

## SUPPORTING INFORMATION

### **Comparative proteomic analysis of slime from the striped pyjama squid, *Sepioloidea lineolata* and the southern bottletail squid, *Sepiadarium austrinum* (Cephalopoda: Sepiadariidae)**

Nikeisha J. Caruana<sup>a</sup>, Jan M. Strugnell<sup>b,a</sup>, Pierre Faou<sup>c</sup>, Julian Finn<sup>d</sup>, Ira R. Cooke<sup>e,c</sup>

<sup>a</sup>Department of Ecology, Environment and Evolution, La Trobe University, Melbourne, VIC, 3086, Australia

<sup>b</sup>Centre for Sustainable Tropical Fisheries and Aquaculture, James Cook University, Townsville, QLD, 4811, Australia

<sup>c</sup> Department of Biochemistry and Genetics, La Trobe Institute for Molecular Sciences, La Trobe University, Melbourne, Vic 3086, Australia

<sup>d</sup> Sciences, Museums Victoria, Carlton, Vic 3053, Australia

<sup>e</sup> Department of Molecular and Cell Biology, James Cook University, Townsville, QLD, 4811, Australia

Corresponding author: Nikeisha J. Caruana

Corresponding author email: [njcaruana@students.latrobe.edu.au](mailto:njcaruana@students.latrobe.edu.au)

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**Supporting Table 2** – ProteinGroups.txt file from *MaxQuant* showing all identified protein groups and relating information. Provided as a separate file, SupportingTable2.xlsx

**Supporting Table 3** - All protein groups identified by *MaxQuant* as having a deamidation probability as well as the number of samples the deamidation was identified in, if it was found in proteins from the control samples and if the protein was likely to be glycosylated. Provided as a separate file, SupportingTable3.xlsx

**Supporting Figure 1: Relative abundance of orthologous proteins found in *Su. austrinum* and *So. lineolata* by KEGG Brite category.**

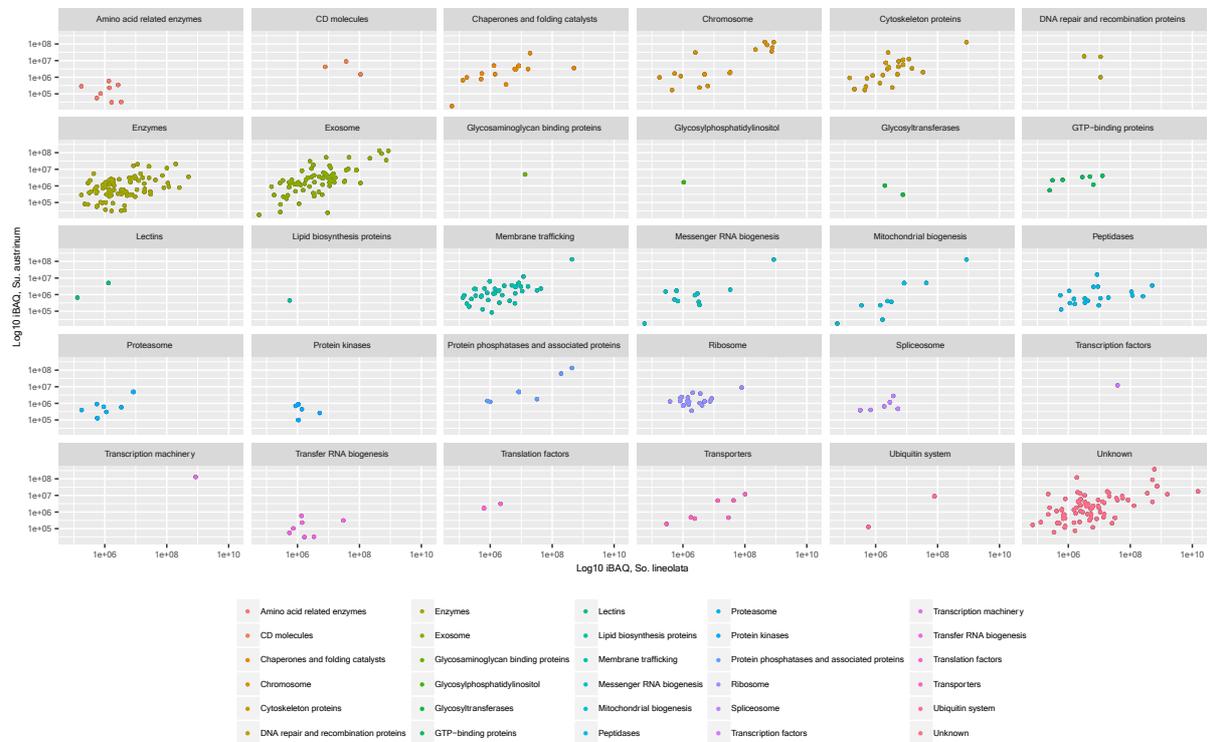
**Supporting Figure 2: Sample clustering based on iBAQ abundance measurements of orthologous proteins between *Su. austrinum* and *So. lineolata*.** Points represent individual slime samples with colours indicating differences between species and shape indicating whether the samples were treated with PNGase-F. Axes are principle components based on a matrix of iBAQ intensities from 77 orthologous proteins with measurements across all samples. Note that for *S. lineolata* sample 3 is not shown as it was a strong outlier and its inclusion would obscure relationships between all other samples.

**Supporting Figure 3A-D: LC-MS/MS mass spectra of a formerly N-glycosylated peptides.** Peptide identified is A – KQGYN\*VSMMFHQAENFFTSIGLKK (m/z 1815.90) from a potential calmodulin protein. B- NVMN\*LTPAETQQLHAALESQ LSPGELAK (m/z 460.19) from a novel secreted protein. C- WFSGISSLFPKPDVSSSSSIEDIN\*GTK (m/z 420.21) from a potential HSP20 protein. D - SLGENPTDAELKDMINEVDADGN\*GTIDFAEFLTLMSQK (m/z 1815.90) from a potential calmodulin protein. The asterisk (\*) denotes the site of N-glycosylation. Spectra generated using the Lorikeet Spectra Viewer.

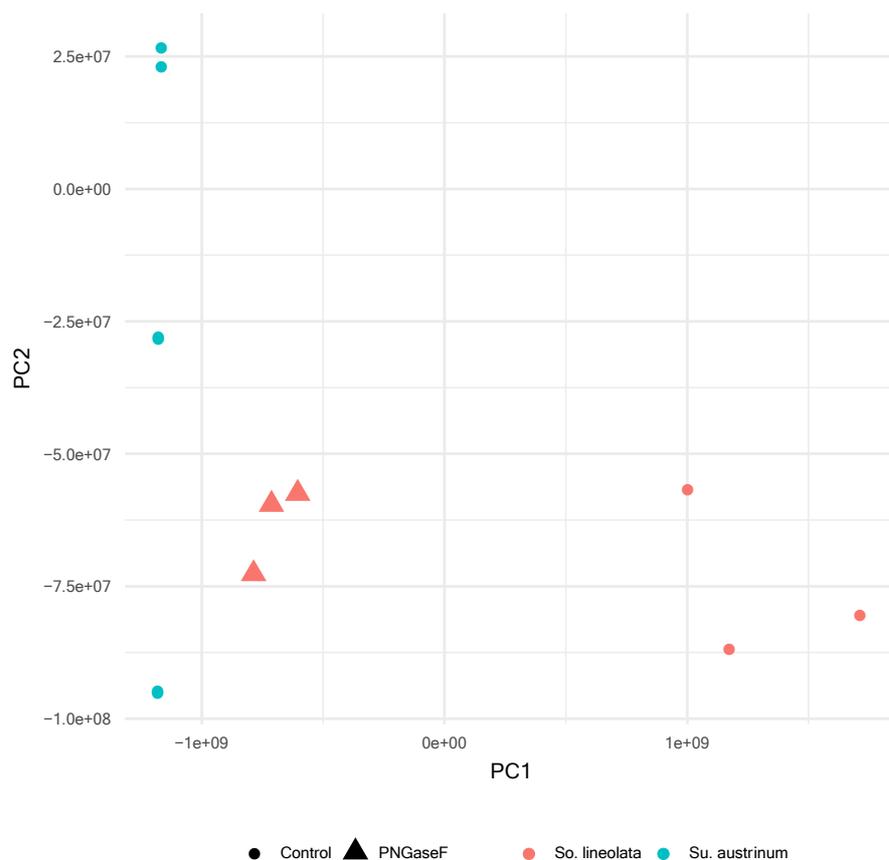
**Supporting Table 1** – Number of sequenced paired-end reads (in millions) for each tissue library and associated SRA accession numbers.

<b>Sample Tissue</b>	<b>SRA Accession</b>	<b>Read Pairs (Mil)</b>
Slimeolata_Brain	SRR5396792	18
Slimeolata_Arms	SRR5396791	19
Slimeolata_Ventral	SRR5396790	20
Slimeolata_Dorsal	SRR5396789	19
Slimeolata_Slime	SRR5396788	19

## Supporting Figure 1: Relative abundance of orthologous proteins found in *Su. austrinum* and *So. lineolata* by KEGG Brite category.

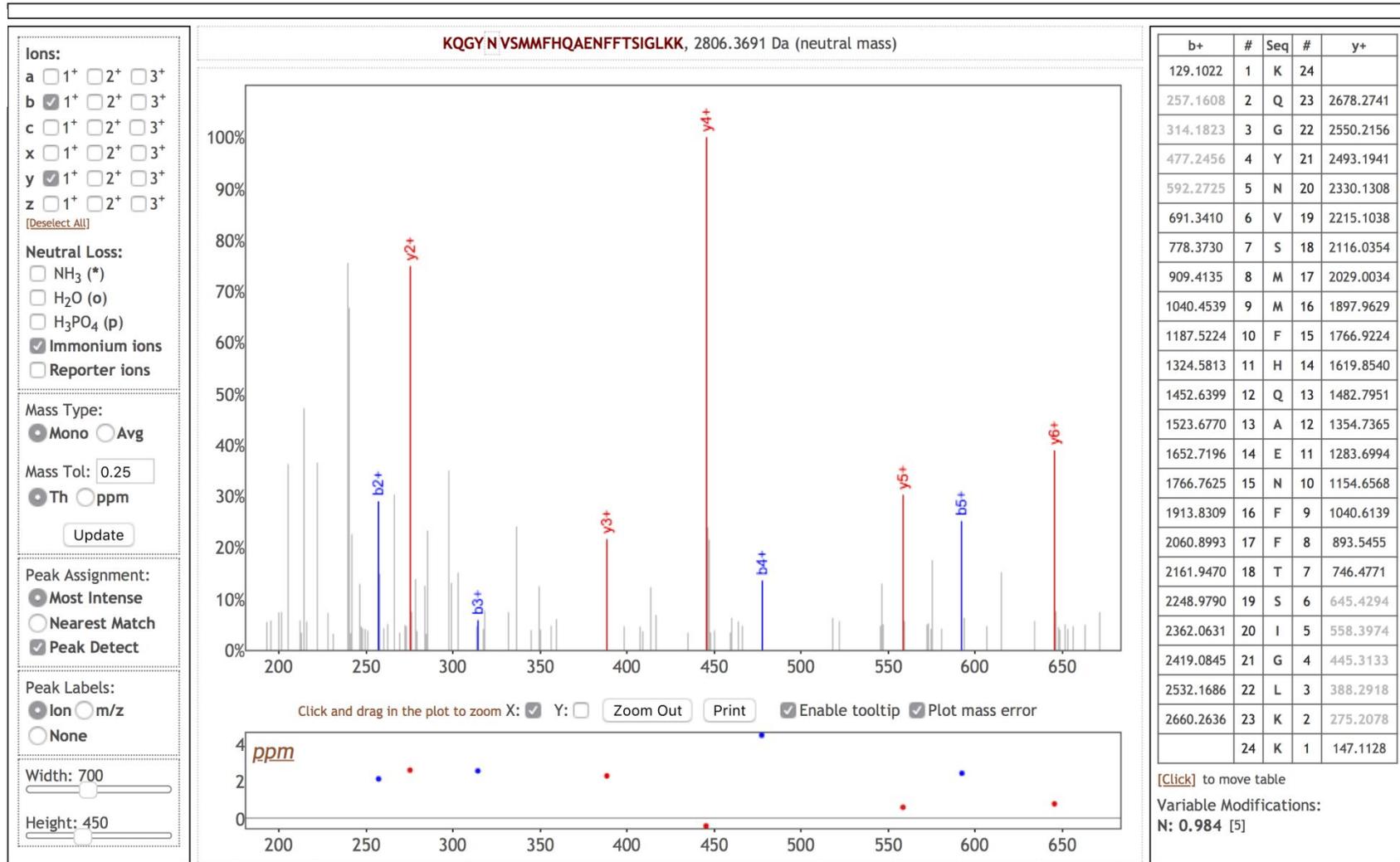


**Supporting Figure 2: Sample clustering based on iBAQ abundance measurements of orthologous proteins between *Su. austrinum* and *So. lineolata*.** Points represent individual slime samples with colours indicating differences between species and shape indicating whether the samples were treated with PNGase-F. Axes are principle components based on a matrix of iBAQ intensities from 77 orthologous proteins with measurements across all samples. Note that for *So. lineolata* sample 3 is not shown as it was a strong outlier and its inclusion would obscure relationships between all other samples.



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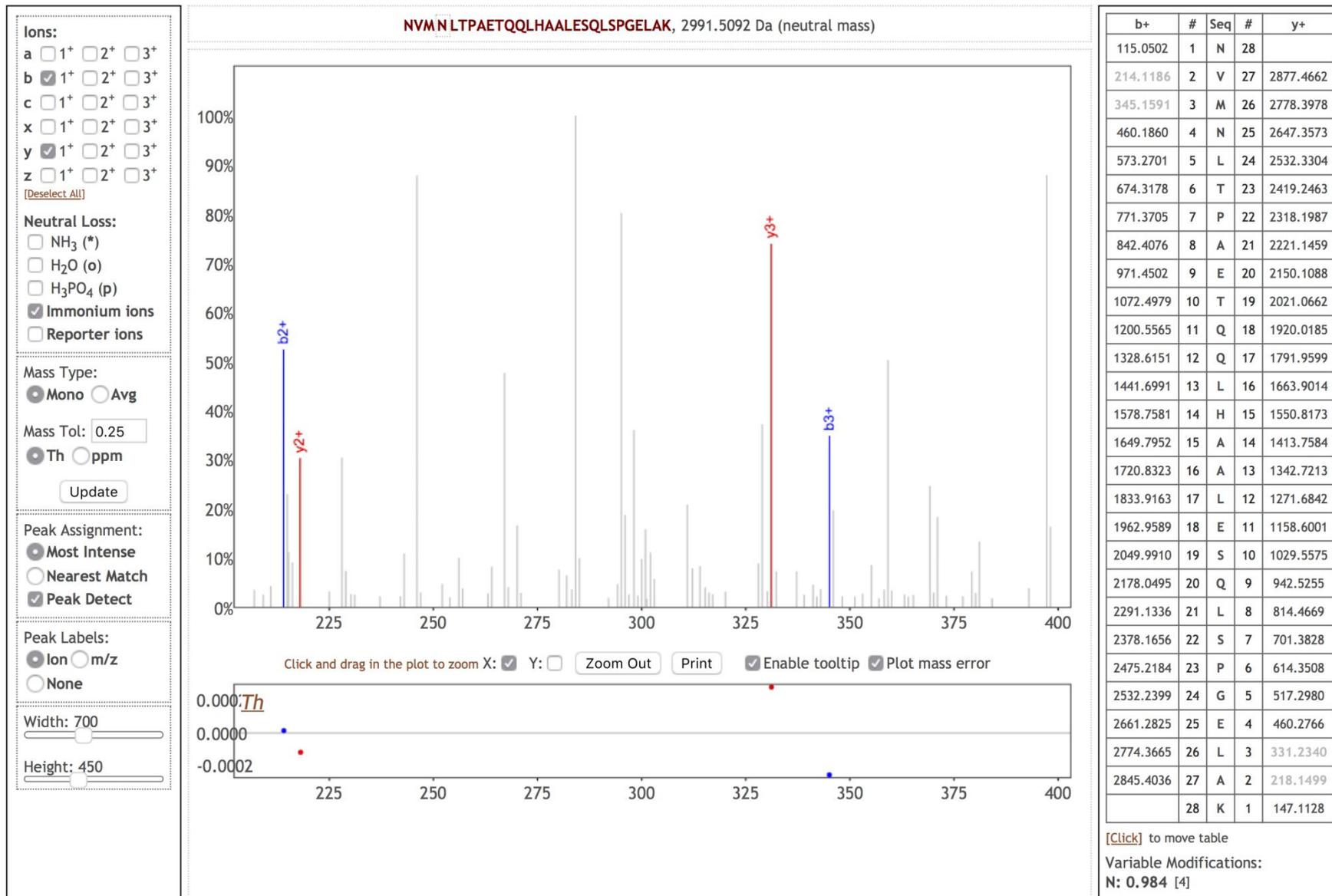
A



**Lorikeet** by vsharma@uw.edu

Lorikeet Spectrum Viewer is a Javascript plugin for JQuery that uses a modified version of the Flot plotting library.

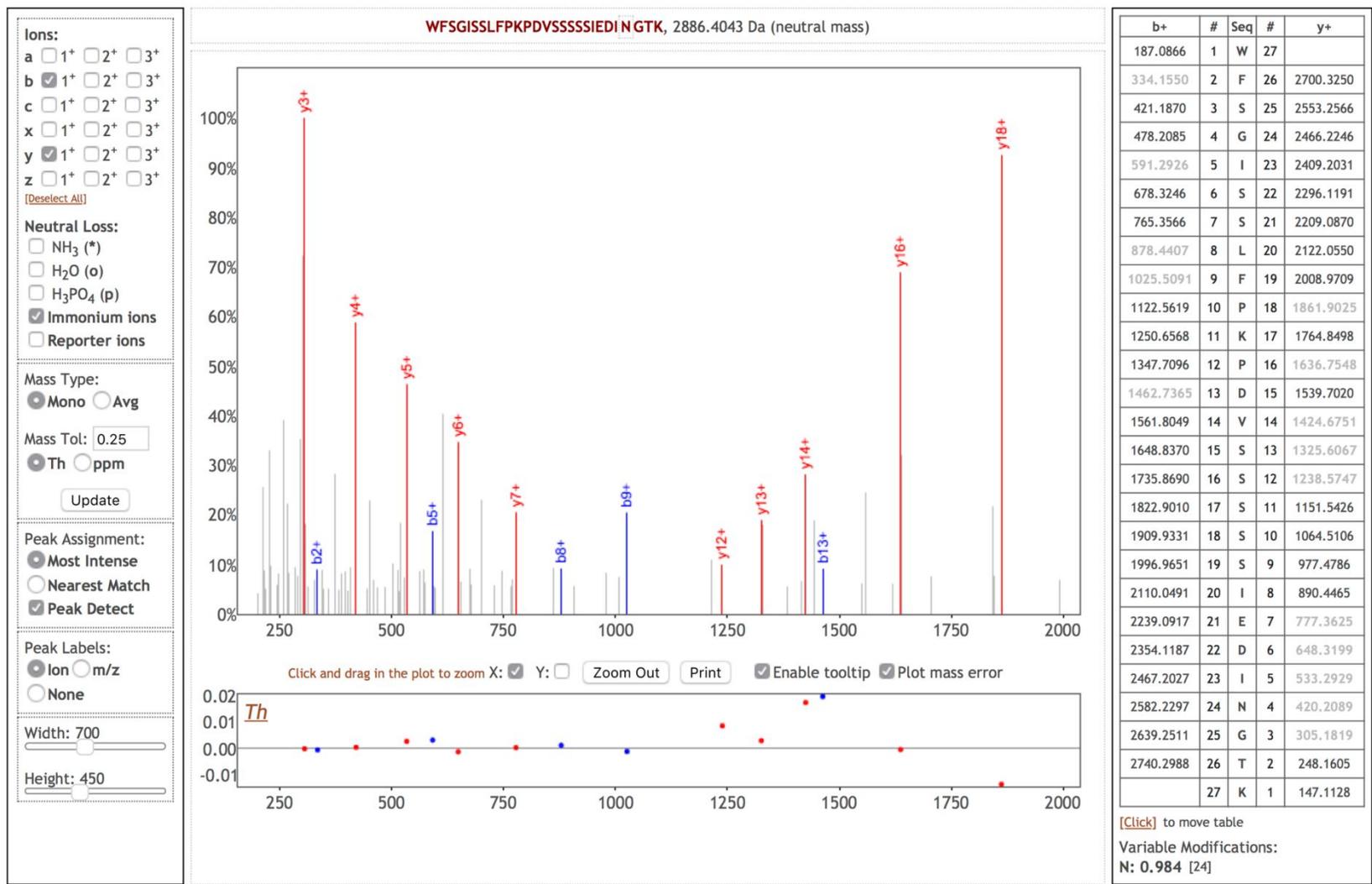
B



**Lorikeet** by vsharma@uw.edu

Lorikeet Spectrum Viewer is a Javascript plugin for JQuery that uses a modified version of the Flot plotting library.

C



[\[Click\]](#) to move table

Variable Modifications:

N: 0.984 [24]

**Lorikeet** by [vsharma@uw.edu](mailto:vsharma@uw.edu)

Lorikeet Spectrum Viewer is a Javascript plugin for [jQuery](#) that uses a modified version of the [Flot](#) plotting library.

D

**Ions:**

a  1+  2+  3+

b  1+  2+  3+

c  1+  2+  3+

x  1+  2+  3+

y  1+  2+  3+

z  1+  2+  3+

[\(Deselect All\)](#)

**Neutral Loss:**

NH<sub>3</sub> (\*)

H<sub>2</sub>O (o)

H<sub>3</sub>PO<sub>4</sub> (p)

Immonium ions

Reporter ions

**Mass Type:**

Mono  Avg

Mass Tol:

Th  ppm

**Peak Assignment:**

Most Intense

Nearest Match

Peak Detect

**Peak Labels:**

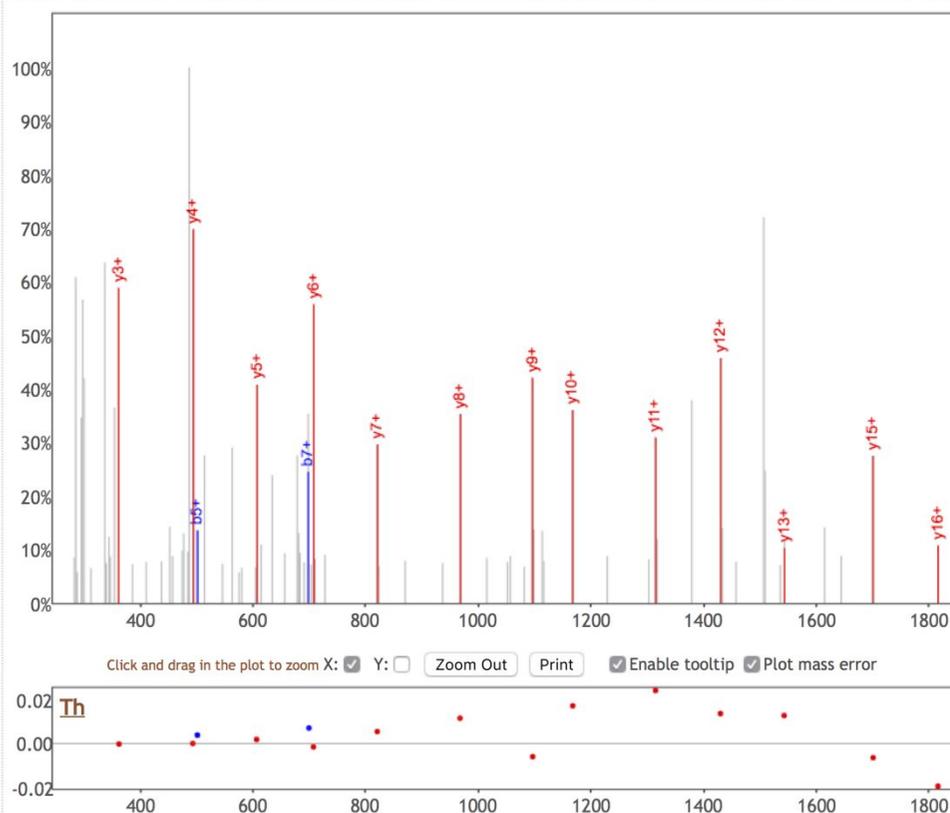
Ion  m/z

None

Width:

Height:

SLGENPTDAELKDMINEVDADG N'GTIDFAEFLTMSQK, 4129.9104 Da (neutral mass)



b+	#	Seq	#	y+
88.0393	1	S	38	
201.1234	2	L	37	4042.8784
258.1448	3	G	36	3929.7943
387.1874	4	E	35	3872.7728
501.2304	5	N	34	3743.7302
598.2831	6	P	33	3629.6873
699.3308	7	T	32	3532.6346
814.3577	8	D	31	3431.5869
885.3949	9	A	30	3316.5599
1014.4374	10	E	29	3245.5228
1127.5215	11	L	28	3116.4802
1255.6165	12	K	27	3003.3962
1370.6434	13	D	26	2875.3012
1501.6839	14	M	25	2760.2743
1614.7680	15	I	24	2629.2338
1728.8109	16	N	23	2516.1497
1857.8535	17	E	22	2402.1068
1956.9219	18	V	21	2273.0642
2071.9488	19	D	20	2173.9958
2142.9860	20	A	19	2058.9688
2258.0129	21	D	18	1987.9317
2315.0344	22	G	17	1872.9048
2430.0613	23	N	16	1815.8833
2487.0828	24	G	15	1700.8564
2588.1304	25	T	14	1643.8349
2701.2145	26	I	13	1542.7872
2816.2414	27	D	12	1429.7032
2963.3099	28	F	11	1314.6762
3034.3470	29	A	10	1167.6078
3163.3896	30	E	9	1096.5707
3310.4580	31	F	8	967.5281
3423.5420	32	L	7	820.4597
3524.5897	33	T	6	707.3756
3637.6738	34	L	5	606.3280
3768.7143	35	M	4	493.2439
3855.7463	36	S	3	362.2034
3983.8049	37	Q	2	275.1714
	38	K	1	147.1128

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Variable Modifications:  
N: 0.984 [23]

