Supplementary Information

Identification of lysine succinylation as a new post-translational modification

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Supplementary Methods

Purification of recombinant proteins from *E. coli* and *S. cerevisiae*

E. coli cells expressing a His-tagged protein of interest were obtained from ASKA library [1]. The cells were grown in LB medium (0.5% yeast extract (w/v), 1% tryptone (w/v), 1% NaCl (w/v)) at 37 ˚C on a rotary shaker (250 rpm). When cultures reached an OD_{600} of 0.7- 0.8, cells were induced by isopropyl-β-d-thiogalactoside (IPTG) (a final concentration of 0.01 mM) for 4 hrs at 30 ˚C. The cells were harvested by centrifugation at 5,000 × g for 10 min and resuspended in cold lysis buffer (10 mM NaH_2PO_4, 300 mM NaCl, 10 mM imidazole, pH 8.0). The cells were broken by 4 cycles of sonication employing 10-second bursts at 200–300 W followed by a 30-second cooling period between each burst. After the removal of cell debris , the supernatant was incubated with Ni-NTA agarose beads at 4 ˚C for 1 hr with gentle rotation. The Ni-NTA beads were then pelleted by centrifugation and washed three times with a washing buffer (10 mM NaH_2PO_4, 300 mM NaCl, 20 mM imidazole, pH 8.0). The His-tagged protein was eluted from the beads with an elution buffer (10 mM NaH_2PO_4, 300 mM NaCl, 250 mM imidazole, pH 8.0). The GST-fused glycerol-3-phosphate dehydrogenase (GAPDH) of *Saccharomyces cerevisiae* was purified by affinity chromatography.

Protein in-gel tryptic digestion

The gel band was washed with 50% ethanol for 1 hr, followed by a second, overnight washing. The destained gel band was washed with water twice and was cut into small pieces. The gel pieces were reduced with 10 mM dithiothreitol at 56 °C for 1 hr and alkylated with 55 mM iodoacetamide at room temperature in the dark for 45 min. Three hundred nanograms of trypsin in 50 mM ammonium bicarbonate was added to the gels and incubated overnight at 37 °C. Tryptic peptides were sequentially extracted from the gel pieces with 50% acetonitrile (acetonitrile/water/TFA, 50:45:5, v/v/v) and 75% acetonitrile (acetonitrile/water/TFA, 75:24:1, v/v/v). The peptide extracts were pooled, dried in a SpeedVac, and desalted using a μ-C18 ZipTip prior to HPLC/MS/MS analysis.

Circular dichroism (CD) spectroscopic analysis

The CD spectra of the wild type, K100R and K100E mutants were measured with an AVIV model 202 CD spectrometer (Aviv Biomedical, Lakewood, NJ). Spectra were collected over a wavelength range of 190 – 260 nm using 1-nm step spacing. A final concentration of 20 μM (in 50 mM sodium phosphate buffer containing 50 mM sodium chloride, pH 8.0) of each sample was used for CD analysis. In each experiment, 3 scans were averaged per sample for enhanced signal-to-noise ratio. All the data were acquired at 24 °C in a 0.1-cm path length quartz cuvette, and were analyzed using the Globalworks software (Olis, Inc., Bogart, GA). The secondary structures of the proteins were calculated from the corresponding CD spectra using the CONTINLL algorithm (with basis set number 10).

Supplementary Results:

Supplementary Figure 1. Three His-tagged proteins, isocitrate dehydrogenase (Icda), GADPH (GapA) and serine hydroxymethyltransferase (GlyA), isolated and resolved by SDS-PAGE and stained by Coomassie blue staining.

Supplementary Figure 2. MS/MS Spectra of *in vivo*, synthetic FTEGAF$^{\text{succ}}$KDWGYQLAR, and their mixture. (a) MS/MS spectrum of FTEGAF$^{\text{succ}}$KDWGYQLAR from isocitrate dehydrogenase led to the identification of a mass shift of 100.0186 Da at its lysine residue. Inset shows its precursor ion mass. The label Δ designates b or y ions with water and/or ammonia loss. (b) MS/MS spectrum of the synthetic peptide corresponding to the sequence identified in (a) with lysine succinylation. (c) MS/MS spectrum of a peptide mixture of the *in vivo*-derived isocitrate dehydrogenase tryptic peptides and its synthetic counterpart as indicated in (b).

Supplementary Figure 3. MS/MS Spectra of synthetic methylmalonyllysine peptide, FTEGAF$^{\text{MeMal}}$KDWGYQLAR. Inset shows its precursor ion mass. The label Δ designates b or y ions with water and/or ammonia loss.

Supplementary Figure 4. MS/MS Spectra of *in vivo* and synthetic GGSEELY$^{\text{Succ}}$KK, and their mixture. MS/MS spectrum of GGSEELY$^{\text{Succ}}$KK from serine hydromethyltransferase. The label Δ designates b or y ions with water and/or ammonia loss. (b) MS/MS spectrum of the synthetic peptide corresponding to the sequence identified in (a) with lysine succinylation. (c) MS/MS spectrum of a mixture of the *in vivo*-derived tryptic peptides and its synthetic counterpart as indicated in (b).

Supplementary Figure 5. Mass spectrometric identification and verification of NLTG$^{\mathrm{Succ}}$KEADAALGR from serine hydromethyltransferase. (a) MS/MS spectrum of a doubly charged tryptic peptide (NLTGKEADAALGR) from serine hydromethyltransferase led to the identification of a mass shift of 100.0057 Da at its lysine residue. Inset shows its precursor ion mass. The label Δ designates b or y ions with water and/or ammonia loss. (b) MS/MS spectrum of the synthetic peptide corresponding to the sequence identified in (a) with lysine succinylation. (c) MS/MS spectrum of a peptide mixture of the *in vivo*-derived tryptic peptides and its synthetic counterpart as indicated in (b). (d) Extracted ion chromatogram (XIC) of the *in vivo*-derived peptide. (e) XIC of the synthetic peptide corresponding to the sequence identified in (a) bearing lysine succinylation, showing a similar retention time. (f) XIC of a mixture of the peptide from in vivo-derived tryptic peptides and its synthetic counterpart as indicated in (b), showing coelution of the two peptides from an HPLC column.

Supplementary Figure 6. Mass spectrometric identification and verification of a lysine succinylated peptide from glyceraldehyde-3-phosphate dehydrogenase (GADPH). (a) MS/MS spectrum of a doubly charged tryptic peptide (GASQNIIPSSTGAAKAVGK) from GADPH led to the identification of a mass shift of 100.0176 Da at its lysine residue. Inset shows its precursor ion mass. The label Δ designates b or y ions with water and/or ammonia loss. (b) MS/MS spectrum of the synthetic peptide corresponding to the sequence identified in (a) with lysine succinylation. (c) MS/MS spectrum of a peptide mixture of the *in vivo*-derived tryptic peptides and its synthetic counterpart as indicated in (b). (d) Extracted ion chromatogram (XIC) of the *in vivo*-derived peptide. (e) XIC of the synthetic peptide corresponding to the sequence identified in (a) bearing lysine succinylation. (f) XIC of a mixture of the peptide from *in vivo*-derived tryptic peptides and its synthetic counterpart as indicated in (b).

Supplementary Figure 7. Isocitrate dehydrogenase sequence annotation (Uniprot ID P08200). The information was obtained from Uniprot database (http://www.uniprot.org/). K100 and K242 are succinylated, but they are not known to be directly involved in substrate binding, catalysis or NADP binding in *E. coli*.

Supplementary Figure 8. Multiple sequence alignment, sequence annotation, and localization of the succinyllysines in serine hydroxymethyltransferase. (a) ClustalW (2.0.12) alignment of serine hydroxymethyltransferase homologs from *H. sapiens* (gi: 703093), *M. musculus* (gi: 74141789), *D. melanogaster* (gi: 24640005), *C. elegans* (gi: 25144732), *A. thaliana* (gi: 14030719), *S. cerevisiae* (gi: 408368) and *E. coli* (gi: 170082161). Conserved sites are shaded with gray and black. Conserved and non-conserved succinyllysine residues are indicated by red and blue triangles, respectively. The positions are labeled corresponding to the *E. coli* sequence. (b) Serine hydroxymethyltransferase sequence annotation (Uniprot ID P0A825). The information was obtained from Uniprot database (http://www.uniprot.org/). Both lysine succinylation and lysine acetylation sites were indicated. K250 are also reported to be acetylated. (c) Localization of the succinyllysines and functional sites in serine hydroxymethyltransferase. The 3-D structure was obtained from the MMDB (MMDB id 77977) and viewed by Cn3D (v4.1). Succinylated and known functionally important sites are indicated by red and yellow arrows, respectively. The superscripts FS and SUCC on the labeled residues refer to function-important residues and succinylated residues, respectively. (d) Localization of the succinyllysines and functional sites in serine hydroxymethyltransferase. The 3-D structure was visualized from another side from (c). All of the succinylated sites (K62, K242, K250, 277, 293, 331, 346, and 354) are more than 5 angstroms away from the major functional residues (R235 and Y55), which has been reported to be important for substrate binding.[2] Succinylated lysines are predominantly located in the loops and alpha helices.

Supplementary Figure 9. Multiple sequence alignment, sequence annotation, and localization of the succinyllysines in glyceraldehyde-3-phosphate dehydrogenase A. (a) ClustalW (2.0.12) alignment of glyceraldehyde-3-phosphate dehydrogenase A homologs from *H. sapiens* (gi: 7669492), *M. musculus* (gi: 149259607), *D. melanogaster* (gi: 22023983), *C. elegans* (gi:

17568413), *A. thaliana* (gi: 21618027), *S. cerevisiae* (gi: 6322409) and *E. coli* (gi: 170081435). Conserved sites are shaded with gray and black. Conserved and non-conserved succinyllysine residues are indicated by red and blue triangles, respectively. The positions are labeled corresponding to the *E. coli* sequence. Seven out of the eleven of these sites are highly conserved among the species investigated. (b) Glyceraldehyde-3-phosphate dehydrogenase A sequence annotation (Uniprot ID P0A9B2). The information was obtained from Uniprot database (http://www.uniprot.org/). (c) Localization of the succinyllysines and functional sites in glyceraldehyde-3-phosphate dehydrogenase A. The 3-D structure of O-P dimer of the protein was obtained from the MMDB (MMDB ID 4433) and viewed by Cn3D (v4.1). Succinylated and known functionally important sites (Uniprot ID P0A9B2) are labeled on the O-subunit and indicated by red and yellow arrows, respectively. The superscripts SB, NB, CAT and SUCC on the labeled residues refer to substrate binding, NAD binding, catalytic sites and succinylated lysine residues, respectively. (d) Localization of the succinyllysines and functional sites in glyceraldehyde-3-phosphate dehydrogenase A. The 3-D structure was visualized from another side from (c). These succinylated lysines are predominantly located in the loops and alpha helices. None of the succinylated sites (K115, 124, 132, 192, 213, 217, 225, 249, 257, 261 and 331) are close (> 5 angstroms) to known major functional important residues, which suggests they are less likely to have direct interaction with them.

Supplementary Figure 10. Circular dichroism (CD) spectrum of wild type,

K100R and K100E mutants of isocitrate dehydrogenase.

Supplementary Figure 11. Mascot-annotated MS/MS spectrum of VLPELQG^{Succ}KLTGMAFR identified from yeast glyceraldehyde-3-phosphate dehydrogenase.

Supplementary Figure 12. Differential succinyllysine profiles in cancer cell lines. Western blotting analysis (left panel) and Ponceau S staining of protein whole-cell lysate (right panel) of cancer cell lines. Total cellular extract (30 µg/lane) was resolved in Tris-Glycine 4% - 20% gradient gel. *Lane 1*, HeLa, adenocarcinoma; *lane 2*, HCT116, colorectal carcinoma; *lane 3*, A549, lung carcinoma; *lane 4*, A375, skin melanoma; *lane 5*, HepG2, hepatocellular carcinoma; *lane 6*, MG-63, osteosarcoma; *lane 7*, Du145, brain carcinoma; *lane 8*, MDA-MB-231, adenocarcinoma ; *lane 9*, HEK293T, human embryonic kidney cells. Red arrows indicate those proteins that have different levels of lysine succinylation.

Supplementary Figure 13. HPLC analysis (extracted ion chromatogram) and purity of synthetic peptides. All the targeted peptides can be unambiguously identified based on their MS/MS spectra.

Supplementary Table 1. A list of H_4 and D_4-labeled succinyllysine peptide sequences identified from D_4-succinate treated *E. coli* sample.

Supplementary Table 2. Primers used for site-specific mutagenesis.

Supplementary Table 3. A list of *E. coli* succinyllysine peptide sequences identified by affinity purification using anti-succinyllysine pan antibody and mass spectrometry.

Supplementary Data 1. MS/MS spectra for H_4 and D_4-labeled succinyllysine peptide sequences identified from D_4-succinate treated *E. coli* sample.

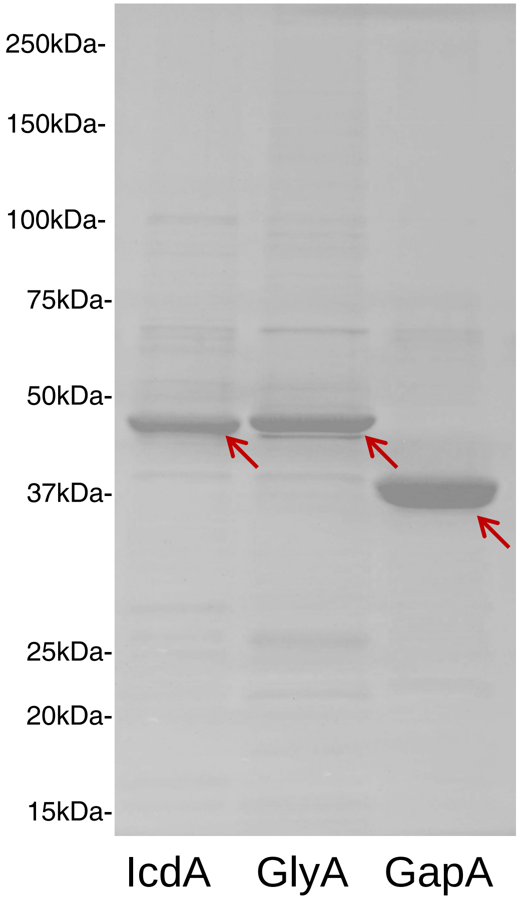
Supplementary Data 2. MS/MS spectra of succinyllysine peptides identified by affinity purification using anti-succinyllysine pan antibody and mass spectrometry.

SUPPLEMENTARY REFERENCES:

1. Kitagawa, M. et al. Complete set of ORF clones of *Escherichia coli* ASKA library (a complete set of E. coli K-12 ORF archive): unique resources for biological research. *DNA Res* 12, 291-299 (2005)

2. Vivoli, M. *et al.* Role of a conserved active site cation-pi interaction in *Escherichia coli* serine hydroxymethyltransferase. *Biochemistry* 48, 12034-12046 (2009).

Supplementary Figure 1:



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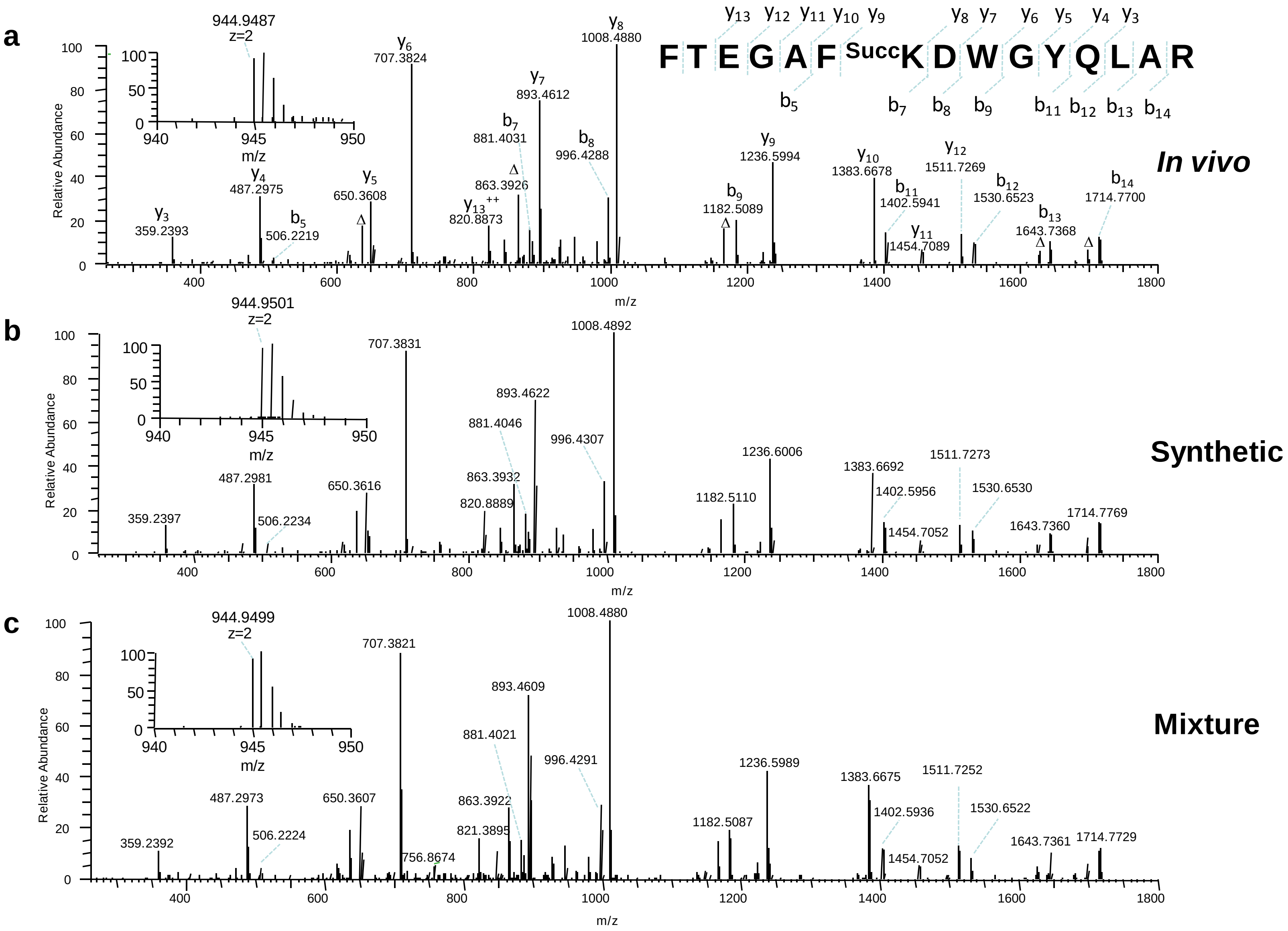

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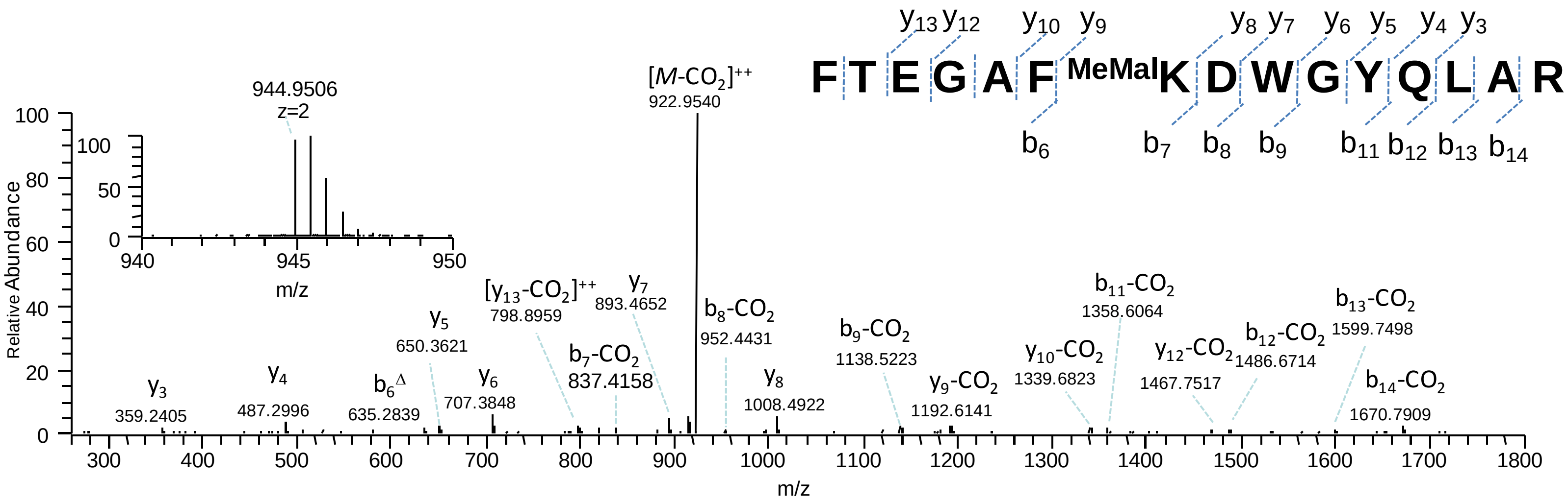

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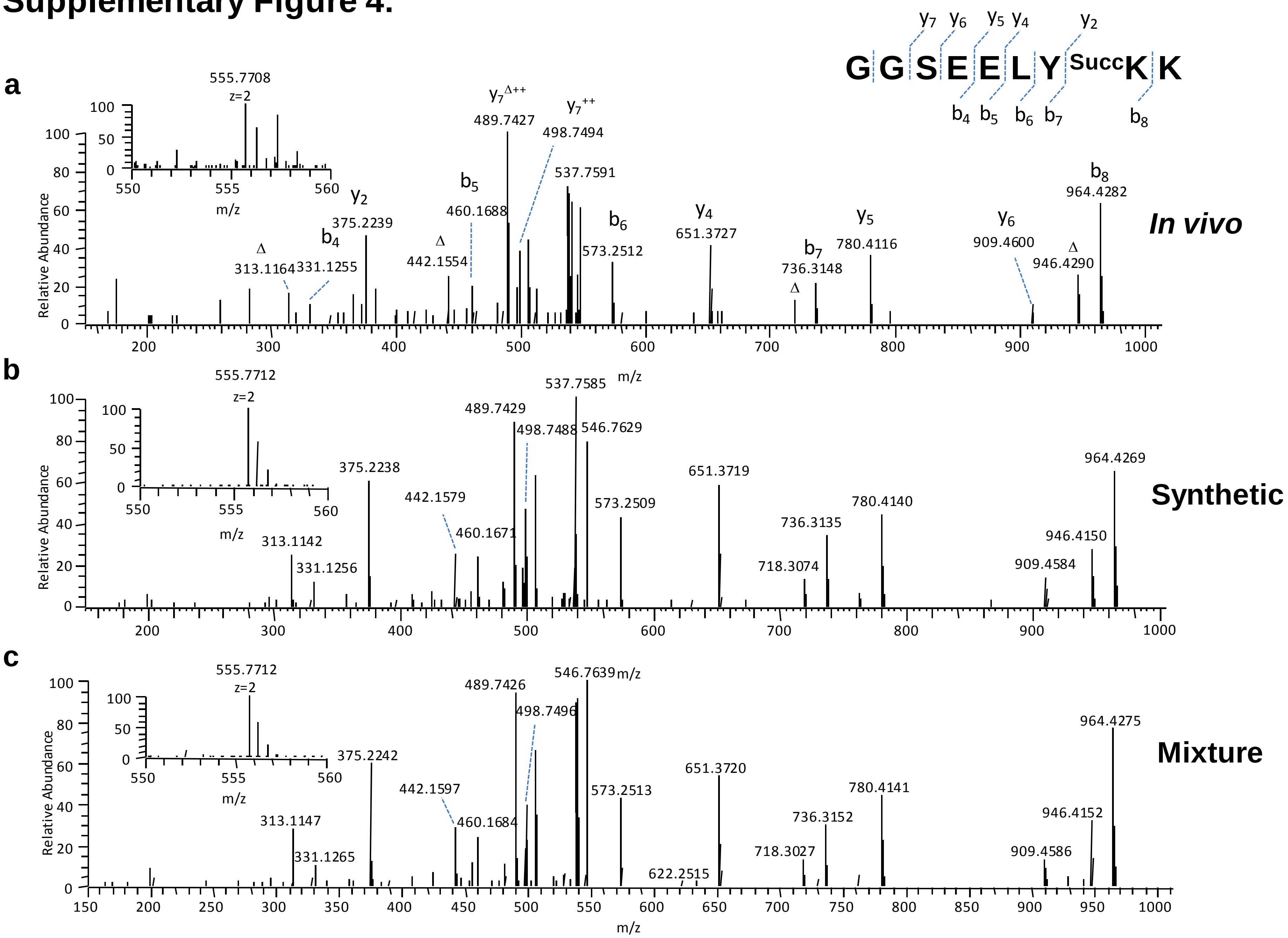

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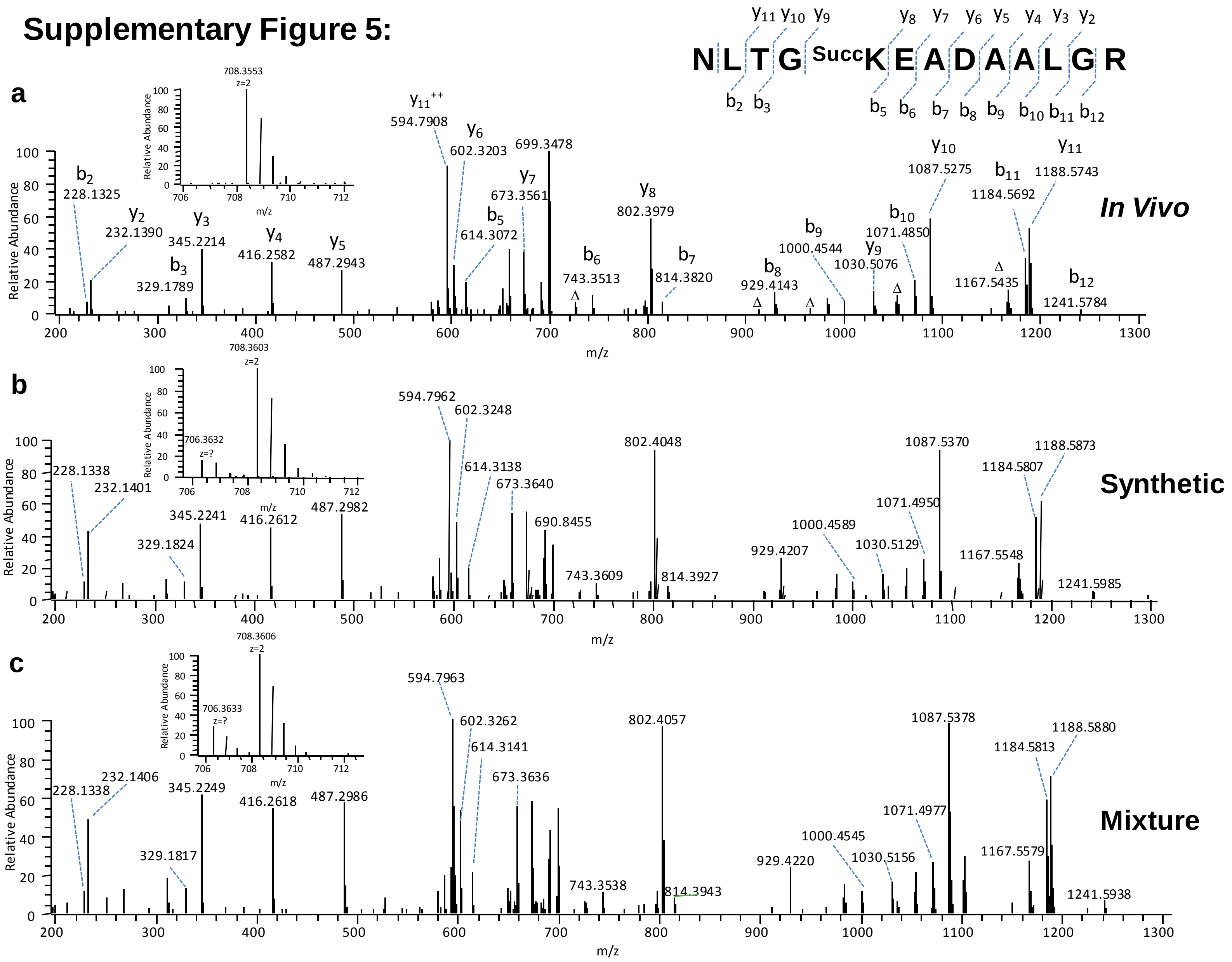

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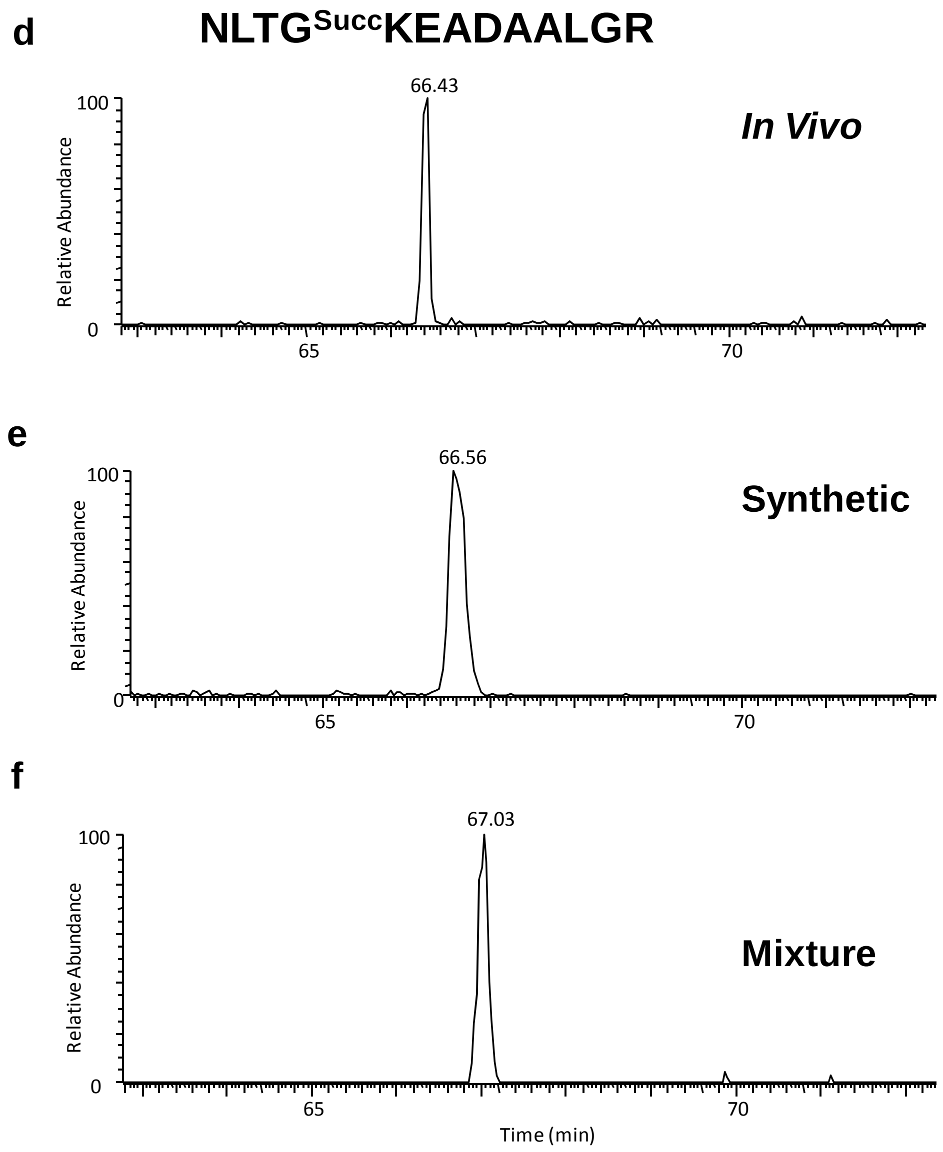

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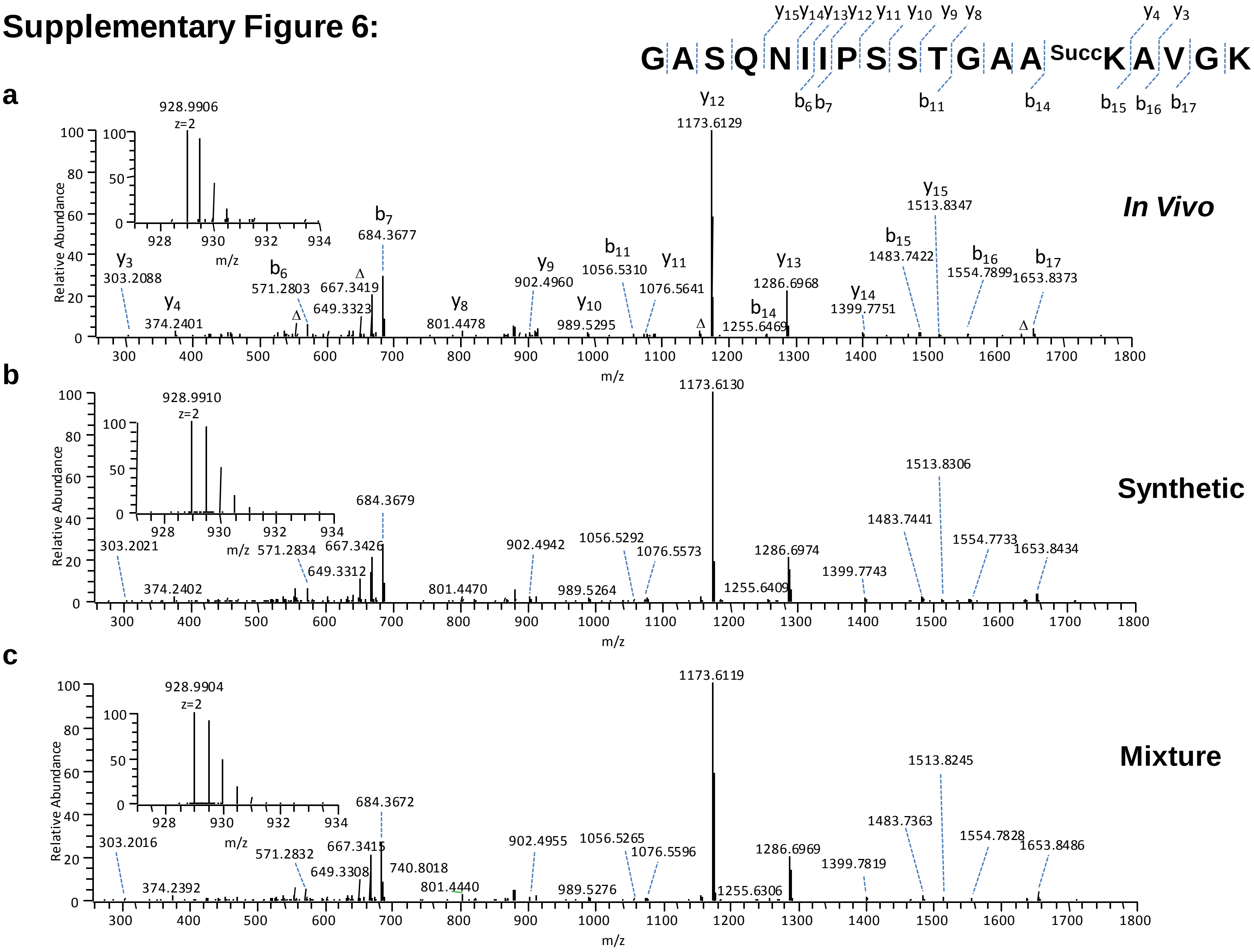

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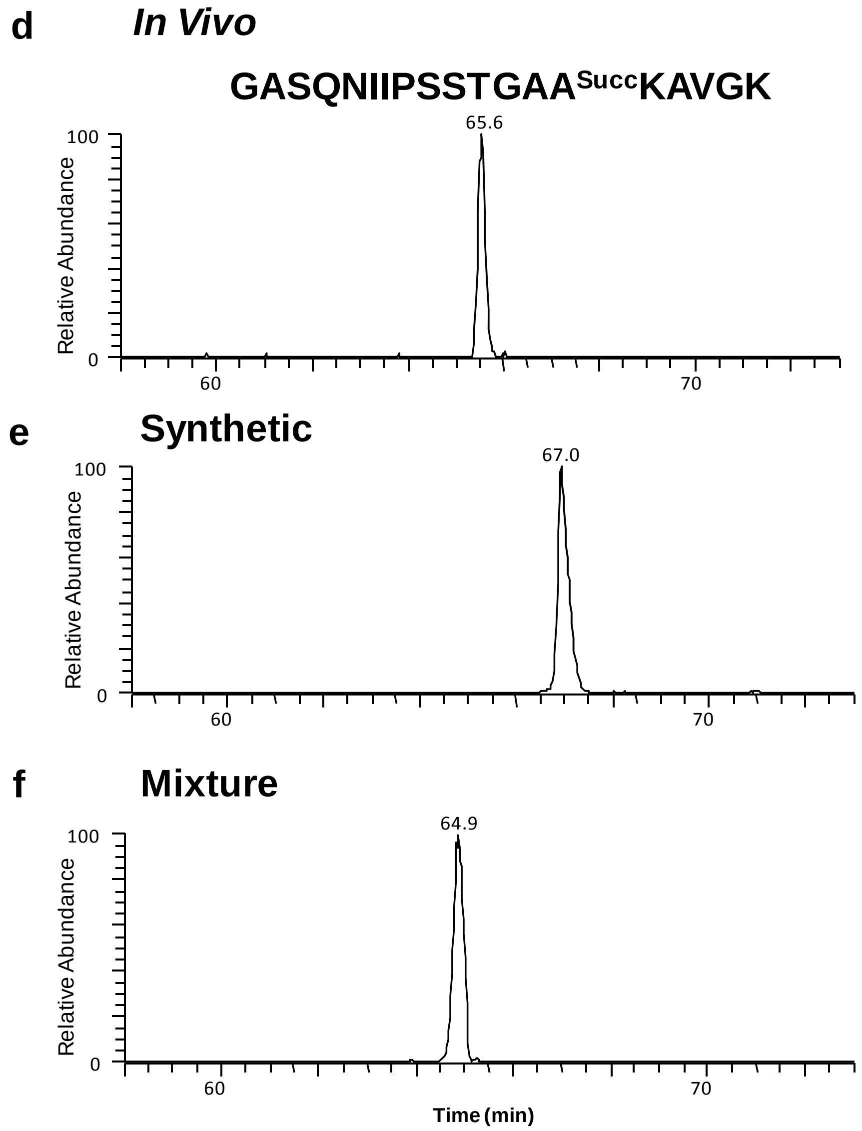

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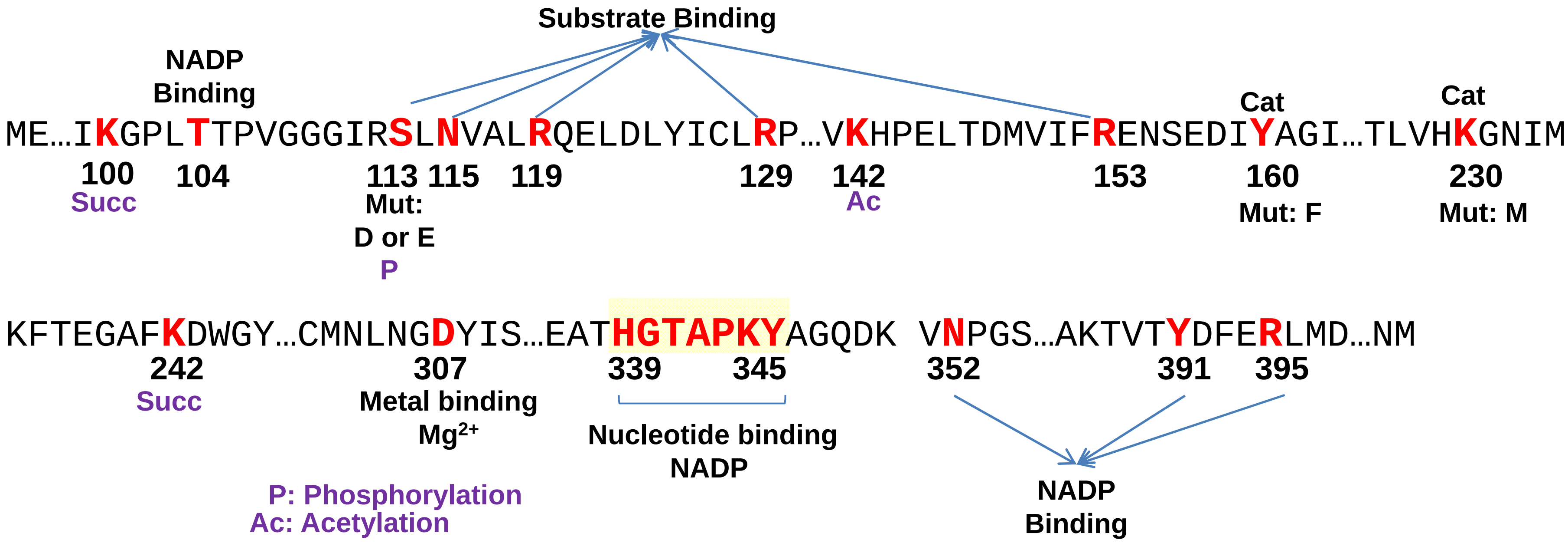


Substrate Binding

NADP Binding

Cat

Cat

ME…I**K**GPL**T**TPVGGGIR**S**L**N**VAL**R**QELDLYICL**R**P…V**K**HPELTDMVIF**R**ENSEDI**Y**AGI…TLVH**K**GNIM

100 Succ

104

113 115 Mut: D or E P

119

129

142 Ac

153

160 Mut: F

230 Mut: M

KFTEGAF**K**DWGY…CMNLNG**D**YIS…EAT**HGTAPKY**AGQDK V**N**PGS…AKTVT**Y**DFE**R**LMD…NM

242 Succ

307 Metal binding Mg^{2+}

339 345 Nucleotide binding NADP

352

391

395

NADP Binding

P: Phosphorylation

Ac: Acetylation

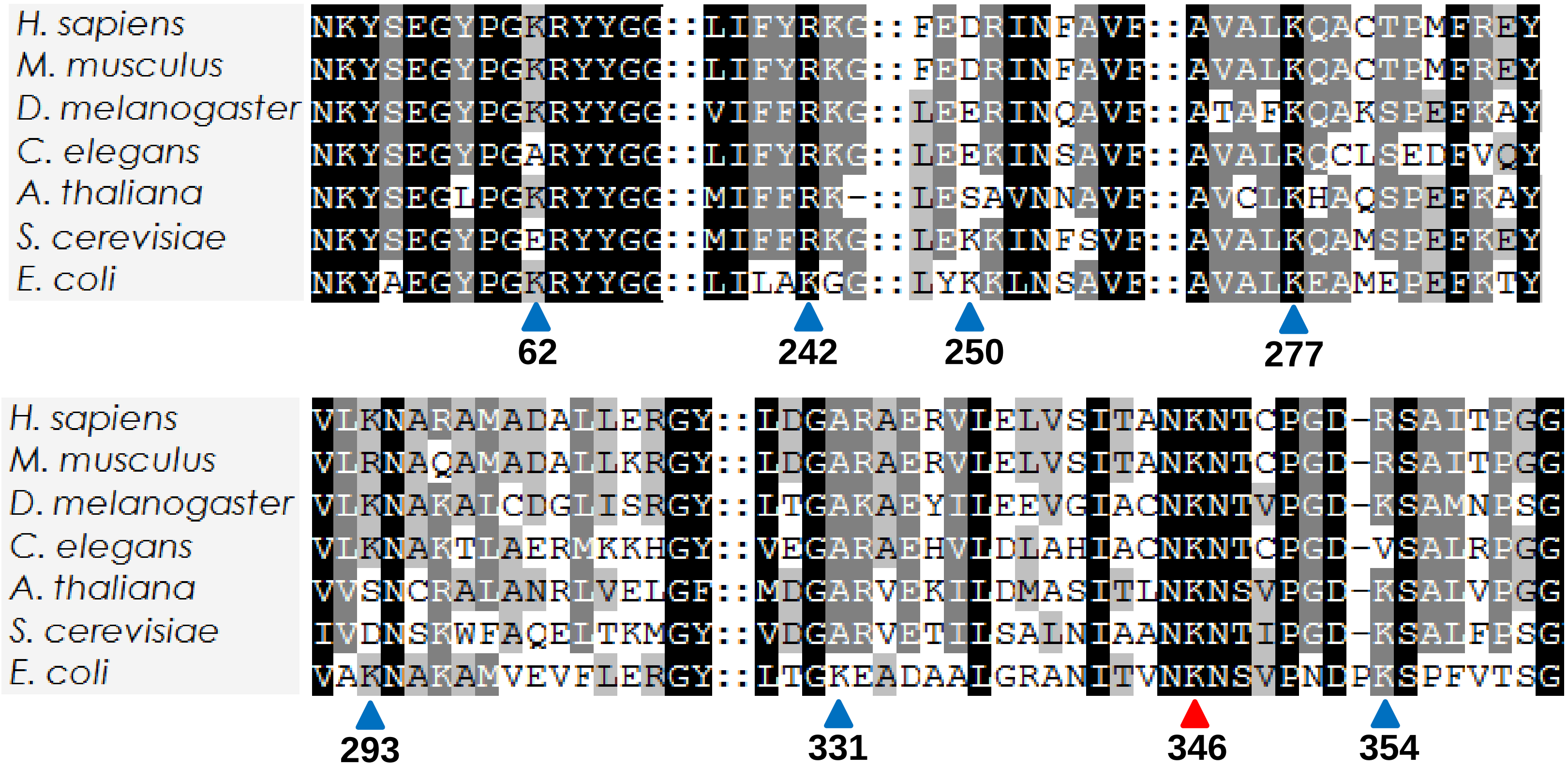
Succ: Succinylation

Mut: mutagenesis

Cat: catalysis

Supplementary Figure 8:

a **Serine hydroxymethyltransferase**



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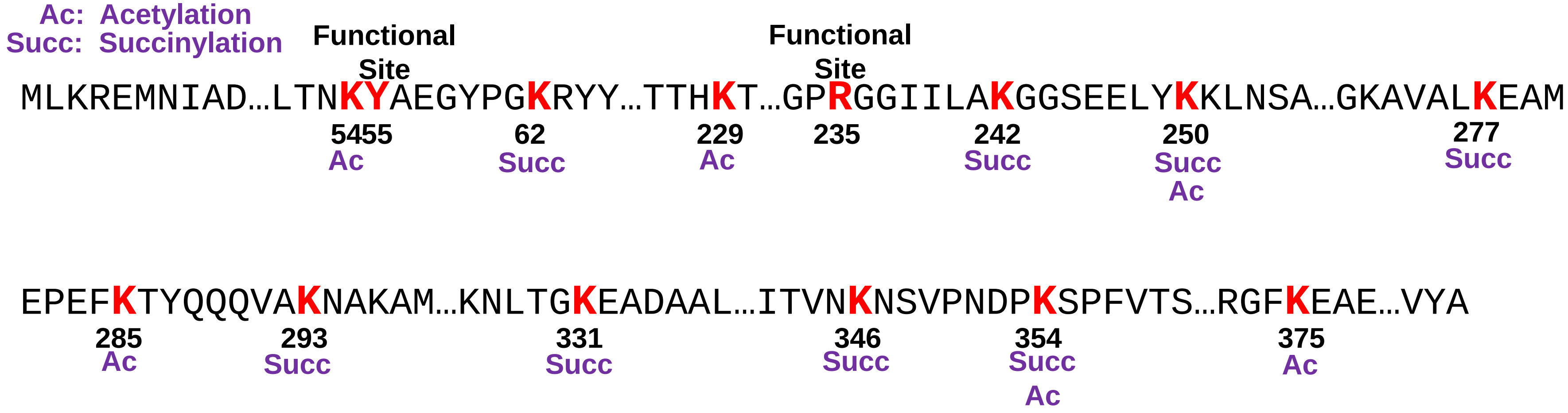
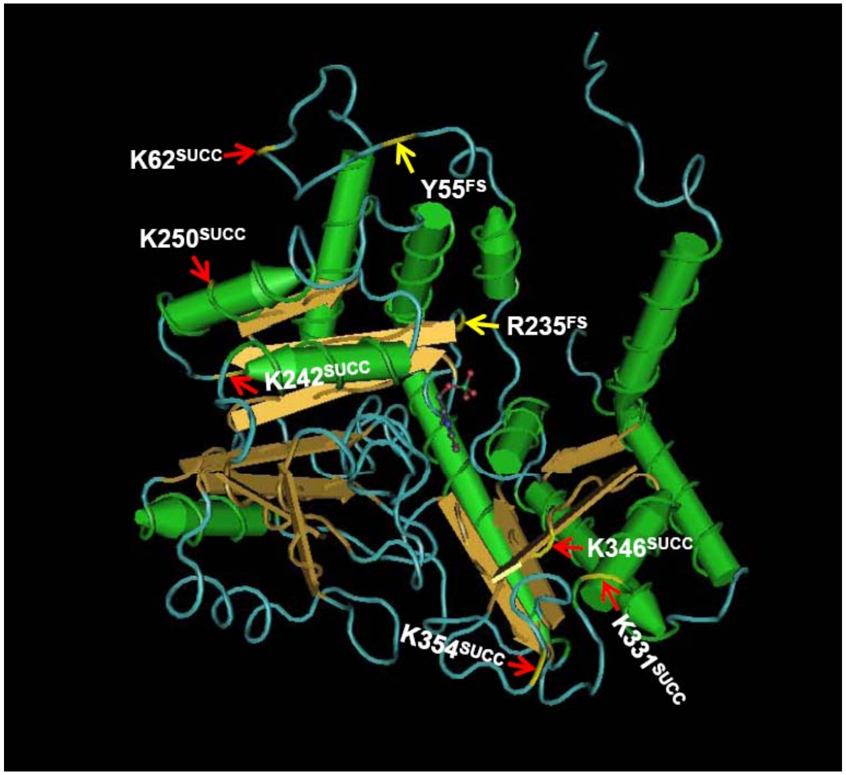


Nature Chemical Biology: doi: 10.1038/nchembio.495

c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K250SUCC
R235FS
K242SUCC
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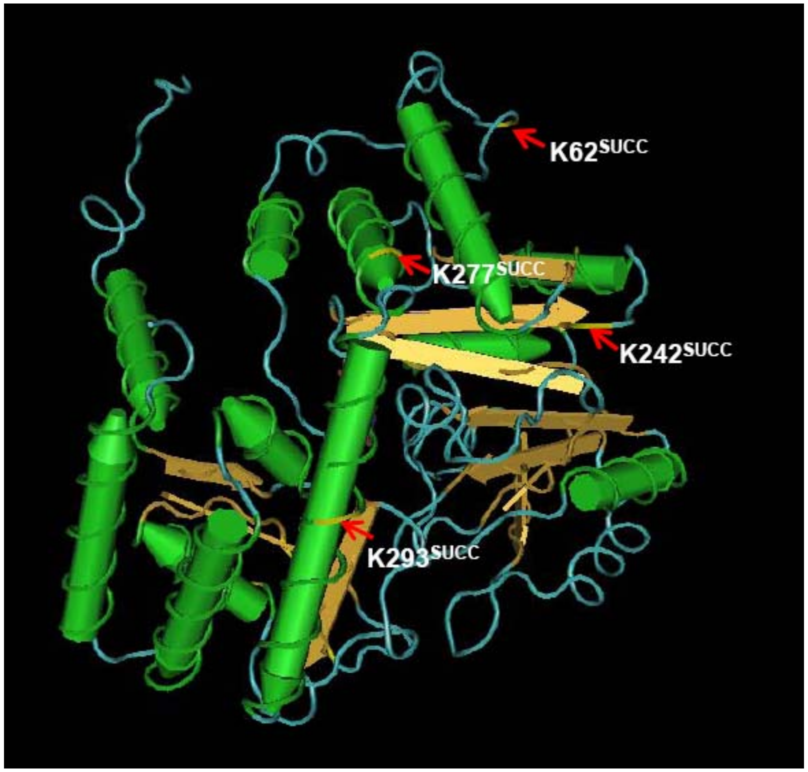
K354SUCC
K331SUCC

d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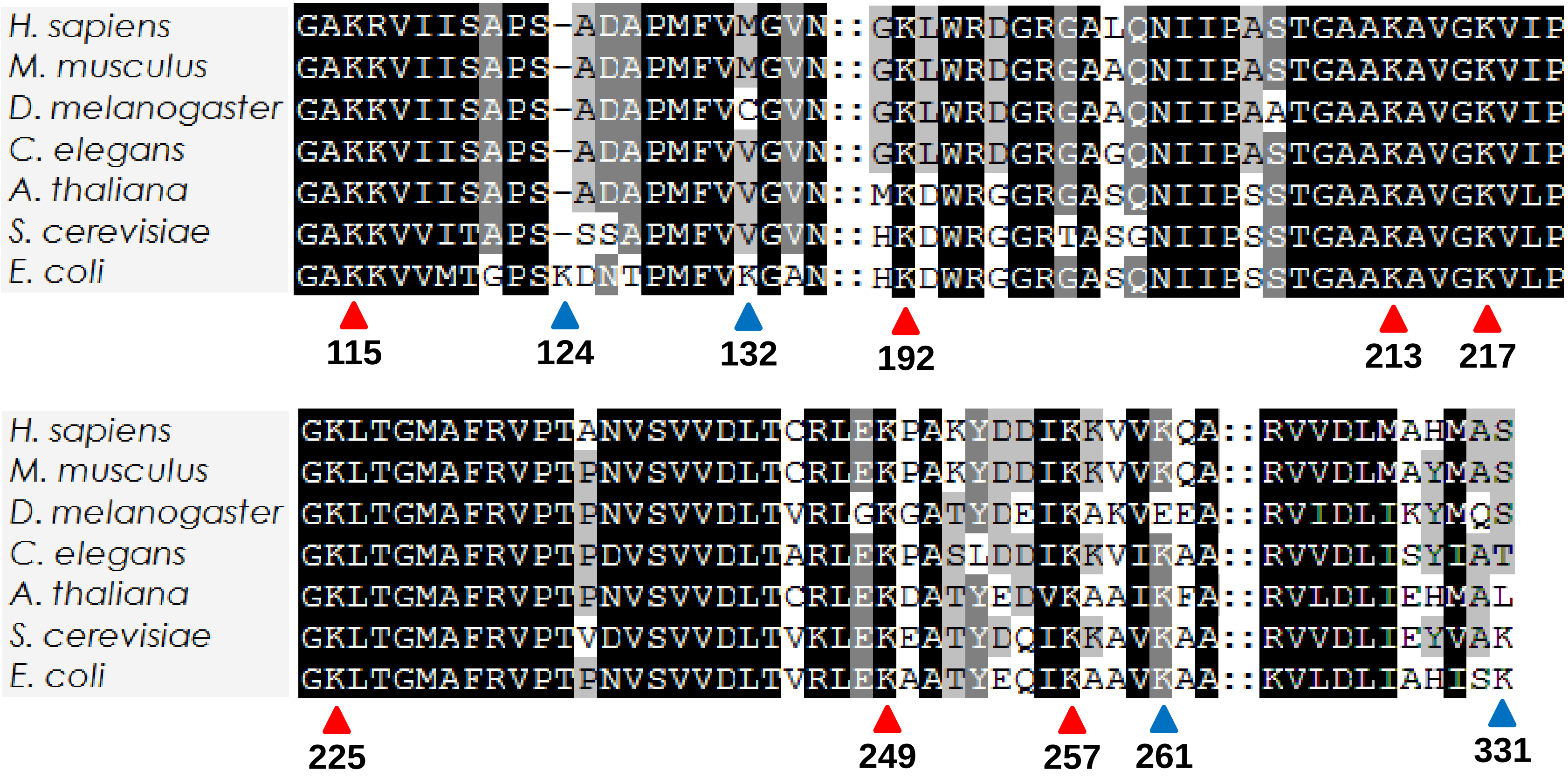
K277SUCC
K242SUCC
K293SUCC

Supplementary Figure 9:

a Glyceraldehyde-3-phosphate dehydrogenase A



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M. musculus	GAKKVIISAPS-ADAPMFVMGVN::GKLWRDGRGAAQNIIPASTGAAKAVGKVIP
D. melanogaster	GAKKVIISAPS-ADAPMFVCGVN::GKLWRDGRGAAQNIIPAATGAAKAVGKVIP
C. elegans	GAKKVIISAPS-ADAPMFVVGVN::GKLWRDGRGAGQNIIPASTGAAKAVGKVIP
A. thaliana	GAKKVIISAPS-ADAPMFVVGVN::MKDWRGGRGASQNIIPSSTGAAKAVGKVLP
S. cerevisiae	GAKKVVITAPS-SSAPMFVVGVN::HKDWRGGRTASGNIIPSSTGAAKAVGKVLP
E. coli	GAKKVVMTGPSKDNTPMFVKGAN::HKDWRGGRGASQNIIPSSTGAAKAVGKVLP

H. sapiens	GKLTGMAFRVPTANVSVVDLTCRLEKPAKYDDIKKVVKQA::RVVDLMAHMAS
M. musculus	GKLTGMAFRVPTPNVSVVDLTCRLEKPAKYDDIKKVVKQA::RVVDLMAYMAS
D. melanogaster	GKLTGMAFRVPTPNVSVVDLTVRLGKGATYDEIKAKVEEA::RVIDLIKYMQS
C. elegans	GKLTGMAFRVPTPDVSVVDLTARLEKPASLDDIKKVIKAA::RVVDLISYIAT
A. thaliana	GKLTGMAFRVPTPNVSVVDLTCRLEKDATYEDVKAAIKFA::RVLDLIEHMAL
S. cerevisiae	GKLTGMAFRVPTVDVSVVDLTVKLEKEATYDQIKKAVKAA::RVVDLIEYVAK
E. coli	GKLTGMAFRVPTPNVSVVDLTVRLEKAATYEQIKAAVKAA::KVLDLIAHISK

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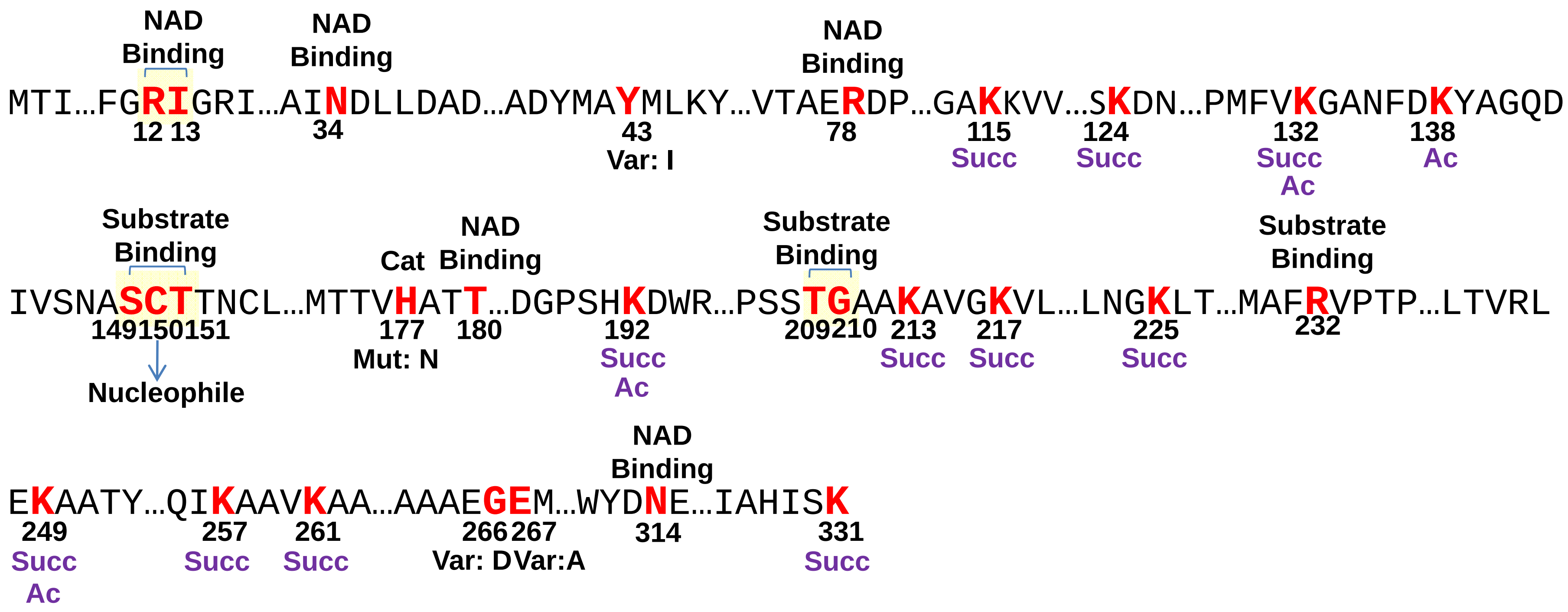
b



Ac: Acetylation
Succ: Succinylation

Var: natrual varient
Cat: catalysis
Mut: mutagenesis

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c
K331SUCC
K115SUCC
K217SUCC
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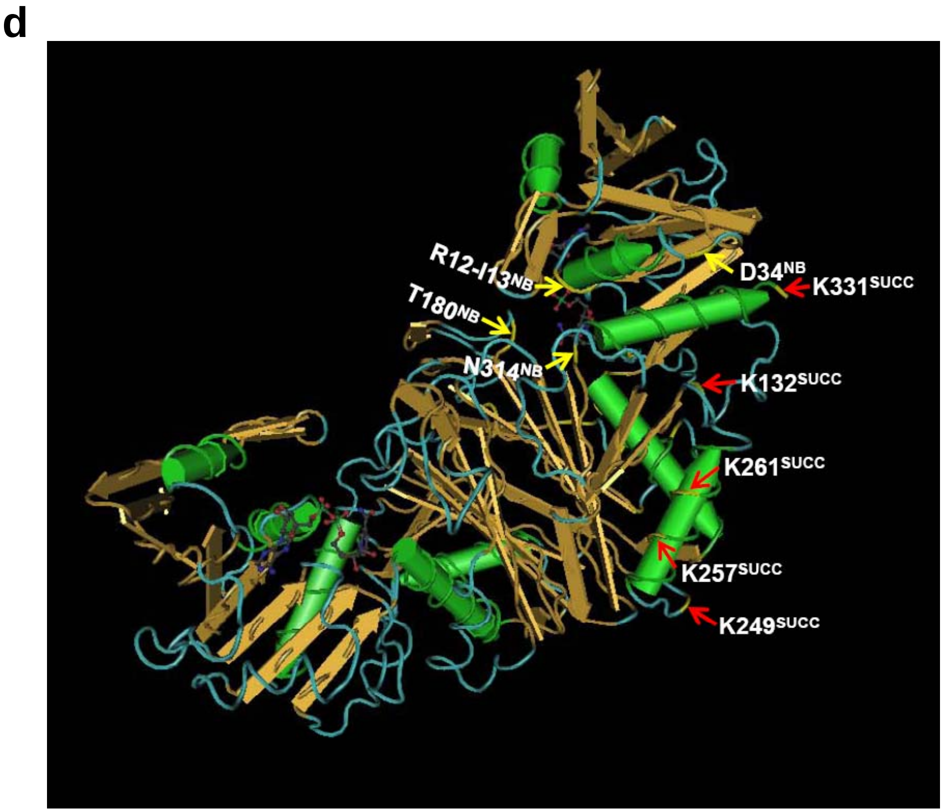
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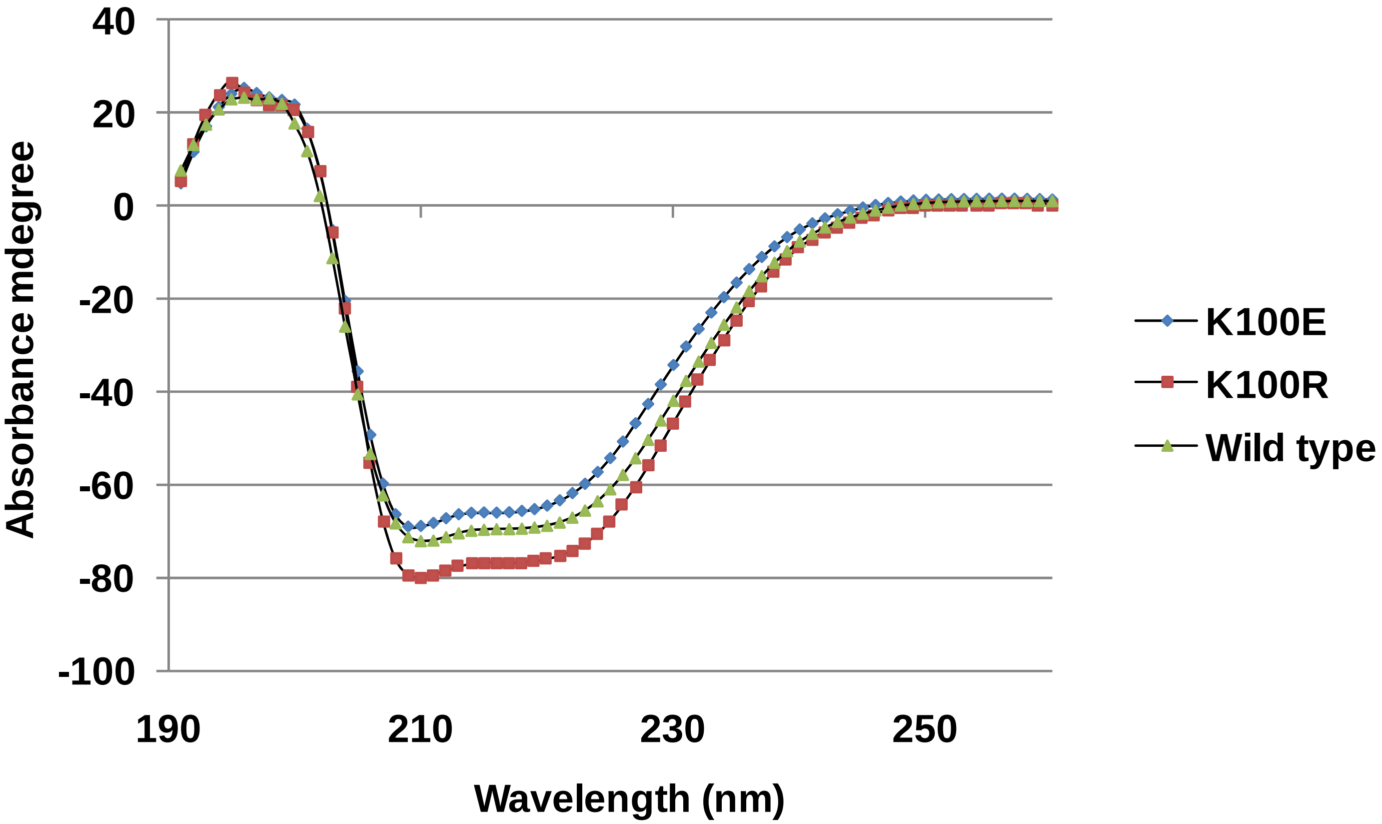

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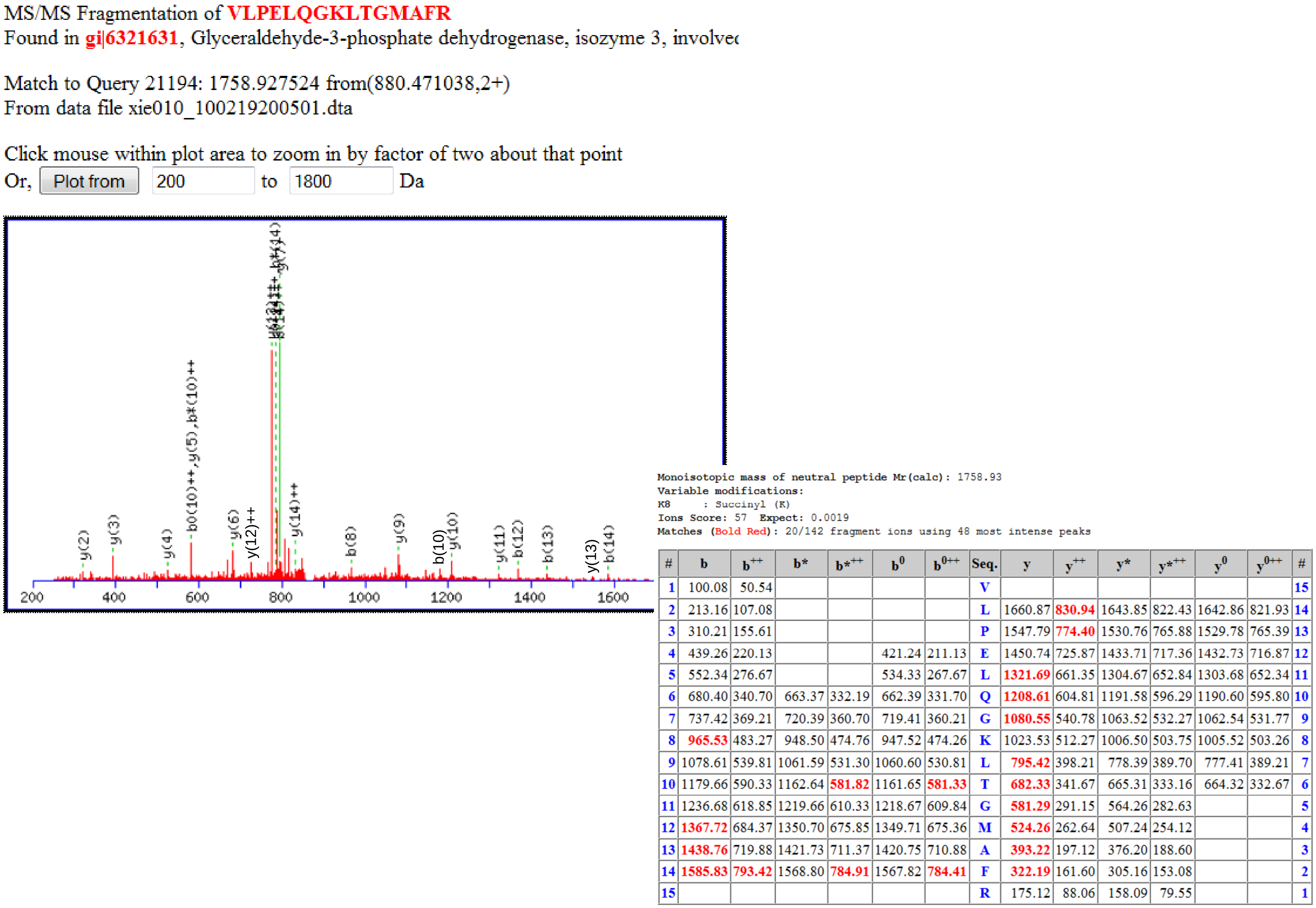
Supplementary Figure 11:

VLPELQG^{Succ}KLTGMAFR K255



MS/MS Fragmentation of **VLPELQGKLTGMAFR**
Found in **gi|6321631**, Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involve

Match to Query 21194: 1758.927524 from(880.471038,2+)
From data file xie010_100219200501.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da

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Monoisotopic mass of neutral peptide Mr(calc): 1758.93
Variable modifications:
K8      : Succinyl (K)
Ions Score: 57  Expect: 0.0019
Matches (Bold Red): 20/142 fragment ions using 48 most intense peaks
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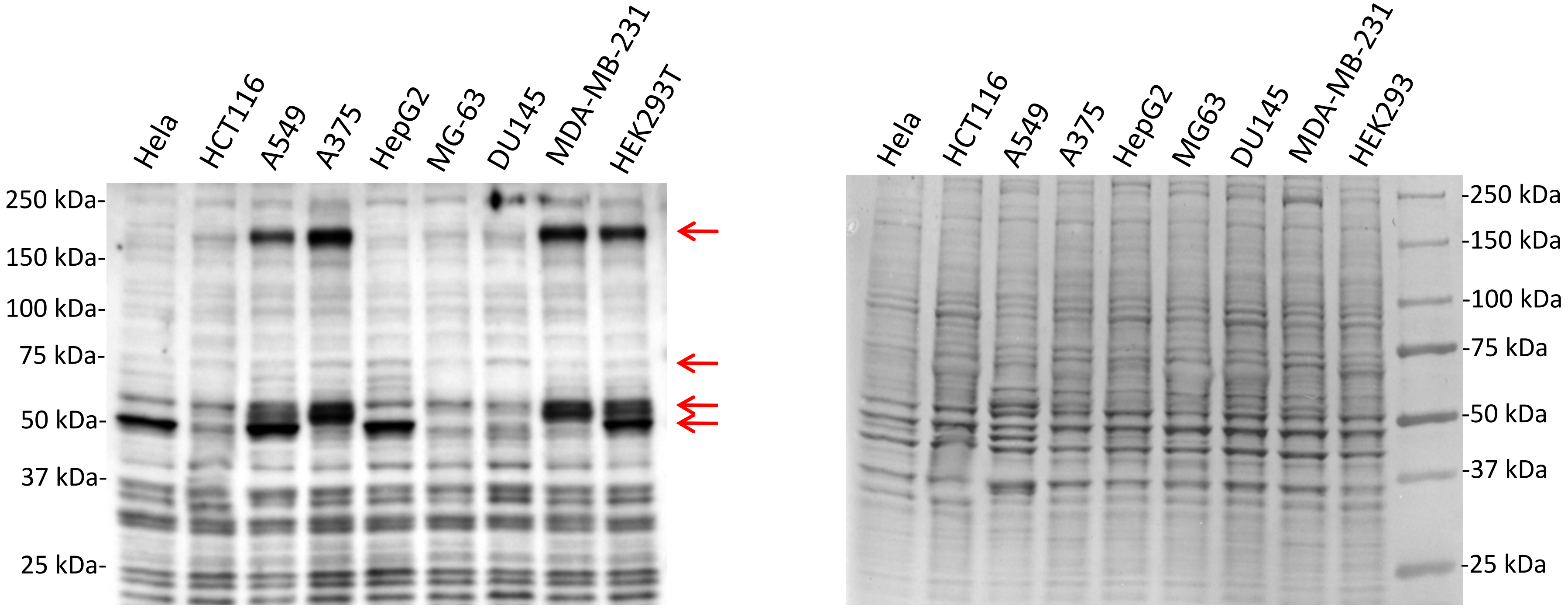
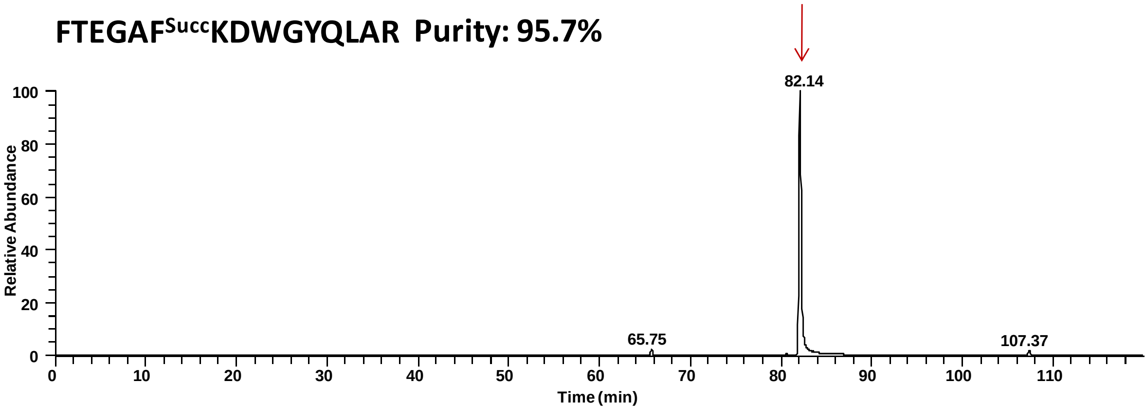
#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.08	50.54					V							15
2	213.16	107.08					L	1660.87	**830.94**	1643.85	822.43	1642.86	821.93	14
3	310.21	155.61					P	1547.79	**774.40**	1530.76	765.88	1529.78	765.39	13
4	439.26	220.13			421.24	211.13	E	1450.74	725.87	1433.71	717.36	1432.73	716.87	12
5	552.34	276.67			534.33	267.67	L	**1321.69**	661.35	1304.67	652.84	1303.68	652.34	11
6	680.40	340.70	663.37	332.19	662.39	331.70	Q	**1208.61**	604.81	1191.58	596.29	1190.60	595.80	10
7	737.42	369.21	720.39	360.70	719.41	360.21	G	**1080.55**	540.78	1063.52	532.27	1062.54	531.77	9
8	**965.53**	483.27	948.50	474.76	947.52	474.26	K	1023.53	512.27	1006.50	503.75	1005.52	503.26	8
9	1078.61	539.81	1061.59	531.30	1060.60	530.81	L	**795.42**	398.21	778.39	389.70	777.41	389.21	7
10	1179.66	590.33	1162.64	**581.82**	1161.65	**581.33**	T	**682.33**	341.67	665.31	333.16	664.32	332.67	6
11	1236.68	618.85	1219.66	610.33	1218.67	609.84	G	**581.29**	291.15	564.26	282.63			5
12	**1367.72**	684.37	1350.70	675.85	1349.71	675.36	M	**524.26**	262.64	507.24	254.12			4
13	**1438.76**	719.88	1421.73	711.37	1420.75	710.88	A	**393.22**	197.12	376.20	188.60			3
14	**1585.83**	**793.42**	1568.80	**784.91**	1567.82	**784.41**	F	**322.19**	161.60	305.16	153.08			2
15							R	175.12	88.06	158.09	79.55			1

Supplementary Figure 12:

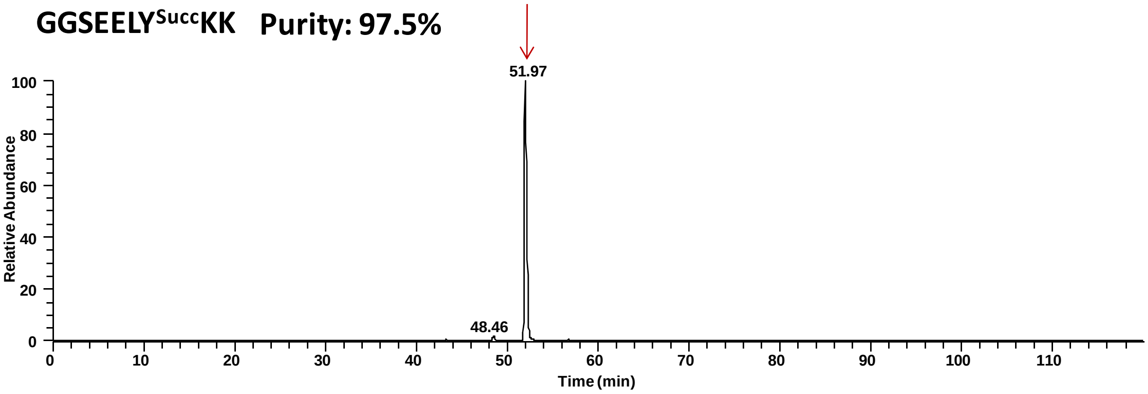


Supplementary Figure 13:

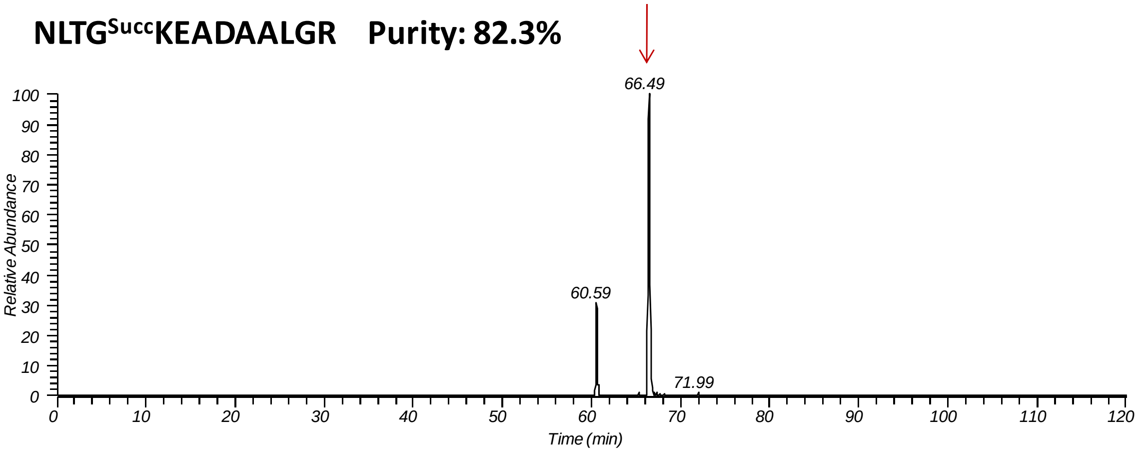
FTEGAF$^{\text{Succ}}$KDWGYQLAR Purity: 95.7%



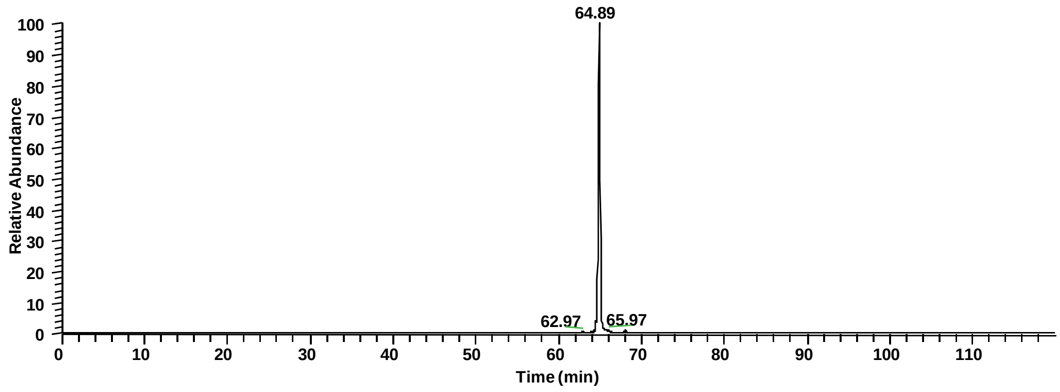
GGSEELY$^{\text{Succ}}$KK Purity: 97.5%



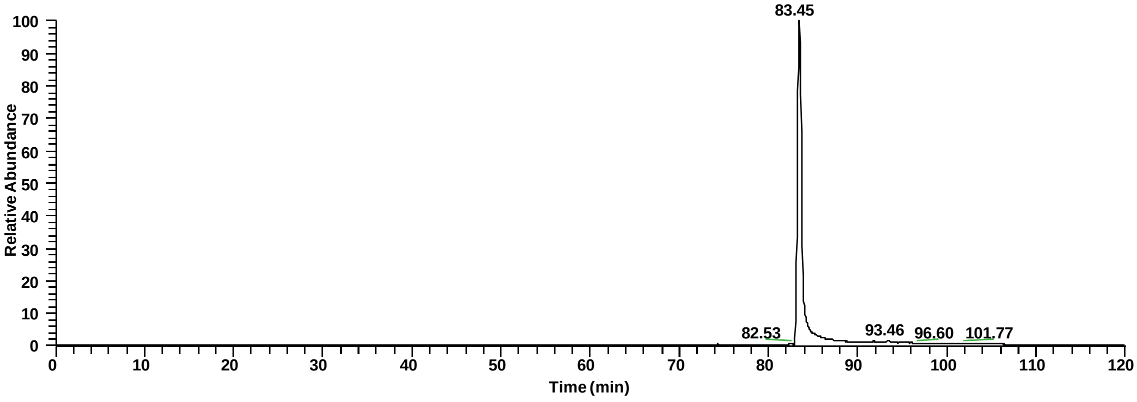
NLTG$^{\text{Succ}}$KEADAALGR Purity: 82.3%



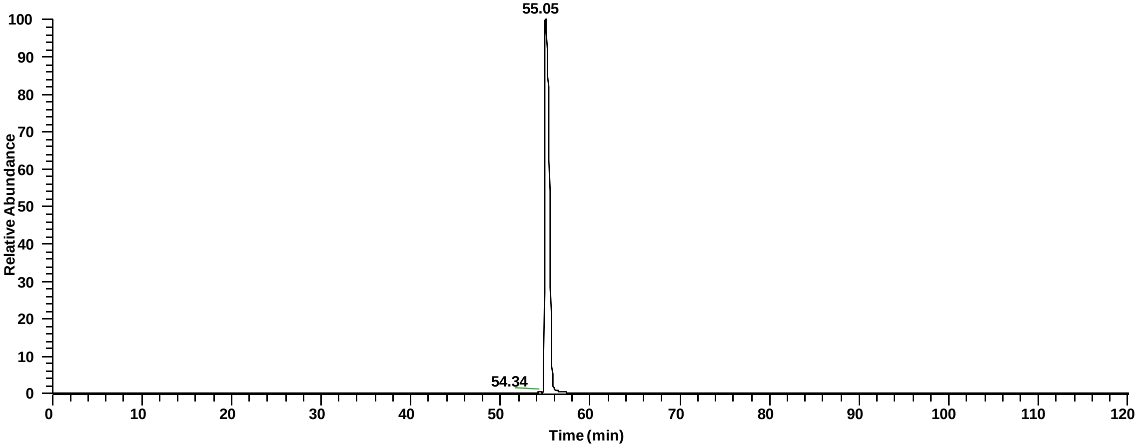
GASQNIIPSSTGAA$^{\text{Succ}}$KAVGK Purity: 99.6%



FTEGAF$^{\text{MeMal}}$KDWGYQLAR Purity: 98.5%



GGSEELY$^{\text{MeMal}}$KK Purity: 99.6%



Supplementary Table 1:

H_4 and D_4-labeled succinyllysine peptide sequences indentified from D4-succinate treated *E. Coli* sample by mass spectrometry*

Protein Name	GI#	site	peptide sequence	Spectral No. of H4-succinyllysine peptide	Spectral No. of D4-succinyllysine peptide
isocitrate dehydrogenase (IcdA)	170080787	K100	R.VAIKGPLTTPVGGGIR.S	1	0
isocitrate dehydrogenase (IcdA)	170080787	K242	K.FTEGAFKDWGYQLAR.E	0	1
serine hydroxymethyltransferase (GlyA)	170082161	K242	R.GGLILAKGGSEELYK.K	1	2
serine hydroxymethyltransferase (GlyA)	170082161	K250	K.GGSEELYKK.L	2	0
serine hydroxymethyltransferase (GlyA)	170082161	K277	K.AVALKEAMEPEFK.T	2	0
serine hydroxymethyltransferase (GlyA)	170082161	K293	K.TYQQQVAKNAK.A	1	1
serine hydroxymethyltransferase (GlyA)	170082161	K331	K.NLTGKEADAALGR.A	2	2
serine hydroxymethyltransferase (GlyA)	170082161	K346	R.ANITVNKNSVPNDPK.S	1	1
glyceraldehyde-3-phosphate dehydrogenase A(GapA)	170081435	K124	K.VVMTGPSKDNTPMFVK.G	10	9
glyceraldehyde-3-phosphate dehydrogenase A(GapA)	170081435	K132	K.DNTPMFVKGANFDK.Y	2	3
glyceraldehyde-3-phosphate dehydrogenase A(GapA)	170081435	K213	R.GASQNIIPSSTGAAKAVGK.V	2	4
glyceraldehyde-3-phosphate dehydrogenase A(GapA)	170081435	K217	K.AVGKVLPELNGK.L	1	0
glyceraldehyde-3-phosphate dehydrogenase A(GapA)	170081435	K225	K.VLPELNGKLTGMAFR.V	1	0
glyceraldehyde-3-phosphate dehydrogenase A(GapA)	170081435	K257	K.AATYEQIKAAVK.A	2	2
glyceraldehyde-3-phosphate dehydrogenase A(GapA)	170081435	K261	K.AAVKAAAEGEMK.G	2	1
glyceraldehyde-3-phosphate dehydrogenase A(GapA)	170081435	K331	K.VLDLIAHISK.-	3	0

*Results were based on Mascot sequence alignment using ion score cutoff 30.

Supplementary Table 2:

Primers used for site specific mutagenesis (mutated bases are shown in bold)

Mutation		Primer
K242R	Forward	5' GTTCACCGAAGGAGCGTTT**CGT**GACTGGGGCTACCAGCTG 3'
	Reverse	5' CAGCTGGTAGCCCCAGTC**ACG**AAACGCTCCTTCGGTGAAC 3'
K242E	Forward	5' CACCGAAGGAGCGTTT**G**AAGACTGGGGCTACC 3'
	Reverse	5' GGTAGCCCCAGTCTT**C**AAACGCTCCTTCGGTG 3'
K100R	Forward	5' GAATATCGCGTTGCCATT**CGT**GGTCCGCTGACCACTCCGG 3'
	Reverse	5' CCGGAGTGGTCAGCGGACC**ACG**AATGGCAACGCGATATTC 3'
K100E	Forward	5' GAATATCGCGTTGCCATT**G**AAGGTCCGCTGACCACTC 3'
	Reverse	5' GAGTGGTCAGCGGACCTT**C**AATGGCAACGCGATATTC 3'

Supplementary Table 3

E. Coli succinyllysine peptide sequences indentified by affinity purification using anti-succinyllysine pan antibody and mass spectrometry.

Peptide	Position	GI#	Succinylation Site	Protein Name
R.VAIKGPLTTPVGGGIR.S	4	170080787	100	isocitrate dehydrogenase, specific for NADP+
K.FTEGAFKDWGYQLAR.E	7	170080787	242	isocitrate dehydrogenase, specific for NADP+
K.YAEGYPGKR.Y	8	170082161	62	serine hydroxymethyltransferase
R.GGLILAKGGSEELYK.K	7	170082161	242	serine hydroxymethyltransferase
K.GGSEELYKK.L	8	170082161	250	serine hydroxymethyltransferase
K.AVALKEAMEPEFK.T	5	170082161	277	serine hydroxymethyltransferase
K.TYQQQVAKNAK.A	8	170082161	293	serine hydroxymethyltransferase
K.NLTGKEADAALGR.A	5	170082161	331	serine hydroxymethyltransferase
R.ANITVNKNSVPNDPK.S	7	170082161	346	serine hydroxymethyltransferase
K.NSVPNDPKSPFVTSGIR.V	8	170082161	354	serine hydroxymethyltransferase
K.HITAGAKK.V	7	170081435	115	glyceraldehyde-3-phosphate dehydrogenase A
K.VVMTGPSKDNTPMFVK.G	8	170081435	124	glyceraldehyde-3-phosphate dehydrogenase A
K.DNTPMFVKGANFDK.Y	8	170081435	132	glyceraldehyde-3-phosphate dehydrogenase A
K.TVDGPSHKDWR.G	8	170081435	192	glyceraldehyde-3-phosphate dehydrogenase A
R.GASQNIIPSSTGAAKAVGK.V	15	170081435	213	glyceraldehyde-3-phosphate dehydrogenase A
K.AVGKVLPELNGK.L	4	170081435	217	glyceraldehyde-3-phosphate dehydrogenase A
K.VLPELNGKLTGMAFR.V	8	170081435	225	glyceraldehyde-3-phosphate dehydrogenase A
R.LEKAATYEQIK.A	3	170081435	249	glyceraldehyde-3-phosphate dehydrogenase A
K.AATYEQIKAAVK.A	8	170081435	257	glyceraldehyde-3-phosphate dehydrogenase A
K.AAVKAAAEGEMK.G	4	170081435	261	glyceraldehyde-3-phosphate dehydrogenase A
K.VLDLIAHISK.	10	170081435	331	glyceraldehyde-3-phosphate dehydrogenase A
K.IFDFVKPGVITGDDVQK.V	6	170082482	9	fructose-bisphosphate aldolase, class II
K.APVIVQFSNGGASFIAGKGVK.S	18	170082482	72	fructose-bisphosphate aldolase, class II
K.KLLPWIDGLLDAGEK.H	1	170082482	115	fructose-bisphosphate aldolase, class II
R.FTIAASFGNVHGVYKPGNVVLTPTILR.D	15	170082482	231	fructose-bisphosphate aldolase, class II
R.DSQEYVSKK.H	8	170082482	251	fructose-bisphosphate aldolase, class II
K.ANEAYLQGQLGNPKGEDQPNKK.Y	14	170082482	319	fructose-bisphosphate aldolase, class II
K.GEDQPNKK.Y	7	170082482	326	fructose-bisphosphate aldolase, class II
R.LEKAFQELNAIDVL.	3	170082482	348	fructose-bisphosphate aldolase, class II

Peptide	Position	GI #	Succinylation Site	Protein Name
K.TTLTAAITTVLAKTYGGAAR.A	13	170083440	38	protein chain elongation factor EF-Tu (duplicate of tufA)
R.GSALKALEGDAEWEAK.I	5	170083440	177	protein chain elongation factor EF-Tu (duplicate of tufA)
K.VGEEVEIVGIKETQK.S	13	170083440	249	protein chain elongation factor EF-Tu (duplicate of tufA)
K.ETQKSTCTGVEMFR.K	4	170083440	253	protein chain elongation factor EF-Tu (duplicate of tufA)
R.GQVLAKPGTIKPHTK.F	5	170083440	295	protein chain elongation factor EF-Tu (duplicate of tufA)
K.FESEVYILSKDEGGR.H	10	170083440	314	protein chain elongation factor EF-Tu (duplicate of tufA)
K.VMEGVKLENR.T	6	170080561	63	pyruvate formate lyase I
K.IVGLQTEAPLKR.A	11	170080561	107	pyruvate formate lyase I
R.ALIPFGGIKMIEGSCK.A	9	170080561	117	pyruvate formate lyase I
K.MIEGSCKAYNR.E	7	170080561	124	pyruvate formate lyase I
R.VALYGIDYLMKDK.L	11	170080561	195	pyruvate formate lyase I
K.TMLYAINGGVDEKLK.M	13	170080561	454	pyruvate formate lyase I
K.SEPIKGDVLNYDEVMER.M	5	170080561	467	pyruvate formate lyase I
K.GAVASLTSVAKLPFAYAK.D	11	170080561	654	pyruvate formate lyase I
K.AAGAELVGMEDLADQIKK.G	17	170083444	105	50S ribosomal subunit protein L1
K.VGTVTPNVAEAVKNAK.A	13	170083444	154	50S ribosomal subunit protein L1
K.LKENLEALLVALK.K	2	170083444	186	50S ribosomal subunit protein L1
K.ENLEALLVALKK.A	11	170083444	197	50S ribosomal subunit protein L1
R.QAVTNPQNTLFAIKR.L	14	170079677	70	chaperone Hsp70, co-chaperone with DnaJ
R.LINYLVEEFKK.D	10	170079677	245	chaperone Hsp70, co-chaperone with DnaJ
K.KDQGIDLR.N	1	170079677	246	chaperone Hsp70, co-chaperone with DnaJ
R.AKLESLVEDLVNR.S	2	170079677	304	chaperone Hsp70, co-chaperone with DnaJ
K.VAEFFGKEPR.K	7	170079677	359	chaperone Hsp70, co-chaperone with DnaJ
K.ITIKASSGLNEDEIQK.M	4	170079677	502	chaperone Hsp70, co-chaperone with DnaJ
R.KFEELVQTR.N	1	170079677	528	chaperone Hsp70, co-chaperone with DnaJ
K.AAIEAKMQELAQVSQK.L	4	170079677	587	chaperone Hsp70, co-chaperone with DnaJ
K.VTLGPKGR.N	6	170083592	34	Cpn60 chaperonin GroEL, large subunit of GroESL
K.SFGAPTITKDGVSVAR.E	9	170083592	51	Cpn60 chaperonin GroEL, large subunit of GroESL
K.AVAAGMNPMDLKR.G	12	170083592	117	Cpn60 chaperonin GroEL, large subunit of GroESL
K.VAAVKAPGFGDR.R	5	170083592	277	Cpn60 chaperonin GroEL, large subunit of GroESL
K.ATLEDLGQAKR.V	10	170083592	321	Cpn60 chaperonin GroEL, large subunit of GroESL
K.VGAATEVEMKEK.K	10	170083592	390	Cpn60 chaperonin GroEL, large subunit of GroESL
R.SFTFVTKTPPAAVLLK.K	7	170083443	72	50S ribosomal subunit protein L11
K.TPPAAVLLKK.A	9	170083443	81	50S ribosomal subunit protein L11
R.VTQVKDLANDGYR.A	5	170082839	38	50S ribosomal subunit protein L3
R.LKDLETQSQDGTFDK.L	2	170079805	115	30S ribosomal subunit protein S2
K.SAGGIVLTGSAAAKSTR.G	14	170083591	34	Cpn10 chaperonin GroES, small subunit of GroESL
K.INALETVTIASKAGDEGK.L	12	170083648	83	50S ribosomal subunit protein L9
R.AEKINALETVTIASK.A	3	170083648	71	50S ribosomal subunit protein L9
R.DIADAVTAAGVEVAKSEVR.L	15	170083648	112	50S ribosomal subunit protein L9

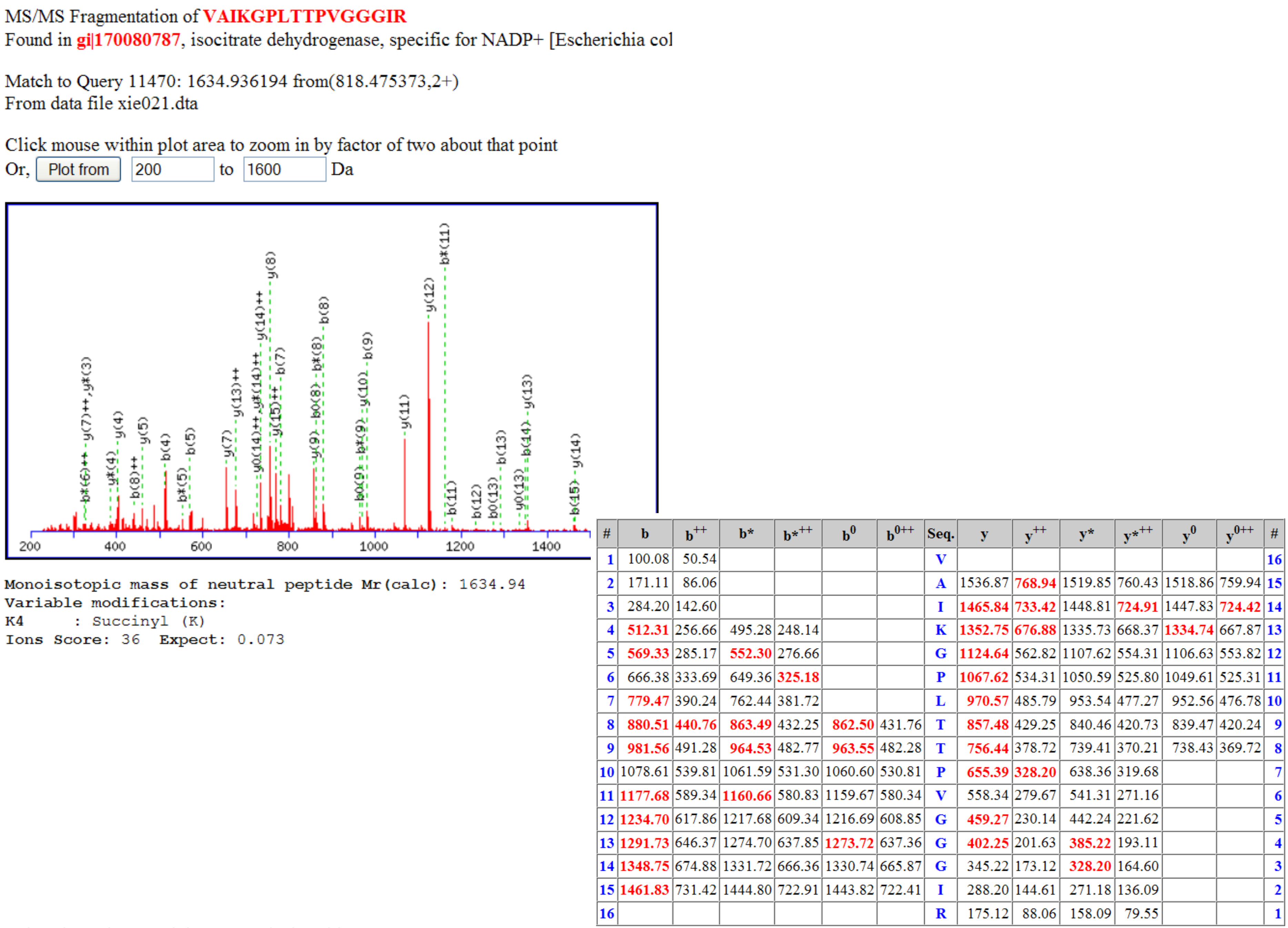
Supplementary Data 1:

MS/MS spectra indentified from 2,2,3,3-D_4-succinate treated and immunoprecipitation-enriched sample using anti-succinyllysine antibody

Note: D_4-succinyllysine and H_4-succinyllysine peptides might be coeluted together.
Results were based on Mascot sequence alignment using ion score cutoff 30.

Isocitrate dehydrogenase K100

VAI^{Succ}KGPLTTPVGGGIR



MS/MS Fragmentation of **VAIKGPLTTPVGGGIR**
Found in **gi|170080787**, isocitrate dehydrogenase, specific for NADP+ [Escherichia col

Match to Query 11470: 1634.936194 from(818.475373,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1634.94
Variable modifications:
K4      : Succinyl (K)
Ions Score: 36  Expect: 0.073
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#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.08	50.54					V							16
2	171.11	86.06					A	1536.87	768.94	1519.85	760.43	1518.86	759.94	15
3	284.20	142.60					I	1465.84	733.42	1448.81	724.91	1447.83	724.42	14
4	512.31	256.66	495.28	248.14			K	1352.75	676.88	1335.73	668.37	1334.74	667.87	13
5	569.33	285.17	552.30	276.66			G	1124.64	562.82	1107.62	554.31	1106.63	553.82	12
6	666.38	333.69	649.36	325.18			P	1067.62	534.31	1050.59	525.80	1049.61	525.31	11
7	779.47	390.24	762.44	381.72			L	970.57	485.79	953.54	477.27	952.56	476.78	10
8	880.51	440.76	863.49	432.25	862.50	431.76	T	857.48	429.25	840.46	420.73	839.47	420.24	9
9	981.56	491.28	964.53	482.77	963.55	482.28	T	756.44	378.72	739.41	370.21	738.43	369.72	8
10	1078.61	539.81	1061.59	531.30	1060.60	530.81	P	655.39	328.20	638.36	319.68			7
11	1177.68	589.34	1160.66	580.83	1159.67	580.34	V	558.34	279.67	541.31	271.16			6
12	1234.70	617.86	1217.68	609.34	1216.69	608.85	G	459.27	230.14	442.24	221.62			5
13	1291.73	646.37	1274.70	637.85	1273.72	637.36	G	402.25	201.63	385.22	193.11			4
14	1348.75	674.88	1331.72	666.36	1330.74	665.87	G	345.22	173.12	328.20	164.60			3
15	1461.83	731.42	1444.80	722.91	1443.82	722.41	I	288.20	144.61	271.18	136.09			2
16							R	175.12	88.06	158.09	79.55			1

Nature Chemical Biology: doi: 10.1038/nchembio.495

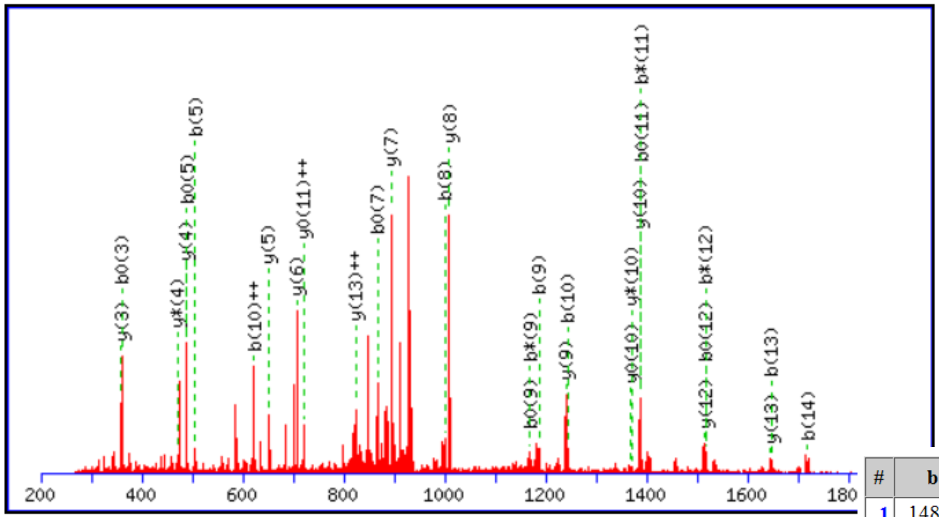
Isocitrate dehydrogenase K242

$\text{FTEGAF}^{\text{Succ-D4}}\text{KDWGYQLAR}$

MS/MS Fragmentation of **FTEGAFKDWGYQLAR**
Found in **gi|170080787**, isocitrate dehydrogenase, specific for NADP+ [Escherichia coli

Match to Query 14390: 1891.902254 from(946.958403,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da



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Monoisotopic mass of neutral peptide Mr(calc): 1891.90
Variable modifications:
K7      : Succinyl (K-D4)
Ions Score: 30  Expect: 0.11
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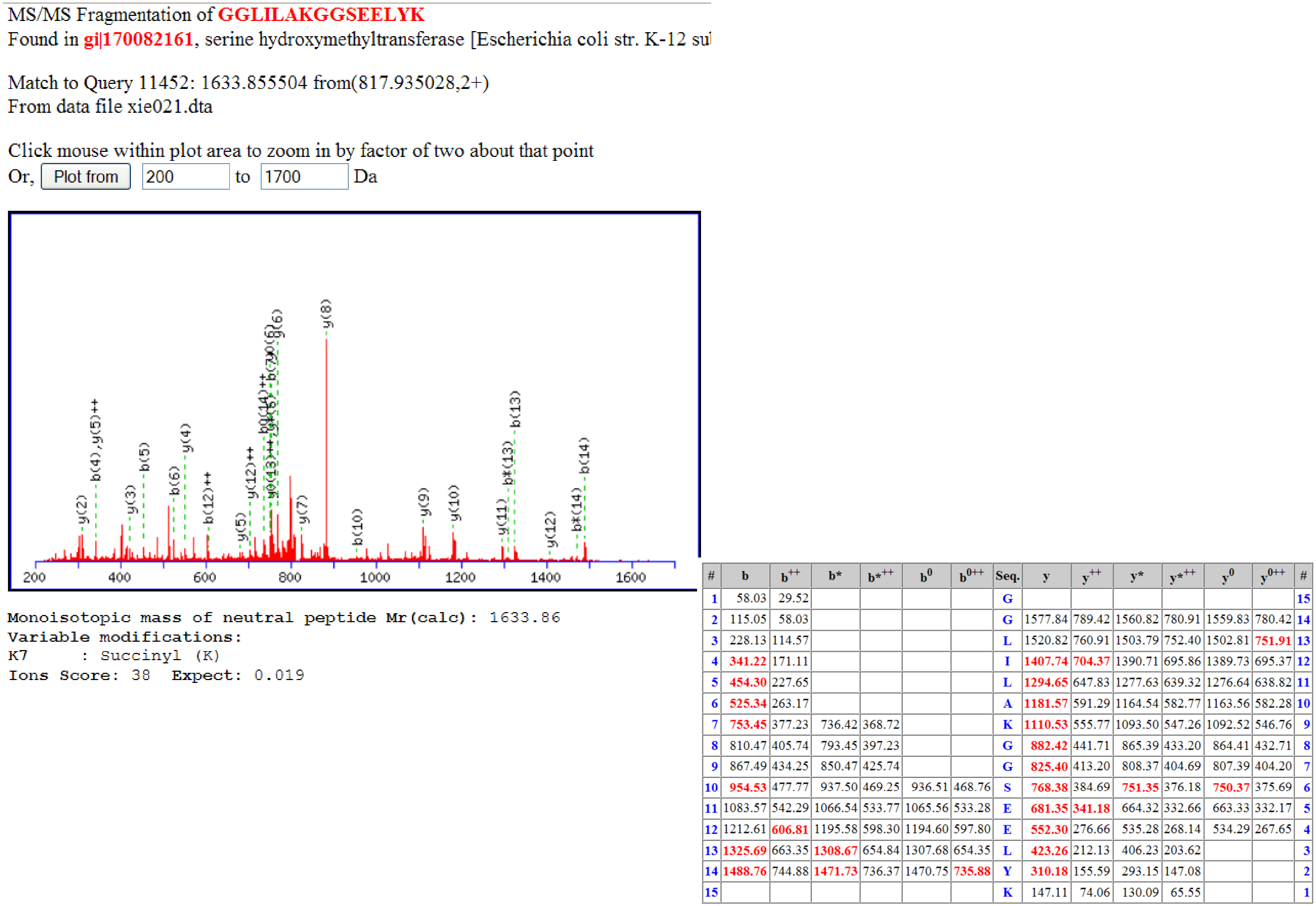
1	148.08	74.54					F							15
2	249.12	125.07			231.11	116.06	T	1745.84	873.43	1728.82	864.91	1727.83	864.42	14
3	378.17	189.59			**360.16**	180.58	E	**1644.80**	**822.90**	1627.77	814.39	1626.78	813.90	13
4	435.19	218.10			417.18	209.09	G	**1515.75**	758.38	1498.73	749.87	1497.74	749.37	12
5	**506.22**	253.62			**488.21**	244.61	A	1458.73	729.87	1441.70	721.36	1440.72	**720.86**	11
6	653.29	327.15			635.28	318.14	F	**1387.69**	694.35	**1370.67**	685.84	**1369.68**	685.35	10
7	885.43	443.22	868.40	434.70	**867.42**	434.21	K	**1240.63**	620.82	1223.60	612.30	1222.62	611.81	9
8	**1000.46**	500.73	983.43	492.22	982.45	491.73	D	**1008.49**	504.75	991.46	496.24	990.48	495.74	8
9	**1186.54**	593.77	**1169.51**	585.26	**1168.52**	584.77	W	**893.46**	447.24	876.44	438.72			7
10	**1243.56**	**622.28**	1226.53	613.77	1225.55	613.28	G	**707.38**	354.20	690.36	345.68			6
11	1406.62	703.81	**1389.59**	695.30	**1388.61**	694.81	Y	**650.36**	325.68	633.34	317.17			5
12	1534.68	767.84	**1517.65**	759.33	**1516.67**	758.84	Q	**487.30**	244.15	**470.27**	235.64			4
13	**1647.76**	824.39	1630.74	815.87	1629.75	815.38	L	**359.24**	180.12	342.21	171.61			3
14	**1718.80**	859.90	1701.77	851.39	1700.79	850.90	A	246.16	123.58	229.13	115.07			2
15							R	175.12	88.06	158.09	79.55			1

serine hydroxymethyltransferase K242 GGLILA^{Succ}KGGSEELYK



MS/MS Fragmentation of **GGLILAKGGSEELYK**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 su

Match to Query 11452: 1633.855504 from(817.935028,2+)
From data file xie021.dta

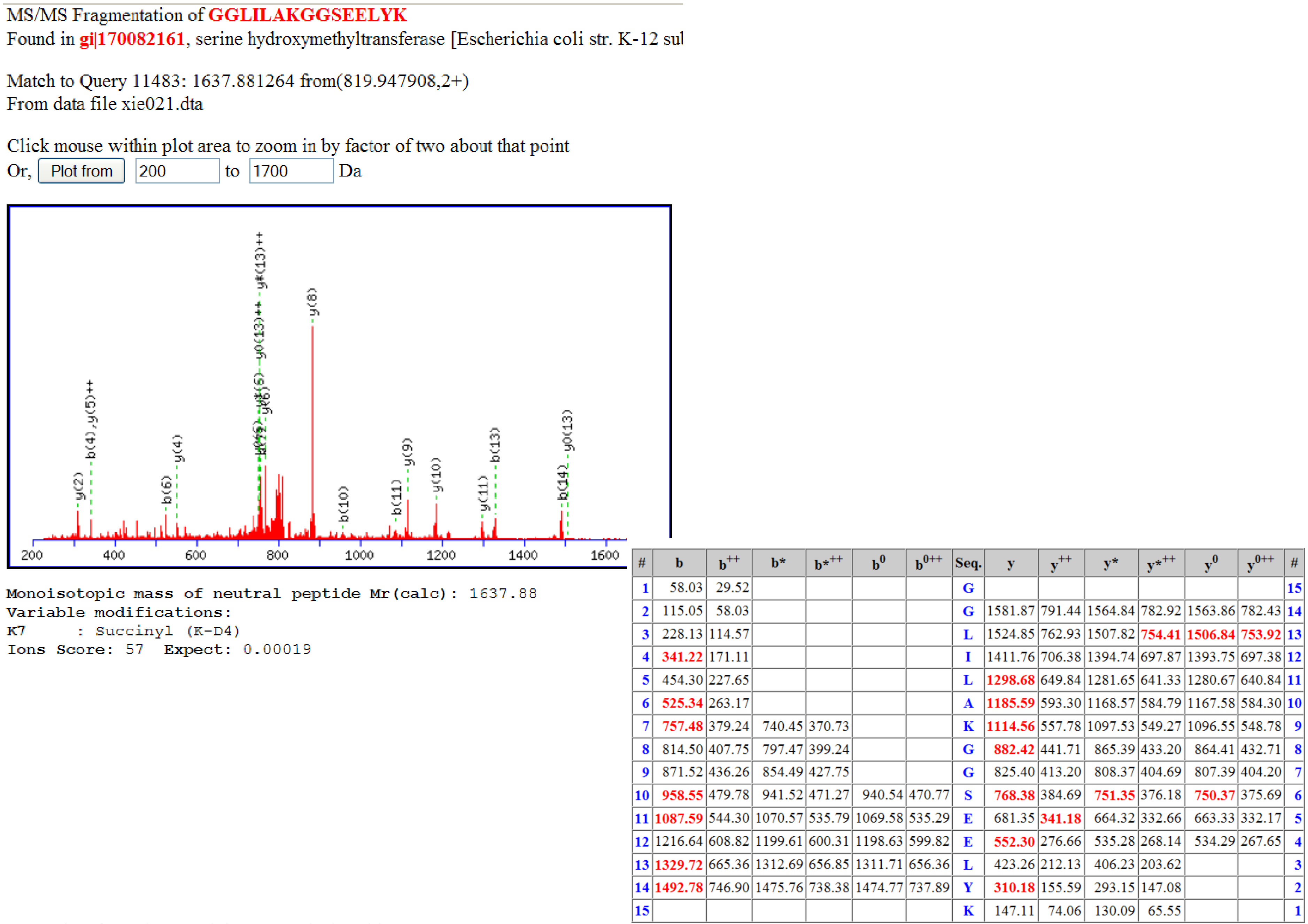
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1633.86
Variable modifications:
K7      : Succinyl (K)
Ions Score: 38  Expect: 0.019
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.03	29.52					G							15
2	115.05	58.03					G	1577.84	789.42	1560.82	780.91	1559.83	780.42	14
3	228.13	114.57					L	1520.82	760.91	1503.79	752.40	1502.81	751.91	13
4	341.22	171.11					I	1407.74	704.37	1390.71	695.86	1389.73	695.37	12
5	454.30	227.65					L	1294.65	647.83	1277.63	639.32	1276.64	638.82	11
6	525.34	263.17					A	1181.57	591.29	1164.54	582.77	1163.56	582.28	10
7	753.45	377.23	736.42	368.72			K	1110.53	555.77	1093.50	547.26	1092.52	546.76	9
8	810.47	405.74	793.45	397.23			G	882.42	441.71	865.39	433.20	864.41	432.71	8
9	867.49	434.25	850.47	425.74			G	825.40	413.20	808.37	404.69	807.39	404.20	7
10	954.53	477.77	937.50	469.25	936.51	468.76	S	768.38	384.69	751.35	376.18	750.37	375.69	6
11	1083.57	542.29	1066.54	533.77	1065.56	533.28	E	681.35	341.18	664.32	332.66	663.33	332.17	5
12	1212.61	606.81	1195.58	598.30	1194.60	597.80	E	552.30	276.66	535.28	268.14	534.29	267.65	4
13	1325.69	663.35	1308.67	654.84	1307.68	654.35	L	423.26	212.13	406.23	203.62			3
14	1488.76	744.88	1471.73	736.37	1470.75	735.88	Y	310.18	155.59	293.15	147.08			2
15							K	147.11	74.06	130.09	65.55			1

Nature Chemical Biology: doi: 10.1038/nchembio.495

serine hydroxymethyltransferase K242 GGLILA$^{Succ\text{-}D4}$KGGSEELYK



MS/MS Fragmentation of **GGLILAKGGSEELYK**

Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 sul

Match to Query 11483: 1637.881264 from(819.947908,2+)

From data file xie021.dta

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

Or, Plot from 200 to 1700 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1637.88
Variable modifications:
K7      : Succinyl (K-D4)
Ions Score: 57  Expect: 0.00019
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.03	29.52					G							15
2	115.05	58.03					G	1581.87	791.44	1564.84	782.92	1563.86	782.43	14
3	228.13	114.57					L	1524.85	762.93	1507.82	**754.41**	**1506.84**	**753.92**	13
4	**341.22**	171.11					I	1411.76	706.38	1394.74	697.87	1393.75	697.38	12
5	454.30	227.65					L	**1298.68**	649.84	1281.65	641.33	1280.67	640.84	11
6	**525.34**	263.17					A	**1185.59**	593.30	1168.57	584.79	1167.58	584.30	10
7	**757.48**	379.24	740.45	370.73			K	**1114.56**	557.78	1097.53	549.27	1096.55	548.78	9
8	814.50	407.75	797.47	399.24			G	**882.42**	441.71	865.39	433.20	864.41	432.71	8
9	871.52	436.26	854.49	427.75			G	825.40	413.20	808.37	404.69	807.39	404.20	7
10	**958.55**	479.78	941.52	471.27	940.54	470.77	S	**768.38**	384.69	**751.35**	376.18	**750.37**	375.69	6
11	**1087.59**	544.30	1070.57	535.79	1069.58	535.29	E	681.35	**341.18**	664.32	332.66	663.33	332.17	5
12	1216.64	608.82	1199.61	600.31	1198.63	599.82	E	**552.30**	276.66	535.28	268.14	534.29	267.65	4
13	**1329.72**	665.36	1312.69	656.85	1311.71	656.36	L	423.26	212.13	406.23	203.62			3
14	**1492.78**	746.90	1475.76	738.38	1474.77	737.89	Y	**310.18**	155.59	293.15	147.08			2
15							K	147.11	74.06	130.09	65.55			1

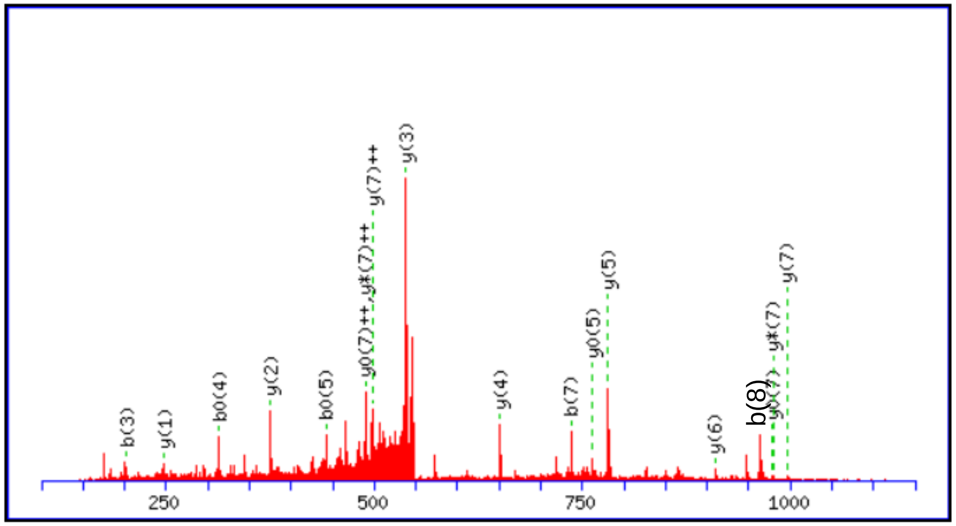
Nature Chemical Biology: doi: 10.1038/nchembio.495

serine hydroxymethyltransferase K250 GGSEELY$^{\text{Succ}}$KK

MS/MS Fragmentation of **GGSEELYKK**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 sub

Match to Query 4032: 1109.524814 from(555.769683,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da

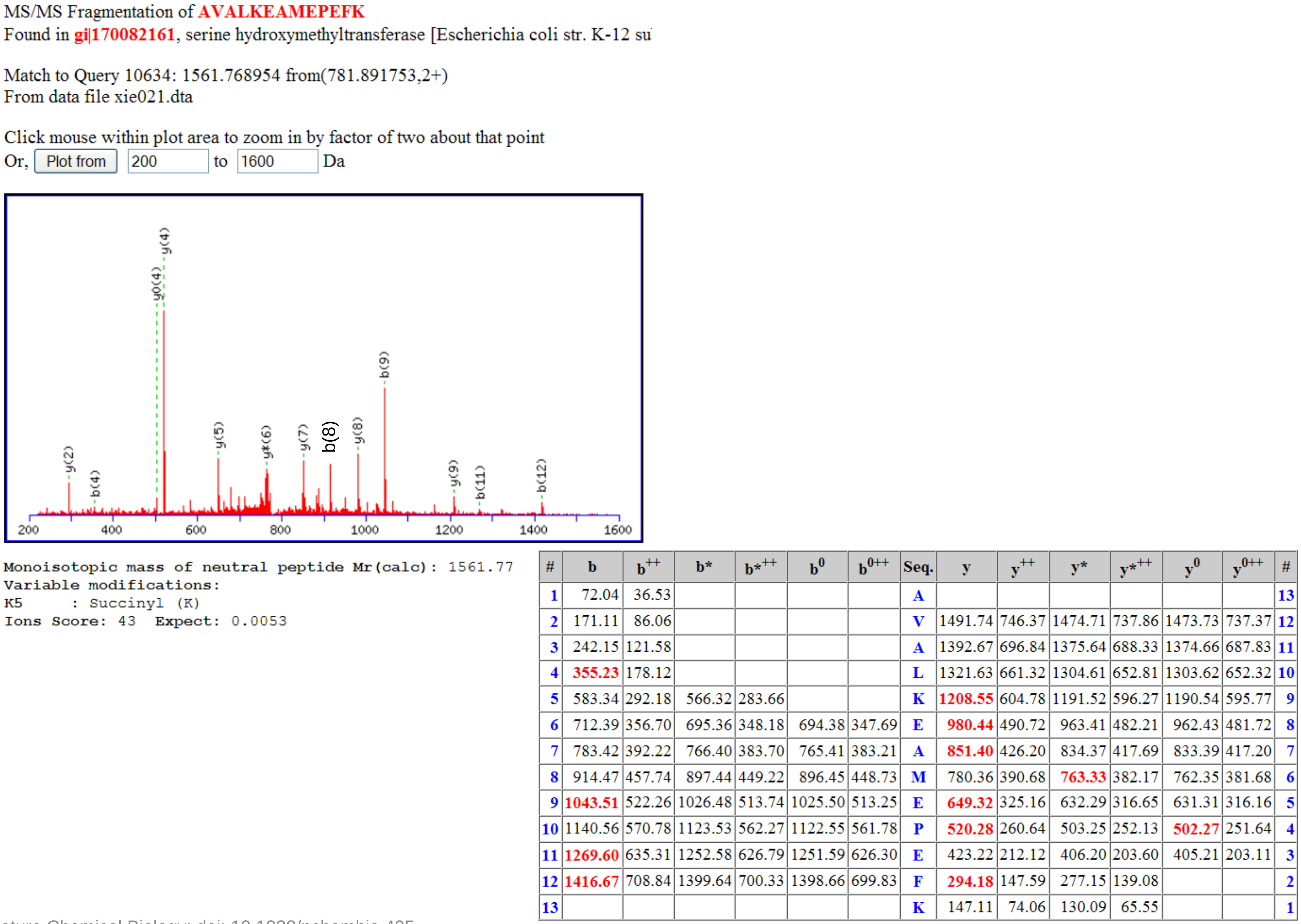


Monoisotopic mass of neutral peptide Mr(calc): 1109.52
Variable modifications:
K8 : Succinyl (K)
Ions Score: 30 Expect: 0.078

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.03	29.52					G							9
2	115.05	58.03					G	1053.51	527.26	1036.48	518.75	1035.50	518.25	8
3	**202.08**	101.54			184.07	92.54	S	**996.49**	**498.75**	**979.46**	**490.23**	**978.48**	**489.74**	7
4	331.12	166.07			**313.11**	157.06	E	**909.46**	455.23	892.43	446.72	891.45	446.23	6
5	460.17	230.59			**442.16**	221.58	E	**780.41**	390.71	763.39	382.20	**762.40**	381.71	5
6	573.25	287.13			555.24	278.12	L	**651.37**	326.19	634.34	317.68			4
7	**736.31**	368.66			718.30	359.66	Y	**538.29**	269.65	521.26	261.13			3
8	**964.41**	432.71	847.38	424.20	846.40	423.70	K	**375.22**	188.12	358.20	179.60			2
9							K	147.13	124.07	230.10	115.55			1

Nature Chemical Biology: doi: 10.1038/nchembio.495

serine hydroxymethyltransferase K277 AVAL^{Succ}KEAMEPEFK



MS/MS Fragmentation of AVALKEAMEPEFK
Found in gi|170082161, serine hydroxymethyltransferase [Escherichia coli str. K-12 su

Match to Query 10634: 1561.768954 from(781.891753,2+)
From data file xie021.dta

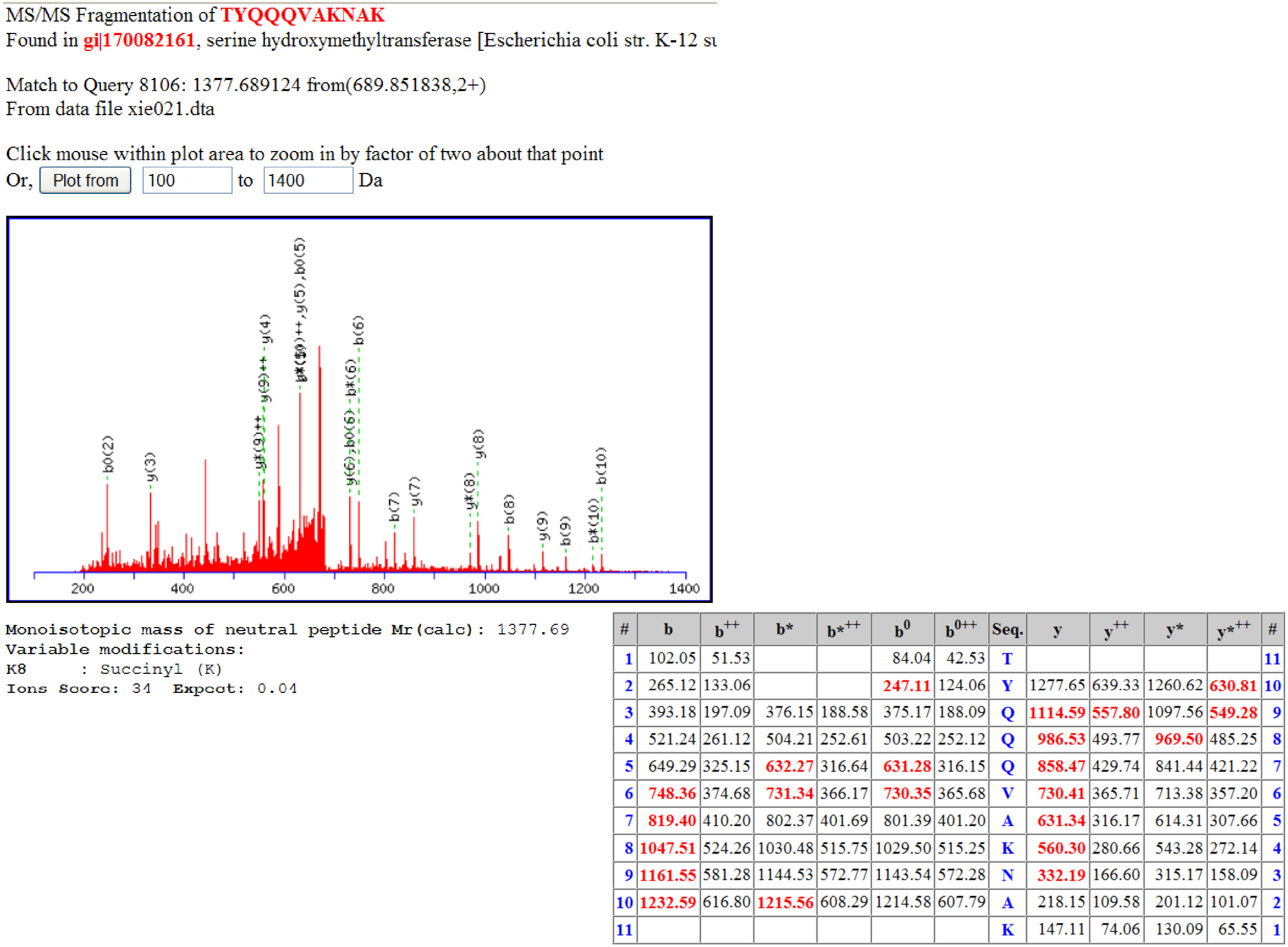
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1561.77
Variable modifications:
K5      : Succinyl (K)
Ions Score: 43  Expect: 0.0053
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.04	36.53					A							13
2	171.11	86.06					V	1491.74	746.37	1474.71	737.86	1473.73	737.37	12
3	242.15	121.58					A	1392.67	696.84	1375.64	688.33	1374.66	687.83	11
4	355.23	178.12					L	1321.63	661.32	1304.61	652.81	1303.62	652.32	10
5	583.34	292.18	566.32	283.66			K	1208.55	604.78	1191.52	596.27	1190.54	595.77	9
6	712.39	356.70	695.36	348.18	694.38	347.69	E	980.44	490.72	963.41	482.21	962.43	481.72	8
7	783.42	392.22	766.40	383.70	765.41	383.21	A	851.40	426.20	834.37	417.69	833.39	417.20	7
8	914.47	457.74	897.44	449.22	896.45	448.73	M	780.36	390.68	763.33	382.17	762.35	381.68	6
9	1043.51	522.26	1026.48	513.74	1025.50	513.25	E	649.32	325.16	632.29	316.65	631.31	316.16	5
10	1140.56	570.78	1123.53	562.27	1122.55	561.78	P	520.28	260.64	503.25	252.13	502.27	251.64	4
11	1269.60	635.31	1252.58	626.79	1251.59	626.30	E	423.22	212.12	406.20	203.60	405.21	203.11	3
12	1416.67	708.84	1399.64	700.33	1398.66	699.83	F	294.18	147.59	277.15	139.08			2
13							K	147.11	74.06	130.09	65.55			1

Nature Chemical Biology: doi: 10.1038/nchembio.495

serine hydroxymethyltransferase K293 TYQQQVA^{Succ}KNAK



MS/MS Fragmentation of **TYQQQVAKNAK**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 su

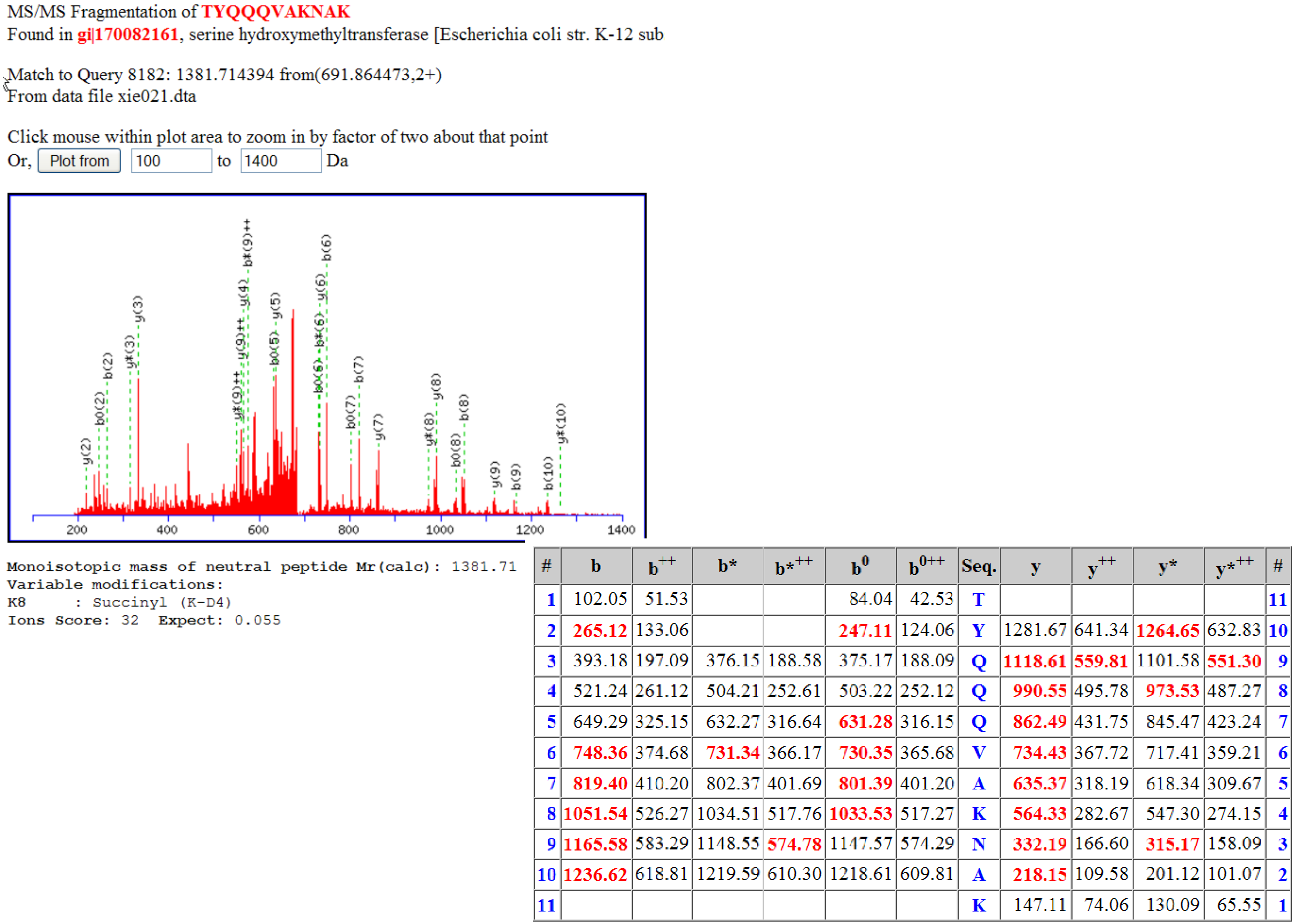
Match to Query 8106: 1377.689124 from(689.851838,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1377.69
Variable modifications:
K8      : Succinyl (K)
Ions Score: 34  Expect: 0.04
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	102.05	51.53			84.04	42.53	T					11
2	265.12	133.06			**247.11**	124.06	Y	1277.65	639.33	1260.62	**630.81**	10
3	393.18	197.09	376.15	188.58	375.17	188.09	Q	**1114.59**	**557.80**	1097.56	**549.28**	9
4	521.24	261.12	504.21	252.61	503.22	252.12	Q	**986.53**	493.77	**969.50**	485.25	8
5	649.29	325.15	**632.27**	316.64	**631.28**	316.15	Q	**858.47**	429.74	841.44	421.22	7
6	**748.36**	374.68	**731.34**	366.17	**730.35**	365.68	V	**730.41**	365.71	713.38	357.20	6
7	**819.40**	410.20	802.37	401.69	801.39	401.20	A	**631.34**	316.17	614.31	307.66	5
8	**1047.51**	524.26	1030.48	515.75	1029.50	515.25	K	**560.30**	280.66	543.28	272.14	4
9	**1161.55**	581.28	1144.53	572.77	1143.54	572.28	N	**332.19**	166.60	315.17	158.09	3
10	**1232.59**	616.80	**1215.56**	608.29	1214.58	607.79	A	218.15	109.58	201.12	101.07	2
11							K	147.11	74.06	130.09	65.55	1

serine hydroxymethyltransferase K293 TYQQQVA$^{\text{Succ-D4}}$KNAK



MS/MS Fragmentation of **TYQQQVAKNAK**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 sub

Match to Query 8182: 1381.714394 from(691.864473,2+)
From data file xie021.dta

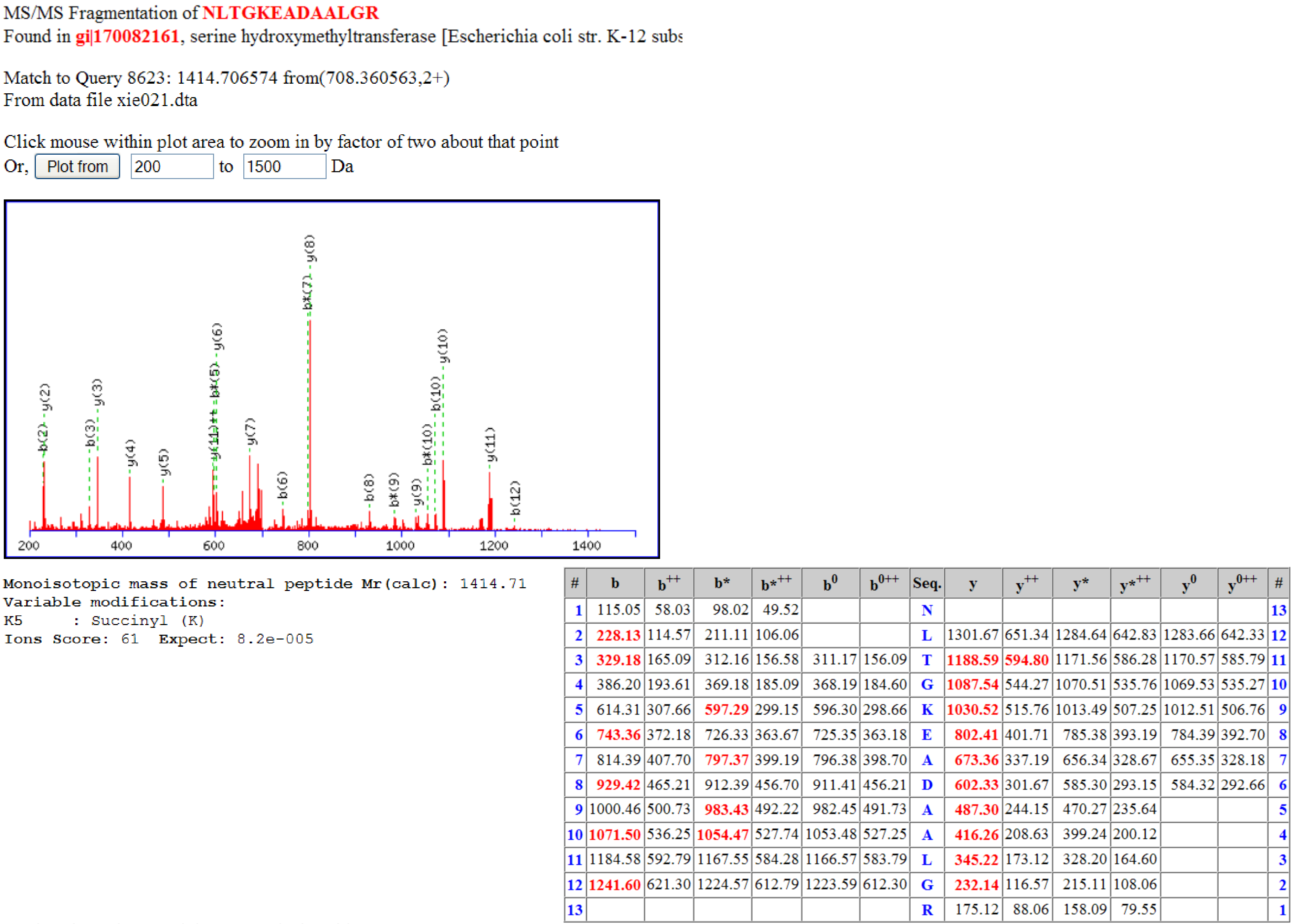
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1381.71
Variable modifications:
K8     : Succinyl (K-D4)
Ions Score: 32  Expect: 0.055
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	102.05	51.53			84.04	42.53	T					11
2	**265.12**	133.06			**247.11**	124.06	Y	1281.67	641.34	**1264.65**	632.83	10
3	393.18	197.09	376.15	188.58	375.17	188.09	Q	**1118.61**	**559.81**	1101.58	**551.30**	9
4	521.24	261.12	504.21	252.61	503.22	252.12	Q	**990.55**	495.78	**973.53**	487.27	8
5	649.29	325.15	632.27	316.64	**631.28**	316.15	Q	**862.49**	431.75	845.47	423.24	7
6	**748.36**	374.68	**731.34**	366.17	**730.35**	365.68	V	**734.43**	367.72	717.41	359.21	6
7	**819.40**	410.20	802.37	401.69	**801.39**	401.20	A	**635.37**	318.19	618.34	309.67	5
8	**1051.54**	526.27	1034.51	517.76	**1033.53**	517.27	K	**564.33**	282.67	547.30	274.15	4
9	**1165.58**	583.29	1148.55	**574.78**	1147.57	574.29	N	**332.19**	166.60	**315.17**	158.09	3
10	**1236.62**	618.81	1219.59	610.30	1218.61	609.81	A	**218.15**	109.58	201.12	101.07	2
11							K	147.11	74.06	130.09	65.55	1

Nature Chemical Biology: doi: 10.1038/nchembio.495

serine hydroxymethyltransferase K331 NLTG^{Succ}KEADAALGR



MS/MS Fragmentation of **NLTGKEADAALGR**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 subs

Match to Query 8623: 1414.706574 from(708.360563,2+)
From data file xie021.dta

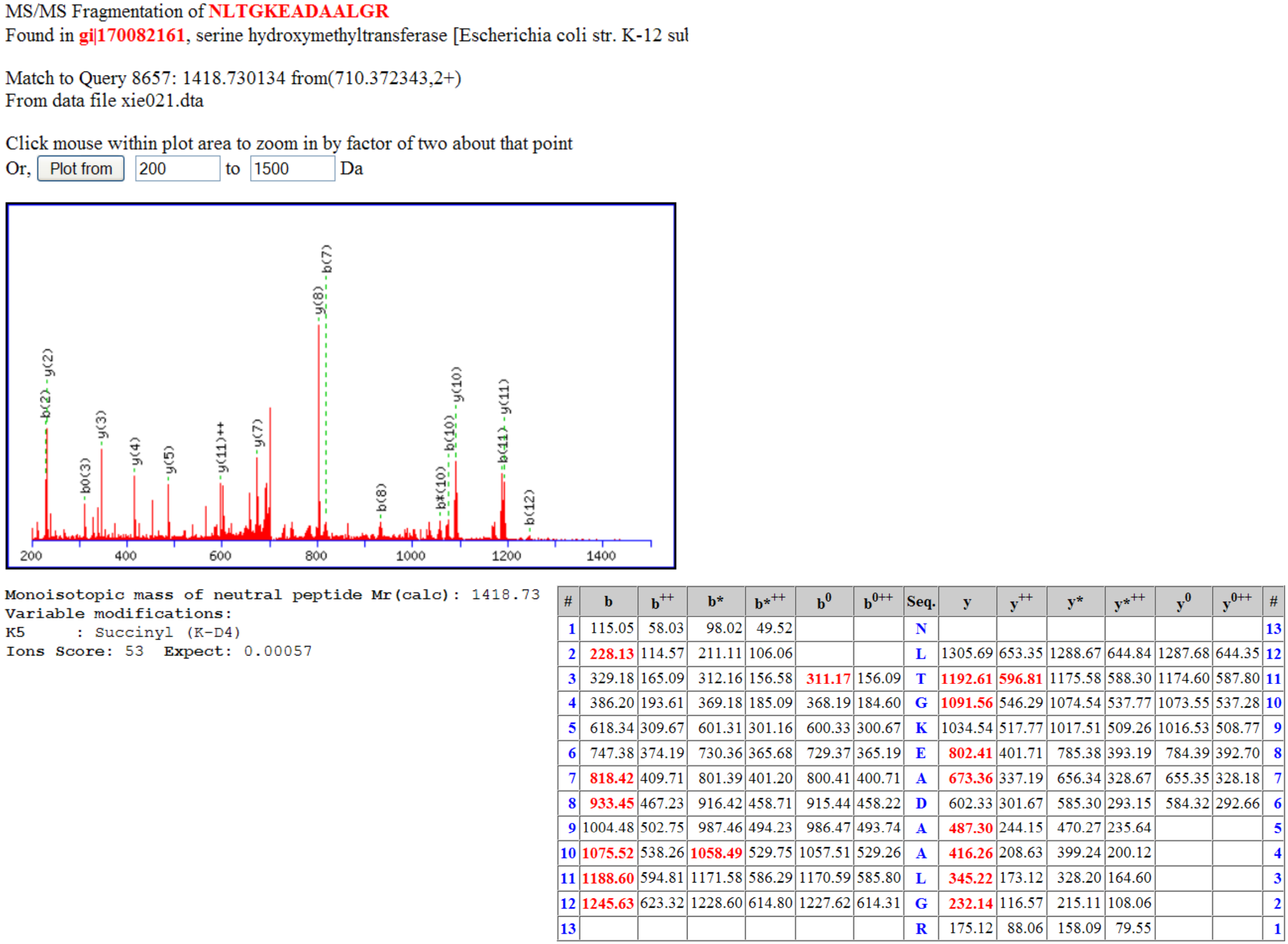
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1414.71
Variable modifications:
K5      : Succinyl (K)
Ions Score: 61  Expect: 8.2e-005
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.05	58.03	98.02	49.52			N							13
2	**228.13**	114.57	211.11	106.06			L	1301.67	651.34	1284.64	642.83	1283.66	642.33	12
3	**329.18**	165.09	312.16	156.58	311.17	156.09	T	**1188.59**	**594.80**	1171.56	586.28	1170.57	585.79	11
4	386.20	193.61	369.18	185.09	368.19	184.60	G	**1087.54**	544.27	1070.51	535.76	1069.53	535.27	10
5	614.31	307.66	**597.29**	299.15	596.30	298.66	K	**1030.52**	515.76	1013.49	507.25	1012.51	506.76	9
6	**743.36**	372.18	726.33	363.67	725.35	363.18	E	**802.41**	401.71	785.38	393.19	784.39	392.70	8
7	814.39	407.70	**797.37**	399.19	796.38	398.70	A	**673.36**	337.19	656.34	328.67	655.35	328.18	7
8	**929.42**	465.21	912.39	456.70	911.41	456.21	D	**602.33**	301.67	585.30	293.15	584.32	292.66	6
9	1000.46	500.73	**983.43**	492.22	982.45	491.73	A	**487.30**	244.15	470.27	235.64			5
10	**1071.50**	536.25	**1054.47**	527.74	1053.48	527.25	A	**416.26**	208.63	399.24	200.12			4
11	1184.58	592.79	1167.55	584.28	1166.57	583.79	L	**345.22**	173.12	328.20	164.60			3
12	**1241.60**	621.30	1224.57	612.79	1223.59	612.30	G	**232.14**	116.57	215.11	108.06			2
13							R	175.12	88.06	158.09	79.55			1

Nature Chemical Biology: doi: 10.1038/nchembio.495

serine hydroxymethyltransferase K331 NLTG$^{Succ\text{-}D4}$KEADAALGR



MS/MS Fragmentation of **NLTGKEADAALGR**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 sul

Match to Query 8657: 1418.730134 from(710.372343,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1418.73
Variable modifications:
K5      : Succinyl (K-D4)
Ions Score: 53  Expect: 0.00057
```

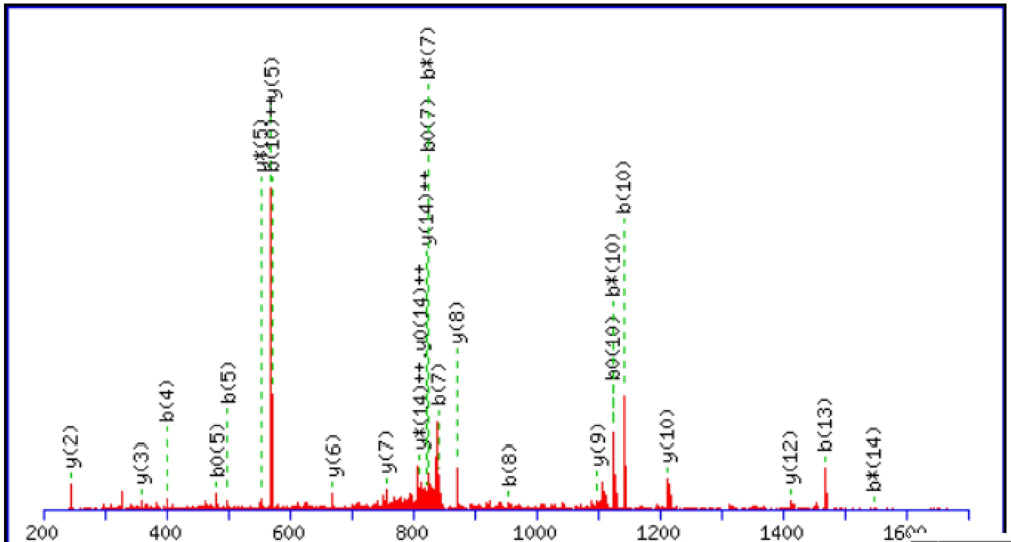
#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.05	58.03	98.02	49.52			N							13
2	**228.13**	114.57	211.11	106.06			L	1305.69	653.35	1288.67	644.84	1287.68	644.35	12
3	329.18	165.09	312.16	156.58	**311.17**	156.09	T	**1192.61**	**596.81**	1175.58	588.30	1174.60	587.80	11
4	386.20	193.61	369.18	185.09	368.19	184.60	G	**1091.56**	546.29	1074.54	537.77	1073.55	537.28	10
5	618.34	309.67	601.31	301.16	600.33	300.67	K	1034.54	517.77	1017.51	509.26	1016.53	508.77	9
6	747.38	374.19	730.36	365.68	729.37	365.19	E	**802.41**	401.71	785.38	393.19	784.39	392.70	8
7	**818.42**	409.71	801.39	401.20	800.41	400.71	A	**673.36**	337.19	656.34	328.67	655.35	328.18	7
8	**933.45**	467.23	916.42	458.71	915.44	458.22	D	602.33	301.67	585.30	293.15	584.32	292.66	6
9	1004.48	502.75	987.46	494.23	986.47	493.74	A	**487.30**	244.15	470.27	235.64			5
10	**1075.52**	538.26	**1058.49**	529.75	1057.51	529.26	A	**416.26**	208.63	399.24	200.12			4
11	**1188.60**	594.81	1171.58	586.29	1170.59	585.80	L	**345.22**	173.12	328.20	164.60			3
12	**1245.63**	623.32	1228.60	614.80	1227.62	614.31	G	**232.14**	116.57	215.11	108.06			2
13							R	175.12	88.06	158.09	79.55			1

serine hydroxymethyltransferase K346 ANITVN^{Succ}KNSVPNDPK

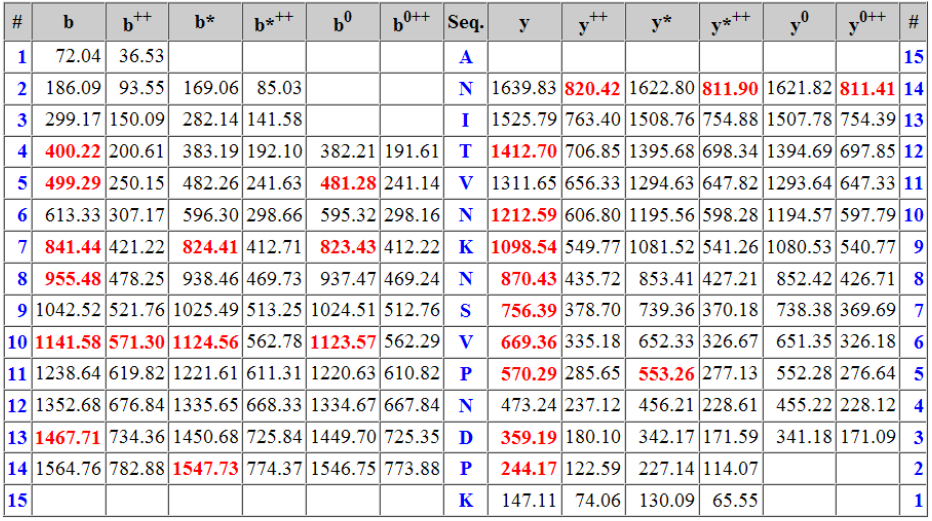
MS/MS Fragmentation of **ANITVNKNSVPNDPK**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 sub

Match to Query 12473: 1709.858674 from(855.936613,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da

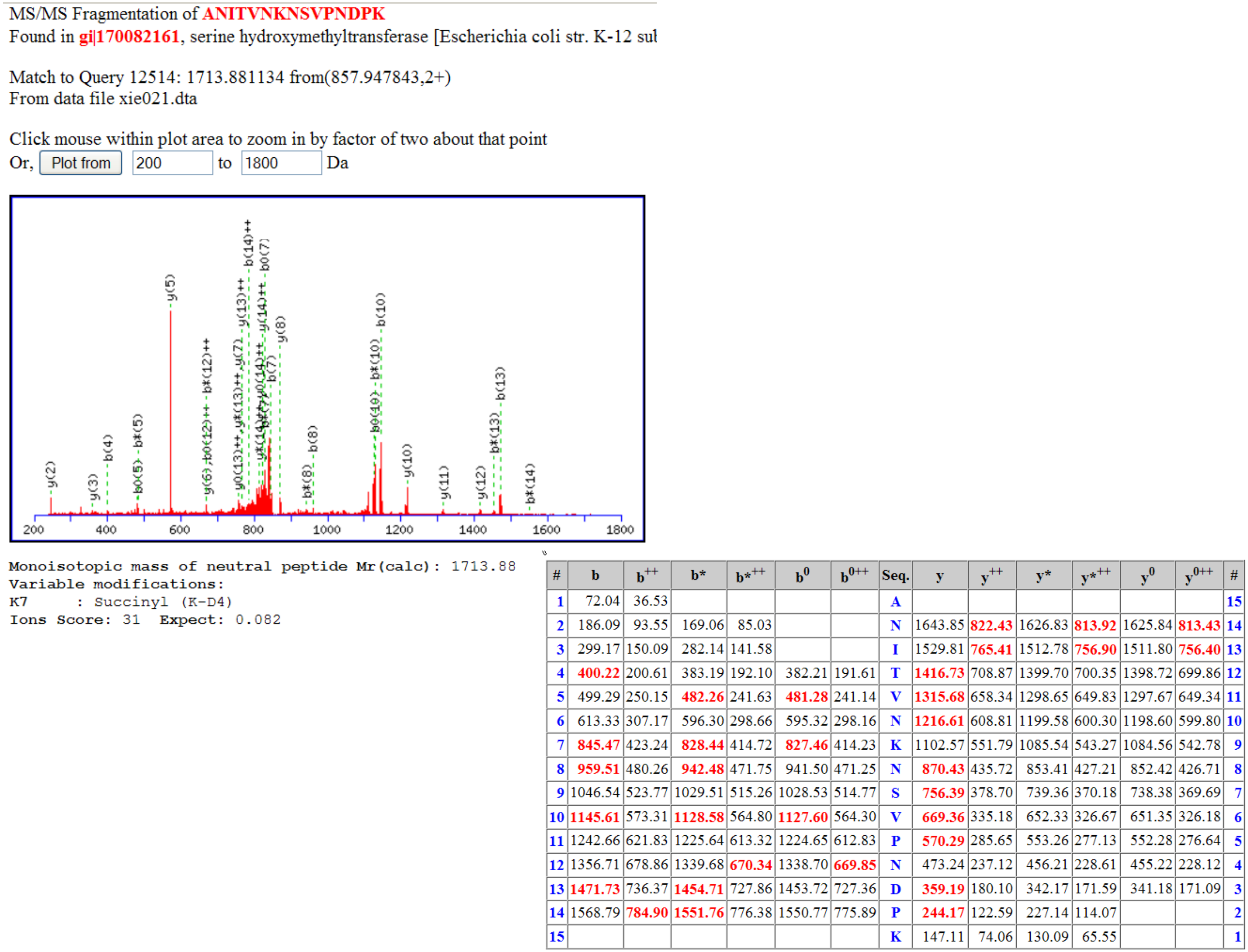


```
Monoisotopic mass of neutral peptide Mr(calc): 1709.86
Variable modifications:
K7      : Succinyl (K)
Ions Score: 39  Expect: 0.015
```



#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.04	36.53					A							15
2	186.09	93.55	169.06	85.03			N	1639.83	**820.42**	1622.80	**811.90**	1621.82	**811.41**	14
3	299.17	150.09	282.14	141.58			I	1525.79	763.40	1508.76	754.88	1507.78	754.39	13
4	**400.22**	200.61	383.19	192.10	382.21	191.61	T	**1412.70**	706.85	1395.68	698.34	1394.69	697.85	12
5	**499.29**	250.15	482.26	241.63	**481.28**	241.14	V	1311.65	656.33	1294.63	647.82	1293.64	647.33	11
6	613.33	307.17	596.30	298.66	595.32	298.16	N	**1212.59**	606.80	1195.56	598.28	1194.57	597.79	10
7	**841.44**	421.22	**824.41**	412.71	**823.43**	412.22	K	**1098.54**	549.77	1081.52	541.26	1080.53	540.77	9
8	**955.48**	478.25	938.46	469.73	937.47	469.24	N	**870.43**	435.72	853.41	427.21	852.42	426.71	8
9	1042.52	521.76	1025.49	513.25	1024.51	512.76	S	**756.39**	378.70	739.36	370.18	738.38	369.69	7
10	**1141.58**	**571.30**	**1124.56**	562.78	**1123.57**	562.29	V	**669.36**	335.18	652.33	326.67	651.35	326.18	6
11	1238.64	619.82	1221.61	611.31	1220.63	610.82	P	**570.29**	285.65	**553.26**	277.13	552.28	276.64	5
12	1352.68	676.84	1335.65	668.33	1334.67	667.84	N	473.24	237.12	456.21	228.61	455.22	228.12	4
13	**1467.71**	734.36	1450.68	725.84	1449.70	725.35	D	**359.19**	180.10	342.17	171.59	341.18	171.09	3
14	1564.76	782.88	**1547.73**	774.37	1546.75	773.88	P	**244.17**	122.59	227.14	114.07			2
15							K	147.11	74.06	130.09	65.55			1

serine hydroxymethyltransferase K346 ANITVN$^{Succ-D4}$KNSVPNDPK



MS/MS Fragmentation of **ANITVNKNSVPNDPK**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 sul

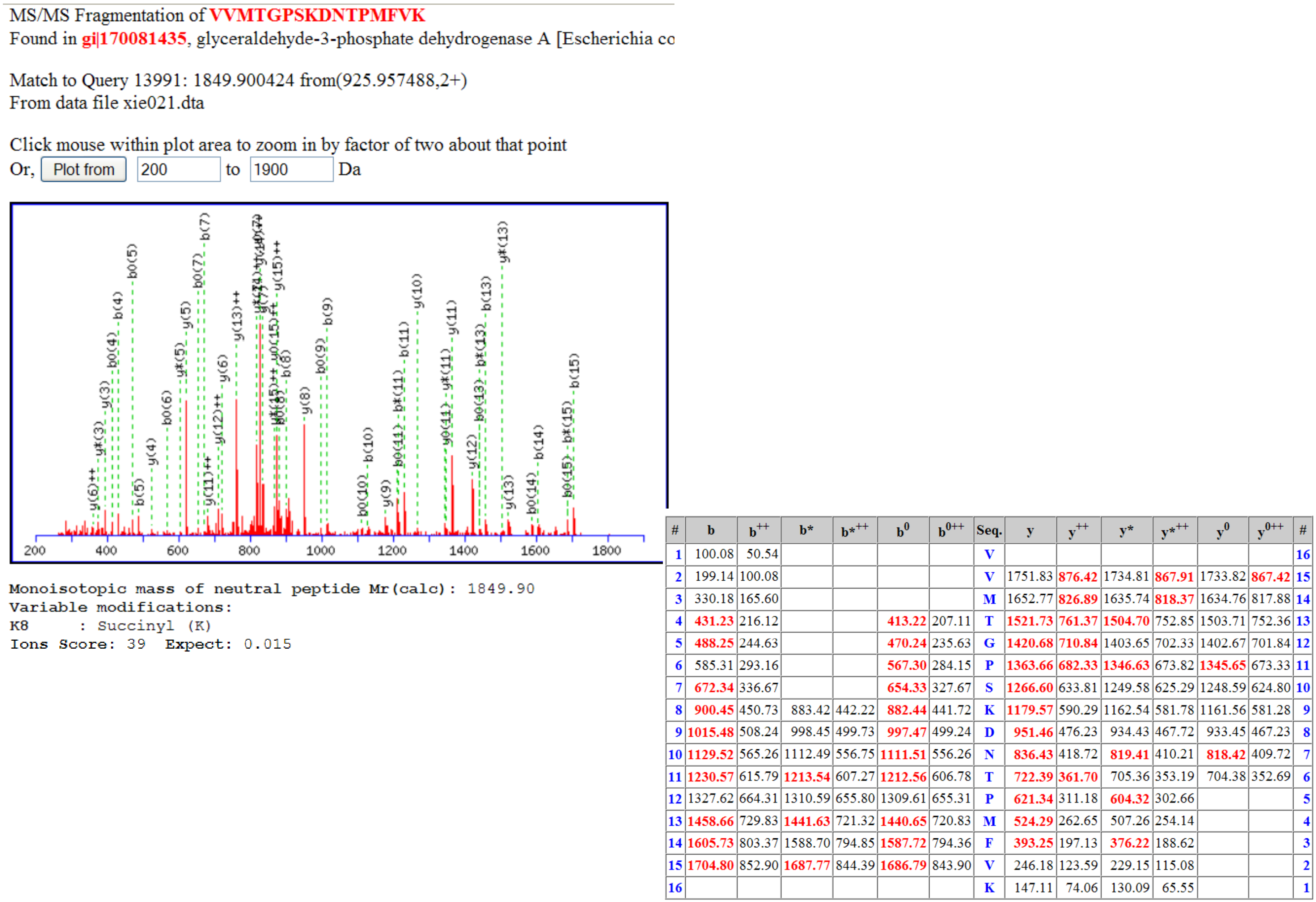
Match to Query 12514: 1713.881134 from(857.947843,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1713.88
Variable modifications:
K7      : Succinyl (K-D4)
Ions Score: 31  Expect: 0.082
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.04	36.53					A							15
2	186.09	93.55	169.06	85.03			N	1643.85	**822.43**	1626.83	**813.92**	1625.84	**813.43**	14
3	299.17	150.09	282.14	141.58			I	1529.81	**765.41**	1512.78	**756.90**	1511.80	**756.40**	13
4	**400.22**	200.61	383.19	192.10	382.21	191.61	T	**1416.73**	708.87	1399.70	700.35	1398.72	699.86	12
5	499.29	250.15	**482.26**	241.63	**481.28**	241.14	V	**1315.68**	658.34	1298.65	649.83	1297.67	649.34	11
6	613.33	307.17	596.30	298.66	595.32	298.16	N	**1216.61**	608.81	1199.58	600.30	1198.60	599.80	10
7	**845.47**	423.24	**828.44**	414.72	**827.46**	414.23	K	1102.57	551.79	1085.54	543.27	1084.56	542.78	9
8	**959.51**	480.26	**942.48**	471.75	941.50	471.25	N	**870.43**	435.72	853.41	427.21	852.42	426.71	8
9	1046.54	523.77	1029.51	515.26	1028.53	514.77	S	**756.39**	378.70	739.36	370.18	738.38	369.69	7
10	**1145.61**	573.31	**1128.58**	564.80	**1127.60**	564.30	V	**669.36**	335.18	652.33	326.67	651.35	326.18	6
11	1242.66	621.83	1225.64	613.32	1224.65	612.83	P	**570.29**	285.65	553.26	277.13	552.28	276.64	5
12	1356.71	678.86	1339.68	**670.34**	1338.70	**669.85**	N	473.24	237.12	456.21	228.61	455.22	228.12	4
13	**1471.73**	736.37	**1454.71**	727.86	1453.72	727.36	D	**359.19**	180.10	342.17	171.59	341.18	171.09	3
14	1568.79	**784.90**	**1551.76**	776.38	1550.77	775.89	P	**244.17**	122.59	227.14	114.07			2
15							K	147.11	74.06	130.09	65.55			1

glyceraldehyde-3-phosphate dehydrogenase A K124 VVMTGPS^{Succ}KDNTPMFVK



MS/MS Fragmentation of **VVMTGPSKDNTPMFVK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia co

Match to Query 13991: 1849.900424 from(925.957488,2+)
From data file xie021.dta

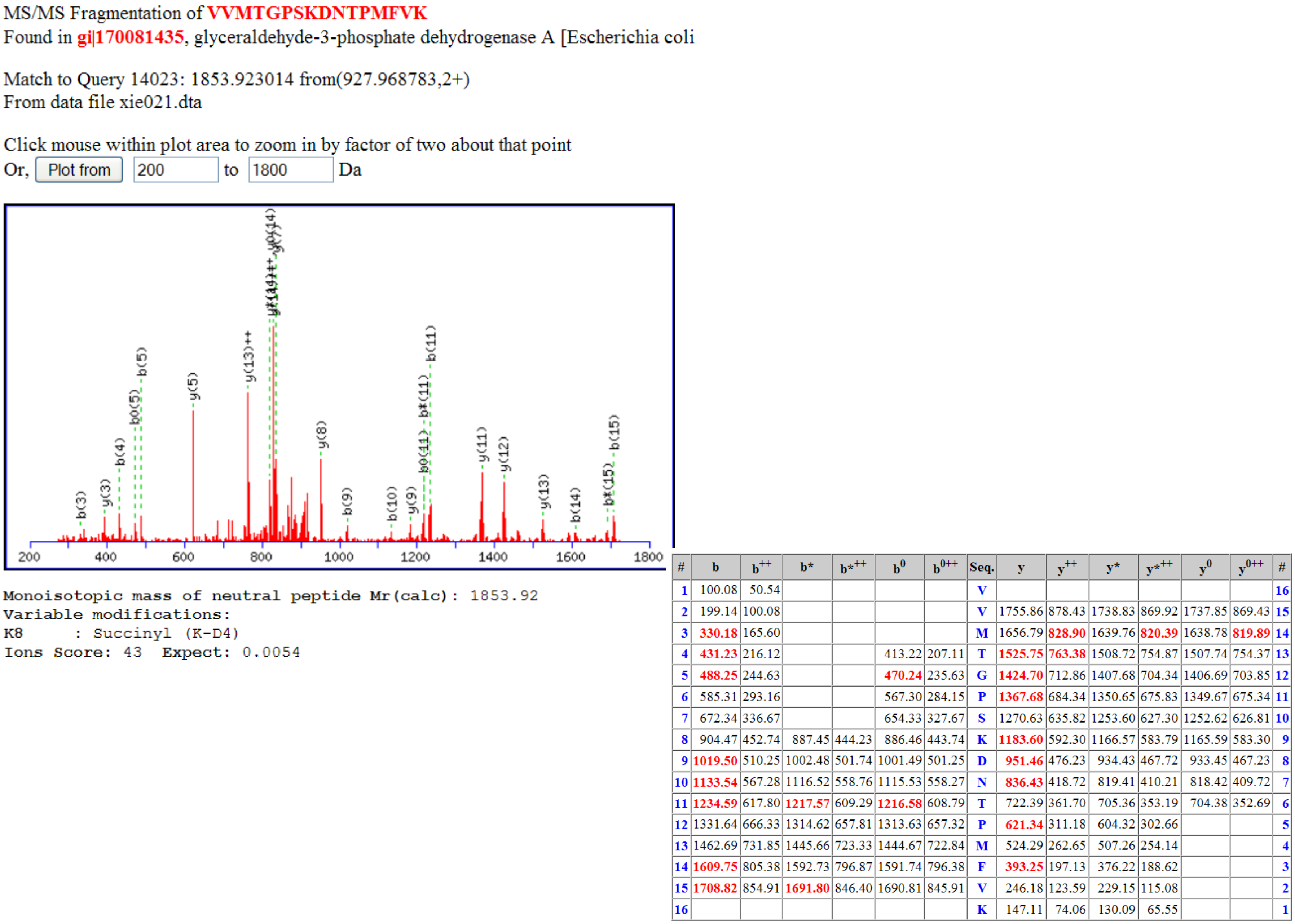
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1849.90
Variable modifications:
K8      : Succinyl (K)
Ions Score: 39   Expect: 0.015
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.08	50.54					V							16
2	199.14	100.08					V	1751.83	**876.42**	1734.81	**867.91**	1733.82	**867.42**	15
3	330.18	165.60					M	1652.77	**826.89**	1635.74	**818.37**	1634.76	817.88	14
4	**431.23**	216.12			**413.22**	207.11	T	**1521.73**	**761.37**	**1504.70**	752.85	1503.71	752.36	13
5	**488.25**	244.63			**470.24**	235.63	G	**1420.68**	**710.84**	1403.65	702.33	1402.67	701.84	12
6	585.31	293.16			**567.30**	284.15	P	**1363.66**	**682.33**	**1346.63**	673.82	**1345.65**	673.33	11
7	**672.34**	336.67			**654.33**	327.67	S	**1266.60**	633.81	1249.58	625.29	1248.59	624.80	10
8	**900.45**	450.73	883.42	442.22	**882.44**	441.72	K	**1179.57**	590.29	1162.54	581.78	1161.56	581.28	9
9	**1015.48**	508.24	998.45	499.73	**997.47**	499.24	D	**951.46**	476.23	934.43	467.72	933.45	467.23	8
10	**1129.52**	565.26	1112.49	556.75	**1111.51**	556.26	N	**836.43**	418.72	**819.41**	410.21	**818.42**	409.72	7
11	**1230.57**	615.79	**1213.54**	607.27	**1212.56**	606.78	T	**722.39**	**361.70**	705.36	353.19	704.38	352.69	6
12	1327.62	664.31	1310.59	655.80	1309.61	655.31	P	**621.34**	311.18	**604.32**	302.66			5
13	**1458.66**	729.83	**1441.63**	721.32	**1440.65**	720.83	M	**524.29**	262.65	507.26	254.14			4
14	**1605.73**	803.37	1588.70	794.85	**1587.72**	794.36	F	**393.25**	197.13	**376.22**	188.62			3
15	**1704.80**	852.90	**1687.77**	844.39	**1686.79**	843.90	V	246.18	123.59	229.15	115.08			2
16							K	147.11	74.06	130.09	65.55			1

Nature Chemical Biology: doi: 10.1038/nchembio.495

glyceraldehyde-3-phosphate dehydrogenase A K124 VVMTGPS$^{Succ\text{-}D4}$KDNTPMFVK



MS/MS Fragmentation of **VVMTGPSKDNTPMFVK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 14023: 1853.923014 from(927.968783,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1853.92
Variable modifications:
K8      : Succinyl (K-D4)
Ions Score: 43  Expect: 0.0054
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.08	50.54					V							16
2	199.14	100.08					V	1755.86	878.43	1738.83	869.92	1737.85	869.43	15
3	**330.18**	165.60					M	1656.79	**828.90**	1639.76	**820.39**	1638.78	**819.89**	14
4	**431.23**	216.12			413.22	207.11	T	**1525.75**	**763.38**	1508.72	754.87	1507.74	754.37	13
5	**488.25**	244.63			**470.24**	235.63	G	**1424.70**	712.86	1407.68	704.34	1406.69	703.85	12
6	585.31	293.16			567.30	284.15	P	**1367.68**	684.34	1350.65	675.83	1349.67	675.34	11
7	672.34	336.67			654.33	327.67	S	1270.63	635.82	1253.60	627.30	1252.62	626.81	10
8	904.47	452.74	887.45	444.23	886.46	443.74	K	**1183.60**	592.30	1166.57	583.79	1165.59	583.30	9
9	**1019.50**	510.25	1002.48	501.74	1001.49	501.25	D	**951.46**	476.23	934.43	467.72	933.45	467.23	8
10	**1133.54**	567.28	1116.52	558.76	1115.53	558.27	N	**836.43**	418.72	819.41	410.21	818.42	409.72	7
11	**1234.59**	617.80	**1217.57**	609.29	**1216.58**	608.79	T	722.39	361.70	705.36	353.19	704.38	352.69	6
12	1331.64	666.33	1314.62	657.81	1313.63	657.32	P	**621.34**	311.18	604.32	302.66			5
13	1462.69	731.85	1445.66	723.33	1444.67	722.84	M	524.29	262.65	507.26	254.14			4
14	**1609.75**	805.38	1592.73	796.87	1591.74	796.38	F	**393.25**	197.13	376.22	188.62			3
15	**1708.82**	854.91	**1691.80**	846.40	1690.81	845.91	V	246.18	123.59	229.15	115.08			2
16							K	147.11	74.06	130.09	65.55			1

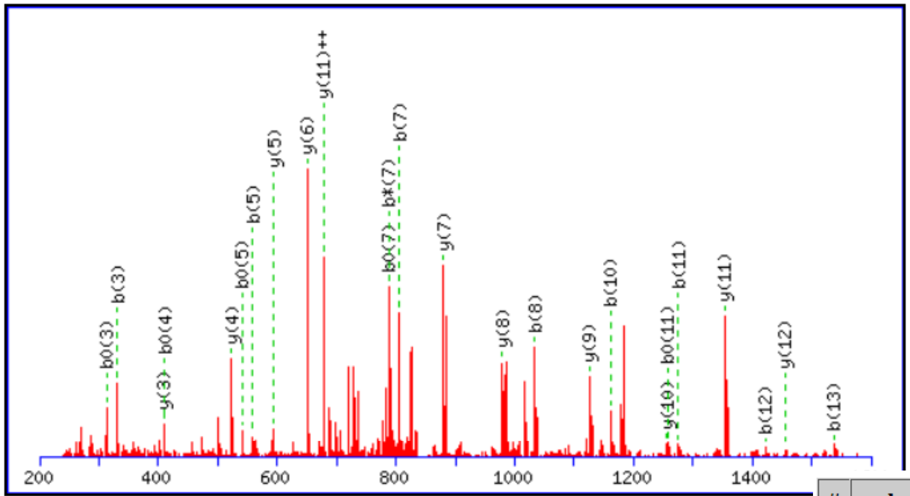
glyceraldehyde-3-phosphate dehydrogenase A K132

DNTPMFV^{Succ}KGANFDK

MS/MS Fragmentation of **DNTPMFVKGANFDK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia cc

Match to Query 12140: 1682.763224 from(842.388888,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da

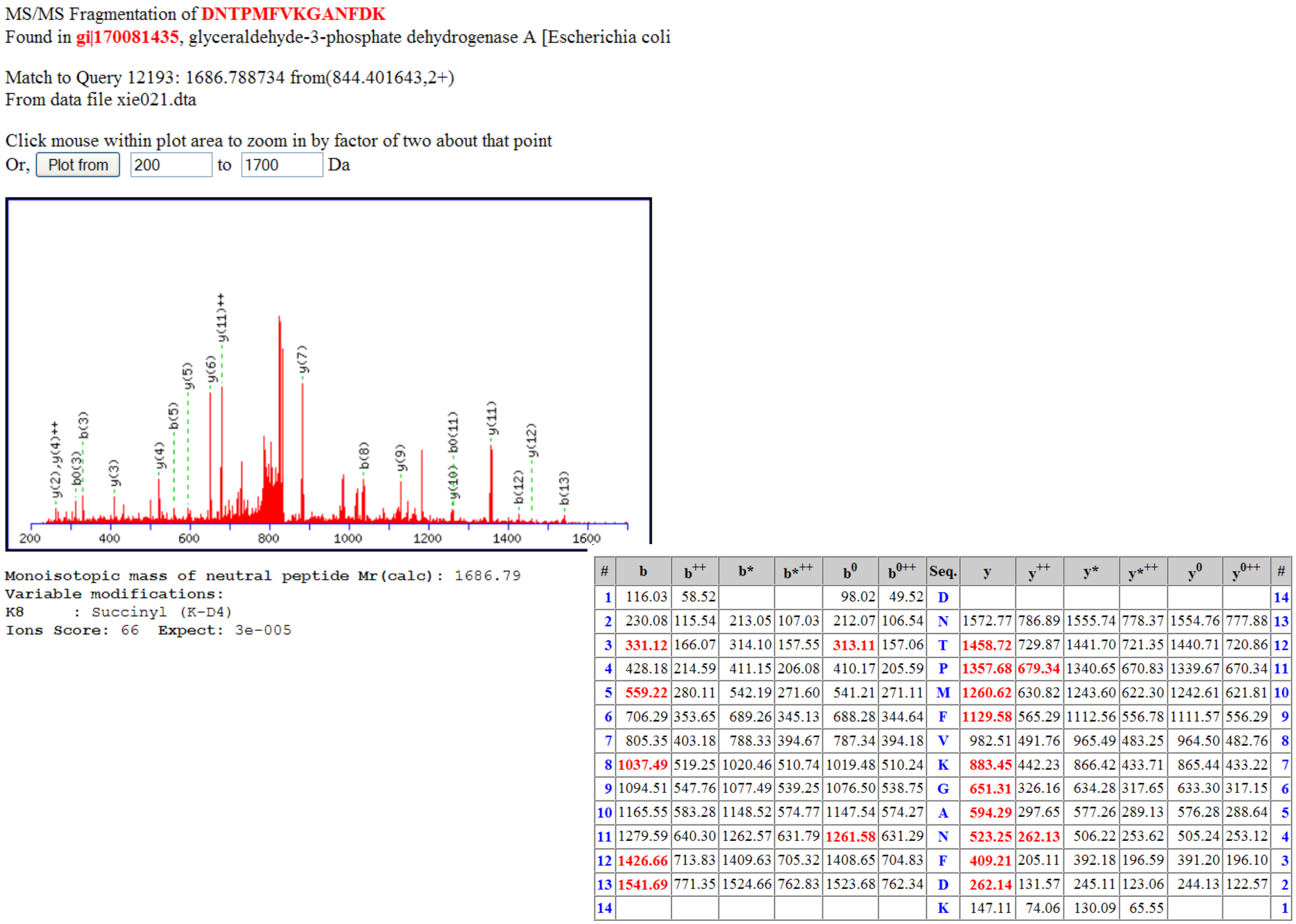


```
Monoisotopic mass of neutral peptide Mr(calc): 1682.76
Variable modifications:
K8     : Succinyl (K)
Ions Score: 57  Expect: 0.00021
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	116.03	58.52			98.02	49.52	D							14
2	230.08	115.54	213.05	107.03	212.07	106.54	N	1568.74	784.87	1551.71	776.36	1550.73	775.87	13
3	331.12	166.07	314.10	157.55	313.11	157.06	T	1454.70	727.85	1437.67	719.34	1436.69	718.85	12
4	428.18	214.59	411.15	206.08	410.17	205.59	P	1353.65	677.33	1336.62	668.82	1335.64	668.32	11
5	559.22	280.11	542.19	271.60	541.21	271.11	M	1256.60	628.80	1239.57	620.29	1238.59	619.80	10
6	706.29	353.65	689.26	345.13	688.28	344.64	F	1125.56	563.28	1108.53	554.77	1107.55	554.28	9
7	805.35	403.18	788.33	394.67	787.34	394.18	V	978.49	489.75	961.46	481.23	960.48	480.74	8
8	1033.47	517.24	1016.44	508.72	1015.46	508.23	K	879.42	440.21	862.39	431.70	861.41	431.21	7
9	1090.49	545.75	1073.46	537.23	1072.48	536.74	G	651.31	326.16	634.28	317.65	633.30	317.15	6
10	1161.52	581.27	1144.50	572.75	1143.51	572.26	A	594.29	297.65	577.26	289.13	576.28	288.64	5
11	1275.57	638.29	1258.54	629.77	1257.56	629.28	N	523.25	262.13	506.22	253.62	505.24	253.12	4
12	1422.64	711.82	1405.61	703.31	1404.63	702.82	F	409.21	205.11	392.18	196.59	391.20	196.10	3
13	1537.66	769.34	1520.64	760.82	1519.65	760.33	D	262.14	131.57	245.11	123.06	244.13	122.57	2
14							K	147.11	74.06	130.09	65.55			1

Nature Chemical Biology: doi: 10.1038/nchembio.495

glyceraldehyde-3-phosphate dehydrogenase A K132 DNTPMFV$^{\text{Succ-D4}}$KGANFDK



MS/MS Fragmentation of **DNTPMFVKGANFDK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 12193: 1686.788734 from(844.401643,2+)
From data file xie021.dta

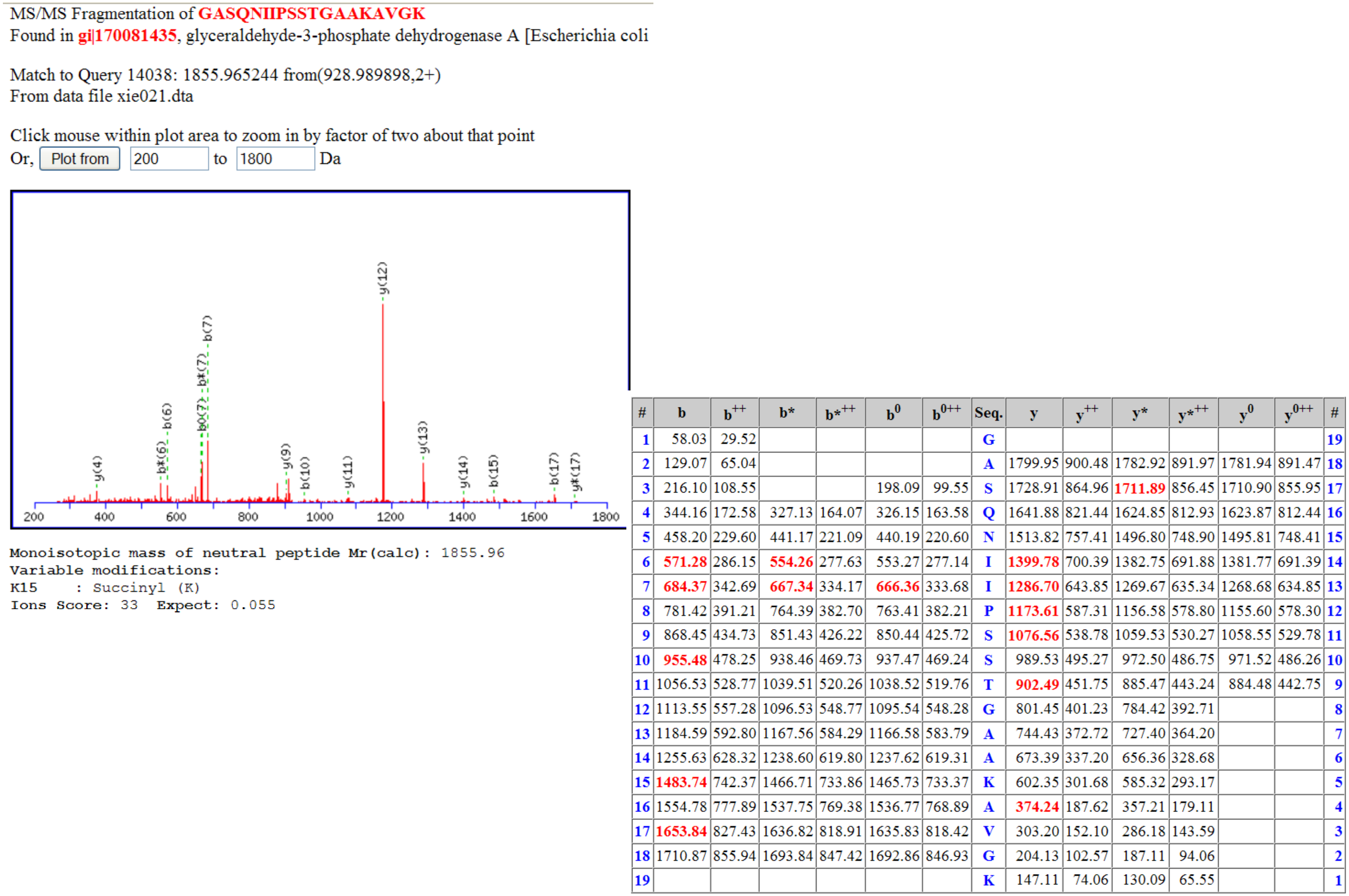
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da

Monoisotopic mass of neutral peptide Mr(calc): 1686.79
Variable modifications:
K8 : Succinyl (K-D4)
Ions Score: 66 Expect: 3e-005

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.03	58.52			98.02	49.52	D							14
2	230.08	115.54	213.05	107.03	212.07	106.54	N	1572.77	786.89	1555.74	778.37	1554.76	777.88	13
3	**331.12**	166.07	314.10	157.55	**313.11**	157.06	T	**1458.72**	729.87	1441.70	721.35	1440.71	720.86	12
4	428.18	214.59	411.15	206.08	410.17	205.59	P	**1357.68**	**679.34**	1340.65	670.83	1339.67	670.34	11
5	**559.22**	280.11	542.19	271.60	541.21	271.11	M	**1260.62**	630.82	1243.60	622.30	1242.61	621.81	10
6	706.29	353.65	689.26	345.13	688.28	344.64	F	**1129.58**	565.29	1112.56	556.78	1111.57	556.29	9
7	805.35	403.18	788.33	394.67	787.34	394.18	V	982.51	491.76	965.49	483.25	964.50	482.76	8
8	**1037.49**	519.25	1020.46	510.74	1019.48	510.24	K	**883.45**	442.23	866.42	433.71	865.44	433.22	7
9	1094.51	547.76	1077.49	539.25	1076.50	538.75	G	**651.31**	326.16	634.28	317.65	633.30	317.15	6
10	1165.55	583.28	1148.52	574.77	1147.54	574.27	A	**594.29**	297.65	577.26	289.13	576.28	288.64	5
11	1279.59	640.30	1262.57	631.79	**1261.58**	631.29	N	**523.25**	**262.13**	506.22	253.62	505.24	253.12	4
12	**1426.66**	713.83	1409.63	705.32	1408.65	704.83	F	**409.21**	205.11	392.18	196.59	391.20	196.10	3
13	**1541.69**	771.35	1524.66	762.83	1523.68	762.34	D	**262.14**	131.57	245.11	123.06	244.13	122.57	2
14							K	147.11	74.06	130.09	65.55			1

Nature Chemical Biology: doi: 10.1038/nchembio.495

glyceraldehyde-3-phosphate dehydrogenase A K213 GASQNIIPSSTGAA^{Succ}KAVGK



MS/MS Fragmentation of **GASQNIIPSSTGAAKAVGK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 14038: 1855.965244 from(928.989898,2+)
From data file xie021.dta

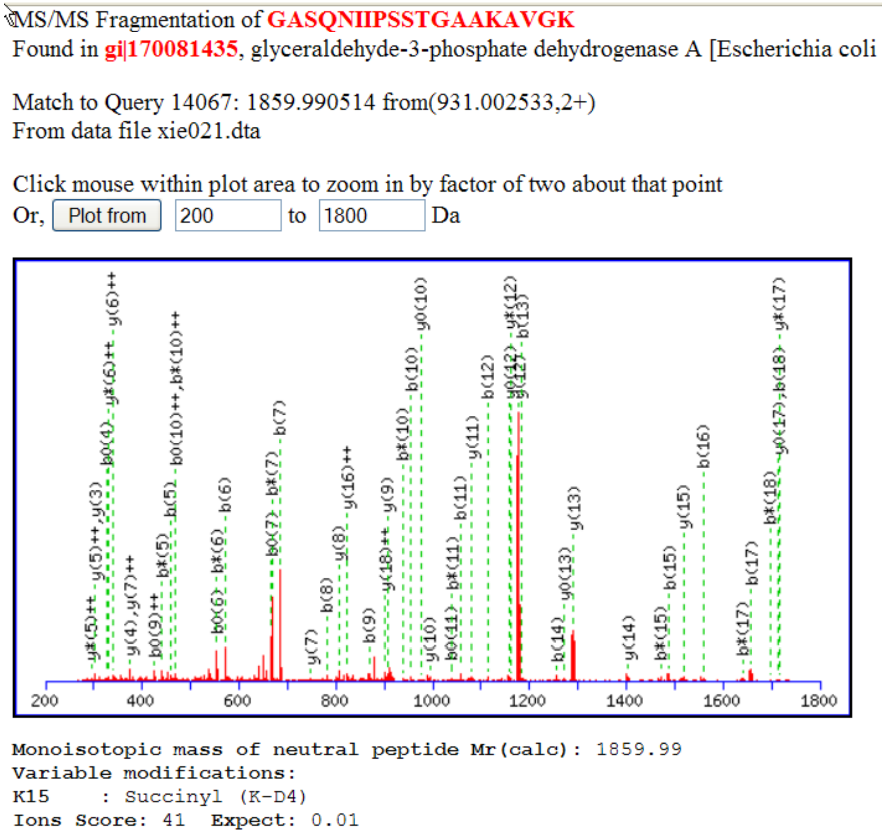
Click mouse within plot area to zoom in by factor of two about that point

```
Monoisotopic mass of neutral peptide Mr(calc): 1855.96
Variable modifications:
K15     : Succinyl (K)
Ions Score: 33  Expect: 0.055
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.03	29.52					G							19
2	129.07	65.04					A	1799.95	900.48	1782.92	891.97	1781.94	891.47	18
3	216.10	108.55			198.09	99.55	S	1728.91	864.96	**1711.89**	856.45	1710.90	855.95	17
4	344.16	172.58	327.13	164.07	326.15	163.58	Q	1641.88	821.44	1624.85	812.93	1623.87	812.44	16
5	458.20	229.60	441.17	221.09	440.19	220.60	N	1513.82	757.41	1496.80	748.90	1495.81	748.41	15
6	**571.28**	286.15	**554.26**	277.63	553.27	277.14	I	**1399.78**	700.39	1382.75	691.88	1381.77	691.39	14
7	**684.37**	342.69	**667.34**	334.17	**666.36**	333.68	I	**1286.70**	643.85	1269.67	635.34	1268.68	634.85	13
8	781.42	391.21	764.39	382.70	763.41	382.21	P	**1173.61**	587.31	1156.58	578.80	1155.60	578.30	12
9	868.45	434.73	851.43	426.22	850.44	425.72	S	**1076.56**	538.78	1059.53	530.27	1058.55	529.78	11
10	**955.48**	478.25	938.46	469.73	937.47	469.24	S	989.53	495.27	972.50	486.75	971.52	486.26	10
11	1056.53	528.77	1039.51	520.26	1038.52	519.76	T	**902.49**	451.75	885.47	443.24	884.48	442.75	9
12	1113.55	557.28	1096.53	548.77	1095.54	548.28	G	801.45	401.23	784.42	392.71			8
13	1184.59	592.80	1167.56	584.29	1166.58	583.79	A	744.43	372.72	727.40	364.20			7
14	1255.63	628.32	1238.60	619.80	1237.62	619.31	A	673.39	337.20	656.36	328.68			6
15	**1483.74**	742.37	1466.71	733.86	1465.73	733.37	K	602.35	301.68	585.32	293.17			5
16	1554.78	777.89	1537.75	769.38	1536.77	768.89	A	**374.24**	187.62	357.21	179.11			4
17	**1653.84**	827.43	1636.82	818.91	1635.83	818.42	V	303.20	152.10	286.18	143.59			3
18	1710.87	855.94	1693.84	847.42	1692.86	846.93	G	204.13	102.57	187.11	94.06			2
19							K	147.11	74.06	130.09	65.55			1

Nature Chemical Biology: doi: 10.1038/nchembio.495

glyceraldehyde-3-phosphate dehydrogenase AK213 GASQNIIPSSTGAA$^{\text{Succ-D4}}$KAVGK

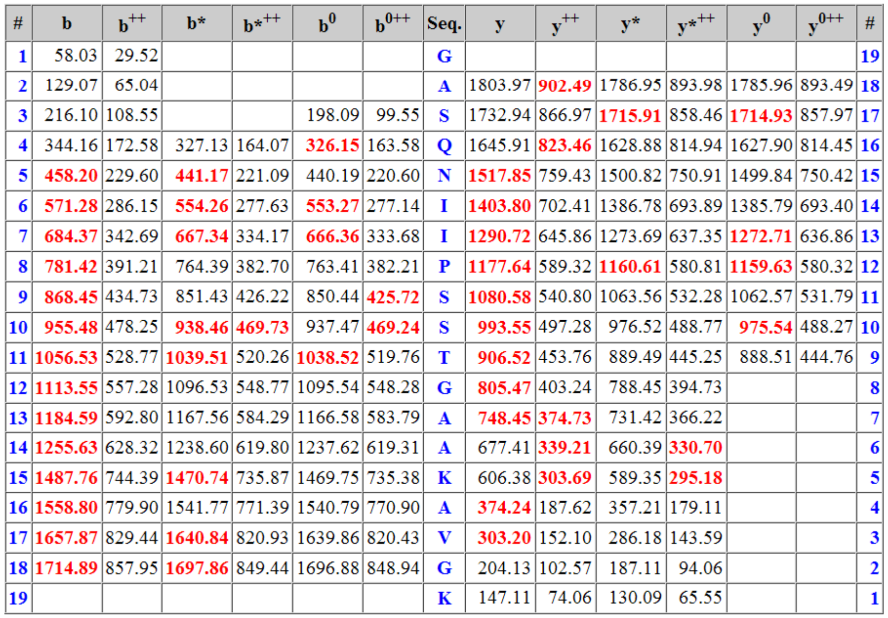


MS/MS Fragmentation of **GASQNIIPSSTGAAKAVGK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 14067: 1859.990514 from(931.002533,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1859.99
Variable modifications:
K15     : Succinyl (K-D4)
Ions Score: 41   Expect: 0.01
```

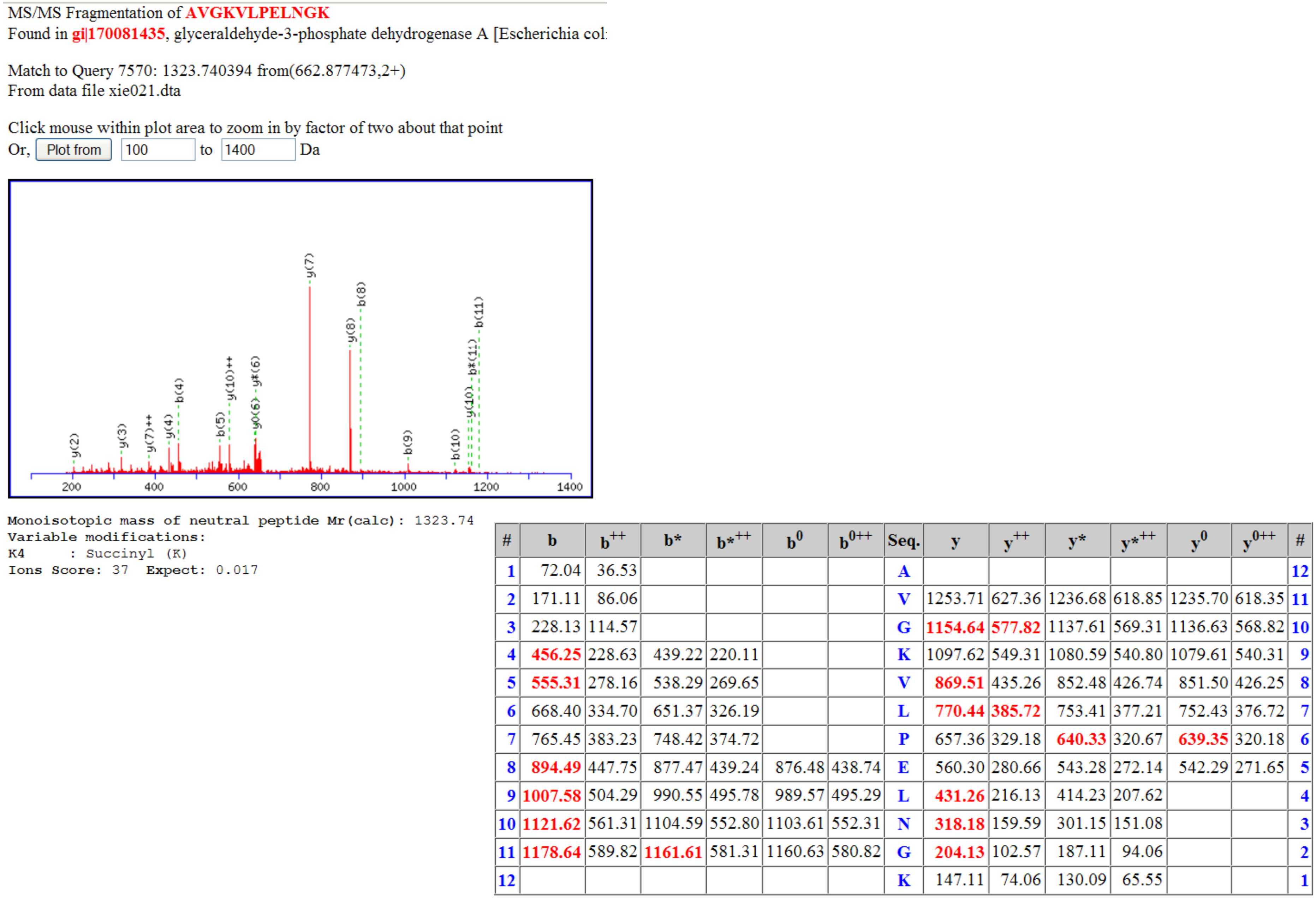


#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.03	29.52					G							19
2	129.07	65.04					A	1803.97	**902.49**	1786.95	893.98	1785.96	893.49	18
3	216.10	108.55			198.09	99.55	S	1732.94	866.97	**1715.91**	858.46	**1714.93**	857.97	17
4	344.16	172.58	327.13	164.07	**326.15**	163.58	Q	1645.91	**823.46**	1628.88	814.94	1627.90	814.45	16
5	**458.20**	229.60	**441.17**	221.09	440.19	220.60	N	**1517.85**	759.43	1500.82	750.91	1499.84	750.42	15
6	**571.28**	286.15	**554.26**	277.63	**553.27**	277.14	I	**1403.80**	702.41	1386.78	693.89	1385.79	693.40	14
7	**684.37**	342.69	**667.34**	334.17	**666.36**	333.68	I	**1290.72**	645.86	1273.69	637.35	**1272.71**	636.86	13
8	**781.42**	391.21	764.39	382.70	763.41	382.21	P	**1177.64**	589.32	**1160.61**	580.81	**1159.63**	580.32	12
9	**868.45**	434.73	851.43	426.22	850.44	**425.72**	S	**1080.58**	540.80	1063.56	532.28	1062.57	531.79	11
10	**955.48**	478.25	**938.46**	**469.73**	937.47	**469.24**	S	**993.55**	497.28	976.52	488.77	**975.54**	488.27	10
11	**1056.53**	528.77	**1039.51**	520.26	**1038.52**	519.76	T	**906.52**	453.76	889.49	445.25	888.51	444.76	9
12	**1113.55**	557.28	1096.53	548.77	1095.54	548.28	G	**805.47**	403.24	788.45	394.73			8
13	**1184.59**	592.80	1167.56	584.29	1166.58	583.79	A	**748.45**	**374.73**	731.42	366.22			7
14	**1255.63**	628.32	1238.60	619.80	1237.62	619.31	A	677.41	**339.21**	660.39	**330.70**			6
15	**1487.76**	744.39	**1470.74**	735.87	1469.75	735.38	K	606.38	**303.69**	589.35	**295.18**			5
16	**1558.80**	779.90	1541.77	771.39	1540.79	770.90	A	**374.24**	187.62	357.21	179.11			4
17	**1657.87**	829.44	**1640.84**	820.93	1639.86	820.43	V	**303.20**	152.10	286.18	143.59			3
18	**1714.89**	857.95	**1697.86**	849.44	1696.88	848.94	G	204.13	102.57	187.11	94.06			2
19							K	147.11	74.06	130.09	65.55			1

Nature Chemical Biology: doi: 10.1038/nchembio.495

glyceraldehyde-3-phosphate dehydrogenase A K217

AVG$^{\mathrm{Succ}}$KVLPELNGK



MS/MS Fragmentation of **AVGKVLPELNGK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia col

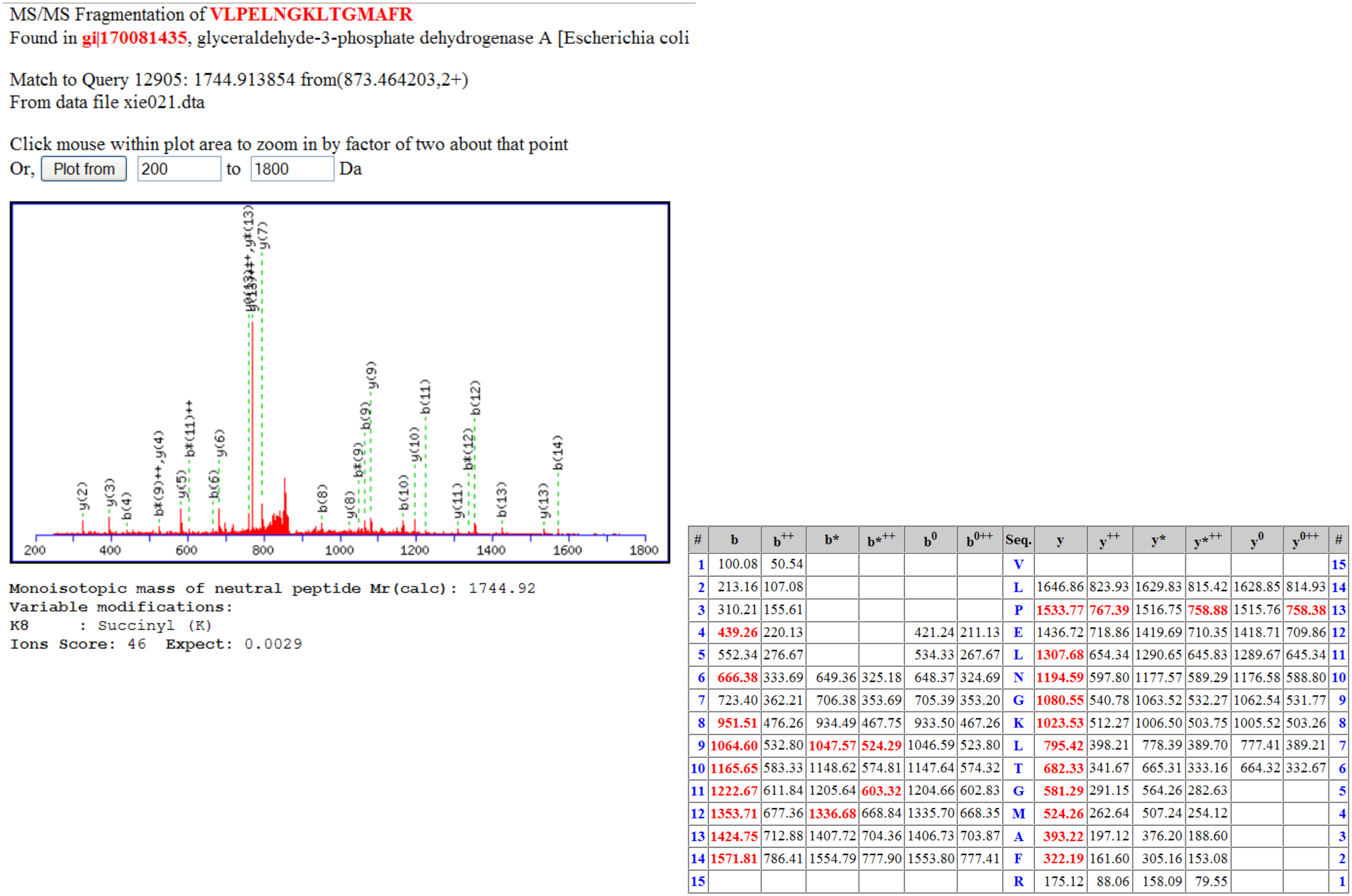
Match to Query 7570: 1323.740394 from(662.877473,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1323.74
Variable modifications:
K4      : Succinyl (K)
Ions Score: 37  Expect: 0.017
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.04	36.53					A							12
2	171.11	86.06					V	1253.71	627.36	1236.68	618.85	1235.70	618.35	11
3	228.13	114.57					G	**1154.64**	**577.82**	1137.61	569.31	1136.63	568.82	10
4	**456.25**	228.63	439.22	220.11			K	1097.62	549.31	1080.59	540.80	1079.61	540.31	9
5	**555.31**	278.16	538.29	269.65			V	**869.51**	435.26	852.48	426.74	851.50	426.25	8
6	668.40	334.70	651.37	326.19			L	**770.44**	**385.72**	753.41	377.21	752.43	376.72	7
7	765.45	383.23	748.42	374.72			P	657.36	329.18	**640.33**	320.67	**639.35**	320.18	6
8	**894.49**	447.75	877.47	439.24	876.48	438.74	E	560.30	280.66	543.28	272.14	542.29	271.65	5
9	**1007.58**	504.29	990.55	495.78	989.57	495.29	L	**431.26**	216.13	414.23	207.62			4
10	**1121.62**	561.31	1104.59	552.80	1103.61	552.31	N	**318.18**	159.59	301.15	151.08			3
11	**1178.64**	589.82	**1161.61**	581.31	1160.63	580.82	G	**204.13**	102.57	187.11	94.06			2
12							K	147.11	74.06	130.09	65.55			1

glyceraldehyde-3-phosphate dehydrogenase A K225 VLPELNG^{Succ}KLTGMAFR



MS/MS Fragmentation of **VLPELNGKLTGMAFR**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 12905: 1744.913854 from(873.464203,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1744.92
Variable modifications:
K8      : Succinyl (K)
Ions Score: 46  Expect: 0.0029
```

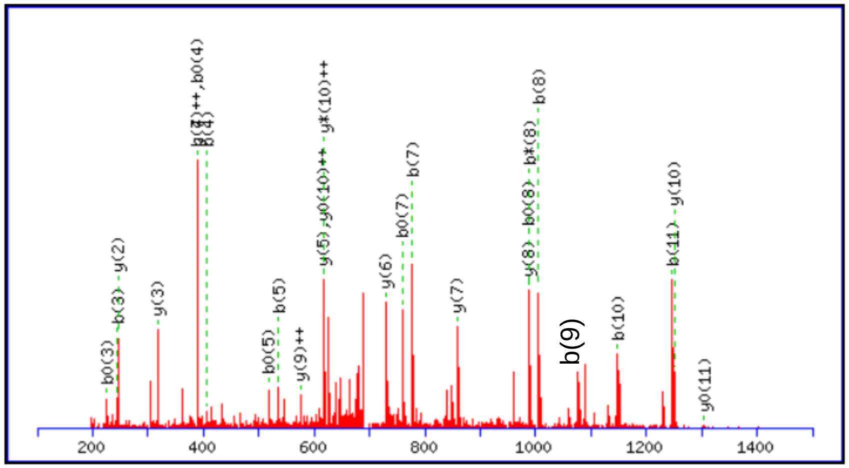
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.08	50.54					V							15
2	213.16	107.08					L	1646.86	823.93	1629.83	815.42	1628.85	814.93	14
3	310.21	155.61					P	**1533.77**	**767.39**	1516.75	**758.88**	1515.76	**758.38**	13
4	**439.26**	220.13			421.24	211.13	E	1436.72	718.86	1419.69	710.35	1418.71	709.86	12
5	552.34	276.67			534.33	267.67	L	**1307.68**	654.34	1290.65	645.83	1289.67	645.34	11
6	**666.38**	333.69	649.36	325.18	648.37	324.69	N	**1194.59**	597.80	1177.57	589.29	1176.58	588.80	10
7	723.40	362.21	706.38	353.69	705.39	353.20	G	**1080.55**	540.78	1063.52	532.27	1062.54	531.77	9
8	**951.51**	476.26	934.49	467.75	933.50	467.26	K	**1023.53**	512.27	1006.50	503.75	1005.52	503.26	8
9	**1064.60**	532.80	**1047.57**	**524.29**	1046.59	523.80	L	**795.42**	398.21	778.39	389.70	777.41	389.21	7
10	**1165.65**	583.33	1148.62	574.81	1147.64	574.32	T	**682.33**	341.67	665.31	333.16	664.32	332.67	6
11	**1222.67**	611.84	1205.64	**603.32**	1204.66	602.83	G	**581.29**	291.15	564.26	282.63			5
12	**1353.71**	677.36	**1336.68**	668.84	1335.70	668.35	M	**524.26**	262.64	507.24	254.12			4
13	**1424.75**	712.88	1407.72	704.36	1406.73	703.87	A	**393.22**	197.12	376.20	188.60			3
14	**1571.81**	786.41	1554.79	777.90	1553.80	777.41	F	**322.19**	161.60	305.16	153.08			2
15							R	175.12	88.06	158.09	79.55			1

glyceraldehyde-3-phosphate dehydrogenase A K257 AATYEQI$^{\text{Succ}}$KAAVK

MS/MS Fragmentation of **AATYEQIKAAVK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 8300: 1391.730744 from(696.872648,2+)
From data file xie021.dta

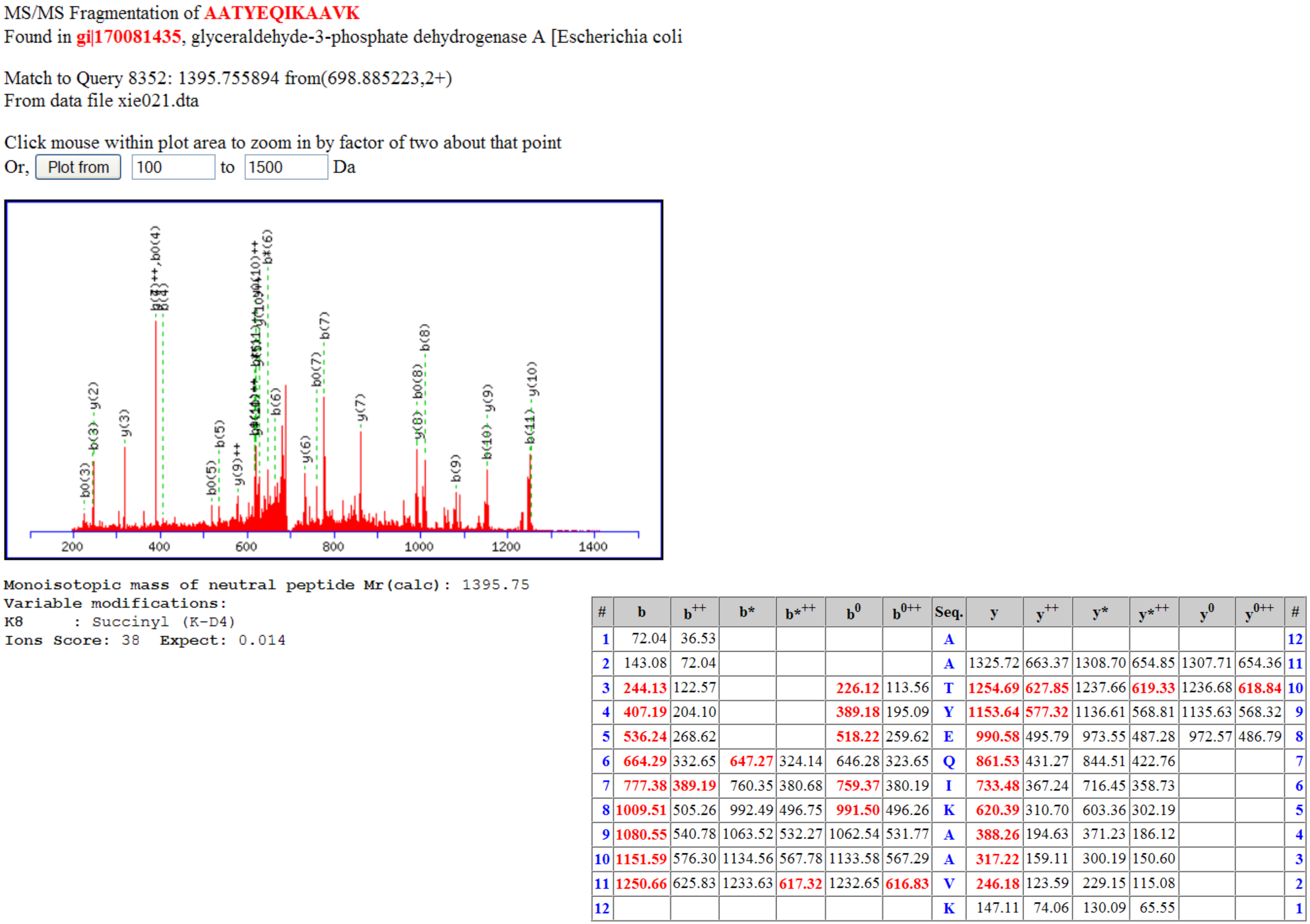
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1500 Da



```
Monoisotopic mass of neutral peptide Mr(calc): 1391.73
Variable modifications:
K8      : Succinyl (K)
Ions Score: 60  Expect: 9.8e-005
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.04	36.53					A							12
2	143.08	72.04					A	1321.70	661.35	1304.67	652.84	**1303.69**	652.35	11
3	**244.13**	122.57			**226.12**	113.56	T	**1250.66**	625.83	1233.64	**617.32**	1232.65	**616.83**	10
4	**407.19**	204.10			**389.18**	195.09	Y	1149.62	**575.31**	1132.59	566.80	1131.60	566.31	9
5	**536.24**	268.62			**518.22**	259.62	E	**986.55**	493.78	969.53	485.27	968.54	484.77	8
6	664.29	332.65	647.27	324.14	646.28	323.65	Q	**857.51**	429.26	840.48	420.74			7
7	**777.38**	**389.19**	760.35	380.68	**759.37**	380.19	I	**729.45**	365.23	712.42	356.72			6
8	**1005.49**	503.25	**988.46**	494.73	**987.48**	494.24	K	**616.37**	308.69	599.34	300.17			5
9	1076.53	538.77	1059.50	530.25	1058.52	529.76	A	**388.26**	194.63	371.23	186.12			4
10	**1147.56**	574.29	1130.54	565.77	1129.55	565.28	A	**317.22**	159.11	300.19	150.60			3
11	**1246.63**	623.82	1229.60	615.31	1228.62	614.81	V	**246.18**	123.59	229.15	115.08			2
12							K	147.11	74.06	130.09	65.55			1

glyceraldehyde-3-phosphate dehydrogenase A K257   AATYEQI$^{\text{Succ-D4}}$KAAVK



MS/MS Fragmentation of **AATYEQIKAAVK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 8352: 1395.755894 from(698.885223,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da

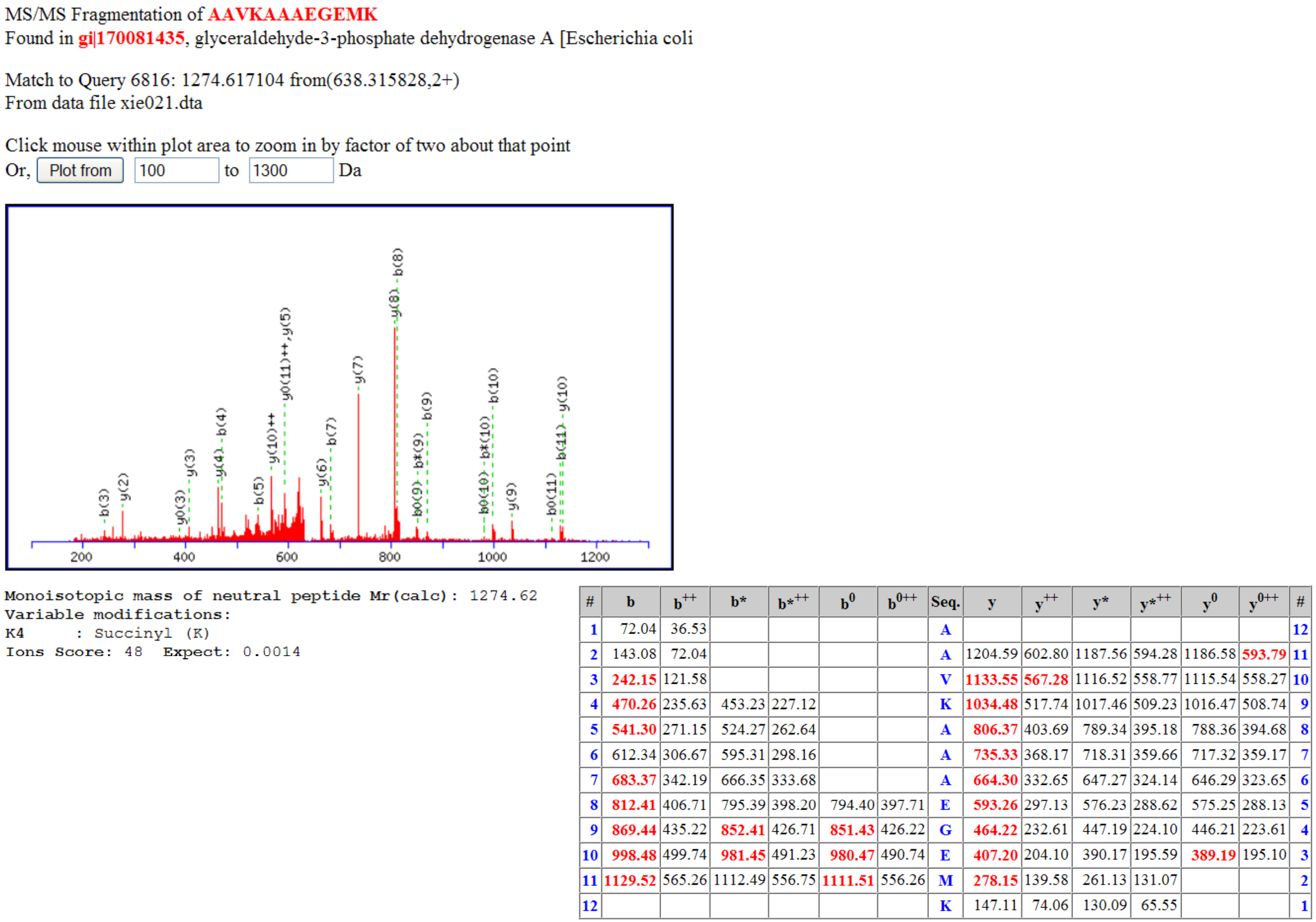
```
Monoisotopic mass of neutral peptide Mr(calc): 1395.75
Variable modifications:
K8      : Succinyl (K-D4)
Ions Score: 38  Expect: 0.014
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.04	36.53					A							12
2	143.08	72.04					A	1325.72	663.37	1308.70	654.85	1307.71	654.36	11
3	**244.13**	122.57			**226.12**	113.56	T	**1254.69**	**627.85**	1237.66	**619.33**	1236.68	**618.84**	10
4	**407.19**	204.10			**389.18**	195.09	Y	**1153.64**	**577.32**	1136.61	568.81	1135.63	568.32	9
5	**536.24**	268.62			**518.22**	259.62	E	**990.58**	495.79	973.55	487.28	972.57	486.79	8
6	**664.29**	332.65	**647.27**	324.14	646.28	323.65	Q	**861.53**	431.27	844.51	422.76			7
7	**777.38**	**389.19**	760.35	380.68	**759.37**	380.19	I	**733.48**	367.24	716.45	358.73			6
8	**1009.51**	505.26	992.49	496.75	**991.50**	496.26	K	**620.39**	310.70	603.36	302.19			5
9	**1080.55**	540.78	1063.52	532.27	1062.54	531.77	A	**388.26**	194.63	371.23	186.12			4
10	**1151.59**	576.30	1134.56	567.78	1133.58	567.29	A	**317.22**	159.11	300.19	150.60			3
11	**1250.66**	625.83	1233.63	**617.32**	1232.65	**616.83**	V	**246.18**	123.59	229.15	115.08			2
12							K	147.11	74.06	130.09	65.55			1

Nature Chemical Biology: doi: 10.1038/nchembio.495

glyceraldehyde-3-phosphate dehydrogenase A K261

AAV^{Succ}KAAAEGEMK



MS/MS Fragmentation of AAVKAAAEGEMK
Found in gi|170081435, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 6816: 1274.617104 from(638.315828,2+)
From data file xie021.dta

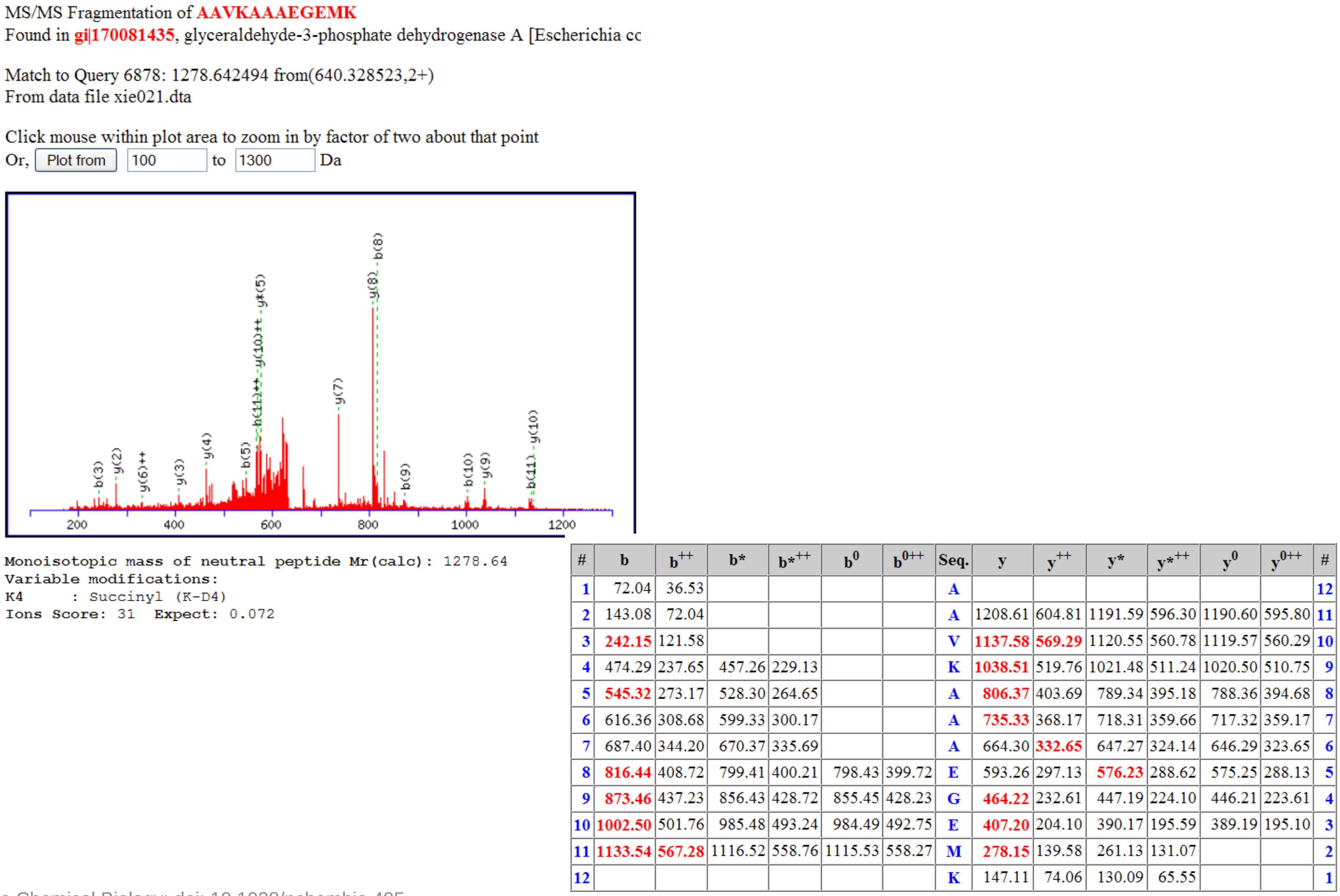
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1274.62
Variable modifications:
K4      : Succinyl (K)
Ions Score: 48   Expect: 0.0014
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.04	36.53					A							12
2	143.08	72.04					A	1204.59	602.80	1187.56	594.28	1186.58	593.79	11
3	242.15	121.58					V	1133.55	567.28	1116.52	558.77	1115.54	558.27	10
4	470.26	235.63	453.23	227.12			K	1034.48	517.74	1017.46	509.23	1016.47	508.74	9
5	541.30	271.15	524.27	262.64			A	806.37	403.69	789.34	395.18	788.36	394.68	8
6	612.34	306.67	595.31	298.16			A	735.33	368.17	718.31	359.66	717.32	359.17	7
7	683.37	342.19	666.35	333.68			A	664.30	332.65	647.27	324.14	646.29	323.65	6
8	812.41	406.71	795.39	398.20	794.40	397.71	E	593.26	297.13	576.23	288.62	575.25	288.13	5
9	869.44	435.22	852.41	426.71	851.43	426.22	G	464.22	232.61	447.19	224.10	446.21	223.61	4
10	998.48	499.74	981.45	491.23	980.47	490.74	E	407.20	204.10	390.17	195.59	389.19	195.10	3
11	1129.52	565.26	1112.49	556.75	1111.51	556.26	M	278.15	139.58	261.13	131.07			2
12							K	147.11	74.06	130.09	65.55			1

Nature Chemical Biology: doi: 10.1038/nchembio.495

glyceraldehyde-3-phosphate dehydrogenase A K261 AAV$^{Succ\text{-}D4}$KAAAEGEMK



MS/MS Fragmentation of **AAVKAAAEGEMK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia cc

Match to Query 6878: 1278.642494 from(640.328523,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1278.64
Variable modifications:
K4      : Succinyl (K-D4)
Ions Score: 31   Expect: 0.072
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.04	36.53					A							12
2	143.08	72.04					A	1208.61	604.81	1191.59	596.30	1190.60	595.80	11
3	242.15	121.58					V	1137.58	569.29	1120.55	560.78	1119.57	560.29	10
4	474.29	237.65	457.26	229.13			K	1038.51	519.76	1021.48	511.24	1020.50	510.75	9
5	545.32	273.17	528.30	264.65			A	806.37	403.69	789.34	395.18	788.36	394.68	8
6	616.36	308.68	599.33	300.17			A	735.33	368.17	718.31	359.66	717.32	359.17	7
7	687.40	344.20	670.37	335.69			A	664.30	332.65	647.27	324.14	646.29	323.65	6
8	816.44	408.72	799.41	400.21	798.43	399.72	E	593.26	297.13	576.23	288.62	575.25	288.13	5
9	873.46	437.23	856.43	428.72	855.45	428.23	G	464.22	232.61	447.19	224.10	446.21	223.61	4
10	1002.50	501.76	985.48	493.24	984.49	492.75	E	407.20	204.10	390.17	195.59	389.19	195.10	3
11	1133.54	567.28	1116.52	558.76	1115.53	558.27	M	278.15	139.58	261.13	131.07			2
12							K	147.11	74.06	130.09	65.55			1

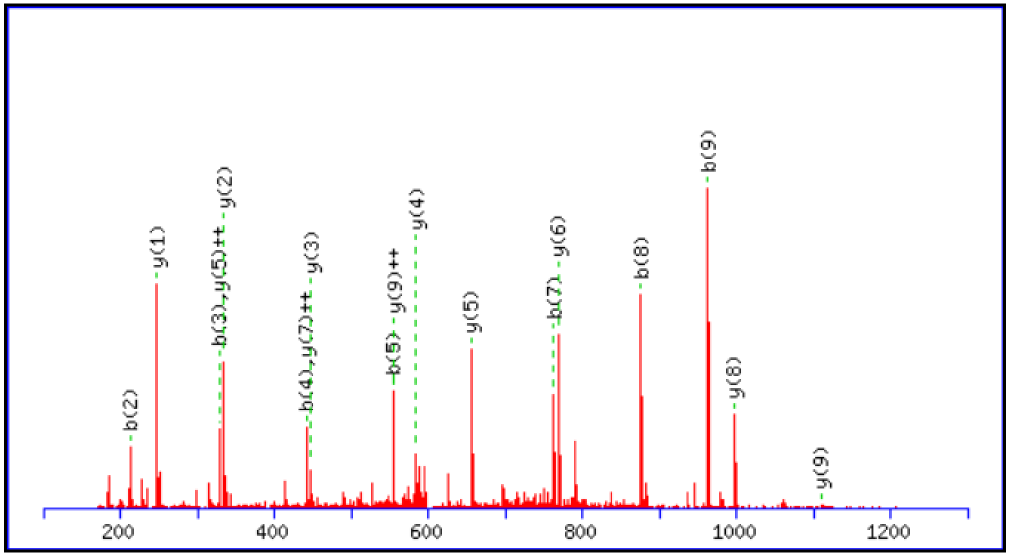
Nature Chemical Biology: doi: 10.1038/nchembio.495

glyceraldehyde-3-phosphate dehydrogenase A K331 VLDLIAHIS^{Succ}K

MS/MS Fragmentation of **VLDLIAHISK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 5564: 1207.683264 from(604.848908,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da



```
Monoisotopic mass of neutral peptide Mr(calc): 1207.68
Variable modifications:
K10     : Succinyl (K)
Ions Score: 53  Expect: 0.00047
```

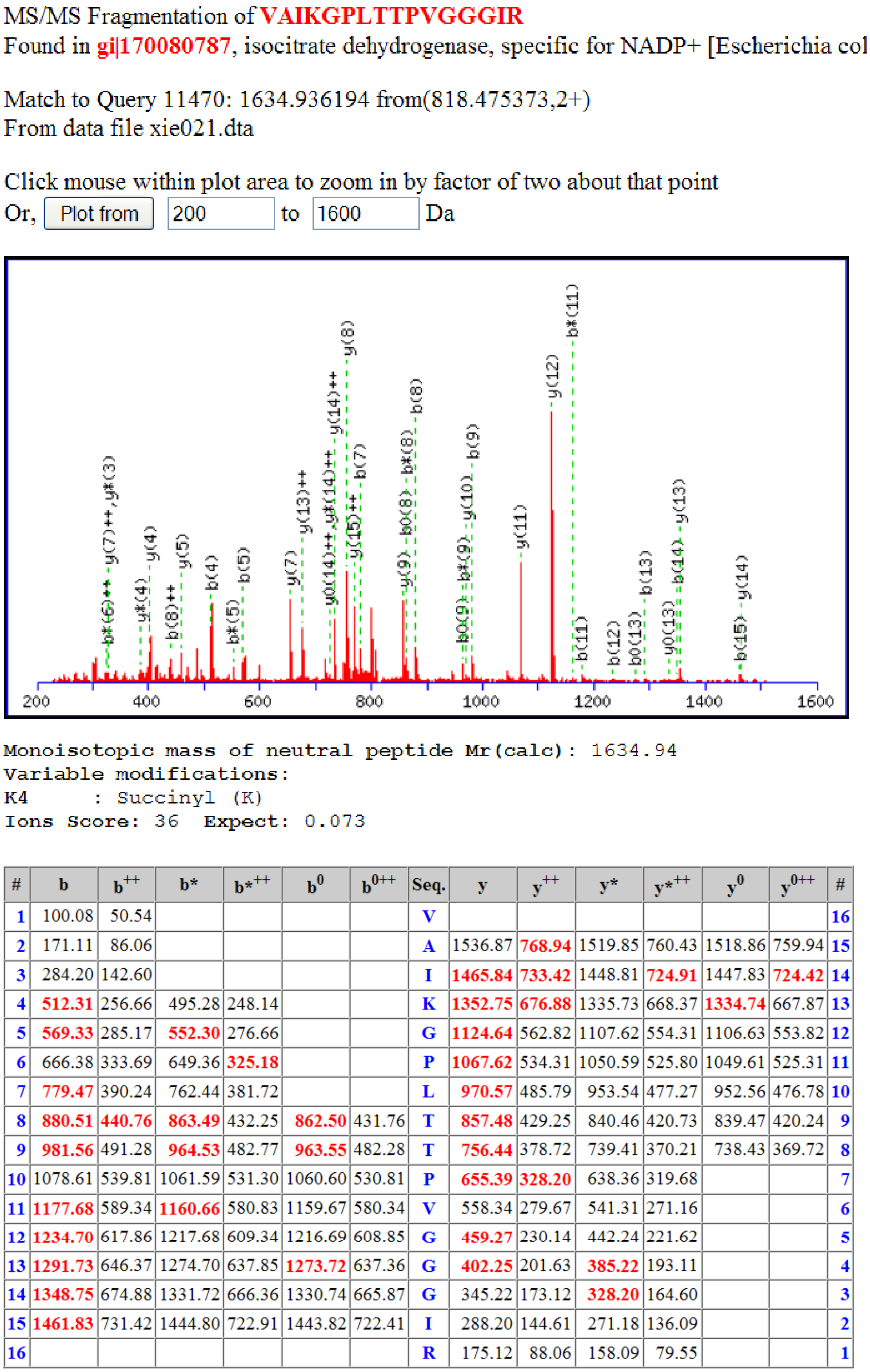
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.08	50.54			V							10
2	213.16	107.08			L	1109.62	555.31	1092.59	546.80	1091.61	546.31	9
3	328.19	164.60	310.18	155.59	D	996.54	498.77	979.51	490.26	978.53	489.77	8
4	441.27	221.14	423.26	212.13	L	881.51	441.26	864.48	432.74	863.50	432.25	7
5	554.35	277.68	536.34	268.68	I	768.43	384.72	751.40	376.20	750.41	375.71	6
6	625.39	313.20	607.38	304.19	A	655.34	328.17	638.31	319.66	637.33	319.17	5
7	762.45	381.73	744.44	372.72	H	584.30	292.66	567.28	284.14	566.29	283.65	4
8	875.53	438.27	857.52	429.27	I	447.24	224.13	430.22	215.61	429.23	215.12	3
9	962.57	481.79	944.56	472.78	S	334.16	167.58	317.13	159.07	316.15	158.58	2
10					K	247.13	124.07	230.10	115.55			1

Supplementary Data 2 :

MS/MS spectra of succinyllysine peptides indentified by affinity purification using anti-succinyllysine pan antibody and mass spectrometry

Isocitrate dehydrogenase K100

VAI^{Succ}KGPLTTPVGGGIR



MS/MS Fragmentation of **VAIKGPLTTPVGGGIR**
Found in **gi|170080787**, isocitrate dehydrogenase, specific for NADP+ [Escherichia col

Match to Query 11470: 1634.936194 from(818.475373,2+)
From data file xie021.dta

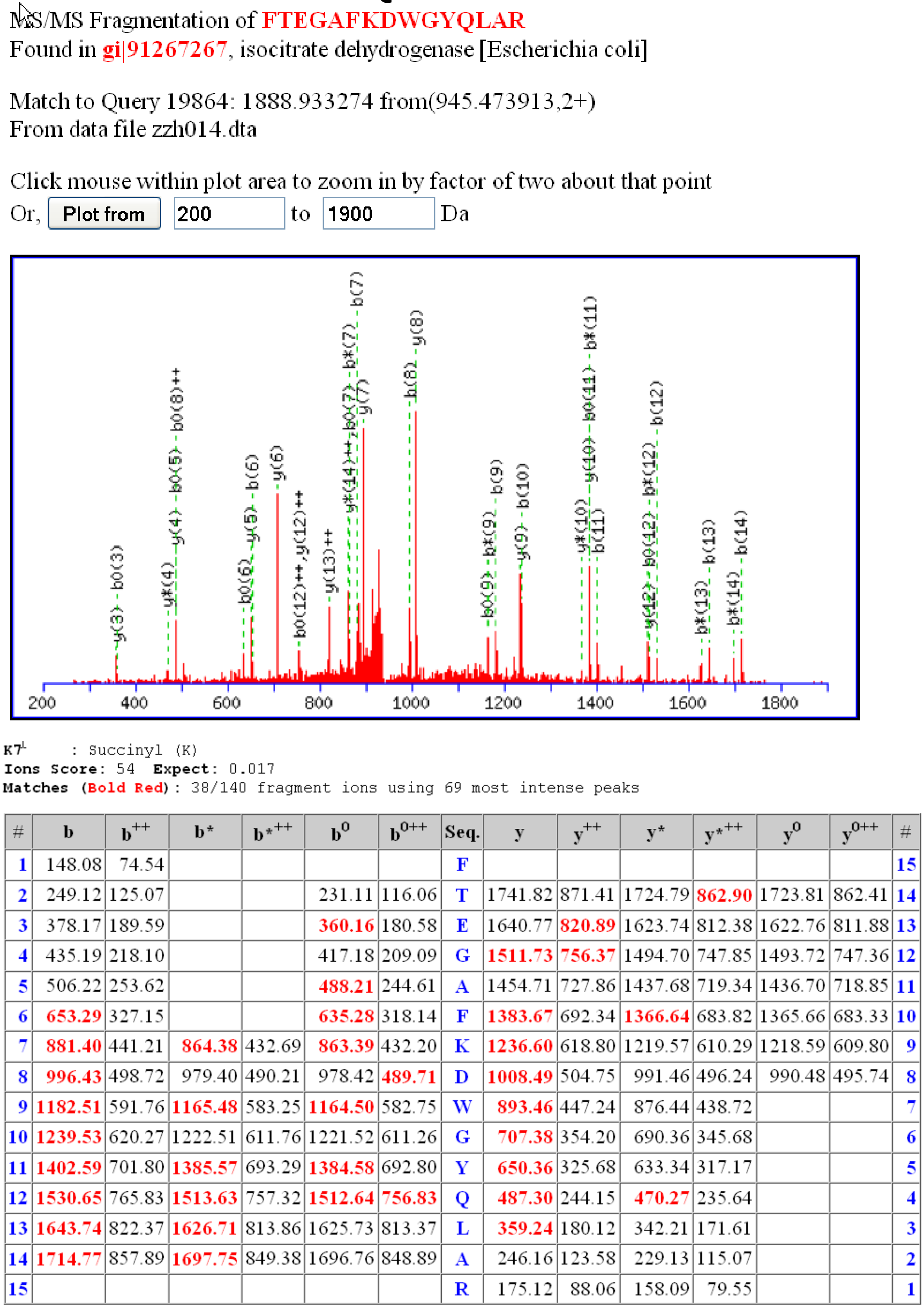
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1634.94
Variable modifications:
K4      : Succinyl (K)
Ions Score: 36   Expect: 0.073
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.08	50.54					V							16
2	171.11	86.06					A	1536.87	**768.94**	1519.85	760.43	1518.86	759.94	15
3	284.20	142.60					I	**1465.84**	**733.42**	1448.81	**724.91**	1447.83	**724.42**	14
4	**512.31**	256.66	495.28	248.14			K	**1352.75**	**676.88**	1335.73	668.37	**1334.74**	667.87	13
5	**569.33**	285.17	**552.30**	276.66			G	**1124.64**	562.82	1107.62	554.31	1106.63	553.82	12
6	666.38	333.69	649.36	**325.18**			P	**1067.62**	534.31	1050.59	525.80	1049.61	525.31	11
7	**779.47**	390.24	762.44	381.72			L	**970.57**	485.79	953.54	477.27	952.56	476.78	10
8	**880.51**	**440.76**	**863.49**	432.25	**862.50**	431.76	T	**857.48**	429.25	840.46	420.73	839.47	420.24	9
9	**981.56**	491.28	**964.53**	482.77	**963.55**	482.28	T	**756.44**	378.72	739.41	370.21	738.43	369.72	8
10	1078.61	539.81	1061.59	531.30	1060.60	530.81	P	**655.39**	**328.20**	638.36	319.68			7
11	**1177.68**	589.34	**1160.66**	580.83	1159.67	580.34	V	558.34	279.67	541.31	271.16			6
12	**1234.70**	617.86	1217.68	609.34	1216.69	608.85	G	**459.27**	230.14	442.24	221.62			5
13	**1291.73**	646.37	1274.70	637.85	**1273.72**	637.36	G	**402.25**	201.63	**385.22**	193.11			4
14	**1348.75**	674.88	1331.72	666.36	1330.74	665.87	G	345.22	173.12	**328.20**	164.60			3
15	**1461.83**	731.42	1444.80	722.91	1443.82	722.41	I	288.20	144.61	271.18	136.09			2
16							R	175.12	88.06	158.09	79.55			1

Isocitrate dehydrogenase K242

FTEGAF^{Succ}KDWGYQLAR



MS/MS Fragmentation of **FTEGAFKDWGYQLAR**
Found in **gi|91267267**, isocitrate dehydrogenase [Escherichia coli]

Match to Query 19864: 1888.933274 from(945.473913,2+)
From data file zzh014.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da

K7$^{\perp}$: Succinyl (K)
Ions Score: 54 **Expect**: 0.017
Matches (Bold Red): 38/140 fragment ions using 69 most intense peaks

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.08	74.54					F							15
2	249.12	125.07			231.11	116.06	T	1741.82	871.41	1724.79	**862.90**	1723.81	862.41	14
3	378.17	189.59			**360.16**	180.58	E	1640.77	**820.89**	1623.74	812.38	1622.76	811.88	13
4	435.19	218.10			417.18	209.09	G	**1511.73**	**756.37**	1494.70	747.85	1493.72	747.36	12
5	506.22	253.62			**488.21**	244.61	A	1454.71	727.86	1437.68	719.34	1436.70	718.85	11
6	**653.29**	327.15			**635.28**	318.14	F	**1383.67**	692.34	**1366.64**	683.82	1365.66	683.33	10
7	**881.40**	441.21	**864.38**	432.69	**863.39**	432.20	K	**1236.60**	618.80	1219.57	610.29	1218.59	609.80	9
8	**996.43**	498.72	979.40	490.21	978.42	**489.71**	D	**1008.49**	504.75	991.46	496.24	990.48	495.74	8
9	**1182.51**	591.76	**1165.48**	583.25	**1164.50**	582.75	W	**893.46**	447.24	876.44	438.72			7
10	**1239.53**	620.27	1222.51	611.76	1221.52	611.26	G	**707.38**	354.20	690.36	345.68			6
11	**1402.59**	701.80	**1385.57**	693.29	**1384.58**	692.80	Y	**650.36**	325.68	633.34	317.17			5
12	**1530.65**	765.83	**1513.63**	757.32	**1512.64**	**756.83**	Q	**487.30**	244.15	**470.27**	235.64			4
13	**1643.74**	822.37	**1626.71**	813.86	1625.73	813.37	L	**359.24**	180.12	342.21	171.61			3
14	**1714.77**	857.89	**1697.75**	849.38	1696.76	848.89	A	246.16	123.58	229.13	115.07			2
15							R	175.12	88.06	158.09	79.55			1

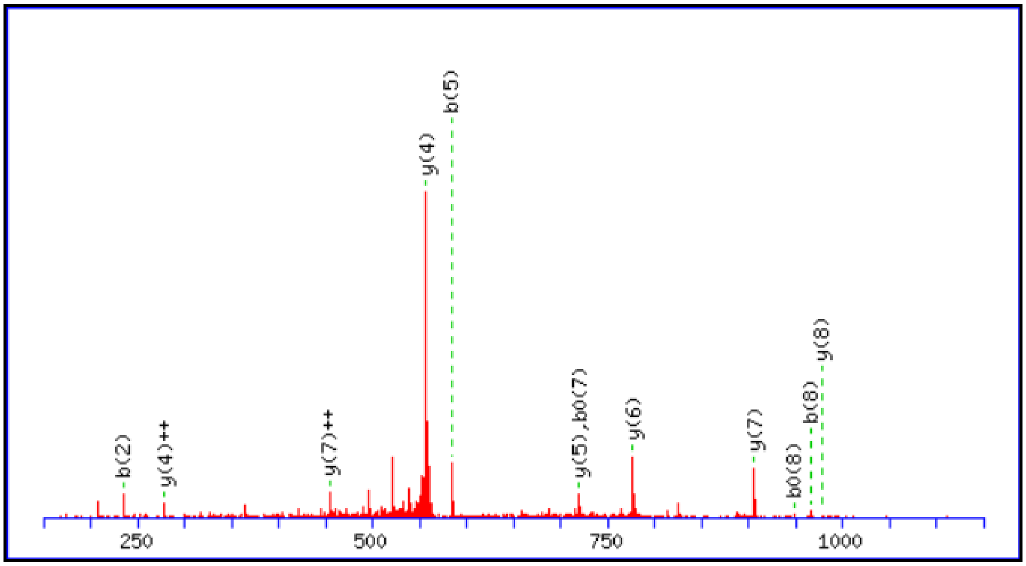
serine hydroxymethyltransferase K62

YAEGYPG^{Succ}KR

MS/MS Fragmentation of **YAEGYPGKR**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 sul

Match to Query 3582: 1139.529694 from(570.772123,2+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da

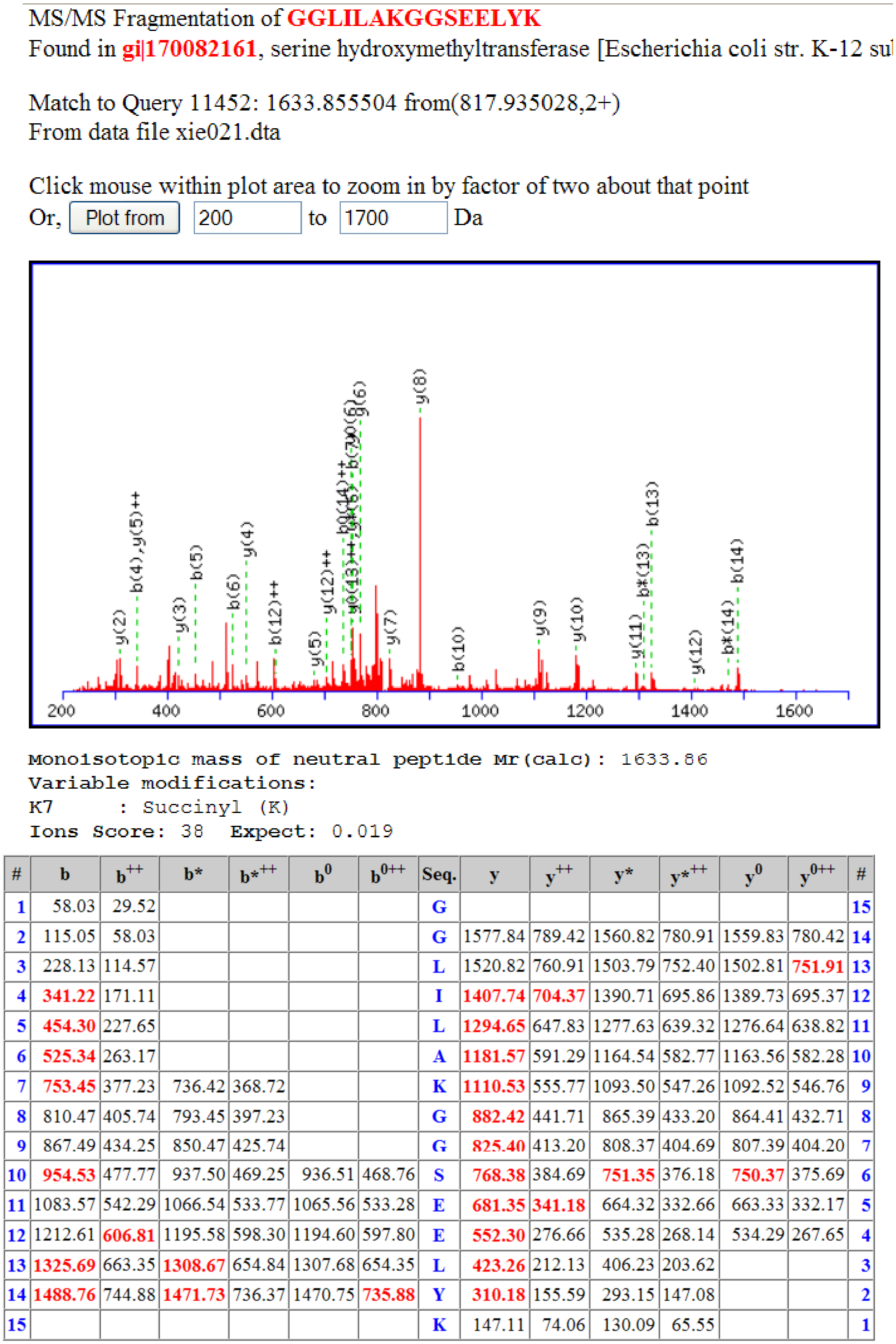


```
Monoisotopic mass of neutral peptide Mr(calc): 1139.52
Variable modifications:
K8      : Succinyl (K)
Ions Score: 43  Expect: 0.0022
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	164.07	82.54					Y							9
2	**235.11**	118.06					A	**977.47**	489.24	960.44	480.72	959.46	480.23	8
3	364.15	182.58			346.14	173.57	E	**906.43**	**453.72**	889.41	445.21	888.42	444.71	7
4	421.17	211.09			403.16	202.08	G	**777.39**	389.20	760.36	380.68			6
5	**584.24**	292.62			566.22	283.62	Y	**720.37**	360.69	703.34	352.17			5
6	681.29	341.15			663.28	332.14	P	**557.30**	**279.16**	540.28	270.64			4
7	738.31	369.66			**720.30**	360.65	G	460.25	230.63	443.22	222.12			3
8	**966.42**	483.71	949.39	475.20	**948.41**	474.71	K	403.23	202.12	386.20	193.61			2
9							R	175.12	88.06	158.09	79.55			1

serine hydroxymethyltransferase K242

GGLILA^{Succ}KGGSEELYK



MS/MS Fragmentation of **GGLILAKGGSEELYK**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 sul

Match to Query 11452: 1633.855504 from(817.935028,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1633.86
Variable modifications:
K7      : Succinyl (K)
Ions Score: 38   Expect: 0.019
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.03	29.52					G							15
2	115.05	58.03					G	1577.84	789.42	1560.82	780.91	1559.83	780.42	14
3	228.13	114.57					L	1520.82	760.91	1503.79	752.40	1502.81	751.91	13
4	341.22	171.11					I	1407.74	704.37	1390.71	695.86	1389.73	695.37	12
5	454.30	227.65					L	1294.65	647.83	1277.63	639.32	1276.64	638.82	11
6	525.34	263.17					A	1181.57	591.29	1164.54	582.77	1163.56	582.28	10
7	753.45	377.23	736.42	368.72			K	1110.53	555.77	1093.50	547.26	1092.52	546.76	9
8	810.47	405.74	793.45	397.23			G	882.42	441.71	865.39	433.20	864.41	432.71	8
9	867.49	434.25	850.47	425.74			G	825.40	413.20	808.37	404.69	807.39	404.20	7
10	954.53	477.77	937.50	469.25	936.51	468.76	S	768.38	384.69	751.35	376.18	750.37	375.69	6
11	1083.57	542.29	1066.54	533.77	1065.56	533.28	E	681.35	341.18	664.32	332.66	663.33	332.17	5
12	1212.61	606.81	1195.58	598.30	1194.60	597.80	E	552.30	276.66	535.28	268.14	534.29	267.65	4
13	1325.69	663.35	1308.67	654.84	1307.68	654.35	L	423.26	212.13	406.23	203.62			3
14	1488.76	744.88	1471.73	736.37	1470.75	735.88	Y	310.18	155.59	293.15	147.08			2
15							K	147.11	74.06	130.09	65.55			1

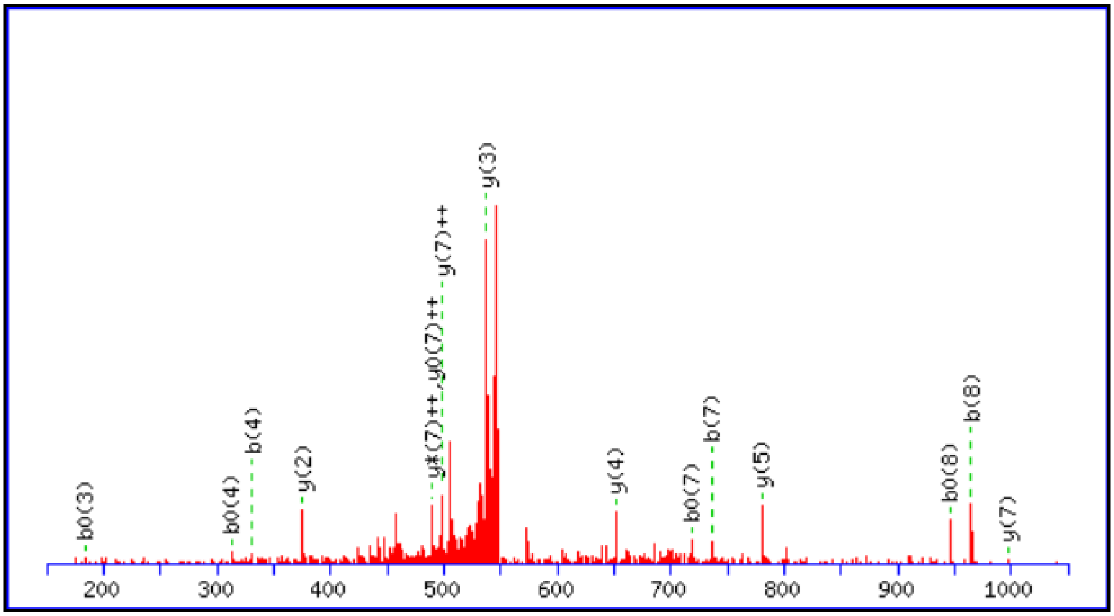
serine hydroxymethyltransferase K250

GGSEELY^{Succ}KK

MS/MS Fragmentation of **GGSEELYKK**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 su

Match to Query 3359: 1109.529084 from(555.771818,2+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da

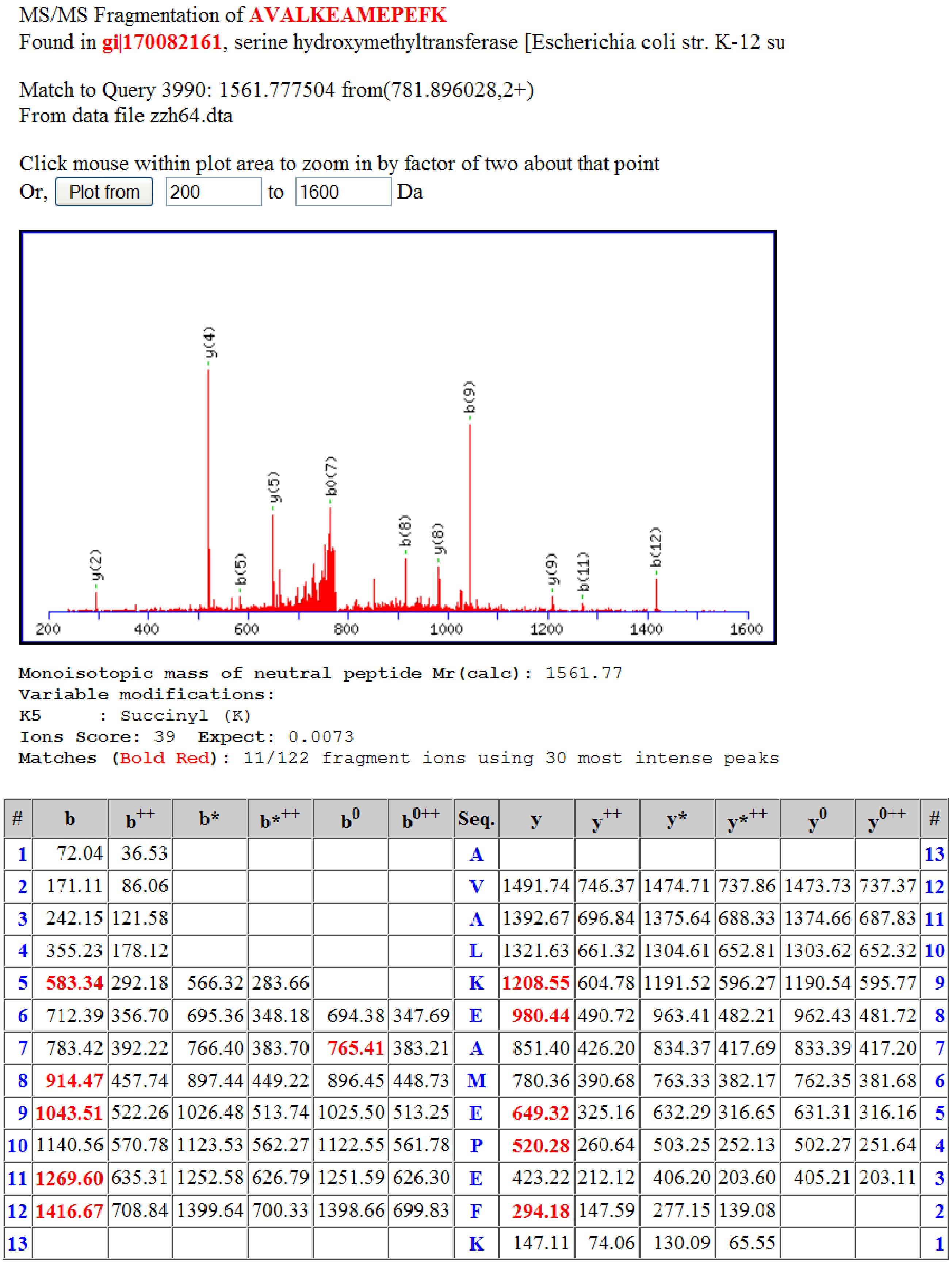


```
Monoisotopic mass of neutral peptide Mr(calc): 1109.52
Variable modifications:
K8      : Succinyl (K)
Ions Score: 34   Expect: 0.016
Matches (Bold Red): 15/70 fragment ions using 29 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.03	29.52					G							9
2	115.05	58.03					G	1053.51	527.26	1036.48	518.75	1035.50	518.25	8
3	202.08	101.54			**184.07**	92.54	S	**996.49**	**498.75**	979.46	**490.23**	978.48	**489.74**	7
4	**331.12**	166.07			**313.11**	157.06	E	909.46	455.23	892.43	446.72	891.45	446.23	6
5	460.17	230.59			442.16	221.58	E	**780.41**	390.71	763.39	382.20	762.40	381.71	5
6	573.25	287.13			555.24	278.12	L	**651.37**	326.19	634.34	317.68			4
7	**736.31**	368.66			**718.30**	359.66	Y	**538.29**	269.65	521.26	261.13			3
8	**964.43**	482.72	947.40	474.20	**946.42**	473.71	K	**375.22**	188.12	358.20	179.60			2
9							K	147.11	74.06	130.09	65.55			1

serine hydroxymethyltransferase K277

AVAL^{Succ}KEAMEPEFK



MS/MS Fragmentation of **AVALKEAMEPEFK**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 su

Match to Query 3990: 1561.777504 from(781.896028,2+)
From data file zzh64.dta

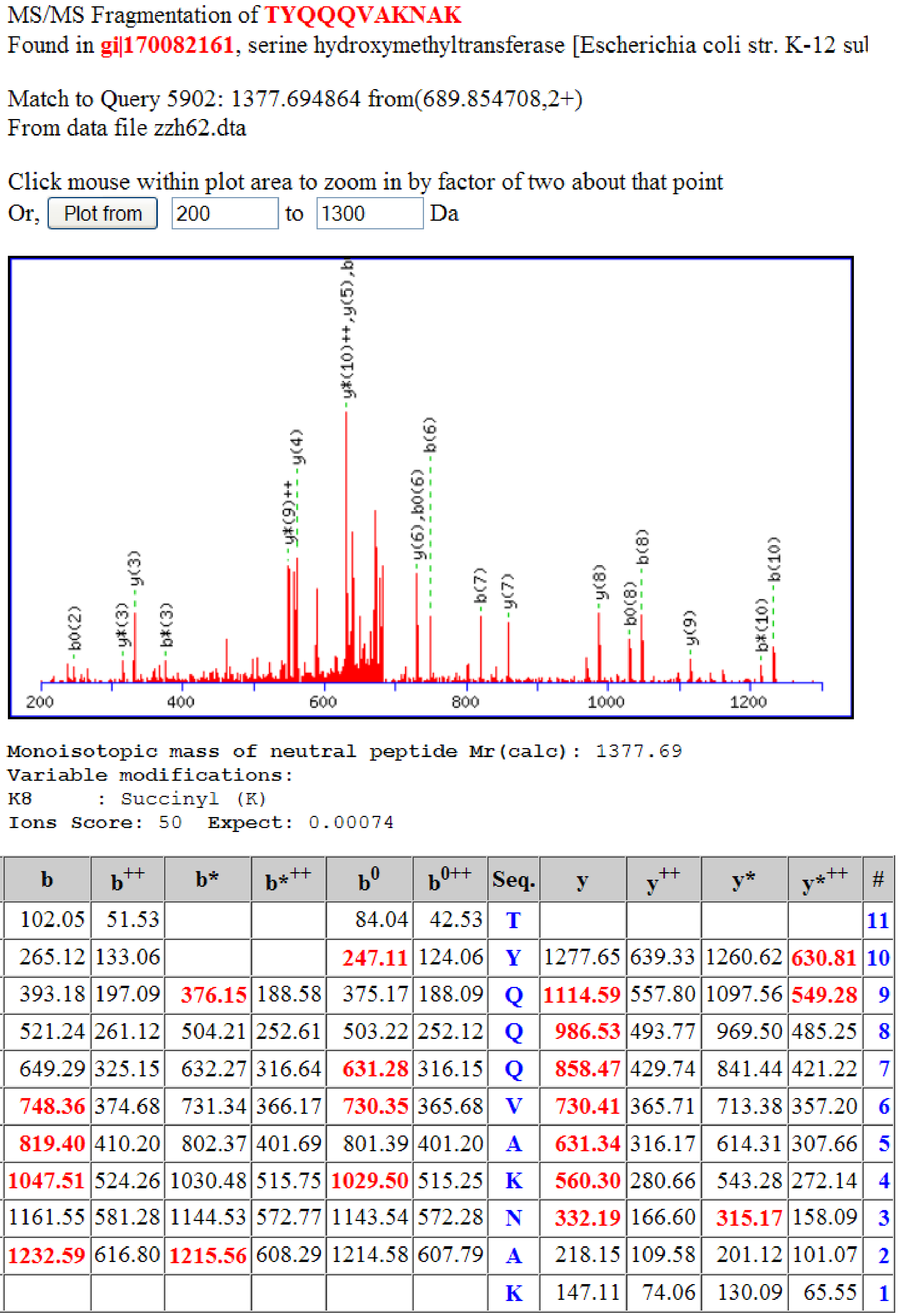
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1561.77
Variable modifications:
K5      : Succinyl (K)
Ions Score: 39  Expect: 0.0073
Matches (Bold Red): 11/122 fragment ions using 30 most intense peaks
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.04	36.53					A							13
2	171.11	86.06					V	1491.74	746.37	1474.71	737.86	1473.73	737.37	12
3	242.15	121.58					A	1392.67	696.84	1375.64	688.33	1374.66	687.83	11
4	355.23	178.12					L	1321.63	661.32	1304.61	652.81	1303.62	652.32	10
5	**583.34**	292.18	566.32	283.66			K	**1208.55**	604.78	1191.52	596.27	1190.54	595.77	9
6	712.39	356.70	695.36	348.18	694.38	347.69	E	**980.44**	490.72	963.41	482.21	962.43	481.72	8
7	783.42	392.22	766.40	383.70	**765.41**	383.21	A	851.40	426.20	834.37	417.69	833.39	417.20	7
8	**914.47**	457.74	897.44	449.22	896.45	448.73	M	780.36	390.68	763.33	382.17	762.35	381.68	6
9	**1043.51**	522.26	1026.48	513.74	1025.50	513.25	E	**649.32**	325.16	632.29	316.65	631.31	316.16	5
10	1140.56	570.78	1123.53	562.27	1122.55	561.78	P	**520.28**	260.64	503.25	252.13	502.27	251.64	4
11	**1269.60**	635.31	1252.58	626.79	1251.59	626.30	E	423.22	212.12	406.20	203.60	405.21	203.11	3
12	**1416.67**	708.84	1399.64	700.33	1398.66	699.83	F	**294.18**	147.59	277.15	139.08			2
13							K	147.11	74.06	130.09	65.55			1

serine hydroxymethyltransferase K293

TYQQQVA^{Succ}KNAK



MS/MS Fragmentation of **TYQQQVAKNAK**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 sul

Match to Query 5902: 1377.694864 from(689.854708,2+)
From data file zzh62.dta

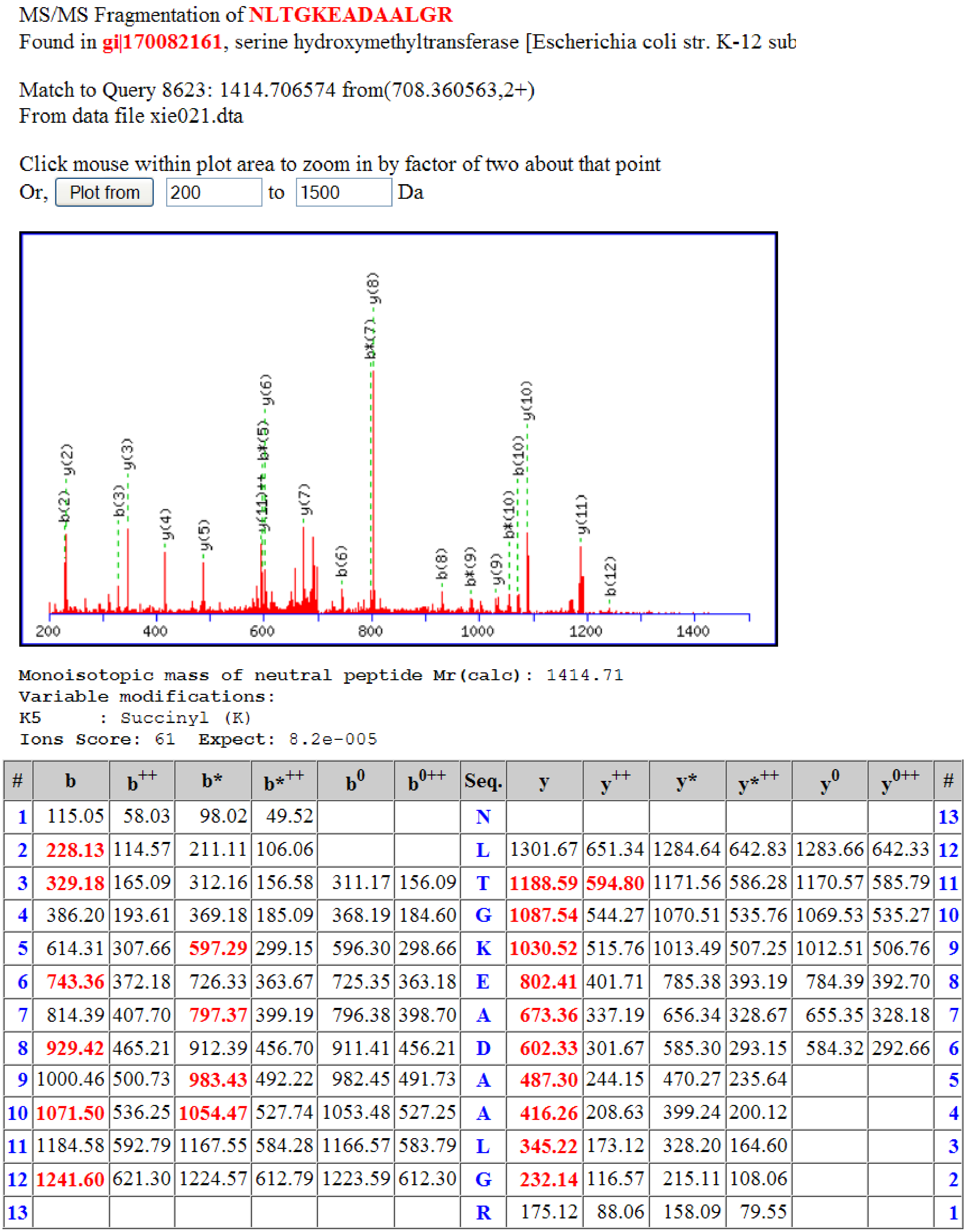
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1377.69
Variable modifications:
K8      : Succinyl (K)
Ions Score: 50   Expect: 0.00074
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	102.05	51.53			84.04	42.53	T					11
2	265.12	133.06			247.11	124.06	Y	1277.65	639.33	1260.62	630.81	10
3	393.18	197.09	376.15	188.58	375.17	188.09	Q	1114.59	557.80	1097.56	549.28	9
4	521.24	261.12	504.21	252.61	503.22	252.12	Q	986.53	493.77	969.50	485.25	8
5	649.29	325.15	632.27	316.64	631.28	316.15	Q	858.47	429.74	841.44	421.22	7
6	748.36	374.68	731.34	366.17	730.35	365.68	V	730.41	365.71	713.38	357.20	6
7	819.40	410.20	802.37	401.69	801.39	401.20	A	631.34	316.17	614.31	307.66	5
8	1047.51	524.26	1030.48	515.75	1029.50	515.25	K	560.30	280.66	543.28	272.14	4
9	1161.55	581.28	1144.53	572.77	1143.54	572.28	N	332.19	166.60	315.17	158.09	3
10	1232.59	616.80	1215.56	608.29	1214.58	607.79	A	218.15	109.58	201.12	101.07	2
11							K	147.11	74.06	130.09	65.55	1

serine hydroxymethyltransferase K331

NLTG^{Succ}KEADAALGR



MS/MS Fragmentation of **NLTGKEADAALGR**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 sub

Match to Query 8623: 1414.706574 from(708.360563,2+)
From data file xie021.dta

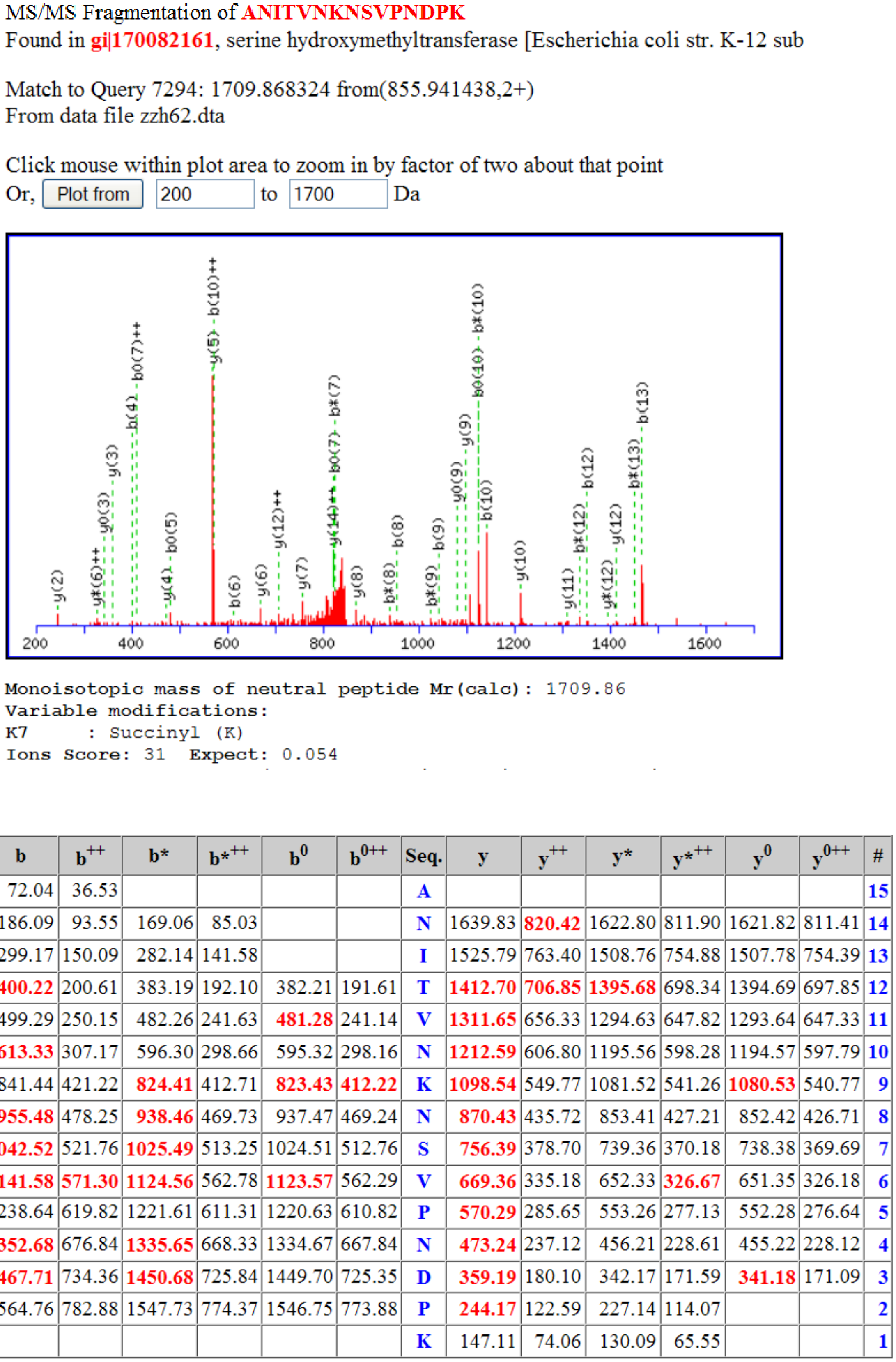
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1414.71
Variable modifications:
K5      : Succinyl (K)
Ions Score: 61  Expect: 8.2e-005
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.05	58.03	98.02	49.52			N							13
2	**228.13**	114.57	211.11	106.06			L	1301.67	651.34	1284.64	642.83	1283.66	642.33	12
3	**329.18**	165.09	312.16	156.58	311.17	156.09	T	**1188.59**	**594.80**	1171.56	586.28	1170.57	585.79	11
4	386.20	193.61	369.18	185.09	368.19	184.60	G	**1087.54**	544.27	1070.51	535.76	1069.53	535.27	10
5	614.31	307.66	**597.29**	299.15	596.30	298.66	K	**1030.52**	515.76	1013.49	507.25	1012.51	506.76	9
6	**743.36**	372.18	726.33	363.67	725.35	363.18	E	**802.41**	401.71	785.38	393.19	784.39	392.70	8
7	814.39	407.70	**797.37**	399.19	796.38	398.70	A	**673.36**	337.19	656.34	328.67	655.35	328.18	7
8	**929.42**	465.21	912.39	456.70	911.41	456.21	D	**602.33**	301.67	585.30	293.15	584.32	292.66	6
9	1000.46	500.73	**983.43**	492.22	982.45	491.73	A	**487.30**	244.15	470.27	235.64			5
10	**1071.50**	536.25	**1054.47**	527.74	1053.48	527.25	A	**416.26**	208.63	399.24	200.12			4
11	1184.58	592.79	1167.55	584.28	1166.57	583.79	L	**345.22**	173.12	328.20	164.60			3
12	**1241.60**	621.30	1224.57	612.79	1223.59	612.30	G	**232.14**	116.57	215.11	108.06			2
13							R	175.12	88.06	158.09	79.55			1

serine hydroxymethyltransferase K346

ANITVN^{Succ}KNSVPNDPK



MS/MS Fragmentation of **ANITVNKNSVPNDPK**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 sub

Match to Query 7294: 1709.868324 from(855.941438,2+)
From data file zzh62.dta

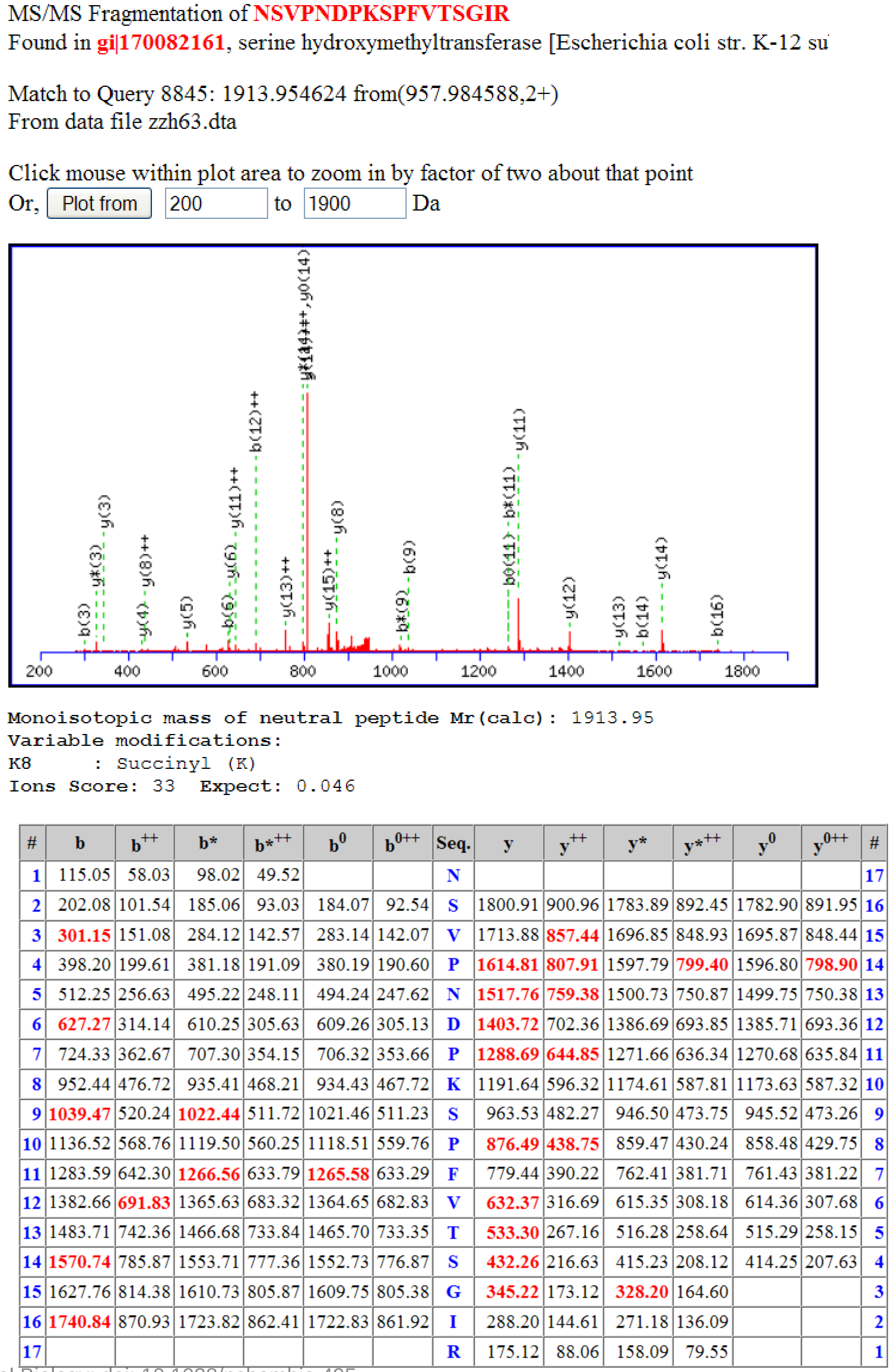
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1709.86
Variable modifications:
K7       : Succinyl (K)
Ions Score: 31   Expect: 0.054
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.04	36.53					A							15
2	186.09	93.55	169.06	85.03			N	1639.83	820.42	1622.80	811.90	1621.82	811.41	14
3	299.17	150.09	282.14	141.58			I	1525.79	763.40	1508.76	754.88	1507.78	754.39	13
4	400.22	200.61	383.19	192.10	382.21	191.61	T	1412.70	706.85	1395.68	698.34	1394.69	697.85	12
5	499.29	250.15	482.26	241.63	481.28	241.14	V	1311.65	656.33	1294.63	647.82	1293.64	647.33	11
6	613.33	307.17	596.30	298.66	595.32	298.16	N	1212.59	606.80	1195.56	598.28	1194.57	597.79	10
7	841.44	421.22	824.41	412.71	823.43	412.22	K	1098.54	549.77	1081.52	541.26	1080.53	540.77	9
8	955.48	478.25	938.46	469.73	937.47	469.24	N	870.43	435.72	853.41	427.21	852.42	426.71	8
9	1042.52	521.76	1025.49	513.25	1024.51	512.76	S	756.39	378.70	739.36	370.18	738.38	369.69	7
10	1141.58	571.30	1124.56	562.78	1123.57	562.29	V	669.36	335.18	652.33	326.67	651.35	326.18	6
11	1238.64	619.82	1221.61	611.31	1220.63	610.82	P	570.29	285.65	553.26	277.13	552.28	276.64	5
12	1352.68	676.84	1335.65	668.33	1334.67	667.84	N	473.24	237.12	456.21	228.61	455.22	228.12	4
13	1467.71	734.36	1450.68	725.84	1449.70	725.35	D	359.19	180.10	342.17	171.59	341.18	171.09	3
14	1564.76	782.88	1547.73	774.37	1546.75	773.88	P	244.17	122.59	227.14	114.07			2
15							K	147.11	74.06	130.09	65.55			1

serine hydroxymethyltransferase K354

NSVPNDP^{Succ}KSPFVTSGIR



MS/MS Fragmentation of **NSVPNDPKSPFVTSGIR**
Found in **gi|170082161**, serine hydroxymethyltransferase [Escherichia coli str. K-12 su

Match to Query 8845: 1913.954624 from(957.984588,2+)
From data file zzh63.dta

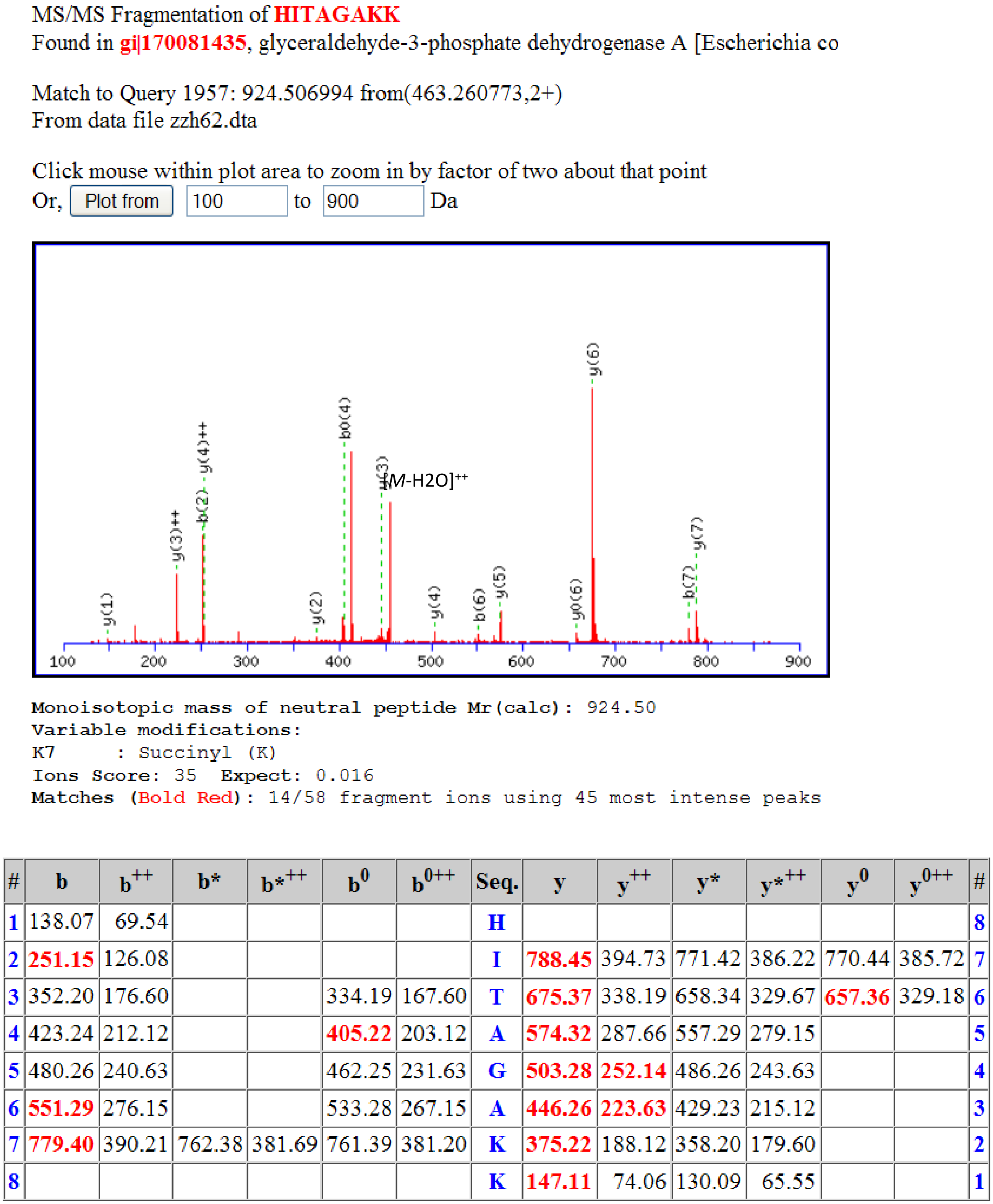
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1913.95
Variable modifications:
K8      : Succinyl (K)
Ions Score: 33  Expect: 0.046
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.05	58.03	98.02	49.52			N							17
2	202.08	101.54	185.06	93.03	184.07	92.54	S	1800.91	900.96	1783.89	892.45	1782.90	891.95	16
3	**301.15**	151.08	284.12	142.57	283.14	142.07	V	1713.88	**857.44**	1696.85	848.93	1695.87	848.44	15
4	398.20	199.61	381.18	191.09	380.19	190.60	P	**1614.81**	**807.91**	1597.79	**799.40**	1596.80	**798.90**	14
5	512.25	256.63	495.22	248.11	494.24	247.62	N	**1517.76**	**759.38**	1500.73	750.87	1499.75	750.38	13
6	**627.27**	314.14	610.25	305.63	609.26	305.13	D	**1403.72**	702.36	1386.69	693.85	1385.71	693.36	12
7	724.33	362.67	707.30	354.15	706.32	353.66	P	**1288.69**	**644.85**	1271.66	636.34	1270.68	635.84	11
8	952.44	476.72	935.41	468.21	934.43	467.72	K	1191.64	596.32	1174.61	587.81	1173.63	587.32	10
9	**1039.47**	520.24	**1022.44**	511.72	1021.46	511.23	S	963.53	482.27	946.50	473.75	945.52	473.26	9
10	1136.52	568.76	1119.50	560.25	1118.51	559.76	P	**876.49**	**438.75**	859.47	430.24	858.48	429.75	8
11	1283.59	642.30	**1266.56**	633.79	**1265.58**	633.29	F	779.44	390.22	762.41	381.71	761.43	381.22	7
12	1382.66	**691.83**	1365.63	683.32	1364.65	682.83	V	**632.37**	316.69	615.35	308.18	614.36	307.68	6
13	1483.71	742.36	1466.68	733.84	1465.70	733.35	T	**533.30**	267.16	516.28	258.64	515.29	258.15	5
14	**1570.74**	785.87	1553.71	777.36	1552.73	776.87	S	**432.26**	216.63	415.23	208.12	414.25	207.63	4
15	1627.76	814.38	1610.73	805.87	1609.75	805.38	G	**345.22**	173.12	**328.20**	164.60			3
16	**1740.84**	870.93	1723.82	862.41	1722.83	861.92	I	288.20	144.61	271.18	136.09			2
17							R	175.12	88.06	158.09	79.55			1

glyceraldehyde-3-phosphate dehydrogenase A K115

HITAGA^{Succ}KK



MS/MS Fragmentation of **HITAGAKK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia co

Match to Query 1957: 924.506994 from(463.260773,2+)
From data file zzh62.dta

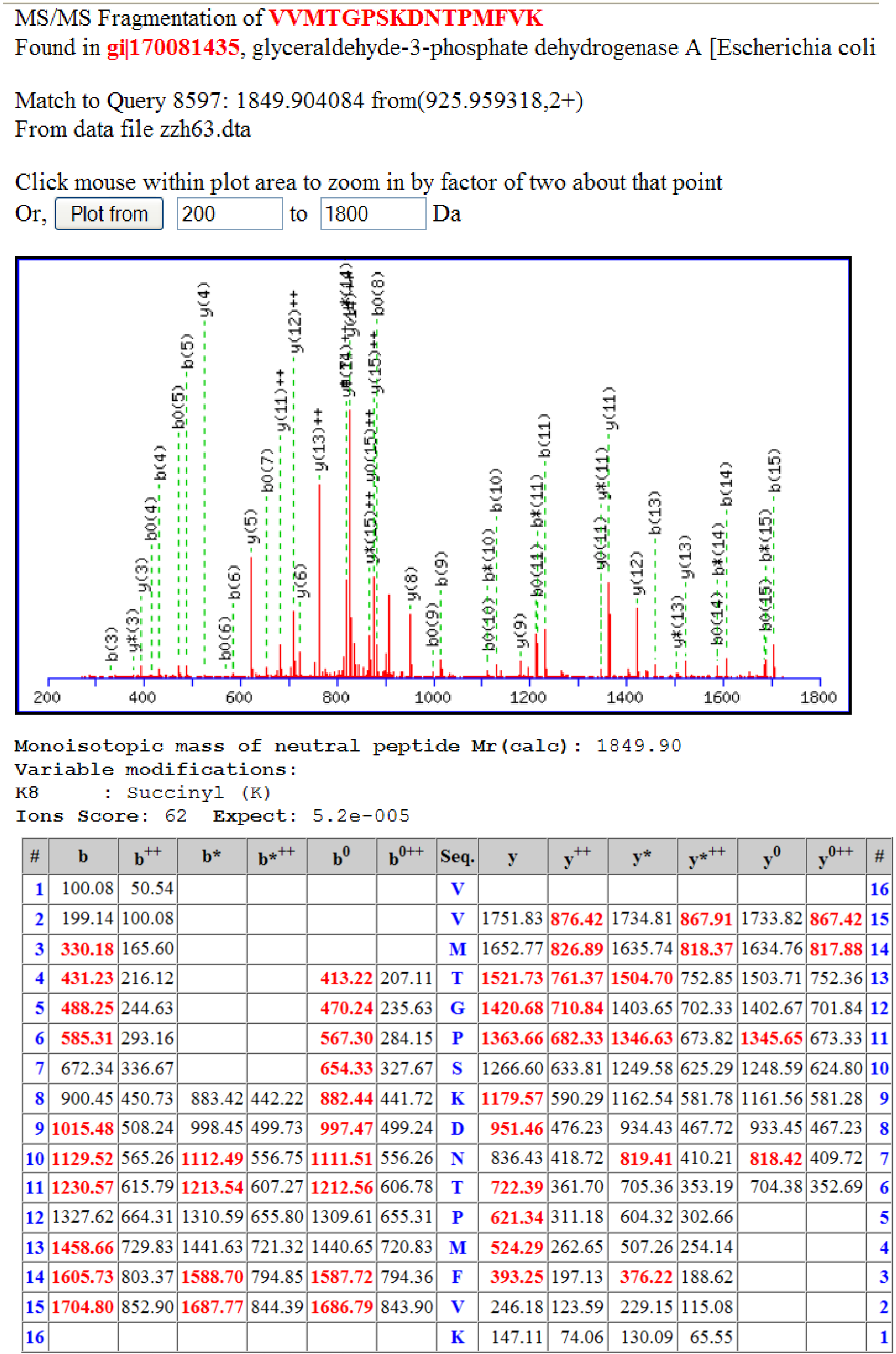
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 924.50
Variable modifications:
K7      : Succinyl (K)
Ions Score: 35  Expect: 0.016
Matches (Bold Red): 14/58 fragment ions using 45 most intense peaks
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.07	69.54					H							8
2	**251.15**	126.08					I	**788.45**	394.73	771.42	386.22	770.44	385.72	7
3	352.20	176.60			334.19	167.60	T	**675.37**	338.19	658.34	329.67	**657.36**	329.18	6
4	423.24	212.12			**405.22**	203.12	A	**574.32**	287.66	557.29	279.15			5
5	480.26	240.63			462.25	231.63	G	**503.28**	**252.14**	486.26	243.63			4
6	**551.29**	276.15			533.28	267.15	A	**446.26**	**223.63**	429.23	215.12			3
7	**779.40**	390.21	762.38	381.69	761.39	381.20	K	**375.22**	188.12	358.20	179.60			2
8							K	**147.11**	74.06	130.09	65.55			1

glyceraldehyde-3-phosphate dehydrogenase A K124

VVMTGPS^{Succ}KDNTPMFVK



MS/MS Fragmentation of **VVMTGPSKDNTPMFVK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 8597: 1849.904084 from(925.959318,2+)
From data file zzh63.dta

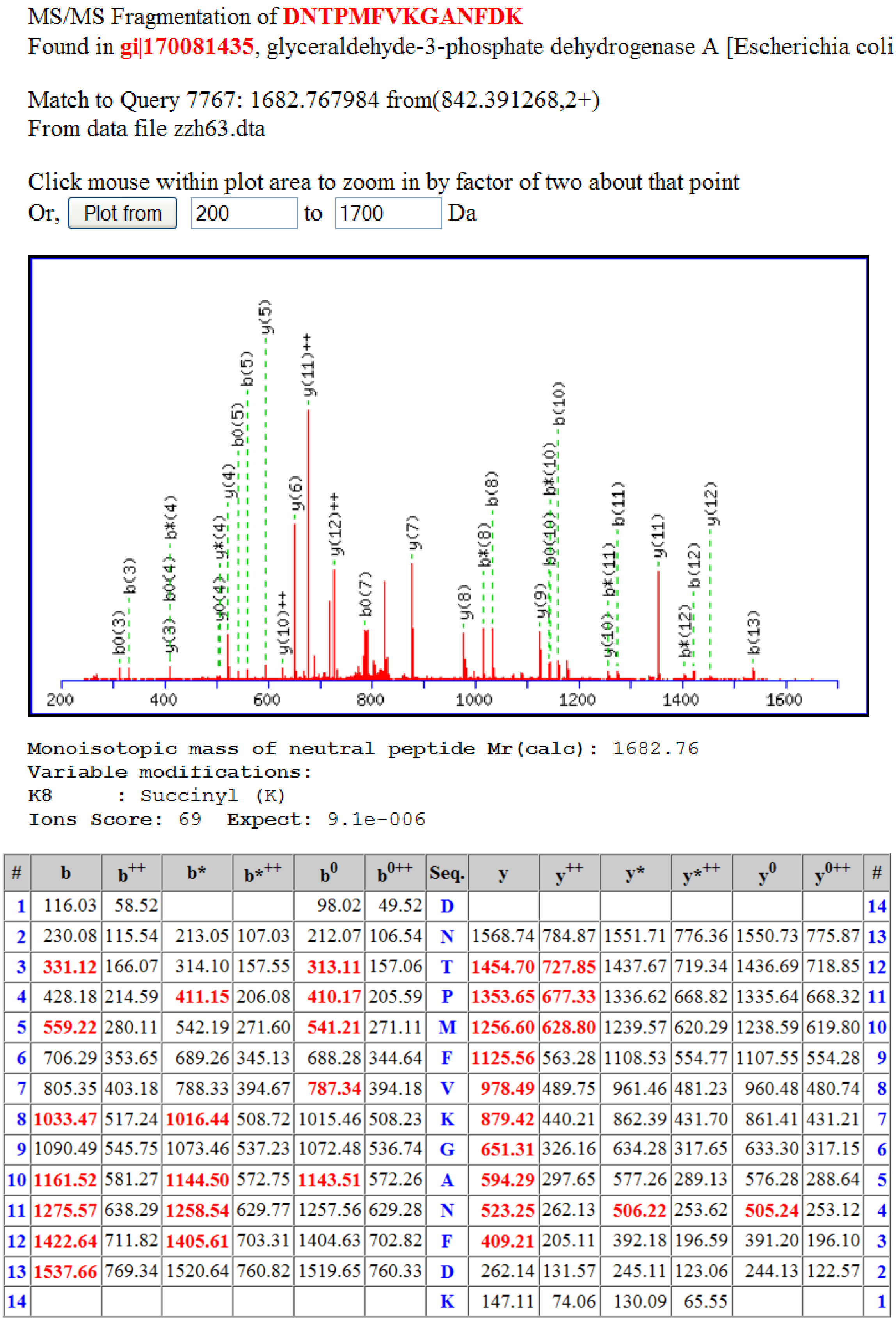
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1849.90
Variable modifications:
K8      : Succinyl (K)
Ions Score: 62  Expect: 5.2e-005
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.08	50.54					V							16
2	199.14	100.08					V	1751.83	876.42	1734.81	867.91	1733.82	867.42	15
3	330.18	165.60					M	1652.77	826.89	1635.74	818.37	1634.76	817.88	14
4	431.23	216.12			413.22	207.11	T	1521.73	761.37	1504.70	752.85	1503.71	752.36	13
5	488.25	244.63			470.24	235.63	G	1420.68	710.84	1403.65	702.33	1402.67	701.84	12
6	585.31	293.16			567.30	284.15	P	1363.66	682.33	1346.63	673.82	1345.65	673.33	11
7	672.34	336.67			654.33	327.67	S	1266.60	633.81	1249.58	625.29	1248.59	624.80	10
8	900.45	450.73	883.42	442.22	882.44	441.72	K	1179.57	590.29	1162.54	581.78	1161.56	581.28	9
9	1015.48	508.24	998.45	499.73	997.47	499.24	D	951.46	476.23	934.43	467.72	933.45	467.23	8
10	1129.52	565.26	1112.49	556.75	1111.51	556.26	N	836.43	418.72	819.41	410.21	818.42	409.72	7
11	1230.57	615.79	1213.54	607.27	1212.56	606.78	T	722.39	361.70	705.36	353.19	704.38	352.69	6
12	1327.62	664.31	1310.59	655.80	1309.61	655.31	P	621.34	311.18	604.32	302.66			5
13	1458.66	729.83	1441.63	721.32	1440.65	720.83	M	524.29	262.65	507.26	254.14			4
14	1605.73	803.37	1588.70	794.85	1587.72	794.36	F	393.25	197.13	376.22	188.62			3
15	1704.80	852.90	1687.77	844.39	1686.79	843.90	V	246.18	123.59	229.15	115.08			2
16							K	147.11	74.06	130.09	65.55			1

glyceraldehyde-3-phosphate dehydrogenase A K132

DNTPMFV^{Succ}KGANFDK



MS/MS Fragmentation of **DNTPMFVKGANFDK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 7767: 1682.767984 from(842.391268,2+)
From data file zzh63.dta

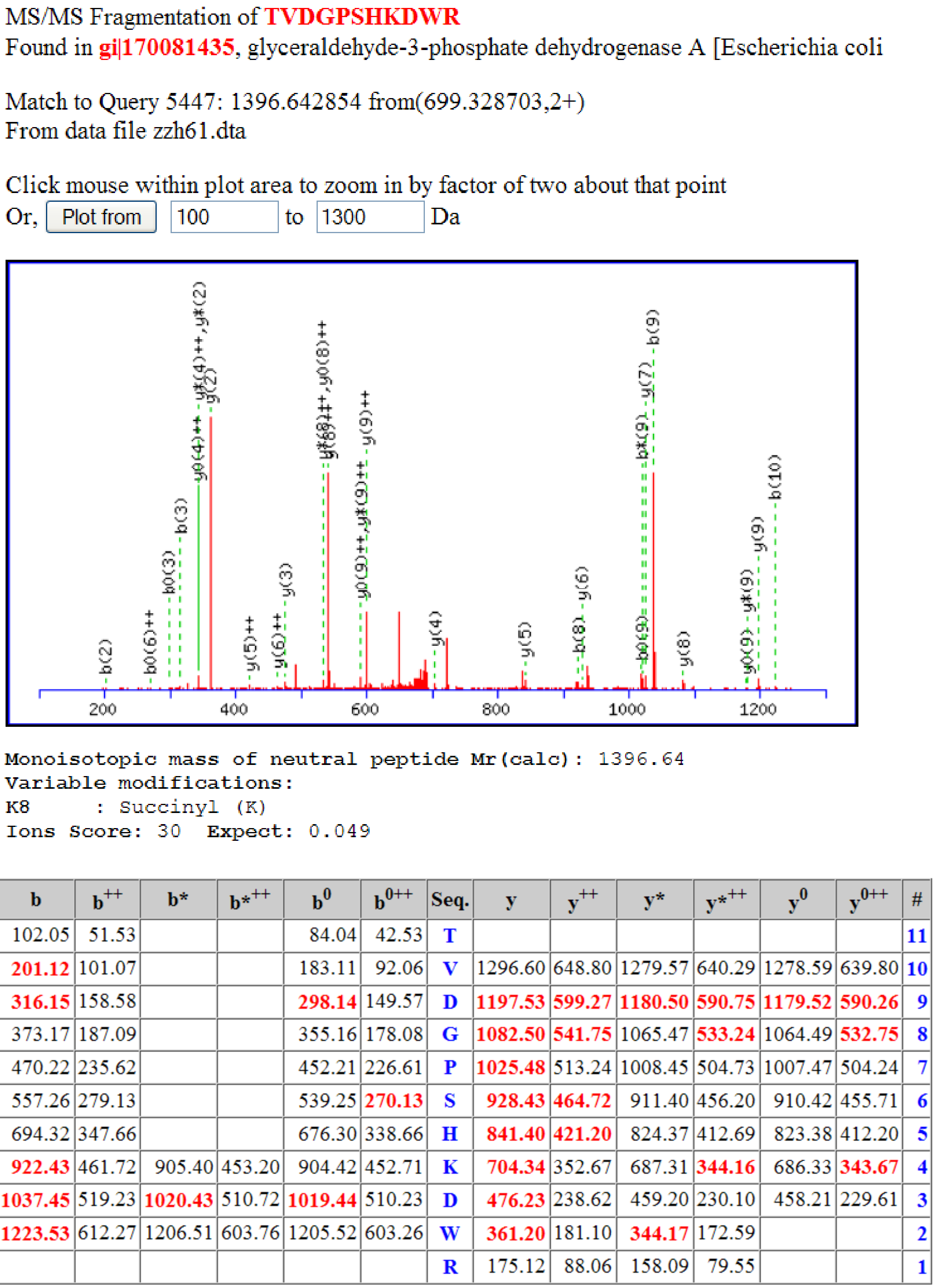
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1682.76
Variable modifications:
K8      : Succinyl (K)
Ions Score: 69  Expect: 9.1e-006
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	116.03	58.52			98.02	49.52	D							14
2	230.08	115.54	213.05	107.03	212.07	106.54	N	1568.74	784.87	1551.71	776.36	1550.73	775.87	13
3	**331.12**	166.07	314.10	157.55	**313.11**	157.06	T	**1454.70**	**727.85**	1437.67	719.34	1436.69	718.85	12
4	428.18	214.59	**411.15**	206.08	**410.17**	205.59	P	**1353.65**	**677.33**	1336.62	668.82	1335.64	668.32	11
5	**559.22**	280.11	542.19	271.60	**541.21**	271.11	M	**1256.60**	**628.80**	1239.57	620.29	1238.59	619.80	10
6	706.29	353.65	689.26	345.13	688.28	344.64	F	**1125.56**	563.28	1108.53	554.77	1107.55	554.28	9
7	805.35	403.18	788.33	394.67	**787.34**	394.18	V	**978.49**	489.75	961.46	481.23	960.48	480.74	8
8	**1033.47**	517.24	**1016.44**	508.72	1015.46	508.23	K	**879.42**	440.21	862.39	431.70	861.41	431.21	7
9	1090.49	545.75	1073.46	537.23	1072.48	536.74	G	**651.31**	326.16	634.28	317.65	633.30	317.15	6
10	**1161.52**	581.27	**1144.50**	572.75	**1143.51**	572.26	A	**594.29**	297.65	577.26	289.13	576.28	288.64	5
11	**1275.57**	638.29	**1258.54**	629.77	1257.56	629.28	N	**523.25**	262.13	**506.22**	253.62	**505.24**	253.12	4
12	**1422.64**	711.82	**1405.61**	703.31	1404.63	702.82	F	**409.21**	205.11	392.18	196.59	391.20	196.10	3
13	**1537.66**	769.34	1520.64	760.82	1519.65	760.33	D	262.14	131.57	245.11	123.06	244.13	122.57	2
14							K	147.11	74.06	130.09	65.55			1

glyceraldehyde-3-phosphate dehydrogenase A K192

TVDGPSH^{Succ}KDWR



MS/MS Fragmentation of **TVDGPSHKDWR**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 5447: 1396.642854 from(699.328703,2+)
From data file zzh61.dta

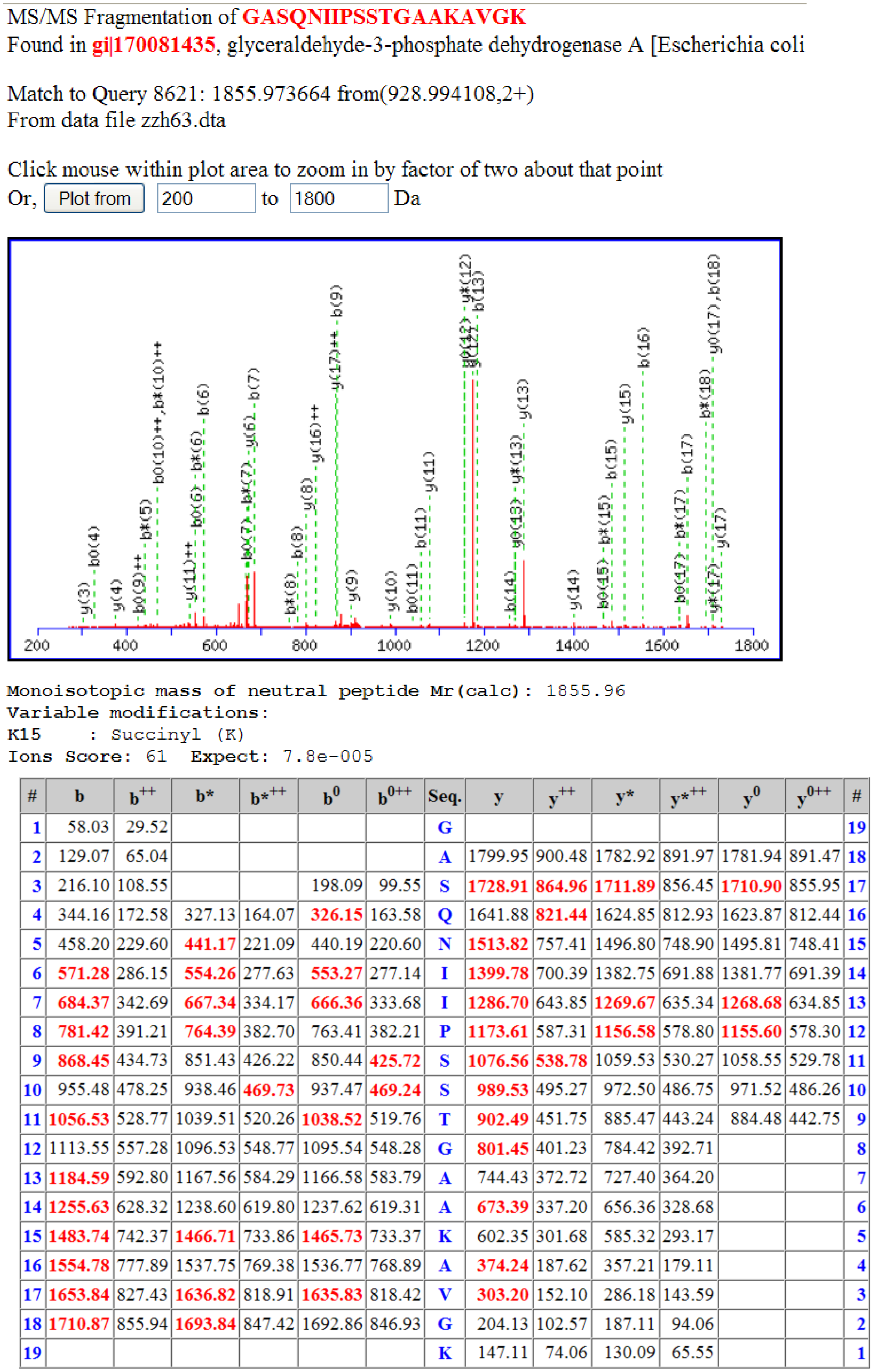
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1396.64
Variable modifications:
K8      : Succinyl (K)
Ions Score: 30   Expect: 0.049
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	102.05	51.53			84.04	42.53	T							11
2	**201.12**	101.07			183.11	92.06	V	1296.60	648.80	1279.57	640.29	1278.59	639.80	10
3	**316.15**	158.58			**298.14**	149.57	D	**1197.53**	**599.27**	**1180.50**	**590.75**	**1179.52**	**590.26**	9
4	373.17	187.09			355.16	178.08	G	**1082.50**	**541.75**	1065.47	**533.24**	1064.49	**532.75**	8
5	470.22	235.62			452.21	226.61	P	**1025.48**	513.24	1008.45	504.73	1007.47	504.24	7
6	557.26	279.13			539.25	**270.13**	S	**928.43**	**464.72**	911.40	456.20	910.42	455.71	6
7	694.32	347.66			676.30	338.66	H	**841.40**	**421.20**	824.37	412.69	823.38	412.20	5
8	**922.43**	461.72	905.40	453.20	904.42	452.71	K	**704.34**	352.67	687.31	**344.16**	686.33	**343.67**	4
9	**1037.45**	519.23	**1020.43**	510.72	**1019.44**	510.23	D	**476.23**	238.62	459.20	230.10	458.21	229.61	3
10	**1223.53**	612.27	1206.51	603.76	1205.52	603.26	W	**361.20**	181.10	**344.17**	172.59			2
11							R	175.12	88.06	158.09	79.55			1

glyceraldehyde-3-phosphate dehydrogenase A K213

GASQNIIPSSTGAA^{Succ}KAVGK


MS/MS Fragmentation of **GASQNIIPSSTGAAKAVGK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 8621: 1855.973664 from(928.994108,2+)
From data file zzh63.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1855.96
Variable modifications:
K15     : Succinyl (K)
Ions Score: 61  Expect: 7.8e-005
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.03	29.52					G							19
2	129.07	65.04					A	1799.95	900.48	1782.92	891.97	1781.94	891.47	18
3	216.10	108.55			198.09	99.55	S	**1728.91**	**864.96**	**1711.89**	856.45	**1710.90**	855.95	17
4	344.16	172.58	327.13	164.07	**326.15**	163.58	Q	1641.88	**821.44**	1624.85	812.93	1623.87	812.44	16
5	458.20	229.60	**441.17**	221.09	440.19	220.60	N	**1513.82**	757.41	1496.80	748.90	1495.81	748.41	15
6	**571.28**	286.15	**554.26**	277.63	**553.27**	277.14	I	**1399.78**	700.39	1382.75	691.88	1381.77	691.39	14
7	**684.37**	342.69	**667.34**	334.17	**666.36**	333.68	I	**1286.70**	643.85	**1269.67**	635.34	**1268.68**	634.85	13
8	**781.42**	391.21	**764.39**	382.70	763.41	382.21	P	**1173.61**	587.31	**1156.58**	578.80	**1155.60**	578.30	12
9	**868.45**	434.73	851.43	426.22	850.44	**425.72**	S	**1076.56**	**538.78**	1059.53	530.27	1058.55	529.78	11
10	955.48	478.25	938.46	**469.73**	937.47	**469.24**	S	**989.53**	495.27	972.50	486.75	971.52	486.26	10
11	**1056.53**	528.77	1039.51	520.26	**1038.52**	519.76	T	**902.49**	451.75	885.47	443.24	884.48	442.75	9
12	1113.55	557.28	1096.53	548.77	1095.54	548.28	G	**801.45**	401.23	784.42	392.71			8
13	**1184.59**	592.80	1167.56	584.29	1166.58	583.79	A	744.43	372.72	727.40	364.20			7
14	**1255.63**	628.32	1238.60	619.80	1237.62	619.31	A	**673.39**	337.20	656.36	328.68			6
15	**1483.74**	742.37	**1466.71**	733.86	**1465.73**	733.37	K	602.35	301.68	585.32	293.17			5
16	**1554.78**	777.89	1537.75	769.38	1536.77	768.89	A	**374.24**	187.62	357.21	179.11			4
17	**1653.84**	827.43	**1636.82**	818.91	**1635.83**	818.42	V	**303.20**	152.10	286.18	143.59			3
18	**1710.87**	855.94	**1693.84**	847.42	1692.86	846.93	G	204.13	102.57	187.11	94.06			2
19							K	147.11	74.06	130.09	65.55			1

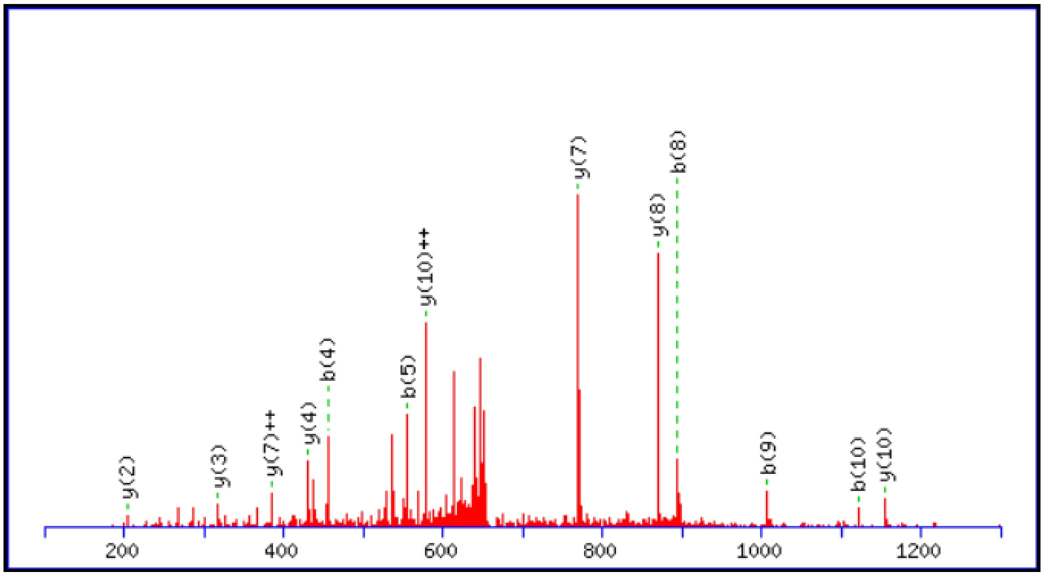
glyceraldehyde-3-phosphate dehydrogenase A K217

AVG^{Succ}KVLPELNGK

MS/MS Fragmentation of **AVGKVLPELNGK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 5028: 1323.746614 from(662.880583,2+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da

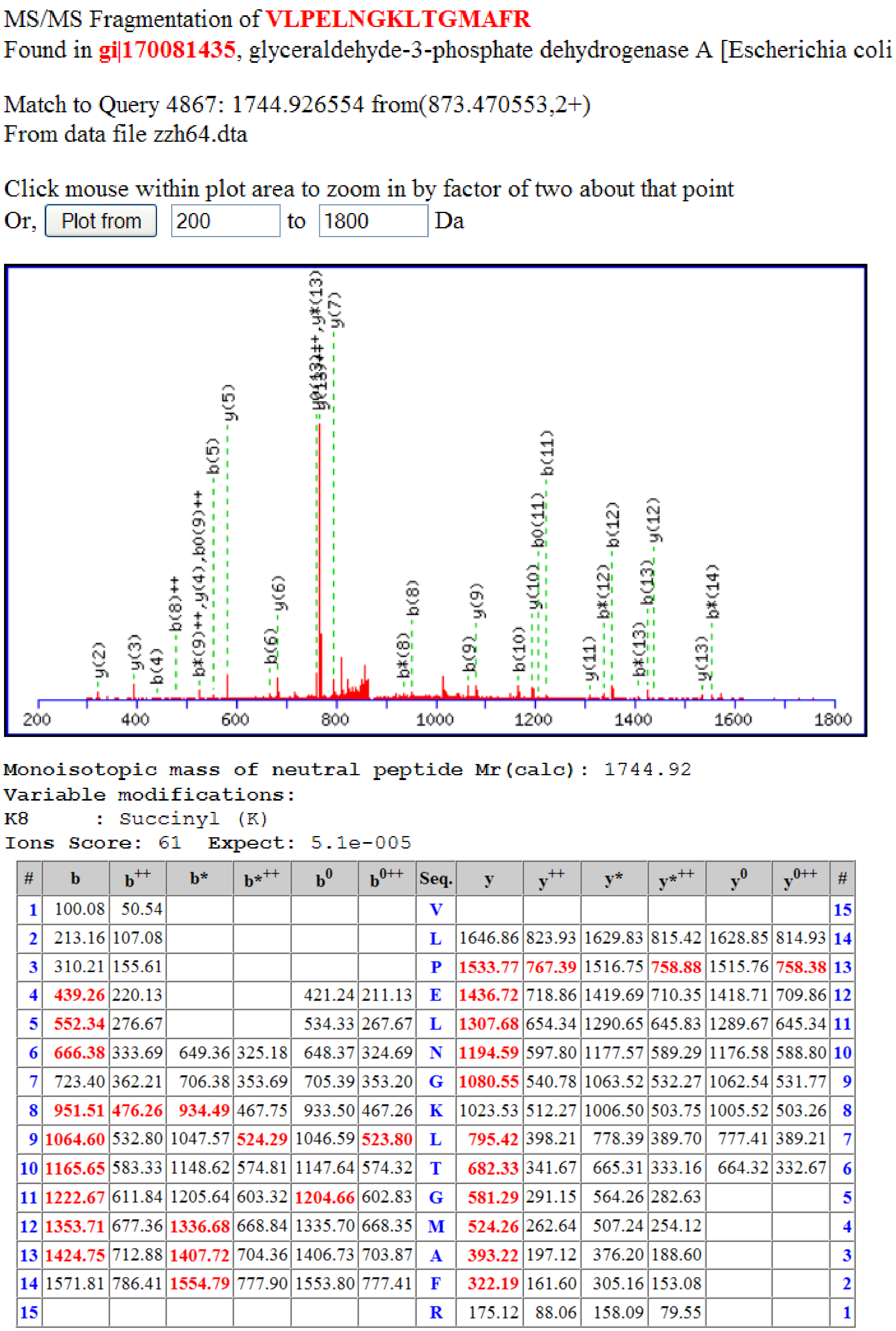


```
Monoisotopic mass of neutral peptide Mr(calc): 1323.74
Variable modifications:
K4       : Succinyl (K)
Ions Score: 34   Expect: 0.021
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.04	36.53					A							12
2	171.11	86.06					V	1253.71	627.36	1236.68	618.85	1235.70	618.35	11
3	228.13	114.57					G	**1154.64**	**577.82**	1137.61	569.31	1136.63	568.82	10
4	**456.25**	228.63	439.22	220.11			K	1097.62	549.31	1080.59	540.80	1079.61	540.31	9
5	**555.31**	278.16	538.29	269.65			V	**869.51**	435.26	852.48	426.74	851.50	426.25	8
6	668.40	334.70	651.37	326.19			L	**770.44**	**385.72**	753.41	377.21	752.43	376.72	7
7	765.45	383.23	748.42	374.72			P	657.36	329.18	640.33	320.67	639.35	320.18	6
8	**894.49**	447.75	877.47	439.24	876.48	438.74	E	560.30	280.66	543.28	272.14	542.29	271.65	5
9	**1007.58**	504.29	990.55	495.78	989.57	495.29	L	**431.26**	216.13	414.23	207.62			4
10	**1121.62**	561.31	1104.59	552.80	1103.61	552.31	N	**318.18**	159.59	301.15	151.08			3
11	1178.64	589.82	1161.61	581.31	1160.63	580.82	G	**204.13**	102.57	187.11	94.06			2
12							K	147.11	74.06	130.09	65.55			1

glyceraldehyde-3-phosphate dehydrogenase A K225

VLPELNG^{Succ}KLTGMAFR



MS/MS Fragmentation of **VLPELNGKLTGMAFR**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 4867: 1744.926554 from(873.470553,2+)
From data file zzh64.dta

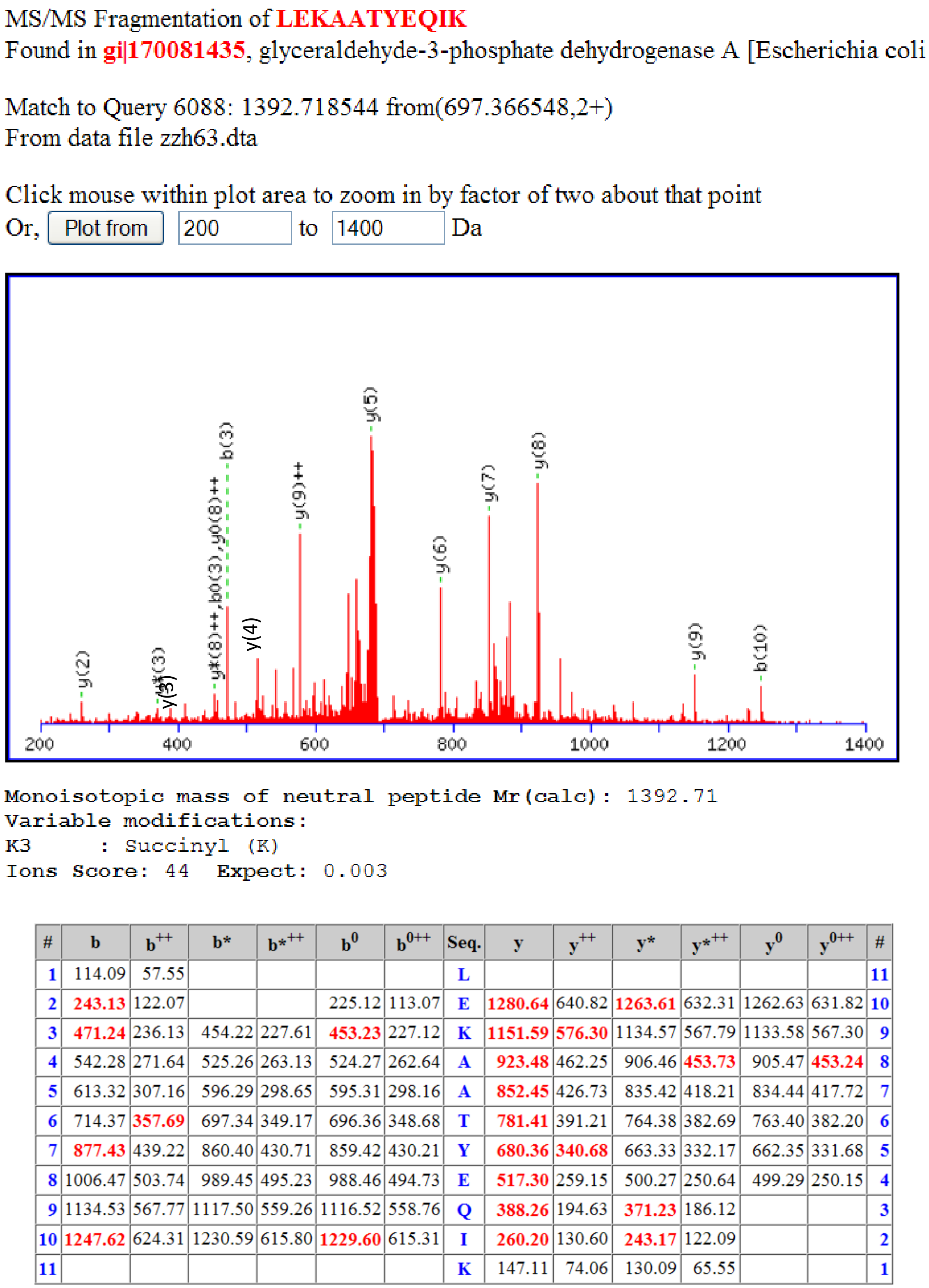
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1744.92
Variable modifications:
K8      : Succinyl (K)
Ions Score: 61  Expect: 5.1e-005
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.08	50.54					V							15
2	213.16	107.08					L	1646.86	823.93	1629.83	815.42	1628.85	814.93	14
3	310.21	155.61					P	**1533.77**	**767.39**	1516.75	**758.88**	1515.76	**758.38**	13
4	**439.26**	220.13			421.24	211.13	E	**1436.72**	718.86	1419.69	710.35	1418.71	709.86	12
5	**552.34**	276.67			534.33	267.67	L	**1307.68**	654.34	1290.65	645.83	1289.67	645.34	11
6	**666.38**	333.69	649.36	325.18	648.37	324.69	N	**1194.59**	597.80	1177.57	589.29	1176.58	588.80	10
7	723.40	362.21	706.38	353.69	705.39	353.20	G	**1080.55**	540.78	1063.52	532.27	1062.54	531.77	9
8	**951.51**	**476.26**	**934.49**	467.75	933.50	467.26	K	1023.53	512.27	1006.50	503.75	1005.52	503.26	8
9	**1064.60**	532.80	1047.57	**524.29**	1046.59	**523.80**	L	**795.42**	398.21	778.39	389.70	777.41	389.21	7
10	**1165.65**	583.33	1148.62	574.81	1147.64	574.32	T	**682.33**	341.67	665.31	333.16	664.32	332.67	6
11	**1222.67**	611.84	1205.64	603.32	**1204.66**	602.83	G	**581.29**	291.15	564.26	282.63			5
12	**1353.71**	677.36	**1336.68**	668.84	1335.70	668.35	M	**524.26**	262.64	507.24	254.12			4
13	**1424.75**	712.88	**1407.72**	704.36	1406.73	703.87	A	**393.22**	197.12	376.20	188.60			3
14	1571.81	786.41	**1554.79**	777.90	1553.80	777.41	F	**322.19**	161.60	305.16	153.08			2
15							R	175.12	88.06	158.09	79.55			1

glyceraldehyde-3-phosphate dehydrogenase A K249

LE^{Succ}KAATYEQIK



MS/MS Fragmentation of **LEKAATYEQIK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 6088: 1392.718544 from(697.366548,2+)
From data file zzh63.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1392.71
Variable modifications:
K3      : Succinyl (K)
Ions Score: 44  Expect: 0.003
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.09	57.55					L							11
2	**243.13**	122.07			225.12	113.07	E	**1280.64**	640.82	**1263.61**	632.31	1262.63	631.82	10
3	**471.24**	236.13	454.22	227.61	**453.23**	227.12	K	**1151.59**	**576.30**	1134.57	567.79	1133.58	567.30	9
4	542.28	271.64	525.26	263.13	524.27	262.64	A	**923.48**	462.25	906.46	**453.73**	905.47	**453.24**	8
5	613.32	307.16	596.29	298.65	595.31	298.16	A	**852.45**	426.73	835.42	418.21	834.44	417.72	7
6	714.37	**357.69**	697.34	349.17	696.36	348.68	T	**781.41**	391.21	764.38	382.69	763.40	382.20	6
7	**877.43**	439.22	860.40	430.71	859.42	430.21	Y	**680.36**	**340.68**	663.33	332.17	662.35	331.68	5
8	1006.47	503.74	989.45	495.23	988.46	494.73	E	**517.30**	259.15	500.27	250.64	499.29	250.15	4
9	1134.53	567.77	1117.50	559.26	1116.52	558.76	Q	**388.26**	194.63	**371.23**	186.12			3
10	**1247.62**	624.31	1230.59	615.80	**1229.60**	615.31	I	**260.20**	130.60	**243.17**	122.09			2
11							K	147.11	74.06	130.09	65.55			1

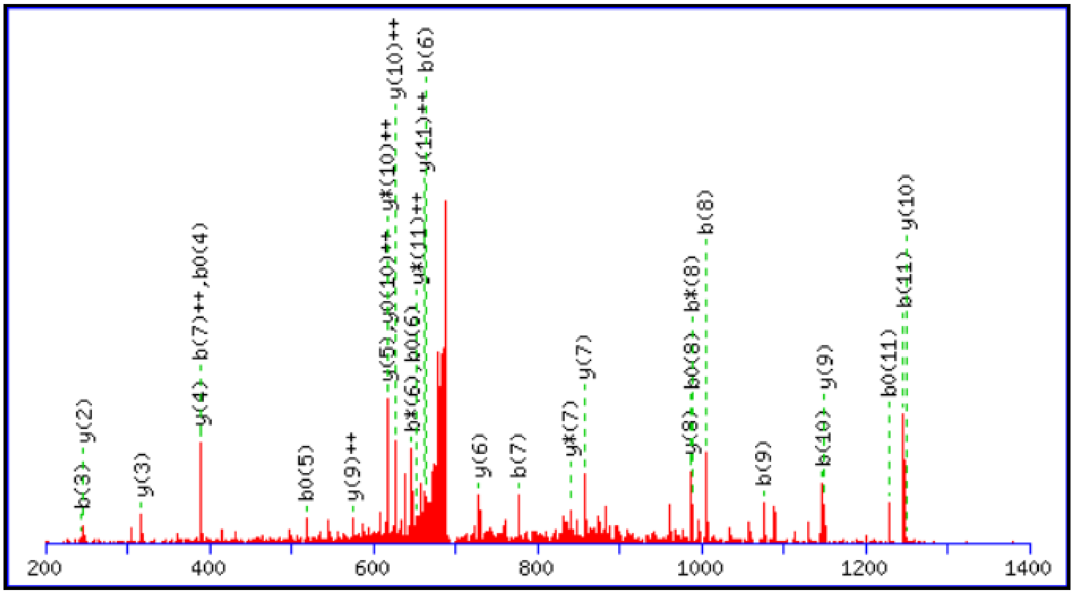
glyceraldehyde-3-phosphate dehydrogenase A K257

AATYEQI^{Succ}KAAVK

MS/MS Fragmentation of **AATYEQIKAAVK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 3316: 1391.735994 from(696.875273,2+)
From data file zzh64.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da

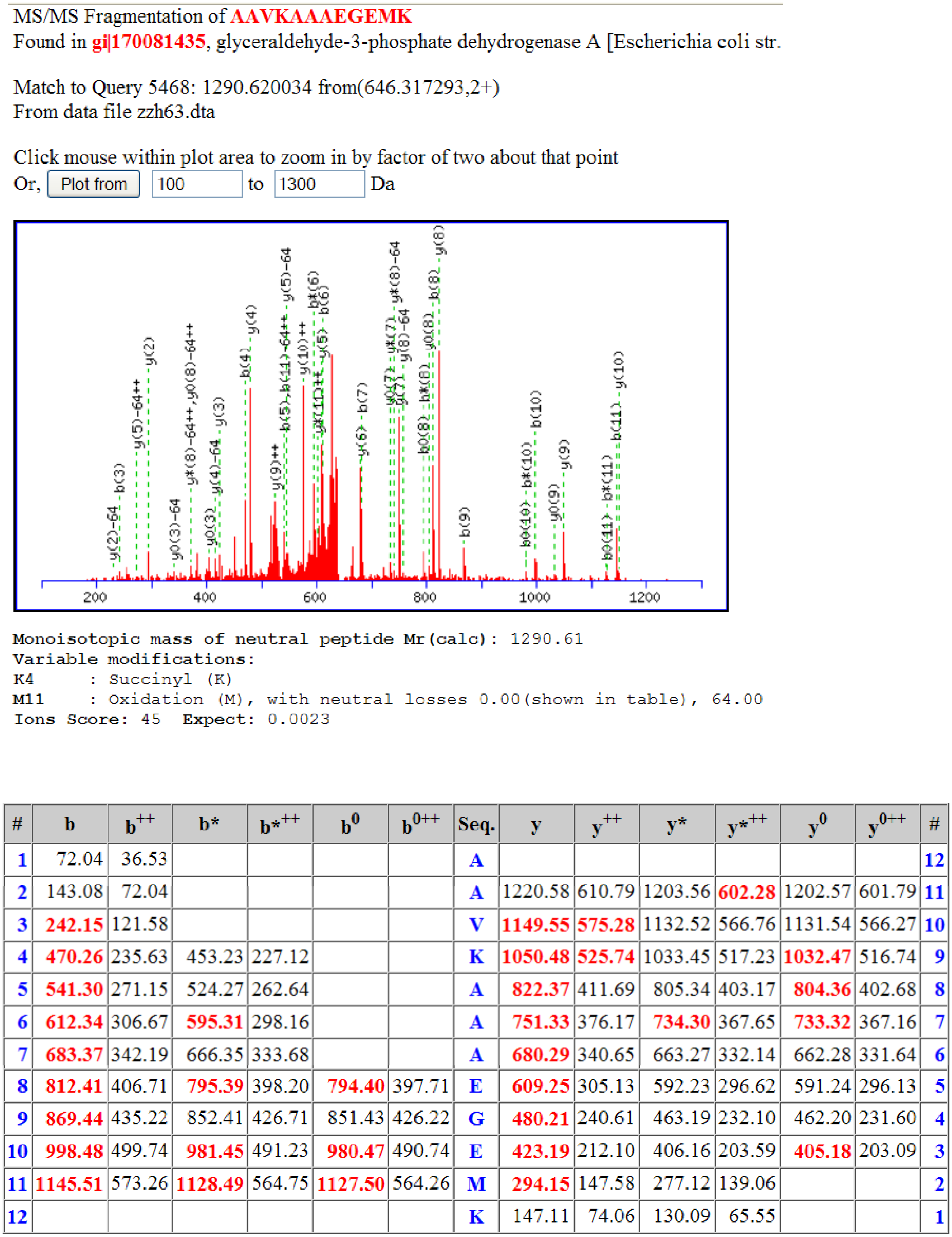


```
Monoisotopic mass of neutral peptide Mr(calc): 1391.73
Variable modifications:
K8      : Succinyl (K)
Ions Score: 45  Expect: 0.0018
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.04	36.53					A							12
2	143.08	72.04					A	1321.70	**661.35**	1304.67	**652.84**	1303.69	652.35	11
3	**244.13**	122.57			226.12	113.56	T	**1250.66**	**625.83**	1233.64	**617.32**	1232.65	**616.83**	10
4	407.19	204.10			**389.18**	195.09	Y	**1149.62**	**575.31**	1132.59	566.80	1131.60	566.31	9
5	536.24	268.62			**518.22**	259.62	E	**986.55**	493.78	969.53	485.27	968.54	484.77	8
6	**664.29**	332.65	**647.27**	324.14	**646.28**	323.65	Q	**857.51**	429.26	**840.48**	420.74			7
7	**777.38**	**389.19**	760.35	380.68	759.37	380.19	I	**729.45**	365.23	712.42	356.72			6
8	**1005.49**	503.25	**988.46**	494.73	**987.48**	494.24	K	**616.37**	308.69	599.34	300.17			5
9	**1076.53**	538.77	1059.50	530.25	1058.52	529.76	A	**388.26**	194.63	371.23	186.12			4
10	**1147.56**	574.29	1130.54	565.77	1129.55	565.28	A	**317.22**	159.11	300.19	150.60			3
11	**1246.63**	623.82	1229.60	615.31	**1228.62**	614.81	V	**246.18**	123.59	229.15	115.08			2
12							K	147.11	74.06	130.09	65.55			1

glyceraldehyde-3-phosphate dehydrogenase A K261

AAV^{Succ}KAAAEGEMK


MS/MS Fragmentation of **AAVKAAAEGEMK**
Found in **gi|170081435**, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli str.

Match to Query 5468: 1290.620034 from(646.317293,2+)
From data file zzh63.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1290.61
Variable modifications:
K4      : Succinyl (K)
M11     : Oxidation (M), with neutral losses 0.00(shown in table), 64.00
Ions Score: 45  Expect: 0.0023
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.04	36.53					A							12
2	143.08	72.04					A	1220.58	610.79	1203.56	**602.28**	1202.57	601.79	11
3	**242.15**	121.58					V	**1149.55**	**575.28**	1132.52	566.76	1131.54	566.27	10
4	**470.26**	235.63	453.23	227.12			K	**1050.48**	**525.74**	1033.45	517.23	**1032.47**	516.74	9
5	**541.30**	271.15	524.27	262.64			A	**822.37**	411.69	805.34	403.17	**804.36**	402.68	8
6	**612.34**	306.67	**595.31**	298.16			A	**751.33**	376.17	**734.30**	367.65	**733.32**	367.16	7
7	**683.37**	342.19	666.35	333.68			A	**680.29**	340.65	663.27	332.14	662.28	331.64	6
8	**812.41**	406.71	**795.39**	398.20	**794.40**	397.71	E	**609.25**	305.13	592.23	296.62	591.24	296.13	5
9	**869.44**	435.22	852.41	426.71	851.43	426.22	G	**480.21**	240.61	463.19	232.10	462.20	231.60	4
10	**998.48**	499.74	**981.45**	491.23	**980.47**	490.74	E	**423.19**	212.10	406.16	203.59	**405.18**	203.09	3
11	**1145.51**	573.26	**1128.49**	564.75	**1127.50**	564.26	M	**294.15**	147.58	277.12	139.06			2
12							K	147.11	74.06	130.09	65.55			1

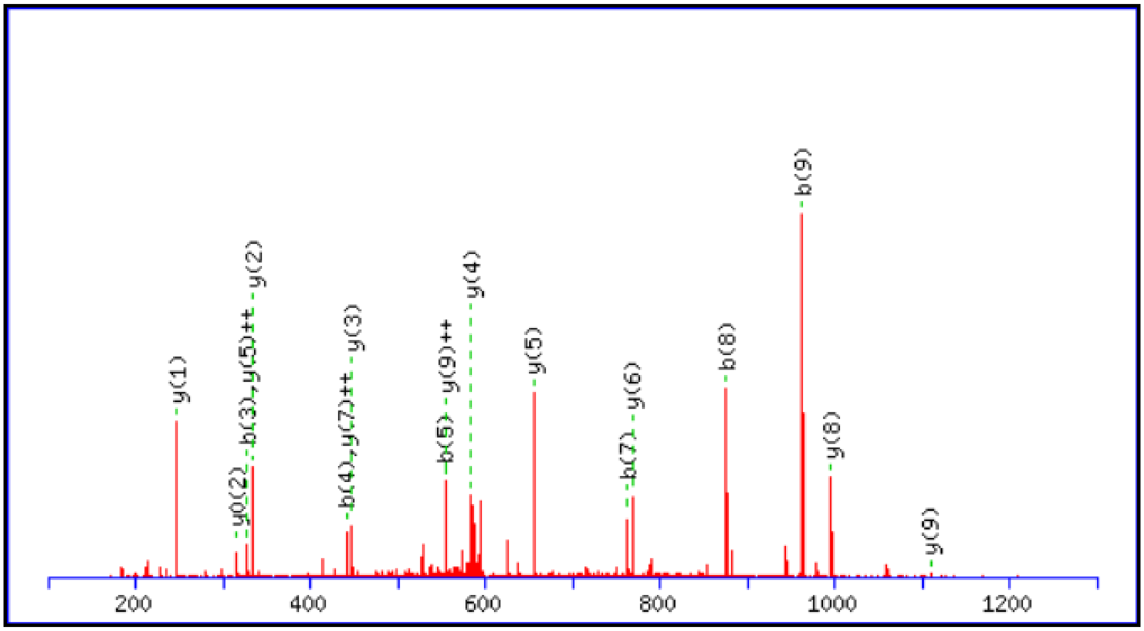
glyceraldehyde-3-phosphate dehydrogenase A K331

VLDLIAHIS$^{\text{Succ}}$K

MS/MS Fragmentation of VLDLIAHISK
Found in gi|170081435, glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli

Match to Query 2410: 1207.686074 from(604.850313,2+)
From data file zzh64.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da



```
Monoisotopic mass of neutral peptide Mr(calc): 1207.68
Variable modifications:
K10     : Succinyl (K)
Ions Score: 70  Expect: 4.9e-006
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.08	50.54			V							10
2	213.16	107.08			L	1109.62	555.31	1092.59	546.80	1091.61	546.31	9
3	328.19	164.60	310.18	155.59	D	996.54	498.77	979.51	490.26	978.53	489.77	8
4	441.27	221.14	423.26	212.13	L	881.51	441.26	864.48	432.74	863.50	432.25	7
5	554.35	277.68	536.34	268.68	I	768.43	384.72	751.40	376.20	750.41	375.71	6
6	625.39	313.20	607.38	304.19	A	655.34	328.17	638.31	319.66	637.33	319.17	5
7	762.45	381.73	744.44	372.72	H	584.30	292.66	567.28	284.14	566.29	283.65	4
8	875.53	438.27	857.52	429.27	I	447.24	224.13	430.22	215.61	429.23	215.12	3
9	962.57	481.79	944.56	472.78	S	334.16	167.58	317.13	159.07	316.15	158.58	2
10					K	247.13	124.07	230.10	115.55			1

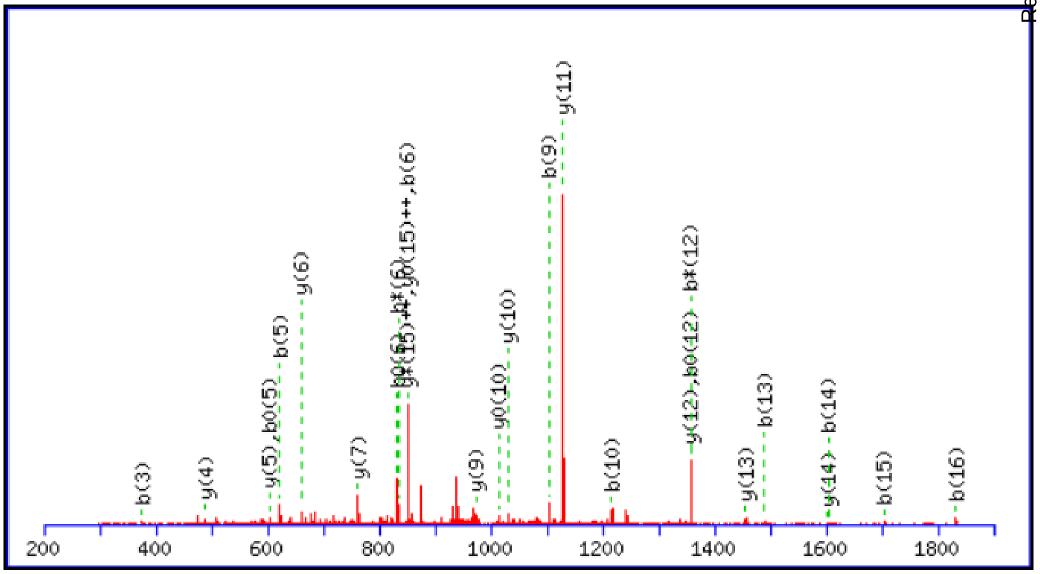
fructose-bisphosphate aldolase, class II K9

IFDFV^{Succ}KPGVITGDDVQK

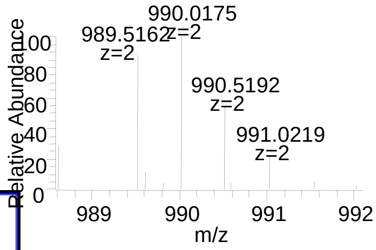
MS/MS Fragmentation of **IFDFVKPGVITGDDVQK**
Found in **gi|170082482**, fructose-bisphosphate aldolase, class II [Escherichia coli str. K

Match to Query 8029: 1978.020914 from(990.017733,2+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da



Precusor Ion



```
Monoisotopic mass of neutral peptide Mr(calc): 1977.01
Variable modifications:
K6      : Succinyl (K)
Ions Score: 52   Expect: 0.00048
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.09	57.55					I							17
2	261.16	131.08					F	1864.93	932.97	1847.91	924.46	1846.92	923.96	16
3	**376.19**	188.60			358.18	179.59	D	1717.86	859.44	1700.84	**850.92**	1699.85	**850.43**	15
4	523.26	262.13			505.24	253.13	F	**1602.84**	801.92	1585.81	793.41	1584.83	792.92	14
5	**622.32**	311.67			**604.31**	302.66	V	**1455.77**	728.39	1438.74	719.87	1437.76	719.38	13
6	**850.43**	425.72	**833.41**	417.21	**832.42**	416.72	K	**1356.70**	678.85	1339.67	670.34	1338.69	669.85	12
7	947.49	474.25	930.46	465.73	929.48	465.24	P	**1128.59**	564.80	1111.56	556.29	1110.58	555.79	11
8	1004.51	502.76	987.48	494.24	986.50	493.75	G	**1031.54**	516.27	1014.51	507.76	**1013.53**	507.27	10
9	**1103.58**	552.29	1086.55	543.78	1085.57	543.29	V	**974.52**	487.76	957.49	479.25	956.50	478.76	9
10	**1216.66**	608.83	1199.63	600.32	1198.65	599.83	I	875.45	438.23	858.42	429.71	857.44	429.22	8
11	1317.71	659.36	1300.68	650.84	1299.70	650.35	T	**762.36**	381.69	745.34	373.17	744.35	372.68	7
12	1374.73	687.87	**1357.70**	679.36	**1356.72**	678.86	G	**661.32**	331.16	644.29	322.65	643.30	322.16	6
13	**1489.76**	745.38	1472.73	736.87	1471.75	736.38	D	**604.29**	302.65	587.27	294.14	586.28	293.65	5
14	**1604.78**	802.90	1587.76	794.38	1586.77	793.89	D	**489.27**	245.14	472.24	236.62	471.26	236.13	4
15	**1703.85**	852.43	1686.83	843.92	1685.84	843.42	V	374.24	187.62	357.21	179.11			3
16	**1831.91**	916.46	1814.88	907.95	1813.90	907.45	Q	275.17	138.09	258.14	129.58			2
17							K	147.11	74.06	130.09	65.55			1

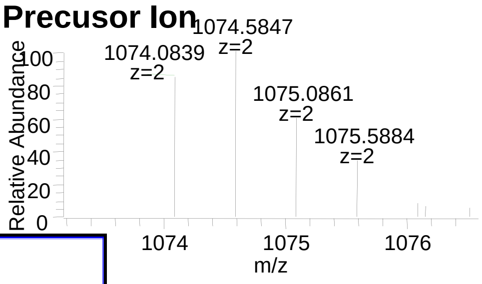
fructose-bisphosphate aldolase, class II K72

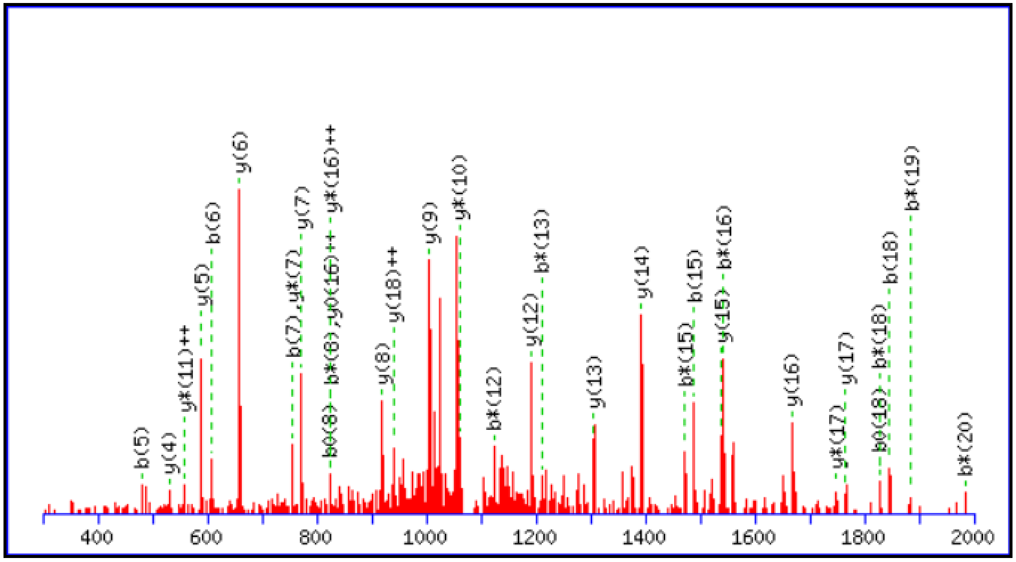
APVIVQFSNGGASFIAG^{Succ}KGVK

MS/MS Fragmentation of **APVIVQFSNGGASFIAGKGVK**
Found in **gi|170082482**, fructose-bisphosphate aldolase, class II [Escherichia coli str. K

Match to Query 8464: 2147.155434 from(1074.584993,2+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da


Precusor Ion



```
Monoisotopic mass of neutral peptide Mr(calc): 2146.14
Variable modifications:
K18      : Succinyl (K)
Ions Scor
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.04	36.53					A							21
2	169.10	85.05					P	2076.11	1038.56	2059.09	1030.05	2058.10	1029.55	20
3	268.17	134.59					V	1979.06	990.03	1962.03	981.52	1961.05	981.03	19
4	381.25	191.13					I	1879.99	**940.50**	1862.96	931.99	1861.98	931.49	18
5	**480.32**	240.66					V	**1766.91**	883.96	**1749.88**	875.44	1748.90	874.95	17
6	**608.38**	304.69	591.35	296.18			Q	**1667.84**	834.42	1650.81	**825.91**	1649.83	**825.42**	16
7	**755.45**	378.23	738.42	369.71			F	**1539.78**	770.39	1522.75	761.88	1521.77	761.39	15
8	842.48	421.74	**825.45**	413.23	**824.47**	412.74	S	**1392.71**	696.86	1375.69	688.35	1374.70	687.85	14
9	956.52	478.76	939.49	470.25	938.51	469.76	N	**1305.68**	653.34	1288.65	644.83	1287.67	644.34	13
10	1013.54	507.27	996.51	498.76	995.53	498.27	G	**1191.64**	596.32	1174.61	587.81	1173.63	587.32	12
11	1070.56	535.79	1053.54	527.27	1052.55	526.78	G	1134.62	567.81	1117.59	**559.30**	1116.60	558.81	11
12	1141.60	571.30	**1124.57**	562.79	1123.59	562.30	A	1077.59	539.30	**1060.57**	530.79	1059.58	530.30	10
13	1228.63	614.82	**1211.61**	606.31	1210.62	605.81	S	**1006.56**	503.78	989.53	495.27	988.55	494.78	9
14	1375.70	688.35	1358.67	679.84	1357.69	679.35	F	**919.52**	460.27	902.50	451.75			8
15	**1488.78**	744.90	**1471.76**	736.38	1470.77	735.89	I	**772.46**	386.73	**755.43**	378.22			7
16	1559.82	780.41	**1542.80**	771.90	1541.81	771.41	A	**659.37**	330.19	642.35	321.68			6
17	1616.84	808.93	1599.82	800.41	1598.83	799.92	G	**588.34**	294.67	571.31	286.16			5
18	**1844.95**	922.98	**1827.93**	914.47	**1826.94**	913.98	K	**531.31**	266.16	514.29	257.65			4
19	1901.98	951.49	**1884.95**	942.98	1883.96	942.49	G	303.20	152.10	286.18	143.59			3
20	2001.04	1001.03	**1984.02**	992.51	1983.03	992.02	V	246.18	123.59	229.15	115.08			2
21							K	147.11	74.06	130.09	65.55			1

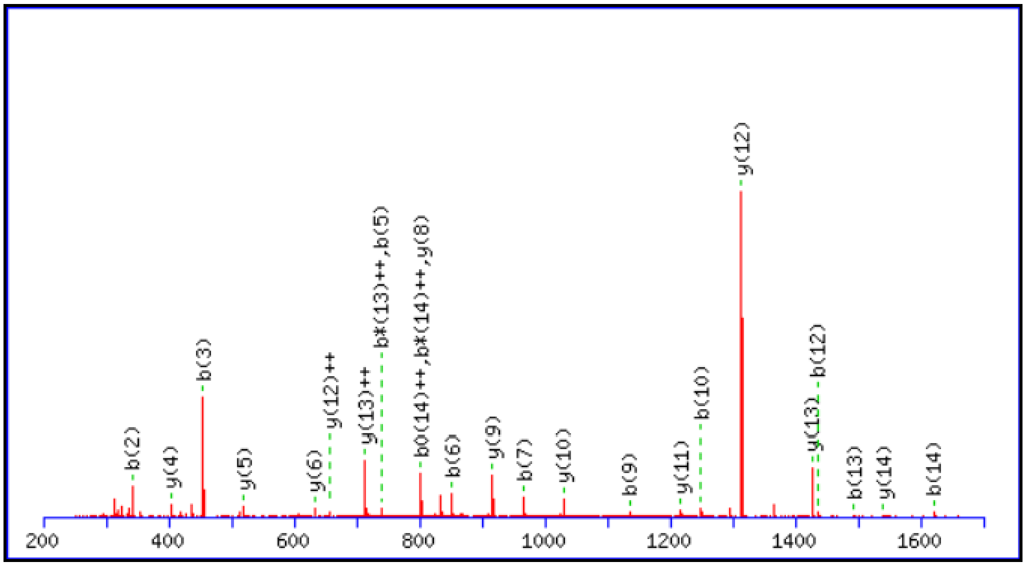
fructose-bisphosphate aldolase, class II K115

^{Succ}KLLPWIDGLLDAGEK

MS/MS Fragmentation of **KLLPWIDGLLDAGEK**
Found in **gi|170082482**, fructose-bisphosphate aldolase, class II [Escherichia coli str. K

Match to Query 7183: 1766.953404 from(884.483978,2+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da



```
Monoisotopic mass of neutral peptide Mr(calc): 1766.95
Variable modifications:
K1      : Succinyl (K)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	229.12	115.06	212.09	106.55			K							15
2	**342.20**	171.60	325.18	163.09			L	**1539.84**	770.42	1522.82	761.91	1521.83	761.42	14
3	**455.29**	228.15	438.26	219.63			L	**1426.76**	**713.88**	1409.73	705.37	1408.75	704.88	13
4	552.34	276.67	535.31	268.16			P	**1313.67**	**657.34**	1296.65	648.83	1295.66	648.34	12
5	**738.42**	369.71	721.39	361.20			W	**1216.62**	608.81	1199.59	600.30	1198.61	599.81	11
6	**851.50**	426.25	834.48	417.74			I	**1030.54**	515.77	1013.51	507.26	1012.53	506.77	10
7	**966.53**	483.77	949.50	475.26	948.52	474.76	D	**917.46**	459.23	900.43	450.72	899.45	450.23	9
8	1023.55	512.28	1006.52	503.77	1005.54	503.27	G	**802.43**	401.72	785.40	393.21	784.42	392.71	8
9	**1136.63**	568.82	1119.61	560.31	1118.62	559.82	L	745.41	373.21	728.38	364.69	727.40	364.20	7
10	**1249.72**	625.36	1232.69	616.85	1231.71	616.36	L	**632.32**	316.67	615.30	308.15	614.31	307.66	6
11	1364.75	682.88	1347.72	674.36	1346.74	673.87	D	**519.24**	260.12	502.21	251.61	501.23	251.12	5
12	**1435.78**	718.40	1418.76	709.88	1417.77	709.39	A	**404.21**	202.61	387.19	194.10	386.20	193.61	4
13	**1492.80**	746.91	1475.78	**738.39**	1474.79	737.90	G	333.18	167.09	316.15	158.58	315.17	158.09	3
14	**1621.85**	811.43	1604.82	**802.91**	1603.84	**802.42**	E	276.16	138.58	259.13	130.07	258.14	129.58	2
15							K	147.11	74.06	130.09	65.55			1

fructose-bisphosphate aldolase, class II K231

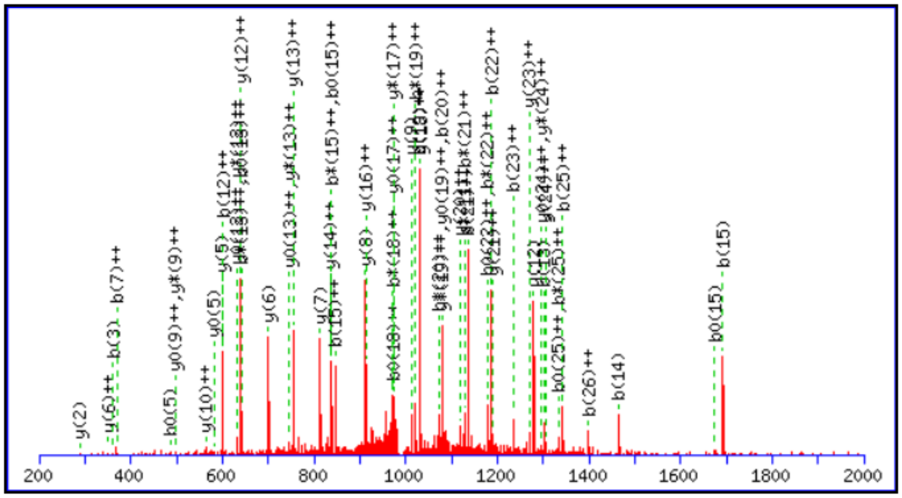
FTIAASFGNVHGVY^Succ^KPGNVVLTPTILR

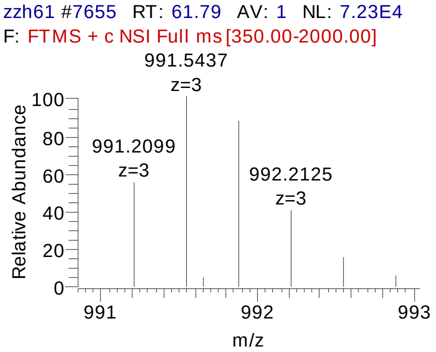
MS/MS Fragmentation of **FTIAASFGNVHGVYKPGNVVLTPTILR**
Found in **gi|170082482**, fructose-bisphosphate aldolase, class II [Escherichia coli str. K

Match to Query 9890: 2971.616781 from(991.546203,3+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da

Precursor ion





```
Monoisotopic mass of neutral peptide Mr(calc): 2970.60
Variable modifications:
K15     : Succinyl (K)
Ions Score: 45   Expect: 0.0038
```

#	b	b^++^	b*	b*^++^	b^0^	b^0++^	Seq.	y	y^++^	y*	y*^++^	y^0^	y^0++^	#
1	148.08	74.54					F							27
2	249.12	125.07			231.11	116.06	T	2824.54	1412.77	2807.51	1404.26	2806.52	1403.77	26
3	**362.21**	181.61			344.20	172.60	I	2723.49	1362.25	2706.46	1353.73	2705.48	1353.24	25
4	433.24	217.13			415.23	208.12	A	2610.40	**1305.71**	2593.38	**1297.19**	2592.39	**1296.70**	24
5	504.28	252.64			**486.27**	243.64	A	2539.37	**1270.19**	2522.34	1261.67	2521.36	1261.18	23
6	591.31	296.16			573.30	287.16	S	2468.33	1234.67	2451.30	1226.16	2450.32	1225.66	22
7	738.38	**369.69**			720.37	360.69	F	2381.30	**1191.15**	2364.27	1182.64	2363.29	1182.15	21
8	795.40	398.21			777.39	389.20	G	2234.23	**1117.62**	2217.20	1109.10	2216.22	1108.61	20
9	909.45	455.23	892.42	446.71	891.44	446.22	N	2177.21	1089.11	2160.18	**1080.59**	2159.20	**1080.10**	19
10	1008.51	504.76	991.49	496.25	990.50	495.76	V	2063.16	**1032.09**	2046.14	1023.57	2045.15	1023.08	18
11	1145.57	573.29	**1128.55**	564.78	1127.56	564.29	H	1964.10	982.55	1947.07	**974.04**	1946.09	**973.55**	17
12	1202.60	**601.80**	1185.57	593.29	1184.58	592.80	G	1827.04	**914.02**	1810.01	905.51	1809.03	905.02	16
13	**1301.66**	651.34	1284.64	**642.82**	1283.65	**642.33**	V	1770.02	885.51	1752.99	877.00	1752.01	876.51	15
14	**1464.73**	732.87	1447.70	724.35	1446.72	723.86	Y	1670.95	**835.98**	1653.92	827.46	1652.94	826.97	14
15	**1692.84**	**846.92**	1675.81	**838.41**	**1674.83**	**837.92**	K	1507.88	**754.45**	1490.86	**745.93**	1489.87	**745.44**	13
16	1789.89	895.45	1772.86	886.94	1771.88	886.44	P	**1279.77**	**640.39**	1262.75	**631.88**	1261.76	**631.38**	12
17	1846.91	923.96	1829.89	915.45	1828.90	914.95	G	1182.72	591.86	1165.69	583.35	1164.71	582.86	11
18	1960.96	980.98	1943.93	**972.47**	1942.94	**971.98**	N	1125.70	**563.35**	1108.67	554.84	1107.69	554.35	10
19	2060.02	**1030.52**	2043.00	**1022.00**	2042.01	1021.51	V	**1011.66**	506.33	994.63	**497.82**	993.65	**497.33**	9
20	2159.09	**1080.05**	2142.07	**1071.54**	2141.08	1071.04	V	**912.59**	456.80	895.56	448.28	894.58	447.79	8
21	2272.18	**1136.59**	2255.15	**1128.08**	2254.17	1127.59	L	**813.52**	407.26	796.49	398.75	795.51	398.26	7
22	2373.22	**1187.12**	2356.20	**1178.60**	2355.21	**1178.11**	T	**700.44**	**350.72**	683.41	342.21	682.42	341.72	6
23	2470.28	**1235.64**	2453.25	1227.13	2452.27	1226.64	P	**599.39**	300.20	582.36	291.68	**581.38**	291.19	5
24	2571.32	1286.17	2554.30	1277.65	2553.31	1277.16	T	502.33	251.67	485.31	243.16	484.32	242.67	4
25	2684.41	**1342.71**	2667.38	**1334.19**	2666.40	**1333.70**	I	401.29	201.15	384.26	192.63			3
26	2797.49	**1399.25**	2780.47	1390.74	2779.48	1390.24	L	**288.20**	144.61	271.18	136.09			2
27							R	175.12	88.06	158.09	79.55			1

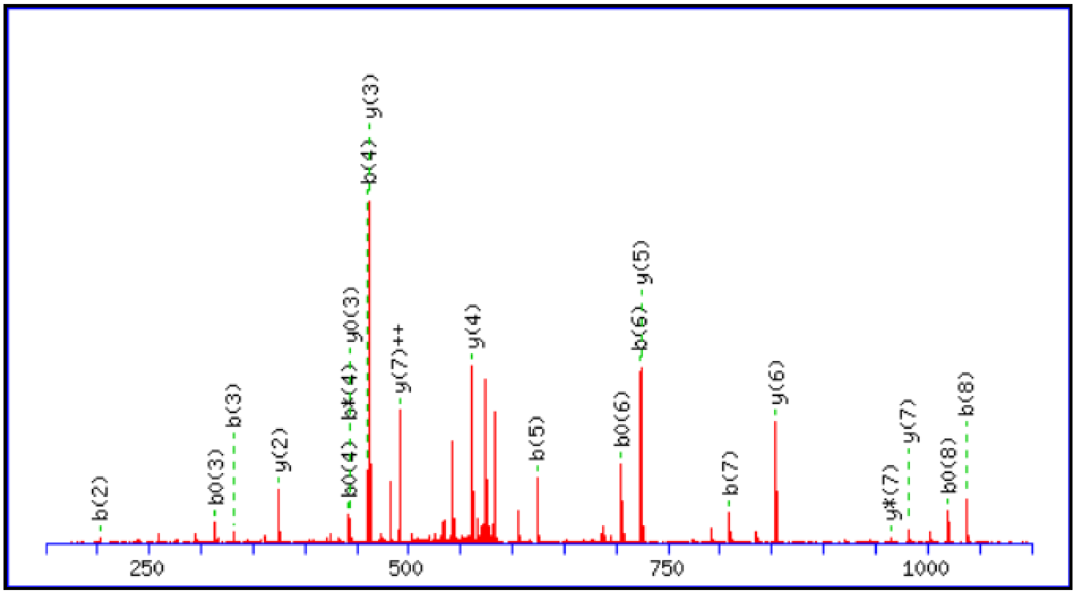
fructose-bisphosphate aldolase, class II K251

DSQEYVS^{Succ}KK

MS/MS Fragmentation of **DSQEYVSKK**
Found in **gi|170082482**, fructose-bisphosphate aldolase, class II [Escherichia coli str. K

Match to Query 3902: 1182.546244 from(592.280398,2+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da



```
Monoisotopic mass of neutral peptide Mr(calc): 1182.54
Variable modifications:
K8      : Succinyl (K)
Ions Score: 45   Expect: 0.0016
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.03	58.52			98.02	49.52	D							9
2	**203.07**	102.04			185.06	93.03	S	1068.52	534.76	1051.49	526.25	1050.51	525.76	8
3	**331.12**	166.07	314.10	157.55	**313.11**	157.06	Q	**981.49**	**491.25**	**964.46**	482.73	963.48	482.24	7
4	**460.17**	230.59	**443.14**	222.07	**442.16**	221.58	E	**853.43**	427.22	836.40	418.71	835.42	418.21	6
5	**623.23**	312.12	606.20	303.61	605.22	303.11	Y	**724.39**	362.70	707.36	354.18	706.38	353.69	5
6	**722.30**	361.65	705.27	353.14	**704.29**	352.65	V	**561.32**	281.17	544.30	272.65	543.31	272.16	4
7	**809.33**	405.17	792.30	396.66	791.32	396.16	S	**462.26**	231.63	445.23	223.12	**444.25**	222.63	3
8	**1037.44**	519.22	1020.42	510.71	**1019.43**	510.22	K	**375.22**	188.12	358.20	179.60			2
9							K	147.11	74.06	130.09	65.55			1

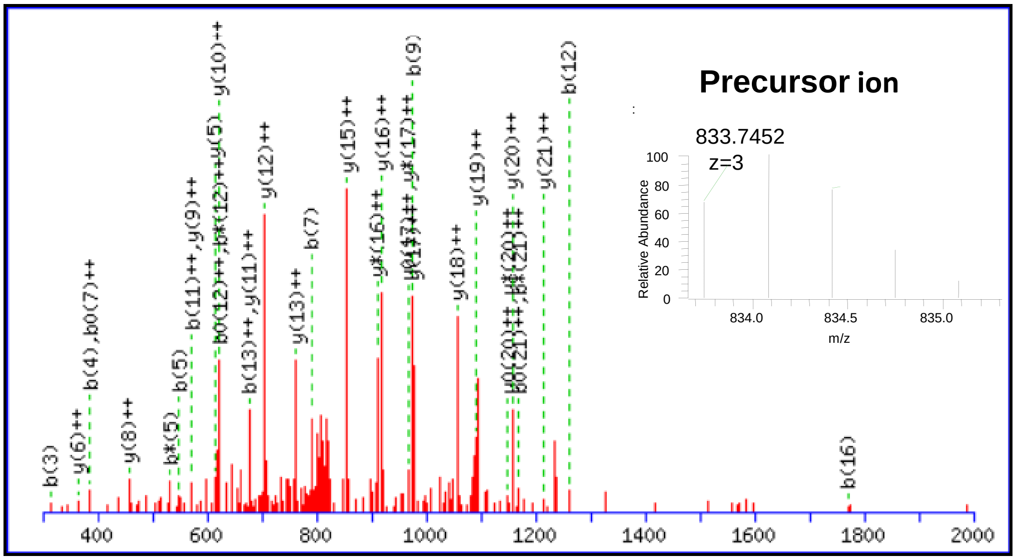
fructose-bisphosphate aldolase, class II K319

ANEAYLQGQLGNPKGEDQPN^{Succ}KK

MS/MS Fragmentation of **ANEAYLQGQLGNPKGEDQPNKK**
Found in **gi|170082482**, fructose-bisphosphate aldolase, class II [Escherichia coli str. K-1

Match to Query 9192: 2499.219501 from(834.080443,3+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da

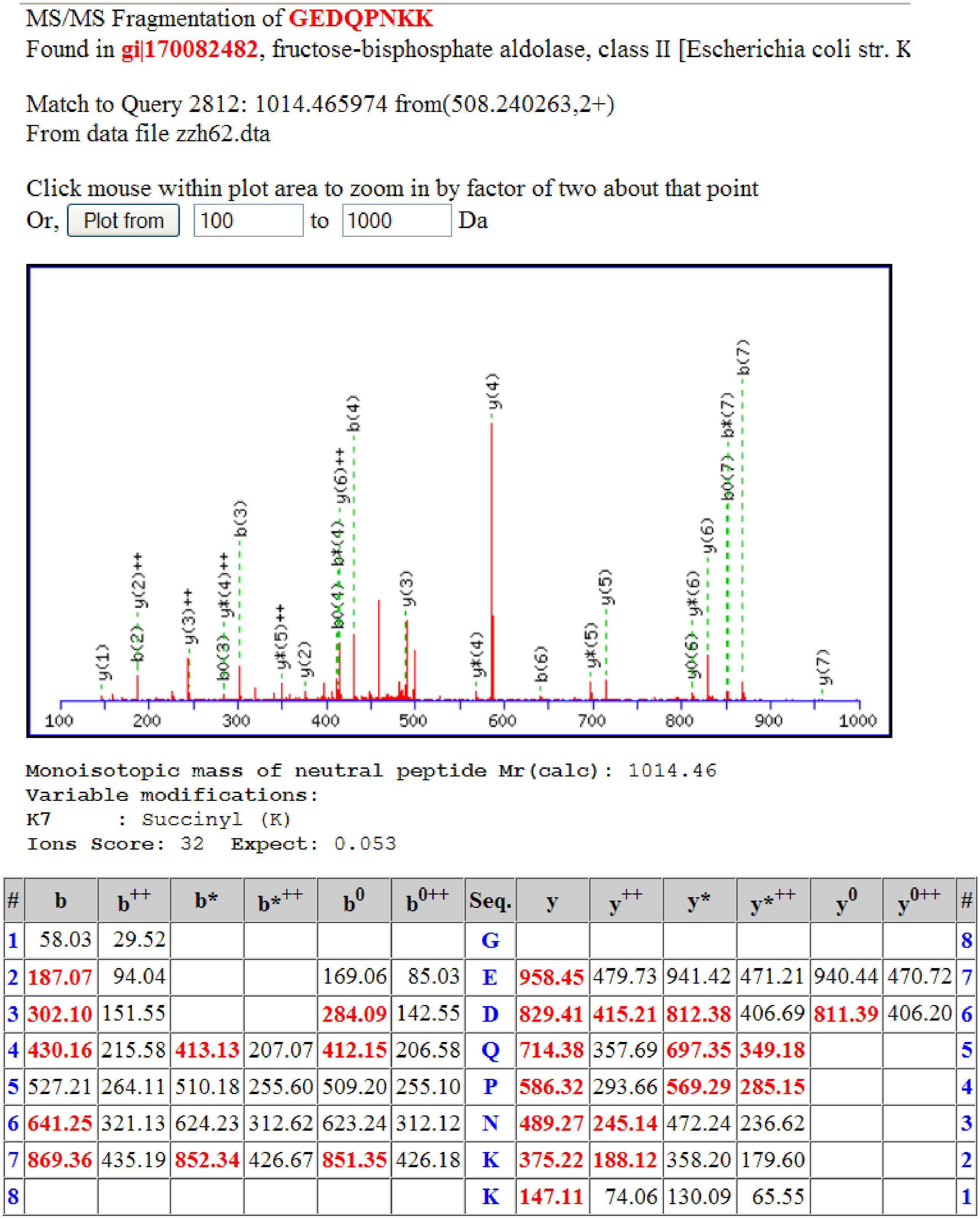


Monoisotopic mass of neutral peptide Mr(calc): 2498.20
Variable modifications:
K14 : Succinyl (K)
Ions Score: 67 Expect: 2e-005

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.04	36.53					A							22
2	186.09	93.55	169.06	85.03			N	2428.17	**1214.59**	2411.15	1206.08	2410.16	1205.59	21
3	**315.13**	158.07	298.10	149.56	297.12	149.06	E	2314.13	**1157.57**	2297.10	**1149.06**	2296.12	**1148.56**	20
4	**386.17**	193.59	369.14	185.07	368.16	184.58	A	2185.09	**1093.05**	2168.06	1084.53	2167.08	1084.04	19
5	**549.23**	275.12	**532.20**	266.61	531.22	266.11	Y	2114.05	**1057.53**	2097.02	1049.02	2096.04	1048.52	18
6	662.31	331.66	645.29	323.15	644.30	322.66	L	1950.99	**976.00**	1933.96	**967.48**	1932.98	**966.99**	17
7	**790.37**	395.69	773.35	387.18	772.36	**386.68**	Q	1837.90	**919.46**	1820.88	**910.94**	1819.89	910.45	16
8	847.39	424.20	830.37	415.69	829.38	415.20	G	1709.85	**855.43**	1692.82	846.91	1691.83	846.42	15
9	**975.45**	488.23	958.43	479.72	957.44	479.22	Q	1652.82	826.92	1635.80	818.40	1634.81	817.91	14
10	1088.54	544.77	1071.51	536.26	1070.53	535.77	L	1524.77	**762.89**	1507.74	754.37	1506.75	753.88	13
11	1145.56	**573.28**	1128.53	564.77	1127.55	564.28	G	1411.68	**706.34**	1394.65	697.83	1393.67	697.34	12
12	**1259.60**	630.30	1242.57	**621.79**	1241.59	**621.30**	N	1354.66	**677.83**	1337.63	669.32	1336.65	668.83	11
13	1356.65	**678.83**	1339.63	670.32	1338.64	669.83	P	1240.62	**620.81**	1223.59	612.30	1222.61	611.81	10
14	1584.77	792.89	1567.74	784.37	1566.75	783.88	K	1143.56	**572.29**	1126.54	563.77	1125.55	563.28	9
15	1641.79	821.40	1624.76	812.88	1623.78	812.39	G	915.45	**458.23**	898.43	449.72	897.44	449.22	8
16	**1770.83**	885.92	1753.80	877.41	1752.82	876.91	E	858.43	429.72	841.41	421.21	840.42	420.71	7
17	1885.86	943.43	1868.83	934.92	1867.85	934.43	D	729.39	**365.20**	712.36	356.68	711.38	356.19	6
18	2013.91	1007.46	1996.89	998.95	1995.90	998.46	Q	**614.36**	307.68	597.34	299.17			5
19	2110.97	1055.99	2093.94	1047.47	2092.96	1046.98	P	486.30	243.66	469.28	235.14			4
20	2225.01	1113.01	2207.98	1104.50	2207.00	1104.00	N	389.25	195.13	372.22	186.62			3
21	2353.11	1177.06	2336.08	**1168.54**	2335.09	**1168.05**	K	275.21	138.11	258.18	129.59			2
22							K	147.11	74.06	130.09	65.55			1

fructose-bisphosphate aldolase, class II K326

GEDQPN^{Succ}KK



MS/MS Fragmentation of **GEDQPNKK**
Found in **gi|170082482**, fructose-bisphosphate aldolase, class II [Escherichia coli str. K

Match to Query 2812: 1014.465974 from(508.240263,2+)
From data file zzh62.dta

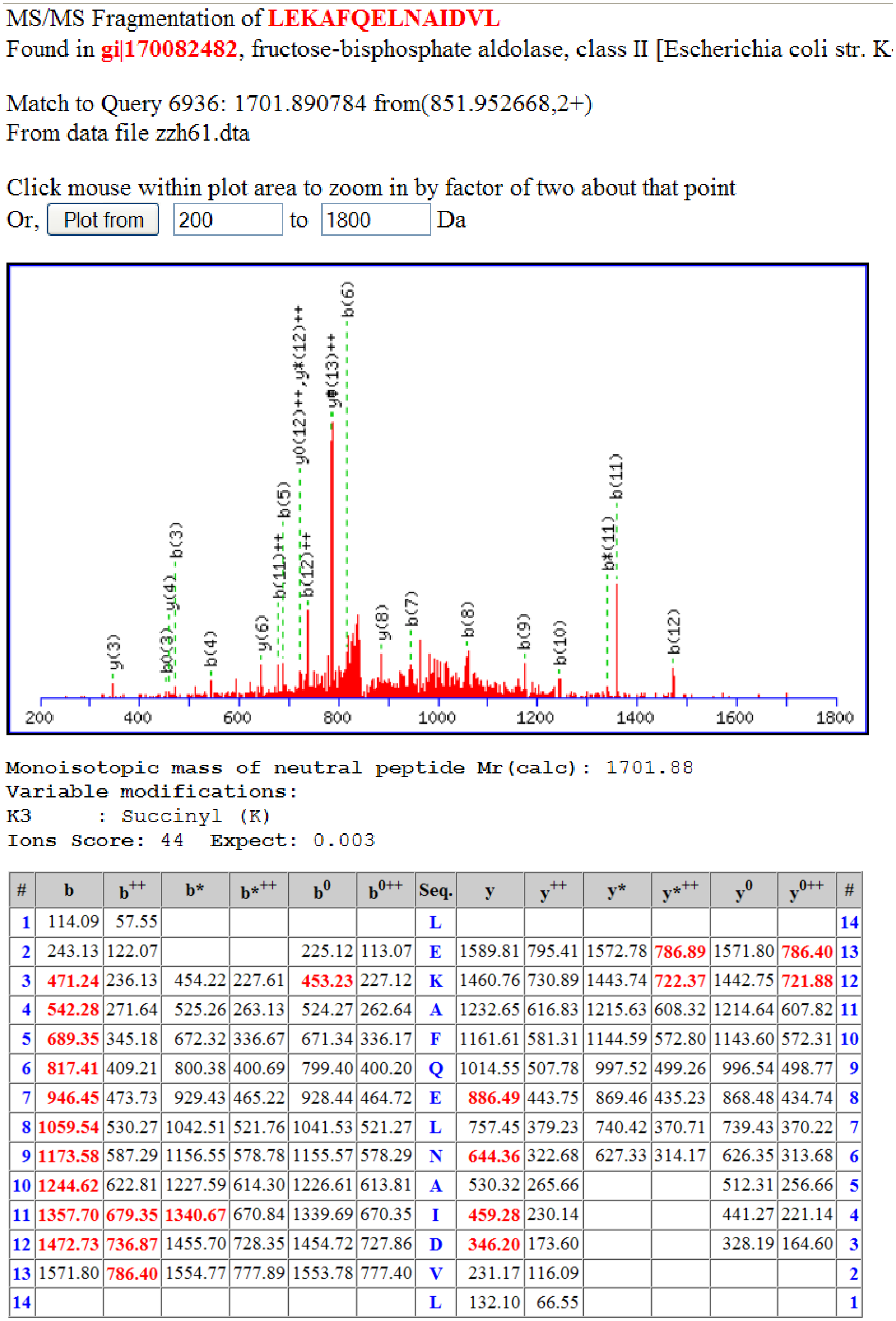
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1014.46
Variable modifications:
K7      : Succinyl (K)
Ions Score: 32  Expect: 0.053
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.03	29.52					G							8
2	**187.07**	94.04			169.06	85.03	E	**958.45**	479.73	941.42	471.21	940.44	470.72	7
3	**302.10**	151.55			**284.09**	142.55	D	**829.41**	**415.21**	**812.38**	406.69	**811.39**	406.20	6
4	**430.16**	215.58	**413.13**	207.07	**412.15**	206.58	Q	**714.38**	357.69	**697.35**	**349.18**			5
5	527.21	264.11	510.18	255.60	509.20	255.10	P	**586.32**	293.66	**569.29**	**285.15**			4
6	**641.25**	321.13	624.23	312.62	623.24	312.12	N	**489.27**	**245.14**	472.24	236.62			3
7	**869.36**	435.19	**852.34**	426.67	**851.35**	426.18	K	**375.22**	**188.12**	358.20	179.60			2
8							K	**147.11**	74.06	130.09	65.55			1

fructose-bisphosphate aldolase, class II K348

LE^{Succ}KAFQELNAIDVL



MS/MS Fragmentation of **LEKAFQELNAIDVL**
Found in **gi|170082482**, fructose-bisphosphate aldolase, class II [Escherichia coli str. K

Match to Query 6936: 1701.890784 from(851.952668,2+)
From data file zzh61.dta

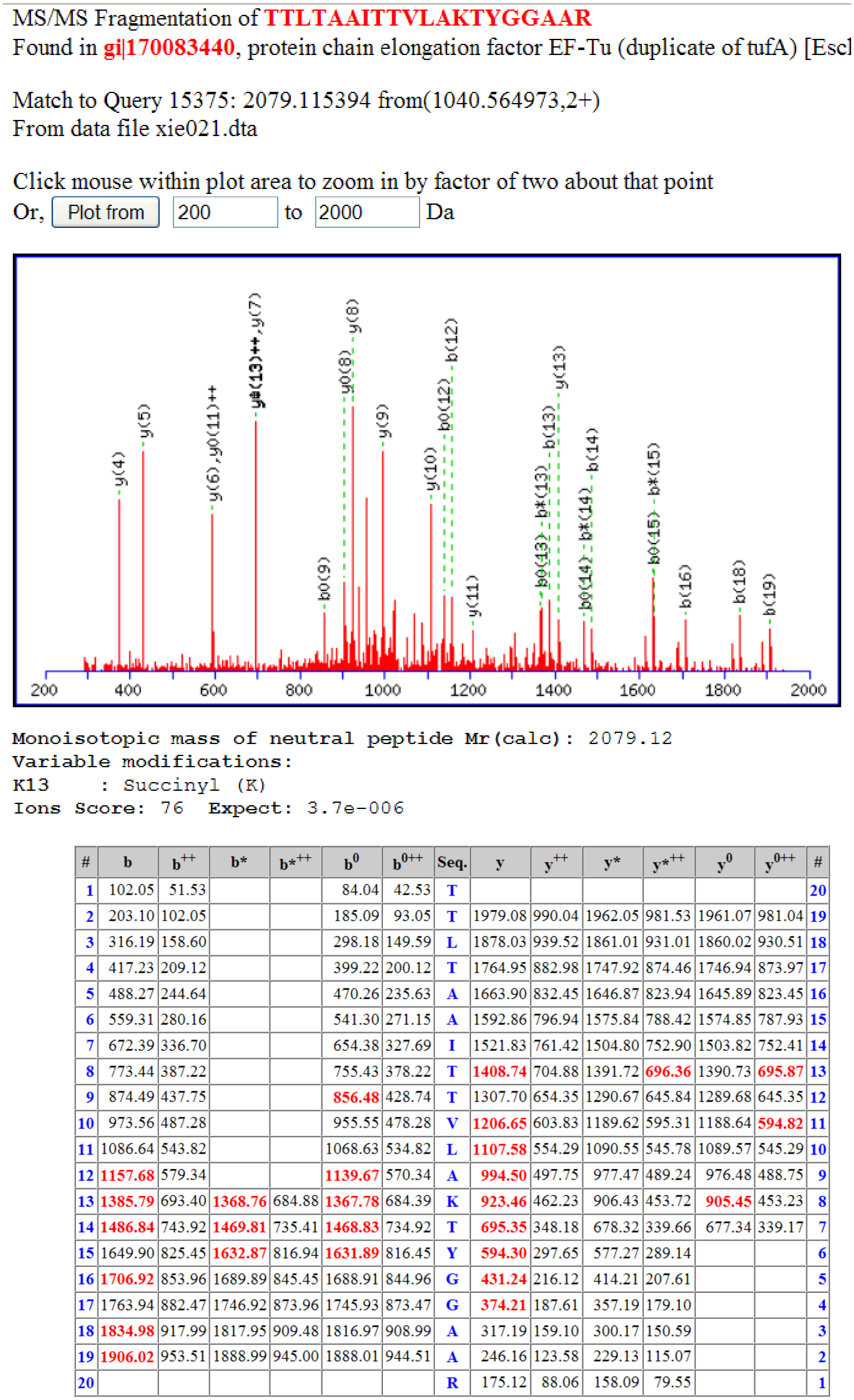
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1701.88
Variable modifications:
K3      : Succinyl (K)
Ions Score: 44  Expect: 0.003
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.09	57.55					L							14
2	243.13	122.07			225.12	113.07	E	1589.81	795.41	1572.78	786.89	1571.80	786.40	13
3	471.24	236.13	454.22	227.61	453.23	227.12	K	1460.76	730.89	1443.74	722.37	1442.75	721.88	12
4	542.28	271.64	525.26	263.13	524.27	262.64	A	1232.65	616.83	1215.63	608.32	1214.64	607.82	11
5	689.35	345.18	672.32	336.67	671.34	336.17	F	1161.61	581.31	1144.59	572.80	1143.60	572.31	10
6	817.41	409.21	800.38	400.69	799.40	400.20	Q	1014.55	507.78	997.52	499.26	996.54	498.77	9
7	946.45	473.73	929.43	465.22	928.44	464.72	E	886.49	443.75	869.46	435.23	868.48	434.74	8
8	1059.54	530.27	1042.51	521.76	1041.53	521.27	L	757.45	379.23	740.42	370.71	739.43	370.22	7
9	1173.58	587.29	1156.55	578.78	1155.57	578.29	N	644.36	322.68	627.33	314.17	626.35	313.68	6
10	1244.62	622.81	1227.59	614.30	1226.61	613.81	A	530.32	265.66			512.31	256.66	5
11	1357.70	679.35	1340.67	670.84	1339.69	670.35	I	459.28	230.14			441.27	221.14	4
12	1472.73	736.87	1455.70	728.35	1454.72	727.86	D	346.20	173.60			328.19	164.60	3
13	1571.80	786.40	1554.77	777.89	1553.78	777.40	V	231.17	116.09					2
14							L	132.10	66.55					1

protein chain elongation factor EF-Tu K38

TTLTAAITTVLA^{Succ}KTYGGAAR



MS/MS Fragmentation of **TTLTAAITTVLAKTYGGAAR**
Found in **gi|170083440**, protein chain elongation factor EF-Tu (duplicate of tufA) [Escl

Match to Query 15375: 2079.115394 from(1040.564973,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 2079.12
Variable modifications:
K13    : Succinyl (K)
Ions Score: 76  Expect: 3.7e-006
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	102.05	51.53			84.04	42.53	T							20
2	203.10	102.05			185.09	93.05	T	1979.08	990.04	1962.05	981.53	1961.07	981.04	19
3	316.19	158.60			298.18	149.59	L	1878.03	939.52	1861.01	931.01	1860.02	930.51	18
4	417.23	209.12			399.22	200.12	T	1764.95	882.98	1747.92	874.46	1746.94	873.97	17
5	488.27	244.64			470.26	235.63	A	1663.90	832.45	1646.87	823.94	1645.89	823.45	16
6	559.31	280.16			541.30	271.15	A	1592.86	796.94	1575.84	788.42	1574.85	787.93	15
7	672.39	336.70			654.38	327.69	I	1521.83	761.42	1504.80	752.90	1503.82	752.41	14
8	773.44	387.22			755.43	378.22	T	1408.74	704.88	1391.72	696.36	1390.73	695.87	13
9	874.49	437.75			856.48	428.74	T	1307.70	654.35	1290.67	645.84	1289.68	645.35	12
10	973.56	487.28			955.55	478.28	V	1206.65	603.83	1189.62	595.31	1188.64	594.82	11
11	1086.64	543.82			1068.63	534.82	L	1107.58	554.29	1090.55	545.78	1089.57	545.29	10
12	1157.68	579.34			1139.67	570.34	A	994.50	497.75	977.47	489.24	976.48	488.75	9
13	1385.79	693.40	1368.76	684.88	1367.78	684.39	K	923.46	462.23	906.43	453.72	905.45	453.23	8
14	1486.84	743.92	1469.81	735.41	1468.83	734.92	T	695.35	348.18	678.32	339.66	677.34	339.17	7
15	1649.90	825.45	1632.87	816.94	1631.89	816.45	Y	594.30	297.65	577.27	289.14			6
16	1706.92	853.96	1689.89	845.45	1688.91	844.96	G	431.24	216.12	414.21	207.61			5
17	1763.94	882.47	1746.92	873.96	1745.93	873.47	G	374.21	187.61	357.19	179.10			4
18	1834.98	917.99	1817.95	909.48	1816.97	908.99	A	317.19	159.10	300.17	150.59			3
19	1906.02	953.51	1888.99	945.00	1888.01	944.51	A	246.16	123.58	229.13	115.07			2
20							R	175.12	88.06	158.09	79.55			1

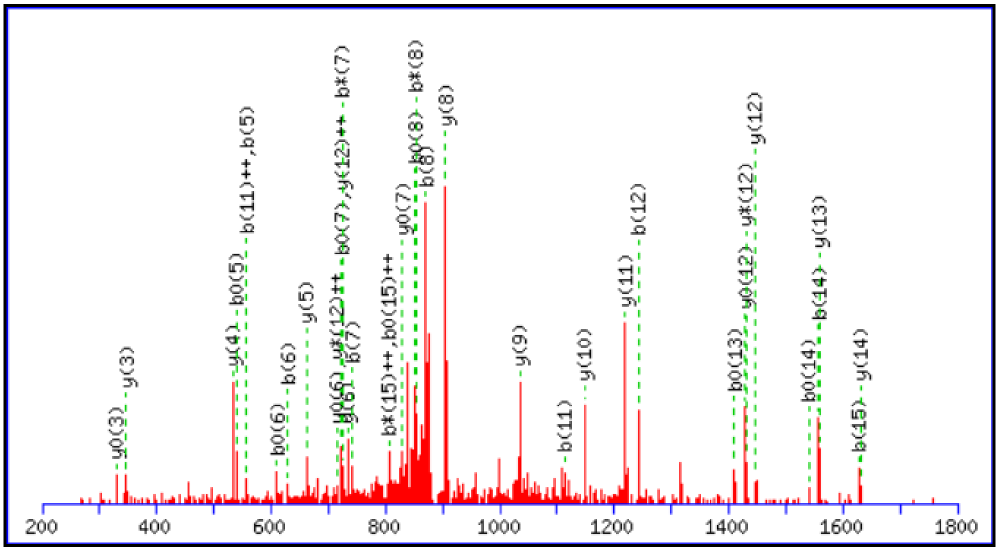
protein chain elongation factor EF-Tu K177

GSAL^{Succ}KALEGDAEWEAK

MS/MS Fragmentation of **GSALKALEGDAEWEAK**
Found in gi|170082857, protein chain elongation factor EF-Tu (duplicate of tufB) [Esch

Match to Query 7225: 1773.847934 from(887.931243,2+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da



```
Monoisotopic mass of neutral peptide Mr(calc): 1773.84
Variable modifications:
K5      : Succinyl (K)
Ions Score: 65   Expect: 2.3e-005
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.03	29.52					G							16
2	145.06	73.03			127.05	64.03	S	1717.83	859.42	1700.80	850.90	1699.82	850.41	15
3	216.10	108.55			198.09	99.55	A	1630.80	815.90	1613.77	807.39	1612.79	806.90	14
4	329.18	165.09			311.17	156.09	L	1559.76	780.38	1542.73	771.87	1541.75	771.38	13
5	557.29	279.15	540.27	270.64	539.28	270.14	K	1446.67	723.84	1429.65	715.33	1428.66	714.84	12
6	628.33	314.67	611.30	306.16	610.32	305.66	A	1218.56	609.79	1201.54	601.27	1200.55	600.78	11
7	741.41	371.21	724.39	362.70	723.40	362.21	L	1147.53	574.27	1130.50	565.75	1129.52	565.26	10
8	870.46	435.73	853.43	427.22	852.45	426.73	E	1034.44	517.72	1017.42	509.21	1016.43	508.72	9
9	927.48	464.24	910.45	455.73	909.47	455.24	G	905.40	453.20	888.37	444.69	887.39	444.20	8
10	1042.51	521.76	1025.48	513.24	1024.49	512.75	D	848.38	424.69	831.35	416.18	830.37	415.69	7
11	1113.54	557.27	1096.52	548.76	1095.53	548.27	A	733.35	367.18	716.32	358.67	715.34	358.17	6
12	1242.58	621.80	1225.56	613.28	1224.57	612.79	E	662.31	331.66	645.29	323.15	644.30	322.66	5
13	1428.66	714.84	1411.64	706.32	1410.65	705.83	W	533.27	267.14	516.25	258.63	515.26	258.13	4
14	1557.71	779.36	1540.68	770.84	1539.70	770.35	E	347.19	174.10	330.17	165.59	329.18	165.09	3
15	1628.74	814.88	1611.72	806.36	1610.73	805.87	A	218.15	109.58	201.12	101.07			2
16							K	147.11	74.06	130.09	65.55			1

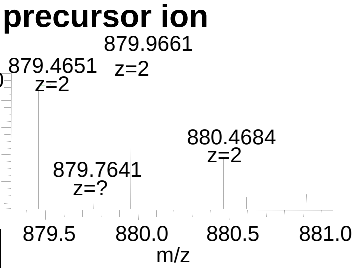
protein chain elongation factor EF-Tu K249

VGEEVEIVGI^{Succ}KETQK

MS/MS Fragmentation of **VGEEVEIVGIKETQK**

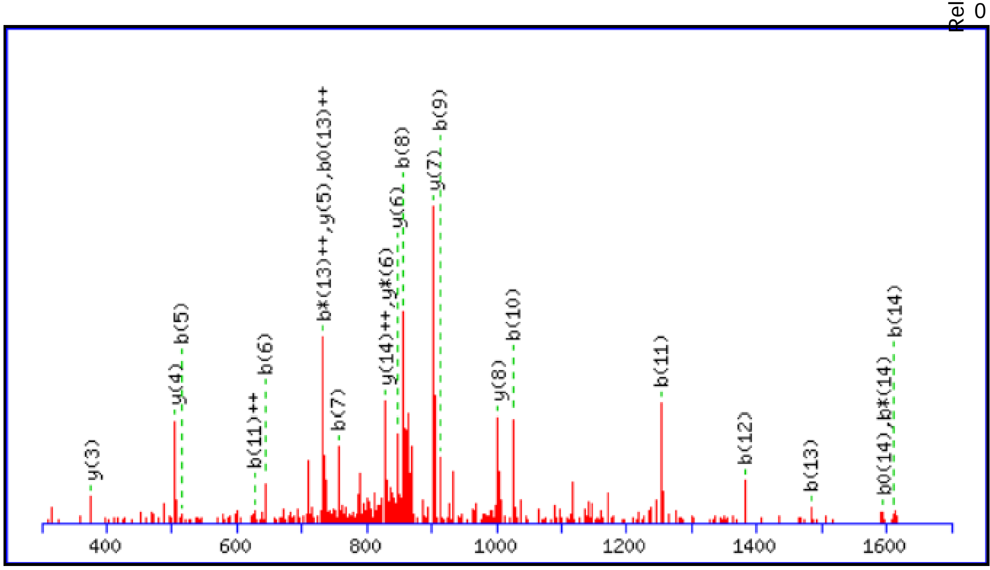
Found in **gi|170082857**, protein chain elongation factor EF-Tu (duplicate of tufB) [Esc

precursor ion



Match to Query 7140: 1757.918124 from(879.966338,2+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1700 Da

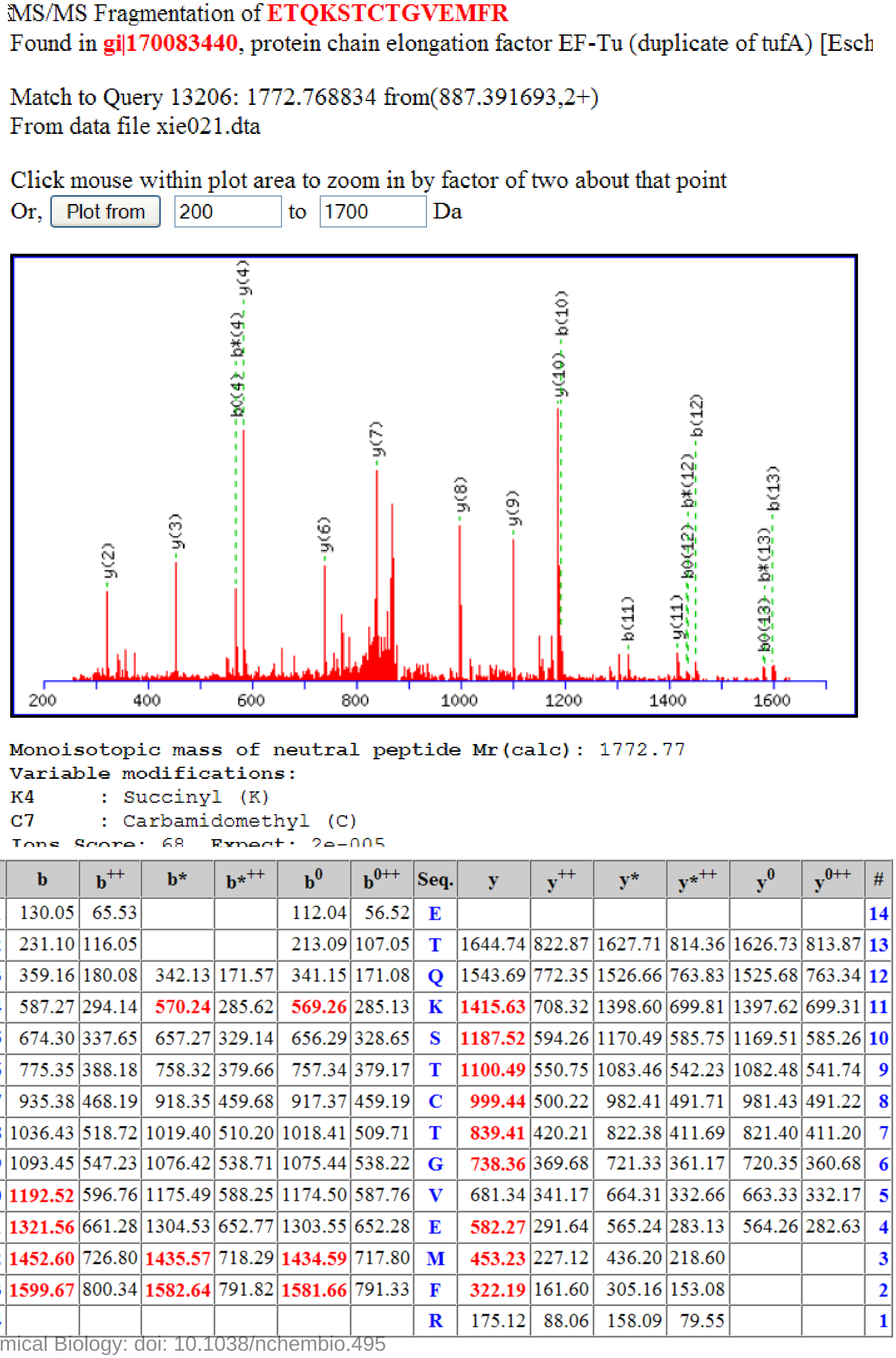


```
Monoisotopic mass of neutral peptide Mr(calc): 1756.91
Variable modifications:
K11     : Succinyl (K)
Ions Score: 67  Expect: 1.5e-005
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.08	50.54					V							15
2	157.10	79.05					G	1658.85	829.93	1641.82	821.41	1640.84	820.92	14
3	286.14	143.57			268.13	134.57	E	1601.83	801.42	1584.80	792.90	1583.82	792.41	13
4	415.18	208.09			397.17	199.09	E	1472.78	736.90	1455.76	728.38	1454.77	727.89	12
5	514.25	257.63			496.24	248.62	V	1343.74	672.37	1326.72	663.86	1325.73	663.37	11
6	643.29	322.15			625.28	313.15	E	1244.67	622.84	1227.65	614.33	1226.66	613.83	10
7	756.38	378.69			738.37	369.69	I	1115.63	558.32	1098.60	549.81	1097.62	549.31	9
8	855.45	428.23			837.44	419.22	V	1002.55	501.78	985.52	493.26	984.54	492.77	8
9	912.47	456.74			894.46	447.73	G	903.48	452.24	886.45	443.73	885.47	443.24	7
10	1025.55	513.28			1007.54	504.27	I	846.46	423.73	829.43	415.22	828.45	414.73	6
11	1253.66	627.33	1236.64	618.82	1235.65	618.33	K	733.37	367.19	716.35	358.68	715.36	358.18	5
12	1382.70	691.86	1365.68	683.34	1364.69	682.85	E	505.26	253.13	488.24	244.62	487.25	244.13	4
13	1483.75	742.38	1466.73	733.87	1465.74	733.37	T	376.22	188.61	359.19	180.10	358.21	179.61	3
14	1611.81	806.41	1594.78	797.90	1593.80	797.40	Q	275.17	138.09	258.14	129.58			2
15							K	147.11	74.06	130.09	65.55			1

protein chain elongation factor EF-Tu K253

ETQ^{Succ}KSTCTGVEMFR



MS/MS Fragmentation of ETQKSTCTGVEMFR
Found in gi|170083440, protein chain elongation factor EF-Tu (duplicate of tufA) [Esch

Match to Query 13206: 1772.768834 from(887.391693,2+)
From data file xie021.dta

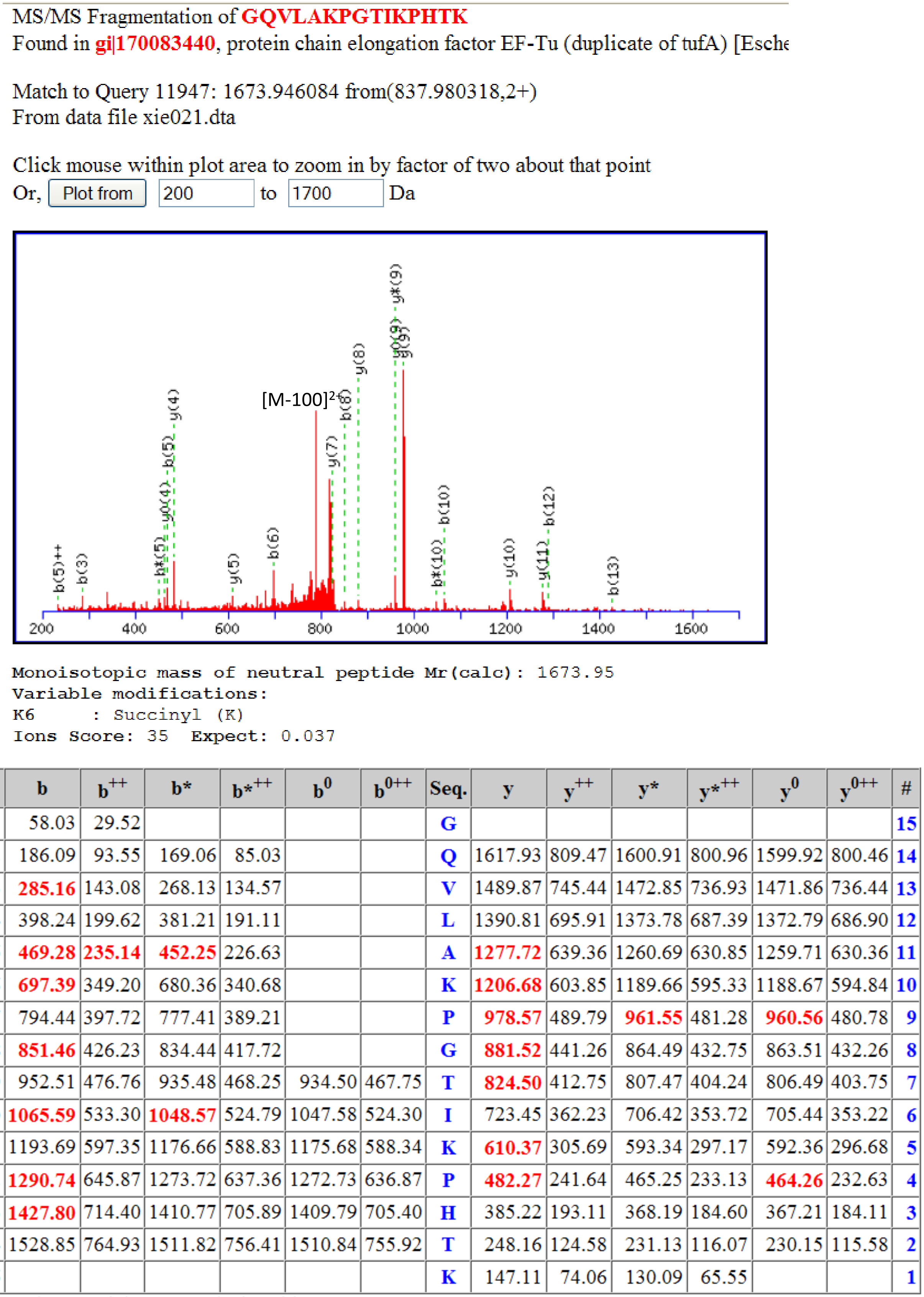
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1772.77
Variable modifications:
K4       : Succinyl (K)
C7       : Carbamidomethyl (C)
Ions Score: 68  Expect: 2e-005
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.05	65.53			112.04	56.52	E							14
2	231.10	116.05			213.09	107.05	T	1644.74	822.87	1627.71	814.36	1626.73	813.87	13
3	359.16	180.08	342.13	171.57	341.15	171.08	Q	1543.69	772.35	1526.66	763.83	1525.68	763.34	12
4	587.27	294.14	570.24	285.62	569.26	285.13	K	1415.63	708.32	1398.60	699.81	1397.62	699.31	11
5	674.30	337.65	657.27	329.14	656.29	328.65	S	1187.52	594.26	1170.49	585.75	1169.51	585.26	10
6	775.35	388.18	758.32	379.66	757.34	379.17	T	1100.49	550.75	1083.46	542.23	1082.48	541.74	9
7	935.38	468.19	918.35	459.68	917.37	459.19	C	999.44	500.22	982.41	491.71	981.43	491.22	8
8	1036.43	518.72	1019.40	510.20	1018.41	509.71	T	839.41	420.21	822.38	411.69	821.40	411.20	7
9	1093.45	547.23	1076.42	538.71	1075.44	538.22	G	738.36	369.68	721.33	361.17	720.35	360.68	6
10	1192.52	596.76	1175.49	588.25	1174.50	587.76	V	681.34	341.17	664.31	332.66	663.33	332.17	5
11	1321.56	661.28	1304.53	652.77	1303.55	652.28	E	582.27	291.64	565.24	283.13	564.26	282.63	4
12	1452.60	726.80	1435.57	718.29	1434.59	717.80	M	453.23	227.12	436.20	218.60			3
13	1599.67	800.34	1582.64	791.82	1581.66	791.33	F	322.19	161.60	305.16	153.08			2
14							R	175.12	88.06	158.09	79.55			1

protein chain elongation factor EF-Tu K295

$\text{GQVLA}^{\text{Succ}}\text{KPGTIKPHTK}$



MS/MS Fragmentation of **GQVLAKPGTIKPHTK**
Found in **gi|170083440**, protein chain elongation factor EF-Tu (duplicate of tufA) [Esche

Match to Query 11947: 1673.946084 from(837.980318,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1673.95
Variable modifications:
K6      : Succinyl (K)
Ions Score: 35  Expect: 0.037
```

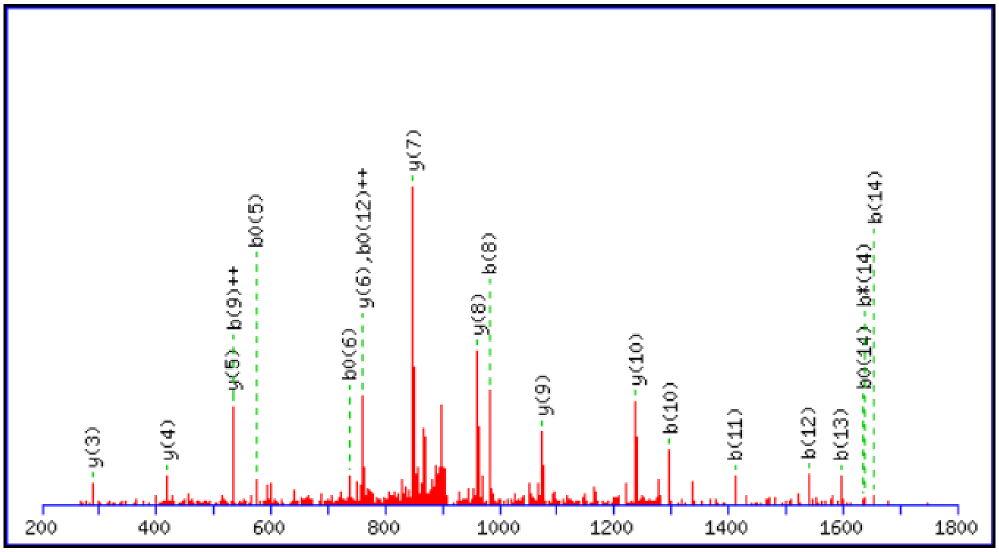
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.03	29.52					G							15
2	186.09	93.55	169.06	85.03			Q	1617.93	809.47	1600.91	800.96	1599.92	800.46	14
3	**285.16**	143.08	268.13	134.57			V	1489.87	745.44	1472.85	736.93	1471.86	736.44	13
4	398.24	199.62	381.21	191.11			L	1390.81	695.91	1373.78	687.39	1372.79	686.90	12
5	**469.28**	**235.14**	**452.25**	226.63			A	**1277.72**	639.36	1260.69	630.85	1259.71	630.36	11
6	**697.39**	349.20	680.36	340.68			K	**1206.68**	603.85	1189.66	595.33	1188.67	594.84	10
7	794.44	397.72	777.41	389.21			P	**978.57**	489.79	**961.55**	481.28	**960.56**	480.78	9
8	**851.46**	426.23	834.44	417.72			G	**881.52**	441.26	864.49	432.75	863.51	432.26	8
9	952.51	476.76	935.48	468.25	934.50	467.75	T	**824.50**	412.75	807.47	404.24	806.49	403.75	7
10	**1065.59**	533.30	**1048.57**	524.79	1047.58	524.30	I	723.45	362.23	706.42	353.72	705.44	353.22	6
11	1193.69	597.35	1176.66	588.83	1175.68	588.34	K	**610.37**	305.69	593.34	297.17	592.36	296.68	5
12	**1290.74**	645.87	1273.72	637.36	1272.73	636.87	P	**482.27**	241.64	465.25	233.13	**464.26**	232.63	4
13	**1427.80**	714.40	1410.77	705.89	1409.79	705.40	H	385.22	193.11	368.19	184.60	367.21	184.11	3
14	1528.85	764.93	1511.82	756.41	1510.84	755.92	T	248.16	124.58	231.13	116.07	230.15	115.58	2
15							K	147.11	74.06	130.09	65.55			1

protein chain elongation factor EF-Tu K314
FESEVYILS^{Succ}KDEGGR

MS/MS Fragmentation of **FESEVYILSKDEGGR**
Found in gi|170082857, protein chain elongation factor EF-Tu (duplicate of tufB) [Esch

Match to Query 7485: 1827.863074 from(914.938813,2+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da

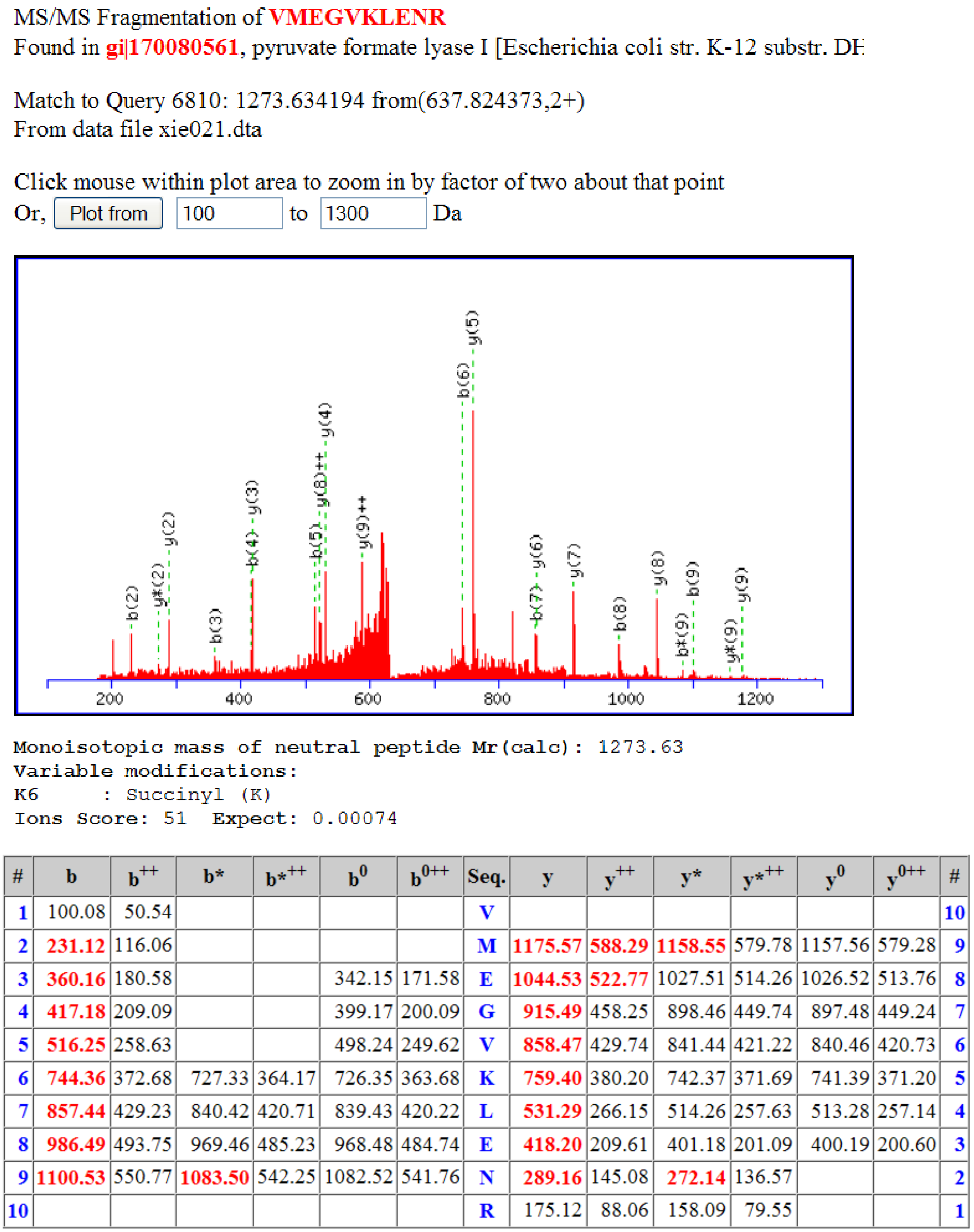


```
Monoisotopic mass of neutral peptide Mr(calc): 1827.85
Variable modifications:
K10     : Succinyl (K)
Ions Score: 72   Expect: 4.1e-006
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.08	74.54					F							15
2	277.12	139.06			259.11	130.06	E	1681.79	841.40	1664.76	832.89	1663.78	832.39	14
3	364.15	182.58			346.14	173.57	S	1552.75	776.88	1535.72	768.36	1534.74	767.87	13
4	493.19	247.10			475.18	238.09	E	1465.72	733.36	1448.69	724.85	1447.71	724.36	12
5	592.26	296.63			574.25	287.63	V	1336.67	668.84	1319.65	660.33	1318.66	659.84	11
6	755.32	378.17			737.31	369.16	Y	1237.61	619.31	1220.58	610.79	1219.60	610.30	10
7	868.41	434.71			850.40	425.70	I	1074.54	537.77	1057.52	529.26	1056.53	528.77	9
8	981.49	491.25			963.48	482.24	L	961.46	481.23	944.43	472.72	943.45	472.23	8
9	1068.52	534.77			1050.51	525.76	S	848.37	424.69	831.35	416.18	830.36	415.69	7
10	1296.64	648.82	1279.61	640.31	1278.63	639.82	K	761.34	381.17	744.32	372.66	743.33	372.17	6
11	1411.66	706.34	1394.64	697.82	1393.65	697.33	D	533.23	267.12	516.20	258.61	515.22	258.11	5
12	1540.71	770.86	1523.68	762.34	1522.69	761.85	E	418.20	209.61	401.18	201.09	400.19	200.60	4
13	1597.73	799.37	1580.70	790.85	1579.72	790.36	G	289.16	145.08	272.14	136.57			3
14	1654.75	827.88	1637.72	819.36	1636.74	818.87	G	232.14	116.57	215.11	108.06			2
15							R	175.12	88.06	158.09	79.55			1

pyruvate formate lyase I K63

VMEGV$^{\text{Succ}}$KLENR



MS/MS Fragmentation of **VMEGVKLENR**
Found in **gi|170080561**, pyruvate formate lyase I [Escherichia coli str. K-12 substr. DH

Match to Query 6810: 1273.634194 from(637.824373,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1273.63
Variable modifications:
K6     : Succinyl (K)
Ions Score: 51  Expect: 0.00074
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.08	50.54					V							10
2	**231.12**	116.06					M	**1175.57**	**588.29**	**1158.55**	579.78	1157.56	579.28	9
3	**360.16**	180.58			342.15	171.58	E	**1044.53**	**522.77**	1027.51	514.26	1026.52	513.76	8
4	**417.18**	209.09			399.17	200.09	G	**915.49**	458.25	898.46	449.74	897.48	449.24	7
5	**516.25**	258.63			498.24	249.62	V	**858.47**	429.74	841.44	421.22	840.46	420.73	6
6	**744.36**	372.68	727.33	364.17	726.35	363.68	K	**759.40**	380.20	742.37	371.69	741.39	371.20	5
7	**857.44**	429.23	840.42	420.71	839.43	420.22	L	**531.29**	266.15	514.26	257.63	513.28	257.14	4
8	**986.49**	493.75	969.46	485.23	968.48	484.74	E	**418.20**	209.61	401.18	201.09	400.19	200.60	3
9	**1100.53**	550.77	**1083.50**	542.25	1082.52	541.76	N	**289.16**	145.08	**272.14**	136.57			2
10							R	175.12	88.06	158.09	79.55			1

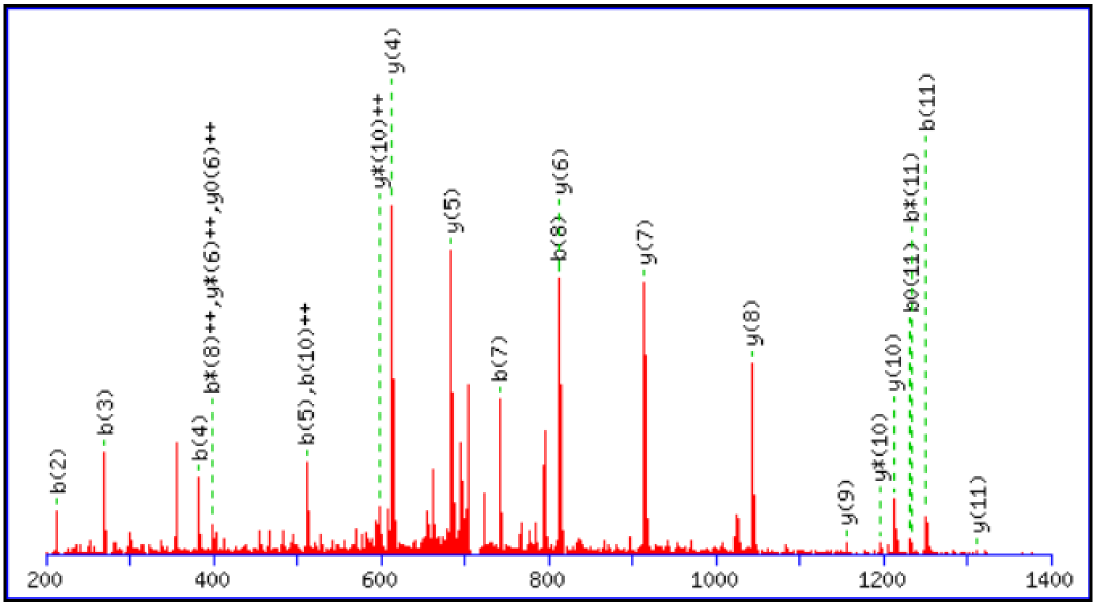
pyruvate formate lyase I K107

IVGLQTEAPL^{Succ}KR

MS/MS Fragmentation of **IVGLQTEAPLKR**
Found in **gi|170080561**, pyruvate formate lyase I [Escherichia coli str. K-12 substr. DH

Match to Query 8719: 1423.805454 from(712.910003,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da

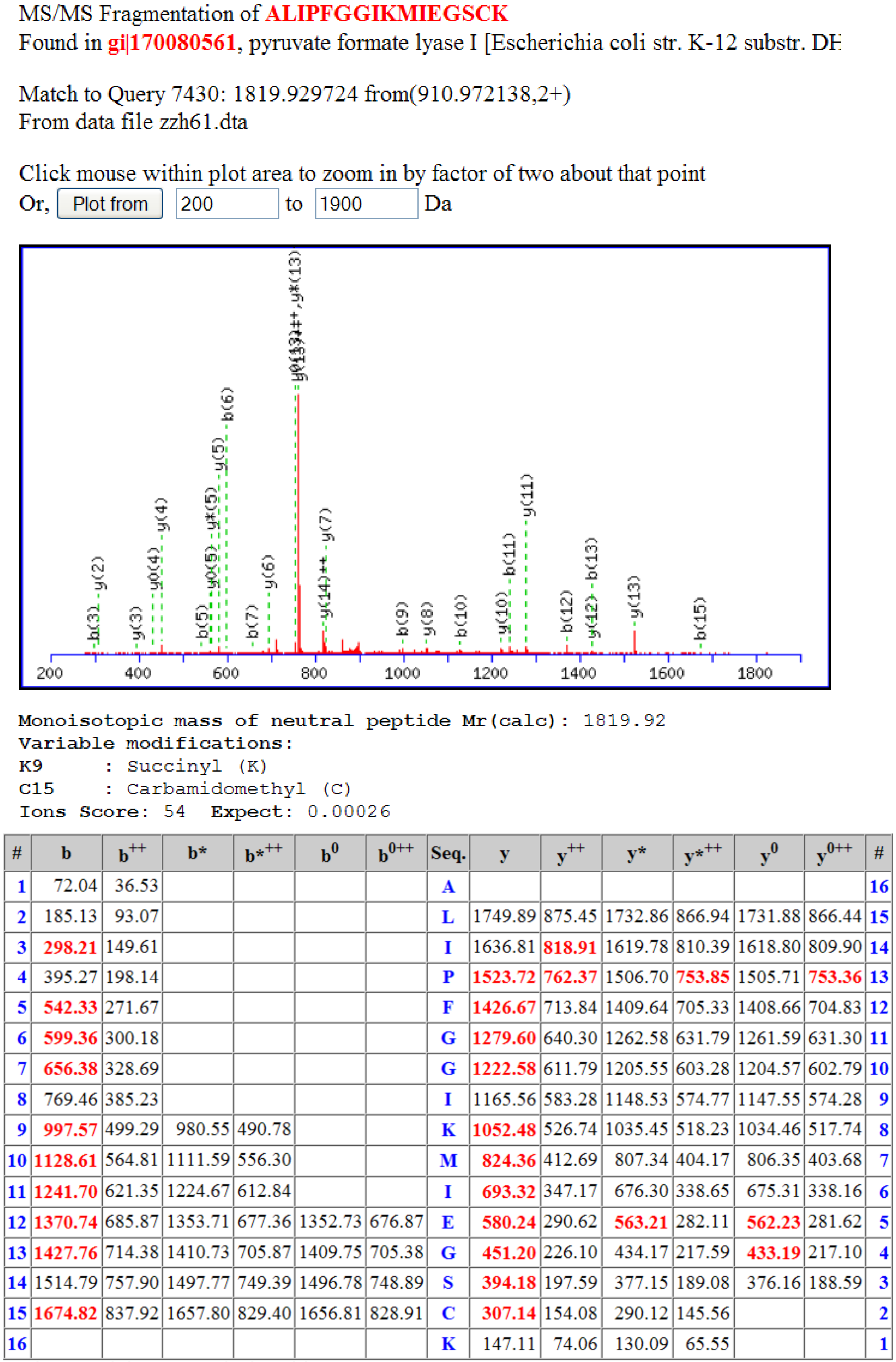


```
Monoisotopic mass of neutral peptide Mr(calc): 1423.80
Variable modifications:
K11     : Succinyl (K)
Ions Score: 60  Expect: 8.5e-005
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.09	57.55					I							12
2	**213.16**	107.08					V	**1311.73**	656.37	1294.70	647.85	1293.72	647.36	11
3	**270.18**	135.59					G	**1212.66**	606.83	**1195.63**	**598.32**	1194.65	597.83	10
4	**383.27**	192.14					L	**1155.64**	578.32	1138.61	569.81	1137.63	569.32	9
5	**511.32**	256.17	494.30	247.65			Q	**1042.55**	521.78	1025.53	513.27	1024.54	512.77	8
6	612.37	306.69	595.34	298.18	594.36	297.68	T	**914.49**	457.75	897.47	449.24	896.48	448.75	7
7	**741.41**	371.21	724.39	362.70	723.40	362.21	E	**813.45**	407.23	796.42	**398.71**	795.44	**398.22**	6
8	**812.45**	406.73	795.42	**398.22**	794.44	397.72	A	**684.40**	342.71	667.38	334.19			5
9	909.50	455.26	892.48	446.74	891.49	446.25	P	**613.37**	307.19	596.34	298.67			4
10	1022.59	**511.80**	1005.56	503.28	1004.58	502.79	L	516.31	258.66	499.29	250.15			3
11	**1250.70**	625.85	**1233.67**	617.34	**1232.69**	616.85	K	403.23	202.12	386.20	193.61			2
12							R	175.12	88.06	158.09	79.55			1

pyruvate formate lyase I K117

ALIPFGGI^{Succ}KMIEGSCK



MS/MS Fragmentation of **ALIPFGGIKMIEGSCK**
Found in **gi|170080561**, pyruvate formate lyase I [Escherichia coli str. K-12 substr. DH

Match to Query 7430: 1819.929724 from(910.972138,2+)
From data file zzh61.dta

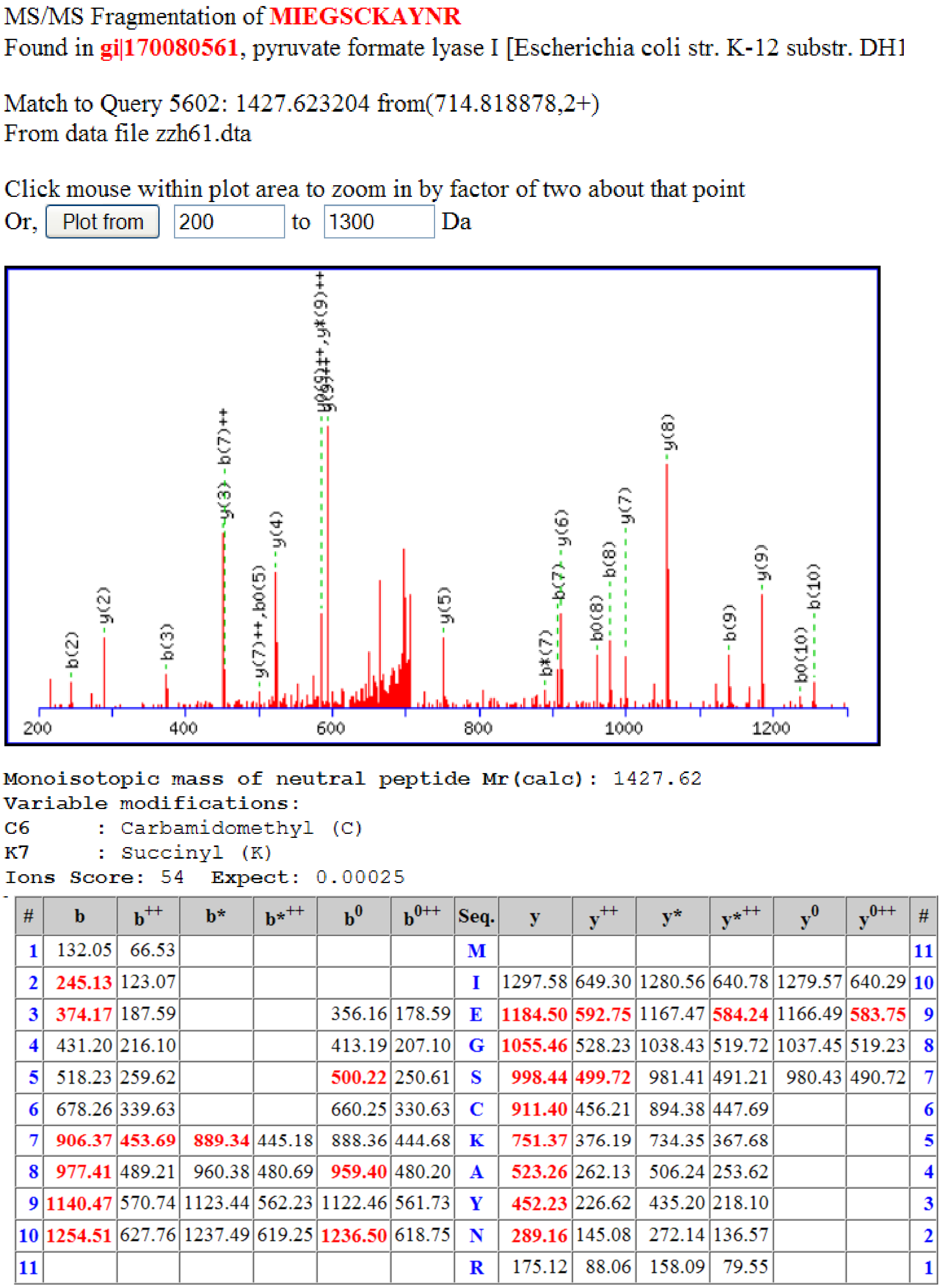
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1819.92
Variable modifications:
K9     : Succinyl (K)
C15    : Carbamidomethyl (C)
Ions Score: 54  Expect: 0.00026
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	72.04	36.53					A							16
2	185.13	93.07					L	1749.89	875.45	1732.86	866.94	1731.88	866.44	15
3	**298.21**	149.61					I	1636.81	**818.91**	1619.78	810.39	1618.80	809.90	14
4	395.27	198.14					P	**1523.72**	**762.37**	1506.70	**753.85**	1505.71	**753.36**	13
5	**542.33**	271.67					F	**1426.67**	713.84	1409.64	705.33	1408.66	704.83	12
6	**599.36**	300.18					G	**1279.60**	640.30	1262.58	631.79	1261.59	631.30	11
7	**656.38**	328.69					G	**1222.58**	611.79	1205.55	603.28	1204.57	602.79	10
8	769.46	385.23					I	1165.56	583.28	1148.53	574.77	1147.55	574.28	9
9	**997.57**	499.29	980.55	490.78			K	**1052.48**	526.74	1035.45	518.23	1034.46	517.74	8
10	**1128.61**	564.81	1111.59	556.30			M	**824.36**	412.69	807.34	404.17	806.35	403.68	7
11	**1241.70**	621.35	1224.67	612.84			I	**693.32**	347.17	676.30	338.65	675.31	338.16	6
12	**1370.74**	685.87	1353.71	677.36	1352.73	676.87	E	**580.24**	290.62	**563.21**	282.11	**562.23**	281.62	5
13	**1427.76**	714.38	1410.73	705.87	1409.75	705.38	G	**451.20**	226.10	434.17	217.59	**433.19**	217.10	4
14	1514.79	757.90	1497.77	749.39	1496.78	748.89	S	**394.18**	197.59	377.15	189.08	376.16	188.59	3
15	**1674.82**	837.92	1657.80	829.40	1656.81	828.91	C	**307.14**	154.08	290.12	145.56			2
16							K	147.11	74.06	130.09	65.55			1

pyruvate formate lyase I K124

MIEGSC^{Succ}KAYNR



MS/MS Fragmentation of **MIEGSCKAYNR**

Found in **gi|170080561**, pyruvate formate lyase I [Escherichia coli str. K-12 substr. DH1

Match to Query 5602: 1427.623204 from(714.818878,2+)

From data file zzh61.dta

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

Or, Plot from 200 to 1300 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1427.62
Variable modifications:
C6      : Carbamidomethyl (C)
K7      : Succinyl (K)
Ions Score: 54  Expect: 0.00025
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	132.05	66.53					M							11
2	**245.13**	123.07					I	1297.58	649.30	1280.56	640.78	1279.57	640.29	10
3	**374.17**	187.59			356.16	178.59	E	**1184.50**	**592.75**	1167.47	**584.24**	1166.49	**583.75**	9
4	431.20	216.10			413.19	207.10	G	**1055.46**	528.23	1038.43	519.72	1037.45	519.23	8
5	518.23	259.62			**500.22**	250.61	S	**998.44**	**499.72**	981.41	491.21	980.43	490.72	7
6	678.26	339.63			660.25	330.63	C	**911.40**	456.21	894.38	447.69			6
7	**906.37**	**453.69**	**889.34**	445.18	888.36	444.68	K	**751.37**	376.19	734.35	367.68			5
8	**977.41**	489.21	960.38	480.69	**959.40**	480.20	A	**523.26**	262.13	506.24	253.62			4
9	**1140.47**	570.74	1123.44	562.23	1122.46	561.73	Y	**452.23**	226.62	435.20	218.10			3
10	**1254.51**	627.76	1237.49	619.25	**1236.50**	618.75	N	**289.16**	145.08	272.14	136.57			2
11							R	175.12	88.06	158.09	79.55			1

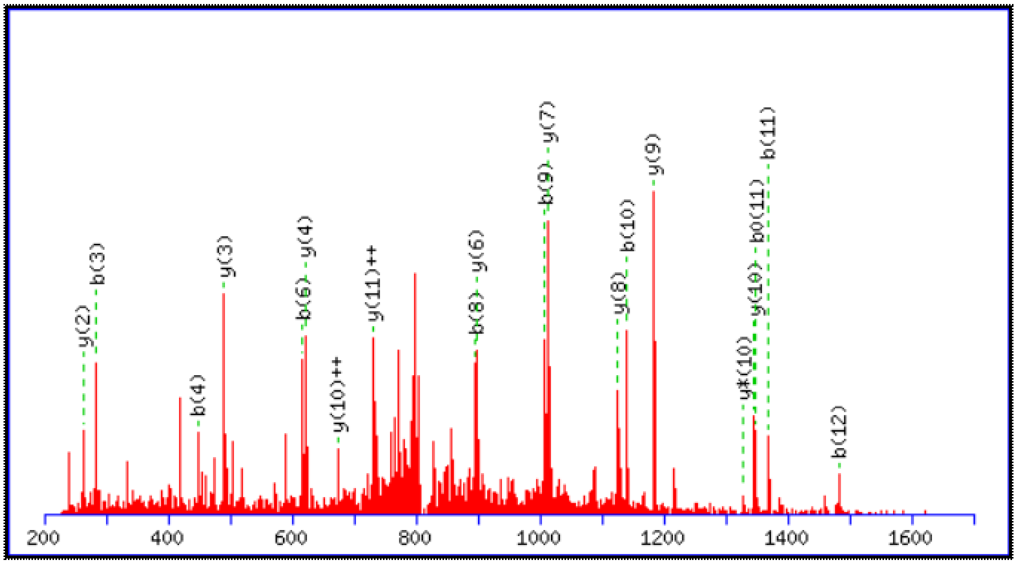
pyruvate formate lyase I K195

VALYGIDYLM^{Succ}KDK

MS/MS Fragmentation of **VALYGIDYLMKDK**
Found in **gi|170080561**, pyruvate formate lyase I [Escherichia coli str. K-12 substr. DH

Match to Query 11365: 1627.818764 from(814.916658,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da



```
Monoisotopic mass of neutral peptide Mr(calc): 1627.82
Variable modifications:
K11     : Succinyl (K)
Ions Score: 49  Expect: 0.0015
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.08	50.54					V							13
2	171.11	86.06					A	1529.76	765.38	1512.73	756.87	1511.75	756.38	12
3	**284.20**	142.60					L	1458.72	**729.86**	1441.69	721.35	1440.71	720.86	11
4	**447.26**	224.13					Y	**1345.63**	**673.32**	**1328.61**	664.81	1327.62	664.32	10
5	504.28	252.64					G	**1182.57**	591.79	1165.54	583.28	1164.56	582.78	9
6	**617.37**	309.19					I	**1125.55**	563.28	1108.52	554.77	1107.54	554.27	8
7	732.39	366.70			714.38	357.69	D	**1012.47**	506.74	995.44	498.22	994.45	497.73	7
8	**895.46**	448.23			877.45	439.23	Y	**897.44**	449.22	880.41	440.71	879.43	440.22	6
9	**1008.54**	504.77			990.53	495.77	L	734.38	367.69	717.35	359.18	716.36	358.69	5
10	**1139.58**	570.29			1121.57	561.29	M	**621.29**	311.15	604.26	302.64	603.28	302.14	4
11	**1367.69**	684.35	1350.66	675.84	**1349.68**	675.34	K	**490.25**	245.63	473.22	237.12	472.24	236.62	3
12	**1482.72**	741.86	1465.69	733.35	1464.71	732.86	D	**262.14**	131.57	245.11	123.06	244.13	122.57	2
13							K	147.11	74.06	130.09	65.55			1

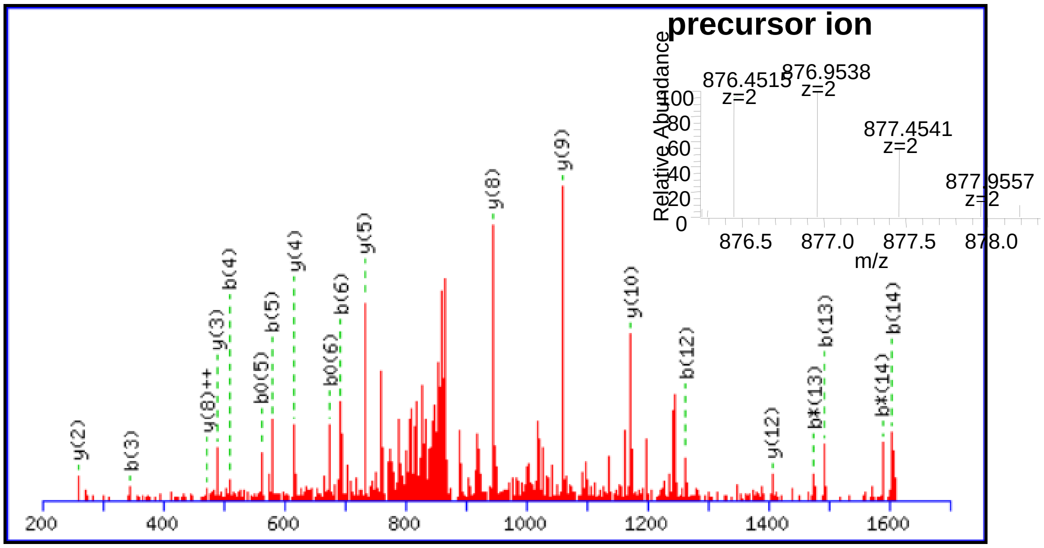
pyruvate formate lyase I   K454

TMLYAINGGVDE^{Succ}KLK

MS/MS Fragmentation of **TMLYAINGGVDEKLK**
Found in **gi|170080561**, pyruvate formate lyase I [Escherichia coli str. K-12 substr. DH10B]

Match to Query 7112: 1751.893594 from(876.954073,2+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da



```
Monoisotopic mass of neutral peptide Mr(calc): 1750.88
Variable modifications:
K13     : Succinyl (K)
Ions Score: 55  Expect: 0.00021
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.05	51.53			84.04	42.53	T							15
2	233.10	117.05			215.08	108.05	M	1650.84	825.92	1633.81	817.41	1632.83	816.92	14
3	**346.18**	173.59			328.17	164.59	L	1519.80	760.40	1502.77	751.89	1501.79	751.40	13
4	**509.24**	255.13			491.23	246.12	Y	**1406.72**	703.86	1389.69	695.35	1388.71	694.86	12
5	**580.28**	290.64			**562.27**	281.64	A	1243.65	622.33	1226.63	613.82	1225.64	613.32	11
6	**693.36**	347.19			**675.35**	338.18	I	**1172.62**	586.81	1155.59	578.30	1154.61	577.81	10
7	807.41	404.21	790.38	395.69	789.40	395.20	N	**1059.53**	530.27	1042.51	521.76	1041.52	521.26	9
8	864.43	432.72	847.40	424.20	846.42	423.71	G	**945.49**	**473.25**	928.46	464.73	927.48	464.24	8
9	921.45	461.23	904.42	452.72	903.44	452.22	G	888.47	444.74	871.44	436.22	870.46	435.73	7
10	1020.52	510.76	1003.49	502.25	1002.51	501.76	V	831.45	416.23	814.42	407.71	813.44	407.22	6
11	1135.55	568.28	1118.52	559.76	1117.53	559.27	D	**732.38**	366.69	715.35	358.18	714.37	357.69	5
12	**1264.59**	632.80	1247.56	624.28	1246.58	623.79	E	**617.35**	309.18	600.32	300.67	599.34	300.17	4
13	**1492.70**	746.85	**1475.67**	738.34	1474.69	737.85	K	**488.31**	244.66	471.28	236.14			3
14	**1605.78**	803.40	**1588.76**	794.88	1587.77	794.39	L	**260.20**	130.60	243.17	122.09			2
15							K	147.11	74.06	130.09	65.55			1

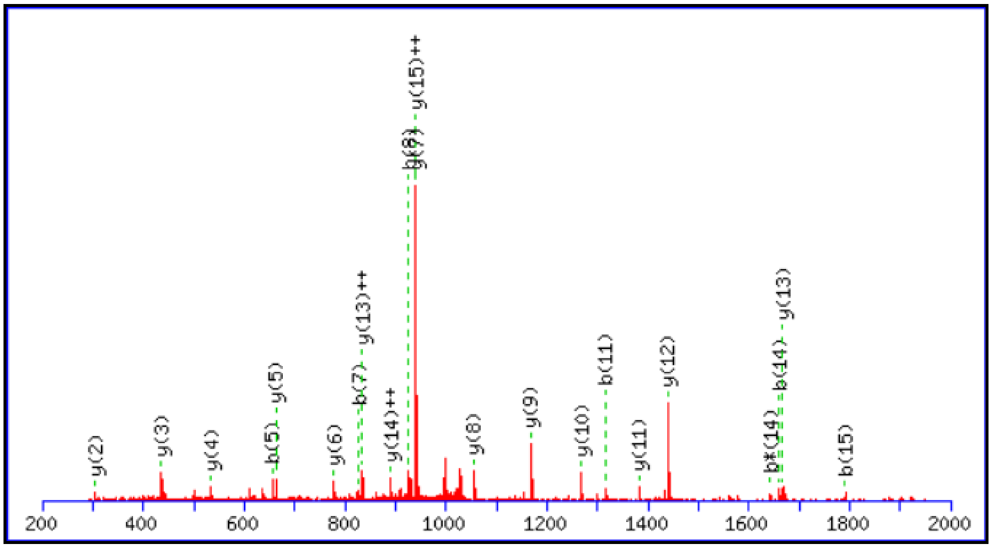
pyruvate formate lyase I K467

SEPI^{Succ}KGDVLNYDEVMER

MS/MS Fragmentation of **SEPIKGDVLNYDEVMER**
Found in **gi|170080561**, pyruvate formate lyase I [Escherichia coli str. K-12 substr. DH10B]

Match to Query 15447: 2092.963294 from(1047.488923,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da



```
Monoisotopic mass of neutral peptide Mr(calc): 2092.96
Variable modifications:
K5      : Succinyl (K)
Ions Score: 57  Expect: 0.00028
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.04	44.52			70.03	35.52	S							17
2	217.08	109.04			199.07	100.04	E	2006.94	1003.97	1989.91	995.46	1988.93	994.97	16
3	314.13	157.57			296.12	148.57	P	1877.89	**939.45**	1860.87	930.94	1859.88	930.45	15
4	427.22	214.11			409.21	205.11	I	1780.84	**890.92**	1763.82	882.41	1762.83	881.92	14
5	**655.33**	328.17	638.30	319.66	637.32	319.16	K	**1667.76**	**834.38**	1650.73	825.87	1649.75	825.38	13
6	712.35	356.68	695.32	348.17	694.34	347.67	G	**1439.65**	720.33	1422.62	711.81	1421.64	711.32	12
7	**827.38**	414.19	810.35	405.68	809.37	405.19	D	**1382.63**	691.82	1365.60	683.30	1364.62	682.81	11
8	**926.45**	463.73	909.42	455.21	908.44	454.72	V	**1267.60**	634.30	1250.57	625.79	1249.59	625.30	10
9	1039.53	520.27	1022.50	511.76	1021.52	511.26	L	**1168.53**	584.77	1151.50	576.26	1150.52	575.76	9
10	1153.57	577.29	1136.55	568.78	1135.56	568.29	N	**1055.45**	528.23	1038.42	519.71	1037.44	519.22	8
11	**1316.64**	658.82	1299.61	650.31	1298.63	649.82	Y	**941.40**	471.21	924.38	462.69	923.39	462.20	7
12	1431.66	716.34	1414.64	707.82	1413.65	707.33	D	**778.34**	389.67	761.31	381.16	760.33	380.67	6
13	1560.71	780.86	1543.68	772.34	1542.70	771.85	E	**663.31**	332.16	646.29	323.65	645.30	323.15	5
14	**1659.77**	830.39	**1642.75**	821.88	1641.76	821.39	V	**534.27**	267.64	517.24	259.13	516.26	258.63	4
15	**1790.82**	895.91	1773.79	887.40	1772.80	886.91	M	**435.20**	218.10	418.18	209.59	417.19	209.10	3
16	1919.86	960.43	1902.83	951.92	1901.85	951.43	E	**304.16**	152.58	287.13	144.07	286.15	143.58	2
17							R	175.12	88.06	158.09	79.55			1

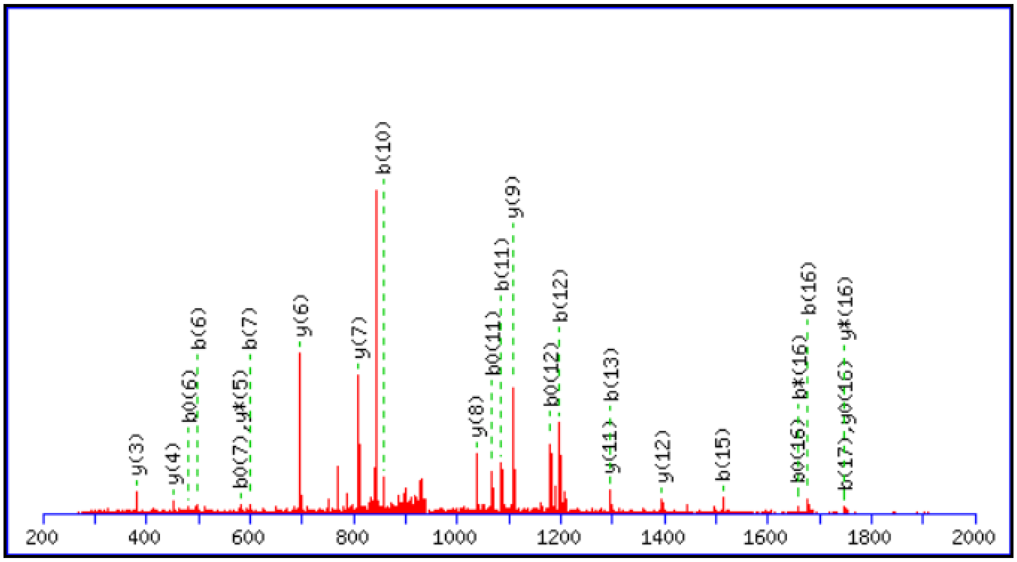
pyruvate formate lyase I K654

GAVASLTSVA^{Succ}KLPFAYAK

MS/MS Fragmentation of **GAVASLTSVAKLPFAYAK**
Found in **gi|170080561**, pyruvate formate lyase I [Escherichia coli str. K-12 substr. DH

Match to Query 14402: 1893.022744 from(947.518648,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da

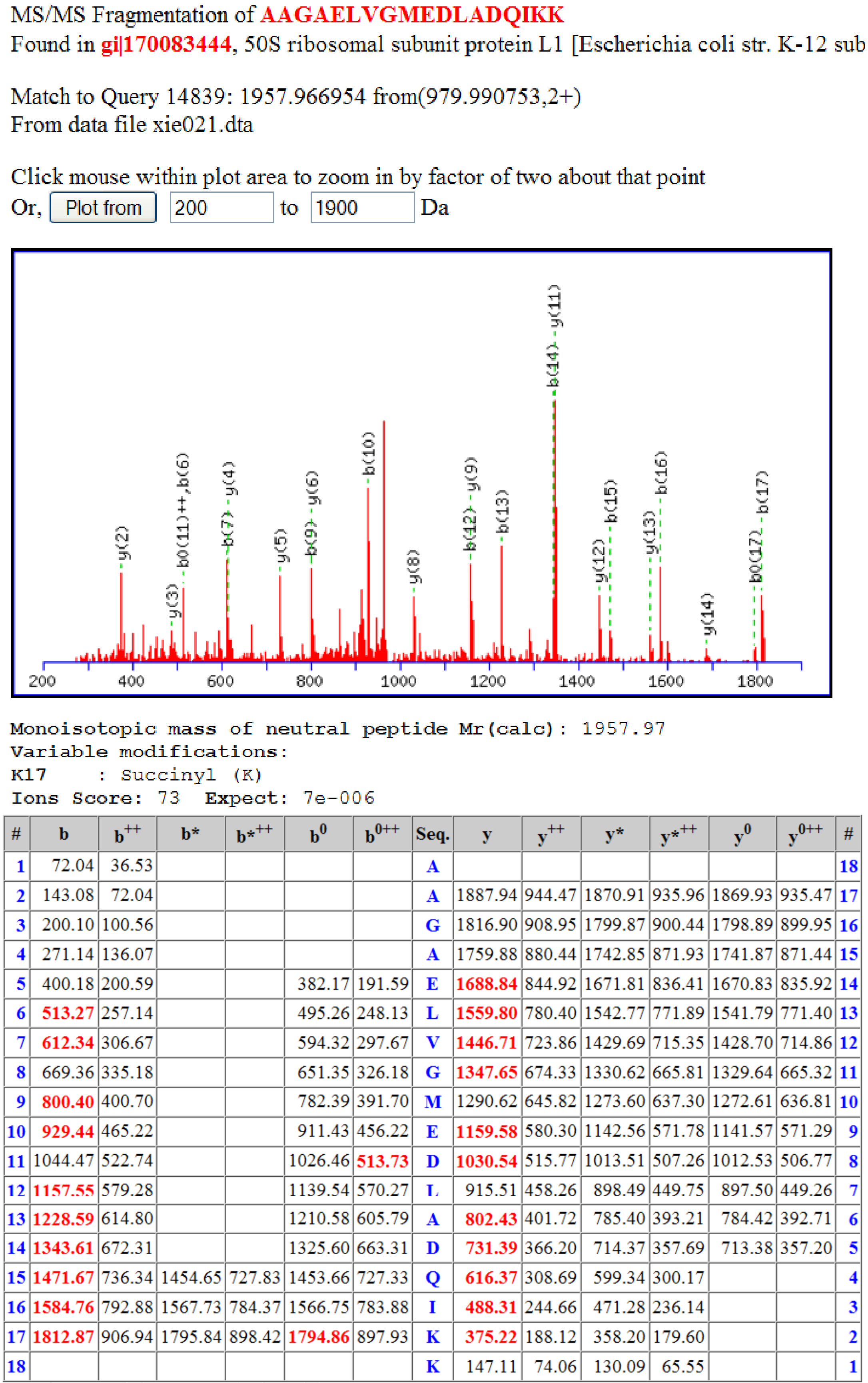


```
Monoisotopic mass of neutral peptide Mr(calc): 1893.02
Variable modifications:
K11     : Succinyl (K)
Ions Score: 46  Expect: 0.0032
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.03	29.52					G							18
2	129.07	65.04					A	1837.01	919.01	1819.98	910.50	1819.00	910.00	17
3	228.13	114.57					V	1765.97	883.49	**1748.95**	874.98	**1747.96**	874.49	16
4	299.17	150.09					A	1666.91	833.96	1649.88	825.44	1648.89	824.95	15
5	386.20	193.61			368.19	184.60	S	1595.87	798.44	1578.84	789.92	1577.86	789.43	14
6	**499.29**	250.15			**481.28**	241.14	L	1508.84	754.92	1491.81	746.41	1490.83	745.92	13
7	**600.34**	300.67			**582.32**	291.67	T	**1395.75**	698.38	1378.73	689.87	1377.74	689.37	12
8	687.37	344.19			669.36	335.18	S	**1294.70**	647.86	1277.68	639.34	1276.69	638.85	11
9	786.44	393.72			768.43	384.72	V	1207.67	604.34	1190.65	595.83			10
10	**857.47**	429.24			839.46	420.23	A	**1108.60**	554.81	1091.58	546.29			9
11	**1085.58**	543.30	1068.56	534.78	**1067.57**	534.29	K	**1037.57**	519.29	1020.54	510.77			8
12	**1198.67**	599.84	1181.64	591.32	**1180.66**	590.83	L	**809.46**	405.23	792.43	396.72			7
13	**1295.72**	648.36	1278.69	639.85	1277.71	639.36	P	**696.37**	348.69	679.34	340.18			6
14	1442.79	721.90	1425.76	713.38	1424.78	712.89	F	599.32	300.16	**582.29**	291.65			5
15	**1513.83**	757.42	1496.80	748.90	1495.82	748.41	A	**452.25**	226.63	435.22	218.12			4
16	**1676.89**	838.95	**1659.86**	830.44	**1658.88**	829.94	Y	**381.21**	191.11	364.19	182.60			3
17	**1747.93**	874.47	1730.90	865.95	1729.92	865.46	A	218.15	109.58	201.12	101.07			2
18							K	147.11	74.06	130.09	65.55			1

50S ribosomal subunit protein L1 K105

AAGAELVGMEDLADQI^{Succ}KK



MS/MS Fragmentation of AAGAELVGMEDLADQIKK
Found in gi|170083444, 50S ribosomal subunit protein L1 [Escherichia coli str. K-12 sub

Match to Query 14839: 1957.966954 from(979.990753,2+)
From data file xie021.dta

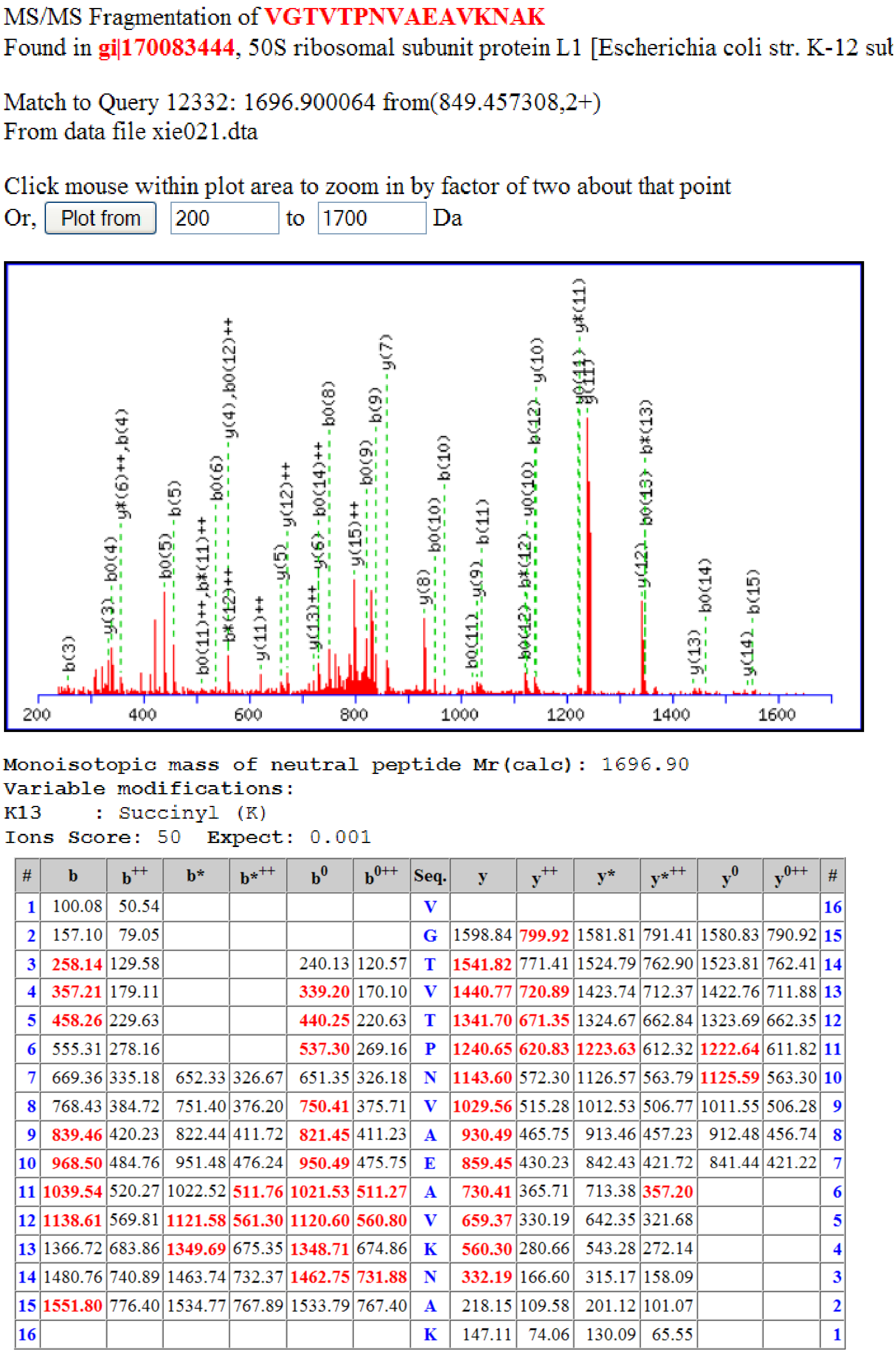
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1957.97
Variable modifications:
K17     : Succinyl (K)
Ions Score: 73  Expect: 7e-006
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.04	36.53					A							18
2	143.08	72.04					A	1887.94	944.47	1870.91	935.96	1869.93	935.47	17
3	200.10	100.56					G	1816.90	908.95	1799.87	900.44	1798.89	899.95	16
4	271.14	136.07					A	1759.88	880.44	1742.85	871.93	1741.87	871.44	15
5	400.18	200.59			382.17	191.59	E	1688.84	844.92	1671.81	836.41	1670.83	835.92	14
6	513.27	257.14			495.26	248.13	L	1559.80	780.40	1542.77	771.89	1541.79	771.40	13
7	612.34	306.67			594.32	297.67	V	1446.71	723.86	1429.69	715.35	1428.70	714.86	12
8	669.36	335.18			651.35	326.18	G	1347.65	674.33	1330.62	665.81	1329.64	665.32	11
9	800.40	400.70			782.39	391.70	M	1290.62	645.82	1273.60	637.30	1272.61	636.81	10
10	929.44	465.22			911.43	456.22	E	1159.58	580.30	1142.56	571.78	1141.57	571.29	9
11	1044.47	522.74			1026.46	513.73	D	1030.54	515.77	1013.51	507.26	1012.53	506.77	8
12	1157.55	579.28			1139.54	570.27	L	915.51	458.26	898.49	449.75	897.50	449.26	7
13	1228.59	614.80			1210.58	605.79	A	802.43	401.72	785.40	393.21	784.42	392.71	6
14	1343.61	672.31			1325.60	663.31	D	731.39	366.20	714.37	357.69	713.38	357.20	5
15	1471.67	736.34	1454.65	727.83	1453.66	727.33	Q	616.37	308.69	599.34	300.17			4
16	1584.76	792.88	1567.73	784.37	1566.75	783.88	I	488.31	244.66	471.28	236.14			3
17	1812.87	906.94	1795.84	898.42	1794.86	897.93	K	375.22	188.12	358.20	179.60			2
18							K	147.11	74.06	130.09	65.55			1

50S ribosomal subunit protein L1 K154

VGTVTPNVAEAV^{Succ}KNAK



MS/MS Fragmentation of **VGTVTPNVAEAVKNAK**
Found in **gi|170083444**, 50S ribosomal subunit protein L1 [Escherichia coli str. K-12 sul

Match to Query 12332: 1696.900064 from(849.457308,2+)
From data file xie021.dta

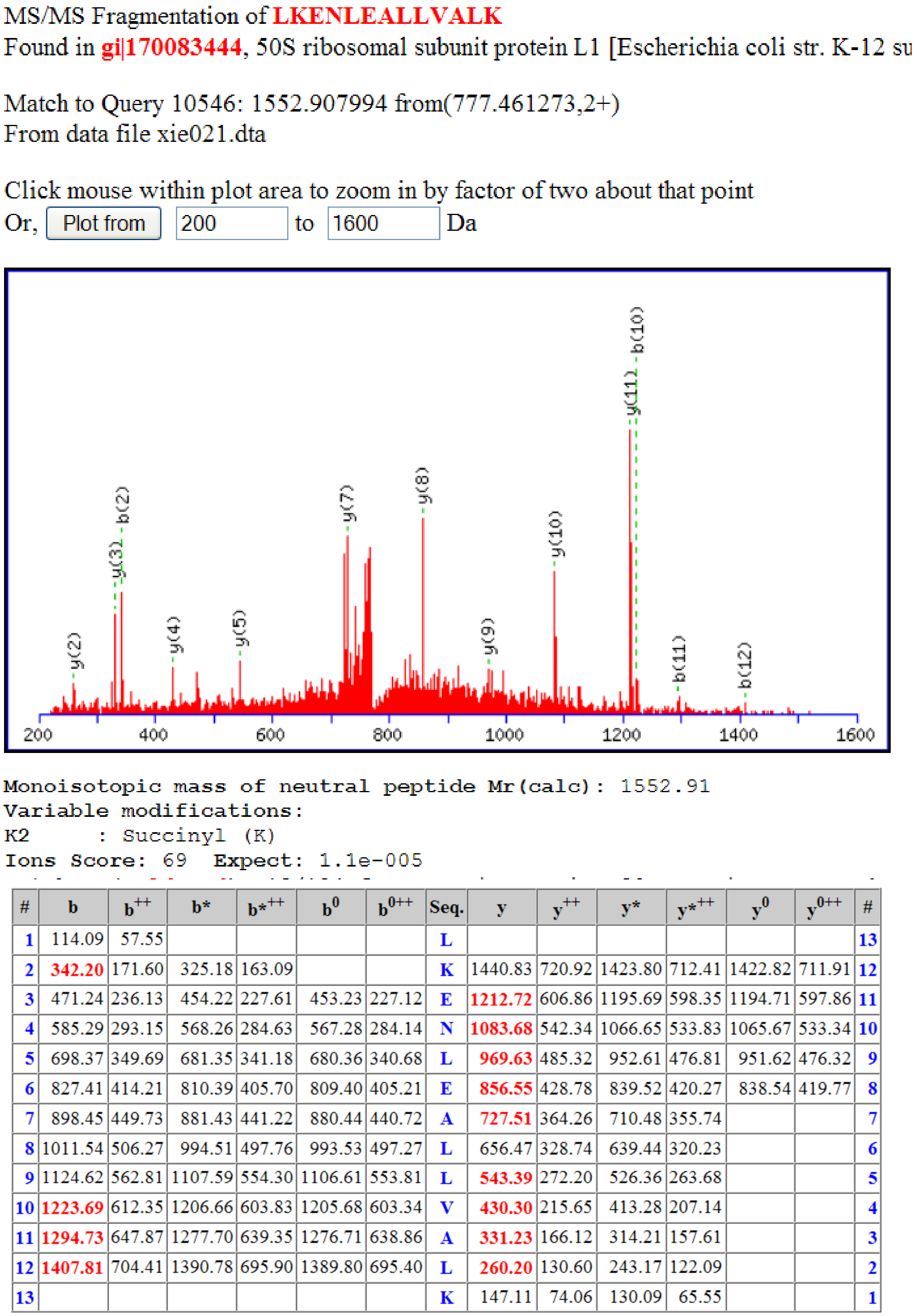
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1696.90
Variable modifications:
K13    : Succinyl (K)
Ions Score: 50  Expect: 0.001
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.08	50.54					V							16
2	157.10	79.05					G	1598.84	**799.92**	1581.81	791.41	1580.83	790.92	15
3	**258.14**	129.58			240.13	120.57	T	**1541.82**	771.41	1524.79	762.90	1523.81	762.41	14
4	**357.21**	179.11			**339.20**	170.10	V	**1440.77**	**720.89**	1423.74	712.37	1422.76	711.88	13
5	**458.26**	229.63			**440.25**	220.63	T	**1341.70**	**671.35**	1324.67	662.84	1323.69	662.35	12
6	555.31	278.16			**537.30**	269.16	P	**1240.65**	**620.83**	**1223.63**	612.32	**1222.64**	611.82	11
7	669.36	335.18	652.33	326.67	651.35	326.18	N	**1143.60**	572.30	1126.57	563.79	**1125.59**	563.30	10
8	768.43	384.72	751.40	376.20	**750.41**	375.71	V	**1029.56**	515.28	1012.53	506.77	1011.55	506.28	9
9	**839.46**	420.23	822.44	411.72	**821.45**	411.23	A	**930.49**	465.75	913.46	457.23	912.48	456.74	8
10	**968.50**	484.76	951.48	476.24	**950.49**	475.75	E	**859.45**	430.23	842.43	421.72	841.44	421.22	7
11	**1039.54**	520.27	1022.52	**511.76**	**1021.53**	**511.27**	A	**730.41**	365.71	713.38	**357.20**			6
12	**1138.61**	569.81	**1121.58**	**561.30**	**1120.60**	**560.80**	V	**659.37**	330.19	642.35	321.68			5
13	1366.72	683.86	**1349.69**	675.35	**1348.71**	674.86	K	**560.30**	280.66	543.28	272.14			4
14	1480.76	740.89	1463.74	732.37	**1462.75**	**731.88**	N	**332.19**	166.60	315.17	158.09			3
15	**1551.80**	776.40	1534.77	767.89	1533.79	767.40	A	218.15	109.58	201.12	101.07			2
16							K	147.11	74.06	130.09	65.55			1

50S ribosomal subunit protein L1 K186

$L^{Succ}KENLEALLVALK$



MS/MS Fragmentation of **LKENLEALLVALK**
Found in **gi|170083444**, 50S ribosomal subunit protein L1 [Escherichia coli str. K-12 su

Match to Query 10546: 1552.907994 from(777.461273,2+)
From data file xie021.dta

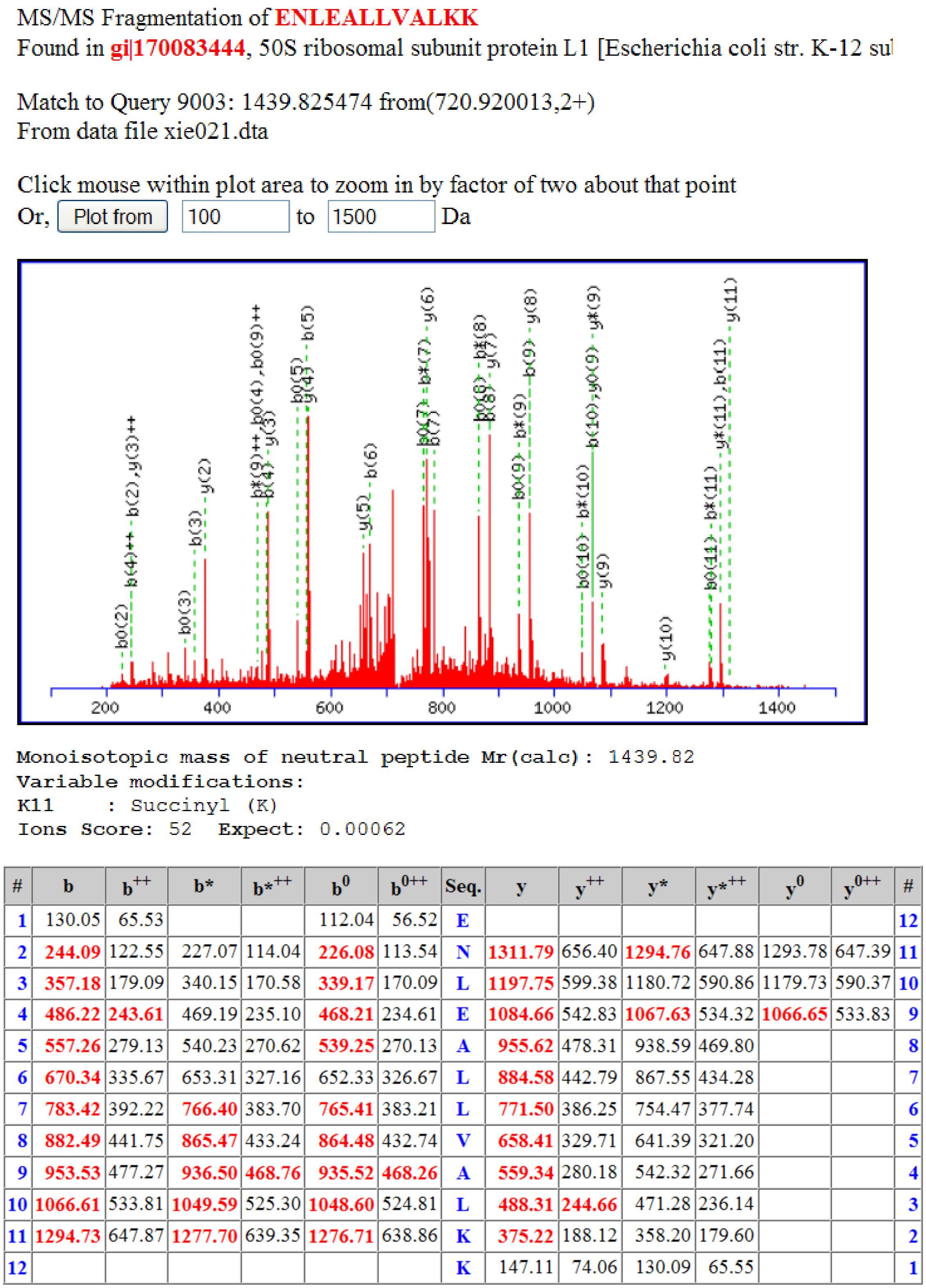
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1552.91
Variable modifications:
K2      : Succinyl (K)
Ions Score: 69   Expect: 1.1e-005
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.09	57.55					L							13
2	**342.20**	171.60	325.18	163.09			K	1440.83	720.92	1423.80	712.41	1422.82	711.91	12
3	471.24	236.13	454.22	227.61	453.23	227.12	E	**1212.72**	606.86	1195.69	598.35	1194.71	597.86	11
4	585.29	293.15	568.26	284.63	567.28	284.14	N	**1083.68**	542.34	1066.65	533.83	1065.67	533.34	10
5	698.37	349.69	681.35	341.18	680.36	340.68	L	**969.63**	485.32	952.61	476.81	951.62	476.32	9
6	827.41	414.21	810.39	405.70	809.40	405.21	E	**856.55**	428.78	839.52	420.27	838.54	419.77	8
7	898.45	449.73	881.43	441.22	880.44	440.72	A	**727.51**	364.26	710.48	355.74			7
8	1011.54	506.27	994.51	497.76	993.53	497.27	L	656.47	328.74	639.44	320.23			6
9	1124.62	562.81	1107.59	554.30	1106.61	553.81	L	**543.39**	272.20	526.36	263.68			5
10	**1223.69**	612.35	1206.66	603.83	1205.68	603.34	V	**430.30**	215.65	413.28	207.14			4
11	**1294.73**	647.87	1277.70	639.35	1276.71	638.86	A	**331.23**	166.12	314.21	157.61			3
12	**1407.81**	704.41	1390.78	695.90	1389.80	695.40	L	**260.20**	130.60	243.17	122.09			2
13							K	147.11	74.06	130.09	65.55			1

50S ribosomal subunit protein L1 K197

ENLEALLVAL$^{\text{Succ}}$KK



MS/MS Fragmentation of **ENLEALLVALKK**
Found in **gi|170083444**, 50S ribosomal subunit protein L1 [Escherichia coli str. K-12 sul

Match to Query 9003: 1439.825474 from(720.920013,2+)
From data file xie021.dta

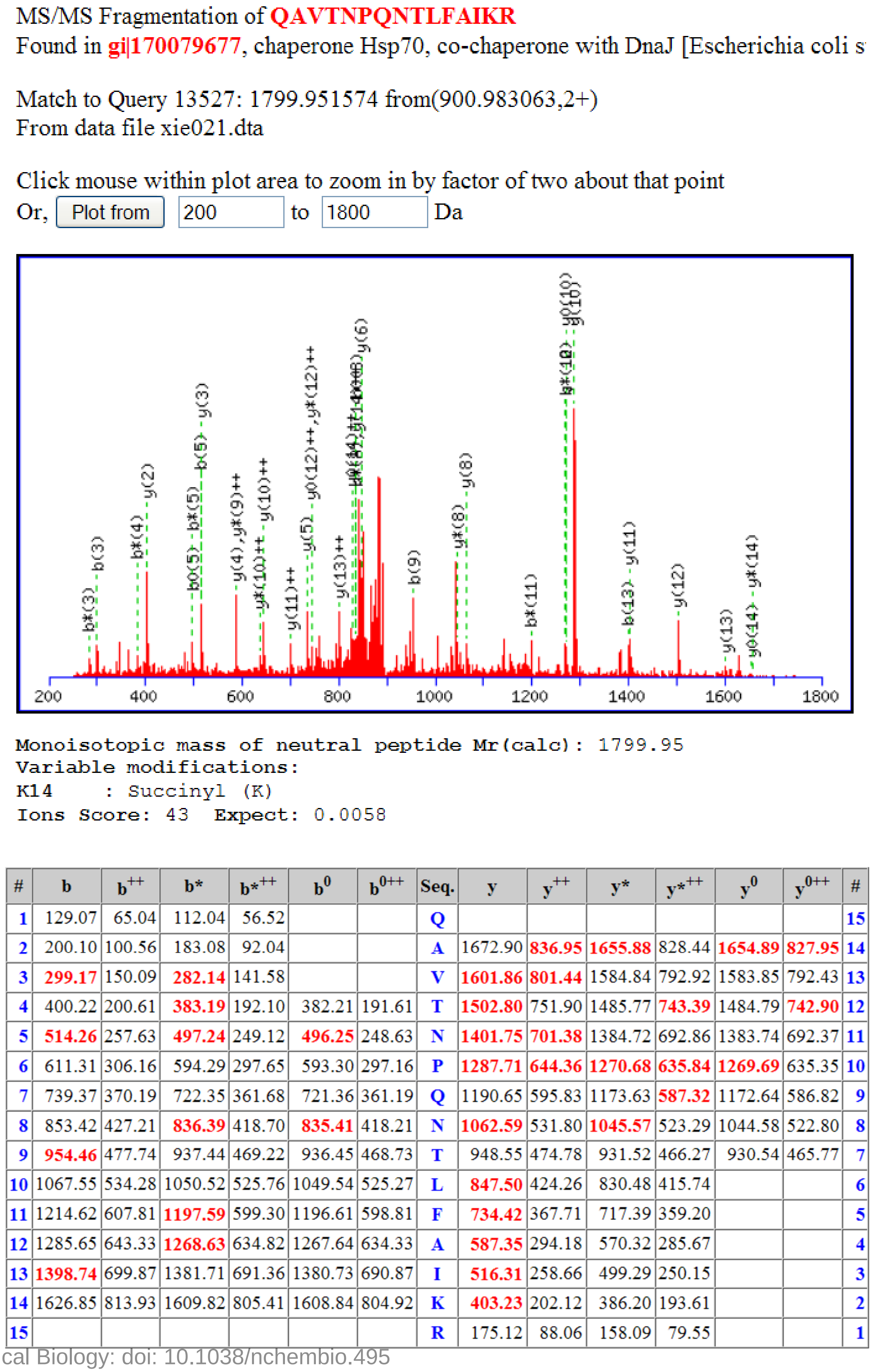
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1439.82
Variable modifications:
K11      : Succinyl (K)
Ions Score: 52   Expect: 0.00062
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.05	65.53			112.04	56.52	E							12
2	**244.09**	122.55	227.07	114.04	**226.08**	113.54	N	**1311.79**	656.40	**1294.76**	647.88	1293.78	647.39	11
3	**357.18**	179.09	340.15	170.58	**339.17**	170.09	L	**1197.75**	599.38	1180.72	590.86	1179.73	590.37	10
4	**486.22**	**243.61**	469.19	235.10	**468.21**	234.61	E	**1084.66**	542.83	**1067.63**	534.32	**1066.65**	533.83	9
5	**557.26**	279.13	540.23	270.62	**539.25**	270.13	A	**955.62**	478.31	938.59	469.80			8
6	**670.34**	335.67	653.31	327.16	652.33	326.67	L	**884.58**	442.79	867.55	434.28			7
7	**783.42**	392.22	**766.40**	383.70	**765.41**	383.21	L	**771.50**	386.25	754.47	377.74			6
8	**882.49**	441.75	**865.47**	433.24	**864.48**	432.74	V	**658.41**	329.71	641.39	321.20			5
9	**953.53**	477.27	**936.50**	**468.76**	**935.52**	**468.26**	A	**559.34**	280.18	542.32	271.66			4
10	**1066.61**	533.81	**1049.59**	525.30	**1048.60**	524.81	L	**488.31**	**244.66**	471.28	236.14			3
11	**1294.73**	647.87	**1277.70**	639.35	**1276.71**	638.86	K	**375.22**	188.12	358.20	179.60			2
12							K	147.11	74.06	130.09	65.55			1

chaperone Hsp70, co-chaperone with DnaJ K70

QAVTNPQNTLFAI^{Succ}KR



MS/MS Fragmentation of **QAVTNPQNTLFAIKR**
Found in **gi|170079677**, chaperone Hsp70, co-chaperone with DnaJ [Escherichia coli s

Match to Query 13527: 1799.951574 from(900.983063,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da

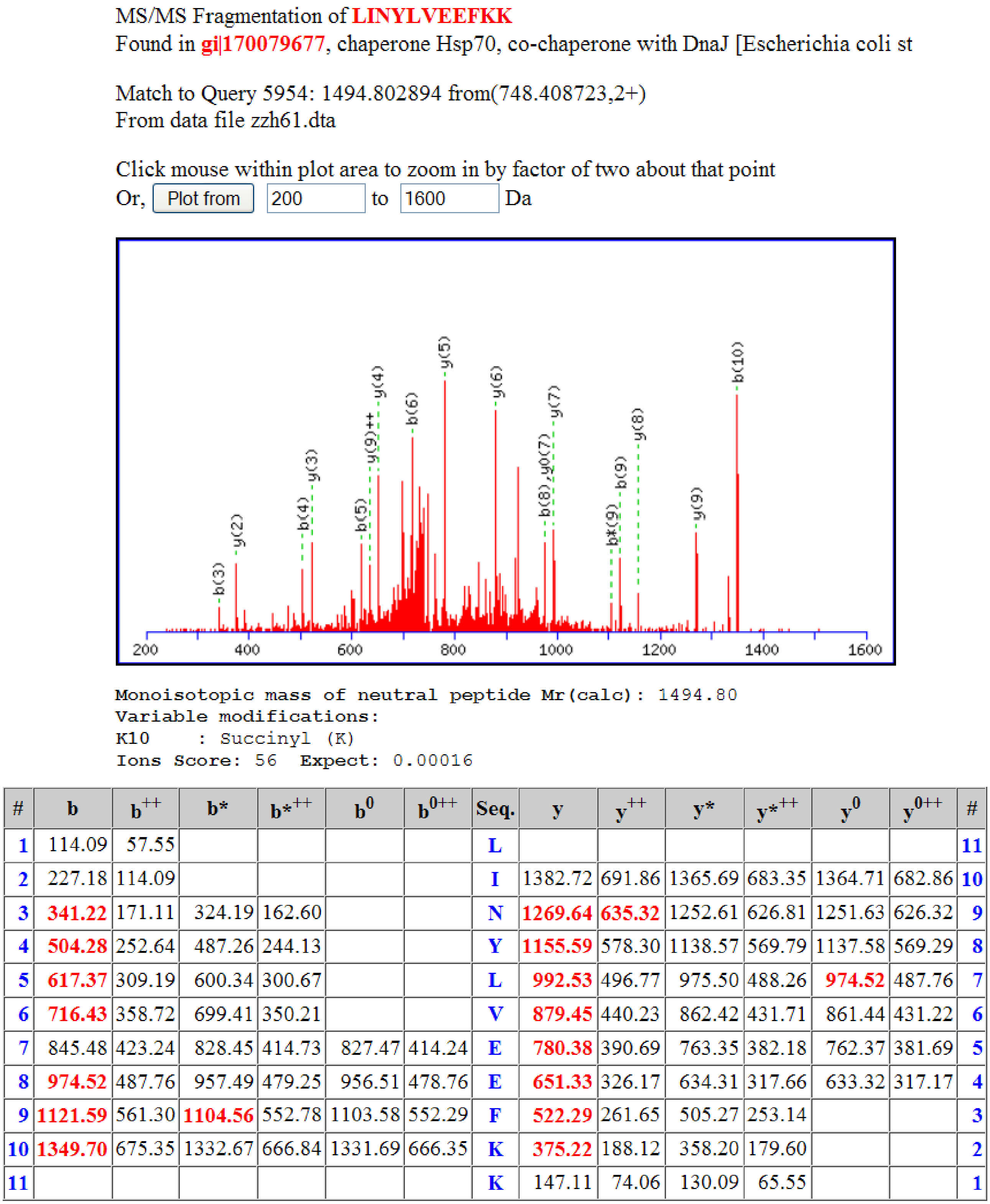
```
Monoisotopic mass of neutral peptide Mr(calc): 1799.95
Variable modifications:
K14     : Succinyl (K)
Ions Score: 43  Expect: 0.0058
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.07	65.04	112.04	56.52			Q							15
2	200.10	100.56	183.08	92.04			A	1672.90	**836.95**	**1655.88**	828.44	**1654.89**	**827.95**	14
3	**299.17**	150.09	**282.14**	141.58			V	**1601.86**	**801.44**	1584.84	792.92	1583.85	792.43	13
4	400.22	200.61	**383.19**	192.10	382.21	191.61	T	**1502.80**	751.90	1485.77	**743.39**	1484.79	**742.90**	12
5	**514.26**	257.63	**497.24**	249.12	**496.25**	248.63	N	**1401.75**	**701.38**	1384.72	692.86	1383.74	692.37	11
6	611.31	306.16	594.29	297.65	593.30	297.16	P	**1287.71**	**644.36**	**1270.68**	**635.84**	**1269.69**	635.35	10
7	739.37	370.19	722.35	361.68	721.36	361.19	Q	1190.65	595.83	1173.63	**587.32**	1172.64	586.82	9
8	853.42	427.21	**836.39**	418.70	**835.41**	418.21	N	**1062.59**	531.80	**1045.57**	523.29	1044.58	522.80	8
9	**954.46**	477.74	937.44	469.22	936.45	468.73	T	948.55	474.78	931.52	466.27	930.54	465.77	7
10	1067.55	534.28	1050.52	525.76	1049.54	525.27	L	**847.50**	424.26	830.48	415.74			6
11	1214.62	607.81	**1197.59**	599.30	1196.61	598.81	F	**734.42**	367.71	717.39	359.20			5
12	1285.65	643.33	**1268.63**	634.82	1267.64	634.33	A	**587.35**	294.18	570.32	285.67			4
13	**1398.74**	699.87	1381.71	691.36	1380.73	690.87	I	**516.31**	258.66	499.29	250.15			3
14	1626.85	813.93	1609.82	805.41	1608.84	804.92	K	**403.23**	202.12	386.20	193.61			2
15							R	175.12	88.06	158.09	79.55			1

chaperone Hsp70, co-chaperone with DnaJ

K245

LINYLVEEF$^{\text{Succ}}$KK



MS/MS Fragmentation of LINYLVEEFKK
Found in gi|170079677, chaperone Hsp70, co-chaperone with DnaJ [Escherichia coli st

Match to Query 5954: 1494.802894 from(748.408723,2+)
From data file zzh61.dta

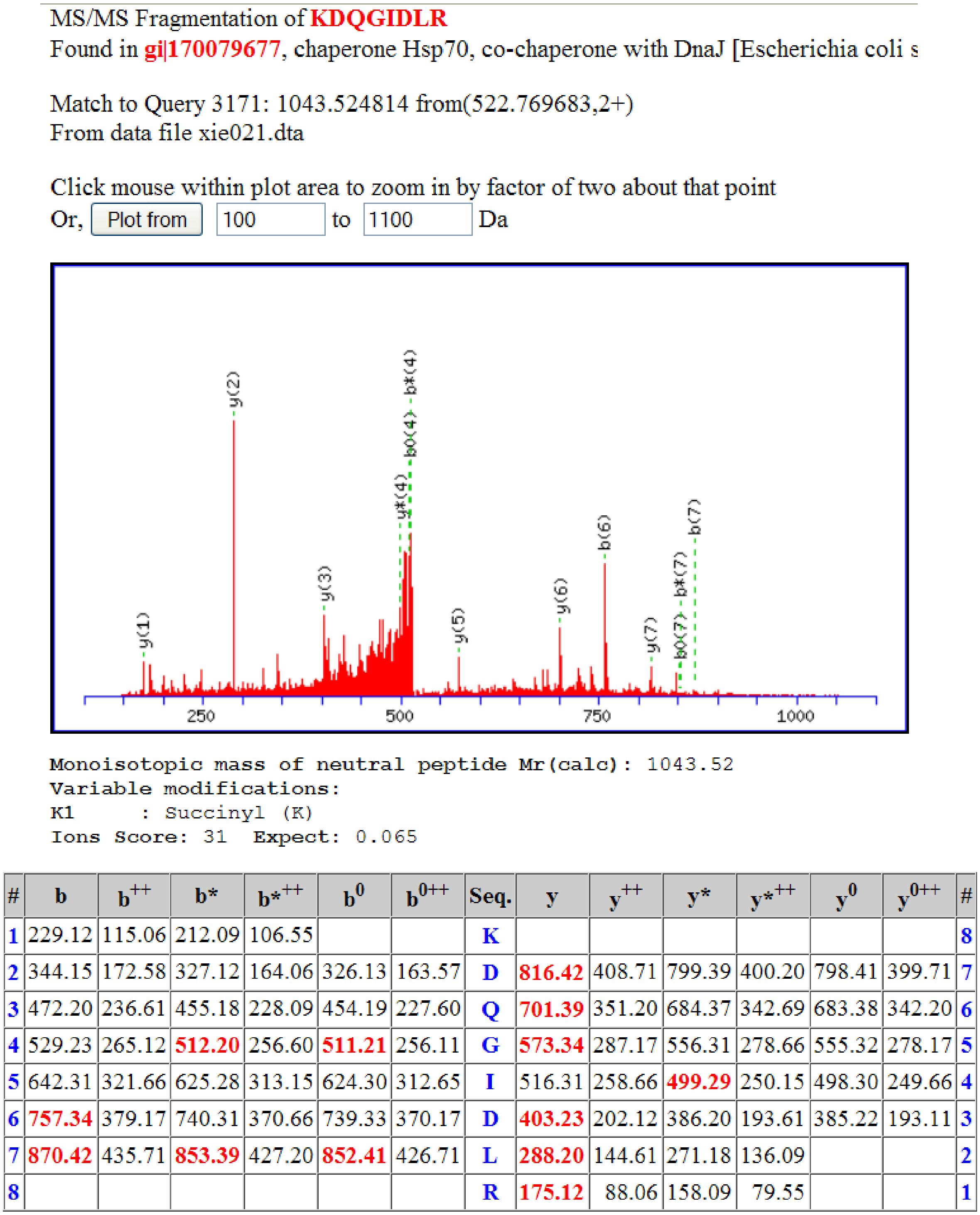
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1494.80
Variable modifications:
K10     : Succinyl (K)
Ions Score: 56   Expect: 0.00016
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.09	57.55					L							11
2	227.18	114.09					I	1382.72	691.86	1365.69	683.35	1364.71	682.86	10
3	341.22	171.11	324.19	162.60			N	1269.64	635.32	1252.61	626.81	1251.63	626.32	9
4	504.28	252.64	487.26	244.13			Y	1155.59	578.30	1138.57	569.79	1137.58	569.29	8
5	617.37	309.19	600.34	300.67			L	992.53	496.77	975.50	488.26	974.52	487.76	7
6	716.43	358.72	699.41	350.21			V	879.45	440.23	862.42	431.71	861.44	431.22	6
7	845.48	423.24	828.45	414.73	827.47	414.24	E	780.38	390.69	763.35	382.18	762.37	381.69	5
8	974.52	487.76	957.49	479.25	956.51	478.76	E	651.33	326.17	634.31	317.66	633.32	317.17	4
9	1121.59	561.30	1104.56	552.78	1103.58	552.29	F	522.29	261.65	505.27	253.14			3
10	1349.70	675.35	1332.67	666.84	1331.69	666.35	K	375.22	188.12	358.20	179.60			2
11							K	147.11	74.06	130.09	65.55			1

chaperone Hsp70, co-chaperone with DnaJ K246

$^{\text{Succ}}$KDQGIDLR



MS/MS Fragmentation of KDQGIDLR
Found in gi|170079677, chaperone Hsp70, co-chaperone with DnaJ [Escherichia coli s

Match to Query 3171: 1043.524814 from(522.769683,2+)
From data file xie021.dta

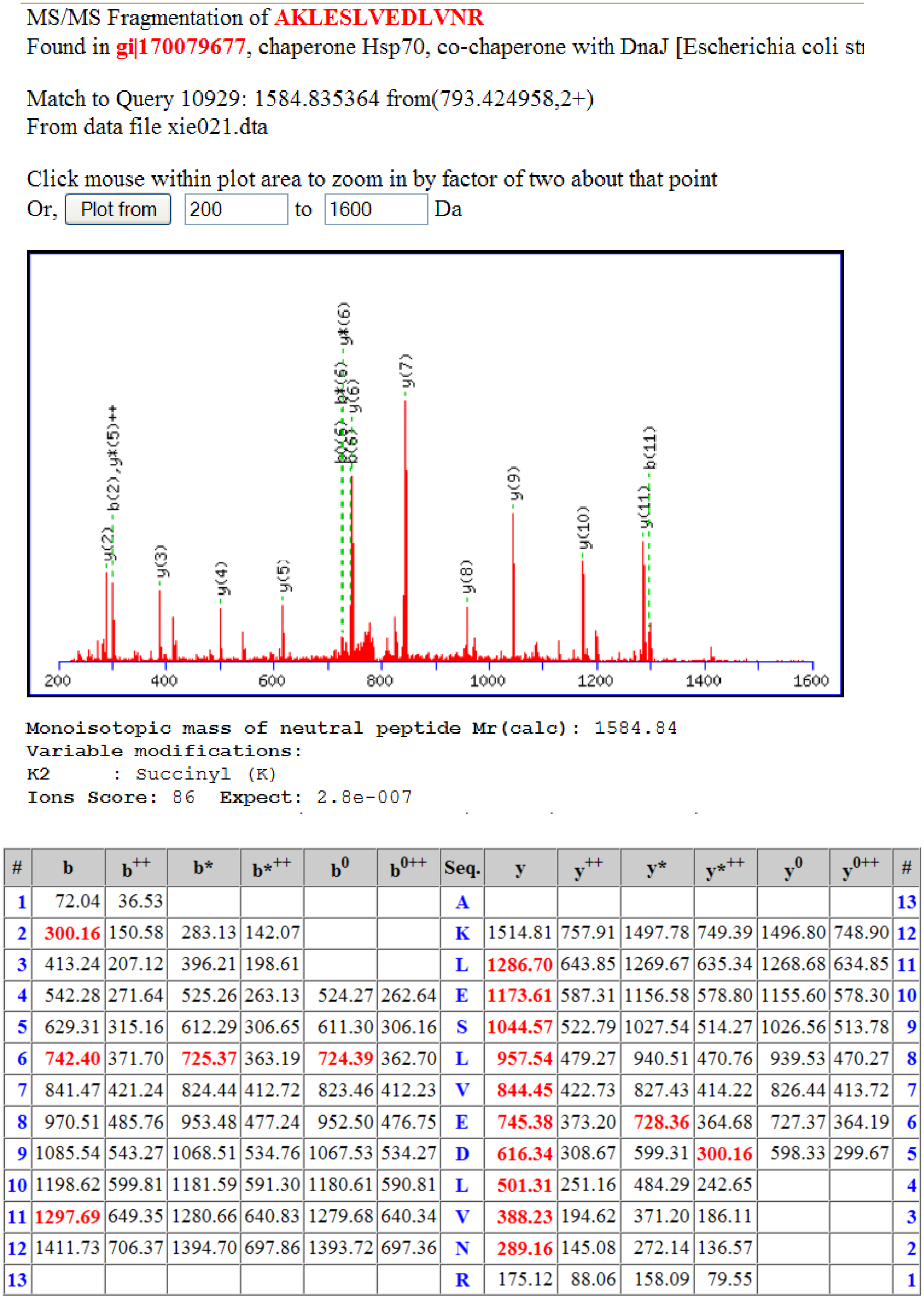
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1043.52
Variable modifications:
K1      : Succinyl (K)
Ions Score: 31  Expect: 0.065
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	229.12	115.06	212.09	106.55			K							8
2	344.15	172.58	327.12	164.06	326.13	163.57	D	816.42	408.71	799.39	400.20	798.41	399.71	7
3	472.20	236.61	455.18	228.09	454.19	227.60	Q	701.39	351.20	684.37	342.69	683.38	342.20	6
4	529.23	265.12	512.20	256.60	511.21	256.11	G	573.34	287.17	556.31	278.66	555.32	278.17	5
5	642.31	321.66	625.28	313.15	624.30	312.65	I	516.31	258.66	499.29	250.15	498.30	249.66	4
6	757.34	379.17	740.31	370.66	739.33	370.17	D	403.23	202.12	386.20	193.61	385.22	193.11	3
7	870.42	435.71	853.39	427.20	852.41	426.71	L	288.20	144.61	271.18	136.09			2
8							R	175.12	88.06	158.09	79.55			1

chaperone Hsp70, co-chaperone with DnaJ K304

A^{Succ}KLESLVEDLVNR



MS/MS Fragmentation of **AKLESLVEDLVNR**

Found in **gi|170079677**, chaperone Hsp70, co-chaperone with DnaJ [Escherichia coli st

Match to Query 10929: 1584.835364 from(793.424958,2+)

From data file xie021.dta

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

Or, 200 to 1600 Da

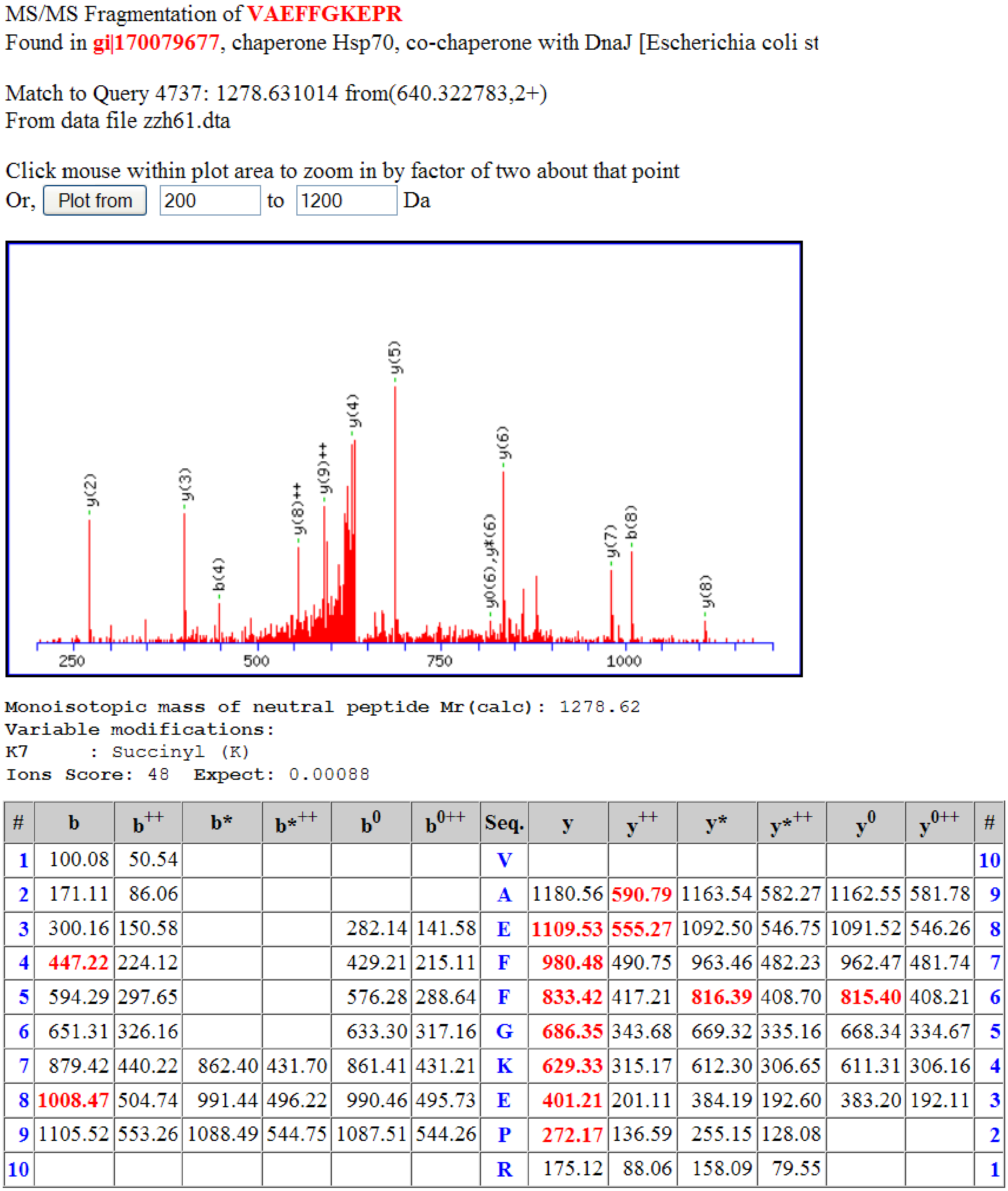
```
Monoisotopic mass of neutral peptide Mr(calc): 1584.84
Variable modifications:
K2      : Succinyl (K)
Ions Score: 86  Expect: 2.8e-007
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.04	36.53					A							13
2	300.16	150.58	283.13	142.07			K	1514.81	757.91	1497.78	749.39	1496.80	748.90	12
3	413.24	207.12	396.21	198.61			L	1286.70	643.85	1269.67	635.34	1268.68	634.85	11
4	542.28	271.64	525.26	263.13	524.27	262.64	E	1173.61	587.31	1156.58	578.80	1155.60	578.30	10
5	629.31	315.16	612.29	306.65	611.30	306.16	S	1044.57	522.79	1027.54	514.27	1026.56	513.78	9
6	742.40	371.70	725.37	363.19	724.39	362.70	L	957.54	479.27	940.51	470.76	939.53	470.27	8
7	841.47	421.24	824.44	412.72	823.46	412.23	V	844.45	422.73	827.43	414.22	826.44	413.72	7
8	970.51	485.76	953.48	477.24	952.50	476.75	E	745.38	373.20	728.36	364.68	727.37	364.19	6
9	1085.54	543.27	1068.51	534.76	1067.53	534.27	D	616.34	308.67	599.31	300.16	598.33	299.67	5
10	1198.62	599.81	1181.59	591.30	1180.61	590.81	L	501.31	251.16	484.29	242.65			4
11	1297.69	649.35	1280.66	640.83	1279.68	640.34	V	388.23	194.62	371.20	186.11			3
12	1411.73	706.37	1394.70	697.86	1393.72	697.36	N	289.16	145.08	272.14	136.57			2
13							R	175.12	88.06	158.09	79.55			1

Nature Chemical Biology: doi: 10.1038/nchembio.495

chaperone Hsp70, co-chaperone with DnaJ K359

VAEFFG$^{\text{Succ}}$KEPR



MS/MS Fragmentation of VAEFFGKEPR
Found in gi|170079677, chaperone Hsp70, co-chaperone with DnaJ [Escherichia coli st

Match to Query 4737: 1278.631014 from(640.322783,2+)
From data file zzh61.dta

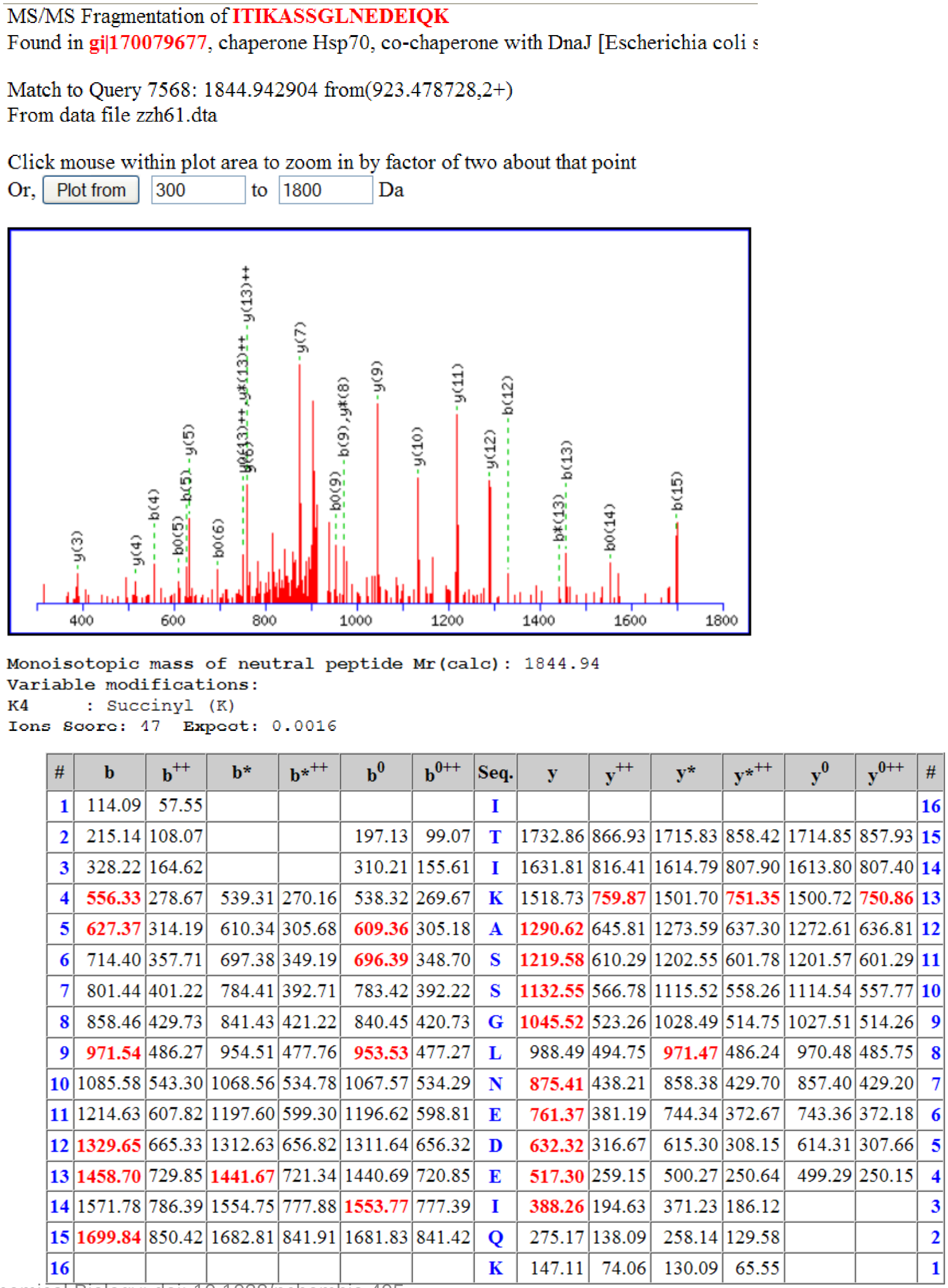
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1200 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1278.62
Variable modifications:
K7      : Succinyl (K)
Ions Score: 48  Expect: 0.00088
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.08	50.54					V							10
2	171.11	86.06					A	1180.56	590.79	1163.54	582.27	1162.55	581.78	9
3	300.16	150.58			282.14	141.58	E	1109.53	555.27	1092.50	546.75	1091.52	546.26	8
4	447.22	224.12			429.21	215.11	F	980.48	490.75	963.46	482.23	962.47	481.74	7
5	594.29	297.65			576.28	288.64	F	833.42	417.21	816.39	408.70	815.40	408.21	6
6	651.31	326.16			633.30	317.16	G	686.35	343.68	669.32	335.16	668.34	334.67	5
7	879.42	440.22	862.40	431.70	861.41	431.21	K	629.33	315.17	612.30	306.65	611.31	306.16	4
8	1008.47	504.74	991.44	496.22	990.46	495.73	E	401.21	201.11	384.19	192.60	383.20	192.11	3
9	1105.52	553.26	1088.49	544.75	1087.51	544.26	P	272.17	136.59	255.15	128.08			2
10							R	175.12	88.06	158.09	79.55			1

chaperone Hsp70, co-chaperone with DnaJ K502

ITI^{Succ}KASSGLNEDEIQK



MS/MS Fragmentation of **ITIKASSGLNEDEIQK**
Found in **gi|170079677**, chaperone Hsp70, co-chaperone with DnaJ [Escherichia coli s

Match to Query 7568: 1844.942904 from(923.478728,2+)
From data file zzh61.dta

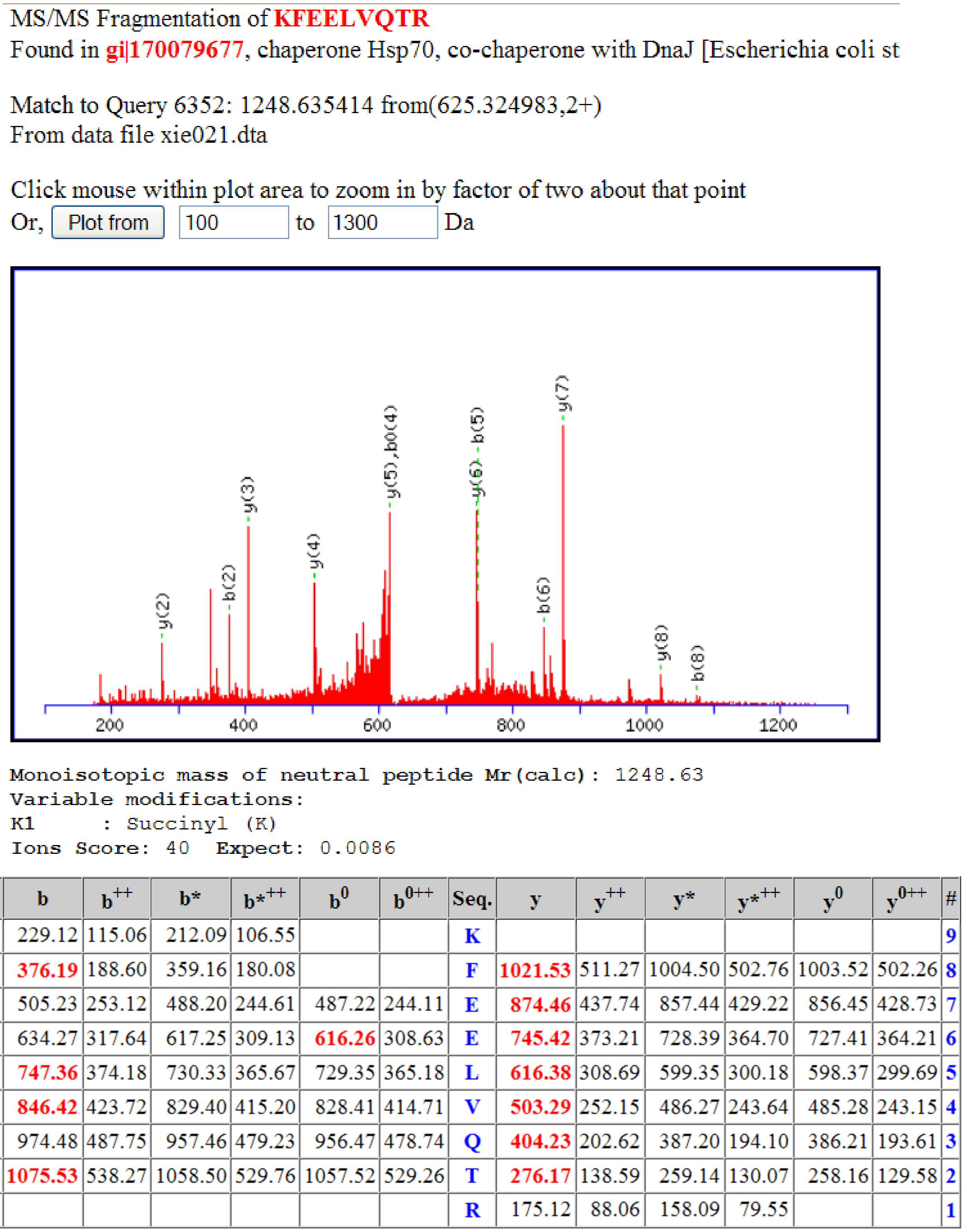
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1800 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1844.94
Variable modifications:
K4      : Succinyl (K)
Ions Score: 47  Expect: 0.0016
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.09	57.55					I							16
2	215.14	108.07			197.13	99.07	T	1732.86	866.93	1715.83	858.42	1714.85	857.93	15
3	328.22	164.62			310.21	155.61	I	1631.81	816.41	1614.79	807.90	1613.80	807.40	14
4	**556.33**	278.67	539.31	270.16	538.32	269.67	K	1518.73	**759.87**	1501.70	**751.35**	1500.72	**750.86**	13
5	**627.37**	314.19	610.34	305.68	**609.36**	305.18	A	**1290.62**	645.81	1273.59	637.30	1272.61	636.81	12
6	714.40	357.71	697.38	349.19	**696.39**	348.70	S	**1219.58**	610.29	1202.55	601.78	1201.57	601.29	11
7	801.44	401.22	784.41	392.71	783.42	392.22	S	**1132.55**	566.78	1115.52	558.26	1114.54	557.77	10
8	858.46	429.73	841.43	421.22	840.45	420.73	G	**1045.52**	523.26	1028.49	514.75	1027.51	514.26	9
9	**971.54**	486.27	954.51	477.76	**953.53**	477.27	L	988.49	494.75	**971.47**	486.24	970.48	485.75	8
10	1085.58	543.30	1068.56	534.78	1067.57	534.29	N	**875.41**	438.21	858.38	429.70	857.40	429.20	7
11	1214.63	607.82	1197.60	599.30	1196.62	598.81	E	**761.37**	381.19	744.34	372.67	743.36	372.18	6
12	**1329.65**	665.33	1312.63	656.82	1311.64	656.32	D	**632.32**	316.67	615.30	308.15	614.31	307.66	5
13	**1458.70**	729.85	**1441.67**	721.34	1440.69	720.85	E	**517.30**	259.15	500.27	250.64	499.29	250.15	4
14	1571.78	786.39	1554.75	777.88	**1553.77**	777.39	I	**388.26**	194.63	371.23	186.12			3
15	**1699.84**	850.42	1682.81	841.91	1681.83	841.42	Q	275.17	138.09	258.14	129.58			2
16							K	147.11	74.06	130.09	65.55			1

chaperone Hsp70, co-chaperone with DnaJ K528

^{Succ}KFEELVQTR



MS/MS Fragmentation of **KFEELVQTR**
Found in **gi|170079677**, chaperone Hsp70, co-chaperone with DnaJ [Escherichia coli st

Match to Query 6352: 1248.635414 from(625.324983,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1248.63
Variable modifications:
K1      : Succinyl (K)
Ions Score: 40   Expect: 0.0086
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	229.12	115.06	212.09	106.55			K							9
2	**376.19**	188.60	359.16	180.08			F	**1021.53**	511.27	1004.50	502.76	1003.52	502.26	8
3	505.23	253.12	488.20	244.61	487.22	244.11	E	**874.46**	437.74	857.44	429.22	856.45	428.73	7
4	634.27	317.64	617.25	309.13	**616.26**	308.63	E	**745.42**	373.21	728.39	364.70	727.41	364.21	6
5	**747.36**	374.18	730.33	365.67	729.35	365.18	L	**616.38**	308.69	599.35	300.18	598.37	299.69	5
6	**846.42**	423.72	829.40	415.20	828.41	414.71	V	**503.29**	252.15	486.27	243.64	485.28	243.15	4
7	974.48	487.75	957.46	479.23	956.47	478.74	Q	**404.23**	202.62	387.20	194.10	386.21	193.61	3
8	**1075.53**	538.27	1058.50	529.76	1057.52	529.26	T	**276.17**	138.59	259.14	130.07	258.16	129.58	2
9							R	175.12	88.06	158.09	79.55			1

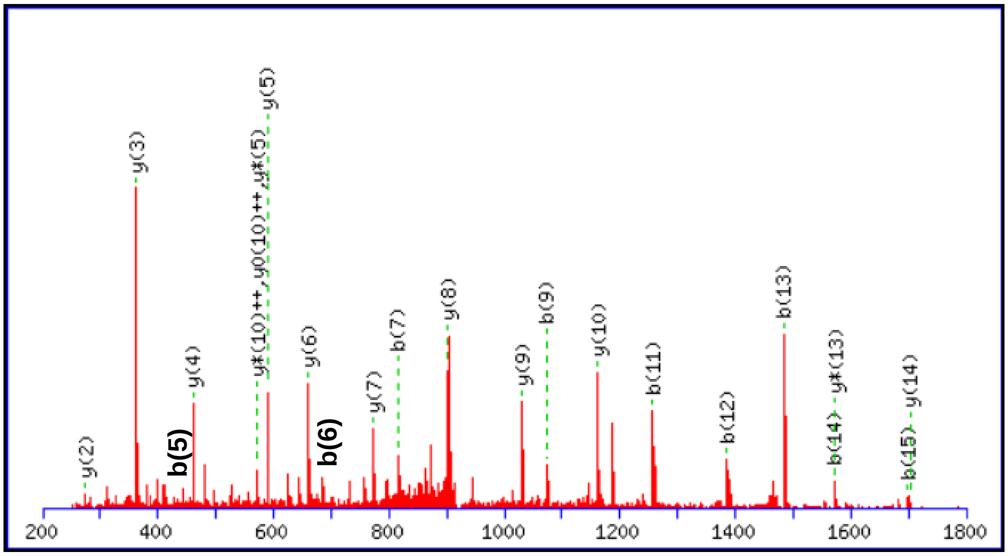
chaperone Hsp70, co-chaperone with DnaJ K587

AAIEA^{Succ}KMQELAQVSQK

MS/MS Fragmentation of **AAIEAKMQELAQVSQK**
Found in **gi|170079677**, chaperone Hsp70, co-chaperone with DnaJ [Escherichia coli s

Match to Query 13954: 1843.932534 from(922.973543,2+)
From data file xie021.dta

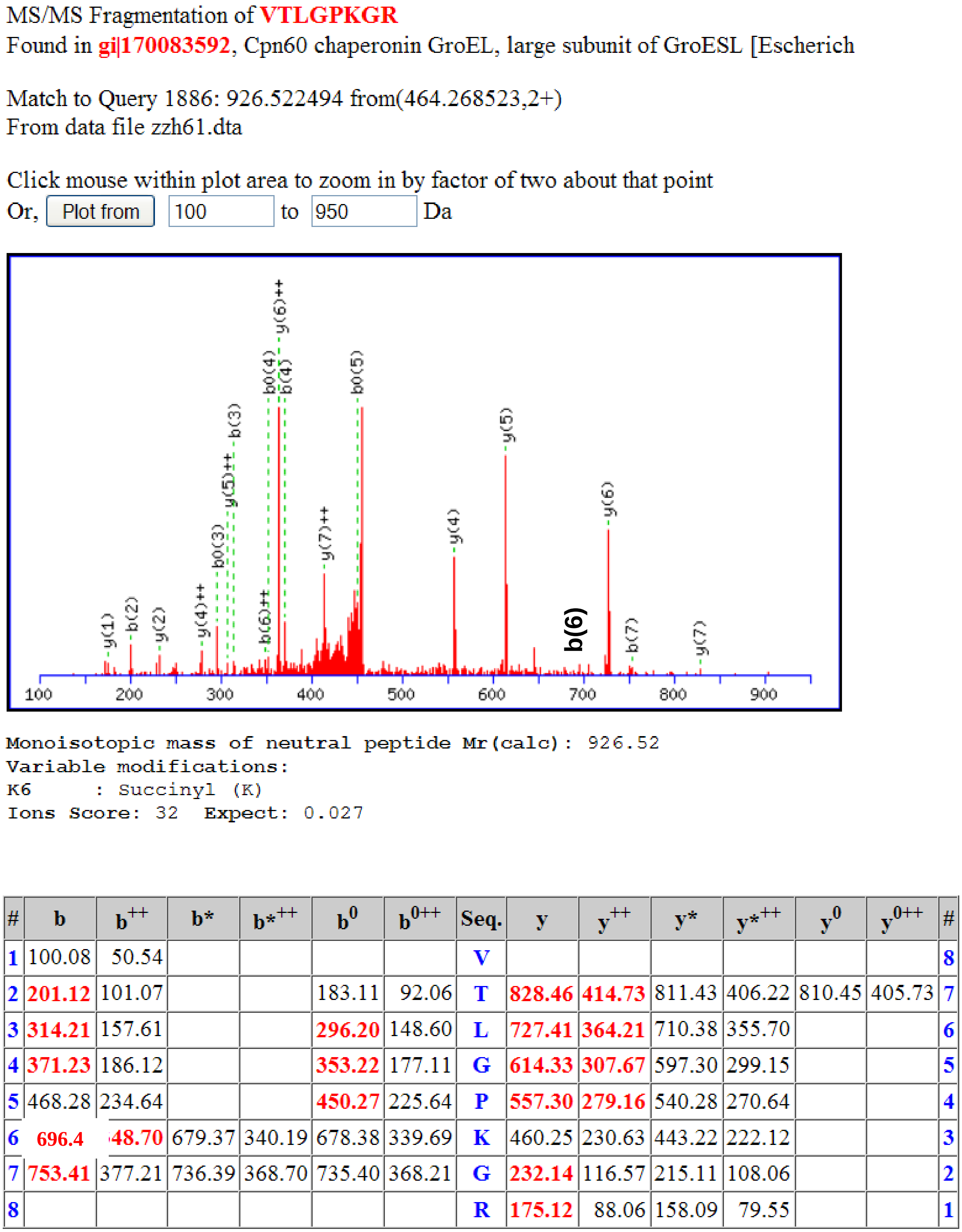
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da



```
Monoisotopic mass of neutral peptide Mr(calc): 1843.93
Variable modifications:
K6      : Succinyl (K)
Ions Score: 53  Expect: 0.00056
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.04	36.53					A							16
2	143.08	72.04					A	1773.91	887.46	1756.88	878.94	1755.89	878.45	15
3	256.17	128.59					I	**1702.87**	851.94	1685.84	843.42	1684.86	842.93	14
4	385.21	193.11			367.20	184.10	E	1589.78	795.40	**1572.76**	786.88	1571.77	786.39	13
5	**456.2**	28.63			438.23	219.62	A	1460.74	730.87	1443.71	722.36	1442.73	721.87	12
6	**684.4**	42.68	667.33	334.17	666.35	333.68	K	1389.70	695.36	1372.68	686.84	1371.69	686.35	11
7	**815.40**	408.20	798.37	399.69	797.39	399.20	M	**1161.59**	581.30	1144.57	**572.79**	1143.58	**572.29**	10
8	943.46	472.23	926.43	463.72	925.44	463.23	Q	**1030.55**	515.78	1013.53	507.27	1012.54	506.77	9
9	**1072.50**	536.75	1055.47	528.24	1054.49	527.75	E	**902.49**	451.75	885.47	443.24	884.48	442.75	8
10	1185.58	593.29	1168.56	584.78	1167.57	584.29	L	**773.45**	387.23	756.43	378.72	755.44	378.22	7
11	**1256.62**	628.81	1239.59	620.30	1238.61	619.81	A	**660.37**	330.69	643.34	322.17	642.36	321.68	6
12	**1384.68**	692.84	1367.65	684.33	1366.67	683.84	Q	**589.33**	295.17	**572.30**	286.66	571.32	286.16	5
13	**1483.75**	742.38	1466.72	733.86	1465.74	733.37	V	**461.27**	231.14	444.25	222.63	443.26	222.13	4
14	**1570.78**	785.89	1553.75	777.38	1552.77	776.89	S	**362.20**	181.61	345.18	173.09	344.19	172.60	3
15	**1698.84**	849.92	1681.81	841.41	1680.83	840.92	Q	**275.17**	138.09	258.14	129.58			2
16							K	147.11	74.06	130.09	65.55			1

Cpn60 chaperonin GroEL, large subunit of GroESL K34 VTLGP^{Succ}KGR



MS/MS Fragmentation of **VTLGPKGR**
Found in **gi|170083592**, Cpn60 chaperonin GroEL, large subunit of GroESL [Escherich

Match to Query 1886: 926.522494 from(464.268523,2+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da

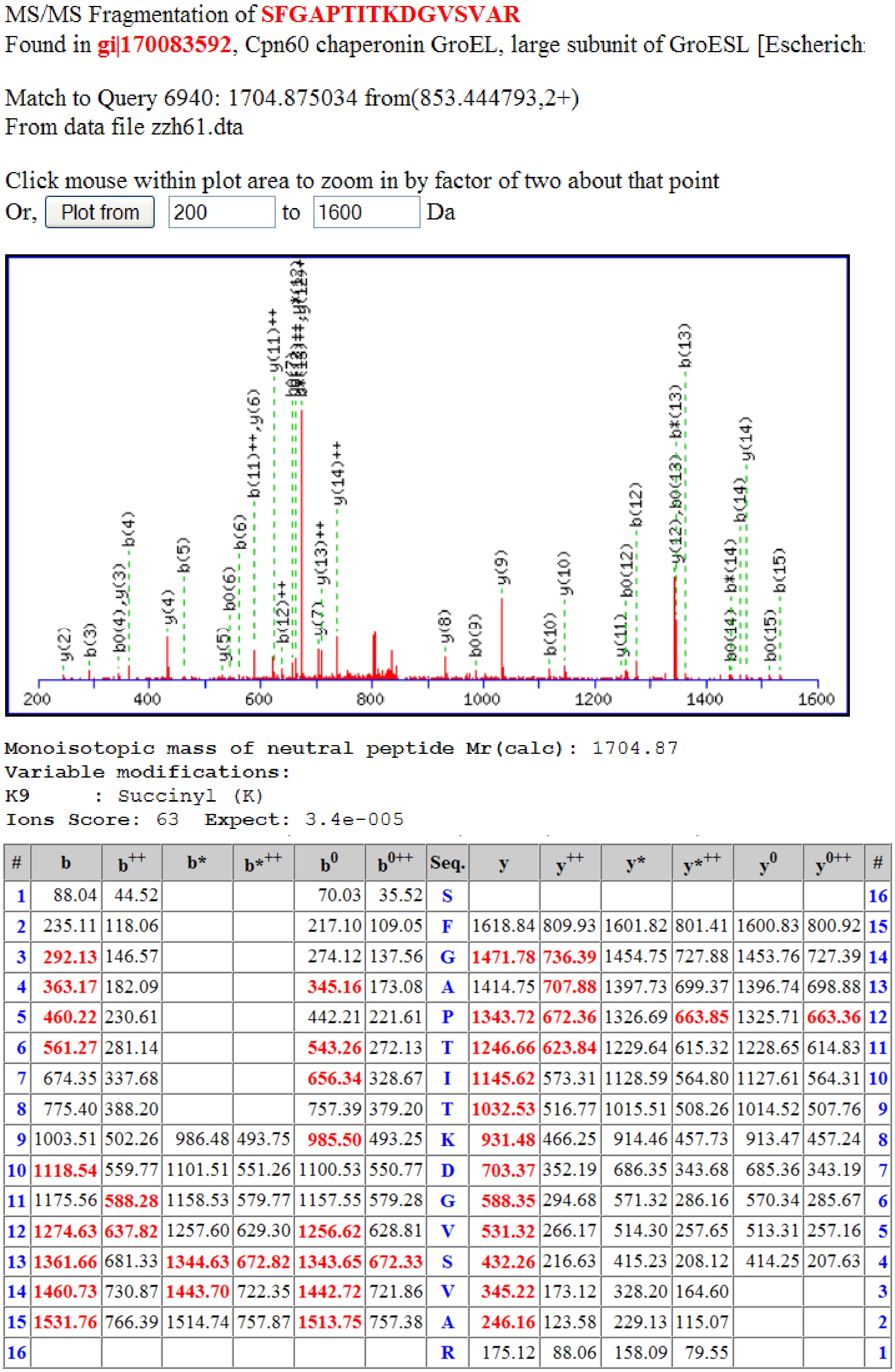
```
Monoisotopic mass of neutral peptide Mr(calc): 926.52
Variable modifications:
K6      : Succinyl (K)
Ions Score: 32   Expect: 0.027
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.08	50.54					V							8
2	**201.12**	101.07			183.11	92.06	T	**828.46**	**414.73**	811.43	406.22	810.45	405.73	7
3	**314.21**	157.61			**296.20**	148.60	L	**727.41**	**364.21**	710.38	355.70			6
4	**371.23**	186.12			**353.22**	177.11	G	**614.33**	**307.67**	597.30	299.15			5
5	468.28	234.64			**450.27**	225.64	P	**557.30**	**279.16**	540.28	270.64			4
6	**696.4**	**48.70**	679.37	340.19	678.38	339.69	K	460.25	230.63	443.22	222.12			3
7	**753.41**	377.21	736.39	368.70	735.40	368.21	G	**232.14**	116.57	215.11	108.06			2
8							R	**175.12**	88.06	158.09	79.55			1

Nature Chemical Biology: doi: 10.1038/nchembio.495

Cpn60 chaperonin GroEL, large subunit of GroESL K51

SFGAPTIT^{Succ}KDGVSVAR



MS/MS Fragmentation of **SFGAPTITKDGVSVAR**
Found in **gi|170083592**, Cpn60 chaperonin GroEL, large subunit of GroESL [Escherich

Match to Query 6940: 1704.875034 from(853.444793,2+)
From data file zzh61.dta

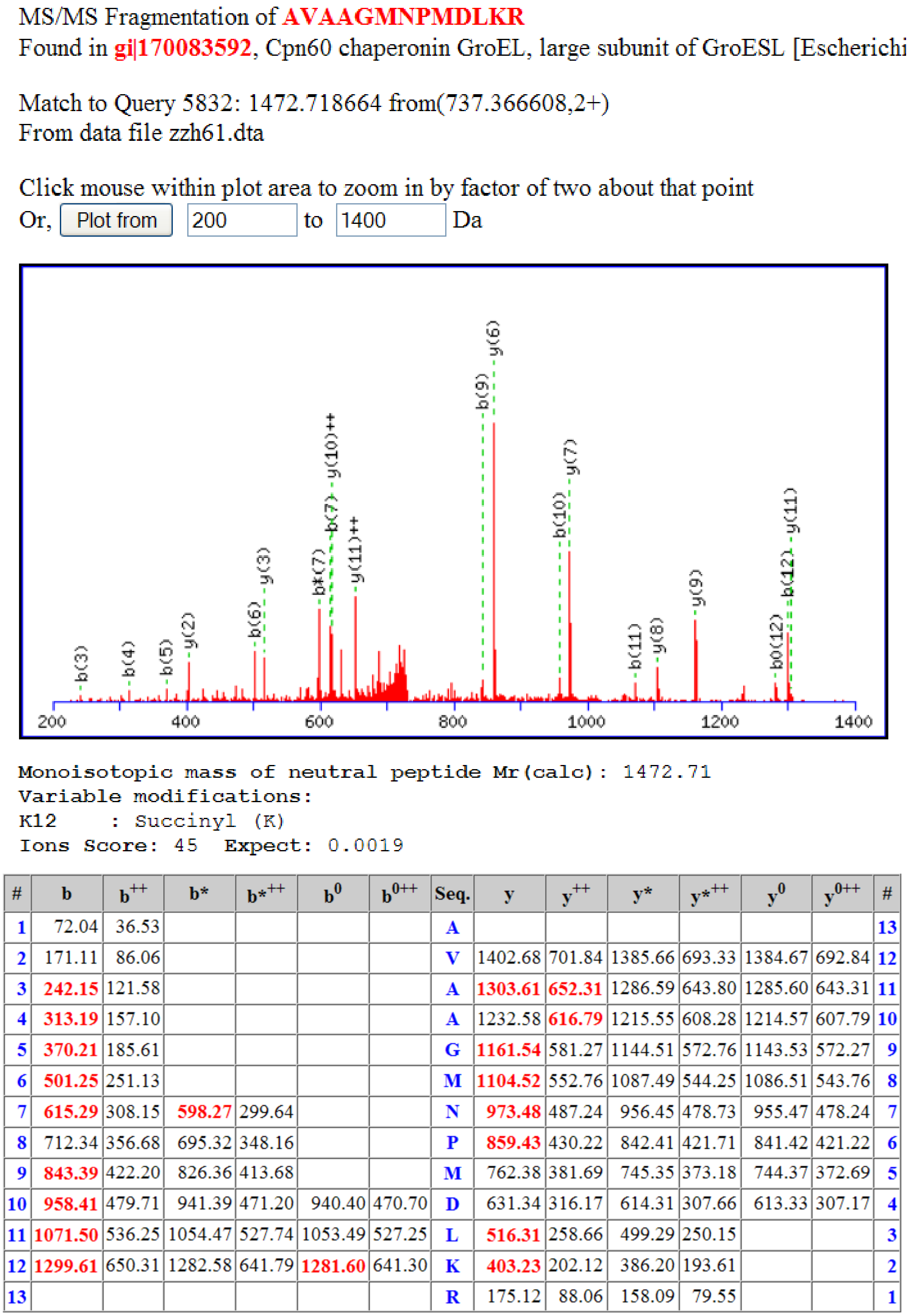
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1704.87
Variable modifications:
K9      : Succinyl (K)
Ions Score: 63  Expect: 3.4e-005
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.04	44.52			70.03	35.52	S							16
2	235.11	118.06			217.10	109.05	F	1618.84	809.93	1601.82	801.41	1600.83	800.92	15
3	**292.13**	146.57			274.12	137.56	G	**1471.78**	**736.39**	1454.75	727.88	1453.76	727.39	14
4	**363.17**	182.09			**345.16**	173.08	A	1414.75	**707.88**	1397.73	699.37	1396.74	698.88	13
5	**460.22**	230.61			442.21	221.61	P	**1343.72**	**672.36**	1326.69	**663.85**	1325.71	**663.36**	12
6	**561.27**	281.14			**543.26**	272.13	T	**1246.66**	**623.84**	1229.64	615.32	1228.65	614.83	11
7	674.35	337.68			**656.34**	328.67	I	**1145.62**	573.31	1128.59	564.80	1127.61	564.31	10
8	775.40	388.20			757.39	379.20	T	**1032.53**	516.77	1015.51	508.26	1014.52	507.76	9
9	1003.51	502.26	986.48	493.75	**985.50**	493.25	K	**931.48**	466.25	914.46	457.73	913.47	457.24	8
10	**1118.54**	559.77	1101.51	551.26	1100.53	550.77	D	**703.37**	352.19	686.35	343.68	685.36	343.19	7
11	1175.56	**588.28**	1158.53	579.77	1157.55	579.28	G	**588.35**	294.68	571.32	286.16	570.34	285.67	6
12	**1274.63**	**637.82**	1257.60	629.30	**1256.62**	628.81	V	**531.32**	266.17	514.30	257.65	513.31	257.16	5
13	**1361.66**	681.33	**1344.63**	**672.82**	**1343.65**	**672.33**	S	**432.26**	216.63	415.23	208.12	414.25	207.63	4
14	**1460.73**	730.87	**1443.70**	722.35	**1442.72**	721.86	V	**345.22**	173.12	328.20	164.60			3
15	**1531.76**	766.39	1514.74	757.87	**1513.75**	757.38	A	**246.16**	123.58	229.13	115.07			2
16							R	175.12	88.06	158.09	79.55			1

Cpn60 chaperonin GroEL, large subunit of GroESL K117

AVAAGMNPMDL^{Succ}KR



MS/MS Fragmentation of **AVAAGMNPMDLKR**
Found in **gi|170083592**, Cpn60 chaperonin GroEL, large subunit of GroESL [Escherichi

Match to Query 5832: 1472.718664 from(737.366608,2+)
From data file zzh61.dta

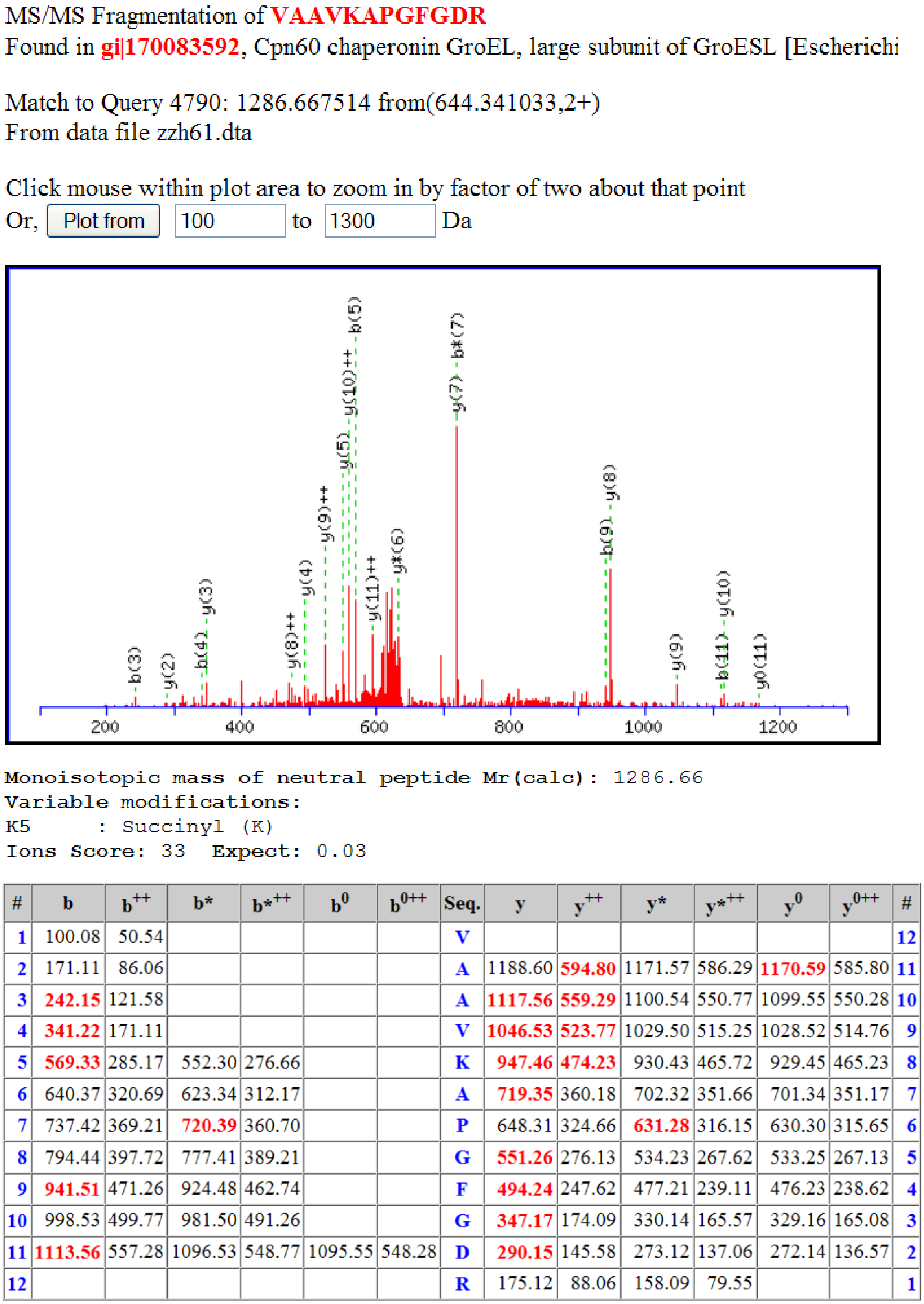
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1472.71
Variable modifications:
K12     : Succinyl (K)
Ions Score: 45   Expect: 0.0019
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.04	36.53					A							13
2	171.11	86.06					V	1402.68	701.84	1385.66	693.33	1384.67	692.84	12
3	**242.15**	121.58					A	**1303.61**	**652.31**	1286.59	643.80	1285.60	643.31	11
4	**313.19**	157.10					A	1232.58	**616.79**	1215.55	608.28	1214.57	607.79	10
5	**370.21**	185.61					G	**1161.54**	581.27	1144.51	572.76	1143.53	572.27	9
6	**501.25**	251.13					M	**1104.52**	552.76	1087.49	544.25	1086.51	543.76	8
7	**615.29**	308.15	**598.27**	299.64			N	**973.48**	487.24	956.45	478.73	955.47	478.24	7
8	712.34	356.68	695.32	348.16			P	**859.43**	430.22	842.41	421.71	841.42	421.22	6
9	**843.39**	422.20	826.36	413.68			M	762.38	381.69	745.35	373.18	744.37	372.69	5
10	**958.41**	479.71	941.39	471.20	940.40	470.70	D	631.34	316.17	614.31	307.66	613.33	307.17	4
11	**1071.50**	536.25	1054.47	527.74	1053.49	527.25	L	**516.31**	258.66	499.29	250.15			3
12	**1299.61**	650.31	1282.58	641.79	**1281.60**	641.30	K	**403.23**	202.12	386.20	193.61			2
13							R	175.12	88.06	158.09	79.55			1

Cpn60 chaperonin GroEL, large subunit of GroESL K277

VAAV^{Succ}KAPGFGDR



MS/MS Fragmentation of **VAAVKAPGFGDR**
Found in **gi|170083592**, Cpn60 chaperonin GroEL, large subunit of GroESL [Escherichi

Match to Query 4790: 1286.667514 from(644.341033,2+)
From data file zzh61.dta

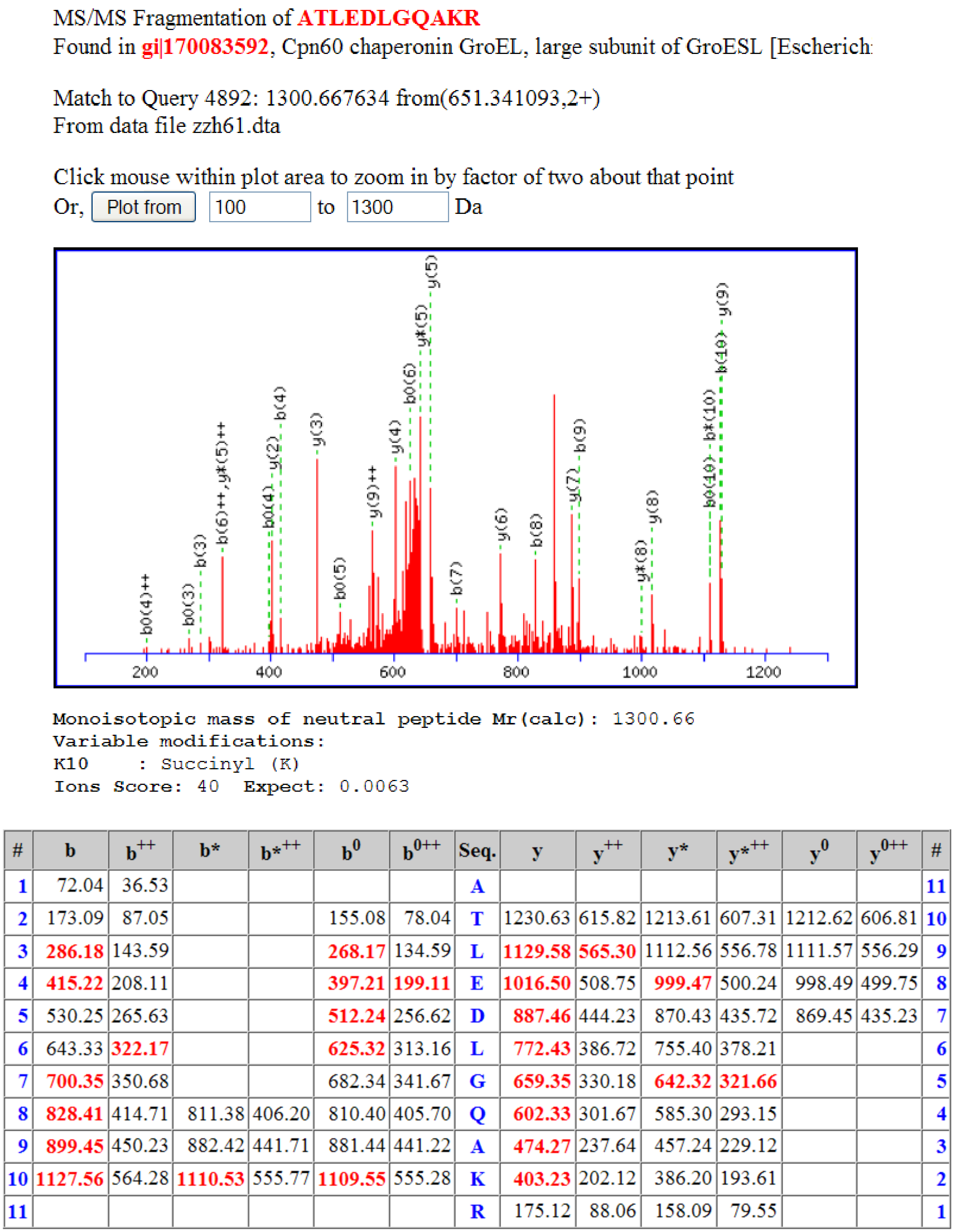
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1286.66
Variable modifications:
K5      : Succinyl (K)
Ions Score: 33   Expect: 0.03
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.08	50.54					V							12
2	171.11	86.06					A	1188.60	**594.80**	1171.57	586.29	**1170.59**	585.80	11
3	**242.15**	121.58					A	**1117.56**	**559.29**	1100.54	550.77	1099.55	550.28	10
4	**341.22**	171.11					V	**1046.53**	**523.77**	1029.50	515.25	1028.52	514.76	9
5	**569.33**	285.17	552.30	276.66			K	**947.46**	**474.23**	930.43	465.72	929.45	465.23	8
6	640.37	320.69	623.34	312.17			A	**719.35**	360.18	702.32	351.66	701.34	351.17	7
7	737.42	369.21	**720.39**	360.70			P	648.31	324.66	**631.28**	316.15	630.30	315.65	6
8	794.44	397.72	777.41	389.21			G	**551.26**	276.13	534.23	267.62	533.25	267.13	5
9	**941.51**	471.26	924.48	462.74			F	**494.24**	247.62	477.21	239.11	476.23	238.62	4
10	998.53	499.77	981.50	491.26			G	**347.17**	174.09	330.14	165.57	329.16	165.08	3
11	**1113.56**	557.28	1096.53	548.77	1095.55	548.28	D	**290.15**	145.58	273.12	137.06	272.14	136.57	2
12							R	175.12	88.06	158.09	79.55			1

Cpn60 chaperonin GroEL, large subunit of GroESL K321

ATLEDLGQA^{Succ}KR



MS/MS Fragmentation of **ATLEDLGQAKR**
Found in **gi|170083592**, Cpn60 chaperonin GroEL, large subunit of GroESL [Escherich

Match to Query 4892: 1300.667634 from(651.341093,2+)
From data file zzh61.dta

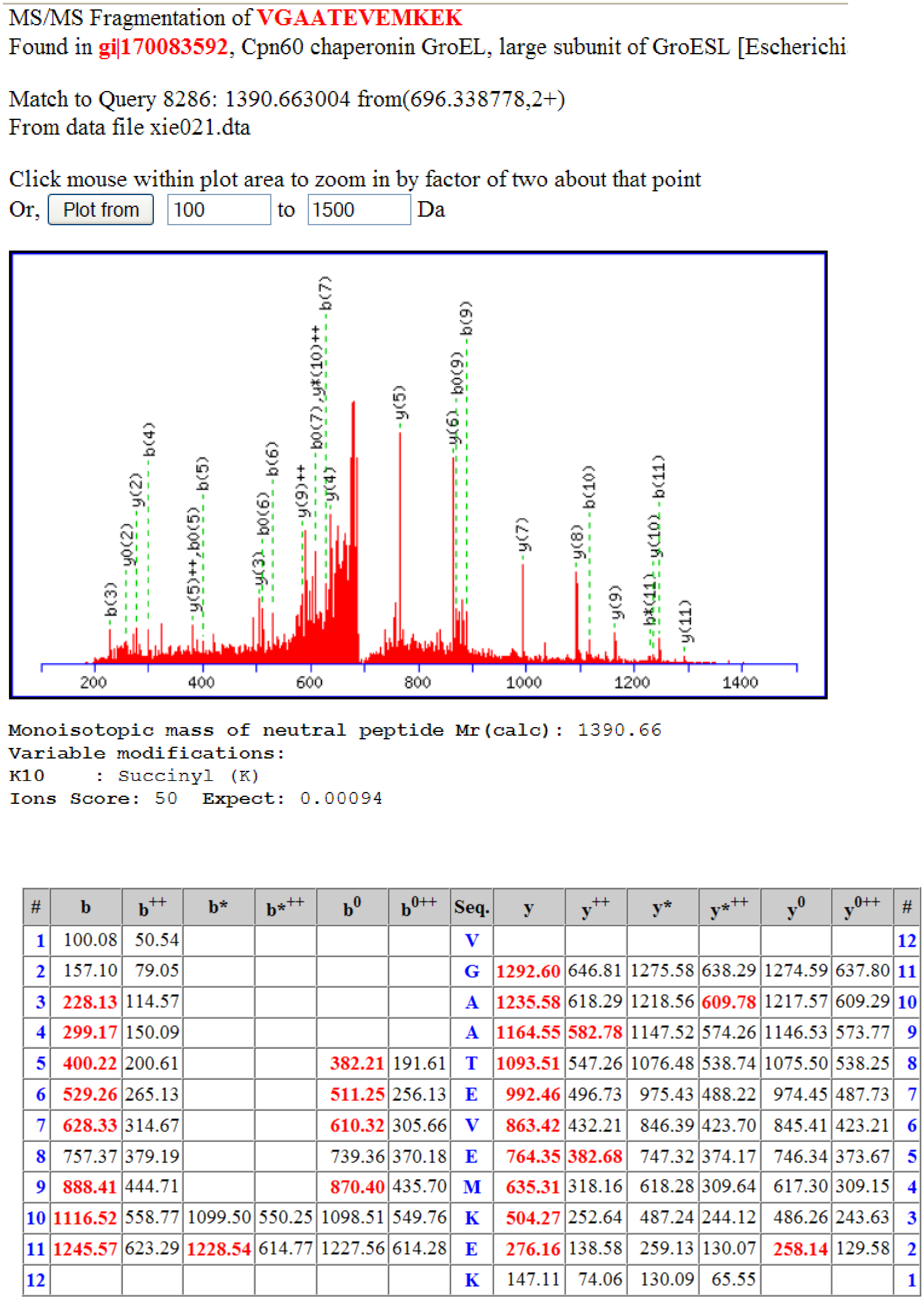
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1300.66
Variable modifications:
K10     : Succinyl (K)
Ions Score: 40   Expect: 0.0063
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.04	36.53					A							11
2	173.09	87.05			155.08	78.04	T	1230.63	615.82	1213.61	607.31	1212.62	606.81	10
3	286.18	143.59			268.17	134.59	L	1129.58	565.30	1112.56	556.78	1111.57	556.29	9
4	415.22	208.11			397.21	199.11	E	1016.50	508.75	999.47	500.24	998.49	499.75	8
5	530.25	265.63			512.24	256.62	D	887.46	444.23	870.43	435.72	869.45	435.23	7
6	643.33	322.17			625.32	313.16	L	772.43	386.72	755.40	378.21			6
7	700.35	350.68			682.34	341.67	G	659.35	330.18	642.32	321.66			5
8	828.41	414.71	811.38	406.20	810.40	405.70	Q	602.33	301.67	585.30	293.15			4
9	899.45	450.23	882.42	441.71	881.44	441.22	A	474.27	237.64	457.24	229.12			3
10	1127.56	564.28	1110.53	555.77	1109.55	555.28	K	403.23	202.12	386.20	193.61			2
11							R	175.12	88.06	158.09	79.55			1

Cpn60 chaperonin GroEL, large subunit of GroESL K390

VGAATEVEM$^{\mathrm{Succ}}$KEK



MS/MS Fragmentation of **VGAATEVEMKEK**
Found in **gi|170083592**, Cpn60 chaperonin GroEL, large subunit of GroESL [Escherichi

Match to Query 8286: 1390.663004 from(696.338778,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1390.66
Variable modifications:
K10     : Succinyl (K)
Ions Score: 50   Expect: 0.00094
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.08	50.54					V							12
2	157.10	79.05					G	1292.60	646.81	1275.58	638.29	1274.59	637.80	11
3	228.13	114.57					A	1235.58	618.29	1218.56	609.78	1217.57	609.29	10
4	299.17	150.09					A	1164.55	582.78	1147.52	574.26	1146.53	573.77	9
5	400.22	200.61			382.21	191.61	T	1093.51	547.26	1076.48	538.74	1075.50	538.25	8
6	529.26	265.13			511.25	256.13	E	992.46	496.73	975.43	488.22	974.45	487.73	7
7	628.33	314.67			610.32	305.66	V	863.42	432.21	846.39	423.70	845.41	423.21	6
8	757.37	379.19			739.36	370.18	E	764.35	382.68	747.32	374.17	746.34	373.67	5
9	888.41	444.71			870.40	435.70	M	635.31	318.16	618.28	309.64	617.30	309.15	4
10	1116.52	558.77	1099.50	550.25	1098.51	549.76	K	504.27	252.64	487.24	244.12	486.26	243.63	3
11	1245.57	623.29	1228.54	614.77	1227.56	614.28	E	276.16	138.58	259.13	130.07	258.14	129.58	2
12							K	147.11	74.06	130.09	65.55			1

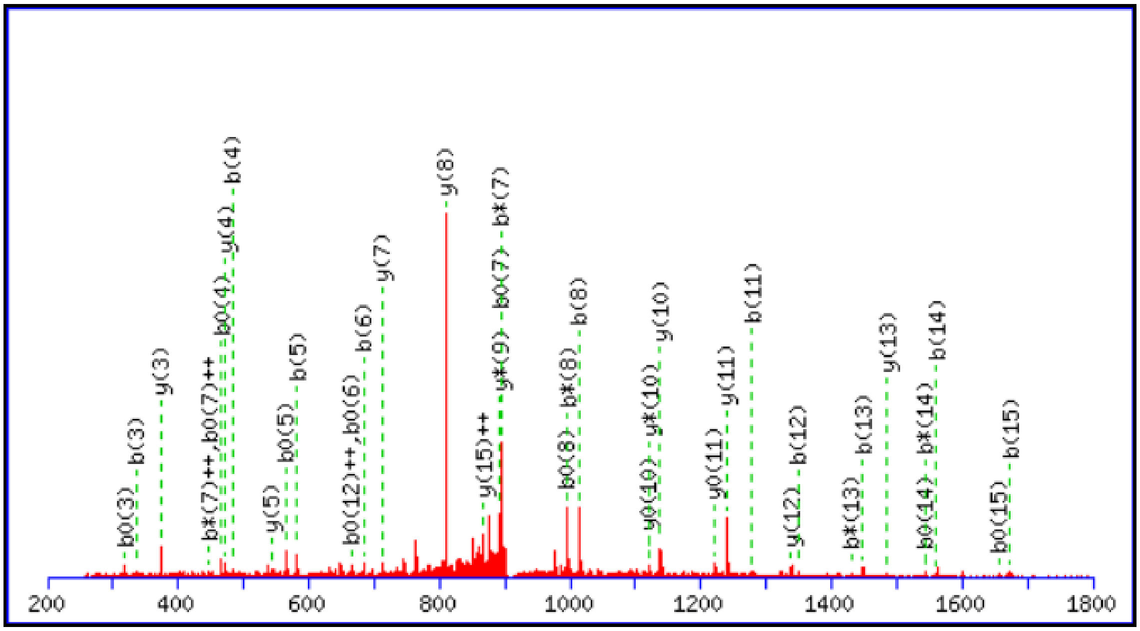
50S ribosomal subunit protein L11 K72

SFTFVT^{Succ}KTPPAAVLLK

MS/MS Fragmentation of **SFTFVTKTPPAAVLLK**
Found in **gi|170083443**, 50S ribosomal subunit protein L11 [Escherichia coli str. K-12

Match to Query 13697: 1819.012124 from(910.513338,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da



```
Monoisotopic mass of neutral peptide Mr(calc): 1819.01
Variable modifications:
K7      : Succinyl (K)
Ions Score: 42  Expect: 0.007
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.04	44.52			70.03	35.52	S							16
2	235.11	118.06			217.10	109.05	F	1732.99	867.00	1715.96	858.48	1714.98	857.99	15
3	336.16	168.58			318.14	159.58	T	1585.92	793.46	1568.89	784.95	1567.91	784.46	14
4	483.22	242.12			465.21	233.11	F	1484.87	742.94	1467.85	734.43	1466.86	733.93	13
5	582.29	291.65			564.28	282.64	V	1337.80	669.41	1320.78	660.89	1319.79	660.40	12
6	683.34	342.17			665.33	333.17	T	1238.74	619.87	1221.71	611.36	1220.72	610.87	11
7	911.45	456.23	894.42	447.72	893.44	447.22	K	1137.69	569.35	1120.66	560.83	1119.68	560.34	10
8	1012.50	506.75	995.47	498.24	994.49	497.75	T	909.58	455.29	892.55	446.78	891.57	446.29	9
9	1109.55	555.28	1092.52	546.77	1091.54	546.27	P	808.53	404.77	791.50	396.25			8
10	1206.60	603.81	1189.58	595.29	1188.59	594.80	P	711.48	356.24	694.45	347.73			7
11	1277.64	639.32	1260.61	630.81	1259.63	630.32	A	614.42	307.72	597.40	299.20			6
12	1348.68	674.84	1331.65	666.33	1330.67	665.84	A	543.39	272.20	526.36	263.68			5
13	1447.75	724.38	1430.72	715.86	1429.74	715.37	V	472.35	236.68	455.32	228.17			4
14	1560.83	780.92	1543.80	772.41	1542.82	771.91	L	373.28	187.14	356.25	178.63			3
15	1673.91	837.46	1656.89	828.95	1655.90	828.46	L	260.20	130.60	243.17	122.09			2
16							K	147.11	74.06	130.09	65.55			1

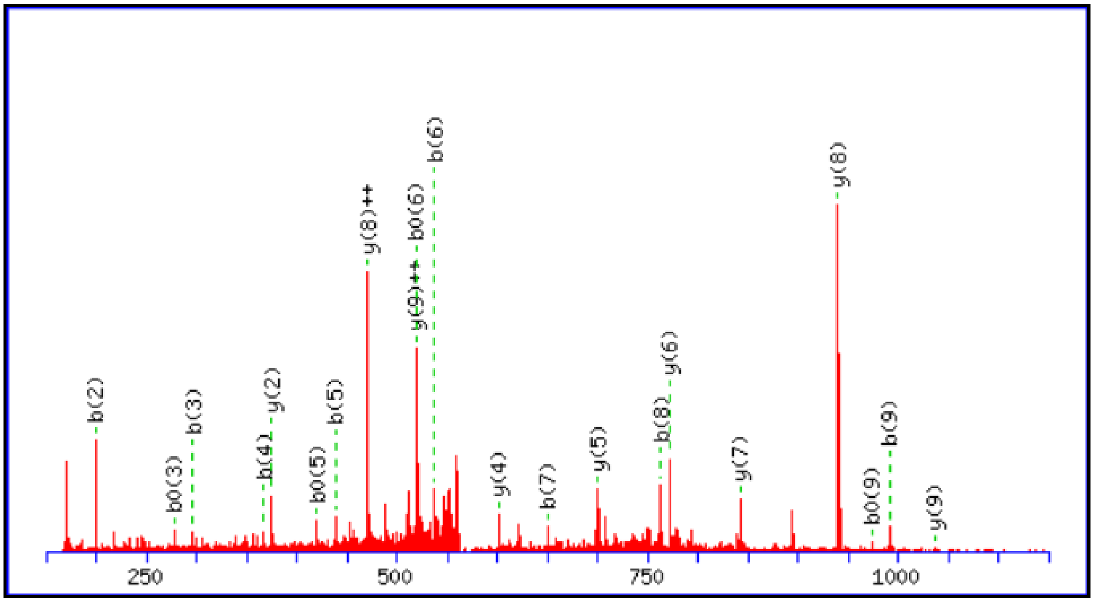
50S ribosomal subunit protein L11 K81

TPPAAVLL^{Succ}KK

MS/MS Fragmentation of **TPPAAVLLKK**
Found in **gi|170083443**, 50S ribosomal subunit protein L11 [Escherichia coli str. K-12

Match to Query 4432: 1136.681674 from(569.348113,2+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da



```
Monoisotopic mass of neutral peptide Mr(calc): 1136.68
Variable modifications:
K9      : Succinyl (K)
Ions Score: 43   Expect: 0.0037
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.05	51.53			84.04	42.53	T					10
2	**199.11**	100.06			181.10	91.05	P	**1036.64**	**518.82**	1019.61	510.31	9
3	**296.16**	148.58			**278.15**	139.58	P	**939.59**	**470.30**	922.56	461.78	8
4	**367.20**	184.10			349.19	175.10	A	**842.53**	421.77	825.51	413.26	7
5	**438.23**	219.62			**420.22**	210.62	A	**771.50**	386.25	754.47	377.74	6
6	**537.30**	269.16			**519.29**	260.15	V	**700.46**	350.73	683.43	342.22	5
7	**650.39**	325.70			632.38	316.69	L	**601.39**	301.20	584.37	292.69	4
8	**763.47**	382.24			745.46	373.23	L	488.31	244.66	471.28	236.14	3
9	**991.58**	496.29	974.56	487.78	**973.57**	487.29	K	**375.22**	188.12	358.20	179.60	2
10							K	147.11	74.06	130.09	65.55	1

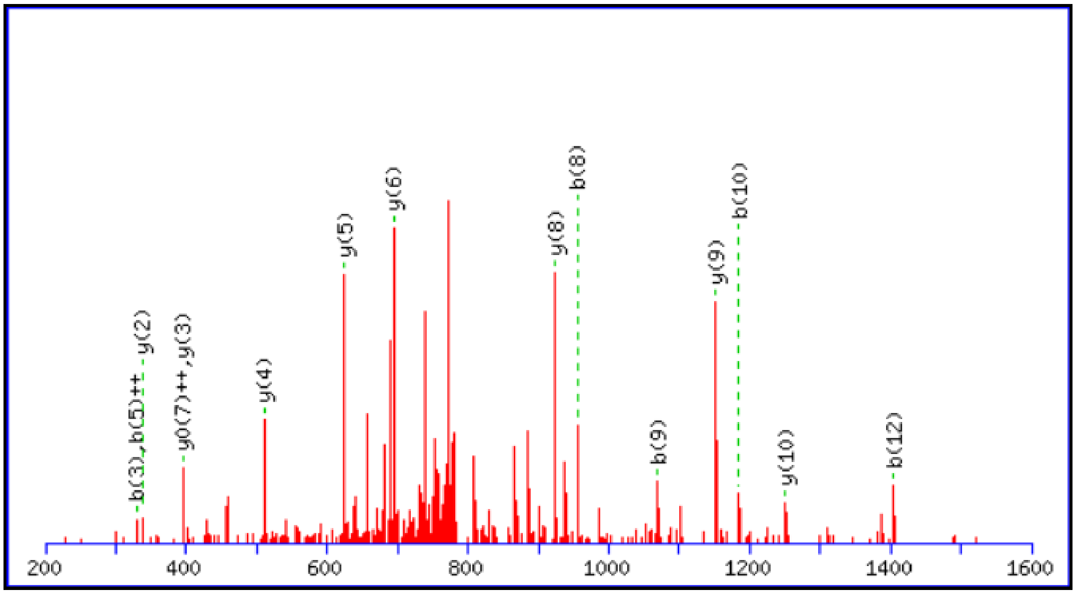
50S ribosomal subunit protein L3 K38

VTQV^{Succ}KDLANDGYR

MS/MS Fragmentation of **VTQVKDLANDGYR**
Found in **gi|170082839**, 50S ribosomal subunit protein L3 [Escherichia coli str. K-12 s

Match to Query 6384: 1577.775304 from(789.894928,2+)
From data file zzh61.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da

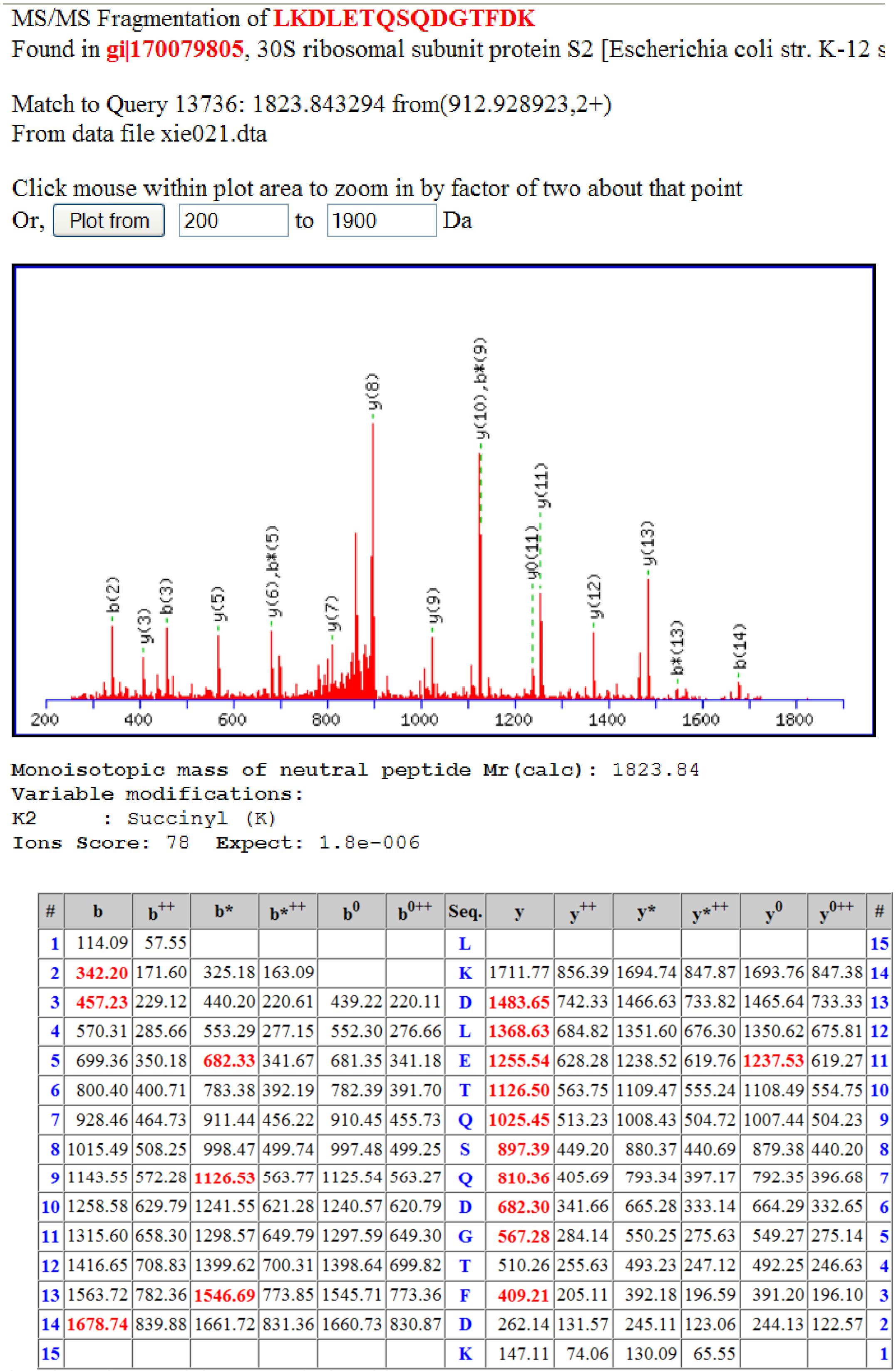


```
Monoisotopic mass of neutral peptide Mr(calc): 1577.77
Variable modifications:
K5      : Succinyl (K)
Ions Score: 62  Expect: 4.2e-005
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.08	50.54					V							13
2	201.12	101.07			183.11	92.06	T	1479.71	740.36	1462.68	731.84	1461.70	731.35	12
3	**329.18**	165.09	312.16	156.58	311.17	156.09	Q	1378.66	689.83	1361.63	681.32	1360.65	680.83	11
4	428.25	214.63	411.22	206.12	410.24	205.62	V	**1250.60**	625.80	1233.57	617.29	1232.59	616.80	10
5	656.36	**328.68**	639.33	320.17	638.35	319.68	K	**1151.53**	576.27	1134.51	567.76	1133.52	567.26	9
6	771.39	386.20	754.36	377.68	753.38	377.19	D	**923.42**	462.21	906.40	453.70	905.41	453.21	8
7	884.47	442.74	867.45	434.23	866.46	433.73	L	808.39	404.70	791.37	396.19	790.38	**395.70**	7
8	**955.51**	478.26	938.48	469.75	937.50	469.25	A	**695.31**	348.16	678.28	339.65	677.30	339.15	6
9	**1069.55**	535.28	1052.53	526.77	1051.54	526.27	N	**624.27**	312.64	607.25	304.13	606.26	303.64	5
10	**1184.58**	592.79	1167.55	584.28	1166.57	583.79	D	**510.23**	255.62	493.20	247.11	492.22	246.61	4
11	1241.60	621.30	1224.57	612.79	1223.59	612.30	G	**395.20**	198.11	378.18	189.59			3
12	**1404.66**	702.84	1387.64	694.32	1386.65	693.83	Y	**338.18**	169.59	321.16	161.08			2
13							R	175.12	88.06	158.09	79.55			1

30S ribosomal subunit protein S2 K115

L^{Succ}KDLETQSQDGTFDK



MS/MS Fragmentation of **LKDLETQSQDGTFDK**
Found in **gi|170079805**, 30S ribosomal subunit protein S2 [Escherichia coli str. K-12 s

Match to Query 13736: 1823.843294 from(912.928923,2+)
From data file xie021.dta

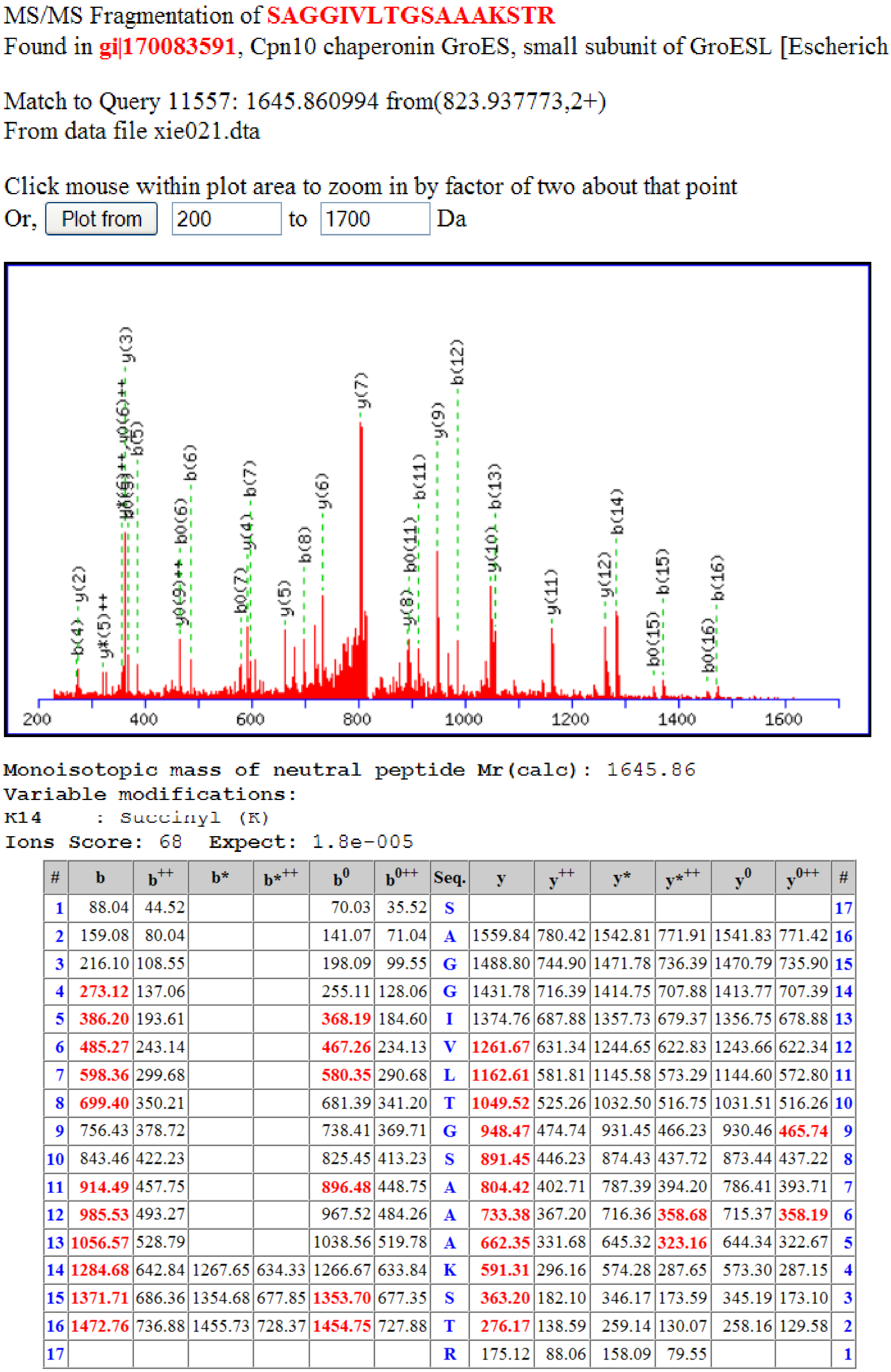
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1823.84
Variable modifications:
K2      : Succinyl (K)
Ions Score: 78  Expect: 1.8e-006
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.09	57.55					L							15
2	**342.20**	171.60	325.18	163.09			K	1711.77	856.39	1694.74	847.87	1693.76	847.38	14
3	**457.23**	229.12	440.20	220.61	439.22	220.11	D	**1483.65**	742.33	1466.63	733.82	1465.64	733.33	13
4	570.31	285.66	553.29	277.15	552.30	276.66	L	**1368.63**	684.82	1351.60	676.30	1350.62	675.81	12
5	699.36	350.18	**682.33**	341.67	681.35	341.18	E	**1255.54**	628.28	1238.52	619.76	**1237.53**	619.27	11
6	800.40	400.71	783.38	392.19	782.39	391.70	T	**1126.50**	563.75	1109.47	555.24	1108.49	554.75	10
7	928.46	464.73	911.44	456.22	910.45	455.73	Q	**1025.45**	513.23	1008.43	504.72	1007.44	504.23	9
8	1015.49	508.25	998.47	499.74	997.48	499.25	S	**897.39**	449.20	880.37	440.69	879.38	440.20	8
9	1143.55	572.28	**1126.53**	563.77	1125.54	563.27	Q	**810.36**	405.69	793.34	397.17	792.35	396.68	7
10	1258.58	629.79	1241.55	621.28	1240.57	620.79	D	**682.30**	341.66	665.28	333.14	664.29	332.65	6
11	1315.60	658.30	1298.57	649.79	1297.59	649.30	G	**567.28**	284.14	550.25	275.63	549.27	275.14	5
12	1416.65	708.83	1399.62	700.31	1398.64	699.82	T	510.26	255.63	493.23	247.12	492.25	246.63	4
13	1563.72	782.36	**1546.69**	773.85	1545.71	773.36	F	**409.21**	205.11	392.18	196.59	391.20	196.10	3
14	**1678.74**	839.88	1661.72	831.36	1660.73	830.87	D	262.14	131.57	245.11	123.06	244.13	122.57	2
15							K	147.11	74.06	130.09	65.55			1

Cpn10 chaperonin GroES, small subunit of GroESL K34

SAGGIVLTGSAAA^{Succ}KSTR



MS/MS Fragmentation of **SAGGIVLTGSAAAKSTR**
Found in **gi|170083591**, Cpn10 chaperonin GroES, small subunit of GroESL [Escherich

Match to Query 11557: 1645.860994 from(823.937773,2+)
From data file xie021.dta

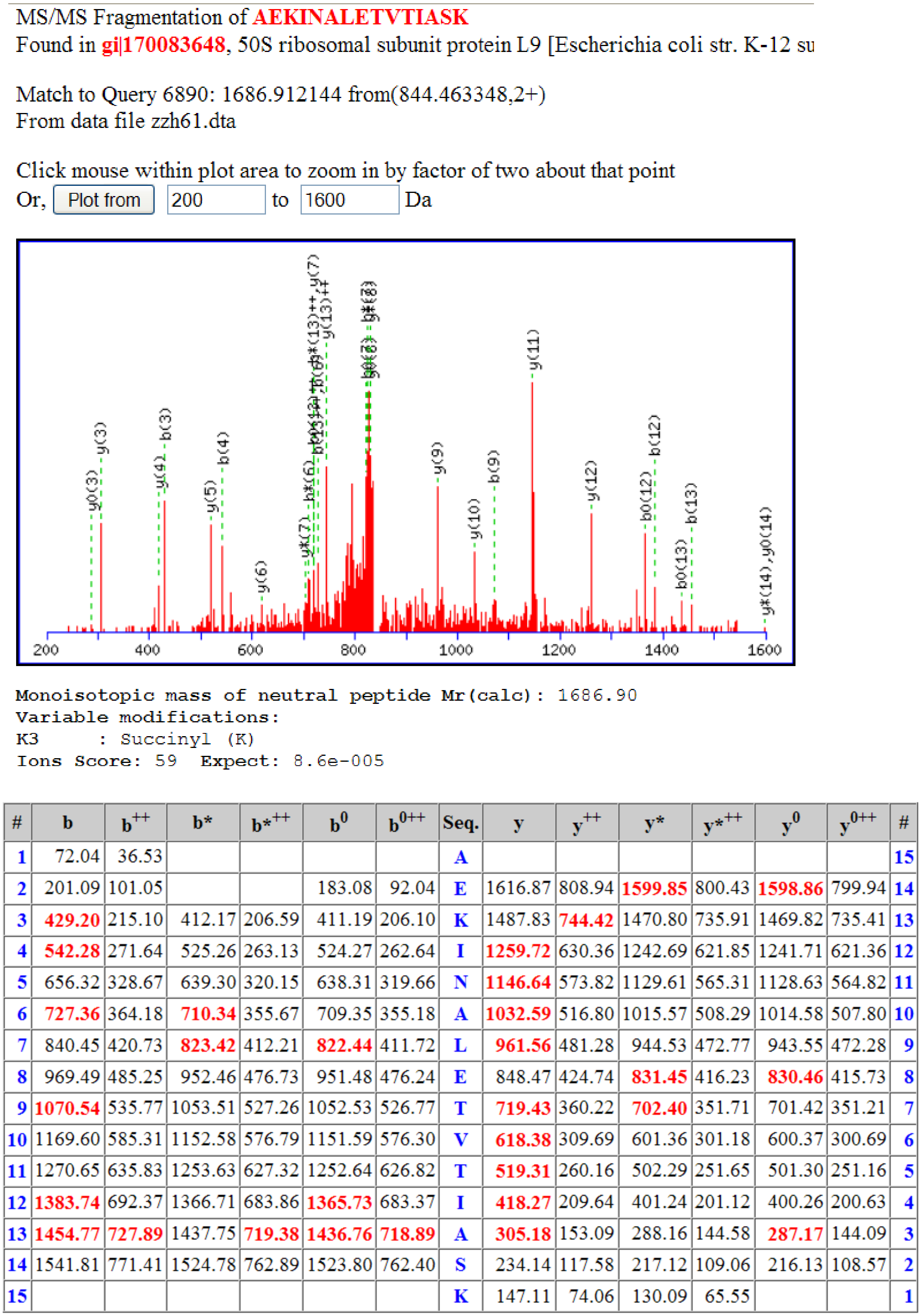
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1645.86
Variable modifications:
K14      : Succinyl (K)
Ions Score: 68   Expect: 1.8e-005
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.04	44.52			70.03	35.52	S							17
2	159.08	80.04			141.07	71.04	A	1559.84	780.42	1542.81	771.91	1541.83	771.42	16
3	216.10	108.55			198.09	99.55	G	1488.80	744.90	1471.78	736.39	1470.79	735.90	15
4	**273.12**	137.06			255.11	128.06	G	1431.78	716.39	1414.75	707.88	1413.77	707.39	14
5	**386.20**	193.61			**368.19**	184.60	I	1374.76	687.88	1357.73	679.37	1356.75	678.88	13
6	**485.27**	243.14			**467.26**	234.13	V	**1261.67**	631.34	1244.65	622.83	1243.66	622.34	12
7	**598.36**	299.68			**580.35**	290.68	L	**1162.61**	581.81	1145.58	573.29	1144.60	572.80	11
8	**699.40**	350.21			681.39	341.20	T	**1049.52**	525.26	1032.50	516.75	1031.51	516.26	10
9	756.43	378.72			738.41	369.71	G	**948.47**	474.74	931.45	466.23	930.46	**465.74**	9
10	843.46	422.23			825.45	413.23	S	**891.45**	446.23	874.43	437.72	873.44	437.22	8
11	**914.49**	457.75			**896.48**	448.75	A	**804.42**	402.71	787.39	394.20	786.41	393.71	7
12	**985.53**	493.27			967.52	484.26	A	**733.38**	367.20	716.36	**358.68**	715.37	**358.19**	6
13	**1056.57**	528.79			1038.56	519.78	A	**662.35**	331.68	645.32	**323.16**	644.34	322.67	5
14	**1284.68**	642.84	1267.65	634.33	1266.67	633.84	K	**591.31**	296.16	574.28	287.65	573.30	287.15	4
15	**1371.71**	686.36	1354.68	677.85	**1353.70**	677.35	S	**363.20**	182.10	346.17	173.59	345.19	173.10	3
16	**1472.76**	736.88	1455.73	728.37	**1454.75**	727.88	T	**276.17**	138.59	259.14	130.07	258.16	129.58	2
17							R	175.12	88.06	158.09	79.55			1

50S ribosomal subunit protein L9 K71

AE^{Succ}KINALETVTIASK



MS/MS Fragmentation of **AEKINALETVTIASK**
Found in **gi|170083648**, 50S ribosomal subunit protein L9 [Escherichia coli str. K-12 su

Match to Query 6890: 1686.912144 from(844.463348,2+)
From data file zzh61.dta

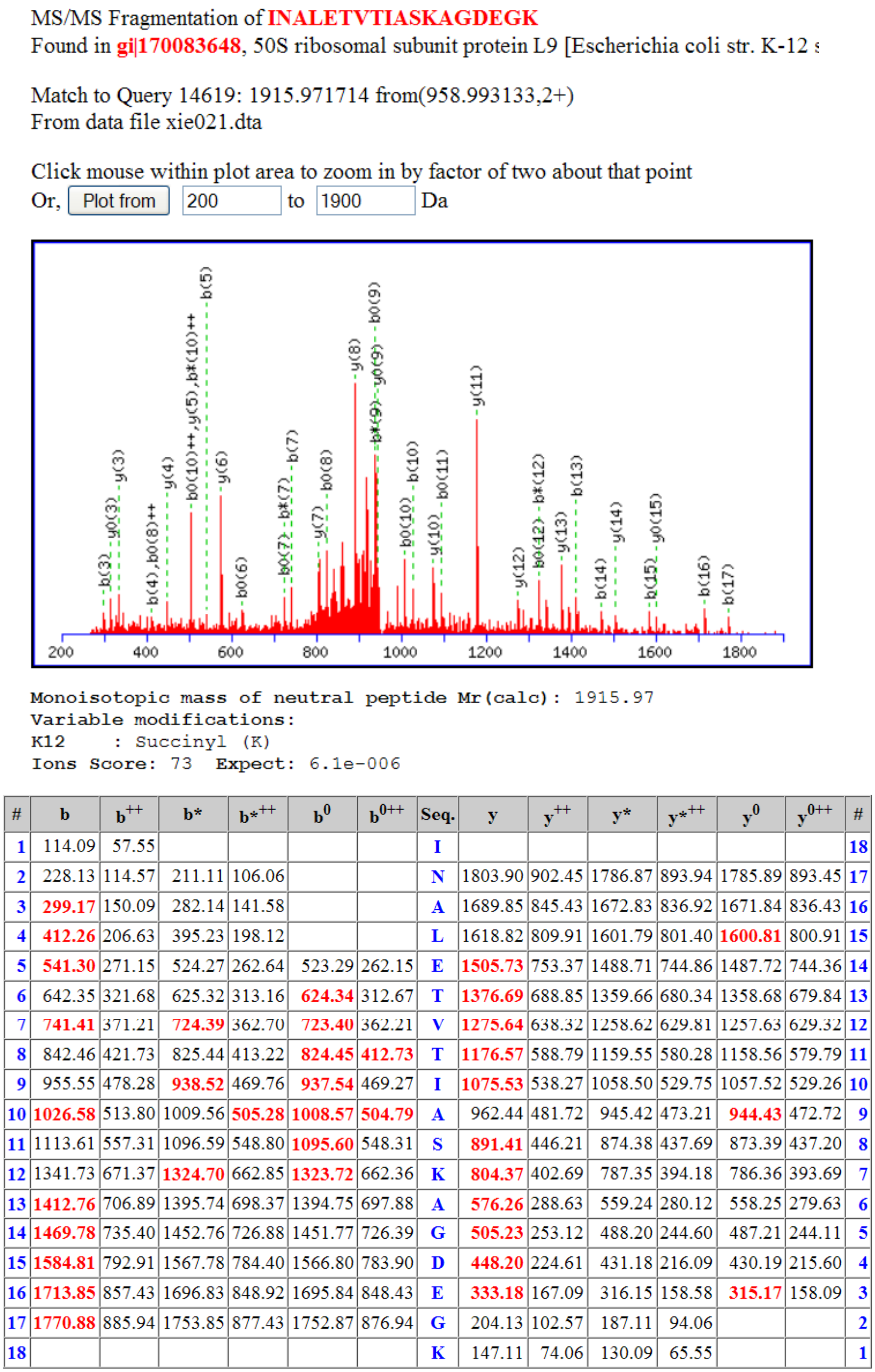
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1600 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1686.90
Variable modifications:
K3      : Succinyl (K)
Ions Score: 59   Expect: 8.6e-005
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.04	36.53					A							15
2	201.09	101.05			183.08	92.04	E	1616.87	808.94	**1599.85**	800.43	**1598.86**	799.94	14
3	**429.20**	215.10	412.17	206.59	411.19	206.10	K	1487.83	**744.42**	1470.80	735.91	1469.82	735.41	13
4	**542.28**	271.64	525.26	263.13	524.27	262.64	I	**1259.72**	630.36	1242.69	621.85	1241.71	621.36	12
5	656.32	328.67	639.30	320.15	638.31	319.66	N	**1146.64**	573.82	1129.61	565.31	1128.63	564.82	11
6	**727.36**	364.18	**710.34**	355.67	709.35	355.18	A	**1032.59**	516.80	1015.57	508.29	1014.58	507.80	10
7	840.45	420.73	**823.42**	412.21	**822.44**	411.72	L	**961.56**	481.28	944.53	472.77	943.55	472.28	9
8	969.49	485.25	952.46	476.73	951.48	476.24	E	848.47	424.74	**831.45**	416.23	**830.46**	415.73	8
9	**1070.54**	535.77	1053.51	527.26	1052.53	526.77	T	**719.43**	360.22	**702.40**	351.71	701.42	351.21	7
10	1169.60	585.31	1152.58	576.79	1151.59	576.30	V	**618.38**	309.69	601.36	301.18	600.37	300.69	6
11	1270.65	635.83	1253.63	627.32	1252.64	626.82	T	**519.31**	260.16	502.29	251.65	501.30	251.16	5
12	**1383.74**	692.37	1366.71	683.86	**1365.73**	683.37	I	**418.27**	209.64	401.24	201.12	400.26	200.63	4
13	**1454.77**	**727.89**	1437.75	**719.38**	**1436.76**	**718.89**	A	**305.18**	153.09	288.16	144.58	**287.17**	144.09	3
14	1541.81	771.41	1524.78	762.89	1523.80	762.40	S	234.14	117.58	217.12	109.06	216.13	108.57	2
15							K	147.11	74.06	130.09	65.55			1

50S ribosomal subunit protein L9 K83

INALETVTIAS^{Succ}KAGDEGK



MS/MS Fragmentation of **INALETVTIASKAGDEGK**
Found in **gi|170083648**, 50S ribosomal subunit protein L9 [Escherichia coli str. K-12 s

Match to Query 14619: 1915.971714 from(958.993133,2+)
From data file xie021.dta

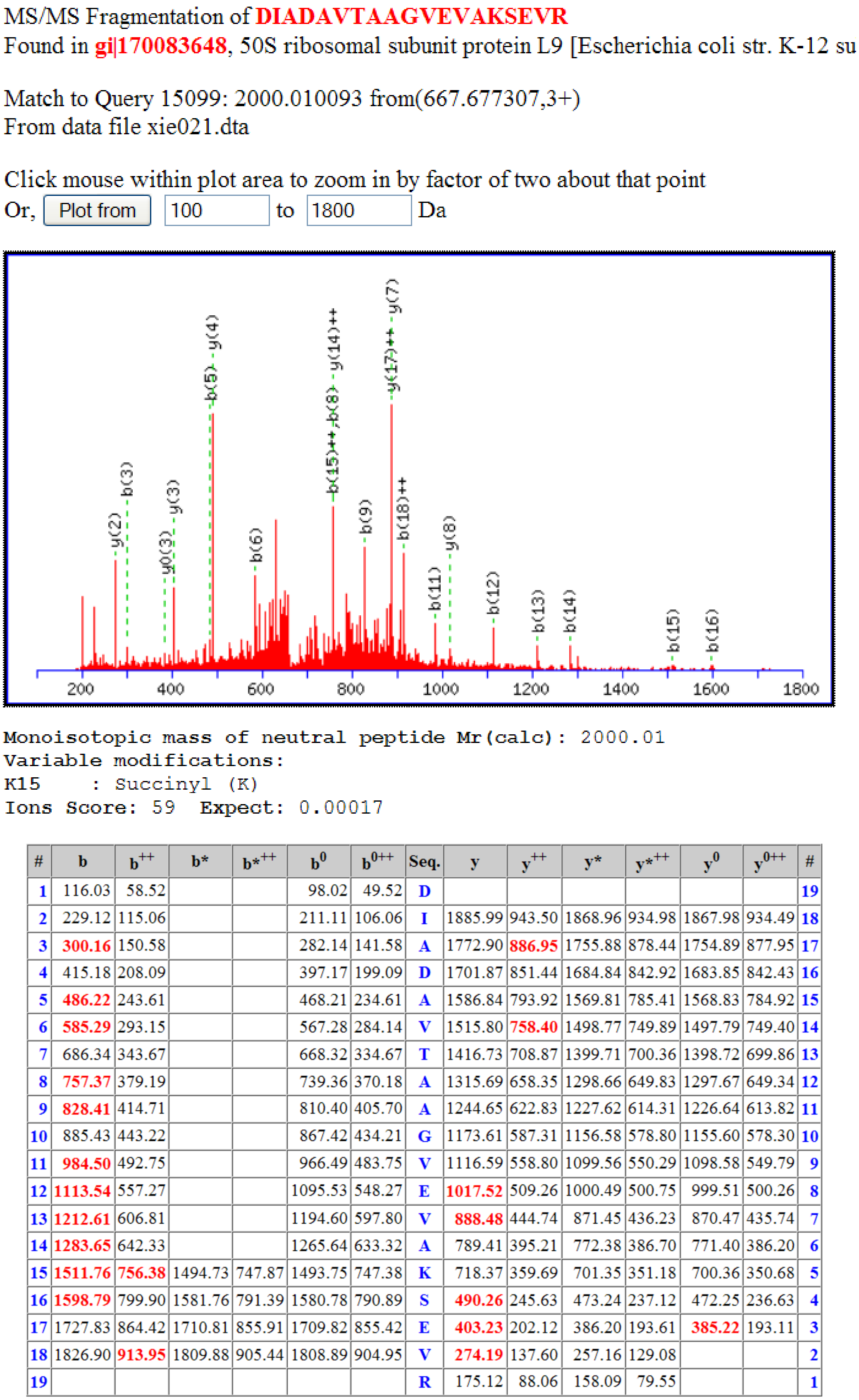
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 1915.97
Variable modifications:
K12     : Succinyl (K)
Ions Score: 73   Expect: 6.1e-006
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	114.09	57.55					I							18
2	228.13	114.57	211.11	106.06			N	1803.90	902.45	1786.87	893.94	1785.89	893.45	17
3	**299.17**	150.09	282.14	141.58			A	1689.85	845.43	1672.83	836.92	1671.84	836.43	16
4	**412.26**	206.63	395.23	198.12			L	1618.82	809.91	1601.79	801.40	**1600.81**	800.91	15
5	**541.30**	271.15	524.27	262.64	523.29	262.15	E	**1505.73**	753.37	1488.71	744.86	1487.72	744.36	14
6	642.35	321.68	625.32	313.16	**624.34**	312.67	T	**1376.69**	688.85	1359.66	680.34	1358.68	679.84	13
7	**741.41**	371.21	**724.39**	362.70	**723.40**	362.21	V	**1275.64**	638.32	1258.62	629.81	1257.63	629.32	12
8	842.46	421.73	825.44	413.22	**824.45**	**412.73**	T	**1176.57**	588.79	1159.55	580.28	1158.56	579.79	11
9	955.55	478.28	**938.52**	469.76	**937.54**	469.27	I	**1075.53**	538.27	1058.50	529.75	1057.52	529.26	10
10	**1026.58**	513.80	1009.56	**505.28**	**1008.57**	**504.79**	A	962.44	481.72	945.42	473.21	**944.43**	472.72	9
11	1113.61	557.31	1096.59	548.80	**1095.60**	548.31	S	**891.41**	446.21	874.38	437.69	873.39	437.20	8
12	1341.73	671.37	**1324.70**	662.85	**1323.72**	662.36	K	**804.37**	402.69	787.35	394.18	786.36	393.69	7
13	**1412.76**	706.89	1395.74	698.37	1394.75	697.88	A	**576.26**	288.63	559.24	280.12	558.25	279.63	6
14	**1469.78**	735.40	1452.76	726.88	1451.77	726.39	G	**505.23**	253.12	488.20	244.60	487.21	244.11	5
15	**1584.81**	792.91	1567.78	784.40	1566.80	783.90	D	**448.20**	224.61	431.18	216.09	430.19	215.60	4
16	**1713.85**	857.43	1696.83	848.92	1695.84	848.43	E	**333.18**	167.09	316.15	158.58	**315.17**	158.09	3
17	**1770.88**	885.94	1753.85	877.43	1752.87	876.94	G	204.13	102.57	187.11	94.06			2
18							K	147.11	74.06	130.09	65.55			1

50S ribosomal subunit protein L9 K112

DIADADVTAAGVEVA^{Succ}KSEVR



MS/MS Fragmentation of **DIADAVTAAGVEVAKSEVR**
Found in **gi|170083648**, 50S ribosomal subunit protein L9 [Escherichia coli str. K-12 su

Match to Query 15099: 2000.010093 from(667.677307,3+)
From data file xie021.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da

```
Monoisotopic mass of neutral peptide Mr(calc): 2000.01
Variable modifications:
K15      : Succinyl (K)
Ions Score: 59   Expect: 0.00017
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.03	58.52			98.02	49.52	D							19
2	229.12	115.06			211.11	106.06	I	1885.99	943.50	1868.96	934.98	1867.98	934.49	18
3	**300.16**	150.58			282.14	141.58	A	1772.90	**886.95**	1755.88	878.44	1754.89	877.95	17
4	415.18	208.09			397.17	199.09	D	1701.87	851.44	1684.84	842.92	1683.85	842.43	16
5	**486.22**	243.61			468.21	234.61	A	1586.84	793.92	1569.81	785.41	1568.83	784.92	15
6	**585.29**	293.15			567.28	284.14	V	1515.80	**758.40**	1498.77	749.89	1497.79	749.40	14
7	686.34	343.67			668.32	334.67	T	1416.73	708.87	1399.71	700.36	1398.72	699.86	13
8	**757.37**	379.19			739.36	370.18	A	1315.69	658.35	1298.66	649.83	1297.67	649.34	12
9	**828.41**	414.71			810.40	405.70	A	1244.65	622.83	1227.62	614.31	1226.64	613.82	11
10	885.43	443.22			867.42	434.21	G	1173.61	587.31	1156.58	578.80	1155.60	578.30	10
11	**984.50**	492.75			966.49	483.75	V	1116.59	558.80	1099.56	550.29	1098.58	549.79	9
12	**1113.54**	557.27			1095.53	548.27	E	**1017.52**	509.26	1000.49	500.75	999.51	500.26	8
13	**1212.61**	606.81			1194.60	597.80	V	**888.48**	444.74	871.45	436.23	870.47	435.74	7
14	**1283.65**	642.33			1265.64	633.32	A	789.41	395.21	772.38	386.70	771.40	386.20	6
15	**1511.76**	**756.38**	1494.73	747.87	1493.75	747.38	K	718.37	359.69	701.35	351.18	700.36	350.68	5
16	**1598.79**	799.90	1581.76	791.39	1580.78	790.89	S	**490.26**	245.63	473.24	237.12	472.25	236.63	4
17	1727.83	864.42	1710.81	855.91	1709.82	855.42	E	**403.23**	202.12	386.20	193.61	**385.22**	193.11	3
18	1826.90	**913.95**	1809.88	905.44	1808.89	904.95	V	**274.19**	137.60	257.16	129.08			2
19							R	175.12	88.06	158.09	79.55			1

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