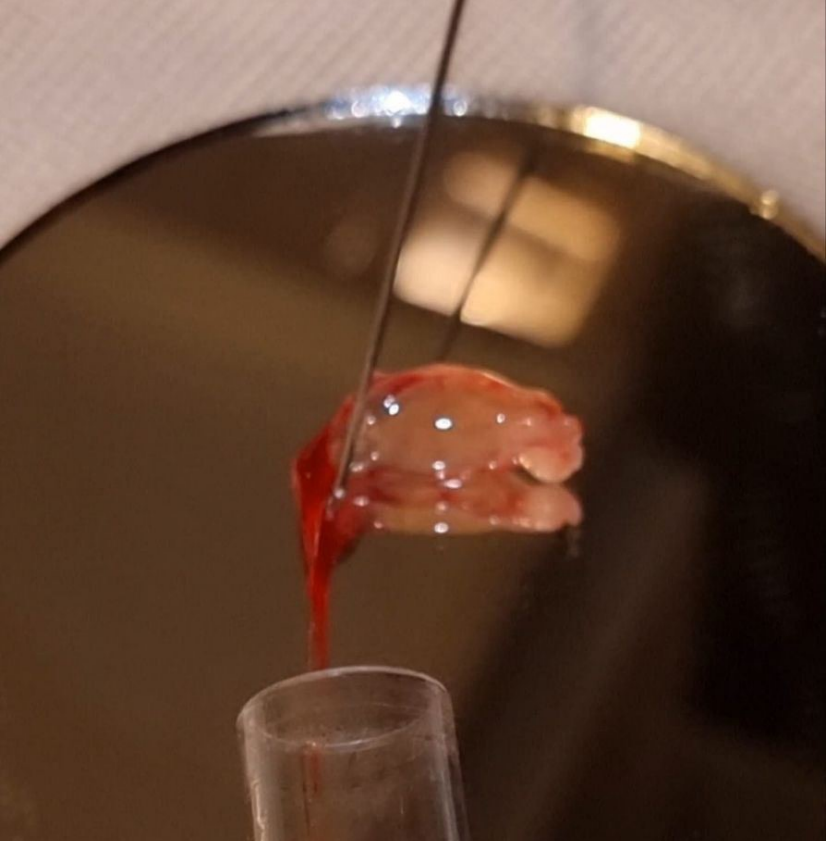
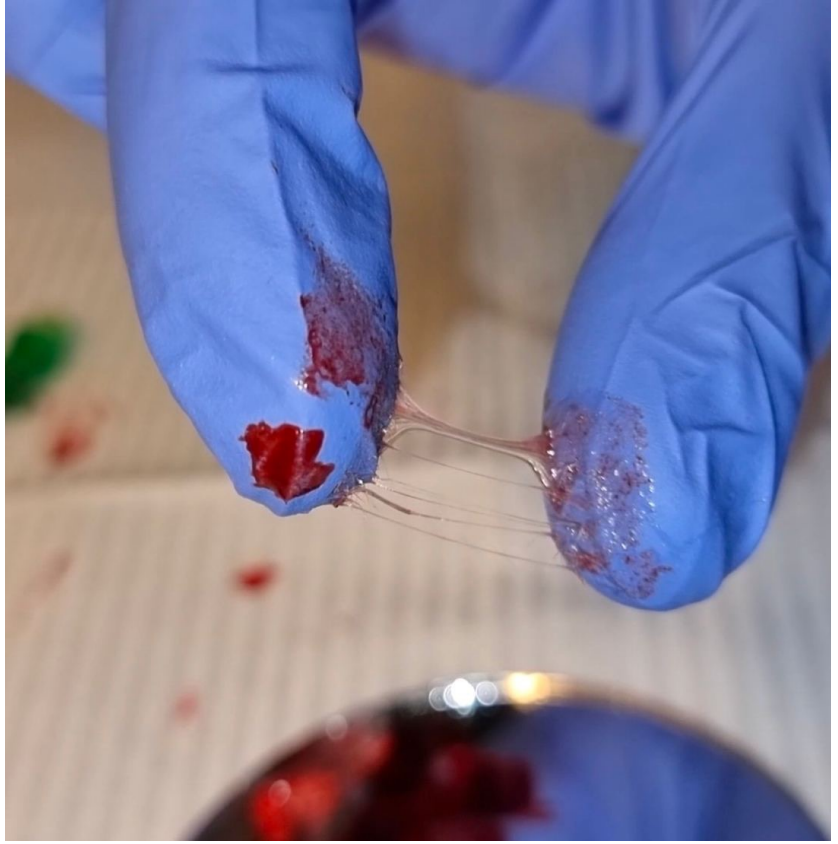
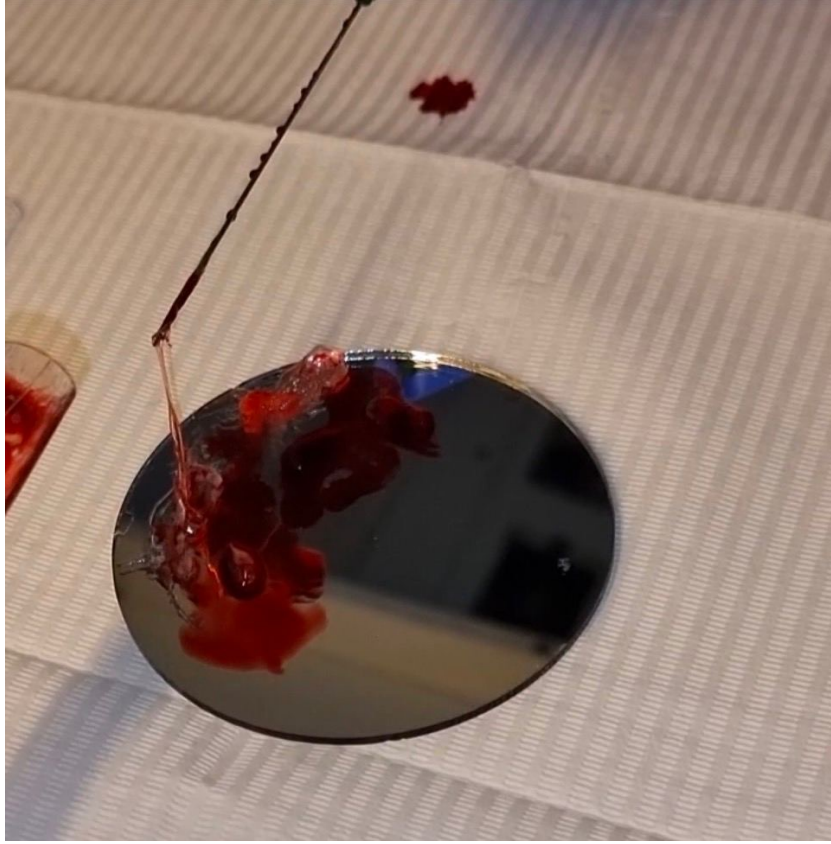
Fibrosis
Clots
&
Augmented
NAC

March, 30 2023







HISTOLOGICAL TISSUE

Microsoft Excel Worksheet

rank	log(e)	log(I)	%/%	#	total	Mr	Accession
1	-83,9	4,5	2.3/4	8	10	792,9	tr | A0A6M6ED C5 | A0A6M6DC55_SARS2 gpmDB | psyt | snap [1/0] homo (5/10309) protein peptide no protein information available
2	-82,8	4,56	1.2/2	4	4	789,8	(kl) tr | A0A3G5BIY8 | A0A3G5BIY8_SARS gpmDB | psyt | snap [1/0] homo (9/10309) protein peptide no protein information available
3	-79,3	4,33	0.5/1	3	3	794,1	(kl) tr | A0A6M4N427 | A0A6M4N427_SARS2 gpmDB | psyt | snap [1/0] homo (15/10309) protein peptide no protein information available
4	-78,1	4,47	0.2/0	1	1	778,1	(kl) tr | A0A6NDVQZ7 | A0A6NDVQZ7_SARS2 gpmDB | psyt | snap [1/0] homo (18/10309) protein peptide no protein information available
5	-75,8	4,37	0.7/1	2	2	793,6	(kl) tr | A0A6N1WHH7 | A0A6N1WHH7_SARS2 gpmDB | psyt | snap [1/0] homo (25/10309) protein peptide no protein information available
6	-75,6	4,33	0.2/0	1	1	793,3	(kl) tr | A0A6M4NGD6 | A0A6M4NGD6_SARS2 gpmDB | psyt | snap [1/0] homo (3/15) protein peptide no protein information available
7	-75,3	4,39	0.4/1	2	2	793,6	(kl) tr | A0A6H2EJD9 | A0A6H2EJD9_SARS2 gpmDB | psyt | snap [1/0] homo (26/10309) protein peptide no protein information available
8	-74,9	4,76	0.4/1	2	2	793,5	(kl) tr | A0A7D7WDX0 | A0A7D7WDX0_SARS2 gpmDB | psyt | snap [1/0] homo (26/10309) protein peptide no protein information available
9	-74,3	4,34	0.4/1	2	3	792,7	(kl) tr | A0A6M5W2S | A0A6M5W2S5_SARS2 gpmDB | psyt | snap [1/0] homo (29/10309) protein peptide no protein information available
10	-74,2	4,35	0.4/1	2	2	793,4	(kl) tr | A0A6M4N231 | A0A6M4N231_SARS2 gpmDB | psyt | snap [1/0] homo (30/10309) protein peptide no protein information available
11	-72,8	4,36	0.9/1	4	4	783,1	(kl) tr | A0A6M3YPE2 | A0A6M3YPE2_SARS2 gpmDB | psyt | snap [1/0] homo (85/10309) protein peptide no protein information available
12	-72	4,81	0.2/0	1	1	793,2	(kl) tr | A0A7D6ES11 | A0A7D6ES11_SARS2 gpmDB | psyt | snap [1/0] homo (93/10309) protein peptide no protein information available
13	-71,7	4,82	0.3/0	1	1	793,8	(kl) tr | A0A7D7U442 | A0A7D7U442_SARS2 gpmDB | psyt | snap [1/0] homo (96/10309) protein peptide no protein information available
14	-69,9	4,34	0.4/1	2	2	793,3	(kl) tr | A0A7D7UDF2 | A0A7D7UDF2_SARS2 gpmDB | psyt | snap [1/0] homo (147/10309) protein peptide no protein information available
15	-68,9	4,47	0.5/1	1	1	793,6	(kl) tr | A0A6M5WW83 | A0A6M5WW83_SARS2 gpmDB | psyt | snap [1/0] homo (159/10309) protein peptide no protein information available
16	-68,5	4,46	0.5/1	1	1	793,6	(kl) tr | A0A6M4MN20 | A0A6M4MN20_SARS2 gpmDB | psyt | snap [1/0] homo (179/10309) protein peptide

s. file: *Histological tissue content*

RESULTS

5. RESULTS OBTAINED

Table 2 shows the degree of aggregation in percent of the complex detected in the absence and presence of Augmented NAC (2 µg/mg).

Table 2: List of samples analyzed

ID	Degree of aggregation % in **absence** of Augmented NAC	Degree of aggregation % in **presence** of Augmented NAC
1	89	32

1. ACRONYMES

H_2O: Deionized water.
ESI: Electrospray ionization.
MS: Mass Spectrometry.
CH_3CN: Acetonitrile.
NH_4HCO_3 : Ammonium bicarbonate.
HCOOH: Formic acid.

2. PURPOSE OF THE ACTIVITY

The aim of the analysis is to measure the degree of aggregation of the histologically derived protein complex in the presence and absence of Augmented NAC.

3. INSTRUMENTATION

Tool	Model	Manufacturer
Centrifuge	MIKRO 120	PBI
Freezer (-20 °C)	DV1	Evermed
Pipette	P20	Metler
Pipette	P100	Metler
Pipette	P1000	Metler
Mass spectrometer	LTQ	Thermofisher
Liquid chromatograph	Surveryor	Thermofisher
Thermoblock	DVV1	PBI

4.3 LC-ESI-MS Instrumentation

The analysis was performed using an HPLC Surveyor (Thermofisher, USA). The column used was a Halo Peptide ES-C18, 2.1 x 50 mm, 2.7 µm. Analyses were performed using a two-phase gradient: Phase A (H_2O+0.2 % Formic Acid (HCOOH)) and Phase C acetonitrile (CH_3CN). The chromatographic gradient used is given in Table 1. The volume of sample injected is equal to 5 µL.

Data acquisition was done using a "SANIST" mass spectrometer. The ionization source used is an ESI.

Table 1: Chromatographic gradient used for the purpose of the feasibility study.

Gradient		
Time (minutes)	% C	Flow (mL/min)
0	2%	0.250
2.5	2%	0.250
3	80%	0.250
7	80%	0.250
8	2%	0.250
15	2%	0.250

4.4 Data Processing

Data processing was performed using SANIST Hb and Mascot packages.

See Lab Report

ZeroSpike is a research project initiated by the non-profit civil society association Federazione Rinascimento Italia (FRI).

The results of our research are available to the international community of like-minded associations and doctors.
Just send us an e-mail: info@zerospike.org

For more information:

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