

Post-translationally modified peptides

Hit	Accession - ID	Description	Score	MW	PI
50	P62988 - UBIQ_HUMAN	Ubiquitin - Homo sapiens (Human)	95.24	8559.62	

[Q5RKT7 \(protein identified with the same set of peptides\)](#)

Query	m/z	Charge	Exp. mass	Theo. mass	Delta	Miss. clv.	Score	pValue	Rank	Sequence	Position
2391	730.8967	2	1459.778848	1459.778305	0.000543	1	70	1.014926088 63851e-005	1	LIFAGKQLEDGR + GlyGly (K)	43-54
3120	865.4885	2	1728.962448	1728.963486	-0.001038	1	33	0.040063779 8197438	1	LIFAGKQLEDGR + LeuArgGlyGly (K)	43-54

MASCOT Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIFAGKQLEDGR**

Found in **UBIQ_HUMAN**, P62988|UBIQ_HUMAN Ubiquitin - Homo sapiens (Human)

Match to Query 2391: 1459.778848 from(730.896700,2+)

Title: OTMPB070622_08.2670.2670.2.dta

Data file D:\data_LTQOrbitrap\Marie-Pierre Bousquet\OTMPB070622_08.RAW

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Monoisotopic mass of neutral peptide Mr(calc): 1459.7783

Variable modifications:

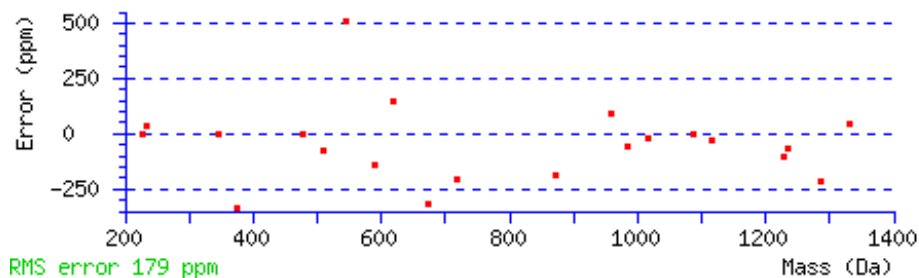
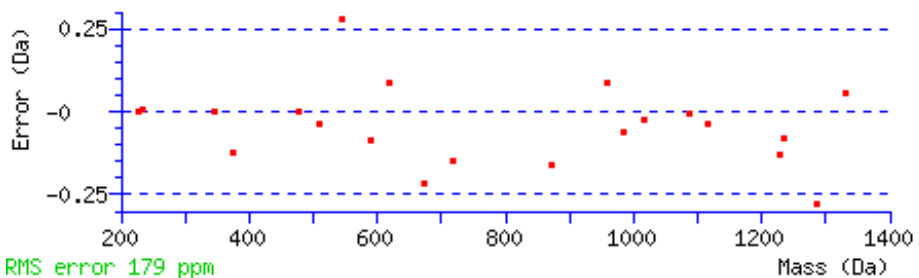
K6 : GlyGly (K)

Ions Score: 71 **Expect:** 1e-005

Matches (Bold Red): 21/102 fragment ions using 40 most intense peaks

#	b	b++	b*	b***	b ⁰	b ⁰⁺⁺	Seq.	y	y++	y*	y***	y ⁰	y ⁰⁺⁺	#
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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	0.0005	LIFAGKQLEDGR
7.9	1459.7816	-0.0028	QAKVRMIAAEAEK
6.8	1459.7857	-0.0069	LIFCSGLVLHR
6.3	1459.7718	0.0071	ILCDRRPPYTAR
4.4	1459.7816	-0.0028	MAALASSLIRQK
3.3	1459.7816	-0.0028	MLLLAREDKK

3.3	1459.7817	-0.0028	TARLECVVSGIK
3.3	1459.7816	-0.0028	IKDISRECALK
2.5	1459.7817	-0.0028	MLKEVLQREGK
1.0	1459.7783	0.0006	AFKESSALTKHK

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIFAGKQLEDGR**

Found in **Q5RKT7_HUMAN**, Q5RKT7|Q5RKT7_HUMAN Ribosomal protein S27a - Homo sapiens (Human)

Match to Query 3120: 1728.962448 from(865.488500,2+)

Title: OTMPB070622_02.2414.2414.2.dta

Data file D:\data_LTQOrbitrap\Marie-Pierre Bousquet\OTMPB070622_02.RAW

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Monoisotopic mass of neutral peptide Mr(calc): 1728.9635

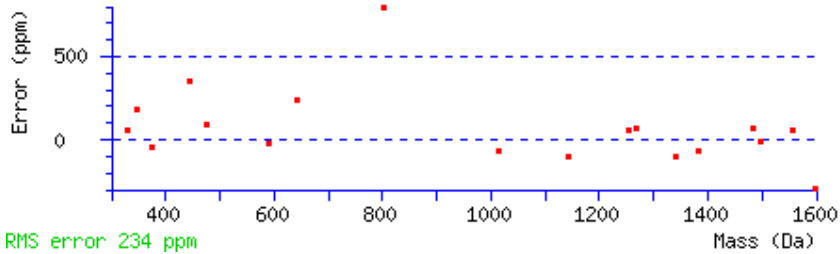
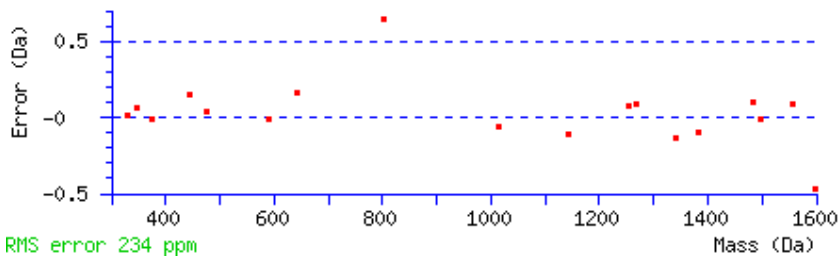
Variable modifications:

K6 : LeuArgGlyGly (K)

Ions Score: 33 **Expect:** 0.04

Matches (Bold Red): 18/102 fragment ions using 78 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	1616.8867	808.9470	1599.8602	800.4337	1598.8762	799.9417	11
3	374.2438	187.6255					F	1503.8027	752.4050	1486.7761	743.8917	1485.7921	743.3997	10
4	445.2809	223.1441					A	1356.7342	678.8708	1339.7077	670.3575	1338.7237	669.8655	9
5	502.3024	251.6548					G	1285.6971	643.3522	1268.6706	634.8389	1267.6866	634.3469	8
6	1013.6255	507.3164	996.5989	498.8031			K	1228.6757	614.8415	1211.6491	606.3282	1210.6651	605.8362	7
7	1141.6840	571.3457	1124.6575	562.8324			Q	717.3526	359.1799	700.3260	350.6667	699.3420	350.1747	6
8	1254.7681	627.8877	1237.7416	619.3744			L	589.2940	295.1506	572.2675	286.6374	571.2835	286.1454	5
9	1383.8107	692.4090	1366.7841	683.8957	1365.8001	683.4037	E	476.2100	238.6086	459.1834	230.0953	458.1994	229.6033	4
10	1498.8376	749.9225	1481.8111	741.4092	1480.8271	740.9172	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
11	1555.8591	778.4332	1538.8326	769.9199	1537.8485	769.4279	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
33.4	1728.9635	-0.0010	LIFAGKQLEDGR
0.6	1728.9635	-0.0011	QLSKPVTTFVDGR
0.5	1728.9675	-0.0051	WLLVSKNSVLPFGR

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