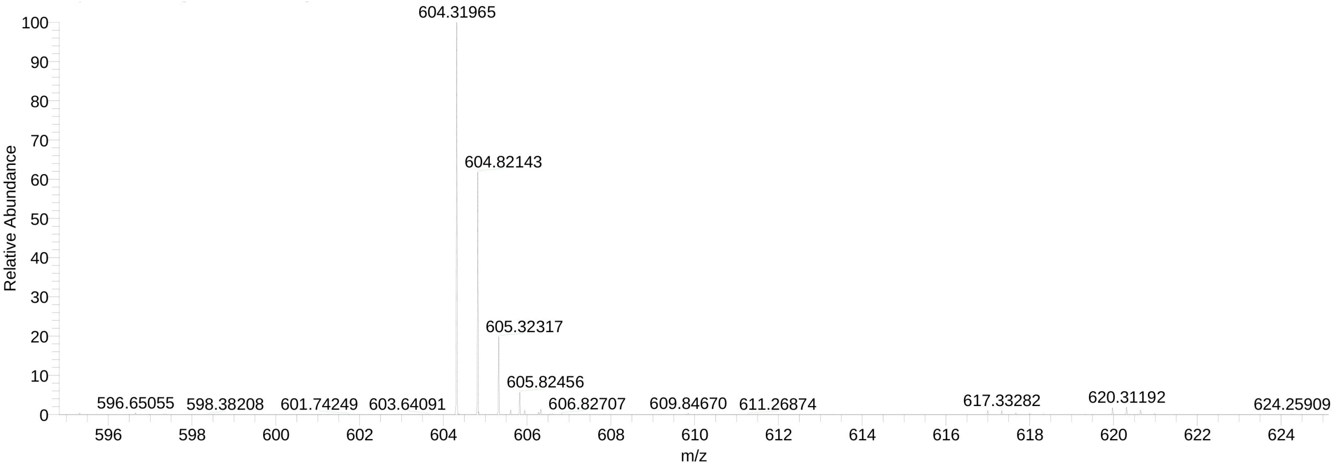
Trypsin digest, peptide 'SLSFLSATEPR'.

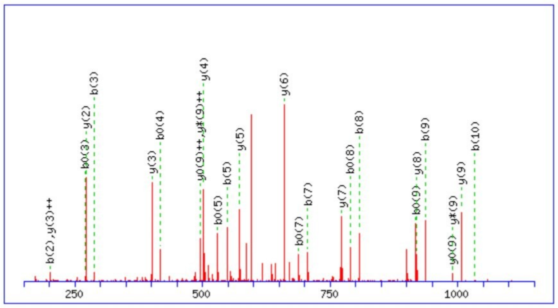
A.



B.

MS/MS Fragmentation of **SLSFLSATEPR**

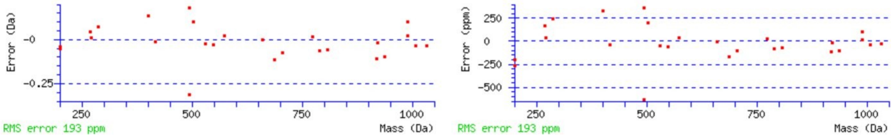
Match to Query 3516: 1206.625034 from(604.319793,2+)



Score	Mr(calc):	Delta	Sequence
60.7	1206.6244	0.0006	SLSFLSATEPR

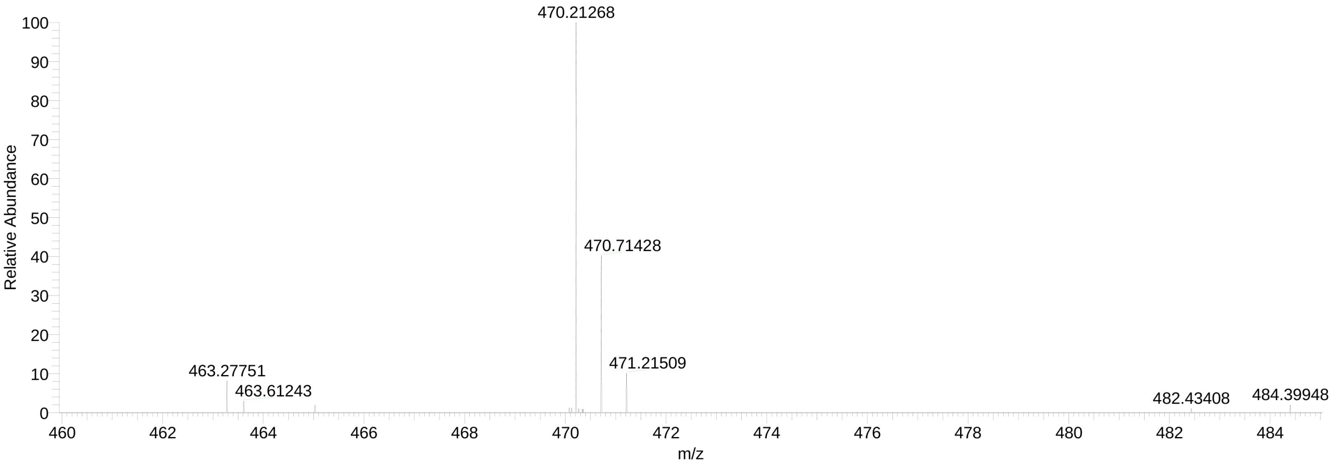
Monoisotopic mass of neutral peptide Mr(calc): 1206.6244
Ions Score: 61 **Expect:** 4.3e-008
Matches (Bold Red): 26/96 fragment ions using 45 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	S							11
2	**201.1234**	101.0653	183.1128	92.0600	L	1120.5997	560.8035	1103.5731	552.2902	1102.5891	551.7982	10
3	**288.1554**	144.5813	**270.1448**	135.5761	S	**1007.5156**	504.2614	**990.4891**	**495.7482**	**989.5051**	**495.2562**	9
4	435.2238	218.1155	**417.2132**	209.1103	F	**920.4836**	460.7454	903.4570	452.2322	902.4730	451.7402	8
5	**548.3079**	274.6576	**530.2973**	265.6523	L	**773.4152**	387.2112	756.3886	378.6980	755.4046	378.2059	7
6	635.3399	318.1736	617.3293	309.1683	S	**660.3311**	330.6692	643.3046	322.1559	642.3206	321.6639	6
7	**706.3770**	353.6921	**688.3664**	344.6869	A	**573.2991**	287.1532	556.2725	278.6399	555.2885	278.1479	5
8	**807.4247**	404.2160	**789.4141**	395.2107	T	**502.2620**	251.6346	485.2354	243.1214	484.2514	242.6293	4
9	**936.4673**	468.7373	**918.4567**	459.7320	E	**401.2143**	**201.1108**	384.1878	192.5975	383.2037	192.1055	3
10	**1033.5200**	517.2637	1015.5095	508.2584	P	**272.1717**	136.5895	255.1452	128.0762			2
11					R	175.1190	88.0631	158.0924	79.5498			1



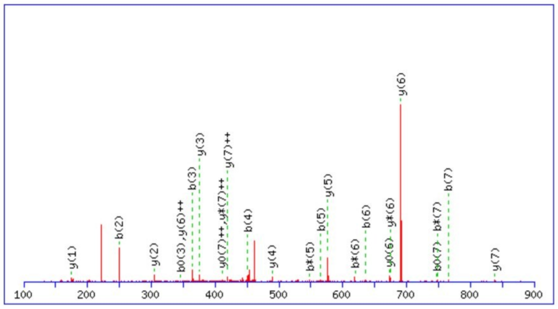
Trypsin digest, peptide 'TFDSNAER'.

A.



B.

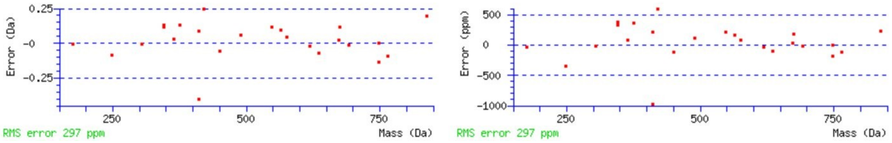
MS/MS Fragmentation of **TFDSNAER**
Match to Query 2625: 938.411354 from(470.212953,2+)



Score	Mr(calc):	Delta	Sequence
47.4	938.4093	0.0020	TFDSNAER

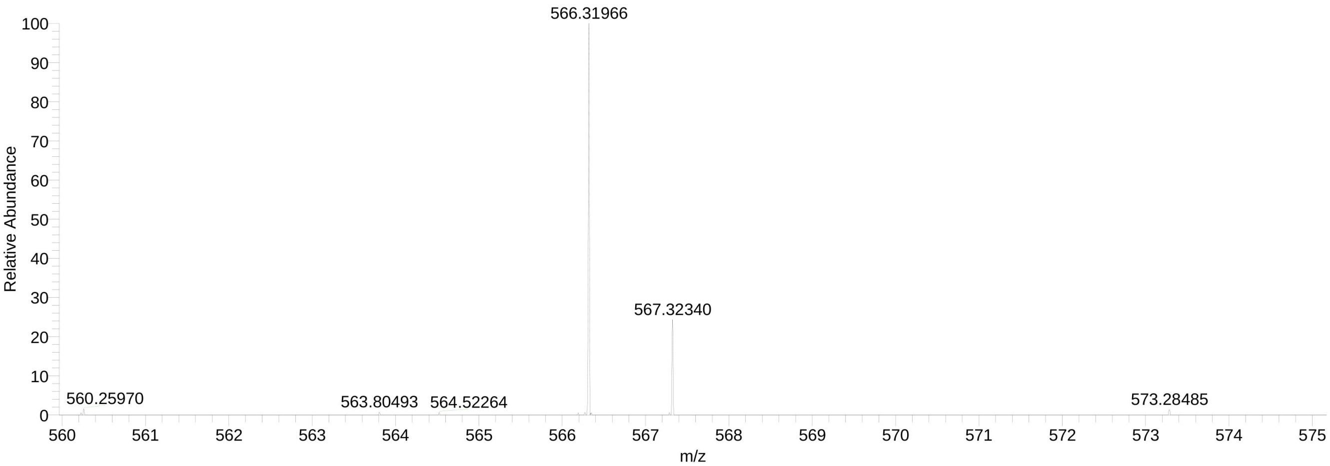
Monoisotopic mass of neutral peptide Mr(calc): 938.4093
Ions Score: 47 **Expect:** 3.7e-006
Matches (Bold Red): 24/74 fragment ions using 43 most intense peaks

#	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							8
2	**249.1234**	125.0653			231.1128	116.0600	F	**838.3690**	**419.6881**	821.3424	**411.1748**	820.3584	**410.6828**	7
3	**364.1503**	182.5788			**346.1397**	173.5735	D	**691.3006**	**346.1539**	**674.2740**	337.6406	**673.2900**	337.1486	6
4	**451.1823**	226.0948			433.1718	217.0895	S	**576.2736**	288.6404	559.2471	280.1272	558.2630	279.6352	5
5	**565.2253**	283.1163	**548.1987**	274.6030	547.2147	274.1110	N	**489.2416**	245.1244	472.2150	236.6112	471.2310	236.1191	4
6	**636.2624**	318.6348	**619.2358**	310.1216	618.2518	309.6295	A	**375.1987**	188.1030	358.1721	179.5897	357.1881	179.0977	3
7	**765.3050**	383.1561	**748.2784**	374.6428	**747.2944**	374.1508	E	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	2
8							R	**175.1190**	88.0631	158.0924	79.5498			1

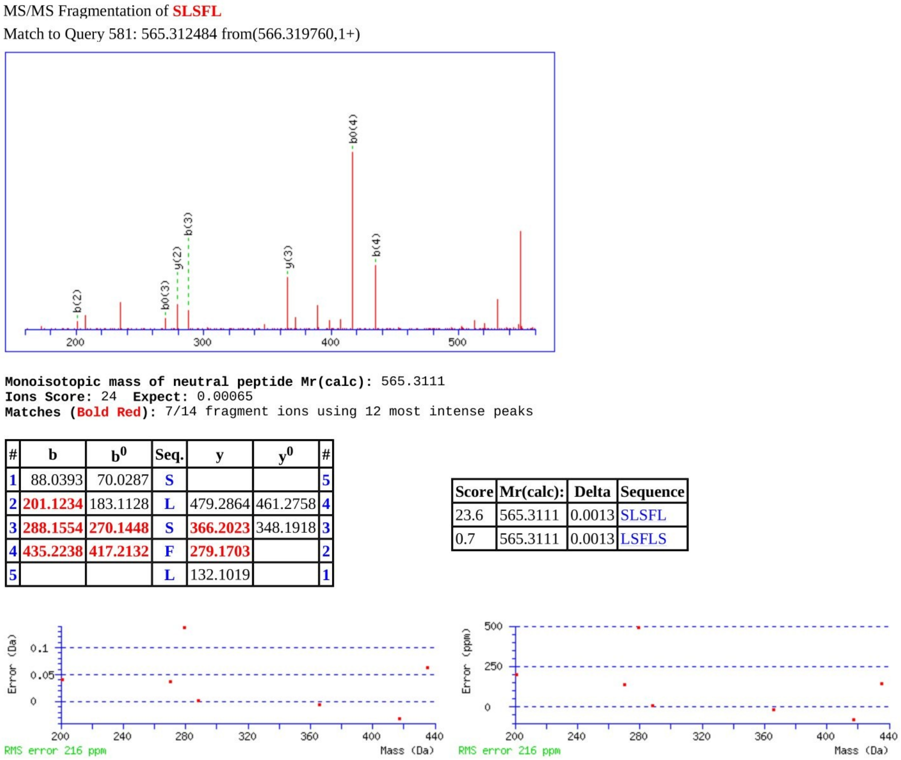


Chymotrypsin digest, peptide 'SLSFL'.

A.



B.



MS/MS Fragmentation of **SLSFL**

Match to Query 581: 565.312484 from(566.319760,1+)

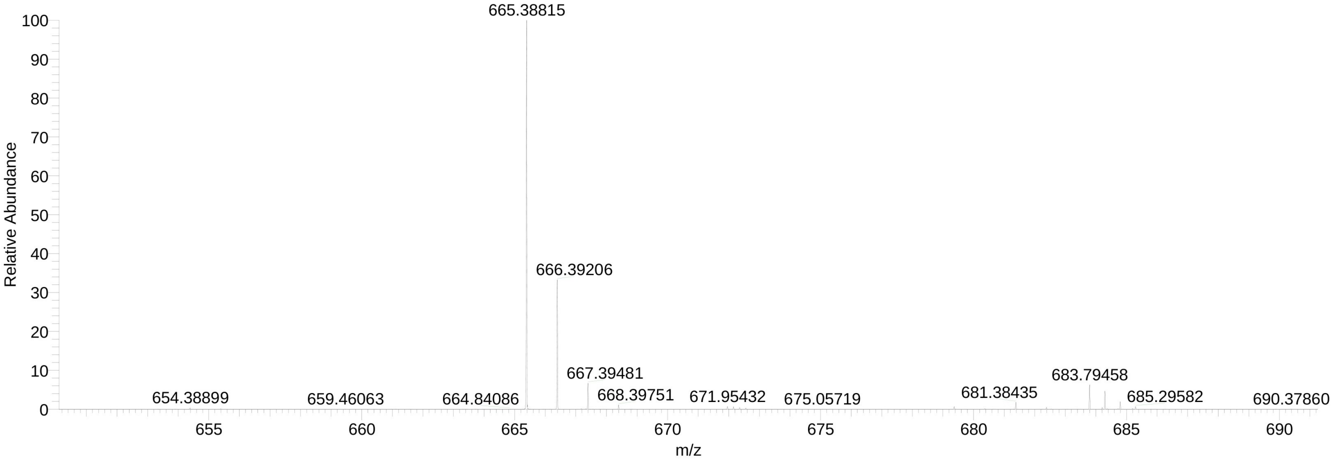
Monoisotopic mass of neutral peptide Mr(calc): 565.3111
Ions Score: 24 **Expect:** 0.00065
Matches (Bold Red): 7/14 fragment ions using 12 most intense peaks

#	b	b^0	Seq.	y	y^0	#
1	88.0393	70.0287	S			5
2	**201.1234**	183.1128	L	479.2864	461.2758	4
3	**288.1554**	**270.1448**	S	**366.2023**	348.1918	3
4	**435.2238**	**417.2132**	F	**279.1703**		2
5			L	132.1019		1

Score	Mr(calc):	Delta	Sequence
23.6	565.3111	0.0013	SLSFL
0.7	565.3111	0.0013	LSFLS

Chymotrypsin digest, peptide 'SLSFLV'.

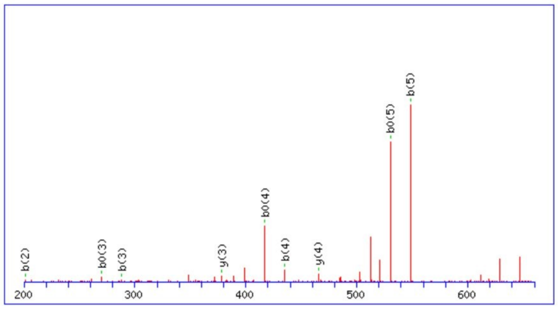
A.



B.

MS/MS Fragmentation of **SLSFLV**

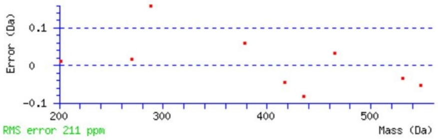
Match to Query 1461: 664.381274 from(665.388550,1+)

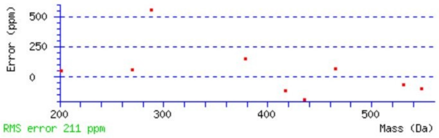


Monoisotopic mass of neutral peptide Mr(calc): 664.3795
Ions Score: 27 **Expect:** 0.00011
Matches (Bold Red): 9/17 fragment ions using 21 most intense peaks

#	b	b^0	Seq.	y	y^0	#
1	88.0393	70.0287	S			6
2	**201.1234**	183.1128	L	578.3548	560.3442	5
3	**288.1554**	**270.1448**	S	**465.2708**	447.2602	4
4	**435.2238**	**417.2132**	F	**378.2387**		3
5	**548.3079**	**530.2973**	L	231.1703		2
6			V	118.0863		1

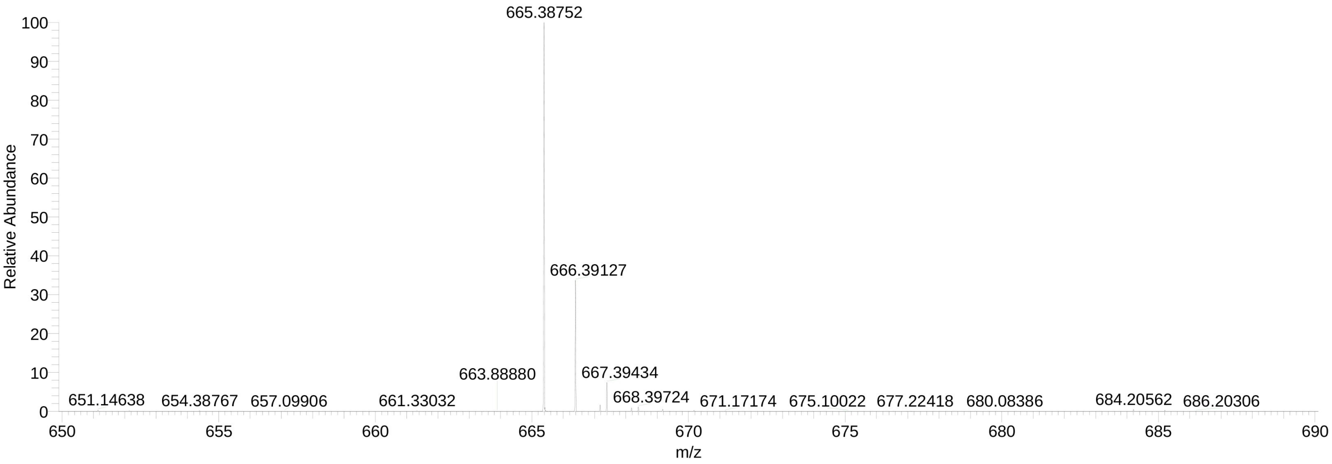
Score	Mr(calc):	Delta	Sequence
26.6	664.3795	0.0017	SLSFLV





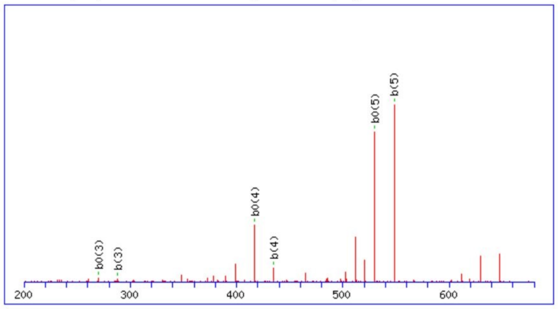
Trypsin digest, peptide 'SLSFLV'.

A.



B.

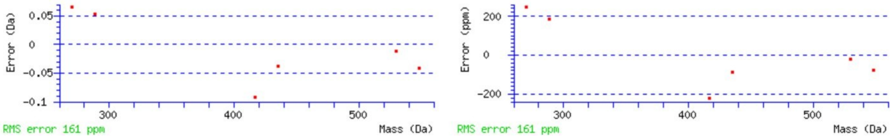
MS/MS Fragmentation of **SLSFLV**
Match to Query 920: 664.380354 from(665.387630,1+)



Monoisotopic mass of neutral peptide Mr(calc): 664.3795
Ions Score: 25 **Expect:** 0.00015
Matches (Bold Red): 6/17 fragment ions using 12 most intense peaks

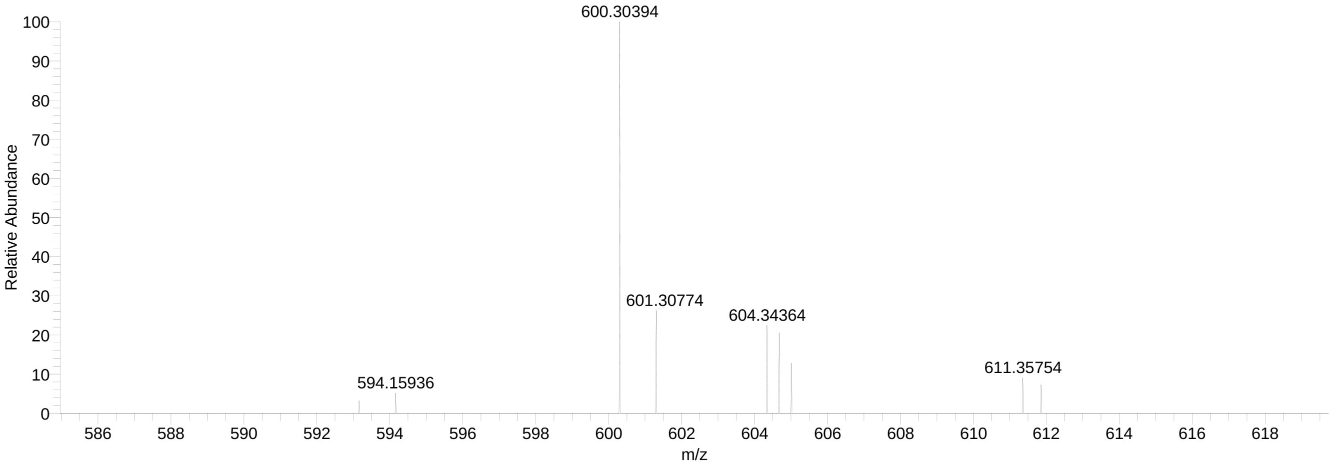
#	b	b^0	Seq.	y	y^0	#
1	88.0393	70.0287	S			6
2	201.1234	183.1128	L	578.3548	560.3442	5
3	**288.1554**	**270.1448**	S	465.2708	447.2602	4
4	**435.2238**	**417.2132**	F	378.2387		3
5	**548.3079**	**530.2973**	L	231.1703		2
6			V	118.0863		1

Score	Mr(calc):	Delta	Sequence
25.1	664.3795	0.0008	SLSFLV



Trypsin digest, peptide 'SLSFF'.

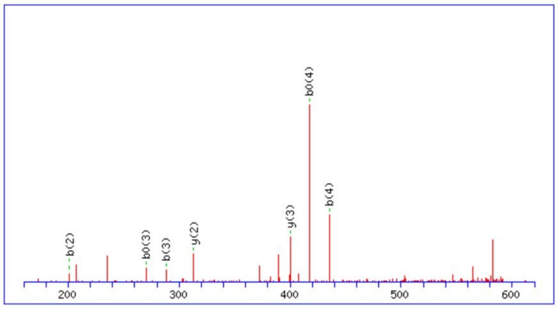
A.



B.

MS/MS Fragmentation of **SLSFF**

Match to Query 545: 599.295944 from(600.303220,1+)



Monoisotopic mass of neutral peptide Mr(calc): 599.2955
Ions Score: 15 **Expect:** 0.0034
Matches (Bold Red): 7/14 fragment ions using 20 most intense peaks

#	b	b^0	Seq.	y	y^0	#
1	88.0393	70.0287	**S**			**5**
2	**201.1234**	183.1128	**L**	513.2708	495.2602	**4**
3	**288.1554**	**270.1448**	**S**	**400.1867**	382.1761	**3**
4	**435.2238**	**417.2132**	**F**	**313.1547**		**2**
5			**F**	166.0863		**1**

Score	Mr(calc):	Delta	Sequence
14.7	599.2955	0.0005	SLSFF