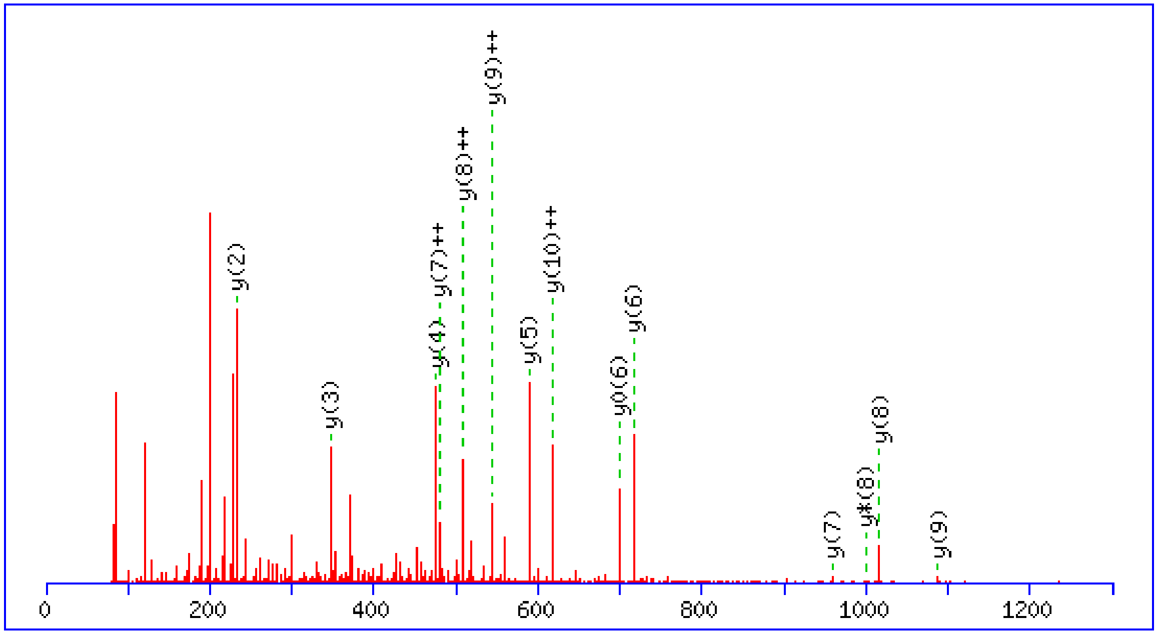
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIFAGKQLEDGR**
Found in **UBIQ_BOVIN**, (P62990) Ubiquitin

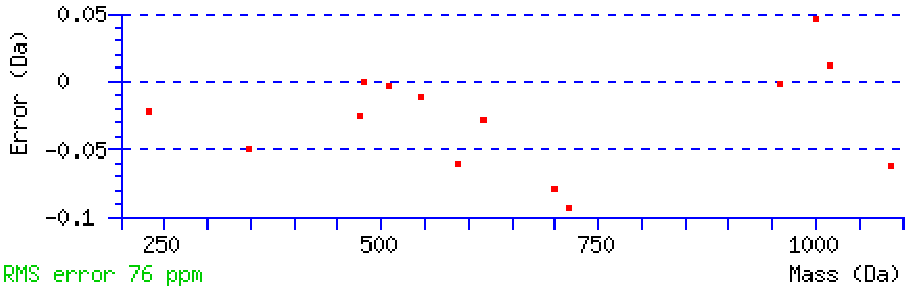
Match to Query 562: 1459.721490 from(487.581106,3+)
Title: File: QSMPB060524001.wiff, Sample: MPB00001A (sample number 1), Elution: 36.341 min, Period: 1, Cycle(s): 985 (Experiment 2)
Data file G:\Donn•es Q-Star\Marie-Pierre Bousquet\LCMSMS060524 et 29 P26S UCLA Lot1 temoin\QSMPB060524001.wiff

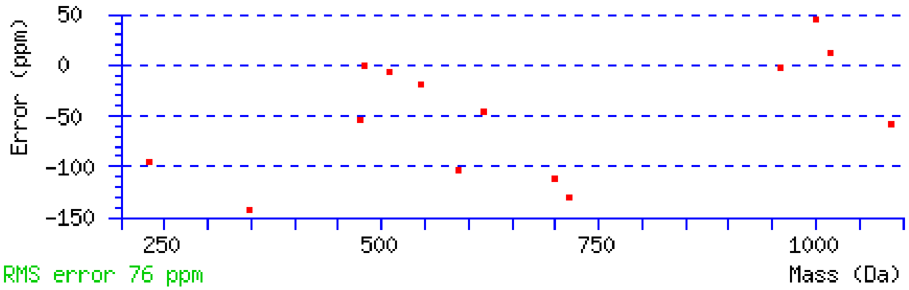
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 1300 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1459.7783
Variable modifications:
K6 : Ubiquitinylated (K)
Ions Score: 53 **Expect:** 0.0077
Matches (Bold Red): 14/102 fragment ions using 31 most intense peaks

#	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	**1016.5120**	**508.7596**	**999.4854**	500.2463	998.5014	499.7543	8
6	744.4403	372.7238	727.4138	364.2105			K	**959.4905**	**480.2489**	942.4640	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**	350.1746	6
8	985.5829	493.2951	968.5564	484.7818			L	**589.2940**	295.1506	572.2675	286.6374	571.2834	286.1454	5
9	1114.6255	557.8164	1097.5990	549.3031	1096.6150	548.8111	E	**476.2099**	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	**347.1673**	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	175.1189	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
53.1	1459.7783	-0.0568	LIFAGKQLEDGR
14.9	1459.7154	0.0061	EGVSEAELGGTGLK
14.8	1459.7783	-0.0568	LDAAAFQKGLQGK

12.2	1459.8293	-0.1078	VATCLQKRVSISR
11.9	1459.6725	0.0490	EAAALQCQLEDGR
11.6	1459.7783	-0.0568	LDAAAFQKGLQGK
10.3	1459.7704	-0.0490	EMKLLEQSGALK
9.7	1459.7639	-0.0424	VVCKQLGCGQAVK
8.6	1459.7313	-0.0098	QRGSASPMAGSGAKR
7.9	1459.7341	-0.0126	MSPKKVGDDIAK

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

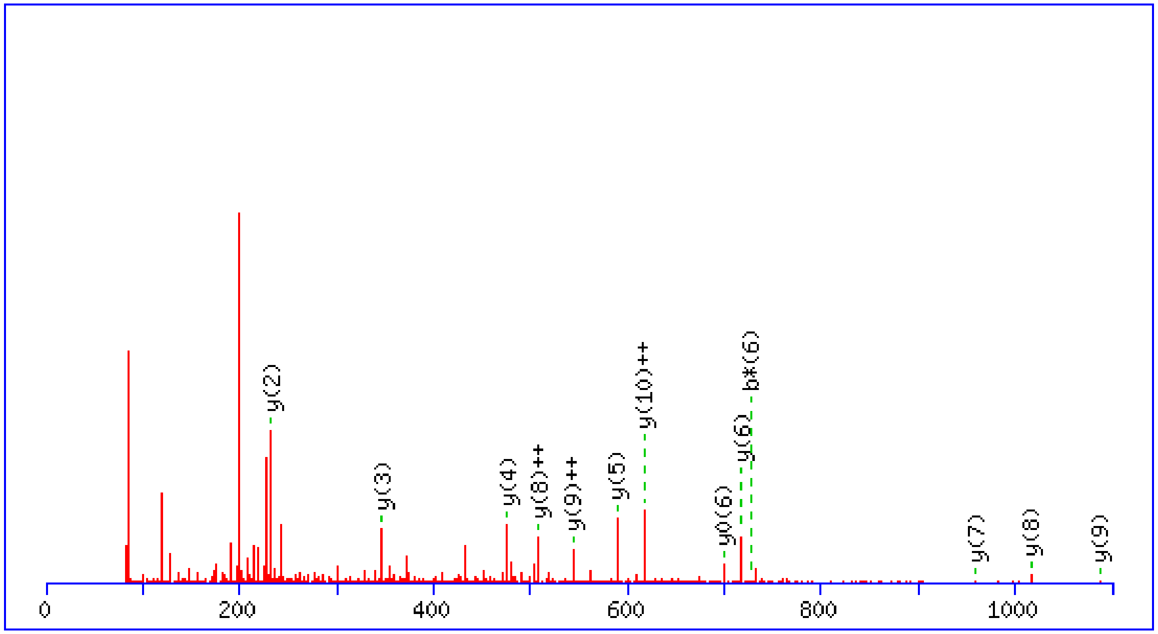
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIFAGKQLEDGR**
Found in **UBIQ_BOVIN**, (P62990) Ubiquitin

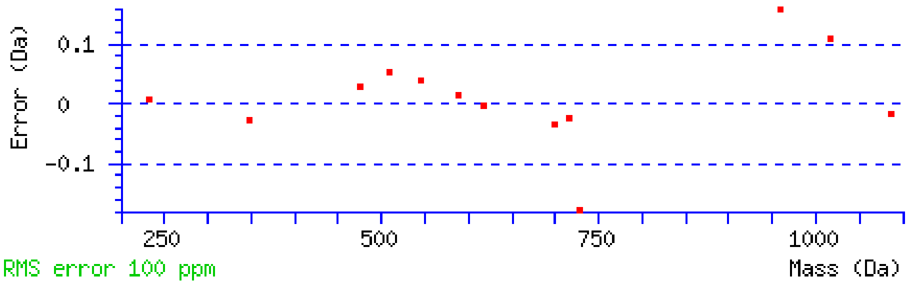
Match to Query 558: 1459.795539 from(487.605789,3+)
Title: File: QSMPB060622001.wiff, Sample: MPB0002A (sample number 1), Elution: 39.185 min, Period: 1, Cycle (s): 1040 (Experiment 3)
Data file G:\Donn•es Q-Star\Marie-Pierre Bousquet\LCMSMS 060620 P26S UCLA Lot1 EtOH\QSMPB060622001.wiff

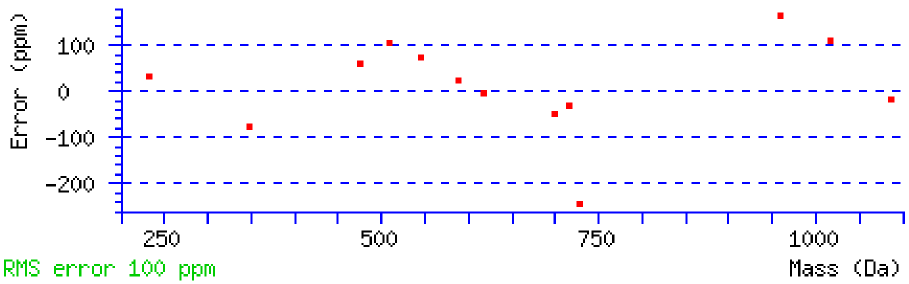
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 1100 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1459.7783
Variable modifications:
K6 : Ubiquitinylated (K)
Ions Score: 50 **Expect:** 0.015
Matches (Bold Red): 13/102 fragment ions using 31 most intense peaks

#	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	**1016.5120**	**508.7596**	999.4854	500.2463	998.5014	499.7543	8
6	744.4403	372.7238	**727.4138**	364.2105			K	**959.4905**	480.2489	942.4640	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**	350.1746	6
8	985.5829	493.2951	968.5564	484.7818			L	**589.2940**	295.1506	572.2675	286.6374	571.2834	286.1454	5
9	1114.6255	557.8164	1097.5990	549.3031	1096.6150	548.8111	E	**476.2099**	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	**347.1673**	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	175.1189	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
50.2	1459.7783	0.0172	LIFAGKQLEDGR
12.1	1459.6763	0.1192	SKDGNGGGGGGGKK
11.6	1459.6725	0.1231	EAAALQCQLEDGR
11.0	1459.7783	0.0172	LDAAAFQKGLQGK

9.3	1459.8035	-0.0079	KIADFGLATQLK
9.1	1459.6763	0.1192	SKDGNGGGGGGGGKK
8.1	1459.7341	0.0615	EEQGCVIEKLK
8.1	1459.7341	0.0615	MSPKKVGDDIAK
7.2	1459.6850	0.1105	NGGAPCVGERHHAR
7.1	1459.7341	0.0615	IGTVTSGCPSPSLK

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