MATRIX SCIENCE Mascot Search Results

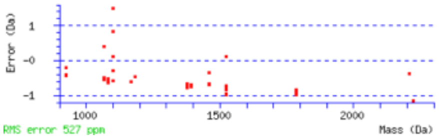
Protein View

```
Match to: YD_RFP-HERPc-Ub Score: 291
YD_RFP-HERPc-Ub
Found in search of C:\Documents and Settings\Safire2\My Documents\20100106_YaelDavid\BIT00737_YD_11_Herp_gp78_G2_merge.mgf

Nominal mass (Mr): 64441; Calculated pI value: 5.86
NCBI BLAST search of YD_RFP-HERPc-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Oxidation (M),GlyGly (K)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 24%

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 ESETEPEPVT
   251 LLVKSPNQRH RDLELSGDRG WSVGHLKAHL SRVYPERPRP EDQRLIYSGK
   301 LLLDHQCLRD LLPKQEKRHV LHLVCNVKSP SKMPEINAKV AESTEEPAGS
   351 NRGQYPEDSS SDGLRQREVL RNLSSPGWEN ISRPEAAQQA FQGLGPGFSG
   401 YTPYGWLQLS WFQQIYARQY YMQYLAATAA SGAFVPPPSA QEIPVVSAPA
   451 PAPIHNQFPA ENQPANQNAA PQVVVNPGAN QNLRMNAQGG PIVEEDDEQI
   501 FVKTLTGKTI TLEVEPSDTI ENVKAKIQDK EGIPPDQQRL IFAGKQLEDG
   551 RTLSDYNIQK ESTLHLVLRL RGG
```

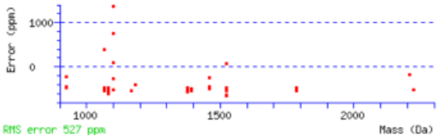
Show predicted peptides also

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

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   57 - 76     1104.3670  2206.7194  2207.1051    -0.3857     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 24)
   91 - 98      462.5310   923.0474   923.4753    -0.4278     0  K.LSFPEGFK.W  (Ions score 35)
   91 - 98      462.5420   923.0694   923.4753    -0.4058     0  K.LSFPEGFK.W  (Ions score 35)
   91 - 98      462.6380   923.2614   923.4753    -0.2138     0  K.LSFPEGFK.W  (Ions score 43)
  132 - 144     688.9350  1375.8554  1376.6395    -0.7840     0  R.GTNFPSDGPVMQK.K  (Ions score 68)
  132 - 144     688.9610  1375.9074  1376.6395    -0.7320     0  R.GTNFPSDGPVMQK.K  (Ions score 46)
  132 - 144     688.9860  1375.9574  1376.6395    -0.6820     0  R.GTNFPSDGPVMQK.K  (Ions score 28)
  132 - 144     689.0010  1375.9874  1376.6395    -0.6520     0  R.GTNFPSDGPVMQK.K  (Ions score 59)
  132 - 144     696.9520  1391.8894  1392.6344    -0.7449     0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 72)
  132 - 144     696.9830  1391.9514  1392.6344    -0.6829     0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 69)
  146 - 155     583.9500  1165.8854  1166.5026    -0.6172     0  K.TMGWEASTER.M  (Ions score 37)
  146 - 155     592.0180  1182.0214  1182.4975    -0.4761     0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 52)
  191 - 200     550.5430  1099.0714  1099.6390    -0.5675     0  K.KPVQLPGAYK.T  (Ions score 48)
  191 - 200    1100.3580  1099.3507  1099.6390    -0.2882     0  K.KPVQLPGAYK.T  (Ions score 32)
  191 - 200     550.8850  1099.7554  1099.6390     0.1165     0  K.KPVQLPGAYK.T  (Ions score 53)
  191 - 200     551.2470  1100.4794  1099.6390     0.8405     0  K.KPVQLPGAYK.T  (Ions score 51)
  191 - 200     551.5770  1101.1394  1099.6390     1.5005     0  K.KPVQLPGAYK.T  (Ions score 51)
  205 - 222    1112.4490  2222.8834  2224.0284    -1.1449     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 23)
  509 - 524     893.9810  1785.9474  1786.9200    -0.9726     0  K.TITLEVEPSDTIENVK.A  (Ions score 19)
  509 - 524     894.0250  1786.0354  1786.9200    -0.8846     0  K.TITLEVEPSDTIENVK.A  (Ions score 52)
  509 - 524     894.0440  1786.0734  1786.9200    -0.8466     0  K.TITLEVEPSDTIENVK.A  (Ions score 48)
  527 - 539    1522.7980  1521.7907  1522.7740    -0.9832     1  K.IQDKEGIPPDQQR.L  (Ions score 41)
  527 - 539     508.2810  1521.8212  1522.7740    -0.9528     1  K.IQDKEGIPPDQQR.L  (Ions score 40)
  527 - 539     761.9790  1521.9434  1522.7740    -0.8305     1  K.IQDKEGIPPDQQR.L  (Ions score 35)
  527 - 539     762.0050  1521.9954  1522.7740    -0.7785     1  K.IQDKEGIPPDQQR.L  (Ions score 30)
  527 - 539     762.0360  1522.0574  1522.7740    -0.7165     1  K.IQDKEGIPPDQQR.L  (Ions score 47)
  527 - 539     762.4520  1522.8894  1522.7740     0.1155     1  K.IQDKEGIPPDQQR.L  (Ions score 50)
  540 - 551     730.5430  1459.0714  1459.7783    -0.7069     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 68)
  540 - 551     730.5700  1459.1254  1459.7783    -0.6529     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 76)
  540 - 551     487.4830  1459.4272  1459.7783    -0.3511     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 35)
  552 - 560     540.9560  1079.8974  1080.5451    -0.6477     0  R.TLSDYNIQK.E  (Ions score 65)
  552 - 560    1080.9510  1079.9437  1080.5451    -0.6014     0  R.TLSDYNIQK.E  (Ions score 17)
  552 - 560     540.9910  1079.9674  1080.5451    -0.5777     0  R.TLSDYNIQK.E  (Ions score 65)
  552 - 560     541.0250  1080.0354  1080.5451    -0.5097     0  R.TLSDYNIQK.E  (Ions score 64)
  561 - 569     534.0320  1066.0494  1066.6135    -0.5640     0  K.ESTLHLVLR.L  (Ions score 61)
  561 - 569     534.0610  1066.1074  1066.6135    -0.5060     0  K.ESTLHLVLR.L  (Ions score 50)
  561 - 569     534.5220  1067.0294  1066.6135     0.4160     0  K.ESTLHLVLR.L  (Ions score 41)
```



RMS error 527 ppm



RMS error 527 ppm

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

Mascot Search Results

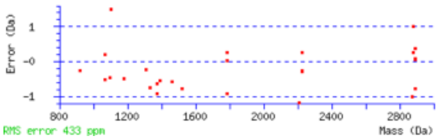
Protein View

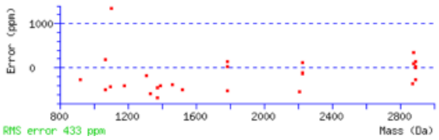
```
Match to: YD_RFP-HERPc-Ub Score: 380
YD_RFP-HERPc-Ub
Found in search of C:\Documents and Settings\Safire2\My Documents\20100106_YaelDavid\BIT00782_YD_14_HerpUb_gp78_G2_merge.mgf

Nominal mass (Mr): 64441; Calculated pI value: 5.86
NCBI BLAST search of YD_RFP-HERPc-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Oxidation (M),GlyGly (K)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 29%

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 ESETEPEPVT
   251 LLVKSPNQRH RDLELSGDRG WSVGHLKAHL SRVYPERPRP EDQRLIYSGK
   301 LLLDHQCLRD LLPKQEKRHV LHLVCNVKSP SKMPEINAKV AESTEEPAGS
   351 NRGQYPEDSS SDGLRQREVL RNLSSPGWEN ISRPEAAQQA FQGLGPGFSG
   401 YTPYGWLQLS WFQQIYARQY YMQYLAATAA SGAFVPPPSA QEIPVVSAPA
   451 PAPIHNQFPA ENQPANQNAA PQVVVNPGAN QNLRMNAQGG PIVEEDDEQI
   501 FVKTLTGKTI TLEVEPSDTI ENVKAKIQDK EGIPPDQQRL IFAGKQLEDG
   551 RTLSDYNIQK ESTLHLVLRL RGG
```

Show predicted peptides also

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

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   57 - 76      1103.9710  2205.9274  2207.1051    -1.1777    0   K.GGPLPFAWDILSPQFQYGSK.A   (Ions score 20)
   91 - 98       462.6210   923.2274   923.4753    -0.2478    0   K.LSFPEGFK.W   (Ions score 47)
  102 - 127     1439.1770  2876.3394  2877.3379    -0.9984    0   R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V   (Ions score 27)
  102 - 127      960.2050  2877.5932  2877.3379     0.2553    0   R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V   (Ions score 55)
  102 - 127     1440.1800  2878.3454  2877.3379     1.0076    0   R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V   (Ions score 66)
  102 - 127     1447.2860  2892.5574  2893.3328    -0.7754    0   R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 36)
  102 - 127      965.4670  2893.3792  2893.3328     0.0464    0   R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 30)
  102 - 127     1447.7230  2893.4314  2893.3328     0.0986    0   R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 80)
  102 - 127      965.5790  2893.7152  2893.3328     0.3824    0   R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 62)
  132 - 144     1376.7230  1375.7157  1376.6395    -0.9237    0   R.GTNFPSDGPVMQK.K   (Ions score 26)
  132 - 144      689.0130  1376.0114  1376.6395    -0.6280    0   R.GTNFPSDGPVMQK.K   (Ions score 60)
  132 - 144      697.0420  1392.0694  1392.6344    -0.5649    0   R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 82)
  145 - 155      656.1940  1310.3734  1310.5925    -0.2190    1   K.KTMGWEASTER.M  Oxidation (M)  (Ions score 83)
  146 - 155      592.0130  1182.0114  1182.4975    -0.4861    0   K.TMGWEASTER.M  Oxidation (M)  (Ions score 62)
  173 - 184     1330.8950  1329.8877  1330.6517    -0.7640    1   K.LKDGGHYDAEVK.T   (Ions score 29)
  191 - 200      550.5930  1099.1714  1099.6390    -0.4675    0   K.KPVQLPGAYK.T   (Ions score 53)
  191 - 200      551.5700  1101.1254  1099.6390     1.4865    0   K.KPVQLPGAYK.T   (Ions score 56)
  205 - 222     1112.8770  2223.7394  2224.0284    -0.2889    0   K.LDITSHNEDYTIVEQYER.A   (Ions score 32)
  205 - 222     1112.8900  2223.7654  2224.0284    -0.2629    0   K.LDITSHNEDYTIVEQYER.A   (Ions score 10)
  205 - 222     1113.1440  2224.2734  2224.0284     0.2451    0   K.LDITSHNEDYTIVEQYER.A   (Ions score 99)
  509 - 524      894.0110  1786.0074  1786.9200    -0.9126    0   K.TITLEVEPSDTIENVK.A   (Ions score 47)
  509 - 524      894.4870  1786.9594  1786.9200     0.0394    0   K.TITLEVEPSDTIENVK.A   (Ions score 47)
  509 - 524      894.6030  1787.1914  1786.9200     0.2714    0   K.TITLEVEPSDTIENVK.A   (Ions score 56)
  527 - 539      762.0100  1522.0054  1522.7740    -0.7685    1   K.IQDKEGIPPDQQR.L   (Ions score 51)
  540 - 551      730.6110  1459.2074  1459.7783    -0.5709    1   R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 70)
  561 - 569      534.0470  1066.0794  1066.6135    -0.5340    0   K.ESTLHLVLR.L   (Ions score 66)
  561 - 569      534.4130  1066.8114  1066.6135     0.1980    0   K.ESTLHLVLR.L   (Ions score 29)
```





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