Mascot Search Results

Protein View

Match to: **IPI00625217** Score: **1095**
Tax_Id=10090 Gene_Symbol=Pax3 Paired box protein Pax-3
Found in search of o63_11jan24_09_uc_90min_neuloss_ms3_pax3_20ul.mgf

Nominal mass (M_r): **53315**; Calculated pI value: **8.92**
NCBI BLAST search of IPI00625217 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Formyl (N-term),Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **38%**

Matched peptides shown in **Bold Red**

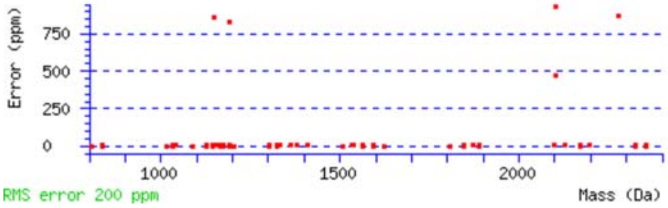
```
  1 MTTLAGAVPR MMRPGPGQNY PRSGFPLEVS TPLGQGRVNQ LGGVFINGRP
 51 LPNHIRHKIV EMAHHGIRPC VISRQLRVSH GCVSKILCRY QETGSIRPGA
101 IGGSKPKQVT TPDVEKKIEE YKRENPGMFS WEIRDKLLKD AVCDRNTVPS
151 VSSISRILRS KFGKGEEEEA DLERKEAEES EKKAKHSIDG ILSERASAPQ
201 SDEGSDIDSE PDLPLKRKQR RSRTTFTAEQ LEELERAFER THYPDIYTRE
251 ELAQRAKLTE ARVQVWFSNR RARWRKQAGA NQLMAFNHLI PGGFPPTAMP
301 TLPTYQLSET SYQPTSIPQA VSDPSSTVHR PQPLPPSTVH QSTIPSNADS
351 SSAYCLPSTR HGFSSYTDSF VPPSGPSNPM NPTIGNGLSP QVMGLLTNHG
401 GVPHQPQTDY ALSPLTGGLE PTTTVSASCS QRLEHMKNVD SLPTSQPYCP
451 PTYSTAGYSM DPVTGYQYGQ YGQSKPWTF
```

Show predicted peptides also

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

```
 Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss Sequence
    38 - 56      526.0518   2100.1782  2100.1705        4     0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 34)
    38 - 56      701.0683   2100.1831  2100.1705        6     0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 55)
    38 - 56     1051.1011   2100.1876  2100.1705        8     0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 16)
    38 - 56      526.2966   2101.1572  2100.1705      470     0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 16)
    38 - 56      526.2967   2101.1577  2100.1705      470     0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 18)
    38 - 56      526.2977   2101.1616  2100.1705      472     0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 36)
    38 - 56      701.3964   2101.1674  2100.1705      475     0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 56)
    38 - 56     1051.5922   2101.1698  2100.1705      476     0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 3)
    38 - 56      526.5427   2102.1416  2100.1705      939     0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 26)
    38 - 56      710.4016   2128.1830  2128.1654        8     0  R.VNQLGGVFINGRPLPNHIR.H  Formyl (N-term) (Ions scor
    59 - 74      473.4999   1889.9704  1889.9716       -1     0  K.IVEMAHHGIRPCVISR.Q  Oxidation (M) (Ions score 10)
    59 - 74      945.9937   1889.9729  1889.9716        1     0  K.IVEMAHHGIRPCVISR.Q  Oxidation (M) (Ions score 15)
    59 - 74      630.9988   1889.9747  1889.9716        2     0  K.IVEMAHHGIRPCVISR.Q  Oxidation (M) (Ions score 23)
    90 - 107     462.2505   1844.9731  1844.9744       -1     0  R.YQETGSIRPGAIGGSKPK.Q  (Ions score 24)
    90 - 107     615.9984   1844.9734  1844.9744       -1     0  R.YQETGSIRPGAIGGSKPK.Q  (Ions score 53)
    90 - 107     923.4977   1844.9808  1844.9744        3     0  R.YQETGSIRPGAIGGSKPK.Q  (Ions score 41)
    90 - 107     625.3336   1872.9790  1872.9694        5     0  R.YQETGSIRPGAIGGSKPK.Q  Formyl (N-term) (Ions score
   108 - 116     508.7664   1015.5183  1015.5186       -0     0  K.QVTTPDVEK.K  (Ions score 14)
   108 - 116     508.7667   1015.5188  1015.5186        0     0  K.QVTTPDVEK.K  (Ions score 20)
   108 - 116    1044.5264   1043.5191  1043.5135        5     0  K.QVTTPDVEK.K  Formyl (N-term) (Ions score 24)
   108 - 117     572.8140   1143.6135  1143.6136       -0     1  K.QVTTPDVEKK.I  (Ions score 39)
   108 - 117     382.2119   1143.6138  1143.6136        0     1  K.QVTTPDVEKK.I  (Ions score 36)
   117 - 122     405.2238    808.4331   808.4330        0     1  K.KIEEYK.R  (Ions score 31)
   117 - 122     809.4408    808.4335   808.4330        1     1  K.KIEEYK.R  (Ions score 1)
   118 - 123     419.2268    836.4391   836.4392       -0     1  K.IEEYKR.E  (Ions score 31)
   118 - 123     419.2271    836.4397   836.4392        1     1  K.IEEYKR.E  (Ions score 12)
   118 - 123     419.2272    836.4399   836.4392        1     1  K.IEEYKR.E  (Ions score 14)
   118 - 123     419.2272    836.4399   836.4392        1     1  K.IEEYKR.E  (Ions score 21)
   118 - 123     837.4491    836.4418   836.4392        3     1  K.IEEYKR.E  (Ions score 14)
   123 - 134     513.2481   1536.7225  1536.7143        5     1  K.RENPGMFSWEIR.D  Oxidation (M) (Ions score 63)
   124 - 134     683.3176   1364.6206  1364.6183        2     0  R.ENPGMFSWEIR.D  (Ions score 43)
   124 - 134     691.3163   1380.6180  1380.6132        3     0  R.ENPGMFSWEIR.D  Oxidation (M) (Ions score 45)
   124 - 134     691.3170   1380.6195  1380.6132        5     0  R.ENPGMFSWEIR.D  Oxidation (M) (Ions score 21)
   124 - 134    1381.6305   1380.6232  1380.6132        7     0  R.ENPGMFSWEIR.D  Oxidation (M) (Ions score 26)
   124 - 134     705.3135   1408.6124  1408.6081        3     0  R.ENPGMFSWEIR.D  Formyl (N-term); Oxidation (M) (Io
   124 - 136     542.2507   1623.7304  1623.7351       -3     1  R.ENPGMFSWEIRDK.L  Oxidation (M) (Ions score 13)
   124 - 136     812.8759   1623.7372  1623.7351        1     1  R.ENPGMFSWEIRDK.L  Oxidation (M) (Ions score 43)
   137 - 145     545.2861   1088.5577  1088.5648       -7     1  K.LLKDAVCDR.N  (Ions score 16)
   137 - 145     545.2886   1088.5626  1088.5648       -2     1  K.LLKDAVCDR.N  (Ions score 48)
   146 - 156     573.8104   1145.6063  1145.6040        2     0  R.NTVPSVSSISR.I  (Ions score 36)
   146 - 156     573.8118   1145.6090  1145.6040        4     0  R.NTVPSVSSISR.I  (Ions score 8)
   146 - 156    1146.6191   1145.6119  1145.6040        7     0  R.NTVPSVSSISR.I  (Ions score 4)
   146 - 156    1147.6035   1146.5962  1145.6040      866     0  R.NTVPSVSSISR.I  (Ions score 23)
```

```
146 - 156     587.8076  1173.6007  1173.5990          1     0  R.NTVPSVSSISR.I  Formyl (N-term) (Ions score 32)
146 - 156     587.8085  1173.6025  1173.5990          3     0  R.NTVPSVSSISR.I  Formyl (N-term) (Ions score 40)
146 - 156    1174.6100  1173.6027  1173.5990          3     0  R.NTVPSVSSISR.I  Formyl (N-term) (Ions score 5)
146 - 156    1174.6113  1173.6041  1173.5990          4     0  R.NTVPSVSSISR.I  Formyl (N-term) (Ions score 12)
146 - 156     587.8098  1173.6050  1173.5990          5     0  R.NTVPSVSSISR.I  Formyl (N-term) (Ions score 11)
162 - 174     503.5661  1507.6766  1507.6790         -2     1  K.FGKGEEEEADLER.K  (Ions score 59)
162 - 174     503.5668  1507.6785  1507.6790         -0     1  K.FGKGEEEEADLER.K  (Ions score 38)
162 - 174     754.8476  1507.6806  1507.6790          1     1  K.FGKGEEEEADLER.K  (Ions score 81)
162 - 174     768.8466  1535.6787  1535.6740          3     1  K.FGKGEEEEADLER.K  Formyl (N-term) (Ions score 61)
165 - 174     588.7541  1175.4936  1175.4942         -0     0  K.GEEEEADLER.K  (Ions score 16)
165 - 174     588.7548  1175.4951  1175.4942          1     0  K.GEEEEADLER.K  (Ions score 63)
165 - 174     588.7551  1175.4956  1175.4942          1     0  K.GEEEEADLER.K  (Ions score 59)
165 - 174    1176.5059  1175.4986  1175.4942          4     0  K.GEEEEADLER.K  (Ions score 46)
165 - 174     602.7515  1203.4884  1203.4891         -1     0  K.GEEEEADLER.K  Formyl (N-term) (Ions score 36)
165 - 175     435.5363  1303.5869  1303.5891         -2     1  K.GEEEEADLERK.E  (Ions score 38)
165 - 175     652.8019  1303.5892  1303.5891          0     1  K.GEEEEADLERK.E  (Ions score 39)
165 - 175     652.8030  1303.5915  1303.5891          2     1  K.GEEEEADLERK.E  (Ions score 50)
165 - 175     666.8007  1331.5869  1331.5841          2     1  K.GEEEEADLERK.E  Formyl (N-term) (Ions score 51)
184 - 195     663.3626  1324.7107  1324.7099          1     1  K.AKHSIDGILSER.A  (Ions score 28)
184 - 195     663.3635  1324.7125  1324.7099          2     1  K.AKHSIDGILSER.A  (Ions score 48)
186 - 195     563.7959  1125.5772  1125.5778         -1     0  K.HSIDGILSER.A  (Ions score 54)
186 - 195     563.7968  1125.5791  1125.5778          1     0  K.HSIDGILSER.A  (Ions score 60)
186 - 195    1126.5876  1125.5804  1125.5778          2     0  K.HSIDGILSER.A  (Ions score 40)
186 - 195     563.8016  1125.5887  1125.5778         10     0  K.HSIDGILSER.A  (Ions score 33)
186 - 195     577.7946  1153.5746  1153.5727          2     0  K.HSIDGILSER.A  Formyl (N-term) (Ions score 16)
186 - 195    1154.5898  1153.5826  1153.5727          9     0  K.HSIDGILSER.A  Formyl (N-term) (Ions score 18)
186 - 195     577.7986  1153.5826  1153.5727          9     0  K.HSIDGILSER.A  Formyl (N-term) (Ions score 5)
196 - 216     724.3375  2169.9907  2169.9913         -0     0  R.ASAPQSDEGSDIDSEPDLPLK.R  (Ions score 80)
196 - 216    1086.0042  2169.9937  2169.9913          1     0  R.ASAPQSDEGSDIDSEPDLPLK.R  (Ions score 96)
196 - 216    1086.0087  2170.0028  2169.9913          5     0  R.ASAPQSDEGSDIDSEPDLPLK.R  (Ions score 69)
196 - 216    1100.0023  2197.9901  2197.9863          2     0  R.ASAPQSDEGSDIDSEPDLPLK.R  Formyl (N-term) (Ions sc
196 - 216     733.6710  2197.9912  2197.9863          2     0  R.ASAPQSDEGSDIDSEPDLPLK.R  Formyl (N-term) (Ions sc
196 - 216     733.6724  2197.9953  2197.9863          4     0  R.ASAPQSDEGSDIDSEPDLPLK.R  Formyl (N-term) (Ions sc
196 - 216    1100.0057  2197.9969  2197.9863          5     0  R.ASAPQSDEGSDIDSEPDLPLK.R  Formyl (N-term) (Ions sc
196 - 216     760.9847  2279.9322  2277.9526        869     0  R.ASAPQSDEGSDIDSEPDLPLK.R  Formyl (N-term); Phospho
196 - 217    1164.0549  2326.0953  2326.0924          1     1  R.ASAPQSDEGSDIDSEPDLPLKR.K  (Ions score 70)
196 - 217     776.3733  2326.0980  2326.0924          2     1  R.ASAPQSDEGSDIDSEPDLPLKR.K  (Ions score 72)
196 - 217     776.3734  2326.0984  2326.0924          3     1  R.ASAPQSDEGSDIDSEPDLPLKR.K  (Ions score 94)
196 - 217     785.7041  2354.0905  2354.0874          1     1  R.ASAPQSDEGSDIDSEPDLPLKR.K  Formyl (N-term) (Ions s
196 - 217    1178.0544  2354.0943  2354.0874          3     1  R.ASAPQSDEGSDIDSEPDLPLKR.K  Formyl (N-term) (Ions s
196 - 217     785.7065  2354.0978  2354.0874          4     1  R.ASAPQSDEGSDIDSEPDLPLKR.K  Formyl (N-term) (Ions s
222 - 236     603.9714  1808.8925  1808.8904          1     1  R.SRTTFTAEQLEELER.A  (Ions score 48)
224 - 236    1566.7635  1565.7563  1565.7573         -1     0  R.TTFTAEQLEELER.A  (Ions score 21)
224 - 236     783.8881  1565.7617  1565.7573          3     0  R.TTFTAEQLEELER.A  (Ions score 74)
224 - 236     783.8886  1565.7625  1565.7573          3     0  R.TTFTAEQLEELER.A  (Ions score 65)
224 - 236     783.8904  1565.7662  1565.7573          6     0  R.TTFTAEQLEELER.A  (Ions score 47)
224 - 236     783.8922  1565.7697  1565.7573          8     0  R.TTFTAEQLEELER.A  (Ions score 45)
224 - 236     797.8843  1593.7541  1593.7522          1     0  R.TTFTAEQLEELER.A  Formyl (N-term) (Ions score 41)
224 - 236     797.8857  1593.7569  1593.7522          3     0  R.TTFTAEQLEELER.A  Formyl (N-term) (Ions score 70)
224 - 236     797.8894  1593.7643  1593.7522          8     0  R.TTFTAEQLEELER.A  Formyl (N-term) (Ions score 35)
241 - 249     389.1922  1164.5548  1164.5564         -1     0  R.THYPDIYTR.E  (Ions score 30)
241 - 249     583.2853  1164.5560  1164.5564         -0     0  R.THYPDIYTR.E  (Ions score 26)
241 - 249     389.1928  1164.5565  1164.5564          0     0  R.THYPDIYTR.E  (Ions score 17)
241 - 249     583.2869  1164.5592  1164.5564          2     0  R.THYPDIYTR.E  (Ions score 12)
241 - 249    1165.5692  1164.5619  1164.5564          5     0  R.THYPDIYTR.E  (Ions score 19)
241 - 249     597.2846  1192.5547  1192.5513          3     0  R.THYPDIYTR.E  Formyl (N-term) (Ions score 13)
263 - 270     518.2718  1034.5290  1034.5298         -1     0  R.VQVWFSNR.R  (Ions score 9)
263 - 270     518.2729  1034.5312  1034.5298          1     0  R.VQVWFSNR.R  (Ions score 29)
263 - 270    1035.5398  1034.5325  1034.5298          3     0  R.VQVWFSNR.R  (Ions score 9)
263 - 271     397.8840  1190.6303  1190.6309         -1     1  R.VQVWFSNRR.A  (Ions score 14)
263 - 271     398.2126  1191.6159  1190.6309        827     1  R.VQVWFSNRR.A  (Ions score 16)
```



```
ID   IPI00625217.1         IPI;      PRT;   479 AA.
AC   IPI00625217;
DT   30-JUL-2005 (IPI Mouse rel. 3.09, Created)
DT   30-JUL-2005 (IPI Mouse rel. 3.09, Last sequence update)
DE   PAIRED BOX PROTEIN PAX-3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
OX   NCBI_TaxID=10090;
CC   -!- GENE_LOCATION: Chr. 1:78097842-78193711:-1.
DR   UniProtKB/Swiss-Prot; P24610; PAX3_MOUSE; M.
DR   REFSEQ_VALIDATED; NP_032807; GI:226958472; -.
DR   ENSEMBL; ENSMUSP00000084320; ENSMUSG00000004872; -.
DR   UniParc; UPI00000E891C; -; -.
DR   MGI; MGI:97487; Pax3; -.
DR   Entrez Gene; 18505; Pax3; -.
DR   UniGene; Mm.1371; -; -.
DR   UniGene; Mm.478746; -; -.
DR   CCDS; CCDS15082.1; -; -.
DR   trome; MTR044593; -; PRT.
DR   Transfac; T00680; -; -.
DR   CleanEx; MM_PAX3; -; -.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR017970; Homeobox_CS.
DR   InterPro; IPR009057; Homeodomain-like.
DR   InterPro; IPR012287; Homeodomain-rel.
DR   InterPro; IPR001523; Paired_box_N.
DR   InterPro; IPR022106; Pax7.
DR   InterPro; IPR011991; WHTH_trsnscrt_rep_DNA-bd.
DR   Pfam; PF00046; Homeobox; 1.
DR   Pfam; PF00292; PAX; 1.
DR   Pfam; PF12360; Pax7; 1.
DR   PRINTS; PR00027; PAIREDBOX.
DR   SMART; SM00389; HOX; 1.
DR   SMART; SM00351; PAX; 1.
DR   PROSITE; PS00027; HOMEOBOX_1; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
DR   PROSITE; PS00034; PAIRED_1; 1.
DR   PROSITE; PS51057; PAIRED_2; 1.
DR   SUPERFAMILY; SSF46689; Homeodomain_like; 2.
DR   GENE3D; G3DSA:1.10.10.10; Wing_hlx_DNA_bd; 2.
DR   GENE3D; G3DSA:1.10.10.60; Homeodomain-rel; 1.
SQ   SEQUENCE   479 AA;  52949 MW;  8806E551FFB755A0 CRC64;
     MTTLAGAVPR MMRPGPGQNY PRSGFPLEVS TPLGQGRVNQ LGGVFINGRP LPNHIRHKIV
     EMAHHGIRPC VISRQLRVSH GCVSKILCRY QETGSIRPGA IGGSKPKQVT TPDVEKKIEE
     YKRENPGMFS WEIRDKLLKD AVCDRNTVPS VSSISRILRS KFGKGEEEEA DLERKEAEES
     EKKAKHSIDG ILSERASAPQ SDEGSDIDSE PDLPLKRKQR RSRTTFTAEQ LEELERAFER
     THYPDIYTRE ELAQRAKLTE ARVQVWFSNR RARWRKQAGA NQLMAFNHLI PGGFPPTAMP
     TLPTYQLSET SYQPTSIPQA VSDPSSTVHR PQPLPPSTVH QSTIPSNADS SSAYCLPSTR
     HGFSSYTDSF VPPSGPSNPM NPTIGNGLSP QVMGLLTNHG GVPHQPQTDY ALSPLTGGLE
     PTTTVSASCS QRLEHMKNVD SLPTSQPYCP PTYSTAGYSM DPVTGYQYGQ YGQSKPWTF
```

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

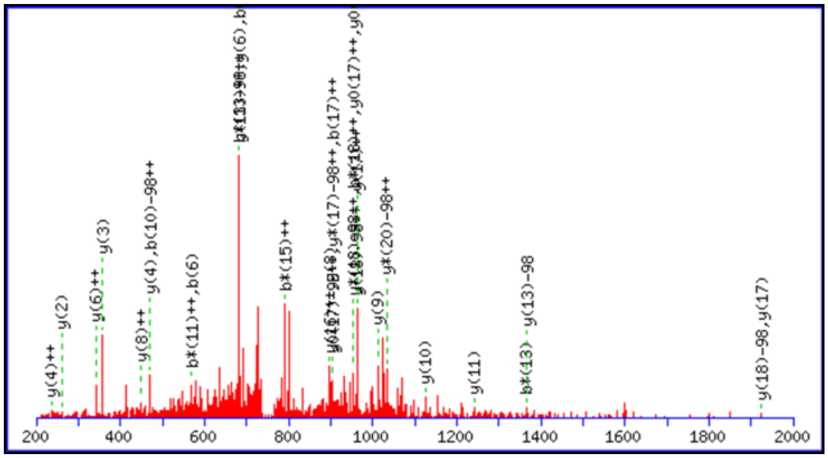
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAPQSDEGSDIDSEPDLPLK**
Found in **IPI00625217**, Tax_Id=10090 Gene_Symbol=Pax3 Paired box protein Pax-3

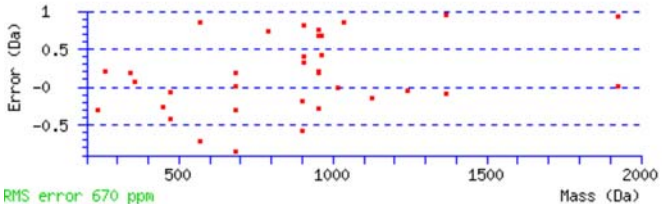
Match to Query 7456: 2279.932212 from(760.984680,3+) intensity(169254.0000) index(2551)
Title: o63_11jan24_09_uc_90min_neuloss_ms3_pax3_20ul.03846.03846.3
Data file o63_11jan24_09_uc_90min_neuloss_ms3_pax3_20ul.mgf

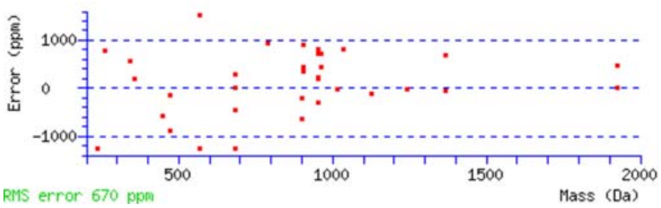
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2277.9526
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Formyl (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 **Expect:** 0.077
Matches : 34/342 fragment ions using 52 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0393	50.5233					A							21
2	187.0713	94.0393			169.0608	85.0340	S	2081.9509	1041.4791	2064.9244	1032.9658	2063.9404	1032.4738	20
3	258.1084	129.5579			240.0979	120.5526	A	1994.9189	997.9631	1977.8924	989.4498	1976.9084	988.9578	19
4	355.1612	178.0842			337.1506	169.0790	P	***1923.8818***	962.4445	1906.8553	953.9313	1905.8712	953.4393	18
5	483.2198	242.1135	466.1932	233.6003	465.2092	233.1083	Q	1826.8290	913.9182	1809.8025	905.4049	1808.8185	904.9129	17
6	570.2518	285.6295	553.2253	277.1163	552.2413	276.6243	S	1698.7705	849.8889	1681.7439	841.3756	1680.7599	840.8836	16
7	685.2788	343.1430	668.2522	334.6297	667.2682	334.1377	D	1611.7384	806.3729	1594.7119	797.8596	1593.7279	797.3676	15
8	814.3214	407.6643	797.2948	399.1510	796.3108	398.6590	E	1496.7115	748.8594	1479.6849	740.3461	1478.7009	739.8541	14
9	871.3428	436.1750	854.3163	427.6618	853.3323	427.1698	G	***1367.6689***	684.3381	1350.6424	675.8248	1349.6583	675.3328	13
10	940.3643	470.6858	923.3377	462.1725	922.3537	461.6805	S	1310.6474	655.8274	1293.6209	647.3141	1292.6369	646.8221	12
11	1055.3912	528.1992	1038.3647	519.6860	1037.3807	519.1940	D	***1241.6260***	621.3166	1224.5994	612.8034	1223.6154	612.3113	11
12	1168.4753	584.7413	1151.4487	576.2280	1150.4647	575.7360	I	***1126.5990***	563.8032	1109.5725	555.2899	1108.5885	554.7979	10
13	1283.5022	642.2548	1266.4757	633.7415	1265.4917	633.2495	D	***1013.5150***	507.2611	996.4884	498.7478	995.5044	498.2558	9
14	1370.5343	685.7708	1353.5077	677.2575	1352.5237	676.7655	S	***898.4880***	449.7477	881.4615	441.2344	880.4775	440.7424	8
15	1499.5769	750.2921	1482.5503	741.7788	1481.5663	741.2868	E	811.4560	406.2316	794.4294	397.7184	793.4454	397.2264	7
16	1596.6296	798.8184	1579.6031	790.3052	1578.6191	789.8132	P	***682.4134***	341.7103	665.3869	333.1971	664.4028	332.7051	6
17	1711.6566	856.3319	1694.6300	847.8186	1693.6460	847.3266	D	585.3606	293.1840	568.3341	284.6707	567.3501	284.1787	5
18	1824.7406	912.8739	1807.7141	904.3607	1806.7301	903.8687	L	***470.3337***	235.6705	453.3071	227.1572			4
19	1921.7934	961.4003	1904.7668	952.8871	1903.7828	952.3950	P	***357.2496***	179.1285	340.2231	170.6152			3
20	2034.8775	1017.9424	2017.8509	1009.4291	2016.8669	1008.9371	L	***260.1969***	130.6021	243.1703	122.0888			2
21							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.6	2277.9526	1.9796	ASAPQSDEGSDIDSEPDLPLK
29.0	2277.9526	1.9796	ASAPQSDEGSDIDSEPDLPLK
21.1	2277.9526	1.9796	ASAPQSDEGSDIDSEPDLPLK
20.7	2278.9703	0.9619	SPSQESSISLSGSSRSASFDR
20.6	2278.9735	0.9587	FPNPFGLASATPATSTPMIR
19.0	2278.9144	1.0178	KASLQSGQEGPGDSPGSQFSK
18.6	2278.9486	0.9836	EMTTKTPYLITIPTATSK
18.4	2277.9338	1.9984	QQVSLESNSSMNSNTPLVR
18.3	2278.8863	1.0459	KVIEGSMSDWAPSDMAMHK
17.9	2277.9573	1.9749	VQEEHMEVEQAQGPSLTSR

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

Mascot Search Results

Protein View

Match to: **IPI00625217** Score: **724**
Tax_Id=10090 Gene_Symbol=Pax3 Paired box protein Pax-3
Found in search of o63_11jan24_09_uc_90min_neuloss_ms3_pax3_20ul.mgf

Nominal mass (M_r): **53315**; Calculated pI value: **8.92**
NCBI BLAST search of IPI00625217 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Formyl (N-term),Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **38%**

Matched peptides shown in **Bold Red**

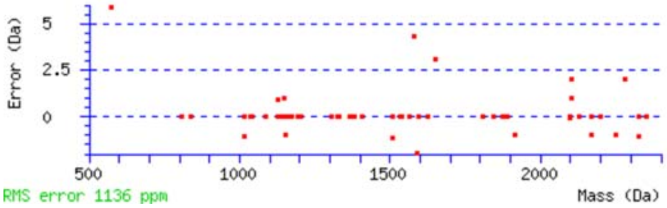
1 MTTLAGAVPR MMRPGPGQNY PRSGFPLEVS TPLGQGR**VNQ** **LGGVFINGRP**
51 **LPNHIR**HK**IV** **EMAHHGIRPC** **VISR**QLRVSH GCVSKILCR**Y** **QETGSIRPGA**
101 **IGGSKPKQVT** **TPDVEKKIEE** **YKRENPGMFS** **WEIRDKLLKD** **AVCDRNTVPS**
151 **VSSISR**ILRS **KFGKGEEEEA** **DLERK**EAEES EKK**AKHSIDG** **ILSERASAPQ**
201 **SDEGSDIDSE** **PDLPLKR**KQR R**SRTTFTAEQ** **LEELER**AFER **THYPDIYTR**E
251 ELAQRAKLTE AR**VQVWFSNR** RARWRKQAGA NQLMAFNHLI PGGFPPTAMP
301 TLPTYQLSET SYQPTSIPQA VSDPSSTVHR PQPLPPSTVH QSTIPSNADS
351 SSAYCLPSTR HGFSSYTDSF VPPSGPSNPM NPTIGNGLSP QVMGLLTNHG
401 GVPHQPQTDY ALSPLTGGLE PTTTVSASCS QRLEHMKNVD SLPTSQPYCP
451 PTYSTAGYSM DPVTGYQYGQ YGQSKPWTF

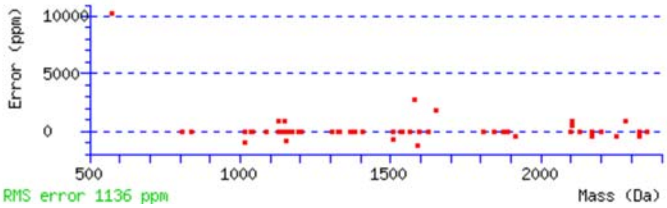
Show predicted peptides also

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

```
Start - End     Observed    Mr(expt)   Mr(calc)     Delta   Miss Sequence
   38 - 56      701.0485   2100.1237  2100.1705   -0.0467    0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 44)
   38 - 56      526.0518   2100.1782  2100.1705    0.0077    0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 34)
   38 - 56      701.0683   2100.1831  2100.1705    0.0126    0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 55)
   38 - 56     1051.1011   2100.1876  2100.1705    0.0171    0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 16)
   38 - 56      526.2977   2101.1616  2100.1705    0.9911    0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 36)
   38 - 56      701.3964   2101.1674  2100.1705    0.9970    0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 56)
   38 - 56      526.5427   2102.1416  2100.1705    1.9711    0  R.VNQLGGVFINGRPLPNHIR.H  (Ions score 26)
   38 - 56      710.4016   2128.1830  2128.1654    0.0176    0  R.VNQLGGVFINGRPLPNHIR.H  Formyl (N-term) (Ions scor
   59 - 74      945.9937   1889.9729  1889.9716    0.0012    0  K.IVEMAHHGIRPCVISR.Q  Oxidation (M) (Ions score 15)
   59 - 74      630.9988   1889.9747  1889.9716    0.0031    0  K.IVEMAHHGIRPCVISR.Q  Oxidation (M) (Ions score 23)
   59 - 74      640.0025   1916.9857  1917.9666   -0.9809    0  K.IVEMAHHGIRPCVISR.Q  Formyl (N-term); Oxidation (M
   90 - 107     462.2505   1844.9731  1844.9744   -0.0014    0  R.YQETGSIRPGAIGGSKPK.Q  (Ions score 24)
   90 - 107     615.9984   1844.9734  1844.9744   -0.0010    0  R.YQETGSIRPGAIGGSKPK.Q  (Ions score 53)
   90 - 107     923.4977   1844.9808  1844.9744    0.0064    0  R.YQETGSIRPGAIGGSKPK.Q  (Ions score 41)
   90 - 107     625.3336   1872.9790  1872.9694    0.0097    0  R.YQETGSIRPGAIGGSKPK.Q  Formyl (N-term) (Ions score
  108 - 116    1015.4998   1014.4925  1015.5186   -1.0261    0  K.QVTTPDVEK.K  (Ions score 24)
  108 - 116     508.7664   1015.5183  1015.5186   -0.0003    0  K.QVTTPDVEK.K  (Ions score 14)
  108 - 116     508.7667   1015.5188  1015.5186    0.0002    0  K.QVTTPDVEK.K  (Ions score 20)
  108 - 116    1044.5264   1043.5191  1043.5135    0.0056    0  K.QVTTPDVEK.K  Formyl (N-term) (Ions score 24)
  108 - 117     572.8140   1143.6135  1143.6136   -0.0001    1  K.QVTTPDVEKK.I  (Ions score 39)
  108 - 117     382.2119   1143.6138  1143.6136    0.0003    1  K.QVTTPDVEKK.I  (Ions score 36)
  117 - 122     405.2238    808.4331   808.4330    0.0001    1  K.KIEEYK.R  (Ions score 31)
  118 - 123     419.2268    836.4391   836.4392   -0.0001    1  K.IEEYKR.E  (Ions score 31)
  118 - 123     837.4491    836.4418   836.4392    0.0026    1  K.IEEYKR.E  (Ions score 14)
  123 - 134     513.2481   1536.7225  1536.7143    0.0082    1  K.RENPGMFSWEIR.D  Oxidation (M) (Ions score 63)
  124 - 134     683.3176   1364.6206  1364.6183    0.0023    0  R.ENPGMFSWEIR.D  (Ions score 43)
  124 - 134     691.3163   1380.6180  1380.6132    0.0048    0  R.ENPGMFSWEIR.D  Oxidation (M) (Ions score 45)
  124 - 134     691.3170   1380.6195  1380.6132    0.0063    0  R.ENPGMFSWEIR.D  Oxidation (M) (Ions score 21)
  124 - 134    1381.6305   1380.6232  1380.6132    0.0100    0  R.ENPGMFSWEIR.D  Oxidation (M) (Ions score 26)
  124 - 134     705.3135   1408.6124  1408.6081    0.0043    0  R.ENPGMFSWEIR.D  Formyl (N-term); Oxidation (M) (Io
  124 - 136     812.8759   1623.7372  1623.7351    0.0020    1  R.ENPGMFSWEIRDK.L  Oxidation (M) (Ions score 43)
  137 - 145     545.2886   1088.5626  1088.5648   -0.0022    1  K.LLKDAVCDR.N  (Ions score 48)
  146 - 156     573.8104   1145.6063  1145.6040    0.0022    0  R.NTVPSVSSISR.I  (Ions score 36)
  146 - 156    1147.6035   1146.5962  1145.6040    0.9922    0  R.NTVPSVSSISR.I  (Ions score 23)
  146 - 156     587.8076   1173.6007  1173.5990    0.0017    0  R.NTVPSVSSISR.I  Formyl (N-term) (Ions score 32)
  146 - 156     587.8085   1173.6025  1173.5990    0.0035    0  R.NTVPSVSSISR.I  Formyl (N-term) (Ions score 40)
  146 - 156    1174.6113   1173.6041  1173.5990    0.0051    0  R.NTVPSVSSISR.I  Formyl (N-term) (Ions score 12)
  146 - 156     526.9125   1577.7156  1573.4306    4.2850    0  R.NTVPSVSSISR.I  Formyl (N-term); 5 Phospho (ST) (I
  160 - 164     572.2136    571.2063   565.3224    5.8839    1  R.SKFGK.G  (Ions score 6)
  162 - 174     754.2815   1506.5484  1507.6790   -1.1306    1  K.FGKGEEEEADLER.K  (Ions score 19)
  162 - 174     503.5661   1507.6766  1507.6790   -0.0025    1  K.FGKGEEEEADLER.K  (Ions score 59)
  162 - 174     503.5668   1507.6785  1507.6790   -0.0005    1  K.FGKGEEEEADLER.K  (Ions score 38)
  162 - 174     754.8476   1507.6806  1507.6790    0.0016    1  K.FGKGEEEEADLER.K  (Ions score 81)
```

```
162 - 174     768.8466  1535.6787  1535.6740     0.0047     1  K.FGKGEEEEADLER.K  Formyl (N-term) (Ions score 61)
165 - 174     588.7541  1175.4936  1175.4942    -0.0006     0  K.GEEEEADLER.K  (Ions score 16)
165 - 174     588.7548  1175.4951  1175.4942     0.0009     0  K.GEEEEADLER.K  (Ions score 63)
165 - 174     588.7551  1175.4956  1175.4942     0.0014     0  K.GEEEEADLER.K  (Ions score 59)
165 - 174    1176.5059  1175.4986  1175.4942     0.0044     0  K.GEEEEADLER.K  (Ions score 46)
165 - 174     602.7515  1203.4884  1203.4891    -0.0007     0  K.GEEEEADLER.K  Formyl (N-term) (Ions score 36)
165 - 175     435.5363  1303.5869  1303.5891    -0.0022     1  K.GEEEEADLERK.E  (Ions score 38)
165 - 175     652.8019  1303.5892  1303.5891     0.0001     1  K.GEEEEADLERK.E  (Ions score 39)
165 - 175     652.8030  1303.5915  1303.5891     0.0024     1  K.GEEEEADLERK.E  (Ions score 50)
165 - 175     666.8007  1331.5869  1331.5841     0.0028     1  K.GEEEEADLERK.E  Formyl (N-term) (Ions score 51)
184 - 195     663.3626  1324.7107  1324.7099     0.0008     1  K.AKHSIDGILSER.A  (Ions score 28)
184 - 195     663.3635  1324.7125  1324.7099     0.0026     1  K.AKHSIDGILSER.A  (Ions score 48)
186 - 195     563.7959  1125.5772  1125.5778    -0.0006     0  K.HSIDGILSER.A  (Ions score 54)
186 - 195     563.7968  1125.5791  1125.5778     0.0013     0  K.HSIDGILSER.A  (Ions score 60)
186 - 195    1126.5876  1125.5804  1125.5778     0.0026     0  K.HSIDGILSER.A  (Ions score 40)
186 - 195     563.8016  1125.5887  1125.5778     0.0109     0  K.HSIDGILSER.A  (Ions score 33)
186 - 195     564.2772  1126.5399  1125.5778     0.9621     0  K.HSIDGILSER.A  (Ions score 13)
186 - 195     577.3014  1152.5882  1153.5727    -0.9845     0  K.HSIDGILSER.A  Formyl (N-term) (Ions score 31)
186 - 195     577.7946  1153.5746  1153.5727     0.0018     0  K.HSIDGILSER.A  Formyl (N-term) (Ions score 16)
186 - 195    1154.5898  1153.5826  1153.5727     0.0098     0  K.HSIDGILSER.A  Formyl (N-term) (Ions score 18)
196 - 216    1085.4990  2168.9835  2169.9913    -1.0078     0  R.ASAPQSDEGSDIDSEPDLPLK.R  (Ions score 40)
196 - 216     724.3375  2169.9907  2169.9913    -0.0006     0  R.ASAPQSDEGSDIDSEPDLPLK.R  (Ions score 80)
196 - 216    1086.0042  2169.9937  2169.9913     0.0024     0  R.ASAPQSDEGSDIDSEPDLPLK.R  (Ions score 96)
196 - 216    1086.0087  2170.0028  2169.9913     0.0114     0  R.ASAPQSDEGSDIDSEPDLPLK.R  (Ions score 69)
196 - 216    1100.0023  2197.9901  2197.9863     0.0038     0  R.ASAPQSDEGSDIDSEPDLPLK.R  Formyl (N-term) (Ions sc
196 - 216     733.6710  2197.9912  2197.9863     0.0050     0  R.ASAPQSDEGSDIDSEPDLPLK.R  Formyl (N-term) (Ions sc
196 - 216    1100.0057  2197.9969  2197.9863     0.0107     0  R.ASAPQSDEGSDIDSEPDLPLK.R  Formyl (N-term) (Ions sc
196 - 216     750.6761  2249.0064  2249.9577    -0.9512     0  R.ASAPQSDEGSDIDSEPDLPLK.R  Phospho (ST) (Ions score
196 - 216     760.9847  2279.9322  2277.9526     1.9796     0  R.ASAPQSDEGSDIDSEPDLPLK.R  Formyl (N-term); Phospho
196 - 217    1163.5406  2325.0667  2326.0924    -1.0257     1  R.ASAPQSDEGSDIDSEPDLPLKR.K  (Ions score 58)
196 - 217     776.0298  2325.0675  2326.0924    -1.0249     1  R.ASAPQSDEGSDIDSEPDLPLKR.K  (Ions score 34)
196 - 217    1164.0549  2326.0953  2326.0924     0.0029     1  R.ASAPQSDEGSDIDSEPDLPLKR.K  (Ions score 70)
196 - 217     776.3733  2326.0980  2326.0924     0.0056     1  R.ASAPQSDEGSDIDSEPDLPLKR.K  (Ions score 72)
196 - 217     776.3734  2326.0984  2326.0924     0.0060     1  R.ASAPQSDEGSDIDSEPDLPLKR.K  (Ions score 94)
196 - 217     785.7041  2354.0905  2354.0874     0.0031     1  R.ASAPQSDEGSDIDSEPDLPLKR.K  Formyl (N-term) (Ions s
196 - 217    1178.0544  2354.0943  2354.0874     0.0070     1  R.ASAPQSDEGSDIDSEPDLPLKR.K  Formyl (N-term) (Ions s
196 - 217     785.7065  2354.0978  2354.0874     0.0104     1  R.ASAPQSDEGSDIDSEPDLPLKR.K  Formyl (N-term) (Ions s
222 - 236     603.9714  1808.8925  1808.8904     0.0021     1  R.SRTTFTAEQLEELER.A  (Ions score 48)
224 - 236    1566.7635  1565.7563  1565.7573    -0.0010     0  R.TTFTAEQLEELER.A  (Ions score 21)
224 - 236     783.8881  1565.7617  1565.7573     0.0044     0  R.TTFTAEQLEELER.A  (Ions score 74)
224 - 236     783.8886  1565.7625  1565.7573     0.0053     0  R.TTFTAEQLEELER.A  (Ions score 65)
224 - 236     783.8904  1565.7662  1565.7573     0.0089     0  R.TTFTAEQLEELER.A  (Ions score 47)
224 - 236     783.8922  1565.7697  1565.7573     0.0125     0  R.TTFTAEQLEELER.A  (Ions score 45)
224 - 236     796.8979  1591.7813  1593.7522    -1.9709     0  R.TTFTAEQLEELER.A  Formyl (N-term) (Ions score 34)
224 - 236     797.8843  1593.7541  1593.7522     0.0019     0  R.TTFTAEQLEELER.A  Formyl (N-term) (Ions score 41)
224 - 236     797.8857  1593.7569  1593.7522     0.0047     0  R.TTFTAEQLEELER.A  Formyl (N-term) (Ions score 70)
224 - 236     797.8894  1593.7643  1593.7522     0.0120     0  R.TTFTAEQLEELER.A  Formyl (N-term) (Ions score 35)
224 - 236     825.3876  1648.7606  1645.7236     3.0370     0  R.TTFTAEQLEELER.A  Phospho (ST) (Ions score 38)
241 - 249     389.1922  1164.5548  1164.5564    -0.0016     0  R.THYPDIYTR.E  (Ions score 30)
241 - 249     583.2853  1164.5560  1164.5564    -0.0004     0  R.THYPDIYTR.E  (Ions score 26)
241 - 249     583.2869  1164.5592  1164.5564     0.0028     0  R.THYPDIYTR.E  (Ions score 12)
241 - 249    1165.5692  1164.5619  1164.5564     0.0056     0  R.THYPDIYTR.E  (Ions score 19)
241 - 249     597.2846  1192.5547  1192.5513     0.0034     0  R.THYPDIYTR.E  Formyl (N-term) (Ions score 13)
263 - 270     518.2729  1034.5312  1034.5298     0.0015     0  R.VQVWFSNR.R  (Ions score 29)
```





```
ID   IPI00625217.1         IPI;      PRT;   479 AA.
AC   IPI00625217;
DT   30-JUL-2005 (IPI Mouse rel. 3.09, Created)
DT   30-JUL-2005 (IPI Mouse rel. 3.09, Last sequence update)
DE   PAIRED BOX PROTEIN PAX-3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
CC   -!- GENE_LOCATION: Chr. 1:78097842-78193711:-1.
DR   UniProtKB/Swiss-Prot; P24610; PAX3_MOUSE; M.
DR   REFSEQ_VALIDATED; NP_032807; GI:226958472; -.
DR   ENSEMBL; ENSMUSP00000084320; ENSMUSG00000004872; -.
DR   UniParc; UPI00000E891C; -; -.
DR   MGI; MGI:97487; Pax3; -.
```

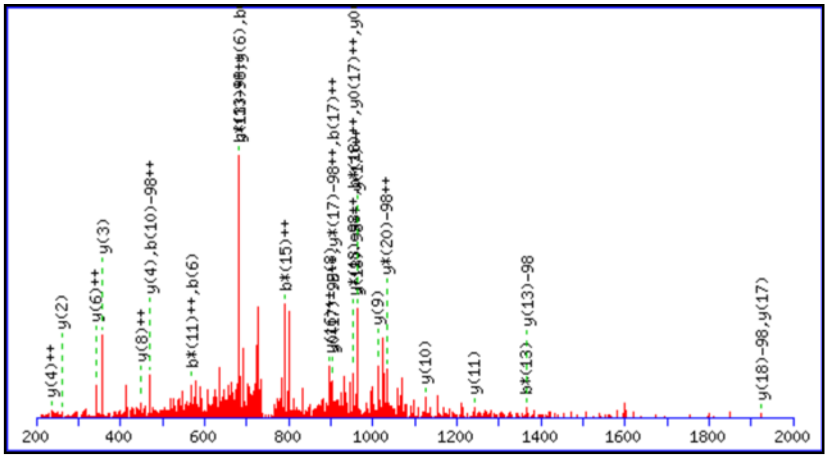
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAPQSDEGSDIDSEPDLPLK**
Found in **IPI00625217**, Tax_Id=10090 Gene_Symbol=Pax3 Paired box protein Pax-3

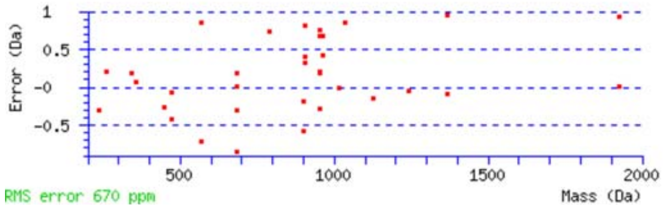
Match to Query 7456: 2279.932212 from(760.984680,3+) intensity(169254.0000) index(2551)
Title: o63_11jan24_09_uc_90min_neuloss_ms3_pax3_20ul.03846.03846.3
Data file o63_11jan24_09_uc_90min_neuloss_ms3_pax3_20ul.mgf

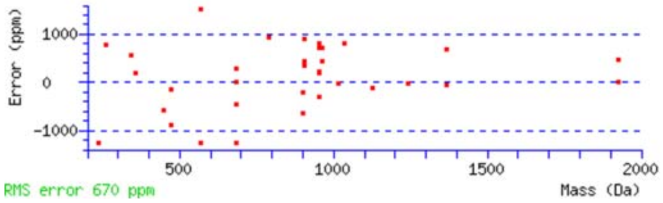
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2277.9526
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Formyl (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 **Expect:** 1.3
Matches : 34/342 fragment ions using 52 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0393	50.5233					A							21
2	187.0713	94.0393			169.0608	85.0340	S	2081.9509	1041.4791	2064.9244	1032.9658	2063.9404	1032.4738	20
3	258.1084	129.5579			240.0979	120.5526	A	1994.9189	997.9631	1977.8924	989.4498	1976.9084	988.9578	19
4	355.1612	178.0842			337.1506	169.0790	P	***1923.8818***	962.4445	1906.8553	953.9313	1905.8712	953.4393	18
5	483.2198	242.1135	466.1932	233.6003	465.2092	233.1083	Q	1826.8290	913.9182	1809.8025	905.4049	1808.8185	904.9129	17
6	570.2518	285.6295	553.2253	277.1163	552.2413	276.6243	S	1698.7705	849.8889	1681.7439	841.3756	1680.7599	840.8836	16
7	685.2788	343.1430	668.2522	334.6297	667.2682	334.1377	D	1611.7384	806.3729	1594.7119	797.8596	1593.7279	797.3676	15
8	814.3214	407.6643	797.2948	399.1510	796.3108	398.6590	E	1496.7115	748.8594	1479.6849	740.3461	1478.7009	739.8541	14
9	871.3428	436.1750	854.3163	427.6618	853.3323	427.1698	G	***1367.6689***	684.3381	1350.6424	675.8248	1349.6583	675.3328	13
10	940.3643	470.6858	923.3377	462.1725	922.3537	461.6805	S	1310.6474	655.8274	1293.6209	647.3141	1292.6369	646.8221	12
11	1055.3912	528.1992	1038.3647	519.6860	1037.3807	519.1940	D	***1241.6260***	621.3166	1224.5994	612.8034	1223.6154	612.3113	11
12	1168.4753	584.7413	1151.4487	576.2280	1150.4647	575.7360	I	***1126.5990***	563.8032	1109.5725	555.2899	1108.5885	554.7979	10
13	1283.5022	642.2548	1266.4757	633.7415	1265.4917	633.2495	D	***1013.5150***	507.2611	996.4884	498.7478	995.5044	498.2558	9
14	1370.5343	685.7708	1353.5077	677.2575	1352.5237	676.7655	S	***898.4880***	449.7477	881.4615	441.2344	880.4775	440.7424	8
15	1499.5769	750.2921	1482.5503	741.7788	1481.5663	741.2868	E	811.4560	406.2316	794.4294	397.7184	793.4454	397.2264	7
16	1596.6296	798.8184	1579.6031	790.3052	1578.6191	789.8132	P	***682.4134***	341.7103	665.3869	333.1971	664.4028	332.7051	6
17	1711.6566	856.3319	1694.6300	847.8186	1693.6460	847.3266	D	585.3606	293.1840	568.3341	284.6707	567.3501	284.1787	5
18	1824.7406	912.8739	1807.7141	904.3607	1806.7301	903.8687	L	***470.3337***	235.6705	453.3071	227.1572			4
19	1921.7934	961.4003	1904.7668	952.8871	1903.7828	952.3950	P	***357.2496***	179.1285	340.2231	170.6152			3
20	2034.8775	1017.9424	2017.8509	1009.4291	2016.8669	1008.9371	L	***260.1969***	130.6021	243.1703	122.0888			2
21							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.5	2276.8948	3.0374	LSTLGSGGESGGDGSPGGAGATAAR
35.8	2276.8948	3.0374	LSTLGSGGESGGDGSPGGAGATAAR
35.8	2276.8948	3.0374	LSTLGSGGESGGDGSPGGAGATAAR
33.6	2277.9526	1.9796	ASAPQSDEGSDIDSEPDLPLK
32.0	2282.8941	-2.9619	HGGLDLTTNNSSSTTSSTTSK
31.8	2276.8948	3.0374	LSTLGSGGESGGDGSPGGAGATAAR
31.8	2276.8948	3.0374	LSTLGSGGESGGDGSPGGAGATAAR
29.2	2281.6964	-1.7642	NSTPNSSGGGGGGSGGNDQLSK
29.1	2276.8948	3.0374	LSTLGSGGESGGDGSPGGAGATAAR
29.0	2277.9526	1.9796	ASAPQSDEGSDIDSEPDLPLK

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

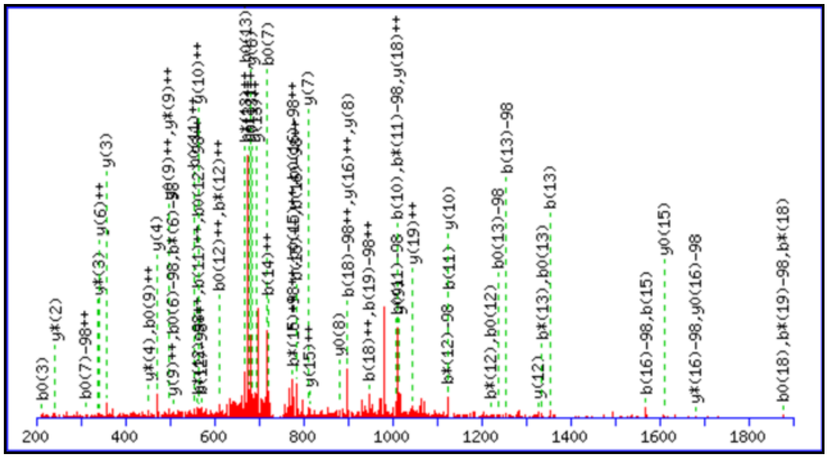
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAPQSDEGSDIDSEPDLPLK**
Found in **IPI00407505**, Tax_Id=10090 Gene_Symbol=Pax3 Putative uncharacterized protein

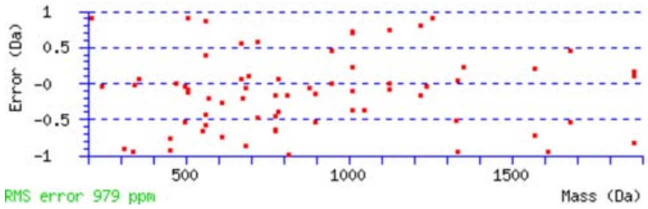
Match to Query 7421: 2249.006430 from(750.676086,3+) intensity(107526.0000) index(2533)
Title: o63_11jan24_09_uc_90min_neuloss_ms3_pax3_20ul.03823.03823.3
Data file o63_11jan24_09_uc_90min_neuloss_ms3_pax3_20ul.mgf

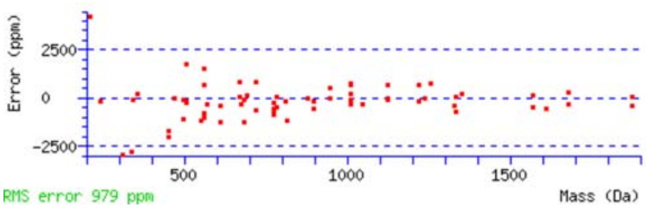
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2249.9577
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6     : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19  Expect: 1.5
Matches : 69/342 fragment ions using 117 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							21
2	159.0764	80.0418			141.0659	71.0366	S	2179.9278	1090.4676	2162.9013	1081.9543	2161.9173	1081.4623	20
3	230.1135	115.5604			212.1030	106.5551	A	2092.8958	1046.9515	2075.8693	1038.4383	2074.8853	1037.9463	19
4	327.1663	164.0868			309.1557	155.0815	P	2021.8587	1011.4330	2004.8322	1002.9197	2003.8481	1002.4277	18
5	455.2249	228.1161	438.1983	219.6028	437.2143	219.1108	Q	1924.8059	962.9066	1907.7794	954.3933	1906.7954	953.9013	17
6	622.2232	311.6153	605.1967	303.1020	604.2127	302.6100	S	1796.7474	898.8773	1779.7208	890.3640	1778.7368	889.8720	16
7	737.2502	369.1287	720.2236	360.6155	719.2396	360.1234	D	1629.7490	815.3781	1612.7225	806.8649	1611.7384	806.3729	15
8	866.2928	433.6500	849.2662	425.1367	848.2822	424.6447	E	1514.7221	757.8647	1497.6955	749.3514	1496.7115	748.8594	14
9	923.3142	462.1608	906.2877	453.6475	905.3037	453.1555	G	1385.6795	693.3434	1368.6529	684.8301	1367.6689	684.3381	13
10	1010.3463	505.6768	993.3197	497.1635	992.3357	496.6715	S	***1328.6580***	664.8326	1311.6315	656.3194	1310.6474	655.8274	12
11	1125.3732	**563.1902**	1108.3467	554.6770	1107.3626	554.1850	D	1241.6260	621.3166	1224.5994	612.8034	1223.6154	612.3113	11
12	1238.4573	619.7323	1221.4307	611.2190	1220.4467	610.7270	I	***1126.5990***	563.8032	1109.5725	555.2899	1108.5885	554.7979	10
13	1353.4842	**677.2457**	1336.4577	668.7325	1335.4736	668.2405	D	***1013.5150***	507.2611	996.4884	498.7478	995.5044	498.2558	9
14	1440.5162	**720.7618**	1423.4897	712.2485	1422.5057	711.7565	S	***898.4880***	449.7477	881.4615	441.2344	880.4775	440.7424	8
15	1569.5588	**785.2831**	1552.5323	776.7698	1551.5483	776.2778	E	***811.4560***	406.2316	794.4294	397.7184	793.4454	397.2264	7
16	1666.6116	833.8094	1649.5850	825.2962	1648.6010	824.8042	P	***682.4134***	341.7103	665.3869	333.1971	664.4028	332.7051	6
17	1781.6385	891.3229	1764.6120	882.8096	1763.6280	882.3176	D	585.3606	293.1840	568.3341	284.6707	567.3501	284.1787	5
18	1894.7226	**947.8649**	1877.6961	939.3517	1876.7120	938.8597	L	***470.3337***	235.6705	453.3071	227.1572			4
19	1991.7754	996.3913	1974.7488	987.8780	1973.7648	987.3860	P	***357.2496***	179.1285	340.2231	170.6152			3
20	2104.8594	1052.9334	2087.8329	1044.4201	2086.8489	1043.9281	L	260.1969	130.6021	243.1703	122.0888			2
21							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
22.0	2248.9192	0.0873	GSDGQPGPPGPPGTAGFPGSPGAK
21.8	2249.0270	-0.0205	LVDVDKLSLPQDTGVFTSK
21.7	2243.0327	5.9737	MNGSLGTKLLLCVSAGSANDK
21.5	2249.9577	-0.9512	ASAPQSDEGSDIDSEPDLPLK
20.4	2246.0596	2.9468	SGGTEGLLAEKLEALITQTR
19.2	2249.9577	-0.9512	ASAPQSDEGSDIDSEPDLPLK
18.9	2249.0270	-0.0205	LVDVDKLSLPQDTGVFTSK
18.6	2249.9341	-0.9277	SSKASLGSLEGEVEAEASSPK
18.6	2249.9341	-0.9277	SSKASLGSLEGEVEAEASSPK
18.6	2249.0270	-0.0205	LVDVDKLSLPQDTGVFTSK

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

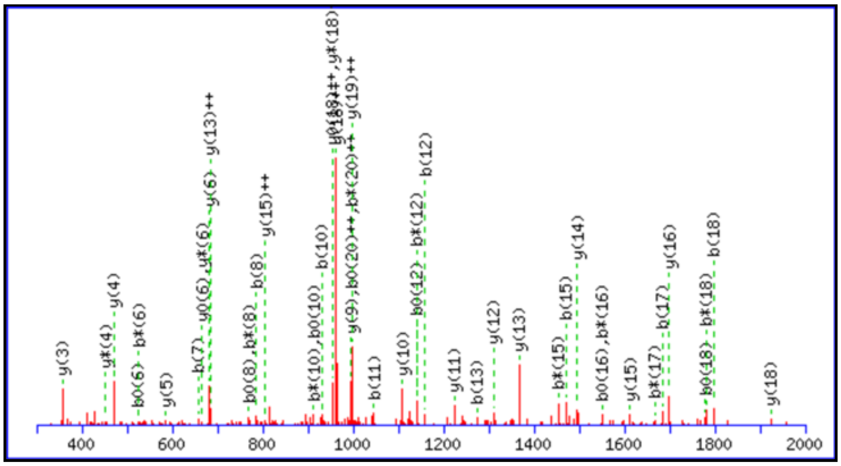
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAPQSDEGSDIDSEPDLPLK**
Found in **IPI00407505**, Tax_Id=10090 Gene_Symbol=Pax3 Putative uncharacterized protein

Match to Query 7262: 2151.994726 from(1077.004639,2+) intensity(92464.2000) index(2825)
Title: o63_11jan24_09_uc_90min_neuloss_ms3_pax3_20ul.04186.04186.2
Data file o63_11jan24_09_uc_90min_neuloss_ms3_pax3_20ul.mgf

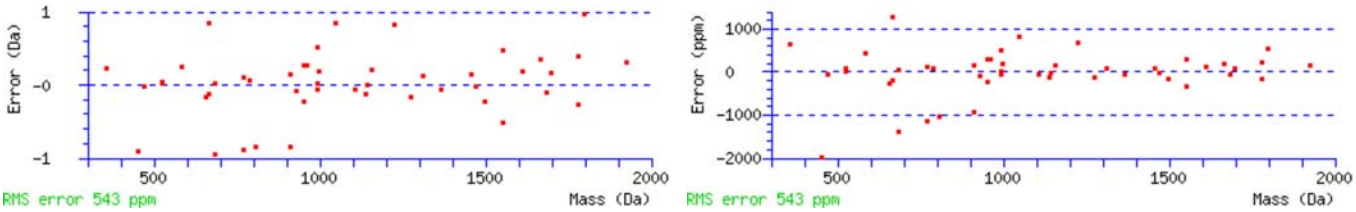
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2151.9808
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Dehydrated (S)
Ions Score: 80 **Expect:** 1.3e-005
Matches : 47/222 fragment ions using 78 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					**A**							**21**
2	159.0764	80.0418			141.0659	71.0366	**S**	2081.9509	1041.4791	2064.9244	1032.9658	2063.9404	1032.4738	**20**
3	230.1135	115.5604			212.1030	106.5551	**A**	1994.9189	997.9631	1977.8924	989.4498	1976.9084	988.9578	**19**
4	327.1663	164.0868			309.1557	155.0815	**P**	***1923.8818***	962.4445	1906.8553	953.9313	1905.8712	953.4393	**18**
5	455.2249	228.1161	438.1983	219.6028	437.2143	219.1108	**Q**	1826.8290	913.9182	1809.8025	905.4049	1808.8185	904.9129	**17**
6	542.2569	271.6321	525.2304	263.1188	524.2463	262.6268	**S**	***1698.7705***	849.8889	1681.7439	841.3756	1680.7599	840.8836	**16**
7	**657.2838**	329.1456	640.2573	320.6323	639.2733	320.1403	**D**	***1611.7384***	806.3729	1594.7119	797.8596	1593.7279	797.3676	**15**
8	**786.3264**	393.6669	769.2999	385.1536	768.3159	384.6616	**E**	***1496.7115***	748.8594	1479.6849	740.3461	1478.7009	739.8541	**14**
9	843.3479	422.1776	826.3214	413.6643	825.3373	413.1723	**G**	***1367.6689***	684.3381	1350.6424	675.8248	1349.6583	675.3328	**13**
10	**930.3799**	465.6936	913.3534	457.1803	912.3694	456.6883	**S**	***1310.6474***	655.8274	1293.6209	647.3141	1292.6369	646.8221	**12**
11	**1045.4069**	523.2071	1028.3803	514.6938	1027.3963	514.2018	**D**	***1223.6154***	612.3113	1206.5889	603.7981	1205.6048	603.3061	**11**
12	**1158.4909**	579.7491	1141.4644	571.2358	1140.4804	570.7438	**I**	***1108.5885***	554.7979	1091.5619	546.2846	1090.5779	545.7926	**10**
13	**1273.5179**	637.2626	1256.4913	628.7493	1255.5073	628.2573	**D**	***995.5044***	498.2558	978.4779	489.7426	977.4938	489.2506	**9**
14	1342.5393	671.7733	1325.5128	663.2600	1324.5288	662.7680	**S**	880.4775	440.7424	863.4509	432.2291	862.4669	431.7371	**8**
15	**1471.5819**	736.2946	1454.5554	727.7813	1453.5714	727.2893	**E**	811.4560	406.2316	794.4294	397.7184	793.4454	397.2264	**7**
16	1568.6347	784.8210	1551.6082	776.3077	1550.6241	775.8157	**P**	***682.4134***	341.7103	665.3869	333.1971	664.4028	332.7051	**6**
17	**1683.6616**	842.3345	1666.6351	833.8212	1665.6511	833.3292	**D**	***585.3606***	293.1840	568.3341	284.6707	567.3501	284.1787	**5**
18	**1796.7457**	898.8765	1779.7192	890.3632	1778.7351	889.8712	**L**	***470.3337***	235.6705	453.3071	227.1572			**4**
19	1893.7985	947.4029	1876.7719	938.8896	1875.7879	938.3976	**P**	***357.2496***	179.1285	340.2231	170.6152			**3**
20	2006.8825	1003.9449	1989.8560	995.4316	1988.8720	994.9396	**L**	260.1969	130.6021	243.1703	122.0888			**2**

21							**K**	147.1128	74.0600	130.0863	65.5468			**1**



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
79.6	2151.9808	0.0139	ASAPQSDEGSDIDSEPDLPLK
59.0	2151.9808	0.0139	ASAPQSDEGSDIDSEPDLPLK
40.0	2151.9808	0.0139	ASAPQSDEGSDIDSEPDLPLK
29.7	2151.9808	0.0139	ASAPQSDEGSDIDSEPDLPLK
26.4	2152.0220	-0.0272	SCESGAAGTVSGTSLAAPDITVR
22.1	2150.0061	1.9886	VQENLLASGVDLVTYITR
22.0	2152.0220	-0.0272	SCESGAAGTVSGTSLAAPDITVR
22.0	2152.0220	-0.0272	SCESGAAGTVSGTSLAAPDITVR
20.9	2151.0292	0.9655	LLGTVMATALMPKQATVMR
19.9	2149.9827	2.0120	VQPQTQMTAPKQTQTPDR

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

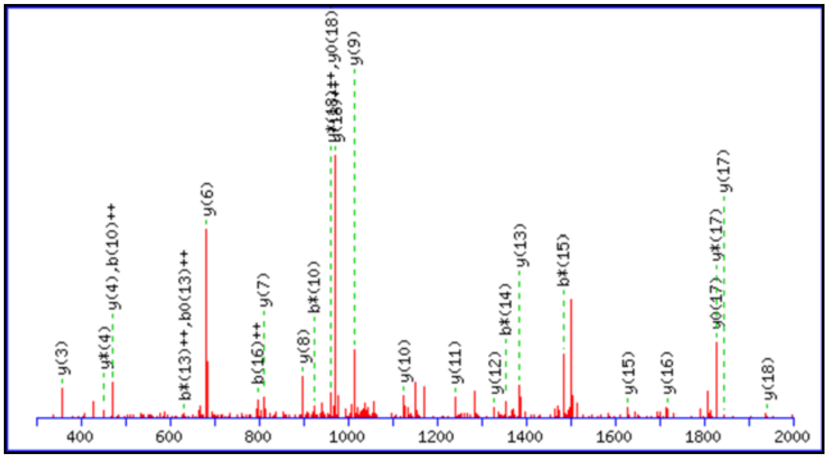
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAPQSDEGSDIDSEPDLPLK**
Found in **IPI00407505**, Tax_Id=10090 Gene_Symbol=Pax3 Putative uncharacterized protein

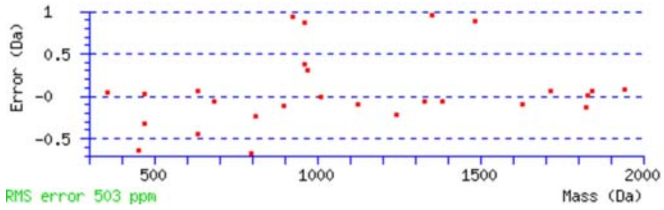
Match to Query 7293: 2181.992772 from(1092.003662,2+) intensity(143534.0000) index(2576)
Title: o63_11jan24_09_uc_90min_neuloss_ms3_pax3_20ul.03879.03879.2
Data file o63_11jan24_09_uc_90min_neuloss_ms3_pax3_20ul.mgf

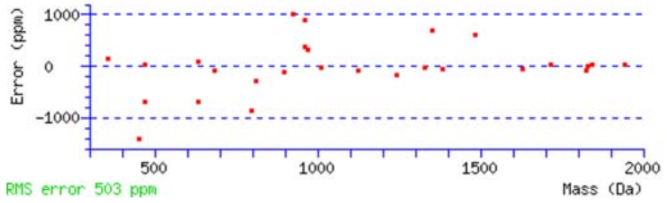
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2179.9757
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Formyl (N-term)
S2 : Dehydrated (S)
Ions Score: 77 **Expect:** 2e-005
Matches : 27/222 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0393	50.5233					**A**							**21**
2	169.0608	85.0340			151.0502	76.0287	**S**	2081.9509	1041.4791	2064.9244	1032.9658	2063.9404	1032.4738	**20**
3	240.0979	120.5526			222.0873	111.5473	**A**	2012.9295	1006.9684	1995.9029	998.4551	1994.9189	997.9631	**19**
4	337.1506	169.0790			319.1401	160.0737	**P**	***1941.8924***	971.4498	1924.8658	962.9365	1923.8818	962.4445	**18**
5	465.2092	233.1083	448.1827	224.5950	447.1987	224.1030	**Q**	***1844.8396***	922.9234	1827.8131	914.4102	1826.8290	913.9182	**17**
6	552.2413	276.6243	535.2147	268.1110	534.2307	267.6190	**S**	***1716.7810***	858.8942	1699.7545	850.3809	1698.7705	849.8889	**16**
7	667.2682	334.1377	650.2416	325.6245	649.2576	325.1325	**D**	***1629.7490***	815.3781	1612.7225	806.8649	1611.7384	806.3729	**15**
8	796.3108	398.6590	779.2842	390.1458	778.3002	389.6537	**E**	1514.7221	757.8647	1497.6955	749.3514	1496.7115	748.8594	**14**
9	853.3323	427.1698	836.3057	418.6565	835.3217	418.1645	**G**	***1385.6795***	693.3434	1368.6529	684.8301	1367.6689	684.3381	**13**
10	940.3643	470.6858	923.3377	462.1725	922.3537	461.6805	**S**	***1328.6580***	664.8326	1311.6315	656.3194	1310.6474	655.8274	**12**
11	1055.3912	528.1992	1038.3647	519.6860	1037.3807	519.1940	**D**	***1241.6260***	621.3166	1224.5994	612.8034	1223.6154	612.3113	**11**
12	1168.4753	584.7413	1151.4487	576.2280	1150.4647	575.7360	**I**	***1126.5990***	563.8032	1109.5725	555.2899	1108.5885	554.7979	**10**
13	1283.5022	642.2548	1266.4757	633.7415	1265.4917	633.2495	**D**	***1013.5150***	507.2611	996.4884	498.7478	995.5044	498.2558	**9**
14	1370.5343	685.7708	1353.5077	677.2575	1352.5237	676.7655	**S**	***898.4880***	449.7477	881.4615	441.2344	880.4775	440.7424	**8**
15	1499.5769	750.2921	1482.5503	741.7788	1481.5663	741.2868	**E**	***811.4560***	406.2316	794.4294	397.7184	793.4454	397.2264	**7**
16	1596.6296	798.8184	1579.6031	790.3052	1578.6191	789.8132	**P**	***682.4134***	341.7103	665.3869	333.1971	664.4028	332.7051	**6**
17	1711.6566	856.3319	1694.6300	847.8186	1693.6460	847.3266	**D**	585.3606	293.1840	568.3341	284.6707	567.3501	284.1787	**5**
18	1824.7406	912.8739	1807.7141	904.3607	1806.7301	903.8687	**L**	***470.3337***	235.6705	453.3071	227.1572			**4**
19	1921.7934	961.4003	1904.7668	952.8871	1903.7828	952.3950	**P**	***357.2496***	179.1285	340.2231	170.6152			**3**
20	2034.8775	1017.9424	2017.8509	1009.4291	2016.8669	1008.9371	**L**	260.1969	130.6021	243.1703	122.0888			**2**
21							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.3	2179.9757	2.0171	ASAPQSDEGSDIDSEPDLPLK
52.4	2179.9757	2.0171	ASAPQSDEGSDIDSEPDLPLK
32.1	2179.9757	2.0171	ASAPQSDEGSDIDSEPDLPLK
26.2	2182.0163	-0.0236	VTQNLPMKEGCTEVSLLR
26.0	2180.9661	1.0267	QSLNSPSPGETEMDLLVTR
23.4	2182.0018	-0.0090	IFSCDSTLLASSASLQTTVK
23.1	2180.0224	1.9704	WTNAKMEIATEEPLNPIK
22.8	2182.0018	-0.0090	IFSCDSTLLASSASLQTTVK
22.8	2180.9674	1.0253	QMQSGVSGFRDLNTEAHVK
22.8	2180.9674	1.0253	QMQSGVSGFRDLNTEAHVK

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

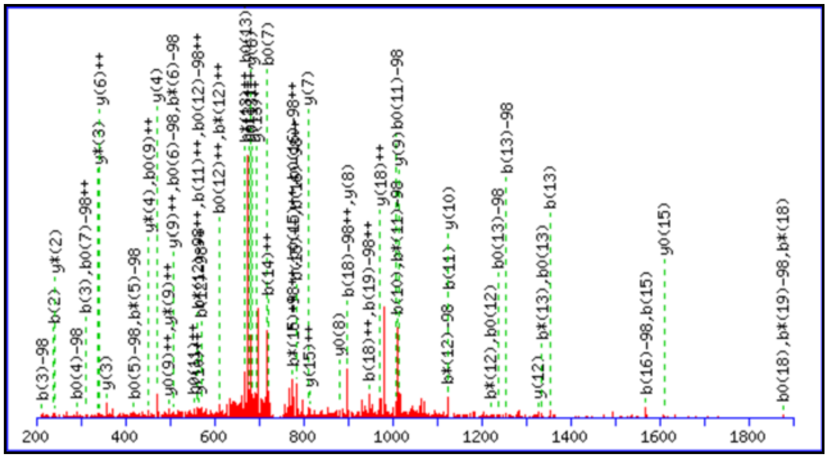
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAPQSDEGSDIDSEPDLPLK**
Found in **IPI00625217**, Tax_Id=10090 Gene_Symbol=Pax3 Paired box protein Pax-3

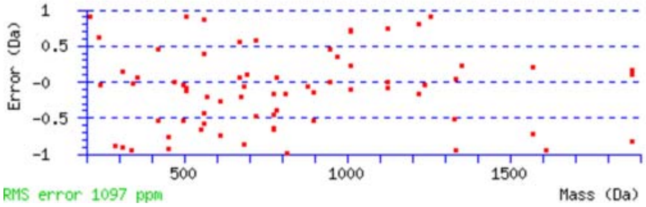
Match to Query 7421: 2249.006430 from(750.676086,3+) intensity(107526.0000) index(2533)
Title: o63_11jan24_09_uc_90min_neuloss_ms3_pax3_20ul.03823.03823.3
Data file o63_11jan24_09_uc_90min_neuloss_ms3_pax3_20ul.mgf

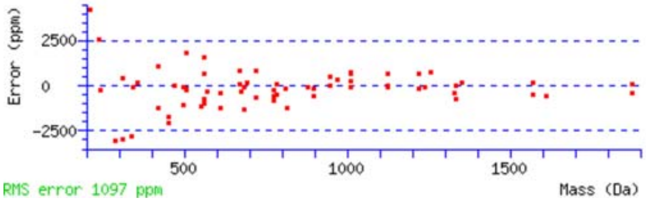
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2249.9577
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2     : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22  Expect: 0.89
Matches : 70/336 fragment ions using 117 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							21
2	***239.0427***	120.0250			221.0322	111.0197	S	2179.9278	1090.4676	2162.9013	1081.9543	2161.9173	1081.4623	20
3	***310.0799***	155.5436			292.0693	146.5383	A	2012.9295	1006.9684	1995.9029	998.4551	1994.9189	997.9631	19
4	407.1326	204.0700			389.1221	195.0647	P	1941.8924	971.4498	1924.8658	962.9365	1923.8818	962.4445	18
5	535.1912	268.0992	518.1647	259.5860	517.1806	259.0940	Q	1844.8396	922.9234	1827.8131	914.4102	1826.8290	913.9182	17
6	622.2232	311.6153	605.1967	303.1020	604.2127	302.6100	S	1716.7810	858.8942	1699.7545	850.3809	1698.7705	849.8889	16
7	737.2502	369.1287	720.2236	360.6155	719.2396	360.1234	D	1629.7490	815.3781	1612.7225	806.8649	1611.7384	806.3729	15
8	866.2928	433.6500	849.2662	425.1367	848.2822	424.6447	E	1514.7221	757.8647	1497.6955	749.3514	1496.7115	748.8594	14
9	923.3142	462.1608	906.2877	453.6475	905.3037	453.1555	G	1385.6795	693.3434	1368.6529	684.8301	1367.6689	684.3381	13
10	***1010.3463***	505.6768	993.3197	497.1635	992.3357	496.6715	S	***1328.6580***	664.8326	1311.6315	656.3194	1310.6474	655.8274	12
11	***1125.3732***	**563.1902**	1108.3467	554.6770	1107.3626	554.1850	D	1241.6260	621.3166	1224.5994	612.8034	1223.6154	612.3113	11
12	1238.4573	619.7323	1221.4307	611.2190	1220.4467	610.7270	I	***1126.5990***	563.8032	1109.5725	555.2899	1108.5885	554.7979	10
13	***1353.4842***	**677.2457**	1336.4577	668.7325	1335.4736	668.2405	D	***1013.5150***	507.2611	996.4884	498.7478	995.5044	498.2558	9
14	1440.5162	**720.7618**	1423.4897	712.2485	1422.5057	711.7565	S	***898.4880***	449.7477	881.4615	441.2344	880.4775	440.7424	8
15	***1569.5588***	**785.2831**	1552.5323	776.7698	1551.5483	776.2778	E	***811.4560***	406.2316	794.4294	397.7184	793.4454	397.2264	7
16	1666.6116	833.8094	1649.5850	825.2962	1648.6010	824.8042	P	***682.4134***	341.7103	665.3869	333.1971	664.4028	332.7051	6
17	1781.6385	891.3229	1764.6120	882.8096	1763.6280	882.3176	D	585.3606	293.1840	568.3341	284.6707	567.3501	284.1787	5
18	1894.7226	**947.8649**	1877.6961	939.3517	1876.7120	938.8597	L	***470.3337***	235.6705	453.3071	227.1572			4
19	1991.7754	996.3913	1974.7488	987.8780	1973.7648	987.3860	P	***357.2496***	179.1285	340.2231	170.6152			3
20	2104.8594	1052.9334	2087.8329	1044.4201	2086.8489	1043.9281	L	260.1969	130.6021	243.1703	122.0888			2
21							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
22.0	2248.9192	0.0873	GSDGQPGPPGPPGTAGFPGSPGAK
21.8	2249.0270	-0.0205	LVDVDKLSLPQDTGVFTSK
21.7	2243.0327	5.9737	MNGSLGTKLLLCVSAGSANDK
21.5	2249.9577	-0.9512	ASAPQSDEGSDIDSEPDLPLK
20.4	2246.0596	2.9468	SGGTEGLLAEKLEALITQTR
19.2	2249.9577	-0.9512	ASAPQSDEGSDIDSEPDLPLK
18.9	2249.0270	-0.0205	LVDVDKLSLPQDTGVFTSK
18.6	2249.9341	-0.9277	SSKASLGSLEGEVEAEASSPK
18.6	2249.9341	-0.9277	SSKASLGSLEGEVEAEASSPK
18.6	2249.0270	-0.0205	LVDVDKLSLPQDTGVFTSK

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

```
DR   Entrez Gene; 18505; Pax3; -.
DR   UniGene; Mm.1371; -; -.
DR   UniGene; Mm.478746; -; -.
DR   CCDS; CCDS15082.1; -; -.
DR   trome; MTR044593; -; PRT.
DR   Transfac; T00680; -; -.
DR   CleanEx; MM_PAX3; -; -.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR017970; Homeobox_CS.
DR   InterPro; IPR009057; Homeodomain-like.
DR   InterPro; IPR012287; Homeodomain-rel.
DR   InterPro; IPR001523; Paired_box_N.
DR   InterPro; IPR022106; Pax7.
DR   InterPro; IPR011991; WHTH_trsnscrt_rep_DNA-bd.
DR   Pfam; PF00046; Homeobox; 1.
DR   Pfam; PF00292; PAX; 1.
DR   Pfam; PF12360; Pax7; 1.
DR   PRINTS; PR00027; PAIREDBOX.
DR   SMART; SM00389; HOX; 1.
DR   SMART; SM00351; PAX; 1.
DR   PROSITE; PS00027; HOMEOBOX_1; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
DR   PROSITE; PS00034; PAIRED_1; 1.
DR   PROSITE; PS51057; PAIRED_2; 1.
DR   SUPERFAMILY; SSF46689; Homeodomain_like; 2.
DR   GENE3D; G3DSA:1.10.10.10; Wing_hlx_DNA_bd; 2.
DR   GENE3D; G3DSA:1.10.10.60; Homeodomain-rel; 1.
SQ   SEQUENCE   479 AA;  52949 MW;  8806E551FFB755A0 CRC64;
     MTTLAGAVPR MMRPGPGQNY PRSGFPLEVS TPLGQGRVNQ LGGVFINGRP LPNHIRHKIV
     EMAHHGIRPC VISRQLRVSH GCVSKILCRY QETGSIRPGA IGGSKPKQVT TPDVEKKIEE
     YKRENPGMFS WEIRDKLLKD AVCDRNTVPS VSSISRILRS KFGKGEEEEA DLERKEAEES
     EKKAKHSIDG ILSERASAPQ SDEGSDIDSE PDLPLKRKQR RSRTTFTAEQ LEELERAFER
     THYPDIYTRE ELAQRAKLTE ARVQVWFSNR RARWRKQAGA NQLMAFNHLI PGGFPPTAMP
     TLPTYQLSET SYQPTSIPQA VSDPSSTVHR PQPLPPSTVH QSTIPSNADS SSAYCLPSTR
     HGFSSYTDSF VPPSGPSNPM NPTIGNGLSP QVMGLLTNHG GVPHQPQTDY ALSPLTGGLE
     PTTTVSASCS QRLEHMKNVD SLPTSQPYCP PTYSTAGYSM DPVTGYQYGQ YGQSKPWTF
```

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