Sample	Substrate	E2
1	RFP-BARD-BRCA-Ub	5C
2	RFP-BARD-BRCA-Ub	D3
3	RFP-BARD-BRCA-Ub	E1
4	RFP-BARD-BRCA-Ub	E2
5	RFP-BARD-BRCA-Ub	E3
6	RFP-BARD-BRCA-Ub	N+V1
7	RFP-BARD-BRCA-Ub	N+V2
8	RFP-BARD-BRCA-Ub	W
9	RFP-BARD-BRCA-Ub	25K
10	RFP-BARD-BRCA-Ub	W+25K
11	RFP-BARD-BRCA-Ub	W+N+V1
12	RFP-BARD-BRCA-Ub	- E2
13	RFP-BARD-BRCA	5C
14	RFP-BARD-BRCA	D3
15	RFP-BARD-BRCA	E1
16	RFP-BARD-BRCA	E2
17	RFP-BARD-BRCA	E3
18	RFP-BARD-BRCA	N+V1
19	RFP-BARD-BRCA	N+V2
20	RFP-BARD-BRCA	W
21	RFP-BARD-BRCA	25K
22	RFP-BARD-BRCA	W+25K
23	RFP-BARD-BRCA	W+N+V1
24	RFP-BARD-BRCA	- E2

Mascot Search Results

Protein View

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Match to: YD_RFP-BARD-BRCA-Ub Score: 4904
YD_RFP-BARD-BRCA-Ub
Found in search of C:\YaelDavid\100203_YaelDavid\BIT00808_YD_2_merge.mgf

Nominal mass (Mr): 60628; Calculated pI value: 6.10
NCBI BLAST search of YD_RFP-BARD-BRCA-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 61%

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 EPDGRGAWAH
   251 SRAALDRLEK LLRCSRCTNI LREPVCLGGC EHIFCSNCVS DCIGTGCPVC
   301 YTPAWIQDLK INRQLDSMIQ LCSKLRNLLH DNELSDLKED GGSGGDLSAL
   351 RVEEVQNVIN AMQKILECPI CLELIKEPVS TKCDHIFCKF CMLKLLNQKK
   401 GPSQCPLCKN DITKRSLQES TRFSQLVEEL LKIICAFQLD TGLEYANSYN
   451 FAKQIFVKTL TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK
   501 QLEDGRTLSD YNIQKESTLH LVLRLRGG
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Show predicted peptides also

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

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 Start - End     Observed   Mr(expt)   Mr(calc)    Delta   Miss Sequence
   24 - 51      1013.5690  3037.6852  3037.3359    0.3492    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 57)
   24 - 51      1520.1810  3038.3474  3037.3359    1.0115    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 38)
   24 - 51      1013.8240  3038.4502  3037.3359    1.1142    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 80)
   24 - 51      1013.8560  3038.5462  3037.3359    1.2102    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 79)
   24 - 51      1013.9050  3038.6932  3037.3359    1.3572    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 79)
   24 - 51      1014.1620  3039.4642  3037.3359    2.1282    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 54)
   24 - 51      1018.5140  3052.5202  3053.3309   -0.8107    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 24)
   24 - 51      1018.8550  3053.5432  3053.3309    0.2123    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 80)
   24 - 51      1018.8930  3053.6572  3053.3309    0.3263    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 48)
   24 - 51      1018.9240  3053.7502  3053.3309    0.4193    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 87)
   24 - 51      1019.1710  3054.4912  3053.3309    1.1603    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 52)
   57 - 76      1104.2640  2206.5134  2207.1051   -0.5917    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 65)
   57 - 76       736.7460  2207.2162  2207.1051    0.1110    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 51)
   57 - 76      1104.6510  2207.2874  2207.1051    0.1823    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 43)
   57 - 76      1104.6700  2207.3254  2207.1051    0.2203    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 66)
   57 - 76      1104.7040  2207.3934  2207.1051    0.2883    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 79)
   57 - 76      1104.7070  2207.3994  2207.1051    0.2943    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 76)
   57 - 76       736.8970  2207.6692  2207.1051    0.5640    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 44)
   81 - 90      1168.6140  1167.6067  1167.5924    0.0143    0  K.HPADIPDYLK.L  (Ions score 41)
   81 - 90      1168.6950  1167.6877  1167.5924    0.0953    0  K.HPADIPDYLK.L  (Ions score 42)
   81 - 90       584.9730  1167.9314  1167.5924    0.3390    0  K.HPADIPDYLK.L  (Ions score 14)
   91 - 98       462.8290   923.6434   923.4753    0.1682    0  K.LSFPEGFK.W  (Ions score 41)
   91 - 98       462.8520   923.6894   923.4753    0.2142    0  K.LSFPEGFK.W  (Ions score 39)
   91 - 98       462.8540   923.6934   923.4753    0.2182    0  K.LSFPEGFK.W  (Ions score 36)
  102 - 127     1439.7090  2877.4034  2877.3379    0.0656    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 61)
  102 - 127      960.2400  2877.6982  2877.3379    0.3603    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 78)
  102 - 127      960.3320  2877.9742  2877.3379    0.6363    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 25)
  102 - 127      960.3680  2878.0822  2877.3379    0.7443    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 92)
  102 - 127     1440.2280  2878.4414  2877.3379    1.1036    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 98)
  102 - 127     1440.3210  2878.6274  2877.3379    1.2896    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 74)
  102 - 127      960.5560  2878.6462  2877.3379    1.3083    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 63)
  102 - 127      960.5790  2878.7152  2877.3379    1.3773    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 110)
  102 - 127      960.6150  2878.8232  2877.3379    1.4853    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 75)
  102 - 127      960.6200  2878.8382  2877.3379    1.5003    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 97)
  102 - 127     1447.7190  2893.4234  2893.3328    0.0906    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 63)
  102 - 127     1447.7540  2893.4934  2893.3328    0.1606    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 100)
  102 - 127     1448.1910  2894.3674  2893.3328    1.0346    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 102)
  102 - 127     1448.2780  2894.5414  2893.3328    1.2086    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 82)
  102 - 127      965.8670  2894.5792  2893.3328    1.2464    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 91)
  102 - 127      965.9070  2894.6992  2893.3328    1.3664    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 84)
  102 - 127      965.9190  2894.7352  2893.3328    1.4024    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 78)
  102 - 127      965.9720  2894.8942  2893.3328    1.5614    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 51)
  132 - 144      688.7800  1375.5454  1376.6395   -1.0940    0  R.GTNFPSDGPVMQK.K  (Ions score 52)
  132 - 144      689.4100  1376.8054  1376.6395    0.1660    0  R.GTNFPSDGPVMQK.K  (Ions score 73)
  132 - 144      689.4400  1376.8654  1376.6395    0.2260    0  R.GTNFPSDGPVMQK.K  (Ions score 70)
  132 - 144      689.4420  1376.8694  1376.6395    0.2300    0  R.GTNFPSDGPVMQK.K  (Ions score 77)
  132 - 144      689.5170  1377.0194  1376.6395    0.3800    0  R.GTNFPSDGPVMQK.K  (Ions score 81)
  132 - 144      697.3720  1392.7294  1392.6344    0.0951    0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 69)
  132 - 144      697.4060  1392.7974  1392.6344    0.1631    0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 62)
  132 - 144      697.4420  1392.8694  1392.6344    0.2351    0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 78)
  132 - 144      697.4470  1392.8794  1392.6344    0.2451    0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 77)
  145 - 155      648.3600  1294.7054  1294.5976    0.1079    1  K.KTMGWEASTER.M  (Ions score 70)
  145 - 155      648.3800  1294.7454  1294.5976    0.1479    1  K.KTMGWEASTER.M  (Ions score 71)
  145 - 155      648.4000  1294.7854  1294.5976    0.1879    1  K.KTMGWEASTER.M  (Ions score 69)
  145 - 155      648.4040  1294.7934  1294.5976    0.1959    1  K.KTMGWEASTER.M  (Ions score 71)
  146 - 155      584.3000  1166.5854  1166.5026    0.0828    0  K.TMGWEASTER.M  (Ions score 52)
  146 - 155      584.3310  1166.6474  1166.5026    0.1448    0  K.TMGWEASTER.M  (Ions score 48)
  146 - 155      584.3550  1166.6954  1166.5026    0.1928    0  K.TMGWEASTER.M  (Ions score 49)
  146 - 155      584.3600  1166.7054  1166.5026    0.2028    0  K.TMGWEASTER.M  (Ions score 52)
  146 - 155      591.7510  1181.4874  1182.4975   -1.0101    0  K.TMGWEASTER.M  Oxidation (M) (Ions score 20)
  146 - 155      592.3010  1182.5874  1182.4975    0.0899    0  K.TMGWEASTER.M  Oxidation (M) (Ions score 57)
  146 - 155      592.3060  1182.5974  1182.4975    0.0999    0  K.TMGWEASTER.M  Oxidation (M) (Ions score 16)
  146 - 155      592.3150  1182.6154  1182.4975    0.1179    0  K.TMGWEASTER.M  Oxidation (M) (Ions score 57)
  146 - 155      592.3490  1182.6834  1182.4975    0.1859    0  K.TMGWEASTER.M  Oxidation (M) (Ions score 62)
  146 - 155      592.3540  1182.6934  1182.4975    0.1959    0  K.TMGWEASTER.M  Oxidation (M) (Ions score 61)
  191 - 200      367.5980  1099.7722  1099.6390    0.1332    0  K.KPVQLPGAYK.T  (Ions score 37)
  191 - 200      550.8940  1099.7734  1099.6390    0.1345    0  K.KPVQLPGAYK.T  (Ions score 51)
  191 - 200      550.9290  1099.8434  1099.6390    0.2045    0  K.KPVQLPGAYK.T  (Ions score 42)
  191 - 200      550.9320  1099.8494  1099.6390    0.2105    0  K.KPVQLPGAYK.T  (Ions score 53)
  191 - 204      558.0370  1671.0892  1670.9355    0.1536    1  K.KPVQLPGAYKTDIK.L  GlyGly (K) (Ions score 42)
  205 - 222      742.1250  2223.3532  2224.0284   -0.6752    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 30)
  205 - 222      742.1640  2223.4702  2224.0284   -0.5582    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 34)
  205 - 222     1113.0860  2224.1574  2224.0284    0.1291    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 28)
  205 - 222      742.3960  2224.1662  2224.0284    0.1378    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 11)
  205 - 222      742.4260  2224.2562  2224.0284    0.2278    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 20)
  205 - 222     1113.1420  2224.2694  2224.0284    0.2411    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 103)
  205 - 222      742.4590  2224.3552  2224.0284    0.3268    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 28)
  205 - 222     1113.1940  2224.3734  2224.0284    0.3451    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 52)
  205 - 222      742.4790  2224.4152  2224.0284    0.3868    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 28)
  205 - 222     1113.2190  2224.4234  2224.0284    0.3951    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 117)
  205 - 222      742.5140  2224.5202  2224.0284    0.4918    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 56)
  205 - 222      742.5530  2224.6372  2224.0284    0.6088    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 34)
  205 - 222      742.5800  2224.7182  2224.0284    0.6898    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 30)
  205 - 222      742.8470  2225.5192  2224.0284    1.4908    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 25)
  205 - 222      742.8650  2225.5732  2224.0284    1.5448    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 30)
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227 - 245   1060.6210  2119.2274  2118.9606    0.2668    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 122)
227 - 245   1060.6520  2119.2894  2118.9606    0.3288    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 144)
227 - 245   1060.7130  2119.4114  2118.9606    0.4508    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 141)
227 - 245    707.4980  2119.4722  2118.9606    0.5115    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 76)
227 - 245   1060.7450  2119.4754  2118.9606    0.5148    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 34)
227 - 245    707.6500  2119.9282  2118.9606    0.9675    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 15)
227 - 245   1061.0740  2120.1334  2118.9606    1.1728    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 124)
227 - 245    707.7840  2120.3302  2118.9606    1.3695    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 51)
314 - 324    661.9220  1321.8294  1321.6370    0.1925    0  R.QLDSMIQLCSK.L  (Ions score 61)
314 - 324    662.0700  1322.1254  1321.6370    0.4885    0  R.QLDSMIQLCSK.L  (Ions score 58)
314 - 324    669.9300  1337.8454  1337.6319    0.2135    0  R.QLDSMIQLCSK.L  Oxidation (M)  (Ions score 45)
314 - 324    669.9500  1337.8854  1337.6319    0.2535    0  R.QLDSMIQLCSK.L  Oxidation (M)  (Ions score 48)
327 - 338    705.9370  1409.8594  1409.7150    0.1444    0  R.NLLHDNELSDLK.E  (Ions score 55)
327 - 338    471.0070  1409.9992  1409.7150    0.2841    0  R.NLLHDNELSDLK.E  (Ions score 35)
327 - 338    706.0190  1410.0234  1409.7150    0.3084    0  R.NLLHDNELSDLK.E  (Ions score 68)
327 - 351   1313.2740  2624.5334  2624.2678    0.2657    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 127)
327 - 351   1313.6840  2625.3534  2624.2678    1.0857    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 118)
327 - 351   1313.6930  2625.3714  2624.2678    1.1037    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 111)
327 - 351    876.1850  2625.5332  2624.2678    1.2654    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 91)
327 - 351    657.4180  2625.6429  2624.2678    1.3751    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 54)
327 - 351    913.9320  2738.7742  2738.3107    0.4635    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  GlyGly (K)  (Ions score 94)
327 - 351    914.1780  2739.5122  2738.3107    1.2015    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  GlyGly (K)  (Ions score 14)
339 - 351    617.3350  1232.6554  1232.5633    0.0921    0  K.EDGGSGGDLSALR.V  (Ions score 84)
339 - 351    617.3410  1232.6674  1232.5633    0.1041    0  K.EDGGSGGDLSALR.V  (Ions score 85)
339 - 351    617.4240  1232.8334  1232.5633    0.2701    0  K.EDGGSGGDLSALR.V  (Ions score 80)
352 - 364    751.5440  1501.0734  1500.7606    0.3128    0  R.VEEVQNVINAMQK.I  (Ions score 109)
352 - 364    751.5450  1501.0754  1500.7606    0.3148    0  R.VEEVQNVINAMQK.I  (Ions score 109)
352 - 364    751.5550  1501.0954  1500.7606    0.3348    0  R.VEEVQNVINAMQK.I  (Ions score 107)
352 - 364    751.5900  1501.1654  1500.7606    0.4048    0  R.VEEVQNVINAMQK.I  (Ions score 107)
352 - 364    759.4490  1516.8834  1516.7555    0.1279    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 13)
352 - 364    759.4640  1516.9134  1516.7555    0.1579    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 95)
352 - 364    759.4860  1516.9574  1516.7555    0.2019    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 95)
352 - 364    759.5050  1516.9954  1516.7555    0.2399    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 99)
352 - 364    759.5080  1517.0014  1516.7555    0.2459    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 91)
352 - 364    759.6320  1517.2494  1516.7555    0.4939    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 76)
352 - 364    760.1270  1518.2394  1516.7555    1.4839    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 50)
365 - 376    750.6660  1499.3174  1499.8091   -0.4917    0  K.ILECPICLELIK.E  (Ions score 61)
365 - 376    751.0770  1500.1394  1499.8091    0.3303    0  K.ILECPICLELIK.E  (Ions score 72)
365 - 376    751.0810  1500.1474  1499.8091    0.3383    0  K.ILECPICLELIK.E  (Ions score 59)
365 - 376    751.0890  1500.1634  1499.8091    0.3543    0  K.ILECPICLELIK.E  (Ions score 61)
423 - 432    602.8930  1203.7714  1204.6703   -0.8989    0  R.FSQLVEELLK.I  (Ions score 81)
423 - 432    603.4790  1204.9434  1204.6703    0.2731    0  R.FSQLVEELLK.I  (Ions score 71)
423 - 432    603.4870  1204.9594  1204.6703    0.2891    0  R.FSQLVEELLK.I  (Ions score 82)
423 - 432    603.4940  1204.9734  1204.6703    0.3031    0  R.FSQLVEELLK.I  (Ions score 84)
423 - 432    603.4980  1204.9814  1204.6703    0.3111    0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    603.5070  1204.9994  1204.6703    0.3291    0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    603.5090  1205.0034  1204.6703    0.3331    0  R.FSQLVEELLK.I  (Ions score 85)
423 - 432    603.5160  1205.0174  1204.6703    0.3471    0  R.FSQLVEELLK.I  (Ions score 89)
423 - 432    603.5300  1205.0454  1204.6703    0.3751    0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    603.5500  1205.0854  1204.6703    0.4151    0  R.FSQLVEELLK.I  (Ions score 80)
423 - 432    604.4200  1206.8254  1204.6703    2.1551    0  R.FSQLVEELLK.I  (Ions score 66)
433 - 453   1219.7580  2437.5014  2437.1624    0.3391    0  K.IICAFQLDTGLEYANSYNFAK.Q  (Ions score 74)
459 - 479    801.5110  2401.5112  2401.2588    0.2524    1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 93)
459 - 479   1201.7640  2401.5134  2401.2588    0.2547    1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 91)
459 - 479   1201.7810  2401.5474  2401.2588    0.2887    1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 98)
459 - 479    801.5810  2401.7212  2401.2588    0.4624    1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 104)
464 - 479    894.0560  1786.0974  1786.9200   -0.8226    0  K.TITLEVEPSDTIENVK.A  (Ions score 81)
464 - 479    894.5100  1787.0054  1786.9200    0.0854    0  K.TITLEVEPSDTIENVK.A  (Ions score 61)
464 - 479    894.5420  1787.0694  1786.9200    0.1494    0  K.TITLEVEPSDTIENVK.A  (Ions score 62)
464 - 479    894.5450  1787.0754  1786.9200    0.1554    0  K.TITLEVEPSDTIENVK.A  (Ions score 61)
464 - 479    894.5730  1787.1314  1786.9200    0.2114    0  K.TITLEVEPSDTIENVK.A  (Ions score 69)
464 - 479    894.5750  1787.1354  1786.9200    0.2154    0  K.TITLEVEPSDTIENVK.A  (Ions score 65)
464 - 479    894.5820  1787.1494  1786.9200    0.2294    0  K.TITLEVEPSDTIENVK.A  (Ions score 66)
464 - 479    894.5870  1787.1594  1786.9200    0.2394    0  K.TITLEVEPSDTIENVK.A  (Ions score 61)
464 - 479    894.5920  1787.1694  1786.9200    0.2494    0  K.TITLEVEPSDTIENVK.A  (Ions score 73)
464 - 479    894.5920  1787.1694  1786.9200    0.2494    0  K.TITLEVEPSDTIENVK.A  (Ions score 66)
464 - 479    894.5970  1787.1794  1786.9200    0.2594    0  K.TITLEVEPSDTIENVK.A  (Ions score 87)
464 - 479    894.6040  1787.1934  1786.9200    0.2734    0  K.TITLEVEPSDTIENVK.A  (Ions score 95)
464 - 479    894.6170  1787.2194  1786.9200    0.2994    0  K.TITLEVEPSDTIENVK.A  (Ions score 72)
464 - 479    894.6280  1787.2414  1786.9200    0.3214    0  K.TITLEVEPSDTIENVK.A  (Ions score 69)
464 - 479    894.6320  1787.2494  1786.9200    0.3294    0  K.TITLEVEPSDTIENVK.A  (Ions score 78)
464 - 479    894.6360  1787.2574  1786.9200    0.3374    0  K.TITLEVEPSDTIENVK.A  (Ions score 61)
464 - 479    894.6610  1787.3074  1786.9200    0.3874    0  K.TITLEVEPSDTIENVK.A  (Ions score 86)
464 - 479    894.6710  1787.3274  1786.9200    0.4074    0  K.TITLEVEPSDTIENVK.A  (Ions score 86)
464 - 479    894.6780  1787.3414  1786.9200    0.4214    0  K.TITLEVEPSDTIENVK.A  (Ions score 86)
464 - 479    894.7190  1787.4234  1786.9200    0.5034    0  K.TITLEVEPSDTIENVK.A  (Ions score 82)
464 - 479    894.9900  1787.9654  1786.9200    1.0454    0  K.TITLEVEPSDTIENVK.A  (Ions score 81)
464 - 481    701.1910  2100.5512  2100.0950    0.4562    1  K.TITLEVEPSDTIENVKAK.I  GlyGly (K)  (Ions score 34)
482 - 494    761.8940  1521.7734  1522.7740   -1.0005    1  K.IQDKEGIPPDQQR.L  (Ions score 51)
482 - 494    762.4620  1522.9094  1522.7740    0.1355    1  K.IQDKEGIPPDQQR.L  (Ions score 51)
482 - 494    762.4650  1522.9154  1522.7740    0.1415    1  K.IQDKEGIPPDQQR.L  (Ions score 31)
482 - 494    762.4660  1522.9174  1522.7740    0.1435    1  K.IQDKEGIPPDQQR.L  (Ions score 56)
482 - 494    762.4720  1522.9294  1522.7740    0.1555    1  K.IQDKEGIPPDQQR.L  (Ions score 47)
482 - 494    762.5060  1522.9974  1522.7740    0.2235    1  K.IQDKEGIPPDQQR.L  (Ions score 58)
482 - 494    546.6930  1637.0572  1636.8169    0.2403    1  K.IQDKEGIPPDQQR.L  GlyGly (K)  (Ions score 23)
486 - 494    520.3020  1038.5894  1038.5094    0.0800    0  K.EGIPPDQQR.L  (Ions score 38)
486 - 494    520.3030  1038.5914  1038.5094    0.0820    0  K.EGIPPDQQR.L  (Ions score 29)
486 - 494    520.3100  1038.6054  1038.5094    0.0960    0  K.EGIPPDQQR.L  (Ions score 33)
486 - 494    520.3200  1038.6254  1038.5094    0.1160    0  K.EGIPPDQQR.L  (Ions score 30)
486 - 494    520.3250  1038.6354  1038.5094    0.1260    0  K.EGIPPDQQR.L  (Ions score 33)
486 - 494    520.3420  1038.6694  1038.5094    0.1600    0  K.EGIPPDQQR.L  (Ions score 29)
486 - 494    520.3500  1038.6854  1038.5094    0.1760    0  K.EGIPPDQQR.L  (Ions score 30)
486 - 494    520.3530  1038.6914  1038.5094    0.1820    0  K.EGIPPDQQR.L  (Ions score 34)
495 - 506    730.3560  1458.6974  1459.7783   -1.0809    1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 71)
495 - 506    487.6410  1459.9012  1459.7783    0.1229    1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 36)
495 - 506    731.0180  1460.0214  1459.7783    0.2431    1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 56)
495 - 506    731.0260  1460.0374  1459.7783    0.2591    1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 74)
495 - 506    487.7030  1460.0872  1459.7783    0.3089    1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 32)
507 - 515    541.3520  1080.6894  1080.5451    0.1443    0  R.TLSDYNIQK.E  (Ions score 51)
507 - 515    541.3560  1080.6974  1080.5451    0.1523    0  R.TLSDYNIQK.E  (Ions score 54)
507 - 515    541.3740  1080.7334  1080.5451    0.1883    0  R.TLSDYNIQK.E  (Ions score 48)
507 - 515    541.3770  1080.7394  1080.5451    0.1943    0  R.TLSDYNIQK.E  (Ions score 57)
507 - 515    541.3860  1080.7574  1080.5451    0.2123    0  R.TLSDYNIQK.E  (Ions score 9)
507 - 515    541.3940  1080.7734  1080.5451    0.2283    0  R.TLSDYNIQK.E  (Ions score 57)
507 - 515    541.3970  1080.7794  1080.5451    0.2343    0  R.TLSDYNIQK.E  (Ions score 28)
507 - 515    541.4060  1080.7974  1080.5451    0.2523    0  R.TLSDYNIQK.E  (Ions score 32)
507 - 524    748.8130  2243.4172  2243.1910    0.2262    1  R.TLSDYNIQKESTLHLVLR.L  GlyGly (K)  (Ions score 53)
507 - 524    748.8300  2243.4682  2243.1910    0.2772    1  R.TLSDYNIQKESTLHLVLR.L  GlyGly (K)  (Ions score 57)
516 - 524    534.3870  1066.7594  1066.6135    0.1460    0  K.ESTLHLVLR.L  (Ions score 65)
516 - 524    534.3890  1066.7634  1066.6135    0.1500    0  K.ESTLHLVLR.L  (Ions score 57)
516 - 524    534.4060  1066.7974  1066.6135    0.1840    0  K.ESTLHLVLR.L  (Ions score 60)
516 - 524    534.4070  1066.7994  1066.6135    0.1860    0  K.ESTLHLVLR.L  (Ions score 57)
516 - 524    534.4210  1066.8274  1066.6135    0.2140    0  K.ESTLHLVLR.L  (Ions score 26)
516 - 524    534.5610  1067.1074  1066.6135    0.4940    0  K.ESTLHLVLR.L  (Ions score 30)
516 - 524    534.9210  1067.8274  1066.6135    1.2140    0  K.ESTLHLVLR.L  (Ions score 34)
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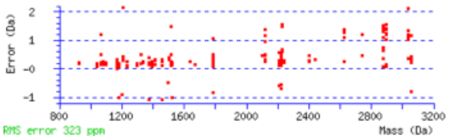
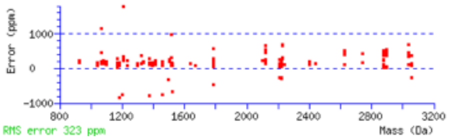




Mascot: http://www.matrixscience.com/

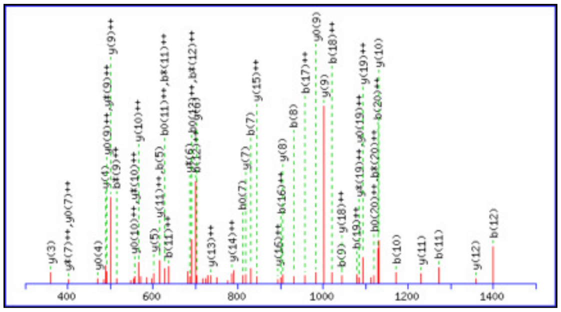
MATRIX SCIENCE Mascot Search Results

Peptide View

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

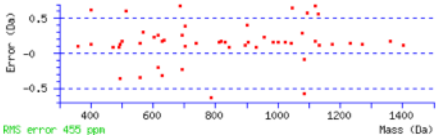
Match to Query 793: 2401.721172 from(801.581000,3+) intensity(3478311.0000)
Title: Cmpd 116, +MSn(802.15), 27.2 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00808_YD_2_merge.mgf

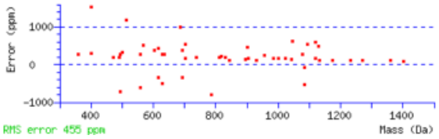
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2401.2588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5 : GlyGly (K)
Ions Score: 104 **Expect:** 2.4e-07
Matches : 52/226 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	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
103.7	2401.2588	0.4624	TLTGKTITLEVEPSDTIENVK
36.8	2401.3039	0.4173	MKKIGSIEVPQEAFLNILK
34.6	2401.2377	0.4835	VFLKDIDGNGLDDDDLIIGLK
34.2	2402.2185	-0.4973	MAKIQEEIAQMEVTGEAGAGLVK
34.0	2401.3216	0.3995	SVNVTASLASLEVWSKKDLIK
31.4	2401.2965	0.4247	RAVEEVFNVKVESVNTINGLGK
30.9	2402.2442	-0.5230	TVIGTPFVEGATVEATVEKQGR
29.0	2401.3216	0.3995	KVNIASYQVKPGDVIEVKEASK
28.3	2400.4257	1.2955	FLIQILVRFVEISNQKLNVK
28.2	2401.3216	0.3995	SVNVTASLASLEVWSKKDLIK

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

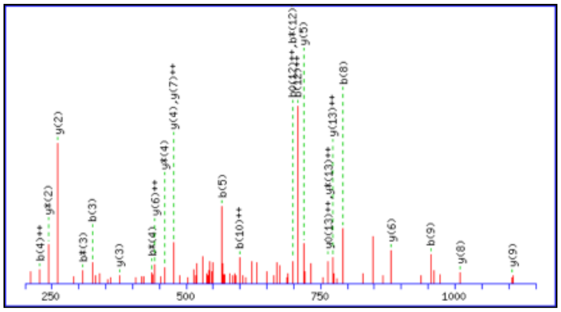
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVQLPGAYKTDIK**
Found in **YD_RFP-BARD-BRCA-Ub**, YD_RFP-BARD-BRCA-Ub

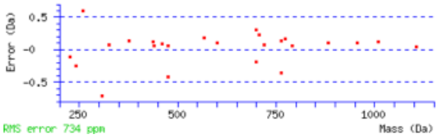
Match to Query 534: 1671.089172 from(558.037000,3+) intensity(612517.0000)
Title: Cmpd 46, +MSn(558.29), 21.2 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00808_YD_2_merge.mgf

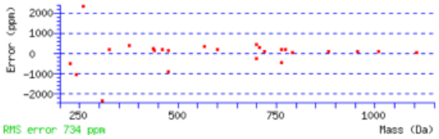
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1670.9355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K10 : GlyGly (K)
Ions Score: 42 **Expect:** 0.012
Matches : 26/132 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							14
2	226.1550	113.5811	209.1285	105.0679			P	1543.8479	772.4276	1526.8213	763.9143	1525.8373	763.4223	13
3	**325.2234**	163.1153	308.1969	154.6021			V	1446.7951	723.9012	1429.7686	715.3879	1428.7845	714.8959	12
4	453.2820	***227.1446***	436.2554	218.6314			Q	1347.7267	674.3670	1330.7001	665.8537	1329.7161	665.3617	11
5	**566.3661**	283.6867	549.3395	275.1734			L	1219.6681	610.3377	1202.6416	601.8244	1201.6576	601.3324	10
6	663.4188	332.2130	646.3923	323.6998			P	***1106.5841***	553.7957	1089.5575	545.2824	1088.5735	544.7904	9
7	720.4403	360.7238	703.4137	352.2105			G	***1009.5313***	505.2693	992.5047	496.7560	991.5207	496.2640	8
8	**791.4774**	396.2423	774.4509	387.7291			A	952.5098	476.7585	935.4833	468.2453	934.4993	467.7533	7
9	**954.5407**	477.7740	937.5142	469.2607			Y	***881.4727***	441.2400	864.4462	432.7267	863.4621	432.2347	6
10	1196.6786	***598.8429***	1179.6521	590.3297			K	***718.4094***	359.7083	701.3828	351.1951	700.3988	350.7030	5
11	1297.7263	649.3668	1280.6998	640.8535	1279.7157	640.3615	T	***476.2715***	238.6394	459.2449	230.1261	458.2609	229.6341	4
12	1412.7532	***706.8803***	1395.7267	698.3670	1394.7427	697.8750	D	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	3
13	1525.8373	***763.4223***	1508.8108	754.9090	1507.8267	754.4170	I	***260.1969***	130.6021	243.1703	122.0888			2
14							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.0	1670.9355	0.1536	KPVQLPGAYKTDIK
28.5	1670.9355	0.1536	KPVQLPGAYKTDIK
20.9	1670.9315	0.1577	VTLNNVALGLGSGKSK
18.9	1671.9236	-0.8344	IFLESKYNTFLGIK
18.6	1670.8951	0.1940	VQVNVGDLEKSKK
17.1	1670.9202	0.1689	EELLKVLQENSKNK
17.0	1669.9502	1.1390	LAVITDSTATLPIDLK
16.3	1670.8151	0.2741	NKYNESESFLEALK
16.2	1671.8679	-0.7787	QIQTLEIELESQK
16.0	1669.7698	1.3194	MSMRATRVGEQMK

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

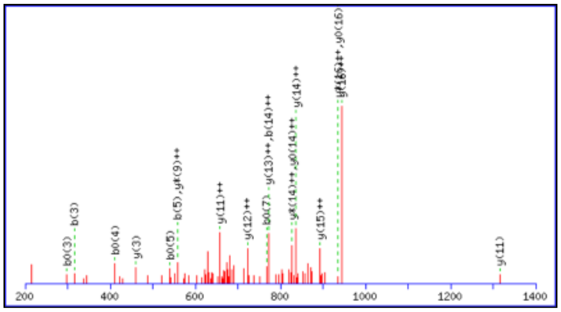
Mascot Search Results

Peptide View

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

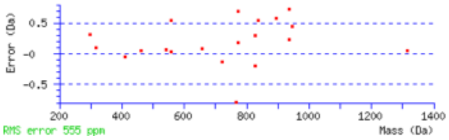
Match to Query 660: 2100.551172 from(701.191000,3+) intensity(337221.0000)
Title: Cmpd 88, +MSn(701.69), 26.4 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00808_YD_2_merge.mgf

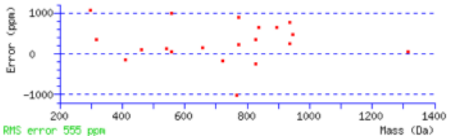
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2100.0950
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K16 : GlyGly (K)
Ions Score: 34 **Expect:** 0.71
Matches : 20/168 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							18
2	215.1390	108.0731			197.1285	99.0679	I	2000.0546	1000.5310	1983.0281	992.0177	1982.0441	991.5257	17
3	**316.1867**	158.5970			298.1761	149.5917	T	1886.9706	943.9889	1869.9440	935.4756	1868.9600	934.9836	16
4	429.2708	215.1390			411.2602	206.1337	L	1785.9229	893.4651	1768.8963	884.9518	1767.9123	884.4598	15
5	**558.3134**	279.6603			540.3028	270.6550	E	1672.8388	836.9230	1655.8123	828.4098	1654.8283	827.9178	14
6	657.3818	329.1945			639.3712	320.1892	V	1543.7962	772.4018	1526.7697	763.8885	1525.7857	763.3965	13
7	786.4244	393.7158			768.4138	384.7105	E	1444.7278	722.8675	1427.7013	714.3543	1426.7172	713.8623	12
8	883.4771	442.2422			865.4666	433.2369	P	**1315.6852**	658.3462	1298.6587	649.8330	1297.6747	649.3410	11
9	970.5092	485.7582			952.4986	476.7529	S	1218.6325	609.8199	1201.6059	601.3066	1200.6219	600.8146	10
10	1085.5361	543.2717			1067.5255	534.2664	D	1131.6004	566.3039	1114.5739	557.7906	1113.5899	557.2986	9
11	1186.5838	593.7955			1168.5732	584.7902	T	1016.5735	508.7904	999.5469	500.2771	998.5629	499.7851	8
12	1299.6678	650.3376			1281.6573	641.3323	I	915.5258	458.2665	898.4993	449.7533	897.5152	449.2613	7
13	1428.7104	714.8589			1410.6999	705.8536	E	802.4417	401.7245	785.4152	393.2112	784.4312	392.7192	6
14	1542.7534	771.8803	1525.7268	763.3670	1524.7428	762.8750	N	673.3991	337.2032	656.3726	328.6899			5
15	1641.8218	821.4145	1624.7952	812.9013	1623.8112	812.4092	V	559.3562	280.1817	542.3297	271.6685			4
16	1883.9597	942.4835	1866.9331	933.9702	1865.9491	933.4782	K	**460.2878**	230.6475	443.2613	222.1343			3
17	1954.9968	978.0020	1937.9702	969.4888	1936.9862	968.9967	A	218.1499	109.5786	201.1234	101.0653			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.5	2100.0950	0.4562	TITLEVEPSDTIENVKAK
34.5	2100.0950	0.4562	TITLEVEPSDTIENVKAK
31.8	2100.1116	0.4396	EWLEQRIDLPVYLRDR
29.9	2101.0287	-0.4775	ELEGEVDAEQKRSAEAVK
25.9	2101.1630	-0.6118	TLSQENLVKLTLESNATLK
23.5	2101.0803	-0.5292	NNSLEDLGWTNLIKKDNK
23.2	2099.0494	1.5017	RGVKTEIEGEQEVAEAIQ
20.2	2099.9728	0.5784	TNGDFSTNMAMQLARVAK
19.9	2100.1579	0.3933	NVTPFLLGKVKELTEGK
19.1	2101.1280	-0.5768	TLTLEAGRFAEQANGAVVVR

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

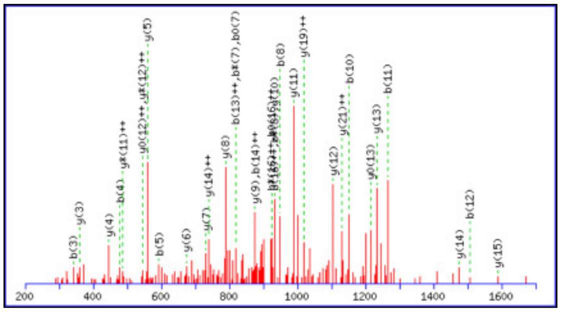
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLLHDNELSDLKEDGGSGGDLSALR**
Found in **YD_RFP-BARD-BRCA-Ub**, YD_RFP-BARD-BRCA-Ub

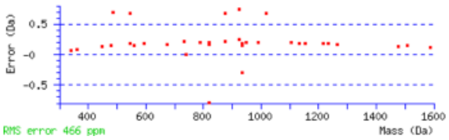
Match to Query 845: 2738.774172 from(913.932000,3+) intensity(1061195.0000)
Title: Cmpd 117, +MSn(914.43), 27.7 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00808_YD_2_merge.mgf

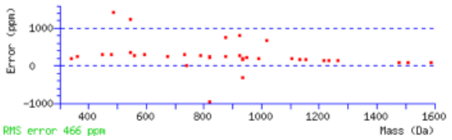
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2738.3107
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K12 : GlyGly (K)
Ions Score: 94 **Expect:** 2.9e-07
Matches : 35/274 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	115.0502	58.0287	98.0237	49.5155			N							25
2	228.1343	114.5708	211.1077	106.0575			L	2625.2751	1313.1412	2608.2485	1304.6279	2607.2645	1304.1359	24
3	***341.2183***	171.1128	324.1918	162.5995			L	2512.1910	1256.5991	2495.1645	1248.0859	2494.1804	1247.5939	23
4	***478.2772***	239.6423	461.2507	231.1290			H	2399.1069	1200.0571	2382.0804	1191.5438	2381.0964	1191.0518	22
5	***593.3042***	297.1557	576.2776	288.6425	575.2936	288.1504	D	2262.0480	1131.5277	2245.0215	1123.0144	2244.0375	1122.5224	21
6	707.3471	354.1772	690.3206	345.6639	689.3365	345.1719	N	2147.0211	1074.0142	2129.9945	1065.5009	2129.0105	1065.0089	20
7	836.3897	418.6985	819.3632	410.1852	818.3791	409.6932	E	2032.9782	1016.9927	2015.9516	1008.4794	2014.9676	1007.9874	19
8	***949.4738***	475.2405	932.4472	466.7272	931.4632	466.2352	L	1903.9356	952.4714	1886.9090	943.9582	1885.9250	943.4661	18
9	1036.5058	518.7565	1019.4792	510.2433	1018.4952	509.7513	S	1790.8515	895.9294	1773.8250	887.4161	1772.8409	886.9241	17
10	***1151.5327***	576.2700	1134.5062	567.7567	1133.5222	567.2647	D	1703.8195	852.4134	1686.7929	843.9001	1685.8089	843.4081	16
11	***1264.6168***	632.8120	1247.5903	624.2988	1246.6062	623.8068	L	***1588.7925***	794.8999	1571.7660	786.3866	1570.7820	785.8946	15
12	***1506.7547***	753.8810	1489.7281	745.3677	1488.7441	744.8757	K	***1475.7085***	738.3579	1458.6819	729.8446	1457.6979	729.3526	14
13	1635.7973	**818.4023**	1618.7707	809.8890	1617.7867	809.3970	E	***1233.5706***	617.2889	1216.5440	608.7757	1215.5600	608.2836	13
14	1750.8242	**875.9158**	1733.7977	867.4025	1732.8137	866.9105	D	***1104.5280***	552.7676	1087.5014	544.2544	1086.5174	543.7624	12
15	1807.8457	904.4265	1790.8191	895.9132	1789.8351	895.4212	G	***989.5010***	495.2542	972.4745	486.7409	971.4905	486.2489	11
16	1864.8672	**932.9372**	1847.8406	924.4239	1846.8566	923.9319	G	***932.4796***	466.7434	915.4530	458.2302	914.4690	457.7381	10
17	1951.8992	976.4532	1934.8726	967.9400	1933.8886	967.4479	S	***875.4581***	438.2327	858.4316	429.7194	857.4476	429.2274	9
18	2008.9207	1004.9640	1991.8941	996.4507	1990.9101	995.9587	G	***788.4261***	394.7167	771.3995	386.2034	770.4155	385.7114	8
19	2065.9421	1033.4747	2048.9156	1024.9614	2047.9315	1024.4694	G	***731.4046***	366.2060	714.3781	357.6927	713.3941	357.2007	7
20	2180.9691	1090.9882	2163.9425	1082.4749	2162.9585	1081.9829	D	***674.3832***	337.6952	657.3566	329.1819	656.3726	328.6899	6
21	2294.0531	1147.5302	2277.0266	1139.0169	2276.0426	1138.5249	L	***559.3562***	280.1817	542.3297	271.6685	541.3457	271.1765	5
22	2381.0851	1191.0462	2364.0586	1182.5329	2363.0746	1182.0409	S	***446.2722***	223.6397	429.2456	215.1264	428.2616	214.6344	4
23	2452.1223	1226.5648	2435.0957	1218.0515	2434.1117	1217.5595	A	***359.2401***	180.1237	342.2136	171.6104			3
24	2565.2063	1283.1068	2548.1798	1274.5935	2547.1958	1274.1015	L	288.2030	144.6051	271.1765	136.0919			2
25							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
93.5	2738.3107	0.4635	NLLHDNELSDLKEDGGSGGDLSALR
23.2	2738.3376	0.4366	MIIPANINHVNLEPMCIGIASQCK
22.6	2738.3448	0.4294	MSRALMIQGTGSNVGKSMLAAGLCR
20.8	2739.2156	-0.4415	KDLNPGDNPEAEFPVEMASDFMVR
20.6	2738.2469	0.5273	AAMGHPEPFELKYVAVGNEDCFK
20.6	2738.3029	0.4713	KQTSTKSIMGGLLVQDTNDSEDK
20.4	2739.3062	-0.5320	FGGQVLDTMAIENFISVQETEGPK
19.6	2737.3415	1.4327	KGKVFVDDQEGMATILAMVNAEK
18.0	2739.2698	-0.4956	EDQVFLGDLPLMTDDGSFVINGADR

17.1	2738.2784	0.4958	DADLGSNTTYKVAEGINPNAFDGQK

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

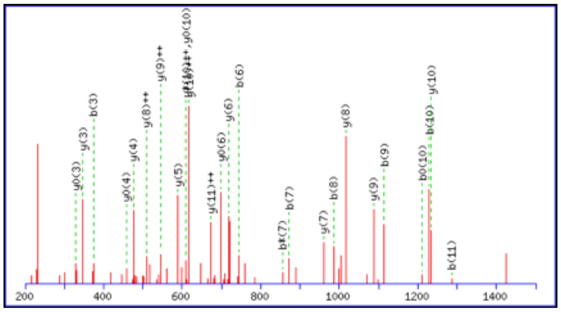
Mascot Search Results

Peptide View

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

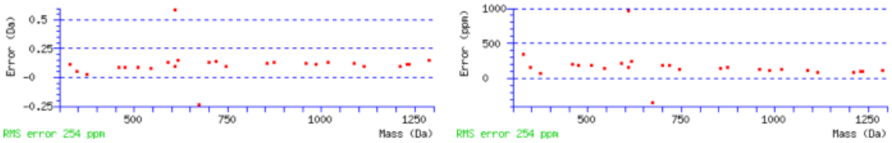
Match to Query 438: 1460.037448 from(731.026000,2+) intensity(2409720.0000)
Title: Cmpd 82, +MSn(731.22), 24.4 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00808_YD_2_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1459.7783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : GlyGly (K)
Ions Score: 74 **Expect:** 4.9e-05
Matches : 26/102 fragment ions using 32 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	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
74.3	1459.7783	0.2591	LIFAGKQLEDGR
27.4	1459.6725	0.3649	EAAALQCQLEDGR
26.6	1460.7987	-0.7613	AGVFKKVDEIK
26.6	1460.7987	-0.7613	AGVFKKVDELK
21.3	1459.6903	0.3472	DEEKKEEVQGR
21.2	1460.7544	-0.7170	NIIEMQQLELSK
20.5	1459.8432	0.1942	SGMVTLKLEKIK
20.2	1459.8293	0.2082	LTRMIRTAGALK
19.8	1459.8068	0.2307	ILQEKMEKAIK
19.2	1459.7307	0.3068	ALENALPYLEDGR

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

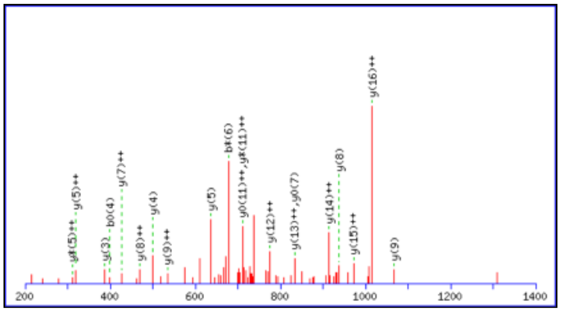
MATRIX SCIENCE Mascot Search Results

Peptide View

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

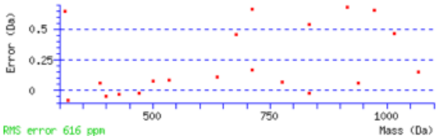
Match to Query 748: 2243.468172 from(748.830000,3+) intensity(240773.0000)
Title: Cmpd 103, +MSn(749.43), 27.7 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00808_YD_2_merge.mgf

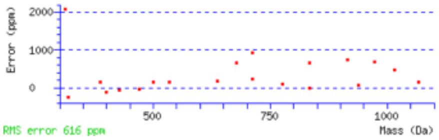
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2243.1910
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K9 : GlyGly (K)
Ions Score: 57 **Expect:** 0.0026
Matches : 20/182 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	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
56.6	2243.1910	0.2772	TLSDYNIQKESTLHLVLR
28.0	2243.9582	-0.4900	EGSPYPMHGEGFTGEPAYFR
18.6	2244.1718	-0.7037	TNQMPNAVQKLLLVMDKR
18.6	2244.1718	-0.7037	TNQMPNAVQKLLLVMDKR
17.3	2244.0667	-0.5985	KFMYQSSIPMTPNGKVDR
17.3	2243.9827	-0.5146	VMGDAEMTLSELGEHFGFSR
17.2	2244.2954	-0.8272	KSLLIKGISYQQAVSVLGAR
16.5	2244.1361	-0.6679	TAKLPFKKPDNCGEIIWGG
15.8	2244.1514	-0.6832	TALMNYLFAKHYNGSFIVR
15.6	2243.8947	-0.4265	GENVTIDEDGFEACMEEQR

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

Mascot Search Results

Protein View

Match to: **YD_RFP-BARD-BRCA-Ub** Score: **4780**
YD_RFP-BARD-BRCA-Ub
Found in search of C:\YaelDavid\100203_YaelDavid\BIT00810_YD_3_merge.mgf

Nominal mass (M_r): **60628**; Calculated pI value: **6.10**
NCBI BLAST search of YD_RFP-BARD-BRCA-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **60%**

Matched peptides shown in **Bold Red**

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  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 EPDGRGAWAH
251 SRAALDRLEK LLRCSRCTNI LREPVCLGGC EHIFCSNCVS DCIGTGCPVC
301 YTPAWIQDLK INRQLDSMIQ LCSKLRNLLH DNELSDLKED GGSGGDLSAL
351 RVEEVQNVIN AMQKILECPI CLELIKEPVS TKCDHIFCKF CMLKLLNQKK
401 GPSQCPLCKN DITKRSLQES TRFSQLVEEL LKIICAFQLD TGLEYANSYN
451 FAKQIFVKTL TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK
501 QLEDGRTLSD YNIQKESTLH LVLRLRGG
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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	1013.6010	3037.7812	3037.3359	0.4452	0	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L (Ions score 45)
24 - 51	760.4930	3037.9429	3037.3359	0.6070	0	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L (Ions score 12)
24 - 51	760.6550	3038.5909	3037.3359	1.2550	0	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L (Ions score 36)
24 - 51	1013.8930	3038.6572	3037.3359	1.3212	0	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L (Ions score 62)
24 - 51	1013.9090	3038.7052	3037.3359	1.3692	0	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L (Ions score 46)
24 - 51	1013.9250	3038.7532	3037.3359	1.4172	0	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L (Ions score 72)
24 - 51	1018.8080	3053.4022	3053.3309	0.0713	0	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L Oxidation (M) (Ions score 58)
24 - 51	1018.8750	3053.6032	3053.3309	0.2723	0	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L Oxidation (M) (Ions score 42)
24 - 51	764.6320	3054.4989	3053.3309	1.1680	0	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L Oxidation (M) (Ions score 32)
24 - 51	1019.1920	3054.5542	3053.3309	1.2233	0	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L Oxidation (M) (Ions score 49)
24 - 51	1019.2590	3054.7552	3053.3309	1.4243	0	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L Oxidation (M) (Ions score 65)
57 - 76	1104.1430	2206.2714	2207.1051	-0.8337	0	K.GGPLPFAWDILSPQFQYGSK.A (Ions score 84)
57 - 76	1104.6520	2207.2894	2207.1051	0.1843	0	K.GGPLPFAWDILSPQFQYGSK.A (Ions score 65)
57 - 76	1104.6570	2207.2994	2207.1051	0.1943	0	K.GGPLPFAWDILSPQFQYGSK.A (Ions score 77)
57 - 76	1104.6630	2207.3114	2207.1051	0.2063	0	K.GGPLPFAWDILSPQFQYGSK.A (Ions score 72)
57 - 76	1104.7410	2207.4674	2207.1051	0.3623	0	K.GGPLPFAWDILSPQFQYGSK.A (Ions score 57)
57 - 76	736.9940	2207.9602	2207.1051	0.8550	0	K.GGPLPFAWDILSPQFQYGSK.A (Ions score 19)
81 - 90	584.3280	1166.6414	1167.5924	-0.9510	0	K.HPADIPDYLK.L (Ions score 34)
81 - 90	584.3420	1166.6694	1167.5924	-0.9230	0	K.HPADIPDYLK.L (Ions score 43)
91 - 98	462.8380	923.6614	923.4753	0.1862	0	K.LSFPEGFK.W (Ions score 43)
91 - 98	462.8580	923.7014	923.4753	0.2262	0	K.LSFPEGFK.W (Ions score 43)
91 - 98	462.8590	923.7034	923.4753	0.2282	0	K.LSFPEGFK.W (Ions score 41)
91 - 98	462.8620	923.7094	923.4753	0.2342	0	K.LSFPEGFK.W (Ions score 39)
102 - 127	960.3930	2878.1572	2877.3379	0.8193	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V (Ions score 119)
102 - 127	1440.2080	2878.4014	2877.3379	1.0636	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V (Ions score 91)
102 - 127	1440.2500	2878.4854	2877.3379	1.1476	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V (Ions score 74)
102 - 127	1440.2950	2878.5754	2877.3379	1.2376	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V (Ions score 102)
102 - 127	960.5980	2878.7722	2877.3379	1.4343	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V (Ions score 104)
102 - 127	960.6140	2878.8202	2877.3379	1.4823	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V (Ions score 111)
102 - 127	960.6410	2878.9012	2877.3379	1.5633	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V (Ions score 67)
102 - 127	1447.7750	2893.5354	2893.3328	0.2026	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V Oxidation (M) (Ions score 92)
102 - 127	965.6470	2893.9192	2893.3328	0.5864	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V Oxidation (M) (Ions score 64)
102 - 127	1448.2270	2894.4394	2893.3328	1.1066	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V Oxidation (M) (Ions score 78)
102 - 127	1448.2650	2894.5154	2893.3328	1.1826	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V Oxidation (M) (Ions score 72)
102 - 127	965.8540	2894.5402	2893.3328	1.2074	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V Oxidation (M) (Ions score 31)
102 - 127	965.8830	2894.6272	2893.3328	1.2944	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V Oxidation (M) (Ions score 73)
102 - 127	1448.3410	2894.6674	2893.3328	1.3346	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V Oxidation (M) (Ions score 61)
102 - 127	965.8980	2894.6722	2893.3328	1.3394	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V Oxidation (M) (Ions score 81)
132 - 144	689.4230	1376.8314	1376.6395	0.1920	0	R.GTNFPSDGPVMQK.K (Ions score 77)
132 - 144	689.4560	1376.8974	1376.6395	0.2580	0	R.GTNFPSDGPVMQK.K (Ions score 73)
132 - 144	689.4630	1376.9114	1376.6395	0.2720	0	R.GTNFPSDGPVMQK.K (Ions score 73)
132 - 144	689.4780	1376.9414	1376.6395	0.3020	0	R.GTNFPSDGPVMQK.K (Ions score 82)
132 - 144	697.3970	1392.7794	1392.6344	0.1451	0	R.GTNFPSDGPVMQK.K Oxidation (M) (Ions score 85)
132 - 144	697.4040	1392.7934	1392.6344	0.1591	0	R.GTNFPSDGPVMQK.K Oxidation (M) (Ions score 64)
132 - 144	697.4060	1392.7974	1392.6344	0.1631	0	R.GTNFPSDGPVMQK.K Oxidation (M) (Ions score 69)
132 - 144	697.4370	1392.8594	1392.6344	0.2251	0	R.GTNFPSDGPVMQK.K Oxidation (M) (Ions score 66)
145 - 155	647.8640	1293.7134	1294.5976	-0.8841	1	K.KTMGWEASTER.M (Ions score 54)
145 - 155	648.3380	1294.6614	1294.5976	0.0639	1	K.KTMGWEASTER.M (Ions score 77)
145 - 155	648.3460	1294.6774	1294.5976	0.0799	1	K.KTMGWEASTER.M (Ions score 75)
145 - 155	648.3620	1294.7094	1294.5976	0.1119	1	K.KTMGWEASTER.M (Ions score 76)
146 - 155	584.3010	1166.5874	1166.5026	0.0848	0	K.TMGWEASTER.M (Ions score 47)
146 - 155	592.2870	1182.5594	1182.4975	0.0619	0	K.TMGWEASTER.M Oxidation (M) (Ions score 59)
146 - 155	592.3180	1182.6214	1182.4975	0.1239	0	K.TMGWEASTER.M Oxidation (M) (Ions score 58)
146 - 155	592.3330	1182.6514	1182.4975	0.1539	0	K.TMGWEASTER.M Oxidation (M) (Ions score 68)
146 - 155	592.3410	1182.6674	1182.4975	0.1699	0	K.TMGWEASTER.M Oxidation (M) (Ions score 65)
191 - 200	367.5870	1099.7392	1099.6390	0.1002	0	K.KPVQLPGAYK.T (Ions score 29)
191 - 200	550.9190	1099.8234	1099.6390	0.1845	0	K.KPVQLPGAYK.T (Ions score 56)
191 - 200	550.9340	1099.8534	1099.6390	0.2145	0	K.KPVQLPGAYK.T (Ions score 54)
191 - 200	550.9340	1099.8534	1099.6390	0.2145	0	K.KPVQLPGAYK.T (Ions score 48)
191 - 200	550.9340	1099.8534	1099.6390	0.2145	0	K.KPVQLPGAYK.T (Ions score 52)
191 - 200	608.4320	1214.8494	1213.6819	1.1676	0	K.KPVQLPGAYK.T GlyGly (K) (Ions score 46)
205 - 222	1113.1000	2224.1854	2224.0284	0.1571	0	K.LDITSHNEDYTIVEQYER.A (Ions score 97)
205 - 222	1113.1240	2224.2334	2224.0284	0.2051	0	K.LDITSHNEDYTIVEQYER.A (Ions score 25)
205 - 222	1113.1430	2224.2714	2224.0284	0.2431	0	K.LDITSHNEDYTIVEQYER.A (Ions score 106)
205 - 222	742.4470	2224.3192	2224.0284	0.2908	0	K.LDITSHNEDYTIVEQYER.A (Ions score 31)
205 - 222	1113.1680	2224.3214	2224.0284	0.2931	0	K.LDITSHNEDYTIVEQYER.A (Ions score 97)
205 - 222	1113.1930	2224.3714	2224.0284	0.3431	0	K.LDITSHNEDYTIVEQYER.A (Ions score 85)
205 - 222	742.4920	2224.4542	2224.0284	0.4258	0	K.LDITSHNEDYTIVEQYER.A (Ions score 16)
205 - 222	742.4920	2224.4542	2224.0284	0.4258	0	K.LDITSHNEDYTIVEQYER.A (Ions score 13)
205 - 222	742.5380	2224.5922	2224.0284	0.5638	0	K.LDITSHNEDYTIVEQYER.A (Ions score 27)
205 - 222	742.5430	2224.6072	2224.0284	0.5788	0	K.LDITSHNEDYTIVEQYER.A (Ions score 32)
205 - 222	742.5640	2224.6702	2224.0284	0.6418	0	K.LDITSHNEDYTIVEQYER.A (Ions score 53)
205 - 222	742.5840	2224.7302	2224.0284	0.7018	0	K.LDITSHNEDYTIVEQYER.A (Ions score 31)
205 - 222	742.6880	2225.0422	2224.0284	1.0138	0	K.LDITSHNEDYTIVEQYER.A (Ions score 24)
205 - 222	742.8640	2225.5702	2224.0284	1.5418	0	K.LDITSHNEDYTIVEQYER.A (Ions score 35)
227 - 245	1060.5800	2119.1454	2118.9606	0.1848	0	R.HSTGAENLYFQGLEEPDGR.G (Ions score 133)
227 - 245	1060.6010	2119.1874	2118.9606	0.2268	0	R.HSTGAENLYFQGLEEPDGR.G (Ions score 139)
227 - 245	1060.6850	2119.3554	2118.9606	0.3948	0	R.HSTGAENLYFQGLEEPDGR.G (Ions score 135)
227 - 245	1060.6980	2119.3814	2118.9606	0.4208	0	R.HSTGAENLYFQGLEEPDGR.G (Ions score 107)
314 - 324	661.9870	1321.9594	1321.6370	0.3225	0	R.QLDSMIQLCSK.L (Ions score 59)
314 - 324	661.9880	1321.9614	1321.6370	0.3245	0	R.QLDSMIQLCSK.L (Ions score 78)
314 - 324	662.0010	1321.9874	1321.6370	0.3505	0	R.QLDSMIQLCSK.L (Ions score 71)
314 - 324	662.0340	1322.0534	1321.6370	0.4165	0	R.QLDSMIQLCSK.L (Ions score 55)
314 - 324	669.9020	1337.7894	1337.6319	0.1575	0	R.QLDSMIQLCSK.L Oxidation (M) (Ions score 52)
327 - 338	470.9780	1409.9122	1409.7150	0.1971	0	R.NLLHDNELSDLK.E (Ions score 28)

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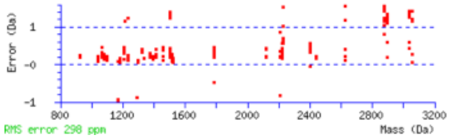
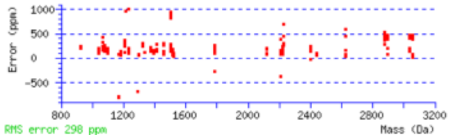
327 - 338     705.9800  1409.9454  1409.7150     0.2304     0  R.NLLHDNELSDLK.E  (Ions score 64)
327 - 338     705.9860  1409.9574  1409.7150     0.2424     0  R.NLLHDNELSDLK.E  (Ions score 50)
327 - 338     705.9980  1409.9814  1409.7150     0.2664     0  R.NLLHDNELSDLK.E  (Ions score 64)
327 - 338     471.0470  1410.1192  1409.7150     0.4041     0  R.NLLHDNELSDLK.E  (Ions score 30)
327 - 351    1313.1970  2624.3794  2624.2678     0.1117     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 105)
327 - 351    1313.2560  2624.4974  2624.2678     0.2297     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 120)
327 - 351    1313.3440  2624.6734  2624.2678     0.4057     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 120)
327 - 351     876.1610  2625.4612  2624.2678     1.1934     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 108)
327 - 351     657.4620  2625.8189  2624.2678     1.5511     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 64)
339 - 351     617.3470  1232.6794  1232.5633     0.1161     0  K.EDGGSGGDLSALR.V  (Ions score 82)
339 - 351     617.3530  1232.6914  1232.5633     0.1281     0  K.EDGGSGGDLSALR.V  (Ions score 84)
339 - 351     617.3880  1232.7614  1232.5633     0.1981     0  K.EDGGSGGDLSALR.V  (Ions score 84)
339 - 351     617.4080  1232.8014  1232.5633     0.2381     0  K.EDGGSGGDLSALR.V  (Ions score 70)
339 - 351     617.9110  1233.8074  1232.5633     1.2441     0  K.EDGGSGGDLSALR.V  (Ions score 78)
352 - 364     751.5070  1500.9994  1500.7606     0.2388     0  R.VEEVQNVINAMQK.I  (Ions score 106)
352 - 364     751.5260  1501.0374  1500.7606     0.2768     0  R.VEEVQNVINAMQK.I  (Ions score 102)
352 - 364     751.5340  1501.0534  1500.7606     0.2928     0  R.VEEVQNVINAMQK.I  (Ions score 109)
352 - 364     751.5700  1501.1254  1500.7606     0.3648     0  R.VEEVQNVINAMQK.I  (Ions score 116)
352 - 364     752.0040  1501.9934  1500.7606     1.2328     0  R.VEEVQNVINAMQK.I  (Ions score 80)
352 - 364     752.0480  1502.0814  1500.7606     1.3208     0  R.VEEVQNVINAMQK.I  (Ions score 104)
352 - 364     752.0900  1502.1654  1500.7606     1.4048     0  R.VEEVQNVINAMQK.I  (Ions score 71)
352 - 364     759.4300  1516.8454  1516.7555     0.0899     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 54)
352 - 364     759.4540  1516.8934  1516.7555     0.1379     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 95)
352 - 364     759.4630  1516.9114  1516.7555     0.1559     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 88)
352 - 364     759.4750  1516.9354  1516.7555     0.1799     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 94)
352 - 364     759.5090  1517.0034  1516.7555     0.2479     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 92)
352 - 364     759.5260  1517.0374  1516.7555     0.2819     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 46)
365 - 376     751.0120  1500.0094  1499.8091     0.2003     0  K.ILECPICLELIK.E  (Ions score 55)
365 - 376     751.0810  1500.1474  1499.8091     0.3383     0  K.ILECPICLELIK.E  (Ions score 77)
365 - 376     751.0860  1500.1574  1499.8091     0.3483     0  K.ILECPICLELIK.E  (Ions score 61)
365 - 376     751.1210  1500.2274  1499.8091     0.4183     0  K.ILECPICLELIK.E  (Ions score 73)
365 - 376     751.1250  1500.2354  1499.8091     0.4263     0  K.ILECPICLELIK.E  (Ions score 62)
423 - 432     603.4170  1204.8194  1204.6703     0.1491     0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432     603.4900  1204.9654  1204.6703     0.2951     0  R.FSQLVEELLK.I  (Ions score 85)
423 - 432     603.4910  1204.9674  1204.6703     0.2971     0  R.FSQLVEELLK.I  (Ions score 63)
423 - 432     603.5000  1204.9854  1204.6703     0.3151     0  R.FSQLVEELLK.I  (Ions score 67)
423 - 432     603.5230  1205.0314  1204.6703     0.3611     0  R.FSQLVEELLK.I  (Ions score 73)
423 - 432     603.5260  1205.0374  1204.6703     0.3671     0  R.FSQLVEELLK.I  (Ions score 82)
423 - 432     603.5430  1205.0714  1204.6703     0.4011     0  R.FSQLVEELLK.I  (Ions score 85)
423 - 432     603.5690  1205.1234  1204.6703     0.4531     0  R.FSQLVEELLK.I  (Ions score 75)
433 - 453    1219.6700  2437.3254  2437.1624     0.1631     0  K.IICAFQLDTGLEYANSYNFAK.Q  (Ions score 127)
433 - 453    1219.6750  2437.3354  2437.1624     0.1731     0  K.IICAFQLDTGLEYANSYNFAK.Q  (Ions score 137)
433 - 453    1219.7020  2437.3894  2437.1624     0.2271     0  K.IICAFQLDTGLEYANSYNFAK.Q  (Ions score 130)
459 - 479    1201.6130  2401.2114  2401.2588    -0.0473     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 75)
459 - 479     801.5350  2401.5832  2401.2588     0.3244     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 105)
459 - 479     801.5450  2401.6132  2401.2588     0.3544     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 93)
459 - 479     801.5590  2401.6552  2401.2588     0.3964     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 70)
459 - 479     801.5930  2401.7572  2401.2588     0.4984     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 78)
459 - 479     801.6200  2401.8382  2401.2588     0.5794     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 44)
464 - 479     894.2320  1786.4494  1786.9200    -0.4706     0  K.TITLEVEPSDTIENVK.A  (Ions score 53)
464 - 479     894.5610  1787.1074  1786.9200     0.1874     0  K.TITLEVEPSDTIENVK.A  (Ions score 55)
464 - 479     894.5680  1787.1214  1786.9200     0.2014     0  K.TITLEVEPSDTIENVK.A  (Ions score 64)
464 - 479     894.5870  1787.1594  1786.9200     0.2394     0  K.TITLEVEPSDTIENVK.A  (Ions score 54)
464 - 479     894.5910  1787.1674  1786.9200     0.2474     0  K.TITLEVEPSDTIENVK.A  (Ions score 63)
464 - 479     894.5910  1787.1674  1786.9200     0.2474     0  K.TITLEVEPSDTIENVK.A  (Ions score 56)
464 - 479     894.5950  1787.1754  1786.9200     0.2554     0  K.TITLEVEPSDTIENVK.A  (Ions score 42)
464 - 479     894.5990  1787.1834  1786.9200     0.2634     0  K.TITLEVEPSDTIENVK.A  (Ions score 74)
464 - 479     894.6120  1787.2094  1786.9200     0.2894     0  K.TITLEVEPSDTIENVK.A  (Ions score 95)
464 - 479     894.6120  1787.2094  1786.9200     0.2894     0  K.TITLEVEPSDTIENVK.A  (Ions score 73)
464 - 479     894.6180  1787.2214  1786.9200     0.3014     0  K.TITLEVEPSDTIENVK.A  (Ions score 65)
464 - 479     894.6210  1787.2274  1786.9200     0.3074     0  K.TITLEVEPSDTIENVK.A  (Ions score 40)
464 - 479     894.6320  1787.2494  1786.9200     0.3294     0  K.TITLEVEPSDTIENVK.A  (Ions score 48)
464 - 479     894.6340  1787.2534  1786.9200     0.3334     0  K.TITLEVEPSDTIENVK.A  (Ions score 64)
464 - 479     894.6700  1787.3254  1786.9200     0.4054     0  K.TITLEVEPSDTIENVK.A  (Ions score 77)
464 - 479     894.6720  1787.3294  1786.9200     0.4094     0  K.TITLEVEPSDTIENVK.A  (Ions score 75)
464 - 479     894.6730  1787.3314  1786.9200     0.4114     0  K.TITLEVEPSDTIENVK.A  (Ions score 67)
464 - 479     894.6950  1787.3754  1786.9200     0.4554     0  K.TITLEVEPSDTIENVK.A  (Ions score 82)
482 - 494     762.4300  1522.8454  1522.7740     0.0715     1  K.IQDKEGIPPDQQR.L  (Ions score 56)
482 - 494     762.4490  1522.8834  1522.7740     0.1095     1  K.IQDKEGIPPDQQR.L  (Ions score 63)
482 - 494     762.4660  1522.9174  1522.7740     0.1435     1  K.IQDKEGIPPDQQR.L  (Ions score 57)
482 - 494     762.4710  1522.9274  1522.7740     0.1535     1  K.IQDKEGIPPDQQR.L  (Ions score 51)
486 - 494     520.3110  1038.6074  1038.5094     0.0980     0  K.EGIPPDQQR.L  (Ions score 32)
486 - 494     520.3210  1038.6274  1038.5094     0.1180     0  K.EGIPPDQQR.L  (Ions score 32)
486 - 494     520.3380  1038.6614  1038.5094     0.1520     0  K.EGIPPDQQR.L  (Ions score 37)
486 - 494     520.3390  1038.6634  1038.5094     0.1540     0  K.EGIPPDQQR.L  (Ions score 30)
486 - 494     520.3430  1038.6714  1038.5094     0.1620     0  K.EGIPPDQQR.L  (Ions score 34)
486 - 494     520.3450  1038.6754  1038.5094     0.1660     0  K.EGIPPDQQR.L  (Ions score 30)
486 - 494     520.3510  1038.6874  1038.5094     0.1780     0  K.EGIPPDQQR.L  (Ions score 33)
486 - 494     520.3660  1038.7174  1038.5094     0.2080     0  K.EGIPPDQQR.L  (Ions score 40)
495 - 506     730.9480  1459.8814  1459.7783     0.1031     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 64)
495 - 506     730.9590  1459.9034  1459.7783     0.1251     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 72)
495 - 506     731.0060  1459.9974  1459.7783     0.2191     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 67)
495 - 506     731.0870  1460.1594  1459.7783     0.3811     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 52)
495 - 506     487.7440  1460.2102  1459.7783     0.4319     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 37)
495 - 506     487.7500  1460.2282  1459.7783     0.4499     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 34)
507 - 515     541.3520  1080.6894  1080.5451     0.1443     0  R.TLSDYNIQK.E  (Ions score 54)
507 - 515     541.3520  1080.6894  1080.5451     0.1443     0  R.TLSDYNIQK.E  (Ions score 54)
507 - 515     541.3530  1080.6914  1080.5451     0.1463     0  R.TLSDYNIQK.E  (Ions score 52)
507 - 515     541.3530  1080.6914  1080.5451     0.1463     0  R.TLSDYNIQK.E  (Ions score 18)
507 - 515     541.3620  1080.7094  1080.5451     0.1643     0  R.TLSDYNIQK.E  (Ions score 57)
507 - 515     541.3980  1080.7814  1080.5451     0.2363     0  R.TLSDYNIQK.E  (Ions score 20)
507 - 515     541.4210  1080.8274  1080.5451     0.2823     0  R.TLSDYNIQK.E  (Ions score 33)
516 - 524     534.4040  1066.7934  1066.6135     0.1800     0  K.ESTLHLVLR.L  (Ions score 57)
516 - 524     534.4090  1066.8034  1066.6135     0.1900     0  K.ESTLHLVLR.L  (Ions score 48)
516 - 524     534.4140  1066.8134  1066.6135     0.2000     0  K.ESTLHLVLR.L  (Ions score 36)
516 - 524     534.4200  1066.8254  1066.6135     0.2120     0  K.ESTLHLVLR.L  (Ions score 57)
516 - 524     534.4210  1066.8274  1066.6135     0.2140     0  K.ESTLHLVLR.L  (Ions score 25)
516 - 524     534.4270  1066.8394  1066.6135     0.2260     0  K.ESTLHLVLR.L  (Ions score 53)
516 - 524     534.4410  1066.8674  1066.6135     0.2540     0  K.ESTLHLVLR.L  (Ions score 37)
516 - 524     534.4840  1066.9534  1066.6135     0.3400     0  K.ESTLHLVLR.L  (Ions score 49)
516 - 524     534.5380  1067.0614  1066.6135     0.4480     0  K.ESTLHLVLR.L  (Ions score 36)
```





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

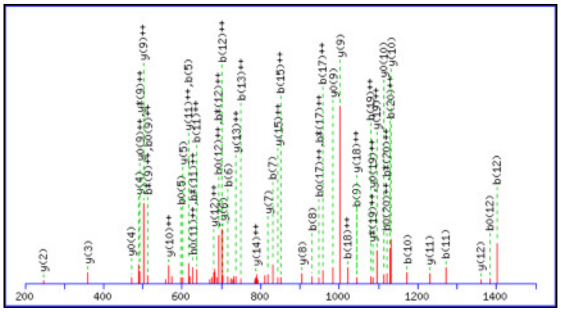
MATRIX SCIENCE Mascot Search Results

Peptide View

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

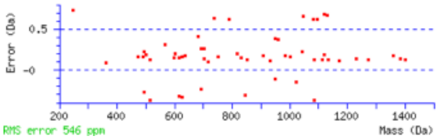
Match to Query 791: 2401.583172 from(801.535000,3+) intensity(1561290.0000)
Title: Cmpd 114, +MSn(801.89), 27.1 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00810_YD_3_merge.mgf

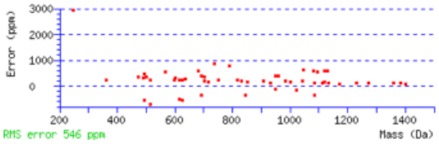
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2401.2588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5 : GlyGly (K)
Ions Score: 105 **Expect:** 1.8e-07
Matches : 55/226 fragment ions using 58 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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
105.0	2401.2588	0.3244	TLTGKTITLEVEPSDTIENVK
32.4	2401.3216	0.2615	KVNIASYQVKPGDVIEVKEASK
30.5	2401.1543	0.4288	SGGNEVSIEERLGAMDIDTHKK
30.4	2401.3953	0.1879	MNATKFLVLLVIGVLCAIVTAR
29.5	2401.2022	0.3810	LADELDLMVGVVEHGLFNGMVK
28.4	2401.1253	0.4579	DMEIAELKKNIEQMDTDHK
26.6	2401.1981	0.3850	GMTMPGHLGSEKTTVQNLEIVK
25.8	2402.1358	-0.5527	MPGNPYSSNEPGIGPLMRDIK
24.4	2401.2965	0.2867	RAVEEVFNVKVESVNTINGLGK
24.1	2400.3273	1.2559	LMMLLTDSPSIRDVILFPALR

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

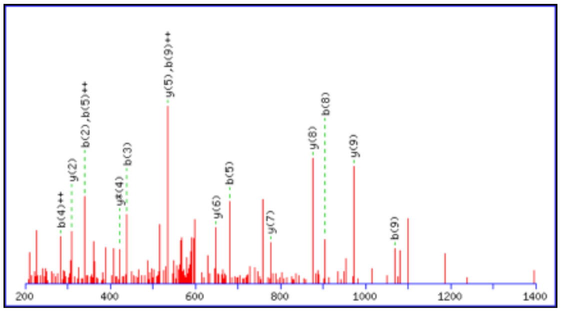
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVQLPGAYK**
Found in **YD_RFP-BARD-BRCA-Ub**, YD_RFP-BARD-BRCA-Ub

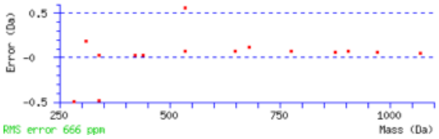
Match to Query 299: 1214.849448 from(608.432000,2+) intensity(258859.0000)
Title: Cmpd 32, +MSn(608.85), 20.4 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00810_YD_3_merge.mgf

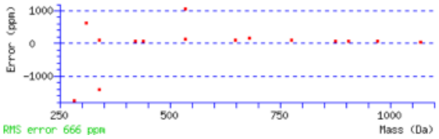
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1213.6819
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : GlyGly (K)
Ions Score: 46 **Expect:** 0.048
Matches : 15/72 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	243.1452	122.0762	226.1186	113.5629	**K**					**10**
2	***340.1979***	170.6026	323.1714	162.0893	**P**	***972.5513***	486.7793	955.5247	478.2660	**9**
3	***439.2663***	220.1368	422.2398	211.6235	**V**	***875.4985***	438.2529	858.4720	429.7396	**8**
4	567.3249	**284.1661**	550.2984	275.6528	**Q**	***776.4301***	388.7187	759.4036	380.2054	**7**
5	***680.4090***	**340.7081**	663.3824	332.1949	**L**	***648.3715***	324.6894	631.3450	316.1761	**6**
6	777.4618	389.2345	760.4352	380.7212	**P**	***535.2875***	268.1474	518.2609	259.6341	**5**
7	834.4832	417.7452	817.4567	409.2320	**G**	438.2347	219.6210	421.2082	211.1077	**4**
8	***905.5203***	453.2638	888.4938	444.7505	**A**	381.2132	191.1103	364.1867	182.5970	**3**
9	***1068.5837***	**534.7955**	1051.5571	526.2822	**Y**	***310.1761***	155.5917	293.1496	147.0784	**2**
10					**K**	147.1128	74.0600	130.0863	65.5468	**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.1	1213.6819	1.1676	KPVQLPGAYK
30.7	1213.5615	1.2879	NFDTGLQEYK
20.4	1213.6203	1.2291	KNHPGKEYK
18.4	1213.6125	1.2369	VTTHQLQEMK
17.3	1214.5311	0.3183	MDECIEKYK
16.6	1213.7394	1.1101	LIIVNNSSVKK
16.6	1212.7230	2.1264	QLPLNLFQIK
15.7	1213.6091	1.2403	KEGIHPEYK
14.8	1213.6495	1.1999	FYKLKDWSK
14.6	1214.7023	0.1472	IPAVAGGIYNIK

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

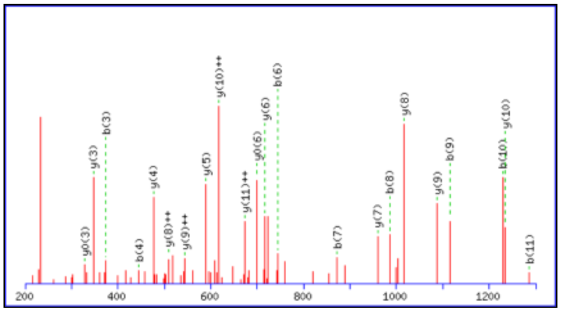
MATRIX SCIENCE Mascot Search Results

Peptide View

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

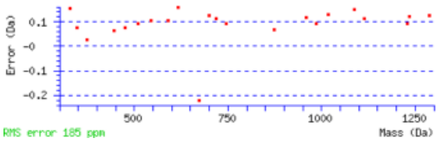
Match to Query 435: 1459.903448 from(730.959000,2+) intensity(727233.0000)
Title: Cmpd 76, +MSn(731.36), 24.5 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00810_YD_3_merge.mgf

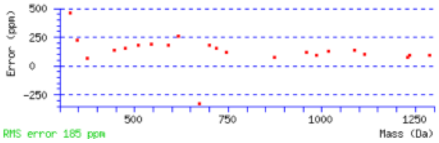
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1459.7783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : GlyGly (K)
Ions Score: 72 **Expect:** 0.00018
Matches : 22/102 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	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
71.8	1459.7783	0.1251	LIFAGKQLEDGR
30.9	1459.7718	0.1316	IIGGGMPVGAFGGRR
26.8	1460.7987	-0.8953	AGVFKKVDEIK
26.8	1460.7987	-0.8953	AGVFKKVDELK
23.8	1459.6725	0.2309	EAAALQCQLEDGR
22.9	1459.8293	0.0742	LTRMIRTAGALK
22.8	1459.7704	0.1330	EMKLLEQSGALK
20.8	1459.8432	0.0602	SGMVTLKLEKIK
20.3	1459.7453	0.1582	KMAQEQEKLK
20.0	1459.7817	0.1218	LLATGMERAGIAK

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

MATRIX SCIENCE Mascot Search Results

Protein View

```
Match to: YD_RFP-BARD-BRCA-Ub Score: 5695
YD_RFP-BARD-BRCA-Ub
Found in search of C:\YaelDavid\100203_YaelDavid\BIT00812_YD_4_merge.mgf

Nominal mass (Mr): 60628; Calculated pI value: 6.10
NCBI BLAST search of YD_RFP-BARD-BRCA-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 55%

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 EPDGRGAWAH
251 SRAALDRLEK LLRCSRCTNI LREPVCLGGC EHIFCSNCVS DCIGTGCPVC
301 YTPAWIQDLK INRQLDSMIQ LCSKLRNLLH DNELSDLKED GGSGGDLSAL
351 RVEEVQNVIN AMQKILECPI CLELIKEPVS TKCDHIFCKF CMLKLLNQKK
401 GPSQCPLCKN DITKRSLQES TRFSQLVEEL LKIICAFQLD TGLEYANSYN
451 FAKQIFVKTL TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK
501 QLEDGRTLSD YNIQKESTLH LVLRLRGG
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Show predicted peptides also

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

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Start - End     Observed   Mr(expt)   Mr(calc)    Delta   Miss Sequence
   24 - 51      760.3810  3037.4949  3037.3359    0.1590    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 43)
   24 - 51     1519.8170  3037.6194  3037.3359    0.2835    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 35)
   24 - 51     1013.6160  3037.8262  3037.3359    0.4902    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 59)
   24 - 51     1013.8520  3038.5342  3037.3359    1.1982    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 92)
   24 - 51     1013.8860  3038.6362  3037.3359    1.3002    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 40)
   24 - 51     1013.9540  3038.8402  3037.3359    1.5042    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 63)
   24 - 51     1014.1200  3039.3382  3037.3359    2.0022    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 34)
   24 - 51      764.3700  3053.4509  3053.3309    0.1200    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 44)
   24 - 51     1019.1690  3054.4852  3053.3309    1.1543    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 31)
   24 - 51     1019.1790  3054.5152  3053.3309    1.1843    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 50)
   24 - 51     1019.2380  3054.6922  3053.3309    1.3613    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 74)
   24 - 51      764.7100  3054.8109  3053.3309    1.4800    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 29)
   24 - 51     1019.5060  3055.4962  3053.3309    2.1653    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 47)
   57 - 76     1104.1630  2206.3114  2207.1051   -0.7937    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 80)
   57 - 76      736.7540  2207.2402  2207.1051    0.1350    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 49)
   57 - 76     1104.6650  2207.3154  2207.1051    0.2103    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 76)
   57 - 76      736.7870  2207.3392  2207.1051    0.2340    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 39)
   57 - 76     1104.6800  2207.3454  2207.1051    0.2403    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 65)
   57 - 76     1104.6860  2207.3574  2207.1051    0.2523    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 84)
   57 - 76      736.7970  2207.3692  2207.1051    0.2640    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 35)
   91 - 98      462.2120   922.4094   923.4753   -1.0658    0  K.LSFPEGFK.W  (Ions score 43)
   91 - 98      462.8030   923.5914   923.4753    0.1162    0  K.LSFPEGFK.W  (Ions score 43)
   91 - 98      462.8210   923.6274   923.4753    0.1522    0  K.LSFPEGFK.W  (Ions score 39)
   91 - 98      462.8790   923.7434   923.4753    0.2682    0  K.LSFPEGFK.W  (Ions score 34)
  102 - 127    1439.7930  2877.5714  2877.3379    0.2336    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 89)
  102 - 127     960.3590  2878.0552  2877.3379    0.7173    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 100)
  102 - 127    1440.2550  2878.4954  2877.3379    1.1576    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 77)
  102 - 127    1440.2550  2878.4954  2877.3379    1.1576    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 92)
  102 - 127    1440.2720  2878.5294  2877.3379    1.1916    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 85)
  102 - 127     960.5880  2878.7422  2877.3379    1.4043    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 96)
  102 - 127     960.7270  2879.1592  2877.3379    1.8213    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 82)
  102 - 127    1447.7500  2893.4854  2893.3328    0.1526    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 102)
  102 - 127    1447.7800  2893.5454  2893.3328    0.2126    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 123)
  102 - 127    1448.2080  2894.4014  2893.3328    1.0686    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 104)
  102 - 127     965.8600  2894.5582  2893.3328    1.2254    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 78)
  102 - 127     965.9140  2894.7202  2893.3328    1.3874    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 67)
  102 - 127     965.9740  2894.9002  2893.3328    1.5674    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 70)
  132 - 144     689.0630  1376.1114  1376.6395   -0.5280    0  R.GTNFPSDGPVMQK.K  (Ions score 18)
  132 - 144     689.4060  1376.7974  1376.6395    0.1580    0  R.GTNFPSDGPVMQK.K  (Ions score 69)
  132 - 144     689.4250  1376.8354  1376.6395    0.1960    0  R.GTNFPSDGPVMQK.K  (Ions score 77)
  132 - 144     689.4580  1376.9014  1376.6395    0.2620    0  R.GTNFPSDGPVMQK.K  (Ions score 77)
  132 - 144     689.4730  1376.9314  1376.6395    0.2920    0  R.GTNFPSDGPVMQK.K  (Ions score 74)
  132 - 144     697.4240  1392.8334  1392.6344    0.1991    0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 56)
  132 - 144     697.4250  1392.8354  1392.6344    0.2011    0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 59)
  132 - 144     697.4500  1392.8854  1392.6344    0.2511    0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 71)
  132 - 144     697.4540  1392.8934  1392.6344    0.2591    0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 48)
  132 - 144     697.4580  1392.9014  1392.6344    0.2671    0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 85)
  145 - 155     648.3340  1294.6534  1294.5976    0.0559    1  K.KTMGWEASTER.M  (Ions score 79)
  145 - 155     648.3700  1294.7254  1294.5976    0.1279    1  K.KTMGWEASTER.M  (Ions score 76)
  145 - 155     648.3920  1294.7694  1294.5976    0.1719    1  K.KTMGWEASTER.M  (Ions score 59)
  145 - 155     648.4030  1294.7914  1294.5976    0.1939    1  K.KTMGWEASTER.M  (Ions score 71)
  146 - 155     584.2730  1166.5314  1166.5026    0.0288    0  K.TMGWEASTER.M  (Ions score 52)
  146 - 155     584.3140  1166.6134  1166.5026    0.1108    0  K.TMGWEASTER.M  (Ions score 48)
  146 - 155     584.3550  1166.6954  1166.5026    0.1928    0  K.TMGWEASTER.M  (Ions score 37)
  146 - 155     584.3680  1166.7214  1166.5026    0.2188    0  K.TMGWEASTER.M  (Ions score 52)
  146 - 155     592.2970  1182.5794  1182.4975    0.0819    0  K.TMGWEASTER.M  Oxidation (M) (Ions score 64)
  146 - 155     592.3070  1182.5994  1182.4975    0.1019    0  K.TMGWEASTER.M  Oxidation (M) (Ions score 57)
  146 - 155     592.3180  1182.6214  1182.4975    0.1239    0  K.TMGWEASTER.M  Oxidation (M) (Ions score 53)
  146 - 155     592.3210  1182.6274  1182.4975    0.1299    0  K.TMGWEASTER.M  Oxidation (M) (Ions score 57)
  191 - 200     367.5690  1099.6852  1099.6390    0.0462    0  K.KPVQLPGAYK.T  (Ions score 40)
  191 - 200     367.5850  1099.7332  1099.6390    0.0942    0  K.KPVQLPGAYK.T  (Ions score 52)
  191 - 200     550.9100  1099.8054  1099.6390    0.1665    0  K.KPVQLPGAYK.T  (Ions score 52)
  191 - 200     550.9220  1099.8294  1099.6390    0.1905    0  K.KPVQLPGAYK.T  (Ions score 51)
  191 - 200     550.9250  1099.8354  1099.6390    0.1965    0  K.KPVQLPGAYK.T  (Ions score 47)
  191 - 200     550.9290  1099.8434  1099.6390    0.2045    0  K.KPVQLPGAYK.T  (Ions score 47)
  191 - 200     607.8800  1213.7454  1213.6819    0.0636    0  K.KPVQLPGAYK.T  GlyGly (K) (Ions score 53)
  191 - 200     607.9000  1213.7854  1213.6819    0.1036    0  K.KPVQLPGAYK.T  GlyGly (K) (Ions score 47)
  191 - 200     607.9010  1213.7874  1213.6819    0.1056    0  K.KPVQLPGAYK.T  GlyGly (K) (Ions score 40)
  191 - 200     607.9270  1213.8394  1213.6819    0.1576    0  K.KPVQLPGAYK.T  GlyGly (K) (Ions score 42)
  191 - 204     558.0350  1671.0832  1670.9355    0.1476    1  K.KPVQLPGAYKTDIK.L  GlyGly (K) (Ions score 42)
  205 - 222    1113.1070  2224.1994  2224.0284    0.1711    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 75)
  205 - 222    1113.1180  2224.2214  2224.0284    0.1931    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 97)
  205 - 222    1113.1800  2224.3454  2224.0284    0.3171    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 27)
  205 - 222    1113.1830  2224.3514  2224.0284    0.3231    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 125)
  205 - 222     742.4740  2224.4002  2224.0284    0.3718    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 36)
  205 - 222    1113.2360  2224.4574  2224.0284    0.4291    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 3)
  205 - 222    1113.2460  2224.4774  2224.0284    0.4491    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 97)
  205 - 222     742.5030  2224.4872  2224.0284    0.4588    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 27)
  205 - 222     742.5160  2224.5262  2224.0284    0.4978    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 42)
  205 - 222     742.5430  2224.6072  2224.0284    0.5788    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 61)
  205 - 222     742.5570  2224.6492  2224.0284    0.6208    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 19)
  205 - 222     742.6340  2224.8802  2224.0284    0.8518    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 55)
  205 - 222     742.7120  2225.1142  2224.0284    1.0858    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 24)
  205 - 222     742.8070  2225.3992  2224.0284    1.3708    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 34)
  205 - 222     742.8310  2225.4712  2224.0284    1.4428    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 42)
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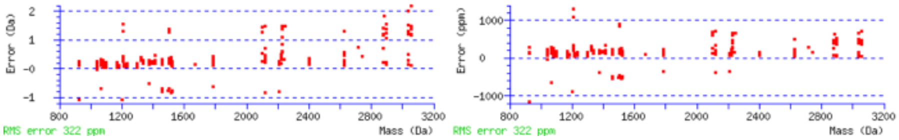
205 - 222    742.8460  2225.5162  2224.0284     1.4878     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 29)
205 - 222    742.8460  2225.5162  2224.0284     1.4878     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 31)
227 - 245   1060.0780  2118.1414  2118.9606    -0.8192     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 43)
227 - 245   1060.5890  2119.1634  2118.9606     0.2028     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 135)
227 - 245   1060.6290  2119.2434  2118.9606     0.2828     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 135)
227 - 245   1060.6590  2119.3034  2118.9606     0.3428     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 115)
227 - 245    707.4760  2119.4062  2118.9606     0.4455     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 34)
227 - 245    707.4780  2119.4122  2118.9606     0.4515     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 35)
227 - 245    707.5620  2119.6642  2118.9606     0.7035     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 52)
227 - 245    707.8270  2120.4592  2118.9606     1.4985     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 40)
314 - 324    661.9630  1321.9114  1321.6370     0.2745     0  R.QLDSMIQLCSK.L  (Ions score 56)
314 - 324    661.9790  1321.9434  1321.6370     0.3065     0  R.QLDSMIQLCSK.L  (Ions score 62)
314 - 324    662.0120  1322.0094  1321.6370     0.3725     0  R.QLDSMIQLCSK.L  (Ions score 59)
314 - 324    662.0280  1322.0414  1321.6370     0.4045     0  R.QLDSMIQLCSK.L  (Ions score 48)
314 - 324    669.9160  1337.8174  1337.6319     0.1855     0  R.QLDSMIQLCSK.L  Oxidation (M)  (Ions score 59)
314 - 324    669.9680  1337.9214  1337.6319     0.2895     0  R.QLDSMIQLCSK.L  Oxidation (M)  (Ions score 76)
327 - 338    705.9610  1409.9074  1409.7150     0.1924     0  R.NLLHDNELSDLK.E  (Ions score 67)
327 - 338    705.9850  1409.9554  1409.7150     0.2404     0  R.NLLHDNELSDLK.E  (Ions score 51)
327 - 338    705.9990  1409.9834  1409.7150     0.2684     0  R.NLLHDNELSDLK.E  (Ions score 64)
327 - 338    706.0170  1410.0194  1409.7150     0.3044     0  R.NLLHDNELSDLK.E  (Ions score 67)
327 - 338    471.0670  1410.1792  1409.7150     0.4641     0  R.NLLHDNELSDLK.E  (Ions score 37)
327 - 351    875.7990  2624.3752  2624.2678     0.1074     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 60)
327 - 351   1313.2430  2624.4714  2624.2678     0.2037     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 115)
327 - 351   1313.2760  2624.5374  2624.2678     0.2697     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 146)
327 - 351   1313.2910  2624.5674  2624.2678     0.2997     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 125)
327 - 351    657.1870  2624.7189  2624.2678     0.4511     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 62)
327 - 351    875.9570  2624.8492  2624.2678     0.5814     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 105)
327 - 351   1313.7960  2625.5774  2624.2678     1.3097     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 127)
327 - 351    913.9210  2738.7412  2738.3107     0.4305     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  GlyGly (K)  (Ions score 50)
339 - 351    617.3260  1232.6374  1232.5633     0.0741     0  K.EDGGSGGDLSALR.V  (Ions score 80)
339 - 351    617.3420  1232.6694  1232.5633     0.1061     0  K.EDGGSGGDLSALR.V  (Ions score 84)
339 - 351    617.3430  1232.6714  1232.5633     0.1081     0  K.EDGGSGGDLSALR.V  (Ions score 94)
339 - 351    617.3800  1232.7454  1232.5633     0.1821     0  K.EDGGSGGDLSALR.V  (Ions score 80)
339 - 351    617.3860  1232.7574  1232.5633     0.1941     0  K.EDGGSGGDLSALR.V  (Ions score 84)
352 - 364    751.0440  1500.0734  1500.7606    -0.6872     0  R.VEEVQNVINAMQK.I  (Ions score 45)
352 - 364    751.4780  1500.9414  1500.7606     0.1808     0  R.VEEVQNVINAMQK.I  (Ions score 102)
352 - 364    751.4820  1500.9494  1500.7606     0.1888     0  R.VEEVQNVINAMQK.I  (Ions score 102)
352 - 364    751.5080  1501.0014  1500.7606     0.2408     0  R.VEEVQNVINAMQK.I  (Ions score 76)
352 - 364    751.5170  1501.0194  1500.7606     0.2588     0  R.VEEVQNVINAMQK.I  (Ions score 74)
352 - 364    751.5420  1501.0694  1500.7606     0.3088     0  R.VEEVQNVINAMQK.I  (Ions score 79)
352 - 364    751.5650  1501.1154  1500.7606     0.3548     0  R.VEEVQNVINAMQK.I  (Ions score 115)
352 - 364    751.5650  1501.1154  1500.7606     0.3548     0  R.VEEVQNVINAMQK.I  (Ions score 109)
352 - 364    752.0270  1502.0394  1500.7606     1.2788     0  R.VEEVQNVINAMQK.I  (Ions score 79)
352 - 364    752.0290  1502.0434  1500.7606     1.2828     0  R.VEEVQNVINAMQK.I  (Ions score 92)
352 - 364    758.9710  1515.9274  1516.7555    -0.8281     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 17)
352 - 364    759.4640  1516.9134  1516.7555     0.1579     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 107)
352 - 364    759.4640  1516.9134  1516.7555     0.1579     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 102)
352 - 364    759.4720  1516.9294  1516.7555     0.1739     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 102)
352 - 364    759.5220  1517.0294  1516.7555     0.2739     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 88)
352 - 364    759.5710  1517.1274  1516.7555     0.3719     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 30)
352 - 364    759.5840  1517.1534  1516.7555     0.3979     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 45)
365 - 376    750.5250  1499.0354  1499.8091    -0.7737     0  K.ILECPICLELIK.E  (Ions score 19)
365 - 376    751.0280  1500.0414  1499.8091     0.2323     0  K.ILECPICLELIK.E  (Ions score 80)
365 - 376    751.0730  1500.1314  1499.8091     0.3223     0  K.ILECPICLELIK.E  (Ions score 64)
365 - 376    751.0940  1500.1734  1499.8091     0.3643     0  K.ILECPICLELIK.E  (Ions score 79)
365 - 376    751.5600  1501.1054  1499.8091     1.2963     0  K.ILECPICLELIK.E  (Ions score 70)
365 - 376    751.5990  1501.1834  1499.8091     1.3743     0  K.ILECPICLELIK.E  (Ions score 67)
423 - 432    602.8080  1203.6014  1204.6703    -1.0689     0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432    603.4740  1204.9334  1204.6703     0.2631     0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    603.4760  1204.9374  1204.6703     0.2671     0  R.FSQLVEELLK.I  (Ions score 73)
423 - 432    603.4810  1204.9474  1204.6703     0.2771     0  R.FSQLVEELLK.I  (Ions score 81)
423 - 432    603.4860  1204.9574  1204.6703     0.2871     0  R.FSQLVEELLK.I  (Ions score 85)
423 - 432    603.4920  1204.9694  1204.6703     0.2991     0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432    603.4980  1204.9814  1204.6703     0.3111     0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    603.5020  1204.9894  1204.6703     0.3191     0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    603.5040  1204.9934  1204.6703     0.3231     0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432    603.5120  1205.0094  1204.6703     0.3391     0  R.FSQLVEELLK.I  (Ions score 85)
423 - 432    603.5160  1205.0174  1204.6703     0.3471     0  R.FSQLVEELLK.I  (Ions score 81)
423 - 432    603.5190  1205.0234  1204.6703     0.3531     0  R.FSQLVEELLK.I  (Ions score 81)
423 - 432    603.5190  1205.0234  1204.6703     0.3531     0  R.FSQLVEELLK.I  (Ions score 71)
423 - 432    603.5500  1205.0854  1204.6703     0.4151     0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432    603.9950  1205.9754  1204.6703     1.3051     0  R.FSQLVEELLK.I  (Ions score 70)
423 - 432    604.1250  1206.2354  1204.6703     1.5651     0  R.FSQLVEELLK.I  (Ions score 66)
459 - 479   1201.7130  2401.4114  2401.2588     0.1527     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 85)
459 - 479    801.4940  2401.4602  2401.2588     0.2014     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 101)
459 - 479   1201.7410  2401.4674  2401.2588     0.2087     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 82)
459 - 479    801.5160  2401.5262  2401.2588     0.2674     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 84)
459 - 479    801.5470  2401.6192  2401.2588     0.3604     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 81)
459 - 481    906.0720  2715.1942  2714.4338     0.7604     2  K.TLTGKTITLEVEPSDTIENVKAK.I  2 GlyGly (K)  (Ions score 71)
464 - 479    894.1540  1786.2934  1786.9200    -0.6266     0  K.TITLEVEPSDTIENVK.A  (Ions score 72)
464 - 479    894.5230  1787.0314  1786.9200     0.1114     0  K.TITLEVEPSDTIENVK.A  (Ions score 69)
464 - 479    894.5510  1787.0874  1786.9200     0.1674     0  K.TITLEVEPSDTIENVK.A  (Ions score 54)
464 - 479    894.5690  1787.1234  1786.9200     0.2034     0  K.TITLEVEPSDTIENVK.A  (Ions score 63)
464 - 479    894.5760  1787.1374  1786.9200     0.2174     0  K.TITLEVEPSDTIENVK.A  (Ions score 100)
464 - 479    894.5760  1787.1374  1786.9200     0.2174     0  K.TITLEVEPSDTIENVK.A  (Ions score 71)
464 - 479    894.5770  1787.1394  1786.9200     0.2194     0  K.TITLEVEPSDTIENVK.A  (Ions score 82)
464 - 479    894.5790  1787.1434  1786.9200     0.2234     0  K.TITLEVEPSDTIENVK.A  (Ions score 86)
464 - 479    894.5810  1787.1474  1786.9200     0.2274     0  K.TITLEVEPSDTIENVK.A  (Ions score 72)
464 - 479    894.5850  1787.1554  1786.9200     0.2354     0  K.TITLEVEPSDTIENVK.A  (Ions score 76)
464 - 479    894.5880  1787.1614  1786.9200     0.2414     0  K.TITLEVEPSDTIENVK.A  (Ions score 91)
464 - 479    894.5890  1787.1634  1786.9200     0.2434     0  K.TITLEVEPSDTIENVK.A  (Ions score 71)
464 - 479    894.5900  1787.1654  1786.9200     0.2454     0  K.TITLEVEPSDTIENVK.A  (Ions score 79)
464 - 479    894.5930  1787.1714  1786.9200     0.2514     0  K.TITLEVEPSDTIENVK.A  (Ions score 62)
464 - 479    894.5960  1787.1774  1786.9200     0.2574     0  K.TITLEVEPSDTIENVK.A  (Ions score 67)
464 - 479    894.6030  1787.1914  1786.9200     0.2714     0  K.TITLEVEPSDTIENVK.A  (Ions score 71)
464 - 479    894.6030  1787.1914  1786.9200     0.2714     0  K.TITLEVEPSDTIENVK.A  (Ions score 85)
464 - 479    894.6030  1787.1914  1786.9200     0.2714     0  K.TITLEVEPSDTIENVK.A  (Ions score 78)
464 - 479    894.6040  1787.1934  1786.9200     0.2734     0  K.TITLEVEPSDTIENVK.A  (Ions score 81)
464 - 479    894.6060  1787.1974  1786.9200     0.2774     0  K.TITLEVEPSDTIENVK.A  (Ions score 76)
464 - 479    894.6090  1787.2034  1786.9200     0.2834     0  K.TITLEVEPSDTIENVK.A  (Ions score 73)
464 - 479    894.6150  1787.2154  1786.9200     0.2954     0  K.TITLEVEPSDTIENVK.A  (Ions score 67)
464 - 479    894.6310  1787.2474  1786.9200     0.3274     0  K.TITLEVEPSDTIENVK.A  (Ions score 50)
464 - 479    894.6370  1787.2594  1786.9200     0.3394     0  K.TITLEVEPSDTIENVK.A  (Ions score 78)
464 - 479    894.6410  1787.2674  1786.9200     0.3474     0  K.TITLEVEPSDTIENVK.A  (Ions score 60)
464 - 479    894.6430  1787.2714  1786.9200     0.3514     0  K.TITLEVEPSDTIENVK.A  (Ions score 86)
464 - 479    894.6680  1787.3214  1786.9200     0.4014     0  K.TITLEVEPSDTIENVK.A  (Ions score 72)
464 - 479    894.6760  1787.3374  1786.9200     0.4174     0  K.TITLEVEPSDTIENVK.A  (Ions score 82)
464 - 479    894.6850  1787.3554  1786.9200     0.4354     0  K.TITLEVEPSDTIENVK.A  (Ions score 74)
464 - 481   1051.1810  2100.3474  2100.0950     0.2524     1  K.TITLEVEPSDTIENVKAK.I  GlyGly (K)  (Ions score 48)
464 - 481    701.2140  2100.6202  2100.0950     0.5252     1  K.TITLEVEPSDTIENVKAK.I  GlyGly (K)  (Ions score 24)
464 - 481    701.4670  2101.3792  2100.0950     1.2842     1  K.TITLEVEPSDTIENVKAK.I  GlyGly (K)  (Ions score 19)
464 - 481    701.5240  2101.5502  2100.0950     1.4552     1  K.TITLEVEPSDTIENVKAK.I  GlyGly (K)  (Ions score 40)
482 - 494    761.9960  1521.9774  1522.7740    -0.7965     1  K.IQDKEGIPPDQQR.L  (Ions score 44)
482 - 494    508.3460  1522.0162  1522.7740    -0.7578     1  K.IQDKEGIPPDQQR.L  (Ions score 39)
482 - 494    762.4420  1522.8694  1522.7740     0.0955     1  K.IQDKEGIPPDQQR.L  (Ions score 51)
482 - 494    762.4480  1522.8814  1522.7740     0.1075     1  K.IQDKEGIPPDQQR.L  (Ions score 52)
482 - 494    762.4740  1522.9334  1522.7740     0.1595     1  K.IQDKEGIPPDQQR.L  (Ions score 56)
482 - 494    508.6860  1523.0362  1522.7740     0.2622     1  K.IQDKEGIPPDQQR.L  (Ions score 42)
486 - 494    520.2490  1038.4834  1038.5094    -0.0260     0  K.EGIPPDQQR.L  (Ions score 34)
486 - 494    520.3050  1038.5954  1038.5094     0.0860     0  K.EGIPPDQQR.L  (Ions score 38)
486 - 494    520.3300  1038.6454  1038.5094     0.1360     0  K.EGIPPDQQR.L  (Ions score 42)
486 - 494    520.3410  1038.6674  1038.5094     0.1580     0  K.EGIPPDQQR.L  (Ions score 35)
486 - 494    520.3650  1038.7154  1038.5094     0.2060     0  K.EGIPPDQQR.L  (Ions score 37)
486 - 494    520.3740  1038.7334  1038.5094     0.2240     0  K.EGIPPDQQR.L  (Ions score 30)
486 - 494    520.3900  1038.7654  1038.5094     0.2560     0  K.EGIPPDQQR.L  (Ions score 33)
```

```
495 - 506     487.3380  1458.9922  1459.7783    -0.7861     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 22)
495 - 506     487.3660  1459.0762  1459.7783    -0.7021     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 31)
495 - 506     487.6450  1459.9132  1459.7783     0.1349     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 32)
495 - 506     730.9740  1459.9334  1459.7783     0.1551     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 72)
495 - 506     730.9960  1459.9774  1459.7783     0.1991     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 71)
495 - 506     731.0060  1459.9974  1459.7783     0.2191     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 71)
495 - 506     731.0370  1460.0594  1459.7783     0.2811     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 71)
495 - 506     487.7080  1460.1022  1459.7783     0.3239     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 31)
507 - 515     541.3020  1080.5894  1080.5451     0.0443     0  R.TLSDYNIQK.E  (Ions score 54)
507 - 515     541.3300  1080.6454  1080.5451     0.1003     0  R.TLSDYNIQK.E  (Ions score 52)
507 - 515     541.3520  1080.6894  1080.5451     0.1443     0  R.TLSDYNIQK.E  (Ions score 57)
507 - 515     541.3780  1080.7414  1080.5451     0.1963     0  R.TLSDYNIQK.E  (Ions score 31)
507 - 515     541.3960  1080.7774  1080.5451     0.2323     0  R.TLSDYNIQK.E  (Ions score 60)
507 - 515     541.3970  1080.7794  1080.5451     0.2343     0  R.TLSDYNIQK.E  (Ions score 41)
507 - 515     541.3980  1080.7814  1080.5451     0.2363     0  R.TLSDYNIQK.E  (Ions score 48)
507 - 515     541.4050  1080.7954  1080.5451     0.2503     0  R.TLSDYNIQK.E  (Ions score 37)
507 - 515     541.4110  1080.8074  1080.5451     0.2623     0  R.TLSDYNIQK.E  (Ions score 38)
507 - 515     541.4170  1080.8194  1080.5451     0.2743     0  R.TLSDYNIQK.E  (Ions score 15)
507 - 524     748.8460  2243.5162  2243.1910     0.3252     1  R.TLSDYNIQKESTLHLVLR.L  GlyGly (K)  (Ions score 72)
507 - 524     749.2290  2244.6652  2243.1910     1.4742     1  R.TLSDYNIQKESTLHLVLR.L  GlyGly (K)  (Ions score 65)
516 - 524     533.9630  1065.9114  1066.6135    -0.7020     0  K.ESTLHLVLR.L  (Ions score 61)
516 - 524     534.3790  1066.7434  1066.6135     0.1300     0  K.ESTLHLVLR.L  (Ions score 55)
516 - 524     534.3890  1066.7634  1066.6135     0.1500     0  K.ESTLHLVLR.L  (Ions score 22)
516 - 524     534.4020  1066.7894  1066.6135     0.1760     0  K.ESTLHLVLR.L  (Ions score 61)
516 - 524     534.4070  1066.7994  1066.6135     0.1860     0  K.ESTLHLVLR.L  (Ions score 53)
516 - 524     534.4100  1066.8054  1066.6135     0.1920     0  K.ESTLHLVLR.L  (Ions score 57)
516 - 524     534.4230  1066.8314  1066.6135     0.2180     0  K.ESTLHLVLR.L  (Ions score 65)
516 - 524     534.4440  1066.8734  1066.6135     0.2600     0  K.ESTLHLVLR.L  (Ions score 37)
516 - 524     534.4600  1066.9054  1066.6135     0.2920     0  K.ESTLHLVLR.L  (Ions score 40)
516 - 524     534.4650  1066.9154  1066.6135     0.3020     0  K.ESTLHLVLR.L  (Ions score 44)
516 - 524     534.4670  1066.9194  1066.6135     0.3060     0  K.ESTLHLVLR.L  (Ions score 55)
516 - 524     534.4680  1066.9214  1066.6135     0.3080     0  K.ESTLHLVLR.L  (Ions score 37)
```



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

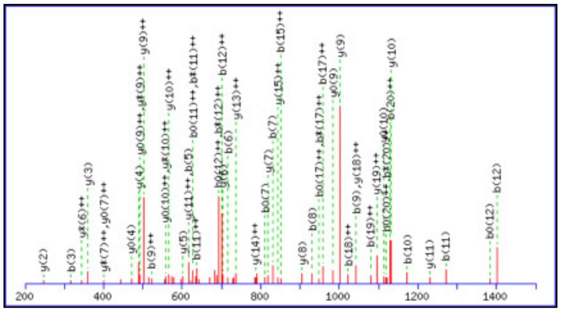
Mascot Search Results

Peptide View

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

Match to Query 826: 2401.460172 from(801.494000,3+) intensity(1539442.0000)
Title: Cmpd 105, +MSn(802.06), 27.2 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00812_YD_4_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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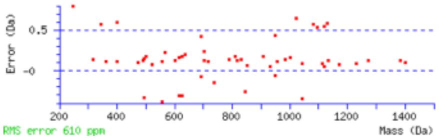
Monoisotopic mass of neutral peptide Mr(calc): 2401.2588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5      : GlyGly (K)
Ions Score: 101  Expect: 4.5e-07
Matches : 55/226 fragment ions using 57 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	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
101.3	2401.2588	0.2014	TLTGKTITLEVEPSDTIENVK
33.9	2402.2199	-0.7597	NVPRYGMGQTAPMVIRSPGEVK
32.9	2401.2410	0.2191	DDMVIPDSKVKIVGDTEALVK
31.9	2400.3273	1.1329	LMMLLTDSPSIRDVILFPALR
28.4	2401.2965	0.1637	RAVEEVFNVKVESVNTINGLGK
28.1	2401.1543	0.3058	SGGNEVSIEERLGAMDIDTHKK
27.8	2401.1981	0.2620	GMTMPGHLGSEKTTVQNLEIVK
25.5	2401.3953	0.0649	MNATKFLVLLVIGVLCAIVTAR
24.8	2401.3039	0.1563	MKKIGSIEVPQEAFLNILK
24.6	2401.1253	0.3349	DMEIAELKKNIEQMDTDHK

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

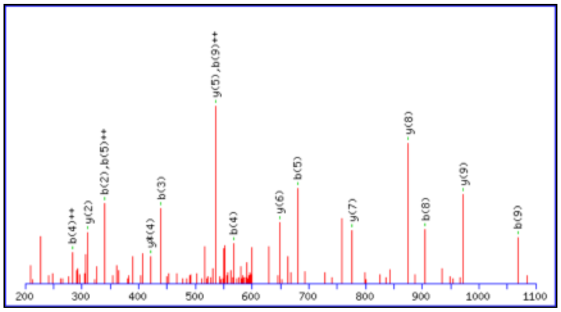
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVQLPGAYK**
Found in **YD_RFP-BARD-BRCA-Ub**, YD_RFP-BARD-BRCA-Ub

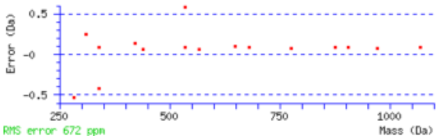
Match to Query 336: 1213.745448 from(607.880000,2+) intensity(337498.0000)
Title: Cmpd 30, +MSn(608.16), 20.5 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00812_YD_4_merge.mgf

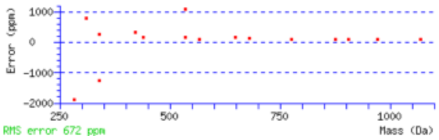
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1213.6819
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : GlyGly (K)
Ions Score: 53 **Expect:** 0.031
Matches : 16/72 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	243.1452	122.0762	226.1186	113.5629	K					10
2	***340.1979***	170.6026	323.1714	162.0893	P	***972.5513***	486.7793	955.5247	478.2660	9
3	***439.2663***	220.1368	422.2398	211.6235	V	***875.4985***	438.2529	858.4720	429.7396	8
4	***567.3249***	**284.1661**	550.2984	275.6528	Q	***776.4301***	388.7187	759.4036	380.2054	7
5	***680.4090***	**340.7081**	663.3824	332.1949	L	***648.3715***	324.6894	631.3450	316.1761	6
6	777.4618	389.2345	760.4352	380.7212	P	***535.2875***	268.1474	518.2609	259.6341	5
7	834.4832	417.7452	817.4567	409.2320	G	438.2347	219.6210	421.2082	211.1077	4
8	***905.5203***	453.2638	888.4938	444.7505	A	381.2132	191.1103	364.1867	182.5970	3
9	***1068.5837***	**534.7955**	1051.5571	526.2822	Y	***310.1761***	155.5917	293.1496	147.0784	2
10					K	147.1128	74.0600	130.0863	65.5468	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.3	1213.6819	0.0636	KPVQLPGAYK
35.7	1213.5615	0.1839	NFDTGLQEYK
24.9	1212.7230	1.0224	QLPLNLFQIK
22.9	1213.6203	0.1251	KNHPGKEYK
21.4	1214.5489	-0.8035	DETSMTPPPPK
20.5	1213.7434	0.0020	LILVPFLNGTK
20.1	1213.6125	0.1329	VTTHQLQEMK
19.6	1213.5649	0.1806	AYGMAGLETSAK
19.4	1214.5311	-0.7857	MDECIEKYK
19.4	1213.7407	0.0047	KPIPKHPRK

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

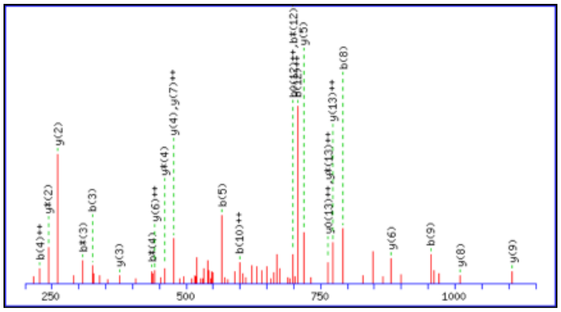
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVQLPGAYKTDIK**
Found in **YD_RFP-BARD-BRCA-Ub**, YD_RFP-BARD-BRCA-Ub

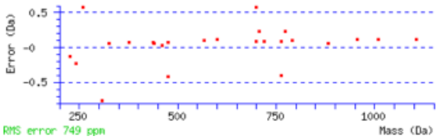
Match to Query 581: 1671.083172 from(558.035000,3+) intensity(390351.0000)
Title: Cmpd 45, +MSn(558.37), 21.2 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00812_YD_4_merge.mgf

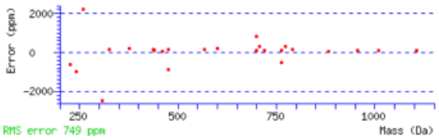
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1670.9355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K10 : GlyGly (K)
Ions Score: 42 **Expect:** 0.01
Matches : 26/132 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							14
2	226.1550	113.5811	209.1285	105.0679			P	1543.8479	772.4276	1526.8213	763.9143	1525.8373	763.4223	13
3	**325.2234**	163.1153	308.1969	154.6021			V	1446.7951	723.9012	1429.7686	715.3879	1428.7845	714.8959	12
4	453.2820	***227.1446***	436.2554	218.6314			Q	1347.7267	674.3670	1330.7001	665.8537	1329.7161	665.3617	11
5	**566.3661**	283.6867	549.3395	275.1734			L	1219.6681	610.3377	1202.6416	601.8244	1201.6576	601.3324	10
6	663.4188	332.2130	646.3923	323.6998			P	***1106.5841***	553.7957	1089.5575	545.2824	1088.5735	544.7904	9
7	720.4403	360.7238	703.4137	352.2105			G	***1009.5313***	505.2693	992.5047	496.7560	991.5207	496.2640	8
8	**791.4774**	396.2423	774.4509	387.7291			A	952.5098	476.7585	935.4833	468.2453	934.4993	467.7533	7
9	**954.5407**	477.7740	937.5142	469.2607			Y	***881.4727***	441.2400	864.4462	432.7267	863.4621	432.2347	6
10	1196.6786	***598.8429***	1179.6521	590.3297			K	***718.4094***	359.7083	701.3828	351.1951	700.3988	350.7030	5
11	1297.7263	649.3668	1280.6998	640.8535	1279.7157	640.3615	T	***476.2715***	238.6394	459.2449	230.1261	458.2609	229.6341	4
12	1412.7532	***706.8803***	1395.7267	698.3670	1394.7427	697.8750	D	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	3
13	1525.8373	***763.4223***	1508.8108	754.9090	1507.8267	754.4170	I	***260.1969***	130.6021	243.1703	122.0888			2
14							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.1	1670.9355	0.1476	KPVQLPGAYKTDIK
26.9	1670.9355	0.1476	KPVQLPGAYKTDIK
20.5	1669.7837	1.2994	SGITMTAGLMLGMNK
19.4	1671.8679	-0.7847	QIQTLEIELESQK
19.2	1671.8072	-0.7241	KLPHACESTQMLK
18.8	1670.8951	0.1880	VQVNVGDLEKSKK
18.1	1671.9229	-0.8398	GDLISGIVVAVQMIK
17.9	1671.7787	-0.6955	EMSKATAYHNDHLR
17.8	1670.9315	0.1517	KLIDQIETSLRK
17.8	1671.8436	-0.7604	HNAMATAIAAKAMDIK

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

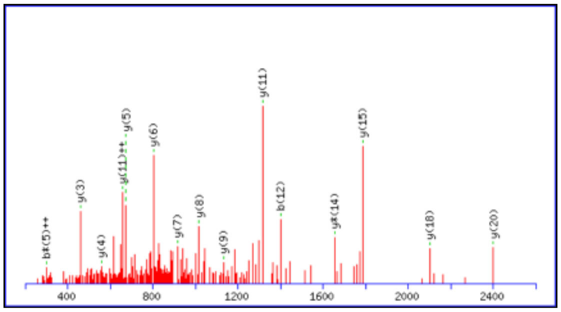
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLTGKTITLEVEPSDTIENVKAK**
Found in **YD_RFP-BARD-BRCA-Ub**, YD_RFP-BARD-BRCA-Ub

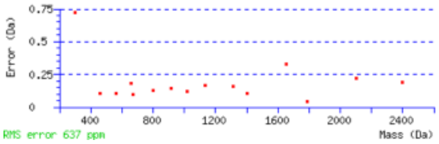
Match to Query 854: 2715.194172 from(906.072000,3+) intensity(386680.0000)
Title: Cmpd 92, +MSn(906.44), 25.9 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00812_YD_4_merge.mgf

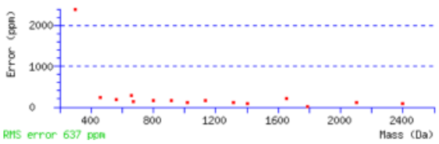
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2714.4338
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5 : GlyGly (K)
K23 : GlyGly (K)
Ions Score: 71 **Expect:** 2.1e-05
Matches : 15/246 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	102.0550	51.5311			84.0444	42.5258	T							23
2	215.1390	108.0731			197.1285	99.0679	L	2614.3934	1307.7003	2597.3669	1299.1871	2596.3828	1298.6951	22
3	316.1867	158.5970			298.1761	149.5917	T	2501.3093	1251.1583	2484.2828	1242.6450	2483.2988	1242.1530	21
4	373.2082	187.1077			355.1976	178.1024	G	***2400.2617***	1200.6345	2383.2351	1192.1212	2382.2511	1191.6292	20
5	615.3461	308.1767	598.3195	299.6634	597.3355	299.1714	K	2343.2402	1172.1237	2326.2136	1163.6105	2325.2296	1163.1185	19
6	716.3937	358.7005	699.3672	350.1872	698.3832	349.6952	T	***2101.1023***	1051.0548	2084.0758	1042.5415	2083.0917	1042.0495	18
7	829.4778	415.2425	812.4512	406.7293	811.4672	406.2373	I	2000.0546	1000.5310	1983.0281	992.0177	1982.0441	991.5257	17
8	930.5255	465.7664	913.4989	457.2531	912.5149	456.7611	T	1886.9706	943.9889	1869.9440	935.4756	1868.9600	934.9836	16
9	1043.6095	522.3084	1026.5830	513.7951	1025.5990	513.3031	L	***1785.9229***	893.4651	1768.8963	884.9518	1767.9123	884.4598	15
10	1172.6521	586.8297	1155.6256	578.3164	1154.6416	577.8244	E	1672.8388	836.9230	1655.8123	828.4098	1654.8283	827.9178	14
11	1271.7205	636.3639	1254.6940	627.8506	1253.7100	627.3586	V	1543.7962	772.4018	1526.7697	763.8885	1525.7857	763.3965	13
12	1400.7631	700.8852	1383.7366	692.3719	1382.7526	691.8799	E	1444.7278	722.8675	1427.7013	714.3543	1426.7172	713.8623	12
13	1497.8159	749.4116	1480.7894	740.8983	1479.8053	740.4063	P	***1315.6852***	658.3462	1298.6587	649.8330	1297.6747	649.3410	11
14	1584.8479	792.9276	1567.8214	784.4143	1566.8374	783.9223	S	1218.6325	609.8199	1201.6059	601.3066	1200.6219	600.8146	10
15	1699.8749	850.4411	1682.8483	841.9278	1681.8643	841.4358	D	***1131.6004***	566.3039	1114.5739	557.7906	1113.5899	557.2986	9
16	1800.9226	900.9649	1783.8960	892.4516	1782.9120	891.9596	T	***1016.5735***	508.7904	999.5469	500.2771	998.5629	499.7851	8
17	1914.0066	957.5069	1896.9801	948.9937	1895.9961	948.5017	I	***915.5258***	458.2665	898.4993	449.7533	897.5152	449.2613	7
18	2043.0492	1022.0282	2026.0227	1013.5150	2025.0386	1013.0230	E	***802.4417***	401.7245	785.4152	393.2112	784.4312	392.7192	6
19	2157.0921	1079.0497	2140.0656	1070.5364	2139.0816	1070.0444	N	***673.3991***	337.2032	656.3726	328.6899			5
20	2256.1605	1128.5839	2239.1340	1120.0706	2238.1500	1119.5786	V	***559.3562***	280.1817	542.3297	271.6685			4
21	2384.2555	1192.6314	2367.2290	1184.1181	2366.2449	1183.6261	K	***460.2878***	230.6475	443.2613	222.1343			3
22	2455.2926	1228.1500	2438.2661	1219.6367	2437.2821	1219.1447	A	332.1928	166.6001	315.1663	158.0868			2
23							K	261.1557	131.0815	244.1292	122.5682			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.7	2714.4338	0.7604	TLTGKTITLEVEPSDTIENVKAK
70.7	2714.4338	0.7604	TLTGKTITLEVEPSDTIENVKAK
19.9	2714.2494	0.9448	AQSETGEVKGHYLNATGGTVEEMYK
15.9	2714.4175	0.7767	KVYNIPGISPDMMKLIIEYAYTR
15.8	2715.1314	0.0628	MDEADPGEAEAAQAEAAQDGAAQDGAAR
14.3	2713.3303	1.8639	EANMLNIPVVAMIDTNANPDVVDVK
13.9	2716.3012	-1.1070	NSTEQSGVNVNGNVLAASNVNNSSVK
12.8	2714.3302	0.8640	IKVCEMLLHECELQSQKLGR
11.8	2715.2666	-0.0724	SMGPDGLKEVTENAVLNANYMMRK
11.4	2713.2912	1.9030	AANGINSSGQQNSSTRFMMQLTLK

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

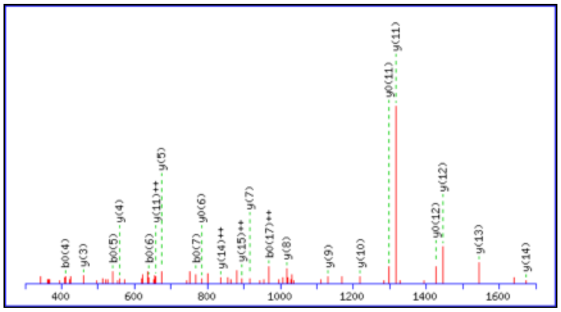
MATRIX SCIENCE Mascot Search Results

Peptide View

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

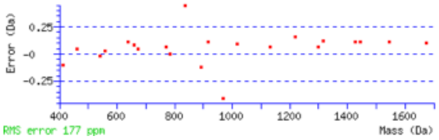
Match to Query 710: 2100.347448 from(1051.181000,2+) intensity(303915.0000)
Title: Cmpd 86, +MSn(1051.60), 26.4 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00812_YD_4_merge.mgf

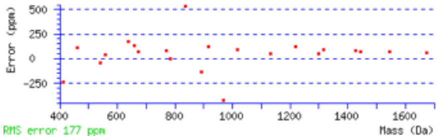
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2100.0950
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K16 : GlyGly (K)
Ions Score: 48 **Expect:** 0.0056
Matches : 22/168 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							18
2	215.1390	108.0731			197.1285	99.0679	I	2000.0546	1000.5310	1983.0281	992.0177	1982.0441	991.5257	17
3	316.1867	158.5970			298.1761	149.5917	T	1886.9706	943.9889	1869.9440	935.4756	1868.9600	934.9836	16
4	429.2708	215.1390			411.2602	206.1337	L	1785.9229	893.4651	1768.8963	884.9518	1767.9123	884.4598	15
5	558.3134	279.6603			540.3028	270.6550	E	***1672.8388***	836.9230	1655.8123	828.4098	1654.8283	827.9178	14
6	657.3818	329.1945			639.3712	320.1892	V	***1543.7962***	772.4018	1526.7697	763.8885	1525.7857	763.3965	13
7	786.4244	393.7158			768.4138	384.7105	E	***1444.7278***	722.8675	1427.7013	714.3543	1426.7172	713.8623	12
8	883.4771	442.2422			865.4666	433.2369	P	***1315.6852***	658.3462	1298.6587	649.8330	1297.6747	649.3410	11
9	970.5092	485.7582			952.4986	476.7529	S	***1218.6325***	609.8199	1201.6059	601.3066	1200.6219	600.8146	10
10	1085.5361	543.2717			1067.5255	534.2664	D	***1131.6004***	566.3039	1114.5739	557.7906	1113.5899	557.2986	9
11	1186.5838	593.7955			1168.5732	584.7902	T	***1016.5735***	508.7904	999.5469	500.2771	998.5629	499.7851	8
12	1299.6678	650.3376			1281.6573	641.3323	I	***915.5258***	458.2665	898.4993	449.7533	897.5152	449.2613	7
13	1428.7104	714.8589			1410.6999	705.8536	E	802.4417	401.7245	785.4152	393.2112	784.4312	392.7192	6
14	1542.7534	771.8803	1525.7268	763.3670	1524.7428	762.8750	N	***673.3991***	337.2032	656.3726	328.6899			5
15	1641.8218	821.4145	1624.7952	812.9013	1623.8112	812.4092	V	***559.3562***	280.1817	542.3297	271.6685			4
16	1883.9597	942.4835	1866.9331	933.9702	1865.9491	933.4782	K	***460.2878***	230.6475	443.2613	222.1343			3
17	1954.9968	978.0020	1937.9702	969.4888	1936.9862	968.9967	A	218.1499	109.5786	201.1234	101.0653			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.9	2100.0950	0.2524	TITLEVEPSDTIENVKAK
47.9	2100.0950	0.2524	TITLEVEPSDTIENVKAK
22.7	2098.9993	1.3481	AQKVDEAIYAFNVMEK
14.4	2100.9505	-0.6031	EVMDKFAMHIPFVCMSK
11.8	2099.0464	1.3010	SLMMLENAAKYLPNLMTK
10.7	2100.0811	0.2664	NVGSSLVEEDKLDLAKR
10.7	2100.1547	0.1927	EVISILMQRQVMVDGKVR
10.6	2099.0323	1.3151	KEDAIFYTYSILGSNHK
10.3	2101.1241	-0.7767	QPTDSEMKALLAQWKIVK
9.7	2100.0851	0.2623	QNFSVNNVDITVIVEAPK

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

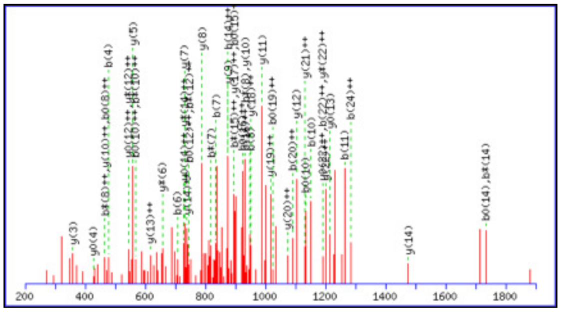
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLLHDNELSDLKEDGGSGGDLSALR**
Found in **YD_RFP-BARD-BRCA-Ub**, YD_RFP-BARD-BRCA-Ub

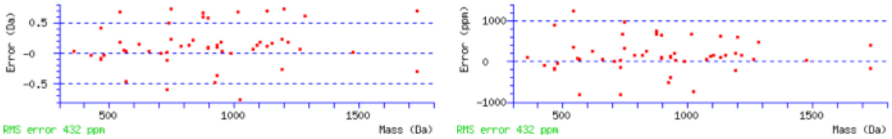
Match to Query 856: 2738.741172 from(913.921000,3+) intensity(3406834.0000)
Title: Cmpd 118, +MSn(914.46), 27.8 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00812_YD_4_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2738.3107
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K12 : GlyGly (K)
Ions Score: 50 **Expect:** 0.0024
Matches : 53/274 fragment ions using 86 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							25
2	228.1343	114.5708	211.1077	106.0575			L	2625.2751	1313.1412	2608.2485	1304.6279	2607.2645	1304.1359	24
3	341.2183	171.1128	324.1918	162.5995			L	2512.1910	1256.5991	2495.1645	1248.0859	2494.1804	1247.5939	23
4	**478.2772**	239.6423	461.2507	231.1290			H	2399.1069	1200.0571	2382.0804	1191.5438	2381.0964	1191.0518	22
5	593.3042	297.1557	576.2776	288.6425	575.2936	288.1504	D	2262.0480	1131.5277	2245.0215	1123.0144	2244.0375	1122.5224	21
6	**707.3471**	354.1772	690.3206	345.6639	689.3365	345.1719	N	2147.0211	1074.0142	2129.9945	1065.5009	2129.0105	1065.0089	20
7	**836.3897**	418.6985	819.3632	410.1852	818.3791	409.6932	E	2032.9782	1016.9927	2015.9516	1008.4794	2014.9676	1007.9874	19
8	**949.4738**	475.2405	932.4472	466.7272	931.4632	466.2352	L	1903.9356	952.4714	1886.9090	943.9582	1885.9250	943.4661	18
9	1036.5058	518.7565	1019.4792	510.2433	1018.4952	509.7513	S	1790.8515	895.9294	1773.8250	887.4161	1772.8409	886.9241	17
10	**1151.5327**	576.2700	1134.5062	567.7567	1133.5222	567.2647	D	1703.8195	852.4134	1686.7929	843.9001	1685.8089	843.4081	16
11	**1264.6168**	632.8120	1247.5903	624.2988	1246.6062	623.8068	L	1588.7925	794.8999	1571.7660	786.3866	1570.7820	785.8946	15
12	1506.7547	753.8810	1489.7281	745.3677	1488.7441	744.8757	K	***1475.7085***	738.3579	1458.6819	729.8446	1457.6979	729.3526	14
13	1635.7973	818.4023	1618.7707	809.8890	1617.7867	809.3970	E	1233.5706	617.2889	1216.5440	608.7757	1215.5600	608.2836	13
14	1750.8242	**875.9158**	1733.7977	867.4025	1732.8137	866.9105	D	***1104.5280***	552.7676	1087.5014	544.2544	1086.5174	543.7624	12
15	1807.8457	904.4265	1790.8191	895.9132	1789.8351	895.4212	G	***989.5010***	495.2542	972.4745	486.7409	971.4905	486.2489	11
16	1864.8672	**932.9372**	1847.8406	924.4239	1846.8566	923.9319	G	***932.4796***	466.7434	915.4530	458.2302	914.4690	457.7381	10
17	1951.8992	976.4532	1934.8726	967.9400	1933.8886	967.4479	S	***875.4581***	438.2327	858.4316	429.7194	857.4476	429.2274	9
18	2008.9207	1004.9640	1991.8941	996.4507	1990.9101	995.9587	G	***788.4261***	394.7167	771.3995	386.2034	770.4155	385.7114	8
19	2065.9421	1033.4747	2048.9156	1024.9614	2047.9315	1024.4694	G	***731.4046***	366.2060	714.3781	357.6927	713.3941	357.2007	7
20	2180.9691	**1090.9882**	2163.9425	1082.4749	2162.9585	1081.9829	D	674.3832	337.6952	657.3566	329.1819	656.3726	328.6899	6
21	2294.0531	1147.5302	2277.0266	1139.0169	2276.0426	1138.5249	L	***559.3562***	280.1817	542.3297	271.6685	541.3457	271.1765	5
22	2381.0851	**1191.0462**	2364.0586	1182.5329	2363.0746	1182.0409	S	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
23	2452.1223	1226.5648	2435.0957	1218.0515	2434.1117	1217.5595	A	***359.2401***	180.1237	342.2136	171.6104			3
24	2565.2063	**1283.1068**	2548.1798	1274.5935	2547.1958	1274.1015	L	288.2030	144.6051	271.1765	136.0919			2
25							R	175.1190	88.0631	158.0924	79.5498			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.7	2738.3107	0.4305	NLLHDNELSDLKEDGGSGGDLSALR
20.9	2737.3996	1.3415	ERLESLVNFSTVMAFIKGTPEEPK
17.4	2739.3109	-0.5697	WSAAKVVIYVGCGERGNEMTDELR
16.3	2738.3116	0.4296	NVCIQTDRETFLKPCDAESKATR
15.2	2739.4555	-0.7143	KPVELKKDSLEAGEVGWLSASIR
15.2	2739.4555	-0.7143	KPVELKKDSLEAGEVGWLSASIR
15.2	2738.4603	0.2809	IVEIYGPESSGKTTLALHAIAQAQK
14.5	2739.3109	-0.5697	AKDTSMTWVVKMNQTENLPFR
14.2	2738.4683	0.2728	IQLQERLGISLQQGDAILGMPMRR

14.2	2739.3915	-0.6503	LVHPSNGNLIWFMDKQAGSKLDR

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

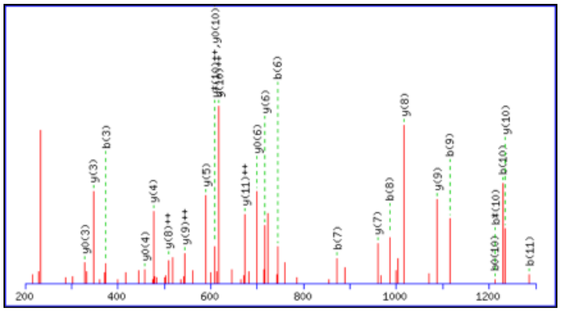
Mascot Search Results

Peptide View

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

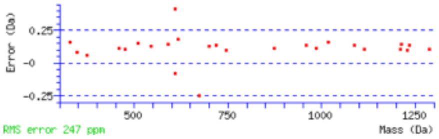
Match to Query 467: 1459.933448 from(730.974000,2+) intensity(2962866.0000)
Title: Cmpd 64, +MSn(731.37), 24.4 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00812_YD_4_merge.mgf

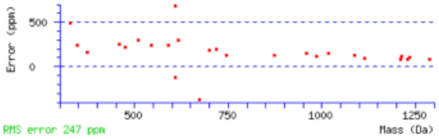
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): `1459.7783`
Fixed modifications: `Carbamidomethyl (C) (apply to specified residues or termini only)`
Variable modifications:
K6 `: GlyGly (K)`
Ions Score: `72` **Expect:** `8.6e-05`
Matches : `26/102 fragment ions using 32 most intense peaks` (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	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
71.6	1459.7783	0.1551	LIFAGKQLEDGR
27.3	1459.6725	0.2609	EAAALQCQLEDGR
23.7	1459.8068	0.1267	ILQEKMEKAIK
22.7	1460.7544	-0.8210	NIIEMQQLELSK
21.6	1459.7307	0.2028	ALENALPYLEDGR
21.3	1459.6903	0.2432	DEEKKEEVQGR
20.2	1459.8293	0.1042	LTRMIRTAGALK
19.9	1459.8610	0.0725	TKTKLSVIESIK
19.9	1459.8610	0.0725	TKTKLSVLESIK
19.9	1459.7718	0.1616	IIGGGMPVGAFGGRR

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

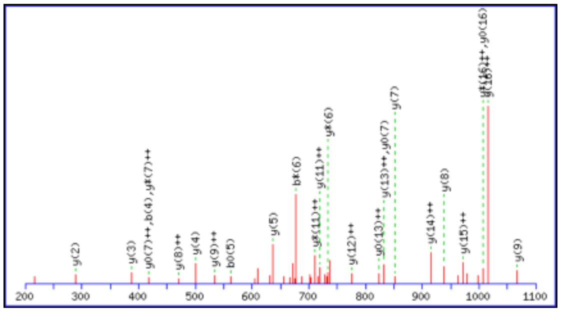
MATRIX SCIENCE Mascot Search Results

Peptide View

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

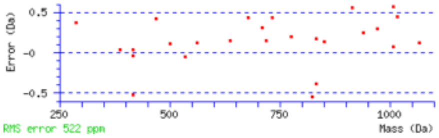
Match to Query 801: 2243.516172 from(748.846000,3+) intensity(584427.0000)
Title: Cmpd 100, +MSn(749.29), 27.4 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00812_YD_4_merge.mgf

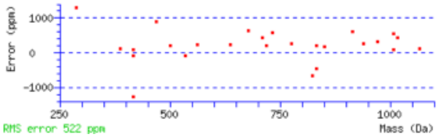
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2243.1910
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K9 : GlyGly (K)
Ions Score: 72 **Expect:** 7.5e-05
Matches : 26/182 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	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
72.0	2243.1910	0.3252	TLSDYNIQKESTLHLVLR
27.1	2243.0713	0.4449	ESMQARGGPDGGNGGKGGDVIIR
21.4	2244.1718	-0.6557	TNQMPNAVQKLLLVMDKR
21.4	2244.1718	-0.6557	TNQMPNAVQKLLLVMDKR
20.1	2243.2056	0.3106	QSSNAVAKPSKMAATKVANVK
18.8	2243.2381	0.2781	ELLSVRELKPILMDGMVIR
18.3	2243.1506	0.3656	TKTNNSGGLQGGISNGEELVIR
17.6	2241.3395	2.1767	LAAKGVKVKPGMVIGYIVLR
17.6	2241.3395	2.1767	LAAKGVKVKPGMVIGYIVLR
17.6	2241.3395	2.1767	LAAKGVKVKPGMVIGYIVLR

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

Mascot Search Results

Protein View

```
Match to: YD_RFP-BARD-BRCA-Ub Score: 5566
YD_RFP-BARD-BRCA-Ub
Found in search of C:\YaelDavid\100203_YaelDavid\BIT00814_YD_5_merge.mgf

Nominal mass (Mr): 60628; Calculated pI value: 6.10
NCBI BLAST search of YD_RFP-BARD-BRCA-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 57%

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 EPDGRGAWAH
   251 SRAALDRLEK LLRCSRCTNI LREPVCLGGC EHIFCSNCVS DCIGTGCPVC
   301 YTPAWIQDLK INRQLDSMIQ LCSKLRNLLH DNELSDLKED GGSGGDLSAL
   351 RVEEVQNVIN AMQKILECPI CLELIKEPVS TKCDHIFCKF CMLKLLNQKK
   401 GPSQCPLCKN DITKRSLQES TRFSQLVEEL LKIICAFQLD TGLEYANSYN
   451 FAKQIFVKTL TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK
   501 QLEDGRTLSD YNIQKESTLH LVLRLRGG
```

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     1013.6210  3037.8412  3037.3359    0.5052     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 83)
   24 - 51     1013.8410  3038.5012  3037.3359    1.1652     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 58)
   24 - 51     1013.8790  3038.6152  3037.3359    1.2792     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 71)
   24 - 51     1018.8660  3053.5762  3053.3309    0.2453     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 70)
   24 - 51     1019.1600  3054.4582  3053.3309    1.1273     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 29)
   24 - 51     1019.2330  3054.6772  3053.3309    1.3463     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 92)
   24 - 51     1019.2370  3054.6892  3053.3309    1.3583     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 49)
   57 - 76     1104.5420  2207.0694  2207.1051   -0.0357     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 63)
   57 - 76     1104.6370  2207.2594  2207.1051    0.1543     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 69)
   57 - 76      736.7670  2207.2792  2207.1051    0.1740     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 65)
   57 - 76     1104.6580  2207.3014  2207.1051    0.1963     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 80)
   57 - 76     1104.6660  2207.3174  2207.1051    0.2123     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 80)
   57 - 76      736.8410  2207.5012  2207.1051    0.3960     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 30)
   57 - 76     1105.3080  2208.6014  2207.1051    1.4963     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 37)
   81 - 90      584.3760  1166.7374  1167.5924   -0.8550     0  K.HPADIPDYLK.L  (Ions score 36)
   91 - 98      462.8230   923.6314   923.4753    0.1562     0  K.LSFPEGFK.W  (Ions score 39)
   91 - 98      462.8290   923.6434   923.4753    0.1682     0  K.LSFPEGFK.W  (Ions score 42)
   91 - 98      462.8370   923.6594   923.4753    0.1842     0  K.LSFPEGFK.W  (Ions score 22)
   91 - 98      462.8390   923.6634   923.4753    0.1882     0  K.LSFPEGFK.W  (Ions score 41)
   91 - 98      462.8660   923.7174   923.4753    0.2422     0  K.LSFPEGFK.W  (Ions score 43)
  102 - 127    1439.8540  2877.6934  2877.3379    0.3556     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 91)
  102 - 127    1440.2540  2878.4934  2877.3379    1.1556     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 89)
  102 - 127    1440.2640  2878.5134  2877.3379    1.1756     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 87)
  102 - 127     960.5530  2878.6372  2877.3379    1.2993     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 92)
  102 - 127     960.5920  2878.7542  2877.3379    1.4163     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 75)
  102 - 127     960.6250  2878.8532  2877.3379    1.5153     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 109)
  102 - 127     960.6790  2879.0152  2877.3379    1.6773     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 92)
  102 - 127     960.6790  2879.0152  2877.3379    1.6773     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 58)
  102 - 127    1447.8140  2893.6134  2893.3328    0.2806     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 115)
  102 - 127     965.5780  2893.7122  2893.3328    0.3794     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 72)
  102 - 127     965.6590  2893.9552  2893.3328    0.6224     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 97)
  102 - 127     965.6650  2893.9732  2893.3328    0.6404     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 67)
  102 - 127    1448.2150  2894.4154  2893.3328    1.0826     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 94)
  102 - 127    1448.2640  2894.5134  2893.3328    1.1806     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 95)
  102 - 127    1448.2850  2894.5554  2893.3328    1.2226     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 104)
  102 - 127     965.9040  2894.6902  2893.3328    1.3574     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 88)
  102 - 127     965.9630  2894.8672  2893.3328    1.5344     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 72)
  132 - 144     688.9150  1375.8154  1376.6395   -0.8240     0  R.GTNFPSDGPVMQK.K  (Ions score 54)
  132 - 144     689.4260  1376.8374  1376.6395    0.1980     0  R.GTNFPSDGPVMQK.K  (Ions score 74)
  132 - 144     689.4630  1376.9114  1376.6395    0.2720     0  R.GTNFPSDGPVMQK.K  (Ions score 74)
  132 - 144     689.4700  1376.9254  1376.6395    0.2860     0  R.GTNFPSDGPVMQK.K  (Ions score 73)
  132 - 144     689.4770  1376.9394  1376.6395    0.3000     0  R.GTNFPSDGPVMQK.K  (Ions score 77)
  132 - 144     697.3670  1392.7194  1392.6344    0.0851     0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 58)
  132 - 144     697.4240  1392.8334  1392.6344    0.1991     0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 85)
  132 - 144     697.4320  1392.8494  1392.6344    0.2151     0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 61)
  132 - 144     697.4320  1392.8494  1392.6344    0.2151     0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 77)
  132 - 144     697.4450  1392.8754  1392.6344    0.2411     0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 82)
  145 - 155     648.3660  1294.7174  1294.5976    0.1199     1  K.KTMGWEASTER.M  (Ions score 62)
  145 - 155     648.3850  1294.7554  1294.5976    0.1579     1  K.KTMGWEASTER.M  (Ions score 77)
  146 - 155     584.3420  1166.6694  1166.5026    0.1668     0  K.TMGWEASTER.M  (Ions score 52)
  146 - 155     584.3490  1166.6834  1166.5026    0.1808     0  K.TMGWEASTER.M  (Ions score 48)
  146 - 155     584.3620  1166.7094  1166.5026    0.2068     0  K.TMGWEASTER.M  (Ions score 48)
  146 - 155     592.2960  1182.5774  1182.4975    0.0799     0  K.TMGWEASTER.M  Oxidation (M) (Ions score 61)
  146 - 155     592.3020  1182.5894  1182.4975    0.0919     0  K.TMGWEASTER.M  Oxidation (M) (Ions score 57)
  146 - 155     592.3090  1182.6034  1182.4975    0.1059     0  K.TMGWEASTER.M  Oxidation (M) (Ions score 57)
  146 - 155     592.3260  1182.6374  1182.4975    0.1399     0  K.TMGWEASTER.M  Oxidation (M) (Ions score 57)
  191 - 200     367.5900  1099.7482  1099.6390    0.1092     0  K.KPVQLPGAYK.T  (Ions score 36)
  191 - 200     550.8820  1099.7494  1099.6390    0.1105     0  K.KPVQLPGAYK.T  (Ions score 52)
  191 - 200     367.5990  1099.7752  1099.6390    0.1362     0  K.KPVQLPGAYK.T  (Ions score 36)
  191 - 200     367.6010  1099.7812  1099.6390    0.1422     0  K.KPVQLPGAYK.T  (Ions score 50)
  191 - 200     550.9190  1099.8234  1099.6390    0.1845     0  K.KPVQLPGAYK.T  (Ions score 44)
  191 - 200     550.9290  1099.8434  1099.6390    0.2045     0  K.KPVQLPGAYK.T  (Ions score 52)
  191 - 200     550.9380  1099.8614  1099.6390    0.2225     0  K.KPVQLPGAYK.T  (Ions score 47)
  191 - 200     607.3280  1212.6414  1213.6819   -1.0404     0  K.KPVQLPGAYK.T  GlyGly (K) (Ions score 45)
  191 - 200     607.9090  1213.8034  1213.6819    0.1216     0  K.KPVQLPGAYK.T  GlyGly (K) (Ions score 46)
  191 - 200     608.3430  1214.6714  1213.6819    0.9896     0  K.KPVQLPGAYK.T  GlyGly (K) (Ions score 35)
  191 - 204     557.8280  1670.4622  1670.9355   -0.4734     1  K.KPVQLPGAYKTDIK.L  GlyGly (K) (Ions score 14)
  191 - 204     836.5960  1671.1774  1670.9355    0.2419     1  K.KPVQLPGAYKTDIK.L  GlyGly (K) (Ions score 29)
  205 - 222    1113.1420  2224.2694  2224.0284    0.2411     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 85)
  205 - 222    1113.1650  2224.3154  2224.0284    0.2871     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 107)
  205 - 222    1113.1870  2224.3594  2224.0284    0.3311     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 106)
  205 - 222     742.4820  2224.4242  2224.0284    0.3958     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 15)
  205 - 222    1113.2370  2224.4594  2224.0284    0.4311     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 66)
  205 - 222     742.5450  2224.6132  2224.0284    0.5848     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 52)
  205 - 222     742.5460  2224.6162  2224.0284    0.5878     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 57)
  205 - 222     742.5470  2224.6192  2224.0284    0.5908     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 55)
  205 - 222     742.6070  2224.7992  2224.0284    0.7708     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 11)
  205 - 222     742.6270  2224.8592  2224.0284    0.8308     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 16)
  205 - 222     742.7830  2225.3272  2224.0284    1.2988     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 60)
  205 - 222     742.8030  2225.3872  2224.0284    1.3588     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 15)
  205 - 222     742.8200  2225.4382  2224.0284    1.4098     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 36)
  205 - 222     742.8440  2225.5102  2224.0284    1.4818     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 51)
  227 - 245    1060.6310  2119.2474  2118.9606    0.2868     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 123)
  227 - 245    1060.6570  2119.2994  2118.9606    0.3388     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 135)
  227 - 245    1060.7030  2119.3914  2118.9606    0.4308     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 131)
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227 - 245   1061.0710  2120.1274  2118.9606     1.1668     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 138)
314 - 324    661.9400  1321.8654  1321.6370     0.2285     0  R.QLDSMIQLCSK.L  (Ions score 62)
314 - 324    661.9770  1321.9394  1321.6370     0.3025     0  R.QLDSMIQLCSK.L  (Ions score 56)
314 - 324    662.0310  1322.0474  1321.6370     0.4105     0  R.QLDSMIQLCSK.L  (Ions score 59)
327 - 338    705.9540  1409.8934  1409.7150     0.1784     0  R.NLLHDNELSDLK.E  (Ions score 69)
327 - 338    706.0020  1409.9894  1409.7150     0.2744     0  R.NLLHDNELSDLK.E  (Ions score 54)
327 - 338    706.0100  1410.0054  1409.7150     0.2904     0  R.NLLHDNELSDLK.E  (Ions score 54)
327 - 338    706.0140  1410.0134  1409.7150     0.2984     0  R.NLLHDNELSDLK.E  (Ions score 67)
327 - 351   1313.2350  2624.4554  2624.2678     0.1877     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 118)
327 - 351   1313.2770  2624.5394  2624.2678     0.2717     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 108)
327 - 351   1313.7150  2625.4154  2624.2678     1.1477     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 140)
327 - 351   1313.7170  2625.4194  2624.2678     1.1517     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 105)
327 - 351    914.2000  2739.5782  2738.3107     1.2675     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  GlyGly (K)  (Ions score 104)
339 - 351    617.3450  1232.6754  1232.5633     0.1121     0  K.EDGGSGGDLSALR.V  (Ions score 84)
339 - 351    617.3730  1232.7314  1232.5633     0.1681     0  K.EDGGSGGDLSALR.V  (Ions score 84)
339 - 351    617.3770  1232.7394  1232.5633     0.1761     0  K.EDGGSGGDLSALR.V  (Ions score 84)
339 - 351    617.4140  1232.8134  1232.5633     0.2501     0  K.EDGGSGGDLSALR.V  (Ions score 84)
339 - 351    617.8960  1233.7774  1232.5633     1.2141     0  K.EDGGSGGDLSALR.V  (Ions score 13)
352 - 364    751.0600  1500.1054  1500.7606    -0.6552     0  R.VEEVQNVINAMQK.I  (Ions score 45)
352 - 364    751.5160  1501.0174  1500.7606     0.2568     0  R.VEEVQNVINAMQK.I  (Ions score 103)
352 - 364    751.5210  1501.0274  1500.7606     0.2668     0  R.VEEVQNVINAMQK.I  (Ions score 109)
352 - 364    751.5390  1501.0634  1500.7606     0.3028     0  R.VEEVQNVINAMQK.I  (Ions score 70)
352 - 364    751.5400  1501.0654  1500.7606     0.3048     0  R.VEEVQNVINAMQK.I  (Ions score 44)
352 - 364    751.5520  1501.0894  1500.7606     0.3288     0  R.VEEVQNVINAMQK.I  (Ions score 96)
352 - 364    751.5870  1501.1594  1500.7606     0.3988     0  R.VEEVQNVINAMQK.I  (Ions score 53)
352 - 364    751.6200  1501.2254  1500.7606     0.4648     0  R.VEEVQNVINAMQK.I  (Ions score 107)
352 - 364    752.0340  1502.0534  1500.7606     1.2928     0  R.VEEVQNVINAMQK.I  (Ions score 61)
352 - 364    752.0820  1502.1494  1500.7606     1.3888     0  R.VEEVQNVINAMQK.I  (Ions score 42)
352 - 364    759.4670  1516.9194  1516.7555     0.1639     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 102)
352 - 364    759.4780  1516.9414  1516.7555     0.1859     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 98)
352 - 364    759.4800  1516.9454  1516.7555     0.1899     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 69)
352 - 364    759.5240  1517.0334  1516.7555     0.2779     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 102)
352 - 364    759.5530  1517.0914  1516.7555     0.3359     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 102)
352 - 364    759.8860  1517.7574  1516.7555     1.0019     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 46)
352 - 364    760.0190  1518.0234  1516.7555     1.2679     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 22)
352 - 364    760.0210  1518.0274  1516.7555     1.2719     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 49)
365 - 376    751.0760  1500.1374  1499.8091     0.3283     0  K.ILECPICLELIK.E  (Ions score 60)
365 - 376    751.0900  1500.1654  1499.8091     0.3563     0  K.ILECPICLELIK.E  (Ions score 64)
365 - 376    751.1170  1500.2194  1499.8091     0.4103     0  K.ILECPICLELIK.E  (Ions score 62)
365 - 376    751.1410  1500.2674  1499.8091     0.4583     0  K.ILECPICLELIK.E  (Ions score 79)
423 - 432    603.4010  1204.7874  1204.6703     0.1171     0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432    603.4690  1204.9234  1204.6703     0.2531     0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    603.4750  1204.9354  1204.6703     0.2651     0  R.FSQLVEELLK.I  (Ions score 68)
423 - 432    603.4950  1204.9754  1204.6703     0.3051     0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    603.4960  1204.9774  1204.6703     0.3071     0  R.FSQLVEELLK.I  (Ions score 72)
423 - 432    603.4990  1204.9834  1204.6703     0.3131     0  R.FSQLVEELLK.I  (Ions score 82)
423 - 432    603.5000  1204.9854  1204.6703     0.3151     0  R.FSQLVEELLK.I  (Ions score 81)
423 - 432    603.5070  1204.9994  1204.6703     0.3291     0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432    603.5220  1205.0294  1204.6703     0.3591     0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432    603.5300  1205.0454  1204.6703     0.3751     0  R.FSQLVEELLK.I  (Ions score 72)
423 - 432    603.5420  1205.0694  1204.6703     0.3991     0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    603.5590  1205.1034  1204.6703     0.4331     0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    603.5630  1205.1114  1204.6703     0.4411     0  R.FSQLVEELLK.I  (Ions score 81)
423 - 432    603.6280  1205.2414  1204.6703     0.5711     0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    604.0690  1206.1234  1204.6703     1.4531     0  R.FSQLVEELLK.I  (Ions score 85)
423 - 432    604.1040  1206.1934  1204.6703     1.5231     0  R.FSQLVEELLK.I  (Ions score 75)
459 - 479   1201.7290  2401.4434  2401.2588     0.1847     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 98)
459 - 479   1201.7520  2401.4894  2401.2588     0.2307     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 100)
459 - 479    801.5310  2401.5712  2401.2588     0.3124     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 88)
459 - 479    801.5570  2401.6492  2401.2588     0.3904     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 97)
459 - 479   1202.1900  2402.3654  2401.2588     1.1067     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 79)
464 - 479    894.1050  1786.1954  1786.9200    -0.7246     0  K.TITLEVEPSDTIENVK.A  (Ions score 66)
464 - 479    894.5310  1787.0474  1786.9200     0.1274     0  K.TITLEVEPSDTIENVK.A  (Ions score 86)
464 - 479    894.5390  1787.0634  1786.9200     0.1434     0  K.TITLEVEPSDTIENVK.A  (Ions score 61)
464 - 479    894.5550  1787.0954  1786.9200     0.1754     0  K.TITLEVEPSDTIENVK.A  (Ions score 61)
464 - 479    894.5680  1787.1214  1786.9200     0.2014     0  K.TITLEVEPSDTIENVK.A  (Ions score 77)
464 - 479    894.5680  1787.1214  1786.9200     0.2014     0  K.TITLEVEPSDTIENVK.A  (Ions score 85)
464 - 479    894.5690  1787.1234  1786.9200     0.2034     0  K.TITLEVEPSDTIENVK.A  (Ions score 56)
464 - 479    894.5720  1787.1294  1786.9200     0.2094     0  K.TITLEVEPSDTIENVK.A  (Ions score 82)
464 - 479    894.5780  1787.1414  1786.9200     0.2214     0  K.TITLEVEPSDTIENVK.A  (Ions score 70)
464 - 479    894.5850  1787.1554  1786.9200     0.2354     0  K.TITLEVEPSDTIENVK.A  (Ions score 83)
464 - 479    894.5850  1787.1554  1786.9200     0.2354     0  K.TITLEVEPSDTIENVK.A  (Ions score 58)
464 - 479    894.5990  1787.1834  1786.9200     0.2634     0  K.TITLEVEPSDTIENVK.A  (Ions score 64)
464 - 479    894.6010  1787.1874  1786.9200     0.2674     0  K.TITLEVEPSDTIENVK.A  (Ions score 73)
464 - 479    894.6120  1787.2094  1786.9200     0.2894     0  K.TITLEVEPSDTIENVK.A  (Ions score 73)
464 - 479    894.6140  1787.2134  1786.9200     0.2934     0  K.TITLEVEPSDTIENVK.A  (Ions score 77)
464 - 479    894.6150  1787.2154  1786.9200     0.2954     0  K.TITLEVEPSDTIENVK.A  (Ions score 86)
464 - 479    894.6210  1787.2274  1786.9200     0.3074     0  K.TITLEVEPSDTIENVK.A  (Ions score 70)
464 - 479    894.6290  1787.2434  1786.9200     0.3234     0  K.TITLEVEPSDTIENVK.A  (Ions score 55)
464 - 479    894.6290  1787.2434  1786.9200     0.3234     0  K.TITLEVEPSDTIENVK.A  (Ions score 88)
464 - 479    894.6300  1787.2454  1786.9200     0.3254     0  K.TITLEVEPSDTIENVK.A  (Ions score 77)
464 - 479    894.6310  1787.2474  1786.9200     0.3274     0  K.TITLEVEPSDTIENVK.A  (Ions score 69)
464 - 479    894.6370  1787.2594  1786.9200     0.3394     0  K.TITLEVEPSDTIENVK.A  (Ions score 73)
464 - 479    894.6430  1787.2714  1786.9200     0.3514     0  K.TITLEVEPSDTIENVK.A  (Ions score 86)
464 - 479    894.6440  1787.2734  1786.9200     0.3534     0  K.TITLEVEPSDTIENVK.A  (Ions score 48)
464 - 479    894.6450  1787.2754  1786.9200     0.3554     0  K.TITLEVEPSDTIENVK.A  (Ions score 73)
464 - 479    894.6480  1787.2814  1786.9200     0.3614     0  K.TITLEVEPSDTIENVK.A  (Ions score 80)
464 - 479    894.6560  1787.2974  1786.9200     0.3774     0  K.TITLEVEPSDTIENVK.A  (Ions score 85)
464 - 479    894.6650  1787.3154  1786.9200     0.3954     0  K.TITLEVEPSDTIENVK.A  (Ions score 68)
464 - 479    894.6700  1787.3254  1786.9200     0.4054     0  K.TITLEVEPSDTIENVK.A  (Ions score 77)
464 - 479    894.6940  1787.3734  1786.9200     0.4534     0  K.TITLEVEPSDTIENVK.A  (Ions score 85)
464 - 479    894.7400  1787.4654  1786.9200     0.5454     0  K.TITLEVEPSDTIENVK.A  (Ions score 82)
464 - 479    895.1370  1788.2594  1786.9200     1.3394     0  K.TITLEVEPSDTIENVK.A  (Ions score 63)
464 - 479    895.1400  1788.2654  1786.9200     1.3454     0  K.TITLEVEPSDTIENVK.A  (Ions score 45)
464 - 481   1051.1380  2100.2614  2100.0950     0.1664     1  K.TITLEVEPSDTIENVKAK.I  GlyGly (K)  (Ions score 28)
464 - 481    701.4820  2101.4242  2100.0950     1.3292     1  K.TITLEVEPSDTIENVKAK.I  GlyGly (K)  (Ions score 14)
482 - 494    761.9800  1521.9454  1522.7740    -0.8285     1  K.IQDKEGIPPDQQR.L  (Ions score 38)
482 - 494    761.9890  1521.9634  1522.7740    -0.8105     1  K.IQDKEGIPPDQQR.L  (Ions score 33)
482 - 494    762.4390  1522.8634  1522.7740     0.0895     1  K.IQDKEGIPPDQQR.L  (Ions score 55)
482 - 494    762.4420  1522.8694  1522.7740     0.0955     1  K.IQDKEGIPPDQQR.L  (Ions score 66)
482 - 494    762.4610  1522.9074  1522.7740     0.1335     1  K.IQDKEGIPPDQQR.L  (Ions score 48)
482 - 494    508.6490  1522.9252  1522.7740     0.1512     1  K.IQDKEGIPPDQQR.L  (Ions score 43)
482 - 494    762.5030  1522.9914  1522.7740     0.2175     1  K.IQDKEGIPPDQQR.L  (Ions score 52)
482 - 494    508.7010  1523.0812  1522.7740     0.3072     1  K.IQDKEGIPPDQQR.L  (Ions score 34)
486 - 494    520.2780  1038.5414  1038.5094     0.0320     0  K.EGIPPDQQR.L  (Ions score 32)
486 - 494    520.3070  1038.5994  1038.5094     0.0900     0  K.EGIPPDQQR.L  (Ions score 31)
486 - 494    520.3280  1038.6414  1038.5094     0.1320     0  K.EGIPPDQQR.L  (Ions score 27)
486 - 494    520.3280  1038.6414  1038.5094     0.1320     0  K.EGIPPDQQR.L  (Ions score 37)
486 - 494    520.3540  1038.6934  1038.5094     0.1840     0  K.EGIPPDQQR.L  (Ions score 30)
486 - 494    520.3560  1038.6974  1038.5094     0.1880     0  K.EGIPPDQQR.L  (Ions score 32)
486 - 494    520.3660  1038.7174  1038.5094     0.2080     0  K.EGIPPDQQR.L  (Ions score 33)
495 - 506    730.9730  1459.9314  1459.7783     0.1531     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 71)
495 - 506    730.9920  1459.9694  1459.7783     0.1911     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 71)
495 - 506    487.6650  1459.9732  1459.7783     0.1949     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 37)
495 - 506    731.0120  1460.0094  1459.7783     0.2311     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 69)
495 - 506    487.6950  1460.0632  1459.7783     0.2849     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 35)
495 - 506    487.6980  1460.0722  1459.7783     0.2939     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 36)
495 - 506    731.0550  1460.0954  1459.7783     0.3171     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 71)
495 - 506    731.0560  1460.0974  1459.7783     0.3191     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 30)
495 - 506    487.7780  1460.3122  1459.7783     0.5339     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 37)
507 - 515    541.3270  1080.6394  1080.5451     0.0943     0  R.TLSDYNIQK.E  (Ions score 33)
507 - 515    541.3470  1080.6794  1080.5451     0.1343     0  R.TLSDYNIQK.E  (Ions score 54)
507 - 515    541.3570  1080.6994  1080.5451     0.1543     0  R.TLSDYNIQK.E  (Ions score 60)
507 - 515    541.3610  1080.7074  1080.5451     0.1623     0  R.TLSDYNIQK.E  (Ions score 44)
507 - 515    541.3740  1080.7334  1080.5451     0.1883     0  R.TLSDYNIQK.E  (Ions score 43)
```

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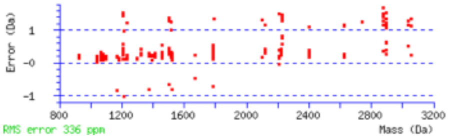
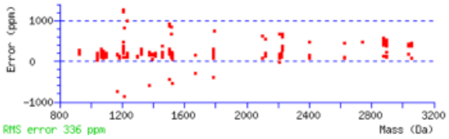
507 - 515     541.3760  1080.7374  1080.5451     0.1923     0  R.TLSDYNIQK.E   (Ions score 52)
507 - 515     541.3800  1080.7454  1080.5451     0.2003     0  R.TLSDYNIQK.E   (Ions score 26)
507 - 515     541.3840  1080.7534  1080.5451     0.2083     0  R.TLSDYNIQK.E   (Ions score 51)
507 - 515     541.4000  1080.7854  1080.5451     0.2403     0  R.TLSDYNIQK.E   (Ions score 41)
507 - 515     541.4150  1080.8154  1080.5451     0.2703     0  R.TLSDYNIQK.E   (Ions score 29)
516 - 524     534.3630  1066.7114  1066.6135     0.0980     0  K.ESTLHLVLR.L   (Ions score 54)
516 - 524     534.3830  1066.7514  1066.6135     0.1380     0  K.ESTLHLVLR.L   (Ions score 39)
516 - 524     534.3960  1066.7774  1066.6135     0.1640     0  K.ESTLHLVLR.L   (Ions score 48)
516 - 524     534.4040  1066.7934  1066.6135     0.1800     0  K.ESTLHLVLR.L   (Ions score 61)
516 - 524     534.4180  1066.8214  1066.6135     0.2080     0  K.ESTLHLVLR.L   (Ions score 61)
516 - 524     534.4280  1066.8414  1066.6135     0.2280     0  K.ESTLHLVLR.L   (Ions score 65)
516 - 524     534.4580  1066.9014  1066.6135     0.2880     0  K.ESTLHLVLR.L   (Ions score 41)
516 - 524     534.4780  1066.9414  1066.6135     0.3280     0  K.ESTLHLVLR.L   (Ions score 41)
```





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

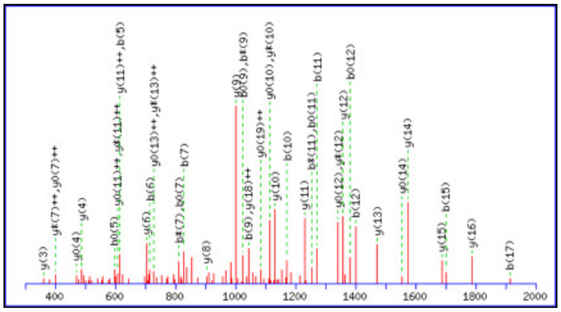
MATRIX SCIENCE Mascot Search Results

Peptide View

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

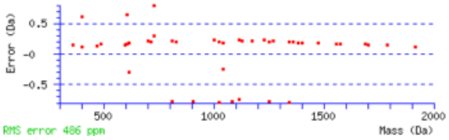
Match to Query 840: 2401.489448 from(1201.752000,2+) intensity(3469580.0000)
Title: Cmpd 130, +MSn(1202.36), 27.2 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00814_YD_5_merge.mgf

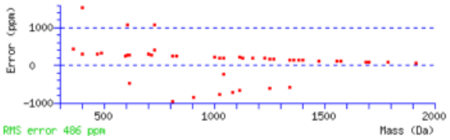
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2401.2588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5 : GlyGly (K)
Ions Score: 100 **Expect:** 1.7e-07
Matches : 44/226 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	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
100.3	2401.2588	0.2307	TLTGKTITLEVEPSDTIENVK
27.0	2401.2887	0.2008	LVSVASTGTPAMVDANNGLVTKLK
25.3	2401.1188	0.3706	RCEKEIIGVSNSAQICYSCK
23.8	2401.1253	0.3641	DMEIAELKKNIEQMDTDHK
22.3	2402.2289	-0.7394	TEEVSKLQSEVQDTKQALQK
22.3	2402.2289	-0.7394	TEEVSKLQSEVQDTKQALQK
21.7	2402.2839	-0.7944	LKTTGLTVDQVMAARVLESEK
21.4	2402.2442	-0.7547	TVIGTPFVEGATVEATVEKQGR
21.4	2399.3094	2.1801	KVMDVGGLISDDIIIGLVKER
20.8	2399.2923	2.1972	SYAYKTTLIIVPMSLLTQWR

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

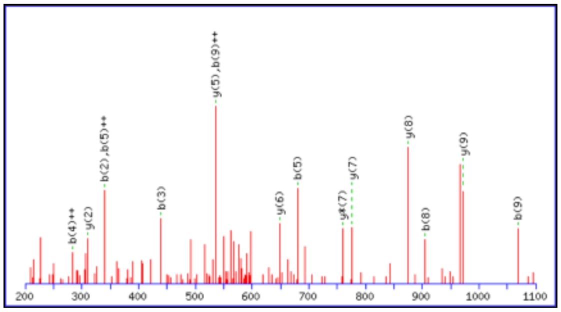
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVQLPGAYK**
Found in **YD_RFP-BARD-BRCA-Ub**, YD_RFP-BARD-BRCA-Ub

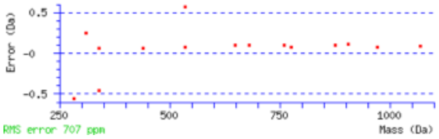
Match to Query 306: 1213.803448 from(607.909000,2+) intensity(405146.0000)
Title: Cmpd 17, +MSn(608.47), 19.1 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00814_YD_5_merge.mgf

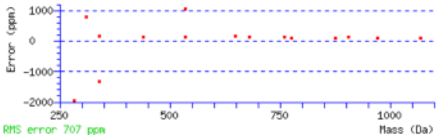
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1213.6819
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : GlyGly (K)
Ions Score: 46 **Expect:** 0.21
Matches : 15/72 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	243.1452	122.0762	226.1186	113.5629	K					10
2	***340.1979***	170.6026	323.1714	162.0893	P	***972.5513***	486.7793	955.5247	478.2660	9
3	***439.2663***	220.1368	422.2398	211.6235	V	***875.4985***	438.2529	858.4720	429.7396	8
4	567.3249	**284.1661**	550.2984	275.6528	Q	***776.4301***	388.7187	759.4036	380.2054	7
5	***680.4090***	**340.7081**	663.3824	332.1949	L	***648.3715***	324.6894	631.3450	316.1761	6
6	777.4618	389.2345	760.4352	380.7212	P	***535.2875***	268.1474	518.2609	259.6341	5
7	834.4832	417.7452	817.4567	409.2320	G	438.2347	219.6210	421.2082	211.1077	4
8	***905.5203***	453.2638	888.4938	444.7505	A	381.2132	191.1103	364.1867	182.5970	3
9	***1068.5837***	**534.7955**	1051.5571	526.2822	Y	***310.1761***	155.5917	293.1496	147.0784	2
10					K	147.1128	74.0600	130.0863	65.5468	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.3	1213.6819	0.1216	KPVQLPGAYK
38.0	1213.7434	0.0600	LILVPFLNGTK
28.5	1213.5615	0.2419	NFDTGLQEYK
23.7	1213.7832	0.0203	ILLVAVSIKMK
23.7	1213.7394	0.0641	LIIVNNSSVKK
23.7	1213.6805	0.1229	LLLVELEEEK
21.0	1213.6091	0.1943	KEGIHPEYK
19.5	1213.5649	0.2386	AYGMAGLETSAK
18.8	1213.7394	0.0641	TLLEKIKQNK
18.2	1213.7645	0.0389	LLLSSINLLTK

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

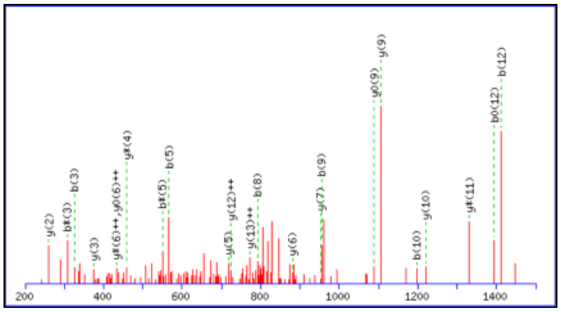
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVQLPGAYKTDIK**
Found in **YD_RFP-BARD-BRCA-Ub**, YD_RFP-BARD-BRCA-Ub

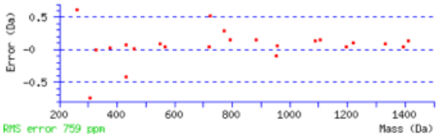
Match to Query 571: 1671.177448 from(836.596000,2+) intensity(1047068.0000)
Title: Cmpd 56, +MSn(836.98), 21.2 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00814_YD_5_merge.mgf

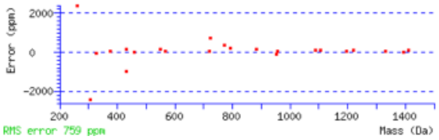
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1670.9355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K10 : GlyGly (K)
Ions Score: 29 **Expect:** 0.11
Matches : 23/132 fragment ions using 51 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.1022	65.0548	112.0757	56.5415			K							14
2	226.1550	113.5811	209.1285	105.0679			P	1543.8479	772.4276	1526.8213	763.9143	1525.8373	763.4223	13
3	***325.2234***	163.1153	308.1969	154.6021			V	1446.7951	723.9012	1429.7686	715.3879	1428.7845	714.8959	12
4	453.2820	227.1446	436.2554	218.6314			Q	1347.7267	674.3670	1330.7001	665.8537	1329.7161	665.3617	11
5	***566.3661***	283.6867	549.3395	275.1734			L	***1219.6681***	610.3377	1202.6416	601.8244	1201.6576	601.3324	10
6	663.4188	332.2130	646.3923	323.6998			P	***1106.5841***	553.7957	1089.5575	545.2824	1088.5735	544.7904	9
7	720.4403	360.7238	703.4137	352.2105			G	1009.5313	505.2693	992.5047	496.7560	991.5207	496.2640	8
8	***791.4774***	396.2423	774.4509	387.7291			A	***952.5098***	476.7585	935.4833	468.2453	934.4993	467.7533	7
9	***954.5407***	477.7740	937.5142	469.2607			Y	***881.4727***	441.2400	864.4462	432.7267	863.4621	432.2347	6
10	***1196.6786***	598.8429	1179.6521	590.3297			K	***718.4094***	359.7083	701.3828	351.1951	700.3988	350.7030	5
11	1297.7263	649.3668	1280.6998	640.8535	1279.7157	640.3615	T	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
12	***1412.7532***	706.8803	1395.7267	698.3670	1394.7427	697.8750	D	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	3
13	1525.8373	763.4223	1508.8108	754.9090	1507.8267	754.4170	I	***260.1969***	130.6021	243.1703	122.0888			2
14							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.0	1670.9355	0.2419	KPVQLPGAYKTDIK
18.1	1671.8176	-0.6402	QGNSVVKINGEDGNK
17.3	1670.8562	0.3212	GASFGRLASMKLDYR
17.3	1670.8199	0.3576	GASFGRLASMQLDYR
16.5	1671.9705	-0.7931	IKVLILMGATKNK
15.1	1670.9355	0.2419	KPVQLPGAYKTDIK
15.0	1671.8865	-0.7091	MLLKETIIPDGANK
12.3	1670.8773	0.3001	AHKEGLTLKQSAMK
12.1	1671.6691	-0.4916	EMFSHADGMTMSAK
11.6	1670.9567	0.2207	TSTVLGIVGAGGIGQTLK

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

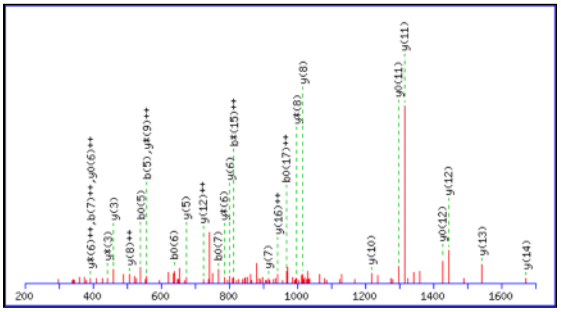
MATRIX SCIENCE Mascot Search Results

Peptide View

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

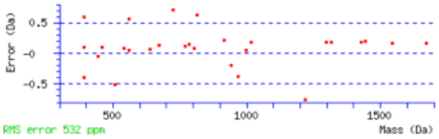
Match to Query 709: 2100.261448 from(1051.138000,2+) intensity(1215853.0000)
Title: Cmpd 115, +MSn(1051.56), 26.2 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00814_YD_5_merge.mgf

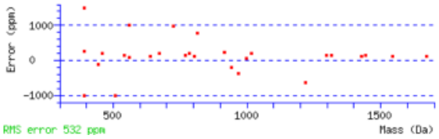
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2100.0950
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K16 : GlyGly (K)
Ions Score: 28 **Expect:** 0.68
Matches : 28/168 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	**T**							**18**
2	215.1390	108.0731			197.1285	99.0679	**I**	2000.0546	1000.5310	1983.0281	992.0177	1982.0441	991.5257	**17**
3	316.1867	158.5970			298.1761	149.5917	**T**	1886.9706	943.9889	1869.9440	935.4756	1868.9600	934.9836	**16**
4	429.2708	215.1390			411.2602	206.1337	**L**	1785.9229	893.4651	1768.8963	884.9518	1767.9123	884.4598	**15**
5	558.3134	279.6603			540.3028	270.6550	**E**	***1672.8388***	836.9230	1655.8123	828.4098	1654.8283	827.9178	**14**
6	657.3818	329.1945			639.3712	320.1892	**V**	***1543.7962***	772.4018	1526.7697	763.8885	1525.7857	763.3965	**13**
7	786.4244	393.7158			768.4138	384.7105	**E**	***1444.7278***	722.8675	1427.7013	714.3543	1426.7172	713.8623	**12**
8	883.4771	442.2422			865.4666	433.2369	**P**	***1315.6852***	658.3462	1298.6587	649.8330	1297.6747	649.3410	**11**
9	970.5092	485.7582			952.4986	476.7529	**S**	***1218.6325***	609.8199	1201.6059	601.3066	1200.6219	600.8146	**10**
10	1085.5361	543.2717			1067.5255	534.2664	**D**	1131.6004	566.3039	1114.5739	557.7906	1113.5899	557.2986	**9**
11	1186.5838	593.7955			1168.5732	584.7902	**T**	***1016.5735***	508.7904	999.5469	500.2771	998.5629	499.7851	**8**
12	1299.6678	650.3376			1281.6573	641.3323	**I**	***915.5258***	458.2665	898.4993	449.7533	897.5152	449.2613	**7**
13	1428.7104	714.8589			1410.6999	705.8536	**E**	***802.4417***	401.7245	785.4152	393.2112	784.4312	392.7192	**6**
14	1542.7534	771.8803	1525.7268	763.3670	1524.7428	762.8750	**N**	***673.3991***	337.2032	656.3726	328.6899			**5**
15	1641.8218	821.4145	1624.7952	812.9013	1623.8112	812.4092	**V**	559.3562	280.1817	542.3297	271.6685			**4**
16	1883.9597	942.4835	1866.9331	933.9702	1865.9491	933.4782	**K**	***460.2878***	230.6475	443.2613	222.1343			**3**
17	1954.9968	978.0020	1937.9702	969.4888	1936.9862	968.9967	**A**	218.1499	109.5786	201.1234	101.0653			**2**
18							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.8	2100.0950	0.1664	TITLEVEPSDTIENVKAK
27.8	2100.0950	0.1664	TITLEVEPSDTIENVKAK
18.9	2100.1435	0.1180	NMVVKIPMTVEGLKAVK
16.0	2100.1136	0.1478	LDILMAEVEDIELSAGRVK
13.3	2098.0782	2.1832	QHGMNSEVFVIFHLAKK
13.3	2098.0782	2.1832	QHGMNSEVFVIFHLAKK
13.1	2099.0464	1.2150	SLMMLENAAKYLPNLMTK
13.1	2099.0464	1.2150	SLMMLENAAKYLPNLMTK
13.0	2099.0494	1.2120	EAQVKVAEVEGEKVDNK
12.7	2101.1241	-0.8627	EIKMGEVANFTIPVVLEGR

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

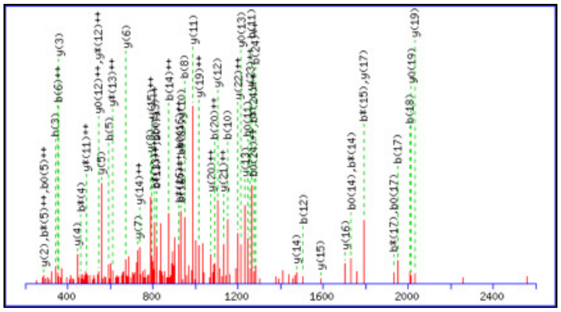
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLLHDNELSDLKEDGGSGGDLSALR**
Found in **YD_RFP-BARD-BRCA-Ub**, YD_RFP-BARD-BRCA-Ub

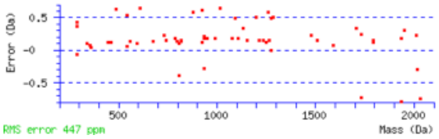
Match to Query 864: 2739.578172 from(914.200000,3+) intensity(3627246.0000)
Title: Cmpd 144, +MSn(914.42), 28.6 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00814_YD_5_merge.mgf

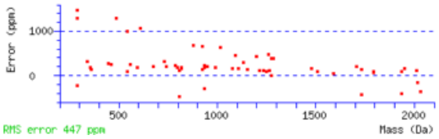
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2738.3107
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K12     : GlyGly (K)
Ions Score: 104  Expect: 7.4e-09
Matches : 60/274 fragment ions using 75 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							25
2	228.1343	114.5708	211.1077	106.0575			L	2625.2751	1313.1412	2608.2485	1304.6279	2607.2645	1304.1359	24
3	**341.2183**	171.1128	324.1918	162.5995			L	2512.1910	1256.5991	2495.1645	1248.0859	2494.1804	1247.5939	23
4	478.2772	239.6423	461.2507	231.1290			H	2399.1069	1200.0571	2382.0804	1191.5438	2381.0964	1191.0518	22
5	**593.3042**	297.1557	576.2776	288.6425	575.2936	288.1504	D	2262.0480	1131.5277	2245.0215	1123.0144	2244.0375	1122.5224	21
6	707.3471	**354.1772**	690.3206	345.6639	689.3365	345.1719	N	2147.0211	1074.0142	2129.9945	1065.5009	2129.0105	1065.0089	20
7	836.3897	418.6985	819.3632	410.1852	818.3791	409.6932	E	***2032.9782***	1016.9927	2015.9516	1008.4794	2014.9676	1007.9874	19
8	**949.4738**	475.2405	932.4472	466.7272	931.4632	466.2352	L	1903.9356	952.4714	1886.9090	943.9582	1885.9250	943.4661	18
9	1036.5058	518.7565	1019.4792	510.2433	1018.4952	509.7513	S	***1790.8515***	895.9294	1773.8250	887.4161	1772.8409	886.9241	17
10	**1151.5327**	576.2700	1134.5062	567.7567	1133.5222	567.2647	D	***1703.8195***	852.4134	1686.7929	843.9001	1685.8089	843.4081	16
11	**1264.6168**	632.8120	1247.5903	624.2988	1246.6062	623.8068	L	***1588.7925***	794.8999	1571.7660	786.3866	1570.7820	785.8946	15
12	**1506.7547**	753.8810	1489.7281	745.3677	1488.7441	744.8757	K	***1475.7085***	738.3579	1458.6819	729.8446	1457.6979	729.3526	14
13	1635.7973	**818.4023**	1618.7707	809.8890	1617.7867	809.3970	E	***1233.5706***	617.2889	1216.5440	608.7757	1215.5600	608.2836	13
14	1750.8242	**875.9158**	1733.7977	867.4025	1732.8137	866.9105	D	***1104.5280***	552.7676	1087.5014	544.2544	1086.5174	543.7624	12
15	1807.8457	904.4265	1790.8191	895.9132	1789.8351	895.4212	G	***989.5010***	495.2542	972.4745	486.7409	971.4905	486.2489	11
16	1864.8672	**932.9372**	1847.8406	924.4239	1846.8566	923.9319	G	***932.4796***	466.7434	915.4530	458.2302	914.4690	457.7381	10
17	**1951.8992**	976.4532	1934.8726	967.9400	1933.8886	967.4479	S	875.4581	438.2327	858.4316	429.7194	857.4476	429.2274	9
18	**2008.9207**	1004.9640	1991.8941	996.4507	1990.9101	995.9587	G	***788.4261***	394.7167	771.3995	386.2034	770.4155	385.7114	8
19	2065.9421	1033.4747	2048.9156	1024.9614	2047.9315	1024.4694	G	***731.4046***	366.2060	714.3781	357.6927	713.3941	357.2007	7
20	2180.9691	**1090.9882**	2163.9425	1082.4749	2162.9585	1081.9829	D	***674.3832***	337.6952	657.3566	329.1819	656.3726	328.6899	6
21	2294.0531	1147.5302	2277.0266	1139.0169	2276.0426	1138.5249	L	***559.3562***	280.1817	542.3297	271.6685	541.3457	271.1765	5
22	2381.0851	1191.0462	2364.0586	1182.5329	2363.0746	1182.0409	S	***446.2722***	223.6397	429.2456	215.1264	428.2616	214.6344	4
23	2452.1223	1226.5648	2435.0957	1218.0515	2434.1117	1217.5595	A	***359.2401***	180.1237	342.2136	171.6104			3
24	2565.2063	**1283.1068**	2548.1798	1274.5935	2547.1958	1274.1015	L	***288.2030***	144.6051	271.1765	136.0919			2
25							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
104.1	2738.3107	1.2675	NLLHDNELSDLKEDGGSGGDLSALR
16.8	2739.3571	0.2211	IAAVLDCKTSKAAEVMAAGEGYIK
14.6	2739.3062	0.2720	FGGQVLDTMAIENFISVQETEGPK
14.6	2740.3124	-0.7343	SSLASSHSSQDQSKHTSPRSSISSPR
14.4	2738.2599	1.3182	NKNTEGSMASNILVMDVEGTDGRER
14.3	2739.2156	0.3626	YKGLGEMDPEQLWETTMDPETR
14.1	2739.3533	0.2249	LGFSEVEQVQMVVDGVKLMVEMEK
13.9	2739.3459	0.2323	NNCIGLMYNALVIDSDESSSLIIAK
13.0	2738.3446	1.2336	YERGSPNMTIVKVQPDSPPPSPGR

12.9	2738.5113	1.0669	IKVTINTAKPGMVIGRQGAGVEELK

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

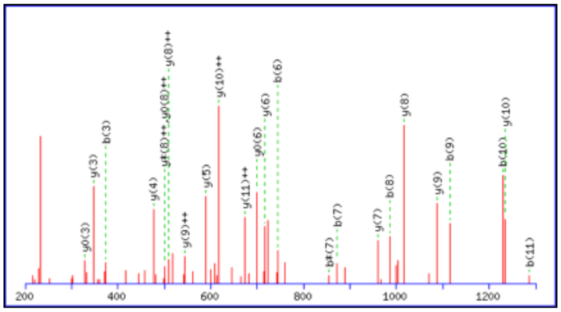
MATRIX SCIENCE Mascot Search Results

Peptide View

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

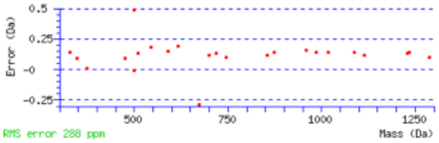
Match to Query 462: 1460.095448 from(731.055000,2+) intensity(5995554.0000)
Title: Cmpd 91, +MSn(731.30), 24.8 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00814_YD_5_merge.mgf

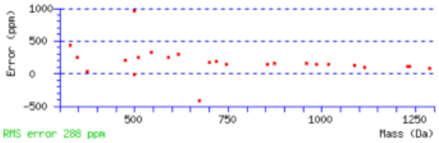
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1459.7783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : GlyGly (K)
Ions Score: 71 **Expect:** 8.9e-05
Matches : 24/102 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	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
71.2	1459.7783	0.3171	LIFAGKQLEDGR
27.1	1460.7544	-0.6590	NIIEMQQLELSK
25.2	1460.7471	-0.6516	TNTNNTINIESIK
25.2	1459.6725	0.4229	EAAALQCQLEDGR
21.9	1459.8610	0.2345	TKTKLSVIESIK
21.9	1459.8610	0.2345	TKTKLSVLESIK
21.3	1459.8293	0.2662	LTRMIRTAGALK
21.2	1459.7307	0.3648	ALENALPYLEDGR
18.9	1459.8432	0.2522	SGMVTLKLEKIK
18.7	1460.7908	-0.6954	TVEMLKAEGIIK

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

Mascot Search Results

Protein View

Match to: **YD_RFP-BARD-BRCA-Ub** Score: **5647**
YD_RFP-BARD-BRCA-Ub
Found in search of C:\YaelDavid\100203_YaelDavid\BIT00816_YD_6_merge.mgf

Nominal mass (M_r): **60628**; Calculated pI value: **6.10**
NCBI BLAST search of YD_RFP-BARD-BRCA-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **57%**

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 EPDGRGAWAH
251 SRAALDRLEK LLRCSRCTNI LREPVCLGGC EHIFCSNCVS DCIGTGCPVC
301 YTPAWIQDLK INRQLDSMIQ LCSKLRNLLH DNELSDLKED GGSGGDLSAL
351 RVEEVQNVIN AMQKILECPI CLELIKEPVS TKCDHIFCKF CMLKLLNQKK
401 GPSQCPLCKN DITKRSLQES TRFSQLVEEL LKIICAFQLD TGLEYANSYN
451 FAKQIFVKTL TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK
501 QLEDGRTLSD YNIQKESTLH LVLRLRGG
```

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     1519.7040  3037.3934  3037.3359   0.0575   0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 50)
   24 - 51     1013.6840  3038.0302  3037.3359   0.6942   0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 71)
   24 - 51     1520.0900  3038.1654  3037.3359   0.8295   0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 52)
   24 - 51     1013.8960  3038.6662  3037.3359   1.3302   0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 91)
   24 - 51     1013.9090  3038.7052  3037.3359   1.3692   0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 59)
   24 - 51     1013.9110  3038.7112  3037.3359   1.3752   0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 81)
   24 - 51     1013.9830  3038.9272  3037.3359   1.5912   0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 76)
   24 - 51      764.6290  3054.4869  3053.3309   1.1560   0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 39)
   24 - 51     1019.1830  3054.5272  3053.3309   1.1963   0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 94)
   24 - 51     1019.2000  3054.5782  3053.3309   1.2473   0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 87)
   24 - 51     1019.2220  3054.6442  3053.3309   1.3133   0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 81)
   24 - 51     1019.2320  3054.6742  3053.3309   1.3433   0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 81)
   57 - 76     1104.1800  2206.3454  2207.1051  -0.7597   0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 85)
   57 - 76     1104.2150  2206.4154  2207.1051  -0.6897   0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 33)
   57 - 76     1104.6740  2207.3334  2207.1051   0.2283   0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 73)
   57 - 76     1104.6740  2207.3334  2207.1051   0.2283   0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 69)
   57 - 76     1104.6840  2207.3534  2207.1051   0.2483   0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 76)
   57 - 76      736.7950  2207.3632  2207.1051   0.2580   0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 47)
   57 - 76      736.8000  2207.3782  2207.1051   0.2730   0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 59)
   57 - 76     1104.7190  2207.4234  2207.1051   0.3183   0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 90)
   57 - 76     1105.1810  2208.3474  2207.1051   1.2423   0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 71)
   57 - 76      737.4590  2209.3552  2207.1051   2.2500   0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 35)
   91 - 98      462.7820   923.5494   923.4753   0.0742   0  K.LSFPEGFK.W  (Ions score 39)
   91 - 98      462.8360   923.6574   923.4753   0.1822   0  K.LSFPEGFK.W  (Ions score 37)
   91 - 98      462.8390   923.6634   923.4753   0.1882   0  K.LSFPEGFK.W  (Ions score 36)
   91 - 98      462.8460   923.6774   923.4753   0.2022   0  K.LSFPEGFK.W  (Ions score 37)
   91 - 98      462.9140   923.8134   923.4753   0.3382   0  K.LSFPEGFK.W  (Ions score 42)
  102 - 127     959.8470  2876.5192  2877.3379  -0.8187   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 54)
  102 - 127     960.1720  2877.4942  2877.3379   0.1563   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 105)
  102 - 127     960.3290  2877.9652  2877.3379   0.6273   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 114)
  102 - 127    1440.2700  2878.5254  2877.3379   1.1876   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 91)
  102 - 127    1440.2810  2878.5474  2877.3379   1.2096   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 113)
  102 - 127    1440.2880  2878.5614  2877.3379   1.2236   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 86)
  102 - 127    1440.2900  2878.5654  2877.3379   1.2276   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 82)
  102 - 127     960.6500  2878.9282  2877.3379   1.5903   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 116)
  102 - 127     960.6650  2878.9732  2877.3379   1.6353   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 118)
  102 - 127     960.9100  2879.7082  2877.3379   2.3703   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 81)
  102 - 127    1447.7710  2893.5274  2893.3328   0.1946   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 112)
  102 - 127    1448.2290  2894.4434  2893.3328   1.1106   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 97)
  102 - 127    1448.2540  2894.4934  2893.3328   1.1606   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 102)
  102 - 127    1448.2670  2894.5194  2893.3328   1.1866   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 95)
  102 - 127     965.8860  2894.6362  2893.3328   1.3034   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 91)
  102 - 127     965.8890  2894.6452  2893.3328   1.3124   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 91)
  102 - 127     965.9450  2894.8132  2893.3328   1.4804   0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 84)
  132 - 144     688.6790  1375.3434  1376.6395  -1.2960   0  R.GTNFPSDGPVMQK.K  (Ions score 66)
  132 - 144     689.4060  1376.7974  1376.6395   0.1580   0  R.GTNFPSDGPVMQK.K  (Ions score 48)
  132 - 144     689.4260  1376.8374  1376.6395   0.1980   0  R.GTNFPSDGPVMQK.K  (Ions score 74)
  132 - 144     689.4560  1376.8974  1376.6395   0.2580   0  R.GTNFPSDGPVMQK.K  (Ions score 78)
  132 - 144     689.4570  1376.8994  1376.6395   0.2600   0  R.GTNFPSDGPVMQK.K  (Ions score 71)
  132 - 144     689.4620  1376.9094  1376.6395   0.2700   0  R.GTNFPSDGPVMQK.K  (Ions score 74)
  132 - 144     689.4750  1376.9354  1376.6395   0.2960   0  R.GTNFPSDGPVMQK.K  (Ions score 74)
  132 - 144     697.4220  1392.8294  1392.6344   0.1951   0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 82)
  132 - 144     697.4240  1392.8334  1392.6344   0.1991   0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 74)
  132 - 144     697.4560  1392.8974  1392.6344   0.2631   0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 75)
  132 - 144     697.4850  1392.9554  1392.6344   0.3211   0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 75)
  145 - 155     647.8480  1293.6814  1294.5976  -0.9161   1  K.KTMGWEASTER.M  (Ions score 68)
  145 - 155     647.8970  1293.7794  1294.5976  -0.8181   1  K.KTMGWEASTER.M  (Ions score 62)
  145 - 155     648.3470  1294.6794  1294.5976   0.0819   1  K.KTMGWEASTER.M  (Ions score 72)
  145 - 155     648.3650  1294.7154  1294.5976   0.1179   1  K.KTMGWEASTER.M  (Ions score 69)
  146 - 155     584.3150  1166.6154  1166.5026   0.1128   0  K.TMGWEASTER.M  (Ions score 50)
  146 - 155     584.3450  1166.6754  1166.5026   0.1728   0  K.TMGWEASTER.M  (Ions score 49)
  146 - 155     584.3700  1166.7254  1166.5026   0.2228   0  K.TMGWEASTER.M  (Ions score 47)
  146 - 155     584.3840  1166.7534  1166.5026   0.2508   0  K.TMGWEASTER.M  (Ions score 51)
  146 - 155     592.0520  1182.0894  1182.4975  -0.4081   0  K.TMGWEASTER.M  Oxidation (M) (Ions score 54)
  146 - 155     592.2970  1182.5794  1182.4975   0.0819   0  K.TMGWEASTER.M  Oxidation (M) (Ions score 55)
  146 - 155     592.3090  1182.6034  1182.4975   0.1059   0  K.TMGWEASTER.M  Oxidation (M) (Ions score 62)
  146 - 155     592.3500  1182.6854  1182.4975   0.1879   0  K.TMGWEASTER.M  Oxidation (M) (Ions score 54)
  191 - 200     550.8690  1099.7234  1099.6390   0.0845   0  K.KPVQLPGAYK.T  (Ions score 61)
  191 - 200     550.8990  1099.7834  1099.6390   0.1445   0  K.KPVQLPGAYK.T  (Ions score 64)
  191 - 200     550.9710  1099.9274  1099.6390   0.2885   0  K.KPVQLPGAYK.T  (Ions score 64)
  191 - 200     550.9740  1099.9334  1099.6390   0.2945   0  K.KPVQLPGAYK.T  (Ions score 53)
  205 - 222    1113.1360  2224.2574  2224.0284   0.2291   0  K.LDITSHNEDYTIVEQYER.A  (Ions score 107)
  205 - 222    1113.1570  2224.2994  2224.0284   0.2711   0  K.LDITSHNEDYTIVEQYER.A  (Ions score 33)
  205 - 222    1113.1610  2224.3074  2224.0284   0.2791   0  K.LDITSHNEDYTIVEQYER.A  (Ions score 123)
  205 - 222    1113.1880  2224.3614  2224.0284   0.3331   0  K.LDITSHNEDYTIVEQYER.A  (Ions score 110)
  205 - 222    1113.1940  2224.3734  2224.0284   0.3451   0  K.LDITSHNEDYTIVEQYER.A  (Ions score 115)
  205 - 222     742.5400  2224.5982  2224.0284   0.5698   0  K.LDITSHNEDYTIVEQYER.A  (Ions score 59)
  205 - 222    1113.3550  2224.6954  2224.0284   0.6671   0  K.LDITSHNEDYTIVEQYER.A  (Ions score 46)
  205 - 222     742.6090  2224.8052  2224.0284   0.7768   0  K.LDITSHNEDYTIVEQYER.A  (Ions score 64)
  205 - 222    1113.6190  2225.2234  2224.0284   1.1951   0  K.LDITSHNEDYTIVEQYER.A  (Ions score 29)
  205 - 222     742.7610  2225.2612  2224.0284   1.2328   0  K.LDITSHNEDYTIVEQYER.A  (Ions score 65)
  205 - 222     742.7980  2225.3722  2224.0284   1.3438   0  K.LDITSHNEDYTIVEQYER.A  (Ions score 58)
  205 - 222     742.8040  2225.3902  2224.0284   1.3618   0  K.LDITSHNEDYTIVEQYER.A  (Ions score 44)
  205 - 222     743.0550  2226.1432  2224.0284   2.1148   0  K.LDITSHNEDYTIVEQYER.A  (Ions score 37)
  205 - 222    1114.1760  2226.3374  2224.0284   2.3091   0  K.LDITSHNEDYTIVEQYER.A  (Ions score 60)
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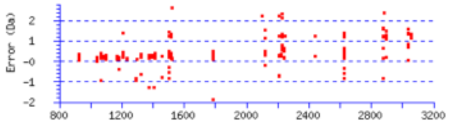
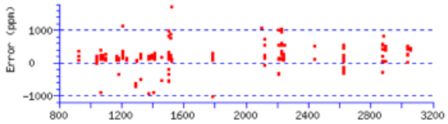
227 - 245   1060.3970  2118.7794  2118.9606   -0.1812     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 27)
227 - 245    707.4360  2119.2862  2118.9606    0.3255     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 39)
227 - 245   1060.7120  2119.4094  2118.9606    0.4488     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 120)
227 - 245   1060.7190  2119.4234  2118.9606    0.4628     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 136)
227 - 245   1060.7480  2119.4814  2118.9606    0.5208     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 113)
227 - 245   1061.0580  2120.1014  2118.9606    1.1408     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 115)
227 - 245    707.8480  2120.5222  2118.9606    1.5615     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 37)
314 - 324    661.5020  1320.9894  1321.6370   -0.6475     0  R.QLDSMIQLCSK.L  (Ions score 59)
314 - 324    661.9210  1321.8274  1321.6370    0.1905     0  R.QLDSMIQLCSK.L  (Ions score 64)
314 - 324    661.9860  1321.9574  1321.6370    0.3205     0  R.QLDSMIQLCSK.L  (Ions score 62)
314 - 324    662.0100  1322.0054  1321.6370    0.3685     0  R.QLDSMIQLCSK.L  (Ions score 69)
327 - 338    705.2180  1408.4214  1409.7150   -1.2936     0  R.NLLHDNELSDLK.E  (Ions score 43)
327 - 338    705.9510  1409.8874  1409.7150    0.1724     0  R.NLLHDNELSDLK.E  (Ions score 65)
327 - 338    705.9530  1409.8914  1409.7150    0.1764     0  R.NLLHDNELSDLK.E  (Ions score 72)
327 - 338    705.9650  1409.9154  1409.7150    0.2004     0  R.NLLHDNELSDLK.E  (Ions score 78)
327 - 338    706.0000  1409.9854  1409.7150    0.2704     0  R.NLLHDNELSDLK.E  (Ions score 64)
327 - 338    706.0220  1410.0294  1409.7150    0.3144     0  R.NLLHDNELSDLK.E  (Ions score 79)
327 - 338    471.0510  1410.1312  1409.7150    0.4161     0  R.NLLHDNELSDLK.E  (Ions score 41)
327 - 351    875.4770  2623.4092  2624.2678   -0.8586     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 63)
327 - 351    875.5740  2623.7002  2624.2678   -0.5676     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 80)
327 - 351    875.6430  2623.9072  2624.2678   -0.3606     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 77)
327 - 351    657.1150  2624.4309  2624.2678    0.1631     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 42)
327 - 351   1313.2240  2624.4334  2624.2678    0.1657     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 108)
327 - 351   1313.2470  2624.4794  2624.2678    0.2117     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 114)
327 - 351    875.8620  2624.5642  2624.2678    0.2964     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 81)
327 - 351   1313.3150  2624.6154  2624.2678    0.3477     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 120)
327 - 351    875.8970  2624.6692  2624.2678    0.4014     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 87)
327 - 351    875.9080  2624.7022  2624.2678    0.4344     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 92)
327 - 351    875.9180  2624.7322  2624.2678    0.4644     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 102)
327 - 351    875.9510  2624.8312  2624.2678    0.5634     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 96)
327 - 351    875.9580  2624.8522  2624.2678    0.5844     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 93)
327 - 351    875.9630  2624.8672  2624.2678    0.5994     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 70)
327 - 351    875.9770  2624.9092  2624.2678    0.6414     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 86)
327 - 351   1313.7300  2625.4454  2624.2678    1.1777     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 144)
327 - 351    876.1720  2625.4942  2624.2678    1.2264     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 114)
327 - 351    876.2210  2625.6412  2624.2678    1.3734     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 81)
327 - 351    876.2250  2625.6532  2624.2678    1.3854     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 101)
327 - 351    876.2300  2625.6682  2624.2678    1.4004     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 88)
339 - 351    617.3450  1232.6754  1232.5633    0.1121     0  K.EDGGSGGDLSALR.V  (Ions score 81)
339 - 351    617.3590  1232.7034  1232.5633    0.1401     0  K.EDGGSGGDLSALR.V  (Ions score 81)
339 - 351    617.3640  1232.7134  1232.5633    0.1501     0  K.EDGGSGGDLSALR.V  (Ions score 81)
339 - 351    617.3750  1232.7354  1232.5633    0.1721     0  K.EDGGSGGDLSALR.V  (Ions score 81)
352 - 364    750.9580  1499.9014  1500.7606   -0.8592     0  R.VEEVQNVINAMQK.I  (Ions score 65)
352 - 364    750.9770  1499.9394  1500.7606   -0.8212     0  R.VEEVQNVINAMQK.I  (Ions score 40)
352 - 364    751.1180  1500.2214  1500.7606   -0.5392     0  R.VEEVQNVINAMQK.I  (Ions score 56)
352 - 364    751.2400  1500.4654  1500.7606   -0.2952     0  R.VEEVQNVINAMQK.I  (Ions score 59)
352 - 364    751.4800  1500.9454  1500.7606    0.1848     0  R.VEEVQNVINAMQK.I  (Ions score 72)
352 - 364    751.5080  1501.0014  1500.7606    0.2408     0  R.VEEVQNVINAMQK.I  (Ions score 94)
352 - 364    751.5200  1501.0254  1500.7606    0.2648     0  R.VEEVQNVINAMQK.I  (Ions score 74)
352 - 364    751.5360  1501.0574  1500.7606    0.2968     0  R.VEEVQNVINAMQK.I  (Ions score 65)
352 - 364    751.5390  1501.0634  1500.7606    0.3028     0  R.VEEVQNVINAMQK.I  (Ions score 98)
352 - 364    751.5400  1501.0654  1500.7606    0.3048     0  R.VEEVQNVINAMQK.I  (Ions score 82)
352 - 364    751.5410  1501.0674  1500.7606    0.3068     0  R.VEEVQNVINAMQK.I  (Ions score 82)
352 - 364    751.5420  1501.0694  1500.7606    0.3088     0  R.VEEVQNVINAMQK.I  (Ions score 92)
352 - 364    751.5540  1501.0934  1500.7606    0.3328     0  R.VEEVQNVINAMQK.I  (Ions score 109)
352 - 364    751.5580  1501.1014  1500.7606    0.3408     0  R.VEEVQNVINAMQK.I  (Ions score 75)
352 - 364    751.5680  1501.1214  1500.7606    0.3608     0  R.VEEVQNVINAMQK.I  (Ions score 61)
352 - 364    751.5810  1501.1474  1500.7606    0.3868     0  R.VEEVQNVINAMQK.I  (Ions score 63)
352 - 364    751.5820  1501.1494  1500.7606    0.3888     0  R.VEEVQNVINAMQK.I  (Ions score 71)
352 - 364    751.6280  1501.2414  1500.7606    0.4808     0  R.VEEVQNVINAMQK.I  (Ions score 59)
352 - 364    752.0120  1502.0094  1500.7606    1.2488     0  R.VEEVQNVINAMQK.I  (Ions score 62)
352 - 364    752.1170  1502.2194  1500.7606    1.4588     0  R.VEEVQNVINAMQK.I  (Ions score 67)
352 - 364    759.4640  1516.9134  1516.7555    0.1579     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 112)
352 - 364    759.4670  1516.9194  1516.7555    0.1639     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 104)
352 - 364    759.5080  1517.0014  1516.7555    0.2459     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 104)
352 - 364    759.5260  1517.0374  1516.7555    0.2819     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 108)
352 - 364    759.5730  1517.1314  1516.7555    0.3759     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 84)
352 - 364    759.9750  1517.9354  1516.7555    1.1799     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 50)
352 - 364    760.0590  1518.1034  1516.7555    1.3479     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 41)
352 - 364    760.6870  1519.3594  1516.7555    2.6039     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 46)
365 - 376    751.0500  1500.0854  1499.8091    0.2763     0  K.ILECPICLELIK.E  (Ions score 77)
365 - 376    751.0860  1500.1574  1499.8091    0.3483     0  K.ILECPICLELIK.E  (Ions score 81)
365 - 376    751.1000  1500.1854  1499.8091    0.3763     0  K.ILECPICLELIK.E  (Ions score 81)
423 - 432    603.4350  1204.8554  1204.6703    0.1851     0  R.FSQLVEELLK.I  (Ions score 61)
423 - 432    603.4450  1204.8754  1204.6703    0.2051     0  R.FSQLVEELLK.I  (Ions score 80)
423 - 432    603.4590  1204.9034  1204.6703    0.2331     0  R.FSQLVEELLK.I  (Ions score 64)
423 - 432    603.4700  1204.9254  1204.6703    0.2551     0  R.FSQLVEELLK.I  (Ions score 85)
423 - 432    603.4830  1204.9514  1204.6703    0.2811     0  R.FSQLVEELLK.I  (Ions score 85)
423 - 432    603.4840  1204.9534  1204.6703    0.2831     0  R.FSQLVEELLK.I  (Ions score 76)
423 - 432    603.4880  1204.9614  1204.6703    0.2911     0  R.FSQLVEELLK.I  (Ions score 83)
423 - 432    603.4920  1204.9694  1204.6703    0.2991     0  R.FSQLVEELLK.I  (Ions score 88)
423 - 432    603.4950  1204.9754  1204.6703    0.3051     0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    603.4960  1204.9774  1204.6703    0.3071     0  R.FSQLVEELLK.I  (Ions score 82)
423 - 432    603.5070  1204.9994  1204.6703    0.3291     0  R.FSQLVEELLK.I  (Ions score 83)
423 - 432    603.5080  1205.0014  1204.6703    0.3311     0  R.FSQLVEELLK.I  (Ions score 72)
423 - 432    603.5130  1205.0114  1204.6703    0.3411     0  R.FSQLVEELLK.I  (Ions score 82)
423 - 432    603.5150  1205.0154  1204.6703    0.3451     0  R.FSQLVEELLK.I  (Ions score 65)
423 - 432    603.5170  1205.0194  1204.6703    0.3491     0  R.FSQLVEELLK.I  (Ions score 83)
423 - 432    603.5370  1205.0594  1204.6703    0.3891     0  R.FSQLVEELLK.I  (Ions score 88)
423 - 432    603.5520  1205.0894  1204.6703    0.4191     0  R.FSQLVEELLK.I  (Ions score 88)
423 - 432    603.5550  1205.0954  1204.6703    0.4251     0  R.FSQLVEELLK.I  (Ions score 72)
423 - 432    603.5620  1205.1094  1204.6703    0.4391     0  R.FSQLVEELLK.I  (Ions score 72)
423 - 432    604.0330  1206.0514  1204.6703    1.3811     0  R.FSQLVEELLK.I  (Ions score 78)
433 - 453   1219.7250  2437.4354  2437.1624    0.2731     0  K.IICAFQLDTGLEYANSYNFAK.Q  (Ions score 130)
433 - 453   1220.2050  2438.3954  2437.1624    1.2331     0  K.IICAFQLDTGLEYANSYNFAK.Q  (Ions score 115)
464 - 479    893.5370  1785.0594  1786.9200   -1.8606     0  K.TITLEVEPSDTIENVK.A  (Ions score 75)
464 - 479    894.5310  1787.0474  1786.9200    0.1274     0  K.TITLEVEPSDTIENVK.A  (Ions score 69)
464 - 479    894.5570  1787.0994  1786.9200    0.1794     0  K.TITLEVEPSDTIENVK.A  (Ions score 71)
464 - 479    894.5640  1787.1134  1786.9200    0.1934     0  K.TITLEVEPSDTIENVK.A  (Ions score 65)
464 - 479    894.5750  1787.1354  1786.9200    0.2154     0  K.TITLEVEPSDTIENVK.A  (Ions score 91)
464 - 479    894.5920  1787.1694  1786.9200    0.2494     0  K.TITLEVEPSDTIENVK.A  (Ions score 71)
464 - 479    894.5940  1787.1734  1786.9200    0.2534     0  K.TITLEVEPSDTIENVK.A  (Ions score 78)
464 - 479    894.5950  1787.1754  1786.9200    0.2554     0  K.TITLEVEPSDTIENVK.A  (Ions score 91)
464 - 479    894.5990  1787.1834  1786.9200    0.2634     0  K.TITLEVEPSDTIENVK.A  (Ions score 79)
464 - 479    894.6000  1787.1854  1786.9200    0.2654     0  K.TITLEVEPSDTIENVK.A  (Ions score 67)
464 - 479    894.6010  1787.1874  1786.9200    0.2674     0  K.TITLEVEPSDTIENVK.A  (Ions score 72)
464 - 479    894.6010  1787.1874  1786.9200    0.2674     0  K.TITLEVEPSDTIENVK.A  (Ions score 66)
464 - 479    894.6030  1787.1914  1786.9200    0.2714     0  K.TITLEVEPSDTIENVK.A  (Ions score 76)
464 - 479    894.6030  1787.1914  1786.9200    0.2714     0  K.TITLEVEPSDTIENVK.A  (Ions score 82)
464 - 479    894.6030  1787.1914  1786.9200    0.2714     0  K.TITLEVEPSDTIENVK.A  (Ions score 84)
464 - 479    894.6040  1787.1934  1786.9200    0.2734     0  K.TITLEVEPSDTIENVK.A  (Ions score 83)
464 - 479    894.6050  1787.1954  1786.9200    0.2754     0  K.TITLEVEPSDTIENVK.A  (Ions score 82)
464 - 479    894.6090  1787.2034  1786.9200    0.2834     0  K.TITLEVEPSDTIENVK.A  (Ions score 87)
464 - 479    894.6100  1787.2054  1786.9200    0.2854     0  K.TITLEVEPSDTIENVK.A  (Ions score 91)
464 - 479    894.6150  1787.2154  1786.9200    0.2954     0  K.TITLEVEPSDTIENVK.A  (Ions score 73)
464 - 479    894.6160  1787.2174  1786.9200    0.2974     0  K.TITLEVEPSDTIENVK.A  (Ions score 72)
464 - 479    894.6170  1787.2194  1786.9200    0.2994     0  K.TITLEVEPSDTIENVK.A  (Ions score 78)
464 - 479    894.6210  1787.2274  1786.9200    0.3074     0  K.TITLEVEPSDTIENVK.A  (Ions score 75)
464 - 479    894.6240  1787.2334  1786.9200    0.3134     0  K.TITLEVEPSDTIENVK.A  (Ions score 77)
464 - 479    894.6300  1787.2454  1786.9200    0.3254     0  K.TITLEVEPSDTIENVK.A  (Ions score 70)
464 - 479    894.6370  1787.2594  1786.9200    0.3394     0  K.TITLEVEPSDTIENVK.A  (Ions score 67)
464 - 479    894.6470  1787.2794  1786.9200    0.3594     0  K.TITLEVEPSDTIENVK.A  (Ions score 87)
464 - 479    894.6490  1787.2834  1786.9200    0.3634     0  K.TITLEVEPSDTIENVK.A  (Ions score 73)
464 - 479    894.6500  1787.2854  1786.9200    0.3654     0  K.TITLEVEPSDTIENVK.A  (Ions score 82)
464 - 479    894.6730  1787.3314  1786.9200    0.4114     0  K.TITLEVEPSDTIENVK.A  (Ions score 88)
```

```
464 - 479     894.6940  1787.3734  1786.9200     0.4534     0  K.TITLEVEPSDTIENVK.A   (Ions score 82)
464 - 479     894.7260  1787.4374  1786.9200     0.5174     0  K.TITLEVEPSDTIENVK.A   (Ions score 76)
464 - 481     701.7810  2102.3212  2100.0950     2.2262     1  K.TITLEVEPSDTIENVKAK.I  GlyGly (K)  (Ions score 44)
482 - 494     762.4400  1522.8654  1522.7740     0.0915     1  K.IQDKEGIPPDQQR.L  (Ions score 55)
482 - 494     762.4440  1522.8734  1522.7740     0.0995     1  K.IQDKEGIPPDQQR.L  (Ions score 62)
482 - 494     762.4540  1522.8934  1522.7740     0.1195     1  K.IQDKEGIPPDQQR.L  (Ions score 58)
482 - 494     762.4650  1522.9154  1522.7740     0.1415     1  K.IQDKEGIPPDQQR.L  (Ions score 63)
482 - 494     762.4730  1522.9314  1522.7740     0.1575     1  K.IQDKEGIPPDQQR.L  (Ions score 55)
482 - 494     762.4750  1522.9354  1522.7740     0.1615     1  K.IQDKEGIPPDQQR.L  (Ions score 48)
486 - 494     520.2600  1038.5054  1038.5094    -0.0040     0  K.EGIPPDQQR.L  (Ions score 31)
486 - 494     520.2890  1038.5634  1038.5094     0.0540     0  K.EGIPPDQQR.L  (Ions score 28)
486 - 494     520.3020  1038.5894  1038.5094     0.0800     0  K.EGIPPDQQR.L  (Ions score 30)
486 - 494     520.3150  1038.6154  1038.5094     0.1060     0  K.EGIPPDQQR.L  (Ions score 31)
486 - 494     520.3200  1038.6254  1038.5094     0.1160     0  K.EGIPPDQQR.L  (Ions score 29)
486 - 494     520.3580  1038.7014  1038.5094     0.1920     0  K.EGIPPDQQR.L  (Ions score 32)
486 - 494     520.3600  1038.7054  1038.5094     0.1960     0  K.EGIPPDQQR.L  (Ions score 30)
486 - 494     520.3650  1038.7154  1038.5094     0.2060     0  K.EGIPPDQQR.L  (Ions score 28)
495 - 506     487.3360  1458.9862  1459.7783    -0.7921     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 39)
495 - 506     487.6810  1460.0212  1459.7783     0.2429     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 42)
507 - 515     541.3500  1080.6854  1080.5451     0.1403     0  R.TLSDYNIQK.E  (Ions score 58)
507 - 515     541.3510  1080.6874  1080.5451     0.1423     0  R.TLSDYNIQK.E  (Ions score 63)
507 - 515     541.3560  1080.6974  1080.5451     0.1523     0  R.TLSDYNIQK.E  (Ions score 63)
507 - 515     541.3890  1080.7634  1080.5451     0.2183     0  R.TLSDYNIQK.E  (Ions score 63)
507 - 515     541.4070  1080.7994  1080.5451     0.2543     0  R.TLSDYNIQK.E  (Ions score 33)
507 - 524    1122.6910  2243.3674  2243.1910     0.1765     1  R.TLSDYNIQKESTLHLVLR.L  GlyGly (K)  (Ions score 101)
507 - 524    1122.7160  2243.4174  2243.1910     0.2265     1  R.TLSDYNIQKESTLHLVLR.L  GlyGly (K)  (Ions score 84)
507 - 524     748.8980  2243.6722  2243.1910     0.4812     1  R.TLSDYNIQKESTLHLVLR.L  GlyGly (K)  (Ions score 75)
507 - 524     748.9500  2243.8282  2243.1910     0.6372     1  R.TLSDYNIQKESTLHLVLR.L  GlyGly (K)  (Ions score 78)
507 - 524    1123.2170  2244.4194  2243.1910     1.2285     1  R.TLSDYNIQKESTLHLVLR.L  GlyGly (K)  (Ions score 101)
516 - 524     533.8360  1065.6574  1066.6135    -0.9560     0  K.ESTLHLVLR.L  (Ions score 64)
516 - 524     534.3830  1066.7514  1066.6135     0.1380     0  K.ESTLHLVLR.L  (Ions score 62)
516 - 524     534.3950  1066.7754  1066.6135     0.1620     0  K.ESTLHLVLR.L  (Ions score 77)
516 - 524     534.3960  1066.7774  1066.6135     0.1640     0  K.ESTLHLVLR.L  (Ions score 64)
516 - 524     534.4340  1066.8534  1066.6135     0.2400     0  K.ESTLHLVLR.L  (Ions score 63)
516 - 524     534.5160  1067.0174  1066.6135     0.4040     0  K.ESTLHLVLR.L  (Ions score 22)
```



RMS error 369 ppm



RMS error 369 ppm

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

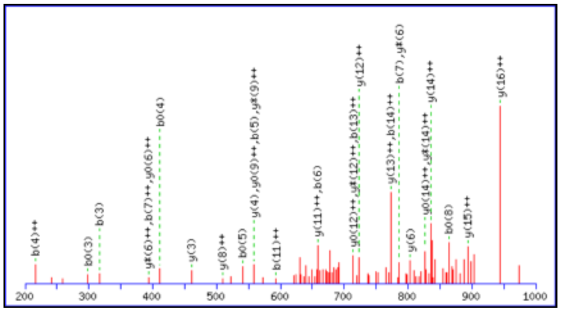
Mascot Search Results

Peptide View

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

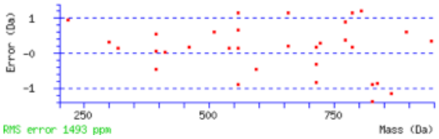
Match to Query 693: 2102.321172 from(701.781000,3+) intensity(392304.0000)
Title: Cmpd 93, +MSn(702.69), 26.4 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00816_YD_6_merge.mgf

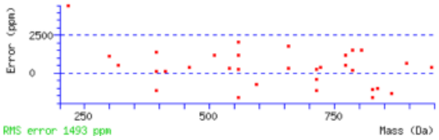
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): `2100.0950`
Fixed modifications: `Carbamidomethyl (C) (apply to specified residues or termini only)`
Variable modifications:
K16 `: GlyGly (K)`
Ions Score: `44` **Expect:** `0.37`
Matches : `33/168 fragment ions using 31 most intense peaks` (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							18
2	**215.1390**	108.0731			197.1285	99.0679	I	2000.0546	1000.5310	1983.0281	992.0177	1982.0441	991.5257	17
3	**316.1867**	158.5970			298.1761	149.5917	T	1886.9706	943.9889	1869.9440	935.4756	1868.9600	934.9836	16
4	429.2708	***215.1390***			411.2602	206.1337	L	1785.9229	893.4651	1768.8963	884.9518	1767.9123	884.4598	15
5	**558.3134**	279.6603			540.3028	270.6550	E	1672.8388	836.9230	1655.8123	828.4098	1654.8283	827.9178	14
6	**657.3818**	329.1945			639.3712	320.1892	V	1543.7962	772.4018	1526.7697	763.8885	1525.7857	763.3965	13
7	**786.4244**	***393.7158***			768.4138	384.7105	E	1444.7278	722.8675	1427.7013	714.3543	1426.7172	713.8623	12
8	883.4771	442.2422			865.4666	433.2369	P	1315.6852	658.3462	1298.6587	649.8330	1297.6747	649.3410	11
9	970.5092	485.7582			952.4986	476.7529	S	1218.6325	609.8199	1201.6059	601.3066	1200.6219	600.8146	10
10	1085.5361	543.2717			1067.5255	534.2664	D	1131.6004	566.3039	1114.5739	557.7906	1113.5899	557.2986	9
11	1186.5838	***593.7955***			1168.5732	584.7902	T	1016.5735	508.7904	999.5469	500.2771	998.5629	499.7851	8
12	1299.6678	650.3376			1281.6573	641.3323	I	915.5258	458.2665	898.4993	449.7533	897.5152	449.2613	7
13	1428.7104	***714.8589***			1410.6999	705.8536	E	**802.4417**	401.7245	785.4152	393.2112	784.4312	392.7192	6
14	1542.7534	***771.8803***	1525.7268	763.3670	1524.7428	762.8750	N	673.3991	337.2032	656.3726	328.6899			5
15	1641.8218	821.4145	1624.7952	812.9013	1623.8112	812.4092	V	**559.3562**	280.1817	542.3297	271.6685			4
16	1883.9597	942.4835	1866.9331	933.9702	1865.9491	933.4782	K	**460.2878**	230.6475	443.2613	222.1343			3
17	1954.9968	978.0020	1937.9702	969.4888	1936.9862	968.9967	A	218.1499	109.5786	201.1234	101.0653			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.7	2104.0874	-1.7662	RYLIDKGLVPMEGDEELK
47.0	2101.0772	1.2440	NVSMQNAVNEPVQKLMRK
44.4	2100.0950	2.2262	TITLEVEPSDTIENVKAK
44.4	2100.0950	2.2262	TITLEVEPSDTIENVKAK
44.3	2100.1361	2.1851	DVITELIAKLGENMNLRR
43.5	2101.2081	1.1131	RGIRPEALYKLMVEIGIK
42.2	2101.1280	1.1932	TLTLEAGRFAEQANGAVVVR
42.0	2102.0831	0.2381	ITCGQVTGSLAPXIPFLRTG
40.7	2102.0491	0.2721	RASEKSGELEDIESSQPLK
40.4	2101.0804	1.2408	GPVSRTFVLAGSADSPELGK

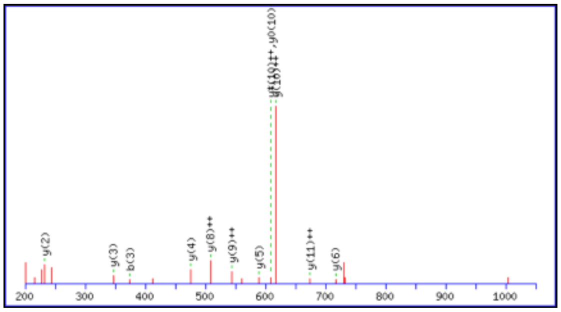
MATRIX SCIENCE Mascot Search Results

Peptide View

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

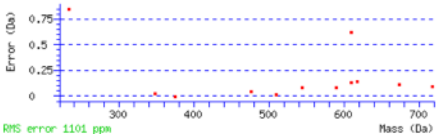
Match to Query 426: 1460.021172 from(487.681000,3+) intensity(2549566.0000)
Title: Cmpd 73, +MSn(487.77), 24.3 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00816_YD_6_merge.mgf

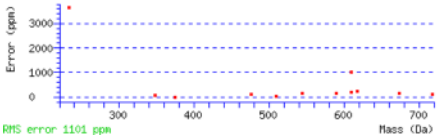
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1459.7783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : GlyGly (K)
Ions Score: 42 **Expect:** 0.72
Matches : 12/102 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	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
47.6	1460.7116	-0.6904	LNGGLGTTMGCVGPK
42.2	1461.7034	-1.6823	IGGGNDKQGFPMK
42.1	1459.7783	0.2429	LIFAGKQLEDGR
38.8	1460.6743	-0.6532	NGGDVTVAGSDDLK
36.7	1460.7147	-0.6935	DIGSAVFPDADLK
34.8	1458.8558	1.1654	NLDLKKGFIGIK
34.8	1459.8398	0.1813	LIIGDKEIFGISR
34.5	1460.6201	-0.5990	AEMDREDSEHVK
34.4	1460.7374	-0.7162	LLFTYQMTYPGK
33.1	1458.8082	1.2129	FPETSGIGIKPVSK

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

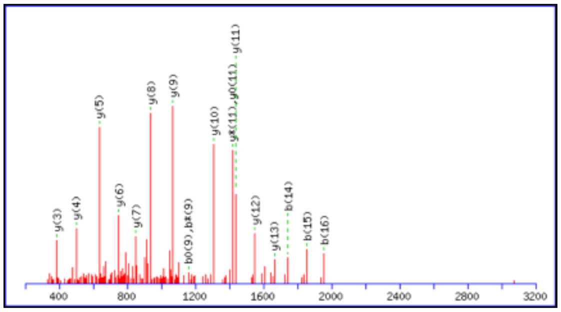
Mascot Search Results

Peptide View

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

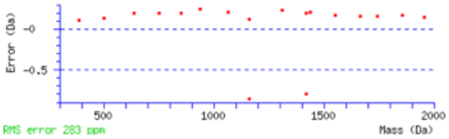
Match to Query 786: 2243.367448 from(1122.691000,2+) intensity(21048710.0000)
Title: Cmpd 103, +MSn(1123.27), 27.3 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00816_YD_6_merge.mgf

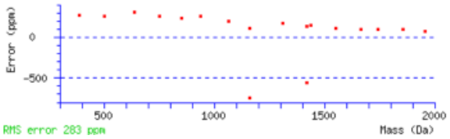
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 3200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2243.1910
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K9 : GlyGly (K)
Ions Score: 101 **Expect:** 7.2e-07
Matches : 18/182 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	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
101.3	2243.1910	0.1765	TLSDYNIQKESTLHLVLR
42.0	2242.1416	1.2259	YGENVPIMAISALRPPDVER
36.6	2242.2507	1.1167	LNAAIIGPGNIGTDLMYKILR
36.6	2243.2247	0.1428	GGVREVLASEALHHLGVRTSR
32.1	2241.1535	2.2139	GLDTHSLAAAKEIEMSRLQR
31.0	2242.2321	1.1353	LTAGGKSLLPIGVTEVQGEFAR
30.8	2243.0416	0.3259	LEELMRQFDEIEDEYLR
30.7	2243.1514	0.2160	IKELQINVQKELNCMNR
30.7	2243.0917	0.2757	GSASDYKDTLTKGSSLSTPSK
29.3	2241.0340	2.3334	AGCPMADMISGAELREFKSR

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

Mascot Search Results

Protein View

```
Match to: YD_RFP-BARD-BRCA-Ub Score: 5113
YD_RFP-BARD-BRCA-Ub
Found in search of C:\YaelDavid\100203_YaelDavid\BIT00820_YD_8_merge.mgf

Nominal mass (Mr): 60628; Calculated pI value: 6.10
NCBI BLAST search of YD_RFP-BARD-BRCA-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 56%

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 EPDGRGAWAH
   251 SRAALDRLEK LLRCSRCTNI LREPVCLGGC EHIFCSNCVS DCIGTGCPVC
   301 YTPAWIQDLK INRQLDSMIQ LCSKLRNLLH DNELSDLKED GGSGGDLSAL
   351 RVEEVQNVIN AMQKILECPI CLELIKEPVS TKCDHIFCKF CMLKLLNQKK
   401 GPSQCPLCKN DITKRSLQES TRFSQLVEEL LKIICAFQLD TGLEYANSYN
   451 FAKQIFVKTL TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK
   501 QLEDGRTLSD YNIQKESTLH LVLRLRGG
```

[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     1519.7300  3037.4454  3037.3359    0.1095     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 42)
   24 - 51     1013.5960  3037.7662  3037.3359    0.4302     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 52)
   24 - 51     1520.2510  3038.4874  3037.3359    1.1515     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 20)
   24 - 51     1013.9070  3038.6992  3037.3359    1.3632     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 88)
   24 - 51     1013.9590  3038.8552  3037.3359    1.5192     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 58)
   24 - 51      764.3400  3053.3309  3053.3309    0.0000     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M)  (Ions score 34)
   24 - 51     1018.9000  3053.6782  3053.3309    0.3473     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M)  (Ions score 87)
   24 - 51     1018.9140  3053.7202  3053.3309    0.3893     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M)  (Ions score 72)
   24 - 51     1019.1810  3054.5212  3053.3309    1.1903     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M)  (Ions score 88)
   57 - 76     1104.1570  2206.2994  2207.1051   -0.8057     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 79)
   57 - 76     1104.6490  2207.2834  2207.1051    0.1783     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 64)
   57 - 76      736.8460  2207.5162  2207.1051    0.4110     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 57)
   57 - 76      737.1270  2208.3592  2207.1051    1.2540     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 22)
   91 - 98      462.8190   923.6234   923.4753    0.1482     0  K.LSFPEGFK.W  (Ions score 41)
   91 - 98      462.8300   923.6454   923.4753    0.1702     0  K.LSFPEGFK.W  (Ions score 41)
   91 - 98      462.8330   923.6514   923.4753    0.1762     0  K.LSFPEGFK.W  (Ions score 35)
   91 - 98      462.8650   923.7154   923.4753    0.2402     0  K.LSFPEGFK.W  (Ions score 43)
  102 - 127    1439.7420  2877.4694  2877.3379    0.1316     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 79)
  102 - 127    1440.2680  2878.5214  2877.3379    1.1836     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 92)
  102 - 127    1440.2800  2878.5454  2877.3379    1.2076     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 89)
  102 - 127    1440.3070  2878.5994  2877.3379    1.2616     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 84)
  102 - 127     960.5430  2878.6072  2877.3379    1.2693     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 86)
  102 - 127     960.5530  2878.6372  2877.3379    1.2993     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 127)
  102 - 127     960.6060  2878.7962  2877.3379    1.4583     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 91)
  102 - 127     965.4870  2893.4392  2893.3328    0.1064     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 70)
  102 - 127    1447.8210  2893.6274  2893.3328    0.2946     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 106)
  102 - 127     965.6100  2893.8082  2893.3328    0.4754     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 79)
  102 - 127    1448.1900  2894.3654  2893.3328    1.0326     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 86)
  102 - 127    1448.2690  2894.5234  2893.3328    1.1906     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 95)
  102 - 127     965.9770  2894.9092  2893.3328    1.5764     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 86)
  132 - 144     689.4230  1376.8314  1376.6395    0.1920     0  R.GTNFPSDGPVMQK.K  (Ions score 70)
  132 - 144     689.4340  1376.8534  1376.6395    0.2140     0  R.GTNFPSDGPVMQK.K  (Ions score 65)
  132 - 144     689.4360  1376.8574  1376.6395    0.2180     0  R.GTNFPSDGPVMQK.K  (Ions score 52)
  132 - 144     689.4540  1376.8934  1376.6395    0.2540     0  R.GTNFPSDGPVMQK.K  (Ions score 77)
  132 - 144     689.4700  1376.9254  1376.6395    0.2860     0  R.GTNFPSDGPVMQK.K  (Ions score 69)
  132 - 144     697.4170  1392.8194  1392.6344    0.1851     0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 64)
  132 - 144     697.4410  1392.8674  1392.6344    0.2331     0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 74)
  132 - 144     697.4480  1392.8814  1392.6344    0.2471     0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 55)
  132 - 144     697.4890  1392.9634  1392.6344    0.3291     0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 65)
  145 - 155     648.3480  1294.6814  1294.5976    0.0839     1  K.KTMGWEASTER.M  (Ions score 75)
  145 - 155     648.3710  1294.7274  1294.5976    0.1299     1  K.KTMGWEASTER.M  (Ions score 69)
  145 - 155     648.4100  1294.8054  1294.5976    0.2079     1  K.KTMGWEASTER.M  (Ions score 68)
  145 - 155     648.4270  1294.8394  1294.5976    0.2419     1  K.KTMGWEASTER.M  (Ions score 75)
  146 - 155     583.7910  1165.5674  1166.5026   -0.9352     0  K.TMGWEASTER.M  (Ions score 48)
  146 - 155     584.2960  1166.5774  1166.5026    0.0748     0  K.TMGWEASTER.M  (Ions score 52)
  146 - 155     584.3080  1166.6014  1166.5026    0.0988     0  K.TMGWEASTER.M  (Ions score 52)
  146 - 155     584.3300  1166.6454  1166.5026    0.1428     0  K.TMGWEASTER.M  (Ions score 52)
  146 - 155     591.9210  1181.8274  1182.4975   -0.6701     0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 52)
  146 - 155     592.2800  1182.5454  1182.4975    0.0479     0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 57)
  146 - 155     592.2850  1182.5554  1182.4975    0.0579     0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 61)
  146 - 155     592.3090  1182.6034  1182.4975    0.1059     0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 61)
  191 - 200     367.5950  1099.7632  1099.6390    0.1242     0  K.KPVQLPGAYK.T  (Ions score 35)
  191 - 200     550.8960  1099.7774  1099.6390    0.1385     0  K.KPVQLPGAYK.T  (Ions score 50)
  191 - 200     550.9020  1099.7894  1099.6390    0.1505     0  K.KPVQLPGAYK.T  (Ions score 49)
  191 - 200     550.9200  1099.8254  1099.6390    0.1865     0  K.KPVQLPGAYK.T  (Ions score 52)
  191 - 200     550.9470  1099.8794  1099.6390    0.2405     0  K.KPVQLPGAYK.T  (Ions score 40)
  205 - 222    1113.1090  2224.2034  2224.0284    0.1751     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 107)
  205 - 222    1113.1100  2224.2054  2224.0284    0.1771     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 102)
  205 - 222    1113.1700  2224.3254  2224.0284    0.2971     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 106)
  205 - 222    1113.1730  2224.3314  2224.0284    0.3031     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 81)
  205 - 222    1113.2000  2224.3854  2224.0284    0.3571     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 98)
  205 - 222     742.4720  2224.3942  2224.0284    0.3658     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 38)
  205 - 222     742.5360  2224.5862  2224.0284    0.5578     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 63)
  205 - 222     742.5420  2224.6042  2224.0284    0.5758     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 57)
  205 - 222     742.5810  2224.7212  2224.0284    0.6928     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 49)
  205 - 222    1113.6370  2225.2594  2224.0284    1.2311     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 63)
  227 - 245    1060.5930  2119.1714  2118.9606    0.2108     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 129)
  227 - 245    1060.6720  2119.3294  2118.9606    0.3688     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 136)
  227 - 245    1060.7530  2119.4914  2118.9606    0.5308     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 119)
  227 - 245    1061.0500  2120.0854  2118.9606    1.1248     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 121)
  227 - 245     707.8550  2120.5432  2118.9606    1.5825     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 32)
  314 - 324     661.9530  1321.8914  1321.6370    0.2545     0  R.QLDSMIQLCSK.L  (Ions score 59)
  314 - 324     661.9640  1321.9134  1321.6370    0.2765     0  R.QLDSMIQLCSK.L  (Ions score 43)
  314 - 324     661.9660  1321.9174  1321.6370    0.2805     0  R.QLDSMIQLCSK.L  (Ions score 58)
  314 - 324     661.9740  1321.9334  1321.6370    0.2965     0  R.QLDSMIQLCSK.L  (Ions score 42)
  314 - 324     669.9090  1337.8034  1337.6319    0.1715     0  R.QLDSMIQLCSK.L  Oxidation (M)  (Ions score 49)
  327 - 338     705.9830  1409.9514  1409.7150    0.2364     0  R.NLLHDNELSDLK.E  (Ions score 59)
  327 - 338     471.0010  1409.9812  1409.7150    0.2661     0  R.NLLHDNELSDLK.E  (Ions score 28)
  327 - 338     706.0070  1409.9994  1409.7150    0.2844     0  R.NLLHDNELSDLK.E  (Ions score 69)
  327 - 338     706.0150  1410.0154  1409.7150    0.3004     0  R.NLLHDNELSDLK.E  (Ions score 49)
  327 - 338     471.0170  1410.0292  1409.7150    0.3141     0  R.NLLHDNELSDLK.E  (Ions score 34)
  327 - 351     875.4060  2623.1962  2624.2678   -1.0716     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 29)
  327 - 351     875.4620  2623.3642  2624.2678   -0.9036     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 56)
  327 - 351    1313.1920  2624.3694  2624.2678    0.1017     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 120)
  327 - 351    1313.2270  2624.4394  2624.2678    0.1717     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 44)
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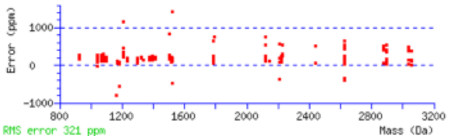
327 - 351   1313.2560  2624.4974  2624.2678    0.2297    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 125)
327 - 351   1313.2840  2624.5534  2624.2678    0.2857    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 122)
327 - 351    875.8810  2624.6212  2624.2678    0.3534    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 77)
327 - 351    875.9200  2624.7382  2624.2678    0.4704    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 88)
327 - 351    875.9340  2624.7802  2624.2678    0.5124    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 90)
327 - 351    875.9680  2624.8822  2624.2678    0.6144    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 77)
327 - 351   1313.7060  2625.3974  2624.2678    1.1297    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 113)
327 - 351    876.1710  2625.4912  2624.2678    1.2234    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 97)
327 - 351    876.2370  2625.6892  2624.2678    1.4214    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 63)
327 - 351    876.3290  2625.9652  2624.2678    1.6974    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 66)
339 - 351    617.3500  1232.6854  1232.5633    0.1221    0  K.EDGGSGGDLSALR.V  (Ions score 80)
339 - 351    617.3560  1232.6974  1232.5633    0.1341    0  K.EDGGSGGDLSALR.V  (Ions score 80)
339 - 351    617.3660  1232.7174  1232.5633    0.1541    0  K.EDGGSGGDLSALR.V  (Ions score 84)
339 - 351    617.4020  1232.7894  1232.5633    0.2261    0  K.EDGGSGGDLSALR.V  (Ions score 84)
352 - 364    751.5120  1501.0094  1500.7606    0.2488    0  R.VEEVQNVINAMQK.I  (Ions score 58)
352 - 364    751.5230  1501.0314  1500.7606    0.2708    0  R.VEEVQNVINAMQK.I  (Ions score 76)
352 - 364    751.5480  1501.0814  1500.7606    0.3208    0  R.VEEVQNVINAMQK.I  (Ions score 106)
352 - 364    751.5600  1501.1054  1500.7606    0.3448    0  R.VEEVQNVINAMQK.I  (Ions score 103)
352 - 364    751.5620  1501.1094  1500.7606    0.3488    0  R.VEEVQNVINAMQK.I  (Ions score 109)
352 - 364    751.5680  1501.1214  1500.7606    0.3608    0  R.VEEVQNVINAMQK.I  (Ions score 74)
352 - 364    751.5880  1501.1614  1500.7606    0.4008    0  R.VEEVQNVINAMQK.I  (Ions score 70)
352 - 364    751.5960  1501.1774  1500.7606    0.4168    0  R.VEEVQNVINAMQK.I  (Ions score 109)
352 - 364    752.0100  1502.0054  1500.7606    1.2448    0  R.VEEVQNVINAMQK.I  (Ions score 44)
352 - 364    759.4510  1516.8874  1516.7555    0.1319    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 87)
352 - 364    759.4720  1516.9294  1516.7555    0.1739    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 99)
352 - 364    759.4900  1516.9654  1516.7555    0.2099    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 43)
352 - 364    759.5270  1517.0394  1516.7555    0.2839    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 88)
352 - 364    759.5430  1517.0714  1516.7555    0.3159    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 98)
352 - 364    760.4670  1518.9194  1516.7555    2.1639    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 47)
365 - 376    751.0490  1500.0834  1499.8091    0.2743    0  K.ILECPICLELIK.E  (Ions score 61)
365 - 376    751.0720  1500.1294  1499.8091    0.3203    0  K.ILECPICLELIK.E  (Ions score 61)
365 - 376    751.1030  1500.1914  1499.8091    0.3823    0  K.ILECPICLELIK.E  (Ions score 57)
365 - 376    751.1220  1500.2294  1499.8091    0.4203    0  K.ILECPICLELIK.E  (Ions score 64)
365 - 376    751.5400  1501.0654  1499.8091    1.2563    0  K.ILECPICLELIK.E  (Ions score 50)
365 - 382   1071.7150  2141.4154  2141.1476    0.2679    1  K.ILECPICLELIKEPVSTK.C  (Ions score 83)
423 - 432    603.4790  1204.9434  1204.6703    0.2731    0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    603.4860  1204.9574  1204.6703    0.2871    0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432    603.4870  1204.9594  1204.6703    0.2891    0  R.FSQLVEELLK.I  (Ions score 81)
423 - 432    603.4910  1204.9674  1204.6703    0.2971    0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    603.5020  1204.9894  1204.6703    0.3191    0  R.FSQLVEELLK.I  (Ions score 72)
423 - 432    603.5040  1204.9934  1204.6703    0.3231    0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432    603.5040  1204.9934  1204.6703    0.3231    0  R.FSQLVEELLK.I  (Ions score 82)
423 - 432    603.5050  1204.9954  1204.6703    0.3251    0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432    603.5120  1205.0094  1204.6703    0.3391    0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432    603.5180  1205.0214  1204.6703    0.3511    0  R.FSQLVEELLK.I  (Ions score 85)
423 - 432    603.5210  1205.0274  1204.6703    0.3571    0  R.FSQLVEELLK.I  (Ions score 85)
423 - 432    603.5230  1205.0314  1204.6703    0.3611    0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432    603.5310  1205.0474  1204.6703    0.3771    0  R.FSQLVEELLK.I  (Ions score 85)
423 - 432    603.5610  1205.1074  1204.6703    0.4371    0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432    603.6130  1205.2114  1204.6703    0.5411    0  R.FSQLVEELLK.I  (Ions score 76)
423 - 432    604.0350  1206.0554  1204.6703    1.3851    0  R.FSQLVEELLK.I  (Ions score 72)
423 - 432    604.0400  1206.0654  1204.6703    1.3951    0  R.FSQLVEELLK.I  (Ions score 74)
433 - 453   1219.6560  2437.2974  2437.1624    0.1351    0  K.IICAFQLDTGLEYANSYNFAK.Q  (Ions score 144)
433 - 453    813.8170  2438.4292  2437.1624    1.2668    0  K.IICAFQLDTGLEYANSYNFAK.Q  (Ions score 71)
464 - 479    894.5120  1787.0094  1786.9200    0.0894    0  K.TITLEVEPSDTIENVK.A  (Ions score 73)
464 - 479    894.5560  1787.0974  1786.9200    0.1774    0  K.TITLEVEPSDTIENVK.A  (Ions score 56)
464 - 479    894.5640  1787.1134  1786.9200    0.1934    0  K.TITLEVEPSDTIENVK.A  (Ions score 57)
464 - 479    894.5670  1787.1194  1786.9200    0.1994    0  K.TITLEVEPSDTIENVK.A  (Ions score 60)
464 - 479    894.5680  1787.1214  1786.9200    0.2014    0  K.TITLEVEPSDTIENVK.A  (Ions score 55)
464 - 479    894.5690  1787.1234  1786.9200    0.2034    0  K.TITLEVEPSDTIENVK.A  (Ions score 77)
464 - 479    894.5870  1787.1594  1786.9200    0.2394    0  K.TITLEVEPSDTIENVK.A  (Ions score 74)
464 - 479    894.5960  1787.1774  1786.9200    0.2574    0  K.TITLEVEPSDTIENVK.A  (Ions score 54)
464 - 479    894.6020  1787.1894  1786.9200    0.2694    0  K.TITLEVEPSDTIENVK.A  (Ions score 66)
464 - 479    894.6060  1787.1974  1786.9200    0.2774    0  K.TITLEVEPSDTIENVK.A  (Ions score 80)
464 - 479    894.6070  1787.1994  1786.9200    0.2794    0  K.TITLEVEPSDTIENVK.A  (Ions score 50)
464 - 479    894.6070  1787.1994  1786.9200    0.2794    0  K.TITLEVEPSDTIENVK.A  (Ions score 63)
464 - 479    894.6150  1787.2154  1786.9200    0.2954    0  K.TITLEVEPSDTIENVK.A  (Ions score 79)
464 - 479    894.6240  1787.2334  1786.9200    0.3134    0  K.TITLEVEPSDTIENVK.A  (Ions score 61)
464 - 479    894.6250  1787.2354  1786.9200    0.3154    0  K.TITLEVEPSDTIENVK.A  (Ions score 61)
464 - 479    894.6290  1787.2434  1786.9200    0.3234    0  K.TITLEVEPSDTIENVK.A  (Ions score 57)
464 - 479    894.6460  1787.2774  1786.9200    0.3574    0  K.TITLEVEPSDTIENVK.A  (Ions score 67)
464 - 479    894.6540  1787.2934  1786.9200    0.3734    0  K.TITLEVEPSDTIENVK.A  (Ions score 66)
464 - 479    894.6560  1787.2974  1786.9200    0.3774    0  K.TITLEVEPSDTIENVK.A  (Ions score 49)
464 - 479    894.6670  1787.3194  1786.9200    0.3994    0  K.TITLEVEPSDTIENVK.A  (Ions score 78)
464 - 479    894.6710  1787.3274  1786.9200    0.4074    0  K.TITLEVEPSDTIENVK.A  (Ions score 73)
464 - 479    894.6780  1787.3414  1786.9200    0.4214    0  K.TITLEVEPSDTIENVK.A  (Ions score 83)
464 - 479    895.0470  1788.0794  1786.9200    1.1594    0  K.TITLEVEPSDTIENVK.A  (Ions score 62)
464 - 479    895.1330  1788.2514  1786.9200    1.3314    0  K.TITLEVEPSDTIENVK.A  (Ions score 68)
482 - 494    762.0250  1522.0354  1522.7740   -0.7385    1  K.IQDKEGIPPDQQR.L  (Ions score 64)
482 - 494    762.4850  1522.9554  1522.7740    0.1815    1  K.IQDKEGIPPDQQR.L  (Ions score 46)
482 - 494    762.4900  1522.9654  1522.7740    0.1915    1  K.IQDKEGIPPDQQR.L  (Ions score 61)
482 - 494    762.5260  1523.0374  1522.7740    0.2635    1  K.IQDKEGIPPDQQR.L  (Ions score 48)
482 - 494    762.5390  1523.0634  1522.7740    0.2895    1  K.IQDKEGIPPDQQR.L  (Ions score 43)
486 - 494    520.2460  1038.4774  1038.5094   -0.0320    0  K.EGIPPDQQR.L  (Ions score 14)
486 - 494    520.3120  1038.6094  1038.5094    0.1000    0  K.EGIPPDQQR.L  (Ions score 26)
486 - 494    520.3360  1038.6574  1038.5094    0.1480    0  K.EGIPPDQQR.L  (Ions score 35)
486 - 494    520.3400  1038.6654  1038.5094    0.1560    0  K.EGIPPDQQR.L  (Ions score 30)
486 - 494    520.3630  1038.7114  1038.5094    0.2020    0  K.EGIPPDQQR.L  (Ions score 28)
486 - 494    520.3630  1038.7114  1038.5094    0.2020    0  K.EGIPPDQQR.L  (Ions score 32)
486 - 494    520.3980  1038.7814  1038.5094    0.2720    0  K.EGIPPDQQR.L  (Ions score 31)
507 - 515    541.3440  1080.6734  1080.5451    0.1283    0  R.TLSDYNIQK.E  (Ions score 60)
507 - 515    541.3640  1080.7134  1080.5451    0.1683    0  R.TLSDYNIQK.E  (Ions score 54)
507 - 515    541.3720  1080.7294  1080.5451    0.1843    0  R.TLSDYNIQK.E  (Ions score 54)
507 - 515    541.3920  1080.7694  1080.5451    0.2243    0  R.TLSDYNIQK.E  (Ions score 15)
507 - 515    541.4350  1080.8554  1080.5451    0.3103    0  R.TLSDYNIQK.E  (Ions score 57)
516 - 524    534.3790  1066.7434  1066.6135    0.1300    0  K.ESTLHLVLR.L  (Ions score 57)
516 - 524    534.3930  1066.7714  1066.6135    0.1580    0  K.ESTLHLVLR.L  (Ions score 46)
516 - 524    534.4010  1066.7874  1066.6135    0.1740    0  K.ESTLHLVLR.L  (Ions score 61)
516 - 524    534.4040  1066.7934  1066.6135    0.1800    0  K.ESTLHLVLR.L  (Ions score 60)
516 - 524    534.4060  1066.7974  1066.6135    0.1840    0  K.ESTLHLVLR.L  (Ions score 61)
516 - 524    534.4520  1066.8894  1066.6135    0.2760    0  K.ESTLHLVLR.L  (Ions score 19)
516 - 524    534.4630  1066.9114  1066.6135    0.2980    0  K.ESTLHLVLR.L  (Ions score 33)
```



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

Mascot Search Results

Protein View

Match to: **YD_RFP-BARD-BRCA-Ub** Score: **4958**
YD_RFP-BARD-BRCA-Ub
Found in search of C:\YaelDavid\100203_YaelDavid\BIT00822_YD_9_merge.mgf

Nominal mass (M_r): **60628**; Calculated pI value: **6.10**
NCBI BLAST search of YD_RFP-BARD-BRCA-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **54%**

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 EPDGRGAWAH
251 SRAALDRLEK LLRCSRCTNI LREPVCLGGC EHIFCSNCVS DCIGTGCPVC
301 YTPAWIQDLK INRQLDSMIQ LCSKLRNLLH DNELSDLKED GGSGGDLSAL
351 RVEEVQNVIN AMQKILECPI CLELIKEPVS TKCDHIFCKF CMLKLLNQKK
401 GPSQCPLCKN DITKRSLQES TRFSQLVEEL LKIICAFQLD TGLEYANSYN
451 FAKQIFVKTL TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK
501 QLEDGRTLSD YNIQKESTLH LVLRLRGG
```

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	760.4050	3037.5909	3037.3359	0.2550	0	**R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L** (Ions score 25)
24 - 51	1013.5520	3037.6342	3037.3359	0.2982	0	**R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L** (Ions score 49)
24 - 51	1013.5620	3037.6642	3037.3359	0.3282	0	**R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L** (Ions score 54)
24 - 51	1520.1990	3038.3834	3037.3359	1.0475	0	**R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L** (Ions score 39)
24 - 51	1013.8590	3038.5552	3037.3359	1.2192	0	**R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L** (Ions score 55)
24 - 51	760.6470	3038.5589	3037.3359	1.2230	0	**R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L** (Ions score 33)
24 - 51	1013.8750	3038.6032	3037.3359	1.2672	0	**R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L** (Ions score 72)
24 - 51	1014.1580	3039.4522	3037.3359	2.1162	0	**R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L** (Ions score 45)
24 - 51	1018.5560	3052.6462	3053.3309	-0.6847	0	**R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L** Oxidation (M) (Ions score 64)
24 - 51	1018.8430	3053.5072	3053.3309	0.1763	0	**R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L** Oxidation (M) (Ions score 68)
24 - 51	1018.8830	3053.6272	3053.3309	0.2963	0	**R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L** Oxidation (M) (Ions score 56)
24 - 51	1019.2410	3054.7012	3053.3309	1.3703	0	**R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L** Oxidation (M) (Ions score 68)
57 - 76	736.5590	2206.6552	2207.1051	-0.4500	0	**K.GGPLPFAWDILSPQFQYGSK.A** (Ions score 48)
57 - 76	1104.6620	2207.3094	2207.1051	0.2043	0	**K.GGPLPFAWDILSPQFQYGSK.A** (Ions score 56)
57 - 76	1104.6980	2207.3814	2207.1051	0.2763	0	**K.GGPLPFAWDILSPQFQYGSK.A** (Ions score 83)
57 - 76	1104.7010	2207.3874	2207.1051	0.2823	0	**K.GGPLPFAWDILSPQFQYGSK.A** (Ions score 33)
91 - 98	462.7980	923.5814	923.4753	0.1062	0	**K.LSFPEGFK.W** (Ions score 41)
91 - 98	462.8160	923.6174	923.4753	0.1422	0	**K.LSFPEGFK.W** (Ions score 41)
91 - 98	462.8270	923.6394	923.4753	0.1642	0	**K.LSFPEGFK.W** (Ions score 39)
91 - 98	462.8310	923.6474	923.4753	0.1722	0	**K.LSFPEGFK.W** (Ions score 37)
91 - 98	462.8800	923.7454	923.4753	0.2702	0	**K.LSFPEGFK.W** (Ions score 20)
102 - 127	960.1780	2877.5122	2877.3379	0.1743	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** (Ions score 121)
102 - 127	960.1940	2877.5602	2877.3379	0.2223	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** (Ions score 53)
102 - 127	960.2170	2877.6292	2877.3379	0.2913	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** (Ions score 21)
102 - 127	1440.2750	2878.5354	2877.3379	1.1976	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** (Ions score 97)
102 - 127	1440.2860	2878.5574	2877.3379	1.2196	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** (Ions score 81)
102 - 127	960.5620	2878.6642	2877.3379	1.3263	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** (Ions score 54)
102 - 127	960.5830	2878.7272	2877.3379	1.3893	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** (Ions score 96)
102 - 127	960.6040	2878.7902	2877.3379	1.4523	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** (Ions score 97)
102 - 127	960.6300	2878.8682	2877.3379	1.5303	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** (Ions score 97)
102 - 127	1447.8170	2893.6194	2893.3328	0.2866	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** Oxidation (M) (Ions score 111)
102 - 127	965.5940	2893.7602	2893.3328	0.4274	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** Oxidation (M) (Ions score 65)
102 - 127	965.6060	2893.7962	2893.3328	0.4634	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** Oxidation (M) (Ions score 53)
102 - 127	965.6570	2893.9492	2893.3328	0.6164	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** Oxidation (M) (Ions score 76)
102 - 127	965.6850	2894.0332	2893.3328	0.7004	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** Oxidation (M) (Ions score 74)
102 - 127	1448.2270	2894.4394	2893.3328	1.1066	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** Oxidation (M) (Ions score 111)
102 - 127	1448.2430	2894.4714	2893.3328	1.1386	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** Oxidation (M) (Ions score 109)
102 - 127	1448.2990	2894.5834	2893.3328	1.2506	0	**R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V** Oxidation (M) (Ions score 111)
132 - 144	688.9610	1375.9074	1376.6395	-0.7320	0	**R.GTNFPSDGPVMQK.K** (Ions score 65)
132 - 144	689.3690	1376.7234	1376.6395	0.0840	0	**R.GTNFPSDGPVMQK.K** (Ions score 21)
132 - 144	689.4260	1376.8374	1376.6395	0.1980	0	**R.GTNFPSDGPVMQK.K** (Ions score 77)
132 - 144	689.4310	1376.8474	1376.6395	0.2080	0	**R.GTNFPSDGPVMQK.K** (Ions score 12)
132 - 144	689.4350	1376.8554	1376.6395	0.2160	0	**R.GTNFPSDGPVMQK.K** (Ions score 73)
132 - 144	689.4450	1376.8754	1376.6395	0.2360	0	**R.GTNFPSDGPVMQK.K** (Ions score 69)
132 - 144	689.4670	1376.9194	1376.6395	0.2800	0	**R.GTNFPSDGPVMQK.K** (Ions score 36)
132 - 144	697.3840	1392.7534	1392.6344	0.1191	0	**R.GTNFPSDGPVMQK.K** Oxidation (M) (Ions score 63)
132 - 144	697.4390	1392.8634	1392.6344	0.2291	0	**R.GTNFPSDGPVMQK.K** Oxidation (M) (Ions score 68)
132 - 144	697.4530	1392.8914	1392.6344	0.2571	0	**R.GTNFPSDGPVMQK.K** Oxidation (M) (Ions score 72)
132 - 144	697.4920	1392.9694	1392.6344	0.3351	0	**R.GTNFPSDGPVMQK.K** Oxidation (M) (Ions score 65)
145 - 155	648.3560	1294.6974	1294.5976	0.0999	1	**K.KTMGWEASTER.M** (Ions score 69)
145 - 155	648.3790	1294.7434	1294.5976	0.1459	1	**K.KTMGWEASTER.M** (Ions score 71)
145 - 155	648.3900	1294.7654	1294.5976	0.1679	1	**K.KTMGWEASTER.M** (Ions score 69)
145 - 155	648.4090	1294.8034	1294.5976	0.2059	1	**K.KTMGWEASTER.M** (Ions score 71)
146 - 155	583.8360	1165.6574	1166.5026	-0.8452	0	**K.TMGWEASTER.M** (Ions score 48)
146 - 155	584.3460	1166.6774	1166.5026	0.1748	0	**K.TMGWEASTER.M** (Ions score 48)
146 - 155	584.3490	1166.6834	1166.5026	0.1808	0	**K.TMGWEASTER.M** (Ions score 44)
146 - 155	592.2940	1182.5734	1182.4975	0.0759	0	**K.TMGWEASTER.M** Oxidation (M) (Ions score 61)
146 - 155	592.2960	1182.5774	1182.4975	0.0799	0	**K.TMGWEASTER.M** Oxidation (M) (Ions score 58)
146 - 155	592.3180	1182.6214	1182.4975	0.1239	0	**K.TMGWEASTER.M** Oxidation (M) (Ions score 58)
191 - 200	367.5780	1099.7122	1099.6390	0.0732	0	**K.KPVQLPGAYK.T** (Ions score 40)
191 - 200	367.5830	1099.7272	1099.6390	0.0882	0	**K.KPVQLPGAYK.T** (Ions score 40)
191 - 200	550.8810	1099.7474	1099.6390	0.1085	0	**K.KPVQLPGAYK.T** (Ions score 52)
191 - 200	550.9090	1099.8034	1099.6390	0.1645	0	**K.KPVQLPGAYK.T** (Ions score 52)
191 - 200	550.9130	1099.8114	1099.6390	0.1725	0	**K.KPVQLPGAYK.T** (Ions score 46)
191 - 200	550.9140	1099.8134	1099.6390	0.1745	0	**K.KPVQLPGAYK.T** (Ions score 52)
191 - 200	367.6130	1099.8172	1099.6390	0.1782	0	**K.KPVQLPGAYK.T** (Ions score 43)
205 - 222	1112.9390	2223.8634	2224.0284	-0.1649	0	**K.LDITSHNEDYTIVEQYER.A** (Ions score 5)
205 - 222	1113.1350	2224.2554	2224.0284	0.2271	0	**K.LDITSHNEDYTIVEQYER.A** (Ions score 128)
205 - 222	1113.1460	2224.2774	2224.0284	0.2491	0	**K.LDITSHNEDYTIVEQYER.A** (Ions score 103)
205 - 222	1113.1620	2224.3094	2224.0284	0.2811	0	**K.LDITSHNEDYTIVEQYER.A** (Ions score 103)
205 - 222	1113.1780	2224.3414	2224.0284	0.3131	0	**K.LDITSHNEDYTIVEQYER.A** (Ions score 94)
205 - 222	742.5220	2224.5442	2224.0284	0.5158	0	**K.LDITSHNEDYTIVEQYER.A** (Ions score 43)
205 - 222	742.5430	2224.6072	2224.0284	0.5788	0	**K.LDITSHNEDYTIVEQYER.A** (Ions score 51)
205 - 222	742.5440	2224.6102	2224.0284	0.5818	0	**K.LDITSHNEDYTIVEQYER.A** (Ions score 53)
205 - 222	742.8180	2225.4322	2224.0284	1.4038	0	**K.LDITSHNEDYTIVEQYER.A** (Ions score 31)
227 - 245	1060.6340	2119.2534	2118.9606	0.2928	0	**R.HSTGAENLYFQGLEEPDGR.G** (Ions score 141)
227 - 245	1060.6420	2119.2694	2118.9606	0.3088	0	**R.HSTGAENLYFQGLEEPDGR.G** (Ions score 119)
227 - 245	1060.7060	2119.3974	2118.9606	0.4368	0	**R.HSTGAENLYFQGLEEPDGR.G** (Ions score 107)
227 - 245	1061.0850	2120.1554	2118.9606	1.1948	0	**R.HSTGAENLYFQGLEEPDGR.G** (Ions score 120)
314 - 324	661.5190	1321.0234	1321.6370	-0.6135	0	**R.QLDSMIQLCSK.L** (Ions score 44)
314 - 324	661.9410	1321.8674	1321.6370	0.2305	0	**R.QLDSMIQLCSK.L** (Ions score 25)
314 - 324	661.9850	1321.9554	1321.6370	0.3185	0	**R.QLDSMIQLCSK.L** (Ions score 45)
314 - 324	661.9910	1321.9674	1321.6370	0.3305	0	**R.QLDSMIQLCSK.L** (Ions score 40)
327 - 338	705.9670	1409.9194	1409.7150	0.2044	0	**R.NLLHDNELSDLK.E** (Ions score 48)
327 - 338	470.9930	1409.9572	1409.7150	0.2421	0	**R.NLLHDNELSDLK.E** (Ions score 35)

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327 - 338     705.9980  1409.9814  1409.7150     0.2664     0  R.NLLHDNELSDLK.E  (Ions score 59)
327 - 338     706.0110  1410.0074  1409.7150     0.2924     0  R.NLLHDNELSDLK.E  (Ions score 53)
327 - 338     471.0380  1410.0922  1409.7150     0.3771     0  R.NLLHDNELSDLK.E  (Ions score 27)
327 - 338     471.0540  1410.1402  1409.7150     0.4251     0  R.NLLHDNELSDLK.E  (Ions score 27)
327 - 351    1313.2240  2624.4334  2624.2678     0.1657     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 110)
327 - 351    1313.2530  2624.4914  2624.2678     0.2237     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 113)
327 - 351    1313.2540  2624.4934  2624.2678     0.2257     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 130)
327 - 351     875.9890  2624.9452  2624.2678     0.6774     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 104)
327 - 351    1313.7380  2625.4614  2624.2678     1.1937     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 119)
327 - 351     876.2330  2625.6772  2624.2678     1.4094     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 60)
327 - 351     876.2840  2625.8302  2624.2678     1.5624     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 66)
339 - 351     616.9610  1231.9074  1232.5633    -0.6559     0  K.EDGGSGGDLSALR.V  (Ions score 81)
339 - 351     617.3890  1232.7634  1232.5633     0.2001     0  K.EDGGSGGDLSALR.V  (Ions score 82)
339 - 351     617.3930  1232.7714  1232.5633     0.2081     0  K.EDGGSGGDLSALR.V  (Ions score 82)
339 - 351     617.4190  1232.8234  1232.5633     0.2601     0  K.EDGGSGGDLSALR.V  (Ions score 77)
339 - 351     617.9010  1233.7874  1232.5633     1.2241     0  K.EDGGSGGDLSALR.V  (Ions score 38)
352 - 364     751.5230  1501.0314  1500.7606     0.2708     0  R.VEEVQNVINAMQK.I  (Ions score 109)
352 - 364     751.5580  1501.1014  1500.7606     0.3408     0  R.VEEVQNVINAMQK.I  (Ions score 109)
352 - 364     751.5650  1501.1154  1500.7606     0.3548     0  R.VEEVQNVINAMQK.I  (Ions score 109)
352 - 364     751.5720  1501.1294  1500.7606     0.3688     0  R.VEEVQNVINAMQK.I  (Ions score 35)
352 - 364     751.5770  1501.1394  1500.7606     0.3788     0  R.VEEVQNVINAMQK.I  (Ions score 107)
352 - 364     751.9770  1501.9394  1500.7606     1.1788     0  R.VEEVQNVINAMQK.I  (Ions score 50)
352 - 364     752.0160  1502.0174  1500.7606     1.2568     0  R.VEEVQNVINAMQK.I  (Ions score 77)
352 - 364     752.0690  1502.1234  1500.7606     1.3628     0  R.VEEVQNVINAMQK.I  (Ions score 76)
352 - 364     758.9390  1515.8634  1516.7555    -0.8921     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 82)
352 - 364     758.9740  1515.9334  1516.7555    -0.8221     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 70)
352 - 364     759.4540  1516.8934  1516.7555     0.1379     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 86)
365 - 376     751.0700  1500.1254  1499.8091     0.3163     0  K.ILECPICLELIK.E  (Ions score 73)
365 - 376     751.1080  1500.2014  1499.8091     0.3923     0  K.ILECPICLELIK.E  (Ions score 76)
365 - 376     751.5390  1501.0634  1499.8091     1.2543     0  K.ILECPICLELIK.E  (Ions score 65)
365 - 376     751.5800  1501.1454  1499.8091     1.3363     0  K.ILECPICLELIK.E  (Ions score 76)
423 - 432     603.4580  1204.9014  1204.6703     0.2311     0  R.FSQLVEELLK.I  (Ions score 80)
423 - 432     603.4780  1204.9414  1204.6703     0.2711     0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432     603.4840  1204.9534  1204.6703     0.2831     0  R.FSQLVEELLK.I  (Ions score 60)
423 - 432     603.5000  1204.9854  1204.6703     0.3151     0  R.FSQLVEELLK.I  (Ions score 78)
423 - 432     603.5000  1204.9854  1204.6703     0.3151     0  R.FSQLVEELLK.I  (Ions score 63)
423 - 432     603.5080  1205.0014  1204.6703     0.3311     0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432     603.5080  1205.0014  1204.6703     0.3311     0  R.FSQLVEELLK.I  (Ions score 72)
423 - 432     603.5140  1205.0134  1204.6703     0.3431     0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432     603.5210  1205.0274  1204.6703     0.3571     0  R.FSQLVEELLK.I  (Ions score 81)
423 - 432     603.5240  1205.0334  1204.6703     0.3631     0  R.FSQLVEELLK.I  (Ions score 75)
423 - 432     603.9700  1205.9254  1204.6703     1.2551     0  R.FSQLVEELLK.I  (Ions score 65)
423 - 432     603.9750  1205.9354  1204.6703     1.2651     0  R.FSQLVEELLK.I  (Ions score 66)
459 - 479    1201.7250  2401.4354  2401.2588     0.1767     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 97)
459 - 479     801.5210  2401.5412  2401.2588     0.2824     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 80)
459 - 479     801.5350  2401.5832  2401.2588     0.3244     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 71)
459 - 479     801.5530  2401.6372  2401.2588     0.3784     1  K.TLTGKTITLEVEPSDTIENVK.A  GlyGly (K)  (Ions score 51)
464 - 479     894.5440  1787.0734  1786.9200     0.1534     0  K.TITLEVEPSDTIENVK.A  (Ions score 67)
464 - 479     894.5580  1787.1014  1786.9200     0.1814     0  K.TITLEVEPSDTIENVK.A  (Ions score 86)
464 - 479     894.5580  1787.1014  1786.9200     0.1814     0  K.TITLEVEPSDTIENVK.A  (Ions score 72)
464 - 479     894.5740  1787.1334  1786.9200     0.2134     0  K.TITLEVEPSDTIENVK.A  (Ions score 61)
464 - 479     894.5760  1787.1374  1786.9200     0.2174     0  K.TITLEVEPSDTIENVK.A  (Ions score 62)
464 - 479     894.5790  1787.1434  1786.9200     0.2234     0  K.TITLEVEPSDTIENVK.A  (Ions score 74)
464 - 479     894.5850  1787.1554  1786.9200     0.2354     0  K.TITLEVEPSDTIENVK.A  (Ions score 91)
464 - 479     894.5880  1787.1614  1786.9200     0.2414     0  K.TITLEVEPSDTIENVK.A  (Ions score 70)
464 - 479     894.5910  1787.1674  1786.9200     0.2474     0  K.TITLEVEPSDTIENVK.A  (Ions score 69)
464 - 479     894.5940  1787.1734  1786.9200     0.2534     0  K.TITLEVEPSDTIENVK.A  (Ions score 55)
464 - 479     894.5960  1787.1774  1786.9200     0.2574     0  K.TITLEVEPSDTIENVK.A  (Ions score 61)
464 - 479     894.6000  1787.1854  1786.9200     0.2654     0  K.TITLEVEPSDTIENVK.A  (Ions score 81)
464 - 479     894.6010  1787.1874  1786.9200     0.2674     0  K.TITLEVEPSDTIENVK.A  (Ions score 90)
464 - 479     894.6020  1787.1894  1786.9200     0.2694     0  K.TITLEVEPSDTIENVK.A  (Ions score 72)
464 - 479     894.6050  1787.1954  1786.9200     0.2754     0  K.TITLEVEPSDTIENVK.A  (Ions score 77)
464 - 479     894.6130  1787.2114  1786.9200     0.2914     0  K.TITLEVEPSDTIENVK.A  (Ions score 69)
464 - 479     894.6180  1787.2214  1786.9200     0.3014     0  K.TITLEVEPSDTIENVK.A  (Ions score 77)
464 - 479     894.6220  1787.2294  1786.9200     0.3094     0  K.TITLEVEPSDTIENVK.A  (Ions score 78)
464 - 479     894.6230  1787.2314  1786.9200     0.3114     0  K.TITLEVEPSDTIENVK.A  (Ions score 85)
464 - 479     894.6290  1787.2434  1786.9200     0.3234     0  K.TITLEVEPSDTIENVK.A  (Ions score 49)
464 - 479     894.6330  1787.2514  1786.9200     0.3314     0  K.TITLEVEPSDTIENVK.A  (Ions score 63)
464 - 479     894.6370  1787.2594  1786.9200     0.3394     0  K.TITLEVEPSDTIENVK.A  (Ions score 63)
464 - 479     894.6380  1787.2614  1786.9200     0.3414     0  K.TITLEVEPSDTIENVK.A  (Ions score 69)
464 - 479     894.6390  1787.2634  1786.9200     0.3434     0  K.TITLEVEPSDTIENVK.A  (Ions score 86)
464 - 479     894.6440  1787.2734  1786.9200     0.3534     0  K.TITLEVEPSDTIENVK.A  (Ions score 61)
464 - 479     894.6490  1787.2834  1786.9200     0.3634     0  K.TITLEVEPSDTIENVK.A  (Ions score 86)
464 - 479     894.6570  1787.2994  1786.9200     0.3794     0  K.TITLEVEPSDTIENVK.A  (Ions score 76)
464 - 479     894.6630  1787.3114  1786.9200     0.3914     0  K.TITLEVEPSDTIENVK.A  (Ions score 60)
464 - 479     894.6640  1787.3134  1786.9200     0.3934     0  K.TITLEVEPSDTIENVK.A  (Ions score 86)
464 - 479     894.6750  1787.3354  1786.9200     0.4154     0  K.TITLEVEPSDTIENVK.A  (Ions score 81)
464 - 479     894.6750  1787.3354  1786.9200     0.4154     0  K.TITLEVEPSDTIENVK.A  (Ions score 82)
464 - 479     895.0960  1788.1774  1786.9200     1.2574     0  K.TITLEVEPSDTIENVK.A  (Ions score 70)
482 - 494     508.3760  1522.1062  1522.7740    -0.6678     1  K.IQDKEGIPPDQQR.L  (Ions score 33)
482 - 494     762.4580  1522.9014  1522.7740     0.1275     1  K.IQDKEGIPPDQQR.L  (Ions score 56)
482 - 494     762.4680  1522.9214  1522.7740     0.1475     1  K.IQDKEGIPPDQQR.L  (Ions score 63)
482 - 494     762.4830  1522.9514  1522.7740     0.1775     1  K.IQDKEGIPPDQQR.L  (Ions score 57)
482 - 494     762.4890  1522.9634  1522.7740     0.1895     1  K.IQDKEGIPPDQQR.L  (Ions score 56)
482 - 494     508.6810  1523.0212  1522.7740     0.2472     1  K.IQDKEGIPPDQQR.L  (Ions score 35)
486 - 494     520.2600  1038.5054  1038.5094    -0.0040     0  K.EGIPPDQQR.L  (Ions score 32)
486 - 494     520.2780  1038.5414  1038.5094     0.0320     0  K.EGIPPDQQR.L  (Ions score 29)
486 - 494     520.3150  1038.6154  1038.5094     0.1060     0  K.EGIPPDQQR.L  (Ions score 40)
486 - 494     520.3490  1038.6834  1038.5094     0.1740     0  K.EGIPPDQQR.L  (Ions score 34)
486 - 494     520.3580  1038.7014  1038.5094     0.1920     0  K.EGIPPDQQR.L  (Ions score 29)
486 - 494     520.3680  1038.7214  1038.5094     0.2120     0  K.EGIPPDQQR.L  (Ions score 31)
486 - 494     520.3700  1038.7254  1038.5094     0.2160     0  K.EGIPPDQQR.L  (Ions score 45)
495 - 500     648.4700   647.4627   647.4006     0.0621     0  R.LIFAGK.Q  (Ions score 19)
495 - 506     487.3470  1459.0192  1459.7783    -0.7591     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 21)
495 - 506     730.9630  1459.9114  1459.7783     0.1331     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 71)
495 - 506     487.6450  1459.9132  1459.7783     0.1349     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 39)
495 - 506     487.6540  1459.9402  1459.7783     0.1619     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 38)
495 - 506     730.9780  1459.9414  1459.7783     0.1631     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 69)
495 - 506     730.9970  1459.9794  1459.7783     0.2011     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 71)
495 - 506     731.0360  1460.0574  1459.7783     0.2791     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 71)
507 - 515     541.3490  1080.6834  1080.5451     0.1383     0  R.TLSDYNIQK.E  (Ions score 28)
507 - 515     541.3570  1080.6994  1080.5451     0.1543     0  R.TLSDYNIQK.E  (Ions score 56)
507 - 515     541.3590  1080.7034  1080.5451     0.1583     0  R.TLSDYNIQK.E  (Ions score 56)
507 - 515     541.3690  1080.7234  1080.5451     0.1783     0  R.TLSDYNIQK.E  (Ions score 60)
507 - 515     541.3690  1080.7234  1080.5451     0.1783     0  R.TLSDYNIQK.E  (Ions score 37)
507 - 515     541.3700  1080.7254  1080.5451     0.1803     0  R.TLSDYNIQK.E  (Ions score 21)
507 - 515     541.3750  1080.7354  1080.5451     0.1903     0  R.TLSDYNIQK.E  (Ions score 30)
507 - 515     541.4060  1080.7974  1080.5451     0.2523     0  R.TLSDYNIQK.E  (Ions score 54)
507 - 515     541.4550  1080.8954  1080.5451     0.3503     0  R.TLSDYNIQK.E  (Ions score 56)
516 - 524     534.0010  1065.9874  1066.6135    -0.6260     0  K.ESTLHLVLR.L  (Ions score 30)
516 - 524     534.0090  1066.0034  1066.6135    -0.6100     0  K.ESTLHLVLR.L  (Ions score 34)
516 - 524     534.1020  1066.1894  1066.6135    -0.4240     0  K.ESTLHLVLR.L  (Ions score 39)
516 - 524     534.3590  1066.7034  1066.6135     0.0900     0  K.ESTLHLVLR.L  (Ions score 32)
516 - 524     534.3610  1066.7074  1066.6135     0.0940     0  K.ESTLHLVLR.L  (Ions score 29)
516 - 524     534.3870  1066.7594  1066.6135     0.1460     0  K.ESTLHLVLR.L  (Ions score 60)
516 - 524     534.4190  1066.8234  1066.6135     0.2100     0  K.ESTLHLVLR.L  (Ions score 74)
516 - 524     534.4220  1066.8294  1066.6135     0.2160     0  K.ESTLHLVLR.L  (Ions score 40)
516 - 524     534.4250  1066.8354  1066.6135     0.2220     0  K.ESTLHLVLR.L  (Ions score 44)
516 - 524     534.4340  1066.8534  1066.6135     0.2400     0  K.ESTLHLVLR.L  (Ions score 33)
516 - 524     534.4420  1066.8694  1066.6135     0.2560     0  K.ESTLHLVLR.L  (Ions score 55)
516 - 524     534.4510  1066.8874  1066.6135     0.2740     0  K.ESTLHLVLR.L  (Ions score 28)
516 - 524     534.4670  1066.9194  1066.6135     0.3060     0  K.ESTLHLVLR.L  (Ions score 22)
516 - 524     534.4700  1066.9254  1066.6135     0.3120     0  K.ESTLHLVLR.L  (Ions score 57)
516 - 524     534.4870  1066.9594  1066.6135     0.3460     0  K.ESTLHLVLR.L  (Ions score 16)
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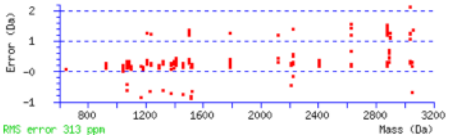
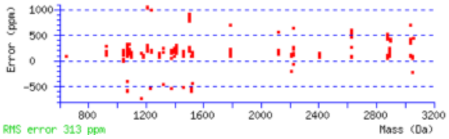




Mascot: http://www.matrixscience.com/

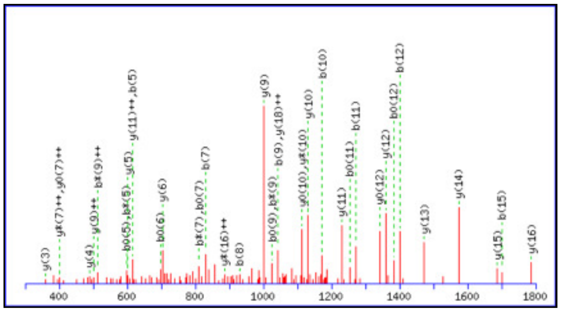
Mascot Search Results

Peptide View

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

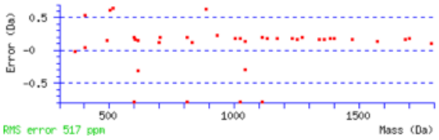
Match to Query 837: 2401.435448 from(1201.725000,2+) intensity(1129620.0000)
Title: Cmpd 117, +MSn(1202.39), 27.1 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00822_YD_9_merge.mgf

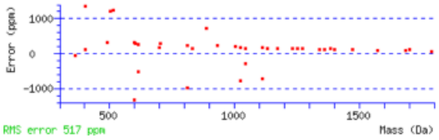
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2401.2588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5     : GlyGly (K)
Ions Score: 97  Expect: 9.2e-08
Matches : 39/226 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							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
96.9	2401.2588	0.1767	TLTGKTITLEVEPSDTIENVK
21.2	2402.1886	-0.7532	MGAEGIKDLLEGLDLDVEIDK
21.1	2402.2839	-0.8484	LKTTGLTVDQVMAARVLESEK
19.9	2401.2675	0.1680	MKIKTVDLEYIQPEKPK
19.9	2401.2675	0.1680	MKIKTVDLEYIQPEKPK
19.6	2401.1730	0.2625	MVNSGTEATMSAVKLARGYTGK
19.0	2402.2693	-0.8339	FPVEEVETVLESITVNVGRTGK
18.4	2401.1972	0.2382	QEDIDSLSDDEIITLAKNLR
18.2	2402.2442	-0.8087	TVIGTPFVEGATVEATVEKQGR
18.1	2401.2060	0.2295	CDISNWNLINKTIDQVLK

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

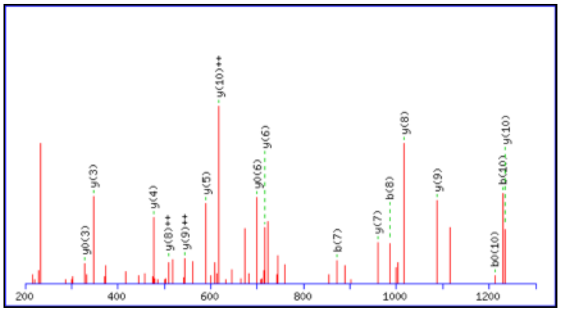
Mascot Search Results

Peptide View

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

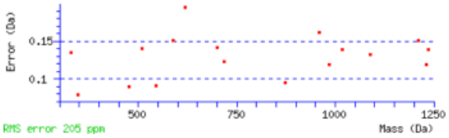
Match to Query 500: 1459.979448 from(730.997000,2+) intensity(17306768.0000)
Title: Cmpd 81, +MSn(731.33), 24.2 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00822_YD_9_merge.mgf

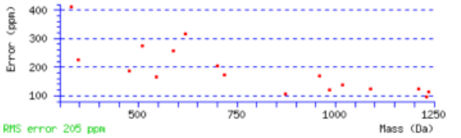
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1459.7783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : GlyGly (K)
Ions Score: 71 **Expect:** 6.9e-05
Matches : 17/102 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	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
70.8	1459.7783	0.2011	LIFAGKQLEDGR
25.5	1459.8293	0.1502	LTRMIRTAGALK
24.2	1460.7544	-0.7750	NIIEMQQLELSK
21.6	1459.7817	0.1978	LLATGMERAGIAK
20.7	1459.8068	0.1726	DMIVNGITVKIK
20.4	1459.7453	0.2342	KMAQEQEKLK
19.9	1459.7307	0.2488	ALENALPYLEDGR
19.5	1459.8068	0.1727	ILQEKMEKAIK
19.2	1457.7950	2.1844	EIEAGKVSVRTR
18.8	1460.7908	-0.8114	TVEMLKAEGIIK

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

Mascot Search Results

Protein View

```
Match to: YD_RFP-BARD-BRCA-Ub Score: 1711
YD_RFP-BARD-BRCA-Ub
Found in search of C:\YaelDavid\100203_YaelDavid\BIT00869_YD_14_merge.mgf

Nominal mass (Mr): 60628; Calculated pI value: 6.10
NCBI BLAST search of YD_RFP-BARD-BRCA-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 48%

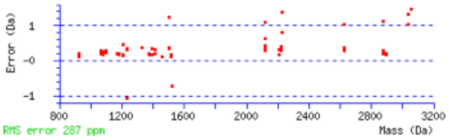
Matched peptides shown in Bold Red

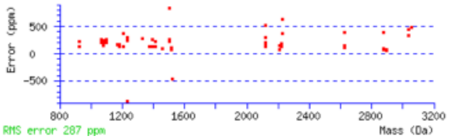
     1 MHHHHHHASS EDVIKEFMRF KVRMEGSVNG HEFEIEGEGE GRPYEGTQTA
    51 KLKVTKGGPL PFAWDILSPQ FQYGSKAYVK HPADIPDYLK LSFPEGFKWE
   101 RVMNFEDGGV VTVTQDSSLQ DGEFIYKVKL RGTNFPSDGP VMQKKTMGWE
   151 ASTERMYPED GALKGEIKMR LKLKDGGHYD AEVKTTYMAK KPVQLPGAYK
   201 TDIKLDITSH NEDYTIVEQY ERAEGRHSTG AENLYFQGLE EPDGRGAWAH
   251 SRAALDRLEK LLRCSRCTNI LREPVCLGGC EHIFCSNCVS DCIGTGCPVC
   301 YTPAWIQDLK INRQLDSMIQ LCSKLRNLLH DNELSDLKED GGSGGDLSAL
   351 RVEEVQNVIN AMQKILECPI CLELIKEPVS TKCDHIFCKF CMLKLLNQKK
   401 GPSQCPLCKN DITKRSLQES TRFSQLVEEL LKIICAFQLD TGLEYANSYN
   451 FAKQIFVKTL TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK
   501 QLEDGRTLSD YNIQKESTLH LVLRLRGG
```

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     1520.1880  3038.3614 3037.3359    1.0255    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 40)
   24 - 51     1013.8980  3038.6722 3037.3359    1.3362    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 52)
   24 - 51     1019.2760  3054.8062 3053.3309    1.4753    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M)  (Ions score 27)
   57 - 76     1104.6430  2207.2714 2207.1051    0.1663    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 60)
   57 - 76     1104.7240  2207.4334 2207.1051    0.3283    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 83)
   91 - 98      924.6090   923.6017  923.4753    0.1265    0  K.LSFPEGFK.W  (Ions score 28)
   91 - 98      462.8460   923.6774  923.4753    0.2022    0  K.LSFPEGFK.W  (Ions score 35)
   91 - 98      462.8510   923.6874  923.4753    0.2122    0  K.LSFPEGFK.W  (Ions score 39)
  102 - 127    1439.7700  2877.5254 2877.3379    0.1876    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 35)
  102 - 127    1439.8210  2877.6274 2877.3379    0.2896    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 57)
  102 - 127    1440.2400  2878.4654 2877.3379    1.1276    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 69)
  102 - 127    1447.7540  2893.4934 2893.3328    0.1606    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 69)
  102 - 127    1447.7800  2893.5454 2893.3328    0.2126    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 75)
  132 - 144     689.4150  1376.8154 1376.6395    0.1760    0  R.GTNFPSDGPVMQK.K  (Ions score 74)
  132 - 144     689.4220  1376.8294 1376.6395    0.1900    0  R.GTNFPSDGPVMQK.K  (Ions score 73)
  132 - 144     697.4160  1392.8174 1392.6344    0.1831    0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 55)
  132 - 144     697.5020  1392.9894 1392.6344    0.3551    0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 62)
  146 - 155     584.3570  1166.6994 1166.5026    0.1968    0  K.TMGWEASTER.M  (Ions score 54)
  146 - 155     592.3380  1182.6614 1182.4975    0.1639    0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 52)
  146 - 155     592.3540  1182.6934 1182.4975    0.1959    0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 52)
  146 - 155     592.3550  1182.6954 1182.4975    0.1979    0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 62)
  173 - 184     444.6850  1331.0332 1330.6517    0.3815    1  K.LKDGGHYDAEVK.T  (Ions score 40)
  191 - 200     550.9350  1099.8554 1099.6390    0.2165    0  K.KPVQLPGAYK.T  (Ions score 48)
  191 - 200     550.9680  1099.9214 1099.6390    0.2825    0  K.KPVQLPGAYK.T  (Ions score 51)
  205 - 222    1113.1580  2224.3014 2224.0284    0.2731    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 7)
  205 - 222    1113.2060  2224.3974 2224.0284    0.3691    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 102)
  205 - 222    1113.2190  2224.4234 2224.0284    0.3951    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 50)
  205 - 222    1113.2260  2224.4374 2224.0284    0.4091    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 74)
  205 - 222     742.6220  2224.8442 2224.0284    0.8158    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 41)
  205 - 222    1113.7200  2225.4254 2224.0284    1.3971    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 85)
  227 - 245    1060.6260  2119.2374 2118.9606    0.2768    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 59)
  227 - 245    1060.6710  2119.3274 2118.9606    0.3668    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 21)
  227 - 245    1060.6980  2119.3814 2118.9606    0.4208    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 155)
  227 - 245     707.4750  2119.4032 2118.9606    0.4425    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 56)
  227 - 245     707.5390  2119.5952 2118.9606    0.6345    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 59)
  227 - 245    1061.0420  2120.0694 2118.9606    1.1088    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 104)
  327 - 338     705.9590  1409.9034 1409.7150    0.1884    0  R.NLLHDNELSDLK.E  (Ions score 66)
  327 - 338     471.0160  1410.0262 1409.7150    0.3111    0  R.NLLHDNELSDLK.E  (Ions score 31)
  327 - 351    1313.2810  2624.5474 2624.2678    0.2797    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 140)
  327 - 351    1313.3280  2624.6414 2624.2678    0.3737    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 132)
  327 - 351    1313.6560  2625.2974 2624.2678    1.0297    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 25)
  339 - 351     616.7560  1231.4974 1232.5633   -1.0659    0  K.EDGGSGGDLSALR.V  (Ions score 77)
  339 - 351     617.4430  1232.8714 1232.5633    0.3081    0  K.EDGGSGGDLSALR.V  (Ions score 85)
  339 - 351     617.4670  1232.9194 1232.5633    0.3561    0  K.EDGGSGGDLSALR.V  (Ions score 81)
  352 - 364     751.5610  1501.1074 1500.7606    0.3468    0  R.VEEVQNVINAMQK.I  (Ions score 105)
  352 - 364     751.5780  1501.1414 1500.7606    0.3808    0  R.VEEVQNVINAMQK.I  (Ions score 109)
  352 - 364     752.0090  1502.0034 1500.7606    1.2428    0  R.VEEVQNVINAMQK.I  (Ions score 89)
  352 - 364     759.4440  1516.8734 1516.7555    0.1179    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 92)
  352 - 364     759.4660  1516.9174 1516.7555    0.1619    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 95)
  423 - 432     603.4190  1204.8234 1204.6703    0.1531    0  R.FSQLVEELLK.I  (Ions score 76)
  423 - 432     603.4250  1204.8354 1204.6703    0.1651    0  R.FSQLVEELLK.I  (Ions score 72)
  423 - 432     603.4260  1204.8374 1204.6703    0.1671    0  R.FSQLVEELLK.I  (Ions score 79)
  423 - 432     603.5680  1205.1214 1204.6703    0.4511    0  R.FSQLVEELLK.I  (Ions score 74)
  482 - 494     762.0380  1522.0614 1522.7740   -0.7125    1  K.IQDKEGIPPDQQR.L  (Ions score 24)
  495 - 506     730.9590  1459.9034 1459.7783    0.1251    1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 77)
  507 - 515     541.3650  1080.7154 1080.5451    0.1703    0  R.TLSDYNIQK.E  (Ions score 60)
  507 - 515     541.3670  1080.7194 1080.5451    0.1743    0  R.TLSDYNIQK.E  (Ions score 60)
  507 - 515     541.3950  1080.7754 1080.5451    0.2303    0  R.TLSDYNIQK.E  (Ions score 56)
  507 - 515     541.4080  1080.8014 1080.5451    0.2563    0  R.TLSDYNIQK.E  (Ions score 43)
  516 - 524     534.4180  1066.8214 1066.6135    0.2080    0  K.ESTLHLVLR.L  (Ions score 57)
  516 - 524     534.4550  1066.8954 1066.6135    0.2820    0  K.ESTLHLVLR.L  (Ions score 60)
```





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

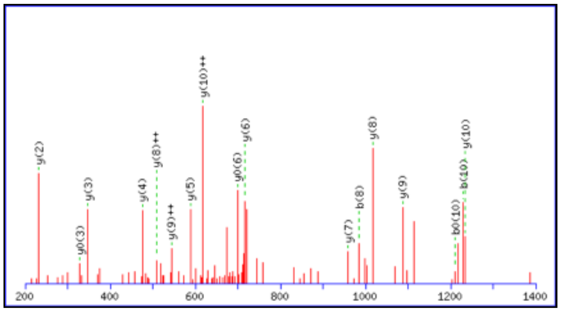
MATRIX SCIENCE Mascot Search Results

Peptide View

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

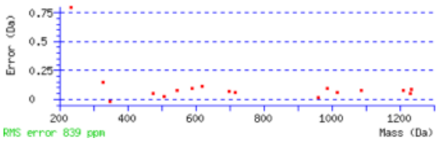
Match to Query 151: 1459.903448 from(730.959000,2+) intensity(1157459.0000)
Title: Cmpd 61, +MSn(731.07), 22.6 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00869_YD_14_merge.mgf

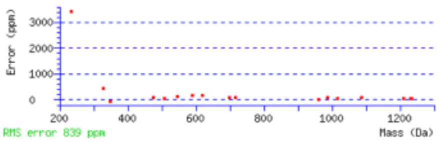
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1459.7783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : GlyGly (K)
Ions Score: 77 **Expect:** 5.7e-05
Matches : 17/102 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	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
77.1	1459.7783	0.1251	LIFAGKQLEDGR
30.7	1458.7929	1.1105	AASDAVLDKLESLK
30.1	1458.7467	1.1568	AAPFIAGTAALEDGR
29.3	1459.6725	0.2309	EAAALQCQLEDGR
23.0	1459.7307	0.1728	ALENALPYLEDGR
21.6	1457.7474	2.1561	KEAQVKAEAEK
20.8	1457.7263	2.1771	AVLTHGYVVDGDGR
20.6	1459.7718	0.1316	VKGSRTGWIPMGR
20.4	1459.8398	0.0636	LLFAIAEKGNKEK
20.0	1460.7471	-0.8436	STQEAIDKITNK

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

Mascot Search Results

Protein View

```
Match to: YD_RFP-BARD-BRCA-Ub Score: 2013
YD_RFP-BARD-BRCA-Ub
Found in search of C:\YaelDavid\100203_YaelDavid\BIT00871_YD_15_merge.mgf

Nominal mass (Mr): 60628; Calculated pI value: 6.10
NCBI BLAST search of YD_RFP-BARD-BRCA-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 57%

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 EPDGRGAWAH
   251 SRAALDRLEK LLRCSRCTNI LREPVCLGGC EHIFCSNCVS DCIGTGCPVC
   301 YTPAWIQDLK INRQLDSMIQ LCSKLRNLLH DNELSDLKED GGSGGDLSAL
   351 RVEEVQNVIN AMQKILECPI CLELIKEPVS TKCDHIFCKF CMLKLLNQKK
   401 GPSQCPLCKN DITKRSLQES TRFSQLVEEL LKIICAFQLD TGLEYANSYN
   451 FAKQIFVKTL TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK
   501 QLEDGRTLSD YNIQKESTLH LVLRLRGG
```

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     1519.7600  3037.5054  3037.3359    0.1695     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 50)
    24 - 51     1013.6090  3037.8052  3037.3359    0.4692     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 33)
    24 - 51     1013.6150  3037.8232  3037.3359    0.4872     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 12)
    24 - 51     1018.5160  3052.5262  3053.3309   -0.8047     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M)  (Ions score 7)
    24 - 51     1527.7300  3053.4454  3053.3309    0.1146     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M)  (Ions score 28)
    24 - 51     1527.8270  3053.6394  3053.3309    0.3086     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M)  (Ions score 23)
    57 - 76     1104.6720  2207.3294  2207.1051    0.2243     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 76)
    57 - 76     1104.7150  2207.4154  2207.1051    0.3103     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 23)
    57 - 76     1104.7210  2207.4274  2207.1051    0.3223     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 61)
    57 - 76     1105.2390  2208.4634  2207.1051    1.3583     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 3)
    57 - 76     1105.2910  2208.5674  2207.1051    1.4623     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 4)
    91 - 98      462.3260   922.6374   923.4753   -0.8378     0  K.LSFPEGFK.W  (Ions score 34)
    91 - 98      462.8240   923.6334   923.4753    0.1582     0  K.LSFPEGFK.W  (Ions score 34)
    91 - 101     698.4540  1394.8934  1394.6983    0.1952     1  K.LSFPEGFKWER.V  (Ions score 46)
   102 - 127    1439.8670  2877.7194  2877.3379    0.3816     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 84)
   102 - 127    1440.2260  2878.4374  2877.3379    1.0996     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 63)
   102 - 127     960.6050  2878.7932  2877.3379    1.4553     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 67)
   102 - 127     960.6480  2878.9222  2877.3379    1.5843     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 63)
   102 - 127    1447.2150  2892.4154  2893.3328   -0.9174     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 17)
   102 - 127     965.5320  2893.5742  2893.3328    0.2414     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 50)
   102 - 127    1448.2560  2894.4974  2893.3328    1.1646     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 101)
   102 - 127    1448.2750  2894.5354  2893.3328    1.2026     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 96)
   102 - 127     965.9870  2894.9392  2893.3328    1.6064     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 74)
   132 - 144     689.4850  1376.9554  1376.6395    0.3160     0  R.GTNFPSDGPVMQK.K  (Ions score 70)
   132 - 144     689.5070  1376.9994  1376.6395    0.3600     0  R.GTNFPSDGPVMQK.K  (Ions score 77)
   132 - 144     697.4170  1392.8194  1392.6344    0.1851     0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 56)
   132 - 144     697.4190  1392.8234  1392.6344    0.1891     0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 74)
   132 - 145     761.5370  1521.0594  1520.7293    0.3301     1  R.GTNFPSDGPVMQKK.T  Oxidation (M)  (Ions score 17)
   145 - 155     648.3820  1294.7494  1294.5976    0.1519     1  K.KTMGWEASTER.M  (Ions score 59)
   145 - 155     648.4170  1294.8194  1294.5976    0.2219     1  K.KTMGWEASTER.M  (Ions score 26)
   146 - 155     584.3540  1166.6934  1166.5026    0.1908     0  K.TMGWEASTER.M  (Ions score 54)
   146 - 155     584.3670  1166.7194  1166.5026    0.2168     0  K.TMGWEASTER.M  (Ions score 50)
   146 - 155     592.2850  1182.5554  1182.4975    0.0579     0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 61)
   146 - 155     592.3130  1182.6114  1182.4975    0.1139     0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 65)
   173 - 184     666.4340  1330.8534  1330.6517    0.2017     1  K.LKDGGHYDAEVK.T  (Ions score 72)
   191 - 200     550.9040  1099.7934  1099.6390    0.1545     0  K.KPVQLPGAYK.T  (Ions score 23)
   191 - 200     550.9370  1099.8594  1099.6390    0.2205     0  K.KPVQLPGAYK.T  (Ions score 48)
   191 - 200     550.9420  1099.8694  1099.6390    0.2305     0  K.KPVQLPGAYK.T  (Ions score 55)
   205 - 222    1112.6660  2223.3174  2224.0284   -0.7109     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 37)
   205 - 222    1113.1530  2224.2914  2224.0284    0.2631     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 45)
   205 - 222    1113.1910  2224.3674  2224.0284    0.3391     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 105)
   205 - 222    1113.1960  2224.3774  2224.0284    0.3491     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 68)
   205 - 222    1113.2090  2224.4034  2224.0284    0.3751     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 6)
   205 - 222    1113.2110  2224.4074  2224.0284    0.3791     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 101)
   205 - 222    1113.7020  2225.3894  2224.0284    1.3611     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 28)
   227 - 245    1060.3420  2118.6694  2118.9606   -0.2912     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 12)
   227 - 245    1060.4460  2118.8774  2118.9606   -0.0832     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 21)
   227 - 245    1060.6750  2119.3354  2118.9606    0.3748     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 61)
   227 - 245     707.4720  2119.3942  2118.9606    0.4335     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 35)
   227 - 245    1061.0780  2120.1414  2118.9606    1.1808     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 127)
   253 - 260     458.3520   914.6894   914.5185    0.1710     1  R.AALDRLEK.L  (Ions score 23)
   253 - 260     458.3590   914.7034   914.5185    0.1850     1  R.AALDRLEK.L  (Ions score 41)
   253 - 260     458.3610   914.7074   914.5185    0.1890     1  R.AALDRLEK.L  (Ions score 37)
   327 - 338     705.9570  1409.8994  1409.7150    0.1844     0  R.NLLHDNELSDLK.E  (Ions score 59)
   327 - 338     470.9800  1409.9182  1409.7150    0.2031     0  R.NLLHDNELSDLK.E  (Ions score 23)
   327 - 338     706.0520  1410.0894  1409.7150    0.3744     0  R.NLLHDNELSDLK.E  (Ions score 64)
   327 - 351    1313.3420  2624.6694  2624.2678    0.4017     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 117)
   327 - 351    1313.3530  2624.6914  2624.2678    0.4237     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 111)
   327 - 351     876.0940  2625.2602  2624.2678    0.9924     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 101)
   327 - 351     657.4100  2625.6109  2624.2678    1.3431     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 38)
   327 - 351     876.2680  2625.7822  2624.2678    1.5144     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 97)
   339 - 351     617.3680  1232.7214  1232.5633    0.1581     0  K.EDGGSGGDLSALR.V  (Ions score 80)
   339 - 351     617.3870  1232.7594  1232.5633    0.1961     0  K.EDGGSGGDLSALR.V  (Ions score 63)
   339 - 351     617.4130  1232.8114  1232.5633    0.2481     0  K.EDGGSGGDLSALR.V  (Ions score 84)
   352 - 364     751.4710  1500.9274  1500.7606    0.1668     0  R.VEEVQNVINAMQK.I  (Ions score 109)
   352 - 364     751.5940  1501.1734  1500.7606    0.4128     0  R.VEEVQNVINAMQK.I  (Ions score 107)
   352 - 364     759.4630  1516.9114  1516.7555    0.1559     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 82)
   352 - 364     759.5170  1517.0194  1516.7555    0.2639     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 71)
   352 - 364     759.5580  1517.1014  1516.7555    0.3459     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 94)
   352 - 364     760.0650  1518.1154  1516.7555    1.3599     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 78)
   423 - 432     603.4690  1204.9234  1204.6703    0.2531     0  R.FSQLVEELLK.I  (Ions score 78)
   423 - 432     603.5140  1205.0134  1204.6703    0.3431     0  R.FSQLVEELLK.I  (Ions score 72)
   423 - 432     603.5410  1205.0674  1204.6703    0.3971     0  R.FSQLVEELLK.I  (Ions score 80)
   423 - 432     604.0150  1206.0154  1204.6703    1.3451     0  R.FSQLVEELLK.I  (Ions score 84)
   423 - 432     604.1040  1206.1934  1204.6703    1.5231     0  R.FSQLVEELLK.I  (Ions score 85)
   433 - 453    1220.2120  2438.4094  2437.1624    1.2471     0  K.IICAFQLDTGLEYANSYNFAK.Q  (Ions score 84)
   464 - 479     894.6530  1787.2914  1786.9200    0.3714     0  K.TITLEVEPSDTIENVK.A  (Ions score 53)
   482 - 494     761.9270  1521.8394  1522.7740   -0.9345     1  K.IQDKEGIPPDQQR.L  (Ions score 14)
   482 - 494     762.5540  1523.0934  1522.7740    0.3195     1  K.IQDKEGIPPDQQR.L  (Ions score 53)
   482 - 494     508.7190  1523.1352  1522.7740    0.3612     1  K.IQDKEGIPPDQQR.L  (Ions score 36)
   482 - 494     762.5780  1523.1414  1522.7740    0.3675     1  K.IQDKEGIPPDQQR.L  (Ions score 56)
   486 - 494     520.3630  1038.7114  1038.5094    0.2020     0  K.EGIPPDQQR.L  (Ions score 32)
   486 - 494     520.3630  1038.7114  1038.5094    0.2020     0  K.EGIPPDQQR.L  (Ions score 28)
   486 - 494     520.3800  1038.7454  1038.5094    0.2360     0  K.EGIPPDQQR.L  (Ions score 28)
   495 - 506     731.0180  1460.0214  1459.7783    0.2431     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 58)
```

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507 - 515     541.3520  1080.6894  1080.5451     0.1443     0  R.TLSDYNIQK.E  (Ions score 54)
507 - 515     541.4180  1080.8214  1080.5451     0.2763     0  R.TLSDYNIQK.E  (Ions score 51)
516 - 524     534.4120  1066.8094  1066.6135     0.1960     0  K.ESTLHLVLR.L  (Ions score 43)
516 - 524     534.4520  1066.8894  1066.6135     0.2760     0  K.ESTLHLVLR.L  (Ions score 43)
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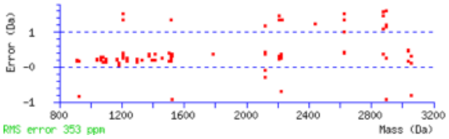
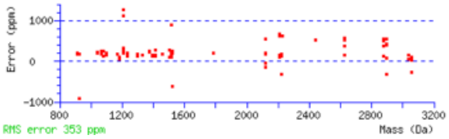




Mascot: http://www.matrixscience.com/

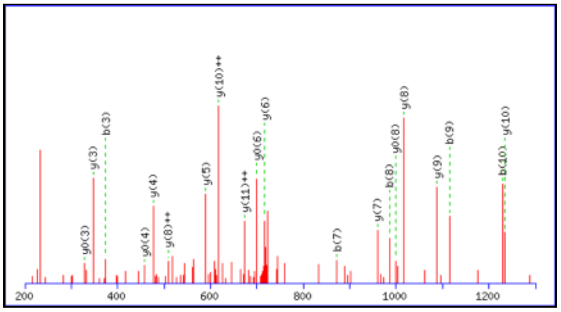
MATRIX SCIENCE Mascot Search Results

Peptide View

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

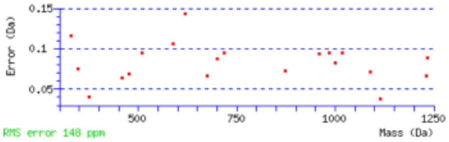
Match to Query 151: 1460.021448 from(731.018000,2+) intensity(1426711.0000)
Title: Cmpd 78, +MSn(731.11), 22.7 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00871_YD_15_merge.mgf

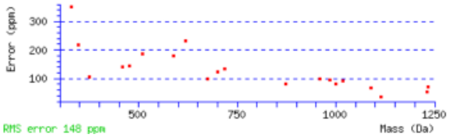
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1459.7783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : GlyGly (K)
Ions Score: 58 **Expect:** 0.00027
Matches : 20/102 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	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
57.6	1459.7783	0.2431	LIFAGKQLEDGR
19.1	1460.7116	-0.6901	LNGGLGTTMGCVGPK
18.4	1459.8398	0.1816	LLFAIAEKGNKEK
18.0	1460.7987	-0.7773	AGVFKKVDEIK
18.0	1460.7987	-0.7773	AGVFKKVDELK
15.9	1459.8293	0.1922	LTRMIRTAGALK
15.7	1459.8610	0.1605	TKTKLSVIESIK
15.7	1459.8610	0.1605	TKTKLSVLESIK
15.7	1459.7718	0.2496	VKGSRTGWIPMGR
15.1	1459.8181	0.2034	IMIKGGGAALTREK

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

Mascot Search Results

Protein View

```
Match to: YD_RFP-BARD-BRCA-Ub Score: 1742
YD_RFP-BARD-BRCA-Ub
Found in search of C:\YaelDavid\100203_YaelDavid\BIT00873_YD_16_merge.mgf

Nominal mass (Mr): 60628; Calculated pI value: 6.10
NCBI BLAST search of YD_RFP-BARD-BRCA-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 49%

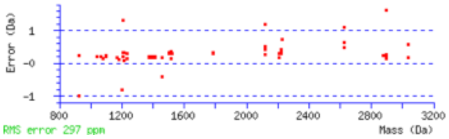
Matched peptides shown in Bold Red

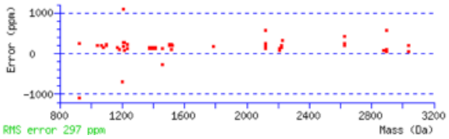
     1 MHHHHHHASS EDVIKEFMRF KVRMEGSVNG HEFEIEGEGE GRPYEGTQTA
    51 KLKVTKGGPL PFAWDILSPQ FQYGSKAYVK HPADIPDYLK LSFPEGFKWE
   101 RVMNFEDGGV VTVTQDSSLQ DGEFIYKVKL RGTNFPSDGP VMQKKTMGWE
   151 ASTERMYPED GALKGEIKMR LKLKDGGHYD AEVKTTYMAK KPVQLPGAYK
   201 TDIKLDITSH NEDYTIVEQY ERAEGRHSTG AENLYFQGLE EPDGRGAWAH
   251 SRAALDRLEK LLRCSRCTNI LREPVCLGGC EHIFCSNCVS DCIGTGCPVC
   301 YTPAWIQDLK INRQLDSMIQ LCSKLRNLLH DNELSDLKED GGSGGDLSAL
   351 RVEEVQNVIN AMQKILECPI CLELIKEPVS TKCDHIFCKF CMLKLLNQKK
   401 GPSQCPLCKN DITKRSLQES TRFSQLVEEL LKIICAFQLD TGLEYANSYN
   451 FAKQIFVKTL TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK
   501 QLEDGRTLSD YNIQKESTLH LVLRLRGG
```

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     1519.7660  3037.5174  3037.3359   0.1815    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 38)
    24 - 51     1013.6410  3037.9012  3037.3359   0.5652    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 11)
    57 - 76     1104.6500  2207.2854  2207.1051   0.1803    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 54)
    57 - 76     1104.7090  2207.4034  2207.1051   0.2983    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 57)
    91 - 98      462.2410   922.4674   923.4753  -1.0078    0  K.LSFPEGFK.W  (Ions score 41)
    91 - 98      462.8580   923.7014   923.4753   0.2262    0  K.LSFPEGFK.W  (Ions score 41)
    91 - 101     698.4390  1394.8634  1394.6983   0.1652    1  K.LSFPEGFKWER.V  (Ions score 38)
   102 - 127    1439.7910  2877.5674  2877.3379   0.2296    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 70)
   102 - 127    1439.7940  2877.5734  2877.3379   0.2356    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 78)
   102 - 127     965.5010  2893.4812  2893.3328   0.1484    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 34)
   102 - 127    1447.7720  2893.5294  2893.3328   0.1966    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 106)
   102 - 127    1447.8140  2893.6134  2893.3328   0.2806    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 84)
   102 - 127     965.9940  2894.9602  2893.3328   1.6274    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 40)
   132 - 144     689.4130  1376.8114  1376.6395   0.1720    0  R.GTNFPSDGPVMQK.K  (Ions score 66)
   132 - 144     689.4250  1376.8354  1376.6395   0.1960    0  R.GTNFPSDGPVMQK.K  (Ions score 69)
   132 - 144     697.4130  1392.8114  1392.6344   0.1771    0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 57)
   132 - 144     697.4290  1392.8434  1392.6344   0.2091    0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 50)
   146 - 155     584.3420  1166.6694  1166.5026   0.1668    0  K.TMGWEASTER.M  (Ions score 49)
   146 - 155     584.3420  1166.6694  1166.5026   0.1668    0  K.TMGWEASTER.M  (Ions score 52)
   146 - 155     592.3100  1182.6054  1182.4975   0.1079    0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 55)
   146 - 155     592.3130  1182.6114  1182.4975   0.1139    0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 59)
   191 - 200     550.9320  1099.8494  1099.6390   0.2105    0  K.KPVQLPGAYK.T  (Ions score 44)
   191 - 200     550.9510  1099.8874  1099.6390   0.2485    0  K.KPVQLPGAYK.T  (Ions score 47)
   191 - 200     607.8900  1213.7654  1213.6819   0.0836    0  K.KPVQLPGAYK.T  GlyGly (K)  (Ions score 42)
   191 - 200     608.0200  1214.0254  1213.6819   0.3436    0  K.KPVQLPGAYK.T  GlyGly (K)  (Ions score 44)
   205 - 222    1113.1780  2224.3414  2224.0284   0.3131    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 112)
   205 - 222    1113.2090  2224.4034  2224.0284   0.3751    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 106)
   205 - 222    1113.2380  2224.4614  2224.0284   0.4331    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 58)
   205 - 222     742.5930  2224.7572  2224.0284   0.7288    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 51)
   227 - 245     707.4180  2119.2322  2118.9606   0.2715    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 65)
   227 - 245    1060.6250  2119.2354  2118.9606   0.2748    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 47)
   227 - 245    1060.6950  2119.3754  2118.9606   0.4148    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 20)
   227 - 245    1060.7490  2119.4834  2118.9606   0.5228    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 137)
   227 - 245    1061.0930  2120.1714  2118.9606   1.2108    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 146)
   327 - 338     705.9600  1409.9054  1409.7150   0.1904    0  R.NLLHDNELSDLK.E  (Ions score 69)
   327 - 338     705.9630  1409.9114  1409.7150   0.1964    0  R.NLLHDNELSDLK.E  (Ions score 67)
   327 - 351    1313.3910  2624.7674  2624.2678   0.4997    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 137)
   327 - 351     875.9740  2624.9002  2624.2678   0.6324    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 90)
   327 - 351    1313.6930  2625.3714  2624.2678   1.1037    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 127)
   339 - 351     617.3690  1232.7234  1232.5633   0.1601    0  K.EDGGSGGDLSALR.V  (Ions score 85)
   339 - 351     617.4320  1232.8494  1232.5633   0.2861    0  K.EDGGSGGDLSALR.V  (Ions score 90)
   352 - 364     751.5390  1501.0634  1500.7606   0.3028    0  R.VEEVQNVINAMQK.I  (Ions score 106)
   352 - 364     751.5590  1501.1034  1500.7606   0.3428    0  R.VEEVQNVINAMQK.I  (Ions score 112)
   352 - 364     759.4600  1516.9054  1516.7555   0.1499    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 98)
   352 - 364     759.5630  1517.1114  1516.7555   0.3559    0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 92)
   423 - 432     602.9290  1203.8434  1204.6703  -0.8269    0  R.FSQLVEELLK.I  (Ions score 73)
   423 - 432     603.4400  1204.8654  1204.6703   0.1951    0  R.FSQLVEELLK.I  (Ions score 77)
   423 - 432     603.5010  1204.9874  1204.6703   0.3171    0  R.FSQLVEELLK.I  (Ions score 82)
   423 - 432     604.0020  1205.9894  1204.6703   1.3191    0  R.FSQLVEELLK.I  (Ions score 63)
   464 - 479     894.6170  1787.2194  1786.9200   0.2994    0  K.TITLEVEPSDTIENVK.A  (Ions score 49)
   464 - 479     894.6320  1787.2494  1786.9200   0.3294    0  K.TITLEVEPSDTIENVK.A  (Ions score 56)
   482 - 494     762.5430  1523.0714  1522.7740   0.2975    1  K.IQDKEGIPPDQQR.L  (Ions score 21)
   486 - 494     520.3620  1038.7094  1038.5094   0.2000    0  K.EGIPPDQQR.L  (Ions score 27)
   495 - 506     730.6930  1459.3714  1459.7783  -0.4069    1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 37)
   495 - 506     730.9840  1459.9534  1459.7783   0.1751    1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 71)
   495 - 506     730.9910  1459.9674  1459.7783   0.1891    1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 69)
   507 - 515     541.3540  1080.6934  1080.5451   0.1483    0  R.TLSDYNIQK.E  (Ions score 52)
   507 - 515     541.3580  1080.7014  1080.5451   0.1563    0  R.TLSDYNIQK.E  (Ions score 57)
   516 - 524     534.4160  1066.8174  1066.6135   0.2040    0  K.ESTLHLVLR.L  (Ions score 57)
   516 - 524     534.4230  1066.8314  1066.6135   0.2180    0  K.ESTLHLVLR.L  (Ions score 57)
```





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

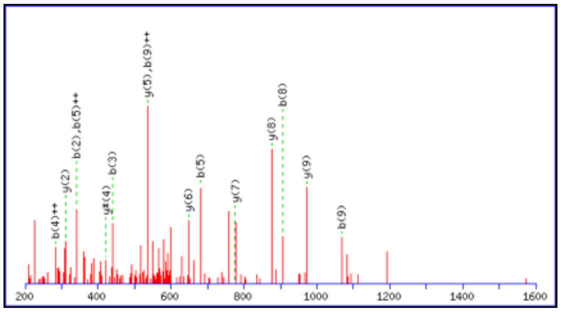
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVQLPGAYK**
Found in **YD_RFP-BARD-BRCA-Ub**, YD_RFP-BARD-BRCA-Ub

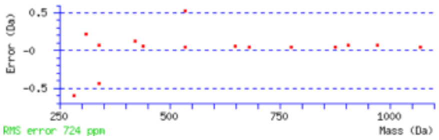
Match to Query 81: 1214.025448 from(608.020000,2+) intensity(408861.0000)
Title: Cmpd 20, +MSn(608.31), 18.8 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00873_YD_16_merge.mgf

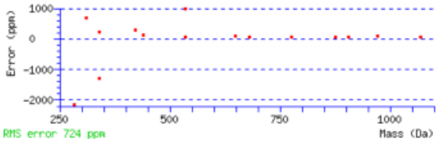
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1213.6819
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : GlyGly (K)
Ions Score: 44 **Expect:** 0.085
Matches : 15/72 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	243.1452	122.0762	226.1186	113.5629	K					10
2	***340.1979***	170.6026	323.1714	162.0893	P	***972.5513***	486.7793	955.5247	478.2660	9
3	***439.2663***	220.1368	422.2398	211.6235	V	***875.4985***	438.2529	858.4720	429.7396	8
4	567.3249	**284.1661**	550.2984	275.6528	Q	***776.4301***	388.7187	759.4036	380.2054	7
5	***680.4090***	**340.7081**	663.3824	332.1949	L	***648.3715***	324.6894	631.3450	316.1761	6
6	777.4618	389.2345	760.4352	380.7212	P	***535.2875***	268.1474	518.2609	259.6341	5
7	834.4832	417.7452	817.4567	409.2320	G	438.2347	219.6210	421.2082	211.1077	4
8	***905.5203***	453.2638	888.4938	444.7505	A	381.2132	191.1103	364.1867	182.5970	3
9	***1068.5837***	**534.7955**	1051.5571	526.2822	Y	***310.1761***	155.5917	293.1496	147.0784	2
10					K	147.1128	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of KPVQLPGAYK
(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	1213.6819	0.3436	KPVQLPGAYK
31.6	1213.5615	0.4639	NFDTGLQEYK
22.4	1213.7434	0.2820	LILVPFLNGTK
21.5	1213.7394	0.2861	TLLEKIKQNK
17.5	1213.6203	0.4051	KNHPGKEYK
17.1	1213.7407	0.2847	KPIPKHPRK
17.1	1213.6455	0.3799	KPLQPFQDK
16.8	1213.7832	0.2423	ILLVAVSIKMK
16.8	1213.7394	0.2861	LIIVNNSSVKK
16.8	1213.6805	0.3449	LLLVELEEEK

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

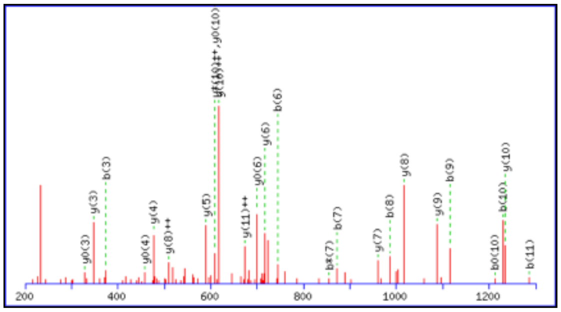
Mascot Search Results

Peptide View

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

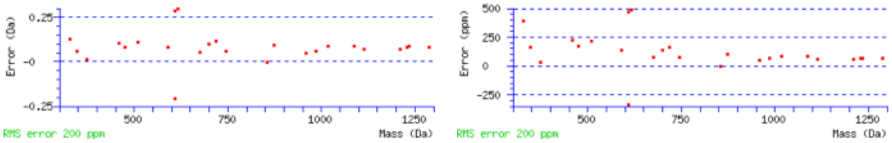
Match to Query 141: 1459.953448 from(730.984000,2+) intensity(5187925.0000)
Title: Cmpd 70, +MSn(731.30), 22.9 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00873_YD_16_merge.mgf

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
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : GlyGly (K)
Ions Score: 71 **Expect:** 0.00012
Matches : 25/102 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	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
71.4	1459.7783	0.1751	LIFAGKQLEDGR
28.4	1460.7987	-0.8453	AGVFKKVDEIK
28.4	1460.7987	-0.8453	AGVFKKVDELK
26.7	1459.6725	0.2809	EAAALQCQLEDGR
20.6	1460.7987	-0.8453	AGVFKKVDEIK
20.6	1460.7987	-0.8453	AGVFKKVDELK
20.2	1459.7089	0.2445	ATAITMPKADDGR
19.5	1459.8432	0.1102	SGMVTLKLEKIK
18.4	1459.7307	0.2228	ALENALPYLEDGR
18.4	1459.7817	0.1718	LLATGMERAGIAK

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

Mascot Search Results

Protein View

```
Match to: YD_RFP-BARD-BRCA-Ub Score: 1715
YD_RFP-BARD-BRCA-Ub
Found in search of C:\YaelDavid\100203_YaelDavid\BIT00875_YD_17_merge.mgf

Nominal mass (Mr): 60628; Calculated pI value: 6.10
NCBI BLAST search of YD_RFP-BARD-BRCA-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 51%

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 EPDGRGAWAH
   251 SRAALDRLEK LLRCSRCTNI LREPVCLGGC EHIFCSNCVS DCIGTGCPVC
   301 YTPAWIQDLK INRQLDSMIQ LCSKLRNLLH DNELSDLKED GGSGGDLSAL
   351 RVEEVQNVIN AMQKILECPI CLELIKEPVS TKCDHIFCKF CMLKLLNQKK
   401 GPSQCPLCKN DITKRSLQES TRFSQLVEEL LKIICAFQLD TGLEYANSYN
   451 FAKQIFVKTL TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK
   501 QLEDGRTLSD YNIQKESTLH LVLRLRGG
```

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     1013.9540  3038.8402  3037.3359     1.5042    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 40)
   24 - 51     1019.3290  3054.9652  3053.3309     1.6343    0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M) (Ions score 50)
   57 - 76     1104.1840  2206.3534  2207.1051    -0.7517    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 54)
   57 - 76     1104.7230  2207.4314  2207.1051     0.3263    0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 78)
   91 - 98      462.8330   923.6514   923.4753     0.1762    0  K.LSFPEGFK.W  (Ions score 37)
   91 - 98      462.8470   923.6794   923.4753     0.2042    0  K.LSFPEGFK.W  (Ions score 32)
   91 - 101     698.4590  1394.9034  1394.6983     0.2052    1  K.LSFPEGFKWER.V  (Ions score 40)
   91 - 101     698.5040  1394.9934  1394.6983     0.2952    1  K.LSFPEGFKWER.V  (Ions score 45)
  102 - 127    1439.7360  2877.4574  2877.3379     0.1196    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 60)
  102 - 127    1439.8260  2877.6374  2877.3379     0.2996    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 67)
  102 - 127    1439.8410  2877.6674  2877.3379     0.3296    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 75)
  102 - 127    1447.1880  2892.3614  2893.3328    -0.9714    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 48)
  102 - 127     965.7210  2894.1412  2893.3328     0.8084    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 19)
  102 - 127    1448.2770  2894.5394  2893.3328     1.2066    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 105)
  102 - 127    1448.2830  2894.5514  2893.3328     1.2186    0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M) (Ions score 99)
  130 - 145     896.0210  1790.0274  1789.9145     0.1129    2  K.LRGTNFPSDGPVMQKK.T  Oxidation (M) (Ions score 27)
  132 - 144     689.4190  1376.8234  1376.6395     0.1840    0  R.GTNFPSDGPVMQK.K  (Ions score 73)
  132 - 144     689.4930  1376.9714  1376.6395     0.3320    0  R.GTNFPSDGPVMQK.K  (Ions score 73)
  132 - 144     697.4180  1392.8214  1392.6344     0.1871    0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 62)
  132 - 144     697.4190  1392.8234  1392.6344     0.1891    0  R.GTNFPSDGPVMQK.K  Oxidation (M) (Ions score 64)
  145 - 155     648.4190  1294.8234  1294.5976     0.2259    1  K.KTMGWEASTER.M  (Ions score 61)
  145 - 155     648.4550  1294.8954  1294.5976     0.2979    1  K.KTMGWEASTER.M  (Ions score 48)
  146 - 155     584.3460  1166.6774  1166.5026     0.1748    0  K.TMGWEASTER.M  (Ions score 48)
  146 - 155     592.3090  1182.6034  1182.4975     0.1059    0  K.TMGWEASTER.M  Oxidation (M) (Ions score 56)
  146 - 155     592.3250  1182.6354  1182.4975     0.1379    0  K.TMGWEASTER.M  Oxidation (M) (Ions score 57)
  191 - 200     550.9490  1099.8834  1099.6390     0.2445    0  K.KPVQLPGAYK.T  (Ions score 52)
  191 - 200     550.9600  1099.9054  1099.6390     0.2665    0  K.KPVQLPGAYK.T  (Ions score 52)
  205 - 222    1113.2090  2224.4034  2224.0284     0.3751    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 80)
  205 - 222    1113.2300  2224.4454  2224.0284     0.4171    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 124)
  205 - 222    1113.2350  2224.4554  2224.0284     0.4271    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 97)
  205 - 222     742.4970  2224.4692  2224.0284     0.4408    0  K.LDITSHNEDYTIVEQYER.A  (Ions score 35)
  227 - 245    1060.2970  2118.5794  2118.9606    -0.3812    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 24)
  227 - 245    1060.7350  2119.4554  2118.9606     0.4948    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 113)
  227 - 245    1061.0830  2120.1514  2118.9606     1.1908    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 146)
  227 - 245     707.7390  2120.1952  2118.9606     1.2345    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 61)
  227 - 245    1061.1750  2120.3354  2118.9606     1.3748    0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 73)
  253 - 260     458.3770   914.7394   914.5185     0.2210    1  R.AALDRLEK.L  (Ions score 39)
  327 - 338     706.0260  1410.0374  1409.7150     0.3224    0  R.NLLHDNELSDLK.E  (Ions score 65)
  327 - 338     471.0240  1410.0502  1409.7150     0.3351    0  R.NLLHDNELSDLK.E  (Ions score 29)
  327 - 338     706.0600  1410.1054  1409.7150     0.3904    0  R.NLLHDNELSDLK.E  (Ions score 61)
  327 - 351    1313.3010  2624.5874  2624.2678     0.3197    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 124)
  327 - 351     875.9890  2624.9452  2624.2678     0.6774    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 81)
  327 - 351    1313.7400  2625.4654  2624.2678     1.1977    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 132)
  327 - 351    1313.7440  2625.4734  2624.2678     1.2057    1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 33)
  339 - 351     617.9740  1233.9334  1232.5633     1.3701    0  K.EDGGSGGDLSALR.V  (Ions score 75)
  352 - 364     751.4820  1500.9494  1500.7606     0.1888    0  R.VEEVQNVINAMQK.I  (Ions score 98)
  352 - 364     751.5700  1501.1254  1500.7606     0.3648    0  R.VEEVQNVINAMQK.I  (Ions score 107)
  352 - 364     759.4840  1516.9534  1516.7555     0.1979    0  R.VEEVQNVINAMQK.I  Oxidation (M) (Ions score 45)
  352 - 364     759.5500  1517.0854  1516.7555     0.3299    0  R.VEEVQNVINAMQK.I  Oxidation (M) (Ions score 98)
  352 - 364     759.5580  1517.1014  1516.7555     0.3459    0  R.VEEVQNVINAMQK.I  Oxidation (M) (Ions score 20)
  352 - 364     759.5720  1517.1294  1516.7555     0.3739    0  R.VEEVQNVINAMQK.I  Oxidation (M) (Ions score 96)
  423 - 432     603.4370  1204.8594  1204.6703     0.1891    0  R.FSQLVEELLK.I  (Ions score 78)
  423 - 432     603.4820  1204.9494  1204.6703     0.2791    0  R.FSQLVEELLK.I  (Ions score 85)
  423 - 432     603.5020  1204.9894  1204.6703     0.3191    0  R.FSQLVEELLK.I  (Ions score 79)
  464 - 479     894.6320  1787.2494  1786.9200     0.3294    0  K.TITLEVEPSDTIENVK.A  (Ions score 60)
  482 - 494     762.0150  1522.0154  1522.7740    -0.7585    1  K.IQDKEGIPPDQQR.L  (Ions score 20)
  482 - 494     762.5400  1523.0654  1522.7740     0.2915    1  K.IQDKEGIPPDQQR.L  (Ions score 52)
  495 - 506     731.0450  1460.0754  1459.7783     0.2971    1  R.LIFAGKQLEDGR.T  GlyGly (K) (Ions score 62)
  507 - 515     541.3620  1080.7094  1080.5451     0.1643    0  R.TLSDYNIQK.E  (Ions score 52)
  507 - 515     541.3710  1080.7274  1080.5451     0.1823    0  R.TLSDYNIQK.E  (Ions score 60)
  516 - 524     534.4090  1066.8034  1066.6135     0.1900    0  K.ESTLHLVLR.L  (Ions score 32)
  516 - 524     534.4140  1066.8134  1066.6135     0.2000    0  K.ESTLHLVLR.L  (Ions score 55)
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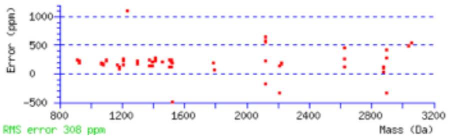


Mascot: http://www.matrixscience.com/

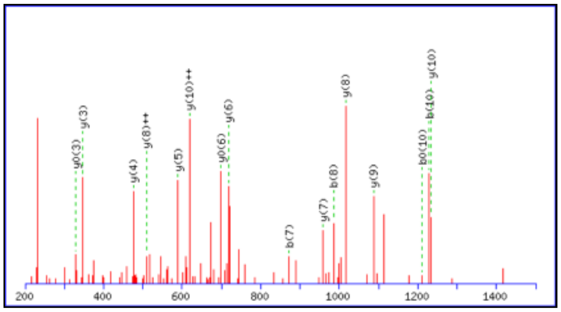
MATRIX SCIENCE Mascot Search Results

Peptide View

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

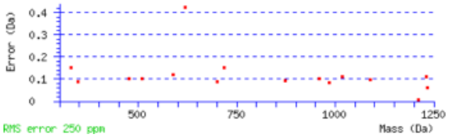
Match to Query 123: 1460.075448 from(731.045000,2+) intensity(1467660.0000)
Title: Cmpd 66, +MSn(731.47), 22.8 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00875_YD_17_merge.mgf

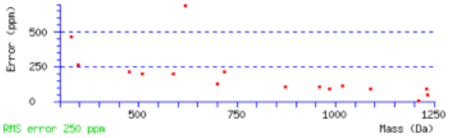
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1459.7783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : GlyGly (K)
Ions Score: 62 **Expect:** 0.00012
Matches : 16/102 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	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
62.0	1459.7783	0.2971	LIFAGKQLEDGR
19.6	1459.6725	0.4029	EAAALQCQLEDGR
18.6	1460.7987	-0.7232	LAFNSLLEKAEAR
18.1	1459.8293	0.2462	LTRMIRTAGALK
17.9	1459.7453	0.3302	KMAQEQEKLK
16.9	1459.7671	0.3084	GINYPTALEGALK
16.5	1460.7987	-0.7233	AGVFKKVDEIK
16.5	1460.7987	-0.7233	AGVFKKVDELK
16.4	1459.8610	0.2145	TKTKLSVIESIK
16.4	1459.8610	0.2145	TKTKLSVLESIK

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

Mascot Search Results

Protein View

Match to: **YD_RFP-BARD-BRCA-Ub** Score: **1956**
YD_RFP-BARD-BRCA-Ub
Found in search of C:\YaelDavid\100203_YaelDavid\BIT00877_YD_18_merge.mgf

Nominal mass (M_r): **60628**; Calculated pI value: **6.10**
NCBI BLAST search of YD_RFP-BARD-BRCA-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **53%**

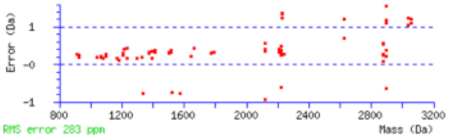
Matched peptides shown in **Bold Red**

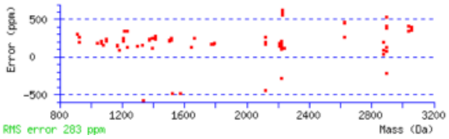
1 MHHHHHHASS EDVIKEFMRF KVR**MEGSVNG HEFEIEGEGE GRPYEGTQTA**
51 **K**LKVTK**GGPL PFAWDILSPQ FQYGSK**AYVK HPADIPDYLK **LSFPEGFK**WE
101 R**VMNFEDGGV VTVTQDSSLQ DGEFIYK**VK**L RGTNFPSDGP VMQKKTMGWE**
151 **ASTER**MYPED GALKGEIKMR **LKLKDGGHYD AEVK**TTYMAK **KPVQLPGAYK**
201 TDIK**LDITSH NEDYTIVEQY ER**AEGR**HSTG AENLYFQGLE EPDGR**GAWAH
251 SR**AALDRLEK** LLRCSRCTNI LREPVCLGGC EHIFCSNCVS DCIGTGCPVC
301 YTPAWIQDLK INR**QLDSMIQ LCSK**LR**NLLH DNELSDLKED GGSGGDLSAL**
351 **RVEEVQNVIN AMQK**ILECPI CLELIKEPVS TKCDHIFCKF CMLKLLNQKK
401 GPSQCPLCKN DITKRSLQES TR**FSQLVEEL LK**IICAFQLD TGLEYANSYN
451 FAKQIFVKTL TGK**TITLEVE PSDTIENVK**A K**IQDKEGIPP DQQR**LIFAGK
501 QLEDGR**TLSD YNIQKESTLH LVLR**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     1520.2040  3038.3934  3037.3359    1.0575     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 32)
   24 - 51     1013.8670  3038.5792  3037.3359    1.2432     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 35)
   24 - 51     1528.2260  3054.4374  3053.3309    1.1066     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M)  (Ions score 41)
   24 - 51     1528.2720  3054.5294  3053.3309    1.1986     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M)  (Ions score 46)
   57 - 76     1104.7180  2207.4214  2207.1051    0.3163     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 49)
   57 - 76     1104.7590  2207.5034  2207.1051    0.3983     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 102)
   91 - 98      462.8380   923.6614   923.4753    0.1862     0  K.LSFPEGFK.W  (Ions score 37)
   91 - 98      462.8660   923.7174   923.4753    0.2422     0  K.LSFPEGFK.W  (Ions score 36)
  102 - 127    1439.7200  2877.4254  2877.3379    0.0876     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 12)
  102 - 127    1439.8040  2877.5934  2877.3379    0.2556     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 75)
  102 - 127    1439.8070  2877.5994  2877.3379    0.2616     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 85)
  102 - 127     960.3040  2877.8902  2877.3379    0.5523     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 50)
  102 - 127     960.3060  2877.8962  2877.3379    0.5583     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 61)
  102 - 127    1447.3490  2892.6834  2893.3328   -0.6494     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 23)
  102 - 127    1447.7900  2893.5654  2893.3328    0.2326     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 36)
  102 - 127     965.5810  2893.7212  2893.3328    0.3884     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 47)
  102 - 127    1448.2290  2894.4434  2893.3328    1.1106     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 74)
  102 - 127    1448.2380  2894.4614  2893.3328    1.1286     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 103)
  102 - 127    1448.2720  2894.5294  2893.3328    1.1966     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 75)
  102 - 127     965.9680  2894.8822  2893.3328    1.5494     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 69)
  130 - 144     824.0250  1646.0354  1645.8246    0.2108     1  K.LRGTNFPSDGPVMQK.K  (Ions score 46)
  130 - 144     555.0880  1662.2422  1661.8195    0.4226     1  K.LRGTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 22)
  130 - 145     888.1220  1774.2294  1773.9196    0.3099     2  K.LRGTNFPSDGPVMQKK.T  (Ions score 34)
  130 - 145     896.1300  1790.2454  1789.9145    0.3309     2  K.LRGTNFPSDGPVMQKK.T  Oxidation (M)  (Ions score 30)
  132 - 144     689.4830  1376.9514  1376.6395    0.3120     0  R.GTNFPSDGPVMQK.K  (Ions score 73)
  132 - 144     689.4870  1376.9594  1376.6395    0.3200     0  R.GTNFPSDGPVMQK.K  (Ions score 70)
  132 - 144     697.4100  1392.8054  1392.6344    0.1711     0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 64)
  132 - 144     697.4960  1392.9774  1392.6344    0.3431     0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 54)
  132 - 145     753.5310  1505.0474  1504.7344    0.3130     1  R.GTNFPSDGPVMQKK.T  (Ions score 43)
  145 - 155     648.3950  1294.7754  1294.5976    0.1779     1  K.KTMGWEASTER.M  (Ions score 71)
  146 - 155     584.3460  1166.6774  1166.5026    0.1748     0  K.TMGWEASTER.M  (Ions score 54)
  146 - 155     584.3470  1166.6794  1166.5026    0.1768     0  K.TMGWEASTER.M  (Ions score 54)
  146 - 155     592.3060  1182.5974  1182.4975    0.0999     0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 74)
  146 - 155     592.3070  1182.5994  1182.4975    0.1019     0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 60)
  171 - 184     786.5370  1571.0594  1571.8307   -0.7713     2  R.LKLKDGGHYDAEVK.T  (Ions score 78)
  173 - 184     666.4340  1330.8534  1330.6517    0.2017     1  K.LKDGGHYDAEVK.T  (Ions score 69)
  191 - 200     550.9430  1099.8714  1099.6390    0.2325     0  K.KPVQLPGAYK.T  (Ions score 50)
  191 - 200     550.9600  1099.9054  1099.6390    0.2665     0  K.KPVQLPGAYK.T  (Ions score 58)
  191 - 200     608.0540  1214.0934  1213.6819    0.4116     0  K.KPVQLPGAYK.T  GlyGly (K)  (Ions score 24)
  205 - 222    1112.7100  2223.4054  2224.0284   -0.6229     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 5)
  205 - 222    1113.1380  2224.2614  2224.0284    0.2331     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 58)
  205 - 222    1113.1810  2224.3474  2224.0284    0.3191     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 8)
  205 - 222    1113.2010  2224.3874  2224.0284    0.3591     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 111)
  205 - 222     742.4750  2224.4032  2224.0284    0.3748     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 29)
  205 - 222    1113.2590  2224.5034  2224.0284    0.4751     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 106)
  205 - 222     742.7610  2225.2612  2224.0284    1.2328     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 39)
  205 - 222    1113.6890  2225.3634  2224.0284    1.3351     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 42)
  205 - 222    1113.7110  2225.4074  2224.0284    1.3791     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 33)
  227 - 245     707.0140  2118.0202  2118.9606   -0.9405     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 59)
  227 - 245    1060.6670  2119.3194  2118.9606    0.3588     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 39)
  227 - 245    1060.6740  2119.3334  2118.9606    0.3728     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 15)
  227 - 245     707.4660  2119.3762  2118.9606    0.4155     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 54)
  227 - 245    1060.7700  2119.5254  2118.9606    0.5648     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 119)
  227 - 245    1060.7740  2119.5334  2118.9606    0.5728     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 135)
  253 - 260     458.4050   914.7954   914.5185    0.2770     1  R.AALDRLEK.L  (Ions score 39)
  314 - 324     669.4370  1336.8594  1337.6319   -0.7725     0  R.QLDSMIQLCSK.L  Oxidation (M)  (Ions score 26)
  327 - 338     706.0320  1410.0494  1409.7150    0.3344     0  R.NLLHDNELSDLK.E  (Ions score 65)
  327 - 338     706.0610  1410.1074  1409.7150    0.3924     0  R.NLLHDNELSDLK.E  (Ions score 66)
  327 - 351     875.9940  2624.9602  2624.2678    0.6924     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 97)
  327 - 351    1313.7410  2625.4674  2624.2678    1.1997     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 23)
  327 - 351    1313.7440  2625.4734  2624.2678    1.2057     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 120)
  339 - 351     617.3720  1232.7294  1232.5633    0.1661     0  K.EDGGSGGDLSALR.V  (Ions score 72)
  339 - 351     617.5040  1232.9934  1232.5633    0.4301     0  K.EDGGSGGDLSALR.V  (Ions score 84)
  352 - 364     751.5490  1501.0834  1500.7606    0.3228     0  R.VEEVQNVINAMQK.I  (Ions score 105)
  352 - 364     751.5540  1501.0934  1500.7606    0.3328     0  R.VEEVQNVINAMQK.I  (Ions score 109)
  352 - 364     759.5540  1517.0934  1516.7555    0.3379     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 29)
  352 - 364     759.5690  1517.1234  1516.7555    0.3679     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 102)
  352 - 364     759.5780  1517.1414  1516.7555    0.3859     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 102)
  423 - 432     603.4660  1204.9174  1204.6703    0.2471     0  R.FSQLVEELLK.I  (Ions score 73)
  423 - 432     603.4760  1204.9374  1204.6703    0.2671     0  R.FSQLVEELLK.I  (Ions score 75)
  423 - 432     603.4970  1204.9794  1204.6703    0.3091     0  R.FSQLVEELLK.I  (Ions score 81)
  464 - 479     894.6250  1787.2354  1786.9200    0.3154     0  K.TITLEVEPSDTIENVK.A  (Ions score 66)
  482 - 494     762.0250  1522.0354  1522.7740   -0.7385     1  K.IQDKEGIPPDQQR.L  (Ions score 15)
  486 - 494     520.3590  1038.7034  1038.5094    0.1940     0  K.EGIPPDQQR.L  (Ions score 26)
  507 - 515     541.3630  1080.7114  1080.5451    0.1663     0  R.TLSDYNIQK.E  (Ions score 57)
  507 - 515     541.3640  1080.7134  1080.5451    0.1683     0  R.TLSDYNIQK.E  (Ions score 57)
  507 - 524    1122.7390  2243.4634  2243.1910    0.2725     1  R.TLSDYNIQKESTLHLVLR.L  GlyGly (K)  (Ions score 83)
  516 - 524     534.4130  1066.8114  1066.6135    0.1980     0  K.ESTLHLVLR.L  (Ions score 56)
  516 - 524     534.4300  1066.8454  1066.6135    0.2320     0  K.ESTLHLVLR.L  (Ions score 57)
```





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

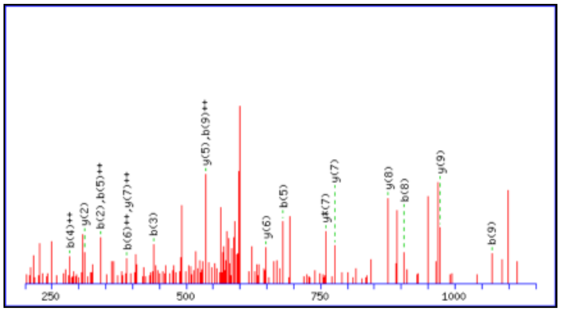
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVQLPGAYK**
Found in **YD_RFP-BARD-BRCA-Ub**, YD_RFP-BARD-BRCA-Ub

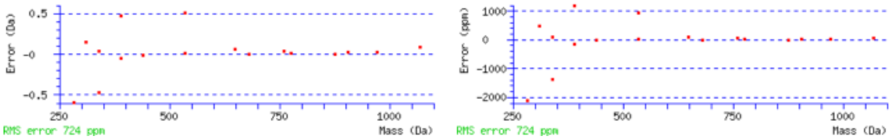
Match to Query 76: 1214.093448 from(608.054000,2+) intensity(124534.0000)
Title: Cmpd 19, +MSn(608.59), 18.7 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00877_YD_18_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1213.6819
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : GlyGly (K)
Ions Score: 24 **Expect:** 0.77
Matches : 17/72 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	243.1452	122.0762	226.1186	113.5629	K					10
2	***340.1979***	170.6026	323.1714	162.0893	P	***972.5513***	486.7793	955.5247	478.2660	9
3	***439.2663***	220.1368	422.2398	211.6235	V	***875.4985***	438.2529	858.4720	429.7396	8
4	567.3249	**284.1661**	550.2984	275.6528	Q	***776.4301***	388.7187	759.4036	380.2054	7
5	***680.4090***	**340.7081**	663.3824	332.1949	L	***648.3715***	324.6894	631.3450	316.1761	6
6	777.4618	**389.2345**	760.4352	380.7212	P	***535.2875***	268.1474	518.2609	259.6341	5
7	834.4832	417.7452	817.4567	409.2320	G	438.2347	219.6210	421.2082	211.1077	4
8	***905.5203***	453.2638	888.4938	444.7505	A	381.2132	191.1103	364.1867	182.5970	3
9	***1068.5837***	**534.7955**	1051.5571	526.2822	Y	***310.1761***	155.5917	293.1496	147.0784	2
10					K	147.1128	74.0600	130.0863	65.5468	1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
23.7	1213.6819	0.4116	KPVQLPGAYK
21.6	1213.7434	0.3500	LILVPFLNGTK
18.8	1213.6190	0.4744	VLDQLLNLGDD
15.1	1213.6091	0.4843	KEGIHPEYK
13.0	1213.6125	0.4809	VTTHQLQEMK
12.5	1213.7142	0.3792	KPVAKSTKK
11.8	1213.6918	0.4016	DKIVVPSDLTK
11.6	1214.5092	-0.4157	VESFNEGFGTE
11.6	1213.7832	0.3103	ILLVAVSIKMK
11.6	1213.7394	0.3541	LIIVNNSSVKK

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

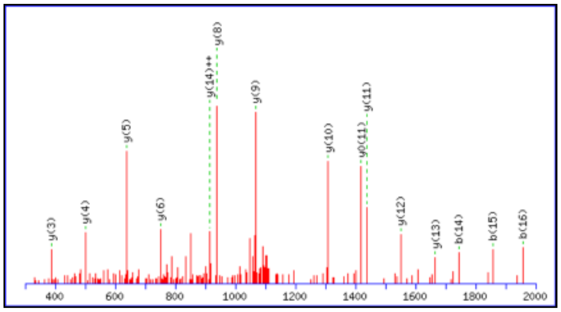
Mascot Search Results

Peptide View

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

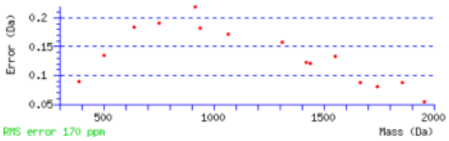
Match to Query 313: 2243.463448 from(1122.739000,2+) intensity(2095379.0000)
Title: Cmpd 91, +MSn(1123.19), 25.5 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00877_YD_18_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

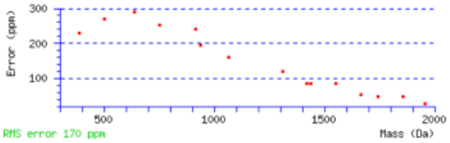


Monoisotopic mass of neutral peptide Mr(calc): 2243.1910
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K9 : GlyGly (K)
Ions Score: 83 **Expect:** 1.7e-06
Matches : 15/182 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	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



RMS error 170 ppm



RMS error 170 ppm

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
83.0	2243.1910	0.2725	TLSDYNIQKESTLHLVLR
20.6	2244.1175	-0.6540	VSDYTAFINQGKLIEYNR
17.3	2244.0555	-0.5920	CKPPPNLQLLDPYMDDGQK
16.7	2244.0191	-0.5556	SMEDLVNEFDEKLNVCFR
16.3	2243.1011	0.3624	KEFFLWSEEIERNFQK
16.1	2242.9882	0.4753	RMGRYCGADMPPTGSTTGSK
15.4	2243.1580	0.3055	SIGNTISPQDVMNKLGGDILR
15.1	2244.0811	-0.6176	YFAIAQIQQDQAESYADRK
14.4	2243.2677	0.1957	NLKIGYENLFIEVPIVIR
14.3	2243.0865	0.3769	DPGAVRNPQNQYPSELMRR

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

Mascot Search Results

Protein View

Match to: **YD_RFP-BARD-BRCA-Ub** Score: **1819**
YD_RFP-BARD-BRCA-Ub
Found in search of C:\YaelDavid\100203_YaelDavid\BIT00881_YD_20_merge.mgf

Nominal mass (M_r): **60628;** Calculated pI value: **6.10**
NCBI BLAST search of YD_RFP-BARD-BRCA-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **43%**

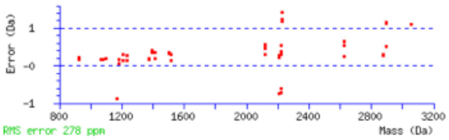
Matched peptides shown in **Bold Red**

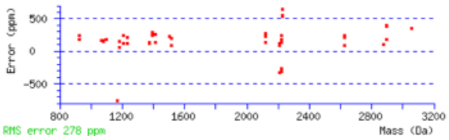
1 MHHHHHHASS EDVIKEFMRF KVR**MEGSVNG HEFEIEGEGE GRPYEGTQTA**
51 **K**LKVTK**GGPL PFAWDILSPQ FQYGSK**AYVK **HPADIPDYLK LSFPEGFKWE**
101 **RVMNFEDGGV VTVTQDSSLQ DGEFIYK**VKL R**GTNFPSDGP VMQK**K**TMGWE**
151 **ASTER**MYPED GALKGEIKMR LKLKDGGHYD AEVKTTYMAK **KPVQLPGAYK**
201 TDIK**LDITSH NEDYTIVEQY ER**AEGR**HSTG AENLYFQGLE EPDGR**GAWAH
251 SRAALDRLEK LLRCSRCTNI LREPVCLGGC EHIFCSNCVS DCIGTGCPVC
301 YTPAWIQDLK INRQLDSMIQ LCSKLR**NLLH DNELSDLKED GGSGGDLSAL**
351 **RVEEVQNVIN AMQK**ILECPI CLELIKEPVS TKCDHIFCKF CMLKLLNQKK
401 GPSQCPLCKN DITKRSLQES TR**FSQLVEEL LK**IICAFQLD TGLEYANSYN
451 FAKQIFVKTL TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK
501 QLEDGR**TLSD YNIQKESTLH LVLR**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	1528.2220	3054.4294	3053.3309	1.0986	0	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L Oxidation (M) (Ions score 26)
57 - 76	1104.1910	2206.3674	2207.1051	-0.7377	0	K.GGPLPFAWDILSPQFQYGSK.A (Ions score 67)
57 - 76	1104.6640	2207.3134	2207.1051	0.2083	0	K.GGPLPFAWDILSPQFQYGSK.A (Ions score 71)
57 - 76	1104.6980	2207.3814	2207.1051	0.2763	0	K.GGPLPFAWDILSPQFQYGSK.A (Ions score 68)
81 - 90	584.3630	1166.7114	1167.5924	-0.8810	0	K.HPADIPDYLK.L (Ions score 38)
91 - 98	462.8260	923.6374	923.4753	0.1622	0	K.LSFPEGFK.W (Ions score 36)
91 - 98	462.8590	923.7034	923.4753	0.2282	0	K.LSFPEGFK.W (Ions score 37)
91 - 101	698.5600	1395.1054	1394.6983	0.4072	1	K.LSFPEGFKWER.V (Ions score 45)
102 - 127	1439.8170	2877.6194	2877.3379	0.2816	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V (Ions score 70)
102 - 127	1439.8220	2877.6294	2877.3379	0.2916	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V (Ions score 74)
102 - 127	965.6240	2893.8502	2893.3328	0.5174	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V Oxidation (M) (Ions score 57)
102 - 127	1448.2330	2894.4514	2893.3328	1.1186	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V Oxidation (M) (Ions score 83)
102 - 127	1448.2500	2894.4854	2893.3328	1.1526	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V Oxidation (M) (Ions score 67)
102 - 127	1448.2520	2894.4894	2893.3328	1.1566	0	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V Oxidation (M) (Ions score 81)
132 - 144	689.4060	1376.7974	1376.6395	0.1580	0	R.GTNFPSDGPVMQK.K (Ions score 77)
132 - 144	689.4190	1376.8234	1376.6395	0.1840	0	R.GTNFPSDGPVMQK.K (Ions score 70)
132 - 144	697.4970	1392.9794	1392.6344	0.3451	0	R.GTNFPSDGPVMQK.K Oxidation (M) (Ions score 52)
132 - 144	697.5000	1392.9854	1392.6344	0.3511	0	R.GTNFPSDGPVMQK.K Oxidation (M) (Ions score 65)
146 - 155	592.2860	1182.5574	1182.4975	0.0599	0	K.TMGWEASTER.M Oxidation (M) (Ions score 53)
146 - 155	592.3450	1182.6754	1182.4975	0.1779	0	K.TMGWEASTER.M Oxidation (M) (Ions score 62)
191 - 200	550.9270	1099.8394	1099.6390	0.2005	0	K.KPVQLPGAYK.T (Ions score 48)
205 - 222	1112.6660	2223.3174	2224.0284	-0.7109	0	K.LDITSHNEDYTIVEQYER.A (Ions score 30)
205 - 222	1112.7170	2223.4194	2224.0284	-0.6089	0	K.LDITSHNEDYTIVEQYER.A (Ions score 18)
205 - 222	742.4500	2224.3282	2224.0284	0.2998	0	K.LDITSHNEDYTIVEQYER.A (Ions score 44)
205 - 222	1113.2170	2224.4194	2224.0284	0.3911	0	K.LDITSHNEDYTIVEQYER.A (Ions score 107)
205 - 222	742.5340	2224.5802	2224.0284	0.5518	0	K.LDITSHNEDYTIVEQYER.A (Ions score 24)
205 - 222	1113.6120	2225.2094	2224.0284	1.1811	0	K.LDITSHNEDYTIVEQYER.A (Ions score 52)
205 - 222	1113.6170	2225.2194	2224.0284	1.1911	0	K.LDITSHNEDYTIVEQYER.A (Ions score 106)
205 - 222	1113.6380	2225.2614	2224.0284	1.2331	0	K.LDITSHNEDYTIVEQYER.A (Ions score 110)
205 - 222	1113.7330	2225.4514	2224.0284	1.4231	0	K.LDITSHNEDYTIVEQYER.A (Ions score 42)
227 - 245	1060.6330	2119.2514	2118.9606	0.2908	0	R.HSTGAENLYFQGLEEPDGR.G (Ions score 105)
227 - 245	707.4840	2119.4302	2118.9606	0.4695	0	R.HSTGAENLYFQGLEEPDGR.G (Ions score 68)
227 - 245	1060.7430	2119.4714	2118.9606	0.5108	0	R.HSTGAENLYFQGLEEPDGR.G (Ions score 117)
227 - 245	1060.7480	2119.4814	2118.9606	0.5208	0	R.HSTGAENLYFQGLEEPDGR.G (Ions score 102)
227 - 245	707.5200	2119.5382	2118.9606	0.5775	0	R.HSTGAENLYFQGLEEPDGR.G (Ions score 66)
327 - 338	705.9630	1409.9114	1409.7150	0.1964	0	R.NLLHDNELSDLK.E (Ions score 65)
327 - 338	706.0440	1410.0734	1409.7150	0.3584	0	R.NLLHDNELSDLK.E (Ions score 67)
327 - 351	1313.2640	2624.5134	2624.2678	0.2457	1	R.NLLHDNELSDLKEDGGSGGDLSALR.V (Ions score 137)
327 - 351	1313.4110	2624.8074	2624.2678	0.5397	1	R.NLLHDNELSDLKEDGGSGGDLSALR.V (Ions score 123)
327 - 351	875.9760	2624.9062	2624.2678	0.6384	1	R.NLLHDNELSDLKEDGGSGGDLSALR.V (Ions score 101)
339 - 351	617.3600	1232.7054	1232.5633	0.1421	0	K.EDGGSGGDLSALR.V (Ions score 94)
339 - 351	617.3640	1232.7134	1232.5633	0.1501	0	K.EDGGSGGDLSALR.V (Ions score 84)
339 - 351	617.4200	1232.8254	1232.5633	0.2621	0	K.EDGGSGGDLSALR.V (Ions score 84)
352 - 364	751.5560	1501.0974	1500.7606	0.3368	0	R.VEEVQNVINAMQK.I (Ions score 102)
352 - 364	751.5590	1501.1034	1500.7606	0.3428	0	R.VEEVQNVINAMQK.I (Ions score 102)
352 - 364	759.4520	1516.8894	1516.7555	0.1339	0	R.VEEVQNVINAMQK.I Oxidation (M) (Ions score 98)
352 - 364	759.4580	1516.9014	1516.7555	0.1459	0	R.VEEVQNVINAMQK.I Oxidation (M) (Ions score 99)
352 - 364	759.5330	1517.0514	1516.7555	0.2959	0	R.VEEVQNVINAMQK.I Oxidation (M) (Ions score 82)
352 - 364	759.5340	1517.0534	1516.7555	0.2979	0	R.VEEVQNVINAMQK.I Oxidation (M) (Ions score 98)
423 - 432	603.4160	1204.8174	1204.6703	0.1471	0	R.FSQLVEELLK.I (Ions score 85)
423 - 432	603.4870	1204.9594	1204.6703	0.2891	0	R.FSQLVEELLK.I (Ions score 71)
507 - 515	541.3640	1080.7134	1080.5451	0.1683	0	R.TLSDYNIQK.E (Ions score 57)
507 - 515	541.3690	1080.7234	1080.5451	0.1783	0	R.TLSDYNIQK.E (Ions score 30)
516 - 524	534.4010	1066.7874	1066.6135	0.1740	0	K.ESTLHLVLR.L (Ions score 34)





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

Mascot Search Results

Protein View

```
Match to: YD_RFP-BARD-BRCA-Ub Score: 2003
YD_RFP-BARD-BRCA-Ub
Found in search of C:\YaelDavid\100203_YaelDavid\BIT00883_YD_21_merge.mgf

Nominal mass (Mr): 60628; Calculated pI value: 6.10
NCBI BLAST search of YD_RFP-BARD-BRCA-Ub against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: GlyGly (K),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 54%

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 EPDGRGAWAH
   251 SRAALDRLEK LLRCSRCTNI LREPVCLGGC EHIFCSNCVS DCIGTGCPVC
   301 YTPAWIQDLK INRQLDSMIQ LCSKLRNLLH DNELSDLKED GGSGGDLSAL
   351 RVEEVQNVIN AMQKILECPI CLELIKEPVS TKCDHIFCKF CMLKLLNQKK
   401 GPSQCPLCKN DITKRSLQES TRFSQLVEEL LKIICAFQLD TGLEYANSYN
   451 FAKQIFVKTL TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK
   501 QLEDGRTLSD YNIQKESTLH LVLRLRGG
```

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     1013.6630  3037.9672  3037.3359    0.6312     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 21)
   24 - 51     1013.9520  3038.8342  3037.3359    1.4982     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  (Ions score 28)
   24 - 51     1528.2350  3054.4554  3053.3309    1.1246     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M)  (Ions score 49)
   24 - 51     1528.6900  3055.3654  3053.3309    2.0346     0  R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L  Oxidation (M)  (Ions score 16)
   57 - 76     1104.2260  2206.4374  2207.1051   -0.6677     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 63)
   57 - 76     1104.6350  2207.2554  2207.1051    0.1503     0  K.GGPLPFAWDILSPQFQYGSK.A  (Ions score 64)
   91 - 98      462.8320   923.6494   923.4753    0.1742     0  K.LSFPEGFK.W  (Ions score 43)
   91 - 98      462.8660   923.7174   923.4753    0.2422     0  K.LSFPEGFK.W  (Ions score 33)
  102 - 127    1439.7450  2877.4754  2877.3379    0.1376     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 61)
  102 - 127    1439.7840  2877.5534  2877.3379    0.2156     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 85)
  102 - 127     960.2240  2877.6502  2877.3379    0.3123     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 45)
  102 - 127     960.3290  2877.9652  2877.3379    0.6273     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 44)
  102 - 127    1440.2790  2878.5434  2877.3379    1.2056     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  (Ions score 82)
  102 - 127     965.5820  2893.7242  2893.3328    0.3914     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 37)
  102 - 127     965.6810  2894.0212  2893.3328    0.6884     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 34)
  102 - 127    1448.2630  2894.5114  2893.3328    1.1786     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 90)
  102 - 127    1448.2730  2894.5314  2893.3328    1.1986     0  R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V  Oxidation (M)  (Ions score 91)
  132 - 144     689.4210  1376.8274  1376.6395    0.1880     0  R.GTNFPSDGPVMQK.K  (Ions score 73)
  132 - 144     689.4270  1376.8394  1376.6395    0.2000     0  R.GTNFPSDGPVMQK.K  (Ions score 73)
  132 - 144     689.4330  1376.8514  1376.6395    0.2120     0  R.GTNFPSDGPVMQK.K  (Ions score 73)
  132 - 144     697.4090  1392.8034  1392.6344    0.1691     0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 56)
  132 - 144     697.4250  1392.8354  1392.6344    0.2011     0  R.GTNFPSDGPVMQK.K  Oxidation (M)  (Ions score 63)
  146 - 155     584.3450  1166.6754  1166.5026    0.1728     0  K.TMGWEASTER.M  (Ions score 49)
  146 - 155     584.3500  1166.6854  1166.5026    0.1828     0  K.TMGWEASTER.M  (Ions score 54)
  146 - 155     591.7870  1181.5594  1182.4975   -0.9381     0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 57)
  146 - 155     592.2980  1182.5814  1182.4975    0.0839     0  K.TMGWEASTER.M  Oxidation (M)  (Ions score 56)
  173 - 184     666.4290  1330.8434  1330.6517    0.1917     1  K.LKDGGHYDAEVK.T  (Ions score 68)
  191 - 200     550.9190  1099.8234  1099.6390    0.1845     0  K.KPVQLPGAYK.T  (Ions score 48)
  191 - 200     550.9440  1099.8734  1099.6390    0.2345     0  K.KPVQLPGAYK.T  (Ions score 44)
  205 - 222    1113.1280  2224.2414  2224.0284    0.2131     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 53)
  205 - 222    1113.1930  2224.3714  2224.0284    0.3431     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 40)
  205 - 222    1113.2260  2224.4374  2224.0284    0.4091     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 115)
  205 - 222    1113.2260  2224.4374  2224.0284    0.4091     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 7)
  205 - 222    1113.2970  2224.5794  2224.0284    0.5511     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 111)
  205 - 222     742.6490  2224.9252  2224.0284    0.8968     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 20)
  205 - 222     742.8280  2225.4622  2224.0284    1.4338     0  K.LDITSHNEDYTIVEQYER.A  (Ions score 20)
  227 - 245    1060.2290  2118.4434  2118.9606   -0.5172     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 25)
  227 - 245     707.4300  2119.2682  2118.9606    0.3075     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 60)
  227 - 245     707.4570  2119.3492  2118.9606    0.3885     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 59)
  227 - 245    1060.7660  2119.5174  2118.9606    0.5568     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 135)
  227 - 245    1060.7940  2119.5734  2118.9606    0.6128     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 124)
  227 - 245    1061.1470  2120.2794  2118.9606    1.3188     0  R.HSTGAENLYFQGLEEPDGR.G  (Ions score 34)
  253 - 260     458.3690   914.7234   914.5185    0.2050     1  R.AALDRLEK.L  (Ions score 36)
  314 - 324     669.4990  1336.9834  1337.6319   -0.6485     0  R.QLDSMIQLCSK.L  Oxidation (M)  (Ions score 21)
  327 - 338     705.9620  1409.9094  1409.7150    0.1944     0  R.NLLHDNELSDLK.E  (Ions score 61)
  327 - 338     706.0610  1410.1074  1409.7150    0.3924     0  R.NLLHDNELSDLK.E  (Ions score 61)
  327 - 351    1312.7550  2623.4954  2624.2678   -0.7723     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 29)
  327 - 351    1312.9090  2623.8034  2624.2678   -0.4643     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 42)
  327 - 351    1313.3830  2624.7514  2624.2678    0.4837     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 123)
  327 - 351    1313.3980  2624.7814  2624.2678    0.5137     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 135)
  327 - 351     875.9350  2624.7832  2624.2678    0.5154     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 109)
  327 - 351    1313.7560  2625.4974  2624.2678    1.2297     1  R.NLLHDNELSDLKEDGGSGGDLSALR.V  (Ions score 122)
  339 - 351     617.3940  1232.7734  1232.5633    0.2101     0  K.EDGGSGGDLSALR.V  (Ions score 89)
  339 - 351     617.4570  1232.8994  1232.5633    0.3361     0  K.EDGGSGGDLSALR.V  (Ions score 71)
  352 - 364     751.5250  1501.0354  1500.7606    0.2748     0  R.VEEVQNVINAMQK.I  (Ions score 27)
  352 - 364     751.5440  1501.0734  1500.7606    0.3128     0  R.VEEVQNVINAMQK.I  (Ions score 98)
  352 - 364     751.5900  1501.1654  1500.7606    0.4048     0  R.VEEVQNVINAMQK.I  (Ions score 109)
  352 - 364     759.4650  1516.9154  1516.7555    0.1599     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 98)
  352 - 364     759.4810  1516.9474  1516.7555    0.1919     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 89)
  352 - 364     759.5390  1517.0634  1516.7555    0.3079     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 54)
  352 - 364     759.5710  1517.1274  1516.7555    0.3719     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 88)
  352 - 364    1518.8900  1517.8827  1516.7555    1.1272     0  R.VEEVQNVINAMQK.I  Oxidation (M)  (Ions score 19)
  423 - 432     603.4220  1204.8294  1204.6703    0.1591     0  R.FSQLVEELLK.I  (Ions score 75)
  423 - 432     603.4970  1204.9794  1204.6703    0.3091     0  R.FSQLVEELLK.I  (Ions score 64)
  423 - 432     603.5000  1204.9854  1204.6703    0.3151     0  R.FSQLVEELLK.I  (Ions score 79)
  423 - 432     604.0800  1206.1454  1204.6703    1.4751     0  R.FSQLVEELLK.I  (Ions score 84)
  464 - 479     894.6100  1787.2054  1786.9200    0.2854     0  K.TITLEVEPSDTIENVK.A  (Ions score 74)
  464 - 479     894.6150  1787.2154  1786.9200    0.2954     0  K.TITLEVEPSDTIENVK.A  (Ions score 83)
  482 - 494     762.0660  1522.1174  1522.7740   -0.6565     1  K.IQDKEGIPPDQQR.L  (Ions score 11)
  495 - 506     731.0020  1459.9894  1459.7783    0.2111     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 67)
  495 - 506     731.0780  1460.1414  1459.7783    0.3631     1  R.LIFAGKQLEDGR.T  GlyGly (K)  (Ions score 71)
  507 - 515     541.3670  1080.7194  1080.5451    0.1743     0  R.TLSDYNIQK.E  (Ions score 54)
  507 - 515     541.3680  1080.7214  1080.5451    0.1763     0  R.TLSDYNIQK.E  (Ions score 60)
  516 - 524     533.9150  1065.8154  1066.6135   -0.7980     0  K.ESTLHLVLR.L  (Ions score 48)
  516 - 524     534.4790  1066.9434  1066.6135    0.3300     0  K.ESTLHLVLR.L  (Ions score 60)
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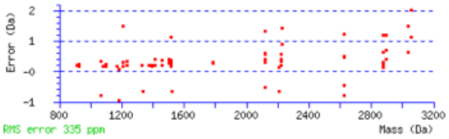
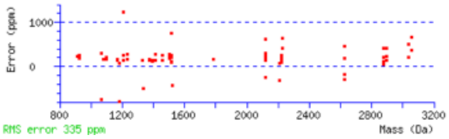




Mascot: http://www.matrixscience.com/

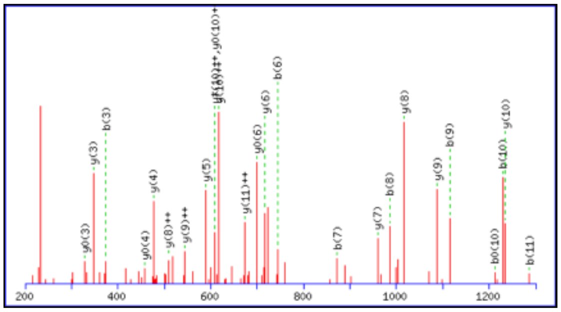
Mascot Search Results

Peptide View

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

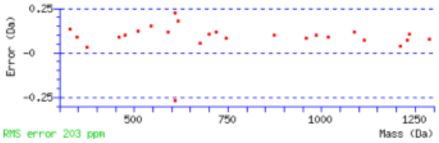
Match to Query 128: 1460.141448 from(731.078000,2+) intensity(7836799.0000)
Title: Cmpd 58, +MSn(731.45), 22.6 min
Data file C:\YaelDavid\100203_YaelDavid\BIT00883_YD_21_merge.mgf

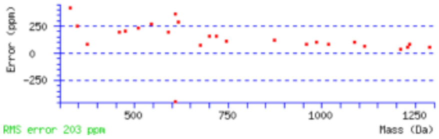
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1459.7783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : GlyGly (K)
Ions Score: 71 **Expect:** 0.0001
Matches : 25/102 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	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
71.4	1459.7783	0.3631	LIFAGKQLEDGR
28.0	1460.7987	-0.6573	AGVFKKVDEIK
28.0	1460.7987	-0.6573	AGVFKKVDELK
25.8	1459.6725	0.4689	EAAALQCQLEDGR
22.7	1459.8068	0.3347	ILQEKMEKAIK
22.5	1459.8432	0.2982	MNITIITVGKIK
22.5	1459.8432	0.2982	MNITLITVGKLK
22.4	1460.7544	-0.6130	NIIEMQQLELSK
21.9	1459.7704	0.3710	EMKLLEQSGALK
21.4	1459.7307	0.4108	ALENALPYLEDGR

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

Referenc #10						P (pro)	Sf	Score	Coverage	MW	Acsn.	Peptide (Hits)	
Scan(s)	Peptide	MH+	DeltaM	z	Type	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions	Count
1 RFP-BARD-BRCA			(ppm)			7.77E-15	35.35	456.27	58.40	51667.6		46 (44 2 0 0 0)	
5890	K.AYVKHPADIPDYLK.L	1629.86352	-0.57436	3	CID	6.83E-10	0.93	3.31	0.60	1092.2	1	25/52	1
1317	K.DGGHYDAEVK.T	1090.47998	1.54412	3	CID	3.57E-02	0.66	2.50	0.46	307.5	1	16/36	1
4271	K.EDGGSGGDLSALR.V	1233.57058	0.41172	2	CID	4.91E-05	0.87	2.41	0.61	748.8	1	14/24	
7392	K.FCM*LK~LLNQK.K	1353.70196	1.16483	2	CID	2.64E-02	0.62	2.17	0.33	221.0	1	11/18	
10336	R.FSQLVEELLK.I	1205.67762	1.65647	2	CID	1.18E-06	0.97	2.85	0.77	1543.1	1	16/18	
12893	K.GGPLPFAWDILSPQFQ.Y	1772.90063	0.37217	2	CID	5.42E-08	0.85	2.50	0.58	587.4	1	16/30	1
12347	K.GGPLPFAWDILSPQFQYGSK.A	2208.11242	1.40825	2	CID	8.70E-11	0.86	2.72	0.30	1038.0	1	20/38	1
905	G.GHYDAEVK.T	918.43157	-1.53485	2	CID	4.48E-02	0.85	2.34	0.40	565.0	1	11/14	1
1047	H.HASSEDVIK.E	985.49490	1.50683	2	CID	3.40E-04	0.88	2.08	0.67	508.9	1	12/16	1
5847	K.HPADIPDYLK.L	1168.59970	0.17217	2	CID	9.26E-07	0.90	2.11	0.80	259.5	1	14/18	1
10950	K.HPADIPDYLK~LSFPEGFK.W	2117.07040	2.30828	3	CID	8.29E-05	0.59	2.63	0.38	407.5	1	18/68	2
8072	R.HSTGAENLYFQGLEE.E	1694.76566	-0.78226	2	CID	4.07E-04	0.72	2.08	0.61	485.3	1	12/28	1
7313	R.HSTGAENLYFQGLEEPDGR.G	2119.96794	0.52103	2	CID	7.77E-15	0.98	5.44	0.65	1388.3	1	22/36	
7289	R.HSTGAENLYFQGLEEPDGRG.A	2176.98940	0.29258	2	CID	4.09E-08	0.89	2.86	0.69	479.6	1	18/38	
11236	K.IICAFQLDTGLEYANSYNFAK.E	2438.16971	1.70867	2	CID	8.88E-15	0.98	4.77	0.45	2172.8	1	25/40	
10896	K.IICAFQLDTGLEYAN@SYNFAK.E	2439.15373	1.15451	2	CID	4.92E-10	0.85	2.71	0.03	1606.6	1	21/40	
1449	L.KDGGHYDAEVK.T	1218.57494	0.54768	2	CID	1.12E-05	0.53	2.10	0.39	336.9	1	10/20	1
1083	K.KGPSQCPLCK.N	1174.57080	-0.16445	2	CID	1.56E-05	0.90	2.85	0.55	670.4	1	12/18	
1424	K.KGPSQ@CPLCK.N	1175.55481	-2.03958	2	CID	3.02E-01	0.56	2.47	0.48	202.6	1	8/18	
8105	K.LDITSHN@EDYTIVEQYER.A	2226.01970	0.60437	2	CID	5.17E-11	0.75	2.53	0.14	891.0	1	18/34	1
1444	K.LK~D^GGHYDAEVK.T	1388.68066	0.47982	2	CID	3.10E-02	0.62	2.43	0.43	185.4	1	11/22	2
1385	K.LKDGGHYDAEVK.T	1331.65901	-1.30028	2	CID	7.07E-08	0.95	3.50	0.44	1360.1	1	17/22	1
1629	K.LK#DGGHYDAEVK.T	1445.70091	-0.37402	2	CID	1.59E-03	0.82	2.89	0.41	476.4	1	13/22	1
7272	N.LLHDNELSDLKEDGGSGGDLSALR.V	2511.23215	-0.36435	3	CID	5.01E-09	0.79	3.48	0.55	245.2	1	21/92	
5905	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3038.34323	1.78824	3	CID	4.51E-12	0.61	2.52	0.36	448.6	1	24/108	1
6850	H.NEDYTIVEQYER.A	1558.70199	0.44372	2	CID	3.40E-10	0.96	2.85	0.77	1195.5	1	17/22	1
6524	R.NLLHDNELSDLK.E	1410.72233	3.89629	2	CID	3.33E-05	0.81	2.62	0.32	647.2	1	14/22	
6699	R.NLLHDNELSDLKED.G	1654.79187	1.50400	2	CID	4.99E-06	0.76	2.80	0.21	757.2	1	14/26	
9082	R.NLLHDNELSDLK~EDGGSGGDLSALR.V	2668.28108	3.66863	3	CID	4.25E-07	0.73	3.73	0.06	908.3	1	27/96	
8235	R.NLLHDNELSDLKEDGGSGGDLSALR.V	2625.27508	3.24757	3	CID	5.55E-11	0.75	3.60	0.20	666.6	1	25/96	
10980	R.NLLHDNELSDLKEDGGSGGDLSALRVEEVQN	4108.02514	2.11618	4	CID	2.22E-09	0.66	3.54	0.25	347.5	1	28/222	
6752	H.PADIPDYLK.L	1031.54079	1.80515	2	CID	3.90E-05	0.94	2.65	0.61	976.4	1	14/16	1
6695	T.QDSSLQDGEFIYK.V	1529.71183	1.76245	2	CID	4.00E-05	0.62	2.74	0.11	389.0	1	14/24	1
7491	R.QLDSM*IQLCSK~LR.N	1650.83041	3.52508	2	CID	8.09E-04	0.24	2.22	0.04	254.6	1	11/24	
8117	F.QLDTGLEYANSYNFAK.E	1833.86537	1.74946	2	CID	1.49E-05	0.84	2.84	0.54	487.3	1	15/30	
6452	D.SSLQDGEFIYK.V	1286.62631	3.28937	2	CID	1.52E-06	0.91	2.08	0.60	975.0	1	15/20	1
8258	H.STGAENLYFQGLEEPDGR.G	1982.90903	3.91865	2	CID	8.66E-10	0.95	3.75	0.68	984.3	1	17/34	
8268	S.TGAENLYFQGLEEPDGR.G	1895.87700	3.67208	2	CID	1.37E-06	0.91	2.84	0.55	1028.4	1	17/32	
6797	D.TGLEYAN@SYNFAK.E	1478.67980	0.12046	2	CID	2.83E-02	0.24	2.05	0.14	331.8	1	10/24	
4389	K.TMGWEASTER.M	1167.50990	2.74981	2	CID	8.93E-03	0.88	2.25	0.55	693.0	1	13/18	1
2812	K.TM*GWEASTER.M	1183.50481	3.91492	2	CID	5.67E-04	0.93	2.43	0.67	868.2	1	14/18	2
10304	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V	2878.34513	2.14024	3	CID	2.03E-06	0.72	3.09	0.42	406.8	1	22/100	1
6914	T.VTQDSSLQDGEFIYK.V	1729.82792	2.33279	2	CID	2.45E-08	0.94	2.93	0.68	1100.2	1	17/28	1
5754	L.YFQGLEEPDGR.G	1310.60116	-1.14413	2	CID	2.34E-06	0.94	2.72	0.69	955.0	1	14/20	
6994	A.YVK#HPADIPDYLK.L	1672.86831	1.91421	2	CID	5.03E-03	0.14	2.13	0.02	131.1	1	10/24	1
2 gi|51703339|sp|P62988.1|UBIQ_HUMAN Ubiquitin						1.10E-09	8.37	116.18	86.80	8559.6	51703339	12 (10 2 0 0 0)	
1765	K.AKIQDKEGIPPDQQR.L	1722.91332	3.36182	2	CID	1.10E-09	0.84	2.72	0.29	696.1	1	18/28	
6239	K.ESTLHLVLR.L	1067.62077	1.72016	2	CID	6.75E-07	0.93	2.74	0.81	225.9	1	13/16	
4159	K.IQDK~EGIPPDQQR.L	1566.78725	3.29331	2	CID	1.11E-03	0.38	2.25	0.17	193.3	1	12/24	
1810	K.IQDKEGIPPDQQR.L	1523.78125	2.91778	2	CID	5.68E-09	0.93	3.19	0.63	566.6	1	17/24	
1785	K.IQD^K~EGIPPDQQR.L	1580.80290	3.71162	2	CID	3.93E-02	0.19	2.26	0.00	174.4	1	9/24	
7398	R.LIFAGK$Q@LEDGR.T	1389.74849	1.99789	2	CID	4.24E-06	0.87	3.11	0.60	1138.5	1	17/22	
7398	R.LIFAGK~QLEDGR.T	1389.74868	1.86549	2	CID	1.64E-06	0.88	3.19	0.02	1138.5	1	17/22	

7763	K.TITLEVEPSDTIEN@VK.A	1788.91132	3.33544	2	CID	3.72E-04	0.90	3.12	0.47	727.9	1	18/30
8139	K.TITLEVEPSDTIENVK.A	1787.92730	2.65856	2	CID	1.84E-07	0.90	2.57	0.56	688.4	1	19/30
8075	R.TLSDYNIQK#ESTLHLVLR.L	2244.19724	0.79237	2	CID	1.09E-08	0.72	2.75	0.12	814.6	1	16/34
8975	K.TLTGK~TITLEVEPSDTIENVK.A	2331.22915	1.73864	2	CID	1.27E-08	0.63	2.95	0.17	484.5	1	16/40