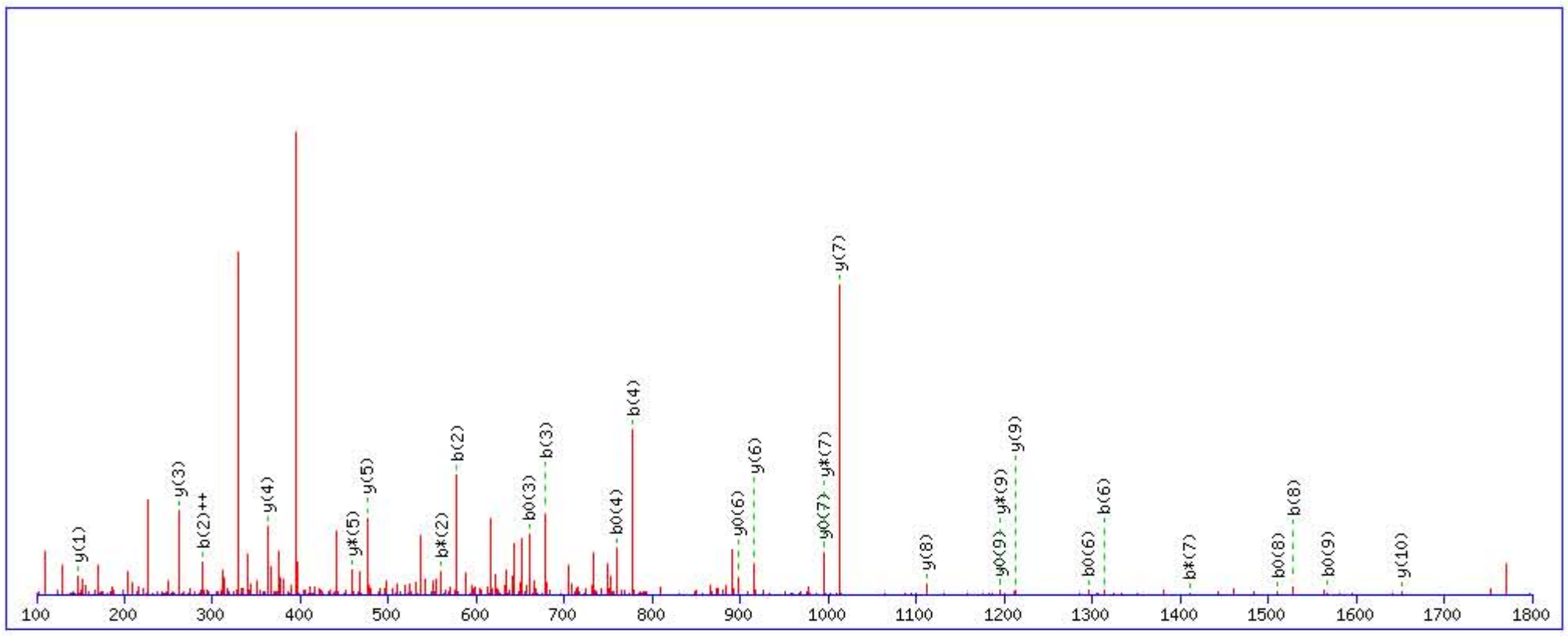
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HQTVPQNTGGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

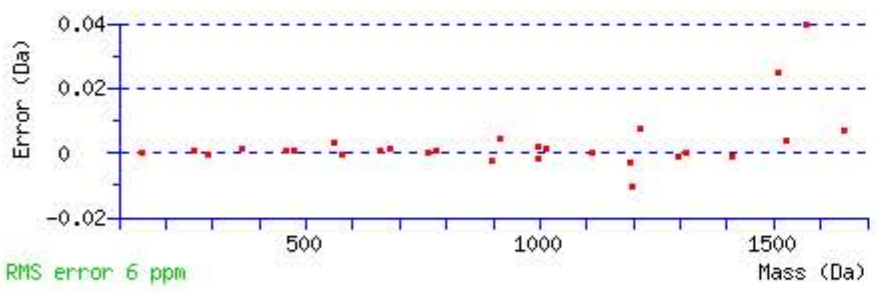
Match to Query 39985: 1787.916462 from(596.979430,3+) rtinseconds(1568) index(63938)
Title: Locus:1.1.1.1821.10 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

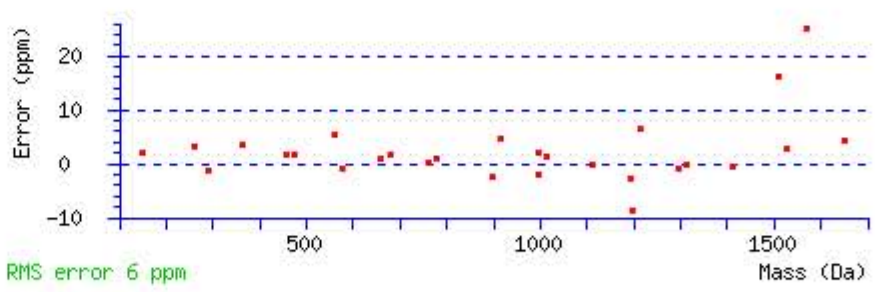
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1787.917496
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 37 **Expect:** 0.00049
**Matches :** 28/108 fragment ions using 64 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 11 |
| 2 | **577.291514** | **289.149395** | 560.264965 | 280.636121 | | | Q | *1651.865847* | 826.436562 | 1634.839298 | 817.923287 | 1633.855282 | 817.431279 | 10 |
| 3 | **678.339193** | 339.673235 | 661.312644 | 331.159960 | 660.328628 | 330.667952 | T | *1212.640521* | 606.823899 | 1195.613972 | 598.310624 | 1194.629956 | 597.818616 | 9 |
| 4 | **777.407607** | 389.207442 | 760.381058 | 380.694167 | 759.397042 | 380.202159 | V | *1111.592842* | 556.300059 | 1094.566293 | 547.786785 | 1093.582277 | 547.294777 | 8 |
| 5 | 874.460371 | 437.733824 | 857.433822 | 429.220549 | 856.449806 | 428.728541 | P | *1012.524428* | 506.765852 | 995.497879 | 498.252578 | 994.513863 | 497.760570 | 7 |
| 6 | **1313.685697** | 657.346487 | 1296.659148 | 648.833212 | 1295.675132 | 648.341204 | Q | *915.471664* | 458.239470 | 898.445115 | 449.726196 | 897.461099 | 449.234188 | 6 |
| 7 | 1427.728624 | 714.367950 | 1410.702075 | 705.854676 | 1409.718059 | 705.362668 | N | *476.246338* | 238.626807 | 459.219789 | 230.113532 | 458.235773 | 229.621524 | 5 |
| 8 | **1528.776303** | 764.891790 | 1511.749754 | 756.378515 | 1510.765738 | 755.886507 | T | *362.203411* | 181.605343 | 345.176862 | 173.092069 | 344.192846 | 172.600061 | 4 |
| 9 | 1585.797767 | 793.402522 | 1568.771218 | 784.889247 | 1567.787202 | 784.397239 | G | *261.155732* | 131.081504 | 244.129183 | 122.568229 | | | 3 |
| 10 | 1642.819231 | 821.913254 | 1625.792682 | 813.399979 | 1624.808666 | 812.907971 | G | 204.134268 | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 11 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 36.9 | 1787.917496 | -0.001034 | HQTVPQNTGGK |
| 1.6 | 1787.943115 | -0.026653 | TPVNDGKYHVVRFTR |

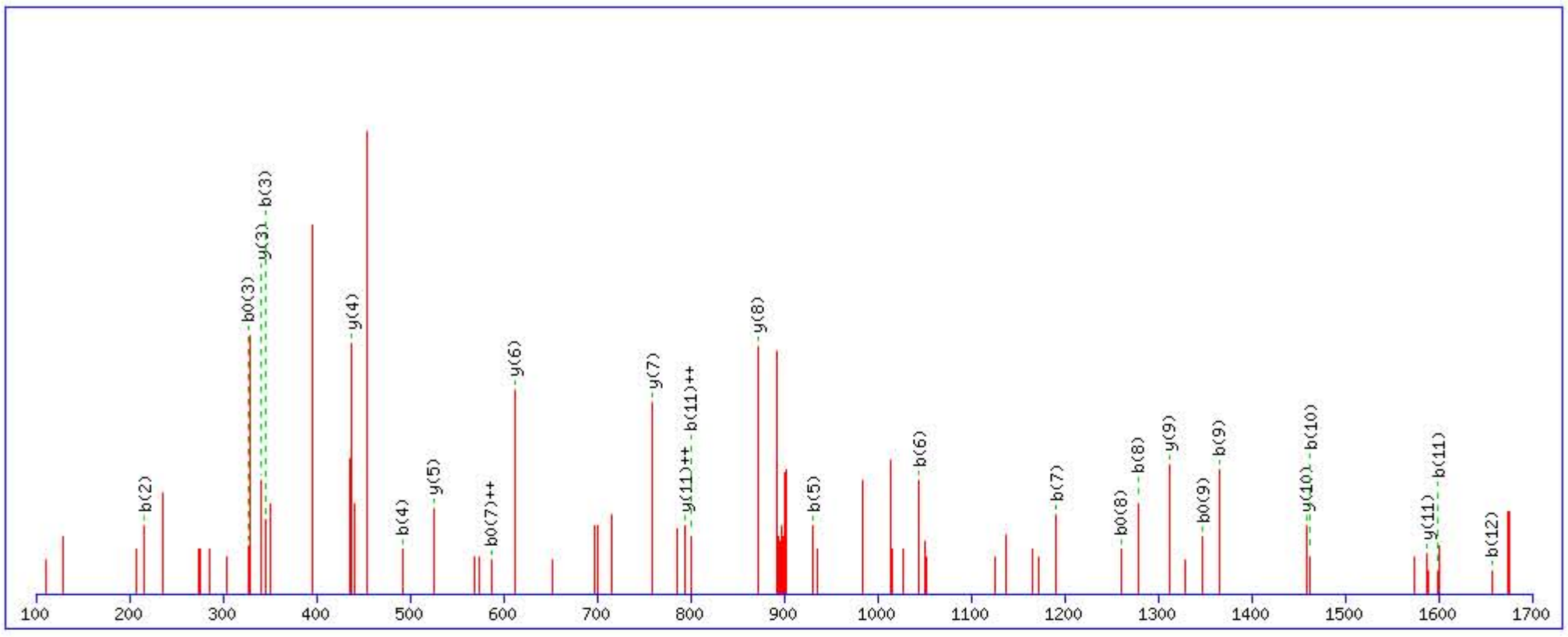
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SKEFQLFSSPHGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

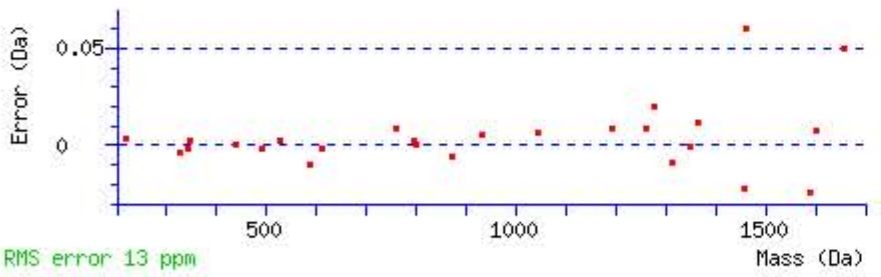
Match to Query 40284: 1801.919128 from(901.966840,2+) rtinseconds(1779) index(65072)
Title: Locus:1.1.1.1894.14 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

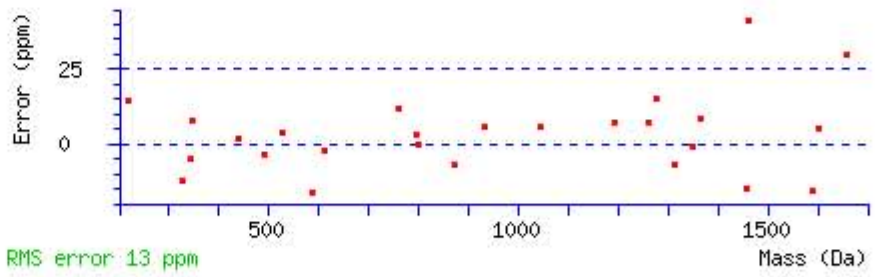
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1801.918518
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.00028
**Matches :** 26/134 fragment ions using 71 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 13 |
| 2 | *216.134267* | 108.570771 | 199.107718 | 100.057497 | 198.123702 | 99.565489 | K | 1715.893774 | 858.450525 | 1698.867225 | 849.937251 | 1697.883209 | 849.445243 | 12 |
| 3 | *345.176860* | 173.092068 | 328.150311 | 164.578793 | 327.166295 | 164.086785 | E | 1587.798811 | 794.403044 | 1570.772262 | 785.889769 | 1569.788246 | 785.397761 | 11 |
| 4 | *492.245274* | 246.626275 | 475.218725 | 238.113000 | 474.234709 | 237.620992 | F | 1458.756218 | 729.881747 | 1441.729669 | 721.368473 | 1440.745653 | 720.876465 | 10 |
| 5 | *931.470600* | 466.238938 | 914.444051 | 457.725664 | 913.460035 | 457.233656 | Q | 1311.687804 | 656.347540 | 1294.661255 | 647.834266 | 1293.677239 | 647.342258 | 9 |
| 6 | *1044.554664* | 522.780970 | 1027.528115 | 514.267696 | 1026.544099 | 513.775688 | L | 872.462478 | 436.734877 | 855.435929 | 428.221603 | 854.451913 | 427.729595 | 8 |
| 7 | *1191.623078* | 596.315177 | 1174.596529 | 587.801903 | 1173.612513 | 587.309895 | F | 759.378414 | 380.192845 | 742.351865 | 371.679571 | 741.367849 | 371.187563 | 7 |
| 8 | *1278.655106* | 639.831191 | 1261.628557 | 631.317917 | 1260.644541 | 630.825909 | S | 612.310000 | 306.658638 | 595.283451 | 298.145364 | 594.299435 | 297.653356 | 6 |
| 9 | *1365.687134* | 683.347205 | 1348.660585 | 674.833931 | 1347.676569 | 674.341923 | S | 525.277972 | 263.142624 | 508.251423 | 254.629350 | 507.267407 | 254.137342 | 5 |
| 10 | *1462.739898* | 731.873587 | 1445.713349 | 723.360313 | 1444.729333 | 722.868305 | P | 438.245944 | 219.626610 | 421.219395 | 211.113335 | | | 4 |
| 11 | *1599.798810* | 800.403043 | 1582.772261 | 791.889769 | 1581.788245 | 791.397761 | H | 341.193180 | 171.100228 | 324.166631 | 162.586953 | | | 3 |
| 12 | *1656.820274* | 828.913775 | 1639.793725 | 820.400501 | 1638.809709 | 819.908493 | G | 204.134268 | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 13 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 44.4 | 1801.918518 | 0.000610 | SKEFQLFSSPHGK |
| 6.5 | 1801.928421 | -0.009293 | KFMTLDPVSQDALPPK |

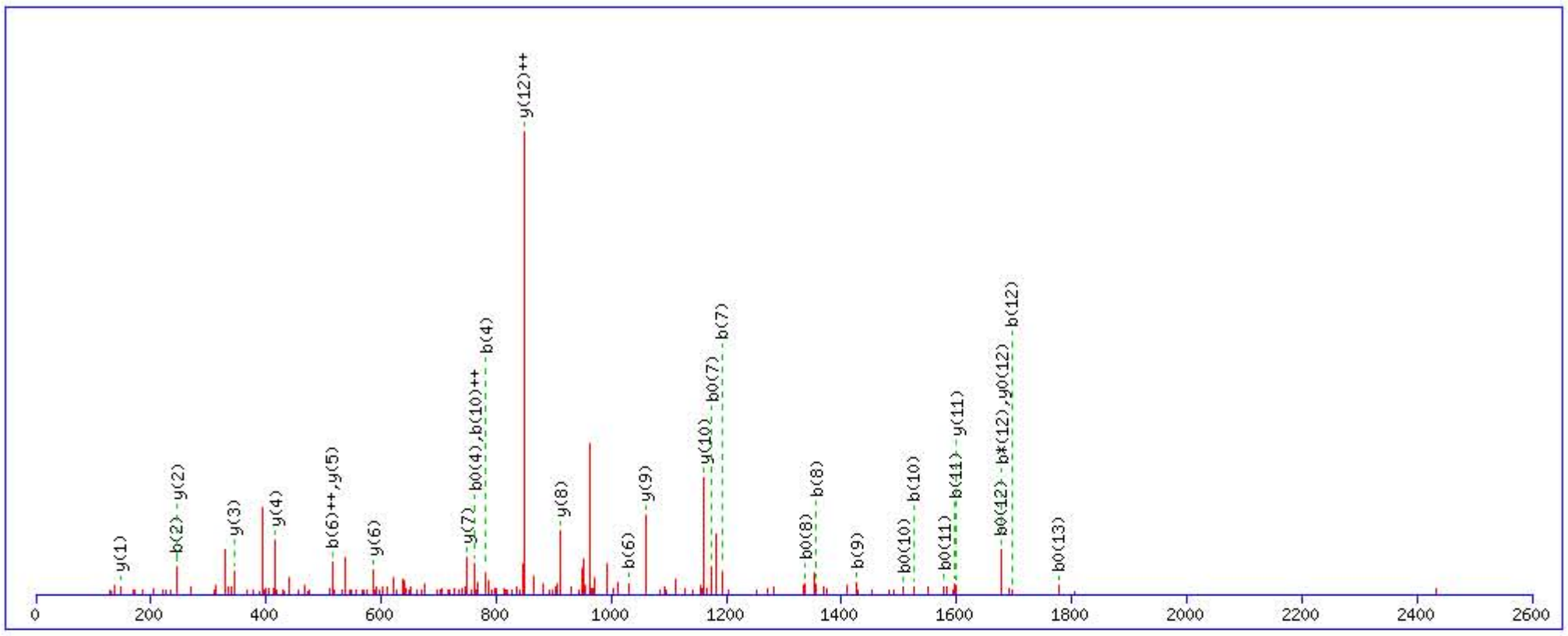
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EDPQTFYYAVAVVK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

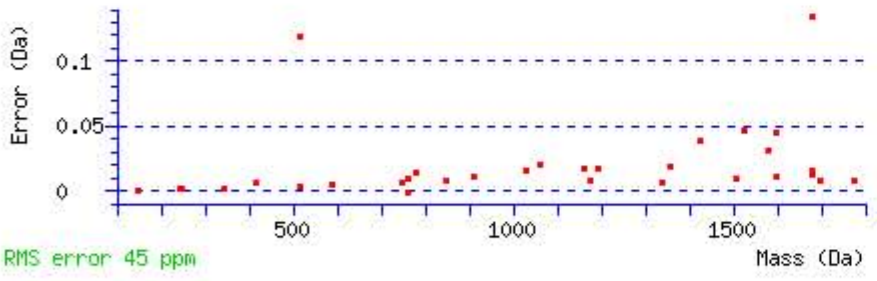
Match to Query 42933: 1940.003128 from(971.008840,2+) rtinseconds(2563) index(69598)
Title: Locus:1.1.1.2168.15 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

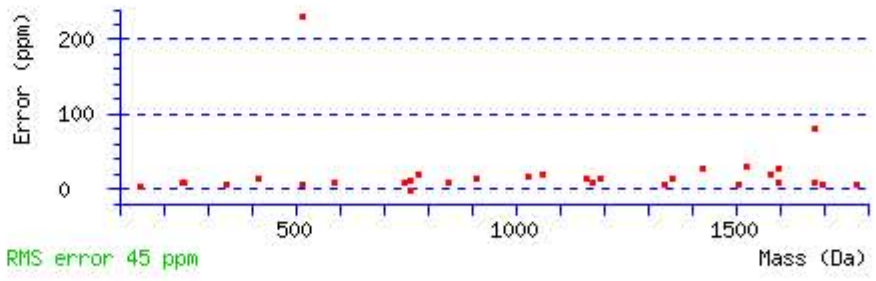
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1939.975372
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 56 **Expect:** 1.2e-005
**Matches :** 32/132 fragment ions using 65 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 14 |
| 2 | **245.076812** | 123.042044 | | | 227.066247 | 114.036762 | D | 1811.940058 | 906.473667 | 1794.913509 | 897.960393 | 1793.929493 | 897.468385 | 13 |
| 3 | 342.129576 | 171.568426 | | | 324.119011 | 162.563144 | P | 1696.913115 | 848.960196 | 1679.886566 | 840.446921 | 1678.902550 | 839.954913 | 12 |
| 4 | **781.354902** | 391.181089 | 764.328353 | 382.667815 | 763.344337 | 382.175807 | Q | ***1599.860351*** | 800.433814 | 1582.833802 | 791.920539 | 1581.849786 | 791.428531 | 11 |
| 5 | 882.402581 | 441.704929 | 865.376032 | 433.191654 | 864.392016 | 432.699646 | T | ***1160.635025*** | 580.821151 | 1143.608476 | 572.307876 | 1142.624460 | 571.815868 | 10 |
| 6 | **1029.470995** | **515.239136** | 1012.444446 | 506.725861 | 1011.460430 | 506.233853 | F | ***1059.587346*** | 530.297311 | 1042.560797 | 521.784037 | | | 9 |
| 7 | **1192.534324** | 596.770800 | 1175.507775 | 588.257526 | 1174.523759 | 587.765518 | Y | ***912.518932*** | 456.763104 | 895.492383 | 448.249830 | | | 8 |
| 8 | **1355.597653** | 678.302465 | 1338.571104 | 669.789190 | 1337.587088 | 669.297182 | Y | ***749.455603*** | 375.231440 | 732.429054 | 366.718165 | | | 7 |
| 9 | **1426.634767** | 713.821022 | 1409.608218 | 705.307747 | 1408.624202 | 704.815739 | A | ***586.392274*** | 293.699775 | 569.365725 | 285.186501 | | | 6 |
| 10 | **1525.703181** | **763.355229** | 1508.676632 | 754.841954 | 1507.692616 | 754.349946 | V | ***515.355160*** | 258.181218 | 498.328611 | 249.667944 | | | 5 |
| 11 | **1596.740295** | 798.873786 | 1579.713746 | 790.360511 | 1578.729730 | 789.868503 | A | ***416.286746*** | 208.647011 | 399.260197 | 200.133737 | | | 4 |
| 12 | **1695.808709** | 848.407993 | 1678.782160 | 839.894718 | 1677.798144 | 839.402710 | V | ***345.249632*** | 173.128454 | 328.223083 | 164.615180 | | | 3 |
| 13 | 1794.877123 | 897.942200 | 1777.850574 | 889.428925 | 1776.866558 | 888.936917 | V | ***246.181218*** | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 14 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 55.8 | 1939.975372 | 0.027756 | EDPQTFYYAVAVVK |
| 3.4 | 1939.993851 | 0.009277 | VSGVTPQHMVGATPFAVAR |
| 2.8 | 1939.982605 | 0.020523 | SVVGIDLGFQSCYVAVAR |

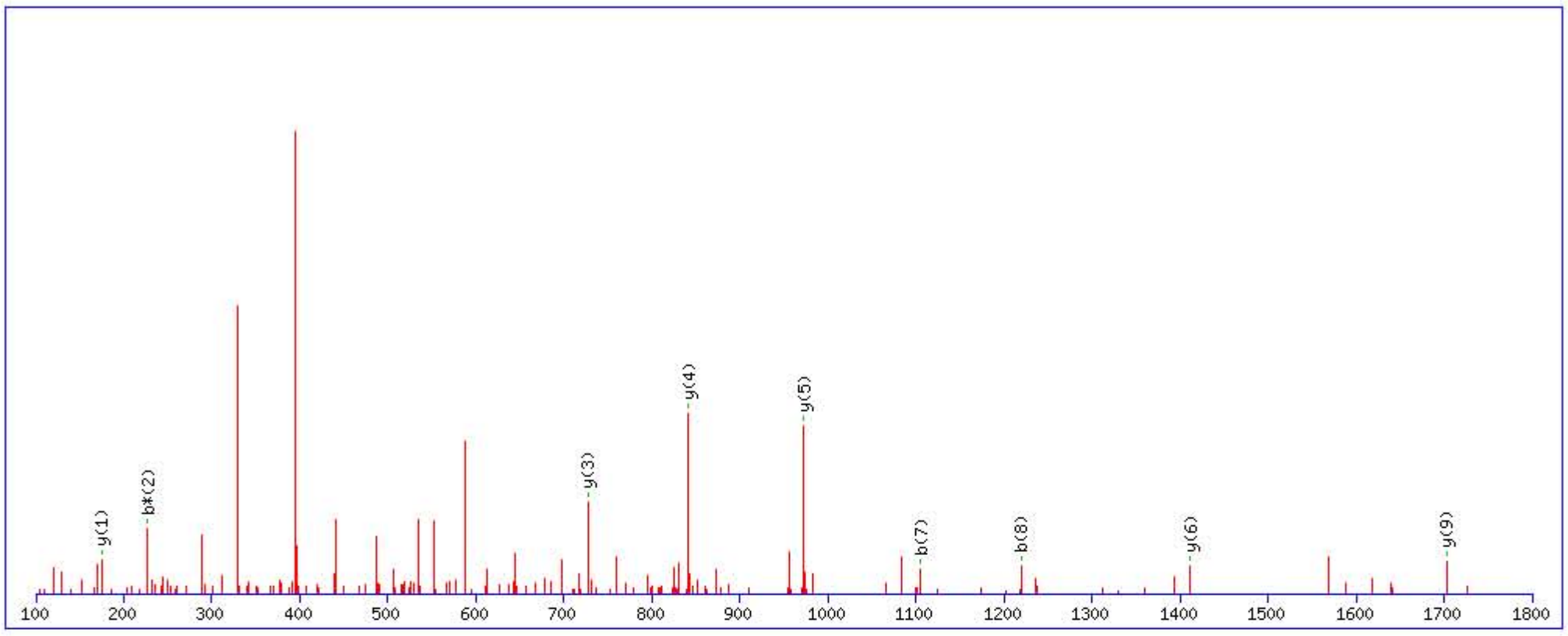
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KDSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

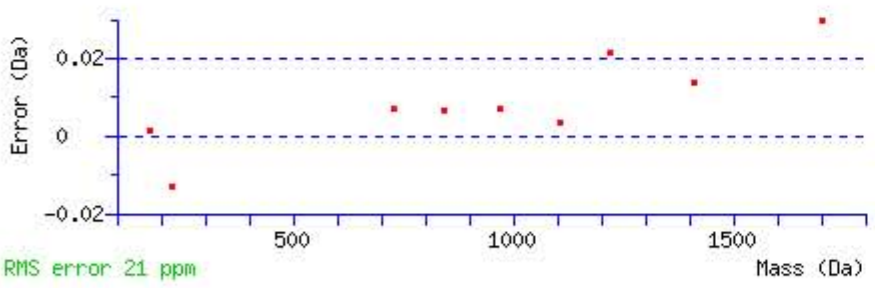
Match to Query 43002: 1944.980022 from(649.333950,3+) rtinseconds(2080) index(66884)
Title: Locus:1.1.1.1999.10 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

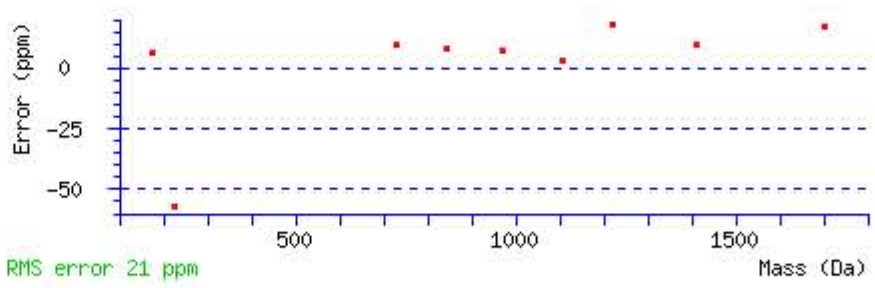
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1944.973602
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 28 **Expect:** 0.048
**Matches :** 9/102 fragment ions using 17 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.102239 | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 11 |
| 2 | 244.129182 | 122.568229 | 227.102633 | 114.054955 | 226.118617 | 113.562947 | D | 1817.885929 | 909.446603 | 1800.859380 | 900.933328 | 1799.875364 | 900.441320 | 10 |
| 3 | 331.161210 | 166.084243 | 314.134661 | 157.570969 | 313.150645 | 157.078961 | S | *1702.858986* | 851.933131 | 1685.832437 | 843.419857 | 1684.848421 | 842.927848 | 9 |
| 4 | 388.182674 | 194.594975 | 371.156125 | 186.081701 | 370.172109 | 185.589693 | G | 1615.826958 | 808.417117 | 1598.800409 | 799.903843 | | | 8 |
| 5 | 535.251088 | 268.129182 | 518.224539 | 259.615908 | 517.240523 | 259.123900 | F | 1558.805494 | 779.906385 | 1541.778945 | 771.393111 | | | 7 |
| 6 | 974.476414 | 487.741845 | 957.449865 | 479.228571 | 956.465849 | 478.736563 | Q | *1411.737080* | 706.372178 | 1394.710531 | 697.858904 | | | 6 |
| 7 | **1105.516899** | 553.262088 | 1088.490350 | 544.748813 | 1087.506334 | 544.256805 | M | *972.511754* | 486.759515 | 955.485205 | 478.246241 | | | 5 |
| 8 | **1219.559826** | 610.283551 | 1202.533277 | 601.770277 | 1201.549261 | 601.278268 | N | *841.471269* | 421.239273 | 824.444720 | 412.725998 | | | 4 |
| 9 | 1658.785152 | 829.896214 | 1641.758603 | 821.382940 | 1640.774587 | 820.890932 | Q | *727.428342* | 364.217809 | 710.401793 | 355.704535 | | | 3 |
| 10 | 1771.869216 | 886.438246 | 1754.842667 | 877.924972 | 1753.858651 | 877.432964 | L | 288.203016 | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 27.5 | 1944.973602 | 0.006420 | KDSGFQMNQLR |

**Mascot:** http://www.matrixscience.com/

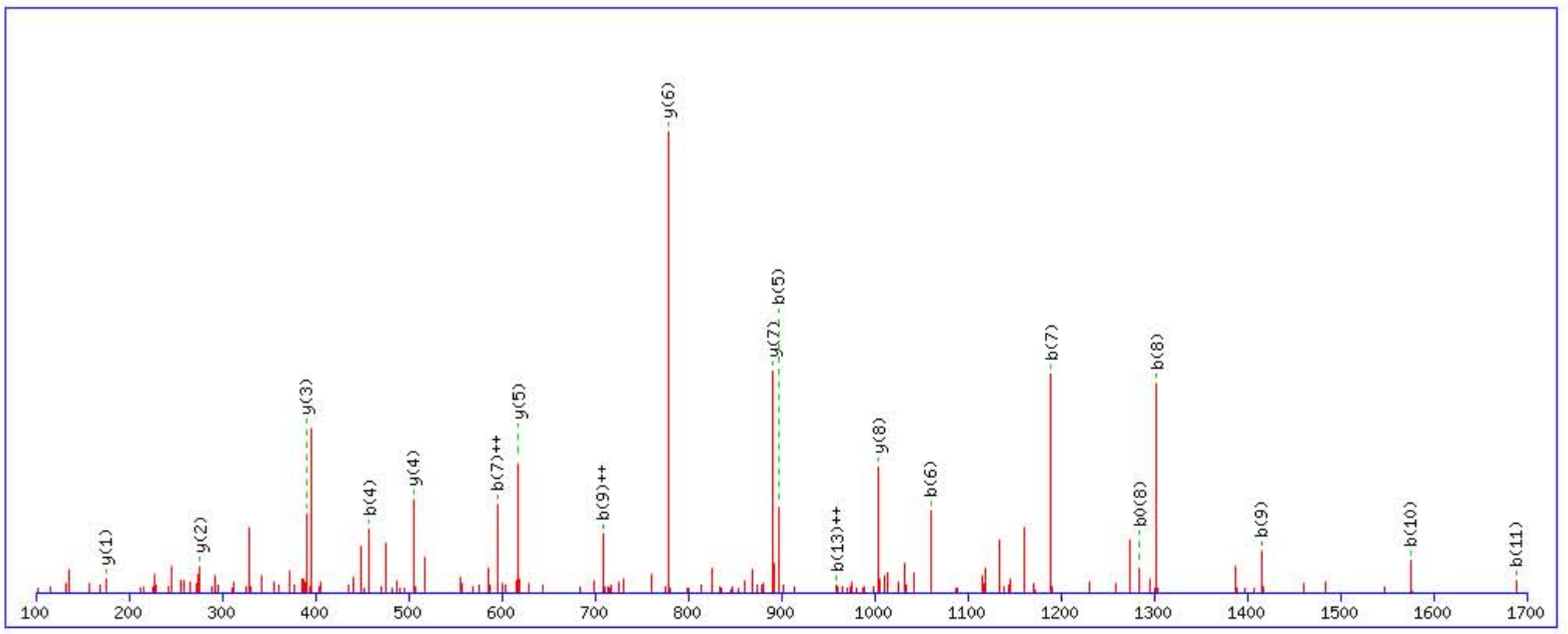
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ADRDQYELLCLDNTR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

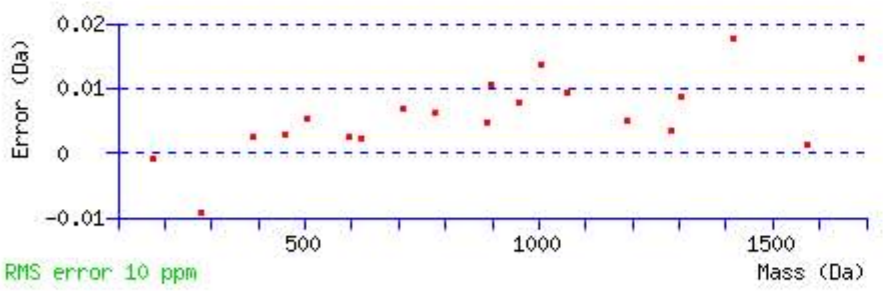
Match to Query 48320: 2192.050542 from(731.690790,3+) rtinseconds(2203) index(67647)
Title: Locus:1.1.1.2042.14 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

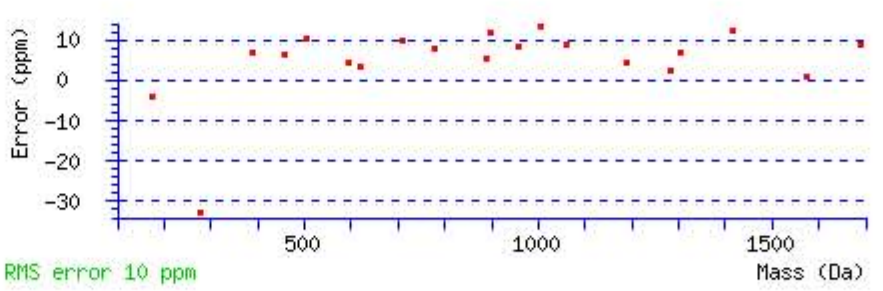
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2192.035400
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 60 **Expect:** 2e-005
**Matches :** 20/160 fragment ions using 31 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 15 |
| 2 | 187.071333 | 94.039304 | | | 169.060768 | 85.034022 | D | 2122.005587 | 1061.506431 | 2104.979038 | 1052.993157 | 2103.995022 | 1052.501149 | 14 |
| 3 | 343.172444 | 172.089860 | 326.145895 | 163.576585 | 325.161879 | 163.084577 | R | 2006.978644 | 1003.992960 | 1989.952095 | 995.479685 | 1988.968079 | 994.987677 | 13 |
| 4 | *458.199387* | 229.603332 | 441.172838 | 221.090057 | 440.188822 | 220.598049 | D | 1850.877533 | 925.942404 | 1833.850984 | 917.429130 | 1832.866968 | 916.937122 | 12 |
| 5 | *897.424713* | 449.215995 | 880.398164 | 440.702720 | 879.414148 | 440.210712 | Q | 1735.850590 | 868.428933 | 1718.824041 | 859.915658 | 1717.840025 | 859.423650 | 11 |
| 6 | *1060.488042* | 530.747659 | 1043.461493 | 522.234385 | 1042.477477 | 521.742376 | Y | 1296.625264 | 648.816270 | 1279.598715 | 640.302995 | 1278.614699 | 639.810987 | 10 |
| 7 | *1189.530635* | **595.268955** | 1172.504086 | 586.755681 | 1171.520070 | 586.263673 | E | 1133.561935 | 567.284605 | 1116.535386 | 558.771331 | 1115.551370 | 558.279323 | 9 |
| 8 | *1302.614699* | 651.810987 | 1285.588150 | 643.297713 | 1284.604134 | 642.805705 | L | *1004.519342* | 502.763309 | 987.492793 | 494.250034 | 986.508777 | 493.758026 | 8 |
| 9 | *1415.698763* | **708.353019** | 1398.672214 | 699.839745 | 1397.688198 | 699.347737 | L | *891.435278* | 446.221277 | 874.408729 | 437.708002 | 873.424713 | 437.215994 | 7 |
| 10 | *1575.729412* | 788.368344 | 1558.702863 | 779.855069 | 1557.718847 | 779.363061 | C | *778.351214* | 389.679245 | 761.324665 | 381.165971 | 760.340649 | 380.673963 | 6 |
| 11 | *1688.813476* | 844.910376 | 1671.786927 | 836.397101 | 1670.802911 | 835.905093 | L | *618.320565* | 309.663921 | 601.294016 | 301.150646 | 600.310000 | 300.658638 | 5 |
| 12 | 1803.840419 | 902.423847 | 1786.813870 | 893.910573 | 1785.829854 | 893.418565 | D | *505.236501* | 253.121888 | 488.209952 | 244.608614 | 487.225936 | 244.116606 | 4 |
| 13 | 1917.883346 | **959.445311** | 1900.856797 | 950.932036 | 1899.872781 | 950.440028 | N | *390.209558* | 195.608417 | 373.183009 | 187.095142 | 372.198993 | 186.603134 | 3 |
| 14 | 2018.931025 | 1009.969150 | 2001.904476 | 1001.455876 | 2000.920460 | 1000.963868 | T | *276.166631* | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 60.2 | 2192.035400 | 0.015142 | ADRDQYELLCLDNTR |

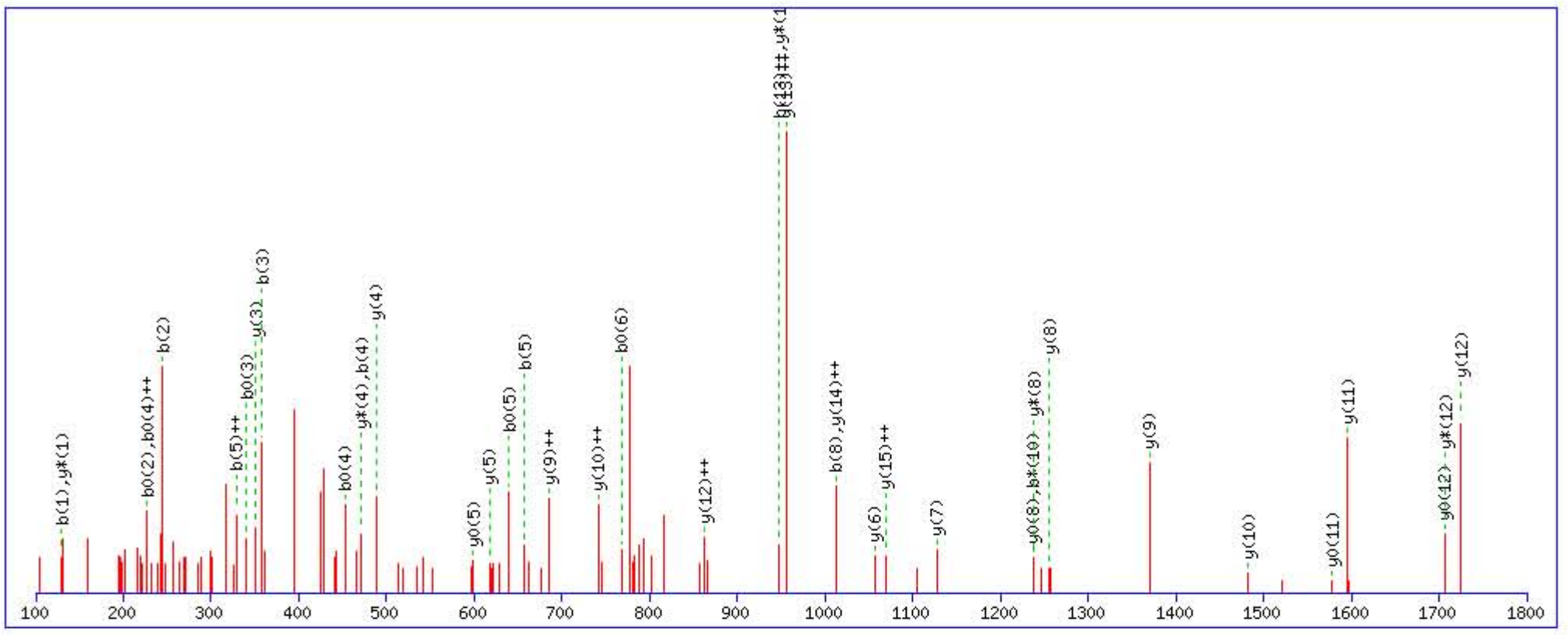
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EDLIWELLNQAQEHFGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

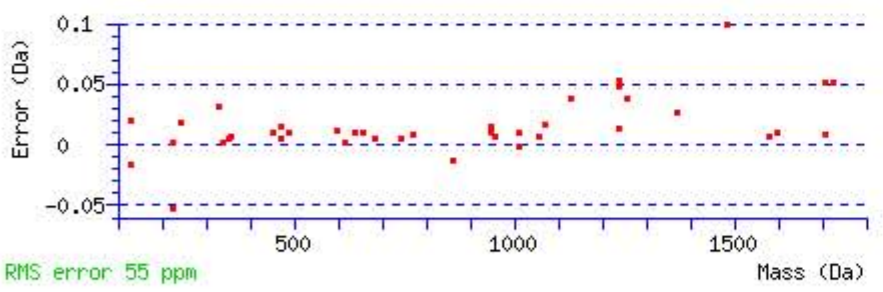
Match to Query 51635: 2380.216752 from(794.412860,3+) rtinseconds(3295) index(74082)
Title: Locus:1.1.1.2417.9 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

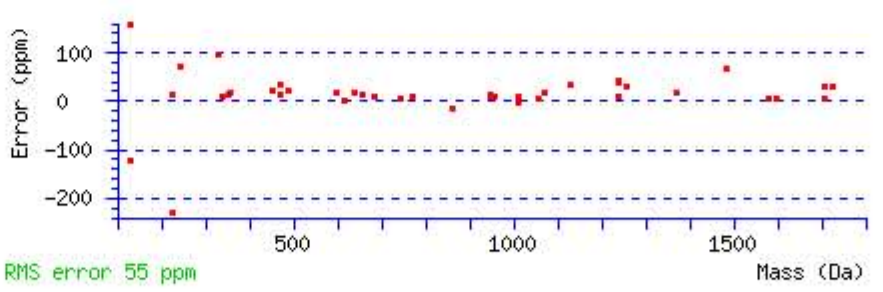
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2380.188522
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.00022
**Matches :** 40/168 fragment ions using 73 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *130.049869* | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 17 |
| 2 | *245.076812* | 123.042044 | | | 227.066247 | 114.036762 | D | 2252.153237 | 1126.580256 | 2235.126688 | 1118.066982 | 2234.142672 | 1117.574974 | 16 |
| 3 | *358.160876* | 179.584076 | | | 340.150311 | 170.578794 | L | 2137.126294 | 1069.066785 | 2120.099745 | 1060.553510 | 2119.115729 | 1060.061502 | 15 |
| 4 | *471.244940* | 236.126108 | | | 453.234375 | 227.120826 | I | 2024.042230 | 1012.524753 | 2007.015681 | 1004.011479 | 2006.031665 | 1003.519470 | 14 |
| 5 | *657.324253* | **329.165765** | | | 639.313688 | 320.160482 | W | 1910.958166 | 955.982721 | 1893.931617 | 947.469447 | 1892.947601 | 946.977438 | 13 |
| 6 | 786.366846 | 393.687061 | | | 768.356281 | 384.681779 | E | *1724.878853* | 862.943064 | 1707.852304 | 854.429790 | 1706.868288 | 853.937782 | 12 |
| 7 | 899.450910 | 450.229093 | | | 881.440345 | 441.223811 | L | *1595.836260* | 798.421768 | 1578.809711 | 789.908493 | 1577.825695 | 789.416485 | 11 |
| 8 | *1012.534974* | 506.771125 | | | 994.524409 | 497.765843 | L | *1482.752196* | 741.879736 | 1465.725647 | 733.366461 | 1464.741631 | 732.874453 | 10 |
| 9 | 1126.577901 | 563.792589 | 1109.551352 | 555.279314 | 1108.567336 | 554.787306 | N | *1369.668132* | 685.337704 | 1352.641583 | 676.824429 | 1351.657567 | 676.332421 | 9 |
| 10 | 1254.636479 | 627.821878 | 1237.609930 | 619.308603 | 1236.625914 | 618.816595 | Q | *1255.625205* | 628.316240 | 1238.598656 | 619.802966 | 1237.614640 | 619.310958 | 8 |
| 11 | 1325.673593 | 663.340435 | 1308.647044 | 654.827160 | 1307.663028 | 654.335152 | A | *1127.566627* | 564.286951 | 1110.540078 | 555.773677 | 1109.556062 | 555.281669 | 7 |
| 12 | 1764.898919 | 882.953098 | 1747.872370 | 874.439823 | 1746.888354 | 873.947815 | Q | *1056.529513* | 528.768395 | 1039.502964 | 520.255120 | 1038.518948 | 519.763112 | 6 |
| 13 | 1893.941512 | **947.474394** | 1876.914963 | 938.961120 | 1875.930947 | 938.469112 | E | *617.304187* | 309.155732 | 600.277638 | 300.642457 | 599.293622 | 300.150449 | 5 |
| 14 | 2031.000424 | 1016.003850 | 2013.973875 | 1007.490576 | 2012.989859 | 1006.998568 | H | *488.261594* | 244.634435 | 471.235045 | 236.121160 | | | 4 |
| 15 | 2178.068838 | 1089.538057 | 2161.042289 | 1081.024782 | 2160.058273 | 1080.532774 | F | *351.202682* | 176.104979 | 334.176133 | 167.591704 | | | 3 |
| 16 | 2235.090302 | 1118.048789 | 2218.063753 | 1109.535514 | 2217.079737 | 1109.043506 | G | 204.134268 | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 17 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 44.1 | 2380.188522 | 0.028230 | EDLIWELLNQAQEHFGK |
| 37.8 | 2380.188522 | 0.028230 | EDLIWELLNQAQEHFGK |
| 5.1 | 2380.199814 | 0.016938 | GEPGLQGFPGKPGFLGEVGPPGMR |

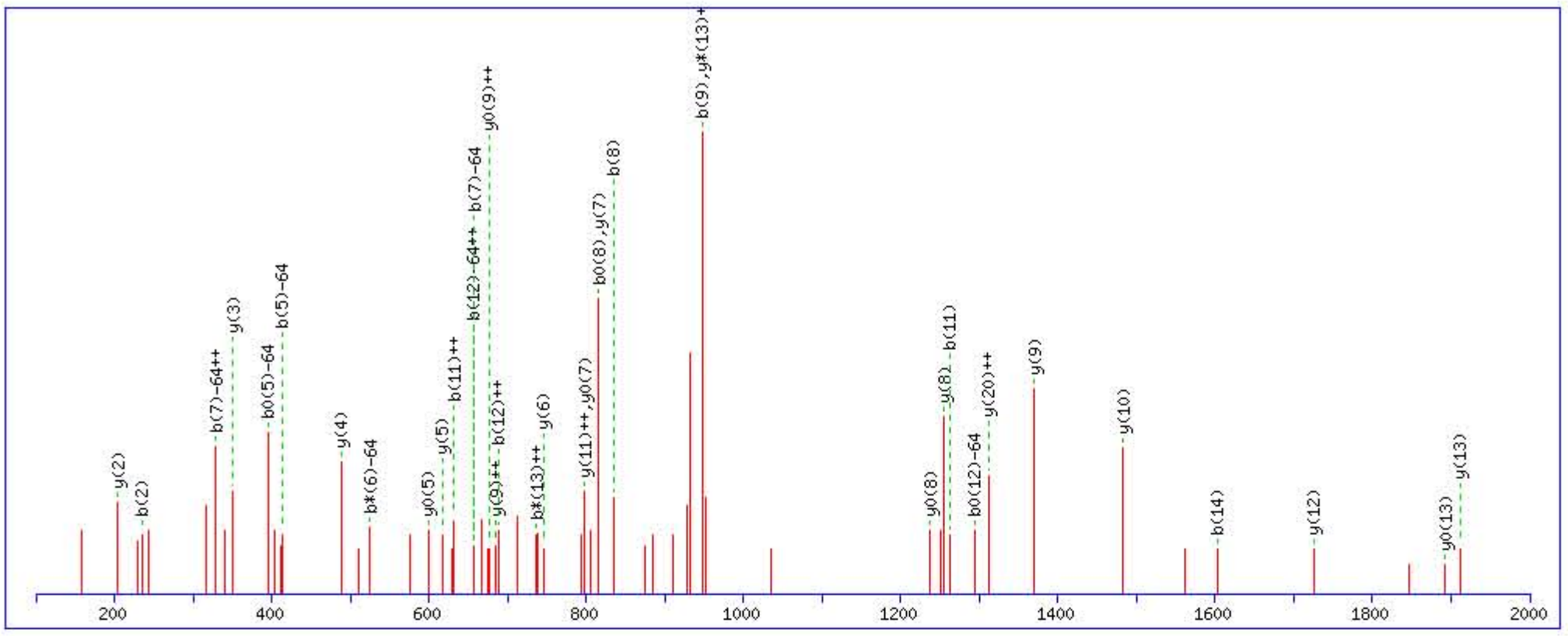
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SMGGKEDLIWELLNQAQEHFGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

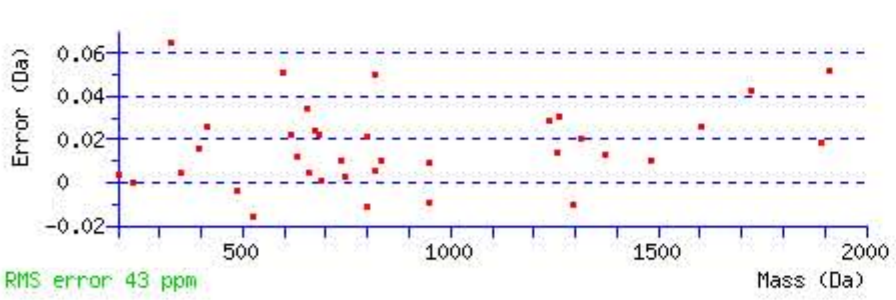
Match to Query 58590: 2856.433902 from(953.151910,3+) rtinseconds(2951) index(72569)
Title: Locus:1.1.1.2300.19 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

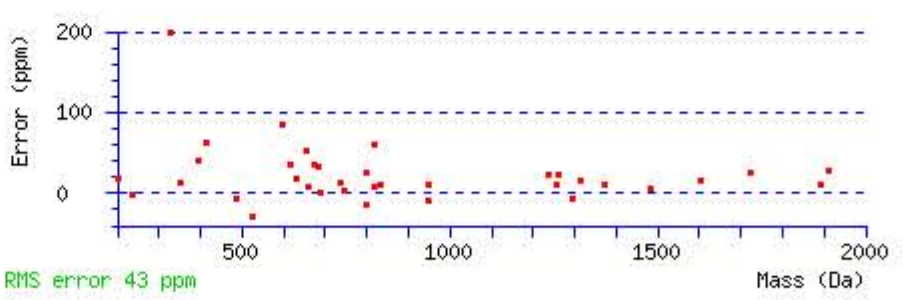
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2856.393845
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
M2 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q15 : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 0.00049
**Matches :** 36/356 fragment ions using 61 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 22 |
| 2 | **235.074704** | 118.040990 | | | 217.064139 | 109.035707 | M | 2770.369121 | 1385.688198 | 2753.342572 | 1377.174924 | 2752.358556 | 1376.682916 | 21 |
| 3 | 292.096168 | 146.551722 | | | 274.085603 | 137.546439 | G | 2623.333721 | 1312.170498 | 2606.307172 | 1303.657224 | 2605.323156 | 1303.165216 | 20 |
| 4 | 349.117632 | 175.062454 | | | 331.107067 | 166.057171 | G | 2566.312257 | 1283.659766 | 2549.285708 | 1275.146492 | 2548.301692 | 1274.654484 | 19 |
| 5 | 477.212595 | 239.109935 | 460.186046 | 230.596661 | 459.202030 | 230.104653 | K | 2509.290793 | 1255.149034 | 2492.264244 | 1246.635760 | 2491.280228 | 1246.143752 | 18 |
| 6 | 606.255188 | 303.631232 | 589.228639 | 295.117958 | 588.244623 | 294.625950 | E | 2381.195830 | 1191.101553 | 2364.169281 | 1182.588278 | 2363.185265 | 1182.096270 | 17 |
| 7 | 721.282131 | 361.144704 | 704.255582 | 352.631429 | 703.271566 | 352.139421 | D | 2252.153237 | 1126.580256 | 2235.126688 | 1118.066982 | 2234.142672 | 1117.574974 | 16 |
| 8 | **834.366195** | 417.686736 | 817.339646 | 409.173461 | 816.355630 | 408.681453 | L | 2137.126294 | 1069.066785 | 2120.099745 | 1060.553510 | 2119.115729 | 1060.061502 | 15 |
| 9 | **947.450259** | 474.228768 | 930.423710 | 465.715493 | 929.439694 | 465.223485 | I | 2024.042230 | 1012.524753 | 2007.015681 | 1004.011479 | 2006.031665 | 1003.519471 | 14 |
| 10 | 1133.529572 | 567.268424 | 1116.503023 | 558.755150 | 1115.519007 | 558.263142 | W | ***1910.958166*** | 955.982721 | 1893.931617 | 947.469447 | 1892.947601 | 946.977439 | 13 |
| 11 | **1262.572165** | **631.789721** | 1245.545616 | 623.276446 | 1244.561600 | 622.784438 | E | ***1724.878853*** | 862.943065 | 1707.852304 | 854.429790 | 1706.868288 | 853.937782 | 12 |
| 12 | 1375.656229 | **688.331753** | 1358.629680 | 679.818478 | 1357.645664 | 679.326470 | L | 1595.836260 | 798.421768 | 1578.809711 | 789.908494 | 1577.825695 | 789.416486 | 11 |
| 13 | 1488.740293 | 744.873785 | 1471.713744 | 736.360510 | 1470.729728 | 735.868502 | L | ***1482.752196*** | 741.879736 | 1465.725647 | 733.366462 | 1464.741631 | 732.874454 | 10 |
| 14 | **1602.783220** | 801.895248 | 1585.756671 | 793.381974 | 1584.772655 | 792.889966 | N | ***1369.668132*** | 685.337704 | 1352.641583 | 676.824430 | 1351.657567 | 676.332422 | 9 |
| 15 | 2042.008546 | 1021.507911 | 2024.981997 | 1012.994637 | 2023.997981 | 1012.502629 | Q | ***1255.625205*** | 628.316241 | 1238.598656 | 619.802966 | 1237.614640 | 619.310958 | 8 |
| 16 | 2113.045660 | 1057.026468 | 2096.019111 | 1048.513193 | 2095.035095 | 1048.021186 | A | ***816.399879*** | 408.703578 | 799.373330 | 400.190303 | 798.389314 | 399.698295 | 7 |
| 17 | 2241.104238 | 1121.055757 | 2224.077689 | 1112.542483 | 2223.093673 | 1112.050475 | Q | ***745.362765*** | 373.185021 | 728.336216 | 364.671746 | 727.352200 | 364.179738 | 6 |
| 18 | 2370.146831 | 1185.577054 | 2353.120282 | 1177.063779 | 2352.136266 | 1176.571771 | E | ***617.304187*** | 309.155732 | 600.277638 | 300.642457 | 599.293622 | 300.150449 | 5 |
| 19 | 2507.205743 | 1254.106510 | 2490.179194 | 1245.593235 | 2489.195178 | 1245.101227 | H | ***488.261594*** | 244.634435 | 471.235045 | 236.121160 | | | 4 |
| 20 | 2654.274157 | 1327.640717 | 2637.247608 | 1319.127442 | 2636.263592 | 1318.635434 | F | ***351.202682*** | 176.104979 | 334.176133 | 167.591704 | | | 3 |
| 21 | 2711.295621 | 1356.151449 | 2694.269072 | 1347.638174 | 2693.285056 | 1347.146166 | G | ***204.134268*** | 102.570772 | 187.107719 | 94.057497 | | | 2 |
| 22 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 47.7 | 2856.393845 | 0.040057 | SMGGKEDLIWELLNQAQEHFGK |
| 37.6 | 2856.393845 | 0.040057 | SMGGKEDLIWELLNQAQEHFGK |

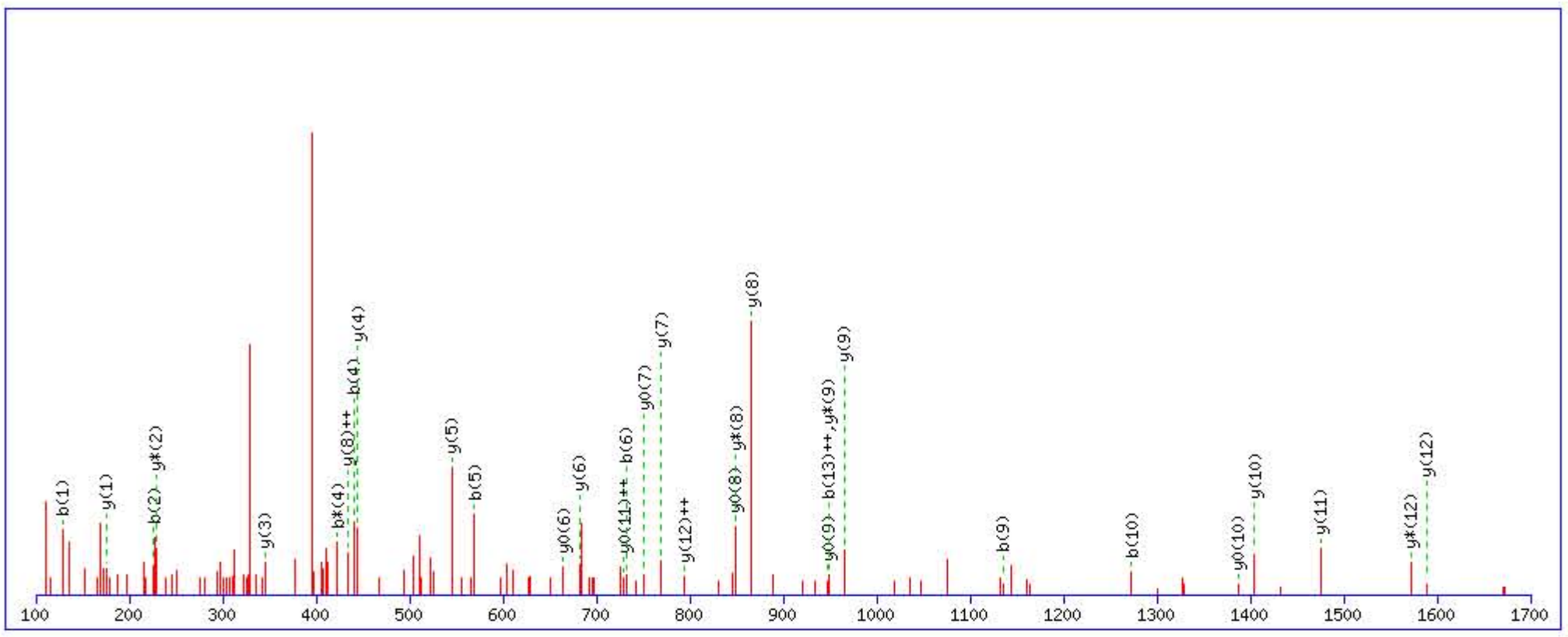
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KPVDEYKDCHLAQVPSHTVVAR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

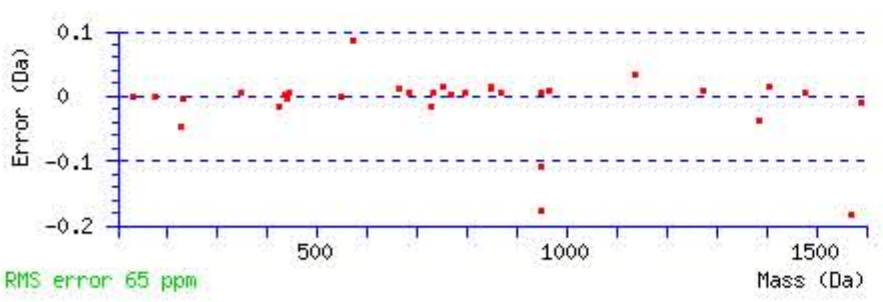
Match to Query 58643: 2859.453120 from(572.897900,5+) rtinseconds(1491) index(63449)
Title: Locus:1.1.1.1794.6 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

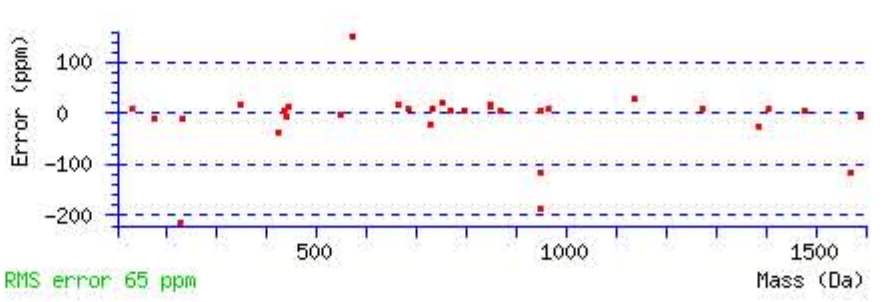
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2859.452393
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 0.0005
**Matches :** 32/238 fragment ions using 76 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *129.102239* | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 22 |
| 2 | *226.155003* | 113.581139 | 209.128454 | 105.067865 | | | P | 2732.364705 | 1366.685990 | 2715.338156 | 1358.172716 | 2714.354140 | 1357.680708 | 21 |
| 3 | 325.223417 | 163.115346 | 308.196868 | 154.602072 | | | V | 2635.311941 | 1318.159608 | 2618.285392 | 1309.646334 | 2617.301376 | 1309.154326 | 20 |
| 4 | *440.250360* | 220.628818 | 423.223811 | 212.115544 | 422.239795 | 211.623536 | D | 2536.243527 | 1268.625401 | 2519.216978 | 1260.112127 | 2518.232962 | 1259.620119 | 19 |
| 5 | *569.292953* | 285.150115 | 552.266404 | 276.636840 | 551.282388 | 276.144832 | E | 2421.216584 | 1211.111930 | 2404.190035 | 1202.598655 | 2403.206019 | 1202.106647 | 18 |
| 6 | *732.356282* | 366.681779 | 715.329733 | 358.168505 | 714.345717 | 357.676497 | Y | 2292.173991 | 1146.590633 | 2275.147442 | 1138.077359 | 2274.163426 | 1137.585351 | 17 |
| 7 | 860.451245 | 430.729261 | 843.424696 | 422.215986 | 842.440680 | 421.723978 | K | 2129.110662 | 1065.058969 | 2112.084113 | 1056.545694 | 2111.100097 | 1056.053686 | 16 |
| 8 | 975.478188 | 488.242732 | 958.451639 | 479.729458 | 957.467623 | 479.237450 | D | 2001.015699 | 1001.011487 | 1983.989150 | 992.498213 | 1983.005134 | 992.006205 | 15 |
| 9 | *1135.508837* | 568.258057 | 1118.482288 | 559.744782 | 1117.498272 | 559.252774 | C | 1885.988756 | 943.498016 | 1868.962207 | 934.984741 | 1867.978191 | 934.492733 | 14 |
| 10 | *1272.567749* | 636.787513 | 1255.541200 | 628.274238 | 1254.557184 | 627.782230 | H | 1725.958107 | 863.482691 | 1708.931558 | 854.969417 | 1707.947542 | 854.477409 | 13 |
| 11 | 1385.651813 | 693.329545 | 1368.625264 | 684.816270 | 1367.641248 | 684.324262 | L | *1588.899195* | 794.953235 | 1571.872646 | 786.439961 | 1570.888630 | 785.947953 | 12 |
| 12 | 1456.688927 | 728.848101 | 1439.662378 | 720.334827 | 1438.678362 | 719.842819 | A | *1475.815131* | 738.411203 | 1458.788582 | 729.897929 | 1457.804566 | 729.405921 | 11 |
| 13 | 1895.914253 | 948.460765 | 1878.887704 | 939.947490 | 1877.903688 | 939.455482 | Q | *1404.778017* | 702.892646 | 1387.751468 | 694.379372 | 1386.767452 | 693.887364 | 10 |
| 14 | 1994.982667 | 997.994972 | 1977.956118 | 989.481697 | 1976.972102 | 988.989689 | V | *965.552691* | 483.279983 | 948.526142 | 474.766709 | 947.542126 | 474.274701 | 9 |
| 15 | 2092.035431 | 1046.521353 | 2075.008882 | 1038.008079 | 2074.024866 | 1037.516071 | P | *866.484277* | 433.745776 | 849.457728 | 425.232502 | 848.473712 | 424.740494 | 8 |
| 16 | 2179.067459 | 1090.037367 | 2162.040910 | 1081.524093 | 2161.056894 | 1081.032085 | S | *769.431513* | 385.219394 | 752.404964 | 376.706120 | 751.420948 | 376.214112 | 7 |
| 17 | 2316.126371 | 1158.566823 | 2299.099822 | 1150.053549 | 2298.115806 | 1149.561541 | H | *682.399485* | 341.703380 | 665.372936 | 333.190106 | 664.388920 | 332.698098 | 6 |
| 18 | 2417.174050 | 1209.090663 | 2400.147501 | 1200.577388 | 2399.163485 | 1200.085380 | T | *545.340573* | 273.173924 | 528.314024 | 264.660650 | 527.330008 | 264.168642 | 5 |
| 19 | 2516.242464 | 1258.624870 | 2499.215915 | 1250.111595 | 2498.231899 | 1249.619587 | V | *444.292894* | 222.650085 | 427.266345 | 214.136810 | | | 4 |
| 20 | 2615.310878 | 1308.159077 | 2598.284329 | 1299.645802 | 2597.300313 | 1299.153794 | V | *345.224480* | 173.115878 | 328.197931 | 164.602603 | | | 3 |
| 21 | 2686.347992 | 1343.677634 | 2669.321443 | 1335.164359 | 2668.337427 | 1334.672351 | A | 246.156066 | 123.581671 | 229.129517 | 115.068397 | | | 2 |
| 22 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 47.7 | 2859.452393 | 0.000727 | KPVDEYKDCHLAQVPSHTVVAR |

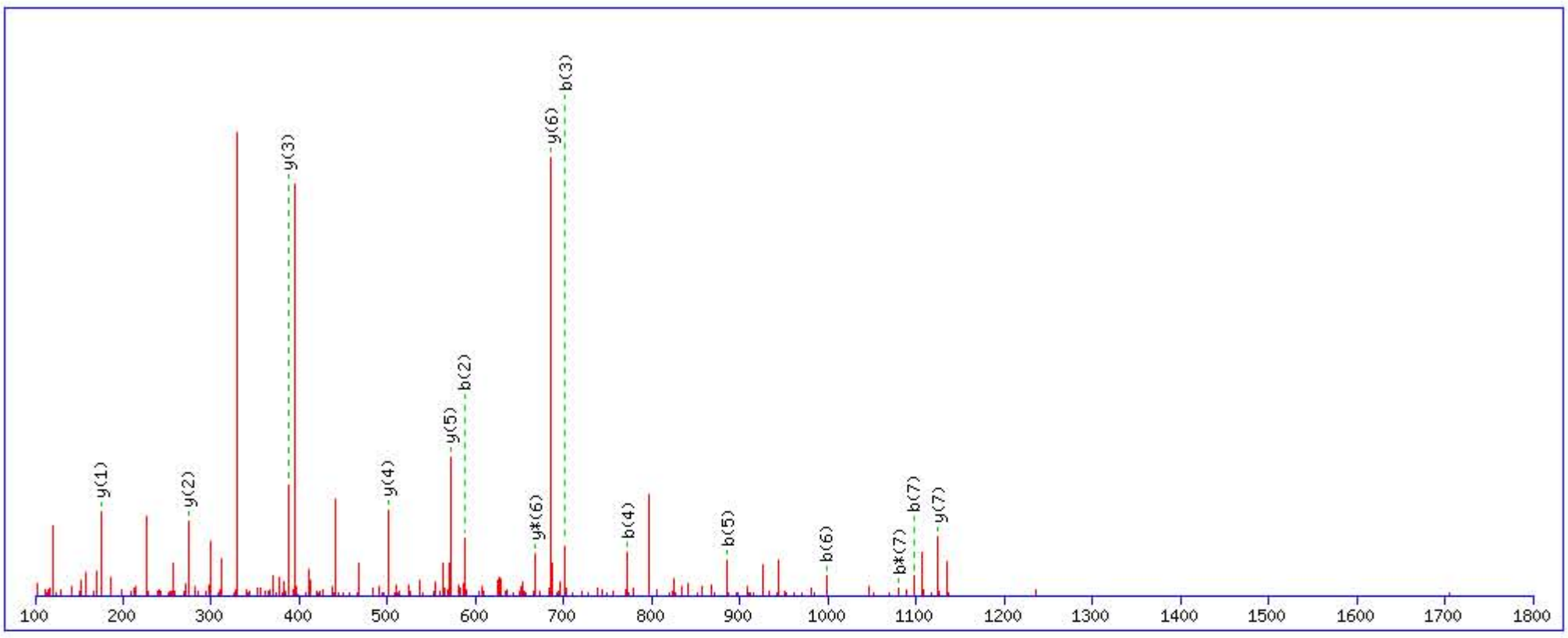
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FQNALLVR**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

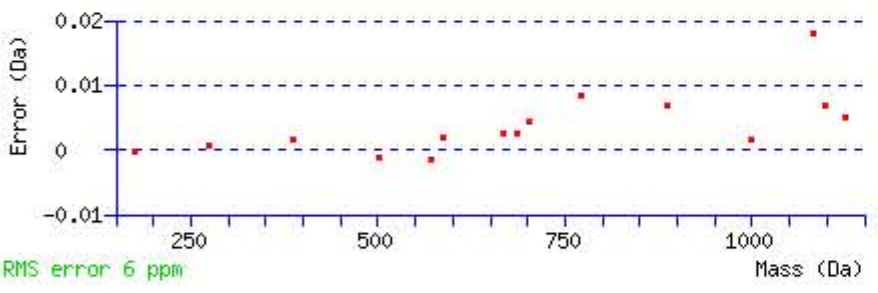
Match to Query 22473: 1270.729008 from(636.371780,2+) rtinseconds(2090) index(20782)
Title: Locus:1.1.1.3110.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

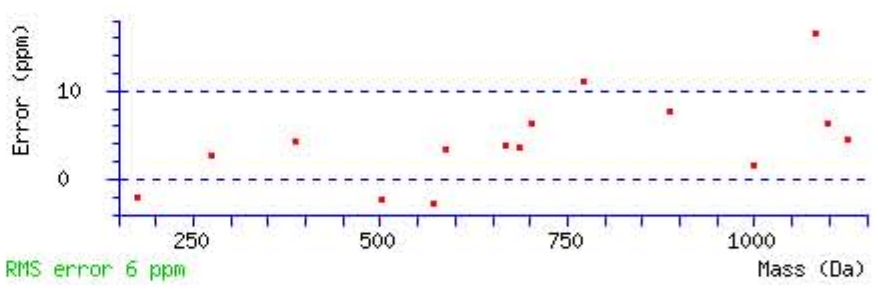
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1270.721985
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 35 **Expect:** 0.0043
**Matches :** 15/54 fragment ions using 34 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | F | | | | | 8 |
| 2 | 587.301016 | 294.154146 | 570.274467 | 285.640872 | Q | *1124.660861* | 562.834068 | 1107.634312 | 554.320794 | 7 |
| 3 | 701.343943 | 351.175610 | 684.317394 | 342.662335 | N | *685.435535* | 343.221406 | 668.408986 | 334.708131 | 6 |
| 4 | 772.381057 | 386.694166 | 755.354508 | 378.180892 | A | *571.392608* | 286.199942 | 554.366059 | 277.686668 | 5 |
| 5 | 885.465121 | 443.236199 | 868.438572 | 434.722924 | L | *500.355494* | 250.681385 | 483.328945 | 242.168110 | 4 |
| 6 | 998.549185 | 499.778231 | 981.522636 | 491.264956 | L | *387.271430* | 194.139353 | 370.244881 | 185.626078 | 3 |
| 7 | 1097.617599 | 549.312437 | 1080.591050 | 540.799163 | V | *274.187366* | 137.597321 | 257.160817 | 129.084046 | 2 |
| 8 | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 35.3 | 1270.721985 | 0.007023 | FQNALLVR |
| 13.1 | 1270.735687 | -0.006679 | KEAELRSGIIR |
| 8.8 | 1270.733215 | -0.004207 | MFHIRAVILR |
| 7.8 | 1270.722000 | 0.007008 | FQIAQVVR |
| 6.8 | 1270.733215 | -0.004207 | FQRQILR |
| 3.8 | 1270.717957 | 0.011051 | QLSRTLSR |
| 3.2 | 1270.739761 | -0.010753 | QVVNIPSFIVR |
| 3.2 | 1270.735733 | -0.006725 | EILGRGVSSVVR |
| 2.7 | 1270.725357 | 0.003651 | QKVMAIVR |
| 1.6 | 1270.710541 | 0.018467 | AVNSKAEVARAR |

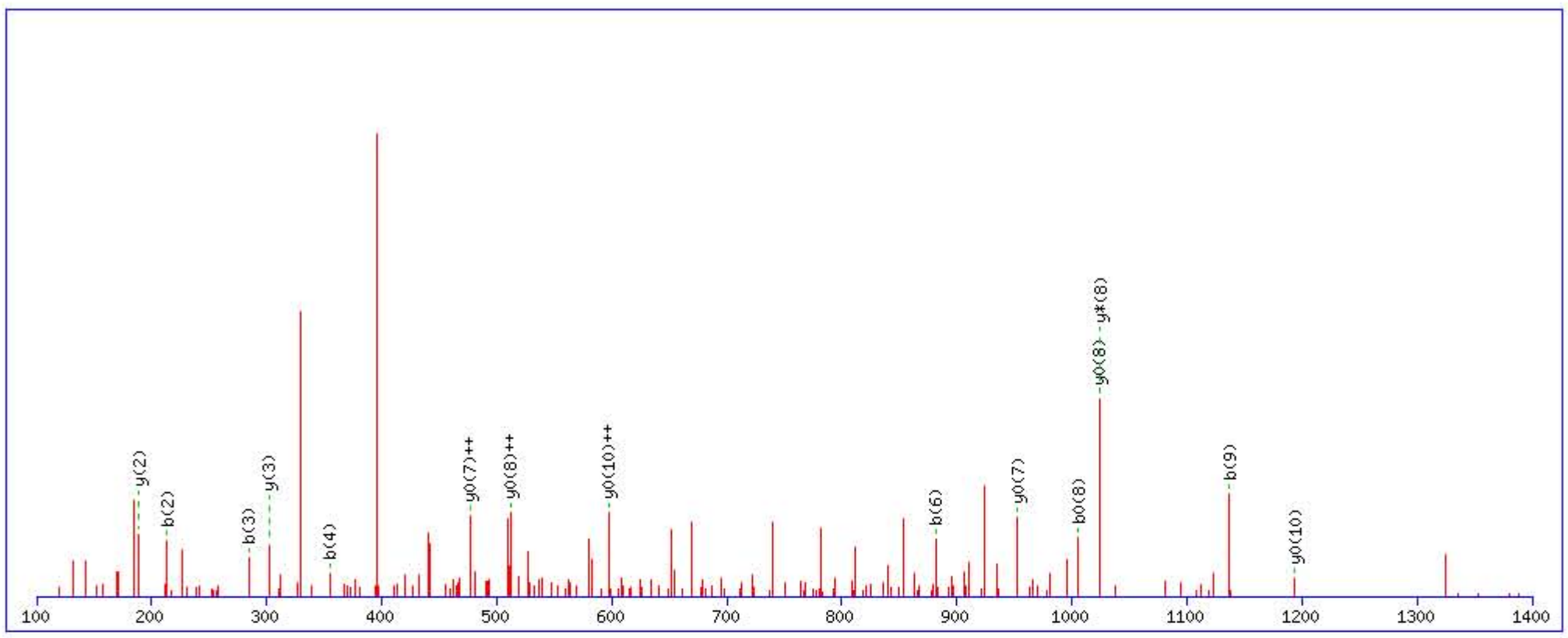
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LVAASQAALGL**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

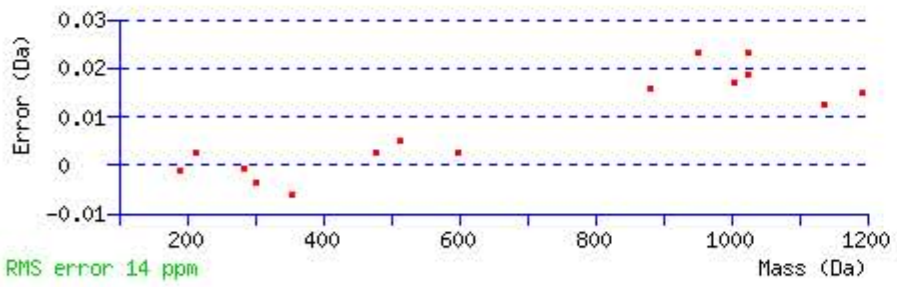
Match to Query 23735: 1323.772348 from(662.893450,2+) rtinseconds(2524) index(23331)
Title: Locus:1.1.1.3261.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

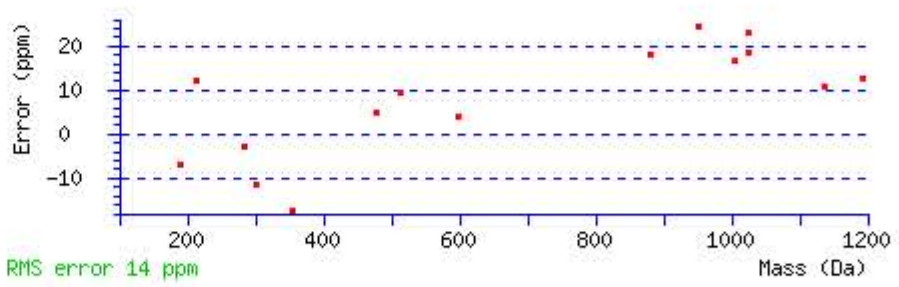
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1323.758423
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.00022
**Matches :** 21/80 fragment ions using 33 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 11 |
| 2 | *213.159754* | 107.083515 | | | | | V | 1211.681657 | 606.344466 | 1194.655108 | 597.831192 | 1193.671092 | 597.339184 | 10 |
| 3 | *284.196868* | 142.602072 | | | | | A | 1112.613243 | 556.810259 | 1095.586694 | 548.296985 | 1094.602678 | 547.804977 | 9 |
| 4 | *355.233982* | 178.120629 | | | | | A | 1041.576129 | 521.291702 | 1024.549580 | 512.778428 | 1023.565564 | 512.286420 | 8 |
| 5 | 442.266010 | 221.636643 | | | 424.255445 | 212.631361 | S | 970.539015 | 485.773145 | 953.512466 | 477.259871 | 952.528450 | 476.767863 | 7 |
| 6 | *881.491336* | 441.249306 | 864.464787 | 432.736032 | 863.480771 | 432.244024 | Q | 883.506987 | 442.257131 | 866.480438 | 433.743857 | | | 6 |
| 7 | *952.528450* | **476.767863** | 935.501901 | 468.254589 | 934.517885 | 467.762581 | A | 444.281661 | 222.644468 | | | | | 5 |
| 8 | *1023.565564* | **512.286420** | 1006.539015 | 503.773146 | 1005.554999 | 503.281138 | A | 373.244547 | 187.125911 | | | | | 4 |
| 9 | *1136.649628* | 568.828452 | 1119.623079 | 560.315178 | 1118.639063 | 559.823169 | L | **302.207433** | 151.607354 | | | | | 3 |
| 10 | *1193.671092* | **597.339184** | 1176.644543 | 588.825909 | 1175.660527 | 588.333901 | G | **189.123369** | 95.065322 | | | | | 2 |
| 11 | | | | | | | L | 132.101905 | 66.554590 | | | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 44.7 | 1323.758423 | 0.013925 | LVAASQAALGL |
| 5.7 | 1323.780899 | -0.008551 | MLGVPANRIVVR |

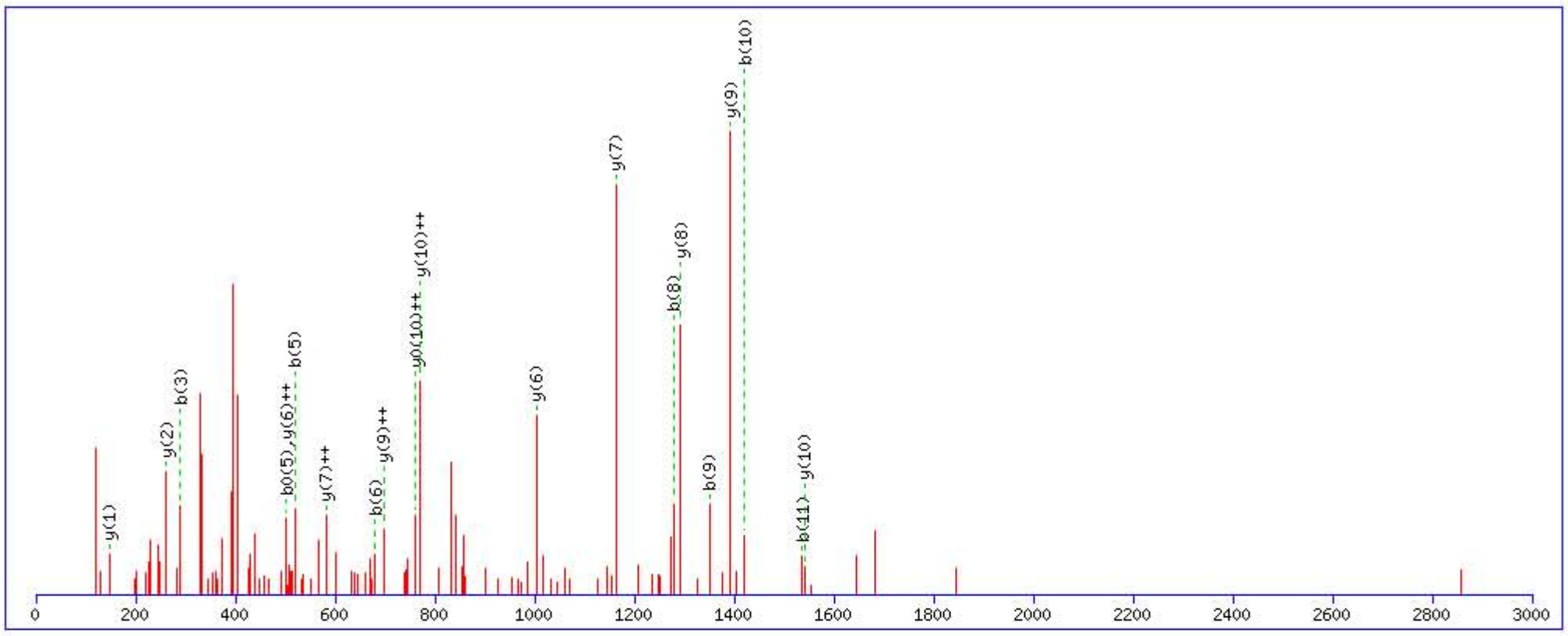
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AAFTECCQAADK**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

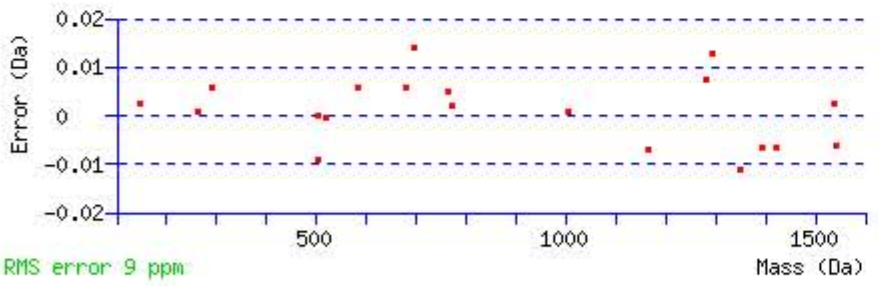
Match to Query 37579: 1681.731328 from(841.872940,2+) rtinseconds(1593) index(17561)
Title: Locus:1.1.1.2937.13 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

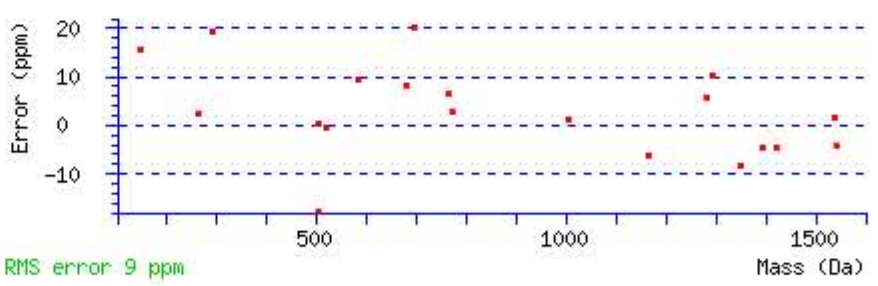
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1681.726227
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 2.6e-005
**Matches :** 20/110 fragment ions using 30 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 12 |
| 2 | 143.081504 | 72.044390 | | | | | A | 1611.696399 | 806.351838 | 1594.669850 | 797.838563 | 1593.685834 | 797.346555 | 11 |
| 3 | *290.149918* | 145.578597 | | | | | F | *1540.659285* | 770.833281 | 1523.632736 | 762.320006 | 1522.648720 | 761.827998 | 10 |
| 4 | 391.197597 | 196.102437 | | | 373.187032 | 187.097154 | T | *1393.590871* | 697.299074 | 1376.564322 | 688.785799 | 1375.580306 | 688.293791 | 9 |
| 5 | *520.240190* | 260.623733 | | | 502.229625 | 251.618451 | E | *1292.543192* | 646.775234 | 1275.516643 | 638.261960 | 1274.532627 | 637.769952 | 8 |
| 6 | *680.270839* | 340.639058 | | | 662.260274 | 331.633775 | C | *1163.500599* | 582.253938 | 1146.474050 | 573.740663 | 1145.490034 | 573.248655 | 7 |
| 7 | 840.301488 | 420.654382 | | | 822.290923 | 411.649100 | C | *1003.469950* | 502.238613 | 986.443401 | 493.725339 | 985.459385 | 493.233331 | 6 |
| 8 | *1279.526814* | 640.267045 | 1262.500265 | 631.753771 | 1261.516249 | 631.261763 | Q | 843.439301 | 422.223289 | 826.412752 | 413.710014 | 825.428736 | 413.218006 | 5 |
| 9 | *1350.563928* | 675.785602 | 1333.537379 | 667.272328 | 1332.553363 | 666.780320 | A | 404.213975 | 202.610626 | 387.187426 | 194.097351 | 386.203410 | 193.605343 | 4 |
| 10 | *1421.601042* | 711.304159 | 1404.574493 | 702.790885 | 1403.590477 | 702.298877 | A | 333.176861 | 167.092069 | 316.150312 | 158.578794 | 315.166296 | 158.086786 | 3 |
| 11 | *1536.627985* | 768.817631 | 1519.601436 | 760.304356 | 1518.617420 | 759.812348 | D | *262.139747* | 131.573512 | 245.113198 | 123.060237 | 244.129182 | 122.568229 | 2 |
| 12 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 53.1 | 1681.726227 | 0.005101 | AAFTECCQAADK |

**Mascot:** http://www.matrixscience.com/

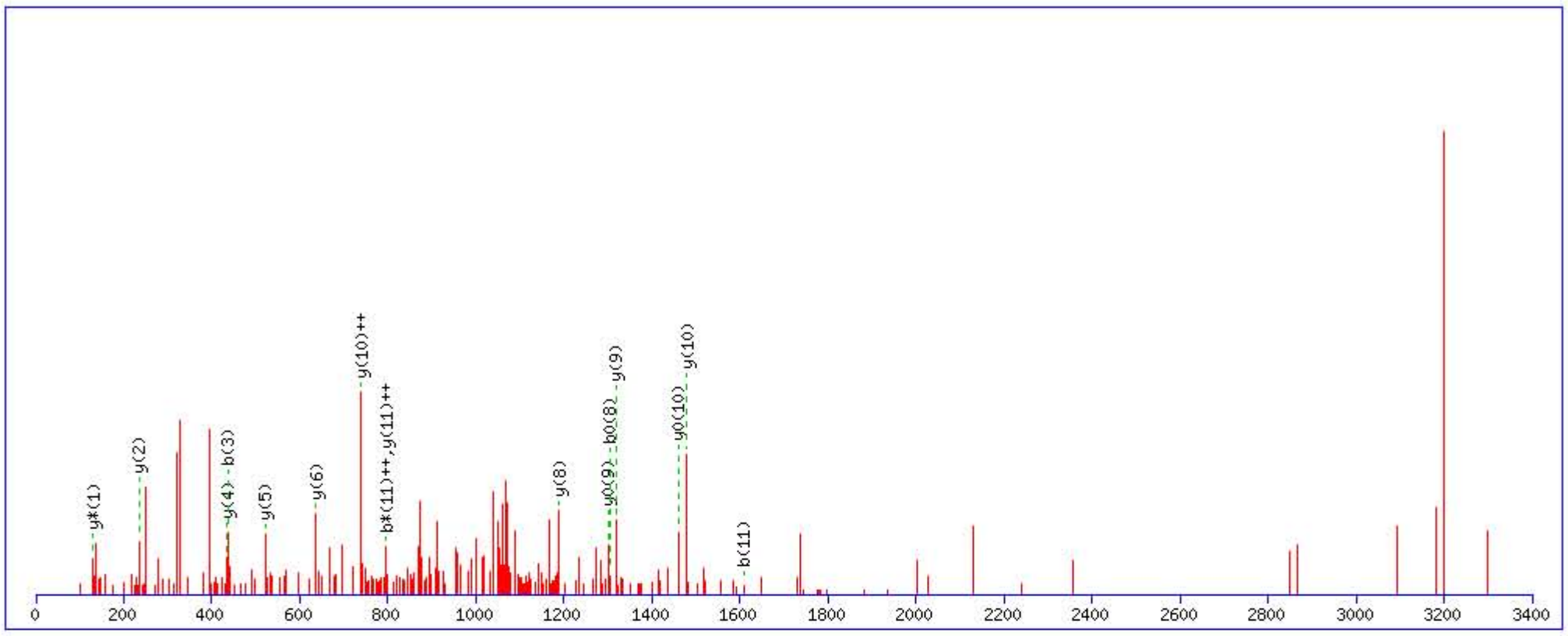
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **YICENQDSISSK**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

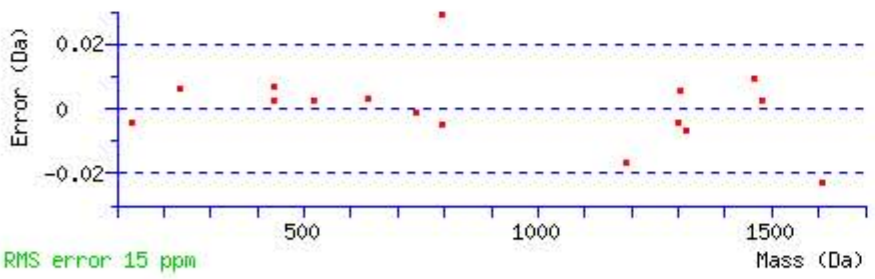
Match to Query 39179: 1753.803828 from(877.909190,2+) rtinseconds(1657) index(17915)
Title: Locus:1.1.1.2959.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

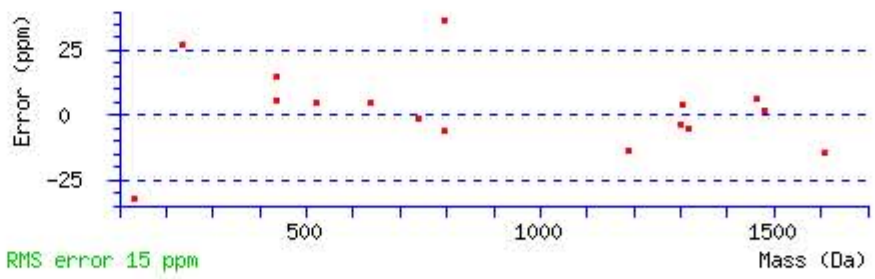
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1753.801483
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 30 **Expect:** 0.012
**Matches :** 16/116 fragment ions using 34 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 164.070605 | 82.538940 | | | | | Y | | | | | | | 12 |
| 2 | 277.154669 | 139.080973 | | | | | I | 1591.745454 | 796.376365 | 1574.718905 | 787.863091 | 1573.734889 | 787.371083 | 11 |
| 3 | **437.185318** | 219.096297 | | | | | C | *1478.661390* | 739.834333 | 1461.634841 | 731.321059 | 1460.650825 | 730.829051 | 10 |
| 4 | 566.227911 | 283.617594 | | | 548.217346 | 274.612311 | E | *1318.630741* | 659.819009 | 1301.604192 | 651.305734 | 1300.620176 | 650.813726 | 9 |
| 5 | 680.270838 | 340.639057 | 663.244289 | 332.125783 | 662.260273 | 331.633775 | N | *1189.588148* | 595.297712 | 1172.561599 | 586.784438 | 1171.577583 | 586.292430 | 8 |
| 6 | 1119.496164 | 560.251720 | 1102.469615 | 551.738446 | 1101.485599 | 551.246437 | Q | 1075.545221 | 538.276249 | 1058.518672 | 529.762974 | 1057.534656 | 529.270966 | 7 |
| 7 | 1234.523107 | 617.765192 | 1217.496558 | 609.251917 | 1216.512542 | 608.759909 | D | *636.319895* | 318.663586 | 619.293346 | 310.150311 | 618.309330 | 309.658303 | 6 |
| 8 | 1321.555135 | 661.281206 | 1304.528586 | 652.767931 | 1303.544570 | 652.275923 | S | *521.292952* | 261.150114 | 504.266403 | 252.636840 | 503.282387 | 252.144832 | 5 |
| 9 | 1434.639199 | 717.823238 | 1417.612650 | 709.309963 | 1416.628634 | 708.817955 | I | *434.260924* | 217.634100 | 417.234375 | 209.120826 | 416.250359 | 208.628818 | 4 |
| 10 | 1521.671227 | 761.339252 | 1504.644678 | 752.825977 | 1503.660662 | 752.333969 | S | 321.176860 | 161.092068 | 304.150311 | 152.578794 | 303.166295 | 152.086786 | 3 |
| 11 | **1608.703255** | 804.855266 | 1591.676706 | 796.341991 | 1590.692690 | 795.849983 | S | *234.144832* | 117.576054 | 217.118283 | 109.062780 | 216.134267 | 108.570772 | 2 |
| 12 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 29.8 | 1753.801483 | 0.002345 | YICENQDSISSK |

**Mascot:** http://www.matrixscience.com/

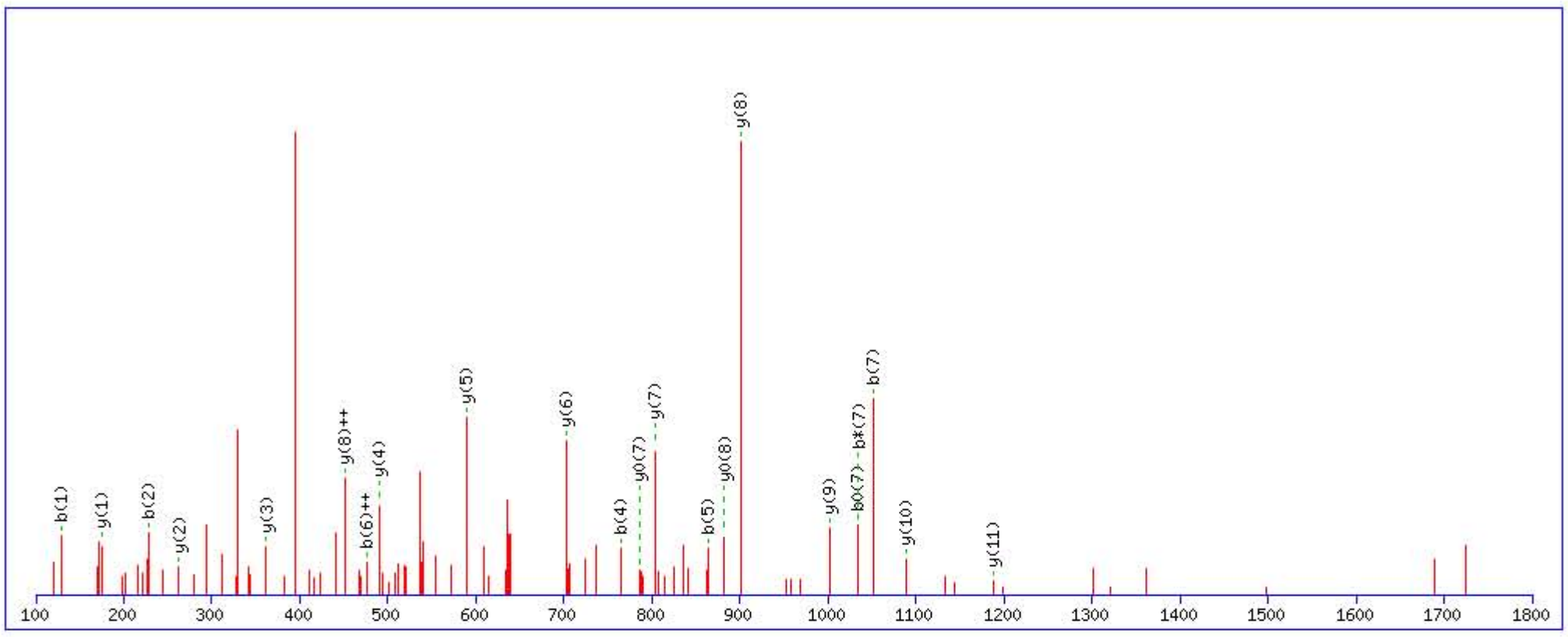
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KVPQVSTPTLVEVSR**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

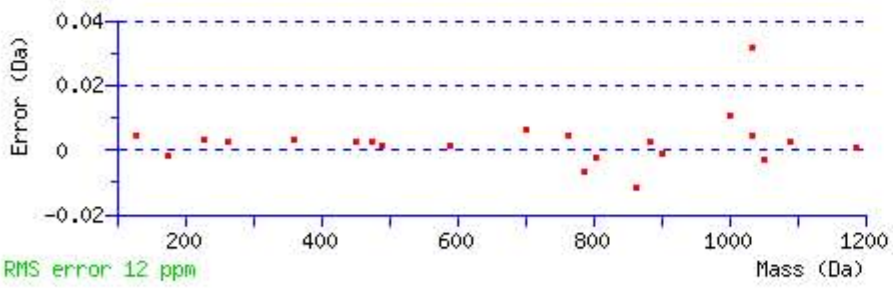
Match to Query 43099: 1950.105972 from(651.042600,3+) rtinseconds(1919) index(65863)
Title: Locus:1.1.1.1943.18 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

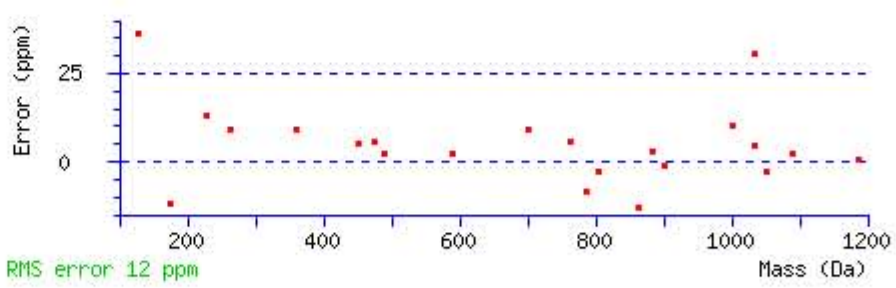
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1950.097229
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 43 **Expect:** 0.0005
**Matches :** 22/156 fragment ions using 61 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.102239 | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 15 |
| 2 | 228.170653 | 114.588965 | 211.144104 | 106.075690 | | | V | 1823.009533 | 912.008404 | 1805.982984 | 903.495130 | 1804.998968 | 903.003122 | 14 |
| 3 | 325.223417 | 163.115346 | 308.196868 | 154.602072 | | | P | 1723.941119 | 862.474197 | 1706.914570 | 853.960923 | 1705.930554 | 853.468915 | 13 |
| 4 | 764.448743 | 382.728010 | 747.422194 | 374.214735 | | | Q | 1626.888355 | 813.947815 | 1609.861806 | 805.434541 | 1608.877790 | 804.942533 | 12 |
| 5 | 863.517157 | 432.262217 | 846.490608 | 423.748942 | | | V | *1187.663029* | 594.335153 | 1170.636480 | 585.821878 | 1169.652464 | 585.329870 | 11 |
| 6 | 950.549185 | 475.778231 | 933.522636 | 467.264956 | 932.538620 | 466.772948 | S | *1088.594615* | 544.800946 | 1071.568066 | 536.287671 | 1070.584050 | 535.795663 | 10 |
| 7 | 1051.596864 | 526.302070 | 1034.570315 | 517.788795 | 1033.586299 | 517.296787 | T | *1001.562587* | 501.284932 | 984.536038 | 492.771657 | 983.552022 | 492.279649 | 9 |
| 8 | 1148.649628 | 574.828452 | 1131.623079 | 566.315178 | 1130.639063 | 565.823169 | P | *900.514908* | 450.761092 | 883.488359 | 442.247818 | 882.504343 | 441.755810 | 8 |
| 9 | 1249.697307 | 625.352291 | 1232.670758 | 616.839017 | 1231.686742 | 616.347009 | T | *803.462144* | 402.234710 | 786.435595 | 393.721436 | 785.451579 | 393.229428 | 7 |
| 10 | 1362.781371 | 681.894323 | 1345.754822 | 673.381049 | 1344.770806 | 672.889041 | L | *702.414465* | 351.710871 | 685.387916 | 343.197596 | 684.403900 | 342.705588 | 6 |
| 11 | 1461.849785 | 731.428530 | 1444.823236 | 722.915256 | 1443.839220 | 722.423248 | V | *589.330401* | 295.168839 | 572.303852 | 286.655564 | 571.319836 | 286.163556 | 5 |
| 12 | 1590.892378 | 795.949827 | 1573.865829 | 787.436552 | 1572.881813 | 786.944544 | E | *490.261987* | 245.634631 | 473.235438 | 237.121357 | 472.251422 | 236.629349 | 4 |
| 13 | 1689.960792 | 845.484034 | 1672.934243 | 836.970759 | 1671.950227 | 836.478751 | V | *361.219394* | 181.113335 | 344.192845 | 172.600061 | 343.208829 | 172.108053 | 3 |
| 14 | 1776.992820 | 889.000048 | 1759.966271 | 880.486774 | 1758.982255 | 879.994765 | S | *262.150980* | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 15 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 43.0 | 1950.097229 | 0.008743 | KVPQVSTPTLVEVSR |

**Mascot:** http://www.matrixscience.com/

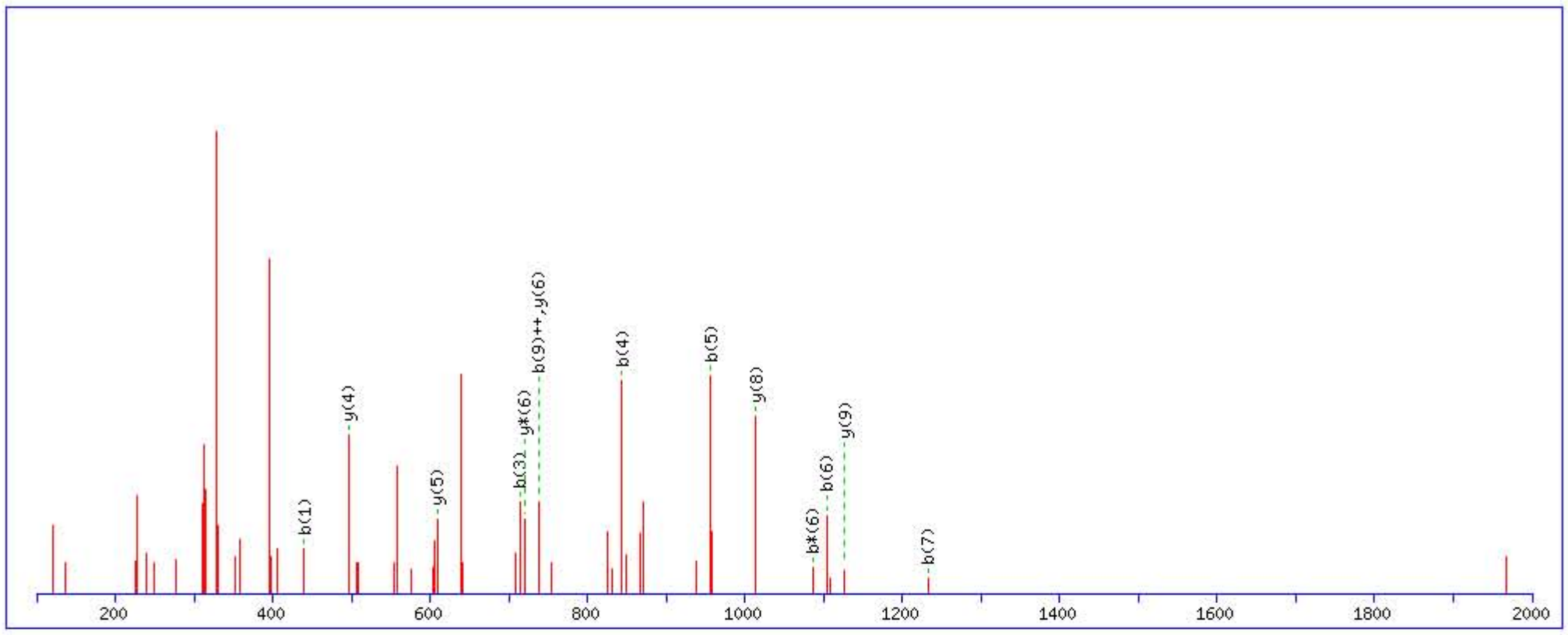
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QNCELFEQLGEYK**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

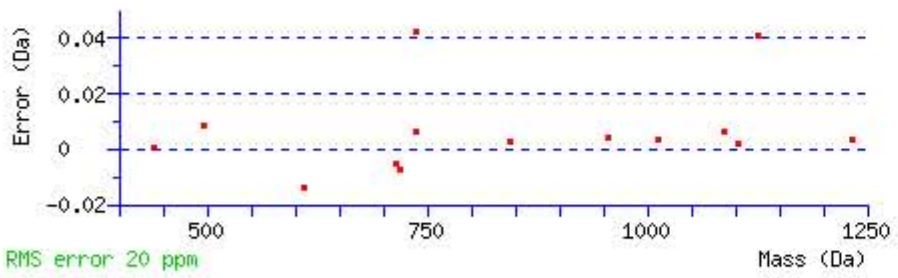
Match to Query 43526: 1967.927742 from(656.983190,3+) rtinseconds(2391) index(7801)
Title: Locus:1.1.1.2110.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

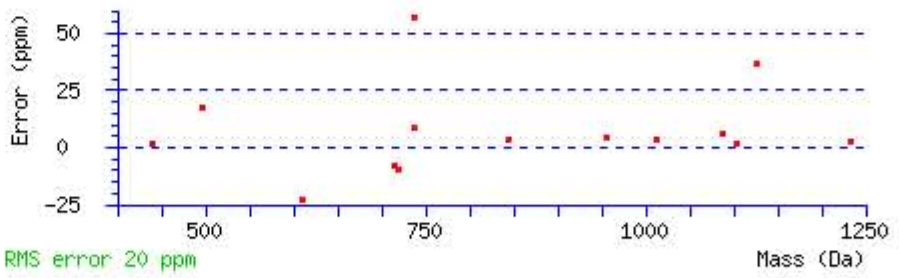
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1967.912094
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q1 : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0084
**Matches :** 14/134 fragment ions using 23 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *440.232602* | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 13 |
| 2 | 554.275529 | 277.641403 | 537.248980 | 269.128128 | | | N | 1529.694072 | 765.350674 | 1512.667523 | 756.837400 | 1511.683507 | 756.345392 | 12 |
| 3 | *714.306178* | 357.656727 | 697.279629 | 349.143453 | | | C | 1415.651145 | 708.329211 | 1398.624596 | 699.815936 | 1397.640580 | 699.323928 | 11 |
| 4 | *843.348771* | 422.178024 | 826.322222 | 413.664749 | 825.338206 | 413.172741 | E | 1255.620496 | 628.313886 | 1238.593947 | 619.800612 | 1237.609931 | 619.308604 | 10 |
| 5 | *956.432835* | 478.720056 | 939.406286 | 470.206781 | 938.422270 | 469.714773 | L | *1126.577903* | 563.792590 | 1109.551354 | 555.279315 | 1108.567338 | 554.787307 | 9 |
| 6 | *1103.501249* | 552.254263 | 1086.474700 | 543.740988 | 1085.490684 | 543.248980 | F | *1013.493839* | 507.250558 | 996.467290 | 498.737283 | 995.483274 | 498.245275 | 8 |
| 7 | *1232.543842* | 616.775559 | 1215.517293 | 608.262285 | 1214.533277 | 607.770277 | E | 866.425425 | 433.716351 | 849.398876 | 425.203076 | 848.414860 | 424.711068 | 7 |
| 8 | 1360.602420 | 680.804848 | 1343.575871 | 672.291574 | 1342.591855 | 671.799566 | Q | *737.382832* | 369.195054 | 720.356283 | 360.681780 | 719.372267 | 360.189772 | 6 |
| 9 | 1473.686484 | 737.346880 | 1456.659935 | 728.833606 | 1455.675919 | 728.341598 | L | *609.324254* | 305.165765 | 592.297705 | 296.652490 | 591.313689 | 296.160482 | 5 |
| 10 | 1530.707948 | 765.857612 | 1513.681399 | 757.344338 | 1512.697383 | 756.852330 | G | *496.240190* | 248.623733 | 479.213641 | 240.110458 | 478.229625 | 239.618450 | 4 |
| 11 | 1659.750541 | 830.378909 | 1642.723992 | 821.865634 | 1641.739976 | 821.373626 | E | 439.218726 | 220.113001 | 422.192177 | 211.599726 | 421.208161 | 211.107718 | 3 |
| 12 | 1822.813870 | 911.910573 | 1805.787321 | 903.397299 | 1804.803305 | 902.905291 | Y | 310.176133 | 155.591705 | 293.149584 | 147.078430 | | | 2 |
| 13 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.1 | 1967.912094 | 0.015648 | QNCELFEQLGEYK |

**Mascot:** http://www.matrixscience.com/

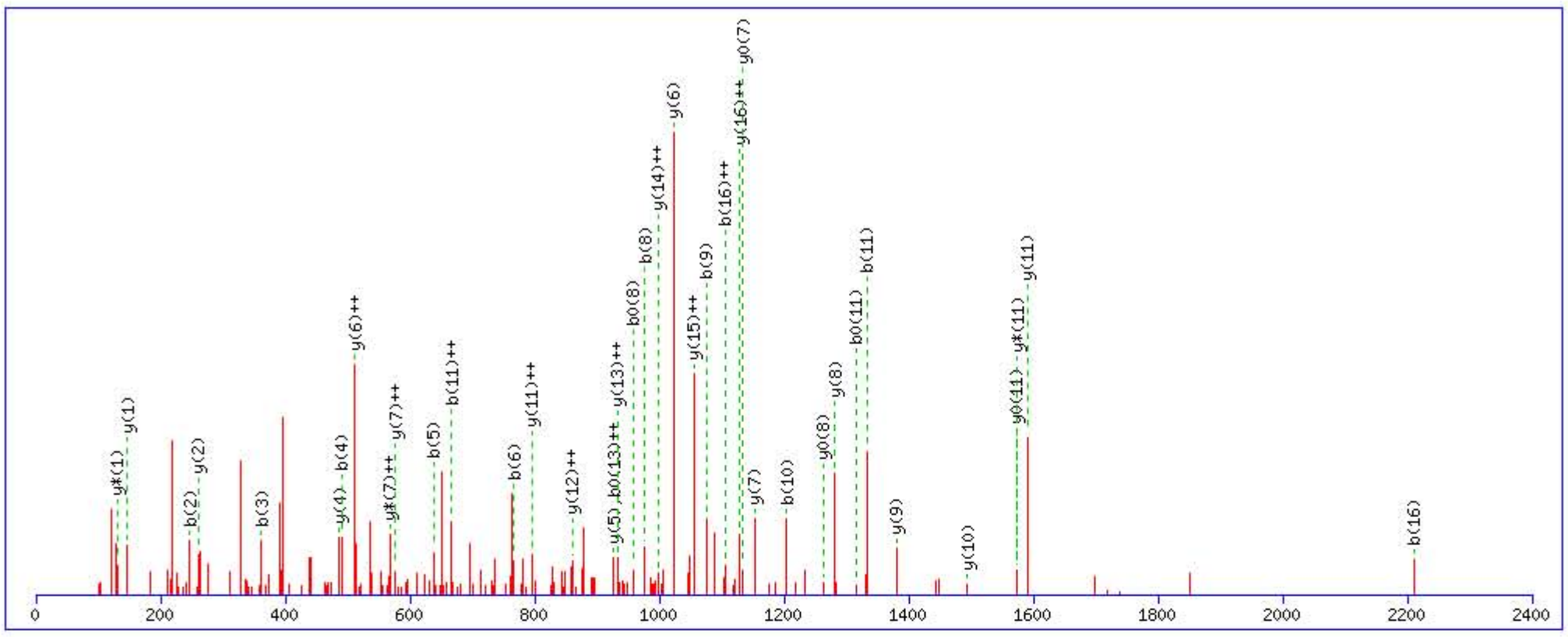
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VFDEFKPLVEEPQNLIK**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

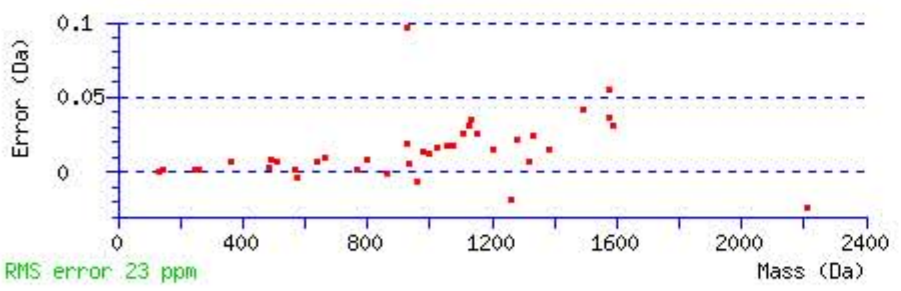
Match to Query 51396: 2355.288072 from(786.103300,3+) rtinseconds(2620) index(23807)
Title: Locus:1.1.1.3294.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

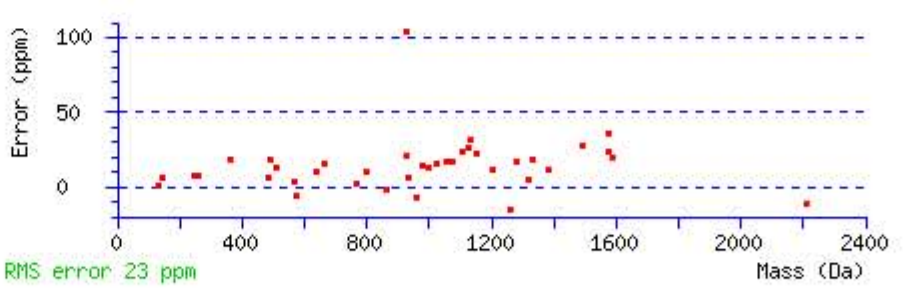
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2355.254822
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q13 : Biotin:Thermo-21345 (Q)
**Ions Score:** 52 **Expect:** 9e-005
**Matches :** 39/166 fragment ions using 77 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 17 |
| 2 | **247.144104** | 124.075690 | | | | | F | 2257.193704 | 1129.100490 | 2240.167155 | 1120.587216 | 2239.183139 | 1120.095208 | 16 |
| 3 | **362.171047** | 181.589161 | | | 344.160482 | 172.583879 | D | 2110.125290 | 1055.566283 | 2093.098741 | 1047.053008 | 2092.114725 | 1046.561000 | 15 |
| 4 | **491.213640** | 246.110458 | | | 473.203075 | 237.105176 | E | 1995.098347 | 998.052812 | 1978.071798 | 989.539537 | 1977.087782 | 989.047529 | 14 |
| 5 | **638.282054** | 319.644665 | | | 620.271489 | 310.639383 | F | 1866.055754 | 933.531515 | 1849.029205 | 925.018241 | 1848.045189 | 924.526233 | 13 |
| 6 | **766.377017** | 383.692147 | 749.350468 | 375.178872 | 748.366452 | 374.686864 | K | 1718.987340 | 859.997308 | 1701.960791 | 851.484034 | 1700.976775 | 850.992026 | 12 |
| 7 | 863.429781 | 432.218529 | 846.403232 | 423.705254 | 845.419216 | 423.213246 | P | ***1590.892377*** | 795.949827 | 1573.865828 | 787.436552 | 1572.881812 | 786.944544 | 11 |
| 8 | **976.513845** | 488.760561 | 959.487296 | 480.247286 | 958.503280 | 479.755278 | L | ***1493.839613*** | 747.423445 | 1476.813064 | 738.910170 | 1475.829048 | 738.418162 | 10 |
| 9 | **1075.582259** | 538.294768 | 1058.555710 | 529.781493 | 1057.571694 | 529.289485 | V | ***1380.755549*** | 690.881413 | 1363.729000 | 682.368138 | 1362.744984 | 681.876130 | 9 |
| 10 | **1204.624852** | 602.816064 | 1187.598303 | 594.302790 | 1186.614287 | 593.810782 | E | ***1281.687135*** | 641.347206 | 1264.660586 | 632.833931 | 1263.676570 | 632.341923 | 8 |
| 11 | **1333.667445** | **667.337361** | 1316.640896 | 658.824086 | 1315.656880 | 658.332078 | E | ***1152.644542*** | 576.825909 | 1135.617993 | 568.312635 | 1134.633977 | 567.820627 | 7 |
| 12 | 1430.720209 | 715.863743 | 1413.693660 | 707.350468 | 1412.709644 | 706.858460 | P | ***1023.601949*** | 512.304613 | 1006.575400 | 503.791338 | | | 6 |
| 13 | 1869.945535 | 935.476406 | 1852.918986 | 926.963131 | 1851.934970 | 926.471123 | Q | ***926.549185*** | 463.778231 | 909.522636 | 455.264956 | | | 5 |
| 14 | 1983.988462 | 992.497869 | 1966.961913 | 983.984595 | 1965.977897 | 983.492587 | N | ***487.323859*** | 244.165568 | 470.297310 | 235.652293 | | | 4 |
| 15 | 2097.072526 | 1049.039901 | 2080.045977 | 1040.526627 | 2079.061961 | 1040.034619 | L | 373.280932 | 187.144104 | 356.254383 | 178.630830 | | | 3 |
| 16 | **2210.156590** | **1105.581933** | 2193.130041 | 1097.068659 | 2192.146025 | 1096.576651 | I | ***260.196868*** | 130.602072 | 243.170319 | 122.088798 | | | 2 |
| 17 | | | | | | | K | ***147.112804*** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.5 | 2355.254822 | 0.033250 | VFDEFKPLVEEPQNLIK |

**Mascot:** http://www.matrixscience.com/

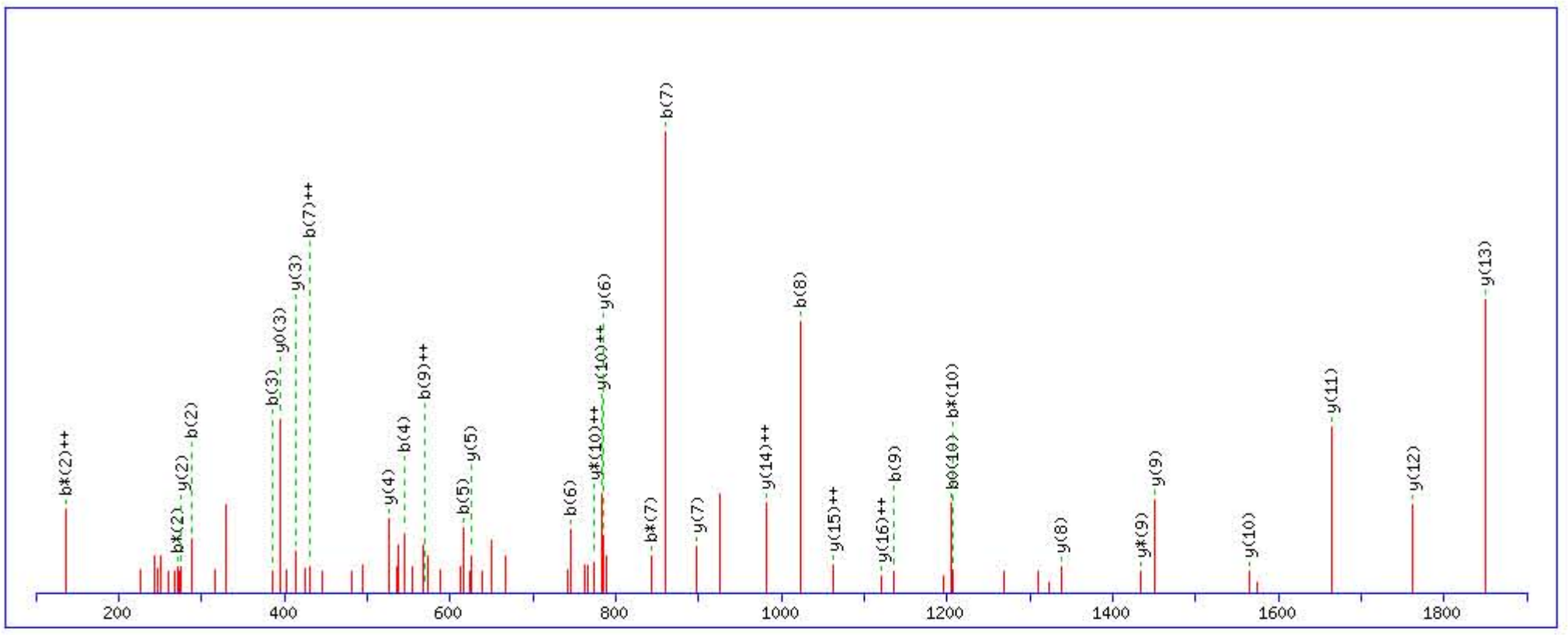
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **RMPCAEDYLSVVLNQLCVLHEK**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

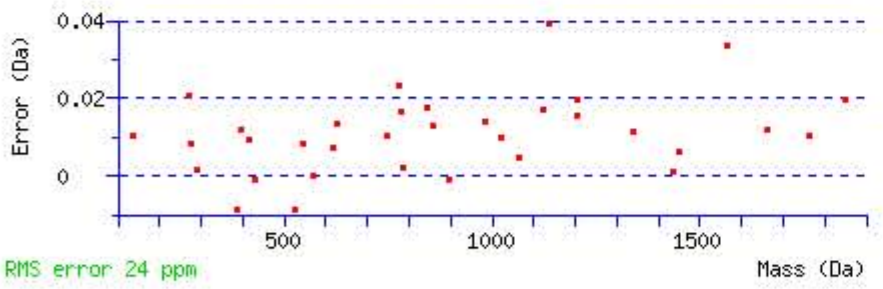
Match to Query 60016: 2984.507656 from(747.134190,4+) rtinseconds(3089) index(26559)
Title: Locus:1.1.1.3455.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

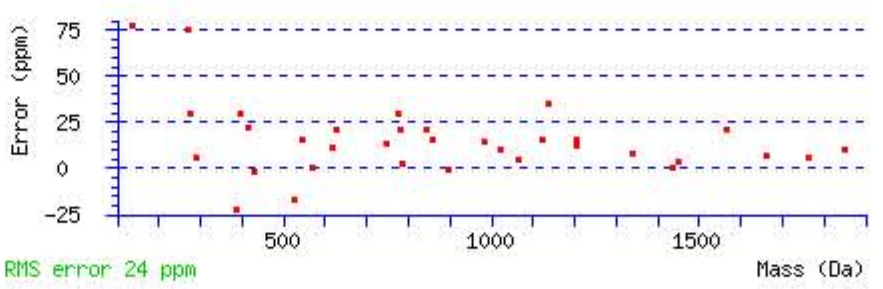
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2984.474426
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q15 : Biotin:Thermo-21345 (Q)
**Ions Score:** 80 **Expect:** 3.5e-008
**Matches :** 34/240 fragment ions using 60 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 157.108387 | 79.057831 | 140.081838 | 70.544557 | | | R | | | | | | | 22 |
| 2 | *288.148872* | 144.578074 | 271.122323 | 136.064799 | | | M | 2829.380614 | 1415.193945 | 2812.354065 | 1406.680670 | 2811.370049 | 1406.188662 | 21 |
| 3 | *385.201636* | 193.104456 | 368.175087 | 184.591181 | | | P | 2698.340129 | 1349.673702 | 2681.313580 | 1341.160428 | 2680.329564 | 1340.668420 | 20 |
| 4 | *545.232285* | 273.119781 | 528.205736 | 264.606506 | | | C | 2601.287365 | 1301.147320 | 2584.260816 | 1292.634046 | 2583.276800 | 1292.142038 | 19 |
| 5 | *616.269399* | 308.638338 | 599.242850 | 300.125063 | | | A | 2441.256716 | 1221.131996 | 2424.230167 | 1212.618721 | 2423.246151 | 1212.126713 | 18 |
| 6 | *745.311992* | 373.159634 | 728.285443 | 364.646360 | 727.301427 | 364.154352 | E | 2370.219602 | 1185.613439 | 2353.193053 | 1177.100164 | 2352.209037 | 1176.608156 | 17 |
| 7 | *860.338935* | **430.673106** | 843.312386 | 422.159831 | 842.328370 | 421.667823 | D | 2241.177009 | 1121.092142 | 2224.150460 | 1112.578868 | 2223.166444 | 1112.086860 | 16 |
| 8 | *1023.402264* | 512.204770 | 1006.375715 | 503.691496 | 1005.391699 | 503.199488 | Y | 2126.150066 | 1063.578671 | 2109.123517 | 1055.065396 | 2108.139501 | 1054.573388 | 15 |
| 9 | *1136.486328* | **568.746802** | 1119.459779 | 560.233528 | 1118.475763 | 559.741519 | L | 1963.086737 | 982.047007 | 1946.060188 | 973.533732 | 1945.076172 | 973.041724 | 14 |
| 10 | 1223.518356 | 612.262816 | 1206.491807 | 603.749542 | 1205.507791 | 603.257534 | S | *1850.002673* | 925.504975 | 1832.976124 | 916.991700 | 1831.992108 | 916.499692 | 13 |
| 11 | 1322.586770 | 661.797023 | 1305.560221 | 653.283749 | 1304.576205 | 652.791741 | V | *1762.970645* | 881.988961 | 1745.944096 | 873.475686 | 1744.960080 | 872.983678 | 12 |
| 12 | 1421.655184 | 711.331230 | 1404.628635 | 702.817956 | 1403.644619 | 702.325948 | V | *1663.902231* | 832.454754 | 1646.875682 | 823.941479 | 1645.891666 | 823.449471 | 11 |
| 13 | 1534.739248 | 767.873262 | 1517.712699 | 759.359988 | 1516.728683 | 758.867980 | L | *1564.833817* | 782.920547 | 1547.807268 | 774.407272 | 1546.823252 | 773.915264 | 10 |
| 14 | 1648.782175 | 824.894726 | 1631.755626 | 816.381451 | 1630.771610 | 815.889443 | N | *1451.749753* | 726.378515 | 1434.723204 | 717.865240 | 1433.739188 | 717.373232 | 9 |
| 15 | 2088.007501 | 1044.507388 | 2070.980952 | 1035.994114 | 2069.996936 | 1035.502106 | Q | *1337.706826* | 669.357051 | 1320.680277 | 660.843777 | 1319.696261 | 660.351769 | 8 |
| 16 | 2201.091565 | 1101.049421 | 2184.065016 | 1092.536146 | 2183.081000 | 1092.044138 | L | *898.481500* | 449.744388 | 881.454951 | 441.231114 | 880.470935 | 440.739106 | 7 |
| 17 | 2361.122214 | 1181.064745 | 2344.095665 | 1172.551470 | 2343.111649 | 1172.059462 | C | *785.397436* | 393.202356 | 768.370887 | 384.689081 | 767.386871 | 384.197073 | 6 |
| 18 | 2460.190628 | 1230.598952 | 2443.164079 | 1222.085677 | 2442.180063 | 1221.593669 | V | *625.366787* | 313.187032 | 608.340238 | 304.673757 | 607.356222 | 304.181749 | 5 |
| 19 | 2573.274692 | 1287.140984 | 2556.248143 | 1278.627709 | 2555.264127 | 1278.135701 | L | *526.298373* | 263.652825 | 509.271824 | 255.139550 | 508.287808 | 254.647542 | 4 |
| 20 | 2710.333604 | 1355.670440 | 2693.307055 | 1347.157165 | 2692.323039 | 1346.665157 | H | *413.214309* | 207.110793 | 396.187760 | 198.597518 | 395.203744 | 198.105510 | 3 |
| 21 | 2839.376197 | 1420.191736 | 2822.349648 | 1411.678462 | 2821.365632 | 1411.186454 | E | *276.155397* | 138.581337 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 22 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 80.0 | 2984.474426 | 0.033230 | RMPCAEDYLSVVLNQLCVLHEK |
| 0.5 | 2984.466171 | 0.041485 | QQMNGLTSFLDASTVYGSSPALERQLR |

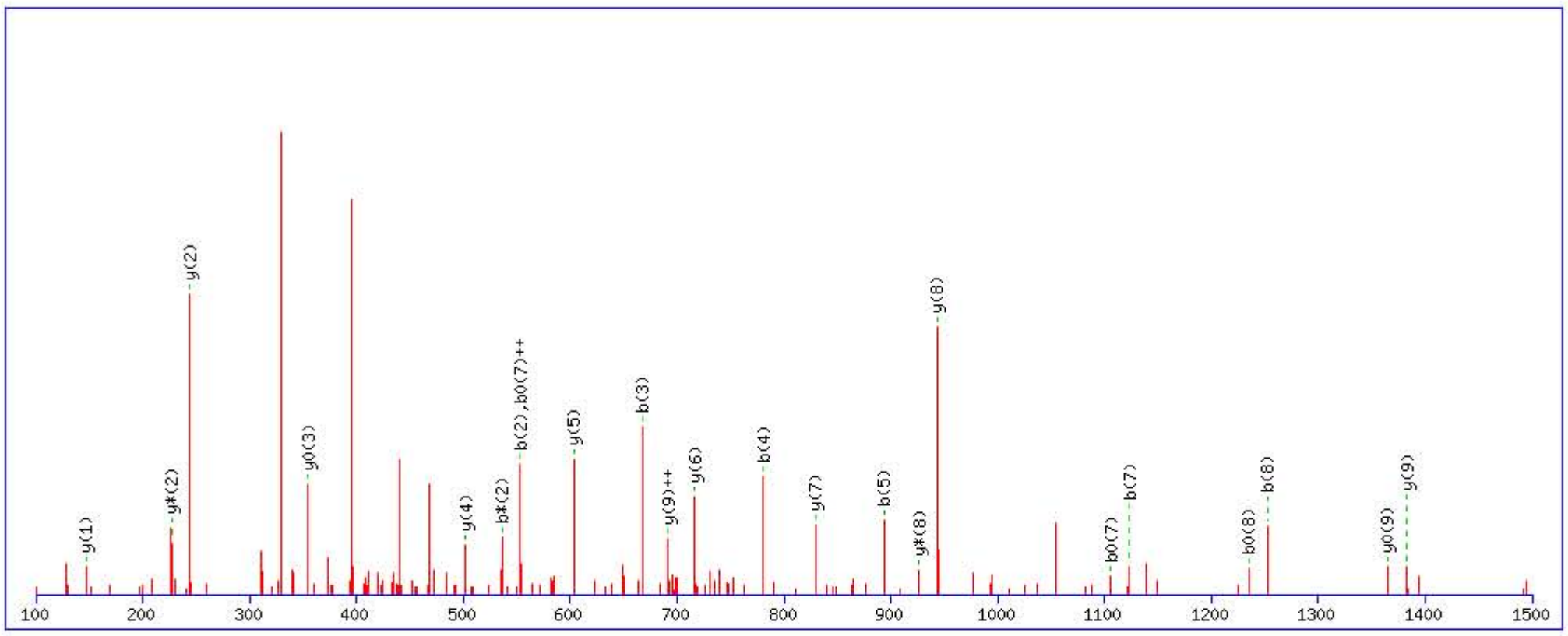
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IQNILTEEPK**
Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

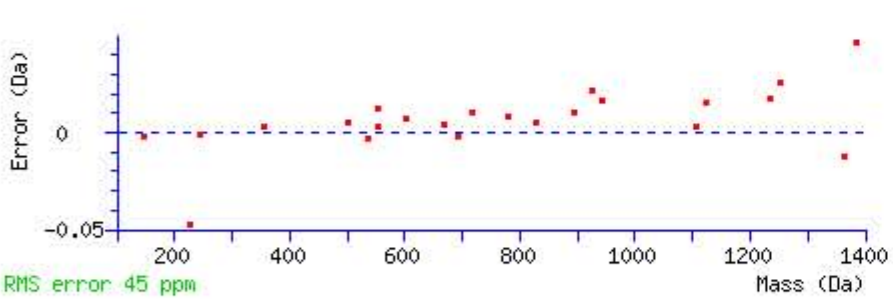
Match to Query 30953: 1494.831908 from(748.423230,2+) rtinseconds(2033) index(50540)
Title: Locus:1.1.1.1945.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

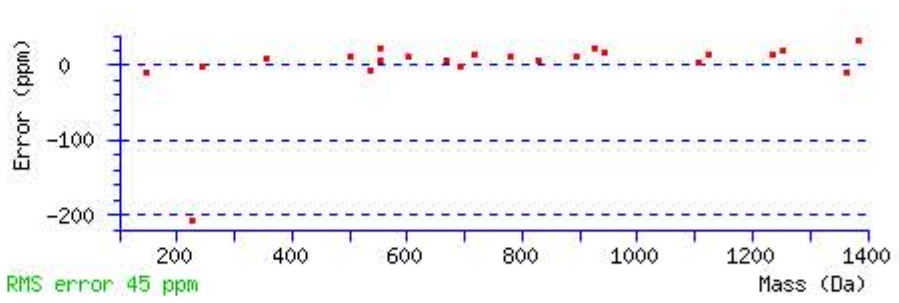
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1494.811569
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 0.0003
**Matches :** 23/92 fragment ions using 40 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 10 |
| 2 | **553.316666** | 277.161971 | 536.290117 | 268.648697 | | | Q | *1382.734814* | 691.871045 | 1365.708265 | 683.357771 | 1364.724249 | 682.865763 | 9 |
| 3 | **667.359593** | 334.183435 | 650.333044 | 325.670160 | | | N | *943.509488* | 472.258382 | 926.482939 | 463.745108 | 925.498923 | 463.253100 | 8 |
| 4 | **780.443657** | 390.725467 | 763.417108 | 382.212192 | | | I | *829.466561* | 415.236919 | 812.440012 | 406.723644 | 811.455996 | 406.231636 | 7 |
| 5 | **893.527721** | 447.267499 | 876.501172 | 438.754224 | | | L | *716.382497* | 358.694887 | 699.355948 | 350.181612 | 698.371932 | 349.689604 | 6 |
| 6 | 994.575400 | 497.791338 | 977.548851 | 489.278064 | 976.564835 | 488.786056 | T | *603.298433* | 302.152855 | 586.271884 | 293.639580 | 585.287868 | 293.147572 | 5 |
| 7 | **1123.617993** | 562.312635 | 1106.591444 | 553.799360 | 1105.607428 | 553.307352 | E | *502.250754* | 251.629015 | 485.224205 | 243.115741 | 484.240189 | 242.623733 | 4 |
| 8 | **1252.660586** | 626.833931 | 1235.634037 | 618.320657 | 1234.650021 | 617.828649 | E | 373.208161 | 187.107719 | 356.181612 | 178.594444 | 355.197596 | 178.102436 | 3 |
| 9 | 1349.713350 | 675.360313 | 1332.686801 | 666.847039 | 1331.702785 | 666.355031 | P | *244.165568* | 122.586422 | 227.139019 | 114.073148 | | | 2 |
| 10 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.0 | 1494.811569 | 0.020339 | IQNILTEEPK |
| 7.0 | 1494.815430 | 0.016478 | KGSTKDSGHLQIPK |
| 6.3 | 1494.834030 | -0.002122 | QLLRALEEGR |
| 3.9 | 1494.822815 | 0.009093 | IIFRTSELMTLR |
| 2.8 | 1494.834030 | -0.002122 | QLNAIRDNIK |

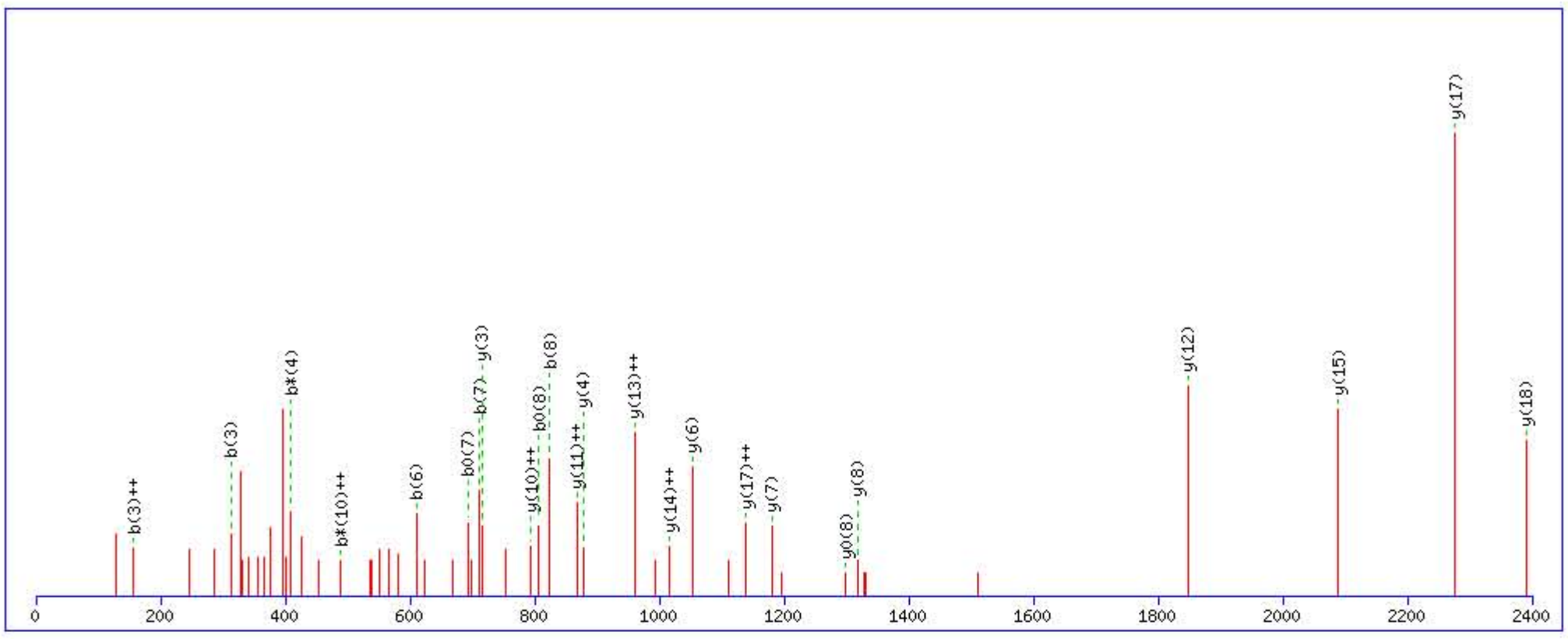
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AKLIALTLLGMGLALFRNHQSSYQTR**
Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

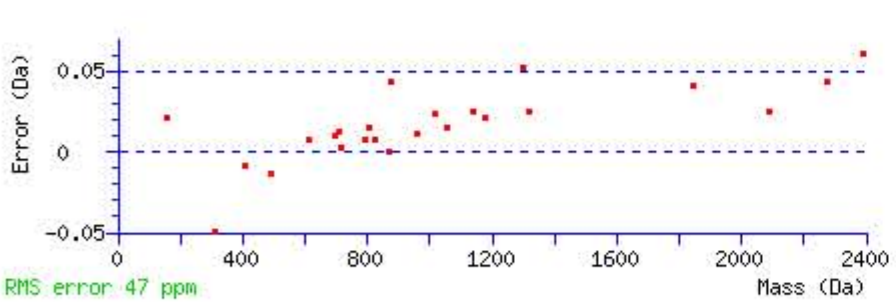
Match to Query 61746: 3212.808020 from(643.568880,5+) rtinseconds(3212) index(58478)
Title: Locus:1.1.1.2350.3 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

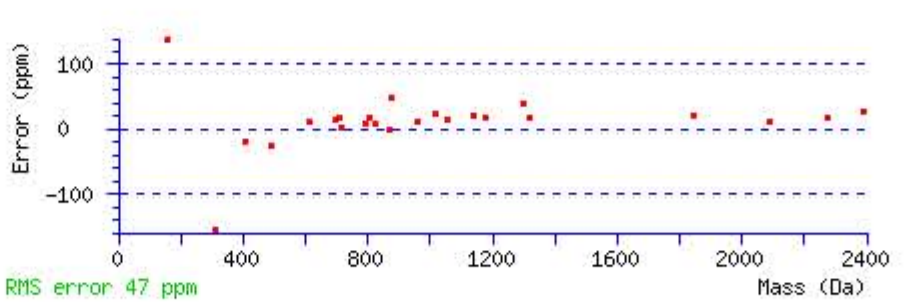
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3212.767807
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q24 : Biotin:Thermo-21345 (Q)
**Ions Score:** 47 **Expect:** 9.9e-005
**Matches :** 24/284 fragment ions using 40 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 26 |
| 2 | 200.139353 | 100.573315 | 183.112804 | 92.060040 | | | K | 3142.738015 | 1571.872645 | 3125.711466 | 1563.359371 | 3124.727450 | 1562.867363 | 25 |
| 3 | **313.223417** | 157.115346 | 296.196868 | 148.602072 | | | L | 3014.643052 | 1507.825164 | 2997.616503 | 1499.311889 | 2996.632487 | 1498.819881 | 24 |
| 4 | 426.307481 | 213.657378 | 409.280932 | 205.144104 | | | I | 2901.558988 | 1451.283132 | 2884.532439 | 1442.769857 | 2883.548423 | 1442.277849 | 23 |
| 5 | 497.344595 | 249.175935 | 480.318046 | 240.662661 | | | A | 2788.474924 | 1394.741100 | 2771.448375 | 1386.227825 | 2770.464359 | 1385.735817 | 22 |
| 6 | **610.428659** | 305.717968 | 593.402110 | 297.204693 | | | L | 2717.437810 | 1359.222543 | 2700.411261 | 1350.709268 | 2699.427245 | 1350.217260 | 21 |
| 7 | **711.476338** | 356.241807 | 694.449789 | 347.728533 | 693.465773 | 347.236525 | T | 2604.353746 | 1302.680511 | 2587.327197 | 1294.167236 | 2586.343181 | 1293.675228 | 20 |
| 8 | **824.560402** | 412.783839 | 807.533853 | 404.270565 | 806.549837 | 403.778557 | L | 2503.306067 | 1252.156671 | 2486.279518 | 1243.643397 | 2485.295502 | 1243.151389 | 19 |
| 9 | 937.644466 | 469.325871 | 920.617917 | 460.812597 | 919.633901 | 460.320589 | L | *2390.222003* | 1195.614639 | 2373.195454 | 1187.101365 | 2372.211438 | 1186.609357 | 18 |
| 10 | 994.665930 | 497.836603 | 977.639381 | 489.323329 | 976.655365 | 488.831321 | G | *2277.137939* | 1139.072607 | 2260.111390 | 1130.559333 | 2259.127374 | 1130.067325 | 17 |
| 11 | 1125.706415 | 563.356846 | 1108.679866 | 554.843571 | 1107.695850 | 554.351563 | M | 2220.116475 | 1110.561875 | 2203.089926 | 1102.048601 | 2202.105910 | 1101.556593 | 16 |
| 12 | 1182.727879 | 591.867578 | 1165.701330 | 583.354303 | 1164.717314 | 582.862295 | G | *2089.075990* | 1045.041633 | 2072.049441 | 1036.528358 | 2071.065425 | 1036.036350 | 15 |
| 13 | 1295.811943 | 648.409609 | 1278.785394 | 639.896335 | 1277.801378 | 639.404327 | L | 2032.054526 | 1016.530901 | 2015.027977 | 1008.017627 | 2014.043961 | 1007.525619 | 14 |
| 14 | 1366.849057 | 683.928166 | 1349.822508 | 675.414892 | 1348.838492 | 674.922884 | A | 1918.970462 | 959.988869 | 1901.943913 | 951.475595 | 1900.959897 | 950.983587 | 13 |
| 15 | 1479.933121 | 740.470198 | 1462.906572 | 731.956924 | 1461.922556 | 731.464916 | L | *1847.933348* | 924.470312 | 1830.906799 | 915.957038 | 1829.922783 | 915.465030 | 12 |
| 16 | 1627.001535 | 814.004405 | 1609.974986 | 805.491131 | 1608.990970 | 804.999123 | F | 1734.849284 | 867.928280 | 1717.822735 | 859.415006 | 1716.838719 | 858.922998 | 11 |
| 17 | 1783.102646 | 892.054961 | 1766.076097 | 883.541686 | 1765.092081 | 883.049678 | R | 1587.780870 | 794.394073 | 1570.754321 | 785.880799 | 1569.770305 | 785.388791 | 10 |
| 18 | 1897.145573 | 949.076424 | 1880.119024 | 940.563150 | 1879.135008 | 940.071142 | N | 1431.679759 | 716.343518 | 1414.653210 | 707.830243 | 1413.669194 | 707.338235 | 9 |
| 19 | 2034.204485 | 1017.605880 | 2017.177936 | 1009.092606 | 2016.193920 | 1008.600598 | H | *1317.636832* | 659.322054 | 1300.610283 | 650.808780 | 1299.626267 | 650.316772 | 8 |
| 20 | 2162.263063 | 1081.635169 | 2145.236514 | 1073.121895 | 2144.252498 | 1072.629887 | Q | *1180.577920* | 590.792598 | 1163.551371 | 582.279324 | 1162.567355 | 581.787316 | 7 |
| 21 | 2249.295091 | 1125.151183 | 2232.268542 | 1116.637909 | 2231.284526 | 1116.145901 | S | *1052.519342* | 526.763309 | 1035.492793 | 518.250035 | 1034.508777 | 517.758027 | 6 |
| 22 | 2336.327119 | 1168.667197 | 2319.300570 | 1160.153923 | 2318.316554 | 1159.661915 | S | 965.487314 | 483.247295 | 948.460765 | 474.734021 | 947.476749 | 474.242013 | 5 |
| 23 | 2499.390448 | 1250.198862 | 2482.363899 | 1241.685587 | 2481.379883 | 1241.193579 | Y | *878.455286* | 439.731281 | 861.428737 | 431.218007 | 860.444721 | 430.725999 | 4 |
| 24 | 2938.615774 | 1469.811525 | 2921.589225 | 1461.298250 | 2920.605209 | 1460.806242 | Q | *715.391957* | 358.199617 | 698.365408 | 349.686342 | 697.381392 | 349.194334 | 3 |
| 25 | 3039.663453 | 1520.335364 | 3022.636904 | 1511.822090 | 3021.652888 | 1511.330082 | T | 276.166631 | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 26 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 46.6 | 3212.767807 | 0.040213 | AKLIALTLLGMGLALFRNHQSSYQTR |
| 34.3 | 3212.767807 | 0.040213 | AKLIALTLLGMGLALFRNHQSSYQTR |

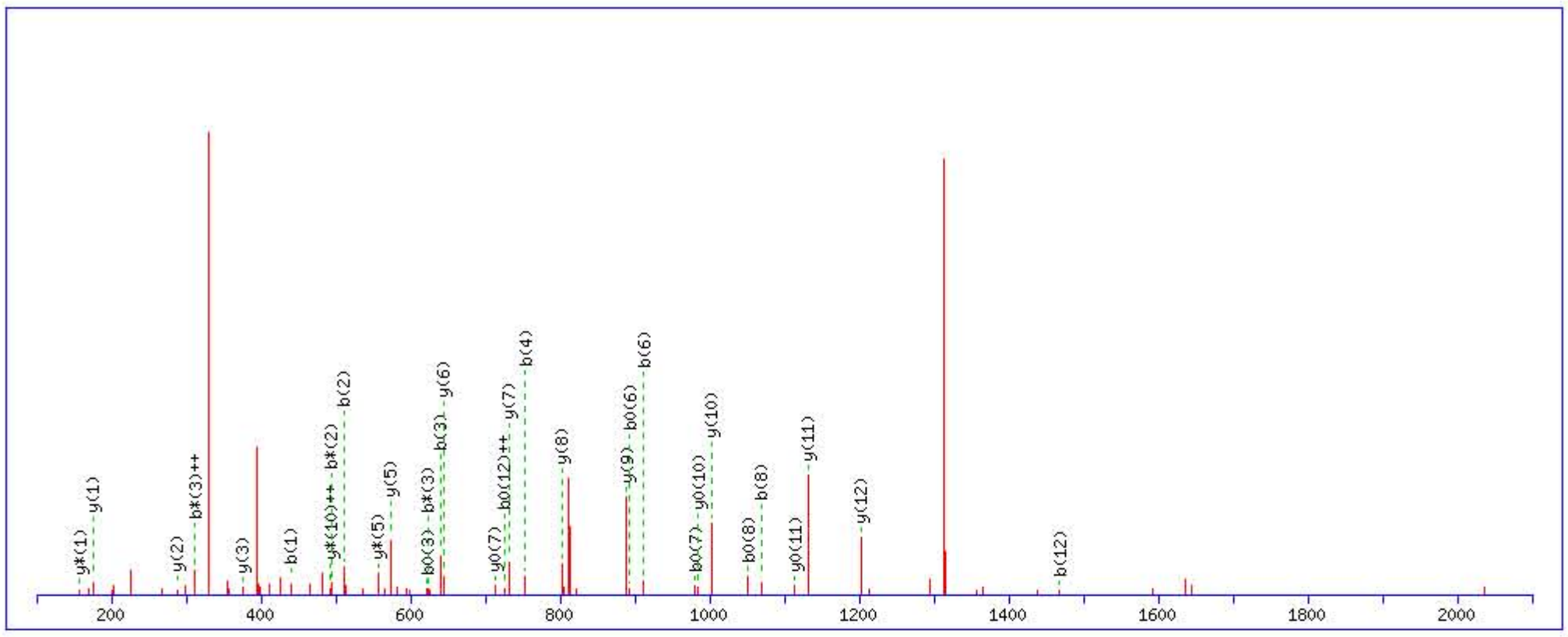
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QAEISASAPTSLR**
Found in **SHBG_HUMAN**, Sex hormone-binding globulin OS=Homo sapiens GN=SHBG PE=1 SV=2

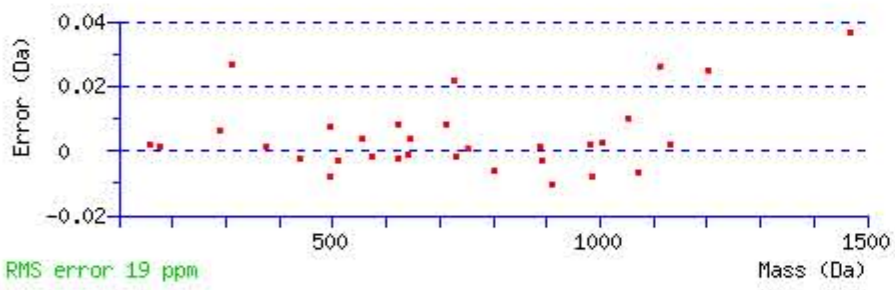
Match to Query 36698: 1640.866728 from(821.440640,2+) rtinseconds(1850) index(4577)
Title: Locus:1.1.1.1921.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

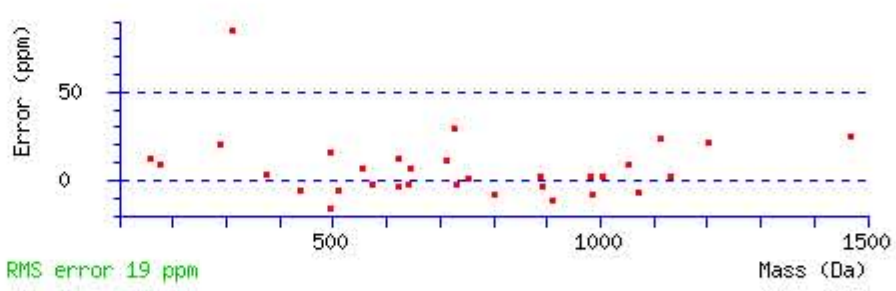
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1640.855560
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 1.2e-005
**Matches** : 32/136 fragment ions using 74 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 13 |
| 2 | 511.269716 | 256.138496 | 494.243167 | 247.625221 | | | A | *1202.637542* | 601.822409 | 1185.610993 | 593.309135 | 1184.626977 | 592.817126 | 12 |
| 3 | 640.312309 | 320.659793 | 623.285760 | 312.146518 | 622.301744 | 311.654510 | E | *1131.600428* | 566.303852 | 1114.573879 | 557.790578 | 1113.589863 | 557.298569 | 11 |
| 4 | 753.396373 | 377.201825 | 736.369824 | 368.688550 | 735.385808 | 368.196542 | I | *1002.557835* | 501.782556 | 985.531286 | 493.269281 | 984.547270 | 492.777273 | 10 |
| 5 | 840.428401 | 420.717839 | 823.401852 | 412.204564 | 822.417836 | 411.712556 | S | *889.473771* | 445.240523 | 872.447222 | 436.727249 | 871.463206 | 436.235241 | 9 |
| 6 | 911.465515 | 456.236396 | 894.438966 | 447.723121 | 893.454950 | 447.231113 | A | *802.441743* | 401.724510 | 785.415194 | 393.211235 | 784.431178 | 392.719227 | 8 |
| 7 | 998.497543 | 499.752410 | 981.470994 | 491.239135 | 980.486978 | 490.747127 | S | *731.404629* | 366.205953 | 714.378080 | 357.692678 | 713.394064 | 357.200670 | 7 |
| 8 | 1069.534657 | 535.270966 | 1052.508108 | 526.757692 | 1051.524092 | 526.265684 | A | *644.372601* | 322.689939 | 627.346052 | 314.176664 | 626.362036 | 313.684656 | 6 |
| 9 | 1166.587421 | 583.797349 | 1149.560872 | 575.284074 | 1148.576856 | 574.792066 | P | *573.335487* | 287.171382 | 556.308938 | 278.658107 | 555.324922 | 278.166099 | 5 |
| 10 | 1267.635100 | 634.321188 | 1250.608551 | 625.807914 | 1249.624535 | 625.315905 | T | 476.282723 | 238.644999 | 459.256174 | 230.131725 | 458.272158 | 229.639717 | 4 |
| 11 | 1354.667128 | 677.837202 | 1337.640579 | 669.323928 | 1336.656563 | 668.831920 | S | *375.235044* | 188.121160 | 358.208495 | 179.607885 | 357.224479 | 179.115877 | 3 |
| 12 | 1467.751192 | 734.379234 | 1450.724643 | 725.865960 | 1449.740627 | 725.373951 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 13 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 57.9 | 1640.855560 | 0.011168 | QAEISASAPTSLR |
| 5.0 | 1640.885422 | -0.018694 | LLKKDLCNTHLMR |
| 3.6 | 1640.855530 | 0.011198 | QAKLEKEEAER |
| 3.4 | 1640.884521 | -0.017793 | EAQKKPAESQKIER |
| 1.8 | 1640.849030 | 0.017698 | AQEMEAAVGRLR |
| 1.7 | 1640.849045 | 0.017683 | QADICVREIAR |
| 1.4 | 1640.848175 | 0.018553 | LLAQPDDSEQTLRR |
| 1.0 | 1640.884537 | -0.017809 | KSSLLAALDEERPGR |
| 0.8 | 1640.852219 | 0.014509 | VTQHFAKETQDPLK |
| 0.6 | 1640.849045 | 0.017683 | GDRIAQLICER |

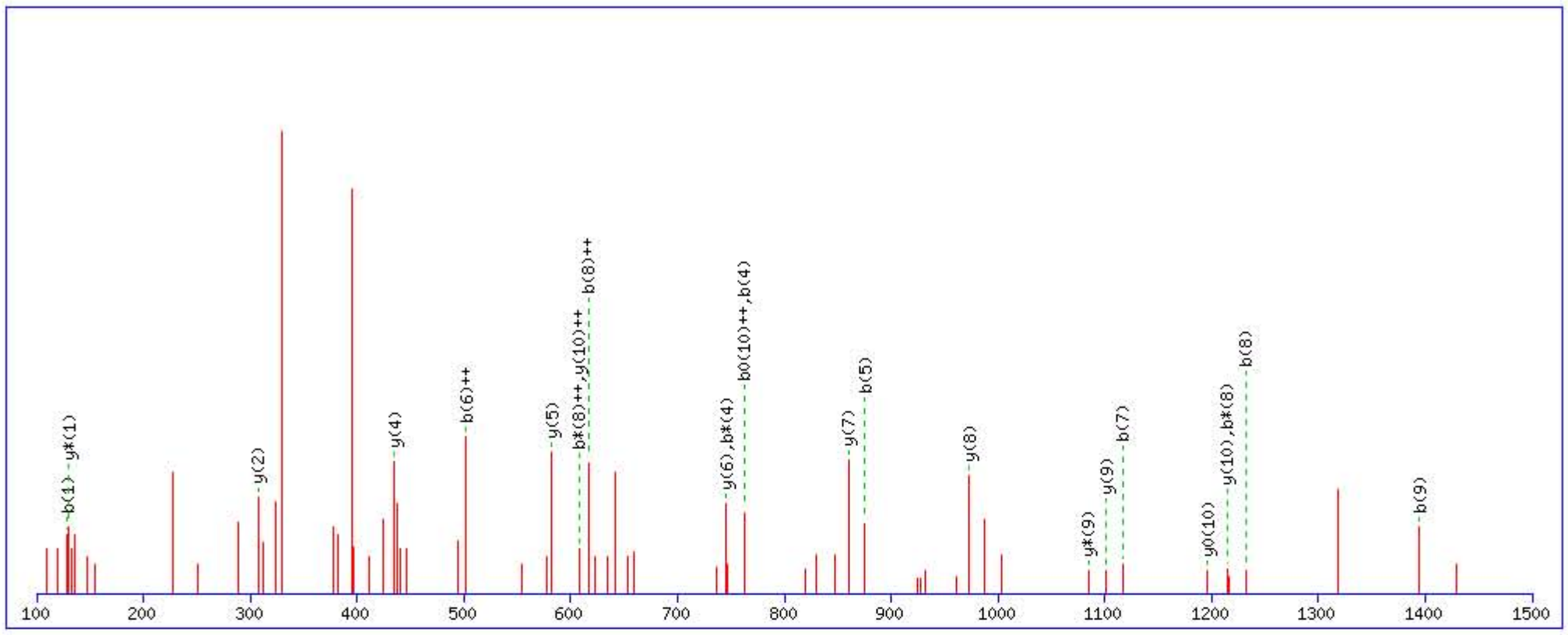
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KGHQLQLDYFGACK**
Found in **SPRL1_HUMAN**, SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2

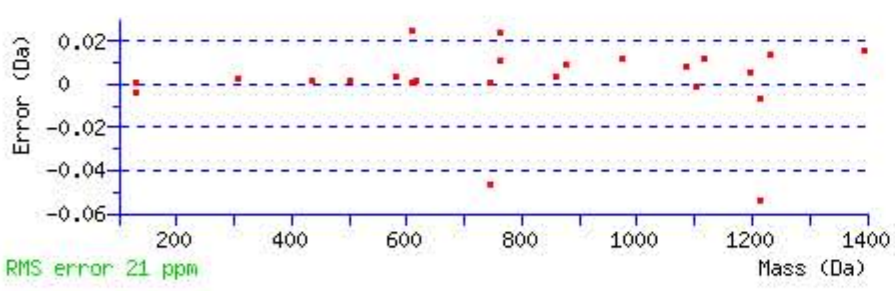
Match to Query 43671: 1974.996012 from(659.339280,3+) rtinseconds(1949) index(49982)
Title: Locus:1.1.1.1916.15 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

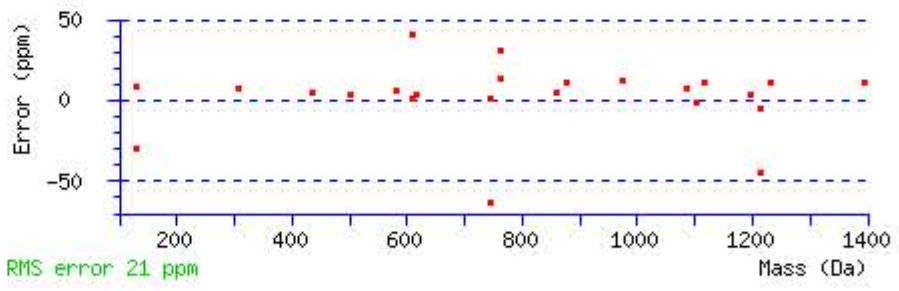
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1974.980804
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 54 **Expect:** 2.4e-005
**Matches :** 24/130 fragment ions using 27 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.102239 | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 14 |
| 2 | 186.123703 | 93.565489 | 169.097154 | 85.052215 | | | G | 1847.893125 | 924.450201 | 1830.866576 | 915.936926 | 1829.882560 | 915.444918 | 13 |
| 3 | 323.182615 | 162.094945 | 306.156066 | 153.581671 | | | H | 1790.871661 | 895.939469 | 1773.845112 | 887.426194 | 1772.861096 | 886.934186 | 12 |
| 4 | 762.407941 | 381.707609 | 745.381392 | 373.194334 | | | Q | 1653.812749 | 827.410013 | 1636.786200 | 818.896738 | 1635.802184 | 818.404730 | 11 |
| 5 | 875.492005 | 438.249641 | 858.465456 | 429.736366 | | | L | *1214.587423* | 607.797350 | 1197.560874 | 599.284075 | 1196.576858 | 598.792067 | 10 |
| 6 | 1003.550583 | 502.278930 | 986.524034 | 493.765655 | | | Q | *1101.503359* | 551.255318 | 1084.476810 | 542.742043 | 1083.492794 | 542.250035 | 9 |
| 7 | 1116.634647 | 558.820962 | 1099.608098 | 550.307687 | | | L | *973.444781* | 487.226029 | 956.418232 | 478.712754 | 955.434216 | 478.220746 | 8 |
| 8 | 1231.661590 | 616.334433 | 1214.635041 | 607.821159 | 1213.651025 | 607.329151 | D | *860.360717* | 430.683997 | 843.334168 | 422.170722 | 842.350152 | 421.678714 | 7 |
| 9 | 1394.724919 | 697.866098 | 1377.698370 | 689.352823 | 1376.714354 | 688.860815 | Y | *745.333774* | 373.170525 | 728.307225 | 364.657251 | | | 6 |
| 10 | 1541.793333 | 771.400305 | 1524.766784 | 762.887030 | 1523.782768 | 762.395022 | F | *582.270445* | 291.638861 | 565.243896 | 283.125586 | | | 5 |
| 11 | 1598.814797 | 799.911037 | 1581.788248 | 791.397762 | 1580.804232 | 790.905754 | G | *435.202031* | 218.104653 | 418.175482 | 209.591379 | | | 4 |
| 12 | 1669.851911 | 835.429594 | 1652.825362 | 826.916319 | 1651.841346 | 826.424311 | A | 378.180567 | 189.593921 | 361.154018 | 181.080647 | | | 3 |
| 13 | 1829.882560 | 915.444918 | 1812.856011 | 906.931644 | 1811.871995 | 906.439636 | C | *307.143453* | 154.075365 | 290.116904 | 145.562090 | | | 2 |
| 14 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 54.3 | 1974.980804 | 0.015208 | KGHQLQLDYFGACK |
| 27.9 | 1974.980804 | 0.015208 | KGHQLQLDYFGACK |
| 4.9 | 1974.966888 | 0.029124 | HMHIHISTVNHAFKCK |

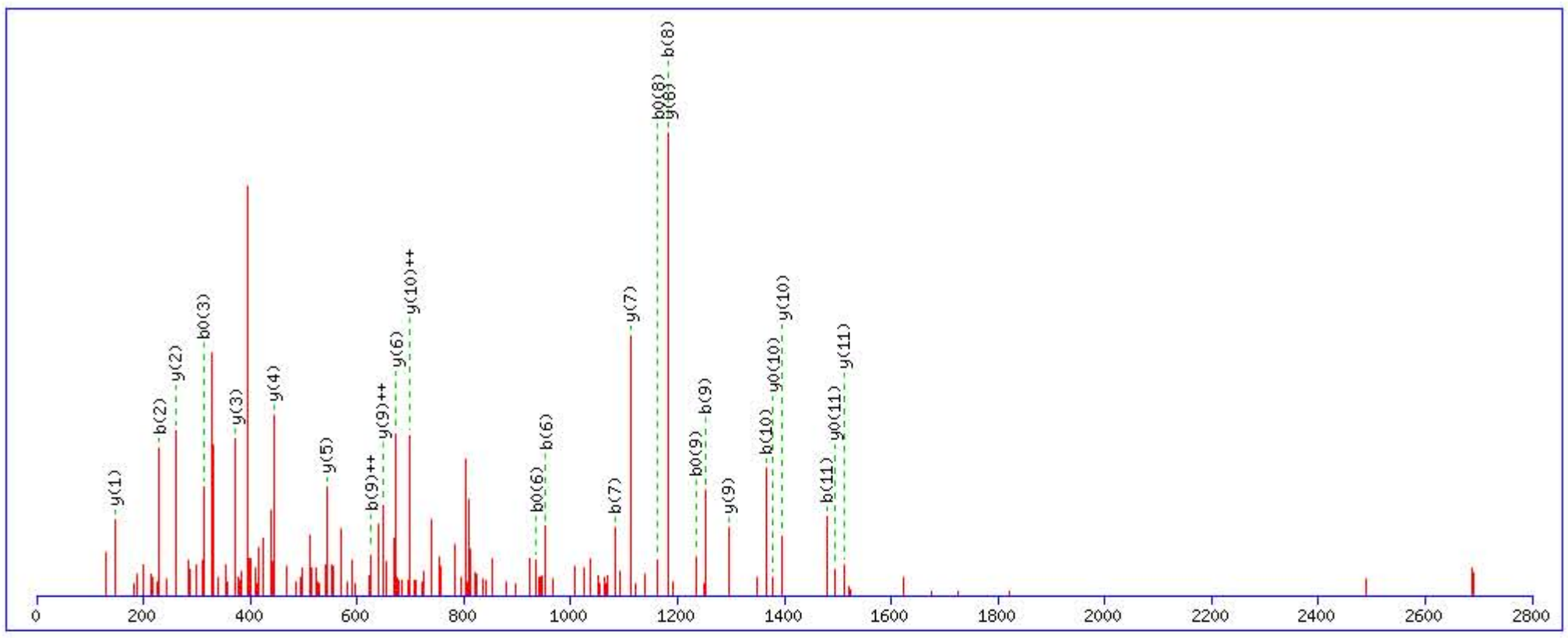
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LDTLAQEVALLK**
Found in **TETN_HUMAN**, Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3

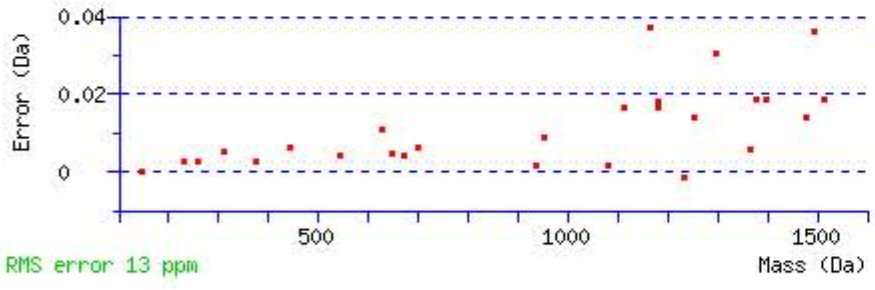
Match to Query 35714: 1623.943448 from(812.979000,2+) rtinseconds(2581) index(8653)
Title: Locus:1.1.1.2176.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

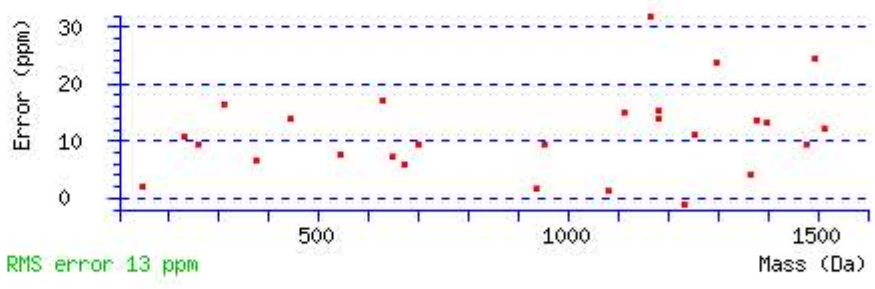
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1623.926941
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 80 **Expect:** 7.4e-008
**Matches :** 27/110 fragment ions using 43 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 12 |
| 2 | **229.118283** | 115.062779 | | | 211.107718 | 106.057497 | D | *1511.850179* | 756.428728 | 1494.823630 | 747.915453 | 1493.839614 | 747.423445 | 11 |
| 3 | 330.165962 | 165.586619 | | | 312.155397 | 156.581336 | T | *1396.823236* | 698.915256 | 1379.796687 | 690.401982 | 1378.812671 | 689.909973 | 10 |
| 4 | 443.250026 | 222.128651 | | | 425.239461 | 213.123369 | L | *1295.775557* | 648.391416 | 1278.749008 | 639.878142 | 1277.764992 | 639.386134 | 9 |
| 5 | 514.287140 | 257.647208 | | | 496.276575 | 248.641926 | A | *1182.691493* | 591.849385 | 1165.664944 | 583.336110 | 1164.680928 | 582.844102 | 8 |
| 6 | **953.512466** | 477.259871 | 936.485917 | 468.746597 | 935.501901 | 468.254589 | Q | *1111.654379* | 556.330827 | 1094.627830 | 547.817553 | 1093.643814 | 547.325545 | 7 |
| 7 | **1082.555059** | 541.781168 | 1065.528510 | 533.267893 | 1064.544494 | 532.775885 | E | *672.429053* | 336.718165 | 655.402504 | 328.204890 | 654.418488 | 327.712882 | 6 |
| 8 | **1181.623473** | 591.315375 | 1164.596924 | 582.802100 | 1163.612908 | 582.310092 | V | *543.386460* | 272.196868 | 526.359911 | 263.683593 | | | 5 |
| 9 | **1252.660587** | 626.833932 | 1235.634038 | 618.320657 | 1234.650022 | 617.828649 | A | *444.318046* | 222.662661 | 427.291497 | 214.149386 | | | 4 |
| 10 | **1365.744651** | 683.375964 | 1348.718102 | 674.862689 | 1347.734086 | 674.370681 | L | *373.280932* | 187.144104 | 356.254383 | 178.630829 | | | 3 |
| 11 | **1478.828715** | 739.917995 | 1461.802166 | 731.404721 | 1460.818150 | 730.912713 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 12 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 80.0 | 1623.926941 | 0.016507 | LDTLAQEVALLK |
| 6.3 | 1623.926956 | 0.016492 | KTLVSMPPLPGLDLK |
| 4.3 | 1623.944702 | -0.001254 | EVELIIQVTPKDIK |
| 3.7 | 1623.957260 | -0.013812 | IFRPKHTRISELK |
| 2.8 | 1623.942001 | 0.001447 | ESKPGGLPRRSSIIK |
| 2.8 | 1623.934799 | 0.008649 | FIQKFSQASSKILK |
| 2.8 | 1623.928284 | 0.015164 | LCHAAFLPSVRLLK |
| 2.8 | 1623.942200 | 0.001248 | LLPVQENFLLK |
| 2.5 | 1623.919556 | 0.023892 | EVSPEPIVSTVARLK |
| 2.3 | 1623.919540 | 0.023908 | KLSLGTAEPQVKEPK |

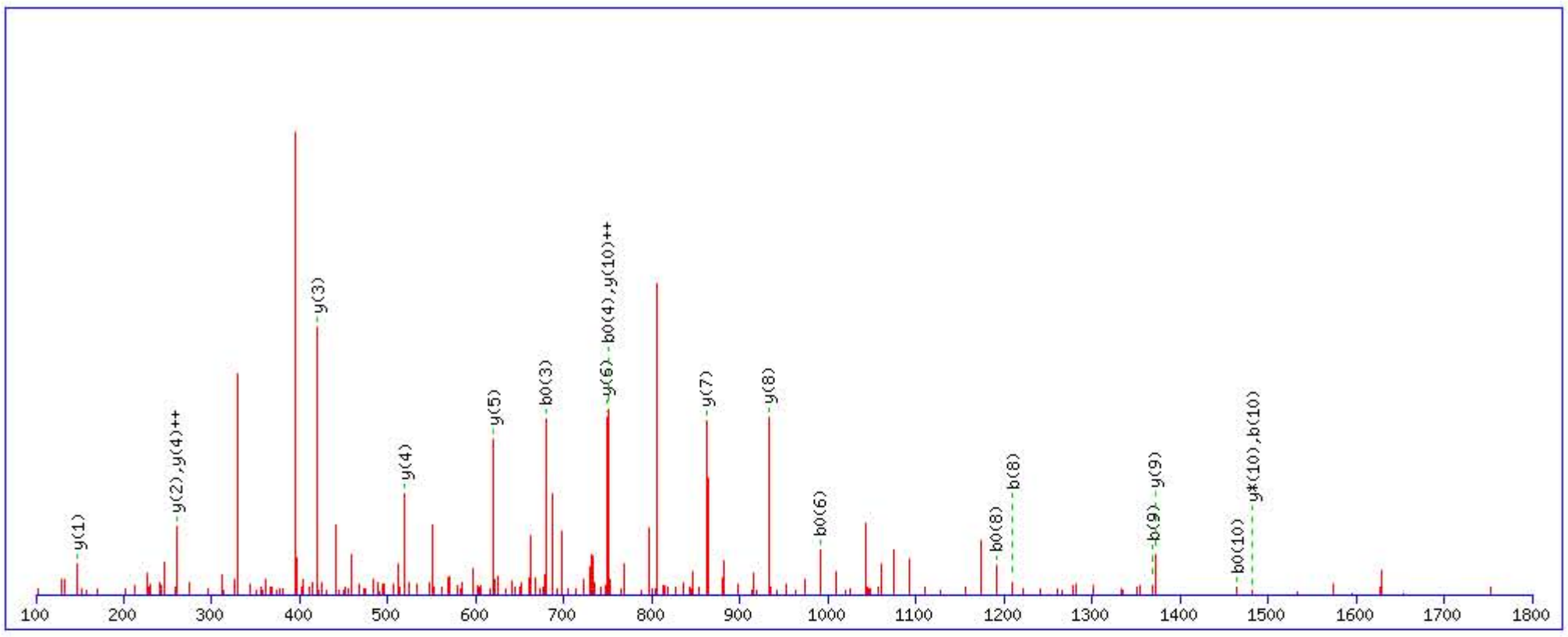
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EQQALQTVCLK**
Found in **TETN_HUMAN**, Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3

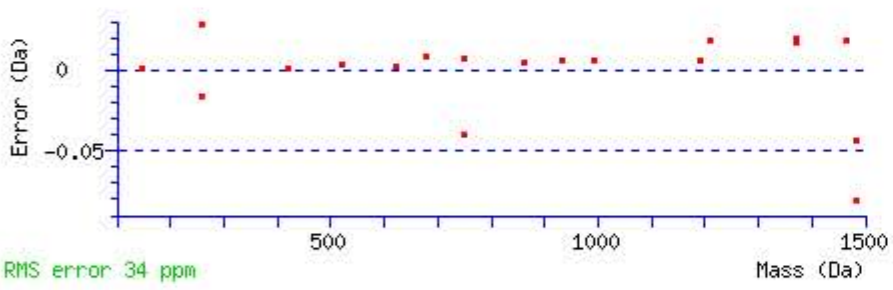
Match to Query 36292: 1627.857608 from(814.936080,2+) rtinseconds(1966) index(5474)
Title: Locus:1.1.1.1961.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

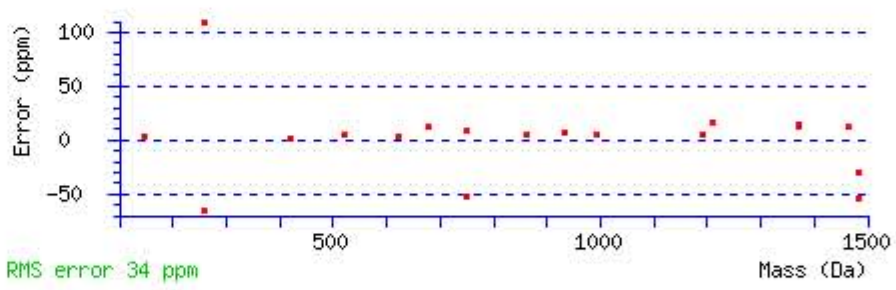
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1627.842575
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 60 **Expect:** 9.1e-006
**Matches :** 20/110 fragment ions using 30 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 11 |
| 2 | 258.108447 | 129.557862 | 241.081898 | 121.044587 | 240.097882 | 120.552579 | Q | 1499.807270 | 750.407273 | 1482.780721 | 741.893999 | 1481.796705 | 741.401991 | 10 |
| 3 | 697.333773 | 349.170525 | 680.307224 | 340.657250 | 679.323208 | 340.165242 | Q | *1371.748692* | 686.377984 | 1354.722143 | 677.864710 | 1353.738127 | 677.372702 | 9 |
| 4 | 768.370887 | 384.689082 | 751.344338 | 376.175807 | 750.360322 | 375.683799 | A | *932.523366* | 466.765321 | 915.496817 | 458.252047 | 914.512801 | 457.760039 | 8 |
| 5 | 881.454951 | 441.231114 | 864.428402 | 432.717839 | 863.444386 | 432.225831 | L | *861.486252* | 431.246764 | 844.459703 | 422.733490 | 843.475687 | 422.241482 | 7 |
| 6 | 1009.513529 | 505.260403 | 992.486980 | 496.747128 | 991.502964 | 496.255120 | Q | *748.402188* | 374.704732 | 731.375639 | 366.191458 | 730.391623 | 365.699450 | 6 |
| 7 | 1110.561208 | 555.784242 | 1093.534659 | 547.270968 | 1092.550643 | 546.778960 | T | *620.343610* | 310.675443 | 603.317061 | 302.162169 | 602.333045 | 301.670161 | 5 |
| 8 | **1209.629622** | 605.318449 | 1192.603073 | 596.805175 | 1191.619057 | 596.313167 | V | *519.295931* | 260.151604 | 502.269382 | 251.638329 | | | 4 |
| 9 | **1369.660271** | 685.333774 | 1352.633722 | 676.820499 | 1351.649706 | 676.328491 | C | *420.227517* | 210.617396 | 403.200968 | 202.104122 | | | 3 |
| 10 | **1482.744335** | 741.875806 | 1465.717786 | 733.362531 | 1464.733770 | 732.870523 | L | *260.196868* | 130.602072 | 243.170319 | 122.088797 | | | 2 |
| 11 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 59.8 | 1627.842575 | 0.015033 | EQQALQTVCLK |
| 51.5 | 1627.842575 | 0.015033 | EQQALQTVCLK |
| 25.0 | 1627.842575 | 0.015033 | EQQALQTVCLK |
| 5.7 | 1627.835159 | 0.022449 | EQVQASREDKK |
| 5.1 | 1627.845688 | 0.011920 | KKEFSLEEIYTNK |
| 5.0 | 1627.835159 | 0.022449 | EQVQASREDKK |
| 5.0 | 1627.853775 | 0.003833 | QEKMQQLREK |
| 4.5 | 1627.875580 | -0.017972 | KPKDLDFAQQK |
| 4.4 | 1627.835159 | 0.022449 | QRPEAKTSGSEK |
| 4.2 | 1627.875580 | -0.017972 | KPKDLDFAQQK |

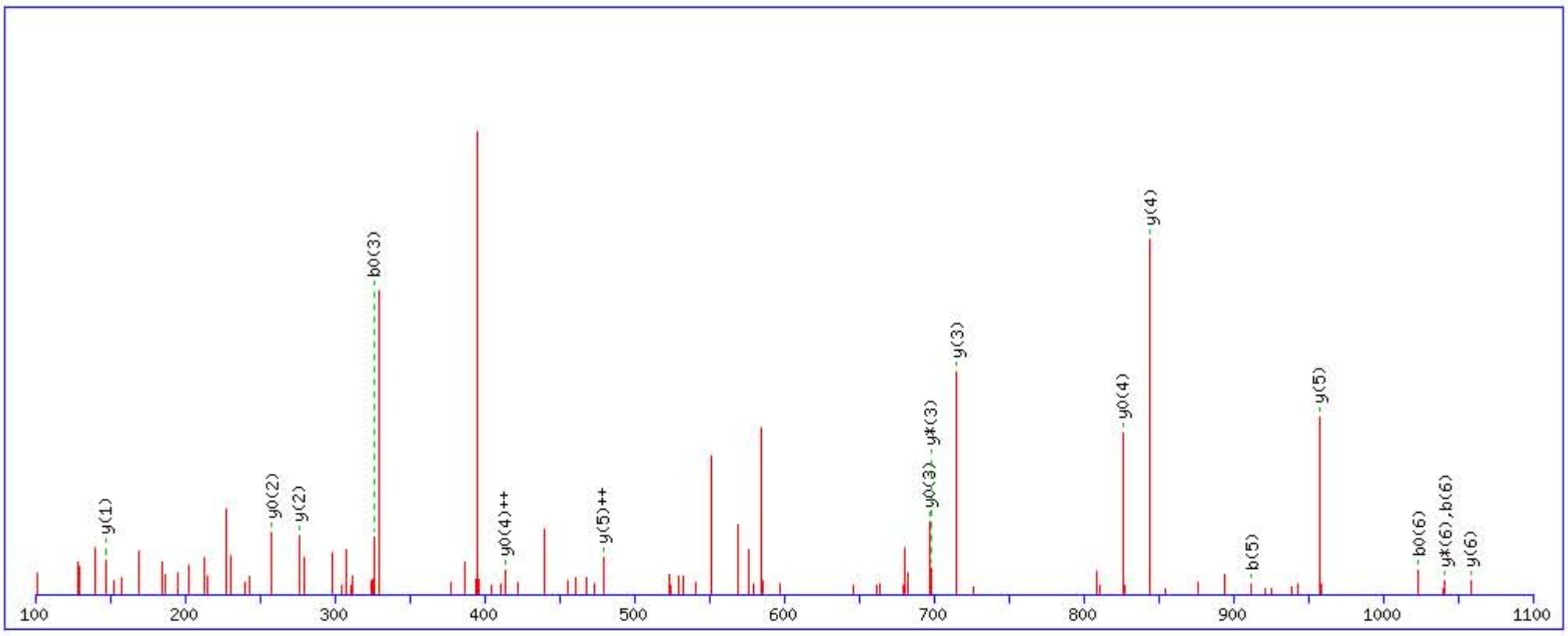
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ETIEQEK**
Found in **TYB10_HUMAN**, Thymosin beta-10 OS=Homo sapiens GN=TMSB10 PE=1 SV=2

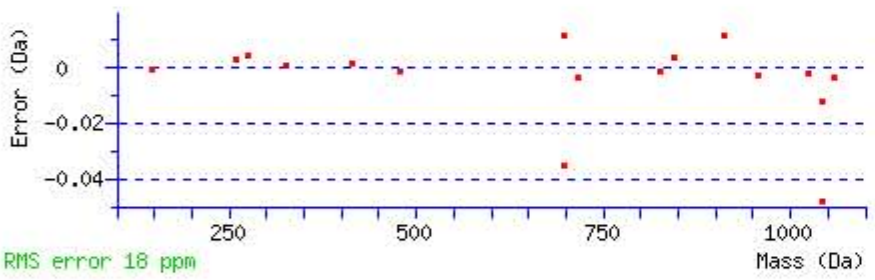
Match to Query 20217: 1186.589968 from(594.302260,2+) rtinseconds(1423) index(62974)
Title: Locus:1.1.1.1770.17 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

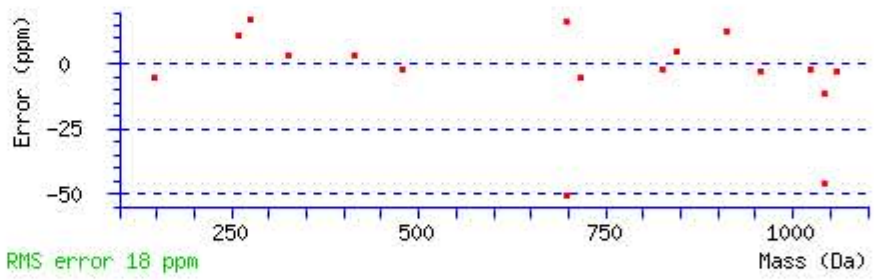
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1186.590347
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q5 : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0068
**Matches :** 17/62 fragment ions using 29 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 7 |
| 2 | 231.097548 | 116.052412 | | | 213.086983 | 107.047130 | T | *1058.555059* | 529.781168 | 1041.528510 | 521.267893 | 1040.544494 | 520.775885 | 6 |
| 3 | 344.181612 | 172.594444 | | | 326.171047 | 163.589162 | I | *957.507380* | 479.257328 | 940.480831 | 470.744054 | 939.496815 | 470.252046 | 5 |
| 4 | 473.224205 | 237.115741 | | | 455.213640 | 228.110458 | E | *844.423316* | 422.715296 | 827.396767 | 414.202022 | 826.412751 | 413.710014 | 4 |
| 5 | **912.449531** | 456.728404 | 895.422982 | 448.215129 | 894.438966 | 447.723121 | Q | *715.380723* | 358.194000 | 698.354174 | 349.680725 | 697.370158 | 349.188717 | 3 |
| 6 | **1041.492124** | 521.249700 | 1024.465575 | 512.736426 | 1023.481559 | 512.244418 | E | *276.155397* | 138.581336 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 7 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.3 | 1186.590347 | -0.000379 | ETIEQEK |
| 9.6 | 1186.572586 | 0.017382 | KEMMKETFK |
| 8.8 | 1186.591721 | -0.001753 | KTVGFHSHMK |
| 8.7 | 1186.572586 | 0.017382 | KEMMKETFK |
| 6.8 | 1186.601578 | -0.011610 | QEQKESK |
| 5.9 | 1186.572617 | 0.017351 | MDVFMKGLSK |
| 5.5 | 1186.590347 | -0.000379 | QEEELTK |
| 5.2 | 1186.605392 | -0.015424 | KEAEQEAARR |
| 4.7 | 1186.601578 | -0.011610 | TNEKQEK |
| 2.6 | 1186.601578 | -0.011610 | EEKQNTK |

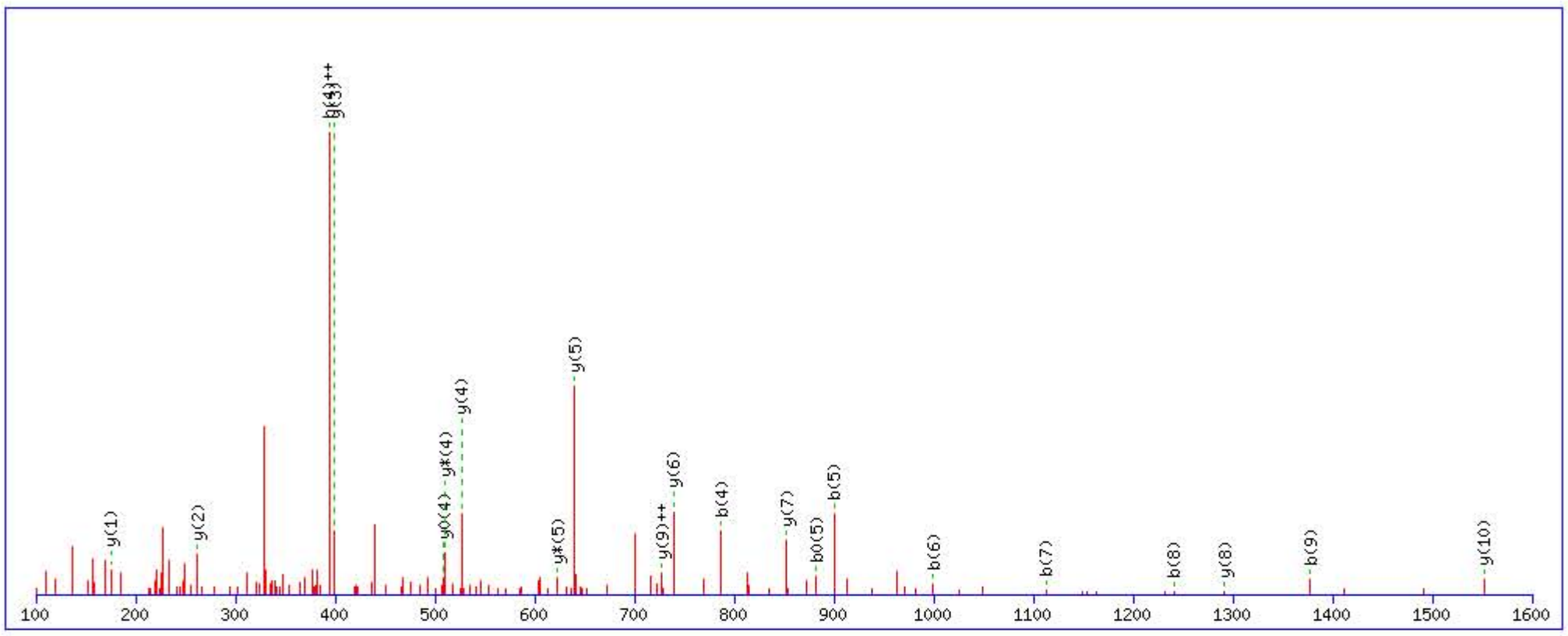
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SPYQLVLQHSR**
Found in **BGH3_HUMAN**, Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1

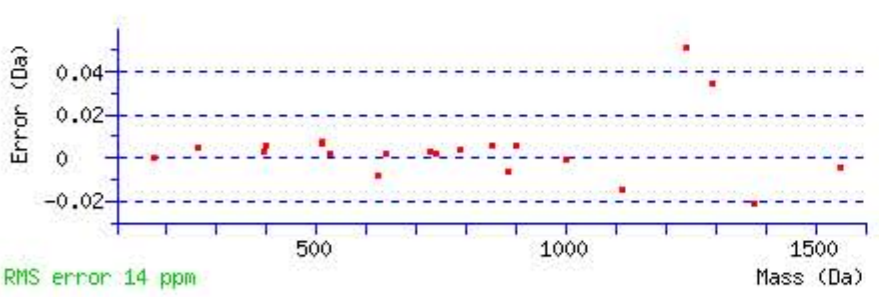
Match to Query 36597: 1637.876022 from(546.965950,3+) rtinseconds(1889) index(19507)
Title: Locus:1.1.1.3040.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

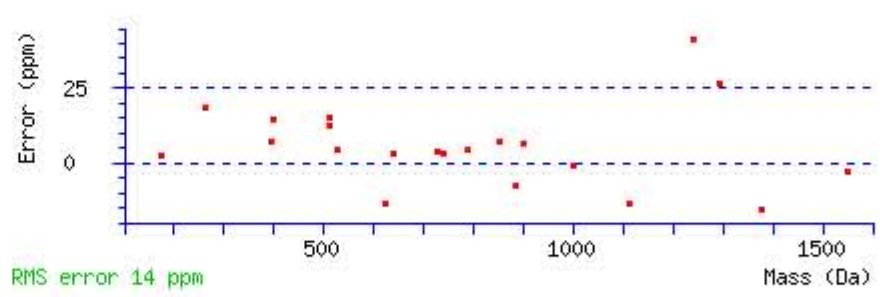
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1637.871170
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 38 **Expect:** 0.00041
**Matches :** 21/112 fragment ions using 50 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 11 |
| 2 | 185.092068 | 93.049672 | | | 167.081503 | 84.044389 | P | *1551.846431* | 776.426853 | 1534.819882 | 767.913579 | 1533.835866 | 767.421571 | 10 |
| 3 | 348.155397 | 174.581336 | | | 330.144832 | 165.576054 | Y | 1454.793667 | 727.900471 | 1437.767118 | 719.387197 | 1436.783102 | 718.895189 | 9 |
| 4 | **787.380723** | 394.194000 | 770.354174 | 385.680725 | 769.370158 | 385.188717 | Q | *1291.730338* | 646.368807 | 1274.703789 | 637.855532 | 1273.719773 | 637.363524 | 8 |
| 5 | **900.464787** | 450.736032 | 883.438238 | 442.222757 | 882.454222 | 441.730749 | L | *852.505012* | 426.756144 | 835.478463 | 418.242869 | 834.494447 | 417.750861 | 7 |
| 6 | **999.533201** | 500.270239 | 982.506652 | 491.756964 | 981.522636 | 491.264956 | V | *739.420948* | 370.214112 | 722.394399 | 361.700837 | 721.410383 | 361.208829 | 6 |
| 7 | **1112.617265** | 556.812270 | 1095.590716 | 548.298996 | 1094.606700 | 547.806988 | L | *640.352534* | 320.679905 | 623.325985 | 312.166630 | 622.341969 | 311.674622 | 5 |
| 8 | **1240.675843** | 620.841559 | 1223.649294 | 612.328285 | 1222.665278 | 611.836277 | Q | *527.268470* | 264.137873 | 510.241921 | 255.624598 | 509.257905 | 255.132590 | 4 |
| 9 | **1377.734755** | 689.371015 | 1360.708206 | 680.857741 | 1359.724190 | 680.365733 | H | *399.209892* | 200.108584 | 382.183343 | 191.595309 | 381.199327 | 191.103301 | 3 |
| 10 | 1464.766783 | 732.887029 | 1447.740234 | 724.373755 | 1446.756218 | 723.881747 | S | *262.150980* | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.0 | 1637.871170 | 0.004852 | SPYQLVLQHSR |
| 1.9 | 1637.855911 | 0.020111 | RTAYSGVPMTILSSR |

**Mascot:** http://www.matrixscience.com/

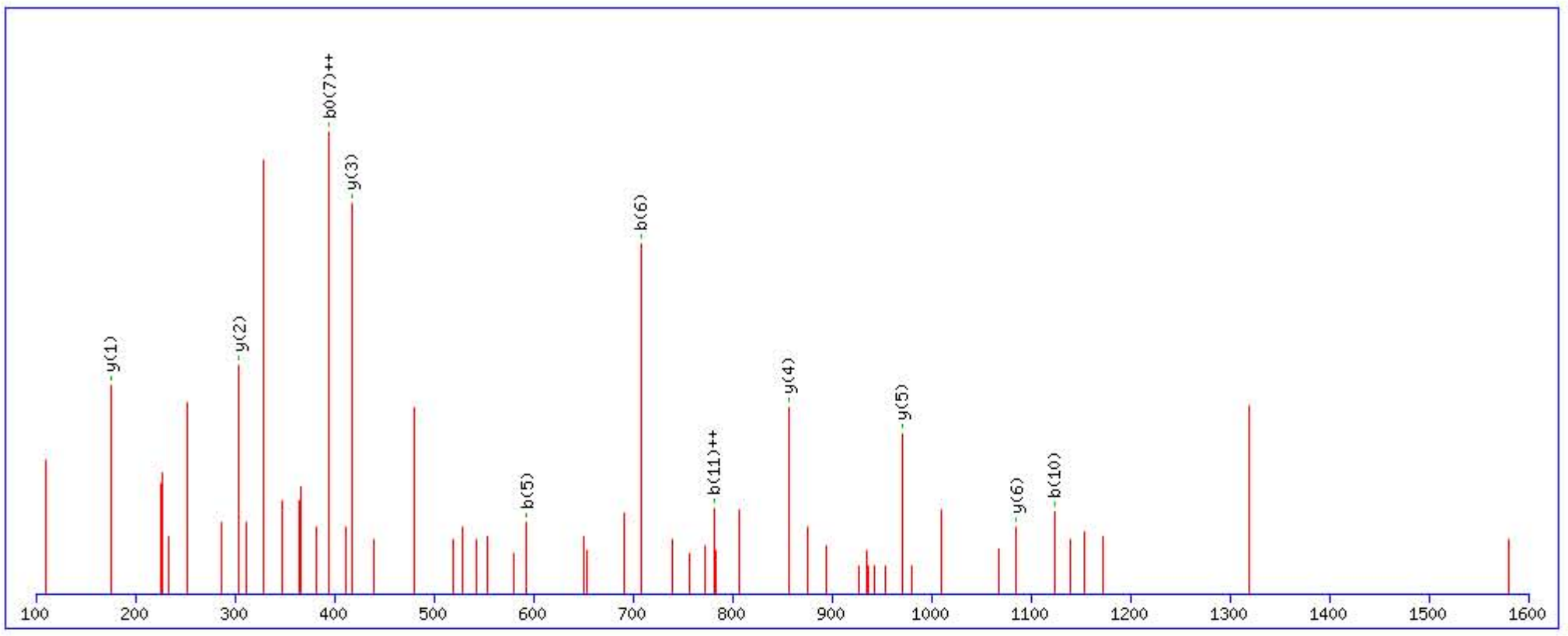
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **NLHDLDVSDNQLER**
Found in **VASN_HUMAN**, Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1

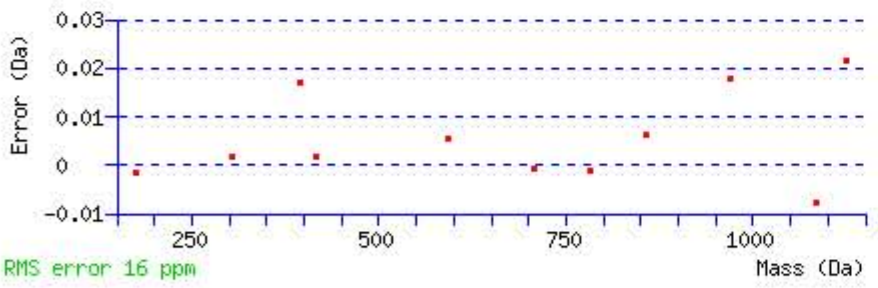
Match to Query 43703: 1977.964422 from(660.328750,3+) rtinseconds(1945) index(5341)
Title: Locus:1.1.1.1954.19 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

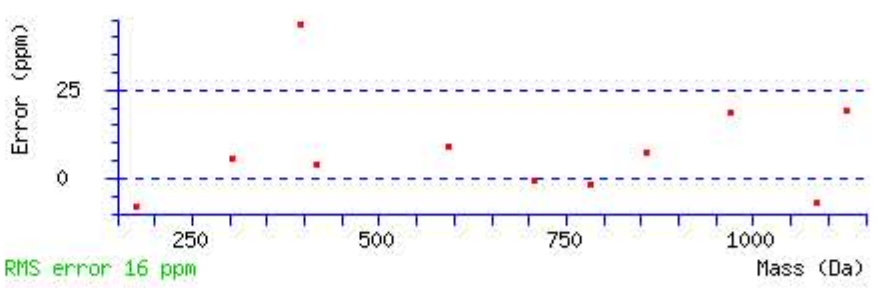
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1977.957809
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 45 **Expect:** 6.7e-005
**Matches :** 11/148 fragment ions using 13 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 115.050203 | 58.028740 | 98.023654 | 49.515465 | | | N | | | | | | | 14 |
| 2 | 228.134267 | 114.570771 | 211.107718 | 106.057497 | | | L | 1864.922173 | 932.964724 | 1847.895624 | 924.451450 | 1846.911608 | 923.959442 | 13 |
| 3 | 365.193179 | 183.100227 | 348.166630 | 174.586953 | | | H | 1751.838109 | 876.422692 | 1734.811560 | 867.909418 | 1733.827544 | 867.417410 | 12 |
| 4 | 480.220122 | 240.613699 | 463.193573 | 232.100425 | 462.209557 | 231.608417 | D | 1614.779197 | 807.893236 | 1597.752648 | 799.379962 | 1596.768632 | 798.887954 | 11 |
| 5 | *593.304186* | 297.155731 | 576.277637 | 288.642457 | 575.293621 | 288.150449 | L | 1499.752254 | 750.379765 | 1482.725705 | 741.866490 | 1481.741689 | 741.374482 | 10 |
| 6 | *708.331129* | 354.669203 | 691.304580 | 346.155928 | 690.320564 | 345.663920 | D | 1386.668190 | 693.837733 | 1369.641641 | 685.324458 | 1368.657625 | 684.832450 | 9 |
| 7 | 807.399543 | 404.203410 | 790.372994 | 395.690135 | 789.388978 | 395.198127 | V | 1271.641247 | 636.324261 | 1254.614698 | 627.810987 | 1253.630682 | 627.318979 | 8 |
| 8 | 894.431571 | 447.719424 | 877.405022 | 439.206149 | 876.421006 | 438.714141 | S | 1172.572833 | 586.790054 | 1155.546284 | 578.276780 | 1154.562268 | 577.784772 | 7 |
| 9 | 1009.458514 | 505.232895 | 992.431965 | 496.719620 | 991.447949 | 496.227612 | D | *1085.540805* | 543.274040 | 1068.514256 | 534.760766 | 1067.530240 | 534.268758 | 6 |
| 10 | *1123.501441* | 562.254358 | 1106.474892 | 553.741084 | 1105.490876 | 553.249076 | N | *970.513862* | 485.760569 | 953.487313 | 477.247294 | 952.503297 | 476.755286 | 5 |
| 11 | 1562.726767 | 781.867021 | 1545.700218 | 773.353747 | 1544.716202 | 772.861739 | Q | *856.470935* | 428.739105 | 839.444386 | 420.225831 | 838.460370 | 419.733823 | 4 |
| 12 | 1675.810831 | 838.409053 | 1658.784282 | 829.895779 | 1657.800266 | 829.403771 | L | *417.245609* | 209.126442 | 400.219060 | 200.613168 | 399.235044 | 200.121160 | 3 |
| 13 | 1804.853424 | 902.930350 | 1787.826875 | 894.417075 | 1786.842859 | 893.925067 | E | *304.161545* | 152.584410 | 287.134996 | 144.071136 | 286.150980 | 143.579128 | 2 |
| 14 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.2 | 1977.957809 | 0.006613 | NLHDLDVSDNQLER |
| 0.7 | 1977.979813 | -0.015391 | TMPRTVPGSTMKMGSLER |

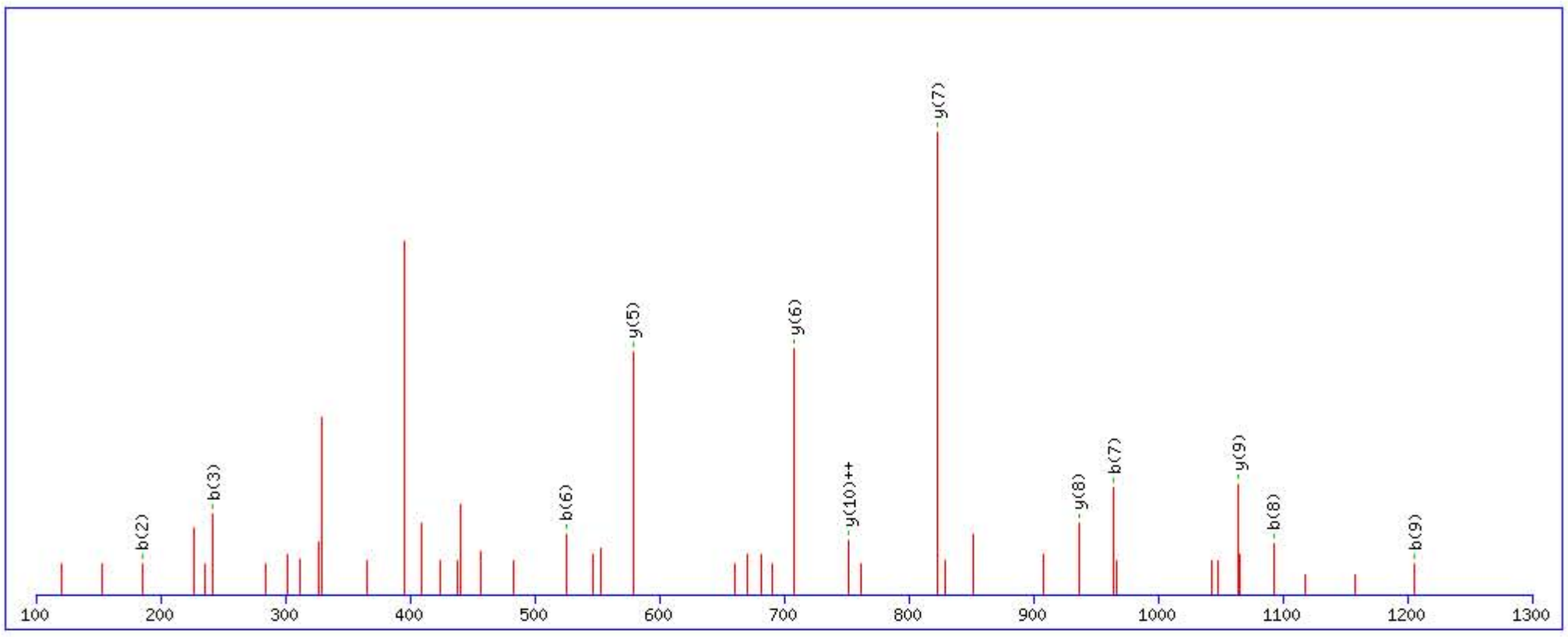
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LAGLGLQQLDEGLFSR**
Found in **VASN_HUMAN**, Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1

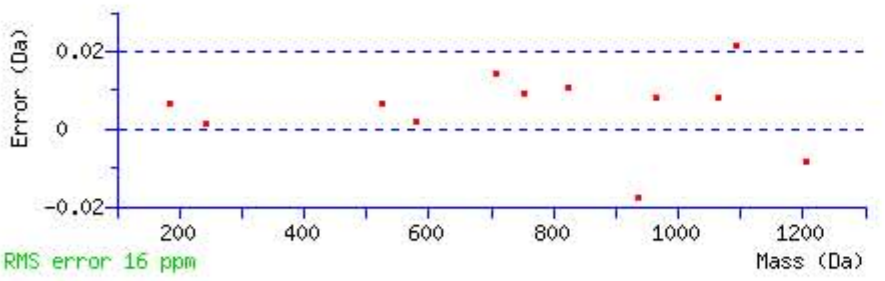
Match to Query 45190: 2027.105622 from(676.709150,3+) rtinseconds(2815) index(9965)
Title: Locus:1.1.1.2257.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

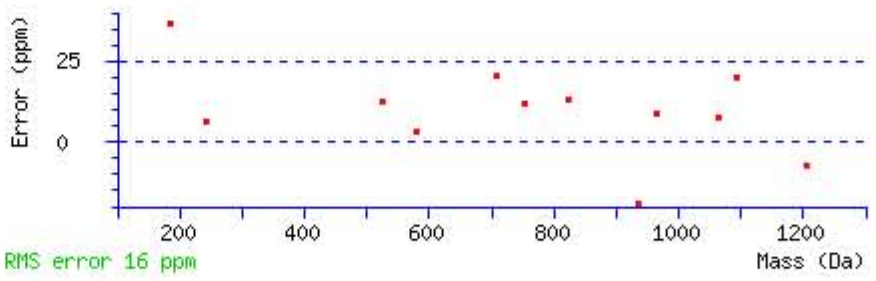
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2027.087372
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.011
**Matches :** 12/148 fragment ions using 22 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 16 |
| 2 | *185.128454* | 93.067865 | | | | | A | 1915.010596 | 958.008936 | 1897.984047 | 949.495662 | 1897.000031 | 949.003654 | 15 |
| 3 | *242.149918* | 121.578597 | | | | | G | 1843.973482 | 922.490379 | 1826.946933 | 913.977105 | 1825.962917 | 913.485097 | 14 |
| 4 | 355.233982 | 178.120629 | | | | | L | 1786.952018 | 893.979647 | 1769.925469 | 885.466373 | 1768.941453 | 884.974364 | 13 |
| 5 | 412.255446 | 206.631361 | | | | | G | 1673.867954 | 837.437615 | 1656.841405 | 828.924341 | 1655.857389 | 828.432333 | 12 |
| 6 | *525.339510* | 263.173393 | | | | | L | 1616.846490 | 808.926883 | 1599.819941 | 800.413609 | 1598.835925 | 799.921601 | 11 |
| 7 | *964.564836* | 482.786056 | 947.538287 | 474.272782 | | | Q | 1503.762426 | 752.384851 | 1486.735877 | 743.871577 | 1485.751861 | 743.379569 | 10 |
| 8 | *1092.623414* | 546.815345 | 1075.596865 | 538.302071 | | | Q | *1064.537100* | 532.772188 | 1047.510551 | 524.258914 | 1046.526535 | 523.766906 | 9 |
| 9 | *1205.707478* | 603.357377 | 1188.680929 | 594.844102 | | | L | *936.478522* | 468.742899 | 919.451973 | 460.229625 | 918.467957 | 459.737617 | 8 |
| 10 | 1320.734421 | 660.870848 | 1303.707872 | 652.357574 | 1302.723856 | 651.865566 | D | *823.394458* | 412.200867 | 806.367909 | 403.687593 | 805.383893 | 403.195585 | 7 |
| 11 | 1449.777014 | 725.392145 | 1432.750465 | 716.878871 | 1431.766449 | 716.386863 | E | *708.367515* | 354.687396 | 691.340966 | 346.174121 | 690.356950 | 345.682113 | 6 |
| 12 | 1506.798478 | 753.902877 | 1489.771929 | 745.389603 | 1488.787913 | 744.897594 | G | *579.324922* | 290.166099 | 562.298373 | 281.652825 | 561.314357 | 281.160817 | 5 |
| 13 | 1619.882542 | 810.444909 | 1602.855993 | 801.931634 | 1601.871977 | 801.439626 | L | 522.303458 | 261.655367 | 505.276909 | 253.142093 | 504.292893 | 252.650085 | 4 |
| 14 | 1766.950956 | 883.979116 | 1749.924407 | 875.465842 | 1748.940391 | 874.973833 | F | 409.219394 | 205.113335 | 392.192845 | 196.600061 | 391.208829 | 196.108053 | 3 |
| 15 | 1853.982984 | 927.495130 | 1836.956435 | 918.981856 | 1835.972419 | 918.489848 | S | 262.150980 | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 16 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 32.2 | 2027.087372 | 0.018250 | LAGLGLQQLDEGLFSR |
| 20.4 | 2027.087372 | 0.018250 | LAGLGLQQLDEGLFSR |

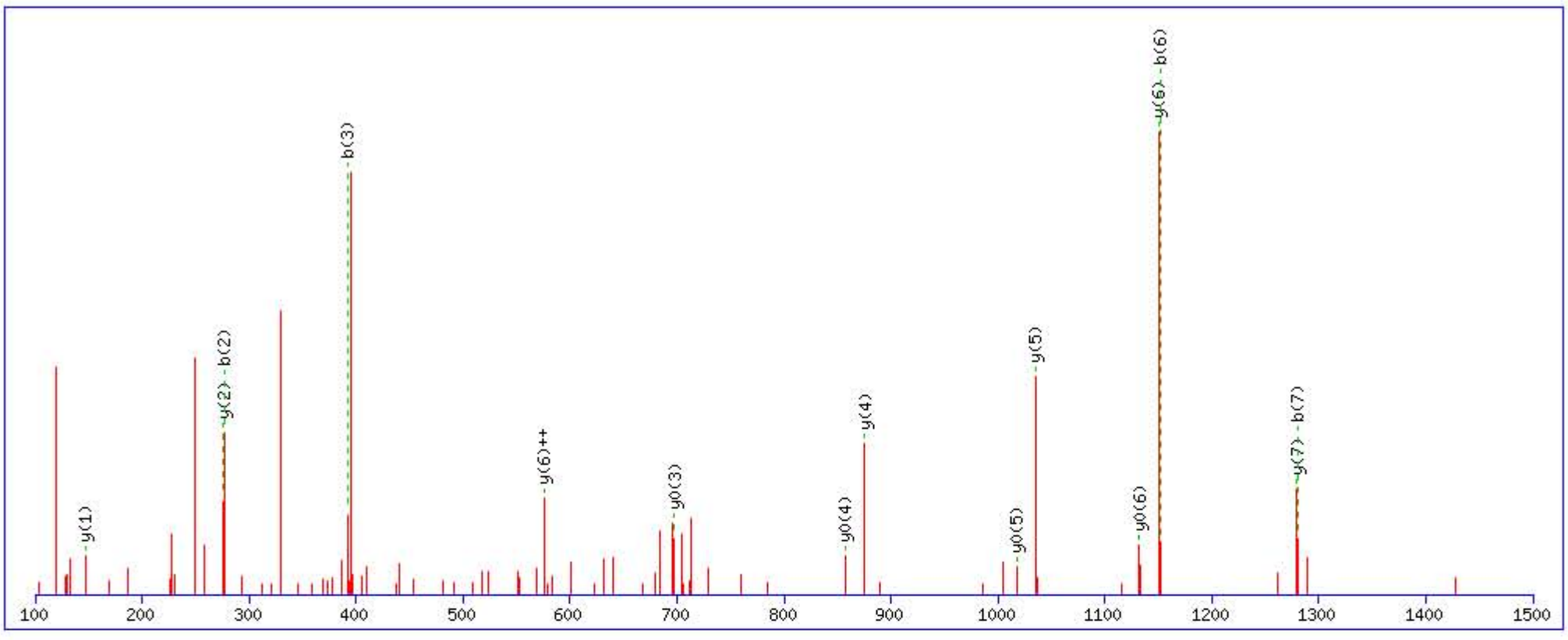
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **FEDCCQEK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

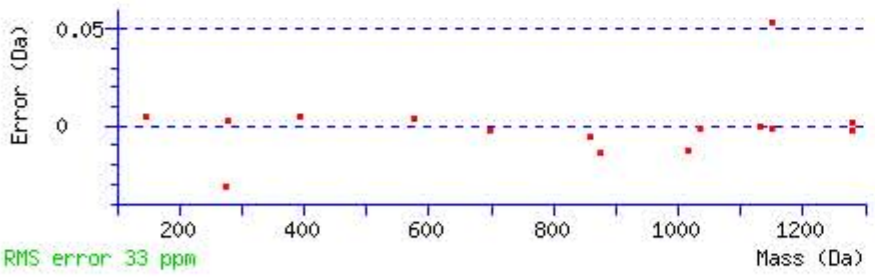
Match to Query 28850: 1425.571328 from(713.792940,2+) rtinseconds(1447) index(16546)
Title: Locus:1.1.1.2886.12 File:"2013-07-02 CLN FXIII 180 min 2nd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

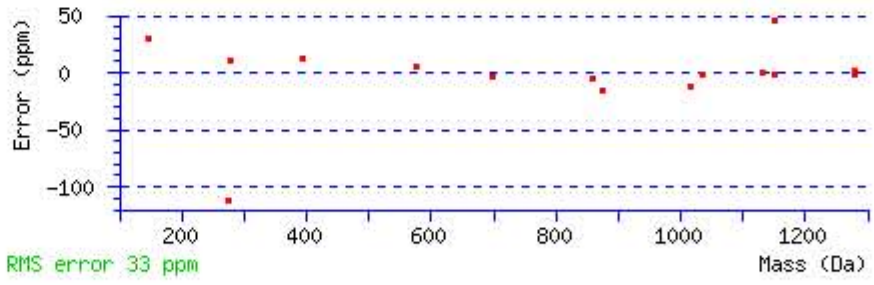
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1425.572693
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q6 : Biotin:Thermo-21345 (Q)
**Ions Score:** 26 **Expect:** 0.0023
**Matches :** 15/70 fragment ions using 34 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 148.075690 | 74.541483 | | | | | F | | | | | | | 8 |
| 2 | **277.118283** | 139.062779 | | | 259.107718 | 130.057497 | E | *1279.511557* | 640.259417 | 1262.485008 | 631.746142 | 1261.500992 | 631.254134 | 7 |
| 3 | **392.145226** | 196.576251 | | | 374.134661 | 187.570968 | D | *1150.468964* | 575.738120 | 1133.442415 | 567.224846 | 1132.458399 | 566.732838 | 6 |
| 4 | 552.175875 | 276.591576 | | | 534.165310 | 267.586293 | C | *1035.442021* | 518.224649 | 1018.415472 | 509.711374 | 1017.431456 | 509.219366 | 5 |
| 5 | 712.206524 | 356.606900 | | | 694.195959 | 347.601618 | C | *875.411372* | 438.209324 | 858.384823 | 429.696050 | 857.400807 | 429.204042 | 4 |
| 6 | **1151.431850** | 576.219563 | 1134.405301 | 567.706289 | 1133.421285 | 567.214281 | Q | 715.380723 | 358.194000 | 698.354174 | 349.680725 | 697.370158 | 349.188717 | 3 |
| 7 | **1280.474443** | 640.740860 | 1263.447894 | 632.227585 | 1262.463878 | 631.735577 | E | *276.155397* | 138.581337 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 8 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 26.4 | 1425.572693 | -0.001365 | FEDCCQEK |

**Mascot:** http://www.matrixscience.com/

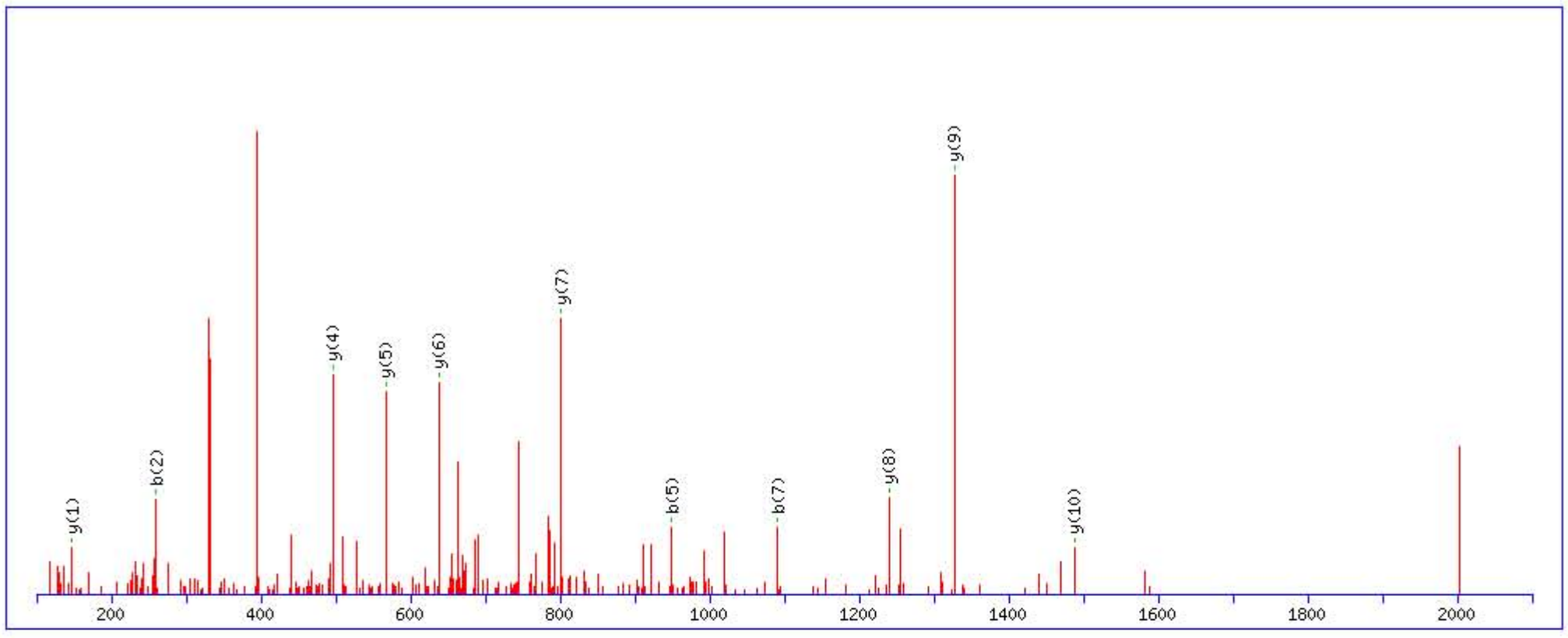
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VCSQYAAYGEK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

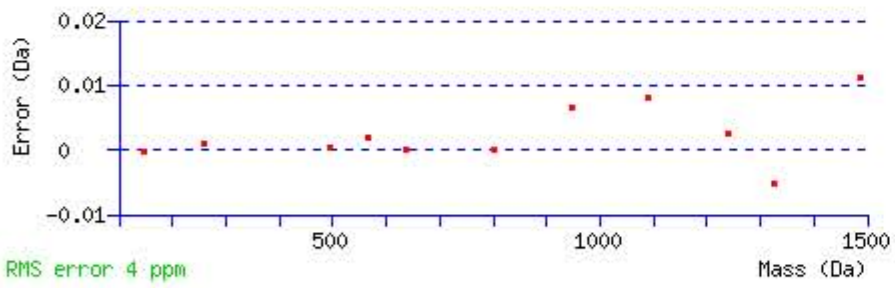
Match to Query 34006: 1585.730508 from(793.872530,2+) rtinseconds(1610) index(64145)
Title: Locus:1.1.1.1835.8 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

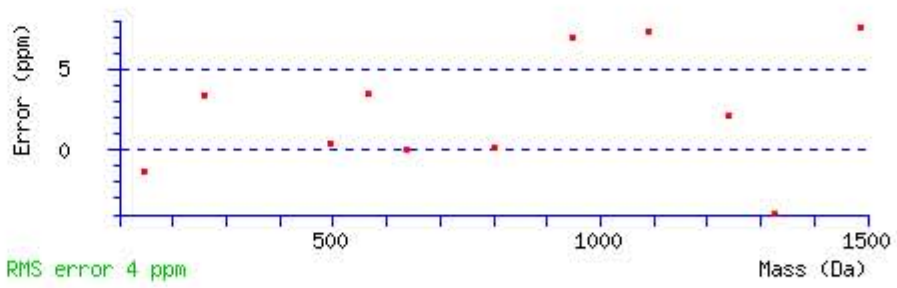
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1585.726868
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 63 **Expect:** 5.4e-006
**Matches :** 11/108 fragment ions using 15 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 11 |
| 2 | **260.106339** | 130.556807 | | | | | C | *1487.665750* | 744.336513 | 1470.639201 | 735.823239 | 1469.655185 | 735.331231 | 10 |
| 3 | 347.138367 | 174.072821 | | | 329.127802 | 165.067539 | S | *1327.635101* | 664.321189 | 1310.608552 | 655.807914 | 1309.624536 | 655.315906 | 9 |
| 4 | 786.363693 | 393.685485 | 769.337144 | 385.172210 | 768.353128 | 384.680202 | Q | *1240.603073* | 620.805175 | 1223.576524 | 612.291900 | 1222.592508 | 611.799892 | 8 |
| 5 | **949.427022** | 475.217149 | 932.400473 | 466.703875 | 931.416457 | 466.211867 | Y | *801.377747* | 401.192512 | 784.351198 | 392.679237 | 783.367182 | 392.187229 | 7 |
| 6 | 1020.464136 | 510.735706 | 1003.437587 | 502.222432 | 1002.453571 | 501.730424 | A | *638.314418* | 319.660847 | 621.287869 | 311.147573 | 620.303853 | 310.655565 | 6 |
| 7 | **1091.501250** | 546.254263 | 1074.474701 | 537.740989 | 1073.490685 | 537.248981 | A | *567.277304* | 284.142290 | 550.250755 | 275.629016 | 549.266739 | 275.137008 | 5 |
| 8 | 1254.564579 | 627.785928 | 1237.538030 | 619.272653 | 1236.554014 | 618.780645 | Y | *496.240190* | 248.623733 | 479.213641 | 240.110459 | 478.229625 | 239.618451 | 4 |
| 9 | 1311.586043 | 656.296660 | 1294.559494 | 647.783385 | 1293.575478 | 647.291377 | G | 333.176861 | 167.092069 | 316.150312 | 158.578794 | 315.166296 | 158.086786 | 3 |
| 10 | 1440.628636 | 720.817956 | 1423.602087 | 712.304682 | 1422.618071 | 711.812674 | E | 276.155397 | 138.581337 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 11 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 62.8 | 1585.726868 | 0.003640 | VCSQYAAYGEK |
| 18.8 | 1585.744614 | -0.014106 | MSVNYAAGLSPYADK |
| 2.1 | 1585.729370 | 0.001138 | LEDYLTSCASNSVK |

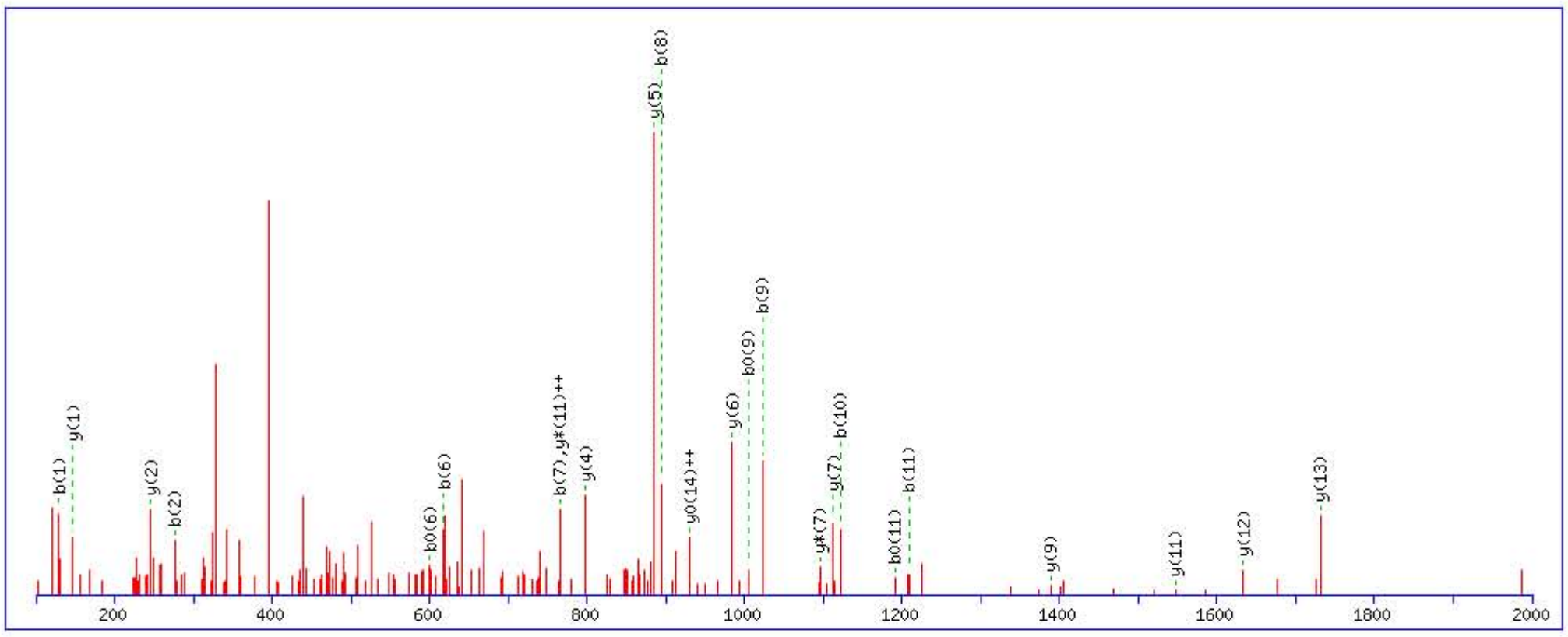
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KFPSGTFEQVSQLVK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

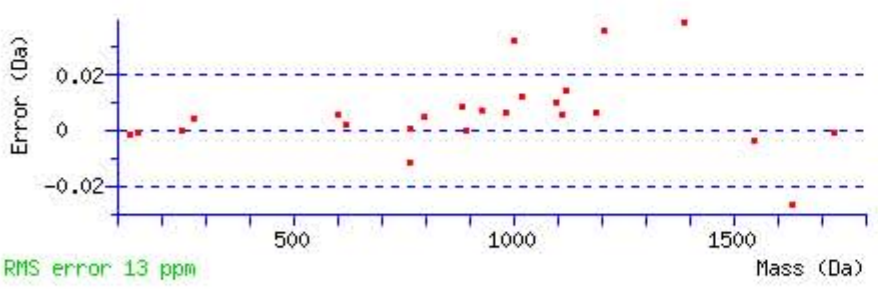
Match to Query 44825: 2005.080822 from(669.367550,3+) rtinseconds(2223) index(67752)
Title: Locus:1.1.1.2049.13 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

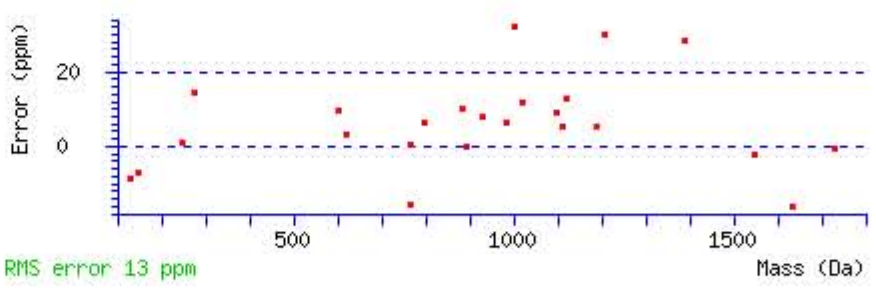
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2005.070679
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q12 : Biotin:Thermo-21345 (Q)
**Ions Score:** 50 **Expect:** 2.5e-005
**Matches :** 25/154 fragment ions using 50 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *129.102239* | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 15 |
| 2 | *276.170653* | 138.588964 | 259.144104 | 130.075690 | | | F | 1877.982984 | 939.495130 | 1860.956435 | 930.981856 | 1859.972419 | 930.489848 | 14 |
| 3 | 373.223417 | 187.115346 | 356.196868 | 178.602072 | | | P | *1730.914570* | 865.960923 | 1713.888021 | 857.447649 | 1712.904005 | 856.955641 | 13 |
| 4 | 460.255445 | 230.631360 | 443.228896 | 222.118086 | 442.244880 | 221.626078 | S | *1633.861806* | 817.434541 | 1616.835257 | 808.921267 | 1615.851241 | 808.429259 | 12 |
| 5 | 517.276909 | 259.142093 | 500.250360 | 250.628818 | 499.266344 | 250.136810 | G | *1546.829778* | 773.918527 | 1529.803229 | 765.405253 | 1528.819213 | 764.913245 | 11 |
| 6 | *618.324588* | 309.665932 | 601.298039 | 301.152658 | 600.314023 | 300.660650 | T | 1489.808314 | 745.407795 | 1472.781765 | 736.894521 | 1471.797749 | 736.402513 | 10 |
| 7 | *765.393002* | 383.200139 | 748.366453 | 374.686865 | 747.382437 | 374.194857 | F | *1388.760635* | 694.883956 | 1371.734086 | 686.370681 | 1370.750070 | 685.878673 | 9 |
| 8 | *894.435595* | 447.721436 | 877.409046 | 439.208161 | 876.425030 | 438.716153 | E | 1241.692221 | 621.349749 | 1224.665672 | 612.836474 | 1223.681656 | 612.344466 | 8 |
| 9 | *1022.494173* | 511.750725 | 1005.467624 | 503.237450 | 1004.483608 | 502.745442 | Q | *1112.649628* | 556.828452 | 1095.623079 | 548.315178 | 1094.639063 | 547.823170 | 7 |
| 10 | *1121.562587* | 561.284932 | 1104.536038 | 552.771657 | 1103.552022 | 552.279649 | V | *984.591050* | 492.799163 | 967.564501 | 484.285889 | 966.580485 | 483.793881 | 6 |
| 11 | *1208.594615* | 604.800946 | 1191.568066 | 596.287671 | 1190.584050 | 595.795663 | S | *885.522636* | 443.264956 | 868.496087 | 434.751682 | 867.512071 | 434.259674 | 5 |
| 12 | 1647.819941 | 824.413609 | 1630.793392 | 815.900334 | 1629.809376 | 815.408326 | Q | *798.490608* | 399.748942 | 781.464059 | 391.235668 | | | 4 |
| 13 | 1760.904005 | 880.955641 | 1743.877456 | 872.442366 | 1742.893440 | 871.950358 | L | 359.265282 | 180.136279 | 342.238733 | 171.623004 | | | 3 |
| 14 | 1859.972419 | 930.489848 | 1842.945870 | 921.976573 | 1841.961854 | 921.484565 | V | *246.181218* | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 15 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 50.0 | 2005.070679 | 0.010143 | KFPSGTFEQVSQLVK |
| 22.6 | 2005.070679 | 0.010143 | KFPSGTFEQVSQLVK |
| 0.9 | 2005.079193 | 0.001629 | RATWLHQALREGTR |

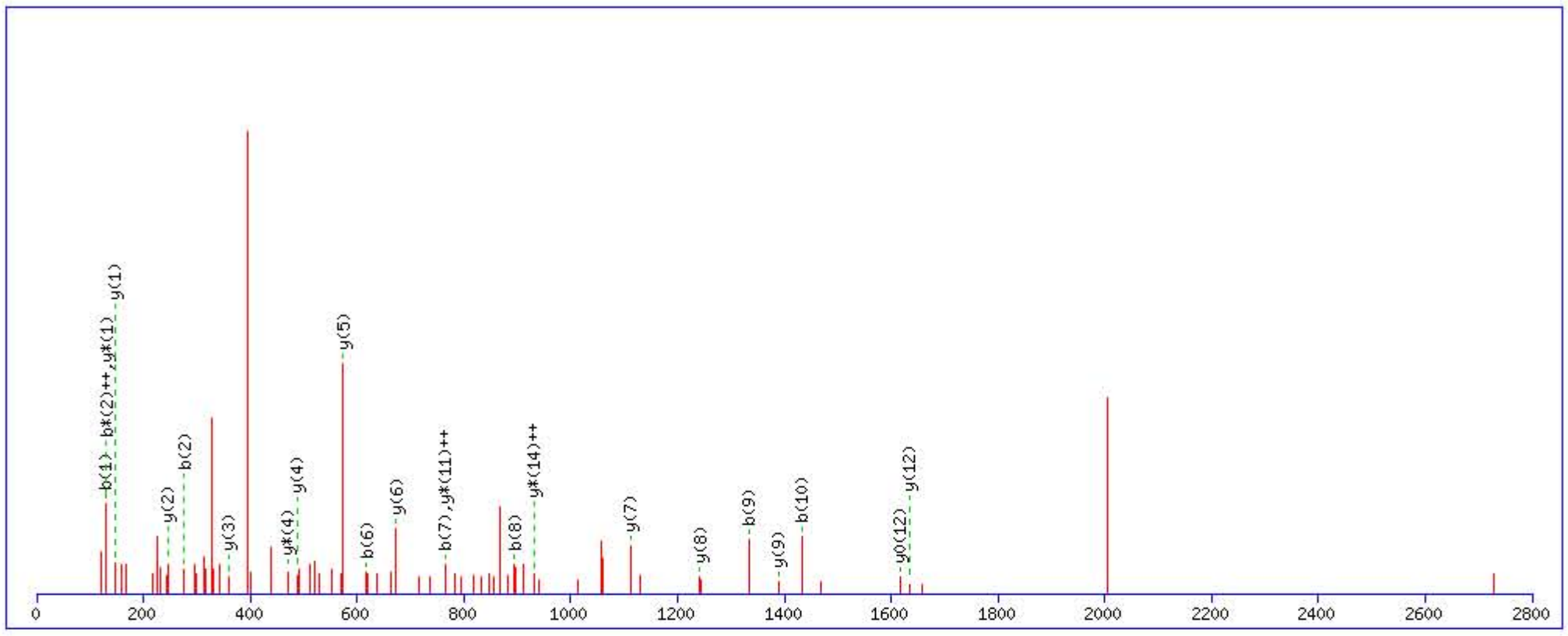
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **KFPSGTFEQVSQLVK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

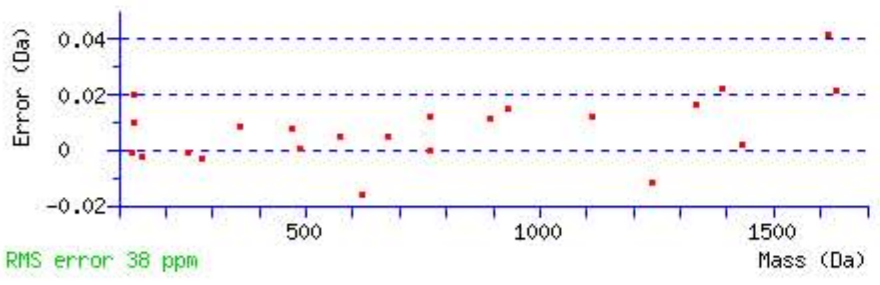
Match to Query 44830: 2005.084332 from(669.368720,3+) rtinseconds(2362) index(68507)
Title: Locus:1.1.1.2097.20 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

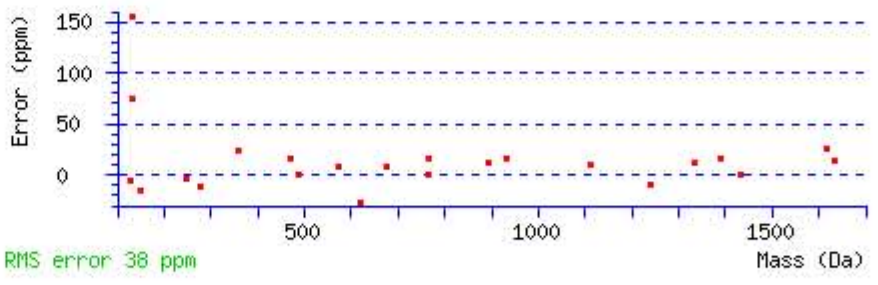
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2005.070679
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 33 **Expect:** 0.0091
**Matches :** 23/154 fragment ions using 63 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *129.102239* | 65.054757 | 112.075690 | 56.541483 | | | K | | | | | | | 15 |
| 2 | *276.170653* | 138.588964 | 259.144104 | 130.075690 | | | F | 1877.982984 | 939.495130 | 1860.956435 | 930.981856 | 1859.972419 | 930.489848 | 14 |
| 3 | 373.223417 | 187.115346 | 356.196868 | 178.602072 | | | P | 1730.914570 | 865.960923 | 1713.888021 | 857.447649 | 1712.904005 | 856.955641 | 13 |
| 4 | 460.255445 | 230.631360 | 443.228896 | 222.118086 | 442.244880 | 221.626078 | S | *1633.861806* | 817.434541 | 1616.835257 | 808.921267 | 1615.851241 | 808.429259 | 12 |
| 5 | 517.276909 | 259.142093 | 500.250360 | 250.628818 | 499.266344 | 250.136810 | G | 1546.829778 | 773.918527 | 1529.803229 | 765.405253 | 1528.819213 | 764.913245 | 11 |
| 6 | *618.324588* | 309.665932 | 601.298039 | 301.152658 | 600.314023 | 300.660650 | T | 1489.808314 | 745.407795 | 1472.781765 | 736.894521 | 1471.797749 | 736.402513 | 10 |
| 7 | *765.393002* | 383.200139 | 748.366453 | 374.686865 | 747.382437 | 374.194857 | F | *1388.760635* | 694.883955 | 1371.734086 | 686.370681 | 1370.750070 | 685.878673 | 9 |
| 8 | *894.435595* | 447.721436 | 877.409046 | 439.208161 | 876.425030 | 438.716153 | E | *1241.692221* | 621.349749 | 1224.665672 | 612.836474 | 1223.681656 | 612.344466 | 8 |
| 9 | *1333.660921* | 667.334098 | 1316.634372 | 658.820824 | 1315.650356 | 658.328816 | Q | *1112.649628* | 556.828452 | 1095.623079 | 548.315178 | 1094.639063 | 547.823169 | 7 |
| 10 | *1432.729335* | 716.868306 | 1415.702786 | 708.355031 | 1414.718770 | 707.863023 | V | *673.424302* | 337.215789 | 656.397753 | 328.702515 | 655.413737 | 328.210507 | 6 |
| 11 | 1519.761363 | 760.384320 | 1502.734814 | 751.871045 | 1501.750798 | 751.379037 | S | *574.355888* | 287.681582 | 557.329339 | 279.168308 | 556.345323 | 278.676300 | 5 |
| 12 | 1647.819941 | 824.413609 | 1630.793392 | 815.900334 | 1629.809376 | 815.408326 | Q | *487.323860* | 244.165568 | 470.297311 | 235.652293 | | | 4 |
| 13 | 1760.904005 | 880.955640 | 1743.877456 | 872.442366 | 1742.893440 | 871.950358 | L | *359.265282* | 180.136279 | 342.238733 | 171.623004 | | | 3 |
| 14 | 1859.972419 | 930.489848 | 1842.945870 | 921.976573 | 1841.961854 | 921.484565 | V | *246.181218* | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 15 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 33.4 | 2005.070679 | 0.013653 | KFPSGTFEQVSQLVK |
| 9.1 | 2005.070679 | 0.013653 | KFPSGTFEQVSQLVK |

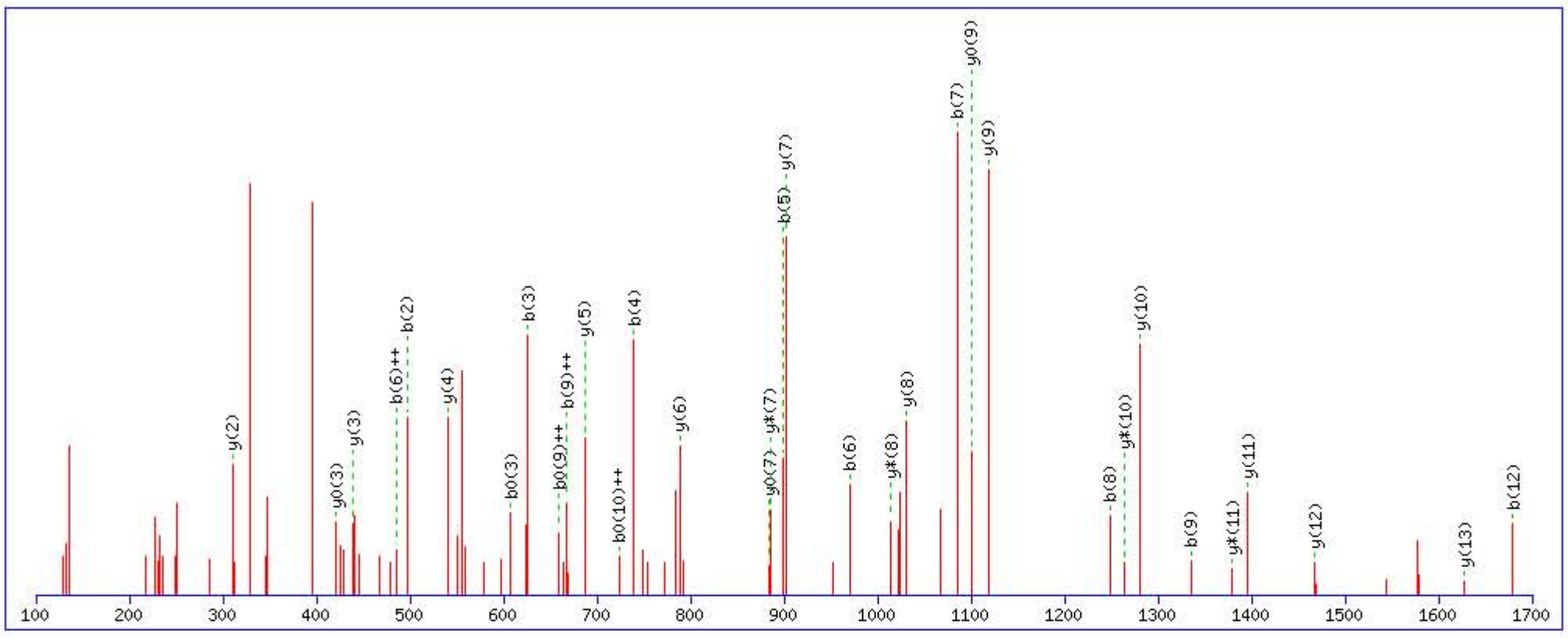
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GQELCADYSENTFTEYK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

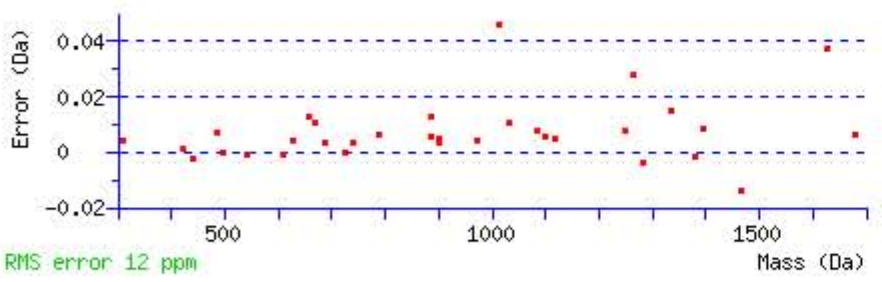
Match to Query 51493: 2365.043412 from(789.355080,3+) rtinseconds(2158) index(67400)
Title: Locus:1.1.1.2026.23 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

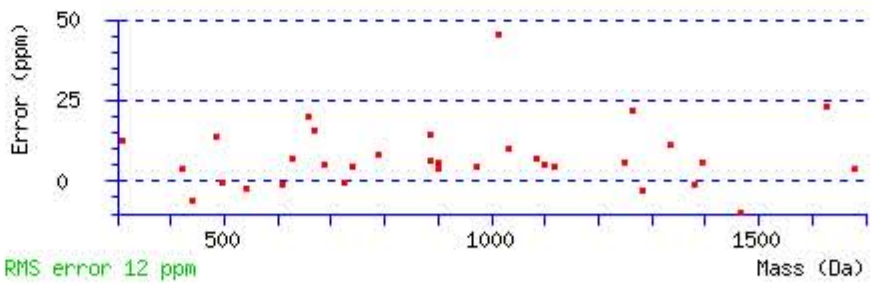
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2365.024231
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 74 **Expect:** 2e-007
**Matches :** 33/182 fragment ions using 53 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 17 |
| 2 | **497.254066** | 249.130671 | 480.227517 | 240.617397 | | | Q | 2309.010064 | 1155.008670 | 2291.983515 | 1146.495395 | 2290.999499 | 1146.003387 | 16 |
| 3 | **626.296659** | 313.651968 | 609.270110 | 305.138693 | 608.286094 | 304.646685 | E | 1869.784738 | 935.396007 | 1852.758189 | 926.882733 | 1851.774173 | 926.390725 | 15 |
| 4 | **739.380723** | 370.194000 | 722.354174 | 361.680725 | 721.370158 | 361.188717 | L | 1740.742145 | 870.874711 | 1723.715596 | 862.361436 | 1722.731580 | 861.869428 | 14 |
| 5 | **899.411372** | 450.209324 | 882.384823 | 441.696050 | 881.400807 | 441.204042 | C | *1627.658081* | 814.332679 | 1610.631532 | 805.819404 | 1609.647516 | 805.327396 | 13 |
| 6 | **970.448486** | **485.727881** | 953.421937 | 477.214607 | 952.437921 | 476.722599 | A | *1467.627432* | 734.317354 | 1450.600883 | 725.804080 | 1449.616867 | 725.312072 | 12 |
| 7 | **1085.475429** | 543.241353 | 1068.448880 | 534.728078 | 1067.464864 | 534.236070 | D | *1396.590318* | 698.798797 | 1379.563769 | 690.285523 | 1378.579753 | 689.793515 | 11 |
| 8 | **1248.538758** | 624.773017 | 1231.512209 | 616.259743 | 1230.528193 | 615.767735 | Y | *1281.563375* | 641.285326 | 1264.536826 | 632.772051 | 1263.552810 | 632.280043 | 10 |
| 9 | **1335.570786** | **668.289031** | 1318.544237 | 659.775757 | 1317.560221 | 659.283749 | S | *1118.500046* | 559.753661 | 1101.473497 | 551.240387 | 1100.489481 | 550.748379 | 9 |
| 10 | 1464.613379 | 732.810328 | 1447.586830 | 724.297053 | 1446.602814 | 723.805045 | E | *1031.468018* | 516.237647 | 1014.441469 | 507.724373 | 1013.457453 | 507.232365 | 8 |
| 11 | 1578.656306 | 789.831791 | 1561.629757 | 781.318517 | 1560.645741 | 780.826509 | N | *902.425425* | 451.716351 | 885.398876 | 443.203076 | 884.414860 | 442.711068 | 7 |
| 12 | **1679.703985** | 840.355631 | 1662.677436 | 831.842356 | 1661.693420 | 831.350348 | T | *788.382498* | 394.694887 | 771.355949 | 386.181613 | 770.371933 | 385.689605 | 6 |
| 13 | 1826.772399 | 913.889838 | 1809.745850 | 905.376563 | 1808.761834 | 904.884555 | F | *687.334819* | 344.171048 | 670.308270 | 335.657773 | 669.324254 | 335.165765 | 5 |
| 14 | 1927.820078 | 964.413677 | 1910.793529 | 955.900403 | 1909.809513 | 955.408395 | T | *540.266405* | 270.636841 | 523.239856 | 262.123566 | 522.255840 | 261.631558 | 4 |
| 15 | 2056.862671 | 1028.934973 | 2039.836122 | 1020.421699 | 2038.852106 | 1019.929691 | E | *439.218726* | 220.113001 | 422.192177 | 211.599726 | 421.208161 | 211.107718 | 3 |
| 16 | 2219.926000 | 1110.466638 | 2202.899451 | 1101.953363 | 2201.915435 | 1101.461355 | Y | *310.176133* | 155.591705 | 293.149584 | 147.078430 | | | 2 |
| 17 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 74.4 | 2365.024231 | 0.019181 | GQELCADYSENTFTEYK |

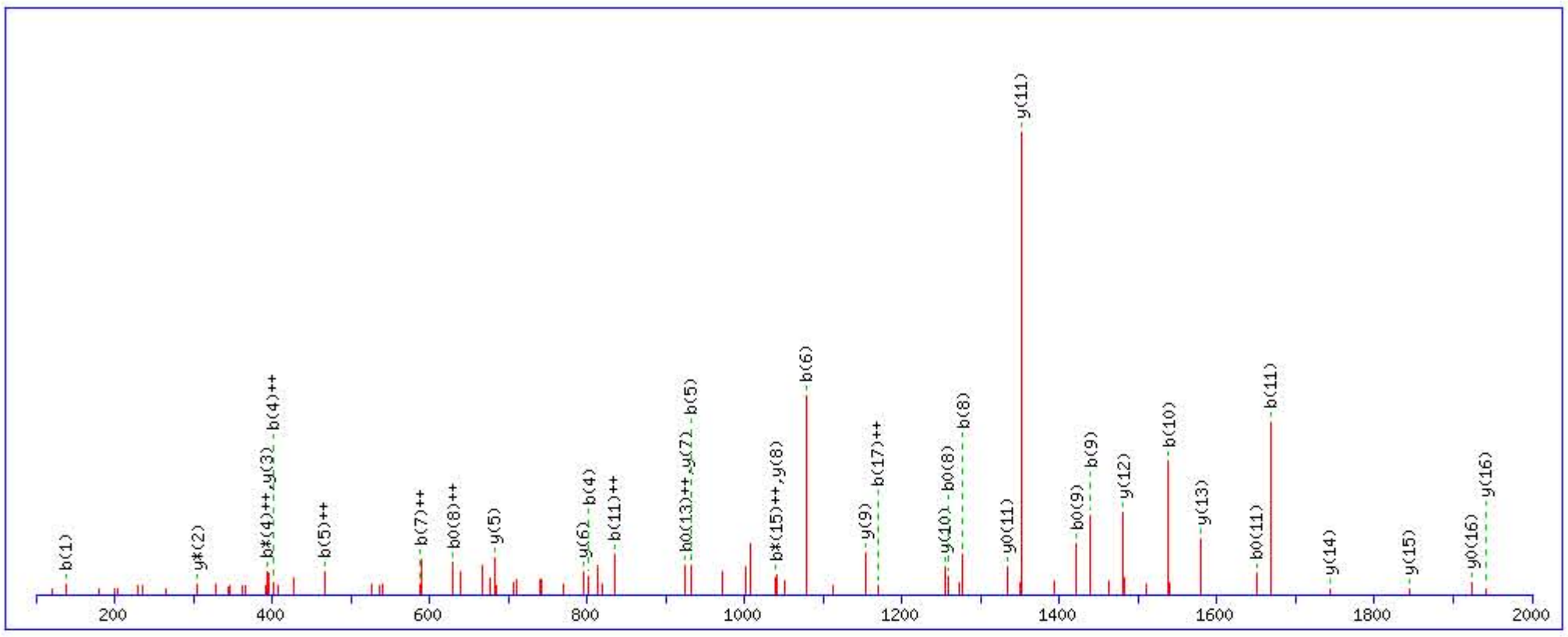
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **HQPQEFPTYVEPTNDEICEAFR**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

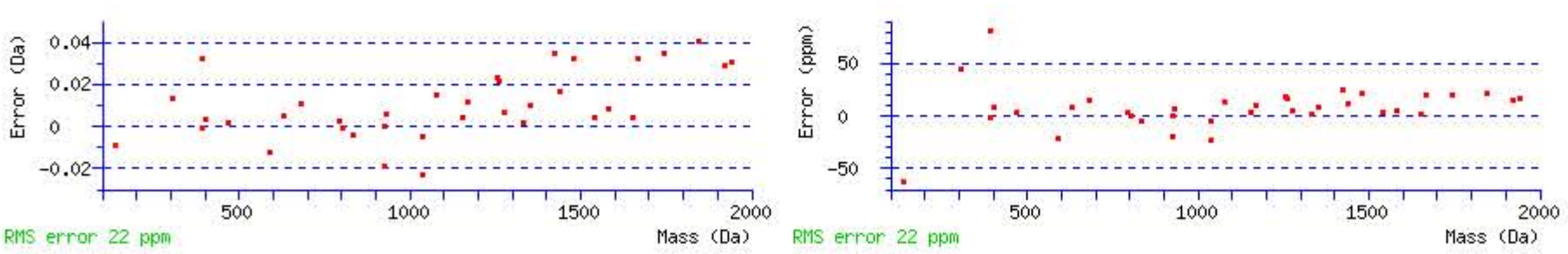
Match to Query 60238: 3017.405622 from(1006.809150,3+) rtinseconds(2354) index(68441)
Title: Locus:1.1.1.2094.26 File:"2013-07-02 CLN FXIII 180 min 2nd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3017.368774
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 82 **Expect:** 2.5e-008
**Matches :** 36/236 fragment ions using 50 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 138.066188 | 69.536732 | | | | | H | | | | | | | 22 |
| 2 | 266.124766 | 133.566021 | 249.098217 | 125.052746 | | | Q | 2881.317146 | 1441.162211 | 2864.290597 | 1432.648936 | 2863.306581 | 1432.156928 | 21 |
| 3 | 363.177530 | 182.092403 | 346.150981 | 173.579129 | | | P | 2753.258568 | 1377.132922 | 2736.232019 | 1368.619647 | 2735.248003 | 1368.127639 | 20 |
| 4 | 802.402856 | 401.705066 | 785.376307 | 393.191792 | | | Q | 2656.205804 | 1328.606540 | 2639.179255 | 1320.093265 | 2638.195239 | 1319.601257 | 19 |
| 5 | 931.445449 | 466.226363 | 914.418900 | 457.713088 | 913.434884 | 457.221080 | E | 2216.980478 | 1108.993877 | 2199.953929 | 1100.480602 | 2198.969913 | 1099.988594 | 18 |
| 6 | 1078.513863 | 539.760570 | 1061.487314 | 531.247295 | 1060.503298 | 530.755287 | F | 2087.937885 | 1044.472580 | 2070.911336 | 1035.959306 | 2069.927320 | 1035.467298 | 17 |
| 7 | 1175.566627 | 588.286952 | 1158.540078 | 579.773677 | 1157.556062 | 579.281669 | P | *1940.869471* | 970.938374 | 1923.842922 | 962.425099 | 1922.858906 | 961.933091 | 16 |
| 8 | 1276.614306 | 638.810791 | 1259.587757 | 630.297517 | 1258.603741 | 629.805509 | T | *1843.816707* | 922.411992 | 1826.790158 | 913.898717 | 1825.806142 | 913.406709 | 15 |
| 9 | 1439.677635 | 720.342456 | 1422.651086 | 711.829181 | 1421.667070 | 711.337173 | Y | *1742.769028* | 871.888152 | 1725.742479 | 863.374878 | 1724.758463 | 862.882870 | 14 |
| 10 | 1538.746049 | 769.876663 | 1521.719500 | 761.363388 | 1520.735484 | 760.871380 | V | *1579.705699* | 790.356488 | 1562.679150 | 781.843213 | 1561.695134 | 781.351205 | 13 |
| 11 | 1667.788642 | 834.397959 | 1650.762093 | 825.884685 | 1649.778077 | 825.392677 | E | *1480.637285* | 740.822281 | 1463.610736 | 732.309006 | 1462.626720 | 731.816998 | 12 |
| 12 | 1764.841406 | 882.924341 | 1747.814857 | 874.411067 | 1746.830841 | 873.919059 | P | *1351.594692* | 676.300984 | 1334.568143 | 667.787710 | 1333.584127 | 667.295702 | 11 |
| 13 | 1865.889085 | 933.448181 | 1848.862536 | 924.934906 | 1847.878520 | 924.442898 | T | *1254.541928* | 627.774602 | 1237.515379 | 619.261328 | 1236.531363 | 618.769320 | 10 |
| 14 | 1979.932012 | 990.469644 | 1962.905463 | 981.956370 | 1961.921447 | 981.464362 | N | *1153.494249* | 577.250763 | 1136.467700 | 568.737488 | 1135.483684 | 568.245480 | 9 |
| 15 | 2094.958955 | 1047.983115 | 2077.932406 | 1039.469841 | 2076.948390 | 1038.977833 | D | *1039.451322* | 520.229299 | 1022.424773 | 511.716025 | 1021.440757 | 511.224017 | 8 |
| 16 | 2224.001548 | 1112.504412 | 2206.974999 | 1103.991137 | 2205.990983 | 1103.499130 | E | *924.424379* | 462.715828 | 907.397830 | 454.202553 | 906.413814 | 453.710545 | 7 |
| 17 | 2337.085612 | 1169.046444 | 2320.059063 | 1160.533170 | 2319.075047 | 1160.041162 | I | *795.381786* | 398.194531 | 778.355237 | 389.681257 | 777.371221 | 389.189249 | 6 |
| 18 | 2497.116261 | 1249.061769 | 2480.089712 | 1240.548494 | 2479.105696 | 1240.056486 | C | *682.297722* | 341.652499 | 665.271173 | 333.139225 | 664.287157 | 332.647217 | 5 |
| 19 | 2626.158854 | 1313.583065 | 2609.132305 | 1305.069791 | 2608.148289 | 1304.577783 | E | 522.267073 | 261.637175 | 505.240524 | 253.123900 | 504.256508 | 252.631892 | 4 |
| 20 | 2697.195968 | 1349.101622 | 2680.169419 | 1340.588348 | 2679.185403 | 1340.096340 | A | *393.224480* | 197.115878 | 376.197931 | 188.602603 | | | 3 |
| 21 | 2844.264382 | 1422.635829 | 2827.237833 | 1414.122555 | 2826.253817 | 1413.630547 | F | 322.187366 | 161.597321 | 305.160817 | 153.084046 | | | 2 |
| 22 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 81.8 | 3017.368774 | 0.036848 | HQPQEFPTYVEPTNDEICEAFR |
| 81.8 | 3017.368774 | 0.036848 | HQPQEFPTYVEPTNDEICEAFR |
| 0.8 | 3017.420258 | -0.014636 | VGWARPGCRPDVELGADDQAFVFEGNR |

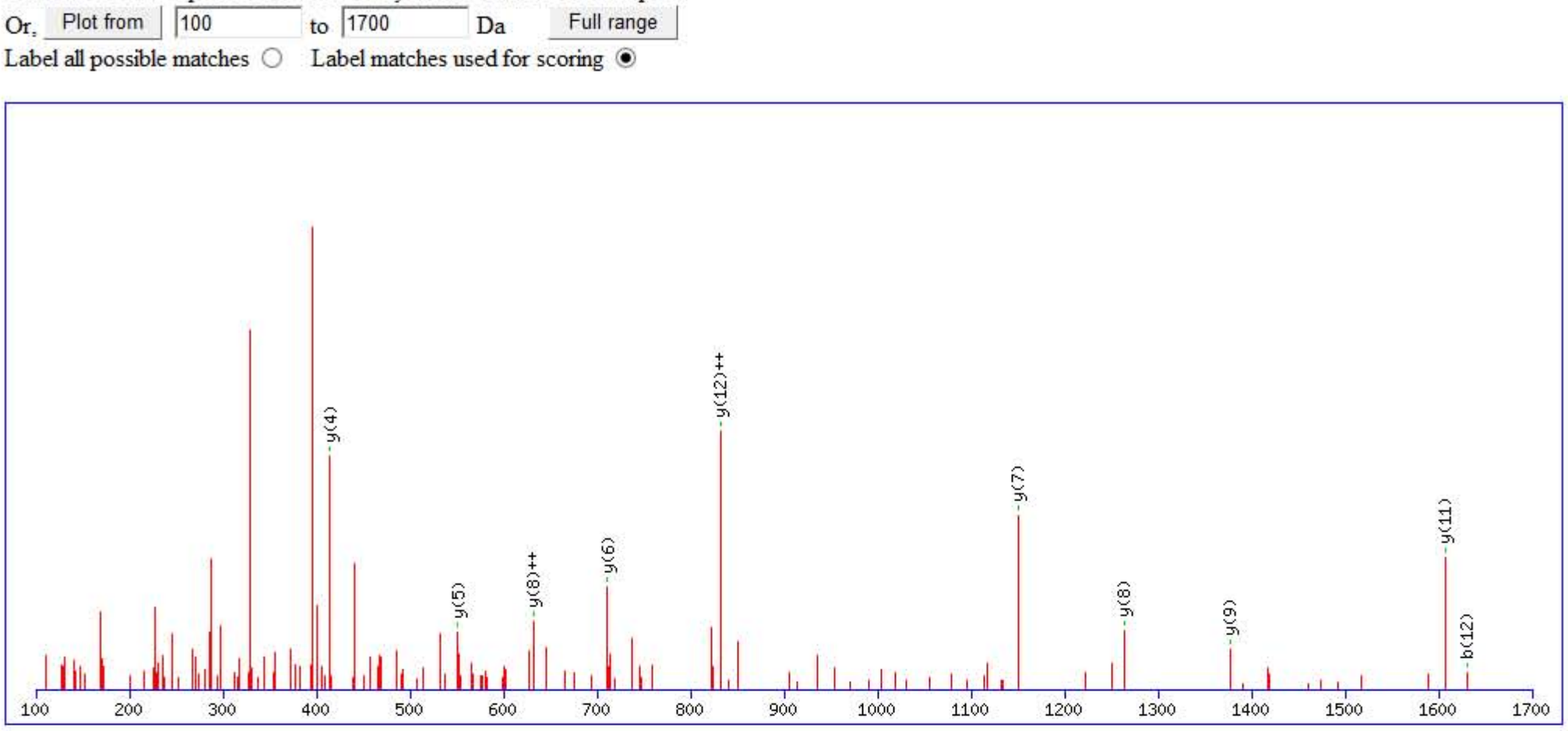
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LGDDLLQCHPAVK**
Found in **PROC_HUMAN**, Vitamin K-dependent protein C OS=Homo sapiens GN=PROC PE=1 SV=1

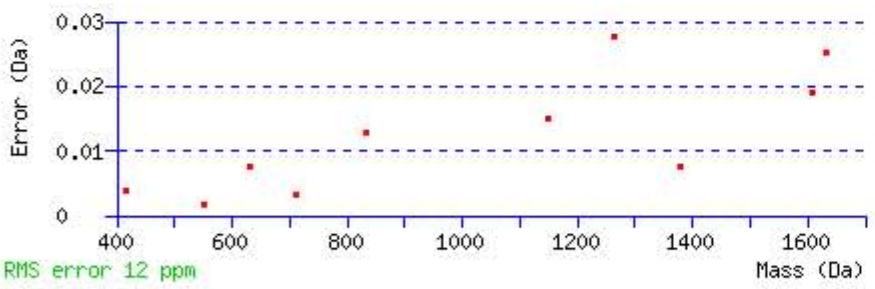
Match to Query 39789: 1775.916372 from(592.979400,3+) rtinseconds(1951) index(50002)
Title: Locus:1.1.1.1917.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

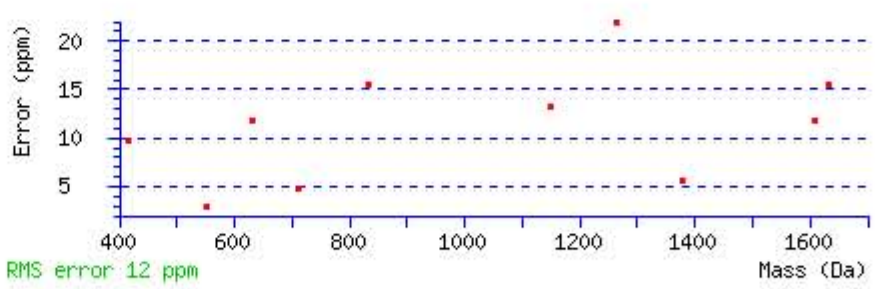
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1775.906250
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 41 **Expect:** 0.00021
**Matches :** 10/110 fragment ions using 16 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | L | | | | | | | 13 |
| 2 | 171.112804 | 86.060040 | | | | | G | 1663.829461 | 832.418369 | 1646.802912 | 823.905094 | 1645.818896 | 823.413086 | 12 |
| 3 | 286.139747 | 143.573512 | | | 268.129182 | 134.568229 | D | *1606.807997* | 803.907637 | 1589.781448 | 795.394362 | 1588.797432 | 794.902354 | 11 |
| 4 | 401.166690 | 201.086983 | | | 383.156125 | 192.081701 | D | 1491.781054 | 746.394165 | 1474.754505 | 737.880891 | 1473.770489 | 737.388883 | 10 |
| 5 | 514.250754 | 257.629015 | | | 496.240189 | 248.623733 | L | *1376.754111* | 688.880694 | 1359.727562 | 680.367419 | | | 9 |
| 6 | 627.334818 | 314.171047 | | | 609.324253 | 305.165765 | L | *1263.670047* | 632.338662 | 1246.643498 | 623.825387 | | | 8 |
| 7 | 1066.560144 | 533.783710 | 1049.533595 | 525.270436 | 1048.549579 | 524.778428 | Q | *1150.585983* | 575.796630 | 1133.559434 | 567.283355 | | | 7 |
| 8 | 1226.590793 | 613.799035 | 1209.564244 | 605.285760 | 1208.580228 | 604.793752 | C | *711.360657* | 356.183967 | 694.334108 | 347.670692 | | | 6 |
| 9 | 1363.649705 | 682.328491 | 1346.623156 | 673.815216 | 1345.639140 | 673.323208 | H | *551.330008* | 276.168642 | 534.303459 | 267.655368 | | | 5 |
| 10 | 1460.702469 | 730.854873 | 1443.675920 | 722.341598 | 1442.691904 | 721.849590 | P | *414.271096* | 207.639186 | 397.244547 | 199.125912 | | | 4 |
| 11 | 1531.739583 | 766.373430 | 1514.713034 | 757.860155 | 1513.729018 | 757.368147 | A | 317.218332 | 159.112804 | 300.191783 | 150.599530 | | | 3 |
| 12 | 1630.807997 | 815.907637 | 1613.781448 | 807.394362 | 1612.797432 | 806.902354 | V | 246.181218 | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 13 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 40.8 | 1775.906250 | 0.010122 | LGDDLLQCHPAVK |
| 1.5 | 1775.935852 | -0.019480 | KRSPYNYLQVAYFK |

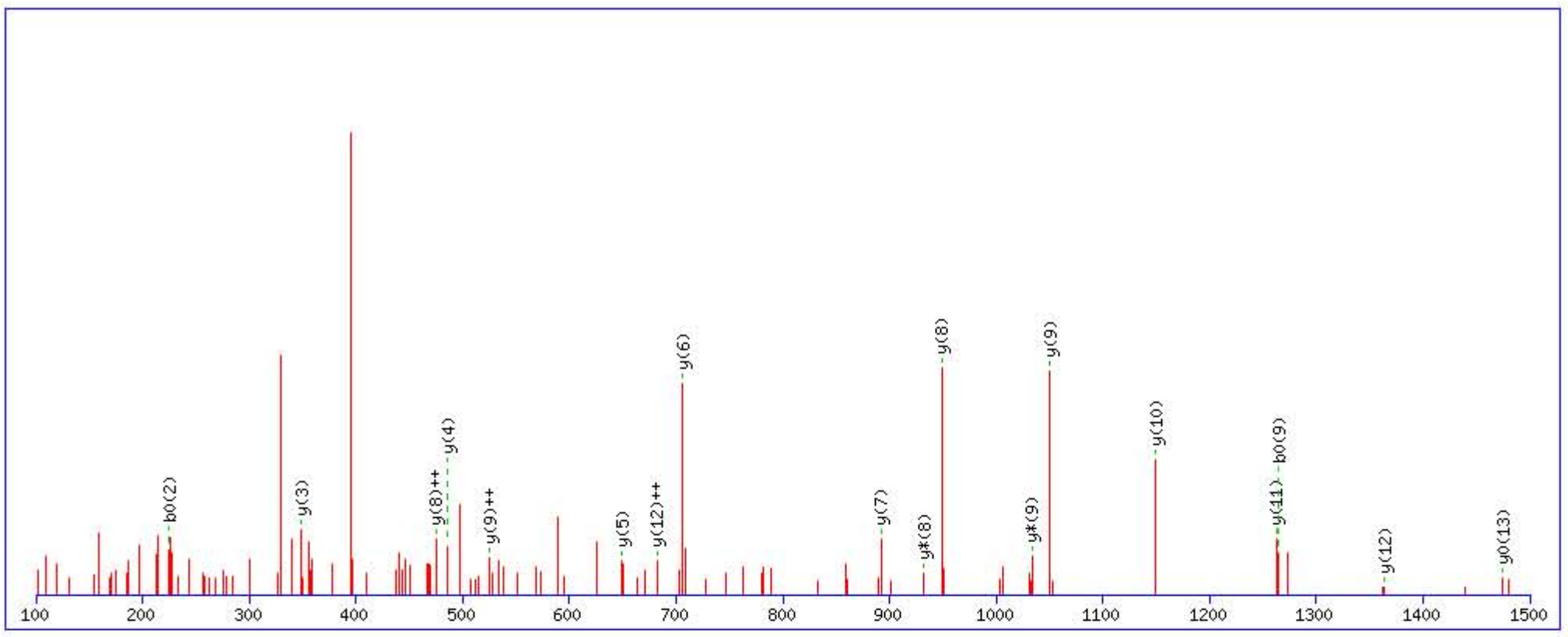
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ELNQAGQETLVTGWGYHSSR**
Found in **PROC_HUMAN**, Vitamin K-dependent protein C OS=Homo sapiens GN=PROC PE=1 SV=1

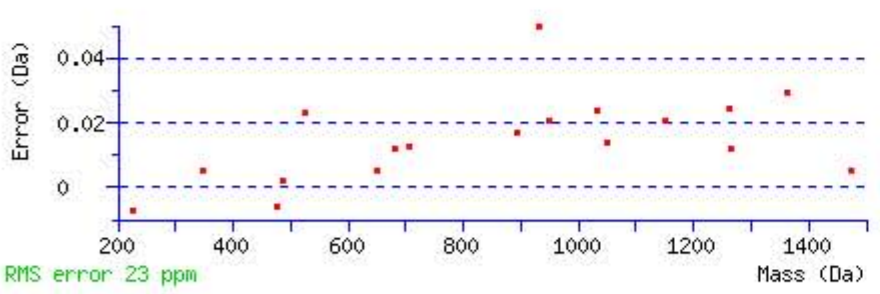
Match to Query 54917: 2543.247696 from(636.819200,4+) rtinseconds(2159) index(51452)
Title: Locus:1.1.1.1989.8 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

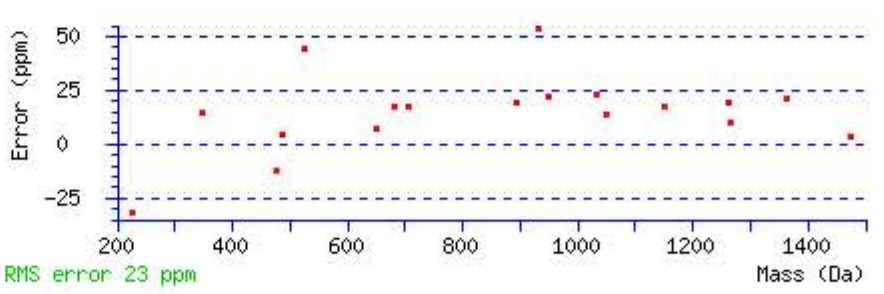
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2543.222702
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 44 **Expect:** 0.0012
**Matches :** 18/222 fragment ions using 39 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 130.049869 | 65.528572 | | | 112.039304 | 56.523290 | E | | | | | | | 20 |
| 2 | 243.133933 | 122.070605 | | | 225.123368 | 113.065322 | L | 2415.187392 | 1208.097334 | 2398.160843 | 1199.584059 | 2397.176827 | 1199.092051 | 19 |
| 3 | 357.176860 | 179.092068 | 340.150311 | 170.578794 | 339.166295 | 170.086786 | N | 2302.103328 | 1151.555302 | 2285.076779 | 1143.042027 | 2284.092763 | 1142.550019 | 18 |
| 4 | 485.235438 | 243.121357 | 468.208889 | 234.608083 | 467.224873 | 234.116075 | Q | 2188.060401 | 1094.533838 | 2171.033852 | 1086.020564 | 2170.049836 | 1085.528556 | 17 |
| 5 | 556.272552 | 278.639914 | 539.246003 | 270.126640 | 538.261987 | 269.634632 | A | 2060.001823 | 1030.504549 | 2042.975274 | 1021.991275 | 2041.991258 | 1021.499267 | 16 |
| 6 | 613.294016 | 307.150646 | 596.267467 | 298.637372 | 595.283451 | 298.145364 | G | 1988.964709 | 994.985993 | 1971.938160 | 986.472718 | 1970.954144 | 985.980710 | 15 |
| 7 | 1052.519342 | 526.763309 | 1035.492793 | 518.250035 | 1034.508777 | 517.758027 | Q | 1931.943245 | 966.475261 | 1914.916696 | 957.961986 | 1913.932680 | 957.469978 | 14 |
| 8 | 1181.561935 | 591.284606 | 1164.535386 | 582.771331 | 1163.551370 | 582.279323 | E | 1492.717919 | 746.862597 | 1475.691370 | 738.349323 | 1474.707354 | 737.857315 | 13 |
| 9 | 1282.609614 | 641.808445 | 1265.583065 | 633.295171 | 1264.599049 | 632.803163 | T | *1363.675326* | 682.341301 | 1346.648777 | 673.828026 | 1345.664761 | 673.336018 | 12 |
| 10 | 1395.693678 | 698.350477 | 1378.667129 | 689.837203 | 1377.683113 | 689.345195 | L | *1262.627647* | 631.817461 | 1245.601098 | 623.304187 | 1244.617082 | 622.812179 | 11 |
| 11 | 1494.762092 | 747.884684 | 1477.735543 | 739.371410 | 1476.751527 | 738.879402 | V | *1149.543583* | 575.275429 | 1132.517034 | 566.762155 | 1131.533018 | 566.270147 | 10 |
| 12 | 1595.809771 | 798.408524 | 1578.783222 | 789.895249 | 1577.799206 | 789.403241 | T | *1050.475169* | 525.741222 | 1033.448620 | 517.227948 | 1032.464604 | 516.735940 | 9 |
| 13 | 1652.831235 | 826.919256 | 1635.804686 | 818.405981 | 1634.820670 | 817.913973 | G | *949.427490* | 475.217383 | 932.400941 | 466.704108 | 931.416925 | 466.212100 | 8 |
| 14 | 1838.910548 | 919.958912 | 1821.883999 | 911.445638 | 1820.899983 | 910.953630 | W | *892.406026* | 446.706651 | 875.379477 | 438.193376 | 874.395461 | 437.701368 | 7 |
| 15 | 1895.932012 | 948.469644 | 1878.905463 | 939.956370 | 1877.921447 | 939.464362 | G | *706.326713* | 353.666994 | 689.300164 | 345.153720 | 688.316148 | 344.661712 | 6 |
| 16 | 2058.995341 | 1030.001308 | 2041.968792 | 1021.488034 | 2040.984776 | 1020.996026 | Y | *649.305249* | 325.156263 | 632.278700 | 316.642988 | 631.294684 | 316.150980 | 5 |
| 17 | 2196.054253 | 1098.530764 | 2179.027704 | 1090.017490 | 2178.043688 | 1089.525482 | H | *486.241920* | 243.624598 | 469.215371 | 235.111324 | 468.231355 | 234.619316 | 4 |
| 18 | 2283.086281 | 1142.046778 | 2266.059732 | 1133.533504 | 2265.075716 | 1133.041496 | S | *349.183008* | 175.095142 | 332.156459 | 166.581868 | 331.172443 | 166.089860 | 3 |
| 19 | 2370.118309 | 1185.562792 | 2353.091760 | 1177.049518 | 2352.107744 | 1176.557510 | S | 262.150980 | 131.579128 | 245.124431 | 123.065854 | 244.140415 | 122.573846 | 2 |
| 20 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 43.7 | 2543.222702 | 0.024994 | ELNQAGQETLVTGWGYHSSR |
| 43.7 | 2543.222702 | 0.024994 | ELNQAGQETLVTGWGYHSSR |

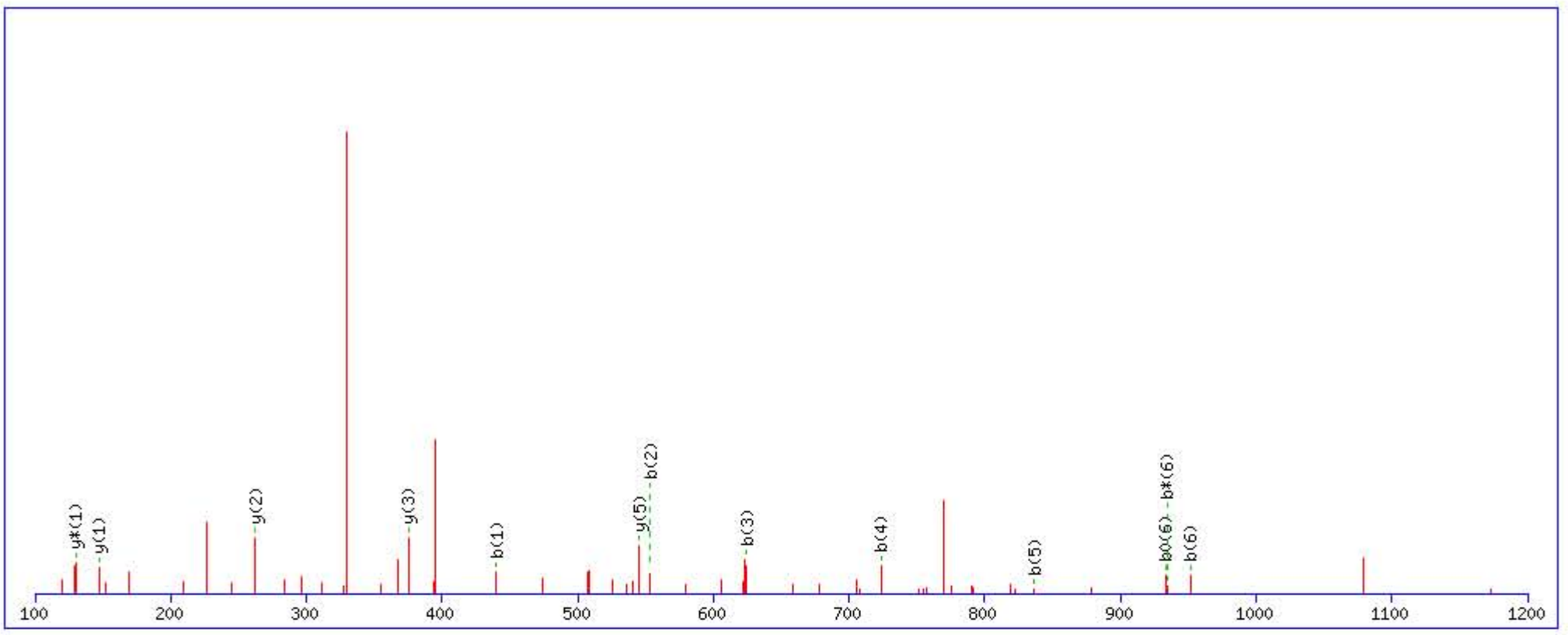
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QLAVLDK**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

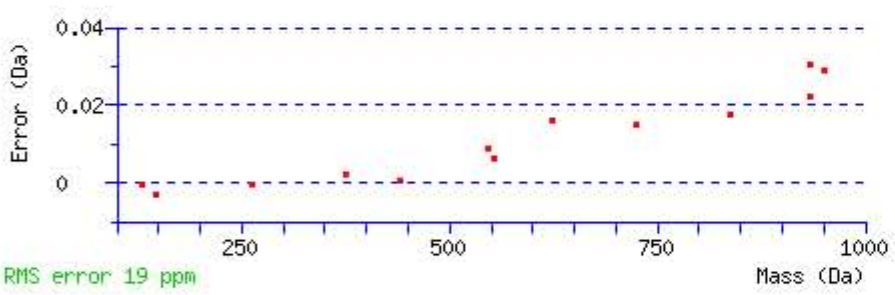
Match to Query 16192: 1096.636108 from(549.325330,2+) rtinseconds(1975) index(50198)
Title: Locus:1.1.1.1925.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

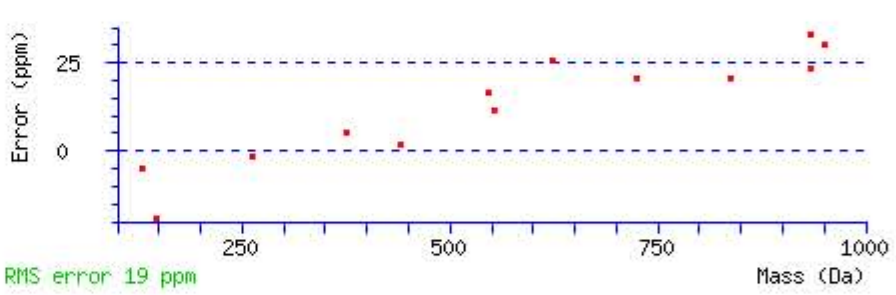
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1096.631439
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.013
**Matches :** 13/60 fragment ions using 28 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | $y^{*}$ | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *440.232602* | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 7 |
| 2 | *553.316666* | 277.161971 | 536.290117 | 268.648697 | | | L | 658.413403 | 329.710340 | 641.386854 | 321.197065 | 640.402838 | 320.705057 | 6 |
| 3 | *624.353780* | 312.680528 | 607.327231 | 304.167254 | | | A | **545.329339** | 273.168308 | 528.302790 | 264.655033 | 527.318774 | 264.163025 | 5 |
| 4 | *723.422194* | 362.214735 | 706.395645 | 353.701461 | | | V | 474.292225 | 237.649750 | 457.265676 | 229.136476 | 456.281660 | 228.644468 | 4 |
| 5 | *836.506258* | 418.756767 | 819.479709 | 410.243493 | | | L | **375.223811** | 188.115543 | 358.197262 | 179.602269 | 357.213246 | 179.110261 | 3 |
| 6 | *951.533201* | 476.270239 | 934.506652 | 467.756964 | 933.522636 | 467.264956 | D | **262.139747** | 131.573511 | 245.113198 | 123.060237 | 244.129182 | 122.568229 | 2 |
| 7 | | | | | | | K | **147.112804** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 30.6 | 1096.631439 | 0.004669 | QLAVLDK |
| 18.3 | 1096.624054 | 0.012054 | KPVDSVPLSR |
| 8.3 | 1096.624023 | 0.012085 | IPRENLLDK |
| 7.9 | 1096.642654 | -0.006546 | QLLREK |
| 7.8 | 1096.639297 | -0.003189 | AHVSPLFKAK |
| 6.1 | 1096.628067 | 0.008041 | YIFVSLLSR |
| 4.9 | 1096.631439 | 0.004669 | GILQLDK |
| 2.8 | 1096.631439 | 0.004669 | QIDVAIK |
| 2.8 | 1096.642654 | -0.006546 | NITMHLLKK |
| 1.2 | 1096.631439 | 0.004669 | QIEGLVK |

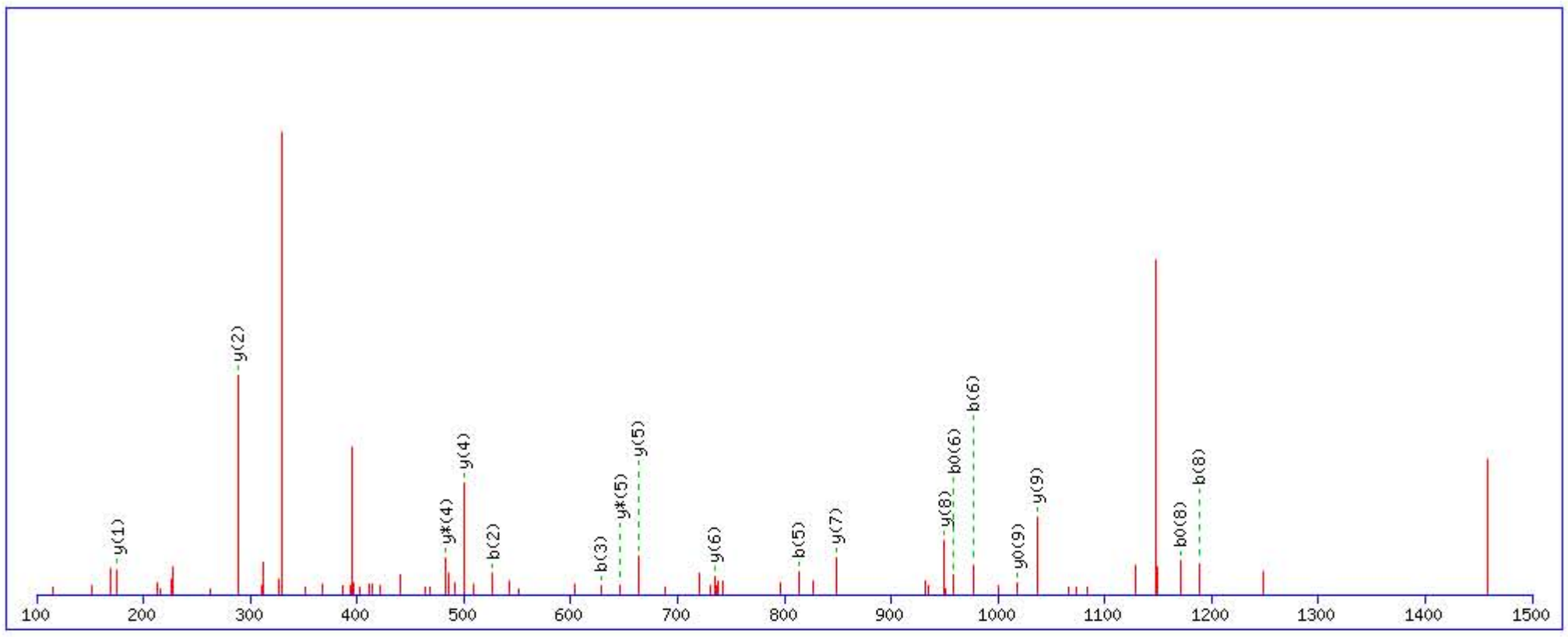
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QSTNAYPDLR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

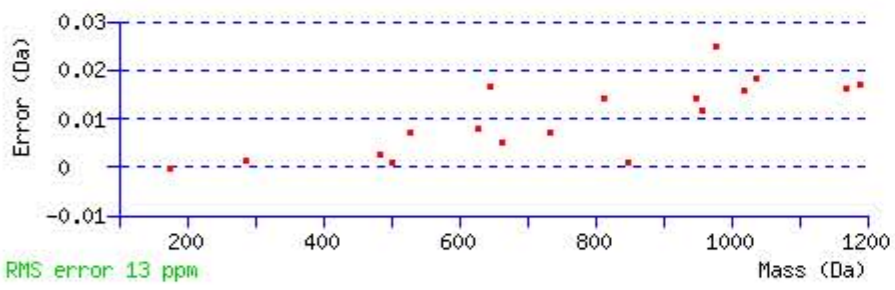
Match to Query 30342: 1474.737428 from(738.375990,2+) rtinseconds(1771) index(32742)
Title: Locus:1.1.1.725.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

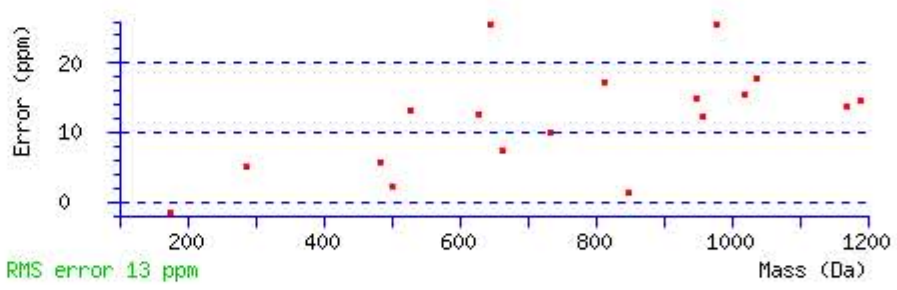
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1474.723831
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 48 **Expect:** 0.00063
**Matches** : 18/102 fragment ions using 34 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 10 |
| 2 | **527.264630** | 264.135953 | 510.238081 | 255.622679 | 509.254065 | 255.130671 | S | *1036.505800* | 518.756538 | 1019.479251 | 510.243263 | 1018.495235 | 509.751255 | 9 |
| 3 | **628.312309** | 314.659793 | 611.285760 | 306.146518 | 610.301744 | 305.654510 | T | *949.473772* | 475.240524 | 932.447223 | 466.727249 | 931.463207 | 466.235241 | 8 |
| 4 | 742.355236 | 371.681256 | 725.328687 | 363.167982 | 724.344671 | 362.675974 | N | *848.426093* | 424.716684 | 831.399544 | 416.203410 | 830.415528 | 415.711402 | 7 |
| 5 | **813.392350** | 407.199813 | 796.365801 | 398.686538 | 795.381785 | 398.194530 | A | *734.383166* | 367.695221 | 717.356617 | 359.181946 | 716.372601 | 358.689938 | 6 |
| 6 | **976.455679** | 488.731477 | 959.429130 | 480.218203 | 958.445114 | 479.726195 | Y | *663.346052* | 332.176664 | 646.319503 | 323.663389 | 645.335487 | 323.171382 | 5 |
| 7 | 1073.508443 | 537.257860 | 1056.481894 | 528.744585 | 1055.497878 | 528.252577 | P | *500.282723* | 250.644999 | 483.256174 | 242.131725 | 482.272158 | 241.639717 | 4 |
| 8 | **1188.535386** | 594.771331 | 1171.508837 | 586.258057 | 1170.524821 | 585.766049 | D | 403.229959 | 202.118617 | 386.203410 | 193.605343 | 385.219394 | 193.113335 | 3 |
| 9 | 1301.619450 | 651.313363 | 1284.592901 | 642.800089 | 1283.608885 | 642.308080 | L | *288.203016* | 144.605146 | 271.176467 | 136.091871 | | | 2 |
| 10 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 48.5 | 1474.723831 | 0.013597 | QSTNAYPDLR |
| 13.4 | 1474.721161 | 0.016267 | QSTHGERGHR |
| 12.8 | 1474.744934 | -0.007506 | LSKEELIQNMDR |
| 8.6 | 1474.748779 | -0.011351 | LQSESTNNGKNKR |
| 8.2 | 1474.745605 | -0.008177 | EPWEELFSIGLR |
| 6.0 | 1474.741592 | -0.004164 | SSLEHGSDVYLLR |
| 4.3 | 1474.735092 | 0.002336 | SFCVLSQLTQHR |
| 1.8 | 1474.726303 | 0.011125 | VQTEKEEKEEAR |
| 1.1 | 1474.757721 | -0.020293 | YQMLAFVHR |
| 1.0 | 1474.757523 | -0.020095 | MGLQARRWASGSR |

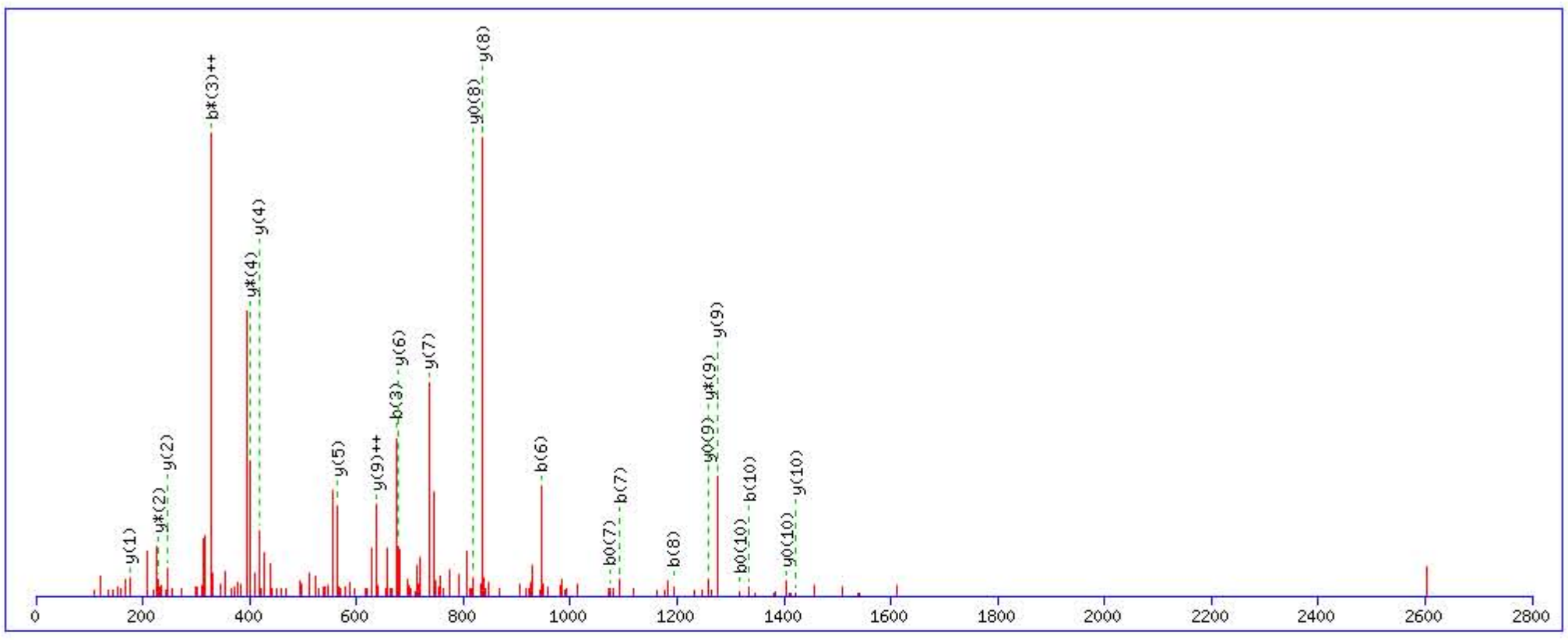
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SFQTGLFTAAR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

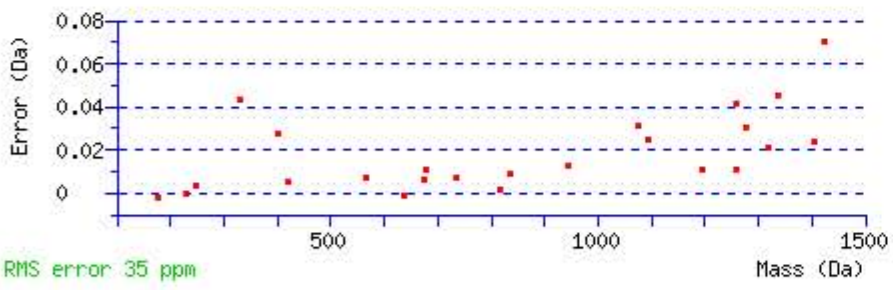
Match to Query 31490: 1508.800388 from(755.407470,2+) rtinseconds(2303) index(52295)
Title: Locus:1.1.1.2039.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

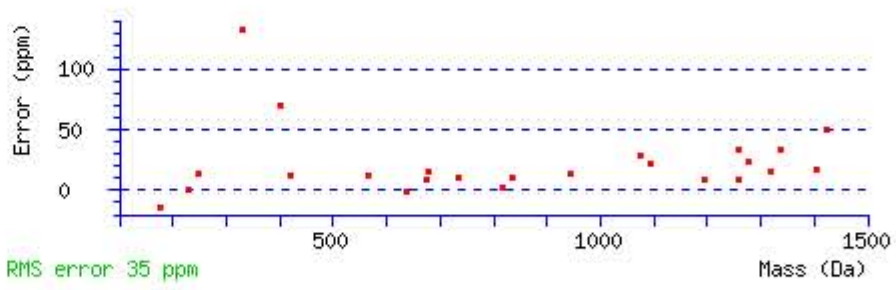
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1508.780975
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 1.9e-005
**Matches :** 24/110 fragment ions using 42 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | | | 11 |
| 2 | 235.107718 | 118.057497 | | | 217.097153 | 109.052214 | F | *1422.756220* | 711.881748 | 1405.729671 | 703.368474 | 1404.745655 | 702.876465 | 10 |
| 3 | **674.333044** | 337.670160 | 657.306495 | 329.156885 | 656.322479 | 328.664877 | Q | *1275.687806* | 638.347541 | 1258.661257 | 629.834267 | 1257.677241 | 629.342259 | 9 |
| 4 | 775.380723 | 388.194000 | 758.354174 | 379.680725 | 757.370158 | 379.188717 | T | *836.462480* | 418.734878 | 819.435931 | 410.221604 | 818.451915 | 409.729596 | 8 |
| 5 | 832.402187 | 416.704732 | 815.375638 | 408.191457 | 814.391622 | 407.699449 | G | *735.414801* | 368.211039 | 718.388252 | 359.697764 | 717.404236 | 359.205756 | 7 |
| 6 | **945.486251** | 473.246764 | 928.459702 | 464.733489 | 927.475686 | 464.241481 | L | *678.393337* | 339.700307 | 661.366788 | 331.187032 | 660.382772 | 330.695024 | 6 |
| 7 | **1092.554665** | 546.780971 | 1075.528116 | 538.267696 | 1074.544100 | 537.775688 | F | *565.309273* | 283.158275 | 548.282724 | 274.645000 | 547.298708 | 274.152992 | 5 |
| 8 | **1193.602344** | 597.304810 | 1176.575795 | 588.791536 | 1175.591779 | 588.299528 | T | *418.240859* | 209.624067 | 401.214310 | 201.110793 | 400.230294 | 200.618785 | 4 |
| 9 | 1264.639458 | 632.823367 | 1247.612909 | 624.310093 | 1246.628893 | 623.818085 | A | 317.193180 | 159.100228 | 300.166631 | 150.586953 | | | 3 |
| 10 | **1335.676572** | 668.341924 | 1318.650023 | 659.828650 | 1317.666007 | 659.336642 | A | *246.156066* | 123.581671 | 229.129517 | 115.068396 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 57.9 | 1508.780975 | 0.019413 | SFQTGLFTAAR |
| 7.3 | 1508.798721 | 0.001667 | SSYGVAAPVDFLRK |
| 2.7 | 1508.805939 | -0.005551 | SSPEHTTILRGGVR |

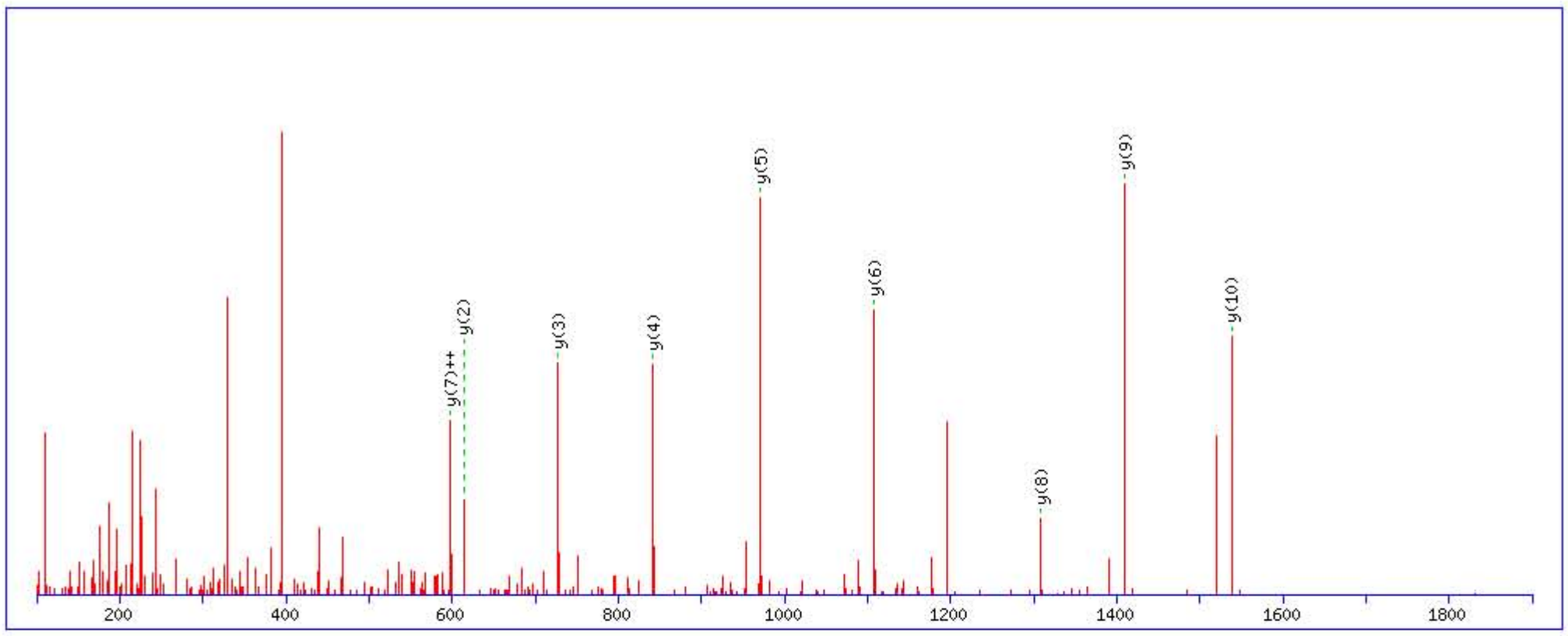
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IETISHEDLQR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

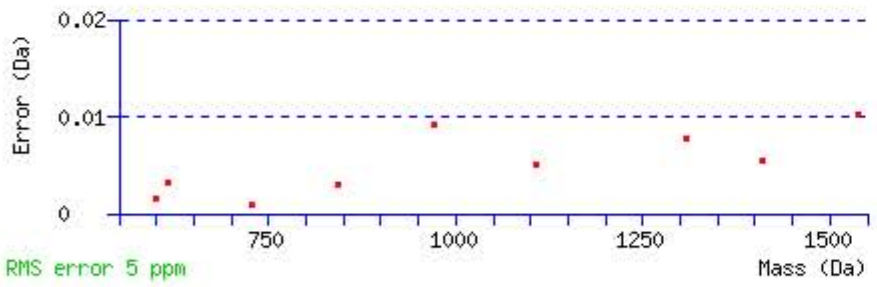
Match to Query 36910: 1650.843342 from(551.288390,3+) rtinseconds(1644) index(47956)
Title: Locus:1.1.1.1810.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

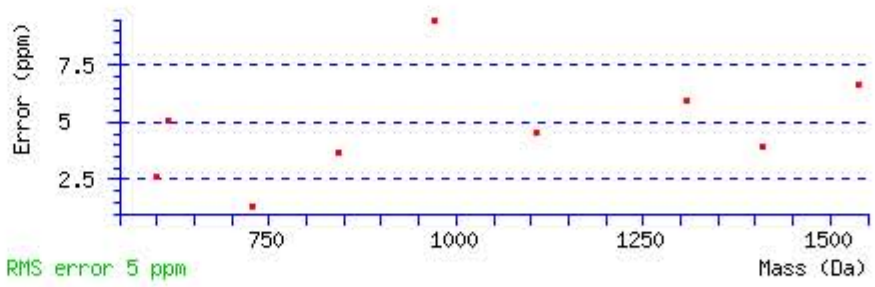
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1650.839920
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 1.8e-005
**Matches :** 9/94 fragment ions using 15 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 11 |
| 2 | 243.133933 | 122.070605 | | | 225.123368 | 113.065322 | E | *1538.763154* | 769.885215 | 1521.736605 | 761.371941 | 1520.752589 | 760.879933 | 10 |
| 3 | 344.181612 | 172.594444 | | | 326.171047 | 163.589162 | T | *1409.720561* | 705.363919 | 1392.694012 | 696.850644 | 1391.709996 | 696.358636 | 9 |
| 4 | 457.265676 | 229.136476 | | | 439.255111 | 220.131194 | I | *1308.672882* | 654.840079 | 1291.646333 | 646.326805 | 1290.662317 | 645.834797 | 8 |
| 5 | 544.297704 | 272.652490 | | | 526.287139 | 263.647208 | S | 1195.588818 | 598.298047 | 1178.562269 | 589.784773 | 1177.578253 | 589.292764 | 7 |
| 6 | 681.356616 | 341.181946 | | | 663.346051 | 332.176664 | H | *1108.556790* | 554.782033 | 1091.530241 | 546.268759 | 1090.546225 | 545.776751 | 6 |
| 7 | 810.399209 | 405.703243 | | | 792.388644 | 396.697960 | E | *971.497878* | 486.252577 | 954.471329 | 477.739303 | 953.487313 | 477.247295 | 5 |
| 8 | 925.426152 | 463.216714 | | | 907.415587 | 454.211432 | D | *842.455285* | 421.731281 | 825.428736 | 413.218006 | 824.444720 | 412.725998 | 4 |
| 9 | 1038.510216 | 519.758746 | | | 1020.499651 | 510.753463 | L | *727.428342* | 364.217809 | 710.401793 | 355.704535 | | | 3 |
| 10 | 1477.735542 | 739.371409 | 1460.708993 | 730.858135 | 1459.724977 | 730.366127 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 11 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 52.8 | 1650.839920 | 0.003422 | IETISHEDLQR |
| 2.3 | 1650.855881 | -0.012539 | MQRTGGGAPRPGR |

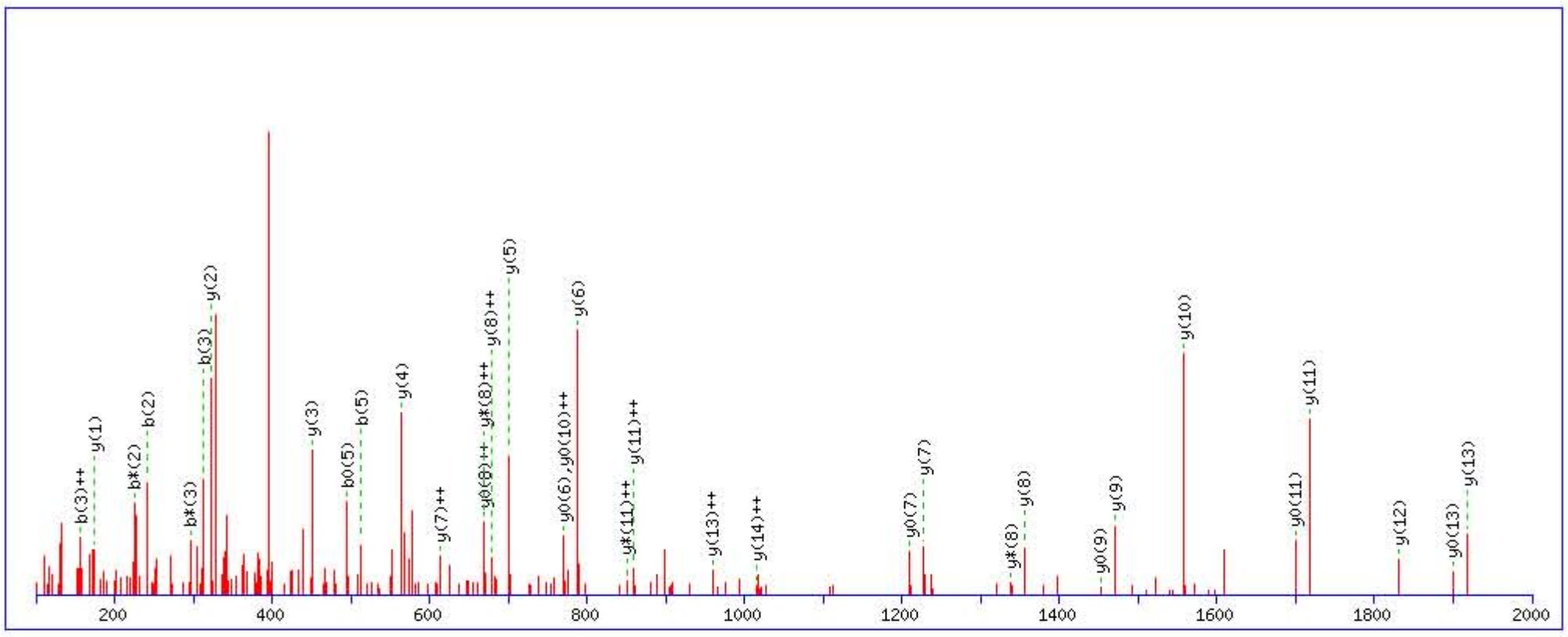
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IQALSLCSDQQSHLEFR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

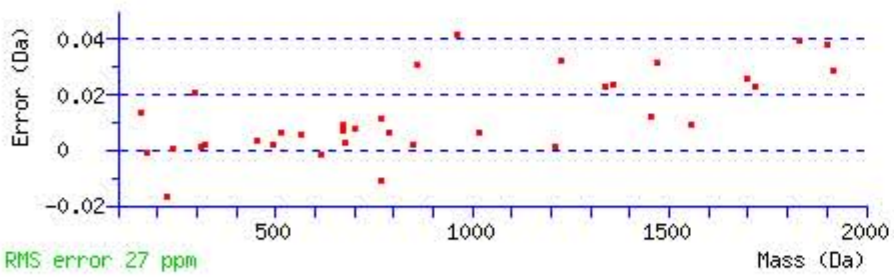
Match to Query 51247: 2342.167136 from(586.549060,4+) rtinseconds(2171) index(51540)
Title: Locus:1.1.1.1993.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

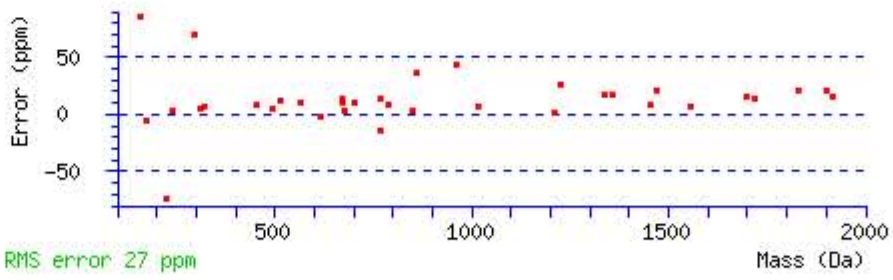
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2342.151108
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q11** : Biotin:Thermo-21345 (Q)
**Ions Score:** 70 **Expect:** 3.5e-006
**Matches :** 35/178 fragment ions using 65 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 17 |
| 2 | **242.149918** | 121.578597 | 225.123369 | 113.065323 | | | Q | 2230.074335 | 1115.540805 | 2213.047786 | 1107.027531 | 2212.063770 | 1106.535523 | 16 |
| 3 | **313.187032** | 157.097154 | 296.160483 | 148.583879 | | | A | 2102.015757 | 1051.511516 | 2084.989208 | 1042.998242 | 2084.005192 | 1042.506234 | 15 |
| 4 | 426.271096 | 213.639186 | 409.244547 | 205.125912 | | | L | 2030.978643 | 1015.992959 | 2013.952094 | 1007.479685 | 2012.968078 | 1006.987677 | 14 |
| 5 | **513.303124** | 257.155200 | 496.276575 | 248.641926 | 495.292559 | 248.149918 | S | *1917.894579* | 959.450927 | 1900.868030 | 950.937653 | 1899.884014 | 950.445645 | 13 |
| 6 | 626.387188 | 313.697232 | 609.360639 | 305.183958 | 608.376623 | 304.691950 | L | *1830.862551* | 915.934913 | 1813.836002 | 907.421639 | 1812.851986 | 906.929631 | 12 |
| 7 | 786.417837 | 393.712557 | 769.391288 | 385.199282 | 768.407272 | 384.707274 | C | *1717.778487* | 859.392881 | 1700.751938 | 850.879607 | 1699.767922 | 850.387599 | 11 |
| 8 | 873.449865 | 437.228571 | 856.423316 | 428.715296 | 855.439300 | 428.223288 | S | *1557.747838* | 779.377557 | 1540.721289 | 770.864282 | 1539.737273 | 770.372274 | 10 |
| 9 | 988.476808 | 494.742042 | 971.450259 | 486.228768 | 970.466243 | 485.736760 | D | *1470.715810* | 735.861543 | 1453.689261 | 727.348268 | *1452.705245* | 726.856260 | 9 |
| 10 | 1116.535386 | 558.771331 | 1099.508837 | 550.258057 | 1098.524821 | 549.766049 | Q | *1355.688867* | 678.348071 | 1338.662318 | 669.834797 | 1337.678302 | 669.342789 | 8 |
| 11 | 1555.760712 | 778.383994 | 1538.734163 | 769.870720 | 1537.750147 | 769.378712 | Q | *1227.630289* | 614.318782 | 1210.603740 | 605.805508 | *1209.619724* | 605.313500 | 7 |
| 12 | 1642.792740 | 821.900008 | 1625.766191 | 813.386734 | 1624.782175 | 812.894726 | S | *788.404963* | 394.706119 | 771.378414 | 386.192845 | *770.394398* | 385.700837 | 6 |
| 13 | 1779.851652 | 890.429464 | 1762.825103 | 881.916190 | 1761.841087 | 881.424182 | H | *701.372935* | 351.190105 | 684.346386 | 342.676831 | 683.362370 | 342.184823 | 5 |
| 14 | 1892.935716 | 946.971496 | 1875.909167 | 938.458222 | 1874.925151 | 937.966213 | L | *564.314023* | 282.660649 | 547.287474 | 274.147375 | 546.303458 | 273.655367 | 4 |
| 15 | 2021.978309 | 1011.492793 | 2004.951760 | 1002.979518 | 2003.967744 | 1002.487510 | E | *451.229959* | 226.118617 | 434.203410 | 217.605343 | 433.219394 | 217.113335 | 3 |
| 16 | 2169.046723 | 1085.026999 | 2152.020174 | 1076.513725 | 2151.036158 | 1076.021717 | F | *322.187366* | 161.597321 | 305.160817 | 153.084046 | | | 2 |
| 17 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 69.5 | 2342.151108 | 0.016028 | IQALSLCSDQQSHLEFR |
| 57.6 | 2342.151108 | 0.016028 | IQALSLCSDQQSHLEFR |

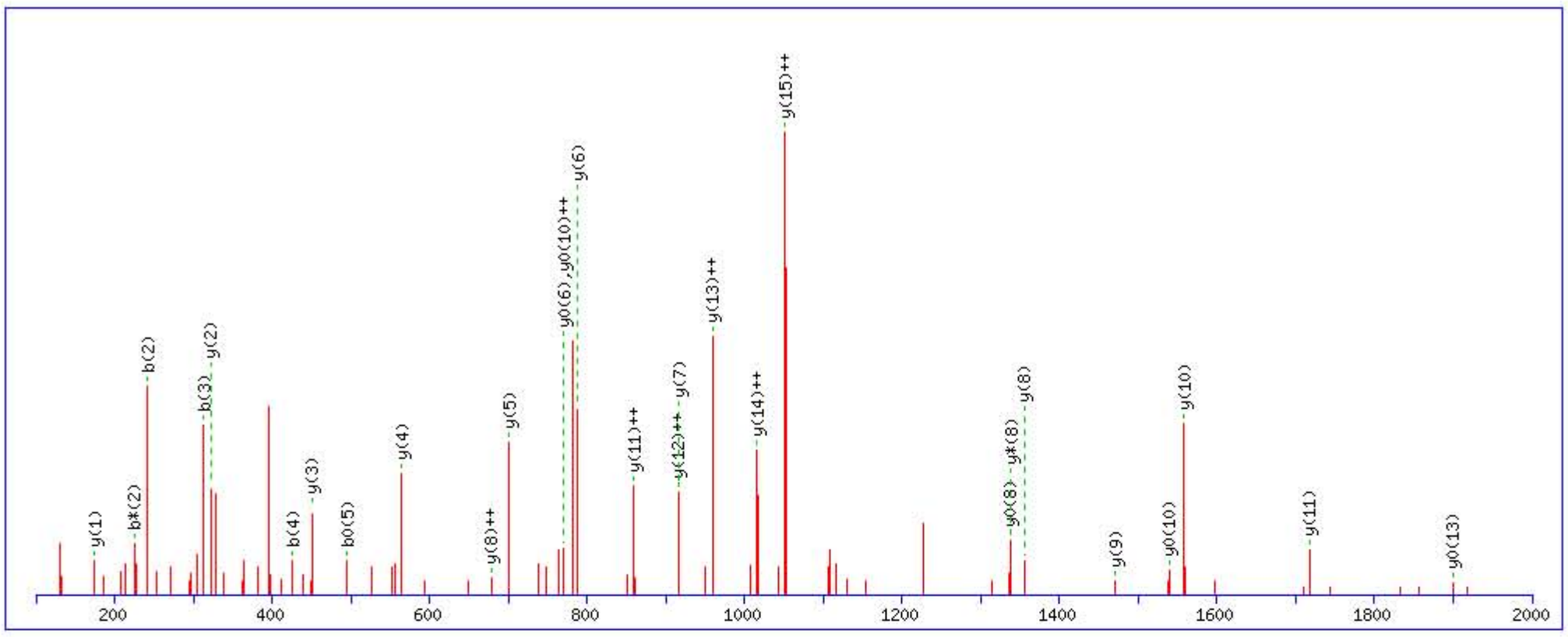
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IQALSLCSDQQSHLEFR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

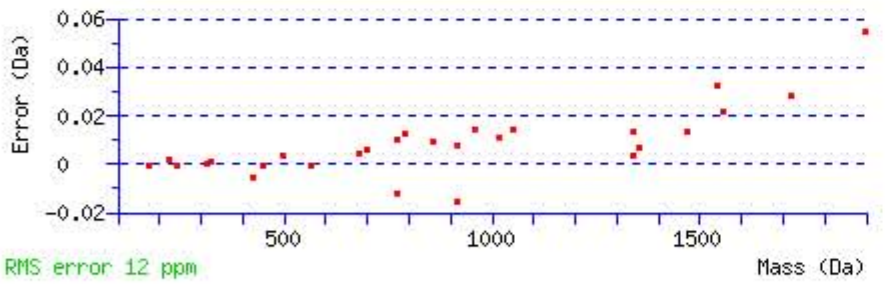
Match to Query 51249: 2342.183682 from(781.735170,3+) rtinseconds(2180) index(51602)
Title: Locus:1.1.1.1996.11 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

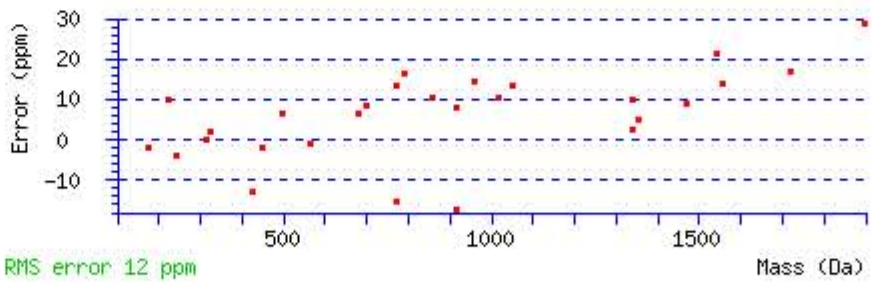
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2342.151108
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 69 **Expect:** 3.7e-006
**Matches :** 28/178 fragment ions using 46 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 17 |
| 2 | **242.149918** | 121.578597 | 225.123369 | 113.065323 | | | Q | 2230.074335 | 1115.540805 | 2213.047786 | 1107.027531 | 2212.063770 | 1106.535523 | 16 |
| 3 | **313.187032** | 157.097154 | 296.160483 | 148.583879 | | | A | 2102.015757 | 1051.511516 | 2084.989208 | 1042.998242 | 2084.005192 | 1042.506234 | 15 |
| 4 | **426.271096** | 213.639186 | 409.244547 | 205.125912 | | | L | 2030.978643 | 1015.992959 | 2013.952094 | 1007.479685 | 2012.968078 | 1006.987677 | 14 |
| 5 | 513.303124 | 257.155200 | 496.276575 | 248.641926 | 495.292559 | 248.149918 | S | 1917.894579 | 959.450927 | 1900.868030 | 950.937653 | 1899.884014 | 950.445645 | 13 |
| 6 | 626.387188 | 313.697232 | 609.360639 | 305.183958 | 608.376623 | 304.691950 | L | 1830.862551 | 915.934913 | 1813.836002 | 907.421639 | 1812.851986 | 906.929631 | 12 |
| 7 | 786.417837 | 393.712557 | 769.391288 | 385.199282 | 768.407272 | 384.707274 | C | *1717.778487* | 859.392881 | 1700.751938 | 850.879607 | 1699.767922 | 850.387599 | 11 |
| 8 | 873.449865 | 437.228571 | 856.423316 | 428.715296 | 855.439300 | 428.223288 | S | *1557.747838* | 779.377557 | 1540.721289 | 770.864282 | 1539.737273 | 770.372274 | 10 |
| 9 | 988.476808 | 494.742042 | 971.450259 | 486.228768 | 970.466243 | 485.736760 | D | *1470.715810* | 735.861543 | 1453.689261 | 727.348268 | 1452.705245 | 726.856260 | 9 |
| 10 | 1427.702134 | 714.354705 | 1410.675585 | 705.841431 | 1409.691569 | 705.349422 | Q | *1355.688867* | 678.348071 | 1338.662318 | 669.834797 | 1337.678302 | 669.342789 | 8 |
| 11 | 1555.760712 | 778.383994 | 1538.734163 | 769.870720 | 1537.750147 | 769.378712 | Q | *916.463541* | 458.735408 | 899.436992 | 450.222134 | 898.452976 | 449.730126 | 7 |
| 12 | 1642.792740 | 821.900008 | 1625.766191 | 813.386734 | 1624.782175 | 812.894726 | S | *788.404963* | 394.706119 | 771.378414 | 386.192845 | 770.394398 | 385.700837 | 6 |
| 13 | 1779.851652 | 890.429464 | 1762.825103 | 881.916190 | 1761.841087 | 881.424182 | H | *701.372935* | 351.190105 | 684.346386 | 342.676831 | 683.362370 | 342.184823 | 5 |
| 14 | 1892.935716 | 946.971496 | 1875.909167 | 938.458222 | 1874.925151 | 937.966213 | L | *564.314023* | 282.660649 | 547.287474 | 274.147375 | 546.303458 | 273.655367 | 4 |
| 15 | 2021.978309 | 1011.492793 | 2004.951760 | 1002.979518 | 2003.967744 | 1002.487510 | E | *451.229959* | 226.118617 | 434.203410 | 217.605343 | 433.219394 | 217.113335 | 3 |
| 16 | 2169.046723 | 1085.026999 | 2152.020174 | 1076.513725 | 2151.036158 | 1076.021717 | F | *322.187366* | 161.597321 | 305.160817 | 153.084046 | | | 2 |
| 17 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 69.0 | 2342.151108 | 0.032574 | IQALSLCSDQQSHLEFR |
| 69.0 | 2342.151108 | 0.032574 | IQALSLCSDQQSHLEFR |
| 3.4 | 2342.151108 | 0.032574 | IQALSLCSDQQSHLEFR |

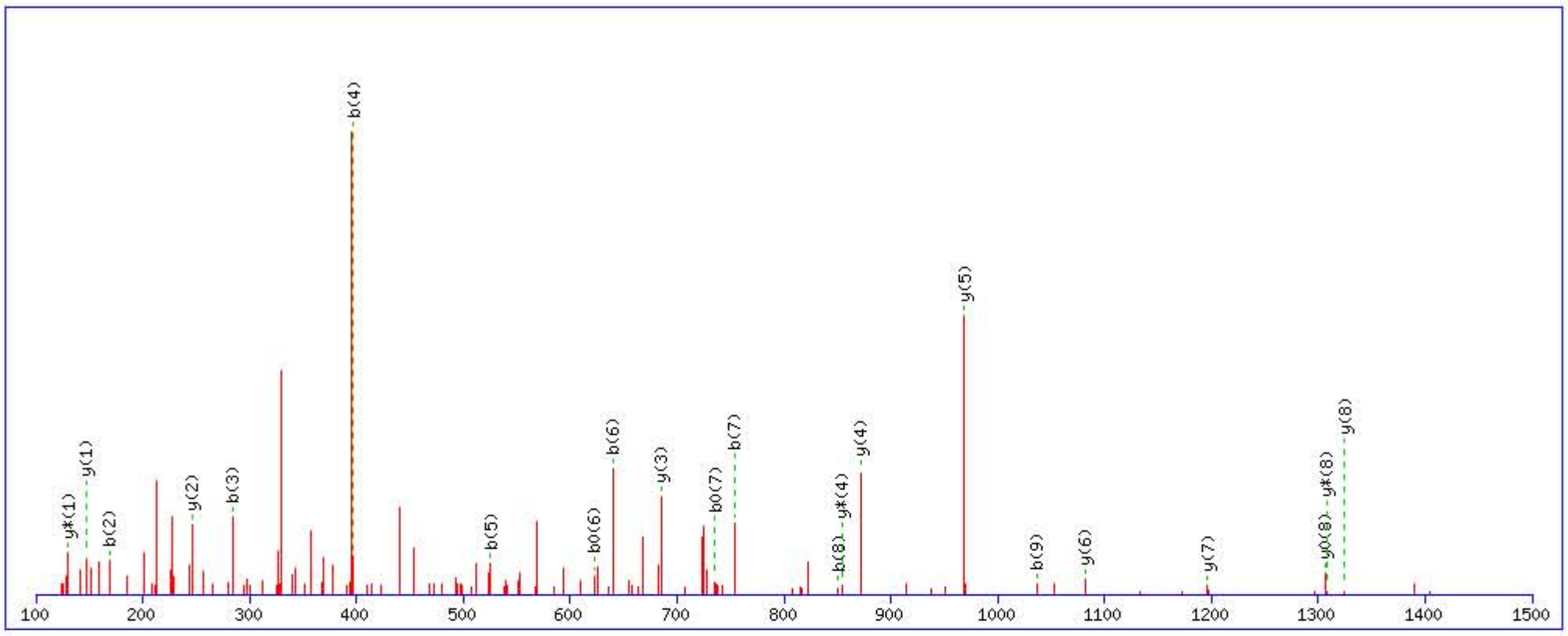
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **APDLQDLPWQVK**
Found in **PROZ_HUMAN**, Vitamin K-dependent protein Z OS=Homo sapiens GN=PROZ PE=1 SV=2

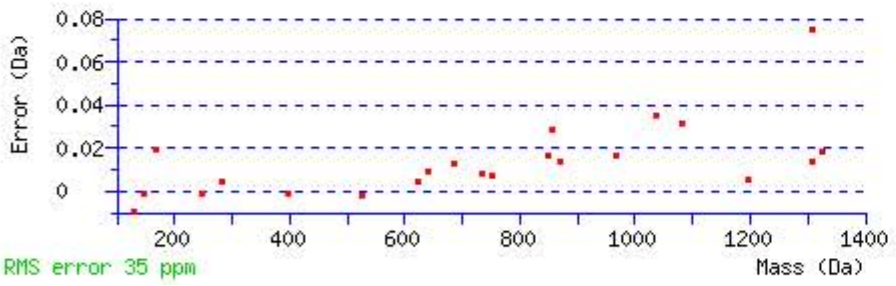
Match to Query 38405: 1719.912042 from(574.311290,3+) rtinseconds(2544) index(53586)
Title: Locus:1.1.1.2123.4 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

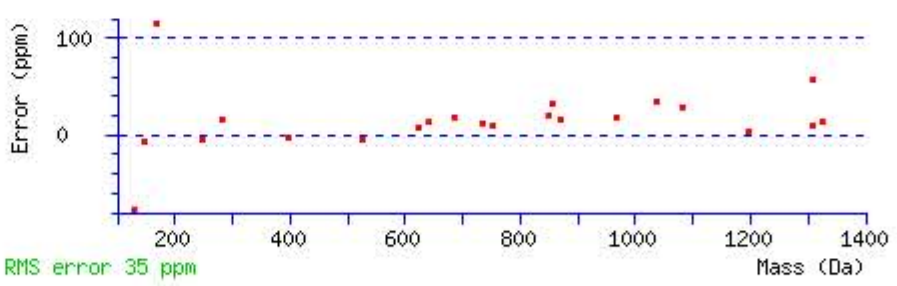
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1719.901810
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q10 : Biotin:Thermo-21345 (Q)
**Ions Score:** 32 **Expect:** 0.0051
**Matches :** 22/108 fragment ions using 58 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 72.044390 | 36.525833 | | | | | A | | | | | | | 12 |
| 2 | *169.097154* | 85.052215 | | | | | P | 1649.871977 | 825.439627 | 1632.845428 | 816.926352 | 1631.861412 | 816.434344 | 11 |
| 3 | *284.124097* | 142.565687 | | | 266.113532 | 133.560404 | D | 1552.819213 | 776.913245 | 1535.792664 | 768.399970 | 1534.808648 | 767.907962 | 10 |
| 4 | *397.208161* | 199.107719 | | | 379.197596 | 190.102436 | L | 1437.792270 | 719.399773 | 1420.765721 | 710.886499 | 1419.781705 | 710.394491 | 9 |
| 5 | *525.266739* | 263.137008 | 508.240190 | 254.623733 | 507.256174 | 254.131725 | Q | *1324.708206* | 662.857741 | 1307.681657 | 654.344467 | 1306.697641 | 653.852459 | 8 |
| 6 | *640.293682* | 320.650479 | 623.267133 | 312.137205 | 622.283117 | 311.645197 | D | *1196.649628* | 598.828452 | 1179.623079 | 590.315178 | 1178.639063 | 589.823170 | 7 |
| 7 | *753.377746* | 377.192511 | 736.351197 | 368.679237 | 735.367181 | 368.187229 | L | *1081.622685* | 541.314981 | 1064.596136 | 532.801706 | | | 6 |
| 8 | *850.430510* | 425.718893 | 833.403961 | 417.205619 | 832.419945 | 416.713611 | P | *968.538621* | 484.772949 | 951.512072 | 476.259674 | | | 5 |
| 9 | *1036.509823* | 518.758550 | 1019.483274 | 510.245275 | 1018.499258 | 509.753267 | W | *871.485857* | 436.246567 | 854.459308 | 427.733292 | | | 4 |
| 10 | 1475.735149 | 738.371213 | 1458.708600 | 729.857938 | 1457.724584 | 729.365930 | Q | *685.406544* | 343.206910 | 668.379995 | 334.693636 | | | 3 |
| 11 | 1574.803563 | 787.905420 | 1557.777014 | 779.392145 | 1556.792998 | 778.900137 | V | *246.181218* | 123.594247 | 229.154669 | 115.080973 | | | 2 |
| 12 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 32.4 | 1719.901810 | 0.010232 | APDLQDLPWQVK |
| 7.7 | 1719.907715 | 0.004327 | VLAGVVMTTGTDVKDAK |
| 3.8 | 1719.897766 | 0.014276 | LVHNKPPTMKPEGEK |

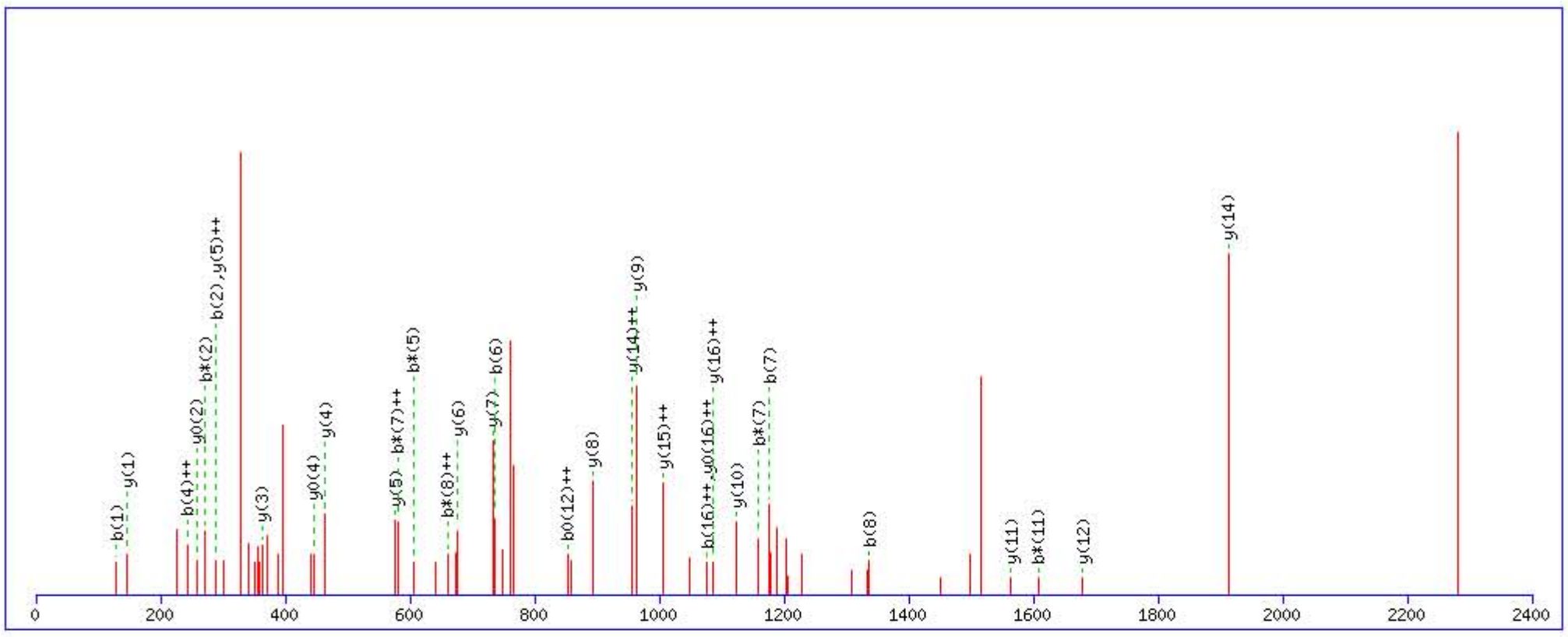
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QCVPHDQCACGVLTSEK**
Found in **PROZ_HUMAN**, Vitamin K-dependent protein Z OS=Homo sapiens GN=PROZ PE=1 SV=2

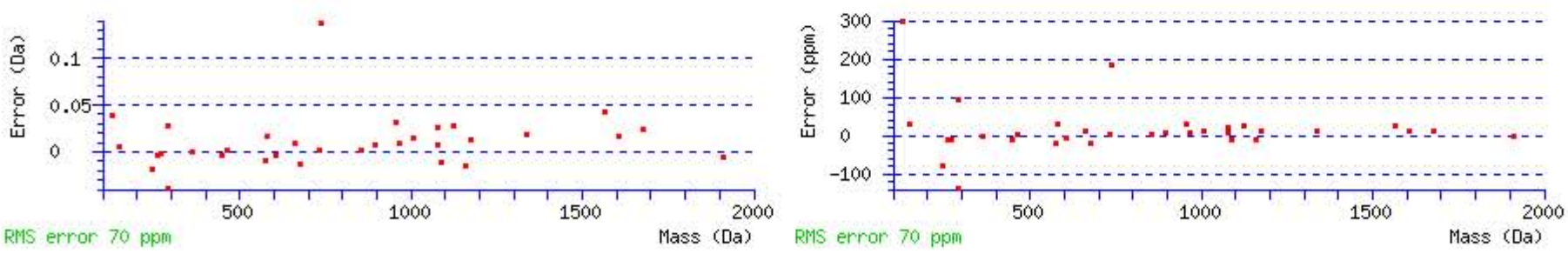
Match to Query 50527: 2299.042722 from(767.354850,3+) rtinseconds(1636) index(47898)
Title: Locus:1.1.1.1807.23 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2299.021790
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q7 : Biotin:Thermo-21345 (Q)
**Ions Score:** 71 **Expect:** 8.6e-007
**Matches :** 33/180 fragment ions using 55 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **129.065854** | 65.036565 | 112.039305 | 56.523291 | | | Q | | | | | | | 17 |
| 2 | **289.096503** | 145.051890 | 272.069954 | 136.538615 | | | C | 2171.970466 | 1086.488871 | 2154.943917 | 1077.975596 | 2153.959901 | 1077.483588 | 16 |
| 3 | 388.164917 | 194.586097 | 371.138368 | 186.072822 | | | V | 2011.939817 | 1006.473547 | 1994.913268 | 997.960272 | 1993.929252 | 997.468264 | 15 |
| 4 | 485.217681 | **243.112479** | 468.191132 | 234.599204 | | | P | *1912.871403* | 956.939340 | 1895.844854 | 948.426065 | 1894.860838 | 947.934057 | 14 |
| 5 | 622.276593 | 311.641935 | 605.250044 | 303.128660 | | | H | 1815.818639 | 908.412958 | 1798.792090 | 899.899683 | 1797.808074 | 899.407675 | 13 |
| 6 | **737.303536** | 369.155406 | 720.276987 | 360.642132 | 719.292971 | 360.150124 | D | *1678.759727* | 839.883502 | 1661.733178 | 831.370227 | 1660.749162 | 830.878219 | 12 |
| 7 | **1176.528862** | 588.768069 | 1159.502313 | 580.254795 | 1158.518297 | 579.762786 | Q | *1563.732784* | 782.370030 | 1546.706235 | 773.856756 | 1545.722219 | 773.364748 | 11 |
| 8 | **1336.559511** | 668.783393 | 1319.532962 | 660.270119 | 1318.548946 | 659.778111 | C | *1124.507458* | 562.757367 | 1107.480909 | 554.244093 | 1106.496893 | 553.752085 | 10 |
| 9 | 1407.596625 | 704.301950 | 1390.570076 | 695.788676 | 1389.586060 | 695.296668 | A | *964.476809* | 482.742043 | 947.450260 | 474.228768 | 946.466244 | 473.736760 | 9 |
| 10 | 1567.627274 | 784.317275 | 1550.600725 | 775.804001 | 1549.616709 | 775.311992 | C | *893.439695* | 447.223486 | 876.413146 | 438.710211 | 875.429130 | 438.218203 | 8 |
| 11 | 1624.648738 | 812.828007 | 1607.622189 | 804.314732 | 1606.638173 | 803.822724 | G | *733.409046* | 367.208161 | 716.382497 | 358.694887 | 715.398481 | 358.202879 | 7 |
| 12 | 1723.717152 | 862.362214 | 1706.690603 | 853.848940 | 1705.706587 | 853.356931 | V | *676.387582* | 338.697429 | 659.361033 | 330.184155 | 658.377017 | 329.692147 | 6 |
| 13 | 1836.801216 | 918.904246 | 1819.774667 | 910.390971 | 1818.790651 | 909.898963 | L | *577.319168* | 289.163222 | 560.292619 | 280.649948 | 559.308603 | 280.157940 | 5 |
| 14 | 1937.848895 | 969.428085 | 1920.822346 | 960.914811 | 1919.838330 | 960.422803 | T | *464.235104* | 232.621190 | 447.208555 | 224.107916 | 446.224539 | 223.615908 | 4 |
| 15 | 2024.880923 | 1012.944100 | 2007.854374 | 1004.430825 | 2006.870358 | 1003.938817 | S | *363.187425* | 182.097351 | 346.160876 | 173.584076 | 345.176860 | 173.092068 | 3 |
| 16 | 2153.923516 | **1077.465396** | 2136.896967 | 1068.952121 | 2135.912951 | 1068.460113 | E | 276.155397 | 138.581337 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 17 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 71.4 | 2299.021790 | 0.020932 | QCVPHDQCACGVLTSEK |
| 35.8 | 2299.021790 | 0.020932 | QCVPHDQCACGVLTSEK |

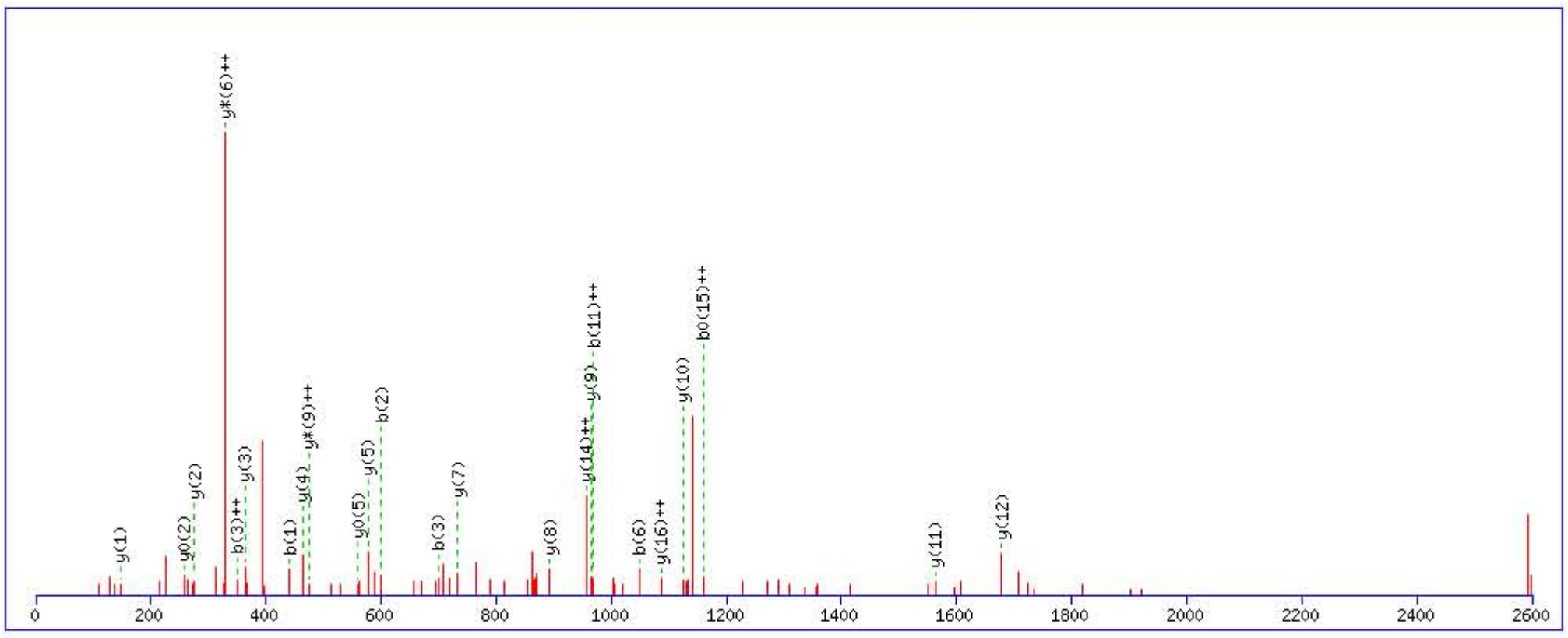
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QCVPHDQCACGVLTSEK**
Found in **PROZ_HUMAN**, Vitamin K-dependent protein Z OS=Homo sapiens GN=PROZ PE=1 SV=2

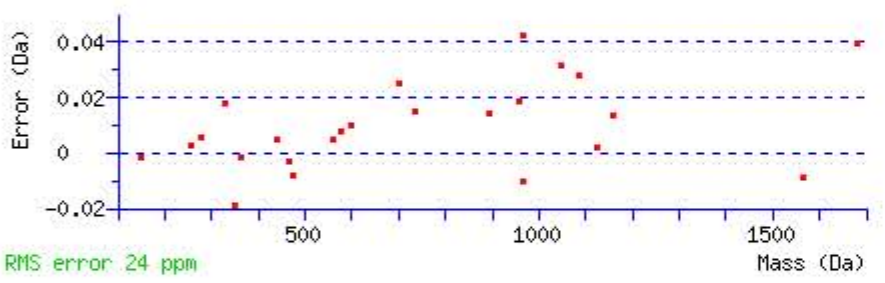
Match to Query 55595: 2610.218172 from(871.080000,3+) rtinseconds(1923) index(49765)
Title: Locus:1.1.1.1907.18 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

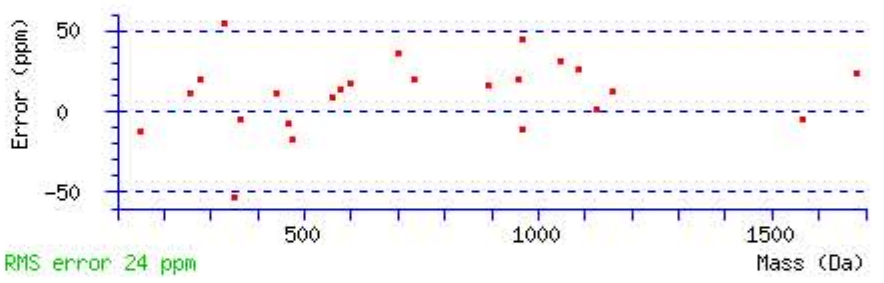
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 2610.188538
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Q7** : Biotin:Thermo-21345 (Q)
**Ions Score:** 30 **Expect:** 0.019
**Matches** : 24/180 fragment ions using 78 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **440.232602** | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 17 |
| 2 | **600.263251** | 300.635264 | 583.236702 | 292.121989 | | | C | 2171.970466 | 1086.488871 | 2154.943917 | 1077.975596 | 2153.959901 | 1077.483588 | 16 |
| 3 | **699.331665** | **350.169471** | 682.305116 | 341.656196 | | | V | 2011.939817 | 1006.473547 | 1994.913268 | 997.960272 | 1993.929252 | 997.468264 | 15 |
| 4 | 796.384429 | 398.695853 | 779.357880 | 390.182578 | | | P | 1912.871403 | 956.939340 | 1895.844854 | 948.426065 | 1894.860838 | 947.934057 | 14 |
| 5 | 933.443341 | 467.225309 | 916.416792 | 458.712034 | | | H | 1815.818639 | 908.412958 | 1798.792090 | 899.899683 | 1797.808074 | 899.407675 | 13 |
| 6 | **1048.470284** | 524.738780 | 1031.443735 | 516.225506 | 1030.459719 | 515.733498 | D | *1678.759727* | 839.883502 | 1661.733178 | 831.370227 | 1660.749162 | 830.878219 | 12 |
| 7 | 1487.695610 | 744.351443 | 1470.669061 | 735.838169 | 1469.685045 | 735.346161 | Q | *1563.732784* | 782.370030 | 1546.706235 | 773.856756 | 1545.722219 | 773.364748 | 11 |
| 8 | 1647.726259 | 824.366768 | 1630.699710 | 815.853493 | 1629.715694 | 815.361485 | C | *1124.507458* | 562.757367 | 1107.480909 | 554.244093 | 1106.496893 | 553.752085 | 10 |
| 9 | 1718.763373 | 859.885325 | 1701.736824 | 851.372050 | 1700.752808 | 850.880042 | A | *964.476809* | 482.742043 | 947.450260 | 474.228768 | 946.466244 | 473.736760 | 9 |
| 10 | 1878.794022 | 939.900649 | 1861.767473 | 931.387375 | 1860.783457 | 930.895367 | C | *893.439695* | 447.223486 | 876.413146 | 438.710211 | 875.429130 | 438.218203 | 8 |
| 11 | 1935.815486 | **968.411381** | 1918.788937 | 959.898107 | 1917.804921 | 959.406098 | G | *733.409046* | 367.208161 | 716.382497 | 358.694887 | 715.398481 | 358.202879 | 7 |
| 12 | 2034.883900 | 1017.945588 | 2017.857351 | 1009.432314 | 2016.873335 | 1008.940306 | V | 676.387582 | 338.697429 | 659.361033 | 330.184155 | 658.377017 | 329.692147 | 6 |
| 13 | 2147.967964 | 1074.487620 | 2130.941415 | 1065.974345 | 2129.957399 | 1065.482337 | L | *577.319168* | 289.163222 | 560.292619 | 280.649948 | 559.308603 | 280.157940 | 5 |
| 14 | 2249.015643 | 1125.011459 | 2231.989094 | 1116.498185 | 2231.005078 | 1116.006177 | T | *464.235104* | 232.621190 | 447.208555 | 224.107915 | 446.224539 | 223.615907 | 4 |
| 15 | 2336.047671 | 1168.527473 | 2319.021122 | 1160.014199 | 2318.037106 | 1159.522191 | S | *363.187425* | 182.097351 | 346.160876 | 173.584076 | 345.176860 | 173.092068 | 3 |
| 16 | 2465.090264 | 1233.048770 | 2448.063715 | 1224.535495 | 2447.079699 | 1224.043487 | E | *276.155397* | 138.581337 | 259.128848 | 130.068062 | 258.144832 | 129.576054 | 2 |
| 17 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 29.6 | 2610.188538 | 0.029634 | QCVPHDQCACGVLTSEK |

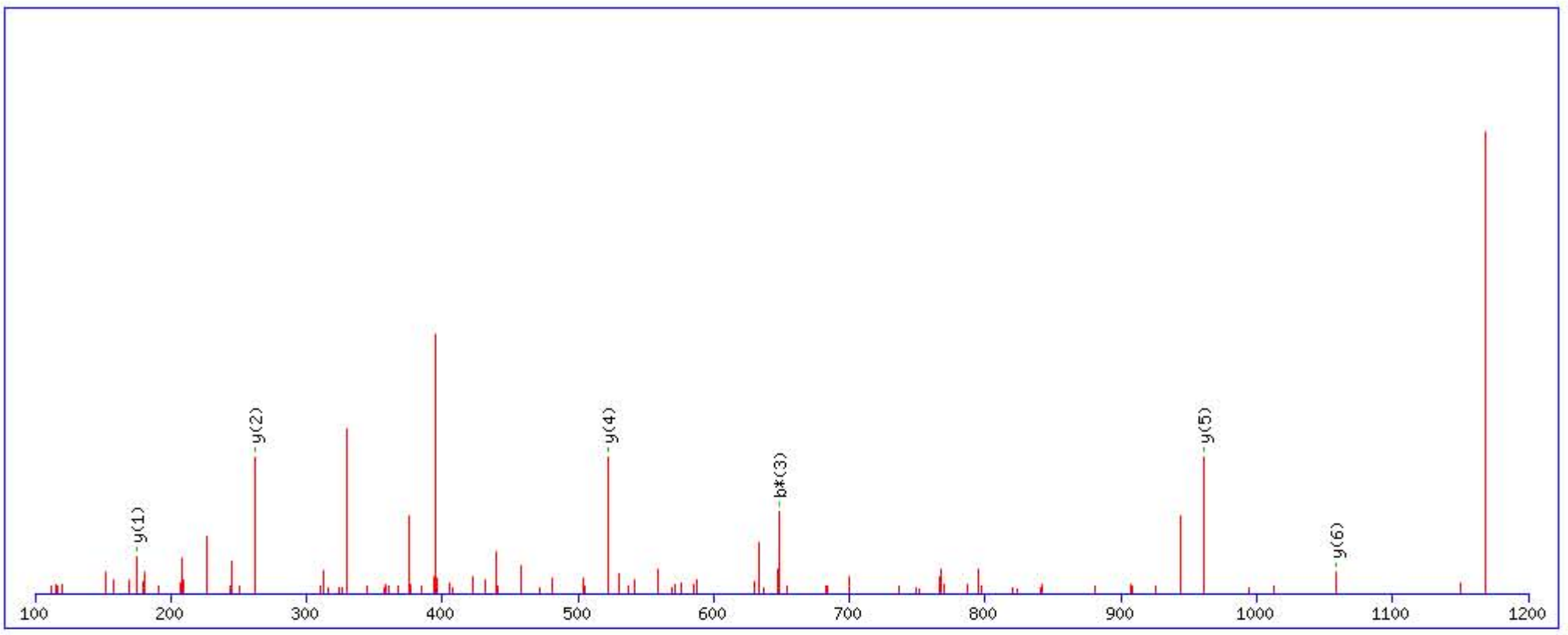
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QPQFISR**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

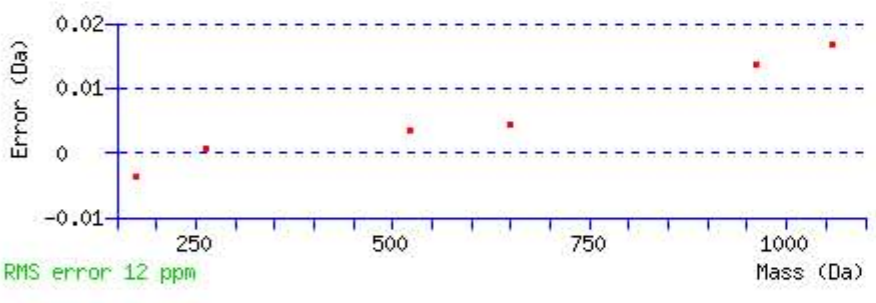
Match to Query 20206: 1185.638728 from(593.826640,2+) rtinseconds(1761) index(48714)
Title: Locus:1.1.1.1851.5 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

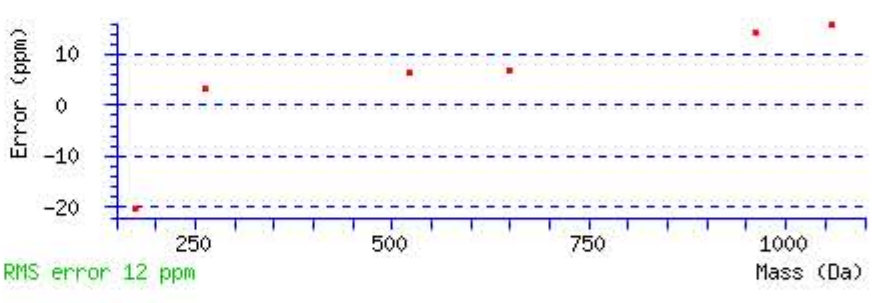
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1185.632843
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 31 **Expect:** 0.02
**Matches :** 6/60 fragment ions using 11 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 129.065854 | 65.036565 | 112.039305 | 56.523291 | | | Q | | | | | | | 7 |
| 2 | 226.118618 | 113.562947 | 209.092069 | 105.049673 | | | P | *1058.581548* | 529.794412 | 1041.554999 | 521.281138 | 1040.570983 | 520.789129 | 6 |
| 3 | 665.343944 | 333.175610 | 648.317395 | 324.662336 | | | Q | *961.528784* | 481.268030 | 944.502235 | 472.754755 | 943.518219 | 472.262747 | 5 |
| 4 | 812.412358 | 406.709817 | 795.385809 | 398.196543 | | | F | *522.303458* | 261.655367 | 505.276909 | 253.142092 | 504.292893 | 252.650084 | 4 |
| 5 | 925.496422 | 463.251849 | 908.469873 | 454.738575 | | | I | 375.235044 | 188.121160 | 358.208495 | 179.607885 | 357.224479 | 179.115877 | 3 |
| 6 | 1012.528450 | 506.767863 | 995.501901 | 498.254589 | 994.517885 | 497.762581 | S | *262.150980* | 131.579128 | 245.124431 | 123.065853 | 244.140415 | 122.573845 | 2 |
| 7 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 30.9 | 1185.632843 | 0.005885 | QPQFISR |
| 18.4 | 1185.646561 | -0.007833 | KPIDSLRDSR |
| 12.9 | 1185.632843 | 0.005885 | QPQFISR |
| 11.8 | 1185.653961 | -0.015233 | LSGALPLCLSR |
| 8.4 | 1185.650604 | -0.011876 | KPVTENVPFR |
| 6.6 | 1185.636200 | 0.002528 | QIAAVMSR |
| 5.6 | 1185.653961 | -0.015233 | ILTASQSR |
| 5.4 | 1185.646561 | -0.007833 | APSAKKPSTGSR |
| 4.5 | 1185.653976 | -0.015248 | TQITLGSR |
| 4.2 | 1185.628799 | 0.009929 | SGKMAPKPQSR |

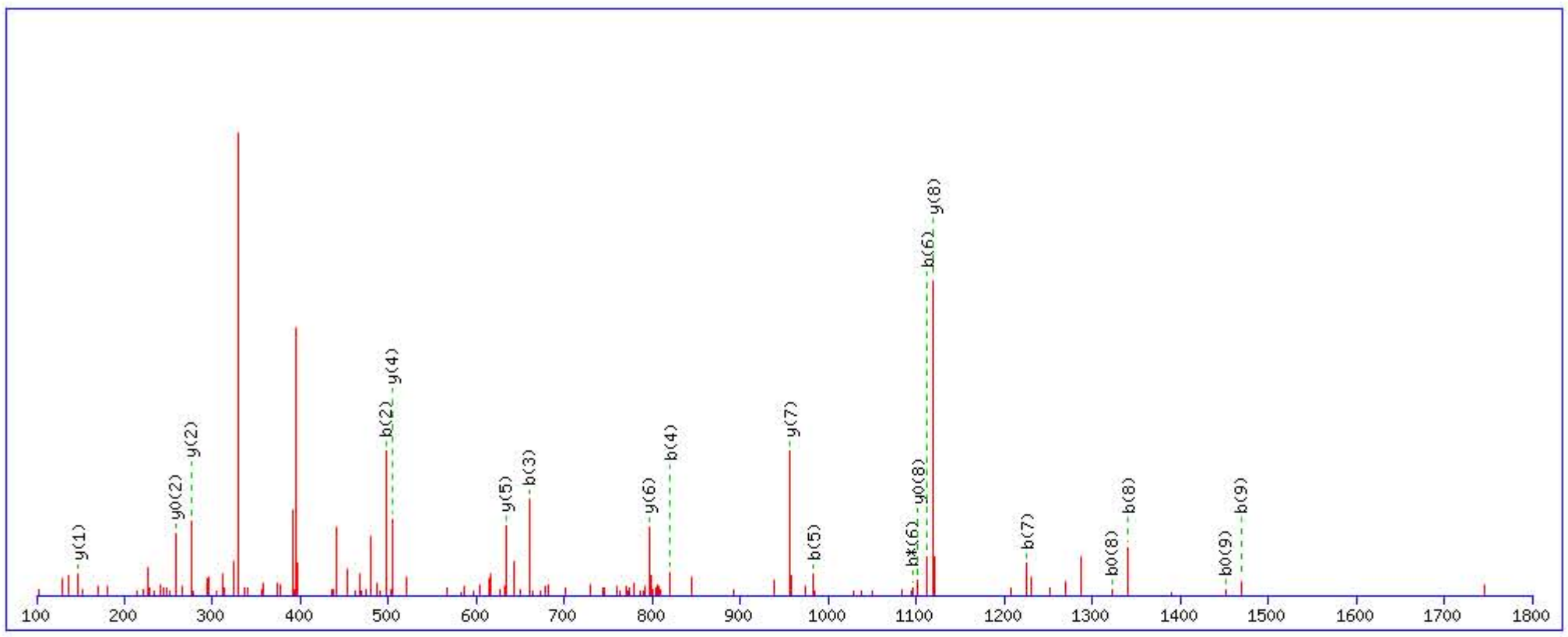
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GQYCYELDEK**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

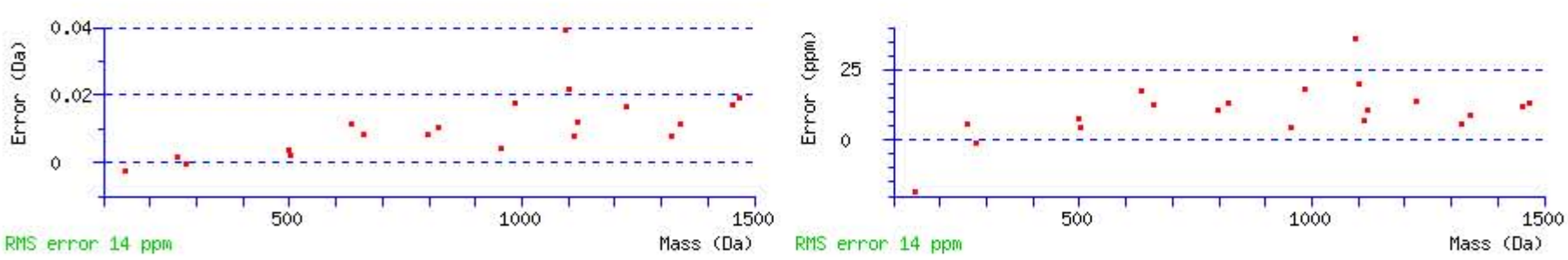
Match to Query 35238: 1614.726548 from(808.370550,2+) rtinseconds(1883) index(33331)
Title: Locus:1.1.1.764.20 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1614.705795
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q2 : Biotin:Thermo-21345 (Q)
**Ions Score:** 59 **Expect:** 8.1e-006
**Matches :** 20/94 fragment ions using 28 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 10 |
| 2 | *497.254066* | 249.130671 | 480.227517 | 240.617397 | | | Q | 1558.691630 | 779.849453 | 1541.665081 | 771.336179 | 1540.681065 | 770.844171 | 9 |
| 3 | *660.317395* | 330.662336 | 643.290846 | 322.149061 | | | Y | **1119.466304** | 560.236790 | 1102.439755 | 551.723516 | **1101.455739** | 551.231508 | 8 |
| 4 | *820.348044* | 410.677660 | 803.321495 | 402.164386 | | | C | **956.402975** | 478.705126 | 939.376426 | 470.191851 | 938.392410 | 469.699843 | 7 |
| 5 | *983.411373* | 492.209325 | 966.384824 | 483.696050 | | | Y | **796.372326** | 398.689801 | 779.345777 | 390.176527 | 778.361761 | 389.684519 | 6 |
| 6 | *1112.453966* | 556.730621 | **1095.427417** | 548.217347 | 1094.443401 | 547.725339 | E | **633.308997** | 317.158137 | 616.282448 | 308.644862 | 615.298432 | 308.152854 | 5 |
| 7 | *1225.538030* | 613.272653 | 1208.511481 | 604.759379 | 1207.527465 | 604.267371 | L | **504.266404** | 252.636840 | 487.239855 | 244.123566 | 486.255839 | 243.631558 | 4 |
| 8 | *1340.564973* | 670.786125 | 1323.538424 | 662.272850 | **1322.554408** | 661.780842 | D | 391.182340 | 196.094808 | 374.155791 | 187.581534 | 373.171775 | 187.089526 | 3 |
| 9 | *1469.607566* | 735.307421 | 1452.581017 | 726.794147 | **1451.597001** | 726.302139 | E | **276.155397** | 138.581337 | 259.128848 | 130.068062 | **258.144832** | 129.576054 | 2 |
| 10 | | | | | | | K | **147.112804** | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.9 | 1614.705795 | 0.020753 | GQYCYELDEK |
| 12.4 | 1614.748520 | -0.021972 | TRAPAEEGAEGPSDTK |
| 7.2 | 1614.717010 | 0.009538 | EYFRMELMHAEK |
| 2.0 | 1614.748535 | -0.021987 | VDNSSLTGESEPQPR |
| 1.7 | 1614.719528 | 0.007020 | KDMYNDTLNGSTEK |
| 1.1 | 1614.738129 | -0.011581 | EKAKADAECYTAMK |
| 0.5 | 1614.702667 | 0.023881 | LWCCTGNSIMVMK |

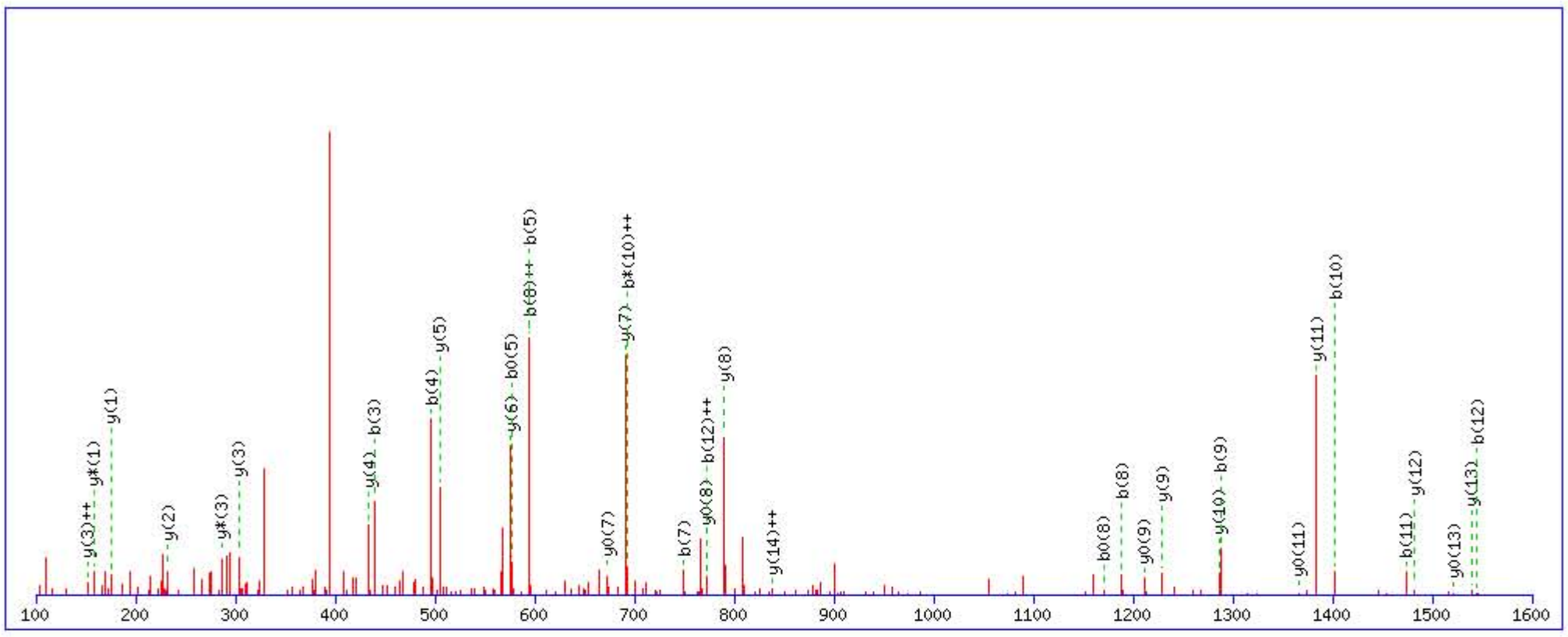
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **DWHGVPGQVDAAMAGR**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

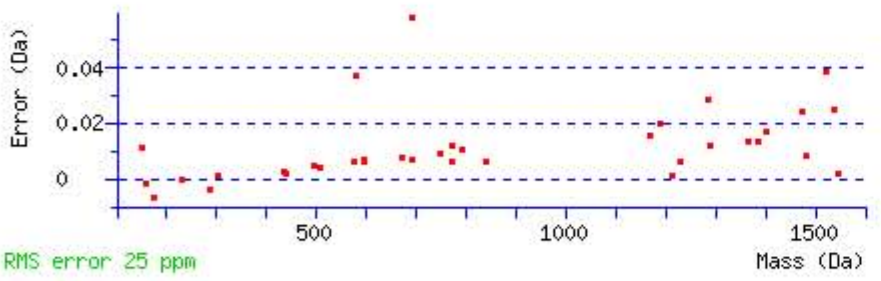
Match to Query 43693: 1976.955702 from(659.992510,3+) rtinseconds(2159) index(51454)
Title: Locus:1.1.1.1989.10 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

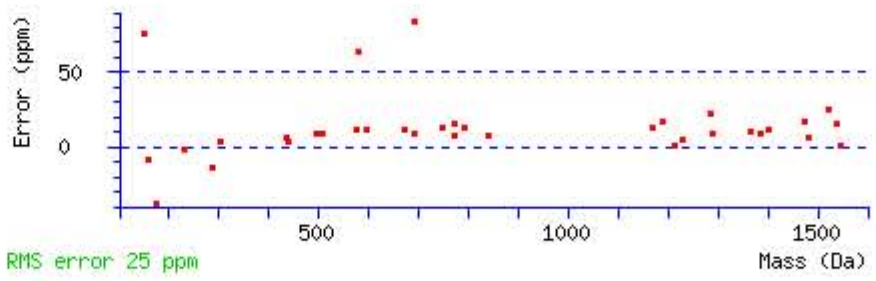
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1976.934937
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 58 **Expect:** 4.2e-006
**Matches :** 36/154 fragment ions using 95 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 116.034219 | 58.520748 | | | 98.023654 | 49.515465 | D | | | | | | | 16 |
| 2 | 302.113532 | 151.560404 | | | 284.102967 | 142.555122 | W | 1862.915257 | 931.961266 | 1845.888708 | 923.447992 | 1844.904692 | 922.955984 | 15 |
| 3 | **439.172444** | 220.089860 | | | 421.161879 | 211.084577 | H | 1676.835944 | 838.921610 | 1659.809395 | 830.408336 | 1658.825379 | 829.916327 | 14 |
| 4 | **496.193908** | 248.600592 | | | 478.183343 | 239.595309 | G | *1539.777032* | 770.392154 | 1522.750483 | 761.878880 | 1521.766467 | 761.386871 | 13 |
| 5 | **595.262322** | 298.134799 | | | 577.251757 | 289.129517 | V | *1482.755568* | 741.881422 | 1465.729019 | 733.368148 | 1464.745003 | 732.876140 | 12 |
| 6 | 692.315086 | 346.661181 | | | 674.304521 | 337.655899 | P | *1383.687154* | 692.347215 | 1366.660605 | 683.833941 | 1365.676589 | 683.341932 | 11 |
| 7 | **749.336550** | 375.171913 | | | 731.325985 | 366.166631 | G | *1286.634390* | 643.820833 | 1269.607841 | 635.307559 | 1268.623825 | 634.815550 | 10 |
| 8 | **1188.561876** | **594.784576** | 1171.535327 | 586.271302 | 1170.551311 | 585.779293 | Q | *1229.612926* | 615.310101 | 1212.586377 | 606.796827 | 1211.602361 | 606.304819 | 9 |
| 9 | **1287.630290** | 644.318783 | 1270.603741 | 635.805509 | 1269.619725 | 635.313501 | V | *790.387600* | 395.697438 | 773.361051 | 387.184164 | 772.377035 | 386.692156 | 8 |
| 10 | **1402.657233** | 701.832255 | 1385.630684 | 693.318980 | 1384.646668 | 692.826972 | D | *691.319186* | 346.163231 | 674.292637 | 337.649956 | 673.308621 | 337.157948 | 7 |
| 11 | **1473.694347** | 737.350812 | 1456.667798 | 728.837537 | 1455.683782 | 728.345529 | A | *576.292243* | 288.649759 | 559.265694 | 280.136485 | | | 6 |
| 12 | **1544.731461** | **772.869369** | 1527.704912 | 764.356094 | 1526.720896 | 763.864086 | A | *505.255129* | 253.131202 | 488.228580 | 244.617928 | | | 5 |
| 13 | 1675.771946 | 838.389611 | 1658.745397 | 829.876337 | 1657.761381 | 829.384329 | M | *434.218015* | 217.612645 | 417.191466 | 209.099371 | | | 4 |
| 14 | 1746.809060 | 873.908168 | 1729.782511 | 865.394894 | 1728.798495 | 864.902886 | A | *303.177530* | 152.092403 | 286.150981 | 143.579128 | | | 3 |
| 15 | 1803.830524 | 902.418900 | 1786.803975 | 893.905626 | 1785.819959 | 893.413617 | G | *232.140416* | 116.573846 | 215.113867 | 108.060571 | | | 2 |
| 16 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 58.0 | 1976.934937 | 0.020765 | DWHGVPGQVDAAMAGR |
| 0.8 | 1976.959854 | -0.004152 | HLTSRHQEAEMAQNAVR |

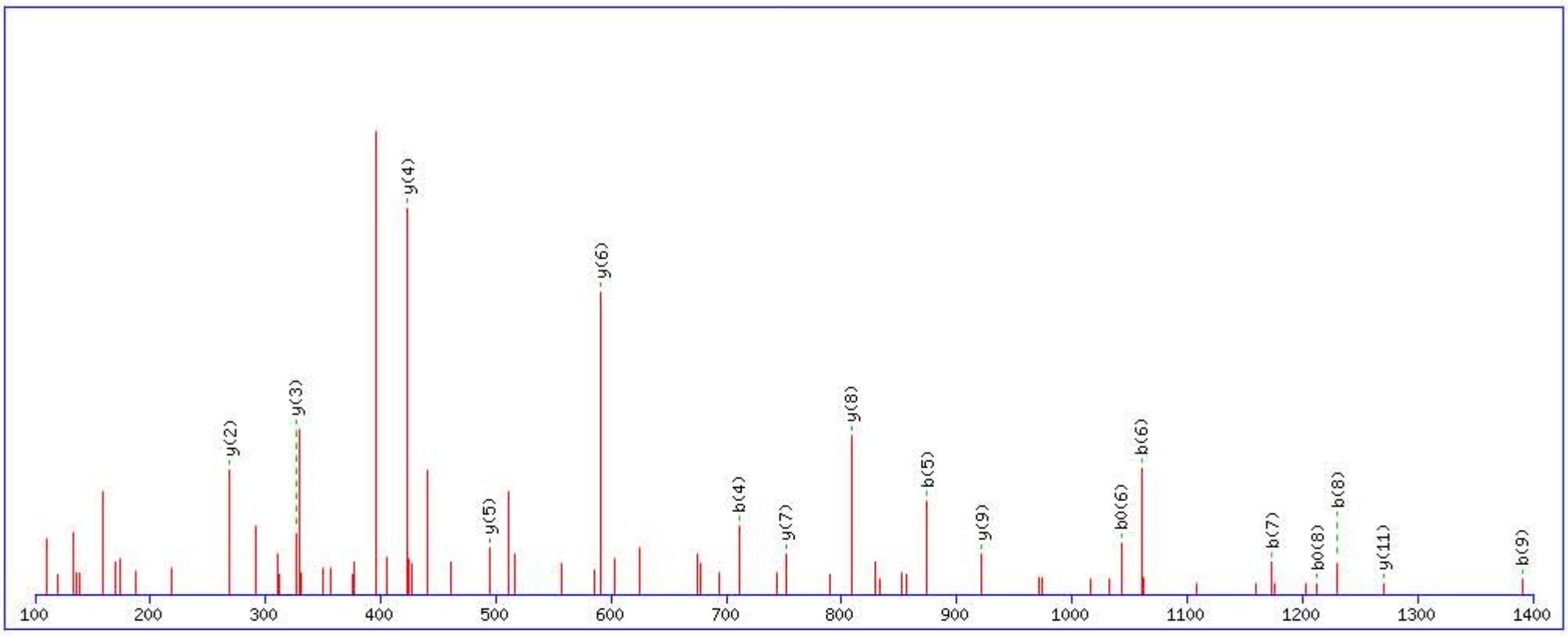
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SIAQYWLGCPAPGHL**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

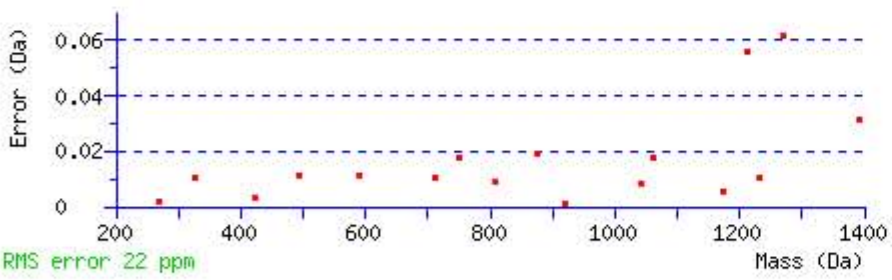
Match to Query 43753: 1979.995962 from(661.005930,3+) rtinseconds(2648) index(54278)
Title: Locus:1.1.1.2159.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

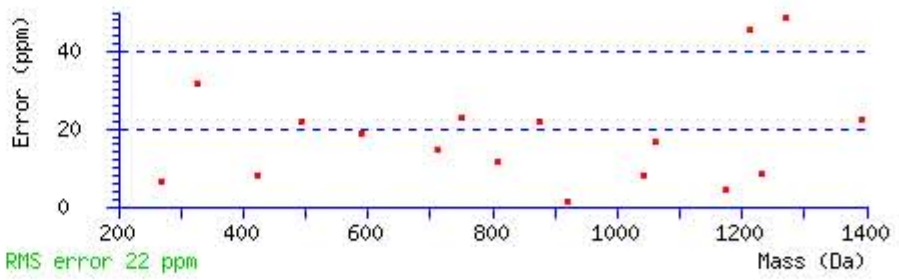
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1979.974991
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 46 **Expect:** 0.00071
**Matches :** 17/112 fragment ions using 37 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 88.039304 | 44.523290 | | | 70.028739 | 35.518008 | S | | | | | 15 |
| 2 | 201.123368 | 101.065322 | | | 183.112803 | 92.060039 | I | 1893.950246 | 947.478761 | 1876.923697 | 938.965486 | 14 |
| 3 | 272.160482 | 136.583879 | | | 254.149917 | 127.578596 | A | 1780.866182 | 890.936729 | 1763.839633 | 882.423454 | 13 |
| 4 | **711.385808** | 356.196542 | 694.359259 | 347.683268 | 693.375243 | 347.191260 | Q | 1709.829068 | 855.418172 | 1692.802519 | 846.904897 | 12 |
| 5 | **874.449137** | 437.728207 | 857.422588 | 429.214932 | 856.438572 | 428.722924 | Y | *1270.603742* | 635.805509 | | | 11 |
| 6 | **1060.528450** | 530.767863 | 1043.501901 | 522.254589 | 1042.517885 | 521.762581 | W | 1107.540413 | 554.273844 | | | 10 |
| 7 | **1173.612514** | 587.309895 | 1156.585965 | 578.796621 | 1155.601949 | 578.304612 | L | *921.461100* | 461.234188 | | | 9 |
| 8 | **1230.633978** | 615.820627 | 1213.607429 | 607.307352 | 1212.623413 | 606.815344 | G | *808.377036* | 404.692156 | | | 8 |
| 9 | **1390.664627** | 695.835951 | 1373.638078 | 687.322677 | 1372.654062 | 686.830669 | C | *751.355572* | 376.181424 | | | 7 |
| 10 | 1487.717391 | 744.362333 | 1470.690842 | 735.849059 | 1469.706826 | 735.357051 | P | *591.324923* | 296.166099 | | | 6 |
| 11 | 1558.754505 | 779.880890 | 1541.727956 | 771.367616 | 1540.743940 | 770.875608 | A | *494.272159* | 247.639717 | | | 5 |
| 12 | 1655.807269 | 828.407272 | 1638.780720 | 819.893998 | 1637.796704 | 819.401990 | P | *423.235045* | 212.121160 | | | 4 |
| 13 | 1712.828733 | 856.918004 | 1695.802184 | 848.404730 | 1694.818168 | 847.912722 | G | *326.182281* | 163.594778 | | | 3 |
| 14 | 1849.887645 | 925.447460 | 1832.861096 | 916.934186 | 1831.877080 | 916.442178 | H | *269.160817* | 135.084046 | | | 2 |
| 15 | | | | | | | L | 132.101905 | 66.554590 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 45.9 | 1979.974991 | 0.020971 | SIAQYWLGCPAPGHL |

**Mascot:** http://www.matrixscience.com/

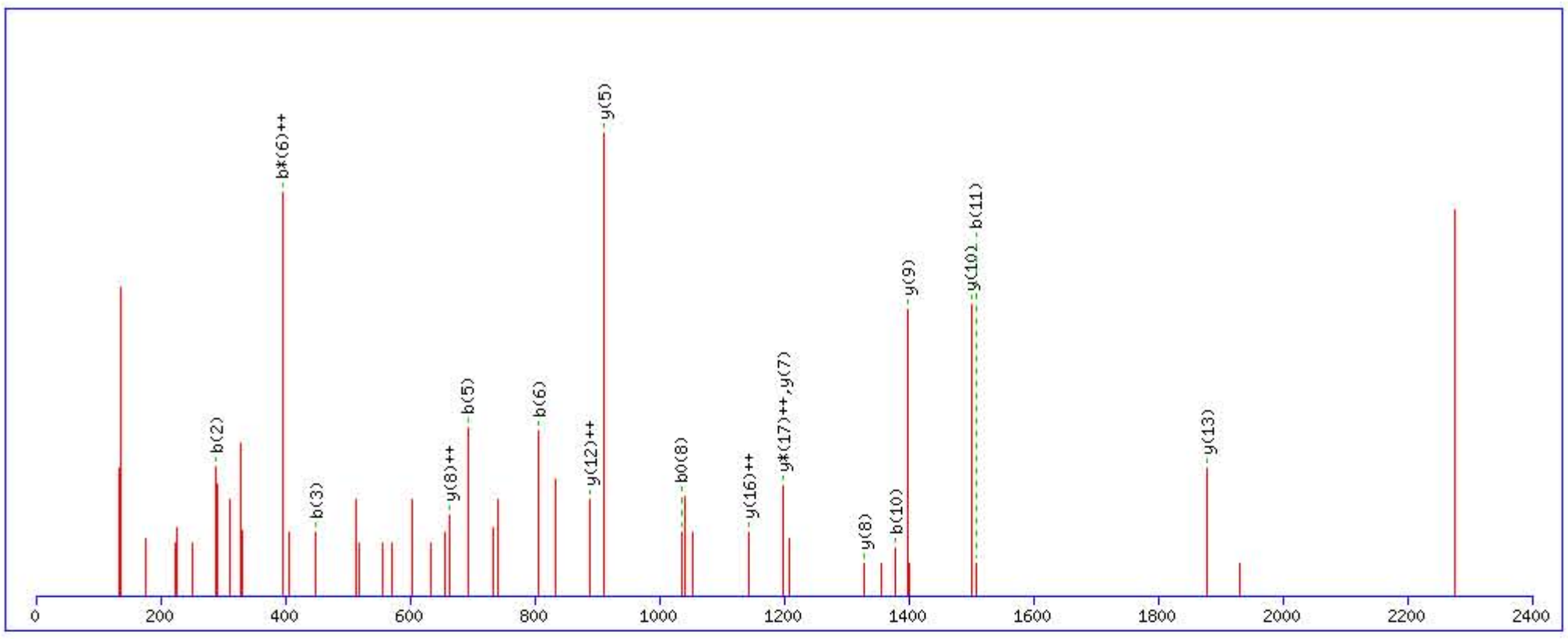
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **CQCDELCSYYQSCCTDYTAECKPQVTR**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

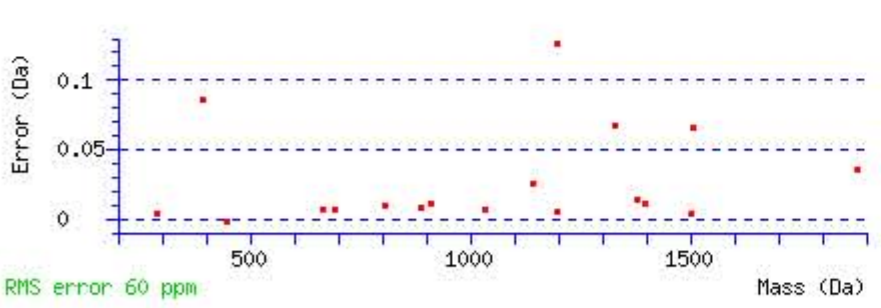
Match to Query 67565: 3792.558470 from(759.518970,5+) rtinseconds(1950) index(49989)
Title: Locus:1.1.1.1916.22 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

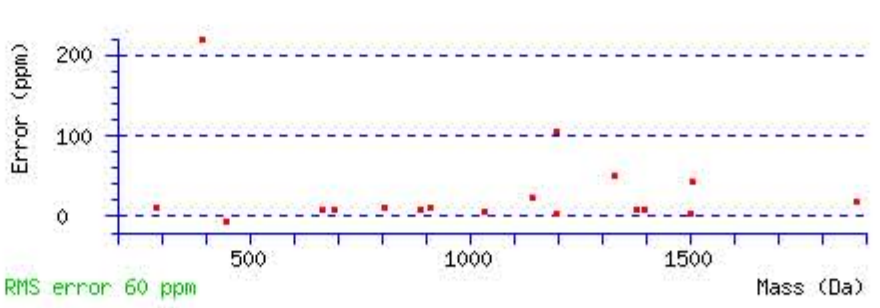
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 3792.511536
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q24 : Biotin:Thermo-21345 (Q)
**Ions Score:** 40 **Expect:** 0.00011
**Matches :** 18/302 fragment ions using 28 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^{0}$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^{0}$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 161.037925 | 81.022600 | | | | | C | | | | | | | 27 |
| 2 | *289.096503* | 145.051890 | 272.069954 | 136.538615 | | | Q | 3633.488150 | 1817.247713 | 3616.461601 | 1808.734438 | 3615.477585 | 1808.242431 | 26 |
| 3 | *449.127152* | 225.067214 | 432.100603 | 216.553940 | | | C | 3505.429572 | 1753.218424 | 3488.403023 | 1744.705149 | 3487.419007 | 1744.213141 | 25 |
| 4 | 564.154095 | 282.580686 | 547.127546 | 274.067411 | 546.143530 | 273.575403 | D | 3345.398923 | 1673.203099 | 3328.372374 | 1664.689825 | 3327.388358 | 1664.197817 | 24 |
| 5 | *693.196688* | 347.101982 | 676.170139 | 338.588708 | 675.186123 | 338.096700 | E | 3230.371980 | 1615.689628 | 3213.345431 | 1607.176353 | 3212.361415 | 1606.684345 | 23 |
| 6 | *806.280752* | 403.644014 | 789.254203 | 395.130740 | 788.270187 | 394.638732 | L | 3101.329387 | 1551.168331 | 3084.302838 | 1542.655057 | 3083.318822 | 1542.163049 | 22 |
| 7 | 966.311401 | 483.659339 | 949.284852 | 475.146064 | 948.300836 | 474.654056 | C | 2988.245323 | 1494.626299 | 2971.218774 | 1486.113025 | 2970.234758 | 1485.621017 | 21 |
| 8 | 1053.343429 | 527.175353 | 1036.316880 | 518.662078 | 1035.332864 | 518.170070 | S | 2828.214674 | 1414.610975 | 2811.188125 | 1406.097700 | 2810.204109 | 1405.605692 | 20 |
| 9 | 1216.406758 | 608.707017 | 1199.380209 | 600.193743 | 1198.396193 | 599.701735 | Y | 2741.182646 | 1371.094961 | 2724.156097 | 1362.581686 | 2723.172081 | 1362.089678 | 19 |
| 10 | *1379.470087* | 690.238682 | 1362.443538 | 681.725407 | 1361.459522 | 681.233399 | Y | 2578.119317 | 1289.563296 | 2561.092768 | 1281.050022 | 2560.108752 | 1280.558014 | 18 |
| 11 | *1507.528665* | 754.267971 | 1490.502116 | 745.754696 | 1489.518100 | 745.262688 | Q | 2415.055988 | 1208.031632 | 2398.029439 | 1199.518357 | 2397.045423 | 1199.026349 | 17 |
| 12 | 1594.560693 | 797.783985 | 1577.534144 | 789.270710 | 1576.550128 | 788.778702 | S | 2286.997410 | 1144.002343 | 2269.970861 | 1135.489068 | 2268.986845 | 1134.997060 | 16 |
| 13 | 1754.591342 | 877.799309 | 1737.564793 | 869.286035 | 1736.580777 | 868.794027 | C | 2199.965382 | 1100.486329 | 2182.938833 | 1091.973054 | 2181.954817 | 1091.481046 | 15 |
| 14 | 1914.621991 | 957.814634 | 1897.595442 | 949.301359 | 1896.611426 | 948.809351 | C | 2039.934733 | 1020.471005 | 2022.908184 | 1011.957730 | 2021.924168 | 1011.465722 | 14 |
| 15 | 2015.669670 | 1008.338473 | 1998.643121 | 999.825199 | 1997.659105 | 999.333191 | T | *1879.904084* | 940.455680 | 1862.877535 | 931.942406 | 1861.893519 | 931.450398 | 13 |
| 16 | 2130.696613 | 1065.851945 | 2113.670064 | 1057.338670 | 2112.686048 | 1056.846662 | D | 1778.856405 | 889.931841 | 1761.829856 | 881.418566 | 1760.845840 | 880.926558 | 12 |
| 17 | 2293.759942 | 1147.383609 | 2276.733393 | 1138.870335 | 2275.749377 | 1138.378327 | Y | 1663.829462 | 832.418369 | 1646.802913 | 823.905095 | 1645.818897 | 823.413086 | 11 |
| 18 | 2394.807621 | 1197.907449 | 2377.781072 | 1189.394174 | 2376.797056 | 1188.902166 | T | *1500.766133* | 750.886704 | 1483.739584 | 742.373430 | 1482.755568 | 741.881422 | 10 |
| 19 | 2465.844735 | 1233.426006 | 2448.818186 | 1224.912731 | 2447.834170 | 1224.420723 | A | *1399.718454* | 700.362865 | 1382.691905 | 691.849591 | 1381.707889 | 691.357583 | 9 |
| 20 | 2594.887328 | 1297.947302 | 2577.860779 | 1289.434028 | 2576.876763 | 1288.942020 | E | *1328.681340* | 664.844308 | 1311.654791 | 656.331033 | 1310.670775 | 655.839025 | 8 |
| 21 | 2754.917977 | 1377.962627 | 2737.891428 | 1369.449352 | 2736.907412 | 1368.957344 | C | *1199.638747* | 600.323011 | 1182.612198 | 591.809737 | 1181.628182 | 591.317729 | 7 |
| 22 | 2883.012940 | 1442.010108 | 2865.986391 | 1433.496834 | 2865.002375 | 1433.004826 | K | 1039.608098 | 520.307687 | 1022.581549 | 511.794412 | 1021.597533 | 511.302404 | 6 |
| 23 | 2980.065704 | 1490.536490 | 2963.039155 | 1482.023216 | 2962.055139 | 1481.531208 | P | *911.513135* | 456.260205 | 894.486586 | 447.746931 | 893.502570 | 447.254923 | 5 |
| 24 | 3419.291030 | 1710.149153 | 3402.264481 | 1701.635879 | 3401.280465 | 1701.143871 | Q | 814.460371 | 407.733823 | 797.433822 | 399.220549 | 796.449806 | 398.728541 | 4 |
| 25 | 3518.359444 | 1759.683360 | 3501.332895 | 1751.170086 | 3500.348879 | 1750.678078 | V | 375.235045 | 188.121160 | 358.208496 | 179.607886 | 357.224480 | 179.115878 | 3 |
| 26 | 3619.407123 | 1810.207200 | 3602.380574 | 1801.693925 | 3601.396558 | 1801.201917 | T | 276.166631 | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 27 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 39.7 | 3792.511536 | 0.046934 | CQCDELCSYYQSCCTDYTAECKPQVTR |
| 5.6 | 3792.511536 | 0.046934 | CQCDELCSYYQSCCTDYTAECKPQVTR |

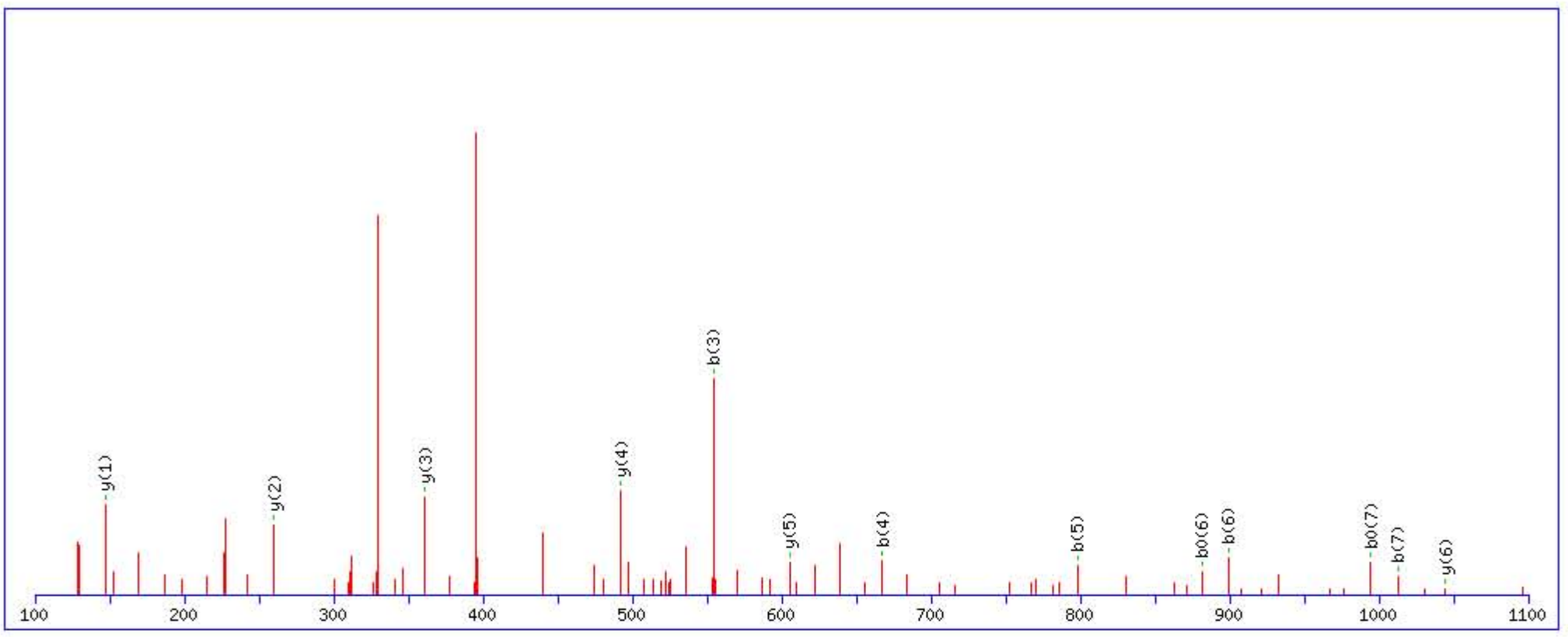
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **GGQIMTLK**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

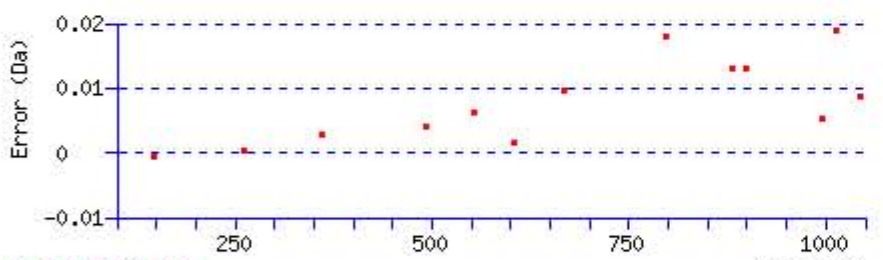
Match to Query 19146: 1157.637348 from(579.825950,2+) rtinseconds(1922) index(49756)
Title: Locus:1.1.1.1907.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

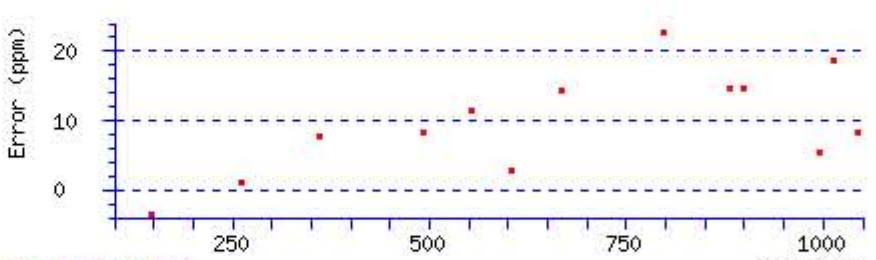
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1157.630066
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q3 : Biotin:Thermo-21345 (Q)
**Ions Score:** 26 **Expect:** 0.046
**Matches :** 13/66 fragment ions using 30 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 58.028740 | 29.518008 | | | | | G | | | | | | | 8 |
| 2 | 115.050204 | 58.028740 | | | | | G | 1101.615886 | 551.311581 | 1084.589337 | 542.798307 | 1083.605321 | 542.306299 | 7 |
| 3 | **554.275530** | 277.641403 | 537.248981 | 269.128129 | | | Q | *1044.594422* | 522.800849 | 1027.567873 | 514.287575 | 1026.583857 | 513.795567 | 6 |
| 4 | **667.359594** | 334.183435 | 650.333045 | 325.670161 | | | I | *605.369096* | 303.188186 | 588.342547 | 294.674912 | 587.358531 | 294.182904 | 5 |
| 5 | **798.400079** | 399.703678 | 781.373530 | 391.190403 | | | M | *492.285032* | 246.646154 | 475.258483 | 238.132880 | 474.274467 | 237.640872 | 4 |
| 6 | **899.447758** | 450.227517 | 882.421209 | 441.714243 | 881.437193 | 441.222235 | T | *361.244547* | 181.125912 | 344.217998 | 172.612637 | 343.233982 | 172.120629 | 3 |
| 7 | **1012.531822** | 506.769549 | 995.505273 | 498.256275 | 994.521257 | 497.764267 | L | *260.196868* | 130.602072 | 243.170319 | 122.088798 | | | 2 |
| 8 | | | | | | | K | *147.112804* | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 26.4 | 1157.630066 | 0.007282 | GGQIMTLK |
| 11.4 | 1157.630051 | 0.007297 | QLSQMLK |
| 11.0 | 1157.636566 | 0.000782 | LLAIMPDELK |
| 10.6 | 1157.647827 | -0.010479 | ALVGGTAPMTIK |
| 8.4 | 1157.640411 | -0.003063 | AQQLLSSGNLK |
| 6.6 | 1157.630081 | 0.007267 | CVTLVQK |
| 6.4 | 1157.640411 | -0.003063 | SPGKNSSIQLK |
| 5.6 | 1157.630051 | 0.007297 | QAGAMLLK |
| 3.5 | 1157.636566 | 0.000782 | ILVEEMAPLK |
| 2.8 | 1157.633209 | 0.004139 | LLDPEPSFLK |

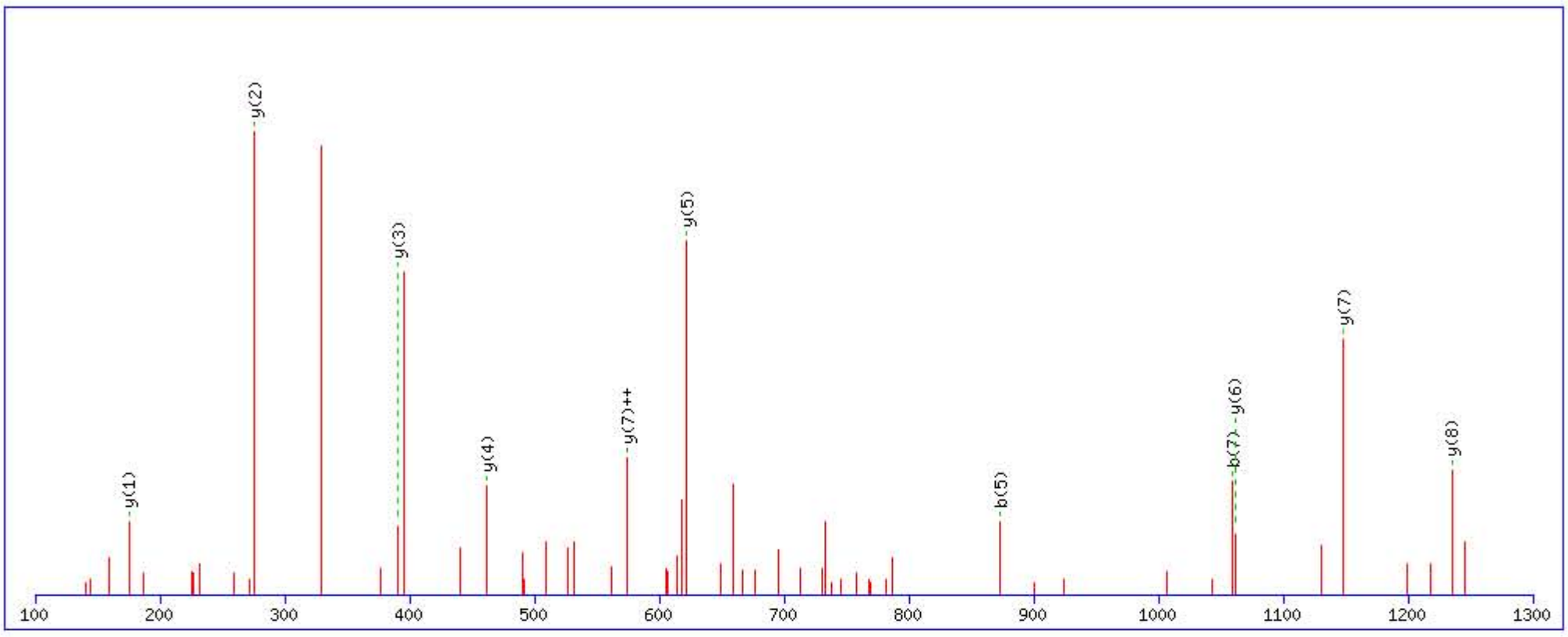
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VSSQCADTR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

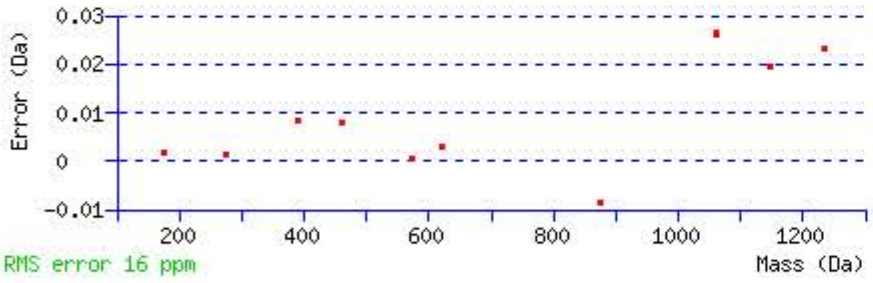
Match to Query 23939: 1333.619708 from(667.817130,2+) rtinseconds(1285) index(29830)
Title: Locus:1.1.1.555.17 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

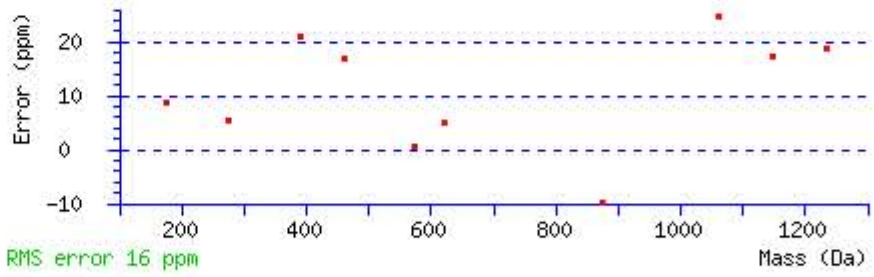
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1333.611862
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q4 : Biotin:Thermo-21345 (Q)
**Ions Score:** 51 **Expect:** 4.9e-005
**Matches :** 11/86 fragment ions using 22 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 9 |
| 2 | 187.107718 | 94.057497 | | | 169.097153 | 85.052214 | S | *1235.550719* | 618.278998 | 1218.524170 | 609.765723 | 1217.540154 | 609.273715 | 8 |
| 3 | 274.139746 | 137.573511 | | | 256.129181 | 128.568229 | S | *1148.518691* | 574.762984 | 1131.492142 | 566.249709 | 1130.508126 | 565.757701 | 7 |
| 4 | 713.365072 | 357.186174 | 696.338523 | 348.672900 | 695.354507 | 348.180892 | Q | *1061.486663* | 531.246970 | 1044.460114 | 522.733695 | 1043.476098 | 522.241687 | 6 |
| 5 | **873.395721** | 437.201499 | 856.369172 | 428.688224 | 855.385156 | 428.196216 | C | *622.261337* | 311.634307 | 605.234788 | 303.121032 | 604.250772 | 302.629024 | 5 |
| 6 | 944.432835 | 472.720056 | 927.406286 | 464.206781 | 926.422270 | 463.714773 | A | *462.230688* | 231.618982 | 445.204139 | 223.105707 | 444.220123 | 222.613700 | 4 |
| 7 | **1059.459778** | 530.233527 | 1042.433229 | 521.720253 | 1041.449213 | 521.228245 | D | *391.193574* | 196.100425 | 374.167025 | 187.587151 | 373.183009 | 187.095143 | 3 |
| 8 | 1160.507457 | 580.757367 | 1143.480908 | 572.244092 | 1142.496892 | 571.752084 | T | *276.166631* | 138.586953 | 259.140082 | 130.073679 | 258.156066 | 129.581671 | 2 |
| 9 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 51.3 | 1333.611862 | 0.007846 | VSSQCADTR |
| 5.0 | 1333.633606 | -0.013898 | LIYNTHMADEK |
| 3.6 | 1333.607117 | 0.012591 | GEIEIESDAPMK |
| 0.9 | 1333.626221 | -0.006513 | GNEIEPNFSATR |

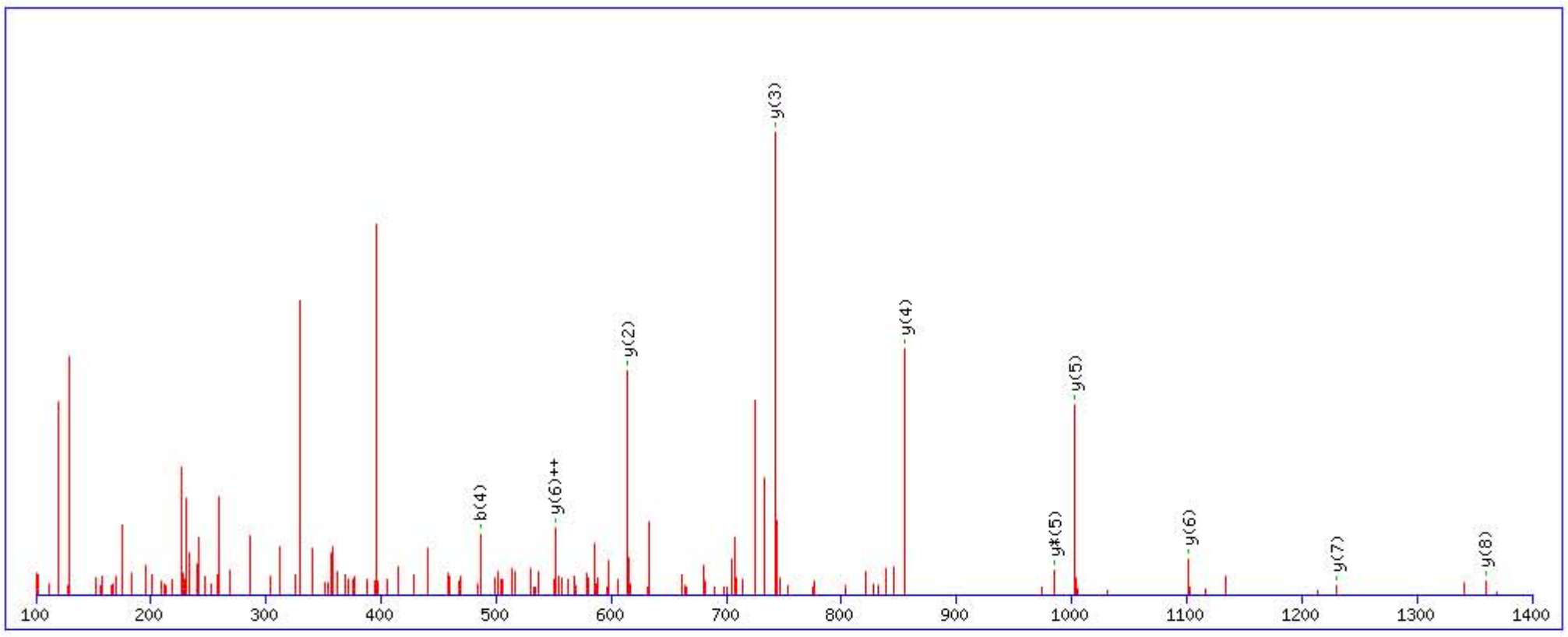
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **VKEEVFIQQR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

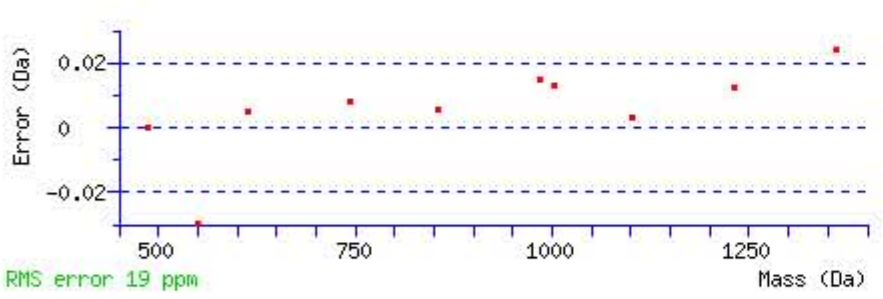
Match to Query 34026: 1585.863822 from(529.628550,3+) rtinseconds(1787) index(32842)
Title: Locus:1.1.1.731.6 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

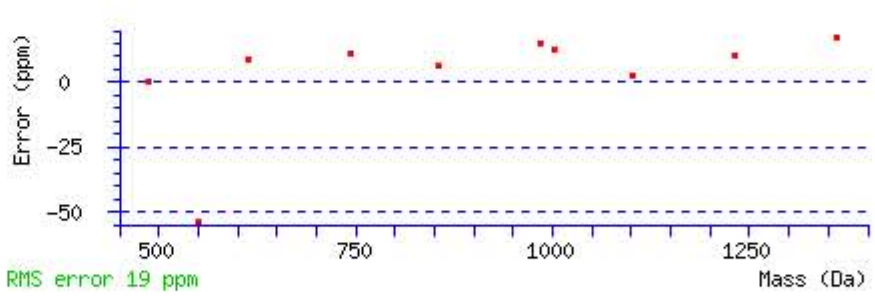
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1585.865021
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q9 : Biotin:Thermo-21345 (Q)
**Ions Score:** 53 **Expect:** 5.9e-005
**Matches :** 10/90 fragment ions using 13 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 100.075690 | 50.541483 | | | | | V | | | | | | | 10 |
| 2 | 228.170653 | 114.588965 | 211.144104 | 106.075690 | | | K | 1487.803897 | 744.405587 | 1470.777348 | 735.892312 | 1469.793332 | 735.400304 | 9 |
| 3 | 357.213246 | 179.110261 | 340.186697 | 170.596987 | 339.202681 | 170.104979 | E | *1359.708934* | 680.358105 | 1342.682385 | 671.844831 | 1341.698369 | 671.352823 | 8 |
| 4 | **486.255839** | 243.631558 | 469.229290 | 235.118283 | 468.245274 | 234.626275 | E | *1230.666341* | 615.836809 | 1213.639792 | 607.323534 | 1212.655776 | 606.831526 | 7 |
| 5 | 585.324253 | 293.165765 | 568.297704 | 284.652490 | 567.313688 | 284.160482 | V | *1101.623748* | 551.315512 | 1084.597199 | 542.802238 | | | 6 |
| 6 | 732.392667 | 366.699972 | 715.366118 | 358.186697 | 714.382102 | 357.694689 | F | *1002.555334* | 501.781305 | 985.528785 | 493.268031 | | | 5 |
| 7 | 845.476731 | 423.242004 | 828.450182 | 414.728729 | 827.466166 | 414.236721 | I | *855.486920* | 428.247098 | 838.460371 | 419.733824 | | | 4 |
| 8 | 973.535309 | 487.271293 | 956.508760 | 478.758018 | 955.524744 | 478.266010 | Q | *742.402856* | 371.705066 | 725.376307 | 363.191792 | | | 3 |
| 9 | 1412.760635 | 706.883956 | 1395.734086 | 698.370681 | 1394.750070 | 697.878673 | Q | *614.344278* | 307.675777 | 597.317729 | 299.162503 | | | 2 |
| 10 | | | | | | | R | 175.118952 | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 53.4 | 1585.865021 | -0.001199 | VKEEVFIQQR |
| 38.5 | 1585.865021 | -0.001199 | VKEEVFIQQR |
| 7.8 | 1585.842392 | 0.021430 | EIQTTTGNQQVLVR |
| 4.0 | 1585.857605 | 0.006217 | QEEVAGIRAKFPNK |
| 0.0 | 1585.842361 | 0.021461 | QSVLVKSNEEGIQR |

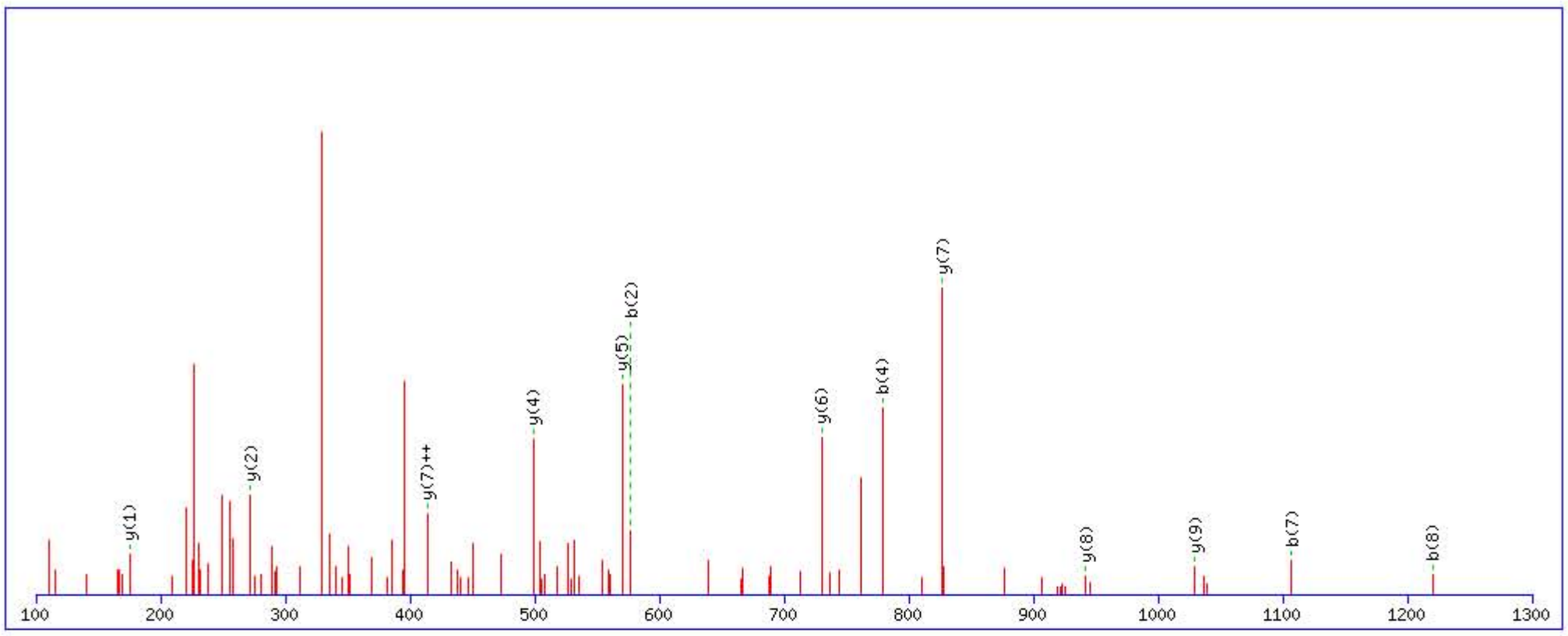
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **QHSDPCALNPR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

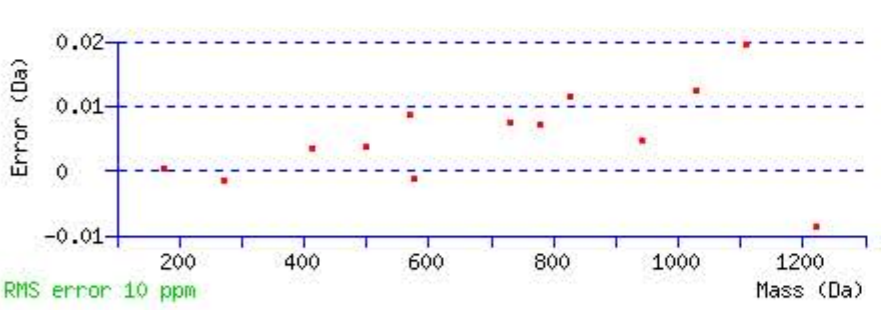
Match to Query 34822: 1604.759022 from(535.926950,3+) rtinseconds(1444) index(30658)
Title: Locus:1.1.1.611.9 File:"2013-07-02 CLN FXIII 180 min 2nd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

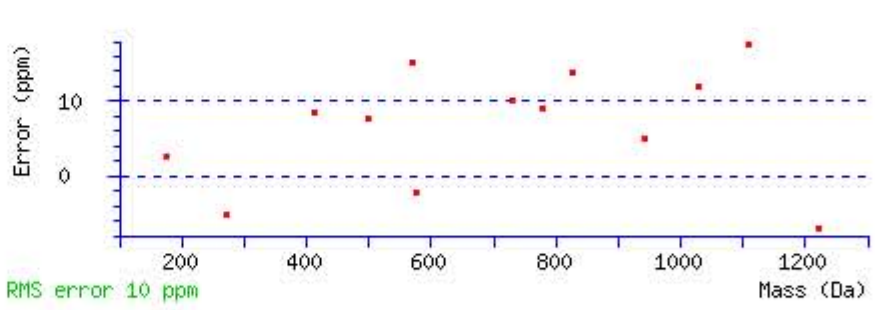
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1604.755157
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
**Q1** : Biotin:Thermo-21345 (Q)
**Ions Score:** 51 **Expect:** 0.00013
**Matches** : 13/102 fragment ions using 21 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 440.232602 | 220.619939 | 423.206053 | 212.106664 | | | Q | | | | | | | 11 |
| 2 | **577.291514** | 289.149395 | 560.264965 | 280.636121 | | | H | 1166.537117 | 583.772196 | 1149.510568 | 575.258922 | 1148.526552 | 574.766914 | 10 |
| 3 | 664.323542 | 332.665409 | 647.296993 | 324.152134 | 646.312977 | 323.660126 | S | *1029.478205* | 515.242740 | 1012.451656 | 506.729466 | 1011.467640 | 506.237458 | 9 |
| 4 | **779.350485** | 390.178880 | 762.323936 | 381.665606 | 761.339920 | 381.173598 | D | *942.446177* | 471.726726 | 925.419628 | 463.213452 | 924.435612 | 462.721444 | 8 |
| 5 | 876.403249 | 438.705263 | 859.376700 | 430.191988 | 858.392684 | 429.699980 | P | *827.419234* | 414.213255 | 810.392685 | 405.699980 | | | 7 |
| 6 | 1036.433898 | 518.720587 | 1019.407349 | 510.207313 | 1018.423333 | 509.715305 | C | *730.366470* | 365.686873 | 713.339921 | 357.173598 | | | 6 |
| 7 | **1107.471012** | 554.239144 | 1090.444463 | 545.725870 | 1089.460447 | 545.233861 | A | *570.335821* | 285.671548 | 553.309272 | 277.158274 | | | 5 |
| 8 | **1220.555076** | 610.781176 | 1203.528527 | 602.267901 | 1202.544511 | 601.775893 | L | *499.298707* | 250.152991 | 482.272158 | 241.639717 | | | 4 |
| 9 | 1334.598003 | 667.802639 | 1317.571454 | 659.289365 | 1316.587438 | 658.797357 | N | 386.214643 | 193.610959 | 369.188094 | 185.097685 | | | 3 |
| 10 | 1431.650767 | 716.329021 | 1414.624218 | 707.815747 | 1413.640202 | 707.323739 | P | *272.171716* | 136.589496 | 255.145167 | 128.076221 | | | 2 |
| 11 | | | | | | | R | *175.118952* | 88.063114 | 158.092403 | 79.549839 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 50.9 | 1604.755157 | 0.003865 | QHSDPCALNPR |
| 12.3 | 1604.782806 | -0.023784 | QEQIINTMTQDLR |
| 3.5 | 1604.736725 | 0.022297 | EGMGWSYLVFCLK |
| 1.2 | 1604.747726 | 0.011296 | IHNEERSYKCNR |
| 0.8 | 1604.769043 | -0.010021 | KEIMYYQQALMR |
| 0.7 | 1604.754288 | 0.004734 | GPSPASSSSSSPPAHPR |

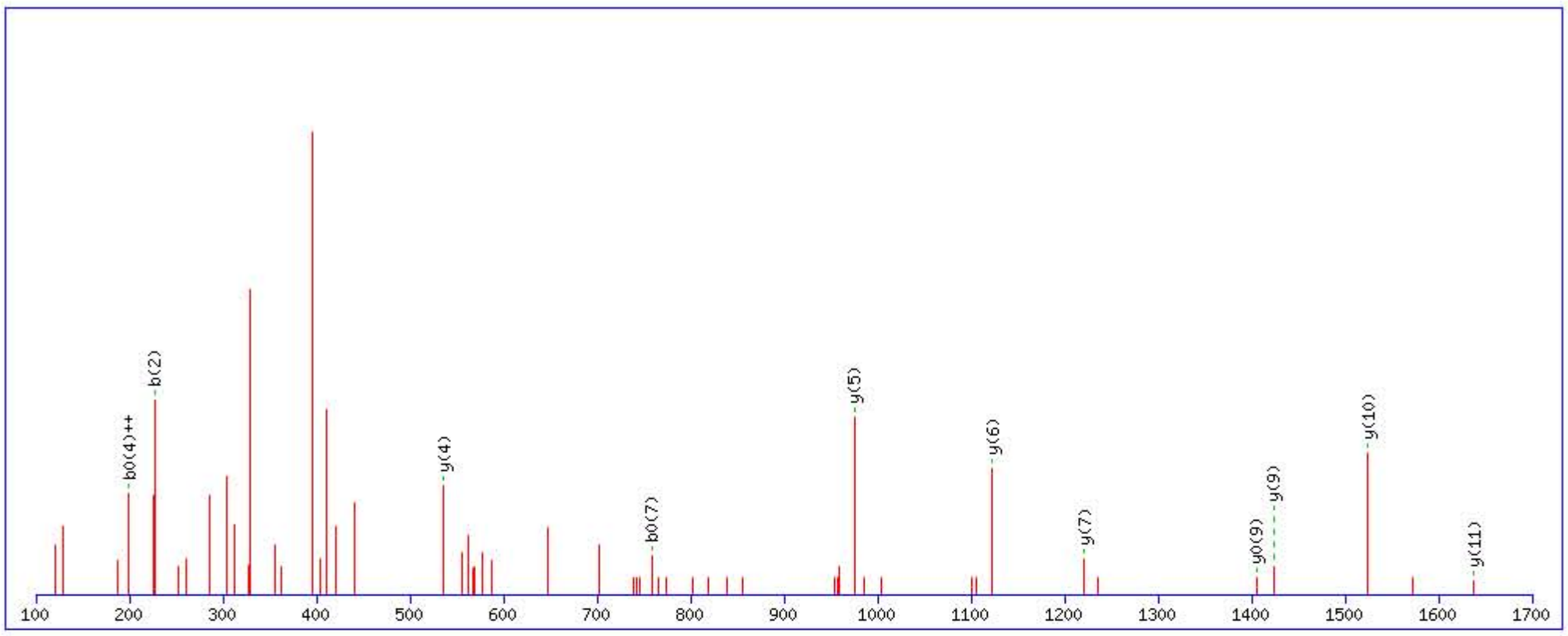
# {MATRIX SCIENCE} Mascot Search Results

## Peptide View

MS/MS Fragmentation of **ILTSDVFQDCNK**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

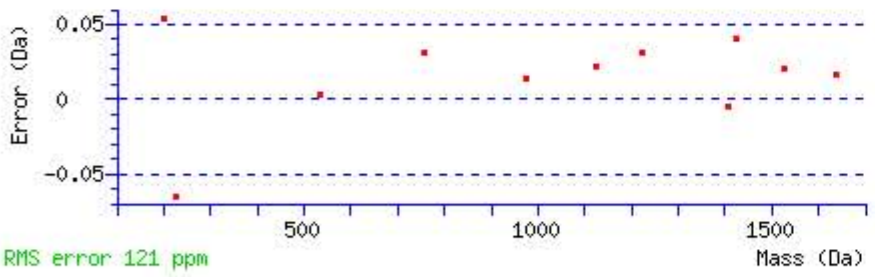
Match to Query 39090: 1749.850272 from(584.290700,3+) rtinseconds(2147) index(51351)
Title: Locus:1.1.1.1985.7 File:"2013-07-02 CLN FXIII 180 min 2nd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\8 FXIII 180 min 2nd\mascot_daemon_merge.mgf

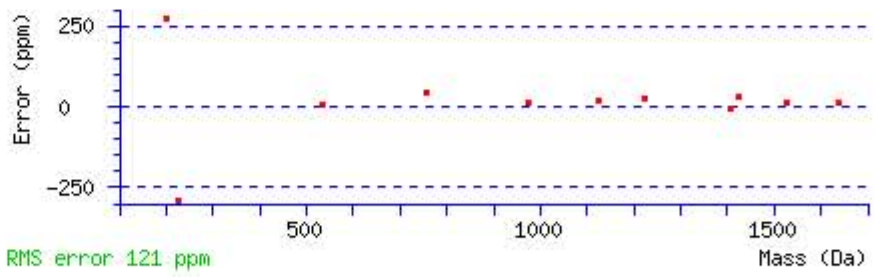
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉




**Monoisotopic mass of neutral peptide Mr(calc):** 1749.842987
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)
**Variable modifications:**
Q8 : Biotin:Thermo-21345 (Q)
**Ions Score:** 39 **Expect:** 0.0029
**Matches :** 11/108 fragment ions using 16 most intense peaks (help)

| # | b | b$^{++}$ | b* | b*$^{++}$ | b$^{0}$ | b$^{0++}$ | Seq. | y | y$^{++}$ | y* | y*$^{++}$ | y$^{0}$ | y$^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.091340 | 57.549308 | | | | | I | | | | | | | 12 |
| 2 | 227.175404 | 114.091340 | | | | | L | *1637.766191* | 819.386734 | 1620.739642 | 810.873459 | 1619.755626 | 810.381451 | 11 |
| 3 | 328.223083 | 164.615179 | | | 310.212518 | 155.609897 | T | *1524.682127* | 762.844702 | 1507.655578 | 754.331427 | 1506.671562 | 753.839419 | 10 |
| 4 | 415.255111 | 208.131193 | | | 397.244546 | 199.125911 | S | *1423.634448* | 712.320862 | 1406.607899 | 703.807588 | 1405.623883 | 703.315580 | 9 |
| 5 | 530.282054 | 265.644665 | | | 512.271489 | 256.639383 | D | 1336.602420 | 668.804848 | 1319.575871 | 660.291574 | 1318.591855 | 659.799565 | 8 |
| 6 | 629.350468 | 315.178872 | | | 611.339903 | 306.173589 | V | *1221.575477* | 611.291377 | 1204.548928 | 602.778102 | 1203.564912 | 602.286094 | 7 |
| 7 | 776.418882 | 388.713079 | | | 758.408317 | 379.707796 | F | *1122.507063* | 561.757170 | 1105.480514 | 553.243895 | 1104.496498 | 552.751887 | 6 |
| 8 | 1215.644208 | 608.325742 | 1198.617659 | 599.812468 | 1197.633643 | 599.320459 | Q | *975.438649* | 488.222963 | 958.412100 | 479.709688 | 957.428084 | 479.217680 | 5 |
| 9 | 1330.671151 | 665.839214 | 1313.644602 | 657.325939 | 1312.660586 | 656.833931 | D | *536.213323* | 268.610300 | 519.186774 | 260.097025 | 518.202758 | 259.605017 | 4 |
| 10 | 1490.701800 | 745.854538 | 1473.675251 | 737.341264 | 1472.691235 | 736.849256 | C | 421.186380 | 211.096828 | 404.159831 | 202.583553 | | | 3 |
| 11 | 1604.744727 | 802.876002 | 1587.718178 | 794.362727 | 1586.734162 | 793.870719 | N | 261.155731 | 131.081503 | 244.129182 | 122.568229 | | | 2 |
| 12 | | | | | | | K | 147.112804 | 74.060040 | 130.086255 | 65.546765 | | | 1 |




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

**All matches to this query**

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 38.5 | 1749.842987 | 0.007285 | ILTSDVFQDCNK |

**Mascot:** http://www.matrixscience.com/