

NEWS & COMMENTARIES



Bombed buildings at Al-Aqsa University’s Khan Younis campus.

By Michele Catanzaro, 2025

These Gaza scientists are keeping research alive amid war, destruction and uncertainty

Researchers in Gaza tell Nature of ‘unwavering commitment to education and knowledge’ as most universities lie damaged or destroyed. The 42-day ceasefire between Hamas and Israel, which took effect on 19 January, provides a vital opportunity to begin to address the devastation from the 15-month war, scientists there have told Nature. The ceasefire might yet prove temporary, and whether or not it holds, the long-term future for the territory and its citizens remains highly uncertain. While daily bombing is suspended, international organizations can complete a detailed assessment of Gaza’s water, food, health and infrastructure needs, the researchers say. *“There’s a need to document what has been happening here in Gaza and to publish [the results] with other researchers worldwide,”* says neuroscientist Khamis Elessi, head of the Evidence-Based Medicine Unit at the Islamic

University of Gaza, who now spends most of his time treating injured people at the Ahli Arab hospital.

<https://www.nature.com/articles/d41586-025-00160-w>



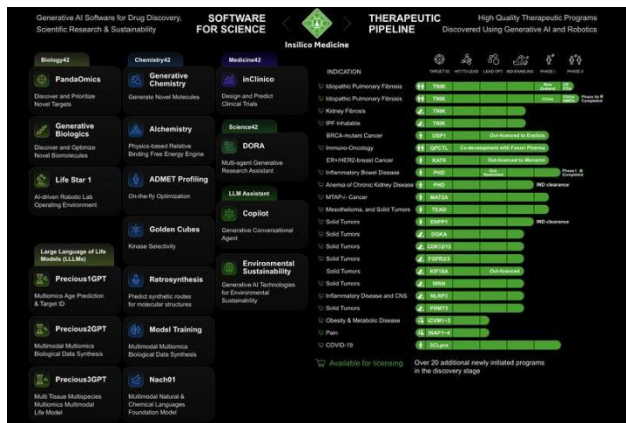
American chaos: standing up for health and medicine

The Lancet, 2025

Withdrawal from WHO and the Paris Agreements. USAID shuttered and aid halted, ceasing health programmes globally. A freeze on US\$3 trillion worth of federal grants and loans, jeopardising the functioning of Medicaid. A sweeping pause on key activities across the National Institutes of Health (the world’s largest biomedical research institution). Stop work orders at the Centers for Disease Control and Prevention (CDC). Denial of gender diversity. The Mexico City policy

reinstated. Communications blackouts, which saw the Morbidity and Mortality Weekly Report not published for the first time in 60 years. Donald Trump’s actions domestically and globally are not a measured reappraisal of US priorities. They are a sweeping and damaging attack on the health of the American people and those dependent on US foreign assistance.

<https://www.thelancet.com/action/showPdf?pii=S0140-6736%2825%2900237-5>



Insilico New look



Welcome our new website! Since we evolved to become a global AI powerhouse

with multiple AI-as-a-Service and Therapeutic-program-as-a-Service products we decided to make the website practical and functional. Pharma executives can now select the many "lego blocks" that can help accelerate every part of their R&D platforms and even expand into novel materials or sustainability and, most importantly, they can choose one or more programs that fit their portfolio strategies for in-licensing. [Check out www.insilico.com](http://www.insilico.com)



RNA gene therapies offer hope for millions with high cholesterol

By Natalie Healey, 2025

Base editing, antisense oligonucleotides and siRNA therapies that target low-density lipoprotein and the genes encoding molecules that regulate it are being tested in several clinical trials.

Since the late 1980s, statins have been the mainstay of cholesterol management, lowering low-density lipoprotein (LDL) levels and preventing countless heart attacks. Yet many patients do not achieve their target LDL cholesterol levels, either because adherence to daily medication is a challenge or because their genetic

profiles make achieving optimal cholesterol levels more difficult. Emerging RNA-based therapies, however, are changing the treatment landscape by targeting cholesterol at the genetic level in the liver (where most cholesterol is made), offering the possibility of long-lasting effects with fewer doses. Although these drugs were initially developed for people with genetic causes of high cholesterol, clinical trials are now testing their wider use.

<https://www.nature.com/articles/d41591-025-00002-2>



FDA Novel Drug Therapy Approvals for 2024

In 2024, CDER approved 50 new drugs never before approved or marketed in the U.S., known as “novel” drugs. We also made other important approval decisions, such as approving previously approved drugs for new uses and broader patient populations. CDER’s novel drug approvals for 2024 are listed below. For more information, download the report.

<https://www.fda.gov/drugs/novel-drug-approvals-fda/novel-drug-approvals-2024>

<https://www.fda.gov/media/184967/download?attachment>



The weight-loss drugs being tested in 2025: will they beat Ozempic?

By **Giorgia Guglielmi, 2025**

Drug companies are trialling a host of medications that they hope will offer benefits beyond weight loss. Several new weight-loss medications are in development, aiming to enhance efficacy and offer additional health benefits. Tirzepatide has demonstrated the ability to reduce heart weight and fat, while Retatrutide has shown significant weight-loss potential in clinical trials. Orforglipron, an oral medication, is emerging as a promising alternative, and MariTide focuses on weight

maintenance post-treatment.

<https://www.nature.com/articles/d41586-025-00376-w>

SELECTED PUBLICATIONS



Expanding the human gut microbiome atlas of Africa

Dylan G. Maghini et al., 2025

<https://doi.org/10.1038/s41586-024-08485-8>

A large-scale gut microbiome study examined 1,801 women across Burkina Faso, Ghana, Kenya, and South Africa, revealing significant geographic and lifestyle-based variations in microbial composition. Urbanization was linked to the loss of *Treponema* and *Cryptobacteroides* species, alongside an increase in *Bifidobacterium* species. Researchers identified 1,005 novel bacterial metagenome-assembled genomes and

discovered a unique microbial signature associated with HIV, including *Dysosmobacter welbionis* and *Enterocloster* species.



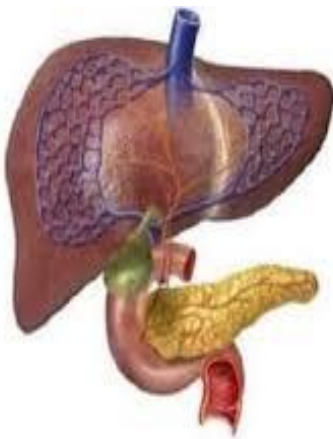
Integration of 168,000 samples reveals global patterns of the human gut microbiome

Richard J. Abdill et al., 2025

DOI: [10.1016/j.cell.2024.12.017](https://doi.org/10.1016/j.cell.2024.12.017)

A comprehensive analysis of 168,464 publicly available gut microbiome samples highlighted significant regional differences, with Central and Southern Asia exhibiting distinct microbial compositions compared to Europe and North America. Additionally, technical factors such as DNA extraction methods and primer selection were found to influence microbiome composition. Machine

learning models trained on this dataset successfully predicted sample origins based on microbiome profiles, underscoring the potential for further microbiome-based research.

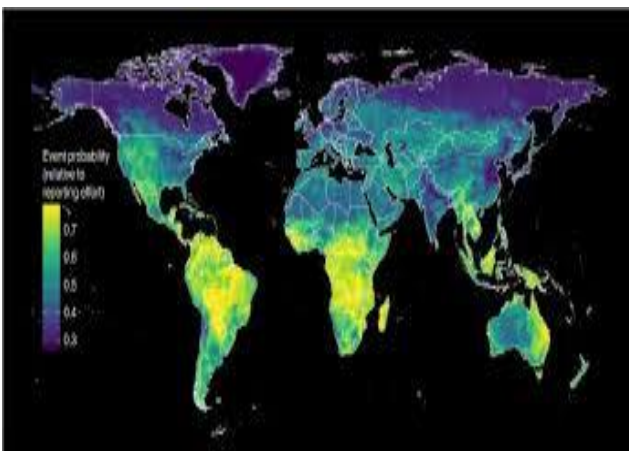


Pregnancy and the liver

Mussarat N Rahim

[https://doi.org/10.1016/S0140-6736\(24\)02351-1](https://doi.org/10.1016/S0140-6736(24)02351-1)

Pregnancy induces physiological liver changes that can exacerbate or alleviate pre-existing liver conditions. The increasing prevalence of conditions such as hypertension, diabetes, and metabolic syndrome has led to a rise in pregnancy-related liver complications. As pregnancy rates among individuals with cirrhosis or post-liver transplantation rise, understanding these changes is crucial. Pregnancy also presents an opportunity for early disease intervention, potentially shaping long-term maternal and fetal health outcomes.



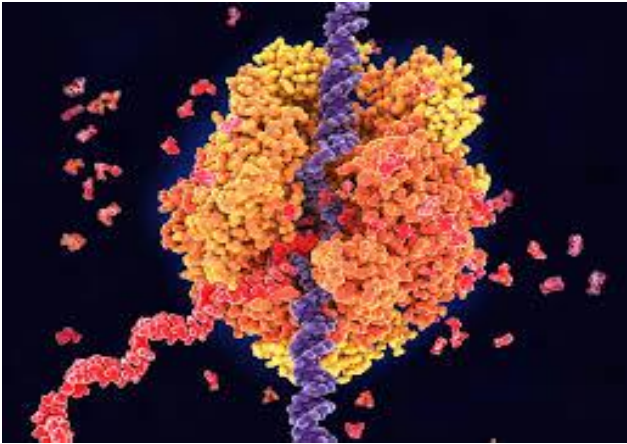
Mapping hotspots of zoonotic pathogen emergence: an integrated model-based and participatory-based approach

Julianne Meisner et al., 2025

[https://doi.org/10.1016/S2542-5196\(24\)00309-7](https://doi.org/10.1016/S2542-5196(24)00309-7)

An increase in pandemics of zoonotic origin has led to a growing interest in using statistical prediction to identify hotspots of zoonotic emergence. However, the rare nature of pathogen emergence requires modellers to impose simplifying assumptions, which limit the model's validity. We present a novel approach to

hotspot mapping that aims to improve validity by combining model-based insights with expert knowledge. This approach shows potential for refining deployment of countermeasures to prevent future pandemics.

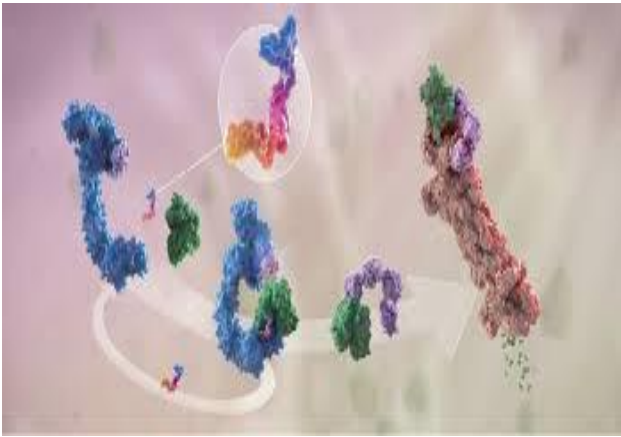


RNA polymerase II at histone genes predicts outcome in human cancer

Steven Henikoff et al., 2025
[doi:10.1126/science.ads2169](https://doi.org/10.1126/science.ads2169)

Genome-wide hypertranscription is a hallmark of cancer and a predictor of poor prognosis, but how does it drive tumor progression? Using a novel method to map RNA polymerase II (RNAPII) in clinical samples, researchers found widespread RNAPII elevations in gliomas and various human tumors. Notably, RNAPII hyperactivity at histone genes correlated with tumor grade, recurrence risk, and chromosomal instability.

These findings suggest that histone gene hypertranscription may fuel cancer overproliferation and aneuploidy, offering new insights for precision oncology.



A PROTAC degrader suppresses oncogenic functions of PTK6, inducing apoptosis of breast cancer cells

Criseyda Martinez et al., 2025
[doi:10.1016/j.chembiol.2024.10.008](https://doi.org/10.1016/j.chembiol.2024.10.008)

Protein tyrosine kinase 6 (PTK6) is a key oncogenic driver, but existing kinase inhibitors have failed in clinical translation. This study introduces MS105, a PROTAC-based PTK6 degrader, which effectively inhibits breast cancer cell growth and induces apoptosis—effects not seen with kinase inhibitors alone. While both approaches reduce cell migration, MS105

fully mimics PTK6 downregulation, highlighting the importance of targeting PTK6 beyond its kinase activity.

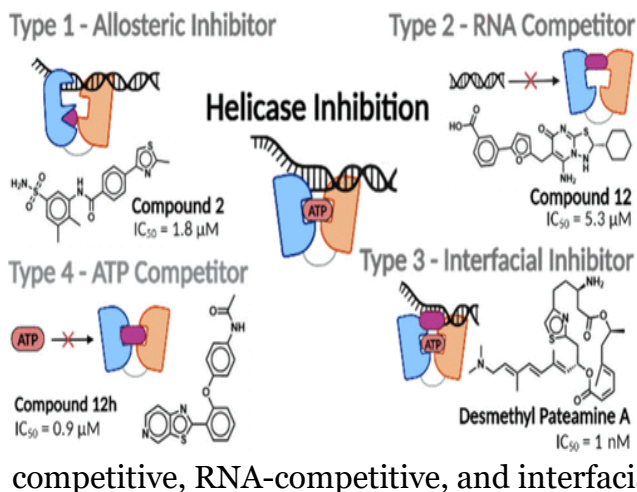


Bat-infecting merbecovirus HKU5-CoV lineage 2 can use human ACE2 as a cell entry receptor

Chen et al. 2025
[Doi:10.1016/j.cell.2025.01.042](https://doi.org/10.1016/j.cell.2025.01.042)

Researchers have identified HKU5-CoV-2, a novel merbecovirus in bats, that efficiently binds to human ACE2, suggesting a potential spillover risk. Structural analysis reveals a unique receptor-binding mode, distinct from other ACE2-using merbecoviruses but sharing key features with sarbecoviruses and NL63.

Functional studies show HKU5-CoV-2 can infect human cells and organoids, highlighting its strong adaptation to human hosts. These findings emphasize the need for ongoing surveillance of animal coronaviruses with zoonotic potential



Structural Chemistry of Helicase Inhibition

Lakshi Selvaratnam, Timothy M. Willson, Matthieu Schapira

Doi: [10.1021/acs.jmedchem.4c01909#](https://doi.org/10.1021/acs.jmedchem.4c01909)

Helicases are essential for genome maintenance and play critical roles in cancer, viral infections, and neurodegenerative diseases. Despite their therapeutic potential, drug discovery remains challenging due to their dynamic nature and conserved active sites. Structural analysis of helicase-inhibitor complexes reveals four inhibition mechanisms: allosteric, ATP-competitive, RNA-competitive, and interfacial binding.



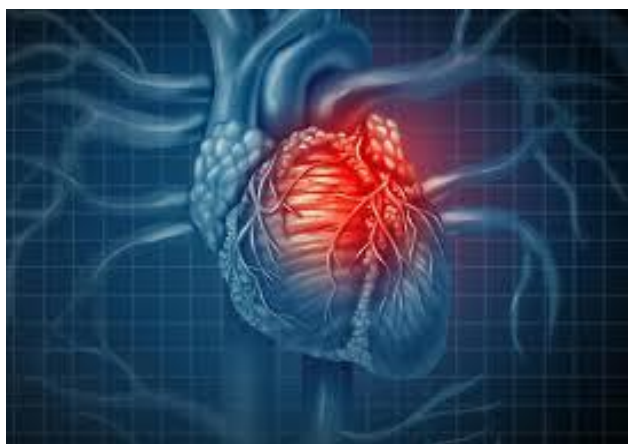
Structural insights into human brachyury DNA recognition and discovery of progressible binders for cancer therapy

Joseph A. Newman et al., 2025

<https://doi.org/10.1038/s41467-025-56213-1>

Brachyury, a key driver of chordoma and other solid tumors, has long been considered undruggable due to its lack of ligands. This study challenges that notion by resolving the structure of human brachyury alone and bound to DNA, offering insights into its function and a disease-associated mutation. Using crystallographic

fragment screening, researchers identified multiple binding hotspots and developed a thiazole-based chemical series with promising low μM potency



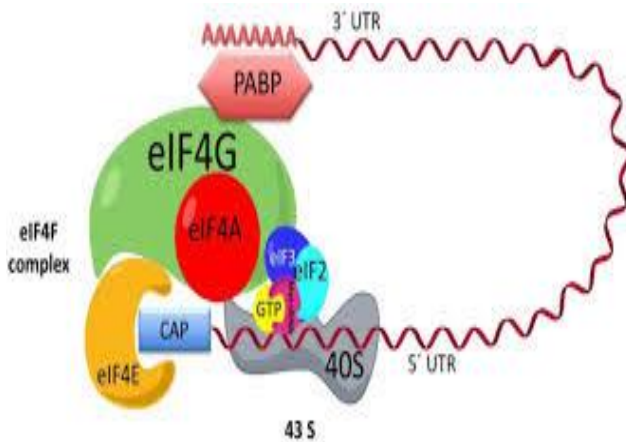
An FDA-approved drug structurally and phenotypically corrects the K210del mutation in genetic cardiomyopathy models

Ping Wang et al., 2025

<https://doi.org/10.1172/JCI174081>

Dilated cardiomyopathy (DCM) linked to genetic disorders leads to reduced heart muscle contractility, which significantly contributes to high rates of illness and death. We have determined the crystal structure of the troponin complex with the K210del mutation. This mutation causes an allosteric shift within the troponin

complex, distorting the activation calcium-binding domain of troponin C (TnnC) at position S69 and resulting in disrupted calcium coordination.



Small-molecule modulators of B56-PP2A restore 4E-BP function to suppress eIF4E-dependent translation in cancer cells

Michelle A. Lum et al., 2025

<https://doi.org/10.1172/JCI176093>

Dysregulated translation mediated by eIF4E plays a crucial role in tumor development and resistance to treatment. The eIF4E-binding proteins (4E-BP1/2/3) serve as key negative regulators of this translation process, yet they often become inactivated in tumors due to inhibitory phosphorylation or reduced expression.

Experiments involving cap-binding and coimmunoprecipitation revealed that the activation of B56-PP2A(s) inhibits the formation of the eIF4F translation initiation complex, while cap-dependent translation assays validated the translation-inhibitory impact of SMAPs. Consequently, B56-PP2A(s) manage a program that suppresses translation, which includes the transcriptional activation of 4E-BP1. Together, these insights, along with SMAPs' capability to modulate 4E-BP1 in living organisms, underscore the promising potential of PP2A activators in cancer treatment and in overcoming therapeutic resistance.

JOBS



PhD fellowship in Computational Aging Research Copenhagen, Hovedstaden (DK)

Agreement between the Danish Ministry of Finance and the Danish Confederation.

Closing date 9 Mar 2025

<https://candidate.hr-manager.net/ApplicationInit.aspx?cid=1307&ProjectId=163492&DepartmentId=19000&MediaId=4638>



**Imperial College
London**

Lecturer in Cell Biology

Imperial College London - Department of Metabolism, Digestion and Reproduction

<https://www.jobs.ac.uk/job/DLV240/lecturer-in-cell-biology>

**We only ask you to co-sponsor scientific event
for the emerging countries contact us:
admin@algeriansca-dz.org**

