Mass spectrometry in wastewater-based epidemiology (WBE) for the determination of small and large molecules as biomarkers of exposure. Needs for COVID-19 testing with environmental proteomics (EP-WBE).

Damiâ Barceló[1,2], Yolanda Picó[3], Manish Kumar[6] Carlos Perez-Lopez[1], Antoni Ginebreda[1], Roma Tauler[1] , Roberto Parra [5] Montserrat Carrascal[4], Joaquin Abian[4]

[1] IDAEA-CSIC, Barcelona, Spain

[2] Catalan Institute for Water Research (ICRA-CERCA), Girona, Spain

[3] CIDE, University of Valencia, Moncada, Spain.

[4] IIBB-CSIC/IDIBAPS, Barcelona, Spain and

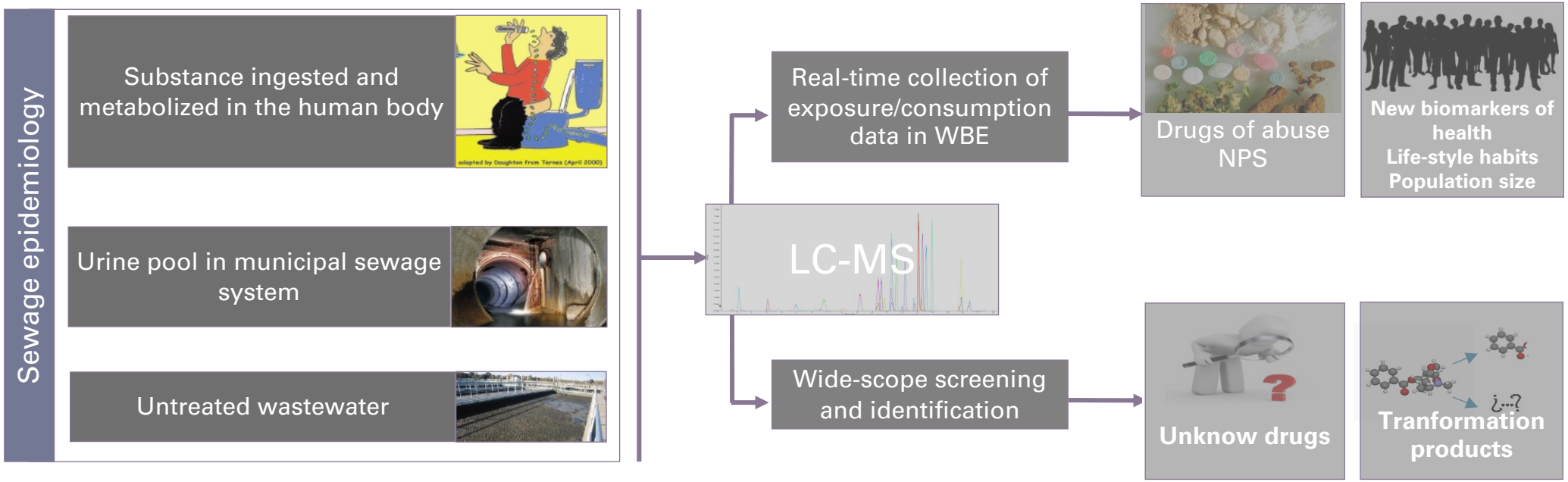
[5]Tecnologico de Monterrey,Mexico

6Indian Inst.of tech Gandhingar,Gujarat, India

EBNet Seminar-Webinar- November 11,2021

C.G. Daughton. Pharmaceuticals and Personal Care Products in the Environment, Scientific and Regulatory Issues, C.G. Daughton, T.L. Jones-Lepp (Eds.), American Chemical Society, Washington (2001), pp. 348-364

E. Zuccato, C. Chiabrando, S. Castiglioni, D. Calamari, R. Bagnati, S. Schiarea, R. Fanelli, Cocaine in surface waters: a new evidence-based tool to monitor community drug abuse, Environ. Health, 4 (2005), p. 14



França: La imatge de Sarkozy cau en picat per la pèrdua del poder adquisitiu **P11**

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Diàleg, P20

Salvador Cardús:
Tots seran vots en blanc

'Sortim'
Ja és el temps per a la ruta del xató ■ **Suplement**

Cultura
Najat El Hachmi guanya el Llull de novel·la ■ **P34**

Barcelona esnifa cada dia 70.000 dosis de cocaïna

INFORME • Les aigües residuals porten les restes de droga a la depuradora del Baix Llobregat

AUGMENT • Els caps de setmana l'arribada dels residus es dobla respecte als altres dies ■ **P23**

Science of the Total Environment 609 (2017) 916–926

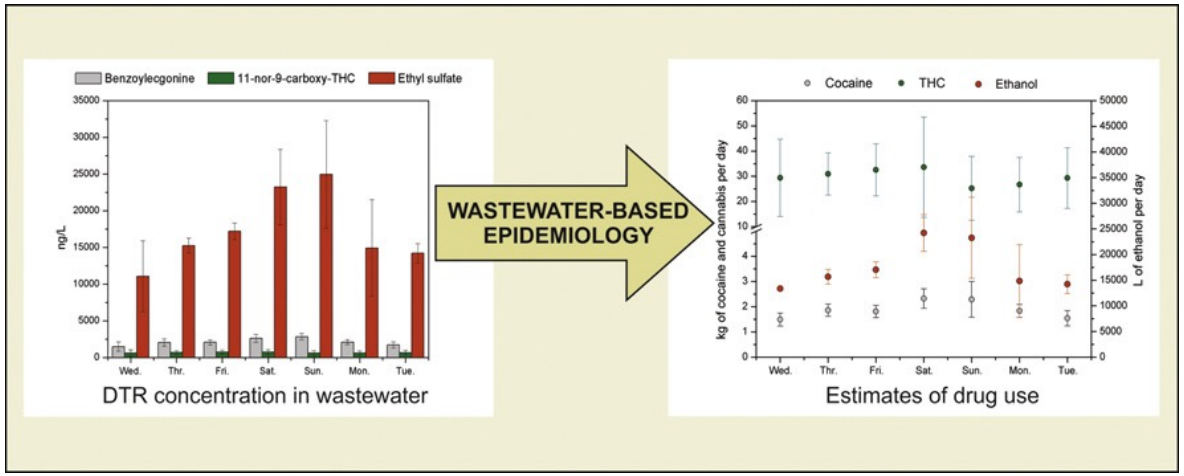
Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

Five-year monitoring of 19 illicit and legal substances of abuse at the inlet of a wastewater treatment plant in Barcelona (NE Spain) and estimation of drug consumption patterns and trends

Nicola Mastroianni [a], Ester López-García [a], Cristina Postigo [a,*], Damià Barceló [a,b], Miren López de Alda [a]



- Drug use in Barcelona during 5 years assessed using WBE.
- Alcohol, cannabis and cocaine were the most consumed drugs.
- Drug use increased from 2011 to 2015, contrary to national official data.
- Temporal trends of drug use were in agreement with regional official data.
- Consumption of alcohol, cocaine and MDMA increased during the weekend.

Contents lists available at ScienceDirect

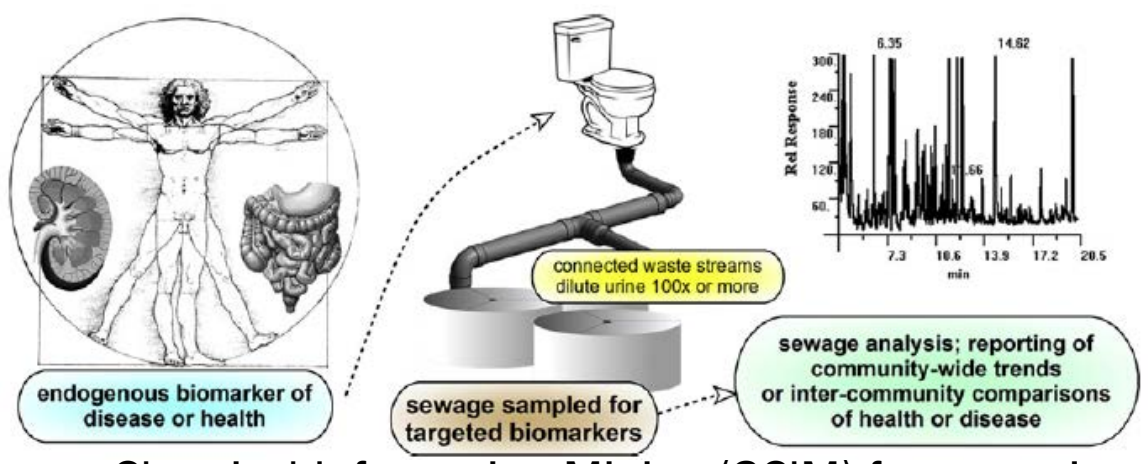
Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

Monitoring wastewater for assessing community health: Sewage Chemical-Information Mining (SCIM)

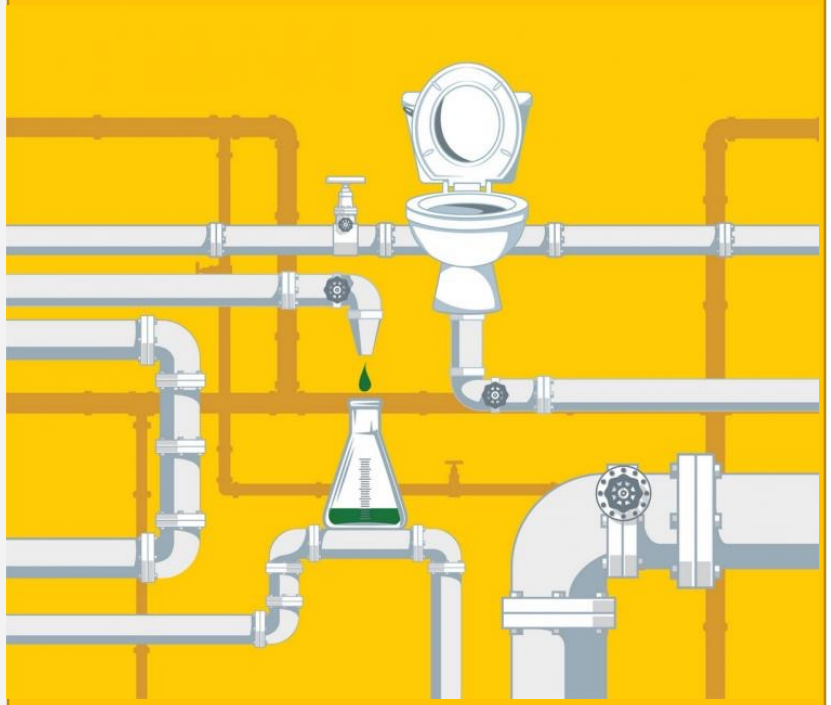
Christian G. Daughton

Environmental Futures Analysis Branch, Systems Exposure Division, National Exposure Research Laboratory, Office of Research and Development, U.S. Environmental Protection Agency, 944 East Harmon Avenue, Las Vegas 89119, NV, USA



- Update on Sewage Chemical-Information Mining (SCIM) for assessing public health
- Additional endogenous biomarkers are proposed for targeted monitoring with SCIM.
- Challenges for SCIM include confounding aspects of sewage and data normalization.
- A new concept is proposed that avoids the need for data normalization.
- Biomarkers are needed that measure not just disease but also health.

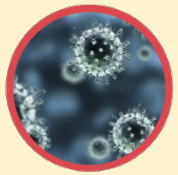
ADVANCES IN WASTEWATER-BASED EPIDEMIOLOGY



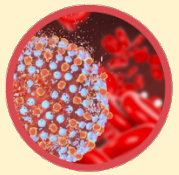
Pharmaceuticals and drugs

Nicotine, alcohol, & environmental contaminants

SARS-CoV-2, zika, & other outbreaks



Hepatitis C, poliovirus, & other asymptomatic diseases



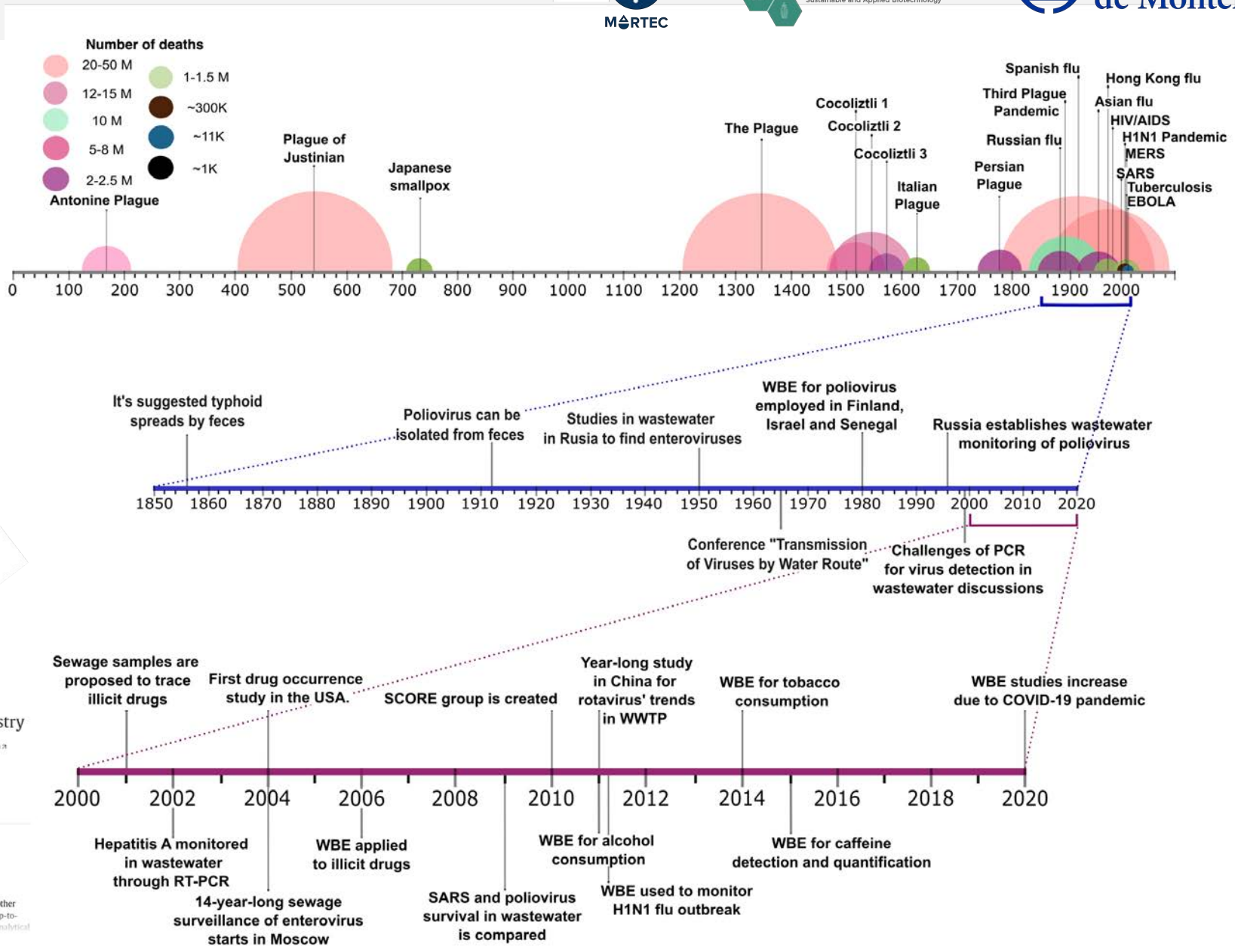
Antibiotic resistant bacteria & healthy microbiome

Diet and nutrition

PAST

FUTURE

Pandemics timeline & WBE timeline



Biosensors for the detection of disease outbreaks through Wastewater-based Epidemiology

Mildred G. Jiménez-Rodríguez[1], Fernando Silva-Lance[1], D. Alejandra Medina-Salazar[2], Manuel Martínez-Ruíz[1], Elda M. Melchor-Martínez[1], María Adriana Martínez-Prado[2], Hafiz M.N. Iqbal[1], Roberto Parra-Saldívar[1,*], Damià Barceló[3,4,5] and Juan Eduardo Sosa-Hernández[1,*]

[1]Tecnologico de Monterrey, School of Engineering and Sciences, Ave. Eugenio Garza Sada 2501, CP 64849, Monterrey, N.L., Mexico.
[2]Tecnológico Nacional de México-Instituto Tecnológico (Chemical and Biochemical Engineering. Blvd. Felipe P Durango, Dgo. 34080, Mexico.
[3]Department of Environmental Chemistry, Institute of Envir (IDAEA-CSIC), Jordi Girona, 18-26, 08034, Barcelona, Spa
[4]Catalan Institute for Water Research (ICRA-CERCA), Par Girona, c/Emili Grahit, 101, Edifici H2O, 17003, Girona, Sp
[5]College of Environmental and Resources Sciences, Zh China.

Under revision at TRAC journal

FIRST STUDY ON WBE IN BELFAST (UK)

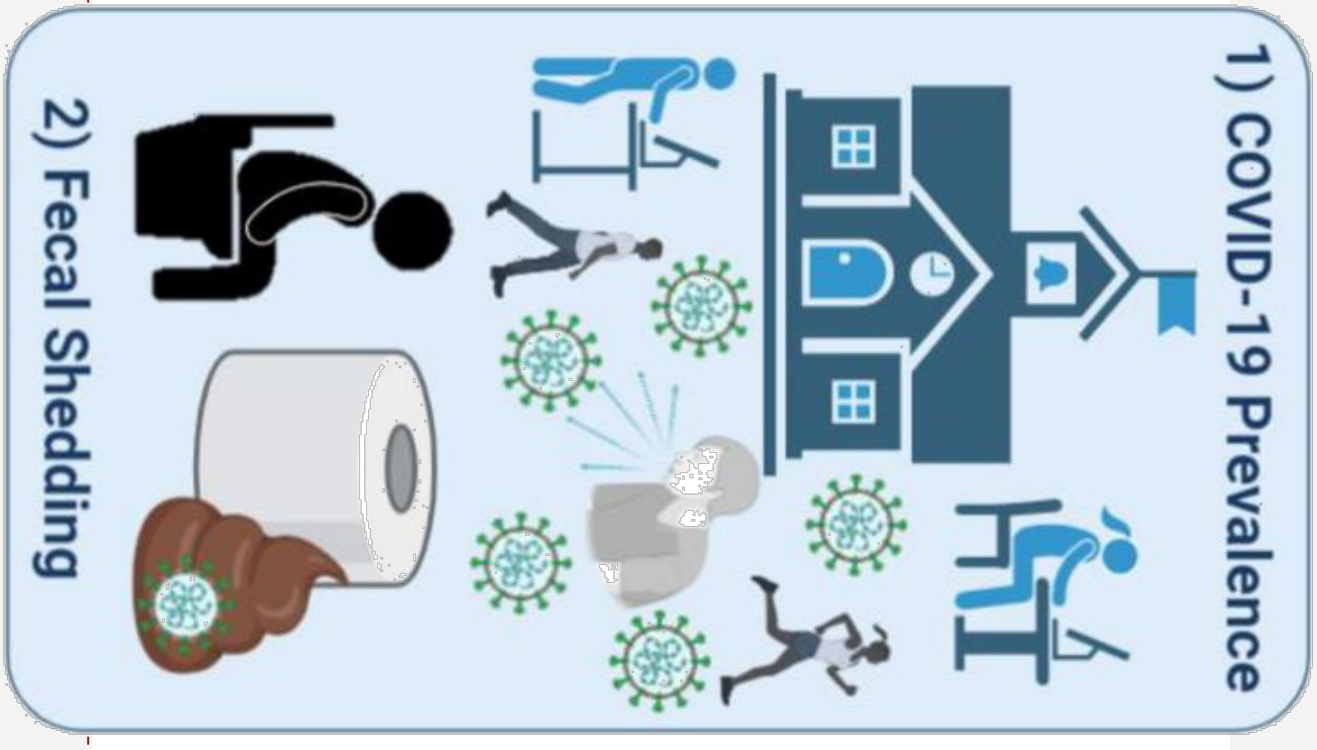
ISOLATION OF *B. THYPOSUS* FROM SEWAGE AND SHELFISH

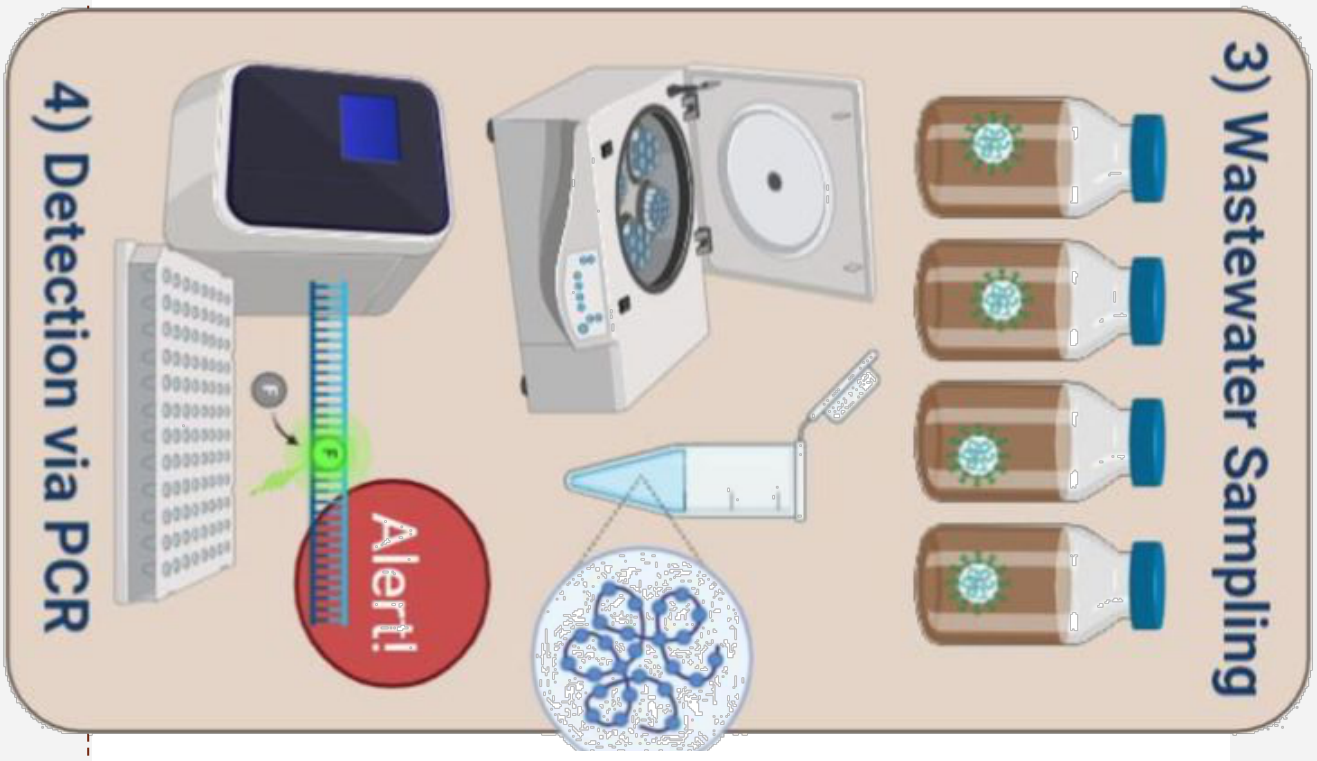
W.James Wilson,M.D, D .Sc.

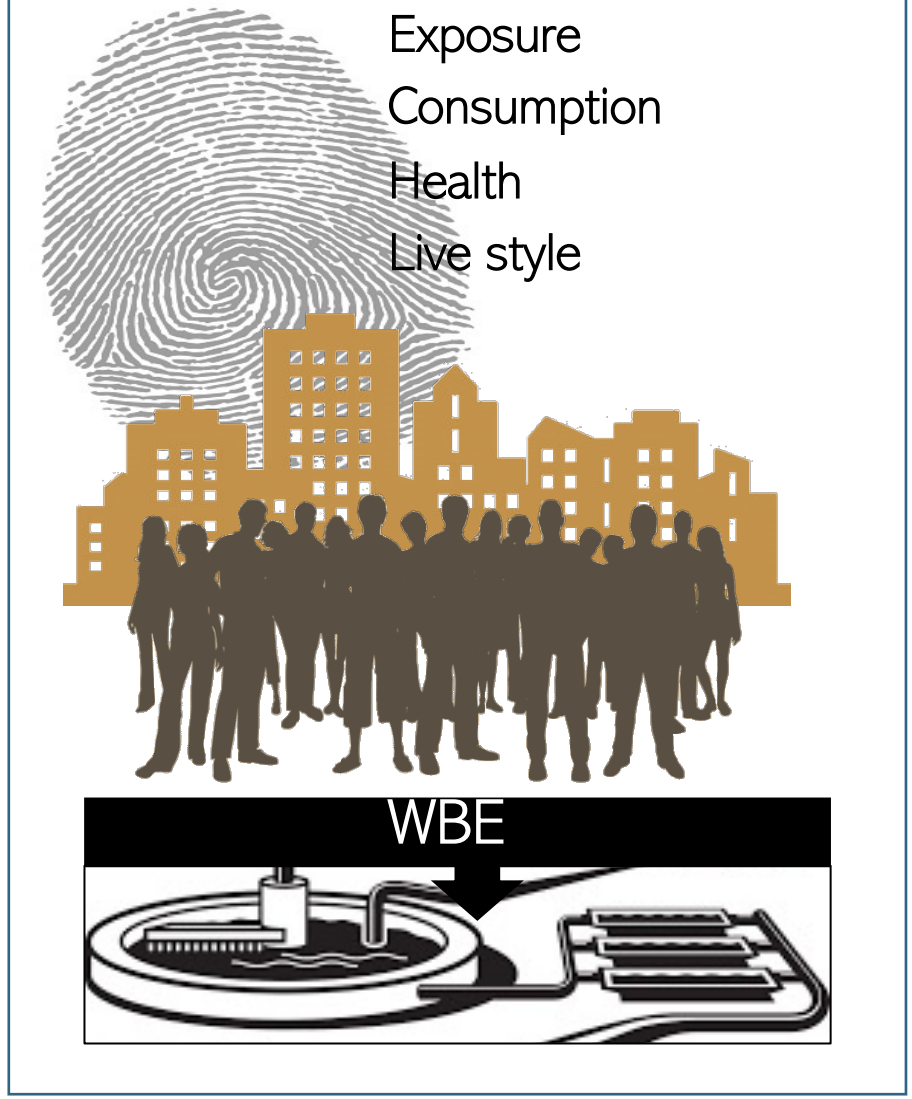
British Medical Journal, (1928)1,1061

by selective methods. The same would apply to water. The success obtained by Wilson (1928) in demonstrating *B. typhosus* in Belfast sewage by his method of selective culture marks a great advance in this branch of bacteriological investigation. I have applied Wilson's technique along with other methods in the examination of sewage in Edinburgh, and the object of this communication is to

WBE also for virus particles. Case study COVID-19 Prevalence







Consumption

Illicit drugs,
PPCPs
Tobacco
Alcohol

Exposure

Pesticides
Phthalates
OPFRs

Health and Live style

Genetic biomarkers

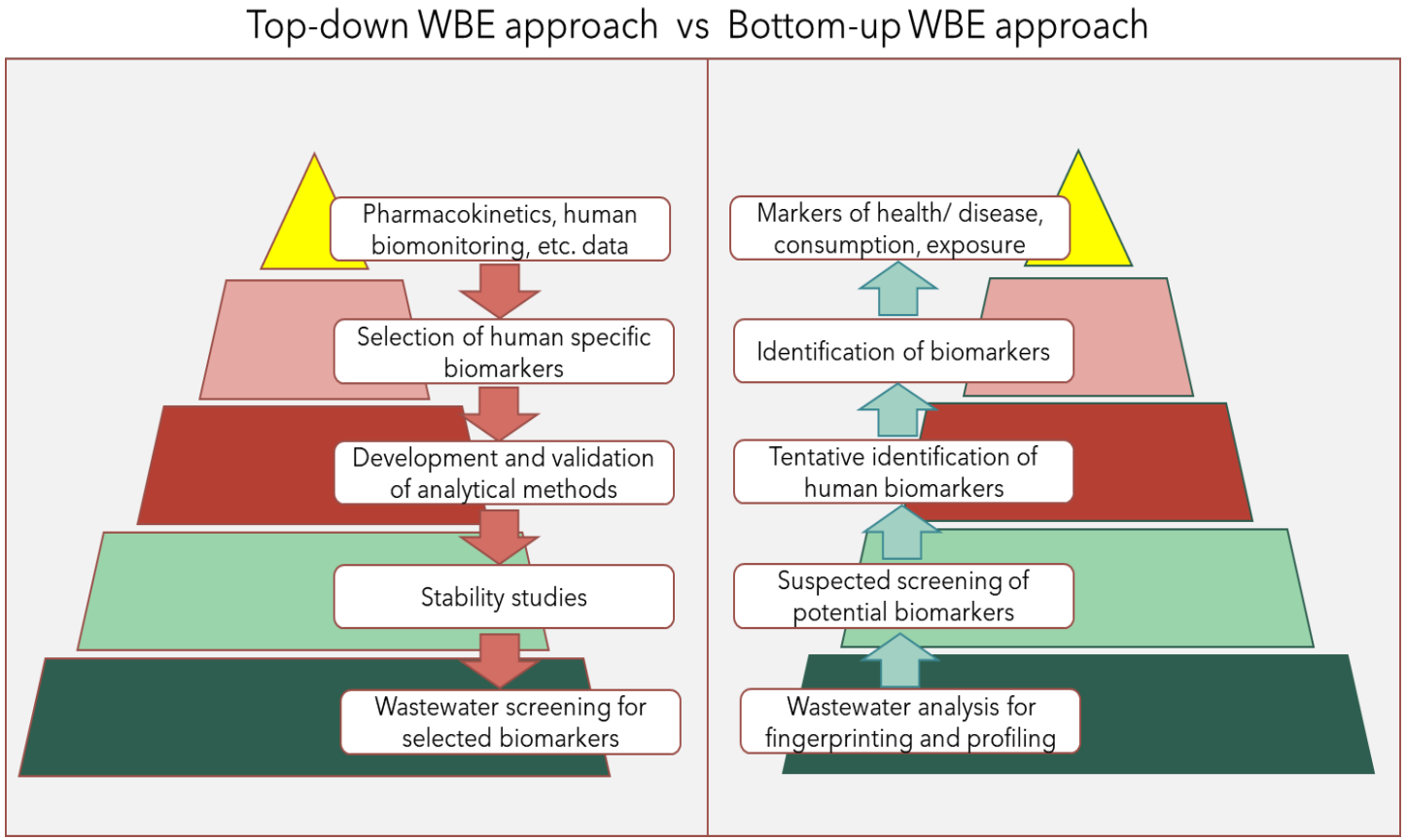
WBE using MS (PCR, Sensors): Lab-based surveillance method totally independent of health-care access

Detection of small molecules as biomarkers

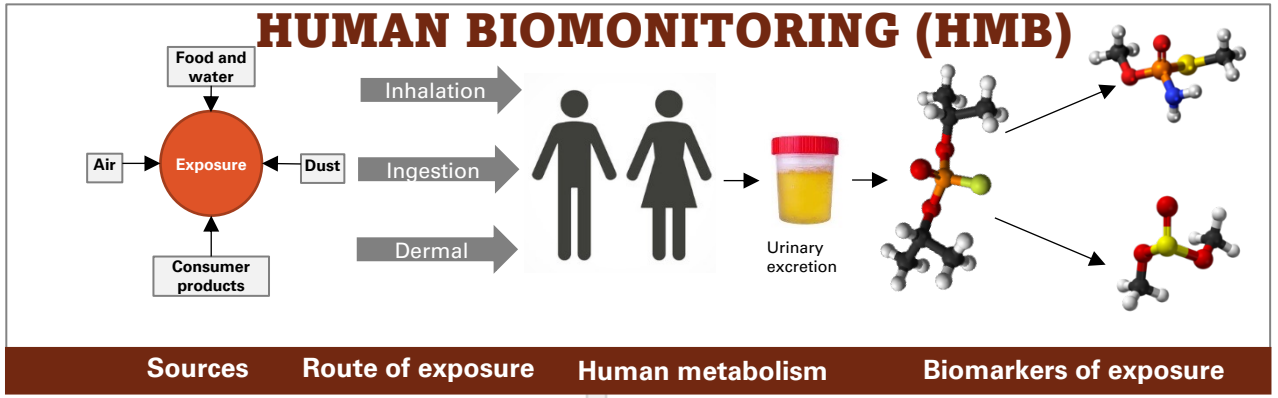
Detection of large molecules as biomarkers

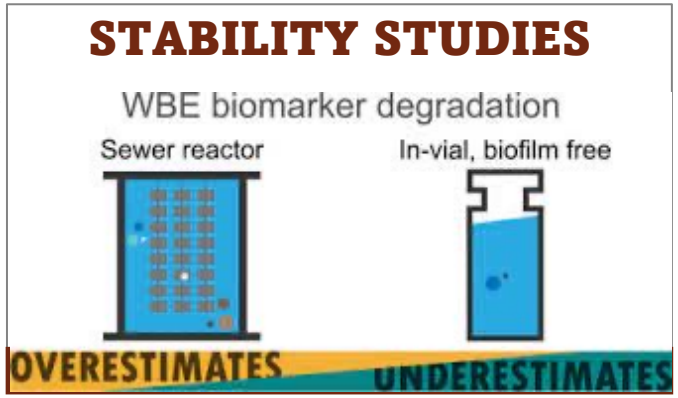
Detection of viral proteins of SARS CoV2 by HRMS

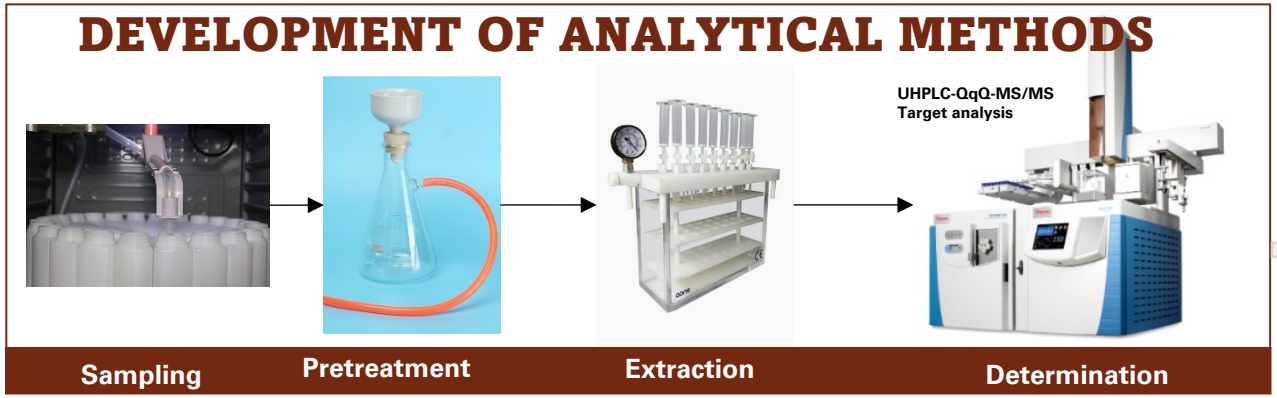
Detection of small molecules

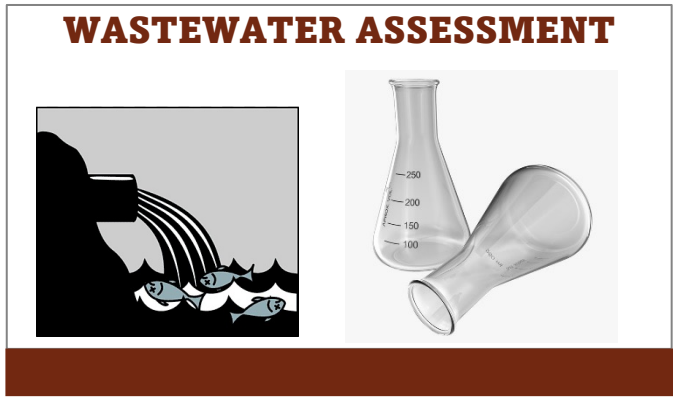


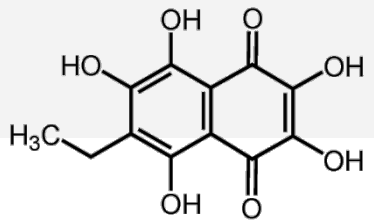
Top-down approach

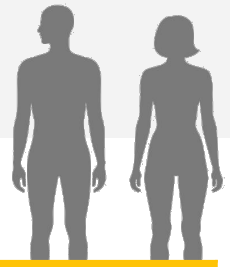










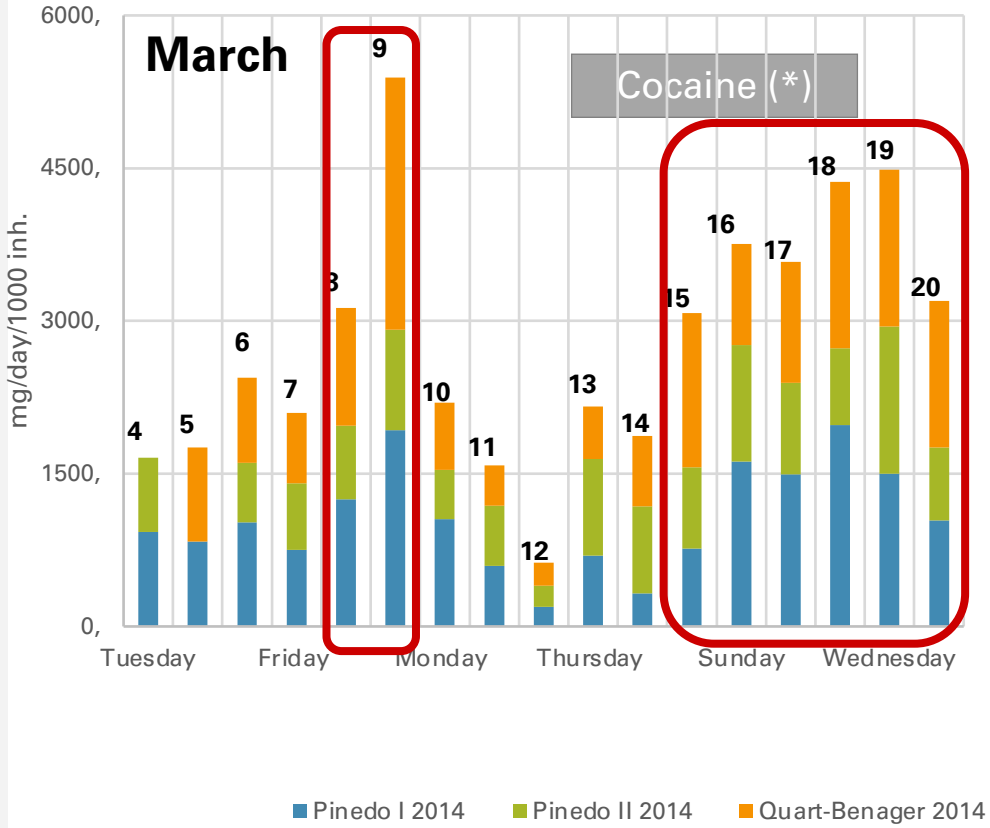


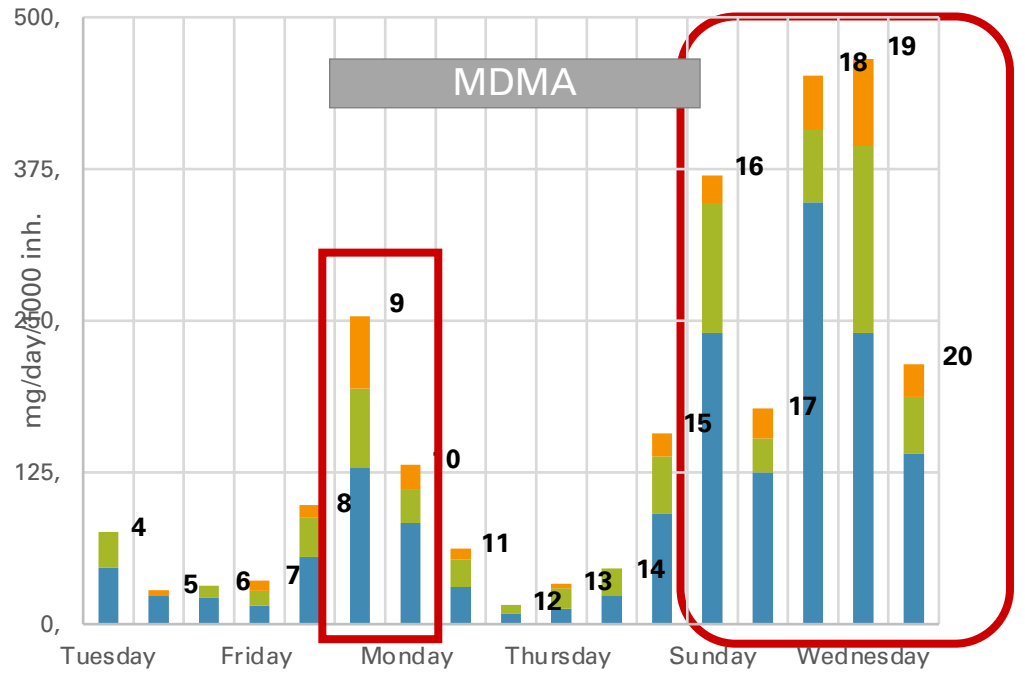
Biomarkers

Compounds	Biomarkers
Consumption of addictive substances	
Illicit drugs	
Cocainics	Human metabolites (> benzoylecgonine)
Opiods	Human metabolites and parent compounds
Cannabis	Human metabolites (> tretrahydrocannabinoic acid)
Amphetaminics	Parent compounds
Tobacco	Parent compound (Nicotine) and HM (cotinine, 3'-hydroxycotinine, anabasine, anatabine)
Alcohol	Human metabolites (ethyl sulfate)
Caffeine	Parent compound (caffeine) and human metabolites (1,7-dimethyluric acid)
New psychoactive compounds	Mostly parent compounds
Consumption of pharmaceuticals	
Pharmaceuticals (NSAIDs, antibiotics, anticancerigens, etc..)	Mostly parent compounds and transformation products, human metabolites in very few cases
Food Consumption	
Artificial sweeteners	As parent compounds (they are neither, metabolized or degraded).
Exposure to contaminants	
Organophosphorus flame retardants	Human metabolites (hydroxylated)
Plasticizers and phthalates	Human metabolites
Pesticides (Triazines, organophosphorus, organochlorine and pyrethroids)	Human metabolites (hydroxylated, dealkyl and acids)
Mycotoxins	Specific metabolites
Prevalence of disease	
Hepatitis B	Lamivuline (pharmaceutical)
Stress	8-iso-prostaglandin F2α (PGF2α), its metabolite dinor-11β-Prostaglandin F2α (dnPGF2α) and Prostaglandin E2 (PGE2)
Diabetes	Metformin (pharmaceutical)
Gout	Oxyallopurinol (metabolite of a pharmaceutical allopurinol)

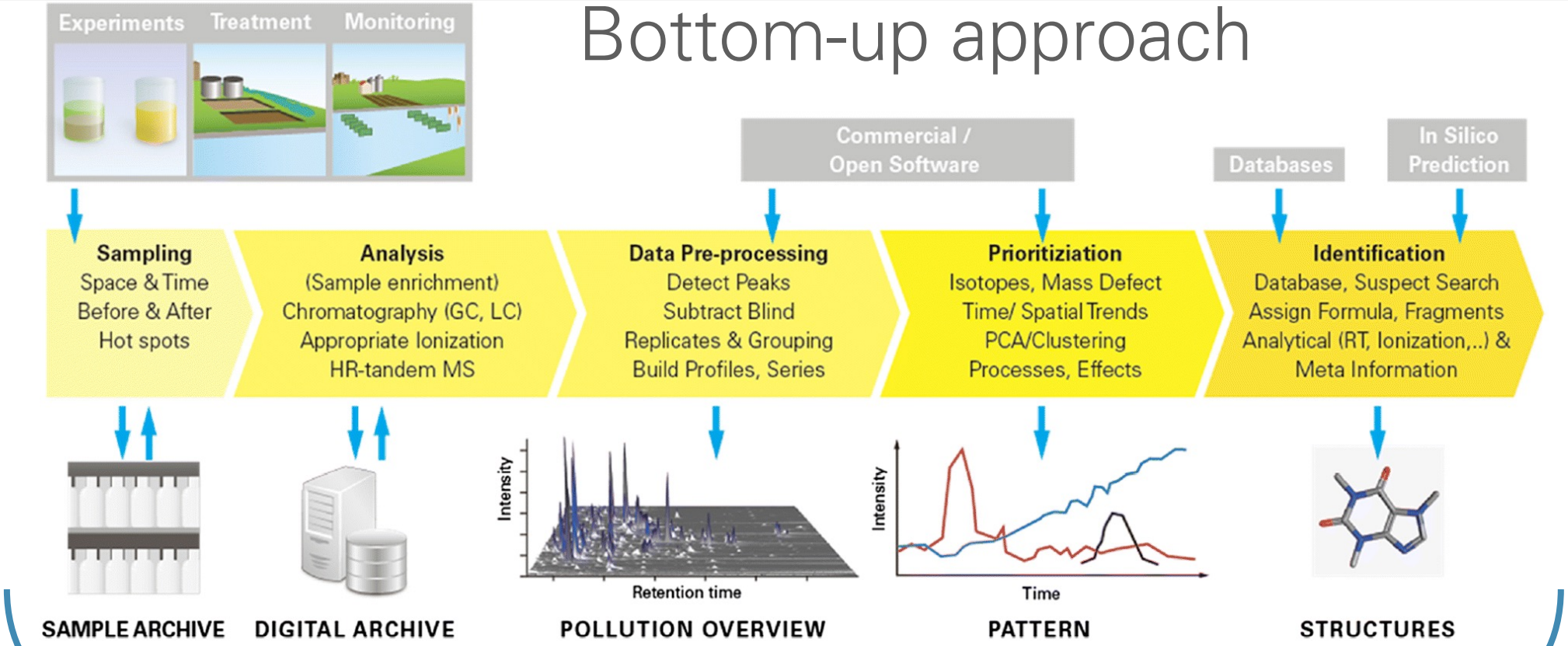
WBE to assess drug consumption: “Fallas of Valencia” as study case

Daily consumption of the investigated drugs of abuse in 2014 in the influent from the WWTPs in the city of Valencia during Fallas 2014.

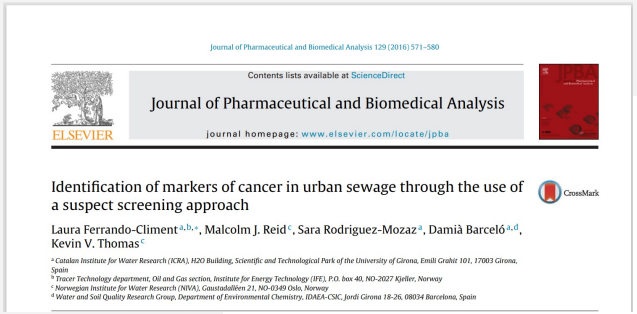




Bottom-up approach



BIOMARKERS IDENTIFICATION



Journal of Pharmaceutical and Biomedical Analysis 129 (2016) 571–580

Contents lists available at ScienceDirect

Journal of Pharmaceutical and Biomedical Analysis

journal homepage: www.elsevier.com/locate/jpba

Identification of markers of cancer in urban sewage through the use of a suspect screening approach

Laura Ferrando-Climent[a,b,*], Malcolm J. Reid[c], Sara Rodriguez-Mozaz[a], Damià Barceló[a,d], Kevin V. Thomas[c]

[a] Catalan Institute for Water Research (ICRA), H2O Building, Scientific and Technological Park of the University of Girona, Emili Grahit 101, 17003 Girona, Spain
[b] Tracer Technology department, Oil and Gas section, Institute for Energy Technology (IFE), P.O. box 40, NO-2027 Kjeller, Norway
[c] Norwegian Institute for Water Research (NIVA), Gaustadalléen 21, NO-0349 Oslo, Norway
[d] Water and Soil Quality Research Group, Department of Environmental Chemistry, IDAEA-CSIC, Jordi Girona 18-26, 08034 Barcelona, Spain

Suspect ion list

a) PACs included in therapy chosen at NORPD database
b) Metabolites and biomarkers which are related with therapy chosen (simulated by Metabolizer or from literature).

More than 1420 compounds

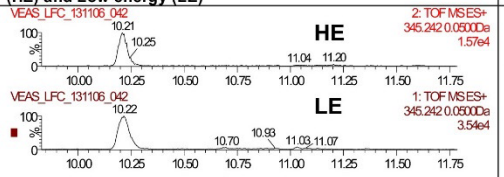
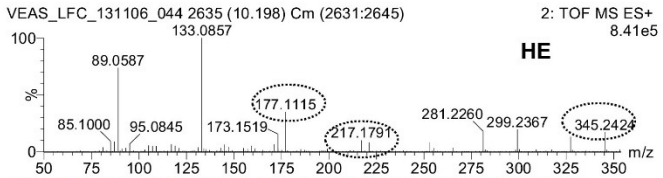
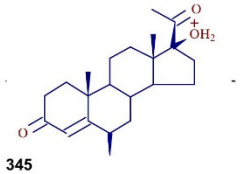
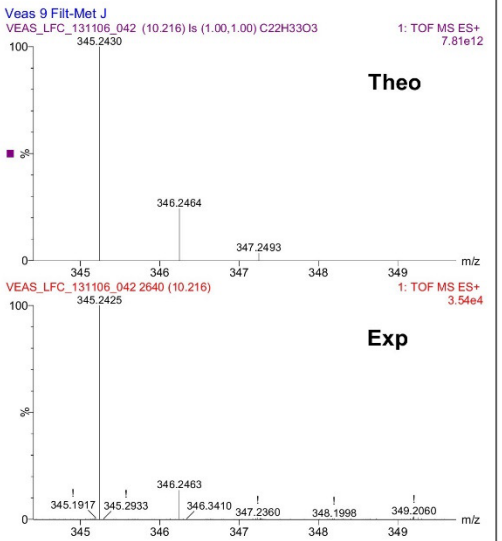
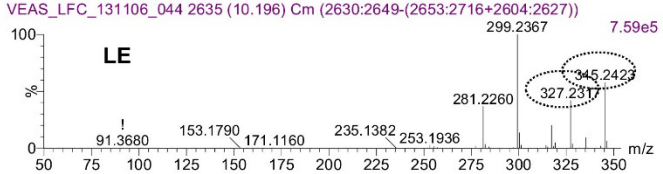
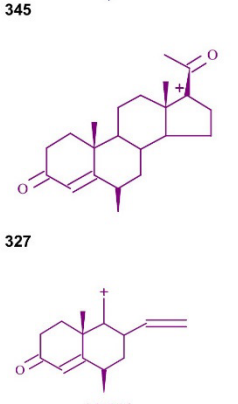
c) Restriction criteria:
- Prescribed in 2013, only in Oslo city and for both sexes.
- DDD (defined daily dose) becomes in detectable concentrations in the input of WWTPs (based on predicted concentrations)

About 600 compounds

d) Limited to those compounds able to be analyzed by:
- LC-HRMS
- Positive Ionization mode
- ESI source
- Automatic solid phase extraction by disk sorbent (using hydrophilic-lipophilic balance sorbent)

Pre-analytical criterion
List of more than 300 compounds

Mass spectrometry criterion for Megestrol identification:

Name	i) XIC at 345.2430 m/z from TOF Full scan at high energy (HE) and Low energy (LE)	ii) TOF MS/MS spectrum at high energy (HE) and Low energy (LE) at 345.2430 m/z	iv) Mass Fragments Suggested
MDG			 345
	iii) Theoric Isotopic Pattern vs. Experimental Isotopic Pattern of C22H33O3 		 327 217 177

Journal of Chromatography A, 1461 (2016) 98–106

Contents lists available at ScienceDirect

Journal of Chromatography A

journal homepage: www.elsevier.com/locate/chroma

Analysis of psychoactive substances in water by information dependent acquisition on a hybrid quadrupole time-of-flight mass spectrometer

María Jesús Andrés-Costa[a,*], Vicente Andreu[b], Yolanda Picó[a]

[a] Environmental and Food Safety Research Group (SAMA-UV), Desertification Research Centre CIDE (CSIC-UV-GV), Faculty of Pharmacy, University of Valencia. Burjassot, Valencia, Spain

[b] Landscape Chemistry and Environmental Forensics Group, CIDE (CSIC-UV-GV), Moncada, Valencia, Spain

Identification of metabolites and transformation products of drugs of abuse

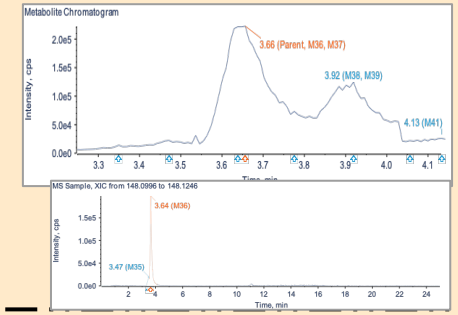
- PI+

- Metabolite Pilot
- Chemspider
- Metlin database

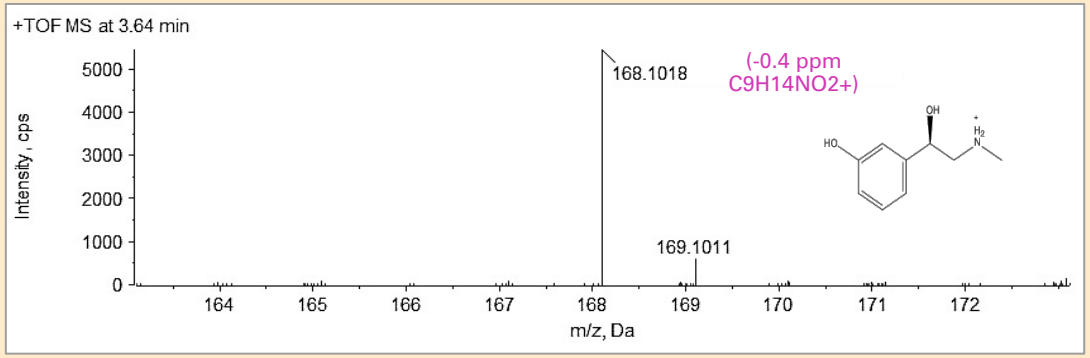
Suspect screening/Identification metabolites

Identification of an EPH metabolite B) MS and C) MS/MS formed by demethylation and oxidation obtained using the software Metabolite Pilot 2.0.

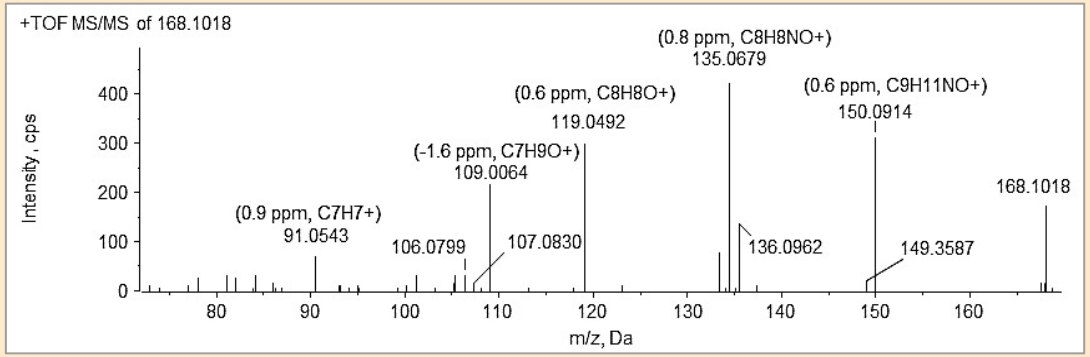
Peak ID	Name	Formula	m/z	ppm	R.T. (min)	Peak Area	% Area	% Score
M36	Loss of CH2 +Oxidation	C9H13NO2	168.1018	-0.4	3.64	1.85E+05	0.1	67.5



B)



C)



Chemical pollutants
(inorganic, pesticides, pharnaceuticals…)

Environmental Pollution

Human Population Waste

WWTP Systems:
- Influent Water
- Water Treatment
- Water Reactor
- .....
- Effluent Water

Sample Extraction Digestion

Sample GC-, LC-HRMS Non-Target Analysis

Pollutants, Metabolites, Peptides, Proteins,

Multi- and Megavariate data

Chemometric data analysis methods

Profiling Quali and Quantitative Information Interpretation Summary

Environmental and Health Risk Assessment

Biological organisms waste

Detection of large molecules

Science of the Total Environment 747 (2020) 141145

Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

Discovery of large molecules as new biomarkers in wastewater using environmental proteomics and suitable polymer probes

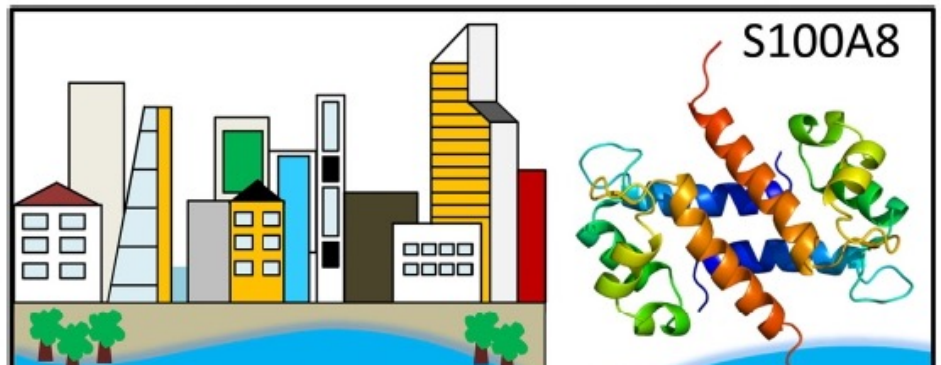
M. Carrascal [a], J. Abian [a,*], A. Ginebreda [b], D. Barceló [b,c]

[a] Proteomics Laboratory CSIC/UAB, Institute of Biomedical Research of Barcelona, Spanish National Research Council (IIBB-CSIC/IDIBAPS), Rosellón 161, E-08036 Barcelona, Spain
[b] Institute of Environmental Assessment and Water Studies (IDAEA-CSIC), Department of Environmental Chemistry, Jordi Girona 18-26, 08034 Barcelona, Spain
[c] Catalan Institute for Water Research (ICRA), Emili Grahit 101, Parc Científic i Tecnològic de la Universitat de Girona, Edifici H2O, 17003 Girona, Spain

HIGHLIGHTS

- Large-scale proteomic analysis of sewage and treated water.
- Proteomics for Wastewater Based Epidemiology.
- Profiling of human proteins in sewage waters for WBE.
- Human uromodulin, α-amylase, and S100A8 identified in urban sewage.

GRAPHICAL ABSTRACT



Objectives: Environmental Proteomics-WBE

- **To design a probe for the evaluation of synthetic organic matter degradation in natural and engineered systems based on a previously selected polymer.**

  Rivas et al. **STOTEN**, (2016), 566–567:27–33

- **To study the degradation patterns of the polymer and its transformation products by MALDI-TOF MS IMAGING and UPLC-HR-MS.**

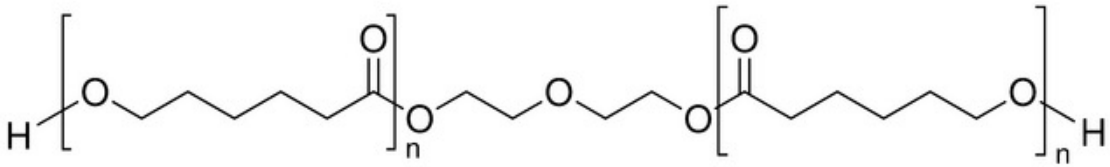
- **To test the polymer probe in the different aquatic environments found in a WWTP :**

  - **Specifically, to examine chemical degradation and microbial community characterization in the influent flow (IN), in the anaerobic/anoxic bioreactor (ANA) and in the oxygen aeration tank (AER).**

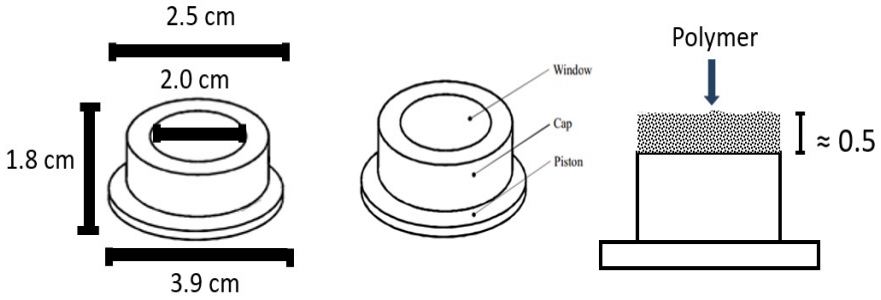
- **To characterize the taxonomical composition of microbial communities present in those aquatic environments, comparing the free-living with the polymer-attached ones.**

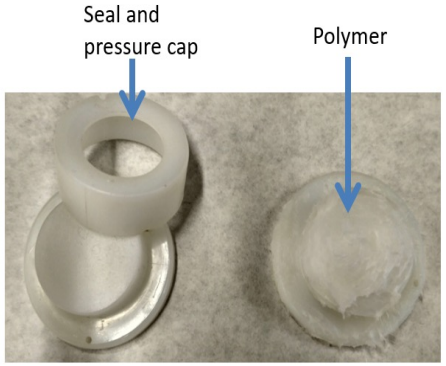
- **To perform Proteomic discovery of the key peptides and related pollution tracers**

Methods: Experimental setup

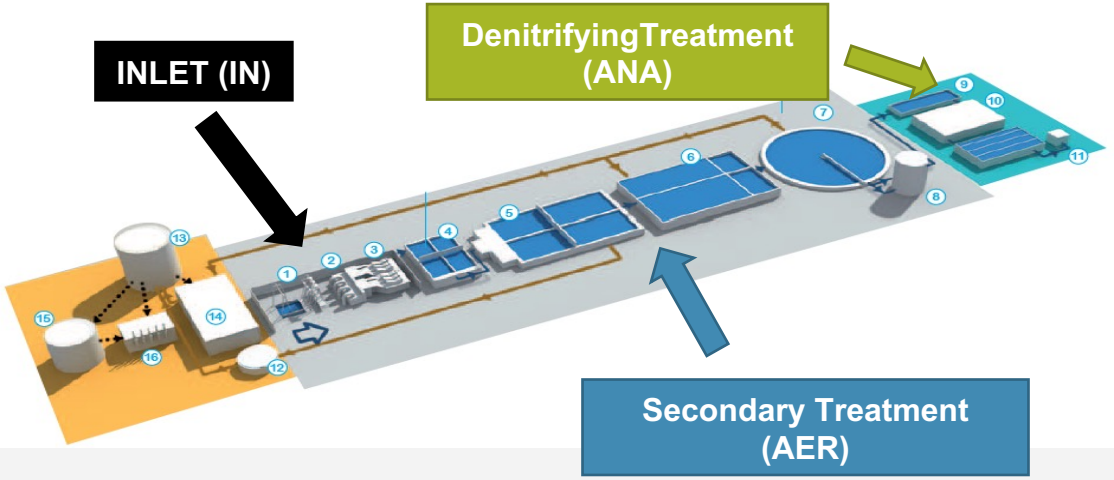


POLYCAPROLACTONEDIOL 1250

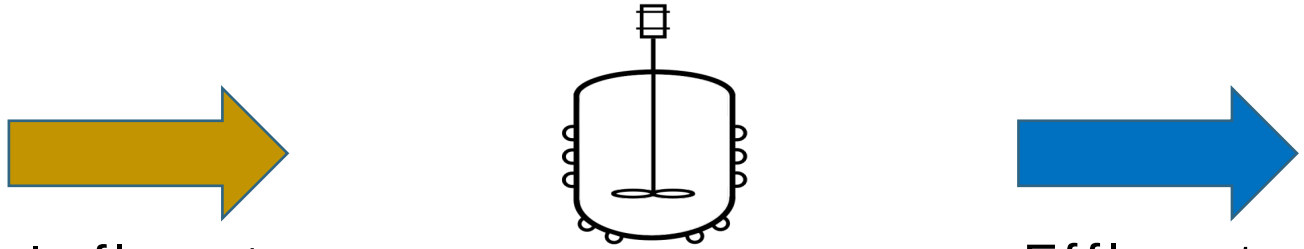




3 replicates per site
5 days + 1 blank (sterile conditions)
5 WWTPs



Water samples from 3 different sites of the Gavà-Viladecans (Barcelona, Spain) wastewater treatment plant were analyzed:



Three devices were placed per sampling point for 11 days

↓

Polymer surfaces were cut and purified

↓ Trypsin digestion

Orbitrap XL

Surface slice
≈ 400 mg

500 µl 2% SDS,
50 mM DTT
75 mM Tris-HCl

Thermomix

30 min 99 ºC
800 rpm

rt 40 min

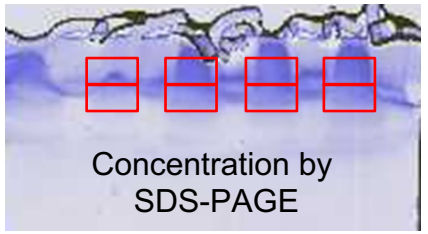
Supernatant

Bullet Blender
250 µl Zr Silicate beads
3 min at 8

centrifuge 7 min

Supernatant
300 µl

150 µl



3 sites
x
3 replicates
x
2 band sections

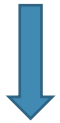
In-gel trypsin digestion

Mix sections

9 runs
Orbitrap
LC-MS/MS

LC-MS/MS SEARCH RESULTS

446 peptides (Proteome Discoverer)
678 peptides (PEAKS)



195 protein groups (Proteome Discoverer)
501 protein groups (PEAKS)

175 protein names (PEAKS)

258 bacterial species (PEAKS)

SEARCH PARAMS

Proteome Discoverer
tryptic
2 miss-cleavages
20 ppm prec/0.8 Da frag
FDR 0.1%

PEAKS
(includes de novo search)
tryptic
2 miss-cleavages
20 ppm prec/0.8 Da frag
FDR 0.1%

DATABASE

Human + Bacteria
Uniprot

Most Abundant Proteins

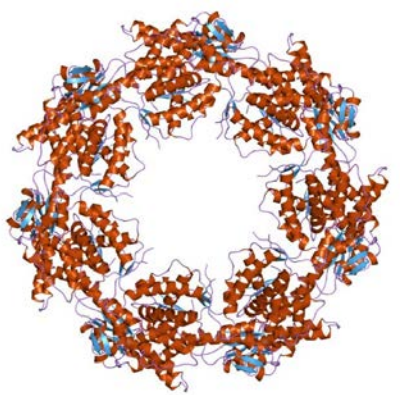
PEAKS search

BACTERIAL	
name	abundance
60 kDa chaperonin	1175
Elongation factor Tu	1152
ATP synthase subunit beta	415
60 kDa chaperonin 2	285
Elongation factor Tu 2	148
ATP synthase subunit alpha	129
60 kDa chaperonin 1	126
Elongation factor Tu 1	89
Malate dehydrogenase	74
Phosphoglycerate kinase	65
RNA-binding protein Hfq	64
Glyceraldehyde-3-phosphate dehydrogenase	52
Enolase	50
Major outer membrane lipoprotein	46
ATP synthase subunit c	42
60 kDa chaperonin 4	41
60 kDa chaperonin 3	39
Outer membrane protein Omp38	36
60 kDa chaperonin 5	34
K(+)-insensitive pyrophosphate-energized proto	34
30S ribosomal protein S5	33
Thioredoxin 1	33
Glycerol kinase	31
Elongation factor Tu-A	31
ATP synthase subunit alpha 1	31
50S ribosomal protein L17	27
50S ribosomal protein L29	25
Elongation factor Tu-B	25
Phosphoenolpyruvate carboxykinase [GTP]	25
Acetoacetyl-CoA reductase	24
30S ribosomal protein S2	24
60 kDa chaperonin 6	22
50S ribosomal protein L5	19
50S ribosomal protein L19	19
30S ribosomal protein S7	16
50S ribosomal protein L7/L12	15

abundance = int(100000 * peptides / mass)

HUMAN	
name	abundance
Keratin type II cytoskeletal 1	84
Chymotrypsin-like elastase family member 3A	74
Keratin type II cytoskeletal 2 epidermal	68
Keratin type I cytoskeletal 10	67
Keratin type I cytoskeletal 9	56
Keratin type II cytoskeletal 5	40
Neutrophil defensin 3	39
Keratin type I cytoskeletal 14	34
Keratin type II cytoskeletal 6A	31
Chymotrypsin-C	27
Keratin type I cytoskeletal 16	27
Keratin type II cytoskeletal 6B	26
Histone H4	26
Small proline-rich protein 2E	25
Chymotrypsin-like elastase family member 3B	23
Protein S100-A8	18
Keratin type II cytoskeletal 2 oral	15
Histone H2B type 1-K	14
Keratin type II cytoskeletal 75	13
Lysozyme C	12
Keratin type II cytoskeletal 79	12
Keratin type II cytoskeletal 78	10
Keratin type II cytoskeletal 1b	9
Defensin-5	9
Keratin type II cytoskeletal 4	8
Dermcidin	8
Keratin type II cytoskeletal 73	8
Keratin type I cytoskeletal 13	8
Trypsin-2	7
Serum albumin	7

60 KDa chaperonin
(GroEL)



GroEL belongs to the chaperonin family of molecular chaperones, and is found in a large number of bacteria. It is required for the proper folding of many proteins. To function properly, GroEL requires the lid-like cochaperonin protein complex GroES.

In eukaryotes the proteins Hsp60 and Hsp10 are structurally and functionally nearly identical to GroEL and GroES, respectively.

ATP synthase

ATP synthase is an enzyme that creates the energy storage molecule adenosine triphosphate (ATP). ATP is the most commonly used "energy currency" of cells for all organisms. It is formed from adenosine diphosphate (ADP) and inorganic phosphate (Pi).

E. coli ATP synthase is the simplest known form of ATP synthase, with 8 different subunit types.

elongation factor Tu

In bacteria, elongation factor Tu plays a central role during the selection of the correct amino acids throughout the elongation phase of translation.

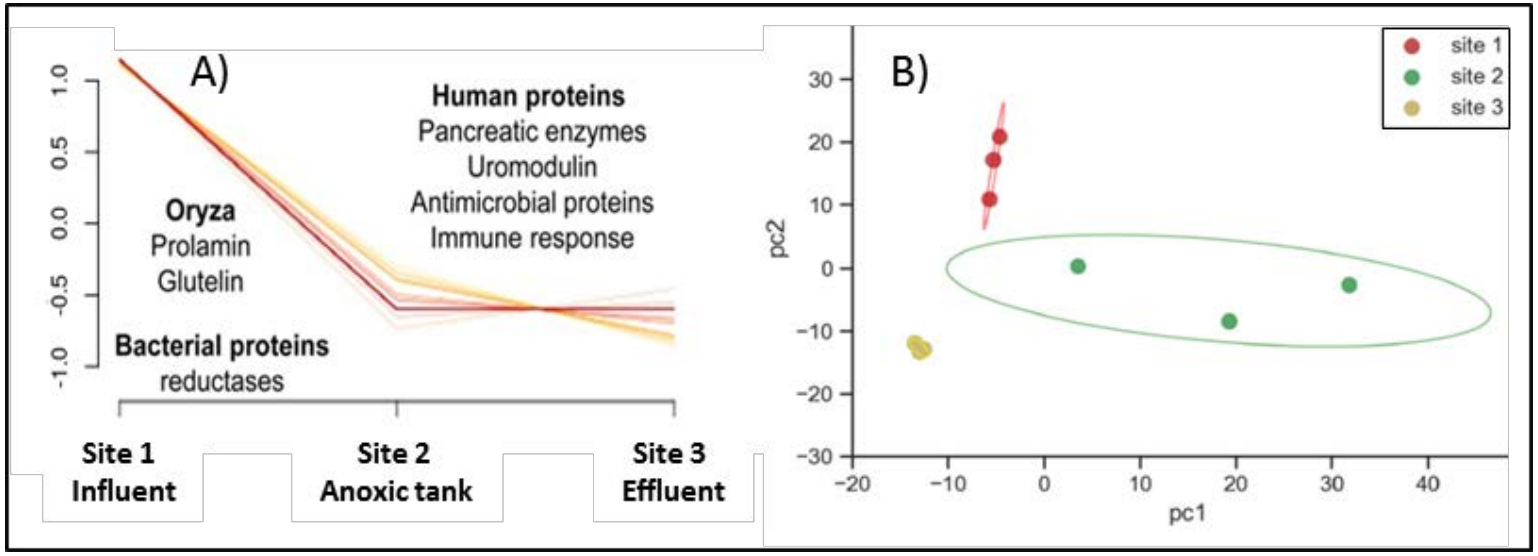
The amount of EF-Tu in the cell is equimolar to that of tRNA, while the total number of EF-Tu molecules is 8–14 times the number of ribosomes depending on growth conditions.2

wikipedia

ASSESSMENT OF HEALTH STATUS, HABITS, AND BEHAVIORS OF THE POPULATION THROUGH WASTEWATER-BASED EPIDEMIOLOGY (WBE) BASED ON PROTEINS.

M.Carrascal, A. Ginebreda, J. Abián, D. Barceló. IIBB/IDAEA-CSIC.

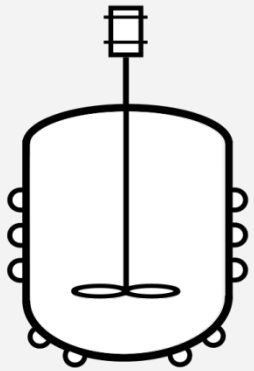
Characterization of human protein biomarkers in sewage waters: presence in urban sewage waters of proteins from diverse origins, including human proteins such as uromodulin, α-amylase, and S100A8, which have been proposed as health → **Wastewater Based Epidemiology (WBE)**.



(Carrascal et al. Stoten,2020 747:141145)

Gavà-Viladecans WWTP

Influent water 1,2,3



Anoxic reactor 4,5,6

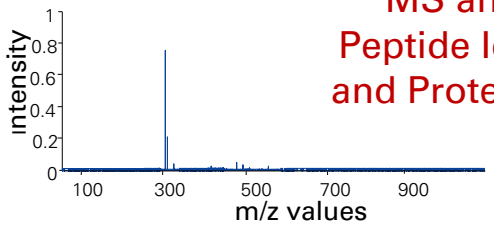
Effluent water 7,8,9

Peptide Analysis

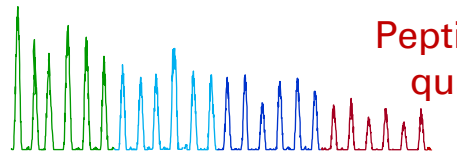
Sample extraction and protein digestion (tripsin)

Orbitrap XL

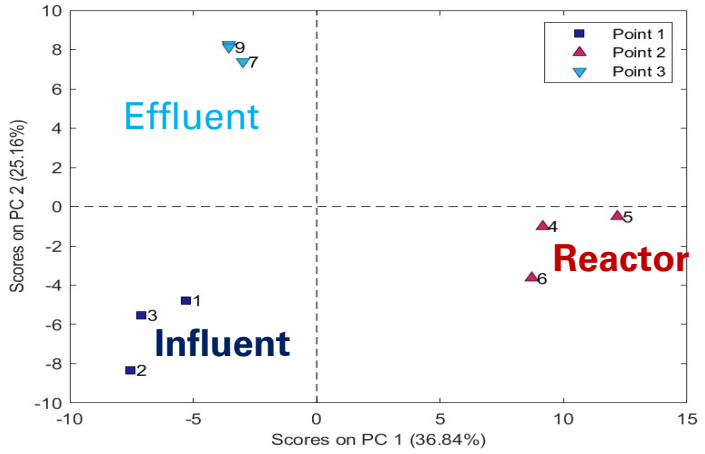
Chemometric Data Analysis



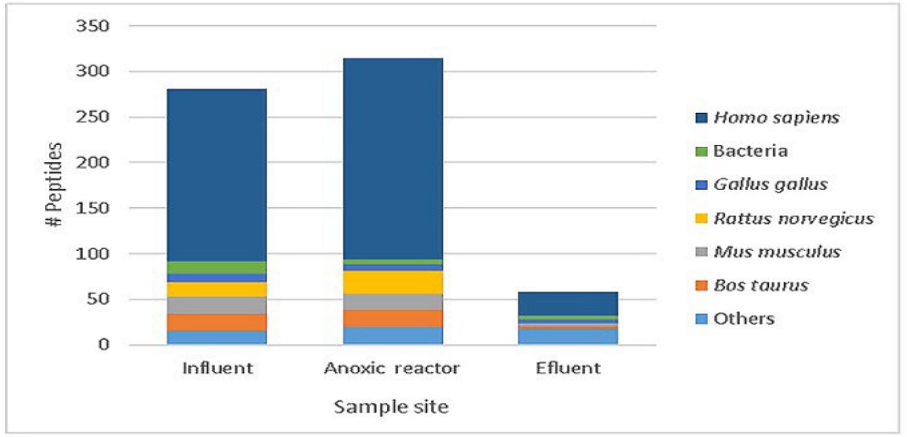
MS and MS/MS
Peptide Identification
and Protein Discovery

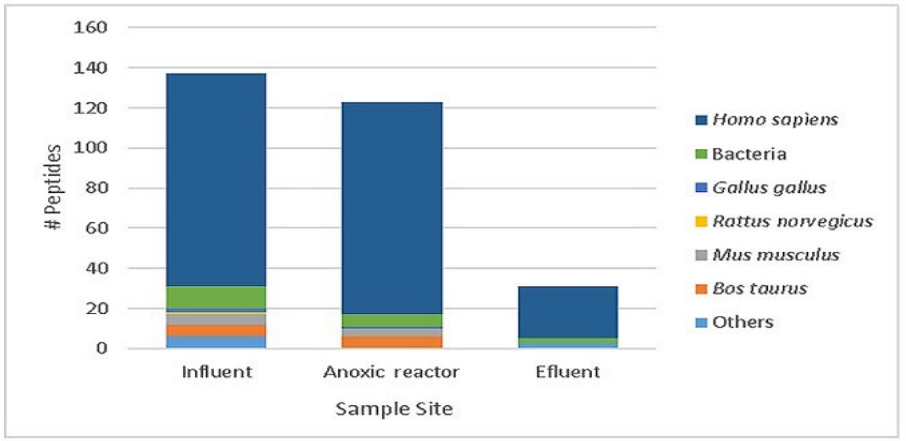


Peptide relative quantitation



Protein assignation

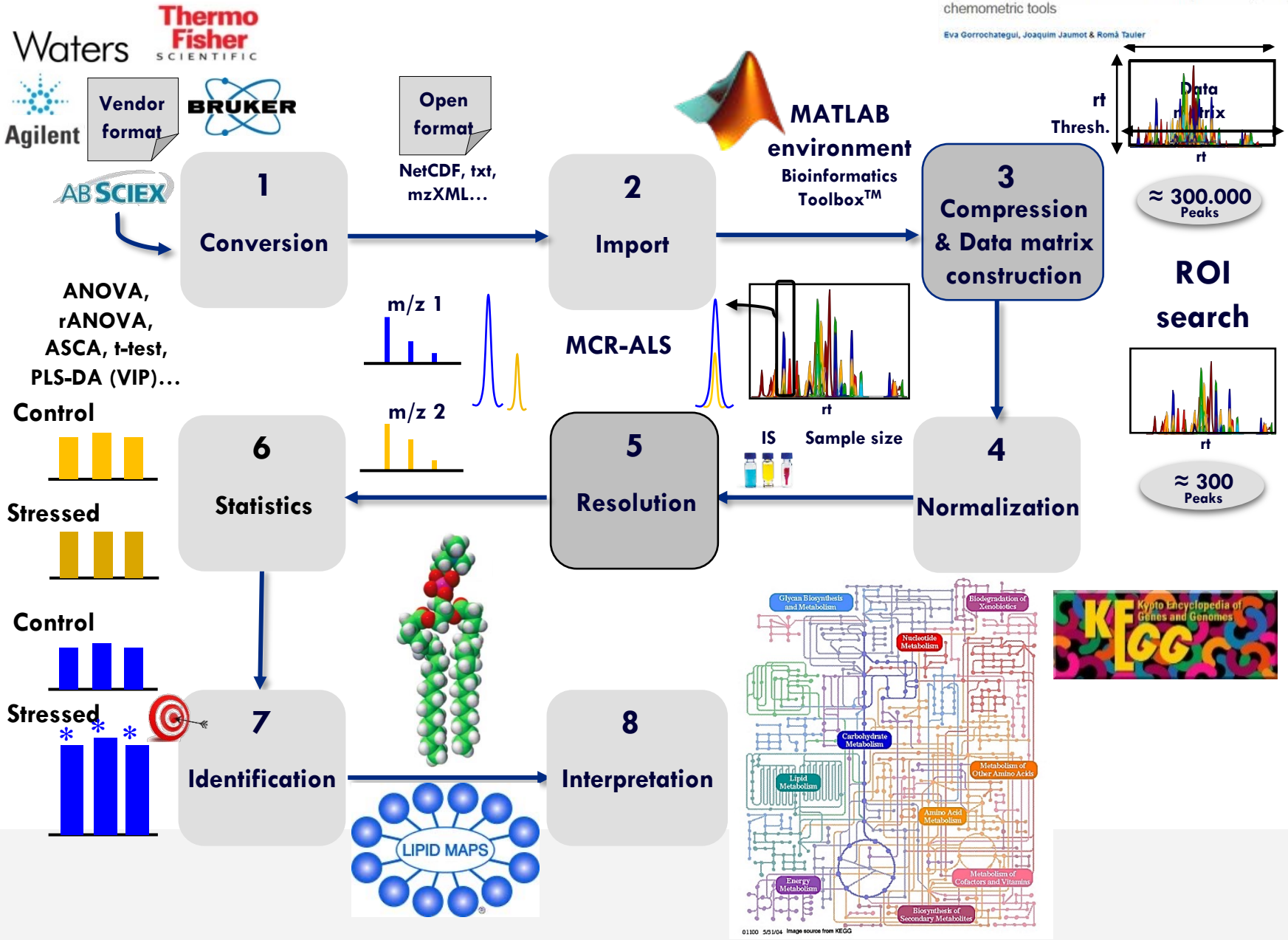




Influent Reactor Effluent

Data analysis (chemometrics) workflow

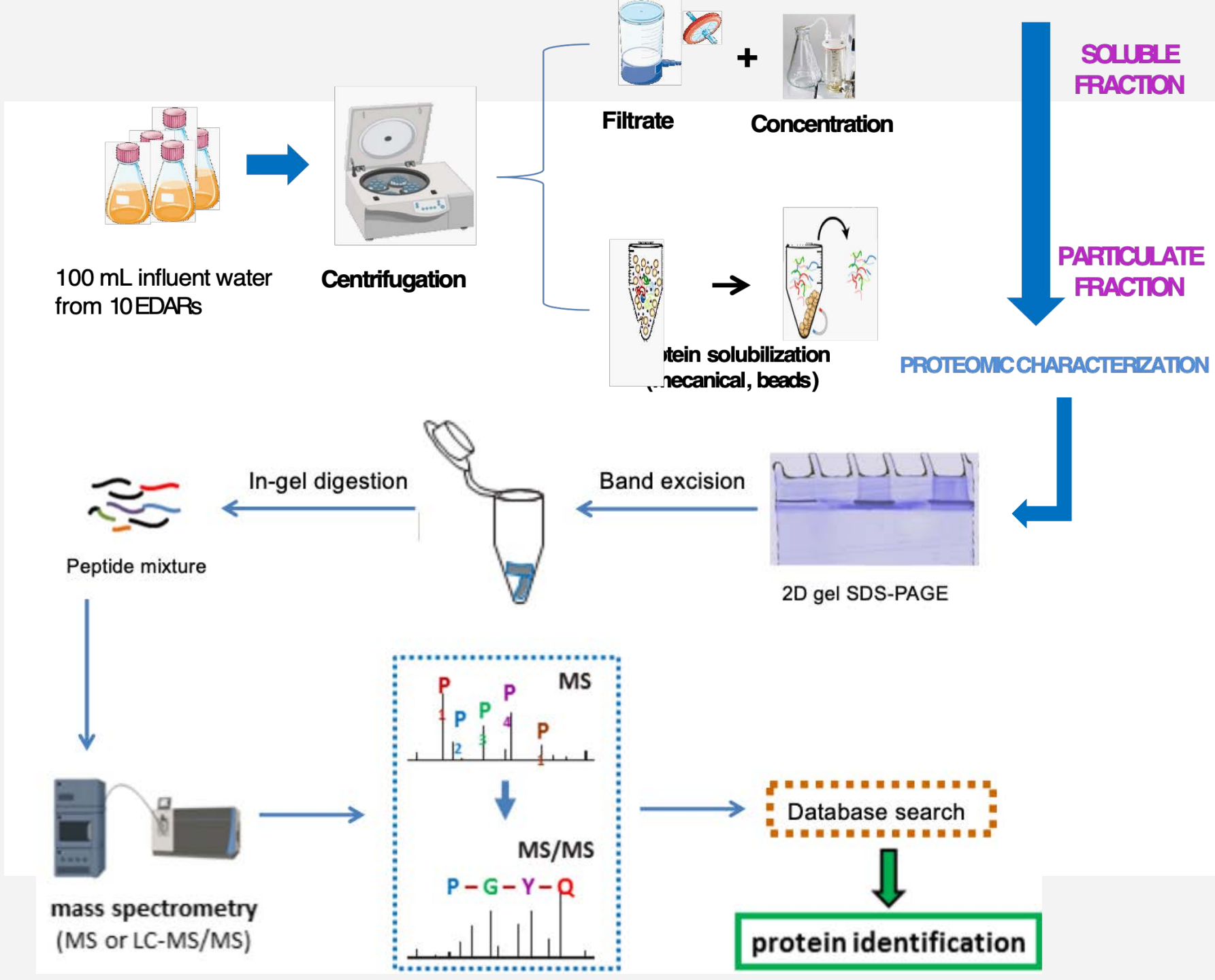
https://www.nature.com/protocolexchange/protocols/4347



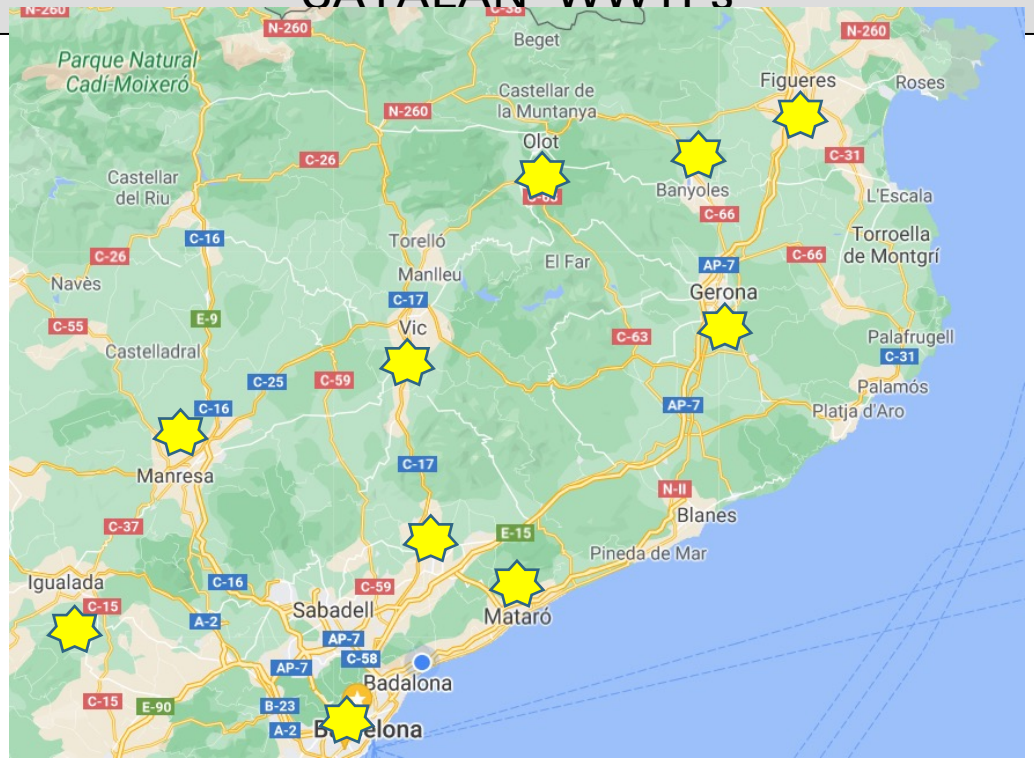
ROIMCR-Regions of Interest-Multivariate Curve Resolution

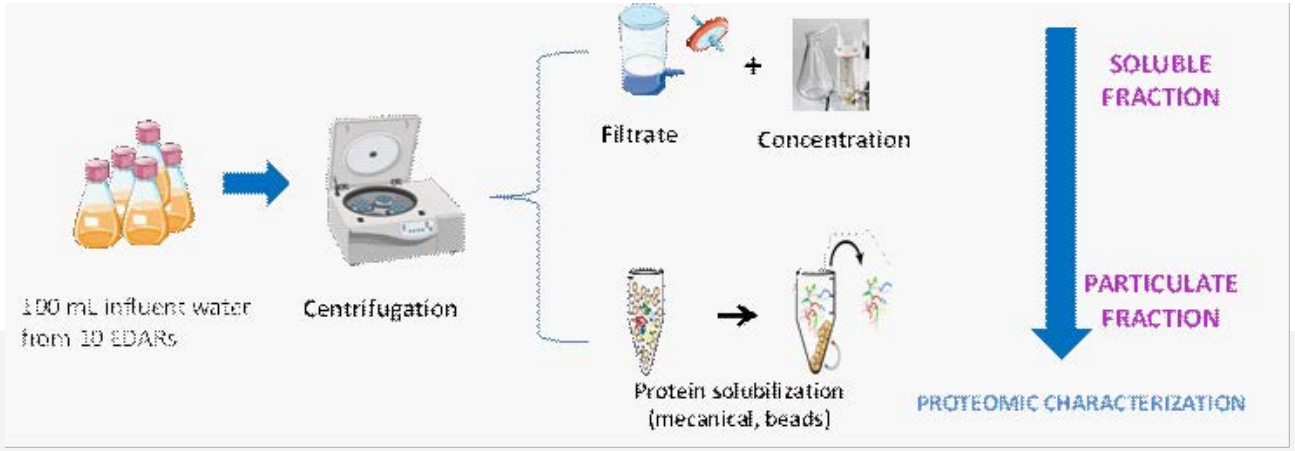
50% of the m/z MS1 spectra from ROIMCR resolution matched MS1 signals- MS2 were taken. When no MS2 fragments were present, no identification by-Protein Discovery 523 Peptides corresponding to 35 different proteins from different eukaryotic species: Human, Chicken, Rat or Mouse, bacterial species

Proteins	Protein name	Organism name	Time 1	Time 2	Time 5
P35908	Keratin, type II cytoskeletal 2 epidermal	Homo sapiens	7	10	5
Q6IFZ6	Keratin, type II cytoskeletal 1b	Mus musculus	7	9	5
P04264	Keratin, type II cytoskeletal 1	Homo sapiens	12	17	6
Q981J9	60 kDa chaperonin 5	Mesorhizobium japonicum	1	1	1
B5YJN3	60 kDa chaperonin	Thermodesulfovibrio yellowstonii	1	1	1
A1K436	60 kDa chaperonin 1	Azoarcus sp.	1	1	1
Q5P7G2	60 kDa chaperonin	Aromatoleum aromaticum	1	1	1
A4G837	60 kDa chaperonin	Herminiimonas arsenicoxydans	1	1	1
Q1H4F2	60 kDa chaperonin	Methylobacillus flagellatus	1	1	1
A4SZV4	60 kDa chaperonin	Polynucleobacter asymbioticus	1	1	1
Q3A0V2	60 kDa chaperonin	Pelobacter carbinolicus	1	1	1
P13645	Keratin, type I cytoskeletal 10	Homo sapiens	1	9	2
P04259	Keratin, type II cytoskeletal 6B	Homo sapiens	2	4	0
A8EV70	ATP synthase subunit beta	Arcobacter butzleri	0	1	0
Q99895	Chymotrypsin-C	Homo sapiens	0	6	0
P01876	Immunoglobulin heavy constant alpha 1	Homo sapiens	0	7	2
Q6FF97	Elongation factor Tu	Acinetobacter baylyi	0	4	0
A3M1F6	Elongation factor Tu	Acinetobacter baumannii	0	4	0
P09093	Chymotrypsin-like elastase family member 3A	Homo sapiens	0	14	0
A5FLS1	ATP synthase subunit beta	Flavobacterium johnsoniae	0	1	0
A1ALL7	ATP synthase subunit beta 1	Pelobacter propionicus	0	1	0
Q82XP8	ATP synthase subunit beta	Nitrosomonas europaea	0	1	0
Q9Y6R7	IgGFc-binding protein	Homo sapiens	0	1	0
Q14533	Keratin, type II cuticular Hb1	Homo sapiens	0	0	1
P78385	Keratin, type II cuticular Hb3	Homo sapiens	0	0	1
P78386	Keratin, type II cuticular Hb5	Homo sapiens	0	0	1
O43790	Keratin, type II cuticular Hb6	Homo sapiens	0	0	1
A5A6M5	Keratin, type I cuticular Ha1	Pan troglodytes	0	0	1
O76009	Keratin, type I cuticular Ha3-I	Homo sapiens	0	0	1

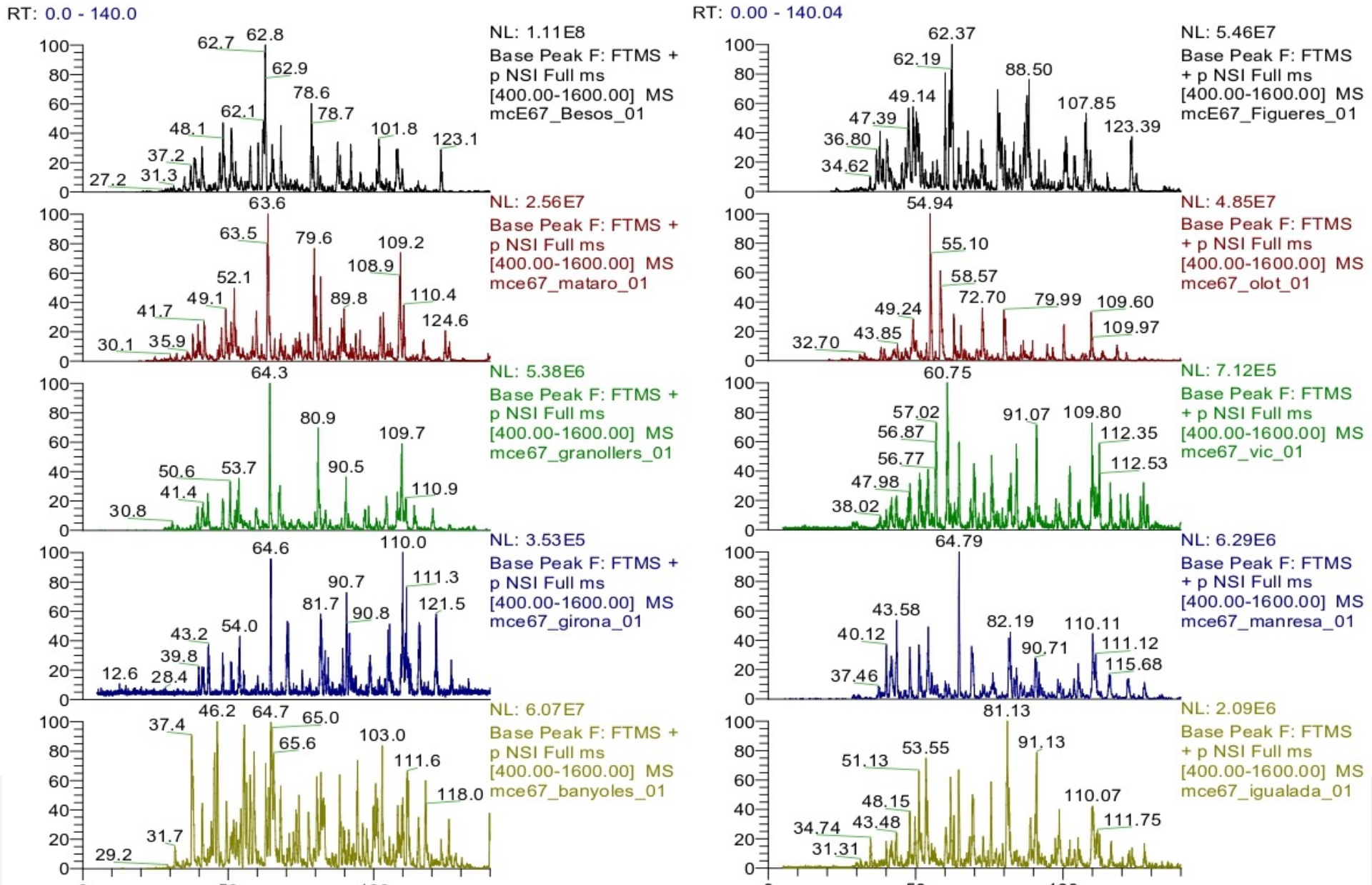

SOLUBLE FRACTION
Filtrate
+
Concentration
100 mL influent water from 10 EDARs
Centrifugation
PARTICULATE FRACTION
tein solubilization
necanical, beads)
PROTEOMIC CHARACTERIZATION
In-gel digestion
Band excision
Peptide mixture
2D gel SDS-PAGE
MS
MS/MS
P – G – Y – Q
mass spectrometry
(MS or LC-MS/MS)
Database search
protein identification

WASTEWATER-BASED EPIDEMIOLOGY (WBE) BASED ON PROTEINS IN 10 CATALAN WWTPs





WASTEWATER-BASED EPIDEMIOLOGY (WBE) BASED ON PROTEINS IN 10 CATALAN WWTPs.



MALDI-TOF of Besos and Olot WWTP

10 (Besos)peaks and 7 (Olot(peaks) match the most abundant proteins

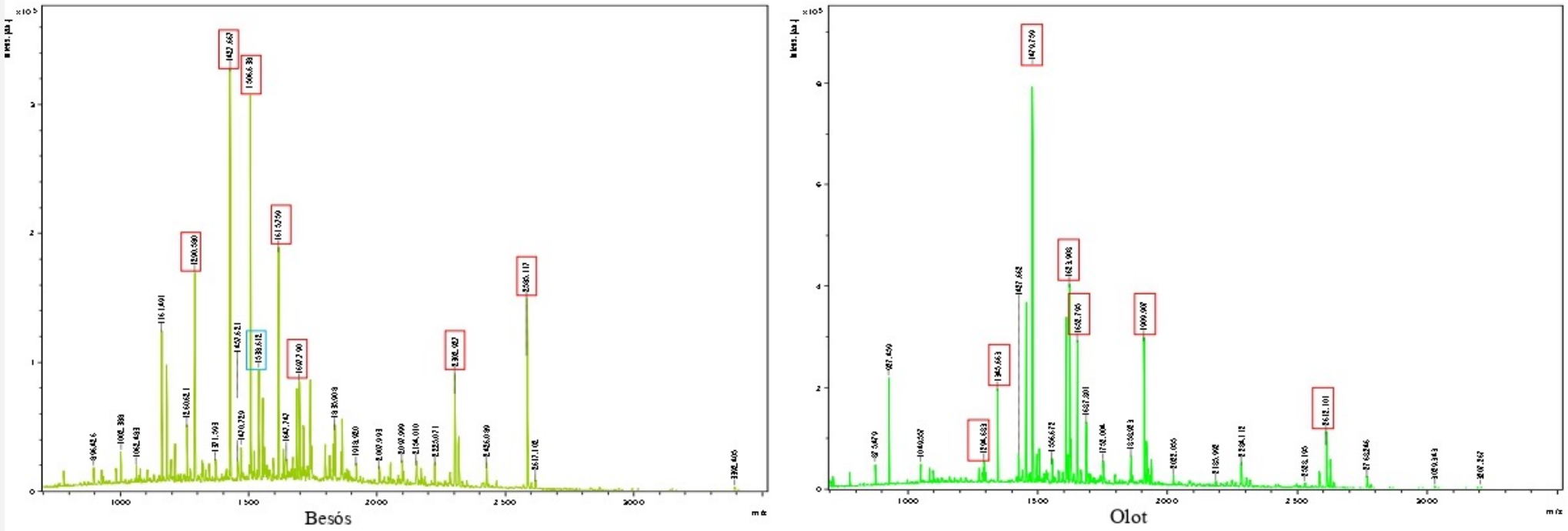


Figure 8. *The spectra of MALDI – ToF of Besós and Olot. Each number represents the molecular weight of each corresponding peptide, the height of peaks indicates the abundance of the corresponding peptide detected in the sample.*

LC/MS/MS of Besos and Olot WWTP: Confirmation of the Proteins detected by MALDI-TOF

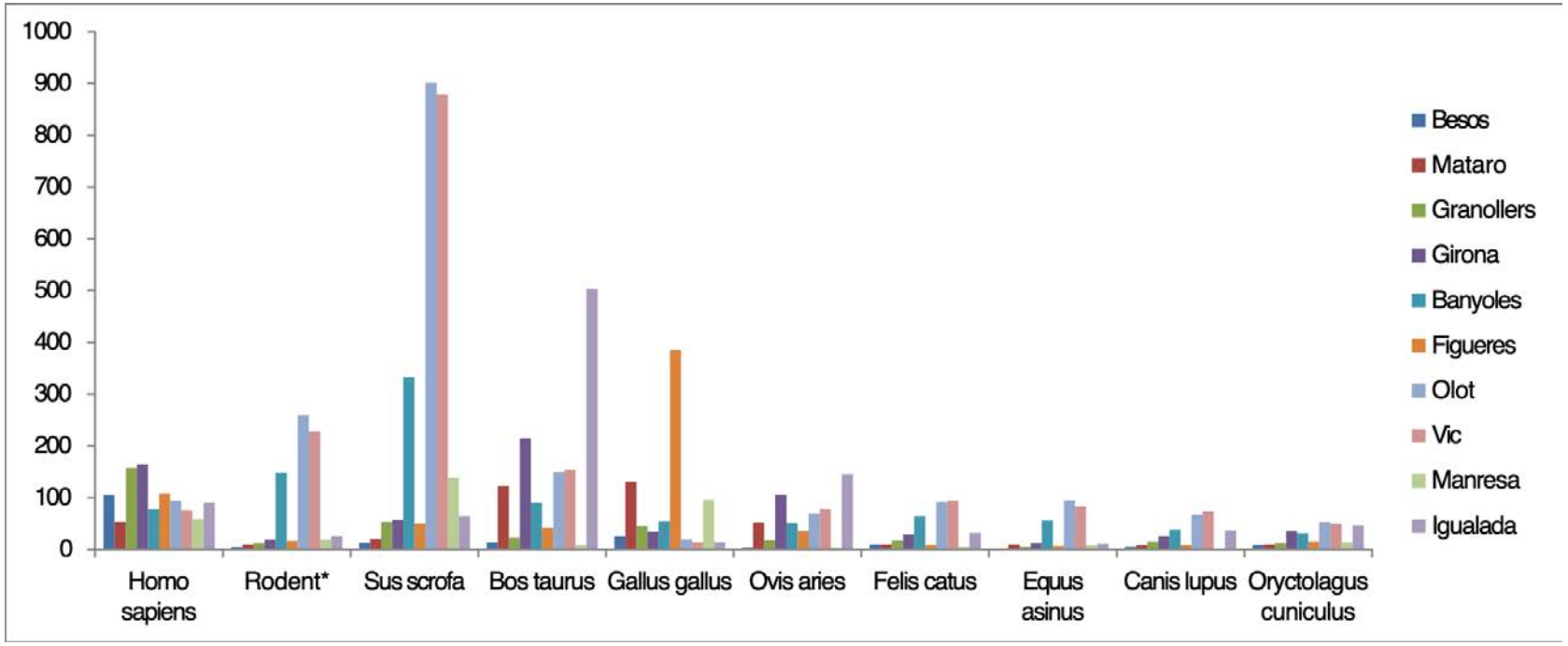
Table 4. *The analytical results of LC – MS/MS of Besós (top) and Olot (bottom). PSMs indicate the abundance of the corresponding proteins detected in the sample.*

Description	Score	Coverage	# Proteins	Unique Peptid	# Peptides	# PSMs
Pancreatic alpha-amylase OS=Homo sapiens C	1689.54	73.97	3	5	34	427
Alpha-amylase 1 OS=Homo sapiens OX=9606	1572.32	72.80	3	7	34	395
Alpha-amylase 2B OS=Homo sapiens OX=960(	1375.19	72.80	4	1	33	361
Maltase-glucoamylase, intestinal OS=Homo sa	532.97	36.51	3	48	52	152
Albumin OS=Homo sapiens OX=9606 GN=ALI	390.23	67.16	6	29	37	107

Description	Score	Coverage	# Proteins	Unique Peptid	# Peptides	# PSMs
Albumin OS=Sus scrofa OX=9823 GN=ALB PE	1519.02	76.11	1	45	58	410
Albumin OS=Bos taurus OX=9913 GN=ALB PE	481.28	64.25	1	16	39	129
Albumin OS=Homo sapiens OX=9606 GN=ALI	454.32	67.00	1	31	38	125
Pancreatic alpha-amylase OS=Homo sapiens C	475.58	64.19	4	5	25	121
Alpha-amylase 1 OS=Homo sapiens OX=9606	451.86	64.19	3	6	25	115

WASTEWATER-BASED EPIDEMIOLOGY (WBE) BASED ON PROTEINS IN 10 CATALAN WWTPs.

Species distribution according to **albumin protein**. Presence of blood from main species (pigs, chicken, cows) in wastewater-illegal discharges to the WWTP . Sampling December 2020.



WASTEWATER-BASED EPIDEMIOLOGY (WBE) BASED ON PROTEINS IN 10 CATALAN WWTPs: IMMUNOGLOBULIN.

Immunoglobulin in feces : tentative biomarker for people infected by SARS-CoV-2 or vaccinated (1 Million vaccinated in Catalonia April 2021) or bacteria, immunodeficiency ,myeloma

Accession	Description	Species
P01834	Immunoglobulin kappa constant OS=Homo sapiens OX=9606 GN=IGKC PE=1 SV=2 - [IGKC	Homo sapiens
P0DOX7	Immunoglobulin kappa light chain OS=Homo sapiens OX=9606 PE=1 SV=1 - [IGK_HUMAN]	Homo sapiens
P01876	Immunoglobulin heavy constant alpha 1 OS=Homo sapiens OX=9606 GN=IGHA1 PE=1 SV=	Homo sapiens
P0DOX2	Immunoglobulin alpha-2 heavy chain OS=Homo sapiens OX=9606 PE=1 SV=2 - [IGA2_HUM	Homo sapiens
P01833	Polymeric immunoglobulin receptor OS=Homo sapiens OX=9606 GN=PIGR PE=1 SV=4 - [P	Homo sapiens
P0DOY2	Immunoglobulin lambda constant 2 OS=Homo sapiens OX=9606 GN=IGLC2 PE=1 SV=1 - [	Homo sapiens
P0CG04	Immunoglobulin lambda constant 1 OS=Homo sapiens OX=9606 GN=IGLC1 PE=1 SV=1 - [	Homo sapiens
P01857	Immunoglobulin heavy constant gamma 1 OS=Homo sapiens OX=9606 GN=IGHG1 PE=1 S	Homo sapiens
A0A075B6P5	Immunoglobulin kappa variable 2-28 OS=Homo sapiens OX=9606 GN=IGKV2-28 PE=3 SV=	Homo sapiens
P01591	Immunoglobulin J chain OS=Homo sapiens OX=9606 GN=JCHAIN PE=1 SV=4 - [IGJ_HUMA	Homo sapiens
P06310	Immunoglobulin kappa variable 2-30 OS=Homo sapiens OX=9606 GN=IGKV2-30 PE=3 SV=	Homo sapiens
P01859	Immunoglobulin heavy constant gamma 2 OS=Homo sapiens OX=9606 GN=IGHG2 PE=1 S	Homo sapiens
P06312	Immunoglobulin kappa variable 4-1 OS=Homo sapiens OX=9606 GN=IGKV4-1 PE=1 SV=1 -	Homo sapiens
P01764	Immunoglobulin heavy variable 3-23 OS=Homo sapiens OX=9606 GN=IGHV3-23 PE=1 SV=	Homo sapiens
P01871	Immunoglobulin heavy constant mu OS=Homo sapiens OX=9606 GN=IGHM PE=1 SV=4 - [	Homo sapiens
P01619	Immunoglobulin kappa variable 3-20 OS=Homo sapiens OX=9606 GN=IGKV3-20 PE=1 SV=	Homo sapiens
P01782	Immunoglobulin heavy variable 3-9 OS=Homo sapiens OX=9606 GN=IGHV3-9 PE=1 SV=2	Homo sapiens
A0A075B6R9	Probable non-functional immunoglobulin kappa variable 2D-24 OS=Homo sapiens OX=9606	Homo sapiens
A0A0C4DH31	Immunoglobulin heavy variable 1-18 OS=Homo sapiens OX=9606 GN=IGHV1-18 PE=3 SV=	Homo sapiens
A0A0C4DH72	Immunoglobulin kappa variable 1-6 OS=Homo sapiens OX=9606 GN=IGKV1-6 PE=3 SV=1 -	Homo sapiens
A0A0A0MT36	Immunoglobulin kappa variable 6D-21 OS=Homo sapiens OX=9606 GN=IGKV6D-21 PE=3 S	Homo sapiens
A0A0C4DH24	Immunoglobulin kappa variable 6-21 OS=Homo sapiens OX=9606 GN=IGKV6-21 PE=3 SV=	Homo sapiens
A0A0B4J2H0	Immunoglobulin heavy variable 1-69D OS=Homo sapiens OX=9606 GN=IGHV1-69D PE=1 S	Homo sapiens
A0A075B6H9	Immunoglobulin lambda variable 4-69 OS=Homo sapiens OX=9606 GN=IGLV4-69 PE=1 SV=	Homo sapiens
P01624	Immunoglobulin kappa variable 3-15 OS=Homo sapiens OX=9606 GN=IGKV3-15 PE=1 SV=	Homo sapiens

WBE of SARS-CoV-2 in India using PCR by, Manish Kumar,Indian Institute of Technology,Gandhinagar, Gujarat, India , IDAEA-CSIC,ICRA, et al. *Chemical Engineering Journal*, 425 (2021)130635.

Can testing waste water help detect coronavirus spread in community?

Joint study by IIT-Gn, GBRC and GPCB to study spread of coronavirus infection among communities in containment zones via presence of genetic material of virus in wastewater

Brendan.Dabhi
@timesgroup.com
TWEETS @BrendanMIRROR

Testing for traces of the genetic material of coronavirus in sewage wastewater may be the next step in identifying transmission and conducting a localised study at a hotspot in Ahmedabad.

Researchers from the Indian Institute of Technology in Gandhinagar (IIT-Gn) are conducting a joint study with the Gujarat Biotechnology Research Centre (GBRC) and the Gujarat Pollution Control Board (GPCB) on the presence of the SARS-CoV-2 virus released into sewage through faeces and other bodily waste of infected persons. Measurement of the amount of genetic material of the virus present therein can help to quantify transmission of infection in the community.

Dr Manish Kumar Singh, Assistant Professor of Earth Sciences at IIT-Gn is leading the study with his students. He said, "The purpose of testing waste water is to find out how much of a certain population is infected by coronavirus. We can thus estimate how many people may be infected in a community. From a certain number of virus copies, we can estimate how many people could be infected."

A similar research is underway in France, Sweden and closer home in Delhi.

Dr Singh said lack of resources and immense population may not allow mass testing of people and this method of community testing through waste water could be a viable alternative. He said, "We cannot test everyone in India. So, we must find ways to do community testing in which this method may be of help."

Team of experts collecting samples

The identification of green, orange and red zones will become easier through this process, claimed the researcher. The study could also help ascertain whether spread of the coronavirus has stopped or not in the population.

There are three parts to this study, each one carried out by a different agency. While the GPCB will collect samples from infected and control groups, the testing of these samples will be carried out at GBRC through the RT-PCR technique. The results will then be studied, quantified and analysed by the team at IIT-Gn.

How the testing is done

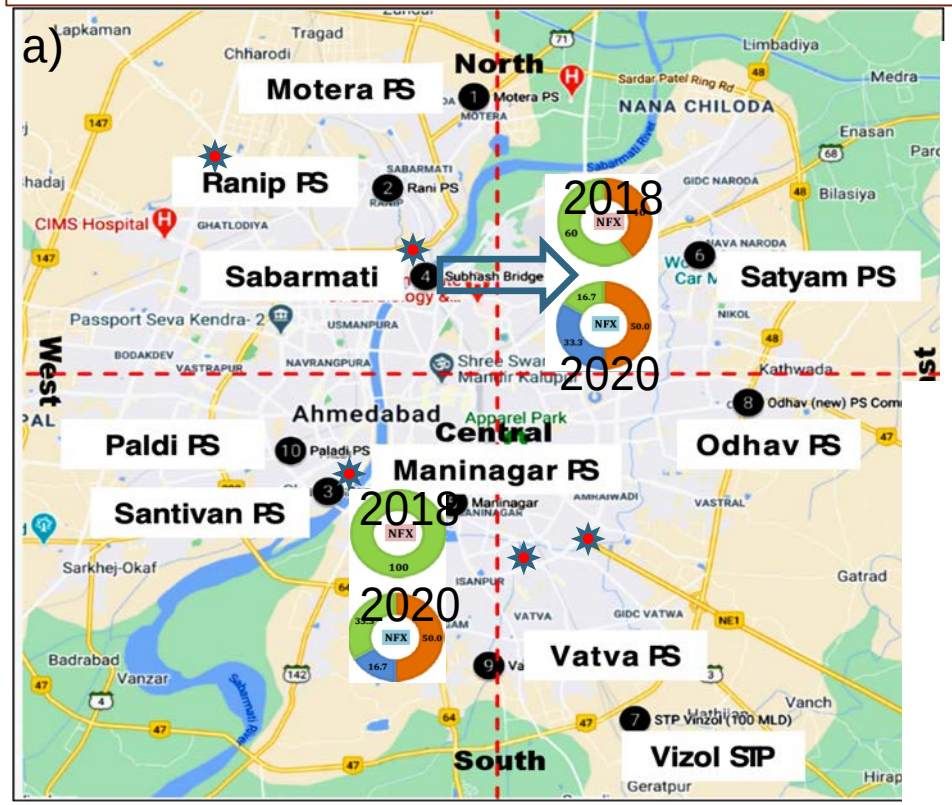
Initially, infected samples are taken from the Ahmedabad Civil Hospital's 106 MLD Sewage Treatment Plant (STP). Control samples are being taken from Zydus Hospital as it is a non-Covid facility so far.

On the process of identifying coronavirus in wastewater, Dr Singh said, "From samples, we will make copies of the genetic material and run it through RT-PCR. We will do a composite sampling over a week for an area to be sure of the results. It also depends on how much MLD sewage water is there. First water sample will be filtered through different methods, catalyst added to filter the sample and extract RNA. We will then polymerase it through RT-PCR and qRT-PCR. We match it through the genetic library to find out the sequencing." The testing of samples will be done at GBRC as it has ICMR approval.

WBE can definitely help in city zonation for effective COVID-19 pandemic preparedness powered by early warning !!

What about effects of population density and condition of sewer systems?

a)



Location from which samples tested for a

Location from which samples tested for S

b)

SARS-CoV-2 Genome Concentration

Journal of Hazardous Materials 416 (2021) 126125

Contents lists available at ScienceDirect

Journal of Hazardous Materials

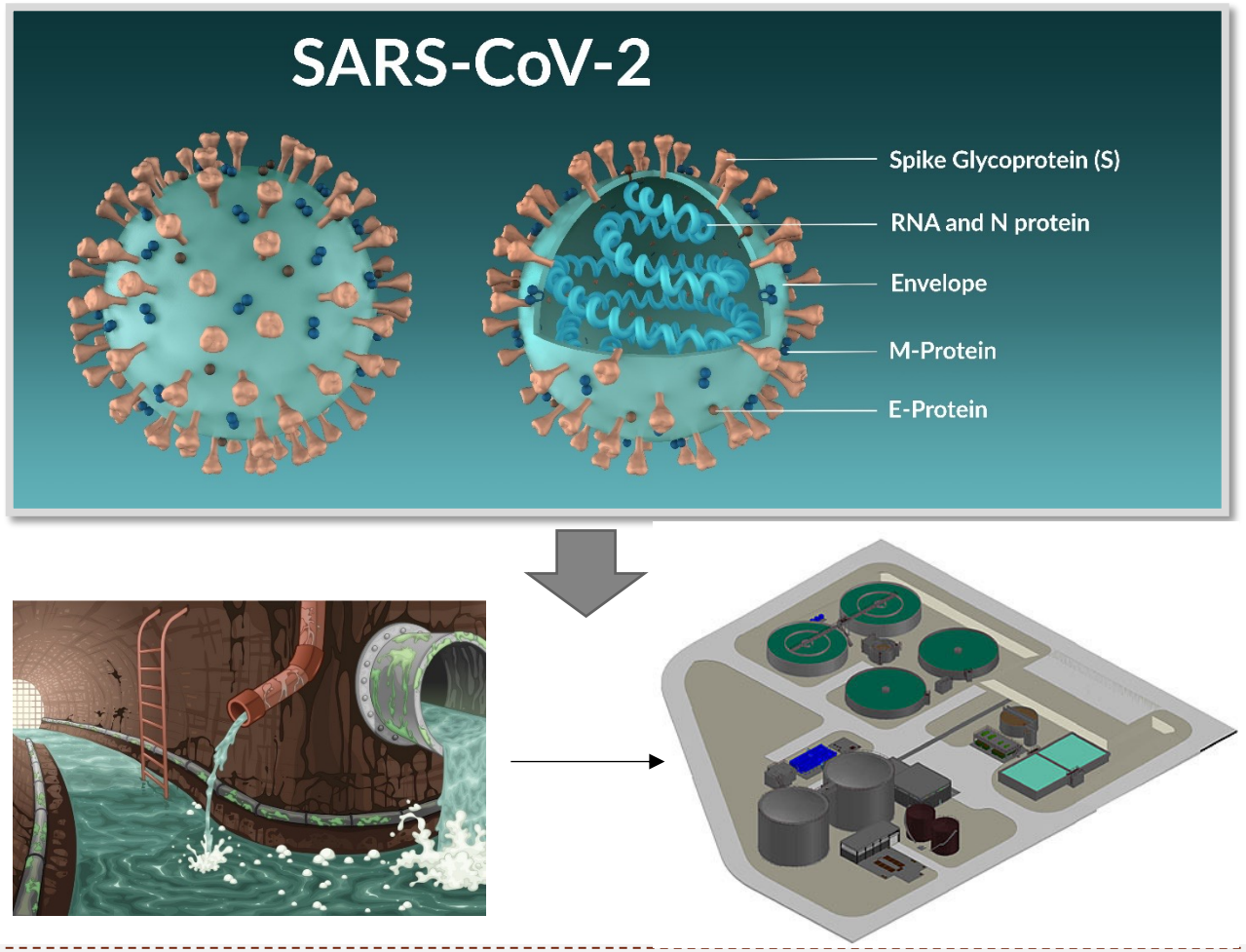
journal homepage: www.elsevier.com/locate/jhazmat

Antidrug resistance in the Indian ambient waters of Ahmedabad during the COVID-19 pandemic

Manish Kumar [a,*], Kiran Dhangar [a], Alok Kumar Thakur [a], Bhagwana Ram [b], Tushara Chaminda [c], Pradeep Sharma [d], Abhay Kumar [e], Nirav Raval [f], Vaibhav Srivastava [f], Jörg Rinklebe [g,h], Keisuke Kuroda [i], Christian Sonne [j], Damia Barcelo [k,l]

[a] Discipline of Earth Science, Indian Institute of Technology Gandhinagar, Gujarat 382355, India
[b] Department of Civil Engineering, Indian Institute of Technology, Gandhinagar, Gujarat, 382355, India
[c] Department of Civil and Environmental Engineering, University of Ruhuna, Galle, Sri Lanka
[d] Department of Environmental Science, Graphic Era Deemed to be University, Dehradun, Uttarakhand, India
[e] NCERT, Sri Aurobindo Marg, New Delhi- 110016, India
[f] Encore Insoltech Pvt. Ltd., Randesan, Gandhinagar, Gujarat 382007, India
[g] University of Wuppertal, School of Architecture and Civil Engineering, Institute of Foundation Engineering, Water and Waste Management, Laboratory of Soil and Groundwater Management, Pauluskirchstraße 7, 42285 Wuppertal, Germany
[h] Department of Environment, Energy and Geoinformatics, University of Sejong, Seoul, Republic of Korea
[i] Department of Environmental and Civil Engineering, Toyama Prefectural University, Imizu 939-9308, Japan
[j] Aarhus University, Department of Bioscience, Arctic Research Centre (ARC), Frederiksborgvej 399, PO Box 358, DK-4000 Roskilde, Denmark
[k] Institute of Environmental Assessment and Water Research, IDAEA-CSIC, C/ Jordi Girona 18-26, 08034 Barcelona, Spain
[l] Catalan Institute for Water Research, ICRA-CERCA, Emili Grahit 101, 17003, Girona, Spain

Detection of viral proteins SARS COVID



Non-structural proteins
(present only in host cells)
- Enzymes
- Transcription factors

Structural proteins
(in the virion particle)
- S (spike)
- E (envelope)
- M (membrane)
- N (nucleocapsid)

Mass Spectrometry Techniques in Emerging Pathogens Studies: COVID-19 Perspectives

Iqbal Mahmud and Timothy J. Garrett*

Journal of the American Society for Mass Spectrometry pubs.acs.org/jasms Account & Perspective

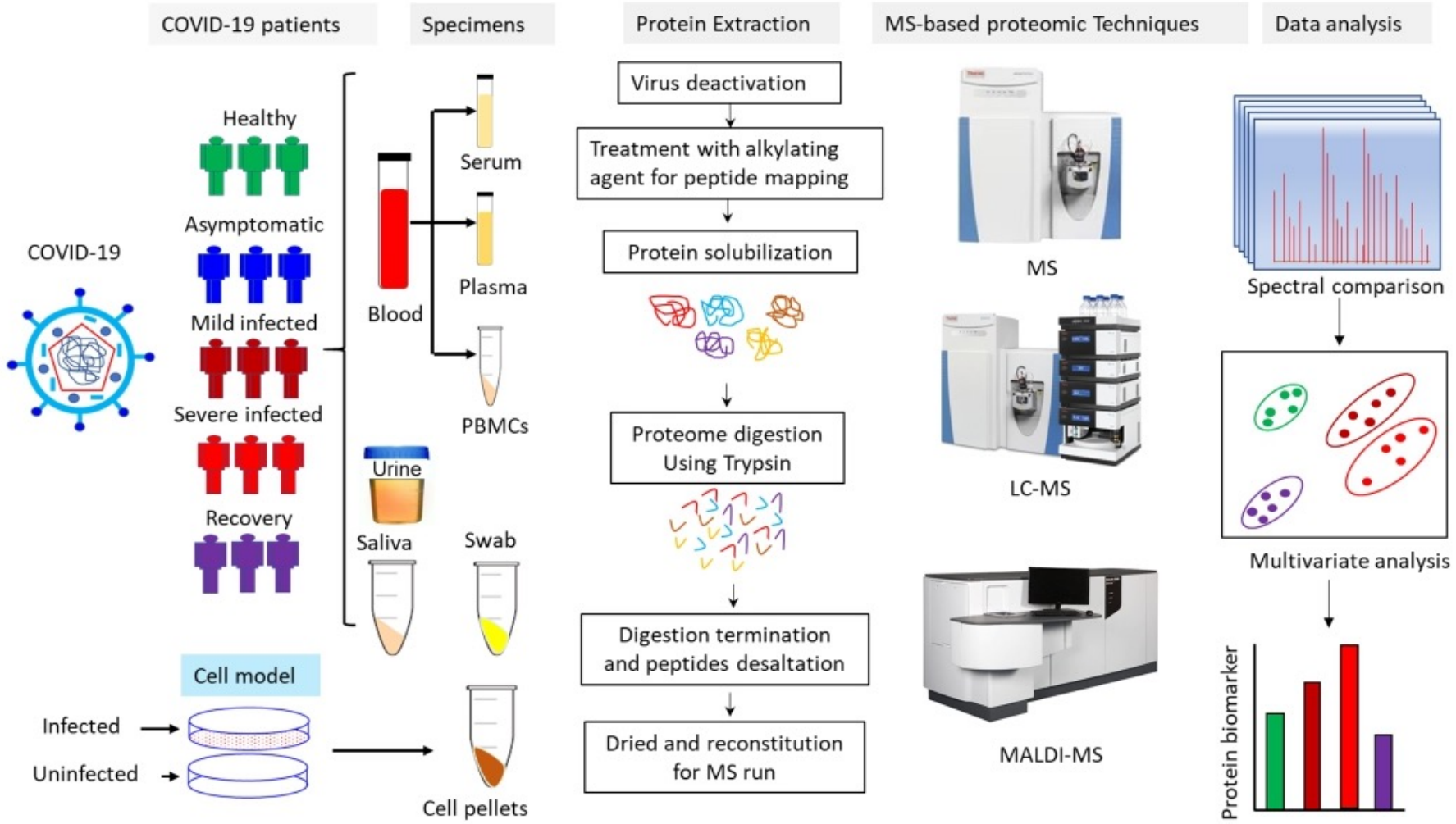
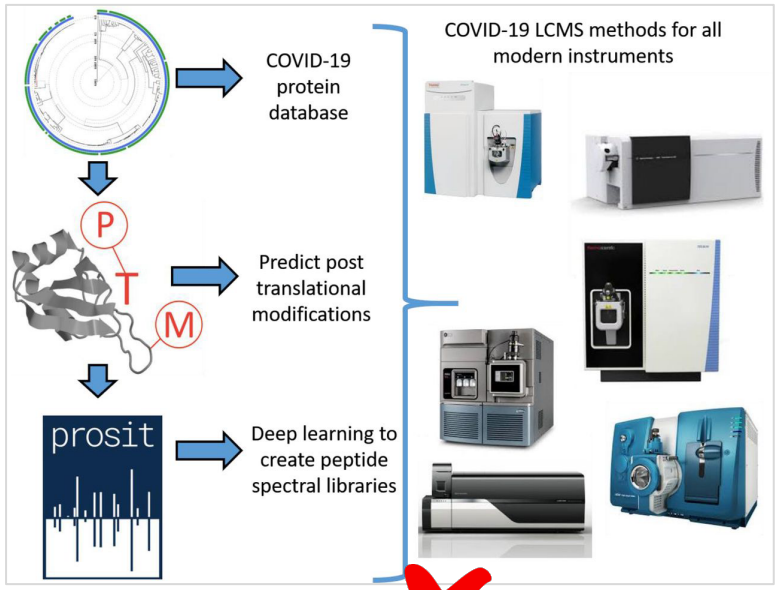
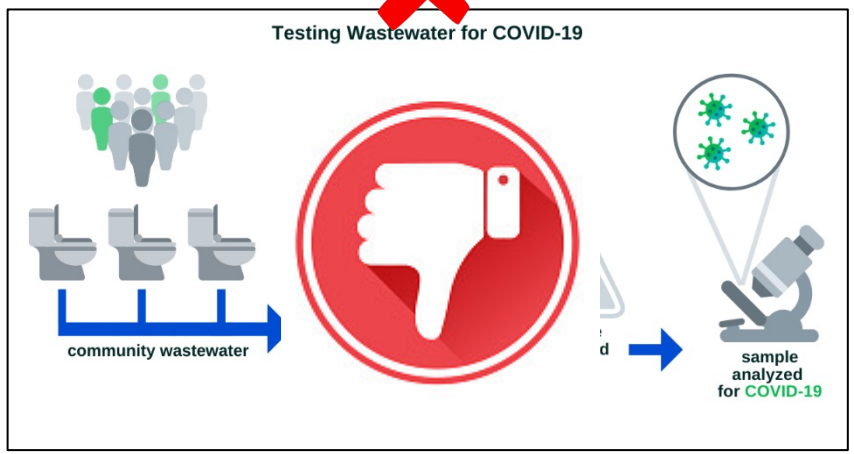
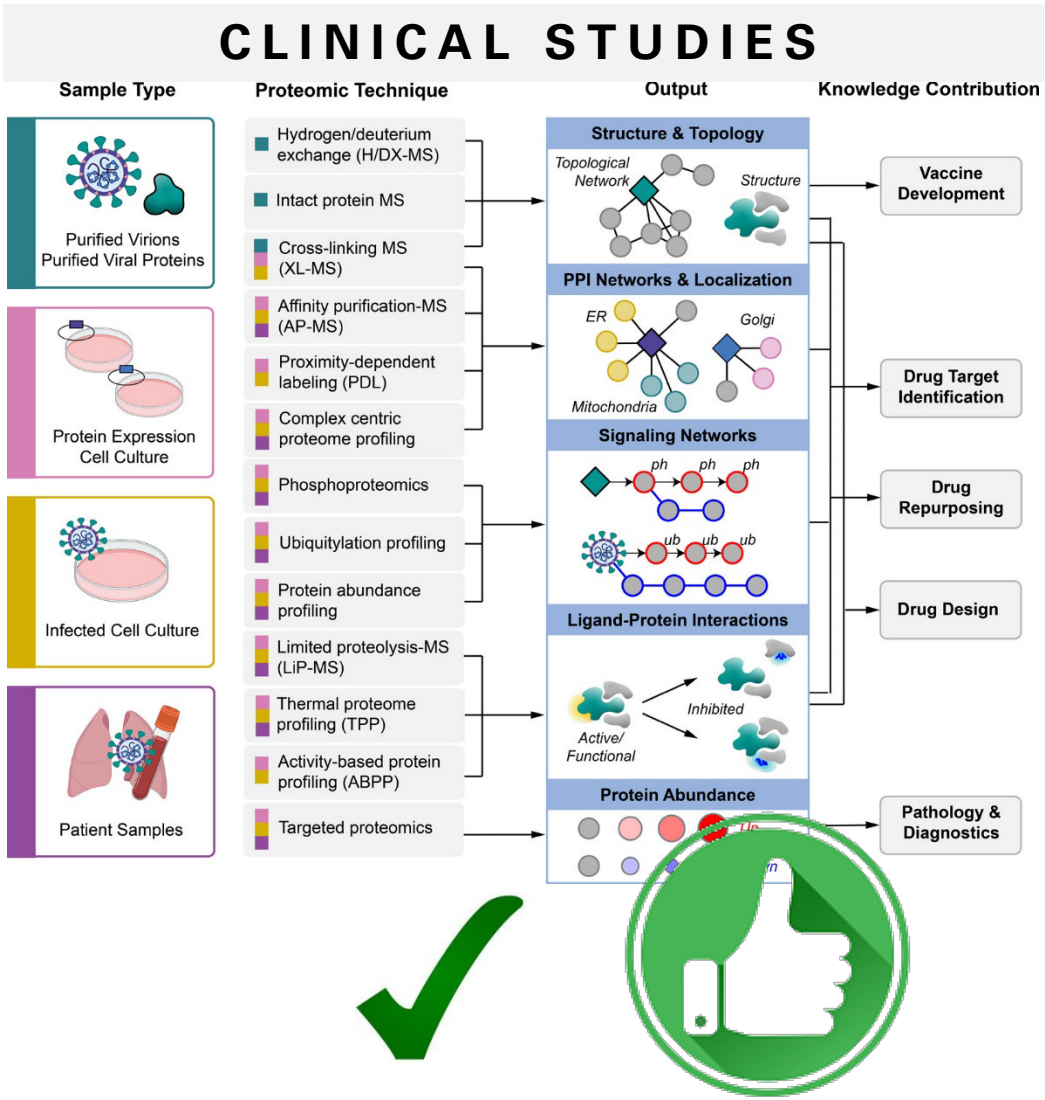


Figure 1. MS-based proteomics to study COVID-19. Workflow developed based on recent proteomic analysis on COVID-19 pandemic. SARS-CoV-2 virus with different symptomatic patient conditions or infected cell model are shown. Typically, serum, plasma, and PBMCs from blood as well as urine, saliva, and nasal swabs have been utilized for targeted or untargeted proteomic analysis in COVID-19 patients. MS spectral comparison followed by multivariate statistical analysis can be applied for biomarker analysis with different levels of COVID-19 severities. For details about different COVID-19 proteomic sample preparation, data collection, and analysis, see Table 1.


COVID-19 LCMS methods for all modern instruments
COVID-19 protein database
P
T
M
Predict post translational modifications
prosit
Deep learning to create peptide spectral libraries


Testing Wastewater for COVID-19
community wastewater
sample analyzed for COVID-19


CLINICAL STUDIES
Sample Type
Proteomic Technique
Output
Knowledge Contribution
Purified Virions Purified Viral Proteins
Protein Expression Cell Culture
Infected Cell Culture
Patient Samples
Hydrogen/deuterium exchange (H/DX-MS)
Intact protein MS
Cross-linking MS (XL-MS)
Affinity purification-MS (AP-MS)
Proximity-dependent labeling (PDL)
Complex centric proteome profiling
Phosphoproteomics
Ubiquitylation profiling
Protein abundance profiling
Limited proteolysis-MS (LiP-MS)
Thermal proteome profiling (TPP)
Activity-based protein profiling (ABPP)
Targeted proteomics
Structure & Topology
Topological Network
Structure
PPI Networks & Localization
ER
Golgi
Mitochondria
Signaling Networks
ph
ub
Ligand-Protein Interactions
Inhibited
Active/ Functional
Protein Abundance
Vaccine Development
Drug Target Identification
Drug Repurposing
Drug Design
Pathology & Diagnostics

analytical chemistry

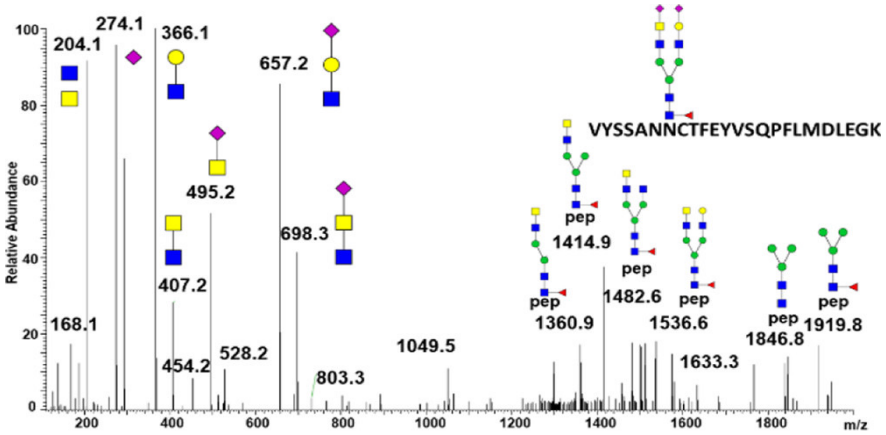
pubs.acs.org/ac Article

N- and O-Glycosylation of the SARS-CoV-2 Spike Protein

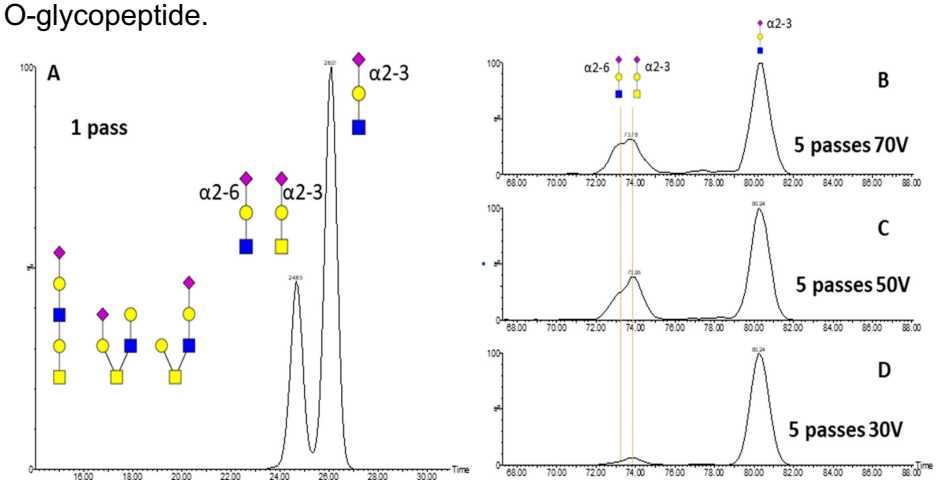
Miloslav Sanda,* Lindsay Morrison, and Radoslav Goldman

Cite This: *Anal. Chem.* 2021, 93, 2003−2009 Read Online

HCD fragmentation of the N165 glycopeptide carrying an asymmetric biantennary glycan with a sialylated LacdiNAc structural motif.



cIMS of the *m/z* 657 fragment produced by fragmentation of the AGC(cam)LIGAEHVNN(dea)SYEC(cam)DIPIGAGIC(cam)ASYQTQTNSPR O-glycopeptide.



roteome
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acs.org/jpr

Article

pteotyping SARS-CoV-2 Virus from Nasopharyngeal Swabs: A oof-of-Concept Focused on a 3 Min Mass Spectrometry Window

rte Gouveia,[¶] Guylaine Miotello,[¶] Fa
rent Bellanger, Jean-Philippe Lavigne,
Jean Armengaud*

Cite This: *J. Proteome Res.* 2020, 19, 4407−4416

CESS | Metrics & More

TRACT: Rapid but yet sensitive, specific, ction of the severe acute respiratory syndrome -2) in clinical samples is key to diagnose infecte ol the spread of the virus. Alternative metho unodiagnostics that would not require specific tigate not only for fighting the COVID-19 pand emergent pathogenic threats. Here, we prop spectrometry to detect SARS-CoV-2 marker al swabs. We documented that the signal from ch samples is low and can be overlooked whe omic data acquired on a restricted windo cape. In this proof-of-concept study, simili d with different quantities of purified SARS-Co

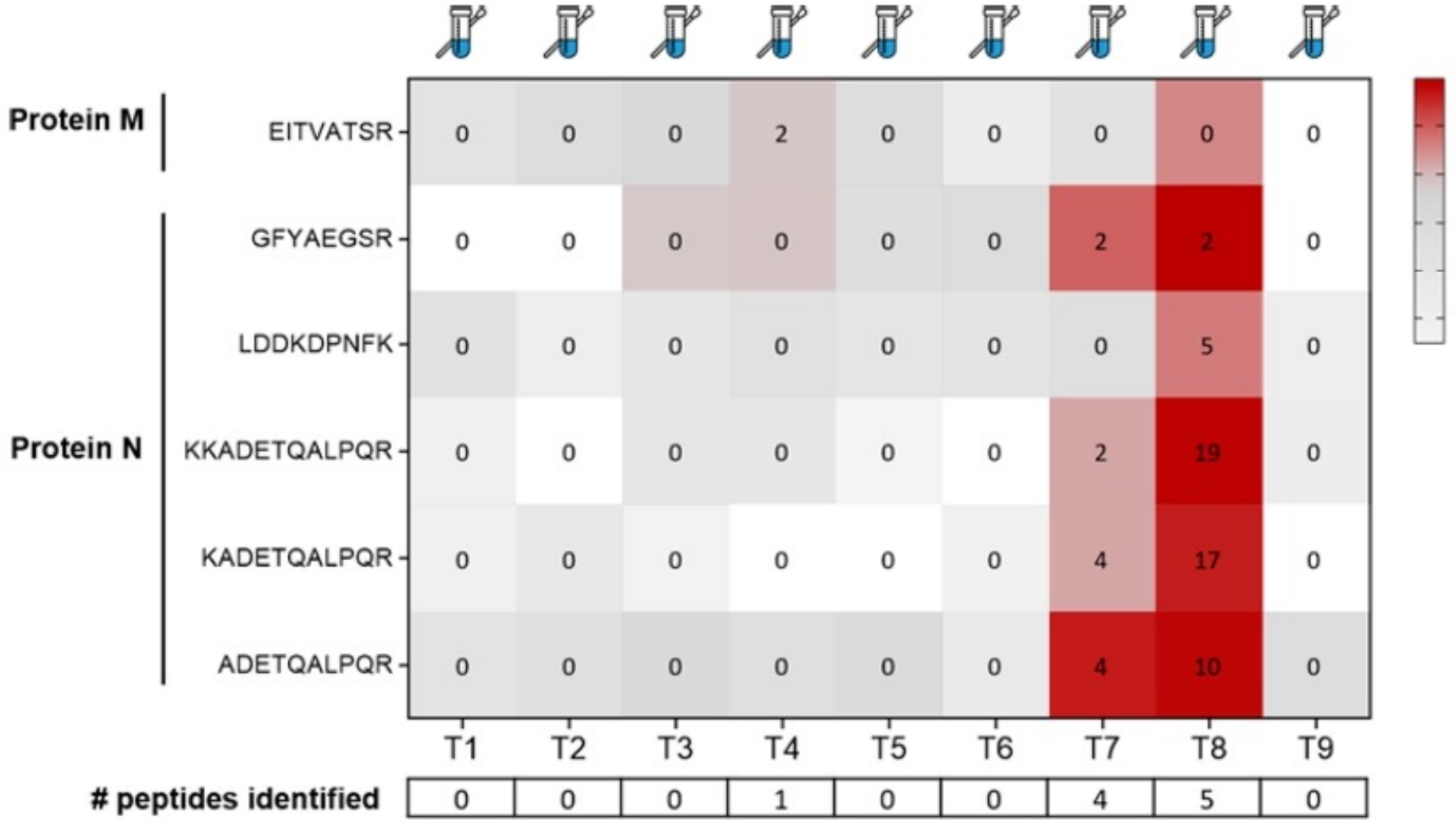


Figure 4. Heatmap of peptide intensities in the clinical nasopharyngeal swabs. Cell color corresponds to MS1 peak area, red bei

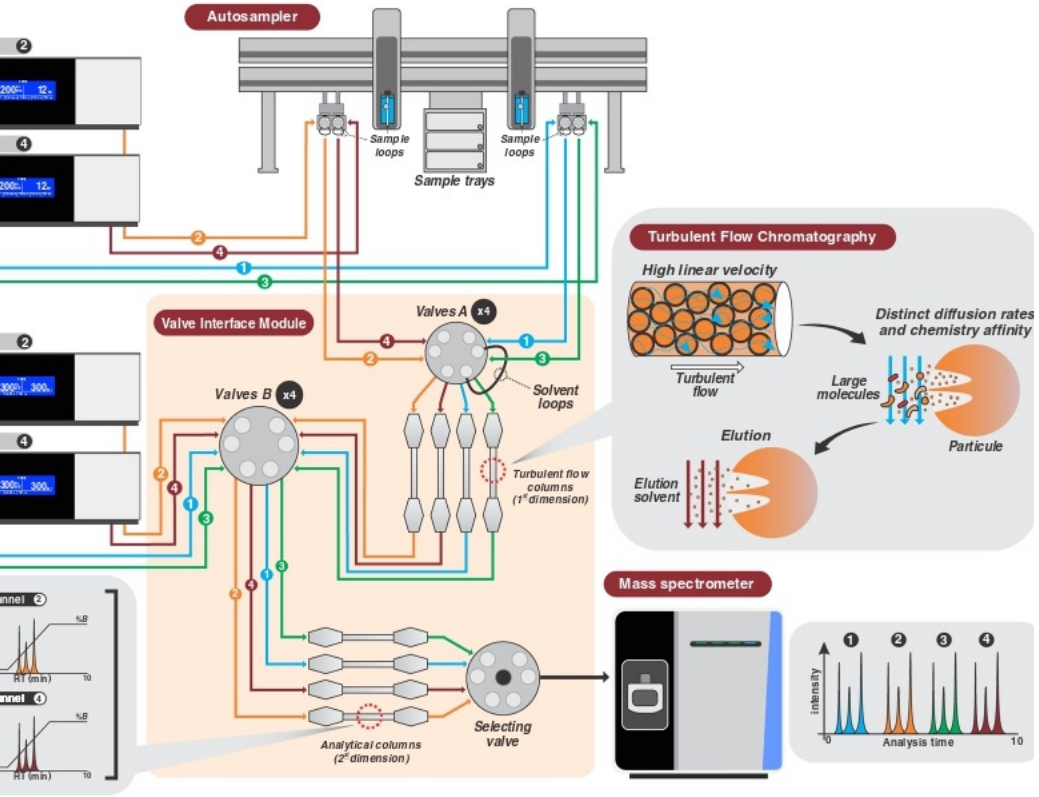
RTICLE

ps://doi.org/10.1038/s41467-020-19925-0 OPEN

Check for updates

stablishing a mass spectrometry-based system for apid detection of SARS-CoV-2 in large clinical ample cohorts

rina Helena Morais Cardozo[1,3], Adriana Lebkuchen[1,3], Guilherme Gonçalves Okai[1,3], drigo Andrade Schuch[1,3], Luciana Godoy Viana[1,3], Aline Nogueira Olive[1], Carolina dos Santos Lazari[2], a Maria Fraga[1], Celso Francisco Hernandes Granato[2], Maria Carolina Tostes Pintão[1] & ldemir Melechco Carvalho[1]✉



bulent flow chromatography (TFC) setup in Transcend TLX-4 system coupled to TSQ Altis triple quadrupole as four independent channels (channel 1: blue, channel 2: orange, channel 3: green and channel 4: red) that can be

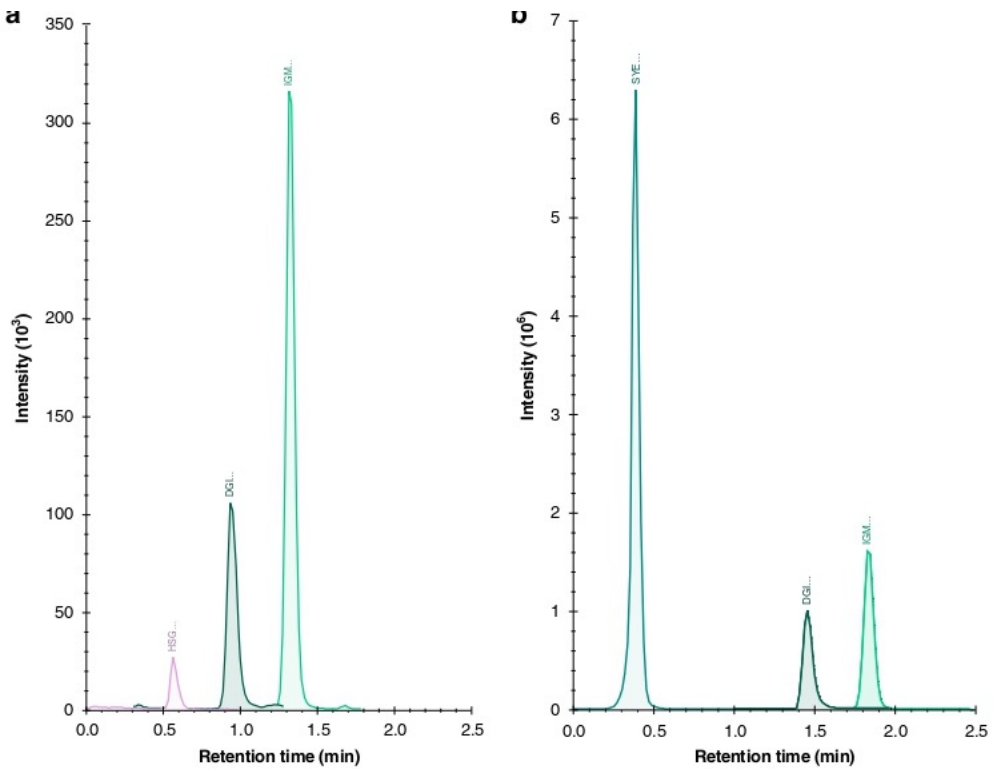


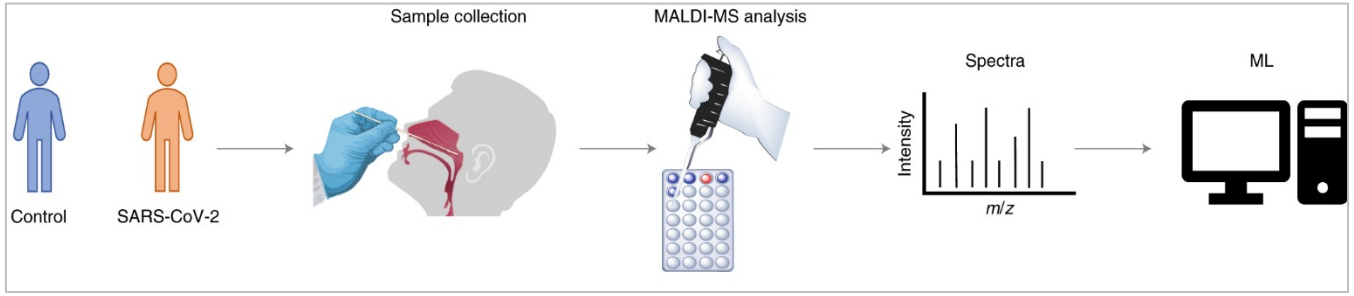
Fig. 3 Selected reaction monitoring chromatograms of SARS-CoV-2-positive clinical respiratory tract specimen showing targeted peptides **a** Qualitative (Tier 3) assay; **b** Quantitative (Tier 1) assay. The first three residues of each peptide are used to label peptide peaks: DGI (DGIIWVATEG and IGM (IGMEVTPSGTWLTYTGAIK) from nucleoprotein; HSG (HSGFEDELSEVLENQSSQAELK) from ^{15}N-labeled surrogate standard chromogra (in Tier 3) and SYE (SYELPDGQVITIGNER) from human beta actin (in Tier 1).

LETTERS
https://doi.org/10.1038/s41587-020-0644-7
nature biotechnology

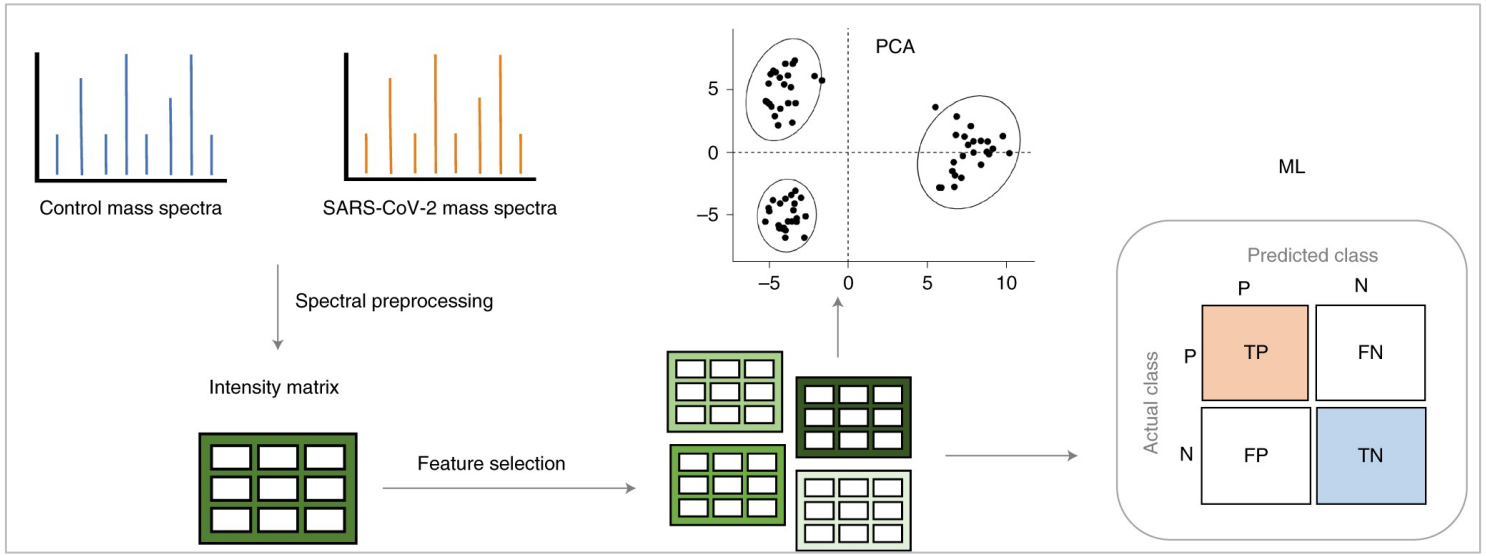
Detection of SARS-CoV-2 in nasal swabs using MALDI-MS

Fabiane M. Nachtigall[1], Alfredo Pereira[2], Oleksandra S. Trofymchuk[3] and Leonardo S. Santos[2]

General scheme for SARS-CoV-2 detection by MALDI-MS and ML



Prediction of SARS-CoV-2 using ML



analytical chemistry

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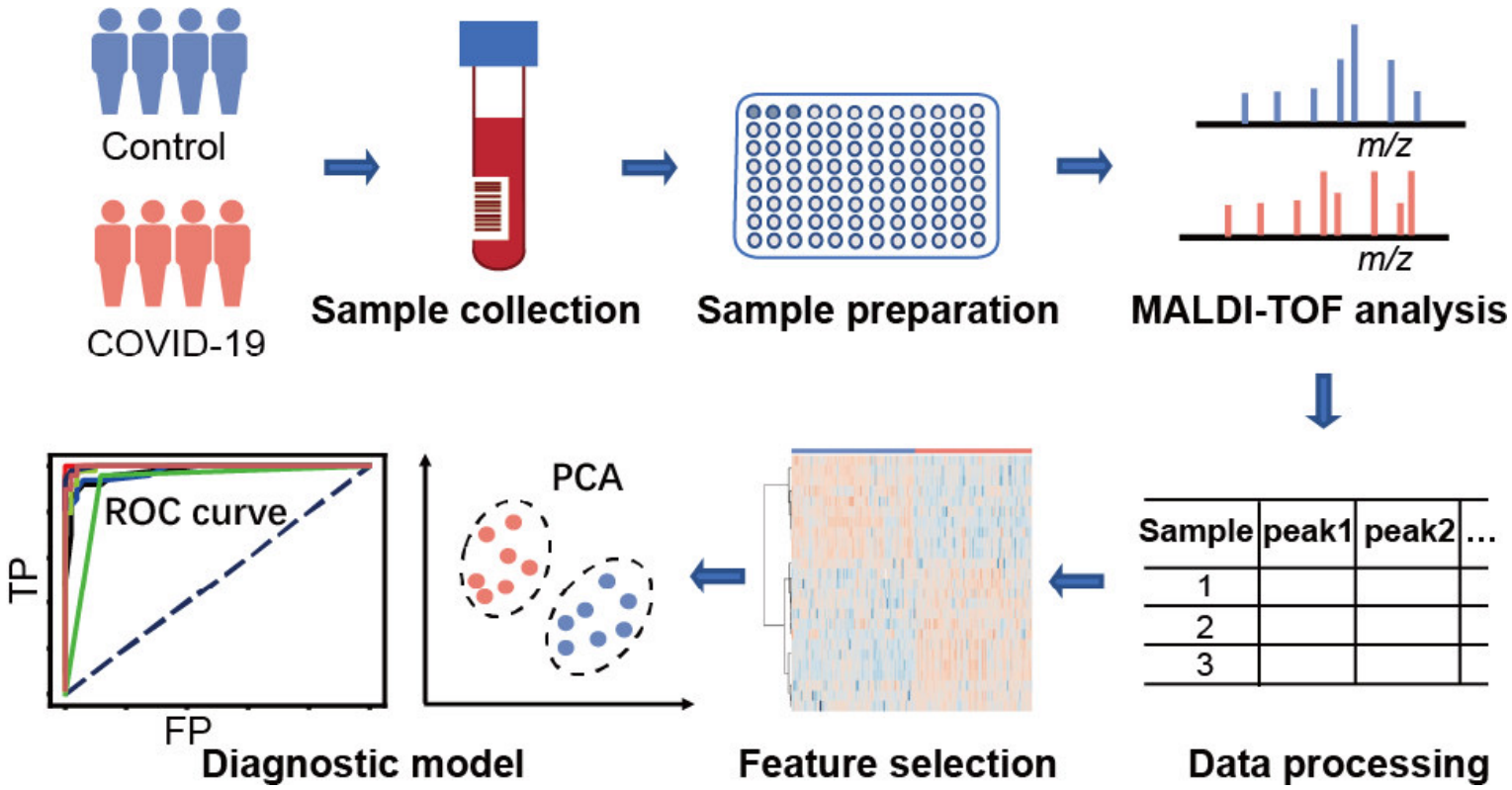
pubs.acs.org/ac Technical Note

Rapid Detection of COVID-19 Using MALDI-TOF-Based Serum Peptidome Profiling

Ling Yan,[▽] Jia Yi,[▽] Changwu Huang,[▽] Jian Zhang,[▽] Shuhui Fu, Zhijie Li, Qian Lyu, Yuan Xu, Kun Wang, Huan Yang, Qingwei Ma, Xiaoping Cui, Liang Qiao,* Wei Sun,* and Pu Liao*

Cite This: *Anal. Chem.* 2021, 93, 4782−4787 Read Online

Scheme of establishing a diagnostic model for rapid screening of COVID-19 patients.



Trends in Analytical Chemistry 142 (2021) 116328

Contents lists available at ScienceDirect

Trends in Analytical Chemistry

Step/parameter	RT-PCR detection [31]	DNA amplicon detection by MS [32, 33]	Viral peptide detection by MALDI-MS [34]	Viral peptide sequencing by LC-ESI-MS/MS [35]
Viral component recovery	RNA	RNA	protein	protein
Recovery time	minutes	minutes	1–2 h	1–2 h
Steps pre-analysis	reverse transcription, denaturation, annealing, amplification[b]	reverse transcription, denaturation, annealing, amplification[b]	proteolytic digestion with/without reduction/alkylation	proteolytic digestion with/without reduction/alkylation
Pre-analysis time	30 min	30 min	4–14 h[c]	4–14 h[c]
Detection time	2–4 h	few minutes	few minutes	30 min – 1 h
Detection limit (copies)	~10	>10–10^2 [32]	> 10^5[d]	10^5–10^6
Reliability/confidence	up to 95%	high (with multiple amplicons detected)	high (with multiple peptides detected)	high (with multiple peptides sequenced)
Analysis cost/sample (USD)	$10	$10-50	$100	$250
Instrument cost (USD)	$20 K+	$100 K+	$100–1000 K+	$250–500 K+

[a] All times and figures are approximate only and depend on specific protocols and equipment employed. Citations are:

1. Da Silva et al. ACS Infect. Dis. 2020, 6, 2319-2336.
2. Xiu et al, J., Front. Microbiol. 2017, 8, 1510.
3. Wandernoth et al. Detection of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) by Mass Spectrometry. 2020, 12, 849.
4. Dollman et al. ACS Infect. Dis. 2020, 6, 3269-3276.
5. Nikolaev et al. J.Proteome Res. 2020, 19, 4393-4397.

[b] According to real-time RT-PCR detection of SARS-CoV-2 protocol, Institute Pasteur, Paris (https://www.who.int/docs/default-source/coronaviruse/real-time-rt-pcr-assays-for-the-detection-of-sars-cov-2-institut-pasteur-paris.pdf).

[c] Improve using immobilized enzyme digestion to 1–2 h.

[d] Improve by one or two orders of magnitude with selected ion monitoring (SIM).

Conclusions and Challenges

1. The **identification** of small molecules used as **biomarkers** is linked to the search of **HBM studies** and to **the advances in MS**
2. Introduction of **HR-MS** and the improvement of raw data **processing**, **identification** systems and applied **bioinformatics** has opened an important door to the discovery of new useful biomarkers directly in wastewater.
3. However, this aspect of WBE is not yet resolved and the **lack of human-specific metabolites** for some compounds and **additional** sources of **transformation products** need to be addressed.
4. Solving these problems can be somewhat **time-consuming** due to the **complexity of wastewater.**

Shall we need to increase/cleanup /sample preparation of the WWTP samples?
Pros and cons to any of the answers should be carefully evaluated on a case-by-case basis.

Conclusions and Challenges

5. Recently, there is an **emerging interest** in complementing the metabolite profile of biomarkers determined in wastewater with **proteomics**.
6. Although the studies are still scarce, **WBE of large molecules using MS** got a lot of possibilities using **HRMS** with **non-target** approaches and **chemometrics**
7. Problems in Proteomics -WBE remain, such as the **prevalence of the bacterial proteome versus human proteomes**, being more difficult for the later.
8. Nevertheless, despite the limited number of studies that exist, several **proteins of human and animal origin** have been **identified** that are related illegal discharges of livestock blood (**Albumin**) , Covid-19 infection **(immunoglobulin**),human proteins identified (**Keratins,pancreatic enzymes,alpha-amylase, uromodulin,S100A8)**
9. **MALDI-TOF is a** fast method to detect the most abundant proteins in WBE with confirmation by LC/MS/MS

Proteins and **peptides related to humans** as well as proteins and peptides from **SARS-other viruses** will be soon identified

Conclusions and Challenges

9. Virus **identification** is the **only field** of **WBE** where **MS is not prevalent**
10. S**ensitivity** still **needs to be resolved** ➔ the **identification** of these proteins in **clinical analysis** is a **reality** of great help in diagnosis.
11. **Biosensors- paper based** and other devices, Little Middle Income Countries (LMICs) lacking WWTP facilities- today´s problem of more than 1 billion people

Should be able to find specific peptides from the nucleocapsid protein responsible of oV-2 infection in WBE?

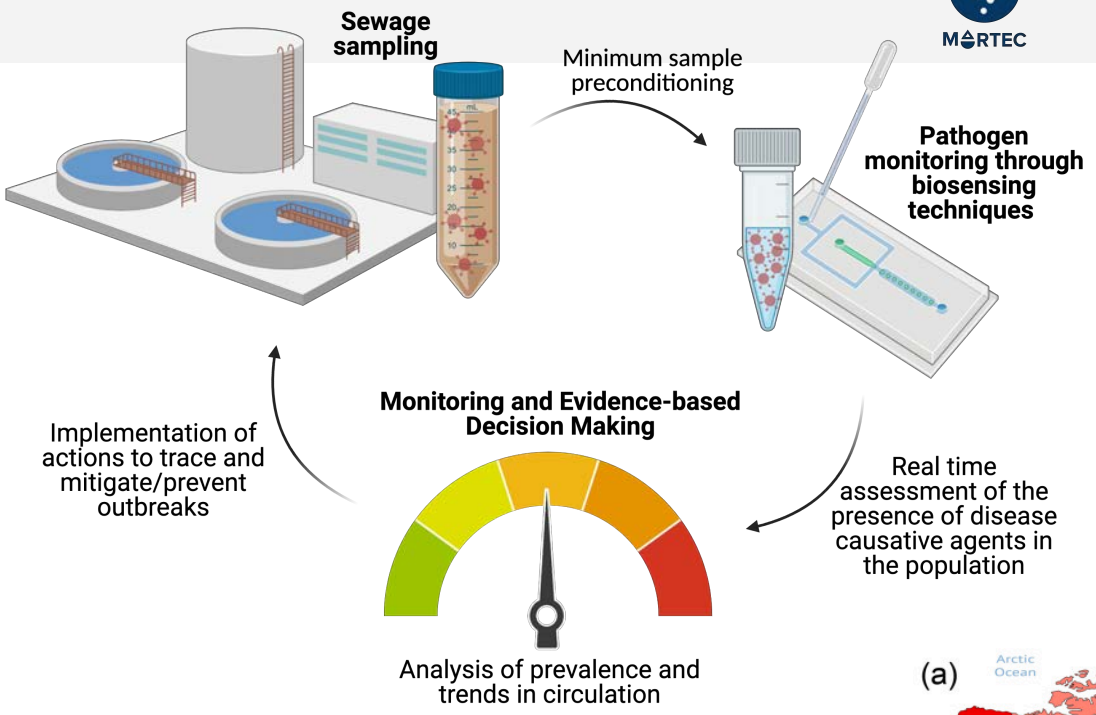
This would always help to improve identification and, **why not?** Future is always going a st rd and this would be of help.

Do we need a more sensitive LC-MS/MS for SARS peptide specific detection in WWTP?

Clearly yes, but the ADVANCES IN MS DOES NOT STOP.

e.g. Ion mobility mass spectrometry and improve workflows in non-target analysis are e anc g sensitivity to unexpected extremes.

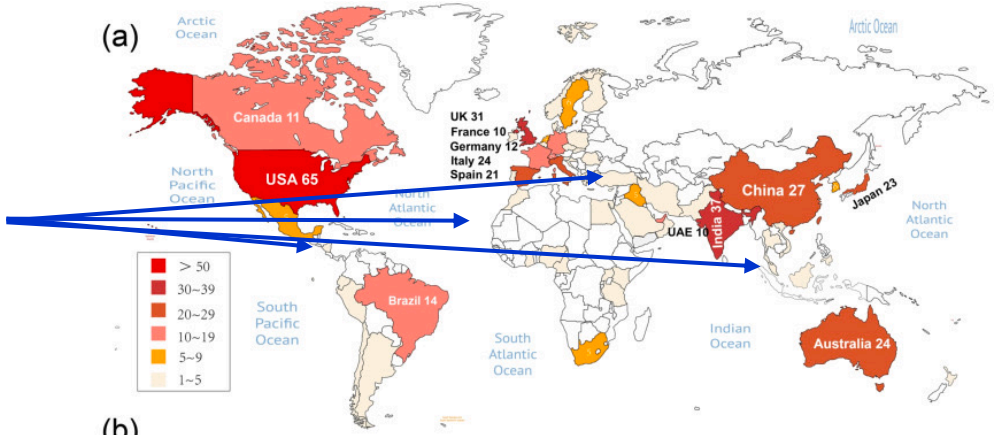
WBE concept & application in the world

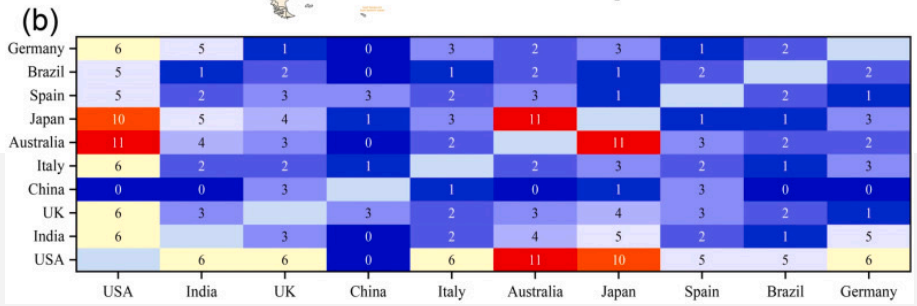


WBE SARS-CoV-2 with PCR, 184 papers, 67 countries. March 2021

Low Middle Income Countries (LMICs),with no WWTP and on-site sanitation facilities require more accessible tools for WBE, i.e, hotspot-based sampling and drainage-based sampling, Biosensors-paper based , others?

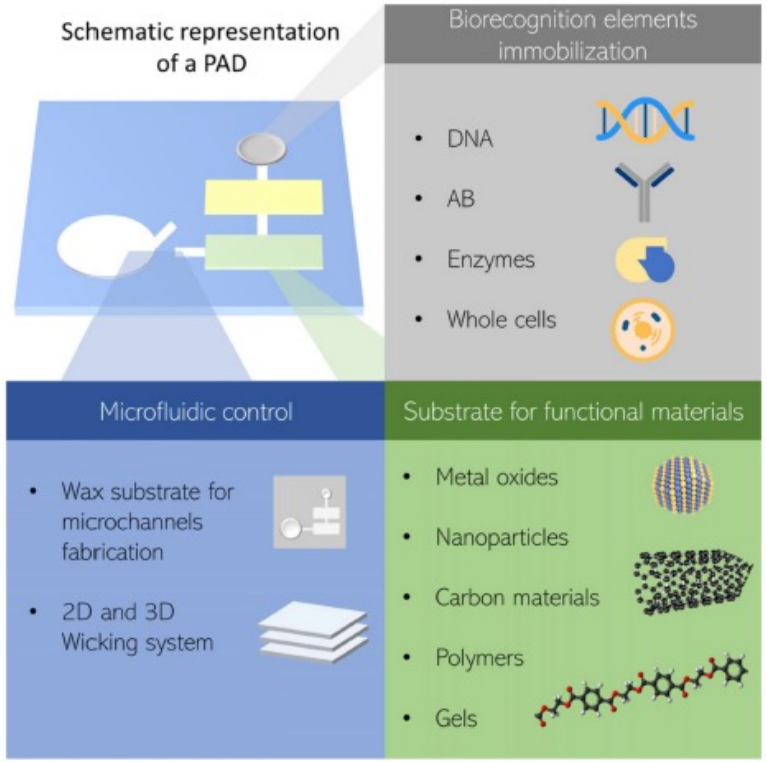
Latin America
Africa
East-Europe
Middle-East
Some points in Asia



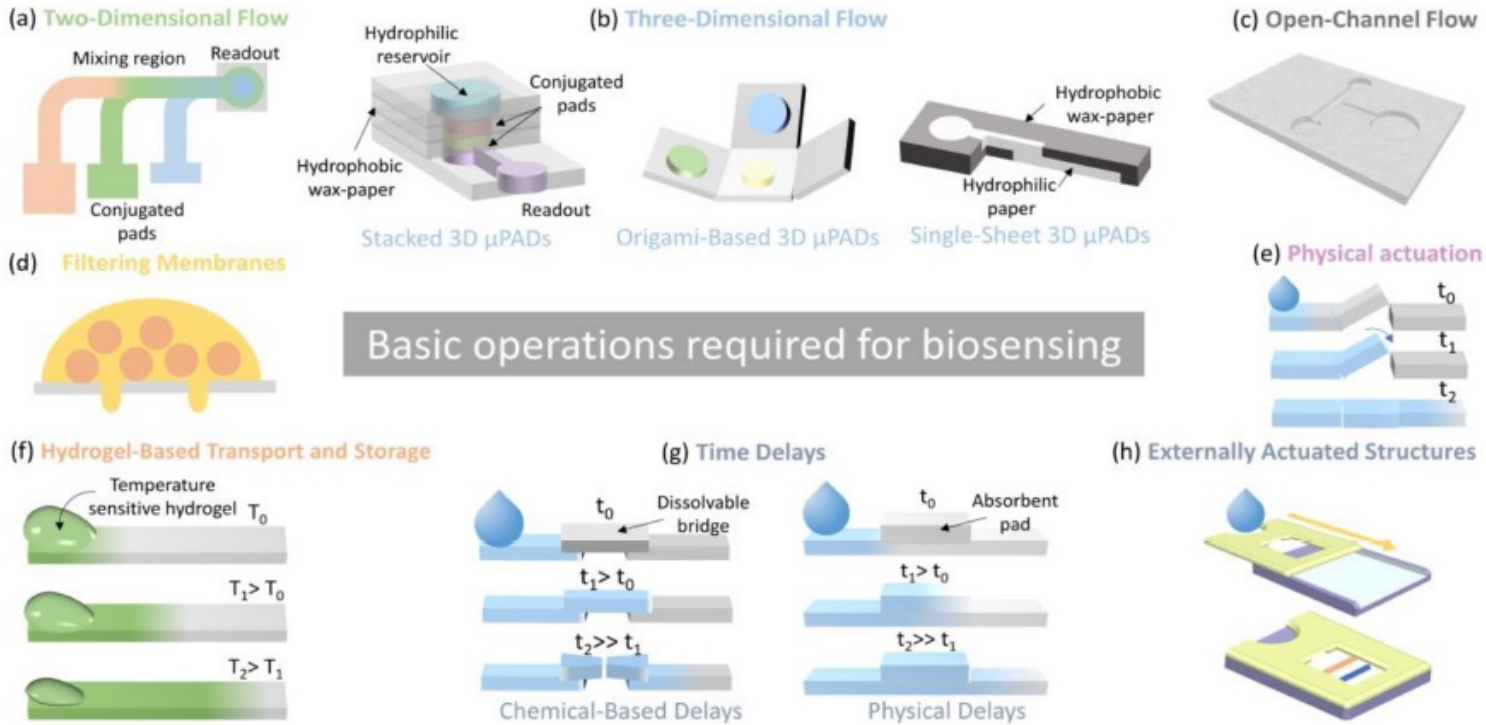


https://doi.org/10.1016/j.jece.2021.105357

Paper and other fibrous materials for biosensing applications



Schematic representation of a paper-based analytical device (PAD) and its primary function as a matrix for biomolecules immobilization, functional materials, and microfluidic control.



a) Two-dimensional flow design for sequential delivery of reagents or mixing; (**b**) three-dimensional flow configurations; (**c**) open-channel microfluidic omniphobic paper; (**d**) Separation membrane; (**e**)"on/off" fluidic switch; (**f**) hydrogel-driven paperbased microfluidics; (**g**) flow time delays using dissolvable bridges and absorbent pads ; (**h**) slip device for one-step point-of-care testing.

https://doi.org/10.3390/bios11050128

Paper-based devices for SARS-CoV-2 in WBE

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Case Studies in Chemical and Environmental Engineering

journal homepage: www.editorialmanager.com/cscee/default.aspx

Paper-based devices for rapid diagnostics and testing sewage for early warning of COVID-19 outbreak

Qingxin Hui, Yuwei Pan, Zhugen Yang *

Cranfield Water Science Institute, School of Water, Energy and Environment, Cranfield University, Cranfield, MK43 0AL, UK

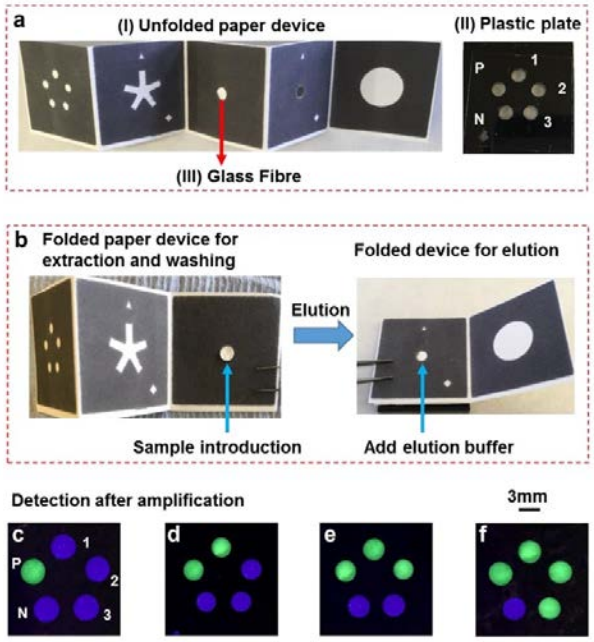


Fig. 3. The schematic diagram of the paper device for the detection of BoHV-1, Brucella and Leptospira [33].

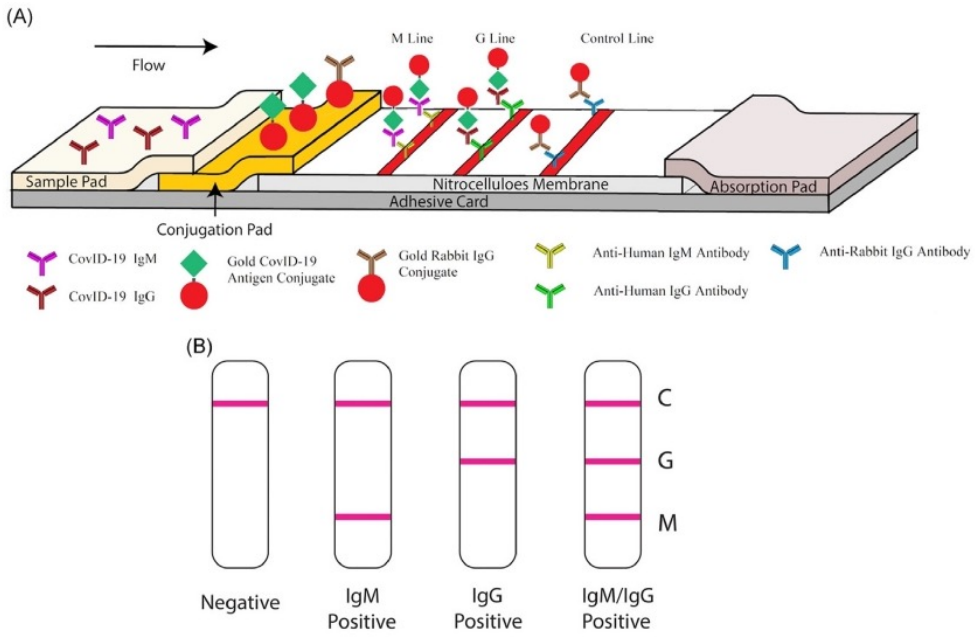


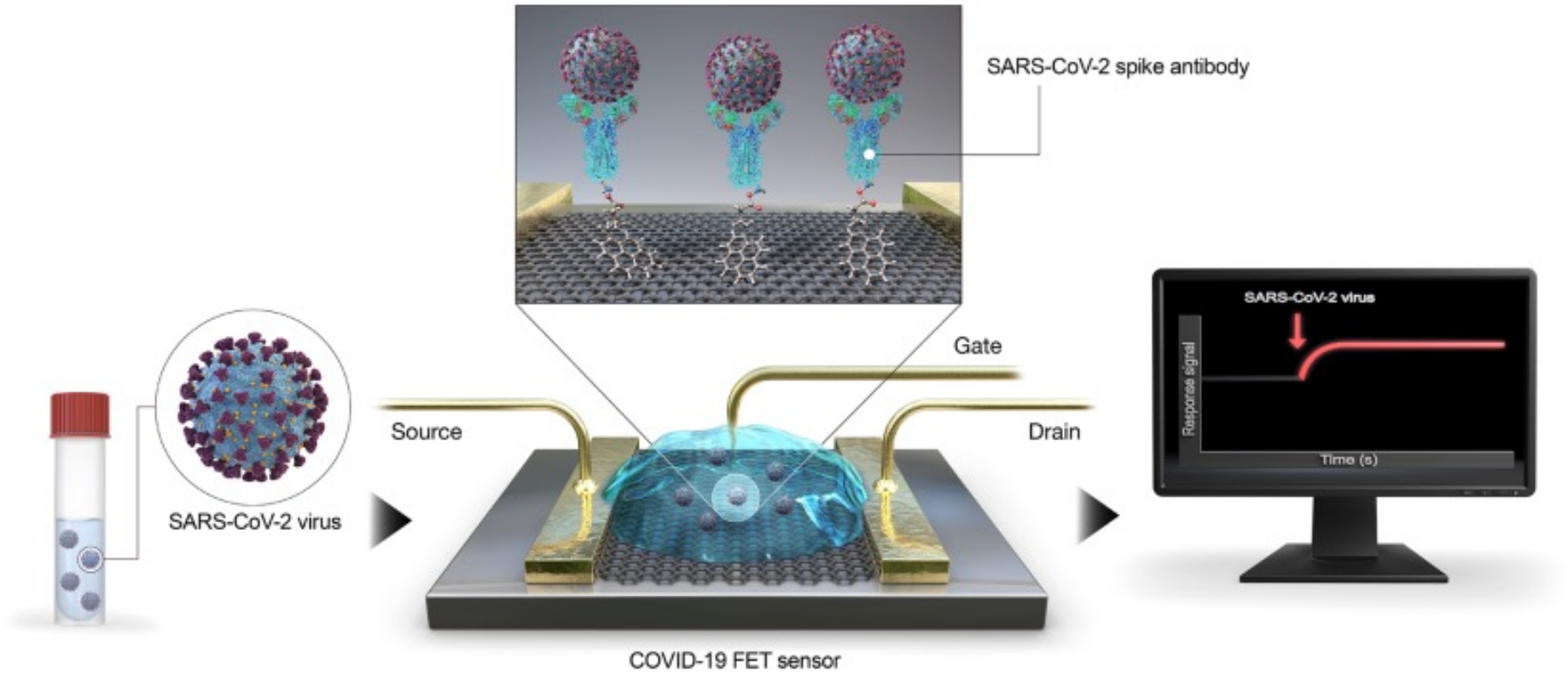
Fig. 4. The schematic illustration of SARS-CoV-2 IgG and IgM test [41]. (A) The detection device. (B) Different test results.

Electrochemical sensing of SARS-CoV-2 amplicons with printed circuit board (PCB) electrodes

SARS-CoV-2 nucleic acid detection workflow. RNA extracted from wastewater is amplified using a low cost thermo cycler and then placed onto PCB electrodes.

https://doi.org/10.1016/j.snb.2021.130169

Field-Effect TransistorBased Biosensor



Schematic diagram of COVID-19 FET sensor operation procedure. Graphene as a sensing material is selected, and SARS-CoV-2 spike antibody is conjugated onto the graphene sheet via 1-pyrenebutyric acid N-hydroxysuccinimide ester, which is an interfacing molecule as a probe linker.

https://doi.org/10.1021/acsnano.0c02823

Acknowledgements

This work has been supported by the Spanish Ministry of Science and Innovation (MICINN, Spain) Projects:

- PID2020-114065RB-C22
- CEX2018-000794-S
- PID2019- 105732GB
- IBERAQUA-NET RED2018-102737-T (http://iberaquanet.com/)

Carlos Perez-Lopez acknowledges the predoctoral Severo Ochoa FPI 2019-090182 scholarship from MICINN.

Many thanks for your attention