

References

Aktuell

BREZNAU 2023

Nate Breznau, Eike Mark Rinke & Alexander Wuttke, *Many-analyst studies should consider effect sizes and CIs, Reply to Mathur et al.* [PNAS 120 \(2023\), e2219555120](#).

Almost a third of the Conclusions our research teams submitted (28.5%) held that the hypothesis was supported—despite the consistently small effect sizes. Support of this hypothesis by the team and the number of their models with a $P < 0.05$ and hypothesis-consistent direction correlate at 0.55–0.66 (with not achieving significance and rejecting the hypothesis). This suggests that statistical significance testing was a key aspect in the teams' own conclusion formation processes.

IRRGANG 2022

Pascal Irrgang, Juliane Gerling, Katharina Kocher, Kilian Schober, Thomas H. Winkler & Matthias Tenbusch et al., *Class switch towards non-inflammatory, spike-specific IgG4 antibodies after repeated SARS-CoV-2 mRNA vaccination.* [SciImm \(2022\), preprint, 1–14](#). [DOI:10.1126/sciimmunol.ade2798](#).

[SciImm2022.12-Irrgang-Supplement.pdf](#)

RNA vaccines are efficient preventive measures to combat the SARS-CoV-2 pandemic. High levels of neutralizing SARS-CoV-2-antibodies are an important component of vaccine-induced immunity. Shortly after the initial two mRNA vaccine doses, the IgG response mainly consists of the pro-inflammatory subclasses IgG1 and IgG3. Here, we report that several months after the second vaccination, SARS-CoV-2-specific antibodies were increasingly composed of non-inflammatory IgG4, which were further boosted by a third mRNA vaccination and/or SARS-CoV-2 variant breakthrough infections. IgG4 antibodies among all spike-specific IgG antibodies rose on average from 0.04% shortly after the second vaccination to 19.27% late after the third vaccination. This induction of IgG4 antibodies was not observed after homologous or heterologous SARS-CoV-2 vaccination with adenoviral vectors. Single-cell sequencing and flow cytometry revealed substantial frequencies of IgG4-switched B cells within the spike-binding memory B-cell population (median 14.4%; interquartile range (IQR) 6.7–18.1%) compared to the overall memory B-cell repertoire (median 1.3%; IQR 0.9–2.2%) after three immunizations. Importantly, this class switch was associated with a reduced capacity of the spike-specific antibodies to mediate antibody-dependent cellular phagocytosis and complement deposition. Since Fc-mediated effector functions are critical for antiviral immunity, these findings may have consequences for the choice and timing of vaccination regimens using mRNA vaccines, including future booster immunizations against SARS-CoV-2.

Pascal Irrgang, Juliane Gerling, Katharina Kocher, Dennis Lapuente, Philipp Steininger, Katharina Habenicht, Monika Wytopil, Stephanie Beileke, Simon Schäfer, Jahn Zhong, George Ssebyatika, Thomas Krey, Valeria Falcone, Christine Schüle, Antonia Sophia Peter, Krystelle Nganou-Makamdop, Hartmut Hengel, Jürgen Held, Christian Bogdan, Klaus Überla, Kilian Schober, Thomas H. Winkler & Matthias Tenbusch

KOZLOV 2023

Max Kozlov, *What happened to the ‘game changing’ Covid drug Paxlovid?* [nature](#) **613** (2023), 224–225.

Insufficient investment and fears about rebound are driving down use of a lifesaving antiviral.

People also perceive COVID-19 as less risky than earlier in the pandemic, Griffin says, making them less likely to seek treatment and physicians less likely to prescribe medications promptly. Paxlovid works by inhibiting viral replication, which mostly occurs early in the disease course. This leaves a narrow window of time for people to receive treatment, which does not mesh well with “this mentality of ‘Let’s wait and see how you do’,” among doctors treating people with COVID-19, says Griffin.

MATHUR 2023

Maya B. Mathur, Christian Covington & Tyler J. VanderWeele, *Variation across analysts in statistical significance, yet consistently small effect sizes.* [PNAS](#) **120** (2023), e2218957120.

A well-known problem with exclusive focus on statistical significance is that, for very large datasets, even a very small point estimate can be significant. Breznau et al.’s teams analyzed a dataset containing tens of thousands of observations, which explains the substantial variation in estimates’ significance even though the estimates themselves were consistently quite small and close to the null.

YONKER 2023

Lael M. Yonker, Zoe Swank, Yannic C. Bartsch, Alessio Fasano & David R. Walt et al., *Circulating Spike Protein Detected in Post-COVID-19 mRNA Vaccine Myocarditis.* [Circulation](#) (2023), preprint, 1–10. DOI:10.1161/CIRCULATIONAHA.122.061025.

Circulation2023.01-Yonker-Supplement.pdf

BACKGROUND: Cases of adolescents and young adults developing myocarditis after vaccination with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)-targeted mRNA vaccines have been reported globally, but the underlying immunoprofiles of these individuals have not been described in detail.

METHODS: From January 2021 through February 2022, we prospectively collected blood from 16 patients who were hospitalized at Massachusetts General for Children or Boston Children’s Hospital for myocarditis, presenting with chest pain with elevated cardiac troponin T after SARS-CoV-2 vaccination. We performed extensive antibody profiling, including tests for SARS-CoV-2-specific humoral responses and assessment for autoantibodies or antibodies against the human-relevant virome, SARS-CoV-2-specific T-cell analysis, and cytokine and SARS-CoV-2 antigen profiling. Results were compared with those from 45 healthy, asymptomatic, age-matched vaccinated control subjects.

RESULTS: Extensive antibody profiling and T-cell responses in the individuals who developed postvaccine myocarditis were essentially indistinguishable from those of vaccinated control subjects, despite a modest increase in cytokine production. A notable finding was that markedly elevated levels of full-length spike protein (33.9 ± 22.4 pg/mL), unbound by antibodies, were detected in the plasma of individuals with postvaccine myocarditis, whereas no free spike was detected in asymptomatic vaccinated control subjects (unpaired t test; $P < 0.0001$).

CONCLUSIONS: Immunoprofiling of vaccinated adolescents and young adults revealed that the mRNA vaccine-induced immune responses did not differ between individuals who developed myocarditis and individuals who did not. However,

free spike antigen was detected in the blood of adolescents and young adults who developed post-mRNA vaccine myocarditis, advancing insight into its potential underlying cause.

Keywords: COVID-19 | mRNA vaccine | myocarditis | spike protein | SARS-CoV-2

Lael M. Yonker, Zoe Swank, Yannic C. Bartsch, Madeleine D. Burns, Abigail Kane, Brittany P. Boribong, Jameson P. Davis, Maggie Loiselle, Tanya Novak, Yasmeen Senussi, MBBS, Chi-An Cheng, Eleanor Burgess, Andrea G. Edlow, Janet Chou, Audrey Dionne, Duraisamy Balaguru, Manuella Lahoud-Rahme, Moshe Arditi, Boris Julg, Adrienne G. Randolph, Galit Alter, Alessio Fasano, David R. Walt

Archäologie

NEWITZ 2021

Annalee Newitz, *Four lost cities, A secret history of the urban age.* (New York 2022).

Klima

HÖRHOOLD 2023

M. Hörhold, T. Münch, S. Weißbach, S. Kipfstuhl, J. Freitag, I. Sassen, G. Lohmann, B. Vinther & T. Laepple, *Modern temperatures in central-north Greenland warmest in past millennium.* [nature 613 \(2023\), 503–507.](#)

The Greenland Ice Sheet has a central role in the global climate system owing to its size, radiative effects and freshwater storage, and as a potential tipping point¹. Weather stations show that the coastal regions are warming², but the imprint of global warming in the central part of the ice sheet is unclear, owing to missing long-term observations. Current ice-core-based temperature reconstructions^{3–5} are ambiguous with respect to isolating global warming signatures from natural variability, because they are too noisy and do not include the most recent decades. By systematically redrilling ice cores, we created a high-quality reconstruction of central and north Greenland temperatures from ad 1000 until 2011. Here we show that the warming in the recent reconstructed decade exceeds the range of the pre-industrial temperature variability in the past millennium with virtual certainty ($P < 0.001$) and is on average 1.5 ± 0.4 degrees Celsius (1 standard error) warmer than the twentieth century. Our findings suggest that these exceptional temperatures arise from the superposition of natural variability with a long-term warming trend, apparent since ad 1800. The disproportionate warming is accompanied by enhanced Greenland meltwater run-off, implying that anthropogenic influence has also arrived in central and north Greenland, which might further accelerate the overall Greenland mass loss.

MILLS 2023

Maria B. Mills & Terhi Riutta et al., *Tropical forests post-logging are a persistent net carbon source to the atmosphere.* [PNAS 120 \(2023\), e2214462120.](#)

[pnas120-e2214462120-Supplement.pdf](#)

Logged and structurally degraded tropical forests are fast becoming one of the most prevalent land-use types throughout the tropics and are routinely assumed to be a net carbon sink because they experience rapid rates of tree regrowth. Yet this assumption is based on forest biomass inventories that record carbon stock recovery but fail to account for the simultaneous losses of carbon from soil and necromass. Here, we used forest plots and an eddy covariance tower to quantify and partition net ecosystem CO₂ exchange in Malaysian Borneo, a region that is a hot spot for deforestation and forest degradation. Our data represent the complete carbon budget for tropical forests measured throughout a logging event and subsequent recovery and found that they constitute a substantial and persistent net carbon source. Consistent with existing literature, our study showed a significantly greater woody biomass gain across moderately and heavily logged forests compared with unlogged forests, but this was counteracted by much larger carbon losses from soil organic matter and deadwood in logged forests. We estimate an average carbon source of 1.75 ± 0.94 Mg C ha⁻¹ yr⁻¹ within moderately logged plots and 5.23 ± 1.23 Mg C ha⁻¹ yr⁻¹ in unsustainably logged and severely degraded plots, with emissions continuing at these rates for at least one-decade post-logging. Our data directly contradict the default assumption that recovering logged and degraded tropical forests are net carbon sinks, implying the amount of carbon being sequestered across the world's tropical forests may be considerably lower than currently estimated.

Keywords: carbon budget | logging | tropical ecology | carbon dynamics | land use

Maria B. Mills, Yadvinder Malhi, Robert M. Ewers, Lip Khoo Kho, Yit Arn Teh, Sabine Both, David F. R. P. Burslem, Noreen Majalap, Reuben Nilus, Walter Huaraca Huasco, Rudi Cruz, Milenka M. Pillco, Edgar C. Turner, Glen Reynolds & Terhi Riutta

Significance: Logged tropical forests are counted as important carbon sinks in global carbon budgets due to the woody biomass they regain when they regrow following disturbance, but this assumption ignores the simultaneous carbon losses from the ecosystem. We found that, when quantifying all the source and sink terms of the ecosystem carbon budget, logged tropical forests are a net source of carbon to the atmosphere. This source persists at least 10 y following logging, meaning rates of carbon sequestration in recovering tropical forests are likely much lower than estimated.

Methoden

O'GRADY 2023

Cathleen O'Grady, *Unlucky Numbers*. [science](#) **379** (2023), 228–228.

Richard Gill is fighting the shoddy statistics that put nurses in prison for serial murder.

But Gill knew the statistician working on the case and considered him a decent, careful person. “So I thought I didn't have to.”

In 2007, convinced of De Berk's innocence, Gill organized a petition to reopen the case. Yet Grünwald says Gill's cheerful fearlessness was crucial. Many Dutch statisticians knew and liked Elffers, he says. “People . . . were afraid to say out loud that he was doing something stupid and nonsensical. Richard had no problems with that at all.”

Thirteen years on, Gill, now retired, is watching the Letby case closely, but his obsession with forensic statistics has begun to subside. He hopes younger statisticians will feel compelled to help when bad statistics lead to injustice, as he did.

Mittelalter

GABRIELE 2021

Matthew Gabriele & David M. Perry, *The bright ages, A new history of medieval Europe*. (New York 2021).

Physik

BROUT 2022

Dillon Brout et al., *The Pantheon+ Analysis: Cosmological Constraints*. [The Astrophysical Journal](#) **938** (2022), 110, 1–24.

We present constraints on cosmological parameters from the Pantheon+ analysis of 1701 light curves of 1550 distinct Type Ia supernovae (SNe Ia) ranging in redshift from $z = 0.001$ to 2.26. This work features an increased sample size from the addition of multiple cross-calibrated photometric systems of SNe covering an increased redshift span, and improved treatments of systematic uncertainties in comparison to the original Pantheon analysis, which together result in a factor of 2 improvement in cosmological constraining power. For a flat Λ CDM model, we find $\Omega_M = 0.334 \pm 0.018$ from SNe Ia alone. For a flat w_0 CDM model, we measure $w_0 = -0.90 \pm 0.14$ from SNe Ia alone, $H_0 = 73.5 \pm 1.1$ km s⁻¹ Mpc⁻¹ when including the Cepheid host distances and covariance (SH0ES), and $w_0 = 0.978 -0.031 +0.024$ when combining the SN likelihood with Planck constraints from the cosmic microwave background (CMB) and baryon acoustic oscillations (BAO); both w_0 values are consistent with a cosmological constant. We also present the most precise measurements to date on the evolution of dark energy in a flat w_0 waCDM universe, and measure $w_a = 0.1 -2.0 +0.9$ from Pantheon+ SNe Ia alone, $H_0 = 73.3 \pm 1.1$ km s⁻¹ Mpc⁻¹ when including SH0ES Cepheid distances, and $w_a = 0.65 -0.32 +0.28$ when combining Pantheon+ SNe Ia with CMB and BAO data. Finally, we find that systematic uncertainties in the use of SNe Ia along the distance ladder comprise less than one-third of the total uncertainty in the measurement of H_0 and cannot explain the present “Hubble tension” between local measurements and early universe predictions from the cosmological model.

Dillon Brout, Dan Scolnic, Brodie Popovic, Adam G. Riess, Anthony Carr, Joe Zuntz, Rick Kessler, Tamara M. Davis, Samuel Hinton, David Jones, W. D’Arcy Kenworthy, Erik R. Peterson, Khaled Said, Georgie Taylor, Noor Ali, Patrick Armstrong, Pranav Charvu, Arianna Dwomoh, Cole Meldorf, Antonella Palmese, Helen Qu, Benjamin M. Rose, Bruno Sanchez, Christopher W. Stubbs, Maria Vincenzi, Charlotte M. Wood, Peter J. Brown, Rebecca Chen, Ken Chambers, David A. Coulter, Mi Dai, Georgios Dimitriadis, Alexei V. Filippenko, Ryan J. Foley, Saurabh W. Jha, Lisa Kelsey, Robert P. Kirshner, Anais Möller, Jessie Muir, Seshadri Nadathur, Yen-Chen Pan, Armin Rest, Cesar Rojas-Bravo, Masao Sako, Matthew R. Siebert, Mat Smith, Benjamin E. Stahl & Phil Wiseman

Story or Book

LIGHTMAN 2023

Bernard Lightman, *Making modern science*. [science](#) **379** (2023), 244.

Victorian values permeate contemporary scientific culture, maintains a historian.

How the Victorians Took Us to the Moon. Iwan Rhys Morus. Pegasus, 2022. 400 pp.

Although Morus develops a complex argument throughout the book, his elegant and accessible writing style will appeal to a variety of audiences, including

historians of science, scientists, and casual readers. His ability to synthesize recent scholarship to present a novel, coherent story is truly impressive.

Men of invention, such as Isambard Kingdom Brunel, John Henry Pepper, and Thomas Edison, were held up as powerful, charismatic, and heroic figures during this era. As Morus points out, however, this image of the scientific loner was an illusion. Scientific discovery and invention were often the product of the efforts of a multitude of expert workers.

Morus ends with a sobering thought: Unreflectingly following the Victorian recipe for future-making sets limitations on how we might remake our own futures.

SCHATTNER-RIESER 2022

Ursula Schattner-Rieser, *The Samaritan Pentateuch*. [Biblische Notizen 195 \(2022\)](#), 142.

Stefan Schorch, *Genesis (The Samaritan Pentateuch)* 451 p., E 119,95, Berlin: De Gruyter 2021, ISBN 978-3110709506.

Die Ausgabe basiert auf den ältesten erhaltenen samaritanischen Pentateuchhandschriften mit Berücksichtigung sämtlicher Varianten und Variationen. Der laufende Bibeltext wird in hebräischer Quadratschrift, die Kapitelbezeichnung und Kolumnentitel, sowie die Schreibernotiz am Endes des Buches in samaritanischer Schrift wiedergegeben. Nicht-samaritanisch ist auch die in masoretischen Texten übliche Kapitel- und Verszählung. Zusätzliche Verse gegenüber dem TM werden mit der Zahl des vorangehenden Verses und nachgestellten Kleinbuchstaben angegeben.