# Mascot Search Results

## Protein View

Match to: **YD_RFP-p53** Score: **317**
**YD_RFP-p53**
Found in search of D:\Merge\20101018_YD\BIT01763_YD_7.mgf

Nominal mass ($M_r$): **70830**; Calculated pI value: **6.14**
NCBI BLAST search of YD_RFP-p53 against nr
Unformatted sequence string for pasting into other applications

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **38%**

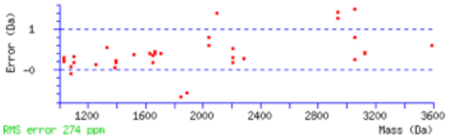
Matched peptides shown in **Bold Red**

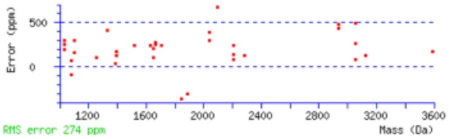
```
  1 MHHHHHHASS EDVIKEFMRF KVRMEGSVNG HEFEIEGEGE GRPYEGTQTA
 51 KLKVTKGGPL PFAWDILSPQ FQYGSKAYVK HPADIPDYLK LSFPEGFKWE
101 RVMNFEDGGV VTVTQDSSLQ DGEFIYKVKL RGTNFPSDGP VMQKKTMGWE
151 ASTERMYPED GALKGEIKMR LKLKDGGHYD AEVKTTYMAK KPVQLPGAYK
201 TDIKLDITSH NEDYTIVEQY ERAEGRHSTG AENLYFQGLE EEPQSDPSVE
251 PPLSQETFSD LWKLLPENNV LSPLPSQAMD DLMLSPDDIE QWFTEDPGPD
301 EAPRMPEAAP RVAPAPAAPT PAAPAPAPSW PLSSSVPSQK TYQGSYGFRL
351 GFLHSGTAKS VTCTYSPALN KMFCQLAKTC PVQLWVDSTP PPGTRVRAMA
401 IYKQSQHMTE VVRRCPHHER CSDSDGLAPP QHLIRVEGNL RVEYLDDRNT
451 FRHSVVVPYE PPEVGSDCTT IHYNYMCNSS CMGGMNRRPI LTIITLEDSS
501 GNLLGRNSFE VHVCACPGRD RRTEEENLRK KGEPHHELPP GSTKRALSNN
551 TSSSPQPKKK PLDGEYFTLQ IRGRERFEMF RELNEALELK DAQAGKEPGG
601 SRAHSSHLKS KKGQSTSRHK KLMFKTEGPD SD
```

Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   20 - 51       897.5670  3586.2389  3585.6318    0.6071    2  R.FKVRMEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  2 Deamidated (NQ); Oxidation (M)  (Ions score 24)
   24 - 51       764.7150  3054.8309  3053.3309    1.5000    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M)  (Ions score 48)
   24 - 51      1019.1930  3054.5572  3054.3149    0.2423    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Deamidated (NQ); Oxidation (M)  (Ions score 44)
   24 - 51       764.7860  3055.1149  3054.3149    0.8000    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Deamidated (NQ); Oxidation (M)  (Ions score 50)
   57 - 76      1104.6540  2207.2934  2207.1051    0.1883    0  K.GGPLPFAWDILSPQFQYGSK.A   (Ions score 77)
   57 - 76      1104.7070  2207.3994  2207.1051    0.2943    0  K.GGPLPFAWDILSPQFQYGSK.A   (Ions score 58)
   57 - 76       736.8850  2207.6332  2207.1051    0.5280    0  K.GGPLPFAWDILSPQFQYGSK.A   (Ions score 56)
   77 - 90       544.0930  1629.2572  1628.8562    0.4010    1  K.AYVKHPADIPDYLK.L   (Ions score 38)
  102 - 129     1041.3110  3120.9112  3120.4962    0.4150    1  R.VMNFEDGGVVTVTQDSSLQDGEFIYKVK.L  Oxidation (M)  (Ions score 106)
  102 - 129     1041.6330  3121.8772  3121.4802    0.3970    1  R.VMNFEDGGVVTVTQDSSLQDGEFIYKVK.L  Deamidated (NQ); Oxidation (M)  (Ions score 52)
  128 - 144      630.8050  1889.3932  1889.9669   -0.5738    2  K.VKLRGTNFPSDGPVMQK.K  Deamidated (NQ); Oxidation (M)  (Ions score 46)
  130 - 144      555.0840  1662.2302  1661.8195    0.4106    1  K.LRGTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 49)
  130 - 144      555.0980  1662.2722  1661.8195    0.4526    1  K.LRGTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 49)
  132 - 144      697.4150  1392.8154  1392.6344    0.1811    0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 69)
  132 - 144      697.4410  1392.8674  1392.6344    0.2331    0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 68)
  132 - 145      508.0410  1521.1012  1520.7293    0.3718    1  R.GTNFPSDGPVMQKK.T  Oxidation (M)  (Ions score 19)
  171 - 190      571.8670  2283.4389  2283.1569    0.2820    3  R.LKLKDGGHYDAEVKTTYMAK.K  Oxidation (M)  (Ions score 38)
  173 - 184      444.7380  1331.1922  1330.6517    0.5405    1  K.LKDGGHYDAEVK.T   (Ions score 24)
  173 - 190      681.8700  2042.5882  2041.9779    0.6103    2  K.LKDGGHYDAEVKTTYMAK.K  Oxidation (M)  (Ions score 51)
  173 - 190      681.9330  2042.7772  2041.9779    0.7993    2  K.LKDGGHYDAEVKTTYMAK.K  Oxidation (M)  (Ions score 58)
  191 - 200      550.9150  1099.8154  1099.6390    0.1765    0  K.KPVQLPGAYK.T   (Ions score 42)
  191 - 200      550.9880  1099.9614  1099.6390    0.3225    0  K.KPVQLPGAYK.T   (Ions score 39)
  341 - 349      539.7050  1077.3954  1077.4880   -0.0925    0  K.TYQGSYGFR.L   (Ions score 48)
  341 - 349      539.7900  1077.5654  1077.4880    0.0775    0  K.TYQGSYGFR.L   (Ions score 51)
  350 - 359      515.8910  1029.7674  1029.5607    0.2067    0  R.LGFLHSGTAK.S   (Ions score 51)
  350 - 359      515.9190  1029.8234  1029.5607    0.2627    0  R.LGFLHSGTAK.S   (Ions score 37)
  350 - 359      344.2970  1029.8692  1029.5607    0.3084    0  R.LGFLHSGTAK.S   (Ions score 39)
  436 - 452      699.8210  2096.4412  2095.0446    1.3965    2  R.VEGNLRVEYLDDRNTFR.H   (Ions score 26)
  545 - 559      922.1320  1842.2494  1842.9183   -0.6689    2  K.RALSNNTSSSPQPKK.K  Deamidated (NQ); 2 GlyGly (K)  (Ions score 17)
  559 - 572      570.1230  1707.3472  1706.9355    0.4116    1  K.KKPLDGEYFTLQIR.G   (Ions score 63)
  577 - 602      980.5720  2938.6942  2937.4290    1.2652    3  R.FEMFRELNEALELKDAQAGKEPGGSR.A  Oxidation (M)  (Ions score 46)
  577 - 602      980.6200  2938.8382  2937.4290    1.4092    3  R.FEMFRELNEALELKDAQAGKEPGGSR.A  Oxidation (M)  (Ions score 59)
  619 - 632      824.9880  1647.9614  1647.7926    0.1688    3  R.HKKLMFKTEGPDSD.-  Oxidation (M)  (Ions score 19)
  619 - 632      550.3880  1648.1422  1647.7926    0.3495    3  R.HKKLMFKTEGPDSD.-  Oxidation (M)  (Ions score 24)
  621 - 632      692.3490  1382.6834  1382.6388    0.0447    2  K.KLMFKTEGPDSD.-  Oxidation (M)  (Ions score 47)
  622 - 632      628.3480  1254.6814  1254.5438    0.1376    1  K.LMFKTEGPDSD.-  Oxidation (M)  (Ions score 52)
```





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

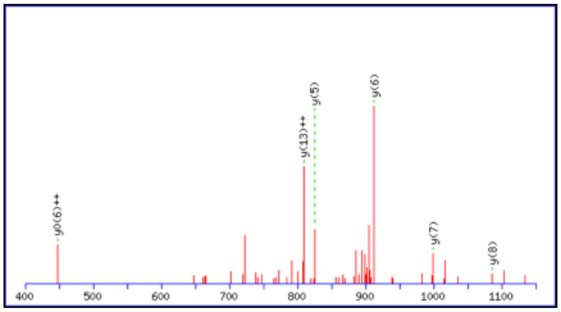
# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **RALSNNTSSSPQPKK**
Found in **YD_RFP-p53**, YD_RFP-p53

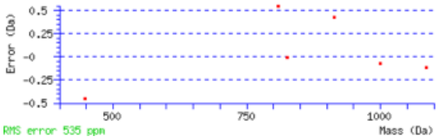
Match to Query 675: 1842.249448 from(922.132000,2+) intensity(16649.0000)
Title: Cmpd 262, +MSn(922.65), 35.4 min
Data file D:\Merge\20101018_YD\BIT01763_YD_7.mgf

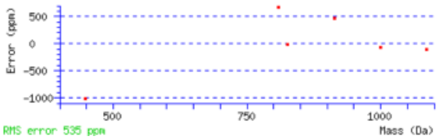
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



**Monoisotopic mass of neutral peptide Mr(calc):** 1842.9183
**Variable modifications:**
**N6** : Deamidated (NQ)
**K14** : GlyGly (K)
**K15** : GlyGly (K)
**Ions Score:** 17 **Expect:** 3.8
**Matches :** 6/152 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 | 157.1084 | 79.0578 | 140.0818 | 70.5446 | | | R | | | | | | | 15 |
| 2 | 228.1455 | 114.5764 | 211.1190 | 106.0631 | | | A | 1687.8246 | 844.4159 | 1670.7980 | 835.9026 | 1669.8140 | 835.4106 | 14 |
| 3 | 341.2296 | 171.1184 | 324.2030 | 162.6051 | | | L | 1616.7875 | 808.8974 | 1599.7609 | 800.3841 | 1598.7769 | 799.8921 | 13 |
| 4 | 428.2616 | 214.6344 | 411.2350 | 206.1212 | 410.2510 | 205.6292 | S | 1503.7034 | 752.3553 | 1486.6768 | 743.8421 | 1485.6928 | 743.3500 | 12 |
| 5 | 542.3045 | 271.6559 | 525.2780 | 263.1426 | 524.2940 | 262.6506 | N | 1416.6714 | 708.8393 | 1399.6448 | 700.3260 | 1398.6608 | 699.8340 | 11 |
| 6 | 657.3315 | 329.1694 | 640.3049 | 320.6561 | 639.3209 | 320.1641 | N | 1302.6284 | 651.8179 | 1285.6019 | 643.3046 | 1284.6179 | 642.8126 | 10 |
| 7 | 758.3791 | 379.6932 | 741.3526 | 371.1799 | 740.3686 | 370.6879 | T | 1187.6015 | 594.3044 | 1170.5749 | 585.7911 | 1169.5909 | 585.2991 | 9 |
| 8 | 845.4112 | 423.2092 | 828.3846 | 414.6959 | 827.4006 | 414.2039 | S | ***1086.5538*** | 543.7805 | 1069.5273 | 535.2673 | 1068.5432 | 534.7753 | 8 |
| 9 | 932.4432 | 466.7252 | 915.4166 | 458.2120 | 914.4326 | 457.7200 | S | ***999.5218*** | 500.2645 | 982.4952 | 491.7513 | 981.5112 | 491.2592 | 7 |
| 10 | 1019.4752 | 510.2413 | 1002.4487 | 501.7280 | 1001.4647 | 501.2360 | S | ***912.4898*** | 456.7485 | 895.4632 | 448.2352 | 894.4792 | 447.7432 | 6 |
| 11 | 1116.5280 | 558.7676 | 1099.5014 | 550.2544 | 1098.5174 | 549.7624 | P | ***825.4577*** | 413.2325 | 808.4312 | 404.7192 | | | 5 |
| 12 | 1244.5866 | 622.7969 | 1227.5600 | 614.2836 | 1226.5760 | 613.7916 | Q | 728.4050 | 364.7061 | 711.3784 | 356.1928 | | | 4 |
| 13 | 1341.6393 | 671.3233 | 1324.6128 | 662.8100 | 1323.6288 | 662.3180 | P | 600.3464 | 300.6768 | 583.3198 | 292.1636 | | | 3 |
| 14 | 1583.7772 | 792.3922 | 1566.7507 | 783.8790 | 1565.7667 | 783.3870 | K | 503.2936 | 252.1504 | 486.2671 | 243.6372 | | | 2 |
| 15 | | | | | | | K | 261.1557 | 131.0815 | 244.1292 | 122.5682 | | | 1 |





NCBI **BLAST** search of RALSNNTSSSPQPKK
(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 | 1842.9046 | -0.6552 | LWTALHSCSDKQVK |
| 21.6 | 1840.8075 | 1.4419 | KGGFFSSSSSSSSSSSK |
| 18.0 | 1841.8665 | 0.3829 | VGKPSWIGSSSCHPNMR |
| 18.0 | 1842.8505 | -0.6011 | VGKPSWIGSSSCHPNMR |
| 17.2 | 1840.5977 | 1.6518 | MDCACATGGSCSCAGSCK |
| 16.9 | 1842.9799 | -0.7304 | AGLKARVQSSINIDQK |
| 16.6 | 1842.9183 | -0.6689 | RALSNNTSSSPQPKK |
| 16.6 | 1842.9183 | -0.6689 | RALSNNTSSSPQPKK |
| 15.8 | 1841.9556 | 0.2938 | EMALKQALLSAIHSDSK |
| 15.8 | 1842.8860 | -0.6366 | EHNPFLSSSDNQLLSR |

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

# Mascot Search Results

## Protein View

Match to: **Q05550** Score: **102**
**RecName: Full=Ubiquitin;**
Found in search of D:\Merge\20101018_YD\BIT01763_YD_7.mgf

Nominal mass ($M_r$): **8544;** Calculated pI value: **6.56**
NCBI BLAST search of Q05550 against nr
Unformatted sequence string for pasting into other applications

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **86%**

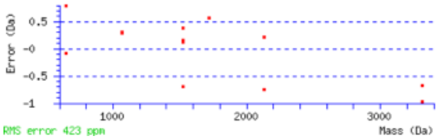
Matched peptides shown in **Bold Red**

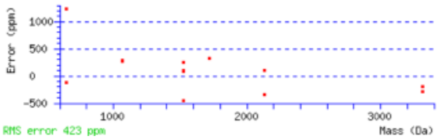
```
     1 MQIFVKTLTG KTIALEVEPS DTIENVKAKI QDKEGIPPDQ QRLIFAGKQL
    51 EEGRTLSDYN IQKESTLHLV LRLRGG
```

Show predicted peptides also

Sort Peptides By   ● Residue Number   ○ Increasing Mass   ○ Decreasing Mass

```
 Start - End     Observed    Mr(expt)   Mr(calc)     Delta   Miss Sequence
     1 - 29      829.9620   3315.8189  3316.7952   -0.9763     3  -.MQIFVKTLTGKTIALEVEPSDTIENVKAK.I  GlyGly (K)  (Ions score 47)
     1 - 29      830.0390   3316.1269  3316.7952   -0.6683     3  -.MQIFVKTLTGKTIALEVEPSDTIENVKAK.I  GlyGly (K)  (Ions score 60)
    28 - 42      575.1660   1722.4762  1721.9060    0.5702     2  K.AKIQDKEGIPPDQQR.L   (Ions score 43)
    30 - 42      508.3650   1522.0732  1522.7740   -0.7008     1  K.IQDKEGIPPDQQR.L   (Ions score 19)
    30 - 42      762.4600   1522.9054  1522.7740    0.1315     1  K.IQDKEGIPPDQQR.L   (Ions score 49)
    30 - 42      762.4720   1522.9294  1522.7740    0.1555     1  K.IQDKEGIPPDQQR.L   (Ions score 58)
    30 - 42      508.7230   1523.1472  1522.7740    0.3732     1  K.IQDKEGIPPDQQR.L   (Ions score 41)
    43 - 48      324.6710    647.3274   647.4006   -0.0732     0  R.LIFAGK.Q   (Ions score 32)
    43 - 48      325.1060    648.1974   647.4006    0.7968     0  R.LIFAGK.Q   (Ions score 34)
    55 - 72     1065.7020   2129.3894  2130.1321   -0.7426     1  R.TLSDYNIQKESTLHLVLR.L  Deamidated (NQ)  (Ions score 30)
    55 - 72      711.1240   2130.3502  2130.1321    0.2181     1  R.TLSDYNIQKESTLHLVLR.L  Deamidated (NQ)  (Ions score 67)
    64 - 72      534.4570   1066.8994  1066.6135    0.2860     0  K.ESTLHLVLR.L   (Ions score 49)
    64 - 72      534.4650   1066.9154  1066.6135    0.3020     0  K.ESTLHLVLR.L   (Ions score 46)
```





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

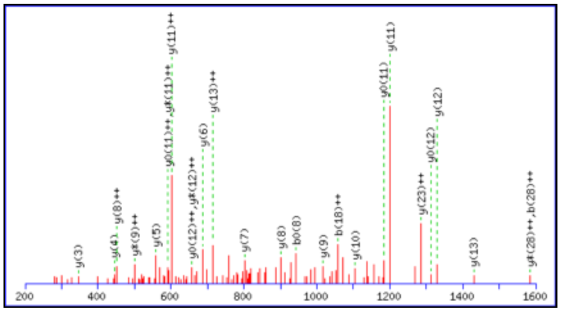
# Mascot Search Results

### Peptide View

MS/MS Fragmentation of **MQIFVKTLTGKTIALEVEPSDTIENVKAK**
Found in **Q05550**, RecName: Full=Ubiquitin;

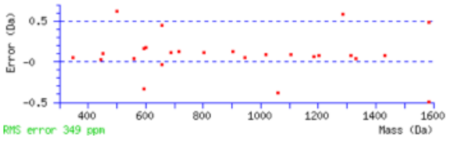
Match to Query 1281: 3316.126896 from(830.039000,4+) intensity(74723.0000)
Title: Cmpd 194, +MSn(830.48), 30.8 min
Data file D:\Merge\20101018_YD\BIT01763_YD_7.mgf

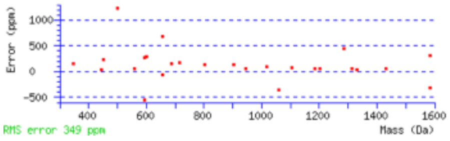
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



**Monoisotopic mass of neutral peptide Mr(calc):** 3316.7952
**Variable modifications:**
**K11** : GlyGly (K)
**Ions Score:** 60 **Expect:** 0.035
**Matches :** 26/312 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 | 132.0478 | 66.5275 | | | | | M | | | | | | | 29 |
| 2 | 260.1063 | 130.5568 | 243.0798 | 122.0435 | | | Q | 3186.7620 | 1593.8846 | 3169.7355 | 1585.3714 | 3168.7515 | 1584.8794 | 28 |
| 3 | 373.1904 | 187.0988 | 356.1639 | 178.5856 | | | I | 3058.7034 | 1529.8554 | 3041.6769 | 1521.3421 | 3040.6929 | 1520.8501 | 27 |
| 4 | 520.2588 | 260.6330 | 503.2323 | 252.1198 | | | F | 2945.6194 | 1473.3133 | 2928.5928 | 1464.8001 | 2927.6088 | 1464.3080 | 26 |
| 5 | 619.3272 | 310.1673 | 602.3007 | 301.6540 | | | V | 2798.5510 | 1399.7791 | 2781.5244 | 1391.2658 | 2780.5404 | 1390.7738 | 25 |
| 6 | 747.4222 | 374.2147 | 730.3956 | 365.7015 | | | K | 2699.4826 | 1350.2449 | 2682.4560 | 1341.7316 | 2681.4720 | 1341.2396 | 24 |
| 7 | 848.4699 | 424.7386 | 831.4433 | 416.2253 | 830.4593 | 415.7333 | T | 2571.3876 | 1286.1974 | 2554.3610 | 1277.6842 | 2553.3770 | 1277.1922 | 23 |
| 8 | 961.5539 | 481.2806 | 944.5274 | 472.7673 | 943.5434 | 472.2753 | L | 2470.3399 | 1235.6736 | 2453.3134 | 1227.1603 | 2452.3293 | 1226.6683 | 22 |
| 9 | 1062.6016 | 531.8044 | 1045.5751 | 523.2912 | 1044.5911 | 522.7992 | T | 2357.2558 | 1179.1316 | 2340.2293 | 1170.6183 | 2339.2453 | 1170.1263 | 21 |
| 10 | 1119.6231 | 560.3152 | 1102.5965 | 551.8019 | 1101.6125 | 551.3099 | G | 2256.2082 | 1128.6077 | 2239.1816 | 1120.0944 | 2238.1976 | 1119.6024 | 20 |
| 11 | 1361.7610 | 681.3841 | 1344.7344 | 672.8708 | 1343.7504 | 672.3788 | K | 2199.1867 | 1100.0970 | 2182.1602 | 1091.5837 | 2181.1761 | 1091.0917 | 19 |
| 12 | 1462.8086 | 731.9080 | 1445.7821 | 723.3947 | 1444.7981 | 722.9027 | T | 1957.0488 | 979.0280 | 1940.0223 | 970.5148 | 1939.0382 | 970.0228 | 18 |
| 13 | 1575.8927 | 788.4500 | 1558.8662 | 779.9367 | 1557.8821 | 779.4447 | I | 1856.0011 | 928.5042 | 1838.9746 | 919.9909 | 1837.9906 | 919.4989 | 17 |
| 14 | 1646.9298 | 823.9686 | 1629.9033 | 815.4553 | 1628.9193 | 814.9633 | A | 1742.9171 | 871.9622 | 1725.8905 | 863.4489 | 1724.9065 | 862.9569 | 16 |
| 15 | 1760.0139 | 880.5106 | 1742.9873 | 871.9973 | 1742.0033 | 871.5053 | L | 1671.8800 | 836.4436 | 1654.8534 | 827.9303 | 1653.8694 | 827.4383 | 15 |
| 16 | 1889.0565 | 945.0319 | 1872.0299 | 936.5186 | 1871.0459 | 936.0266 | E | 1558.7959 | 779.9016 | 1541.7693 | 771.3883 | 1540.7853 | 770.8963 | 14 |
| 17 | 1988.1249 | 994.5661 | 1971.0983 | 986.0528 | 1970.1143 | 985.5608 | V | ***1429.7533*** | 715.3803 | 1412.7268 | 706.8670 | 1411.7427 | 706.3750 | 13 |
| 18 | 2117.1675 | 1059.0874 | 2100.1409 | 1050.5741 | 2099.1569 | 1050.0821 | E | ***1330.6849*** | 665.8461 | 1313.6583 | 657.3328 | 1312.6743 | 656.8408 | 12 |
| 19 | 2214.2203 | 1107.6138 | 2197.1937 | 1099.1005 | 2196.2097 | 1098.6085 | P | ***1201.6423*** | 601.3248 | 1184.6157 | 592.8115 | 1183.6317 | 592.3195 | 11 |
| 20 | 2301.2523 | 1151.1298 | 2284.2257 | 1142.6165 | 2283.2417 | 1142.1245 | S | ***1104.5895*** | 552.7984 | 1087.5630 | 544.2851 | 1086.5790 | 543.7931 | 10 |
| 21 | 2416.2792 | 1208.6433 | 2399.2527 | 1200.1300 | 2398.2687 | 1199.6380 | D | ***1017.5575*** | 509.2824 | 1000.5310 | 500.7691 | 999.5469 | 500.2771 | 9 |
| 22 | 2517.3269 | 1259.1671 | 2500.3004 | 1250.6538 | 2499.3163 | 1250.1618 | T | ***902.5306*** | 451.7689 | 885.5040 | 443.2556 | 884.5200 | 442.7636 | 8 |
| 23 | 2630.4110 | 1315.7091 | 2613.3844 | 1307.1958 | 2612.4004 | 1306.7038 | I | ***801.4829*** | 401.2451 | 784.4563 | 392.7318 | 783.4723 | 392.2398 | 7 |
| 24 | 2759.4536 | 1380.2304 | 2742.4270 | 1371.7171 | 2741.4430 | 1371.2251 | E | ***688.3988*** | 344.7030 | 671.3723 | 336.1898 | 670.3883 | 335.6978 | 6 |
| 25 | 2873.4965 | 1437.2519 | 2856.4699 | 1428.7386 | 2855.4859 | 1428.2466 | N | ***559.3562*** | 280.1817 | 542.3297 | 271.6685 | | | 5 |
| 26 | 2972.5649 | 1486.7861 | 2955.5384 | 1478.2728 | 2954.5543 | 1477.7808 | V | ***445.3133*** | 223.1603 | 428.2867 | 214.6470 | | | 4 |
| 27 | 3100.6599 | 1550.8336 | 3083.6333 | 1542.3203 | 3082.6493 | 1541.8283 | K | ***346.2449*** | 173.6261 | 329.2183 | 165.1128 | | | 3 |
| 28 | 3171.6970 | 1586.3521 | 3154.6704 | 1577.8389 | 3153.6864 | 1577.3468 | A | 218.1499 | 109.5786 | 201.1234 | 101.0653 | | | 2 |
| 29 | | | | | | | K | 147.1128 | 74.0600 | 130.0863 | 65.5468 | | | 1 |





NCBI **BLAST** search of MQIFVKTLTGKTIALEVEPSDTIENVKAK
(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 | 3316.7952 | -0.6683 | MQIFVKTLTGKTIALEVEPSDTIENVKAK |
| 57.2 | 3316.7952 | -0.6683 | MQIFVKTLTGKTIALEVEPSDTIENVKAK |
| 57.2 | 3315.7926 | 0.3343 | QIFVKTLTGKTITLDVEPSDTIENVKAK |
| 57.2 | 3316.7766 | -0.6497 | QIFVKTLTGKTITLDVEPSDTIENVKAK |
| 35.8 | 3314.8312 | 1.2957 | NILDLSPFTVTDLTPMEIVVDIFRKLGLR |
| 34.9 | 3315.5385 | 0.5884 | MEQLKEQGGEGQSEAAEAQRQQAEAQKK |

| | | | |
|---|---|---|---|
| 34.9 | 3315.5385 | 0.5884 | MEQLKEQGGEGQSEAAEAQRQQAEAQKK |
| 34.8 | 3316.5225 | -0.3956 | MEQLKEQGGEGQSEAAEAQRQQAEAQKK |
| 33.9 | 3316.4474 | -0.3205 | CRKENSALKECLTAYYNDPAFYEECK |
| 33.4 | 3315.8329 | 0.2940 | IYQKIVTKARNLVAVGEAIESEFGIPIINK |

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

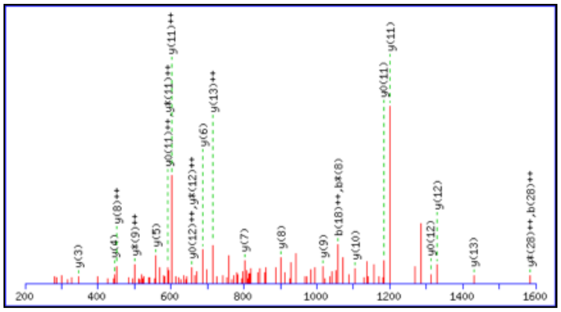
# MATRIX SCIENCE Mascot Search Results

### Peptide View

MS/MS Fragmentation of **MQIFVKTLTGKTIALEVEPSDTIENVKAK**
Found in **Q05550**, RecName: Full=Ubiquitin;

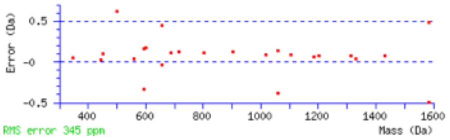
Match to Query 1281: 3316.126896 from(830.039000,4+) intensity(74723.0000)
Title: Cmpd 194, +MSn(830.48), 30.8 min
Data file D:\Merge\20101018_YD\BIT01763_YD_7.mgf

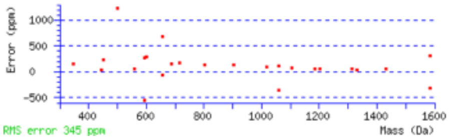
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



**Monoisotopic mass of neutral peptide Mr(calc):** 3316.7952
**Variable modifications:**
**K6** : GlyGly (K)
**Ions Score:** 57 **Expect:** 0.062
**Matches :** 25/312 fragment ions using 35 most intense peaks (help)

| # | b | b++ | b* | b*++ | b0 | b0++ | Seq. | y | y++ | y* | y*++ | y0 | y0++ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 132.0478 | 66.5275 | | | | | M | | | | | | | 29 |
| 2 | 260.1063 | 130.5568 | 243.0798 | 122.0435 | | | Q | 3186.7620 | 1593.8846 | 3169.7355 | 1585.3714 | 3168.7515 | 1584.8794 | 28 |
| 3 | 373.1904 | 187.0988 | 356.1639 | 178.5856 | | | I | 3058.7034 | 1529.8554 | 3041.6769 | 1521.3421 | 3040.6929 | 1520.8501 | 27 |
| 4 | 520.2588 | 260.6330 | 503.2323 | 252.1198 | | | F | 2945.6194 | 1473.3133 | 2928.5928 | 1464.8001 | 2927.6088 | 1464.3080 | 26 |
| 5 | 619.3272 | 310.1673 | 602.3007 | 301.6540 | | | V | 2798.5510 | 1399.7791 | 2781.5244 | 1391.2658 | 2780.5404 | 1390.7738 | 25 |
| 6 | 861.4651 | 431.2362 | 844.4386 | 422.7229 | | | K | 2699.4826 | 1350.2449 | 2682.4560 | 1341.7316 | 2681.4720 | 1341.2396 | 24 |
| 7 | 962.5128 | 481.7600 | 945.4863 | 473.2468 | 944.5022 | 472.7548 | T | 2457.3447 | 1229.1760 | 2440.3181 | 1220.6627 | 2439.3341 | 1220.1707 | 23 |
| 8 | 1075.5969 | 538.3021 | 1058.5703 | 529.7888 | 1057.5863 | 529.2968 | L | 2356.2970 | 1178.6521 | 2339.2704 | 1170.1389 | 2338.2864 | 1169.6468 | 22 |
| 9 | 1176.6445 | 588.8259 | 1159.6180 | 580.3126 | 1158.6340 | 579.8206 | T | 2243.2129 | 1122.1101 | 2226.1864 | 1113.5968 | 2225.2024 | 1113.1048 | 21 |
| 10 | 1233.6660 | 617.3366 | 1216.6395 | 608.8234 | 1215.6554 | 608.3314 | G | 2142.1652 | 1071.5863 | 2125.1387 | 1063.0730 | 2124.1547 | 1062.5810 | 20 |
| 11 | 1361.7610 | 681.3841 | 1344.7344 | 672.8708 | 1343.7504 | 672.3788 | K | 2085.1438 | 1043.0755 | 2068.1172 | 1034.5623 | 2067.1332 | 1034.0702 | 19 |
| 12 | 1462.8086 | 731.9080 | 1445.7821 | 723.3947 | 1444.7981 | 722.9027 | T | 1957.0488 | 979.0280 | 1940.0223 | 970.5148 | 1939.0382 | 970.0228 | 18 |
| 13 | 1575.8927 | 788.4500 | 1558.8662 | 779.9367 | 1557.8821 | 779.4447 | I | 1856.0011 | 928.5042 | 1838.9746 | 919.9909 | 1837.9906 | 919.4989 | 17 |
| 14 | 1646.9298 | 823.9686 | 1629.9033 | 815.4553 | 1628.9193 | 814.9633 | A | 1742.9171 | 871.9622 | 1725.8905 | 863.4489 | 1724.9065 | 862.9569 | 16 |
| 15 | 1760.0139 | 880.5106 | 1742.9873 | 871.9973 | 1742.0033 | 871.5053 | L | 1671.8800 | 836.4436 | 1654.8534 | 827.9303 | 1653.8694 | 827.4383 | 15 |
| 16 | 1889.0565 | 945.0319 | 1872.0299 | 936.5186 | 1871.0459 | 936.0266 | E | 1558.7959 | 779.9016 | 1541.7693 | 771.3883 | 1540.7853 | 770.8963 | 14 |
| 17 | 1988.1249 | 994.5661 | 1971.0983 | 986.0528 | 1970.1143 | 985.5608 | V | ***1429.7533*** | 715.3803 | 1412.7268 | 706.8670 | 1411.7427 | 706.3750 | 13 |
| 18 | 2117.1675 | 1059.0874 | 2100.1409 | 1050.5741 | 2099.1569 | 1050.0821 | E | ***1330.6849*** | 665.8461 | 1313.6583 | 657.3328 | 1312.6743 | 656.8408 | 12 |
| 19 | 2214.2203 | 1107.6138 | 2197.1937 | 1099.1005 | 2196.2097 | 1098.6085 | P | ***1201.6423*** | 601.3248 | 1184.6157 | 592.8115 | 1183.6317 | 592.3195 | 11 |
| 20 | 2301.2523 | 1151.1298 | 2284.2257 | 1142.6165 | 2283.2417 | 1142.1245 | S | ***1104.5895*** | 552.7984 | 1087.5630 | 544.2851 | 1086.5790 | 543.7931 | 10 |
| 21 | 2416.2792 | 1208.6433 | 2399.2527 | 1200.1300 | 2398.2687 | 1199.6380 | D | ***1017.5575*** | 509.2824 | 1000.5310 | 500.7691 | 999.5469 | 500.2771 | 9 |
| 22 | 2517.3269 | 1259.1671 | 2500.3004 | 1250.6538 | 2499.3163 | 1250.1618 | T | ***902.5306*** | 451.7689 | 885.5040 | 443.2556 | 884.5200 | 442.7636 | 8 |
| 23 | 2630.4110 | 1315.7091 | 2613.3844 | 1307.1958 | 2612.4004 | 1306.7038 | I | ***801.4829*** | 401.2451 | 784.4563 | 392.7318 | 783.4723 | 392.2398 | 7 |
| 24 | 2759.4536 | 1380.2304 | 2742.4270 | 1371.7171 | 2741.4430 | 1371.2251 | E | ***688.3988*** | 344.7030 | 671.3723 | 336.1898 | 670.3883 | 335.6978 | 6 |
| 25 | 2873.4965 | 1437.2519 | 2856.4699 | 1428.7386 | 2855.4859 | 1428.2466 | N | ***559.3562*** | 280.1817 | 542.3297 | 271.6685 | | | 5 |
| 26 | 2972.5649 | 1486.7861 | 2955.5384 | 1478.2728 | 2954.5543 | 1477.7808 | V | ***445.3133*** | 223.1603 | 428.2867 | 214.6470 | | | 4 |
| 27 | 3100.6599 | 1550.8336 | 3083.6333 | 1542.3203 | 3082.6493 | 1541.8283 | K | ***346.2449*** | 173.6261 | 329.2183 | 165.1128 | | | 3 |
| 28 | 3171.6970 | 1586.3521 | 3154.6704 | 1577.8389 | 3153.6864 | 1577.3468 | A | 218.1499 | 109.5786 | 201.1234 | 101.0653 | | | 2 |
| 29 | | | | | | | K | 147.1128 | 74.0600 | 130.0863 | 65.5468 | | | 1 |





NCBI **BLAST** search of MQIFVKTLTGKTIALEVEPSDTIENVKAK
(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 | 3316.7952 | -0.6683 | MQIFVKTLTGKTIALEVEPSDTIENVKAK |
| 57.2 | 3316.7952 | -0.6683 | MQIFVKTLTGKTIALEVEPSDTIENVKAK |
| 57.2 | 3315.7926 | 0.3343 | QIFVKTLTGKTITLDVEPSDTIENVKAK |
| 57.2 | 3316.7766 | -0.6497 | QIFVKTLTGKTITLDVEPSDTIENVKAK |
| 35.8 | 3314.8312 | 1.2957 | NILDLSPFTVTDLTPMEIVVDIFRKLGLR |
| 34.9 | 3315.5385 | 0.5884 | MEQLKEQGGEGQSEAAEAQRQQAEAQKK |

| | | | |
|---|---|---|---|
| 34.9 | 3315.5385 | 0.5884 | MEQLKEQGGEGQSEAAEAQRQQAEAQKK |
| 34.8 | 3316.5225 | -0.3956 | MEQLKEQGGEGQSEAAEAQRQQAEAQKK |
| 33.9 | 3316.4474 | -0.3205 | CRKENSALKECLTAYYNDPAFYEECK |
| 33.4 | 3315.8329 | 0.2940 | IYQKIVTKARNLVAVGEAIESEFGIPIINK |

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

# Mascot Search Results

## Protein View

Match to: **YD_RFP-p53-Ub** Score: **724**
**YD_RFP-p53-Ub**
Found in search of D:\Data\2010_10\BIT01711b_YD_14_RC1_01_7727.d\Analysis.mgf

Nominal mass ($M_r$): **79240**; Calculated pI value: **6.17**
NCBI BLAST search of YD_RFP-p53-Ub against nr
Unformatted sequence string for pasting into other applications

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **36%**

Matched peptides shown in **Bold Red**

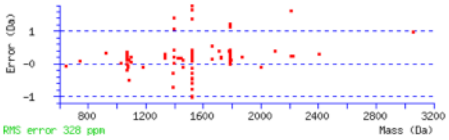
**1** MHHHHHHASS EDVIKEFMRF KVR**MEGSVNG** **HEFEIEGEGE** **GRPYEGTQTA**
**51** **K**LKVTK**GGPL** **PFAWDILSPQ** **FQYGSK**AYVK HPADIPDYLK **LSFPEGFK**WE
**101** RVMNFEDGGV VTVTQDSSLQ DGEFIYKVK**L** **RGTNFPSDGP** **VMQKKTMGWE**
**151** **ASTER**MYPED GALKGEIKMR LK**LKDGGHYD** **AEVK**TTYMAK **KPVQLPGAYK**
**201** TDIK**LDITSH** **NEDYTIVEQY** **ER**AEGRHSTG AENLYFQGLE EEPQSDPSVE
**251** PPLSQETFSD LWKLLPENNV LSPLPSQAMD DLMLSPDDIE QWFTEDPGPD
**301** EAPRMPEAAP RVAPAPAAPT PAAPAPAPSW PLSSSVPSQK **TYQGSYGFRL**
**351** **GFLHSGTAK**S VTCTYSPALN KMFCQLAKTC PVQLWVDSTP PPGTRVRAMA
**401** IYKQSQHMTE VVRRCPHHER CSDSDGLAPP QHLIR**VEGNL** **RVEYLDDRNT**
**451** **FR**HSVVVPYE PPEVGSDCTT IHYNYMCNSS CMGGMNRRPI LTIITLEDSS
**501** GNLLGRNSFE VHVCACPGRD RRTEEENLRK KGEPHHELPP GSTKRALSNN
**551** TSSSPQPK**KK** **PLDGEYFTLQ** **IR**GRER**FEMF** **R**ELNEALELK DAQAGKEPGG
**601** SRAHSSHLKS KKGQSTSRHK **KLMFKTEGPD** **SDQIFVKTLT** **GKTITLEVEP**
**651** **SDTIENVKAK** **IQDKEGIPPD** **QQRLIFAGKQ** **LEDGRTLSDY** **NIQKESTLHL**
**701** **VLR**LRGG

Show predicted peptides also

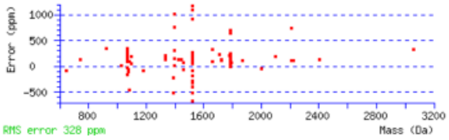
Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

| Start - End | Observed | Mr(expt) | Mr(calc) | Delta | Miss | Sequence |
|---|---|---|---|---|---|---|
| 24 - 51 | 764.5870 | 3054.3189 | 3053.3309 | 0.9880 | 0 | R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L Oxidation (M) (Ions score 63) |
| 57 - 76 | 1104.6760 | 2207.3374 | 2207.1051 | 0.2323 | 0 | K.GGPLPFAWDILSPQFQYGSK.A (Ions score 78) |
| 57 - 76 | 737.2480 | 2208.7222 | 2207.1051 | 1.6170 | 0 | K.GGPLPFAWDILSPQFQYGSK.A (Ions score 29) |
| 91 - 98 | 462.9040 | 923.7934 | 923.4753 | 0.3182 | 0 | K.LSFPEGFK.W (Ions score 39) |
| 130 - 144 | 555.0000 | 1661.9782 | 1661.8195 | 0.1586 | 1 | K.LRGTNFPSDGPVMQK.K Oxidation (M) (Ions score 44) |
| 130 - 144 | 832.1930 | 1662.3714 | 1661.8195 | 0.5519 | 1 | K.LRGTNFPSDGPVMQK.K Oxidation (M) (Ions score 22) |
| 130 - 145 | 896.0220 | 1790.0294 | 1789.9145 | 0.1149 | 2 | K.LRGTNFPSDGPVMQKK.T Oxidation (M) (Ions score 26) |
| 132 - 144 | 696.9610 | 1391.9074 | 1392.6344 | -0.7269 | 0 | R.GTNFPSDGPVMQK.K Oxidation (M) (Ions score 31) |
| 132 - 144 | 697.1770 | 1392.3394 | 1392.6344 | -0.2949 | 0 | R.GTNFPSDGPVMQK.K Oxidation (M) (Ions score 41) |
| 132 - 144 | 697.3290 | 1392.6434 | 1392.6344 | 0.0091 | 0 | R.GTNFPSDGPVMQK.K Oxidation (M) (Ions score 31) |
| 132 - 144 | 697.4290 | 1392.8434 | 1392.6344 | 0.2091 | 0 | R.GTNFPSDGPVMQK.K Oxidation (M) (Ions score 67) |
| 132 - 144 | 697.5420 | 1393.0694 | 1392.6344 | 0.4351 | 0 | R.GTNFPSDGPVMQK.K Oxidation (M) (Ions score 19) |
| 132 - 144 | 697.8540 | 1393.6934 | 1392.6344 | 1.0591 | 0 | R.GTNFPSDGPVMQK.K Oxidation (M) (Ions score 18) |
| 132 - 144 | 698.0270 | 1394.0394 | 1392.6344 | 1.4051 | 0 | R.GTNFPSDGPVMQK.K Oxidation (M) (Ions score 22) |
| 146 - 155 | 592.2020 | 1182.3894 | 1182.4975 | -0.1081 | 0 | K.TMGWEASTER.M Oxidation (M) (Ions score 74) |
| 173 - 184 | 666.4420 | 1330.8694 | 1330.6517 | 0.2177 | 1 | K.LKDGGHYDAEVK.T (Ions score 78) |
| 173 - 184 | 444.6550 | 1330.9432 | 1330.6517 | 0.2915 | 1 | K.LKDGGHYDAEVK.T (Ions score 34) |
| 173 - 184 | 723.4450 | 1444.8754 | 1444.6946 | 0.1808 | 1 | K.LKDGGHYDAEVK.T GlyGly (K) (Ions score 44) |
| 191 - 200 | 367.5760 | 1099.7062 | 1099.6390 | 0.0672 | 0 | K.KPVQLPGAYK.T (Ions score 36) |
| 191 - 200 | 550.9310 | 1099.8474 | 1099.6390 | 0.2085 | 0 | K.KPVQLPGAYK.T (Ions score 49) |
| 205 - 222 | 1113.1450 | 2224.2754 | 2224.0284 | 0.2471 | 0 | K.LDITSHNEDYTIVEQYER.A (Ions score 38) |
| 341 - 349 | 539.7000 | 1077.3854 | 1077.4880 | -0.1025 | 0 | K.TYQGSYGFR.L (Ions score 40) |
| 341 - 349 | 539.7150 | 1077.4154 | 1077.4880 | -0.0725 | 0 | K.TYQGSYGFR.L (Ions score 45) |
| 350 - 359 | 515.7960 | 1029.5774 | 1029.5607 | 0.0167 | 0 | R.LGFLHSGTAK.S (Ions score 50) |
| 350 - 359 | 344.2020 | 1029.5842 | 1029.5607 | 0.0234 | 0 | R.LGFLHSGTAK.S (Ions score 25) |
| 436 - 452 | 699.4830 | 2095.4272 | 2095.0446 | 0.3825 | 2 | R.VEGNLRVEYLDDRNTFR.H (Ions score 24) |
| 442 - 452 | 714.4440 | 1426.8734 | 1426.6841 | 0.1894 | 1 | R.VEYLDDRNTFR.H (Ions score 45) |
| 559 - 572 | 570.1130 | 1707.3172 | 1706.9355 | 0.3816 | 1 | K.KKPLDGEYFTLQIR.G (Ions score 59) |
| 577 - 581 | 373.2180 | 744.4214 | 744.3265 | 0.0950 | 0 | R.FEMFR.E Oxidation (M) (Ions score 29) |
| 621 - 637 | 666.9800 | 1997.9182 | 1998.0132 | -0.0950 | 2 | K.KLMFKTEGPDSDQIFVK.T Oxidation (M) (Ions score 20) |
| 622 - 637 | 936.0630 | 1870.1114 | 1869.9183 | 0.1932 | 1 | K.LMFKTEGPDSDQIFVK.T Oxidation (M) (Ions score 82) |
| 626 - 637 | 668.4090 | 1334.8034 | 1334.6354 | 0.1680 | 0 | K.TEGPDSDQIFVK.T (Ions score 81) |
| 638 - 658 | 801.5300 | 2401.5682 | 2401.2588 | 0.3094 | 1 | K.TLTGKTITLEVEPSDTIENVK.A GlyGly (K) (Ions score 79) |
| 643 - 658 | 894.4650 | 1786.9154 | 1786.9200 | -0.0046 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 51) |
| 643 - 658 | 894.4720 | 1786.9294 | 1786.9200 | 0.0094 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 57) |
| 643 - 658 | 894.4720 | 1786.9294 | 1786.9200 | 0.0094 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 46) |
| 643 - 658 | 894.4780 | 1786.9414 | 1786.9200 | 0.0214 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 61) |
| 643 - 658 | 894.4830 | 1786.9514 | 1786.9200 | 0.0314 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 49) |
| 643 - 658 | 894.4920 | 1786.9694 | 1786.9200 | 0.0494 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 53) |
| 643 - 658 | 894.4950 | 1786.9754 | 1786.9200 | 0.0554 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 60) |
| 643 - 658 | 894.5060 | 1786.9974 | 1786.9200 | 0.0774 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 57) |
| 643 - 658 | 894.5160 | 1787.0174 | 1786.9200 | 0.0974 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 30) |
| 643 - 658 | 894.5360 | 1787.0574 | 1786.9200 | 0.1374 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 31) |
| 643 - 658 | 894.5520 | 1787.0894 | 1786.9200 | 0.1694 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 47) |
| 643 - 658 | 894.5570 | 1787.0994 | 1786.9200 | 0.1794 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 53) |
| 643 - 658 | 894.5650 | 1787.1154 | 1786.9200 | 0.1954 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 53) |
| 643 - 658 | 894.5660 | 1787.1174 | 1786.9200 | 0.1974 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 57) |
| 643 - 658 | 894.5860 | 1787.1574 | 1786.9200 | 0.2374 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 36) |
| 643 - 658 | 894.5950 | 1787.1754 | 1786.9200 | 0.2554 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 60) |
| 643 - 658 | 894.6060 | 1787.1974 | 1786.9200 | 0.2774 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 62) |
| 643 - 658 | 894.6100 | 1787.2054 | 1786.9200 | 0.2854 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 77) |
| 643 - 658 | 894.6160 | 1787.2174 | 1786.9200 | 0.2974 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 66) |
| 643 - 658 | 894.6310 | 1787.2474 | 1786.9200 | 0.3274 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 65) |
| 643 - 658 | 894.6490 | 1787.2834 | 1786.9200 | 0.3634 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 53) |
| 643 - 658 | 894.6790 | 1787.3434 | 1786.9200 | 0.4234 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 82) |
| 643 - 658 | 894.6860 | 1787.3574 | 1786.9200 | 0.4374 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 102) |
| 643 - 658 | 895.0340 | 1788.0534 | 1786.9200 | 1.1334 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 39) |
| 643 - 658 | 895.0470 | 1788.0794 | 1786.9200 | 1.1594 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 40) |
| 643 - 658 | 895.0860 | 1788.1574 | 1786.9200 | 1.2374 | 0 | K.TITLEVEPSDTIENVK.A (Ions score 37) |
| 659 - 673 | 862.0560 | 1722.0974 | 1721.9060 | 0.1914 | 2 | K.AKIQDKEGIPPDQQR.L (Ions score 78) |
| 659 - 673 | 431.5390 | 1722.1269 | 1721.9060 | 0.2209 | 2 | K.AKIQDKEGIPPDQQR.L (Ions score 30) |
| 661 - 673 | 761.8860 | 1521.7574 | 1522.7740 | -1.0165 | 1 | K.IQDKEGIPPDQQR.L (Ions score 11) |
| 661 - 673 | 761.8890 | 1521.7634 | 1522.7740 | -1.0105 | 1 | K.IQDKEGIPPDQQR.L (Ions score 15) |
| 661 - 673 | 762.0100 | 1522.0054 | 1522.7740 | -0.7685 | 1 | K.IQDKEGIPPDQQR.L (Ions score 14) |
| 661 - 673 | 762.0890 | 1522.1634 | 1522.7740 | -0.6105 | 1 | K.IQDKEGIPPDQQR.L (Ions score 29) |
| 661 - 673 | 762.1500 | 1522.2854 | 1522.7740 | -0.4885 | 1 | K.IQDKEGIPPDQQR.L (Ions score 10) |
| 661 - 673 | 762.1800 | 1522.3454 | 1522.7740 | -0.4285 | 1 | K.IQDKEGIPPDQQR.L (Ions score 21) |
| 661 - 673 | 762.2550 | 1522.4954 | 1522.7740 | -0.2785 | 1 | K.IQDKEGIPPDQQR.L (Ions score 29) |
| 661 - 673 | 762.3330 | 1522.6514 | 1522.7740 | -0.1225 | 1 | K.IQDKEGIPPDQQR.L (Ions score 12) |
| 661 - 673 | 762.4400 | 1522.8654 | 1522.7740 | 0.0915 | 1 | K.IQDKEGIPPDQQR.L (Ions score 12) |
| 661 - 673 | 762.4760 | 1522.9374 | 1522.7740 | 0.1635 | 1 | K.IQDKEGIPPDQQR.L (Ions score 56) |
| 661 - 673 | 762.4910 | 1522.9674 | 1522.7740 | 0.1935 | 1 | K.IQDKEGIPPDQQR.L (Ions score 27) |
| 661 - 673 | 762.4980 | 1522.9814 | 1522.7740 | 0.2075 | 1 | K.IQDKEGIPPDQQR.L (Ions score 57) |
| 661 - 673 | 762.5030 | 1522.9914 | 1522.7740 | 0.2175 | 1 | K.IQDKEGIPPDQQR.L (Ions score 53) |
| 661 - 673 | 762.5070 | 1522.9994 | 1522.7740 | 0.2255 | 1 | K.IQDKEGIPPDQQR.L (Ions score 35) |
| 661 - 673 | 762.5460 | 1523.0774 | 1522.7740 | 0.3035 | 1 | K.IQDKEGIPPDQQR.L (Ions score 20) |
| 661 - 673 | 508.7000 | 1523.0782 | 1522.7740 | 0.3042 | 1 | K.IQDKEGIPPDQQR.L (Ions score 21) |
| 661 - 673 | 508.7000 | 1523.0782 | 1522.7740 | 0.3042 | 1 | K.IQDKEGIPPDQQR.L (Ions score 26) |
| 661 - 673 | 508.7100 | 1523.1082 | 1522.7740 | 0.3342 | 1 | K.IQDKEGIPPDQQR.L (Ions score 39) |
| 661 - 673 | 762.6030 | 1523.1914 | 1522.7740 | 0.4175 | 1 | K.IQDKEGIPPDQQR.L (Ions score 14) |
| 661 - 673 | 762.6050 | 1523.1954 | 1522.7740 | 0.4215 | 1 | K.IQDKEGIPPDQQR.L (Ions score 43) |
| 661 - 673 | 763.0900 | 1524.1654 | 1522.7740 | 1.3915 | 1 | K.IQDKEGIPPDQQR.L (Ions score 23) |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 661 - 673 | 763.2260 | 1524.4374 | 1522.7740 | 1.6635 | 1 | K.IQDKEGIPPDQQR.L | | (Ions score 24) |
| 661 - 673 | 763.2840 | 1524.5534 | 1522.7740 | 1.7795 | 1 | K.IQDKEGIPPDQQR.L | | (Ions score 44) |
| 674 - 679 | 324.6790 | 647.3434 | 647.4006 | -0.0572 | 0 | R.LIFAGK.Q | | (Ions score 35) |
| 674 - 685 | 487.5700 | 1459.6882 | 1459.7783 | -0.0901 | 1 | R.LIFAGKQLEDGR.T | GlyGly (K) | (Ions score 37) |
| 674 - 685 | 730.9460 | 1459.8774 | 1459.7783 | 0.0991 | 1 | R.LIFAGKQLEDGR.T | GlyGly (K) | (Ions score 87) |
| 680 - 694 | 594.0940 | 1779.2602 | 1778.8799 | 0.3803 | 1 | K.QLEDGRTLSDYNIQK.E | | (Ions score 21) |
| 686 - 694 | 541.0340 | 1080.0534 | 1080.5451 | -0.4917 | 0 | R.TLSDYNIQK.E | | (Ions score 20) |
| 686 - 694 | 541.3310 | 1080.6474 | 1080.5451 | 0.1023 | 0 | R.TLSDYNIQK.E | | (Ions score 57) |
| 695 - 703 | 534.2230 | 1066.4314 | 1066.6135 | -0.1820 | 0 | K.ESTLHLVLR.L | | (Ions score 58) |
| 695 - 703 | 534.3060 | 1066.5974 | 1066.6135 | -0.0160 | 0 | K.ESTLHLVLR.L | | (Ions score 26) |
| 695 - 703 | 534.3640 | 1066.7134 | 1066.6135 | 0.1000 | 0 | K.ESTLHLVLR.L | | (Ions score 74) |
| 695 - 703 | 534.3700 | 1066.7254 | 1066.6135 | 0.1120 | 0 | K.ESTLHLVLR.L | | (Ions score 65) |
| 695 - 703 | 534.3790 | 1066.7434 | 1066.6135 | 0.1300 | 0 | K.ESTLHLVLR.L | | (Ions score 43) |
| 695 - 703 | 534.3870 | 1066.7594 | 1066.6135 | 0.1460 | 0 | K.ESTLHLVLR.L | | (Ions score 62) |
| 695 - 703 | 534.3950 | 1066.7754 | 1066.6135 | 0.1620 | 0 | K.ESTLHLVLR.L | | (Ions score 55) |
| 695 - 703 | 534.4140 | 1066.8134 | 1066.6135 | 0.2000 | 0 | K.ESTLHLVLR.L | | (Ions score 21) |
| 695 - 703 | 534.4270 | 1066.8394 | 1066.6135 | 0.2260 | 0 | K.ESTLHLVLR.L | | (Ions score 45) |
| 695 - 703 | 534.4600 | 1066.9054 | 1066.6135 | 0.2920 | 0 | K.ESTLHLVLR.L | | (Ions score 20) |
| 695 - 703 | 534.4870 | 1066.9594 | 1066.6135 | 0.3460 | 0 | K.ESTLHLVLR.L | | (Ions score 65) |
| 695 - 703 | 534.5010 | 1066.9874 | 1066.6135 | 0.3740 | 0 | K.ESTLHLVLR.L | | (Ions score 69) |



RMS error 328 ppm



RMS error 328 ppm

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

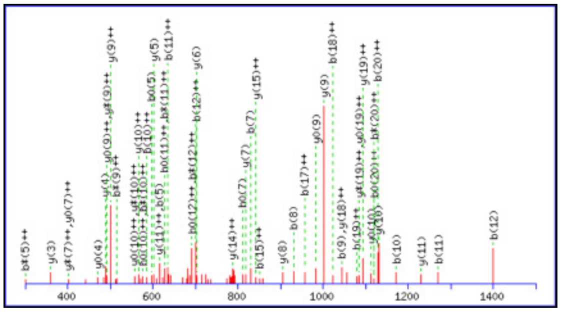
# Mascot Search Results

### Peptide View

MS/MS Fragmentation of **TLTGKTITLEVEPSDTIENVK**
Found in **YD_RFP-p53-Ub**, YD_RFP-p53-Ub

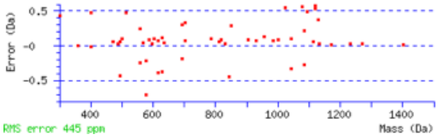
Match to Query 717: 2401.568172 from(801.530000,3+) intensity(782903.0000)
Title: Cmpd 346, +MSn(802.12), 29.0 min
Data file D:\Data\2010_10\BIT01711b_YD_14_RC1_01_7727.d\Analysis.mgf

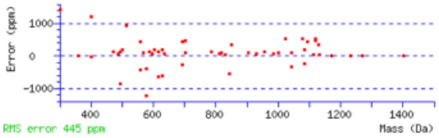
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



**Monoisotopic mass of neutral peptide Mr(calc):** 2401.2588
**Variable modifications:**
**K5** : GlyGly (K)
**Ions Score:** 79 **Expect:** 0.00035
**Matches :** 54/226 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 | 102.0550 | 51.5311 | | | 84.0444 | 42.5258 | T | | | | | | | 21 |
| 2 | 215.1390 | 108.0731 | | | 197.1285 | 99.0679 | L | 2301.2184 | 1151.1128 | 2284.1918 | 1142.5996 | 2283.2078 | 1142.1076 | 20 |
| 3 | 316.1867 | 158.5970 | | | 298.1761 | 149.5917 | T | 2188.1343 | 1094.5708 | 2171.1078 | 1086.0575 | 2170.1238 | 1085.5655 | 19 |
| 4 | 373.2082 | 187.1077 | | | 355.1976 | 178.1024 | G | 2087.0867 | 1044.0470 | 2070.0601 | 1035.5337 | 2069.0761 | 1035.0417 | 18 |
| 5 | ***615.3461*** | 308.1767 | 598.3195 | 299.6634 | 597.3355 | 299.1714 | K | 2030.0652 | 1015.5362 | 2013.0386 | 1007.0230 | 2012.0546 | 1006.5310 | 17 |
| 6 | 716.3937 | 358.7005 | 699.3672 | 350.1872 | 698.3832 | 349.6952 | T | 1787.9273 | 894.4673 | 1770.9008 | 885.9540 | 1769.9167 | 885.4620 | 16 |
| 7 | ***829.4778*** | 415.2425 | 812.4512 | 406.7293 | 811.4672 | 406.2373 | I | 1686.8796 | 843.9434 | 1669.8531 | 835.4302 | 1668.8691 | 834.9382 | 15 |
| 8 | ***930.5255*** | 465.7664 | 913.4989 | 457.2531 | 912.5149 | 456.7611 | T | 1573.7956 | 787.4014 | 1556.7690 | 778.8881 | 1555.7850 | 778.3961 | 14 |
| 9 | ***1043.6095*** | 522.3084 | 1026.5830 | 513.7951 | 1025.5990 | 513.3031 | L | 1472.7479 | 736.8776 | 1455.7213 | 728.3643 | 1454.7373 | 727.8723 | 13 |
| 10 | ***1172.6521*** | ***586.8297*** | 1155.6256 | 578.3164 | 1154.6416 | 577.8244 | E | 1359.6638 | 680.3355 | 1342.6373 | 671.8223 | 1341.6533 | 671.3303 | 12 |
| 11 | ***1271.7205*** | ***636.3639*** | 1254.6940 | 627.8506 | 1253.7100 | 627.3586 | V | ***1230.6212*** | 615.8142 | 1213.5947 | 607.3010 | 1212.6107 | 606.8090 | 11 |
| 12 | ***1400.7631*** | ***700.8852*** | 1383.7366 | 692.3719 | 1382.7526 | 691.8799 | E | ***1131.5528*** | 566.2800 | 1114.5263 | 557.7668 | 1113.5422 | 557.2748 | 10 |
| 13 | 1497.8159 | 749.4116 | 1480.7894 | 740.8983 | 1479.8053 | 740.4063 | P | ***1002.5102*** | 501.7587 | 985.4837 | 493.2455 | 984.4997 | 492.7535 | 9 |
| 14 | 1584.8479 | 792.9276 | 1567.8214 | 784.4143 | 1566.8374 | 783.9223 | S | ***905.4575*** | 453.2324 | 888.4309 | 444.7191 | 887.4469 | 444.2271 | 8 |
| 15 | 1699.8749 | ***850.4411*** | 1682.8483 | 841.9278 | 1681.8643 | 841.4358 | D | ***818.4254*** | 409.7163 | 801.3989 | 401.2031 | 800.4149 | 400.7111 | 7 |
| 16 | 1800.9226 | 900.9649 | 1783.8960 | 892.4516 | 1782.9120 | 891.9596 | T | ***703.3985*** | 352.2029 | 686.3719 | 343.6896 | 685.3879 | 343.1976 | 6 |
| 17 | 1914.0066 | ***957.5069*** | 1896.9801 | 948.9937 | 1895.9961 | 948.5017 | I | ***602.3508*** | 301.6790 | 585.3243 | 293.1658 | 584.3402 | 292.6738 | 5 |
| 18 | 2043.0492 | ***1022.0282*** | 2026.0227 | 1013.5150 | 2025.0386 | 1013.0230 | E | ***489.2667*** | 245.1370 | 472.2402 | 236.6237 | 471.2562 | 236.1317 | 4 |
| 19 | 2157.0921 | ***1079.0497*** | 2140.0656 | 1070.5364 | 2139.0816 | 1070.0444 | N | ***360.2241*** | 180.6157 | 343.1976 | 172.1024 | | | 3 |
| 20 | 2256.1605 | ***1128.5839*** | 2239.1340 | 1120.0706 | 2238.1500 | 1119.5786 | V | 246.1812 | 123.5942 | 229.1547 | 115.0810 | | | 2 |
| 21 | | | | | | | K | 147.1128 | 74.0600 | 130.0863 | 65.5468 | | | 1 |





NCBI **BLAST** search of TLTGKTITLEVEPSDTIENVK
(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 | 2401.2588 | 0.3094 | TLTGKTITLEVEPSDTIENVK |
| 47.6 | 2402.0180 | -0.4498 | TSGNQQSVVTQPSTGTNNDFCSK |
| 41.2 | 2402.2428 | -0.6746 | TLTGKTITLEVEPSDTIENVK |
| 34.8 | 2402.1648 | -0.5966 | EIREACDNAEVIGARYPPGAGSK |
| 34.4 | 2401.2887 | 0.2795 | LVSVASTGTPAMVDANNGLVTKLK |
| 33.0 | 2401.1682 | 0.4000 | ITQSIMDNPEAIEQIAREVK |
| 32.9 | 2401.0340 | 0.5342 | TSGNQQSVVTQPSTGTNNDFCSK |
| 31.6 | 2401.0340 | 0.5342 | TSGNQQSVVTQPSTGTNNDFCSK |
| 31.6 | 2401.0340 | 0.5342 | TSGNQQSVVTQPSTGTNNDFCSK |
| 30.4 | 2401.3216 | 0.2465 | KVNIASYQVKPGDVIEVKEASK |

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

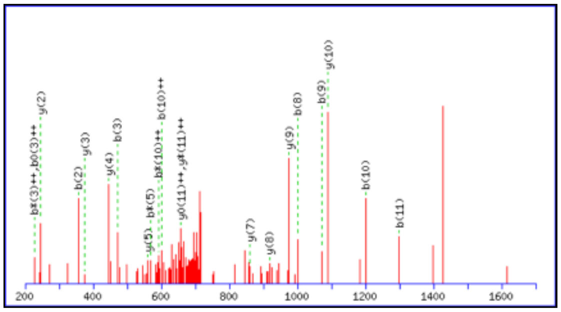
# Mascot Search Results

### Peptide View

MS/MS Fragmentation of **LKDGGHYDAEVK**
Found in **YD_RFP-p53-Ub**, YD_RFP-p53-Ub

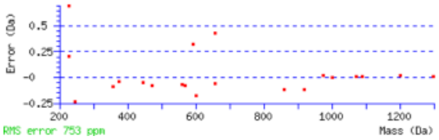
Match to Query 282: 1444.875448 from(723.445000,2+) intensity(29358.0000)
Title: Cmpd 220, +MSn(723.91), 17.2 min
Data file D:\Data\2010_10\BIT01711b_YD_14_RC1_01_7727.d\Analysis.mgf

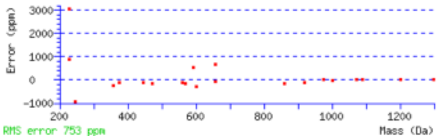
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



**Monoisotopic mass of neutral peptide Mr(calc):** 1444.6946
**Variable modifications:**
**K2** : GlyGly (K)
**Ions Score:** 44 **Expect:** 0.55
**Matches :** 21/122 fragment ions using 36 most intense peaks (help)

| # | b | b++ | b* | b*++ | b0 | b0++ | Seq. | y | y++ | y* | y*++ | y0 | y0++ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.0913 | 57.5493 | | | | | L | | | | | | | 12 |
| 2 | **356.2292** | 178.6183 | 339.2027 | 170.1050 | | | K | 1332.6179 | 666.8126 | 1315.5913 | 658.2993 | 1314.6073 | 657.8073 | 11 |
| 3 | **471.2562** | 236.1317 | 454.2296 | 227.6185 | 453.2456 | 227.1264 | D | ***1090.4800*** | 545.7436 | 1073.4534 | 537.2304 | 1072.4694 | 536.7383 | 10 |
| 4 | 528.2776 | 264.6425 | 511.2511 | 256.1292 | 510.2671 | 255.6372 | G | ***975.4530*** | 488.2302 | 958.4265 | 479.7169 | 957.4425 | 479.2249 | 9 |
| 5 | 585.2991 | 293.1532 | 568.2726 | 284.6399 | 567.2885 | 284.1479 | G | ***918.4316*** | 459.7194 | 901.4050 | 451.2062 | 900.4210 | 450.7141 | 8 |
| 6 | 722.3580 | 361.6826 | 705.3315 | 353.1694 | 704.3474 | 352.6774 | H | ***861.4101*** | 431.2087 | 844.3836 | 422.6954 | 843.3995 | 422.2034 | 7 |
| 7 | 885.4213 | 443.2143 | 868.3948 | 434.7010 | 867.4108 | 434.2090 | Y | 724.3512 | 362.6792 | 707.3246 | 354.1660 | 706.3406 | 353.6740 | 6 |
| 8 | **1000.4483** | 500.7278 | 983.4217 | 492.2145 | 982.4377 | 491.7225 | D | ***561.2879*** | 281.1476 | 544.2613 | 272.6343 | 543.2773 | 272.1423 | 5 |
| 9 | **1071.4854** | 536.2463 | 1054.4589 | 527.7331 | 1053.4748 | 527.2411 | A | ***446.2609*** | 223.6341 | 429.2344 | 215.1208 | 428.2504 | 214.6288 | 4 |
| 10 | **1200.5280** | 600.7676 | 1183.5014 | 592.2544 | 1182.5174 | 591.7624 | E | ***375.2238*** | 188.1155 | 358.1973 | 179.6023 | 357.2132 | 179.1103 | 3 |
| 11 | **1299.5964** | 650.3018 | 1282.5699 | 641.7886 | 1281.5858 | 641.2966 | V | ***246.1812*** | 123.5942 | 229.1547 | 115.0810 | | | 2 |
| 12 | | | | | | | K | 147.1128 | 74.0600 | 130.0863 | 65.5468 | | | 1 |





NCBI **BLAST** search of LKDGGHYDAEVK
(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 | 1444.6946 | 0.1808 | LKDGGHYDAEVK |
| 40.3 | 1444.7409 | 0.1346 | KLDQINDKLDK |
| 36.4 | 1444.7521 | 0.1233 | RAQDEIQKLTDK |
| 31.2 | 1444.7045 | 0.1709 | KLDEAQAQADIK |
| 29.2 | 1444.7158 | 0.1597 | KLDKNGDGQLDK |
| 29.1 | 1444.7522 | 0.1233 | IGGKTQDQTAAINK |
| 29.0 | 1443.6048 | 1.2706 | MNGAPQNTSHGSK |
| 28.8 | 1444.7409 | 0.1346 | KLNQVGSDILNK |
| 28.8 | 1444.7521 | 0.1233 | NQLNQKTKLDK |
| 28.8 | 1444.7521 | 0.1233 | NQLNQKTKLDK |

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

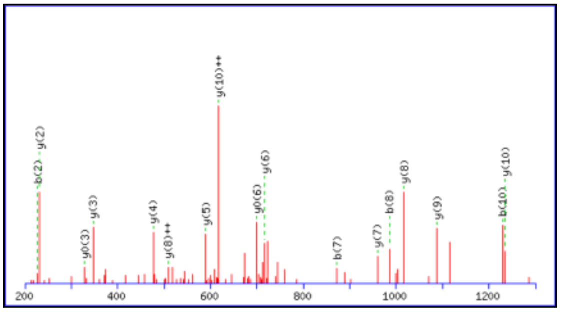
# MATRIX SCIENCE Mascot Search Results

### Peptide View

MS/MS Fragmentation of **LIFAGKQLEDGR**
Found in **YD_RFP-p53-Ub**, YD_RFP-p53-Ub

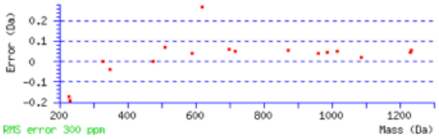
Match to Query 291: 1459.877448 from(730.946000,2+) intensity(1610801.0000)
Title: Cmpd 315, +MSn(731.23), 26.0 min
Data file D:\Data\2010_10\BIT01711b_YD_14_RC1_01_7727.d\Analysis.mgf

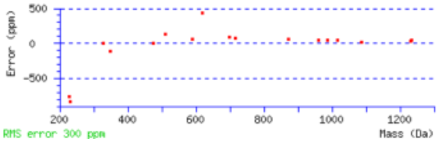
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



**Monoisotopic mass of neutral peptide Mr(calc):** 1459.7783
**Variable modifications:**
**K6** : GlyGly (K)
**Ions Score:** 87 **Expect:** 3.8e-06
**Matches :** 17/102 fragment ions using 20 most intense peaks (help)

| # | b | $b^{++}$ | b* | $b^{*++}$ | $b^0$ | $b^{0++}$ | Seq. | y | $y^{++}$ | y* | $y^{*++}$ | $y^0$ | $y^{0++}$ | # |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 114.0913 | 57.5493 | | | | | L | | | | | | | 12 |
| 2 | **227.1754** | 114.0913 | | | | | I | 1347.7015 | 674.3544 | 1330.6750 | 665.8411 | 1329.6910 | 665.3491 | 11 |
| 3 | 374.2438 | 187.6255 | | | | | F | ***1234.6175*** | 617.8124 | 1217.5909 | 609.2991 | 1216.6069 | 608.8071 | 10 |
| 4 | 445.2809 | 223.1441 | | | | | A | ***1087.5491*** | 544.2782 | 1070.5225 | 535.7649 | 1069.5385 | 535.2729 | 9 |
| 5 | 502.3024 | 251.6548 | | | | | G | ***1016.5119*** | 508.7596 | 999.4854 | 500.2463 | 998.5014 | 499.7543 | 8 |
| 6 | 744.4403 | 372.7238 | 727.4137 | 364.2105 | | | K | ***959.4905*** | 480.2489 | 942.4639 | 471.7356 | 941.4799 | 471.2436 | 7 |
| 7 | **872.4989** | 436.7531 | 855.4723 | 428.2398 | | | Q | ***717.3526*** | 359.1799 | 700.3260 | 350.6667 | 699.3420 | 350.1747 | 6 |
| 8 | **985.5829** | 493.2951 | 968.5564 | 484.7818 | | | L | ***589.2940*** | 295.1506 | 572.2675 | 286.6374 | 571.2835 | 286.1454 | 5 |
| 9 | 1114.6255 | 557.8164 | 1097.5990 | 549.3031 | 1096.6150 | 548.8111 | E | ***476.2100*** | 238.6086 | 459.1834 | 230.0953 | 458.1994 | 229.6033 | 4 |
| 10 | **1229.6525** | 615.3299 | 1212.6259 | 606.8166 | 1211.6419 | 606.3246 | D | ***347.1674*** | 174.0873 | 330.1408 | 165.5740 | 329.1568 | 165.0820 | 3 |
| 11 | 1286.6739 | 643.8406 | 1269.6474 | 635.3273 | 1268.6634 | 634.8353 | G | ***232.1404*** | 116.5738 | 215.1139 | 108.0606 | | | 2 |
| 12 | | | | | | | R | 175.1190 | 88.0631 | 158.0924 | 79.5498 | | | 1 |





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

### All matches to this query

| Score | Mr(calc): | Delta | Sequence |
|---|---|---|---|
| 87.5 | 1459.7783 | 0.0991 | LIFAGKQLEDGR |
| 28.9 | 1459.7307 | 0.1468 | ALENALPYLEDGR |
| 27.6 | 1460.7657 | -0.8882 | MSKALLVLEDGR |
| 27.4 | 1458.8228 | 1.0547 | MAKIGKKLQEAK |
| 25.6 | 1459.7718 | 0.1056 | IIGGGMPVGAFGGRR |
| 25.6 | 1459.6725 | 0.2049 | EAAALQCQLEDGR |
| 25.4 | 1460.7623 | -0.8849 | LIFAGKQLEDGR |
| 25.4 | 1459.8293 | 0.0482 | LTRMIRTAGALK |
| 24.1 | 1459.7704 | 0.1070 | EMKLLEQSGALK |
| 24.0 | 1459.6263 | 0.2512 | GCQFSYAGRSNGR |

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

# Mascot Search Results

## Protein View

Match to: **YD_RFP-p53-Ub** Score: **794**
**YD_RFP-p53-Ub**
Found in search of D:\Data\2010_10\BIT01712b_YD_15_RC2_01_7730.d\Analysis.mgf

Nominal mass ($M_r$): **79240**; Calculated pI value: **6.17**
NCBI BLAST search of YD_RFP-p53-Ub against nr
Unformatted sequence string for pasting into other applications

Variable modifications: Carbamidomethyl (C),Deamidated (NQ),GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **47%**

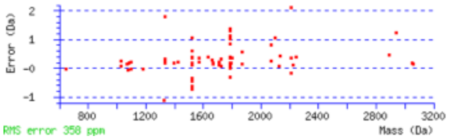
Matched peptides shown in **Bold Red**

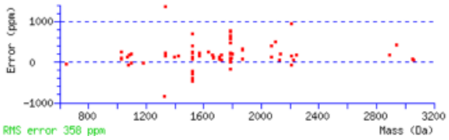
```
  1 MHHHHHHASS EDVIKEFMRF KVRMEGSVNG HEFEIEGEGE GRPYEGTQTA
 51 KLKVTKGGPL PFAWDILSPQ FQYGSKAYVK HPADIPDYLK LSFPEGFKWE
101 RVMNFEDGGV VTVTQDSSLQ DGEFIYKVKL RGTNFPSDGP VMQKKTMGWE
151 ASTERMYPED GALKGEIKMR LKLKDGGHYD AEVKTTYMAK KPVQLPGAYK
201 TDIKLDITSH NEDYTIVEQY ERAEGRHSTG AENLYFQGLE EEPQSDPSVE
251 PPLSQETFSD LWKLLPENNV LSPLPSQAMD DLMLSPDDIE QWFTEDPGPD
301 EAPRMPEAAP RVAPAPAAPT PAAPAPAPSW PLSSSVPSQK TYQGSYGFRL
351 GFLHSGTAKS VTCTYSPALN KMFCQLAKTC PVQLWVDSTP PPGTRVRAMA
401 IYKQSQHMTE VVRRCPHHER CSDSDGLAPP QHLIRVEGNL RVEYLDDRNT
451 FRHSVVVPYE PPEVGSDCTT IHYNYMCNSS CMGGMNRRPI LTIITLEDSS
501 GNLLGRNSFE VHVCACPGRD RRTEEENLRK KGEPHHELPP GSTKRALSNN
551 TSSSPQPKKK PLDGEYFTLQ IRGRERFEMF RELNEALELK DAQAGKEPGG
601 SRAHSSHLKS KKGQSTSRHK KLMFKTEGPD SDQIFVKTLT GKTITLEVEP
651 SDTIENVKAK IQDKEGIPPD QQRLIFAGKQ LEDGRTLSDY NIQKESTLHL
701 VLRLRGG
```

Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
Start - End     Observed   Mr(expt)   Mr(calc)    Delta  Miss  Sequence
  24 - 51      1018.8510  3053.5312  3053.3309   0.2003    0   R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M)  (Ions score 94)
  24 - 51       764.6260  3054.4749  3054.3149   0.1600    0   R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Deamidated (NQ); Oxidation (M)  (Ions score 39)
  57 - 76      1104.7390  2207.4634  2207.1051   0.3583    0   K.GGPLPFAWDILSPQFQYGSK.A   (Ions score 80)
  57 - 76      1105.6100  2209.2054  2207.1051   2.1003    0   K.GGPLPFAWDILSPQFQYGSK.A   (Ions score 50)
  77 - 90       544.0950  1629.2632  1628.8562   0.4070    1   K.AYVKHPADIPDYLK.L   (Ions score 55)
 102 - 127      965.6120  2893.8142  2893.3328   0.4814    0   R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 83)
 130 - 144      555.0380  1662.0922  1661.8195   0.2726    1   K.LRGTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 50)
 130 - 145      896.0550  1790.0954  1789.9145   0.1809    2   K.LRGTNFPSDGPVMQKK.T  Oxidation (M)  (Ions score 27)
 132 - 144      697.4140  1392.8134  1392.6344   0.1791    0   R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 71)
 132 - 145      508.0070  1520.9992  1521.7133  -0.7142    1   R.GTNFPSDGPVMQKK.T  Deamidated (NQ); Oxidation (M)  (Ions score 24)
 146 - 155      592.2410  1182.4674  1182.4975  -0.0301    0   K.TMGWEASTER.M  Oxidation (M)  (Ions score 74)
 171 - 184      787.0390  1572.0634  1571.8307   0.2327    2   R.LKLKDGGHYDAEVK.T   (Ions score 77)
 171 - 184      525.0660  1572.1762  1571.8307   0.3454    2   R.LKLKDGGHYDAEVK.T   (Ions score 38)
 173 - 184      665.7700  1329.5254  1330.6517  -1.1263    1   K.LKDGGHYDAEVK.T   (Ions score 46)
 173 - 184      666.4280  1330.8414  1330.6517   0.1897    1   K.LKDGGHYDAEVK.T   (Ions score 74)
 191 - 200      550.8180  1099.6214  1099.6390  -0.0175    0   K.KPVQLPGAYK.T   (Ions score 41)
 191 - 200      550.9310  1099.8474  1099.6390   0.2085    0   K.KPVQLPGAYK.T   (Ions score 50)
 205 - 222     1113.0800  2224.1454  2224.0284   0.1171    0   K.LDITSHNEDYTIVEQYER.A   (Ions score 36)
 341 - 349      539.7170  1077.4194  1077.4880  -0.0685    0   K.TYQGSYGFR.L   (Ions score 55)
 350 - 359      515.8250  1029.6354  1029.5607   0.0747    0   R.LGFLHSGTAK.S   (Ions score 52)
 350 - 359      344.2210  1029.6412  1029.5607   0.0804    0   R.LGFLHSGTAK.S   (Ions score 24)
 350 - 359      515.8360  1029.6574  1029.5607   0.0967    0   R.LGFLHSGTAK.S   (Ions score 19)
 350 - 359      515.9190  1029.8234  1029.5607   0.2627    0   R.LGFLHSGTAK.S   (Ions score 11)
 436 - 452      699.7080  2096.1022  2095.0446   1.0575    2   R.VEGNLRVEYLDDRNTFR.H   (Ions score 28)
 442 - 452      714.4540  1426.8934  1426.6841   0.2094    1   R.VEYLDDRNTFR.H   (Ions score 47)
 488 - 506     1034.7270  2067.4394  2067.1688   0.2707    0   R.RPILTIITLEDSSGNLLGR.N   (Ions score 83)
 488 - 506      690.3330  2067.9772  2067.1688   0.8084    0   R.RPILTIITLEDSSGNLLGR.N   (Ions score 80)
 530 - 545      600.1140  1797.3202  1796.9645   0.3556    3   R.KKGEPHHELPPGSTKR.A   (Ions score 38)
 531 - 545      835.5190  1669.0234  1668.8696   0.1539    2   K.KGEPHHELPPGSTKR.A   (Ions score 39)
 531 - 545      835.5360  1669.0574  1668.8696   0.1879    2   K.KGEPHHELPPGSTKR.A   (Ions score 55)
 531 - 545      557.3610  1669.0612  1668.8696   0.1916    2   K.KGEPHHELPPGSTKR.A   (Ions score 26)
 559 - 572      570.0260  1707.0562  1706.9355   0.1206    1   K.KKPLDGEYFTLQIR.G   (Ions score 30)
 559 - 572      854.5790  1707.1434  1706.9355   0.2079    1   K.KKPLDGEYFTLQIR.G   (Ions score 87)
 577 - 602      980.5600  2938.6582  2937.4290   1.2292    3   R.FEMFRELNEALELKDAQAGKEPGGSR.A  Oxidation (M)  (Ions score 58)
 582 - 602      737.9880  2210.9422  2211.1131  -0.1709    2   R.ELNEALELKDAQAGKEPGGSR.A   (Ions score 95)
 622 - 637      936.0430  1870.0714  1869.9183   0.1532    1   K.LMFKTEGPDSDQIFVK.T  Oxidation (M)  (Ions score 76)
 622 - 637      624.5040  1870.4902  1869.9183   0.5719    1   K.LMFKTEGPDSDQIFVK.T  Oxidation (M)  (Ions score 75)
 622 - 637      624.5080  1870.5022  1869.9183   0.5839    1   K.LMFKTEGPDSDQIFVK.T  Oxidation (M)  (Ions score 84)
 626 - 637      668.4190  1334.8234  1334.6354   0.1880    0   K.TEGPDSDQIFVK.T   (Ions score 46)
 626 - 637      668.4470  1334.8794  1334.6354   0.2440    0   K.TEGPDSDQIFVK.T   (Ions score 10)
 626 - 637      668.4820  1334.9494  1334.6354   0.3140    0   K.TEGPDSDQIFVK.T   (Ions score 57)
 626 - 637      669.2300  1336.4454  1334.6354   1.8100    0   K.TEGPDSDQIFVK.T   (Ions score 18)
 643 - 658      894.3080  1786.6014  1786.9200  -0.3186    0   K.TITLEVEPSDTIENVK.A   (Ions score 20)
 643 - 658      894.4660  1786.9174  1786.9200  -0.0026    0   K.TITLEVEPSDTIENVK.A   (Ions score 38)
 643 - 658      894.5120  1787.0094  1786.9200   0.0894    0   K.TITLEVEPSDTIENVK.A   (Ions score 23)
 643 - 658      894.5220  1787.0294  1786.9200   0.1094    0   K.TITLEVEPSDTIENVK.A   (Ions score 29)
 643 - 658      894.5560  1787.0974  1786.9200   0.1774    0   K.TITLEVEPSDTIENVK.A   (Ions score 45)
 643 - 658      894.6470  1787.2794  1786.9200   0.3594    0   K.TITLEVEPSDTIENVK.A   (Ions score 33)
 643 - 658      894.6670  1787.3194  1786.9200   0.3994    0   K.TITLEVEPSDTIENVK.A   (Ions score 32)
 643 - 658      894.8970  1787.7794  1786.9200   0.8594    0   K.TITLEVEPSDTIENVK.A   (Ions score 33)
 643 - 658      894.9770  1787.9394  1786.9200   1.0194    0   K.TITLEVEPSDTIENVK.A   (Ions score 27)
 643 - 658      894.9810  1787.9474  1786.9200   1.0274    0   K.TITLEVEPSDTIENVK.A   (Ions score 94)
 643 - 658      895.0090  1788.0034  1786.9200   1.0834    0   K.TITLEVEPSDTIENVK.A   (Ions score 19)
 643 - 658      895.0260  1788.0374  1786.9200   1.1174    0   K.TITLEVEPSDTIENVK.A   (Ions score 32)
 643 - 658      895.0320  1788.0494  1786.9200   1.1294    0   K.TITLEVEPSDTIENVK.A   (Ions score 22)
 643 - 658      895.0360  1788.0574  1786.9200   1.1374    0   K.TITLEVEPSDTIENVK.A   (Ions score 20)
 643 - 658      895.1270  1788.2394  1786.9200   1.3194    0   K.TITLEVEPSDTIENVK.A   (Ions score 29)
 643 - 658      895.1570  1788.2994  1786.9200   1.3794    0   K.TITLEVEPSDTIENVK.A   (Ions score 39)
 659 - 673      861.9970  1721.9794  1721.9060   0.0734    2   K.AKIQDKEGIPPDQQR.L   (Ions score 70)
 659 - 673      575.0020  1721.9842  1721.9060   0.0782    2   K.AKIQDKEGIPPDQQR.L   (Ions score 31)
 659 - 673      862.1200  1722.2254  1721.9060   0.3194    2   K.AKIQDKEGIPPDQQR.L   (Ions score 73)
 661 - 673      762.0350  1522.0554  1522.7740  -0.7185    1   K.IQDKEGIPPDQQR.L   (Ions score 33)
 661 - 673      762.0910  1522.1674  1522.7740  -0.6065    1   K.IQDKEGIPPDQQR.L   (Ions score 7)
 661 - 673      762.1720  1522.3294  1522.7740  -0.4445    1   K.IQDKEGIPPDQQR.L   (Ions score 14)
 661 - 673      762.2270  1522.4394  1522.7740  -0.3345    1   K.IQDKEGIPPDQQR.L   (Ions score 16)
 661 - 673      762.4520  1522.8894  1522.7740   0.1155    1   K.IQDKEGIPPDQQR.L   (Ions score 13)
 661 - 673      762.4530  1522.8914  1522.7740   0.1175    1   K.IQDKEGIPPDQQR.L   (Ions score 48)
 661 - 673      762.4640  1522.9134  1522.7740   0.1395    1   K.IQDKEGIPPDQQR.L   (Ions score 38)
 661 - 673      508.6560  1522.9462  1522.7740   0.1722    1   K.IQDKEGIPPDQQR.L   (Ions score 32)
 661 - 673      508.6630  1522.9672  1522.7740   0.1932    1   K.IQDKEGIPPDQQR.L   (Ions score 35)
 661 - 673      762.5660  1523.1174  1522.7740   0.3435    1   K.IQDKEGIPPDQQR.L   (Ions score 12)
 661 - 673      762.5850  1523.1554  1522.7740   0.3815    1   K.IQDKEGIPPDQQR.L   (Ions score 13)
 661 - 673      762.5920  1523.1694  1522.7740   0.3955    1   K.IQDKEGIPPDQQR.L   (Ions score 23)
 661 - 673      762.7050  1523.3954  1522.7740   0.6215    1   K.IQDKEGIPPDQQR.L   (Ions score 12)
 661 - 673      762.9240  1523.8334  1522.7740   1.0595    1   K.IQDKEGIPPDQQR.L   (Ions score 21)
 674 - 679      324.6950   647.3754   647.4006  -0.0252    0   R.LIFAGK.Q   (Ions score 40)
 686 - 694      541.3730  1080.7314  1080.5451   0.1863    0   R.TLSDYNIQK.E   (Ions score 51)
 686 - 703     1065.6260  2129.2374  2129.1480   0.0894    1   R.TLSDYNIQKESTLHLVLR.L   (Ions score 48)
 686 - 703      710.8720  2129.5942  2129.1480   0.4461    1   R.TLSDYNIQKESTLHLVLR.L   (Ions score 77)
 686 - 703      748.8710  2243.5912  2243.1910   0.4002    1   R.TLSDYNIQKESTLHLVLR.L  GlyGly (K)  (Ions score 66)
 695 - 703      534.3800  1066.7454  1066.6135   0.1320    0   K.ESTLHLVLR.L   (Ions score 66)
```





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

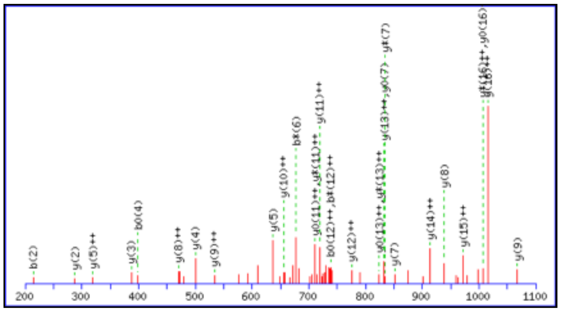
# Mascot Search Results

### Peptide View

MS/MS Fragmentation of **TLSDYNIQKESTLHLVLR**
Found in **YD_RFP-p53-Ub**, YD_RFP-p53-Ub

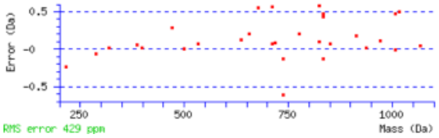
Match to Query 721: 2243.591172 from(748.871000,3+) intensity(718357.0000)
Title: Cmpd 316, +MSn(749.52), 29.0 min
Data file D:\Data\2010_10\BIT01712b_YD_15_RC2_01_7730.d\Analysis.mgf

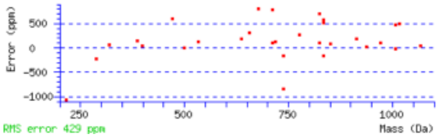
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



**Monoisotopic mass of neutral peptide Mr(calc):** 2243.1910
**Variable modifications:**
**K9** : GlyGly (K)
**Ions Score:** 66 **Expect:** 0.0025
**Matches :** 30/182 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 | 102.0550 | 51.5311 | | | 84.0444 | 42.5258 | T | | | | | | | 18 |
| 2 | 215.1390 | 108.0731 | | | 197.1285 | 99.0679 | L | 2143.1506 | 1072.0789 | 2126.1240 | 1063.5657 | 2125.1400 | 1063.0737 | 17 |
| 3 | 302.1710 | 151.5892 | | | 284.1605 | 142.5839 | S | 2030.0665 | 1015.5369 | 2013.0400 | 1007.0236 | 2012.0560 | 1006.5316 | 16 |
| 4 | 417.1980 | 209.1026 | | | 399.1874 | 200.0974 | D | 1943.0345 | 972.0209 | 1926.0080 | 963.5076 | 1925.0239 | 963.0156 | 15 |
| 5 | 580.2613 | 290.6343 | | | 562.2508 | 281.6290 | Y | 1828.0076 | 914.5074 | 1810.9810 | 905.9941 | 1809.9970 | 905.5021 | 14 |
| 6 | 694.3042 | 347.6558 | 677.2777 | 339.1425 | 676.2937 | 338.6505 | N | 1664.9442 | 832.9758 | 1647.9177 | 824.4625 | 1646.9337 | 823.9705 | 13 |
| 7 | 807.3883 | 404.1978 | 790.3618 | 395.6845 | 789.3777 | 395.1925 | I | 1550.9013 | 775.9543 | 1533.8748 | 767.4410 | 1532.8907 | 766.9490 | 12 |
| 8 | 935.4469 | 468.2271 | 918.4203 | 459.7138 | 917.4363 | 459.2218 | Q | 1437.8172 | 719.4123 | 1420.7907 | 710.8990 | 1419.8067 | 710.4070 | 11 |
| 9 | 1177.5848 | 589.2960 | 1160.5582 | 580.7828 | 1159.5742 | 580.2907 | K | 1309.7587 | 655.3830 | 1292.7321 | 646.8697 | 1291.7481 | 646.3777 | 10 |
| 10 | 1306.6274 | 653.8173 | 1289.6008 | 645.3040 | 1288.6168 | 644.8120 | E | ***1067.6208*** | 534.3140 | 1050.5942 | 525.8007 | 1049.6102 | 525.3087 | 9 |
| 11 | 1393.6594 | 697.3333 | 1376.6329 | 688.8201 | 1375.6488 | 688.3281 | S | ***938.5782*** | 469.7927 | 921.5516 | 461.2795 | 920.5676 | 460.7874 | 8 |
| 12 | 1494.7071 | 747.8572 | 1477.6805 | 739.3439 | 1476.6965 | 738.8519 | T | ***851.5461*** | 426.2767 | 834.5196 | 417.7634 | 833.5356 | 417.2714 | 7 |
| 13 | 1607.7911 | 804.3992 | 1590.7646 | 795.8859 | 1589.7806 | 795.3939 | L | 750.4985 | 375.7529 | 733.4719 | 367.2396 | | | 6 |
| 14 | 1744.8501 | 872.9287 | 1727.8235 | 864.4154 | 1726.8395 | 863.9234 | H | ***637.4144*** | 319.2108 | 620.3879 | 310.6976 | | | 5 |
| 15 | 1857.9341 | 929.4707 | 1840.9076 | 920.9574 | 1839.9236 | 920.4654 | L | ***500.3555*** | 250.6814 | 483.3289 | 242.1681 | | | 4 |
| 16 | 1957.0025 | 979.0049 | 1939.9760 | 970.4916 | 1938.9920 | 969.9996 | V | ***387.2714*** | 194.1394 | 370.2449 | 185.6261 | | | 3 |
| 17 | 2070.0866 | 1035.5469 | 2053.0600 | 1027.0337 | 2052.0760 | 1026.5417 | L | ***288.2030*** | 144.6051 | 271.1765 | 136.0919 | | | 2 |
| 18 | | | | | | | R | 175.1190 | 88.0631 | 158.0924 | 79.5498 | | | 1 |





NCBI **BLAST** search of TLSDYNIQKESTLHLVLR
(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 | 2243.1910 | 0.4002 | TLSDYNIQKESTLHLVLR |
| 66.1 | 2244.1750 | -0.5838 | TLSDYNIQKESTLHLVLR |
| 66.1 | 2244.1750 | -0.5838 | TLSDYNIQKESTLHLVLR |
| 37.0 | 2243.2525 | 0.3387 | VNVDTDQIIPKQFLKSIKR |
| 37.0 | 2243.2525 | 0.3387 | VNVDTDQIIPKQFLKSIKR |
| 37.0 | 2243.2525 | 0.3387 | VNVDTDQIIPKQFLKSIKR |
| 25.1 | 2244.1718 | -0.5807 | TNQMPNAVQKLLLVMDKR |
| 24.7 | 2244.2365 | -0.6453 | VNVDTDQIIPKQFLKSIKR |
| 24.7 | 2243.1181 | 0.4730 | AIENSQKKVEGHNFEIRK |
| 24.5 | 2243.1757 | 0.4155 | DVSDNSIINVSVKVKNVGK |

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

| Sample | Substrate | E2 | E3 | Additional factors |
|---|---|---|---|---|
| 2 | RFP-p53 | E2N/E2V1 | MDM2 | MDMX |
| 3 | RFP-p53 | UBE2D3 | MDM2 | MDMX |
| 4 | RFP-p53-Ub | UBE2D2 | - | - |
| 5 | RFP-p53-Ub | UBE2D2 | MDM2 | - |
| 6 | RFP-p53 | UBE2D2 | MDM2 | - |

| Reference | #2 | | | | | P (pro) | Sf | Score | Coverage | MW | Acsn | Peptide (Hits) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Scan(s)** | **Peptide** | **MH+** | **DeltaM (ppm)** | **z** | **Type** | **P (pep)** | **Sf** | **XC** | **DeltaCn** | **Sp** | **RSp** | **Ions** |
| 1 | gi\|88702791\|ref\|NP_002384.2\| protein Mdm4 [Homo sapiens] | | | | | 1.22E-10 | 34.90 | 488.26 | 73.30 | 54829.6 | 88702791 | 52 (46 1 2 1 2) |
| 971 | K.AGASCPICK.K | 963.43872 | 0.04950 | 2 | CID | 1.66E-03 | 0.88 | 2.53 | 0.69 | 385.2 | 1 | 11/16 |
| 698 | K.AGASCPICKK.E | 1091.53368 | 1.28092 | 2 | CID | 1.23E-01 | 0.57 | 1.81 | 0.37 | 318.6 | 1 | 11/18 |
| 5828 | K.CIHSREDED^LIENLAQDETSR.L | 2544.16312 | 1.58311 | 3 | CID | 9.98E-07 | 0.84 | 4.69 | 0.05 | 993.4 | 1 | 23/80 |
| 5829 | K.CIHSREDEDLIENLAQDETSR.L | 2530.14747 | 0.80569 | 3 | CID | 3.20E-08 | 0.95 | 4.14 | 0.38 | 1652.8 | 1 | 30/80 |
| 1266 | R.DGNIIHGR.T | 881.45879 | 1.24413 | 2 | CID | 3.54E-07 | 0.90 | 2.41 | 0.68 | 439.1 | 1 | 11/14 |
| 7266 | K.DPSPLYDMLR.K | 1206.58234 | 0.39446 | 2 | CID | 6.18E-02 | 0.67 | 2.38 | 0.40 | 317.3 | 1 | 10/18 |
| 6592 | R.EDEDLIENLAQDETSR.L | 1876.84067 | 1.79598 | 2 | CID | 1.26E-07 | 0.96 | 4.00 | 0.67 | 1055.0 | 1 | 17/30 |
| 6748 | K.EVMHYLGQYIMVK.Q | 1610.80693 | 0.07582 | 2 | CID | 1.47E-06 | 0.94 | 3.24 | 0.74 | 603.6 | 1 | 16/24 |
| 6259 | K.EVMHYLGQYIM*VK.Q | 1626.80185 | 0.12433 | 2 | CID | 5.78E-05 | 0.89 | 3.02 | 0.64 | 522.7 | 1 | 13/24 |
| 5771 | K.EVM*HYLGQYIMVK.Q | 1626.80185 | 0.34944 | 2 | CID | 1.44E-02 | 0.72 | 1.87 | 0.54 | 381.4 | 1 | 13/24 |
| 3638 | K.ILHAAGAQGEM*FTVK.E | 1588.81519 | -0.20280 | 2 | CID | 3.00E-08 | 0.91 | 3.00 | 0.59 | 686.1 | 1 | 17/28 |
| 4659 | K.ILHAAGAQGEMFTVK.E | 1572.82027 | 0.59794 | 2 | CID | 4.91E-10 | 0.96 | 3.84 | 0.55 | 1113.6 | 1 | 22/28 |
| 2786 | R.ISPGQINQVRPK.L | 1336.76956 | -0.98979 | 2 | CID | 6.54E-05 | 0.70 | 2.10 | 0.70 | 119.0 | 1 | 11/22 |
| 2499 | R.ISPGQIN@QVRPK.L | 1337.75358 | 2.01681 | 2 | CID | 5.77E-03 | 0.35 | 2.50 | 0.04 | 189.7 | 1 | 12/22 |
| 2031 | R.KDWYSDCSK.L | 1188.49904 | 1.67290 | 2 | CID | 3.62E-02 | 0.84 | 2.42 | 0.50 | 444.3 | 1 | 11/16 |
| 3786 | K.KEIQLVIK.V | 970.62954 | -0.16729 | 2 | CID | 2.02E-02 | 0.92 | 2.55 | 0.69 | 435.1 | 1 | 12/14 |
| 9133 | K.LFDPCNSVEFLDLAHSSESQETISSMGEQLDNLSEQR.T | 4212.89726 | 0.59208 | 3 | CID | 2.44E-06 | 0.79 | 3.60 | 0.48 | 310.9 | 1 | 26/144 |
| 8354 | K.LFD^PCNSVEFLDLAHSSESQETISSM*GEQLDNLSEQR.T | 4242.90782 | 1.80924 | 3 | CID | 6.13E-04 | 0.38 | 3.00 | 0.01 | 392.3 | 1 | 24/144 |
| 8336 | K.LFDPCNSVEFLDLAHSSESQETISSM*GEQLDNLSEQR.T | 4228.89217 | 2.34073 | 3 | CID | 3.07E-04 | 0.89 | 5.16 | 0.13 | 825.8 | 1 | 36/144 |
| 4629 | K.LTHSLSTSDITAIPEK.E | 1712.90651 | -0.80660 | 3 | CID | 5.99E-03 | 0.52 | 2.31 | 0.44 | 309.0 | 1 | 18/60 |
| 4820 | K.LTHSLSTSDITAIPEKENEGNDVPD^CR.R | 3012.42152 | 0.65591 | 3 | CID | 4.58E-03 | 0.52 | 3.15 | 0.14 | 412.5 | 1 | 20/104 |
| 4763 | K.LTHSLSTSDITAIPEKENEGNDVPDCR.R | 2998.40587 | -0.55404 | 3 | CID | 9.64E-07 | 0.90 | 4.21 | 0.54 | 589.3 | 1 | 25/104 |
| 4492 | K.LTHSLSTSDITAIPEKENEGNDVPD^CRR.T | 3168.52263 | 2.05670 | 3 | CID | 8.86E-04 | 0.66 | 3.86 | 0.10 | 423.7 | 1 | 23/108 |
| 5077 | K.LTHSLSTSDITAIPEK$ENEGNDVPDCRR.T | 3197.51280 | 3.01386 | 3 | CID | 4.73E-05 | 0.34 | 3.12 | 0.58 | 218.8 | 1 | 20/108 |
| 4538 | K.LTHSLSTSDITAIPEKENEGN@DVPDCRR.T | 3155.49100 | 2.43408 | 4 | CID | 1.02E-05 | 0.66 | 3.53 | 0.07 | 567.1 | 1 | 35/162 |
| 4443 | K.LTHSLSTSDITAIPEKENEGNDVPDCRR.T | 3154.50698 | 1.60940 | 3 | CID | 6.37E-09 | 0.91 | 4.38 | 0.62 | 546.8 | 1 | 24/108 |
| 4522 | K.LTHSLSTSDITAIPEKEN@EGNDVPDCRR.T | 3155.49100 | 1.37451 | 3 | CID | 1.29E-08 | 0.54 | 2.93 | 0.03 | 663.6 | 1 | 26/108 |
| 8503 | K.NLVTLATATTDAAQTL.A | 1603.85374 | -0.26386 | 2 | CID | 5.51E-02 | 0.50 | 1.94 | 0.66 | 194.1 | 1 | 10/30 |
| 9286 | K.NLVTLATATTDAAQTLALAQDHSMDIPSQDQLK.Q | 3481.74790 | 2.10203 | 3 | CID | 1.53E-03 | 0.44 | 3.25 | 0.02 | 340.5 | 1 | 23/128 |
| 9042 | K.NLVTLATATTDAAQTLALAQ@DHSMD^IPSQDQ@LK.Q | 3497.73159 | 5.93374 | 4 | CID | 4.87E-05 | 0.66 | 3.66 | 0.01 | 687.9 | 1 | 37/192 |
| 9042 | K.NLVTLATATTDAAQTLALAQ@DHSMD^IPSQ@DQLK.Q | 3497.73159 | 5.93374 | 4 | CID | 4.87E-05 | 0.65 | 3.61 | 0.10 | 687.9 | 1 | 37/192 |
| 9010 | K.NLVTLATATTDAAQTLALAQDHSM*DIPSQDQLK$QSAEESST | 4603.20641 | -0.68369 | 4 | CID | 8.94E-02 | 0.33 | 3.14 | 0.34 | 230.0 | 1 | 28/252 |
| 9187 | K.QLYDQQEQHMVYCGGDLLGELLGR.Q | 2822.32366 | -0.15790 | 3 | CID | 7.33E-03 | 0.89 | 3.87 | 0.61 | 569.9 | 1 | 22/92 |
| 8738 | K.QLYD^QQ@EQ@HMVYCGGDLLGELLGR.Q | 2838.30734 | 4.21593 | 3 | CID | 8.77E-05 | 0.72 | 3.64 | 0.09 | 888.6 | 1 | 26/92 |
| 5236 | R.QSFSVKDPSPLYD.M | 1482.71110 | 0.00428 | 2 | CID | 1.98E-06 | 0.52 | 1.89 | 0.38 | 323.3 | 1 | 12/24 |
| 7321 | R.QSFSVKDPSPLYDMLR.K | 1882.93676 | 0.15160 | 3 | CID | 5.53E-05 | 0.44 | 2.81 | 0.09 | 414.3 | 1 | 20/60 |
| 5239 | R.QSFSVKDPSPLYDM*LRK.N | 2027.02664 | -0.20729 | 3 | CID | 9.93E-03 | 0.20 | 2.39 | 0.11 | 185.4 | 1 | 16/64 |
| 6561 | R.QSFSVKDPSPLYDMLRK.N | 2011.03172 | 0.75277 | 3 | CID | 8.18E-04 | 0.53 | 2.73 | 0.18 | 353.4 | 1 | 23/64 |
| 5425 | K.SLSDDTDVEVTSEDEWQCTECK.K | 2633.05022 | 2.45643 | 2 | CID | 2.46E-07 | 0.69 | 2.48 | 0.38 | 511.8 | 1 | 15/42 |
| 5031 | K.SLSDDTDVEVTSEDEWQCTE^CKK.F | 2775.16083 | 1.35186 | 3 | CID | 7.40E-04 | 0.34 | 2.89 | 0.02 | 279.0 | 1 | 21/88 |
| 4471 | R.TDTENM*EDCQNLLKPCSLCEK.R | 2601.09366 | 0.65822 | 3 | CID | 2.56E-04 | 0.67 | 3.24 | 0.00 | 732.0 | 1 | 24/80 |
| 5149 | R.TDTENMEDCQNLLKPCSLCEK.R | 2585.09874 | 0.06465 | 3 | CID | 6.26E-05 | 0.66 | 3.14 | 0.10 | 688.5 | 1 | 24/80 |
| 5238 | R.TDTENMED^CQNLLKPCSLCEK.R | 2599.11439 | -0.08621 | 3 | CID | 2.35E-03 | 0.57 | 3.37 | 0.08 | 469.6 | 1 | 21/80 |
| 2612 | R.TGHLVTCFHCAR.R | 1458.67297 | 1.87549 | 2 | CID | 3.06E-06 | 0.94 | 3.15 | 0.50 | 1021.7 | 1 | 16/22 |
| 2456 | R.TISAPVVRPK.D | 1067.65716 | 2.05510 | 2 | CID | 1.63E-02 | 0.32 | 2.01 | - | 388.2 | 1 | 11/18 |
| 4048 | R.TTEDDIPTLPTSEHK.C | 1683.80719 | 0.28434 | 2 | CID | 1.68E-06 | 0.87 | 3.50 | 0.61 | 283.8 | 1 | 13/28 |
| 1542 | K.VEAADTEQTSEEVGK.V | 1592.72860 | 1.50890 | 2 | CID | 3.61E-10 | 0.98 | 4.16 | 0.70 | 1670.3 | 1 | 21/28 |
| 3073 | K.VEAADTEQTSEEVGK$VSDK.K | 2064.95677 | 1.33396 | 2 | CID | 2.00E-02 | 0.33 | 2.45 | 0.31 | 124.7 | 1 | 11/36 |
| 2289 | K.VEAADTEQTSEEVGKVSDKK.V | 2150.04591 | 3.44419 | 3 | CID | 2.32E-03 | 0.37 | 2.42 | 0.35 | 163.7 | 1 | 17/76 |
| 2828 | K.VIEVGKNDDLEDSK.S | 1560.77516 | 0.80548 | 2 | CID | 1.22E-10 | 0.97 | 4.08 | 0.70 | 1222.3 | 1 | 18/26 |
| 3724 | K.VIEVGK$NDDLEDSK.S | 1603.78097 | 2.02875 | 2 | CID | 1.05E-04 | 0.79 | 2.95 | 0.27 | 446.1 | 1 | 16/26 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2 | His-RFP-p53 | | | | | 1.70E-10 | 32.99 | 446.23 | 56.50 | 70829.9 | | 45 (44 0 1 0 0) |
| 4978 | E.ALELKDAQAGK.E | 1143.63681 | -7.51311 | 2 | CID | 4.61E-02 | 0.34 | 2.15 | 0.23 | 194.8 | 1 | 10/20 |
| 4568 | K.AYVKHPADIPDYLK.L | 1629.86352 | 1.75566 | 2 | CID | 1.94E-04 | 0.94 | 3.39 | 0.58 | 967.3 | 1 | 17/26 |
| 4245 | R.CSD^SDGLAPPQHLIR.V | 1679.81702 | -0.04392 | 2 | CID | 8.80E-04 | 0.48 | 2.79 | 0.17 | 331.6 | 1 | 12/28 |
| 4212 | R.CSDSDGLAPPQHLIR.V | 1665.80137 | 0.55696 | 2 | CID | 4.91E-06 | 0.74 | 2.49 | 0.65 | 240.3 | 1 | 12/28 |
| 1017 | K.DGGHYDAEVK.T | 1090.47998 | 0.82883 | 2 | CID | 1.63E-04 | 0.81 | 2.38 | 0.59 | 388.8 | 1 | 11/18 |
| 7552 | D.DIEQWFTEDPGPDEAPR.M | 2001.88248 | 0.19176 | 2 | CID | 1.53E-02 | 0.83 | 3.22 | 0.58 | 321.0 | 1 | 13/32 |
| 4510 | R.ELNEALELK.D | 1058.57282 | 0.21651 | 2 | CID | 8.16E-03 | 0.39 | 1.85 | 0.38 | 231.5 | 1 | 8/16 |
| 3751 | R.ELNEALELKDAQAGKEPGGSR.A | 2212.12042 | 1.23277 | 3 | CID | 9.28E-07 | 0.73 | 3.38 | 0.20 | 751.9 | 1 | 23/80 |
| 9503 | K.GGPLPFAWDILSPQFQYGSK.A | 2208.11242 | 0.41316 | 2 | CID | 7.80E-08 | 0.92 | 3.46 | 0.32 | 1147.5 | 1 | 21/38 |
| 2762 | R.GTNFPSDGPVM*QK.K | 1393.64164 | -0.95799 | 2 | CID | 9.65E-07 | 0.85 | 3.04 | 0.59 | 352.3 | 1 | 13/24 |
| 3707 | R.GTNFPSDGPVMQK.K | 1377.64673 | 0.30185 | 2 | CID | 1.33E-06 | 0.94 | 3.48 | 0.70 | 624.7 | 1 | 16/24 |
| 2966 | R.GTNFPSDGPVMQKK.T | 1505.74169 | -0.93476 | 2 | CID | 2.80E-02 | 0.31 | 1.87 | 0.39 | 215.5 | 1 | 10/26 |
| 4384 | K.HPADIPDYLK.L | 1168.59970 | 0.27663 | 2 | CID | 2.28E-07 | 0.93 | 2.39 | 0.78 | 376.7 | 1 | 15/18 |
| 6208 | R.HSTGAENLYFQGLEEEPQ.S | 2048.91959 | 0.78099 | 2 | CID | 3.44E-04 | 0.52 | 2.01 | 0.44 | 309.5 | 1 | 13/34 |
| 6111 | R.HSTGAENLYFQGLEEEPQSDPS.V | 2435.06335 | -0.23076 | 2 | CID | 4.66E-05 | 0.87 | 3.11 | 0.59 | 545.0 | 1 | 17/42 |
| 8204 | R.HSTGAENLYFQGLEEEPQSDPSVEPPLSQETF.S | 3562.61324 | 2.02461 | 3 | CID | 1.08E-04 | 0.57 | 2.25 | 0.50 | 235.3 | 1 | 21/124 |
| 5879 | K.KKPLDGEYFTLQIR.G | 1707.94283 | 0.82905 | 3 | CID | 3.43E-05 | 0.76 | 2.53 | 0.52 | 595.8 | 1 | 19/52 |
| 2837 | K.KPVQLPGAYK.T | 1100.64626 | 0.25058 | 2 | CID | 6.04E-05 | 0.89 | 2.61 | 0.58 | 333.9 | 1 | 14/18 |
| 3107 | K.KPVQLPGAYKT.D | 1201.69393 | 0.17039 | 2 | CID | 1.07E-02 | 0.60 | 2.05 | 0.66 | 136.1 | 1 | 9/20 |
| 2525 | K.KTMGWEASTER.M | 1295.60486 | 1.44748 | 2 | CID | 4.22E-04 | 0.83 | 2.62 | 0.50 | 510.1 | 1 | 12/20 |
| 5916 | K.LDITSHNEDYTIVEQYER.A | 2225.03568 | 1.86971 | 2 | CID | 1.70E-10 | 0.96 | 4.56 | 0.57 | 1152.5 | 1 | 20/34 |
| 3226 | R.LGFLHSGTAK.S | 1030.56801 | -1.03219 | 2 | CID | 5.53E-06 | 0.93 | 2.72 | 0.62 | 727.9 | 1 | 14/18 |
| 1283 | K.LKDGGHYDAEVK.T | 1331.65901 | -0.47527 | 2 | CID | 1.35E-04 | 0.88 | 2.96 | 0.41 | 739.2 | 1 | 14/22 |
| 2931 | K.LRGTNFPSDGPVM*QK.K | 1662.82682 | 0.14677 | 3 | CID | 6.44E-04 | 0.85 | 3.54 | 0.58 | 377.9 | 1 | 20/56 |
| 3729 | K.LRGTNFPSDGPVMQK.K | 1646.83190 | 1.59020 | 2 | CID | 1.74E-05 | 0.87 | 2.95 | 0.61 | 388.6 | 1 | 15/28 |
| 5721 | K.LSFPEGFK.W | 924.48254 | 0.31452 | 2 | CID | 3.42E-02 | 0.62 | 1.81 | 0.54 | 290.5 | 1 | 8/14 |
| 6752 | K.LSFPEGFKWER.V | 1395.70556 | -0.05017 | 2 | CID | 4.75E-08 | 0.58 | 2.18 | 0.44 | 215.0 | 1 | 10/20 |
| 4496 | R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L | 3038.34323 | 1.60745 | 3 | CID | 3.95E-08 | 0.84 | 3.28 | 0.41 | 812.7 | 1 | 27/108 |
| 4795 | R.MEGSVN@GHEFEIEGEGEGRPYEGTQTAK.L | 3039.32725 | 0.45989 | 3 | CID | 2.92E-08 | 0.89 | 4.46 | 0.17 | 1011.3 | 1 | 32/108 |
| 4133 | R.M*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L | 3054.33815 | 0.90587 | 3 | CID | 6.65E-03 | 0.46 | 2.21 | 0.36 | 193.4 | 1 | 23/108 |
| 4310 | R.M*EGSVN@GHEFEIEGEGEGRPYEGTQTAK.L | 3055.32216 | 0.90322 | 3 | CID | 2.46E-06 | 0.70 | 3.37 | 0.42 | 159.1 | 1 | 21/108 |
| 5080 | T.QDSSLQDGEFIYK.V | 1529.71183 | 1.68265 | 2 | CID | 5.98E-04 | 0.39 | 2.50 | 0.09 | 286.4 | 1 | 12/24 |
| 8396 | R.RPILTIITLEDSSGNLLGR.N | 2068.17608 | 1.76109 | 3 | CID | 1.22E-02 | 0.64 | 2.52 | 0.62 | 258.7 | 1 | 16/72 |
| 795 | R.RTEEENLR.K | 1046.52251 | -0.12020 | 2 | CID | 3.22E-06 | 0.94 | 3.33 | 0.60 | 456.3 | 1 | 12/14 |
| 4941 | D.SSLQDGEFIYK.V | 1286.62631 | 0.91746 | 2 | CID | 2.38E-06 | 0.94 | 2.82 | 0.68 | 909.2 | 1 | 15/20 |
| 2930 | K.SVTCTYSPALNK.M | 1340.65151 | 0.92774 | 2 | CID | 5.82E-05 | 0.67 | 2.01 | 0.57 | 313.5 | 1 | 11/22 |
| 6590 | K.TCPVQLWVDSTPPPGTR.V | 1910.94294 | 1.71113 | 2 | CID | 2.20E-07 | 0.93 | 3.57 | 0.63 | 604.4 | 1 | 18/32 |
| 2189 | K.TM*GWEASTER.M | 1183.50481 | -0.10766 | 2 | CID | 5.19E-06 | 0.97 | 3.13 | 0.65 | 1235.0 | 1 | 17/18 |
| 3192 | K.TYQGSYGFR.L | 1078.49523 | 0.50094 | 2 | CID | 6.13E-04 | 0.85 | 2.68 | 0.37 | 482.0 | 1 | 12/16 |
| 5116 | R.VEGNLRVEYLDDRNTFR.H | 2096.05194 | -1.61469 | 3 | CID | 9.87E-06 | 0.67 | 2.76 | 0.61 | 199.6 | 1 | 15/64 |
| 7376 | R.VM*NFEDGGVVTVTQDSSLQDGEFIYK.V | 2894.34005 | 1.97095 | 2 | CID | 1.44E-06 | 0.57 | 2.78 | 0.16 | 452.4 | 1 | 17/50 |
| 8001 | R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V | 2878.34513 | 0.74071 | 3 | CID | 4.53E-06 | 0.88 | 4.18 | 0.41 | 665.5 | 1 | 25/100 |
| 5426 | A.YVK#HPADIPDYLK.L | 1672.86831 | 2.20609 | 2 | CID | 2.95E-04 | 0.73 | 2.39 | 0.66 | 144.5 | 1 | 11/24 |
| 3 | gi\|260080636\|gb\|ACX31156.1\| MDM2 [Homo sapiens] | | | | | 4.42E-12 | 7.65 | 146.26 | 38.80 | 52436.5 | 260080636 | 15 (13 2 0 0 0) |
| 2593 | R.AISETEENSDELSGER.Q | 1765.77226 | 0.41893 | 2 | CID | 3.72E-07 | 0.94 | 3.04 | 0.58 | 1214.9 | 1 | 18/30 |
| 3450 | K.AKLENSTQAEEGFDVPD^CKK.T | 2280.08129 | 3.44588 | 3 | CID | 5.97E-06 | 0.89 | 4.58 | 0.27 | 687.7 | 1 | 27/76 |
| 3357 | K.AKLENSTQAEEGFDVPDCKK.T | 2266.06564 | -0.56193 | 3 | CID | 8.67E-10 | 0.89 | 4.94 | 0.08 | 889.6 | 1 | 29/76 |
| 4794 | R.CHLE^GGSDQKDLVQELQEEKPSSSHLVSRPSTSSR.R | 3921.89958 | 0.84593 | 5 | CID | 1.08E-03 | 0.71 | 3.80 | 0.08 | 635.2 | 1 | 44/272 |
| 5142 | K.DLVQELQEEKPSSSHLVSRPSTSSR.R | 2796.41224 | 0.94772 | 3 | CID | 4.38E-07 | 0.55 | 2.47 | 0.33 | 444.6 | 1 | 21/96 |
| 4313 | S.DQ@K#DLVQELQEE^K.P | 1730.84327 | -1.38938 | 2 | CID | 9.85E-02 | 0.40 | 2.07 | 0.21 | 353.7 | 1 | 11/24 |
| 4313 | S.DQ@K#DLVQELQE^EK.P | 1730.84327 | -1.38938 | 2 | CID | 9.85E-02 | 0.40 | 2.07 | 0.00 | 353.7 | 1 | 11/24 |
| 9139 | R.ENWLPEDKGKDK$GEISE^KAK.L | 2357.20957 | -0.64664 | 3 | CID | 1.30E-01 | 0.21 | 2.37 | 0.10 | 251.4 | 1 | 16/76 |
| 3393 | R.NLVVVNQQESSDSGTSVSENR.C | 2249.06402 | 2.60083 | 2 | CID | 4.42E-12 | 0.98 | 5.22 | 0.37 | 1908.2 | 1 | 26/40 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 9295 | K.QQHIVYCSNDLLGDLFGVPSFSVK.E | 2723.34980 | 1.33233 | 3 | CID | 1.21E-03 | 0.50 | 3.11 | 0.10 | 435.1 | 1 | 21/92 |
| | 4126 | K.TGHLMACFTCAK.K | 1396.61710 | 1.14867 | 2 | CID | 2.62E-05 | 0.70 | 2.53 | 0.35 | 419.4 | 1 | 12/22 |
| | 8463 | T.VYQAGESDTDSFEEDPEISLADYWK.C | 2894.25267 | 1.54001 | 2 | CID | 1.31E-09 | 0.35 | 1.84 | 0.19 | 326.6 | 1 | 17/48 |
| 4 | gi\|51703339\|sp\|P62988.1\|UBIQ_HUMAN Ubiquitin | | | | | | 1.79E-09 | 7.70 | 110.21 | 89.50 | 8559.6 | 51703339 | 11 (11 0 0 0 0) |
| | 1438 | K.AKIQDKEGIPPDQQR.L | 1722.91332 | 0.31522 | 2 | CID | 7.54E-04 | 0.70 | 2.65 | 0.58 | 254.9 | 1 | 11/28 |
| | 4718 | K.ESTLHLVLR.L | 1067.62077 | -1.71000 | 2 | CID | 4.23E-07 | 0.78 | 2.10 | 0.69 | 151.5 | 1 | 10/16 |
| | 1469 | K.IQDKEGIPPDQQR.L | 1523.78125 | 0.35425 | 2 | CID | 1.79E-09 | 0.96 | 3.86 | 0.65 | 720.6 | 1 | 19/24 |
| | 5625 | R.LIFAGK$QLEDGR.T | 1389.74849 | -0.11018 | 2 | CID | 4.51E-05 | 0.93 | 3.18 | 0.62 | 599.9 | 1 | 16/22 |
| | 6658 | R.LIFAGK$QLEDGRTLSDYNIQK.E | 2452.28307 | 0.11962 | 3 | CID | 1.25E-02 | 0.53 | 2.29 | 0.43 | 269.9 | 1 | 20/80 |
| | 6113 | K.TITLEVEPSDTIENVK.A | 1787.92730 | 1.36134 | 2 | CID | 4.50E-08 | 0.94 | 3.15 | 0.62 | 839.0 | 1 | 20/30 |
| | 6234 | K.TITLEVEPSDTIEN@VK$AK.I | 2030.06519 | 1.88340 | 2 | CID | 5.65E-06 | 0.48 | 2.60 | 0.13 | 346.6 | 1 | 15/34 |
| | 6228 | R.TLSDYNIQK#ESTLHLVLR.L | 2244.19724 | 0.13964 | 2 | CID | 6.15E-08 | 0.68 | 3.04 | 0.15 | 541.0 | 1 | 15/34 |
| | 6110 | R.TLSDYNIQKESTLHLVLR.L | 2130.15534 | -1.59299 | 3 | CID | 7.47E-06 | 0.82 | 2.93 | 0.54 | 505.7 | 1 | 24/68 |
| | 6921 | K.TLTGK$TITLEVEPSDTIENVK.A | 2331.22896 | -1.01003 | 2 | CID | 4.52E-02 | 0.17 | 2.91 | 0.12 | 107.4 | 1 | 8/40 |
| | 5793 | F.VK#TLTGK$TITLEVEPSDTIENVK.A | 2671.45023 | 1.28088 | 3 | CID | 2.10E-04 | 0.70 | 4.27 | 0.01 | 485.1 | 1 | 23/88 |

M* +15.99492) (KS# +114.04190) (NQ@ +0.98402) (DE^ +14.01565) (STY~ +79.96633) (K$ +42.02180) C=160.03068  Enzyme:None selected

| | Referen | #3 | | | | | P (pro) | Sf | Score | Coverage | MW | Accession | Peptide (Hits) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Scan(s)** | **Peptide** | **MH+** | **DeltaM (ppm)** | **z** | **Type** | **P (pep)** | **Sf** | **XC** | **DeltaCn** | **Sp** | **RSp** | **Ions** |
| 1 | His-RFP-p53 | | | | | | 2.94E-11 | 31.82 | 440.22 | 44.90 | 70829.9 | | 44 (44 0 0 0 0) |
| | 4291 | K.AYVKHPADIPDYLK.L | 1629.86352 | -1.47312 | 3 | CID | 1.81E-03 | 0.84 | 3.01 | 0.63 | 553.4 | 1 | 19/52 |
| | 4027 | R.CSDSDGLAPPQHLIR.V | 1665.80137 | -0.10256 | 2 | CID | 1.10E-05 | 0.67 | 2.11 | 0.63 | 242.5 | 1 | 12/28 |
| | 4048 | R.CSD^SDGLAPPQHLIR.V | 1679.81702 | 0.24676 | 2 | CID | 8.82E-04 | 0.28 | 2.36 | 0.21 | 256.8 | 1 | 10/28 |
| | 3919 | K.DAQ@AGKEPGGSRAH.S | 1381.64548 | -3.30374 | 2 | CID | 8.66E-02 | 0.11 | 1.82 | 0.37 | 113.3 | 1 | 7/26 |
| | 956 | K.DGGHYDAEVK.T | 1090.47998 | 0.26912 | 2 | CID | 1.45E-04 | 0.83 | 2.38 | 0.51 | 501.7 | 1 | 12/18 |
| | 4284 | R.ELNEALELK.D | 1058.57282 | -0.24476 | 2 | CID | 6.34E-04 | 0.60 | 1.99 | 0.41 | 383.0 | 1 | 9/16 |
| | 3604 | R.ELNEALELKDAQAGKEPGGSR.A | 2212.12042 | 0.15671 | 3 | CID | 5.34E-09 | 0.81 | 3.93 | 0.13 | 883.2 | 1 | 26/80 |
| | 4184 | R.ERFEMFR.E | 1014.48256 | -0.09095 | 2 | CID | 1.49E-04 | 0.67 | 1.85 | 0.51 | 130.6 | 1 | 8/12 |
| | 3528 | R.GTNFPSDGPVMQK.K | 1377.64673 | 2.33983 | 2 | CID | 4.14E-08 | 0.96 | 3.97 | 0.67 | 729.3 | 1 | 18/24 |
| | 2686 | R.GTNFPSDGPVM*QK.K | 1393.64164 | 0.79383 | 2 | CID | 2.05E-08 | 0.95 | 3.76 | 0.52 | 808.9 | 1 | 18/24 |
| | 3794 | R.GTNFPSDGPVMQK$K.T | 1548.74751 | 0.30148 | 2 | CID | 6.45E-02 | 0.11 | 1.86 | 0.00 | 197.7 | 1 | 11/26 |
| | 2854 | R.GTNFPSDGPVMQKK.T | 1505.74169 | -0.04299 | 2 | CID | 2.67E-02 | 0.42 | 2.09 | 0.46 | 197.9 | 1 | 10/26 |
| | 4138 | K.HPADIPDYLK.L | 1168.59970 | 0.27663 | 2 | CID | 3.89E-07 | 0.93 | 2.33 | 0.83 | 357.8 | 1 | 15/18 |
| | 5676 | R.HSTGAENLYFQGLEEEPQ.S | 2048.91959 | 0.90014 | 2 | CID | 1.31E-06 | 0.94 | 3.65 | 0.53 | 797.6 | 1 | 20/34 |
| | 5609 | R.HSTGAENLYFQGLEEEPQSDPS.V | 2435.06335 | 1.37341 | 2 | CID | 3.49E-07 | 0.89 | 3.21 | 0.59 | 623.2 | 1 | 18/42 |
| | 6490 | R.HSTGAENLYFQGLEEEPQSDPSVEPPLSQET.F | 3415.54483 | 1.87757 | 3 | CID | 2.78E-02 | 0.56 | 2.40 | 0.44 | 251.7 | 1 | 20/120 |
| | 5405 | K.KKPLDGEYFTLQIR.G | 1707.94283 | 0.18580 | 3 | CID | 5.31E-05 | 0.91 | 3.47 | 0.71 | 672.5 | 1 | 20/52 |
| | 2794 | K.KPVQLPGAYK.T | 1100.64626 | -0.41487 | 2 | CID | 2.24E-06 | 0.92 | 2.76 | 0.70 | 409.3 | 1 | 14/18 |
| | 2949 | K.KPVQLPGAYKTD.I | 1316.72088 | -0.18911 | 2 | CID | 2.69E-05 | 0.60 | 2.11 | 0.39 | 292.4 | 1 | 12/22 |
| | 2355 | K.KTMGWEASTER.M | 1295.60486 | 0.69373 | 2 | CID | 4.16E-06 | 0.72 | 2.12 | 0.51 | 259.9 | 1 | 12/20 |
| | 5462 | K.LDITSHNEDYTIVEQYER.A | 2225.03568 | 1.32109 | 2 | CID | 2.94E-11 | 0.94 | 4.01 | 0.52 | 933.5 | 1 | 18/34 |
| | 3043 | R.LGFLHSGTAK.S | 1030.56801 | 0.98145 | 2 | CID | 1.01E-04 | 0.84 | 2.32 | 0.44 | 578.4 | 1 | 13/18 |
| | 1151 | K.LKDGGHYDAEVK.T | 1331.65901 | -0.29194 | 2 | CID | 4.38E-08 | 0.93 | 3.23 | 0.41 | 1066.5 | 1 | 16/22 |
| | 3572 | K.LRGTNFPSDGPVMQK.K | 1646.83190 | 0.62658 | 2 | CID | 1.89E-06 | 0.45 | 2.12 | 0.44 | 203.9 | 1 | 11/28 |
| | 2850 | K.LRGTNFPSDGPVM*QK.K | 1662.82682 | -1.06452 | 3 | CID | 2.34E-03 | 0.51 | 2.52 | 0.19 | 554.3 | 1 | 20/56 |
| | 5304 | K.LSFPEGFK.W | 924.48254 | -0.08160 | 2 | CID | 7.17E-05 | 0.82 | 1.93 | 0.60 | 426.2 | 1 | 10/14 |
| | 6084 | K.LSFPEGFKWER.V | 1395.70556 | -0.92478 | 2 | CID | 2.02E-08 | 0.83 | 2.05 | 0.53 | 404.0 | 1 | 14/20 |
| | 4538 | R.MEGSVN@GHEFEIEGEGEGRPYEGTQTAK.L | 3039.32725 | 0.27916 | 3 | CID | 3.65E-09 | 0.83 | 3.83 | 0.25 | 755.2 | 1 | 29/108 |
| | 4118 | R.M*EGSVN@GHEFEIEGEGEGRPYEGTQTAK.L | 3055.32216 | 0.00427 | 3 | CID | 1.21E-05 | 0.78 | 3.50 | 0.42 | 313.9 | 1 | 26/108 |
| | 3946 | R.M*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L | 3054.33815 | 2.58445 | 3 | CID | 1.09E-03 | 0.41 | 2.53 | 0.24 | 235.0 | 1 | 21/108 |
| | 4261 | R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L | 3038.34323 | 2.02930 | 3 | CID | 1.69E-06 | 0.93 | 4.20 | 0.60 | 881.3 | 1 | 30/108 |
| | 4925 | R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK$LK.V | 3323.51209 | 0.59159 | 4 | CID | 8.28E-06 | 0.78 | 4.38 | 0.02 | 756.6 | 1 | 35/174 |
| | 4826 | H.PADIPDYLK.L | 1031.54079 | 1.09512 | 2 | CID | 1.36E-03 | 0.75 | 2.05 | 0.38 | 481.7 | 1 | 11/16 |
| | 3593 | K.PVQLPGAYK.T | 972.55129 | 0.33842 | 2 | CID | 2.03E-04 | 0.84 | 2.11 | 0.55 | 597.5 | 1 | 11/16 |
| | 4797 | T.QDSSLQDGEFIYK.V | 1529.71183 | 1.20385 | 2 | CID | 3.52E-04 | 0.33 | 2.61 | 0.07 | 254.5 | 1 | 11/24 |
| | 710 | R.RTEEENLR.K | 1046.52251 | -0.58677 | 2 | CID | 1.34E-06 | 0.85 | 2.28 | 0.65 | 268.5 | 1 | 10/14 |
| | 4673 | D.SSLQDGEFIYK.V | 1286.62631 | 0.25333 | 2 | CID | 1.99E-06 | 0.91 | 2.71 | 0.70 | 565.7 | 1 | 13/20 |
| | 2884 | K.SVTCTYSPALNK.M | 1340.65151 | 0.38142 | 2 | CID | 1.37E-07 | 0.88 | 2.76 | 0.62 | 522.3 | 1 | 13/22 |
| | 5983 | K.TCPVQLWVDSTPPPGTR.V | 1910.94294 | 0.49741 | 2 | CID | 2.09E-08 | 0.82 | 2.38 | 0.63 | 428.7 | 1 | 16/32 |
| | 2159 | K.TM*GWEASTER.M | 1183.50481 | -0.62337 | 2 | CID | 1.08E-04 | 0.84 | 2.32 | 0.60 | 529.3 | 1 | 11/18 |
| | 3116 | K.TMGWEASTER.M | 1167.50990 | -0.17776 | 2 | CID | 2.66E-04 | 0.93 | 2.61 | 0.66 | 756.6 | 1 | 14/18 |
| | 3738 | R.VEYLDDRNTFR.H | 1427.69137 | 0.23082 | 2 | CID | 6.59E-05 | 0.61 | 1.97 | 0.54 | 203.5 | 1 | 10/20 |
| | 5065 | A.YVK#HPADIPDYLK.L | 1672.86831 | 0.38183 | 2 | CID | 2.94E-04 | 0.52 | 2.12 | 0.50 | 151.3 | 1 | 10/24 |
| 2 | gi\|88702791\|ref\|NP_002384.2\| protein Mdm4 [Homo sapiens] | | | | | | 2.80E-12 | 23.60 | 348.24 | 48.20 | 54829.6 | 88702791 | 35 (34 1 0 0 0) |
| | 902 | K.AGASCPICK.K | 963.43872 | -1.28088 | 2 | CID | 2.44E-04 | 0.89 | 2.56 | 0.74 | 346.8 | 1 | 11/16 |
| | 5375 | K.CIHSRE^DEDLIENLAQDETSR.L | 2544.16312 | 0.07172 | 3 | CID | 3.10E-05 | 0.88 | 4.74 | 0.03 | 1064.1 | 1 | 27/80 |
| | 5375 | K.CIHSRED^EDLIENLAQDETSR.L | 2544.16312 | 0.07172 | 3 | CID | 3.10E-05 | 0.86 | 4.58 | 0.10 | 1064.1 | 1 | 27/80 |
| | 989 | R.DGNIIHGR.T | 881.45879 | 0.13624 | 2 | CID | 3.10E-05 | 0.93 | 2.53 | 0.66 | 612.8 | 1 | 12/14 |
| | 6484 | K.DPSPLYDMLR.K | 1206.58234 | -0.21257 | 2 | CID | 1.71E-01 | 0.62 | 1.96 | 0.33 | 397.8 | 1 | 11/18 |
| | 5995 | R.EDEDLIENLAQDETSR.L | 1876.84067 | 1.53582 | 2 | CID | 1.23E-08 | 0.96 | 3.22 | 0.63 | 1502.6 | 1 | 20/30 |
| | 5701 | K.EVMHYLGQYIM*VK.Q | 1626.80185 | 1.55003 | 2 | CID | 8.63E-05 | 0.92 | 3.05 | 0.60 | 676.2 | 1 | 15/24 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  | 6085 | K.EVMHYLGQYIMVK.Q | 1610.80693 | 0.37895 | 2 | CID | 1.44E-06 | 0.94 | 3.08 | 0.68 | 855.7 | 1 | 15/24 |
|  | 5342 | K.EVM*HYLGQYIMVK.Q | 1626.80185 | 0.19936 | 2 | CID | 2.21E-05 | 0.61 | 2.24 | 0.54 | 246.2 | 1 | 10/24 |
|  | 4396 | K.ILHAAGAQGEMFTVK.E | 1572.82027 | 0.90838 | 2 | CID | 4.67E-10 | 0.91 | 3.46 | 0.34 | 845.9 | 1 | 18/28 |
|  | 3473 | K.ILHAAGAQGEM*FTVK.E | 1588.81519 | 1.25699 | 2 | CID | 1.64E-06 | 0.95 | 3.10 | 0.64 | 1037.4 | 1 | 19/28 |
|  | 2707 | R.ISPGQINQVRPK.L | 1336.76956 | -0.07662 | 2 | CID | 8.38E-04 | 0.74 | 2.02 | 0.79 | 116.1 | 1 | 11/22 |
|  | 2407 | R.ISPGQIN@QVRPK.L | 1337.75358 | 0.28305 | 2 | CID | 2.30E-03 | 0.31 | 2.21 | 0.08 | 178.7 | 1 | 12/22 |
|  | 3562 | K.KEIQLVIK.V | 970.62954 | -0.73323 | 2 | CID | 1.62E-02 | 0.86 | 1.84 | 0.78 | 366.2 | 1 | 10/14 |
|  | 3157 | K.K$VIEVGKNDDLEDSK.S | 1731.87594 | 0.96685 | 2 | CID | 8.41E-05 | 0.62 | 2.60 | 0.42 | 123.1 | 1 | 13/28 |
|  | 2263 | K.KVIEVGKNDDLEDSK.S | 1688.87012 | 1.39946 | 2 | CID | 6.14E-06 | 0.66 | 2.58 | 0.57 | 163.2 | 1 | 11/28 |
|  | 4388 | K.LTHSLSTSDITAIPEK.E | 1712.90651 | 1.22445 | 3 | CID | 2.33E-03 | 0.43 | 2.52 | 0.41 | 258.3 | 1 | 14/60 |
|  | 4521 | K.LTHSLSTSDITAIPEKENEGNDVPDCR.R | 2998.40587 | 0.66731 | 3 | CID | 9.69E-06 | 0.91 | 4.05 | 0.62 | 709.8 | 1 | 25/104 |
|  | 4575 | K.LTHSLSTSDITAIPEKENEGNDVPD^CR.R | 3012.42152 | 0.35199 | 3 | CID | 1.50E-08 | 0.62 | 2.37 | 0.26 | 700.8 | 1 | 26/104 |
|  | 4257 | K.LTHSLSTSDITAIPEKENEGNDVPD^CRR.T | 3168.52263 | 1.01650 | 3 | CID | 1.40E-05 | 0.36 | 2.39 | 0.17 | 299.3 | 1 | 21/108 |
|  | 4288 | K.LTHSLSTSDITAIPEKENEGN@DVPDCRR.T | 3155.49100 | 2.12460 | 4 | CID | 2.56E-05 | 0.66 | 3.75 | 0.06 | 499.0 | 1 | 32/162 |
|  | 4215 | K.LTHSLSTSDITAIPEKENEGNDVPDCRR.T | 3154.50698 | 1.60940 | 3 | CID | 2.80E-12 | 0.92 | 4.33 | 0.54 | 732.5 | 1 | 30/108 |
|  | 6350 | A.QGE^MFTVKEVMHYLGQY~IM*V.K | 2513.13145 | -4.20580 | 3 | CID | 1.67E-01 | 0.42 | 2.60 | 0.25 | 366.5 | 1 | 22/114 |
|  | 6521 | R.QSFSVKDPSPLYDMLR.K | 1882.93676 | 1.90914 | 2 | CID | 1.95E-03 | 0.17 | 1.87 | 0.16 | 202.1 | 1 | 11/30 |
|  | 5956 | R.QSFSVKDPSPLYDMLRK.N | 2011.03172 | 0.11542 | 3 | CID | 3.49E-03 | 0.39 | 2.47 | 0.27 | 231.7 | 1 | 18/64 |
|  | 4741 | K.SLSDDTDVEVTSEDEWQCTE^CKK.F | 2775.16083 | 1.74774 | 3 | CID | 5.50E-03 | 0.14 | 2.26 | 0.06 | 138.4 | 1 | 15/88 |
|  | 4837 | R.TDTENMEDCQNLLKPCSLCEK.R | 2585.09874 | 0.77296 | 3 | CID | 5.66E-05 | 0.33 | 2.34 | 0.02 | 524.1 | 1 | 22/80 |
|  | 4857 | R.TDTENMEDCQNLLKPCSLCE^K.R | 2599.11439 | 1.60457 | 3 | CID | 1.37E-04 | 0.44 | 2.49 | 0.22 | 383.1 | 1 | 19/80 |
|  | 4285 | R.TDTENM*EDCQNLLKPCSLCEK.R | 2601.09366 | 0.44703 | 3 | CID | 2.90E-03 | 0.23 | 2.26 | 0.03 | 386.2 | 1 | 19/80 |
|  | 2448 | R.TGHLVTCFHCAR.R | 1458.67297 | -0.87444 | 3 | CID | 3.36E-08 | 0.93 | 3.42 | 0.69 | 671.6 | 1 | 25/44 |
|  | 3874 | R.TTEDDIPTLPTSEHK.C | 1683.80719 | 1.29929 | 2 | CID | 2.98E-02 | 0.62 | 2.40 | 0.45 | 295.9 | 1 | 12/28 |
|  | 1522 | K.VEAADTEQTSEEVGK.V | 1592.72860 | 1.73883 | 2 | CID | 3.35E-11 | 0.97 | 3.81 | 0.70 | 1769.6 | 1 | 21/28 |
|  | 2515 | K.VEAADTEQTSEEVGKVSDK.K | 2021.95095 | 1.22014 | 2 | CID | 1.41E-07 | 0.74 | 3.75 | 0.03 | 590.2 | 1 | 17/36 |
|  | 3626 | K.VIEVGK$NDDLEDSK.S | 1603.78097 | 0.35424 | 2 | CID | 3.35E-04 | 0.71 | 2.85 | 0.34 | 350.1 | 1 | 13/26 |
|  | 2752 | K.VIEVGKNDDLEDSK.S | 1560.77516 | 0.49263 | 2 | CID | 3.69E-08 | 0.95 | 3.32 | 0.65 | 946.1 | 1 | 18/26 |
| 3 | gi\|51703339\|sp\|P62988.1\|UBIQ_HUMAN Ubiquitin |  |  |  |  |  | 4.30E-11 | 9.57 | 120.21 | 89.50 | 8559.6 | 51703339 | 12 (12 0 0 0 0) |
|  | 1340 | K.AKIQDKEGIPPDQQR.L | 1722.91332 | 1.09459 | 2 | CID | 3.24E-05 | 0.92 | 3.45 | 0.58 | 659.1 | 1 | 16/28 |
|  | 4494 | K.ESTLHLVLR.L | 1067.62077 | 0.34809 | 2 | CID | 1.20E-06 | 0.93 | 2.86 | 0.76 | 252.6 | 1 | 13/16 |
|  | 1407 | K.IQDKEGIPPDQQR.L | 1523.78125 | -1.00762 | 2 | CID | 4.30E-11 | 0.96 | 3.92 | 0.70 | 726.9 | 1 | 19/24 |
|  | 4363 | R.LIFAGK#QLEDGR.T | 1460.78458 | 1.51633 | 2 | CID | 3.90E-08 | 0.90 | 2.95 | 0.56 | 727.2 | 1 | 13/22 |
|  | 5239 | R.LIFAGK$QLEDGR.T | 1389.74849 | 1.20736 | 2 | CID | 1.64E-06 | 0.97 | 4.12 | 0.70 | 802.4 | 1 | 18/22 |
|  | 3708 | K.QLEDGRTLSDYNIQK.E | 1779.88717 | -0.13016 | 3 | CID | 1.27E-02 | 0.50 | 2.38 | 0.47 | 249.7 | 1 | 15/56 |
|  | 4427 | E.STLHLVLR.L | 938.57818 | -0.71962 | 2 | CID | 2.41E-07 | 0.86 | 2.28 | 0.78 | 309.3 | 1 | 9/14 |
|  | 5621 | K.TITLEVEPSDTIENVK.A | 1787.92730 | 1.90754 | 2 | CID | 3.85E-05 | 0.94 | 3.60 | 0.60 | 766.1 | 1 | 19/30 |
|  | 5716 | K.TITLEVEPSDTIENVK$AK.I | 2030.06519 | 1.04157 | 2 | CID | 1.10E-03 | 0.21 | 2.19 | 0.05 | 249.2 | 1 | 13/34 |
|  | 2840 | R.TLSDYNIQK.E | 1081.55242 | 0.00036 | 2 | CID | 1.95E-06 | 0.90 | 2.05 | 0.63 | 479.1 | 1 | 14/16 |
|  | 5547 | K.TLTGK#TITLEVEPSDTIENVK.A | 2402.26505 | 1.07274 | 2 | CID | 4.61E-05 | 0.80 | 3.67 | 0.09 | 743.3 | 1 | 18/40 |
|  | 5337 | F.VK#TLTGK($-1)TITLEVEPSDTIENVK.A | 2671.45023 | 1.76068 | 3 | CID | 4.75E-03 | 0.69 | 3.90 | 0.02 | 545.0 | 1 | 26/88 |
| 4 | gi\|260080636\|gb\|ACX31156.1\| MDM2 [Homo sapiens] |  |  |  |  |  | 1.08E-11 | 2.62 | 30.23 | 12.20 | 52436.5 | 260080636 | 3 (3 0 0 0 0) |
|  | 2551 | R.AISETEENSDELSGER.Q | 1765.77226 | 0.28067 | 2 | CID | 5.70E-08 | 0.86 | 2.57 | 0.41 | 763.9 | 1 | 18/30 |
|  | 3324 | K.AKLENSTQAEEGFDVPD^CKK.T | 2280.08129 | 0.79577 | 3 | CID | 8.06E-05 | 0.78 | 4.25 | 0.20 | 342.9 | 1 | 24/76 |
|  | 3315 | R.NLVVVNQQESSDSGTSVSENR.C | 2249.06402 | 2.27518 | 2 | CID | 1.08E-11 | 0.98 | 4.64 | 0.43 | 2255.9 | 1 | 27/40 |

M* +15.99492) (KS# +114.04190) (NQ@ +0.98402) (DE^ +14.01565) (STY~ +79.96633) (K$ +43.006) C=160.03068  Enzyme:None selected

|  | Reference | #4 |  |  |  |  | P (pro) | Sf | Score | Coverage | MW | Accession | Peptide (Hits) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  | Scan(s) | Peptide | MH+ | DeltaM (ppm) | z | Type | P (pep) | Sf | XC | DeltaCn | Sp | RSp | Ions |
| 1 | His-RFP-p53 |  |  |  |  |  | 2.21E-11 | 21.07 | 260.26 | 40.30 | 70829.9 |  | 26 (26 0 0 0 0) |
|  | 4443 | K.AYVKHPADIPDYLK.L | 1629.86352 | -0.46202 | 3 | CID | 2.85E-04 | 0.83 | 2.86 | 0.43 | 785.8 | 1 | 22/52 |
|  | 4167 | R.CSDSDGLAPPQHLIR.V | 1665.80137 | -0.07399 | 3 | CID | 1.36E-03 | 0.74 | 2.79 | 0.55 | 361.0 | 1 | 19/56 |
|  | 2031 | E.D^GALK#GEIKM.R | 1189.62351 | -2.10248 | 3 | CID | 2.83E-03 | 0.60 | 2.30 | 0.26 | 640.8 | 1 | 16/36 |
|  | 956 | K.DGGHYDAEVK.T | 1090.47998 | 0.38106 | 2 | CID | 3.34E-04 | 0.70 | 2.08 | 0.43 | 399.5 | 1 | 11/18 |
|  | 3746 | R.ELNEALELKDAQAGKEPGGSR.A | 2212.12042 | 0.40503 | 3 | CID | 5.92E-05 | 0.78 | 4.46 | 0.11 | 643.6 | 1 | 21/80 |
|  | 2739 | R.GTNFPSDGPVM*QK.K | 1393.64164 | 4.03469 | 2 | CID | 4.02E-06 | 0.91 | 3.42 | 0.59 | 592.0 | 1 | 14/24 |
|  | 3682 | R.GTNFPSDGPVMQK.K | 1377.64673 | 2.16261 | 2 | CID | 2.45E-05 | 0.82 | 2.72 | 0.65 | 321.1 | 1 | 12/24 |
|  | 4295 | K.HPADIPDYLK.L | 1168.59970 | 0.59000 | 2 | CID | 1.28E-07 | 0.93 | 2.41 | 0.82 | 373.9 | 1 | 15/18 |
|  | 6193 | R.HSTGAENLYFQGLEEEPQ.S | 2048.91959 | 0.54268 | 2 | CID | 1.36E-06 | 0.90 | 3.62 | 0.46 | 686.1 | 1 | 16/34 |
|  | 2757 | K.KPVQLPGAYK.T | 1100.64626 | 4.68689 | 2 | CID | 2.02E-04 | 0.88 | 2.65 | 0.64 | 396.2 | 1 | 12/18 |
|  | 5931 | K.LDITSHNEDYTIVEQYER.A | 2225.03568 | -0.43450 | 2 | CID | 4.47E-10 | 0.91 | 3.46 | 0.55 | 664.1 | 1 | 17/34 |
|  | 3028 | R.LGFLHSGTAK.S | 1030.56801 | -0.67685 | 2 | CID | 1.20E-04 | 0.92 | 2.89 | 0.64 | 669.0 | 1 | 13/18 |
|  | 1089 | K.LKDGGHYDAEVK.T | 1331.65901 | -0.10860 | 2 | CID | 1.96E-08 | 0.93 | 3.43 | 0.50 | 928.9 | 1 | 15/22 |
|  | 2955 | K.LRGTNFPSDGPVM*QK.K | 1662.82682 | -0.28561 | 2 | CID | 7.56E-02 | 0.44 | 1.81 | 0.45 | 220.0 | 1 | 12/28 |
|  | 6696 | K.LSFPEGFKWER.V | 1395.70556 | 1.26175 | 2 | CID | 2.08E-09 | 0.48 | 2.07 | 0.38 | 150.6 | 1 | 10/20 |
|  | 4336 | R.M*EGSVN@GHEFEIEGEGEGRPYEGTQTAK.L | 3055.32216 | -0.31976 | 4 | CID | 3.13E-10 | 0.89 | 3.98 | 0.53 | 715.9 | 1 | 36/162 |
|  | 4484 | R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L | 3038.34323 | 2.75248 | 3 | CID | 8.89E-07 | 0.95 | 5.17 | 0.58 | 787.7 | 1 | 29/108 |
|  | 4128 | R.M*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L | 3054.33815 | -0.03774 | 4 | CID | 1.63E-03 | 0.76 | 3.31 | 0.50 | 350.2 | 1 | 24/162 |
|  | 4642 | R.MEGSVN@GHEFEIEGEGEGRPYEGTQTAK.L | 3039.32725 | 2.50381 | 4 | CID | 2.93E-08 | 0.83 | 3.79 | 0.42 | 487.3 | 1 | 36/162 |
|  | 656 | R.RTEEENLR.K | 1046.52251 | -0.47013 | 2 | CID | 1.46E-05 | 0.93 | 3.12 | 0.53 | 562.9 | 1 | 12/14 |
|  | 4921 | D.SSLQDGEFIYK.V | 1286.62631 | 0.82258 | 2 | CID | 6.73E-05 | 0.71 | 2.27 | 0.55 | 225.1 | 1 | 11/20 |
|  | 2991 | K.SVTCTYSPALNK.M | 1340.65151 | -1.62175 | 2 | CID | 6.07E-06 | 0.85 | 2.56 | 0.60 | 487.5 | 1 | 13/22 |
|  | 6563 | K.TCPVQLWVDSTPPPGTR.V | 1910.94294 | 1.00845 | 2 | CID | 2.21E-11 | 0.93 | 3.66 | 0.67 | 535.5 | 1 | 17/32 |
|  | 2141 | K.TM*GWEASTER.M | 1183.50481 | 0.40806 | 2 | CID | 1.75E-05 | 0.87 | 2.51 | 0.67 | 488.0 | 1 | 11/18 |
|  | 3232 | K.TMGWEASTER.M | 1167.50990 | 0.76325 | 2 | CID | 1.59E-02 | 0.90 | 2.69 | 0.70 | 523.9 | 1 | 12/18 |
|  | 7307 | R.VM*NFEDGGVVTVTQDSSLQDGEFIYK.V | 2894.34005 | 0.70104 | 3 | CID | 1.25E-03 | 0.68 | 3.64 | 0.08 | 568.9 | 1 | 26/100 |
| 2 | gi\|51703339\|sp\|P62988.1\|UBIQ_HUMAN Ubiquitin |  |  |  |  |  | 7.04E-13 | 11.55 | 154.22 | 89.50 | 8559.6 | 51703339 | 16 (13 3 0 0 0) |
|  | 1352 | K.AKIQDKEGIPPDQQR.L | 1722.91332 | -1.07418 | 3 | CID | 1.08E-04 | 0.84 | 3.23 | 0.55 | 467.7 | 1 | 21/56 |
|  | 4614 | K.ESTLHLVLR.L | 1067.62077 | 0.23376 | 2 | CID | 3.93E-07 | 0.92 | 2.55 | 0.78 | 255.6 | 1 | 13/16 |
|  | 1606 | K.IQDKEGIPPDQQR.L | 1523.78125 | 0.91502 | 2 | CID | 7.53E-10 | 0.97 | 3.99 | 0.69 | 828.2 | 1 | 20/24 |
|  | 4603 | R.LIFAGK#QLEDGR.T | 1460.78458 | 2.76980 | 2 | CID | 2.52E-06 | 0.93 | 2.99 | 0.66 | 622.5 | 1 | 16/22 |
|  | 5609 | R.LIFAGK$QLEDGR.T | 1389.74849 | 0.85602 | 2 | CID | 1.23E-05 | 0.92 | 3.47 | 0.66 | 437.9 | 1 | 14/22 |
|  | 3888 | K.QLEDGRTLSDYNIQK.E | 1779.88717 | -0.29406 | 2 | CID | 1.30E-04 | 0.39 | 2.04 | 0.41 | 127.7 | 1 | 11/28 |
|  | 5947 | K.TITLEVEPSDTIEN@VK.A | 1788.91132 | -4.37536 | 2 | CID | 8.66E-04 | 0.74 | 3.20 | 0.26 | 455.6 | 1 | 14/30 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 6119 | K.TITLEVEPSDTIENVK.A | 1787.92730 | 0.95169 | 2 | CID | 1.80E-08 | 0.96 | 3.95 | 0.69 | 834.7 | 1 | 20/30 |
| 6238 | K.TITLEVEPSDTIENVK$AK.I | 2030.06519 | 0.80104 | 2 | CID | 3.60E-04 | 0.68 | 2.05 | 0.37 | 498.9 | 1 | 17/34 |
| 5547 | K.TITLEVEPSDTIENVK#AK.I it is either this or the peptide below | 2101.10128 | -0.40022 | 3 | CID | 7.23E-05 | 0.33 | 2.95 | 0.03 | 320.1 | 1 | 20/68 |
| 5547 | K.TITLEVEPSDTIENVKAK#.I | 2101.10128 | -0.40022 | 3 | CID | 7.23E-05 | 0.35 | 2.97 | 0.01 | 320.1 | 1 | 20/68 |
| 2868 | R.TLSDYNIQK.E | 1081.55242 | -2.36982 | 2 | CID | 1.17E-05 | 0.93 | 2.61 | 0.69 | 493.8 | 1 | 14/16 |
| 6066 | R.TLSDYNIQKESTLHLVLR.L | 2130.15534 | 0.29810 | 3 | CID | 7.04E-13 | 0.88 | 3.19 | 0.66 | 451.7 | 1 | 27/68 |
| 6861 | K.TLTGK$TITLEVEPSDTIENVK.A | 2331.22896 | 0.66559 | 2 | CID | 4.68E-03 | 0.16 | 2.35 | 0.20 | 140.4 | 1 | 9/40 |
| 6014 | K.TLTGK#TITLEVEPSDTIENVK.A | 2402.26505 | 0.56459 | 2 | CID | 4.34E-05 | 0.80 | 3.64 | 0.04 | 803.8 | 1 | 19/40 |
| 5745 | F.VK#TLTGK$TITLEVEPSDTIENVK.A | 2671.45023 | -0.15849 | 3 | CID | 9.06E-06 | 0.74 | 4.38 | 0.63 | 517.6 | 1 | 26/88 |

| Reference | #5 | | | | | P (pro) | Sf | Score | Coverage | MW | Accession | Peptide (Hits) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Scan(s) | Peptide | MH+ | DeltaM (ppm) | z | Type | P (pep) | Sf | XC | DeltaCn | Sp | RSp | Ions |
| 1 His-RFP-p53 | | | | | | 2.66E-14 | 33.10 | 458.25 | 46.40 | 70829.9 | | 46 (45 1 0 0 0) |
| 5311 | K.AYVKHPADIPDYLK.L | 1629.86352 | -1.92249 | 3 | CID | 7.14E-04 | 0.70 | 2.41 | 0.46 | 568.2 | 1 | 19/52 |
| 1331 | K.DGGHYDAEVK.T | 1090.47998 | -0.06670 | 2 | CID | 4.28E-03 | 0.77 | 2.16 | 0.55 | 399.8 | 1 | 11/18 |
| 5260 | R.ELNEALELK.D | 1058.57282 | -0.70602 | 2 | CID | 9.32E-04 | 0.44 | 1.91 | 0.42 | 225.8 | 1 | 8/16 |
| 4435 | R.ELNEALELKDAQAGKEPGGSR.A | 2212.12042 | -1.00212 | 3 | CID | 1.11E-04 | 0.59 | 3.29 | 0.14 | 561.8 | 1 | 21/80 |
| 10615 | K.GGPLPFAWDILSPQFQYGSK.A | 2208.11242 | 0.63429 | 2 | CID | 2.74E-08 | 0.88 | 3.51 | 0.41 | 609.4 | 1 | 18/38 |
| 3318 | R.GTNFPSDGPVM*QK.K | 1393.64164 | 0.61864 | 2 | CID | 1.20E-09 | 0.94 | 3.41 | 0.61 | 804.1 | 1 | 17/24 |
| 4425 | R.GTNFPSDGPVMQK.K | 1377.64673 | 0.30185 | 2 | CID | 5.66E-07 | 0.90 | 3.10 | 0.61 | 471.0 | 1 | 15/24 |
| 3527 | R.GTNFPSDGPVM*QK$K.T | 1564.74242 | 1.51980 | 2 | CID | 1.91E-02 | 0.06 | 1.86 | 0.03 | 115.2 | 1 | 9/26 |
| 3499 | R.GTNFPSDGPVMQKK.T | 1505.74169 | -0.41674 | 3 | CID | 4.80E-02 | 0.45 | 2.75 | 0.43 | 158.6 | 1 | 13/52 |
| 5096 | K.HPADIPDYLK.L | 1168.59970 | -1.29025 | 2 | CID | 9.79E-07 | 0.94 | 2.30 | 0.83 | 438.1 | 1 | 16/18 |
| 7186 | R.HSTGAENLYFQGLEEEPQ.S | 2048.91959 | 1.73423 | 2 | CID | 9.19E-08 | 0.94 | 3.99 | 0.47 | 889.6 | 1 | 20/34 |
| 7095 | R.HSTGAENLYFQGLEEEPQSDPS.V | 2435.06335 | 1.27315 | 2 | CID | 7.72E-07 | 0.90 | 3.32 | 0.63 | 623.3 | 1 | 17/42 |
| 9278 | R.HSTGAENLYFQGLEEEPQSDPSVEPPLSQETF.S | 3562.61324 | 0.68830 | 3 | CID | 1.70E-07 | 0.67 | 2.80 | 0.54 | 203.0 | 1 | 19/124 |
| 6779 | K.KKPLDGEYFTLQIR.G | 1707.94283 | -1.85116 | 3 | CID | 1.87E-03 | 0.83 | 3.09 | 0.58 | 558.0 | 1 | 18/52 |
| 3419 | K.KPVQLPGAYK.T | 1100.64626 | 1.35966 | 2 | CID | 5.25E-03 | 0.75 | 1.95 | 0.61 | 277.1 | 1 | 11/18 |
| 3627 | K.KPVQLPGAYKT.D | 1201.69393 | 1.08463 | 2 | CID | 6.06E-02 | 0.62 | 2.26 | 0.61 | 168.4 | 1 | 9/20 |
| 2877 | K.KTMGWEASTER.M | 1295.60486 | -0.62533 | 2 | CID | 1.02E-04 | 0.90 | 2.77 | 0.64 | 500.5 | 1 | 13/20 |
| 6186 | K.LDITSHNEDYTIVEQ.Y | 1776.82865 | 0.48718 | 2 | CID | 4.52E-02 | 0.31 | 2.00 | 0.40 | 214.2 | 1 | 9/28 |
| 6863 | K.LDITSHNEDYTIVEQYER.A | 2225.03568 | 2.52805 | 2 | CID | 2.66E-14 | 0.97 | 4.99 | 0.59 | 1193.1 | 1 | 21/34 |
| 3695 | R.LGFLHSGTAK.S | 1030.56801 | -0.55840 | 2 | CID | 6.24E-05 | 0.95 | 3.31 | 0.65 | 627.6 | 1 | 15/18 |
| 1350 | K.LKDGGHYDAEVK.T | 1331.65901 | 0.80808 | 2 | CID | 1.30E-08 | 0.95 | 3.54 | 0.44 | 1328.2 | 1 | 17/22 |
| 4426 | K.LRGTNFPSDGPVMQK.K | 1646.83190 | 0.84895 | 2 | CID | 2.65E-05 | 0.74 | 3.06 | 0.48 | 256.5 | 1 | 12/28 |
| 3487 | K.LRGTNFPSDGPVM*QK.K | 1662.82682 | 0.36700 | 3 | CID | 6.18E-05 | 0.54 | 2.63 | 0.26 | 465.4 | 1 | 19/56 |
| 6603 | K.LSFPEGFK.W | 924.48254 | 0.90871 | 2 | CID | 5.00E-02 | 0.71 | 2.02 | 0.47 | 356.5 | 1 | 9/14 |
| 7775 | K.LSFPEGFKWER.V | 1395.70556 | -1.53701 | 2 | CID | 1.13E-06 | 0.47 | 2.26 | 0.31 | 181.1 | 1 | 10/20 |
| 5269 | R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L | 3038.34323 | 0.22136 | 3 | CID | 2.66E-07 | 0.90 | 4.46 | 0.54 | 421.0 | 1 | 25/108 |
| 4862 | R.M*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L | 3054.33815 | -0.95256 | 3 | CID | 7.22E-09 | 0.64 | 3.45 | 0.20 | 254.7 | 1 | 26/108 |
| 5467 | R.MEGSVN@GHEFEIEGEGEGRPYEGTQTAK.L | 3039.32725 | 1.78529 | 3 | CID | 1.52E-07 | 0.82 | 4.46 | 0.23 | 441.1 | 1 | 26/108 |
| 5105 | R.M*EGSVN@GHEFEIEGEGEGRPYEGTQTAK.L | 3055.32216 | -0.59503 | 3 | CID | 1.72E-08 | 0.83 | 3.70 | 0.41 | 459.2 | 1 | 29/108 |
| 4415 | K.PVQLPGAYK.T | 972.55129 | -0.85398 | 2 | CID | 2.43E-04 | 0.82 | 1.96 | 0.57 | 512.9 | 1 | 11/16 |
| 5945 | T.QDSSLQDGEFIYK.V | 1529.71183 | -0.23254 | 2 | CID | 3.49E-05 | 0.30 | 2.40 | 0.17 | 227.0 | 1 | 10/24 |
| 6809 | F.RE^LNEALELK#DAQ.A | 1656.85411 | 1.21611 | 2 | CID | 8.24E-02 | 0.18 | 2.25 | 0.03 | 209.4 | 1 | 10/24 |
| 761 | R.RTEEENLR.K | 1046.52251 | -0.70342 | 2 | CID | 3.78E-06 | 0.91 | 3.07 | 0.57 | 421.9 | 1 | 11/14 |
| 5781 | D.SSLQDGEFIYK.V | 1286.62631 | 1.48672 | 2 | CID | 3.66E-04 | 0.92 | 2.57 | 0.69 | 645.2 | 1 | 14/20 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 3545 | K.SVTCTYSPALNK.M | 1340.65151 | 0.10826 | 2 | CID | 3.52E-06 | 0.77 | 2.68 | 0.56 | 340.6 | 1 | 11/22 |
| | 7599 | K.TCPVQLWVDSTPPPGTR.V | 1910.94294 | 0.88069 | 2 | CID | 8.94E-10 | 0.85 | 3.40 | 0.61 | 306.7 | 1 | 13/32 |
| | 7418 | K.TDIKLDITSHNEDYTIVEQYER.A | 2682.28933 | 0.59034 | 4 | CID | 7.84E-05 | 0.74 | 3.17 | 0.42 | 439.9 | 1 | 26/126 |
| | 2535 | K.TM*GWEASTER.M | 1183.50481 | -0.82966 | 2 | CID | 5.15E-04 | 0.92 | 2.61 | 0.62 | 768.7 | 1 | 13/18 |
| | 3847 | K.TMGWEASTER.M | 1167.50990 | 0.86780 | 2 | CID | 4.10E-05 | 0.94 | 3.12 | 0.66 | 640.1 | 1 | 14/18 |
| | 3096 | R.VEYLDDR.N | 909.43124 | 0.42835 | 2 | CID | 2.47E-05 | 0.90 | 1.84 | 0.66 | 468.3 | 1 | 11/12 |
| | 9075 | R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V | 2878.34513 | 1.50409 | 3 | CID | 2.02E-08 | 0.94 | 4.77 | 0.41 | 1038.7 | 1 | 30/100 |
| | 8480 | R.VM*NFEDGGVVTVTQDSSLQDGEFIYK.V | 2894.34005 | 2.13965 | 2 | CID | 8.35E-06 | 0.62 | 3.19 | 0.13 | 418.1 | 1 | 17/50 |
| | 4769 | K.VRM*EGSVN@GHEFEIEGEGEGRPYEGTQTAK.L | 3310.49169 | 2.33221 | 4 | CID | 2.47E-06 | 0.85 | 3.56 | 0.51 | 608.0 | 1 | 34/174 |
| | 6292 | A.YVK#HPADIPDYLK.L | 1672.86831 | 2.93580 | 2 | CID | 6.24E-03 | 0.67 | 2.50 | 0.61 | 103.3 | 1 | 10/24 |
| 2 | gi\|51703339\|sp\|P62988.1\|UBIQ_HUMAN Ubiquitin | | | | | | 4.31E-10 | 13.45 | 220.26 | 89.50 | 8559.6 | 51703339 | 22 (22 0 0 0 0) |
| | 1564 | K.AKIQDKEGIPPDQQR.L | 1722.91332 | 0.51997 | 3 | CID | 4.09E-03 | 0.57 | 2.55 | 0.52 | 237.3 | 1 | 15/56 |
| | 5587 | K.ESTLHLVLR.L | 1067.62077 | 0.91979 | 2 | CID | 5.82E-08 | 0.92 | 2.77 | 0.84 | 202.1 | 1 | 12/16 |
| | 2479 | K.IQDKEGIPPDQQR.L | 1523.78125 | 1.15535 | 2 | CID | 9.38E-10 | 0.95 | 3.69 | 0.70 | 638.7 | 1 | 18/24 |
| | 2831 | K.IQDK$EGIPPDQQR.L | 1566.78706 | 1.61879 | 2 | CID | 2.84E-01 | 0.36 | 2.34 | 0.28 | 164.6 | 1 | 10/24 |
| | 1680 | K.IQD^K$EGIPPDQQR.L | 1580.80271 | 1.27974 | 2 | CID | 9.84E-02 | 0.56 | 2.53 | 0.24 | 333.3 | 1 | 12/24 |
| | 6553 | R.LIFAGK$QLEDGR.T | 1389.74849 | -0.28585 | 2 | CID | 3.31E-08 | 0.97 | 3.97 | 0.72 | 975.7 | 1 | 18/22 |
| | 5198 | R.LIFAGK$QLE^DGR.T | 1403.76414 | -1.69216 | 2 | CID | 7.68E-04 | 0.48 | 2.39 | 0.07 | 321.7 | 1 | 13/22 |
| | 5466 | R.LIFAGK#QLEDGR.T | 1460.78458 | 1.68346 | 2 | CID | 2.14E-08 | 0.96 | 3.70 | 0.64 | 1006.0 | 1 | 18/22 |
| | 4954 | K.QLEDGRTLSDYNIQK.E | 1779.88717 | 0.48709 | 3 | CID | 2.51E-03 | 0.28 | 2.44 | 0.28 | 198.9 | 1 | 13/56 |
| | 1537 | L.SDYNIQK.E | 867.42067 | -1.65537 | 2 | CID | 2.54E-02 | 0.80 | 2.15 | 0.49 | 312.4 | 1 | 9/12 |
| | 5430 | E.STLHLVLR.L | 938.57818 | -2.41039 | 2 | CID | 2.02E-05 | 0.79 | 2.02 | 0.45 | 495.8 | 1 | 10/14 |
| | 6991 | K.TITLEVEPSDTIENVK.A | 1787.92730 | 0.81515 | 2 | CID | 4.31E-10 | 0.96 | 3.84 | 0.64 | 880.3 | 1 | 21/30 |
| | 6953 | K.TITLEVEPSDTIE^NVK$.A | 1844.94877 | 1.59389 | 2 | CID | 1.84E-01 | 0.20 | 2.35 | 0.15 | 191.9 | 1 | 10/30 |
| | 7229 | K.TITLEVEPSDTIENVK$AK.I | 2030.06519 | 1.70301 | 2 | CID | 5.95E-04 | 0.56 | 3.01 | 0.12 | 347.4 | 1 | 15/34 |
| | 6358 | K.TITLEVEPSDTIE^NVK$AK.I | 2044.08084 | -0.35792 | 3 | CID | 1.50E-01 | 0.18 | 2.54 | 0.01 | 196.1 | 1 | 18/68 |
| | 3385 | R.TLSDYNIQK.E | 1081.55242 | 0.11322 | 2 | CID | 2.68E-06 | 0.93 | 2.56 | 0.69 | 467.5 | 1 | 14/16 |
| | 6753 | R.TLSDYNIQK$ESTL.H | 1554.76460 | 1.79211 | 2 | CID | 2.89E-02 | 0.21 | 2.17 | 0.11 | 233.2 | 1 | 10/24 |
| | 7204 | R.TLSDYNIQK#ESTLHLVLR.L | 2244.19724 | 1.03115 | 3 | CID | 3.86E-02 | 0.20 | 2.48 | 0.05 | 151.3 | 1 | 18/68 |
| | 7012 | K.TLTGK#TITLEVEPSDTIENVK.A | 2402.26505 | 5.13791 | 2 | CID | 4.14E-08 | 0.96 | 5.18 | 0.57 | 936.8 | 1 | 20/40 |
| | 7925 | K.TLTGK$TITLEVEPSDTIENVK.A | 2331.22896 | 0.87504 | 2 | CID | 1.36E-01 | 0.08 | 1.85 | 0.21 | 116.4 | 1 | 8/40 |
| | 7182 | K.TLTGK#TITLEVEPSDTIENVK$AK.I | 2644.40294 | 1.10248 | 3 | CID | 2.74E-06 | 0.76 | 4.02 | 0.04 | 751.4 | 1 | 26/88 |
| | 6665 | F.VK#TLTGK$TITLEVEPSDTIENVK.A | 2671.45023 | 2.24047 | 3 | CID | 2.13E-07 | 0.74 | 3.63 | 0.07 | 689.1 | 1 | 29/88 |
| 3 | gi\|260080636\|gb\|ACX31156.1\| MDM2 [Homo sapiens] | | | | | | 8.99E-14 | 4.13 | 78.27 | 23.40 | 52436.5 | 260080636 | 9 (6 1 1 1 0) |
| | 3149 | R.AISETEENSDELSGER.Q | 1765.77226 | 0.55720 | 2 | CID | 1.53E-09 | 0.98 | 3.77 | 0.58 | 2173.8 | 1 | 23/30 |
| | 5990 | K.DLVQELQEEKPSSSHLVSRPSTSSR.R | 2796.41224 | 1.99538 | 3 | CID | 2.54E-11 | 0.52 | 2.63 | 0.21 | 474.2 | 1 | 23/96 |
| | 4121 | R.NLVVVNQQESSDSDGTSVSENR.C | 2249.06402 | 4.88043 | 2 | CID | 8.99E-14 | 0.98 | 5.32 | 0.48 | 2217.8 | 1 | 26/40 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2743 | R.RAISETEENSDELSGER.Q | 1921.87337 | 2.33476 | 2 | CID | 1.34E-03 | 0.90 | 3.26 | 0.63 | 471.3 | 1 | 17/32 |