Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

be judged from the peer-reviewed scientific output in the near future.

The response to the crisis was data-driven, thanks to a single institutional data platform fed by a single information system, providing important decision making parameters (eg, length of stay, treatment, clinical pathway) in real time.

Large-scale initiatives were rapidly developed. Each day, a farm of 63 3D printers manufactured 1000 parts of various medical devices, bypassing a slow supply chain and avoiding disabled equipment. The Covidom telemedicine platform monitored more than 50 000 patients at home (appendix).[3]

A region-wide patient-tracing programme, COVISAN, was set up.[4] Devised by AP-HP under the umbrella of the regional health authority, the COVISAN programme brought together local authorities, general practitioners, non-governmental organisations, and private companies, which helped to secure the national lockdown exit plan.

All this was made possible because of extraordinary mobilisation and joint efforts of medical, paramedical, and administrative staff and with reinforcements from other regions (appendix). The COVID-19 crisis hit an institution that already had a shortage of nurses. A substantial number of health-care professionals became infected. We wish to acknowledge the tireless work of the highly motivated personnel at AP-HP. The COVID-19 crisis is not yet behind us; nevertheless, at a time when virtually every health system in the world is facing unprecedented challenges, we hope others will find our initial lessons helpful.

Members of the COVID19-APHP Group are listed in the appendix. We declare no competing interests.

The COVID19-APHP Group
martin.hirsch@aphp.fr

Assistance-Publique-Hôpitaux de Paris, 75004 Paris, France

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The COVID-19 MS Coalition—accelerating diagnostics, prognostics, and treatment

Rapid and comprehensive genetic sequencing has shed light on the origin of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and allowed timely implementation of PCR tests to determine the presence of viral RNA. PCR tests for SARS-CoV-2 are some way from being reliably qualitative and will never indicate how the disease might progress in an individual. As COVID-19 becomes endemic, there is a concomitant need for accurate serological assays to detect antibodies to SARS-CoV-2 antigens and ultimately tests for prognostic markers to target treatment options.[1,2] With this considerable genetic insight, and the emerging structural information, comes associated questions regarding the molecular descriptors that contribute to disease progression, especially when we consider spread across different populations. The power of mass spectrometry to generate rapid, precise, and reproducible diagnostic information that complements genomic information and accelerates our understanding of the disease, is now becoming a reality.[3,4]

Mass spectrometry-based analysis can answer questions broadly falling into two categories. The first concerns multi-omic profiling of the host response, correlating prognosis with disease severity. Robust biomarkers will further our understanding of disease mechanisms and the susceptibility of certain clinical groups. The most valuable of these prognostic markers will be those indicating the transition from a beneficial immune response to one that is harmful, ultimately resulting in respiratory distress. Such data will facilitate public health efforts for population screening, defining high-risk patients, tracking disease progression, and identifying sources of vulnerability that will permit treatment stratification and minimise or prevent future coronavirus pandemics.

The second category concerns the SARS-CoV-2 viral spike glycoprotein, which is not only key for host-cell attachment but is also a major target for neutralising antibodies elicited through vaccination. Although RNA sequencing is extraordinarily informative for viral mutation or adaptation via immune selective pressure, it cannot inform on a critical feature of enveloped viruses: viral spike glycosylation. The functional role of SARS-CoV-2 spike glycans, of which there are 66 per trimer,[5] is undetermined yet, along with associated conformational dynamics that shape receptor or antibody binding, a key factor for vaccine design. Investigating spike glycosylation and plasticity with advanced mass spectrometry methods on recombinant preparations and comparing this to wild type viral proteins is crucial to this effort.

The COVID-19 MS Coalition is a collective mass spectrometry effort that will provide molecular level information on SARS-CoV-2 in the human host and reveal pathophysiological and structural information to treat and minimise COVID-19 infection. Collaboration with colleagues at pace involves sharing of optimised methods for

For the **Covidom application** see https://www.nouveal.com/covidom-le-suivi-des-patients-porteurs-du-covid-19/

For the **COVISAN programme** see https://www.aphp.fr/actualite/lancement-de-covisan-un-dispositif-de-suivi-renforce-des-personnes-covid

Published **Online** May 27, 2020 https://doi.org/10.1016/S0140-6736(20)31211-3

For the **COVID-19 MS Coalition** see http://covid19-msc.org/

sample collection and data generation, processing and formatting for maximal information gain. Open datasets will enable ready access to this valuable information by the computational community to help understand antigen response mechanisms, inform vaccine development, and enable antiviral drug design. As countries across the world increase widespread testing to confirm SARS-CoV-2 exposure and assess immunity, mass spectrometry has a significant role in fighting the disease. Through collaborative actions, and the collective efforts of the COVID-19 MS Coalition, a molecular level quantitative understanding of SARS-CoV-2 and its effect will benefit all.

We declare no competing interests.

*Weston Struwe, Edward Emmott, Melanie Bailey, Michal Sharon, Andrea Sinz, Fernando J Corrales, Kostas Thalassinos, Julian Braybrook, Clare Mills, *Perdita Barran, on behalf of the COVID-19 MS Coalition*

perdita.barran@manchester.ac.uk

Department of Chemistry and Oxford Glycobiology Institute, Department of Biochemistry, University of Oxford, Oxford, UK (WS); Centre for Proteome Research, Institute for Integrative Biology and Department of Biochemistry, University of Liverpool, Liverpool, UK (EE); Department of Chemistry and Surrey Ion Beam Centre, University of Surrey, Surrey, UK (MB); Department of Biomolecular Sciences, Weizmann Institute of Science, Rehovot, Israel (MS); Department of Pharmaceutical Chemistry & Bioanalytics, Institute of Pharmacy, Charles Tanford Protein Center, Martin-Luther University Halle-Wittenberg, Halle, Germany (AS); Proteomics Unit, Centro Nacional de Biotecnología, Madrid, Spain (FJC); ProteoRed-ISCIII, Madrid, Spain (FJC); Institute of Structural and Molecular Biology, Department of Structural and Molecular Biology, University College London, London, UK (KT); National Measurement Laboratory, LGC, Teddington, Middlesex, UK (JB); Division of Infection, Immunity and Respiratory Medicine, Manchester Academic Health Science Centre, Manchester, UK (CM); and Michael Barber Centre for Collaborative Mass Spectrometry, Manchester Institute of Biotechnology (CM, PB) and Department of Chemistry (PB), University of Manchester, Manchester M1 7DN, UK

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Department of Error

Grasselli G, Zanella A. Critically ill patients with COVID-19 in New York City. Lancet *2020; **395:** 1740–41*—In this Comment, the number of participants should have been 86 (33%) women and 171 (67%) men, and median respiratory system compliance should have been 27 mL/cm water. These corrections have been made to the online version as of June 4, 2020, and the printed version is correct.

Reiner RC Jr, Hay SI. Mapping geographical inequalities in childhood diarrhoeal morbidity and mortality in low-income and middle-income countries, 2000–17: analysis for the Global Burden of Disease Study 2017. Lancet *2020; **395:** 1779–801*—In this Article, the author byline has been amended to Local Burden of Disease Diarrhoea Collaborators. This correction has been made to the online version as of June 4, 2020, and the printed version is correct.

Watts N, Amann M, Arnell N, et al. The 2018 report of The Lancet *Countdown on health and climate change: shaping the health of nations for centuries to come.* Lancet *2018; **392:** 2479–514*—In this Review, the methodology for indicator 5.1 (figure 25) has been updated to address concerns regarding the use of relying on the same search string in multiple databases to produce this data. Newspaper databases interpret search strings differently and use different algorithms to search and return articles. The updated methodology ensures that the searches are more uniformly interpreted across databases and removed certain terms that were found to not represent the concepts intended to be captured. In due course, the most up-to-date findings will be available at www.lancetcountdown.org/data-platform. This correction has been made to the online version as of June 4, 2020.

Watts N, Amann M, Ayeb-Karlsson S, et al. The 2017 report of The Lancet *Countdown on health and climate change: from 25 years of inaction to a global transformation for public health.* Lancet *2017; **391:** 581–630*—In this Review, the methodology for indicator 5.1 (figure 40) has been updated to address concerns regarding the use of relying on the same search string in multiple databases to produce this data. Newspaper databases interpret search strings differently and use different algorithms to search and return articles. The updated methodology ensures that the searches are more uniformly interpreted across databases and removed certain terms that were found to not represent the concepts intended to be captured. In due course, the most up-to-date findings will be available at www.lancetcountdown.org/data-platform. This correction has been made to the online version as of June 4, 2020.