ESCMID 2026

ESCMID Global reaffirms itself not only as a platform for cutting-edge science, but as a unifying force in an increasingly complex world

Review of the European Society of Clinical Microbiology and Infectious Diseases (ESCMID) Global Congress 2026

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THIS SPRING, Munich, Germany, hosted the 36th European Society of Clinical Microbiology and Infectious Diseases (ESCMID) Global Congress from 17th–21st April, bringing together a global community of infectious diseases experts at a time marked by geopolitical tension, rising healthcare costs, and eroding public trust in science.

ESCMID's growing community now includes more than **14,500** members worldwide, with over a third based outside Europe

In his opening address, ESCMID President Robert Leo Skov acknowledged the ongoing global conflicts and divisions shaping the healthcare landscape, as well as the enduring impact of misinformation following the COVID-19 pandemic, particularly around vaccines. Coupled with funding cuts affecting scientific research, Skov warned that, "in this climate of growing uncertainty and distrust, science itself is under attack." He framed the current moment as a dual battle against infectious diseases and misinformation.

Skov outlined a clear path forward rooted in several key priorities. First, he emphasised the need to double down on scientific research, particularly in vaccinology. Reflecting this commitment, Maheshi Ramasamy, University of Oxford, UK; and Joint Committee on Vaccination and Immunisation, has been appointed as ESCMID's first Vaccines Subcommittee Director. At the same time, ESCMID continues to broaden its scientific reach, launching five new study groups spanning AI and digitalisation, mobile genetic elements and plasmids, urinary tract infections, sexually transmitted infections, and maternal and child health. With 37 study groups now active, the society reflects the scale and importance of international scientific collaboration. Efforts to tackle antimicrobial resistance (AMR) have also intensified, including the co-founding of the Global AMR Innovators Conference.

Equally important is the need to bridge science and policy. ESCMID has joined forces with organisations such as the Infectious Diseases Society of America (IDSA), the American Society for Microbiology (ASM), and the AMR Action Fund in calling on the G7 to adopt a One Health diagnostics compact, aimed at improving access to diagnostics, strengthening stewardship, and accelerating research and development. At the European level, the society contributes to advisory work for the Health Emergency Preparedness and Response Authority, while its AMR Science Policy Forums support alignment between national strategies and global commitments.

Global collaboration remains a defining feature of the society. ESCMID's growing community now includes more than 14,500 members worldwide, with over a third based outside Europe and 14% in low- and middle-income countries. The ESCMID Local Champions initiative, now

comprising 100 representatives across 88 countries, continues to strengthen regional engagement and knowledge exchange. Skov emphasised that progress in infectious diseases is built incrementally through shared achievements over time. He closed by calling for unity and collective responsibility in the face of future challenges.

The opening ceremony also celebrated excellence across the field. The ESCMID Award for Outstanding Contributions in Infection was presented to Leonard Leibovici, Tel Aviv University, Israel, for his pioneering work in neutropenia and sepsis. The Award for Excellence in Science went to Nicholas Day, Director of the Mahidol Oxford Tropical Medicine Research Unit, Bangkok, Thailand, recognising more than 3 decades of research in low-resource settings.

The Lifetime Achievement Award honoured Murat Akova of Hacettepe University School of Medicine, Türkiye, whose work has shaped the understanding of infections in immunocompromised patients and clinical ethics.

Finally, ESCMID Young Investigator Awards were presented to Sarah Delliere, Université Paris Cité and Hôpital Saint-Louis, France; Iris K. Minichmayr, Medical University of Vienna, Austria; Clark D. Russell, University of Edinburgh Centre for Inflammation Research in the Institute for Regeneration and Repair, UK; Daniel Pan, University of Leicester and University Hospitals of Leicester, UK; and Grace O. Androga, Malawi Liverpool Wellcome Programme, Blantyre, Malawi, highlighting the next generation of leaders in infectious diseases.

As the Congress unfolds, ESCMID Global reaffirms itself not only as a platform for cutting-edge science, but as a unifying force in an increasingly complex world. Read on for key insights from this year's meeting, and be sure to follow next year's coverage of ESCMID Global 2027.

High-Dose Influenza Vaccine Shows Consistent Benefit in Immunosuppressed Older Adults

FINDINGS from a prespecified analysis of the DANFLU-2 trial, presented at ESCMID Global 2026, provide important real-world evidence on influenza vaccine effectiveness in immunosuppressed older adults, a population at heightened risk of severe outcomes and often reduced vaccine responsiveness.[1]

This pragmatic, registry-based, randomised trial included 332,438 adults aged ≥65 years across the 2022/23–2024/25 influenza seasons. Participants were randomised 1:1 to receive either high-dose inactivated influenza vaccine (HD-IIV) or standard-dose vaccine (SD-IIV).

A total of 14,315 individuals (4.3%) met predefined criteria for immunosuppression, with 7,187 assigned to HD-IIV and 7,128 to SD-IIV. Baseline characteristics were well balanced between groups, although immunosuppressed participants had a higher burden of comorbidities and consistently higher event rates.

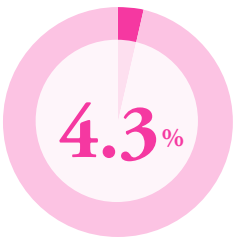
For the primary endpoint (hospitalisation for influenza or pneumonia), HD-IIV and SD-IIV showed comparable effectiveness across immunosuppression strata. However, HD-IIV was associated with fewer influenza-related hospitalisations overall, with a relative vaccine effectiveness (rVE) of 42.1% (95% CI: −16.5–72.3%) in immunosuppressed participants and 43.9% (95% CI: 26.5–57.3%) in non-immunosuppressed individuals.

Reductions were also observed in cardiorespiratory hospitalisations, with rVE estimates of 12.3% (95% CI: −2.2–24.7%) in immunosuppressed participants and 5.1% (95% CI: 0.5–10.7%) in those without immunosuppression.

Notably, a potential differential effect emerged for cardiovascular hospitalisations, where HD-IIV was associated with a greater reduction among immunosuppressed individuals (rVE: 26.7%; 95% CI: 6.3–42.9%) compared with non-immunosuppressed participants (rVE: 5.8%; 95% CI: −0.1–11.4%).

Across all endpoints, immunosuppressed participants experienced higher absolute rates of hospitalisation, highlighting their vulnerability despite vaccination.

Overall, these findings suggest that while high-dose and standard-dose influenza vaccines offer broadly similar protection against the primary endpoint, HD-IIV may provide additional benefits in reducing influenza-related and cardiorespiratory hospitalisations, with a possible enhanced effect on cardiovascular outcomes in immunosuppressed patients.



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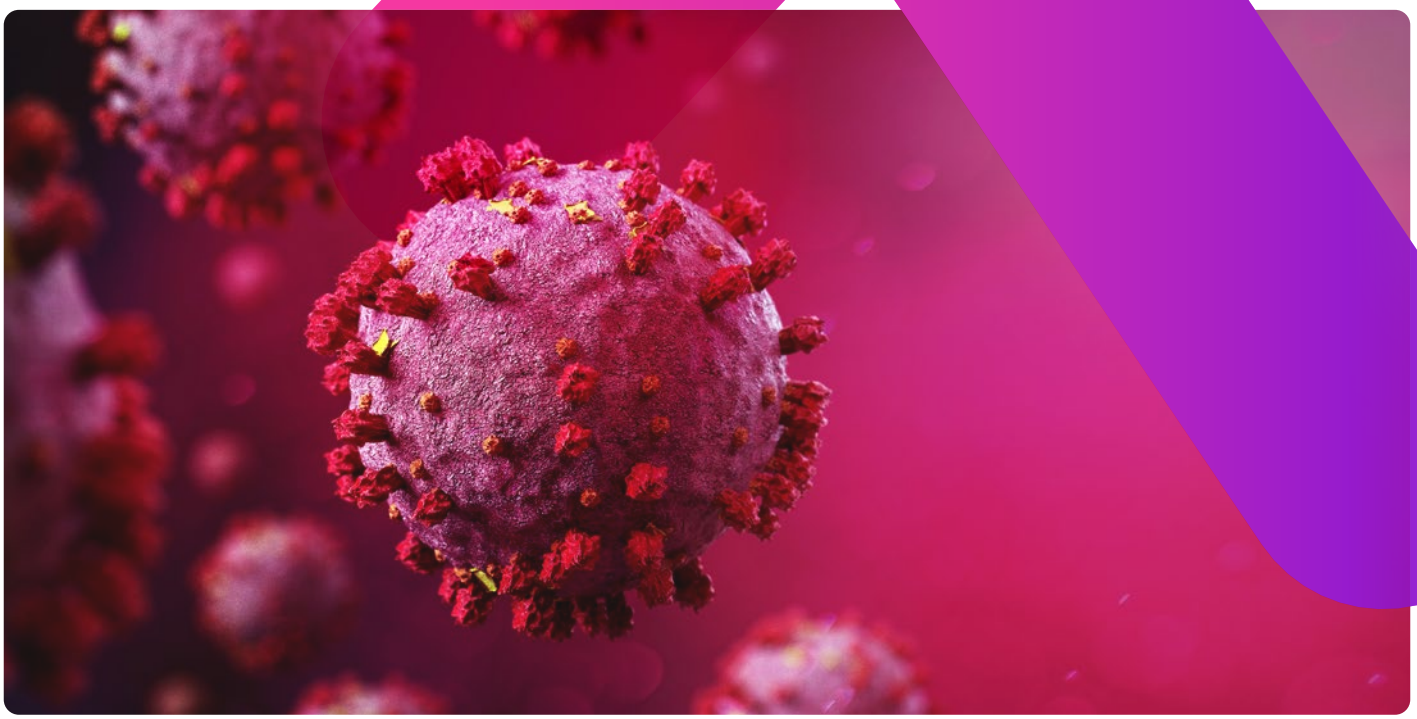

IgG4 Rise Linked to Repeated SARS-CoV-2 Exposure

RESEARCH presented at ESCMID Global 2026 suggests that repeated SARS-CoV-2 vaccination and infection drive a sustained shift in antibody responses, characterised by increasing IgG4 levels.[2]

The study analysed a cohort of healthcare workers with multiple immunological exposures (≥6 vaccination or infection events), using longitudinal serum samples to assess antibody subclasses, neutralisation capacity, and Fc-mediated functions. Individuals who were infection-naïve prior to vaccination developed a distinct immune profile from the third mRNA dose onwards, marked by a sharp and persistent rise in anti-spike IgG4. Those with hybrid immunity showed a similar trend, although more gradual.

IgG4 levels continued to increase with successive exposures, including against nucleocapsid protein following breakthrough infections, indicating broader class switching beyond spike-specific responses. Despite this shift, IgG4 appeared to have minimal impact on Fc effector functions, as its depletion did not significantly alter antibody-dependent cellular cytotoxicity.

Notably, while correlations between IgG1–3 and neutralisation of newer variants weakened, IgG4 maintained a stable association, suggesting a potential role in cross-reactive immunity.

> **Individuals who were infection-naïve prior to vaccination developed a distinct immune profile from the third mRNA dose onwards**

Overall, the findings indicate that the sequence and frequency of SARS-CoV-2 exposures shape long-term antibody profiles, with IgG4 emerging as a consistent feature of repeated immunisation. The clinical implications of this shift, whether beneficial or potentially dampening protective immunity, remain to be determined.

Global Surveillance Identifies Diverse Nairoviruses in Ixodes Ticks

RESEARCHERS at ESCMID Global 2026 reported that Ixodes ticks harbour substantial viral diversity across countries and host species, including known nairoviruses and previously unidentified variants, highlighting the value of early surveillance to detect emerging vector-borne pathogens as climate change reshapes disease spread.[3]

Research has shown that climate change is impacting ecological systems, animal behaviour, vector distribution, and microbial equilibria. These changes enable disease vectors to spread into new regions, with concerns rising that emerging viruses may spread unnoticed. Researchers within the ARBO-WATCH preparedness network sought to investigate the epidemiogenetics of members of the Nairoviridae in ticks collected globally.

Researchers designed a pan-orthonairovirus hemi-nested reverse-transcriptase-PCR targeting a 347 bp region of the RNA-dependent RNA polymerase gene. The assay was applied to RNA extracted from single ticks or pooled samples collected from vertebrate hosts or the environment. Positive samples underwent Sanger sequencing, while full genomes were generated through metagenomics. Maximum-likelihood phylogenetic analyses were then performed across the Nairoviridae family. Overall, 1,916 ticks from 14 species were analysed from 11 countries spanning six continents. Completion numbers were the full tested sample set, with all positive pools sequenced.

Fifteen Ixodes pools tested positive, containing five viruses from four genera. Sulina virus was identified in a Danish pool with nucleotide identity of 96.3–97.3% versus reference strains. Taggert virus was detected in Ixodes uriae from Antarctica with 93.8% identity. A relative of South Bay virus was found in Mongolian Ixodes persulcatus with 74.7% identity. Two Grotenhout virus variants were identified in Ixodes ricinus from Denmark, Italy, and Poland, with identities of 96.3–98.6%. Most notably, two variants representing a novel genus were discovered in 14 of 31 Danish Ixodes hexagonus ticks, equivalent to 45.2%. Their bisegmented genomes were fully sequenced and named Esrum virus 1 and 2. Full RNA-dependent RNA polymerase sequences showed less than 50% identity to reference viruses.

Researchers concluded that Ixodes ticks harbour substantial viral diversity across countries and host species. Early findings suggest strong tick species specificity, which may help model future spillover and emergence pathways. Continued international surveillance could improve early warning systems, guide ecological risk assessment, and strengthen preparedness for future vector-borne threats.

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Drug-Resistant *Klebsiella* Evades Meropenem–Durlobactam

A NEWLY characterised clinical strain of *Klebsiella pneumoniae* is raising concerns after demonstrating non-susceptibility to the antibiotic combination meropenem–durlobactam, a therapy designed to overcome resistance in some of the most difficult-to-treat infections, as shown by results presented at ESCMID Global 2026.[4]

Carbapenem-resistant *Klebsiella pneumoniae* (CRKP) is recognised as a major global health threat, often associated with high mortality in hospital settings. Durlobactam, a diazabicyclooctane β-lactamase inhibitor, has been developed to restore the activity of β-lactam antibiotics such as meropenem by blocking enzymes like KPC and OXA-48 carbapenemases that degrade them. However, new findings suggest that resistance mechanisms beyond β-lactamase activity may undermine this approach.

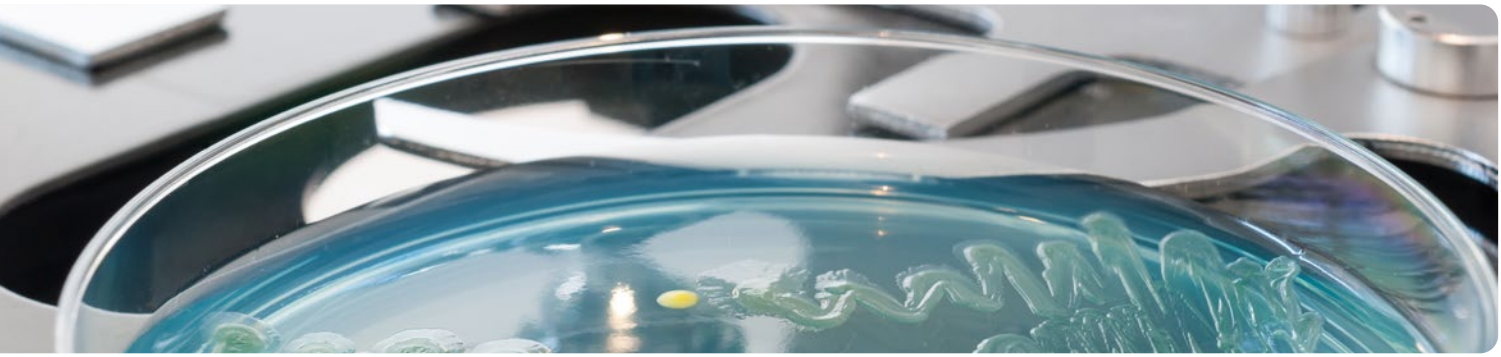
In this study, researchers analysed a CRKP strain isolated from a bile sample. Laboratory testing revealed extremely high minimum inhibitory concentrations for both meropenem–durlobactam and sulbactam–durlobactam, indicating poor susceptibility despite the presence of the inhibitor. Genomic sequencing showed that the strain belonged to sequence Type 11 and capsular Type 64, and carried the carbapenemase gene bla_{KPC-2}.

Importantly, the strain also possessed several virulence factors, including genes linked to aerobactin and yersiniabactin production, as well as regulators associated with a hypermucoid phenotype. These features suggest that the bacterium may not only be resistant, but also potentially more capable of causing severe disease.

Further analysis identified structural changes in the bacterial outer membrane that may explain the reduced antibiotic susceptibility. The *lamB* gene, which encodes a porin responsible for the uptake of small molecules, including certain antibiotics, was truncated. Loss of LamB function is known to reduce antibiotic entry into bacterial cells. In addition, the strain lacked the gene encoding AsmA, a protein involved in assembling another key porin, OmpK35. Disruption of these membrane channels likely limits drug penetration, reducing the effectiveness of meropenem even when protected by durlobactam.

The findings highlight a growing challenge in antimicrobial resistance: even novel inhibitor combinations may fail when multiple resistance mechanisms converge. Researchers emphasise the need for continued surveillance and deeper investigation into non-enzymatic resistance pathways, particularly those affecting membrane permeability.

As new therapies are introduced to combat multidrug-resistant pathogens, this study underscores the adaptability of CRKP and the importance of staying ahead of emerging resistance mechanisms.



LC16m8 Vaccine Generates Strong Immunity but Limited Mpox Coverage

A NEW study presented at ESCMID Global 2026 has shown that the replicating smallpox vaccine LC16m8 generated strong and durable antibody responses in high-risk populations during mpox vaccine deployment in Colombia, although cross-protection against circulating mpox strains appeared limited.[5]

The research addressed a critical evidence gap regarding the immunogenicity of LC16m8 outside Japan, particularly in populations at elevated risk of mpox infection, including people living with HIV. Understanding how effectively this vaccine stimulates immune responses is essential for informing outbreak preparedness and vaccination strategies.

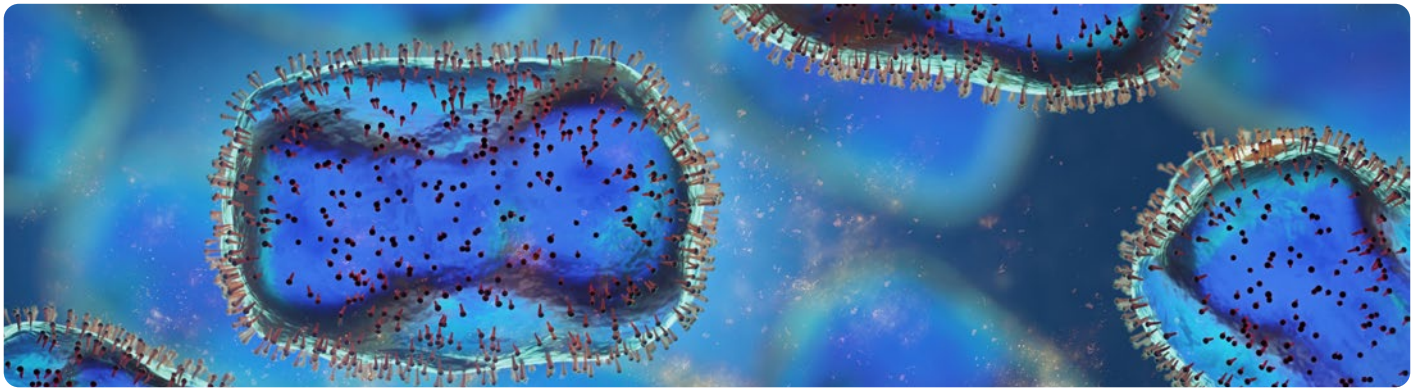
Investigators conducted a hybrid study combining a randomised delayed vaccination trial with an observational cohort across three centres in Bogotá, Colombia. Adults aged 18–50 years at increased risk of mpox infection were enrolled, including individuals receiving antiretroviral therapy, pre-exposure prophylaxis users, and those reporting high-risk sexual behaviours. A predefined immunogenicity sub-study analysed neutralising antibody responses in 60 participants, with serum samples collected at baseline and at 14, 30, and 180 days following vaccination.

Findings showed that neutralising antibody responses against the vaccine strain increased rapidly after immunisation. Geometric mean titres rose from 9.8 at baseline to 359.8 at Day 14 and peaked at 2220.9 at Day 30 before declining to 899.4 at Day 180, remaining well above baseline levels. Seroconversion rates were consistently high, reaching 100.0% at Day 14, 98.3% at Day 30, and 100.0% at Day 180, demonstrating robust and sustained homologous immune responses.

In contrast, cross-neutralising responses against the mpox virus clade IIb strain were modest. Antibody titres increased only slightly, from 8.9 at baseline to 23.2 at Day 30, and fell to 12.6 at Day 180. Correspondingly, seroconversion peaked at 33.9% before declining to 12.1% at 6 months, indicating limited cross-reactivity.

The authors noted that while LC16m8 elicited strong immune responses against its own strain, the comparatively weak neutralisation of mpox virus highlights challenges in assessing cross-protection using current assays.

Overall, the findings supported the immunogenic potential of LC16m8 in high-risk populations, including people living with HIV, but underscored the need for further research to better understand its effectiveness against circulating mpox strains and to optimise vaccination strategies in outbreak settings.



mRNA Embecovirus Spike and HE Antigens Induce Cross-Reactive Antibody Responses

PRECLINICAL data presented at ESCMID Global 2026 provide important insights into next-generation vaccine strategies targeting embecoviruses, a clinically relevant and evolutionarily diverse subgroup of betacoronaviruses that includes human seasonal pathogens, such as OC43 and HKU1, as well as animal reservoir viruses.[6]

The study evaluated mRNA-based immunogens encoding codon-optimised spike and haemagglutinin esterase (HE) proteins from multiple embecoviruses, including OC43, HKU1, human enteric coronavirus (HECV), and murine hepatitis virus (MHV). Using lipid nanoparticle-delivered mRNA vaccines, BALB/c mice were immunised in a prime-boost regimen, and sera were assessed for cross-reactive binding and neutralising activity across a phylogenetically diverse panel of human and animal embecoviruses.

Overall, the vaccine constructs were immunogenic but elicited distinct antigen-specific patterns of cross-reactivity. OC43 and HECV spike proteins generated broad heterotypic antibody binding responses against multiple animal reservoir spikes, although cross-reactivity was reduced against HKU1 and MHV. In contrast, the MHV spike induced more limited responses, with weak or negligible cross-reactivity to OC43 and HKU1.

HE antigens showed a divergent profile. OC43 and HECV HE proteins produced cross-reactive binding responses broadly similar to their spike counterparts, but did not bind MHV targets. Notably, MHV HE induced narrower antibody breadth compared with spike. Despite these differences, HE antigens demonstrated functional relevance in neutralisation assays: OC43 and HECV HEs generated broader and more potent heterotypic neutralisation, including activity against porcine coronavirus, whereas MHV HE was non-neutralising.

In contrast, OC43 and HECV spike proteins induced strong homotypic neutralising responses but more limited heterotypic neutralisation. MHV spike retained homotypic neutralisation capacity, while HKU1 spike and HE failed to elicit detectable antibody responses under the study conditions.

These findings highlight important antigen-specific differences in breadth and function of immune responses induced by embecovirus proteins delivered via mRNA platforms. Importantly, the data identify HE as an underexplored antigen capable of mediating cross-reactive neutralisation, supporting its potential inclusion in broadly protective betacoronavirus vaccine strategies.

The study provides crucial preclinical evidence to inform the rational design of pan-betacoronavirus vaccines aimed at improving antigenic coverage across human and zoonotic reservoirs.

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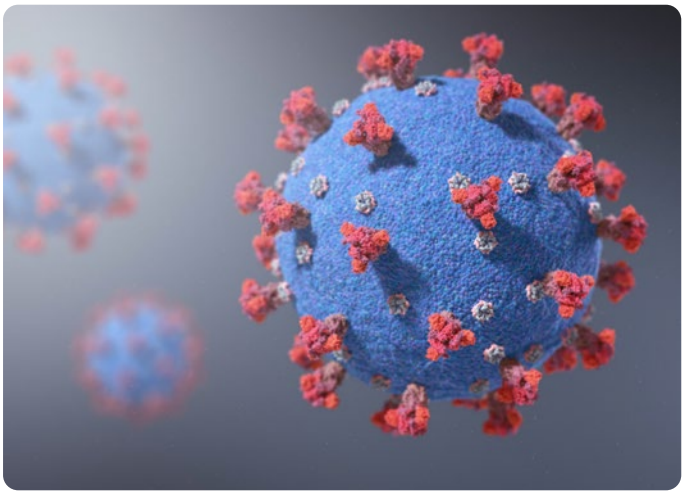

Updated COVID-19 Vaccines Elicit Strong Responses in At-Risk Groups

INTERIM data, presented at ESCMID Global 2026, suggest that updated mRNA vaccines continue to strengthen immune protection against COVID-19 in at-risk populations.[7]

COVID-19, caused by the SARS-CoV-2 virus, remains a significant health concern, particularly for older adults and individuals with underlying conditions who are more likely to experience severe outcomes. As the virus continues to evolve genetically, vaccines are periodically updated to better match circulating variants and maintain protection.

Interim data from two ongoing clinical studies evaluating variant-targeted vaccines show encouraging immune responses. These Phase IIIb/IV open-label studies assessed updated formulations designed to target the LP.8.1 variant of COVID-19. Participants included adults aged 65 years and over, as well as individuals aged 12–64 years with at least one risk factor for severe illness.

Across both studies, 660 participants aged 65 years and older and 662 participants aged 12–64 years with at least one risk condition for severe COVID-19 were enrolled. Researchers measured neutralising antibody levels at baseline (Day 1) and again at Day 29 post-vaccination to assess immune response.

Results showed a substantial rise in antibody levels following vaccination, with increases ranging from 15.4- to 53.0-fold. These findings indicate that updated vaccines can effectively stimulate the immune system against the targeted variant, with responses exceeding the fourfold increase predefined as the study's primary immunogenicity objective. No serious adverse events were reported during this interim analysis, supporting a favourable safety profile in the populations studied.

While the interim results are descriptive and based on early data from a limited subset of participants, longer-term outcomes, including durability of protection and real-world effectiveness, are still being evaluated.

These results highlight the potential of updated mRNA vaccines to maintain protection as SARS-CoV-2 continues to evolve, particularly for those most vulnerable to severe disease. Future analyses could help clarify how these immune responses translate into clinical protection and inform future vaccination strategies.

Phage Therapy Breakthrough: P49 Kills Multiple Drug-Resistant Bacteria

A NEWLY identified bacteriophage, P49, shows promise as a broad-spectrum therapeutic candidate against drug-resistant bacteria according to recent research, presented at ESCMID Global 2026, investigating alternatives to antibiotics for *Klebsiella pneumoniae* (KP) infections.[8]

KP is a major cause of hospital-acquired infections, and many phages that target it are highly specific, often limited to a single capsule type. This narrow host range has restricted their clinical usefulness. To address this, researchers isolated phage P49 from wastewater using KP strains resistant to existing phages (P04 and P40).

Laboratory testing revealed that P49 effectively lysed mutant KP strains that were resistant to other phages, forming clear plaques that ranged from 1.0–2.0 mm in diameter, though it could not infect the original non-resistant strain. Electron microscopy showed that P49 has a long, noncontractile tail typical of certain double-stranded DNA phages. It also demonstrated strong biological properties, including stability across a range of temperatures and pH levels, rapid adsorption to host cells, and a high burst size, all desirable traits for therapeutic use.

Genomic analysis showed that P49 has a genome of approximately 114 kb and, importantly, does not carry genes associated with antimicrobial resistance or virulence, supporting its safety profile. Phylogenetic analysis placed P49 within the genus Epseptimavirus, closely related to phages that infect *Salmonella* and *Escherichia coli*.

Notably, P49 exhibited an unusually broad host range. Beyond targeting resistant KP mutants, it was capable of lysing multiple bacterial species, including *E. coli*, *Salmonella enterica*, *Kluyvera tianfuensis*, and *Enterobacter ludwigii*. In growth inhibition experiments, P49 suppressed *E. coli* for up to 11 hours and other tested species for 16 to over 24 hours.

This cross-species activity is uncommon among phages and suggests potential for wider clinical application, particularly in treating mixed or difficult-to-diagnose infections involving multiple pathogens.

Overall, the findings position P49 as a strong candidate for further development in phage therapy, offering a potential tool against multidrug-resistant infections where current treatments are failing.

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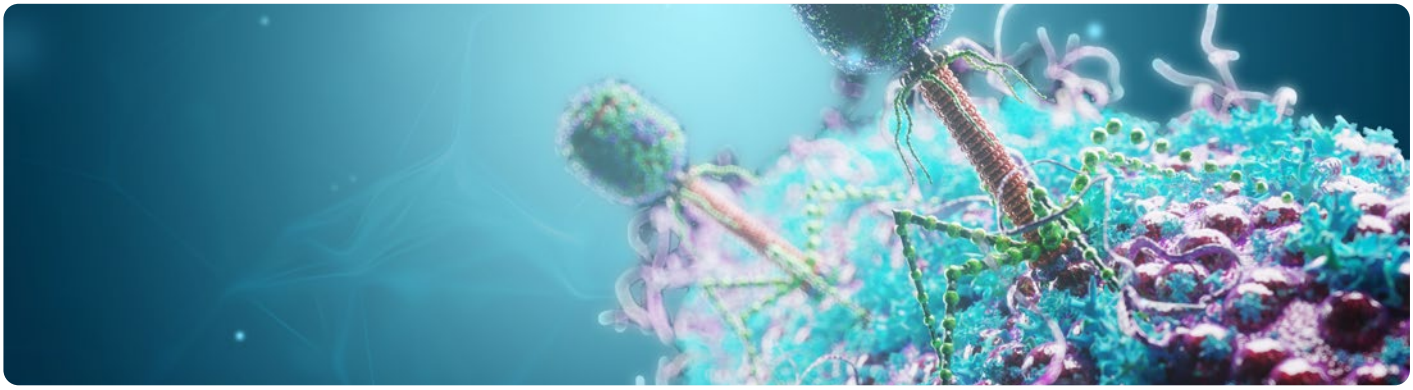

New *Staphylococcus aureus* Panel Captures Resistance and Virulence Diversity

A GENETICALLY DIVERSE panel of 95 *Staphylococcus aureus* isolates has been developed to enhance and standardise antimicrobial resistance research, comprised of isolates collected from 18 countries, as stated in the abstract presentation at ESCMID Global 2026.[9]

S. aureus is a versatile pathogen responsible for infections ranging from skin and soft tissue disease to life-threatening sepsis. Due to its ability to acquire resistance to multiple antibiotics, it has been a persistent contributor to the global antimicrobial resistance crisis.

In response to this crisis, efforts have focused on providing the scientific community with well-characterised bacterial isolate panels for research. The panel was derived from 6,484 isolates collected across 18 countries over a 20-year period. A two-step selection process combined k-medoid clustering (to maximise genetic distance between isolates) with manual curation to retain strains with distinctive metadata, including date, country, and site, as well as major resistance and virulence biomarkers.

All 95 isolates underwent whole-genome sequencing using Oxford Nanopore (Oxford Nanopore Technologies, Oxford, UK) technology, alongside antibiotic susceptibility testing in a College of American Pathologists (CAP)-accredited laboratory.

The resulting panel included 69 sequence types, 74 *S. aureus* protein A types, and six Staphylococcal cassette chromosome mec types. It included 47 methicillin-susceptible and 48 methicillin-resistant isolates, ensuring balanced representation of clinically relevant phenotypes.

Resistance profiling identified isolates with reduced susceptibility to linezolid, co-trimoxazole, and rifampin, amongst other clinically relevant antibiotics. One isolate was classified as extensively drug-resistant, while four isolates remained fully susceptible to all antibiotics tested. A total of 55 distinct antimicrobial resistance and antiseptic/disinfectant resistance genes, as well as 35 characterised mutations, were detected across the panel.

Virulence analysis revealed 50 distinct virulence factors, including Panton–Valentine leukocidin in 25% of isolates and toxic-shock syndrome toxin-1 in 8.4%.

While not intended to directly guide treatment decisions, this standardised panel offers a reproducible platform for evaluating diagnostics, therapeutics, and surveillance tools. Limitations include its fixed size and curated selection, which may not capture all emerging resistance mechanisms.

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Nirsevimab Shows Consistent Protection Against Severe RSV Outcomes Across Seasons

REAL-WORLD data presented at ESCMID Global 2026 provide important insights into the effectiveness of nirsevimab across successive respiratory syncytial virus (RSV) seasons in infants with bronchiolitis following its introduction in Italy in 2024.[10]

The study evaluated nirsevimab, a long-acting monoclonal antibody targeting RSV, using a single-centre test-negative case–control design. Infants aged 1–12 months presenting with bronchiolitis to a tertiary paediatric emergency department (ED) in Milan, Italy, were included. Infants who were RSV-positive were classified as cases and those who were RSV-negative were classified as controls, with immunisation status assessed at admission. Vaccine effectiveness (VE) was estimated against RSV-associated ED-attended illness, RSV-related hospitalisation, and paediatric ICU (PICU) admission. Epidemiological outcomes from November–January in the 2025–2026 season were compared with the same period in 2024–2025.

Overall, VE estimates during the second RSV season varied by clinical severity and were associated with wide CIs due to reduced case numbers. VE was 19.3% (95% CI: −137.0–72.6) against RSV-associated ED-attended illness, 75.0% (95% CI: −33.7–95.3) against RSV-related hospitalisation, and 75.0% (95% CI: −1498.0–99.6) against PICU admission.

In parallel, notable reductions in bronchiolitis burden were observed across seasons. ED visits for bronchiolitis decreased from 147 in 2024–2025 to 89 in 2025–2026 (−39.5%). RSV-positive ED visits declined from 63 to 33 (−47.6%; p<0.001), while RSV-negative visits decreased from 84 to 56 (−33.3%). Overall hospital admissions fell from 79 to 54. Among infants who were RSV-positive, hospitalisations decreased from 43 to 28 (−34.9%), although hospitalisation rates remained similar between seasons (68.3% versus 84.8%; p=0.08).

These findings highlight a gradient in observed effectiveness, with lower VE against ED-attended illness and higher VE against more severe outcomes, including hospitalisation and PICU admission. This pattern is consistent with stronger protection against severe disease and may also reflect selection and threshold effects inherent to ED-based test-negative designs, where vaccinated infants presenting to care may represent a higher-risk subgroup with differing healthcare-seeking and testing behaviours.

Collectively, these real-world data support the continued implementation of nirsevimab and underscore the importance of robust surveillance systems to inform RSV prevention strategies and policy decisions.

References

1. AM Reimer Jensen et al. High-dose vs standard-dose influenza vaccine effectiveness in immunosuppressed older adults: a prespecified analysis of the DANFLU-2 trial. Abstract 06036. ESCMID Global, 17-21 April, 2026.
2. Perisse T et al. History of vaccination and infection shapes the humoral response to SARS-CoV-2 through IgG4 class switching. Abstract 03143. ESCMID Global, 17-21 April, 2026.
3. Bianchi S et al. Identifying emerging vector-borne pathogens in a time of climate change, the ARBO-WATCH network. Abstract 08522. ESCMID Global, 17-21 April, 2026.
4. Zong Z et al. Carbapenem-resistant Klebsiella pneumoniae non-susceptible to mero-penem/durlobactam. Abstract 09287. ESCMID Global, 17-21 April, 2026.
5. Hernandez J et al. Humoral immunogenicity of the replicating smallpox vaccine LC16m8 during mpox vaccine deployment in high-risk populations in Colombia. Abstract 09306. ESCMID Global, 17-21 April, 2026.
6. George C et al. mRNA delivered embecovirus spike and haemagglutinin esterase antigens elicit cross-reactive humoral immunity to divergent human and animal coronaviruses. Abstract 09328. ESCMID Global, 17-21 April, 2026.
7. Chalkias S et al. Effectiveness and safety of variant-updated COVID-19 vaccines. Abstract 09326. ESCMID Global, 17-21 April, 2026.
8. Yin X, Feng Y. The biological and genomic characteristics of a broad-spectrum phage target Klebsiella pneumoniae. Abstract 09452. ESCMID Global, 17-21 April, 2026.
9. Vargas-Cuebas GG et al. A panel of global and genetically distinct Staphylococcus aureus isolates for research and development. Abstract 04666. ESCMID Global, 17-21 April, 2026.
10. Pisano EM et al. Consistency of nirsevimab effectiveness across successive RSV seasons in infants with bronchiolitis: a test-negative study. Abstract 09278. ESCMID Global, 17–21 April, 2026.