

Sequence	-log q-...	-log PEP	Search Engr...	Score	Delta Score	z	Theoretic...	Measured...	Mass Err...	Fixed Mo...	Variable ...	Project	Experiment
<b>MS<sup>2</sup></b> K.SSAAMAK.A	2.0898	-99	Mascot	26.98	4.39	2	736.4728	736.4657	-9.62	Dimethyl:2...		Munoz_M...	IPS_Singa...
<b>MS<sup>2</sup></b> K.SSAAMAK.A	2.0898	-99	Mascot	26.98	4.39	2	736.4728	736.4657	-9.62	Dimethyl:2...		Munoz_M...	IPS_Singa...
<b>MS<sup>2</sup></b> K.SSAAMAK.A	2.0898	-99	Mascot	26.98	4.39	2	736.4728	736.4657	-9.62	Dimethyl:2...		Munoz_M...	IPS_Singa...

> Reference spectrum

> Fragments

Select All Deselect All

a:  1+  2+  3+

b:  1+  2+  3+

c:  1+  2+  3+

x:  1+  2+  3+

y:  1+  2+  3+

z:  1+  2+  3+

yb:

IM:

M[H]:

Neutral loss:

CH4O  NH3  C3H6S

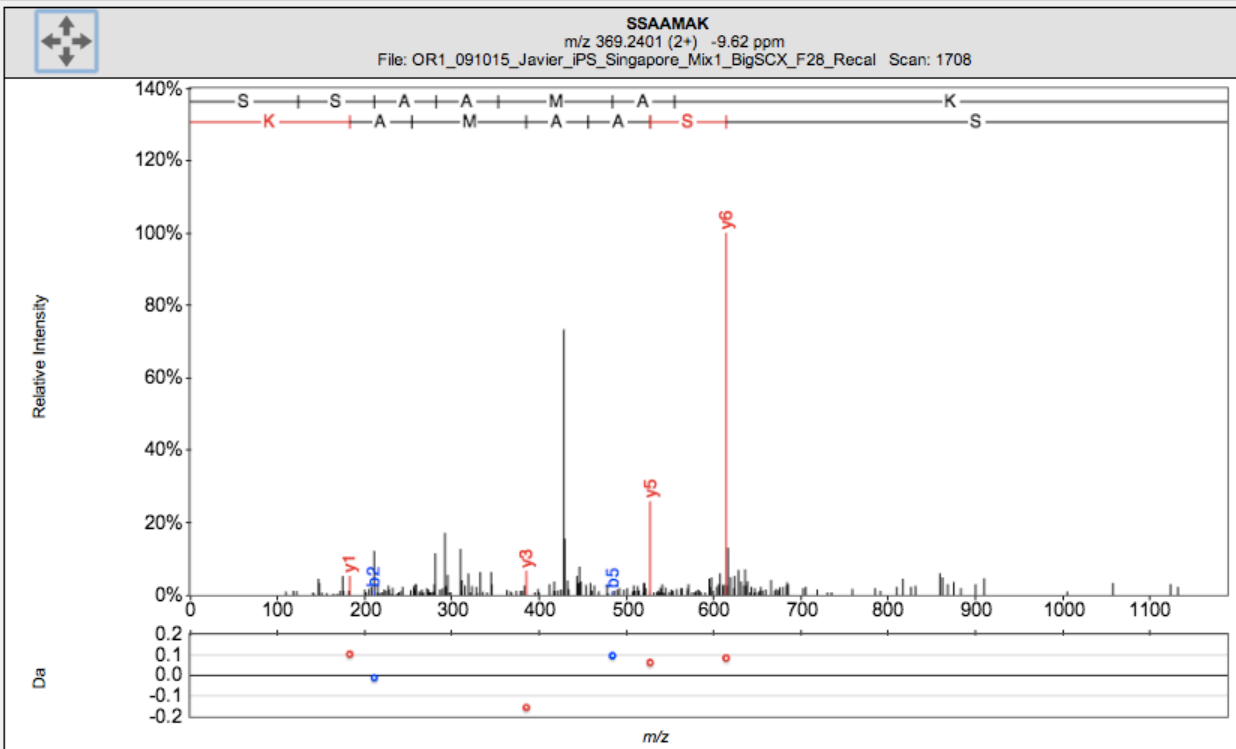
C2H4S  H2O  CO

Max neutral loss count: 3

Mass tolerance: 0.4 Da

Expert Mode:  on  off

> Configuration



b1+	#	Seq #	y1+
124.115	1	S	7
<b>211.147</b>	2	S	<b>614.3723</b>
282.1841	3	A	<b>527.3403</b>
353.2212	4	A	456.3032
<b>484.2617</b>	5	M	<b>385.2661</b>
555.2988	6	A	254.2256
	7	K	<b>183.1885</b>

Sequence	-log q...	-log PEP	Search Engl...	Score	Delta Score	z	Theoretic...	Measured...	Mass Err...	Fixed Mo...	Variable ...	Project	Experiment
<input type="checkbox"/> MS <sup>2</sup> R.AVFDLSSK.T	2.3667	1.56	Andromeda	63.49	11.49	2	873.4687	865.4545	-9175.15	Label:13C...		Geiger_C...	HMELonza
<input type="checkbox"/> MS <sup>2</sup> R.AVFDLSSK.T	2.3667	1.56	Andromeda	63.49	11.49	2	873.4687	865.4545	-9175.15	Label:13C...		Geiger_C...	HMELonza
<input checked="" type="checkbox"/> MS <sup>2</sup> R.AVFDLSSK.T	2.0768	1.43	Andromeda	98.52	29.33	2	865.4545	865.4545	-0.01			Joshi_MS...	Label-free ...
<input type="checkbox"/> MS <sup>2</sup> R.AVFDLSSK.T	2.0755	1.43	Andromeda	82.45	6.42	2	865.4545	865.4545	-0.01			CPTAC_C...	Clinical_pr...
<input type="checkbox"/> MS <sup>2</sup> R.AVFDLSSK.T	2.4811	1.41	Andromeda	60.59	18.48	2	873.4687	865.4545	-9175.15	Label:13C...		Geiger_C...	HCC1937

< 1 2 >

> Reference spectrum

> Fragments

Select All Deselect All

a:  1+  2+  3+

b:  1+  2+  3+

c:  1+  2+  3+

x:  1+  2+  3+

y:  1+  2+  3+

z:  1+  2+  3+

yb:

IM:

M[H]:

Neutral loss:

H2O  NH3  C2O

C4H9N  CH4O  C3H9N

CO  C4H8  C2H5N

C5H11N  C4H11N  C3H6

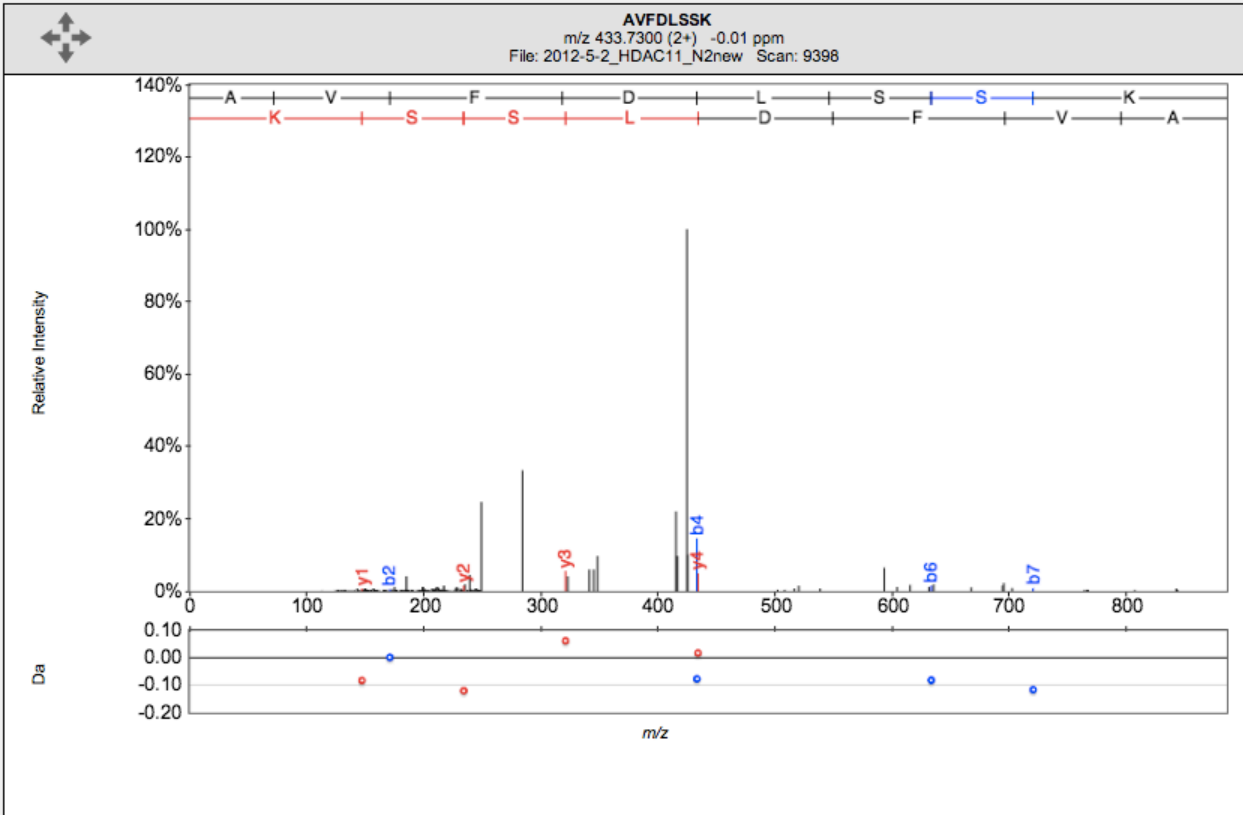
C2H4O2

Max neutral loss count: 3

Mass tolerance: 0.4 Da

Expert Mode:  on  off

> Configuration



b1+	#	Seq	#	y1+
72.0444	1	A	8	
171.1128	2	V	7	795.4247
318.1812	3	F	6	696.3563
433.2082	4	D	5	549.2879
546.2922	5	L	4	434.2609
633.3243	6	S	3	321.1769
720.3563	7	S	2	234.1448
	8	K	1	147.1128

Sequence	-log q-...	-log PEP	Search Engr...	Score	Delta Score	z	Theoretic...	Measured...	Mass Err...	Fixed Mo...	Variable ...	Project	Experiment
<b>MS<sup>2</sup></b> R.VFQSGQGGMGIKA	2.07	0.21	Mascot	29.98	10.36	3	1222.6380	1222.6315	-5.34	Dimethyl...	Oxidation...	Munoz_E...	Comparis...
<b>MS<sup>2</sup></b> R.VFQSGQGGMGIKA	2.07	0.21	Mascot	29.98	10.36	3	1222.6380	1222.6315	-5.34	Dimethyl...	Oxidation...	Munoz_E...	Compariso...

> Reference spectrum

> Fragments

Select All   Deselect All

a:  1+  2+  3+

b:  1+  2+  3+

c:  1+  2+  3+

x:  1+  2+  3+

y:  1+  2+  3+

z:  1+  2+  3+

yb:

IM:

M[H]:

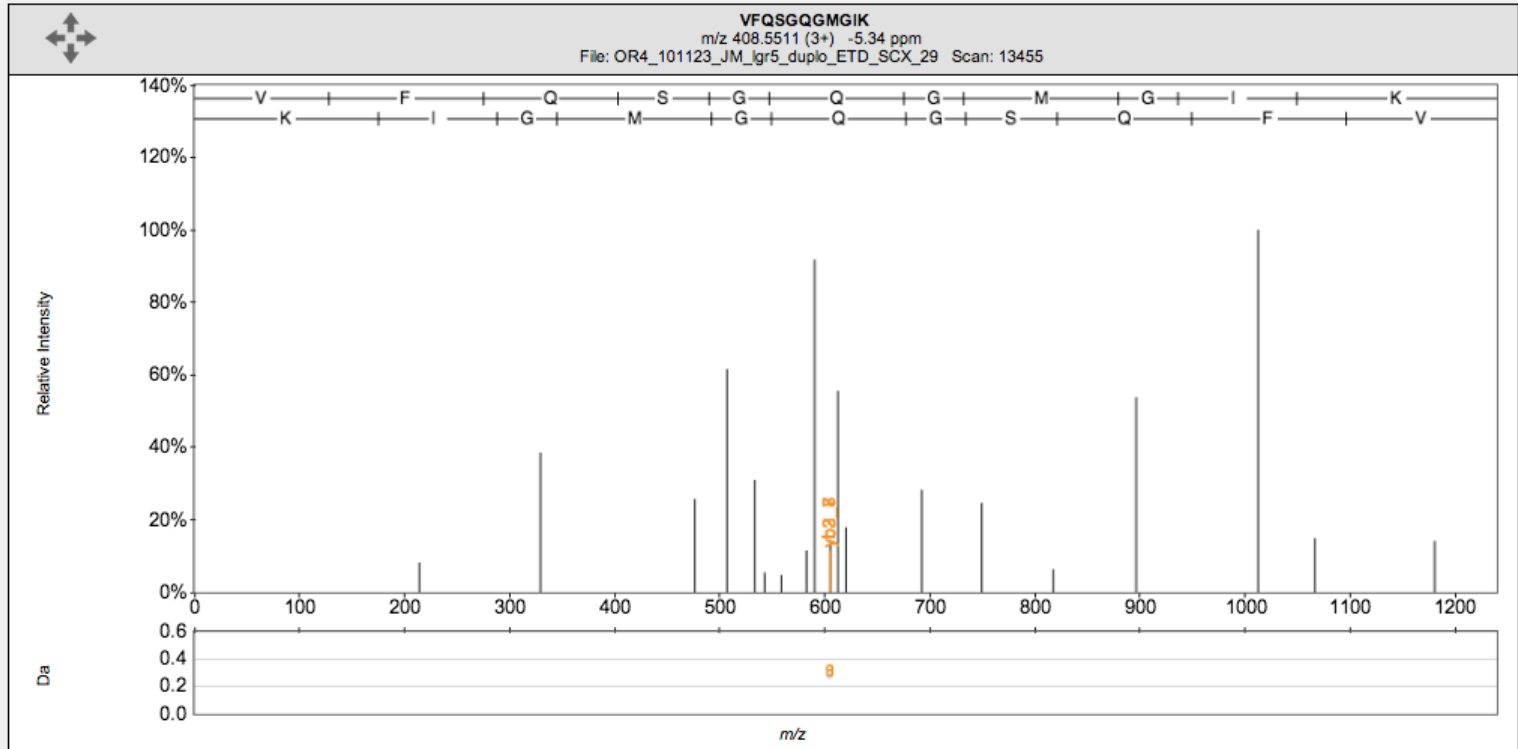
Neutral loss:

Max neutral loss count: 3

Mass tolerance: 0.4 Da

Expert Mode:  on  off

> Configuration



Fragment Ion Table

Sequence	-log q...	-log PEP	Search Engl...	Score	Delta Score	z	Theoretic...	Measured...	Mass Err...	Fixed Mo...	Variable ...	Project	Experiment
<b>MS<sup>2</sup></b> K.QIQEGVIK.F	2.346	1.88	Andromeda	93.43	2.36	2	913.5233	913.5233	0.01			Maier_MC...	tissue_pro...
<b>MS<sup>2</sup></b> K.QIQEGVIK.F	5	1	Mascot	38.48	1.72	2	913.5233	914.5187	1089.7			Nagaraj_...	Deep prot...
<b>MS<sup>2</sup></b> K.QIQEGVIK.F	3.0218	0.39	Mascot	49.95	2.07	2	913.5233	914.5184	1089.31			Human_b...	Proteome ...
<b>MS<sup>2</sup></b> K.QIQEGVIK.F	3.0687	0.31	Mascot	51.09	2.27	2	913.5233	914.5179	1088.74			Human_b...	Proteome ...
<b>MS<sup>2</sup></b> K.QIQEGVIK.F	2.0583	0.15	Mascot	24.22	7.65	2	913.5233	913.5237	0.51			Human_b...	Proteome ...

> Reference spectrum

> Fragments

Select All Deselect All

a:  1+  2+  3+

b:  1+  2+  3+

c:  1+  2+  3+

x:  1+  2+  3+

y:  1+  2+  3+

z:  1+  2+  3+

yb:

IM:

M[H]:

Neutral loss:

H2O  C3H6  NH3

C2H5NO  C2H5N  C5H11N

C3H9N  C3H5NO  CH3NO

C2H4  C4H9N  C4H11N

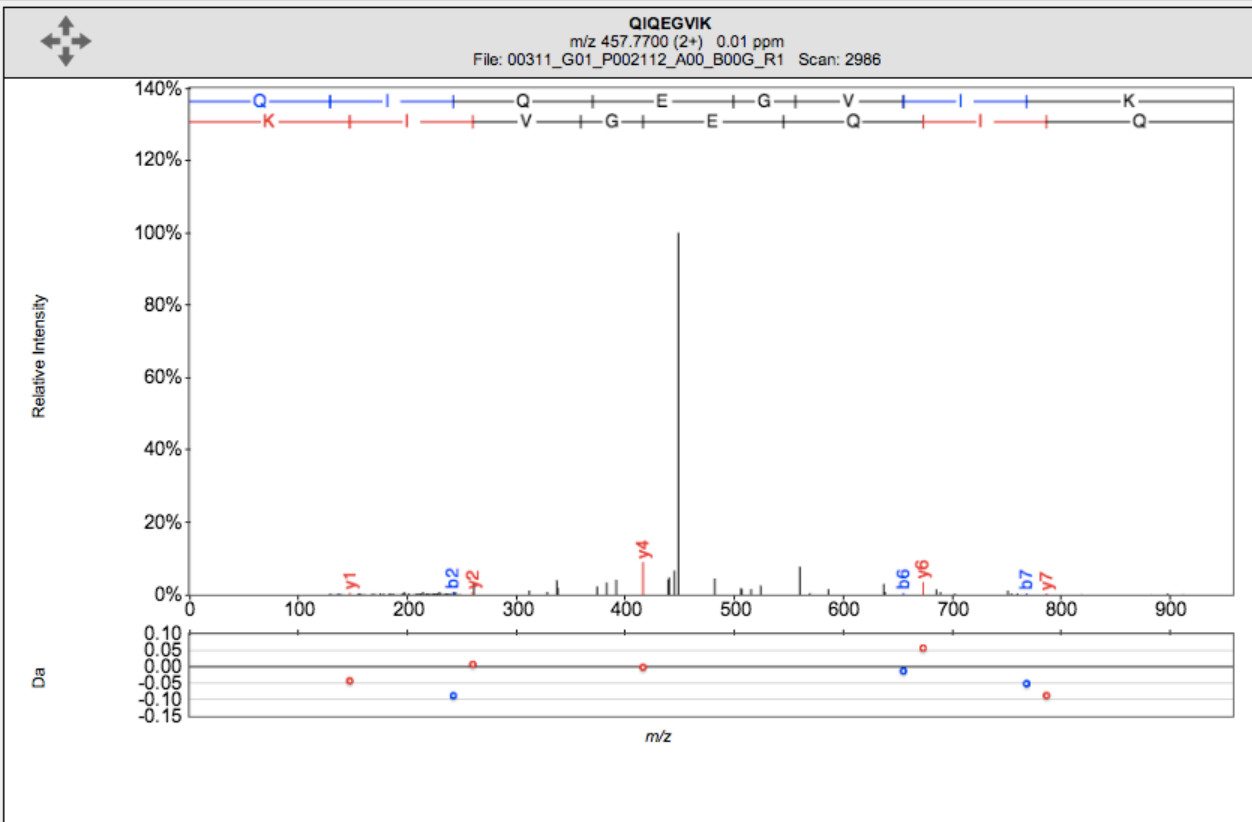
CO

Max neutral loss count: 3

Mass tolerance: 0.4 Da

Expert Mode:  on  off

> Configuration



b1+	#	Seq #	y1+
129.0659	1	Q	8
242.1499	2	I	7 <b>786.472</b>
370.2085	3	Q	6 <b>673.3879</b>
499.2511	4	E	5 545.3293
556.2726	5	G	4 <b>416.2867</b>
655.341	6	V	3 359.2653
768.425	7	I	2 <b>260.1969</b>
	8	K	1 <b>147.1128</b>

Sequence	-log q-...	-log PEP	Search Engi...	Score	Delta Score	z	Theoretic...	Measured...	Mass Err...	Fixed Mo...	Variable ...	Project	Experiment
<b>MS<sup>2</sup></b> K.EFKNALK.K	2.6669	1.16	Andromeda	97.07	10.2	2	848.4756	848.4756	0			Cutler_Pe...	Roche_hu...
<b>MS<sup>2</sup></b> K.EFKNALK.K	2.6711	0.93	Andromeda	94.26	24.26	2	848.4756	848.4756	0			Cutler_Pe...	Roche_hu...
<b>MS<sup>2</sup></b> K.EFKNALK.K	2.2728	0.6	Andromeda	76.85	6.85	2	848.4756	848.4756	0			IEC_prote...	colon
<b>MS<sup>2</sup></b> K.EFKNALK.K	2.0411	0.66	Andromeda	76.85	5.5	2	848.4756	848.4756	0			Moghadda...	full proteo...
<b>MS<sup>2</sup></b> K.EFKNALK.K	2.3445	0.58	Andromeda	76.04	6.65	2	848.4756	848.4756	0			Cutler_Pe...	Roche_hu...

< 1 2 3 >

> Reference spectrum

> Fragments

Select All Deselect All

a:  1+  2+  3+

b:  1+  2+  3+

c:  1+  2+  3+

x:  1+  2+  3+

y:  1+  2+  3+

z:  1+  2+  3+

yb:

IM:

M[H]:

Neutral loss:

C5H11N  NH3  C4H8

H2O  C2H5N  C4H9N

C3H6  C4H11N  C3H9N

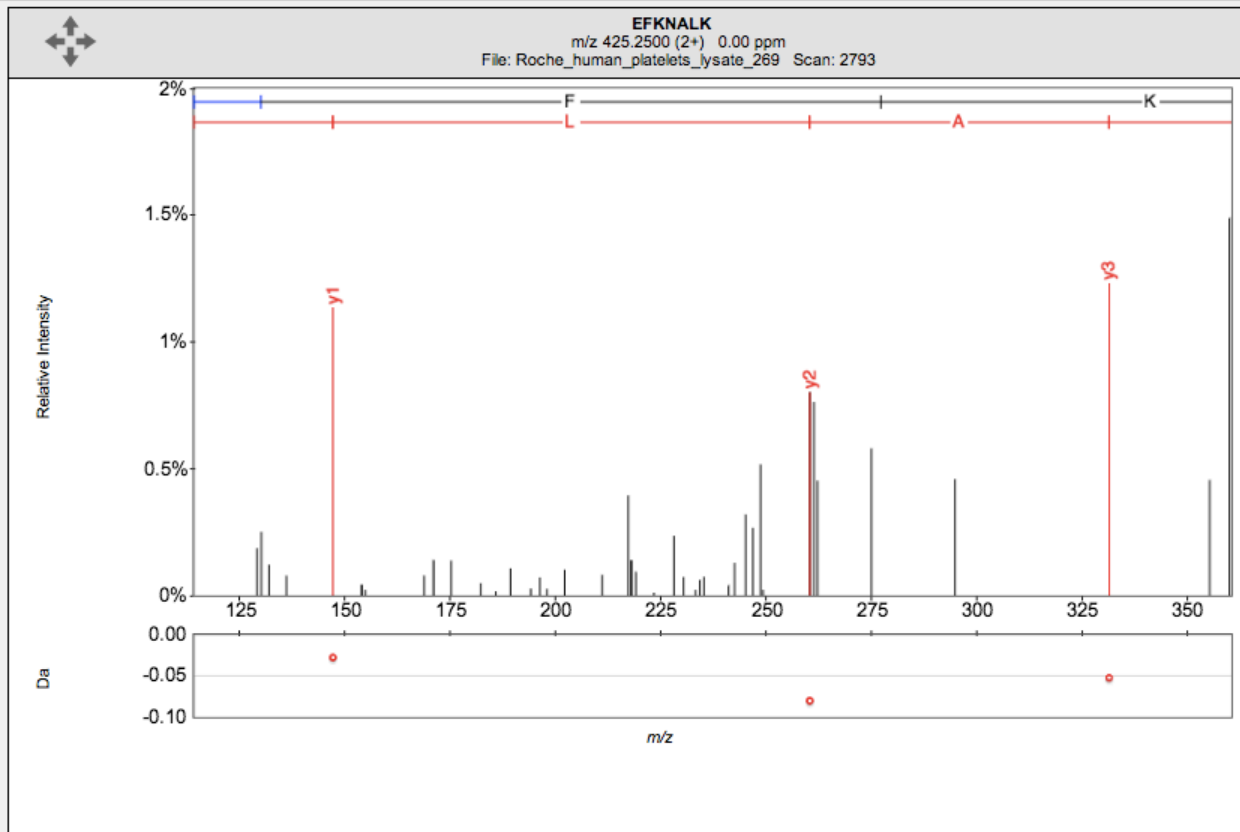
C2H4O2

Max neutral loss count: 3

Mass tolerance: 0.4 Da

Expert Mode:  on  off

> Configuration



b1+	#	Seq	#	y1+
130.0499	1	E	7	
277.1183	2	F	6	720.4403
405.2132	3	K	5	573.3719
519.2562	4	N	4	445.2769
590.2933	5	A	3	331.234
703.3774	6	L	2	260.1969
	7	K	1	147.1128

Sequence	-log q-...	-log PEP	Search Engi...	Score	Delta Score	z	Theoretic...	Measured...	Mass Err...	Fixed Mo...	Variable ...	Project	Experiment
<b>MS<sup>2</sup></b> R.NTDVQGALCQLLVGKR.S	2.2539	0.53	Andromeda	81.45	4.86	3	1827.0037	1770.9411	-30685.54	Carbamid...		Munoz_M...	4Skin_Mix...
<b>MS<sup>2</sup></b> R.NTDVQGALCQLLVGKR.S	2.2539	0.53	Andromeda	81.45	4.86	3	1827.0037	1770.9411	-30685.54	Carbamid...		Munoz_M...	4Skin_Mix...
<b>MS<sup>2</sup></b> R.NTDVQGALCQLLVGKR.S	2.2539	0.53	Andromeda	81.45	4.86	3	1827.0037	1770.9411	-30685.54	Carbamid...		Munoz_M...	4Skin_Mix...

[Click for peptide details](#)

> Reference spectrum

> Fragments

Select All   Deselect All

a:  1+  2+  3+

b:  1+  2+  3+

c:  1+  2+  3+

x:  1+  2+  3+

y:  1+  2+  3+

z:  1+  2+  3+

yb:

IM:

M[H]:

Neutral loss:

CH3NO  C2H4O  CO2

NH3  CH2N2  C3H6

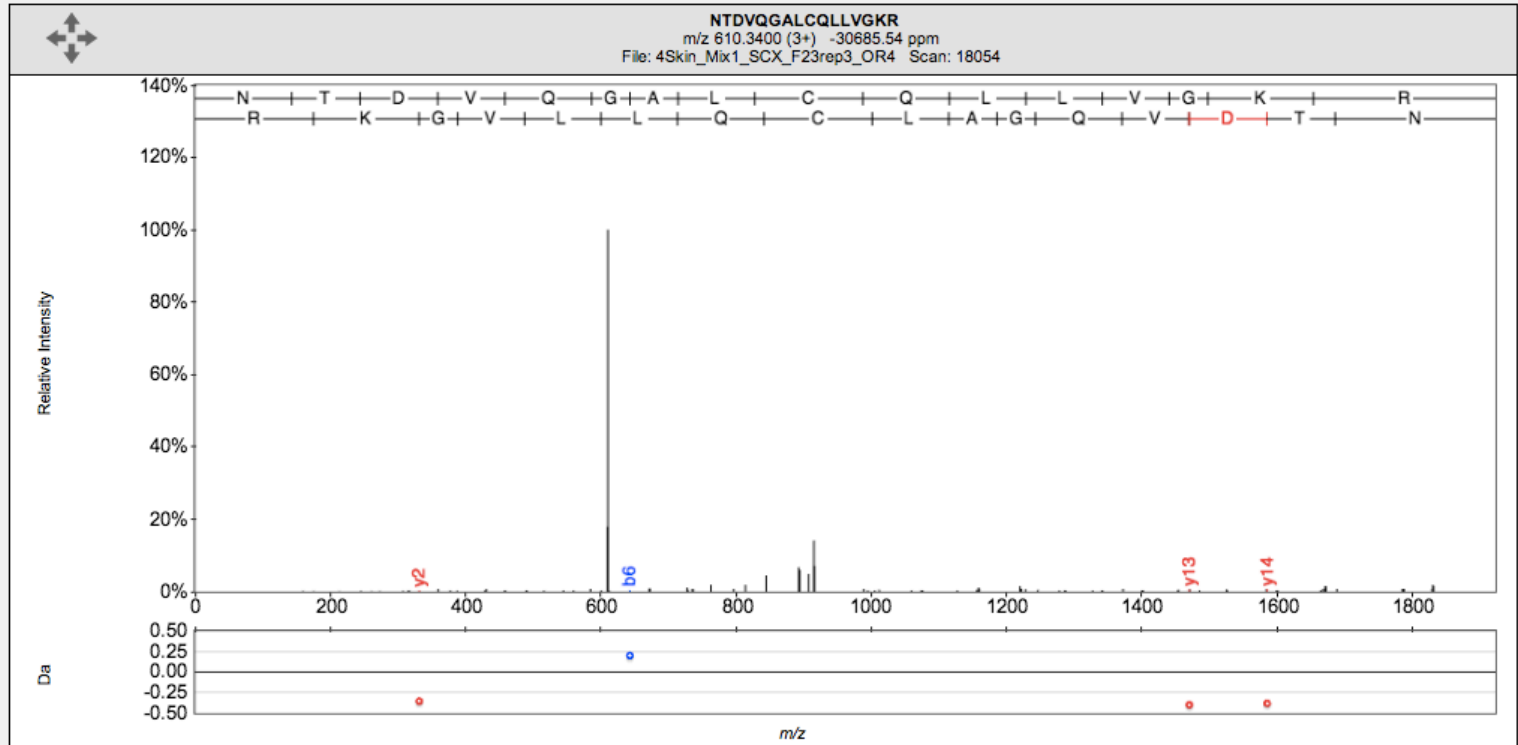
C2H5NO  C3H9N3

Max neutral loss count:

Mass tolerance:  Da

Expert Mode:  on  off

> Configuration



Fragment Ion Table