



# Comparative Analysis of Fibronectin Using *In Situ* ToF-SIMS, SPI-MS, and dropDESI-MS in a Microfluidic Reactor



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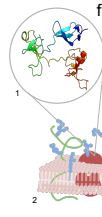
<sup>2</sup> Pacific Northwest National Laboratory

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## Introduction

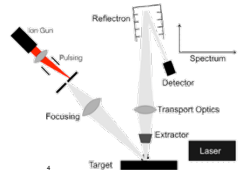
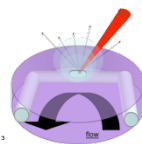
Fibronectin is a protein within the extracellular matrix of animal cells. It is an important biomolecule due to its role in cell differentiation, growth, kinesis and adhesion. Biological responses as such occur within aqueous environments and are mediated through membrane recognition and signaling; where fibronectin is found to play a role.



Studying the outer molecular surface of fibronectin, a model system for proteins, in aqueous solution allows deeper insight into the micro-biochemical reactions that occur during these processes. *In situ* mass spectrometry (MS) comparative analysis in aqueous solution accurately represents fibronectin's chemical components, made possible by the vacuum compatible microfluidic reactor.

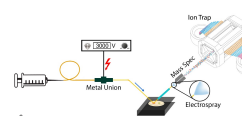
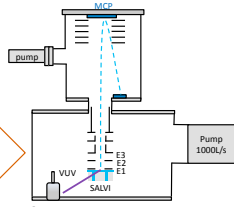
## Experimental Design

System for Analysis at the Liquid Vacuum Interface (SALVI). PDMS microfluidic block placed in vacuum chamber enabling *in situ* liquid MS.  
- Microfluidic channel  
- Aperture for direct liquid probing



Time-of-flight secondary ion mass spectrometer (ToF-SIMS)  
- Interface surface technique  
- Bismuth liquid metal ion beam  
- Monitors positive and negative emitted ions

Advanced light source single photon ionization mass spectrometer (ALS SPI-MS)  
- Interface surface technique  
- Synchrotron vacuum ultraviolet (VUV) photon beam  
- Determines appearance energy (AE)



Drop desorption electrospray ionization mass spectrometer (dropDESI-MS)  
- Ambient conditions  
- Electrode spray ion source  
- Capillary generates charged micro droplets

## Results

### ToF-SIMS

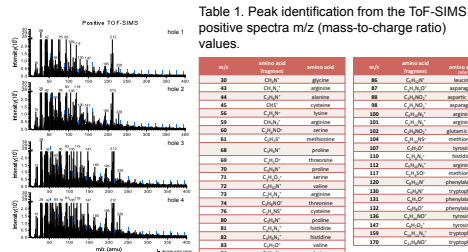


Table 1. Peak identification from the ToF-SIMS positive spectra  $m/z$  (mass-to-charge ratio) values.

$m/z$	amino acid	amino acid	$m/z$	amino acid	amino acid
39	OH <sup>+</sup>	glycine	86	CA <sup>+</sup>	histidine
40	OH <sup>+</sup>	glycine	87	CA <sup>+</sup>	histidine
44	CA <sup>+</sup>	alanine	88	CA <sup>+</sup>	aspartic acid
45	OH <sup>+</sup>	alanine	89	CA <sup>+</sup>	aspartic acid
56	CA <sup>+</sup>	lysine	100	CA <sup>+</sup>	arginine
58	CA <sup>+</sup>	lysine	101	CA <sup>+</sup>	arginine
60	OH <sup>+</sup>	arginine	105	CA <sup>+</sup>	arginine
61	CA <sup>+</sup>	arginine	106	CA <sup>+</sup>	arginine
61	CA <sup>+</sup>	methionine	106	CA <sup>+</sup>	arginine
68	CA <sup>+</sup>	methionine	107	CA <sup>+</sup>	methionine
69	CA <sup>+</sup>	threonine	110	CA <sup>+</sup>	histidine
70	CA <sup>+</sup>	threonine	112	CA <sup>+</sup>	arginine
71	CA <sup>+</sup>	alanine	117	CA <sup>+</sup>	methionine
71	CA <sup>+</sup>	alanine	118	CA <sup>+</sup>	phenylalanine
71	CA <sup>+</sup>	valine	118	CA <sup>+</sup>	tyrosine
71	CA <sup>+</sup>	alanine	119	CA <sup>+</sup>	phenylalanine
76	CA <sup>+</sup>	threonine	122	CA <sup>+</sup>	phenylalanine
76	CA <sup>+</sup>	threonine	123	CA <sup>+</sup>	phenylalanine
81	CA <sup>+</sup>	lysine	147	CA <sup>+</sup>	lysine
81	CA <sup>+</sup>	proline	147	CA <sup>+</sup>	lysine
81	CA <sup>+</sup>	histidine	158	CA <sup>+</sup>	tyrosine
81	CA <sup>+</sup>	valine	159	CA <sup>+</sup>	tyrosine
84	CA <sup>+</sup>	lysine	159	CA <sup>+</sup>	tyrosine

### SPI-MS

The  $m/z$  spectral plot for photoionization efficiencies (PIE) from 8.0 to 11.0 eV with a step size of 0.1 eV.

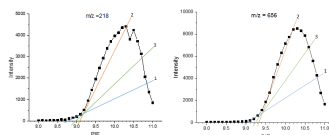
Table 2. Possible peak identification from the SPI-MS positive spectra.

$m/z$	amino acid fragment	amino acid
14	NH <sup>+</sup>	ammonium
41	CA <sup>+</sup>	alanine fragment
56	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	amino acid fragment
80	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	histidine fragment
101	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	glutamic acid
148	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	methionine-ammonium
172	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	tryptophan fragment
218	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Gln-Ala
278	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Gln-Met
292	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Tyr-Leu
350	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Tyr-Arg
353	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Cys-Tyr-Asp-immunium
368	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	PDMS interference (R)
429	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Lys-Ile-Gly-Asp
433	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Cys-Val-Cys-Lys
505	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Asn-Arg-Cys-Asn
580	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Cys-Val-Tyr-Asp-Ser-Gly
595	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Ser-Tyr-Asp-Ile-Gly
656	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Glu-Ser-Lys-Pro-Glu-Ala
732	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Tyr-Asp-Asn-Gly-Lys-His
808	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Gly-Thr-Ser-Tyr-Val-Ile-Gly-Gly
884	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Trp-Met-Val-Asp-Cys-Thr

Table 3. Summary of Estimated AE Values

$m/z$	AE (eV)
56	9.7±0.1
101	8.5±0.1
172	9.8±0.1
218	8.9±0.1
278	8.7±0.1
292	9.2±0.1
353	9.2±0.1
429	9.2±0.1
433	9.3±0.1
505	9.2±0.1
580	9.2±0.1
595	9.2±0.1
656	9.2±0.1
732	9.1±0.1
808	9.1±0.1
884	9.1±0.1

Estimated appearance energies (AE) for selected  $m/z$  values computed. Linear regression analysis was also used. The three colored lines are 1) the onset AE value limit; 2) the extreme PIE value limit; and 3) the average between lines 1 and 2 which estimate the average AE.



### dropDESI-MS

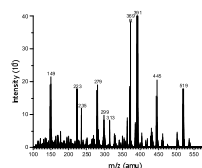


Table 4. Possible peak identification from the drop DESI-MS positive spectra.

$m/z$	amino acid fragment	amino acid
149	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	methionine-ammonium
223	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Tyr-Leu
235	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Asn-Tyr
279	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Gln-Met
299	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Lys-Pro-Gly
313	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Tyr-Met
369	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	PDMS interference (R)
391	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Thr-Tyr-Gly
445	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Gly-Ala-Ile-Thr
519	C <sub>2</sub> H <sub>5</sub> N <sup>+</sup>	Gln-Asp-Thr-Arg

## Discussion

Compounds and constituents of the fibronectin samples show complementary results based on the identified amino acid fragments. Possible  $m/z$  identifications for ALS SPI-MS and dropDESI-MS were calculated based on fibronectin's amino acid sequence, while values for ToF-SIMS were comparable to previously conducted experiments. The microfluidic reactor successfully enabled different MS techniques in aqueous solution. Only fibronectin in aqueous solution has been studied so far in MS. Our results suggest the need for further research of large biomolecules to understand their surface compositions in aqueous solution, accurately representing their natural environment.

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15. Courtesy of LBNL



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