toxic peptide was not detected by software implementing the screening guidelines. The respective order was moved to production. Details are withheld, but IGSC was notified about the threat and potential mitigation methods. The order was canceled for biosecurity reasons following our disclosure.

Many such attacks can be mitigated: first, synthesizers can implement cybersecurity protocols, such as electronic signatures on orders, and adapt to provide intrusion detection approaches, ranging from heuristic signatures to artificial intelligence behavioral analysis, to identify malicious code^{10–12}; second, the current 200-bp screening windows^{13,14} should be reduced to the length of the shortest homology-directed repair template required for deobfuscation; third, fulfilled orders should be revisited when new information arises; fourth, data should be shared (in a privacy-preserving manner)¹⁵ to enable detection of malicious orders deliberately distributed across multiple synthesizers; and fifth, enhanced protocols should be implemented by legislation and regulation¹⁶.

Cyber dangers are spilling over to the physical space, blurring the separation between the digital world and the real

world, especially with increasing levels of automation in the biological lab. Best practices and standards must be woven into operational biological protocols to combat these threats.

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Competing interests

The authors declare no competing interests.

Supporting US public health experts

To the Editor — As CEOs of biotechnology companies, we are writing this letter in support of US National Institutes of Allergy and Infectious Disease (NIAID) director Anthony Fauci and the institutions and organizations that are working tirelessly to combat the COVID-19 pandemic.

The biotechnology industry is the world's greatest innovation engine for creating new medicines and vaccines that improve the human condition. It is a strategic asset to the nation. The past few decades have shown extraordinary progress in our ability to fight disease. This year, our industry has risen to the challenge of overcoming the deadly pandemic that has gripped the world, putting that engine to work at miraculous speed to develop therapies and vaccines.

To do so most effectively requires close collaboration among biopharmaceutical companies; regulatory authorities such as the US Food and Drug Administration (FDA); public health authorities such as the US Centers for Disease Control and Prevention (CDC); federal, state and local

government authorities; scientific and medical institutions, such as the US National Institutes of Health (NIH); and world experts in epidemiology and infectious disease — most prominently, Anthony Fauci. As we come ever closer to producing safe, effective therapies for COVID-19, it is critical that all of these institutions and experts work together to ensure the best, most rapid possible outcomes for all Americans and, indeed, for people worldwide.

The institutions of the CDC, FDA and NIH comprise tens of thousands of men and women who care deeply about society and making the world a better place. These nameless individuals represent our 'United Armed Forces' against COVID-19. They fight with brains instead of weapons, displaying the same courage and dedication as our armed forces in times of war, and they deserve our eternal gratitude. We and the associates of our companies consider that we fight alongside these individuals as part of the same cause, wielding science against our common adversary.

However, we are concerned that various parties in this critical coalition have come under politically motivated attacks. Targets have included, among others, the FDA, the CDC and Dr. Fauci; in Fauci's case this has occurred to the point where he now requires a security detail. Not only are these attacks completely unjustified, they risk intimidating and demoralizing the very people we all are relying on to help end the COVID-19 nightmare. As such, they are irresponsible and a pose danger to us all.

Fauci is a giant of epidemiology, one of the world's most respected scientists in infectious diseases, and an American hero who has served multiple administrations — both Republican and Democratic — for decades. He has recommended measures that have saved likely scores of thousands of lives in our country. Had his counsel been taken more widely, even more lives could have been saved. Unfortunately, the United States today has experienced the largest number of deaths from COVID-19 of any country in the world.

When a public servant of Fauci's caliber is attacked, it puts our collective efforts, and the safety of the American public, at risk. Senator Lamar Alexander (Republican, Tennessee) posted on Twitter: "Dr. Fauci is one of our country's most distinguished public servants" and "If more Americans paid attention to his advice, we'd have fewer cases of COVID-19, & it would be safer to go back to school & back to work & out to eat."

This is the sort of responsible, truthful support that is needed from our public officials. Many of our colleagues and friends are working as part of Operation Warp Speed; we stand united with them, with the many good people at FDA, CDC and NIH, and with Dr. Fauci in upholding the high scientific, medical and ethical principles that will allow us to defeat COVID-19. □

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Competing interests

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Guidelines for reporting single-cell RNA-seq experiments

To the Editor — Single-cell RNA-sequencing (scRNA-seq) has undergone major technological advances in recent years, enabling the conception of various organism-level cell atlas projects. With increasing numbers of datasets being deposited in public archives, there is a need to ensure the reproducibility of such datasets. To this end, we describe the minSCe (Minimum Information about a Single-Cell Experiment) guidelines for a minimum set of metadata needed for robust comparative analyses of scRNA-seq.

scRNA-seq experiments have many advantages over so-called bulk RNA-sequencing and microarray experiments, as they allow researchers to study gene expression at an individual-cell rather than at tissue level¹. As the scRNA-seq technologies are maturing, these experiments are becoming increasingly high-throughput and widespread. Data from an estimated 3,000 scRNA-seq studies have been submitted to NCBI's Gene Expression Omnibus (GEO)², EMBL-EBI's ArrayExpress³ and the European Nucleotide Archive (ENA)⁴ in recent years. Large collaborative efforts are taking off, such as the Human Cell Atlas (HCA)⁵, which aims to uncover the gene expression profiles of all human cell types; the Fly Cell Atlas (<http://flycellatlas.org/>), which has similar aims for *Drosophila*, or the Human Biomolecular Atlas Program (HuBMAP)⁶, as well as organ-specific projects, such as the BRAIN Initiative Cell Census Consortium⁷.

Meta-analyses combining data from independent scRNA-seq studies have been performed, revealing that although overall conclusions from independent studies confirm each other, there are notable differences^{8,9}. To ensure that the results

Fig. 1 | Typical design steps of single-cell transcriptomics experiments with examples for each step. ERCC, External RNA Controls Consortium; FACS, fluorescence-activated cell sorting; PCR, polymerase chain reaction; UMI, unique molecular identifier.

of individual scRNA-seq studies can be reproduced, to allow for reuse of data generated in such experiments, and, more generally, to enable researchers to build on previous discoveries, it is important that necessary minimal information about scRNA-seq experiments is collected and preserved together with the respective data. The community agreement and publication of the Minimum Information About a Microarray Experiment (MIAME)¹⁰ guidelines almost two decades ago was a major milestone in the way functional genomics data have been reported and archived. For the last two decades, the functional genomics data archives at EBI and NCBI have been accepting microarray and bulk RNA-seq datasets; for the latter, the minimal metadata standards

have now been well established in the MINSEQE (Minimum Information about a SEQuencing Experiment) guidelines, but the emergence of protocols that can assay transcriptomics at single-cell resolution brings new requirements.

There is a clear need to establish minimum standards for reporting data and metadata for the various scRNA-seq assays. ArrayExpress and the HCA have published online guidelines for technical information required for scRNA-seq data submissions; however, these are not yet widely adopted community standards. Such standards would serve as the guiding principles and would ensure the reusability of the submitted datasets, guide the adaptation of existing archival resources and enable reproducibility of analysis by the wider