LISTA DE REFERÊNCIAS BIBLIOGRÁFICAS E RESUMOS– COVID -19

Atualizado em: 22 de julho de 2022

Título	Innate immunity to SARS-CoV-2 infection: a review
Autor(es)	Marcos Jessé Abrahão Silva, Yan Corrêa Rodrigues, Karla Valéria Batista Lima, Luana Nepomuceno Gondim Costa Lima
Resumo	The SARS-CoV-2 virus pandemic, first notified in China, has spread around the world causing high morbidity and mortality, which is due to factors such as the subversion of the immune response. The aims of the study are to summarize and present the immunopathological relationship of COVID-19 with innate immunity. This is a systematic review conducted by the National Library of Medicine - National Institutes of Health, USA (PUBMED), Latin American and Caribbean Literature on Health Sciences (LILACS), Medical Literature Analysis and Retrieval System Online (MEDLINE) and Scientific Electronic Library Online (SCIELO) databases with clinical trials, in vitro assays, case-controls, cohort studies, systematic reviews and meta-analyses between February 2020 and July 2021. The version 2 of the Cochrane risk-of-bias tool for RCTs (RoB 2), Joana Briggs Institute (JBI) Critical Appraisal (for the review articles) and the Risk of Bias in Non-randomized Studies of Interventions (ROBINS-I) tools were used to evaluate the quality and the risk of bias of the studies included in this review. The innate immune response through the generation of interferons (IFNs), alternative pathways and complement system lectins and the joint action of innate immune cells and cytokines and chemokines lead to different clinical outcomes, taking into account the exacerbated inflammatory response and pathogenesis. Then, in addition to interacting as a bridge for adaptive immunity, the innate immune response plays an essential role in primary defense and is one of the starting points for immune evasion by SARS-CoV-2.
Referências	SILVA, M. J. A. *et al.* Innate immunity to SARS-CoV-2 infection: a review. **Epidemiology and infection**, [United Kingdom], p. 1–49, July 18, 2022. DOI: 10.1017/S095026882200125X. Disponível em: https://www.cambridge.org/core/journals/epidemiology-and-infection/article/innate-immunity-to-sarscov2-infection-a-review/029C907BB6B3927A6AB00315707C4F59. Acesso em: 22 jul. 2022.
Fonte	https://www.cambridge.org/core/services/aop-cambridge-core/content/view/029C907BB6B3927A6AB00315707C4F59/S095026882200125Xa.pdf/innate-immunity-to-sars-cov-2-infection-a-review.pdf

Título	Moraxella occupied the largest proportion in the nasal microbiome in healthy children, which potential protect them from COVID-19
Autor(es)	Xia Yu, Li Wang, XueMei Zheng, Yizhou Wen, Zhirong Zhang, Lingxia Fan, Qin Zhou, Xiao Yang, Binqian Xue, Yonghong Lin
Resumo	In the prevalence of COVID-19, infection symptoms are different in children and adults. In this study to investigate the differences in the upper respiratory tract microbiome profile between healthy children and adults and to explore which microbiome protect them from COVID-19. Methods: Thirty healthy children and 24 healthy adults were enrolled between October 2020 and January 2021. Nasal and throat swabs were obtained at enrollment, and DNA was extracted. We performed 16S rDNA sequencing to compare the alpha and beta diversity of the nasal and throat microbiomes between children and adults and assessed potential microbiome biomarkers. Results: In the nasal icrobiome, there were significant differences between healthy children and adults, and Moraxella occupied the largest proportion in healthy children. Notably, there was no significant difference between healthy children and adults in the throat microbiome, and it was predominated by Firmicutes. In the function analysis, compared with adults, there was increased enrichment in pathways related to amino acid metabolism and lipid metabolism, in children. Conclusions: In the upper respiratory tract microbiome profiles, Moraxella may be involved in protecting children from COVID-19 infections and may be involved the amino acid metabolism and lipid metabolism.
Referências	XIA, Y. *et al.* Moraxella occupied the largest proportion in the nasal microbiome in healthy children, which potential protect them from COVID-19. **Microbial pathogenesis**, [Netherlands], p. 105685, July 21, 2022. DOI: 10.1016/j.micpath.2022.105685. Disponível em: https://www.sciencedirect.com/science/article/pii/S0882401022002984. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S0882401022002984/pdf

Título	SARS-CoV-2 incidence, signs and symptoms and main risk factors for COVID-19 infection in health care workers: a hospital-wide survey in Salvador, Brazil
Autor(es)	Iris Montanõ-Castellón, Liliane Lins-Kusterer, Estela Luz, Celia Pedroso, Márcia Paz, Carlos Brites
Resumo	Brazil is the third country most affected by Coronavirus Disease 2019 (COVID-19) in the world. Health care workers (HCWs) are at higher risk of infection. Despite the increasing numbers of studies on the topic, There are gaps in the knowledge of characteristics and risk factors for infection of HCWS. This information is important to design preventive strategies and to mitigate the disease impact. The objective of this study was to estimate the incidence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection, to identify factors associated, and to describe symptoms reported by healthcare workers at a tertiary hospital in Salvador, Brazil. Methods: All HCWs were evaluated in a cross-sectional study conducted between May and September 2020, using self-administered questionnaires, and screening all participants for SARS-COV-2 IgG and IgM antibodies by rapid tests. Reactive IgG samples were retested by ELISA and IgM-positive test had a saliva sample retest by RT-PCR. Univariate associations were estimated by a non-adjusted incidence proportion ratio. Variables associated with COVID-19 incidence at $p < 0.20$ were selected for inclusion in a binary logistic regression model. Results: A total of 2083 HCWs were included, mean age 41±10 years, 71.8% women, and 77.8% non-white. Of these, 271 (13.0%) and 25 (1.2%) HCWs tested positive for IgG and IgM SARS-CoV-2 antibodies, respectively, and three had a positive RT-PCR. Ancillary work [Odds Ratio (OR): 4.96], elementary education (OR: 2.91), high school education (OR: 2.89), and catholic religion (OR: 2.16) were associated with an increased likelihood of a positive IgG antibodies against SARS-CoV-2. Anosmia [Incidence Proportion Ratio (IPR): 7.41] and ageusia (IPR:8.51) were the most frequent associated symptoms. Conclusion: HCWs with low mean family income, lower level of schooling or being black had a significantly higher likelihood of

	testing positive for SARS-CoV-2 antibodies. Social vulnerability was an important risk factor for COVID-19 infection.
Referências	MONTAÑO-CASTELLÓN, I. *et al.* SARS-CoV-2 incidence, signs and symptoms and main risk factors for COVID-19 infection in health care workers: a hospital-wide survey in Salvador, Brazil. **The Brazilian journal of infectious diseases**, [Brazil], p. 102387, July 21, 2022. DOI: 10.1016/j.bjid.2022.102387. Disponível em: https://www.sciencedirect.com/science/article/pii/S1413867022000745. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S1413867022000745/pdf

Título	Gamma variant vertically transmitted from a mild symptomatic pregnant woman associated with fatal neonatal COVID
Autor(es)	Walusa Assad Goncalves-Ferri, Cristina Galdonyi Carvalheiro, Marisa Marcia Mussi-Pinhata, Bruna Pinto Dias Cavasin, Benedito Antonio Lopes da Fonseca
Resumo	Herein we describe a mild symptomatic real-time reverse transcriptase- polymerase chain reaction-confirmed coronavirus 2 (SARS-CoV-2) infection in a pregnant woman who gave birth to a preterm infant, 32 weeks gestational age. The neonate was immediately isolated after delivery and developed severe respiratory disease that progressed to multisystem inflammatory syndrome and death on the seventh day of life. Genome sequencing detected the P.1 (gamma) variant in samples obtained at hospital admission (mother) and on the first (10h) and 13th days of life (neonate). Complete homology (mother's and newborn's sequences) confirmed vertical transmission. To our knowledge, this is the first report of vertically-transmitted SARS-CoV-2 P.1 (gamma) variant in a mild symptomatic infection in pregnancy associated with fatal COVID in a neonate.
Referências	GONÇALVES-FERRI, W. A. *et al.* Gamma variant vertically transmitted from a mild symptomatic pregnant woman associated with fatal neonatal COVID. **The Brazilian journal of infectious diseases**, [Brazil], v. 26, n. 4, p. 102385, July 21, 2022. DOI: 10.1016/j.bjid.2022.102385. Disponível em: https://www.sciencedirect.com/science/article/pii/S1413867022000721. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S1413867022000721/pdf

Título	Delineating COVID-19 immunological features using single-cell RNA sequencing
Autor(es)	Wendao Liu, Johnathan Jia, Yulin Daí, Wenhao Chen, Guangsheng Pei, Qiheng Yan, Zhongming Zhao
Resumo	Understanding the molecular mechanisms of COVID-19 pathogenesis and immune response is vital for developing therapies. Single-cell RNA sequencing has been applied to delineate the cellular heterogeneity of the host response towards COVID-19 in multiple tissues and organs. Here, we review the applications and findings from over 80 original COVID-19 single-cell RNA sequencing studies as well as many secondary analysis studies. We describe that single-cell RNA sequencing reveals multiple features of COVID-19 patients with different severity, including cell populations with proportional alteration, COVID-19 induced genes and pathways, SARS-CoV-2 infection in single cells, and adaptation of immune repertoire. We also collect published single-cell RNA sequencing datasets from original studies. Finally, we discuss the limitations in current studies and perspectives for future advance.
Referências	WENDAO, L. *et al.* Delineating COVID-19 immunological features using single-cell RNA sequencing. **The Innovation**, [United States], p. 100289, July 21, 2022. DOI: 10.1016/j.xinn.2022.100289. Disponível em: https://www.sciencedirect.com/science/article/pii/S2666675822000856. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S2666675822000856/pdf

Título	Clinical comparison and agreement of pcr, antigen, and viral culture for the diagnosis of COVID-19: clinical agreement between diagnostics for COVID19
Autor(es)	Amanda Agard, Omar Elsheikh, Drew Bell, Ryan Relich, Bryan Schmitt, Josh Sadowski, William Fadel, Douglas H. Webb, Lana Dbeibo, Kristen Kelley, Mariel Carozza, Guang-Shen Lei, Paul Calkins, Cole Beeler
Resumo	The aim of this study is to compare the COVID-19 nasopharyngeal PCR (NP PCR) to antigen, nasal PCR, and viral culture. One-hundred-and-fourteen risk-stratified patients were tested by culture, nasal PCR, NP PCR, and Ag testing. Twenty (48%) of the high risk and 23 (32%) of the low risk were NP PCR positive. Compared with NP PCR, the sensitivity of nasal PCR, Sofia Ag, BinaxNOW Ag, and culture were 44%, 31%, 37%, and 15%. In the high risk group, the sensitivity of these tests improved to 71%, 37%, 50%, and 22%. Agreement between tests was highest between nasal PCR and both antigen tests. Patients who were NP PCR positive but antigen negative were more likely to have remote prior COVID-19 infection ($p<0.01$). Nasal PCR and antigen positive patients were more likely to have symptoms ($p = 0.01$).
Referências	AGARD, A. *et al.* Clinical comparison and agreement of pcr, antigen, and viral culture for the diagnosis of COVID-19: clinical agreement between diagnostics for COVID19. **Journal of clinical virology plus**, [United Kingdom], p. 100099, July 21, 2022. DOI: 10.1016/j.jcvp.2022.100099. Disponível em: https://www.sciencedirect.com/science/article/pii/S2667038022000382. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S2667038022000382/pdf

Título	An assessment of post-COVID-19 infection pulmonary functions in healthcare professionals
Autor(es)	Pınar Yıldız Gülhan, Peri Meram Arbak, Ali Nihat Annakkaya, Ege Güleç Balbay, Öner Abidin Balbay
Resumo	The medium- and long-term effects of COVID-19 infection on pulmonary function are still unknown. The present study aimed to investigate the pulmonary functions in healthcare professionals who had persistent complaints after contracting COVID-19 and returning to work. Methods: The study included COVID-19-infected healthcare professionals from the Düzce University Medical Faculty Hospital who volunteered to participate. Medical histories, medical records, pulmonary function tests, the diffusing capacity of the lungs for carbon monoxide (DLCO) test, and the 6-minute walk test (6MWT) were used to collect data from all participants. Results: The study included 53 healthcare professionals, with an average age of 38 ± 10 years (min: 24 years and max: 71 years), including 29 female (54.7%) and 24 male (45.3%) participants. Of the participants, 22.6% were smokers, 35.8% (19 individuals) had comorbidities, and 17% (9 individuals) were hospitalized. The mean length of stay was 9 ± 4 days (mean ± standard deviation). The most prevalent symptoms were weakness (88.7%), muscle aches (67.9%), inability to smell/taste (60.4%), headache (54.7%), fever (45.3%), cough (41.5%), and shortness of breath (37.7%). The mean time to return to work after a positive polymerase chain reaction (PCR) test for COVID-19 was 18 ± 13 days. The average time among post-disease pulmonary function, 6MW, and DLCO tests was 89 ± 36 days (min: 15 and max: 205). The DLCO level decreased in 39.6% (21) of the participants. Female participants had a significantly higher rate of decreased DLCO levels than male participants (25% vs. 55.2%, p = 0.026). DLCO levels were significantly higher in participants with long-term persistent complaints (p = 0.043). The later the time to return to work, the lower the DLCO value (r = −0.290 and p = 0.035). The 6MWT distance was positively correlated with hemoglobin and lymphocyte levels at the time of the disease onset and negatively correlated with D-dimer levels. The most prevalent symptoms during the control visits were shortness of breath/effort dyspnea (24.6%), weakness (9.5%), and muscle aches (7.6%). Conclusion: Significant persistent complaints (47.2%) and low DLCO levels (39.6%) were observed in healthcare professionals during control visits at a

Resumo	mean time of 3 months after the COVID-19 infection. Symptoms and spirometry measurements, including DLCO, may be helpful in the follow-up of healthcare professionals who contracted COVID-19. Further comprehensive studies with long-term follow-up periods are required.
Referências	GÜLHAN, P. Y. *et al.* An assessment of post-COVID-19 infection pulmonary functions in healthcare professionals. **American journal of infection control**, [United States], July 20, 2022. DOI: 10.1016/j.ajic.2022.07.003. Disponível em: https://www.sciencedirect.com/science/article/pii/S019665532200534X. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S019665532200534X/pdf

Título	Gastrointestinal prophylaxis for COVID-19: an illustration of severe bias arising from inappropriate comparators in observational studies
Autor(es)	Kueiyu Joshua Lin, William B. Feldman, Shirley Wang, Siddhi Pramod Pramod Umarje, Elvira D'Andrea, Helen Tesfaye, Luke E. Zabotka, Jun Liu, Rishi J. Desai
Resumo	We aimed to use setting-appropriate comparisons to estimate effects of different gastrointestinal (GI) prophylaxis pharmacotherapies for patients hospitalized with COVID-19 and setting-inappropriate comparisons to illustrate how improper design choices could result in biased results. Study Design and Setting: We identified 3,804 hospitalized patients aged ≥18 years with COVID-19 from Mar-Nov 2020. We compared the effects of different gastroprotective agents on clinical improvement of COVID-19 measured by a published severity scale. We used propensity-score-based fine-stratification for confounding adjustment. Based on guidelines, we pre-specified comparisons between agents with clinical equipoise and inappropriate comparisons of users vs. non-users of GI prophylaxis in the intensive care unit (ICU). Results: No benefit was detected when comparing oral famotidine to omeprazole in patients treated in the general ward or ICUs. We also found no associations when comparing intravenous (IV) famotidine to IV pantoprazole. For inappropriate comparisons of users vs. non-users in the ICU, the probability of improvement was reduced by 34 to 43% in famotidine users and 18 to 47% in omeprazole or pantoprazole users. Conclusion: We found no evidence that GI prophylaxis improved outcomes for patients hospitalized with COVID-19 in setting-appropriate comparisons. Improper comparator choice can lead to spurious associations in critically ill patients.
Referências	LIN, K. J. *et al.* Gastrointestinal prophylaxis for COVID-19: an illustration of severe bias arising from inappropriate comparators in observational studies. **Journal of clinical epidemiology**, [United States], July 20, 2022. DOI: 10.1016/j.jclinepi.2022.07.009. Disponível em: https://www.sciencedirect.com/science/article/pii/S0895435622001822. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S0895435622001822/pdf

Título	Inactivation methods for human coronavirus 229E on various food-contact surfaces and foods
Autor(es)	Eun Seo Choi, Sangha Han, Jeong won Son, Gyeong Bae Song, Sang-Do Ha
Resumo	Severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), the cause of the COVID-19 outbreaks, is transmitted by respiratory droplets and has become a life-threatening viral pandemic worldwide. The aim of this study was to evaluate the effects of different chemical (chlorine dioxide [ClO2] and peroxyacetic acid [PAA]) and physical (ultraviolet [UV]-C irradiation) inactivation methods on various food-contact surfaces (stainless steel [SS] and polypropylene [PP]) and foods (lettuce, chicken breast, and salmon) contaminated with human coronavirus 229E (HCoV-229E). Treatments with the maximum concentration of ClO2 (500 ppm) and PAA (200 ppm) for 5 min achieved >99.9% inactivation on SS and PP. At 200 ppm ClO2 for 1 min on lettuce, chicken breast, and salmon, the HCoV-229E titers were 1.19, 3.54, and 3.97 log10 TCID50/mL, respectively. Exposure (5 min) to 80 ppm PAA achieved 1.68 log10 reduction on lettuce, and 2.03 and 1.43 log10 reductions on chicken breast and salmon, respectively, treated with 1500 ppm PAA. In the carrier tests, HCoV-229E titers on food-contact surfaces were significantly decreased ($p < 0.05$) with increased doses of UV-C (0–60 mJ/cm2) and not detected at the maximum UV-C dose (Detection limit: 1.0 log10 TCID50/coupon). The UV-C dose of 900 mJ/cm2 proved more effective on chicken breast (>2 log10 reduction) than on lettuce and salmon (>1 log10 reduction). However, there were no quality changes ($p > 0.05$) in food samples after inactivation treatments except the maximum PAA concentration (5 min) and the UV-C dose (1800 mJ/cm2).
Referências	EUN, S. C. *et al.* Inactivation methods for human coronavirus 229E on various food-contact surfaces and foods. **Food control**, [United Kingdom], p. 109271, 2022. DOI: 10.1016/j.foodcont.2022.109271. Disponível em: https://www.sciencedirect.com/science/article/pii/S0956713522004649. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S0956713522004649/pdf

Título	Antibody responses and SARS-CoV-2 infection after BNT162b2 mRNA booster vaccination among healthcare workers in Japan
Autor(es)	Hidetoshi Igari, Haruna Asano, Shota Murata, Toshihiko Yoshida, Kenji Kawasaki, Takahiro Kageyama, Key Ikeda, Hiromi Koshikawa, Yoshio Okuda, Misao Urushihara, Hitoshi Chiba, Misuzu Yahaba, Toshibumi Taniguchi, Kazuyuki Matsushita, Ichiro Yoshino, Koutaro Yokote, Hiroshi Nakajima
Resumo	Vaccine effectiveness against SARS-CoV-2 infections decreases due to waning immunity, and booster vaccination was therefore introduced. We estimated the anti-spike antibody (AS-ab) recovery by booster vaccination and analyzed the risk factors for SARS-CoV-2 infections. Methods: The subjects were health care workers (HCWs) in a Chiba University Hospital vaccination cohort. They had received two doses of vaccine (BNT162b2) and a booster vaccine (BNT162b2). We retrospectively analyzed AS-ab titers and watched out for SARS-CoV-2 infection for 90 days following booster vaccination. Results: AS-ab titer eight months after two-dose vaccinations had decreased to as low as 587 U/mL (median, IQR (interquartile range) 360-896). AS-ab titer had then increased to 22471 U/mL (15761-32622) three weeks after booster vaccination. There were no significant differences among age groups. A total of 1708 HCWs were analyzed for SARS-CoV-2 infection, and 48 of them proved positive. SARS-CoV-2 infections in the booster-vaccinated and non-booster groups were 1.8% and 4.0%, respectively, and were not significant. However, when restricted to those 20–29 years old, SARS-CoV-2 infections in the booster-vaccinated and non-booster groups were 2.9% and 13.6%, respectively (p = 0.04). After multivariate logistic regression, COVID-19 wards (adjusted odds ratio (aOR):2.9, 95% confidence interval (CI) 1.5–5.6) and those aged 20–49 years (aOR:9.7, 95%CI 1.3–71.2) were risk factors for SARS-CoV-2 infection. Conclusions: Booster vaccination induced the recovery of AS-ab titers. Risk factors for SARS-CoV-2 infection were HCWs of COVID-19 wards and those aged 20–49 years. Increased vaccination coverage, together with implementing infection control, remains the primary means of preventing HCWs from SARS-CoV-2 infection.
Referências	IGARI, H. *et al.* Antibody responses and SARS-CoV-2 infection after BNT162b2 mRNA booster vaccination among healthcare workers in Japan. **Journal of infection and chemotherapy**, [Japan], July 20, 2022. DOI: 10.1016/j.jiac.2022.07.010. Disponível em: https://www.sciencedirect.com/science/article/pii/S1341321X22002069. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S1341321X22002069/pdf

Título	Evidence in decision-making in the context of COVID-19 in Latin America
Autor(es)	Victoria Stanford, Lionel Gresh, Joao Toledo,Jairo Mendez, Sylvain Aldighieri, Ludovic Reveiz
Resumo	The pace of the COVID-19 pandemic poses an unprecedented challenge to the evidence-to-decision process. Latin American countries have responded to COVID-19 by introducing interventions to both mitigate the risk of infection and to treat cases. Understanding how evidence is used to inform government-level decision-making at a national scale is crucial for informing country and regional actors in ongoing response efforts. Objectives: This study was undertaken between February-May 2021 and aims to characterise the best available evidence (BAE) and assess the extent to which it was used to inform decision-making in 21 Latin American countries, in relation to pharmaceutical (PI) and non-pharmaceutical interventions (NPI) related to COVID-19, including the use of therapeutics (corticosteroids, hydroxychloroquine/chloroquine and ivermectin), facemask use in the community setting and the use of diagnostic tests as a requirement for international travel. Method: A three-phase methodology was used to; (i) characterise the BAE for each intervention using an umbrella review, (ii) identify government-level decisions for each intervention through a document review and (iii) assess the use of evidence to inform decisions using a novel adapted framework analysis. Findings: The BAE is characterized by 17 living and non-living systematic reviews as evolving, and particularly uncertain for NPIs. 107 country-level documents show variation in both content and timing of decision outcomes across intervention types, with the majority of decisions taken at a time of evidence uncertainty, with only 5 documents including BAE. Seven out of eight key indicators of an evidence-to-decision process were identified more frequently among PIs than either NPI of facemask use or testing prior to travel. Overall evidence use was reported more frequently among PIs than either NPI of facemask use or travel testing (92%, 28% and 29%, respectively). Interpretation: There are limitations in the extent to which evidence use in decision-making is

	reported across the Latin America region. Institutionalising this process and grounding it in existing and emerging methodologies can facilitate the rapid response in an emergency setting. Funding: No funding was sourced for this work.
Referências	STANFORD, V. *et al.* Evidence in decision-making in the context of COVID-19 in Latin America. **The Lancet regional health. Americas**, [United Kingdom], v. 14, p. 100322, October 2022. DOI: 10.1016/j.lana.2022.100322. Disponível em: https://www.sciencedirect.com/science/article/pii/S2667193X22001399. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S2667193X22001399/pdf

Título	COVID-19 and Indigenous health in the Brazilian Amazon
Autor(es)	Bruno Wichmann, Roberta Wichmann
Resumo	We test whether the COVID-19 pandemic has an ethnicity-differentiated (Indigenous vs non-Indigenous) effect on infant health in the Brazilian Amazon. Using vital statistics data we find that Indigenous infants born during the pandemic are 0.5% more likely to have very low birth weights. Access to health care contributes to health gaps. 13% of mothers travel to deliver their babies. For traveling mothers, having an Indigenous baby during the pandemic increases the probability of very low birth weight by 3%. Indigenous mothers are 7.5% less likely to receive adequate prenatal care. Mothers that travel long distances to deliver their babies and give birth during the pandemic are 35% less likely to receive proper prenatal care. We also find evidence that the pandemic shifts medical resources from rural to urban areas, which disproportionately benefits non-Indigenous mothers. These results highlight the need for policies to reduce health inequalities in the Amazon.
Referências	WICHMANN, B.; WICHMANN, R. COVID-19 and Indigenous health in the Brazilian Amazon. **Economic modelling**, [United Kingdom], p. 105962, July 18, 2022. DOI: 10.1016/j.econmod.2022.105962. Disponível em: https://www.sciencedirect.com/science/article/pii/S0264999322002085. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S0264999322002085/pdf

Título	COVID-19 booster dose induces robust antibody response in pregnant, lactating, and nonpregnant women
Autor(es)	Caroline Atyeo, Lydia L. Shook, Nadege Nziza, Elizabeth A. Deriso, Cordelia Muir, Arantxa Medina Baez, Rosiane S. Lima, Stepan Demidkin, Sara Brigida, Rose M. De Guzman, Madeleine D. Burns, Alejandro B. Balazs, Alessio Fasano, Lael M. Yonker, Kathryn J. Gray, Galit Alter, Andrea G. Edlow
Resumo	While emerging data during the SARS-CoV-2 pandemic have demonstrated robust mRNA vaccine-induced immunogenicity across populations, including pregnant and lactating individuals, the rapid waning of vaccine-induced immunity and the emergence of variants of concern motivated the use of mRNA vaccine booster doses. Whether all populations, including pregnant and lactating individuals, will mount a comparable response to a booster dose is not known. OBJECTIVE: We sought to profile the humoral immune response to a COVID-19 mRNA booster dose in a cohort of pregnant, lactating, and age-matched nonpregnant women. STUDY DESIGN: We characterized the antibody response against ancestral Spike and Omicron in a cohort of 31 pregnant, 12 lactating and 20 nonpregnant age-matched controls who received a BNT162b2 or mRNA-1273 booster dose after primary COVID-19 vaccination. We also examined the vaccine-induced antibody profiles of 15 maternal:cord dyads at delivery. RESULTS: Receipt of a booster dose during pregnancy resulted in increased IgG1 against Omicron Spike (post-primary vaccination vs post-booster, p = 0.03). Pregnant and lactating individuals exhibited equivalent Spike-specific total IgG1, IgM and IgA levels and neutralizing titers against Omicron compared to nonpregnant women. Subtle differences in Fc-receptor binding and antibody subclass profiles were observed in the immune response to a booster dose in pregnant compared to nonpregnant individuals. Analysis of maternal and cord antibody profiles at delivery demonstrated equivalent total Spike-specific IgG1 in maternal and cord blood, yet higher Spike-specific FcγR3a-binding antibodies in the cord relative to maternal blood (p = 0.002), consistent with preferential transfer of highly functional IgG. Spike-specific IgG1 levels in the cord were positively correlated with time elapsed since receipt of the booster dose (Spearman R 0.574, p = 0.035). CONCLUSIONS: These data suggest that receipt of a booster dose during pregnancy induces a robust

Resumo	Spike-specific humoral immune response, including against Omicron. If boosting occurs in the third trimester, higher Spike-specific cord IgG1 levels are achieved with greater time elapsed between receipt of the booster and delivery. Receipt of a booster dose has the potential to augment maternal and neonatal immunity.
Referências	ATYEO, C. *et al.* COVID-19 booster dose induces robust antibody response in pregnant, lactating, and nonpregnant women. **American journal of obstetrics and gynecology**, [United States], July 19, 2022. DOI: 10.1016/j.ajog.2022.07.014. Disponível em: https://www.sciencedirect.com/science/article/pii/S0002937822005622. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S0002937822005622/pdf

Título	Management of severe and critical COVID-19 infection with immunotherapies
Autor(es)	Janhavi Athal, Jolie Gallagher, Lindsay M. Busch
Resumo	Early in the COVID-19 pandemic, clinicians and researchers sought to rapidly repurpose available candidate therapies for SARS-CoV-2 infection pending the development of directed antivirals and novel vaccines. Slowly, anecdotal case series and single-arm observational trials gave way to randomized control trials (RCTs) as the global research community mobilized to design, implement, and analyze studies in the midst of unprecedented pressure on healthcare systems. Despite early controversy surrounding the Emergency Use Authorization (EUA) and politicization of hydroxychloroquine therapy, progress soon followed in the form of remdesivir and dexamethasone, which became standard of care following EUA by the Food and Drug Administration (FDA) in May 2020(1) and release of the RECOVERY trial results in June 2020(2). Propelled by the dramatic impact on mortality conferred by the nonspecific immunosuppression of steroids, earnest investigation into directed immunomodulation soon followed, with modest mortality benefit demonstrated with these agents and an on-going need for larger studies. […]
Referências	ATHALE, J.; GALLAGHER, J.; BUSCH, L. M. Management of severe and critical COVID-19 infection with immunotherapies. **Infectious disease clinics of North America**, [United States], July 19, 2022. DOI: 10.1016/j.idc.2022.07.002. Disponível em: https://www.sciencedirect.com/science/article/pii/S0891552022000538. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S0891552022000538/pdf

Título	Vitamin D deficiency is associated with increased risk of delirium and mortality among critically ill, elderly COVID-19 patients
Autor(es)	Zahra Gholi, Davood Yadegarynia, Hassan Eini-Zeinab, Zahra Vahdat Shariatpanah
Resumo	Data on the associations of vitamin D levels with severe outcomes of coronavirus disease 2019 (COVID-19) among critically ill elderly patients are not conclusive and also no information is available about some outcomes such as delirium. Therefore, the current study was done to assess these associations in critically ill elderly COVID-19 patients. Methods: In total, 310 critically ill COVID-19 patients, aged ≥65 years, were included in the current single center prospective study. All patients were hospitalized in the intensive care unit (ICU). We collected data on demographic characteristics, laboratory parameters, blood pressure, comorbidities, medications, and types of mechanical ventilation at baseline (the first day of ICU admission). Patients were categorized based on serum 25(OH)D3 levels at the baseline [normal levels (>30 ng/mL), insufficiency (20-30 ng/mL), deficiency (<20 ng/mL)]. Data on delirium incidence, mortality, invasive mechanical ventilation (IMV) requirement during treatment, length of ICU and hospital admission, and re-hospitalization were recorded until 45 days after the baseline. Results: Vitamin D deficiency and insufficiency were prevalent among 12% and 37% of study participants, respectively. In terms of baseline differences, patients with vitamin D deficiency were more likely to be older, have organ failure, take propofol, need IMV, and were less likely to need face mask compared to patients with normal levels of vitamin D. A significant positive association was found between vitamin D deficiency and risk of delirium. After controlling for potential confounders, patients with vitamin D deficiency had a 54% higher risk of delirium compared to those with vitamin D sufficiency (HR: 1.54, 95% CI: 1.02-2.33). Such a positive association was also seen for 45-day COVID-19 mortality (HR: 3.95, 95% CI: 1.80-8.67). Also, each 10 ng/mL increase in vitamin D levels was associated with a 45% and 26% lower risk of 45-day mortality (HR: 0.55, 95% CI: 0.40-0.74) and ICU mortality due to COVID-19 (HR: 0.74, 95% CI:

Resumo	0.60-0.92), respectively. In terms of other COVID-19 outcomes including IMV requirement during treatment, prolonged hospitalization, and re-hospitalization, we found no significant association in relation to serum 25(OH)D3 levels either in crude or fully adjusted models. Conclusion: Vitamin D deficiency was associated with an increased risk of delirium and mortality among critically ill elderly COVID-19 patients.
Referências	GHOLI, Z. *et al.* Vitamin D deficiency is associated with increased risk of delirium and mortality among critically ill, elderly COVID-19 patients. **Complementary therapies in medicine**, [United Kingdom], p. 102855, July 19, 2022. DOI: 10.1016/j.ctim.2022.102855. Disponível em: https://www.sciencedirect.com/science/article/pii/S0965229922000577. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S0965229922000577/pdf

Título	Wastewater-based epidemiology: a Brazilian SARS-COV-2 surveillance experience
Autor(es)	Rodrigo de Freitas Bueno, Ieda Carolina Mantovani Claro, Matheus Ribeiro Augusto, Adriana Feliciano Alves Duran, Lívia de Moraes Bomediano Camillo, Aline Diniz Cabral, Fernando Fabriz Sodré, Cristina Celia Silveira Brandão, Carla Simone Vizzotto, Rafaella Silveira, Geovana de Melo Mendes, Andrea Fernandes Arruda, Núbia Natália de Brito, Bruna Aparecida Souza Machado, Gabriela Rodrigues Mendes Duarte, Maria de Lourdes Aguiar-Oliveira
Resumo	Since 2020, developed countries have rapidly shared both publicly and academically relevant wastewater surveillance information. Data on SARS-CoV-2 circulation is pivotal for guiding public health policies and improving the COVID-19 pandemic response. Conversely, low- and middle-income countries, such as Latin America and the Caribbean, showed timid activities in the Wastewater-Based Epidemiology (WBE) context. In these countries, isolated groups perform viral wastewater monitoring, and the data are unevenly shared or accessible to health agencies and the scientific community. This manuscript aims to highlight the relevance of a multiparty effort involving research, public health, and governmental agencies to support usage of WBE methodology to its full potential during the COVID-19 pandemic as part of a joint One Health surveillance approach. Thus, in this study, we explored the results obtained from wastewater surveillance in different regions of Brazil as a part of the COVID-19 Wastewater Monitoring Network ANA (National Water Agency), MCTI (Ministry of Science, Technology, and Innovations) and MS (Ministry of Health). Over the epidemiological weeks of 2021 and early 2022, viral RNA concentrations in wastewater followed epidemiological trends and variations. The highest viral loads in wastewater samples were detected during the second Brazilian wave of COVID-19. Corroborating international reports, our experience demonstrated usefulness of the WBE approach in viral surveillance. Wastewater surveillance allows hotspot identification, and therefore, early public health interventions. In addition, this methodology allows tracking of asymptomatic and oligosymptomatic individuals, who are generally underreported, especially in emerging countries with limited clinical testing capacity. Therefore, WBE undoubtedly contributes to improving public health

	responses in the context of this pandemic, as well as other sanitary emergencies.
Referências	BUENO, R. de F. *et al.* Wastewater-based epidemiology: a Brazilian SARS-COV-2 surveillance experience. **Journal of environmental chemical engineering**, [Netherlands], v. 10, n. 5, p. 108298, October 2022. DOI: 10.1016/j.jece.2022.108298. Disponível em: https://www.sciencedirect.com/science/article/pii/S221334372201171X. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S221334372201171X/pdf

Título	COVID-19 vaccination, incidence, and mortality rates among indigenous populations compared to the general population in Brazil: Describing trends over time
Autor(es)	Fernanda Christina Gomes Machado, Mariana Maleronka Ferron, Maria Tereza da Matta Barddal, Laura Alves Nascimento, Juliana Rosalen, Vivian I. Avelino-Silva
Resumo	Chronic social and health inequities faced by indigenous peoples in Brazil foretell the detrimental impact of COVID-19. Methods: We use de-identified, publicly available data from the Ministry of Health from March/2020 - December/2021 to describe vaccination coverage, cumulative incidence, and cumulative mortality rates due to COVID-19 among indigenous peoples. We also compare vaccination coverage among indigenous peoples with that reported for older adults, who were simultaneously included as a priority group in the vaccination strategy. Finally, we compared COVID-19 incidence and mortality rates in the indigenous population with that reported for the general Brazilian population. Findings: We found important heterogeneities in vaccination coverage across the 34 indigenous districts, and a lower overall coverage among indigenous peoples compared to older adults. We observed higher COVID-19 cumulative incidence rates among indigenous populations compared to the general Brazilian population. Although mortality rates were seemingly lower, data should be interpreted with caution due to a younger age structure and more frequent underreporting of cases and deaths among indigenous populations. After the beginning of COVID-19 vaccination program, we observed a decrease in both incidence and mortality rates among indigenous peoples in all Brazilian regions. Interpretation: The COVID-19 pandemic has had a heavy toll on vulnerable populations. Although social and geographic isolation challenges the implementation of any vaccination program for indigenous populations, prior experience suggests that the COVID-19 vaccination strategy lacked effectiveness. The absence of a coordinated strategy to reinforce the importance of the vaccine and other prevention methods, to guarantee the access to trustworthy information, and to respond with the necessary resources in extreme situations, resulted in lower COVID-19 vaccination coverage, higher incidence rates, and preventable deaths

	due to COVID-19 among indigenous peoples in Brazil. Funding: This work was not supported by specific funding.
Referências	MACHADO, F. C. G. *et al.* COVID-19 vaccination, incidence, and mortality rates among indigenous populations compared to the general population in Brazil: Describing trends over time. **The Lancet regional health. Americas**, [United Kingdom], p. 100319, July 19, 2022. DOI: 10.1016/j.lana.2022.100319. Disponível em: https://www.sciencedirect.com/science/article/pii/S2667193X22001363. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S2667193X22001363/pdf

Título	COVID-19: consequences on pregnant women and neonates
Autor(es)	Kritika S. Sharma, Rekha Sharma, Sapna Nehra, Naresh A. Rajpurohit, Kaushalya Bhakar, Dinesh Kumar
Resumo	Human species is confronting with a gigantic global COVID-19 pandemic. Initially, it was observed in Wuhan, China, that the COVID-19 cases spread across the globe with lightning speed and resulted in the 21st Century pandemic. If scientific reports are taken care of, it is noteworthy that this virus possesses more specific characteristics due to its structure. The distinctive structure has a higher binding affinity with angiotensin-converting enzyme 2 (ACE2) protein, and this is used as an access point to gain access to hosts. Methods: A complete literature search was conducted using PubMed, Google Scholar, SciFinder, and deep-diving Google Search using keywords such as "Pregnancy, COVID-19, Newborn, Fetus, Coronavirus 2019, Neonate, Pregnant women, and vertical transmission". Result & Discussion: The SARS-CoV-2 virus is unlike its former analogs: SARS-CoV, and MERS-CoV in 2002, 2012 respectively, or anything mankind has faced earlier concerning viciousness, global spread, and gravity of a causative agent. The current review has delved into articles published in various journals worldwide including the latest studies on the impact of COVID-19 on pregnant women and neonates and has discussed complications and challenges, psychological health, immunological response, vertical transmission, concurrent disorders, vaccine debate, management recommendations, recent news of the approval of COVID-19 vaccine for 6 months and older babies, and future perspectives.
Referências	SHARMA, K. S. *et al.* COVID-19: consequences on pregnant women and neonates. **Health sciences review**, [United Kingdom], p. 100044, July 19, 2022. DOI: 10.1016/j.hsr.2022.100044. Disponível em: https://www.sciencedirect.com/science/article/pii/S2772632022000332. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S2772632022000332/pdf

Título	Duration of infectious shedding of SARS-CoV-2 omicron variant and its relation with symptoms
Autor(es)	Şiran Keske, Gülen Güney Esken, Cansel Vatansever, Yeşim Beşli, Zeynep Ece Kuloğlu, Zeliş Nergiz, Tayfun Barlas, Özgür Şencanlı, Mert Ahmet Kuşkucu, Erhan Palaoğlu, Füsun Can, Önder Ergönül
Resumo	SARS CoV-2 infections with omicron variants have a high capability of human-to-human transmission. Nevertheless, the duration of isolation for mild cases was shortened to 5-7 days. We aimed to detect the duration of viral shedding among healthcare workers (HCWs) with omicron by using viral culture. Methods: We prospectively included newly diagnosed non-severe, symptomatic SARS CoV-2 positive HCWs. Nasopharyngeal swab samples were obtained consecutively on days 5, 7,10, and 14 of onset of symptoms. The samples were examined by nucleic acid amplification test and viral culture. Results: In total 55 non-severe patients with SARS CoV-2 omicron variant were included. The mean age of the population was 34 (range 23 to 54) and 78% (43/55) were female. The PCR positivity rate on days 5, 7, 10, and 14 was 96.4% (53/55), 87.3% (48/55), 74.6% (41/55), and 41.8% (23/55) consecutively, while viral culture positivity rates were 83% (44/53), 52% (26/50), 13.5% (7/52), and 8% (4/50). Among the patients who became symptom-free, the viral culture positivity rates were 100% (4/4), 58% (7/12), 11% (3/27), and 5% (2/41). Conclusion: We showed that among the SARS-CoV-2 omicron variant infected patients, viral shedding continues for at least ten days in 13.5% of all cases and 11% in symptom-free cases. The decision for cessation of isolation according to the presence of symptoms could be re-considered until further studies disapprove of our results. Meanwhile, the infected HCWs who give care to the high-risk patients for severe COVID-19 might extend their isolations up to 10 days after the onset of symptoms, regardless of their symptoms.
Referências	KESKE, Ş. *et al.* Duration of infectious shedding of SARS-CoV-2 omicron variant and its relation with symptoms. **Clinical microbiology and infection**, [United Kingdom], July 16, 2022. DOI: 10.1016/j.cmi.2022.07.009. Disponível em: https://www.sciencedirect.com/science/article/pii/S1198743X22003731. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S1198743X22003731/pdf

Título	Investigation of the diagnostic performance of the SARS-CoV-2 saliva antigen test: a meta-analysis
Autor(es)	Cheng-Chieh Chen, Ke-Yu Hsiao, Chyi-Huey Bai, Yuan-Hung Wang
Resumo	The COVID-19 pandemic is caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Rapid identification and isolation of patients with COVID-19 are critical strategies to contain COVID-19. The saliva antigen test has the advantages of noninvasiveness and decreased transmission risk to health-care professionals. This meta-analysis investigated the diagnostic accuracy of the saliva antigen test for SARS-CoV-2. Methods: We searched for relevant studies in PubMed, Embase, Cochrane Library, and Biomed Central. Studies evaluating the diagnostic accuracy of saliva antigen tests for SARS-CoV-2 were included. The data of the included studies were used to construct a 2 × 2 table on a per patient basis. The overall sensitivity and specificity of saliva antigen tests were determined using a bivariate random-effects model. Results: Nine studies enrolling 9842 patients were included. The meta-analysis generated a pooled sensitivity of 65.3% and a pooled specificity of 99.7%. A subgroup analysis of the studies performing the chemiluminescent enzyme immunoassay (CLEIA) for participants from airports and public health centers revealed a pooled sensitivity of 93.6%. Conclusion: Our findings demonstrated that the saliva antigen test performed using CLEIA exhibited higher sensitivity for the detection of SARS-CoV-2. Therefore, the saliva antigen test performed using CLEIA might be an effective and noninvasive screening tool for SARS-CoV-2.
Referências	CHENG, C. C. *et al.* Investigation of the diagnostic performance of the SARS-CoV-2 saliva antigen test: a meta-analysis. **Journal of microbiology, immunology and infection**, [Hong Kong], July 16, 2022. DOI: 10.1016/j.jmii.2022.07.003. Disponível em: https://www.sciencedirect.com/science/article/pii/S1684118222001013. Acesso em: 22 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S1684118222001013/pdf

Título	Persisting gastrointestinal symptoms and post-infectious irritable bowel syndrome following SARS-CoV-2 infection: results from the Arizona CoVHORT
Autor(es)	Erika Austhof, Melanie L. Bell, Mark S. Riddle, Collin Catalfamo, Caitlyn McFadden, Kerry Cooper, Elaine Scallan Walter, Elizabeth Jacobs, Kristen Pogreba-Brown
Resumo	In this study we aimed to examine the association between gastrointestinal (GI) symptom presence during acute SARS-CoV-2 infection and the prevalence of GI symptoms and development of post-infectious irritable bowel syndrome (PI-IBS). We used data from a prospective cohort and logistic regression to examine the association between GI symptom status during confirmed SARS-CoV-2 infection and prevalence of persistent gastrointestinal symptoms at ≥45 days. We also report the incidence of PI-IBS following SARS-CoV-2 infection. Of the 1,475 participants in this study, 33.8% (n=499) had GI symptoms during acute infection. Cases with acute GI symptoms had an odds of persisting GI symptoms 4 times higher than cases without acute GI symptoms (OR=4.29, CI: 2.45, 7.53); symptoms lasted on average 8 months following infection. Of those with persisting GI symptoms, 67% sought care for their symptoms and incident PI-IBS occurred in 3.0% (n=15) of participants. Those with acute GI symptoms after SARS-CoV-2 infection are likely to have similar persistent symptoms 45 days and greater. These data indicate that attention to a potential increase in related healthcare needs is warranted.
Referências	AUSTHOF, E. et al. Persisting gastrointestinal symptoms and post-infectious irritable bowel syndrome following SARS-CoV-2 infection: results from the Arizona CoVHORT**. Epidemiology and infection**, [United Kingdom], p. 1–22, July 8, 2022. DOI: 10.1017/S0950268822001200. Disponível em: https://www.cambridge.org/core/journals/epidemiology-and-infection/article/persisting-gastrointestinal-symptoms-and-postinfectious-irritable-bowel-syndrome-following-sarscov2-infection-results-from-the-arizona-covhort/4074EB44B26516F4680171554F6C9CC8. Acesso em: 15 jul. 2022.
Fonte	https://www.cambridge.org/core/services/aop-cambridge-core/content/view/4074EB44B26516F4680171554F6C9CC8/S0950268822001200a.pdf/persisting-gastrointestinal-symptoms-and-post-infectious-irritable-bowel-syndrome-following-sars-cov-2-infection-results-from-the-arizona-covhort.pdf

Título	Emergence of immune escape at dominant SARS-CoV-2 killer T-cell epitope
Autor(es)	Garry Dolton, Cristina Rius, Md Samiul Hasan, Aaron Wall, Barbara Szomolay, Enas Behiry, Thomas Whalley, Joel Southgate, Anna Fuller, The COVID-19 Genomics UK (COG-UK) consortium, Théo Morin, Katie Topley, Li Rong Tan, Philip J.R. Goulder, Owen B. Spiller, Pierre J. Rizkallah, Lucy C. Jones, Thomas R. Connor, Andrew K. Sewell
Resumo	We studied the prevalent cytotoxic CD8 T-cell response mounted against severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) Spike glycoprotein269-277 epitope (sequence YLQPRTFLL) via the most frequent Human Leukocyte Antigen (HLA) class I worldwide, HLA A∗02. The Spike P272L mutation that has arisen in at least 112 different SARS-CoV-2 lineages to date, including in lineages classified as 'variants of concern', was not recognised by the large CD8 T-cell response seen across cohorts of HLA A∗02+ convalescent patients and individuals vaccinated against SARS-CoV-2, despite these responses comprising of over 175 different individual T-cell receptors. Viral escape at prevalent T-cell epitopes restricted by high frequency HLAs may be particularly problematic when vaccine immunity is focussed on a single protein such as SARS-CoV-2 Spike providing a strong argument for inclusion of multiple viral proteins in next generation vaccines and highlighting the need for monitoring T-cell escape in new SARS-CoV-2 variants.
Referências	DOLTON, G. *et al.* Emergence of immune escape at dominant SARS-CoV-2 killer T-cell epitope. **Cell**, [United States], July 14, 2022. DOI: 10.1016/j.cell.2022.07.002. Disponível em: https://www.sciencedirect.com/science/article/pii/S0092867422008492. Acesso em: 15 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S0092867422008492/pdf

Título	Efficacy and safety of a single dose of casirivimab and imdevimab for the prevention of COVID-19 over an 8-month period: a randomised, double-blind, placebo-controlled trial
Autor(es)	Gary A. Herman, Meagan P. O'Brien, Eduardo Forleo-Neto, Neena Sarkar, Flonza Isa, Peijie Hou, Kuo-Chen Chan, Katharine J. Bar, Ruanne V. Barnabas, Dan H. Barouch, Myron S. Cohen, Christopher B. Hurt, Dale R. Burwen, Mary A. Marovich, Bret J. Musser, John D. Davis, Kenneth C. Turner, Adnan Mahmood, Andrea T. Hooper, Jennifer D. Hamilton, Janie Parrino, Danise Subramaniam, Alina Baum, Christos A. Kyratsous, A. Thomas DiCioccio, Neil Stahl, Ned Braunstein, George D. Yancopoulos, David M. Weinreich, for the COVID-19 Phase 3 Prevention Trial Team
Resumo	There is an unmet need for COVID-19 prevention in patient populations who have not mounted or are not expected to mount an adequate immune response to complete COVID-19 vaccination. We previously reported that a single subcutaneous 1200 mg dose of the monoclonal antibody combination casirivimab and imdevimab (CAS+IMD) prevented symptomatic SARS-CoV-2 infections by 81·4% in generally healthy household contacts of SARS-CoV-2-infected individuals over a 1-month efficacy assessment period. Here we present additional results, including the 7-month follow-up period (months 2–8), providing additional insights about the potential for efficacy in pre-exposure prophylaxis settings. Methods This was a randomised, double-blind, placebo-controlled trial done in the USA, Romania, and Moldova in 2020–2021, before the emergence of omicron (B.1.1.529) and omicron-lineage variants. Uninfected and unvaccinated household contacts of infected individuals, judged by the investigator to be in good health, were randomly assigned (1:1) to receive 1200 mg CAS+IMD or placebo by subcutaneous injection according to a central randomisation scheme provided by an interactive web response system; randomisation was stratified per site by the test results of a local diagnostic assay for SARS-CoV-2 and age group at baseline. COVID-19 vaccines were prohibited before randomisation, but participants were allowed to receive COVID-19 vaccination during the follow-up period. Participants who developed COVID-19 symptoms during the follow-up period underwent RT-PCR testing. Prespecified endpoints included the proportion of previously uninfected and baseline-seronegative participants (seronegative-modified full analysis set) who had RT-PCR-confirmed COVID-19 in the follow-up period (post-hoc for the timepoints of months 2–5 and 6–8 only) and underwent seroconversion (ie, became seropositive, considered a proxy for any SARS-CoV-2 infections [symptomatic and asymptomatic]; prespecified up to day 57, post-hoc for all timepoints thereafter). We also assessed the incidence of treatment-emergent adverse events. This study is registered with ClinicalTrials.gov, NCT04452318. Findings From July 13, 2020, to Oct 4, 2021, 2317 participants who were RT-PCR-negative for SARS-CoV-2 were randomly assigned, of whom 1683 (841 assigned to CAS + IMD and 842 assigned to placebo) were seronegative at baseline. During the entirety of the 8-month study, CAS + IMD reduced the risk of COVID-19 by 81·2%

Resumo	(nominal p<0·0001) versus placebo (prespecified analysis). During the 7-month follow-up period, protection was greatest during months 2–5, with a 100% relative risk reduction in COVID-19 (nominal p<0·0001; post-hoc analysis). Efficacy waned during months 6–8 (post-hoc analysis). Seroconversion occurred in 38 (4·5%) of 841 participants in the CAS + IMD group and in 181 (21·5%) of 842 in the placebo group during the 8-month study (79·0% relative risk reduction vs placebo; nominal p<0·0001). Six participants in the placebo group were hospitalised due to COVID-19 versus none who received CAS + IMD. Serious treatment-emergent adverse events (including COVID-19) were reported in 24 (1·7%) of 1439 participants receiving CAS + IMD and in 23 (1·6%) of 1428 receiving placebo. Five deaths were reported, none of which were due to COVID-19 or related to the study drugs. Interpretation CAS+IMD is not authorised in any US region as of Jan 24, 2022, because data show that CAS+IMD is not active against omicron-lineage variants. In this study, done before the emergence of omicron-lineage variants, a single subcutaneous 1200 mg dose of CAS+IMD protected against COVID-19 for up to 5 months of community exposure to susceptible strains of SARS-CoV-2 in the pre-exposure prophylaxis setting, in addition to the postexposure prophylaxis setting that was previously shown.
Referências	HERMAN, G. A. *et al.* Efficacy and safety of a single dose of casirivimab and imdevimab for the prevention of COVID-19 over an 8-month period: a randomised, double-blind, placebo-controlled trial. **The Lancet. Infectious diseases**, [United Kingdom], July 5, 2022. DOI: 10.1016/S1473-3099(22)00416-9. Disponível em: https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(22)00416-9/fulltext. Acesso em: 15 jul. 2022.
Fonte	https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(22)00416-9/fulltext

Título	Estimated number of COVID-19 infections, hospitalizations, and deaths prevented among vaccinated persons in the US, December 2020 to September 2021
Autor(es)	Molly K. Steele, Alexia Couture, Carrie Reed, Danielle Iuliano, Michael Whitaker, Hannah Fast, Aron J. Hall, Adam MacNeil, Betsy Cadwell, Kristin J. Marks, Benjamin J. Silk
Resumo	The number of SARS-CoV-2 infections and COVID-19–associated hospitalizations and deaths prevented among vaccinated persons, independent of the effect of reduced transmission, is a key measure of vaccine impact.To estimate the number of SARS-CoV-2 infections and COVID-19–associated hospitalizations and deaths prevented among vaccinated adults in the US.In this modeling study, a multiplier model was used to extrapolate the number of SARS-CoV-2 infections and COVID-19–associated deaths from data on the number of COVID-19–associated hospitalizations stratified by state, month, and age group (18-49, 50-64, and ≥65 years) in the US from December 1, 2020, to September 30, 2021. These estimates were combined with data on vaccine coverage and effectiveness to estimate the risks of infections, hospitalizations, and deaths. Risks were applied to the US population 18 years or older to estimate the expected burden in that population without vaccination. The estimated burden in the US population 18 years or older given observed levels of vaccination was subtracted from the expected burden in the US population 18 years or older without vaccination (ie, counterfactual) to estimate the impact of vaccination among vaccinated persons.Completion of the COVID-19 vaccination course, defined as 2 doses of messenger RNA (BNT162b2 or mRNA-1273) vaccines or 1 dose of JNJ-78436735 vaccine.Monthly numbers and percentages of SARS-CoV-2 infections and COVID-19–associated hospitalizations and deaths prevented were estimated among those who have been vaccinated in the US.COVID-19 vaccination was estimated to prevent approximately 27 million (95% uncertainty interval [UI], 22 million to 34 million) infections, 1.6 million (95% UI, 1.4 million to 1.8 million) hospitalizations, and 235 000 (95% UI, 175 000–305 000) deaths in the US from December 1, 2020, to September 30, 2021, among vaccinated adults 18 years or older. From September 1 to September 30, 2021, vaccination was estimated to prevent 52%

	(95% UI, 45%–62%) of expected infections, 56% (95% UI, 52%-62%) of expected hospitalizations, and 58% (95% UI, 53%-63%) of expected deaths in adults 18 years or older.These findings indicate that the US COVID-19 vaccination program prevented a substantial burden of morbidity and mortality through direct protection of vaccinated individuals.
Referências	STEELE, M. K. *et al.* Estimated number of COVID-19 infections, hospitalizations, and deaths prevented among vaccinated persons in the US, December 2020 to September 2021. **JAMA network open**, [United States], v. 5, n. 7, p. e2220385, July 6, 2022. DOI: 10.1001/jamanetworkopen.2022.20385. Disponível em: https://jamanetwork.com/journals/jamanetworkopen/fullarticle/2793913. Acesso em: 15 jul. 2022.
Fonte	https://jamanetwork.com/journals/jamanetworkopen/fullarticle/2793913

Título	First nonprescription COVID-19 test that also detects flu and RSV
Autor(es)	Howard D. Larkin
Resumo	The FDA has authorized the first nonprescription diagnostic test that can identify multiple viruses that cause COVID-19–like respiratory symptoms, including respiratory syncytial virus (RSV). FDA officials see it as another step toward diagnostic testing at home for certain viruses. In addition to SARS-CoV-2 and RSV, the Labcorp Seasonal Respiratory Virus RT-PCR DTC Test can detect influenza A and B. Patients can self-collect a nasal swab sample at home and then send the sample to Labcorp for testing without consulting a clinician. Results are delivered through an online portal, and a health care professional follows up for positive or invalid test results. The home sample collection kit can be purchased online or in stores. Adults can collect their own nasal samples but teens aged 14 to 17 years should have adult supervision when they self-collect their samples. An adult should assist children aged 2 years or older in collecting samples. The multianalyte test will enable consumers to more easily determine whether they're infected with SARS-CoV-2, influenza, or RSV. Test results can help consumers determine whether they should self-isolate or take other health care steps after discussion with a medical professional, according to the FDA. "The rapid advances being made in consumer access to diagnostic tests, including the ability to collect your sample at home for flu and RSV without a prescription, brings us one step closer to tests for these viruses that could be performed entirely at home," Jeff Shuren, MD, JD, director of FDA's Center for Devices and Radiological Health, said in a statement.
Referências	LARKIN, H. D. First nonprescription COVID-19 test that also detects flu and RSV. **JAMA**, [United States], v. 328, n. 1, p. 11, July 5, 2022. DOI: 10.1001/jama.2022.11031. Disponível em: https://doi.org/10.1001/jama.2022.11031. Acesso em: 15 jul. 2022.
Fonte	https://jamanetwork.com/journals/jama/fullarticle/2793846

Título	Leading causes of death in the us during the COVID-19 pandemic, March 2020 to October 2021
Autor(es)	Meredith S. Shiels, Anika T. Haque, Amy Berrington de González, Neal D. Freedman
Resumo	In 2020, heart disease and cancer were the leading causes of death in the US, accounting for 1.29 million deaths, followed by COVID-19, accounting for 350 000 deaths. The pandemic may also have indirectly led to increases in other causes of death, including heart disease, diabetes, Alzheimer disease, and unintentional injuries. We examined the leading causes of death in the US, overall and in various age groups, from March 2020 to October 2021.
Referências	SHIELS, M. S. *et al.* Leading causes of death in the us during the covid-19 pandemic, march 2020 to october 2021. **JAMA internal medicine**, [United States], July 5, 2022. DOI: 10.1001/jamainternmed.2022.2476. Disponível em: https://doi.org/10.1001/jamainternmed.2022.2476. Acesso em: 15 jul. 2022.
Fonte	https://jamanetwork.com/journals/jamainternalmedicine/fullarticle/2794043

Título	Asymptomatic severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) infection in adults is uncommon using rigorous symptom characterization and follow-up in an acute care adult hospital Outbreak
Autor(es)	Heidi M. O'Grady, Devika Dixit, Zoha Khawaja, Kate Snedeker, Jennifer Ellison, Joyce Erebor, Peter Jamieson, Amanda Weiss, Daniel Salcedo, Kimberley Roberts, Karen Wiens, Nicholas Etches, Jenine Leal, John M. Conly
Resumo	Asymptomatic COVID-19 has been reported as a significant driver of COVID-19 outbreaks. Our hospital ward outbreak analysis suggests that comprehensive symptoms and signs assessment, in combination with adequate follow-up, allows for a more precise determination of COVID-19 symptoms and revealed asymptomatic infection was quite uncommon amongst adults in this setting.
Referências	O'GRADY, H. M. *et al.* Asymptomatic severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) infection in adults is uncommon using rigorous symptom characterization and follow-up in an acute care adult hospital Outbreak. **Infection control and hospital epidemiology**, [United Kingdom], p. 1–25, July 7, 2022. DOI: 10.1017/ice.2022.168. Disponível em: https://doi.org/10.1017/ice.2022.168. Acesso em: 15 jul. 2022.
Fonte	https://www.cambridge.org/core/journals/infection-control-and-hospital-epidemiology/article/asymptomatic-severe-acute-respiratory-syndrome-coronavirus2-sarscov2-infection-in-adults-is-uncommon-using-rigorous-symptom-characterization-and-followup-in-an-acute-care-adult-hospital-outbreak/15B8F8ED799EBCB622701455A32D8FD1

Título	SARS-CoV-2 brain regional detection, histopathology, gene expression, and immunomodulatory changes in decedents with COVID-19
Autor(es)	Geidy E. Serrano, Jessica E. Walker, Cecilia Tremblay, Ignazio S. Piras, Matthew J. Huentelman, Christine M. Belden, Danielle Goldfarb, David Shprecher, Alireza Atri, Charles H. Adler, Holly A. Shill, Erika Driver-Dunckley, Shyamal H. Mehta, Richard Caselli, Bryan K. Woodruff, Chadwick F. Haarer, Thomas Ruhlen, Maria Torres, Steve Nguyen, Dasan Schmitt, Steven Z. Rapscak, Christian Bime, Joseph L. Peters, Ellie Alevritis, Richard A. Arce, Michael J. Glass, Daisy Vargas, Lucia I. Sue, Anthony J. Intorcia, Courtney M. Nelson, Javon Oliver, Aryck Russell, Katsuko E. Suszczewicz, Claryssa I. Borja, Madison P. Cline, Spencer J. Hemmingsen, Sanaria Qiji, Holly M. Hobgood, Joseph P. Mizgerd, Malaya K. Sahoo, Haiyu Zhang, Daniel Solis, Thomas J. Montine, Gerald J. Berry, Eric M. Reiman, Katharina Ro¨ltgen, Scott D. Boyd, Benjamin A. Pinsky, James L. Zehnder, Pierre Talbot, Marc Desforges, Michael DeTure, Dennis W. Dickson, Thomas G. Beach
Resumo	Brains of 42 COVID-19 decedents and 107 non-COVID-19 controls were studied. RT-PCR screening of 16 regions from 20 COVID-19 autopsies found SARS-CoV-2 E gene viral sequences in 7 regions (2.5% of 320 samples), concentrated in 4/20 subjects (20%). Additional screening of olfactory bulb (OB), amygdala (AMY) and entorhinal area for E, N1, N2, RNA-dependent RNA polymerase, and S gene sequences detected one or more of these in OB in 8/21 subjects (38%). It is uncertain whether these RNA sequences represent viable virus. Significant histopathology was limited to 2/42 cases (4.8%), one with a large acute cerebral infarct and one with hemorrhagic encephalitis. Case-control RNAseq in OB and AMY found more than 5000 and 700 differentially expressed genes, respectively, unrelated to RT-PCR results; these involved immune response, neuronal constituents, and olfactory/taste receptor genes. Olfactory marker protein-1 reduction indicated COVID-19-related loss of OB olfactory mucosa afferents. Iba-1-immunoreactive microglia had reduced area fractions in cerebellar cortex and AMY, and cytokine arrays showed generalized downregulation in AMY and upregulation in blood serum in COVID-19 cases. Although OB is a major brain portal for SARS-CoV-2, COVID-19 brain changes are more likely due to blood-borne immune mediators and trans-synaptic gene expression changes arising from OB deafferentation.

Referências	SERRANO, G. E. *et al.* SARS-CoV-2 brain regional detection, histopathology, gene expression, and immunomodulatory changes in decedents with COVID-19. **Journal of neuropathology and experimental neurology**, [United States], p. nlac056, July 11, 2022. DOI: 10.1093/jnen/nlac056. Disponível em: https://academic.oup.com/jnen/advance-article/doi/10.1093/jnen/nlac056/6639867. Acesso em: 15 jul. 2022.
Fonte	https://academic.oup.com/jnen/advance-article-pdf/doi/10.1093/jnen/nlac056/44828349/nlac056.pdf

Título	Delivering an mRNA vaccine using a lymphatic drug delivery device improves humoral and cellular immunity against SARS-CoV-2
Autor(es)	Runqiang Chen, Hui Xie, Sahba Khorsandzadeh, Madison Smith, Namir Shaabani, Qidong Hu, Xiaoxuan Lyu, Hua Wang, Wan-lin Lim, Haotian Sun, Henry Ji, Brian Cooley, Russell Ross, David M Francis
Resumo	The exploration and identification of safe and effective vaccines for the SARS-CoV-2 pandemic has captured the world's attention and remains an ongoing issue due to concerns of balancing protection against emerging variants of concern (VoCs) while also generating long lasting immunity. Here, we report the synthesis of a novel messenger ribonucleic acid encoding the spike protein in a lipid nanoparticle formulation (STI-7264) that generates robust humoral and cellular immunity following immunization of C57Bl6 mice. In an effort to improve immunity, a clinically-focused lymphatic drug delivery device (MuVaxx) was engineered to modulate immune cells at the injection site (epidermis and dermis) and draining lymph node (LN) and tested to measure adaptive immunity. Using MuVaxx, immune responses were elicited and maintained at a 10-fold dose reduction compared to traditional intramuscular (IM) administration as measured by anti-spike antibodies, cytokine-producing CD8 T cells, neutralizing antibodies against the Washington (wild type) strain and South African (Beta) variants, and LN-resident spike-specific memory B cells. Remarkably, a 4-fold elevated T cell response was observed in MuVaxx administered vaccination compared to that of IM administered vaccination. Thus, these data support further investigation into STI-7264 and lymphatics-mediated delivery using MuVaxx for SARS-CoV-2 and VoC vaccines.
Referências	CHEN, R. *et al.* Delivering an mRNA vaccine using a lymphatic drug delivery device improves humoral and cellular immunity against SARS-CoV-2. **Journal of Molecular Cell Biology**, [United Kingdom], p. mjac041, July 8, 2022. DOI: 10.1093/jmcb/mjac041. Disponível em: https://academic.oup.com/jmcb/advance-article/doi/10.1093/jmcb/mjac041/6634240. Acesso em: 15 jul. 2022.
Fonte	https://academic.oup.com/jmcb/advance-article-pdf/doi/10.1093/jmcb/mjac041/44686042/mjac041.pdf

Título	Epidemiological analysis of the first 1000 cases of SARS-CoV-2 lineage BA.1 (B.1.1.529, Omicron) compared with co-circulating Delta in Wales, UK
Autor(es)	Nicole Pacchiarini, Clare Sawyer, Christopher Williams, Daryn Sutton, Christopher Roberts, Felicity Simkin, Grace King, Victoria McClure, Simon Cottrell, Helen Clayton, Andrew Beazer, Catie Williams, Sara M. Rey, Thomas R. Connor, Catherine Moore
Resumo	The Omicron (lineage B.1.1.529) variant of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was first reported in Wales, UK, on 3 December 2021. The aim of the study was to describe the first 1000 cases of the Omicron variant by demographic, vaccination status, travel and severe outcome status and compare this to contemporaneous cases of the Delta variant. Methods Testing, typing and contact tracing data were collected by Public Health Wales and analysis undertaken by the Communicable Disease Surveillance Centre (CDSC). Risk ratios for demographic factors and symptoms were calculated comparing Omicron cases to Delta cases identified over the same time period. Results By 14 December 2021, 1000 cases of the Omicron variant had been identified in Wales. Of the first 1000, just 3% of cases had a prior history of travel revealing rapid community transmission. A higher proportion of Omicron cases were identified in individuals aged 20–39, and most cases were double vaccinated (65.9%) or boosted (15.7%). Age-adjusted analysis also revealed that Omicron cases were less likely to be hospitalised (0.4%) or report symptoms (60.8%). Specifically a significant reduction was observed in the proportion of Omicron cases reporting anosmia (8.9%). Conclusion Key findings include a lower risk of anosmia and a reduced risk of hospitalisation in the first 1000 Omicron cases compared with co-circulating Delta cases. We also identify that existing measures for travel restrictions to control importations of new variants identified outside the United Kingdom did not prevent the rapid ingress of Omicron within Wales.
Referências	PACCHIARINI, N. *et al.* Epidemiological analysis of the first 1000 cases of SARS-CoV-2 lineage BA.1 (B.1.1.529, Omicron) compared with co-circulating Delta in Wales, UK. **Influenza and other respiratory viruses**, [United Kingdom], v. n/a, n. n/a, DOI: 10.1111/irv.13021. Disponível em: https://onlinelibrary.wiley.com/doi/abs/10.1111/irv.13021. Acesso em: 15 jul. 2022.
Fonte	https://onlinelibrary.wiley.com/doi/epdf/10.1111/irv.13021

Título	Analysis of COVID-19–related croup and SARS-CoV-2 variant predominance in the US
Autor(es)	Brian Lefchak, Amanda Nickel, Shea Lammers, Dave Watson, Gabrielle Z. Hester, Kelly R. Bergmann
Resumo	Introduction...Recent reports have found an association between SARS-CoV-2 and croup.[1-3] We aimed to investigate whether SARS-CoV-2 variants were associated with the proportion of children with croup, as well as hospital and intensive care unit (ICU) admissions and racemic epinephrine (RE) treatment.
Referências	LEFCHAK, B. *et al.* Analysis of COVID-19–related croup and SARS-CoV-2 variant predominance in the US. **JAMA network open**, [United States], v. 5, n. 7, p. e2220060, July 1, 2022. DOI: 10.1001/jamanetworkopen.2022.20060. Disponível em: https://doi.org/10.1001/jamanetworkopen.2022.20060. Acesso em: 8 jul. 2022.
Fonte	https://jamanetwork.com/journals/jamanetworkopen/fullarticle/2793808

Título	Persistent SARS-CoV-2 infection with accumulation of mutations in a patient with poorly controlled HIV infection
Autor(es)	Tongai G Maponga, Montenique Jeffries, Houriiyah Tegally, Andrew Sutherland, Eduan Wilkinson, Richard J Lessells, Nokukhanya Msomi, Gert van Zyl, Tulio de Oliveira, Wolfgang Preiser
Resumo	A 22-year-old female with uncontrolled advanced HIV infection was persistently infected with SARS-CoV-2 beta variant for 9 months, the virus accumulating >20 additional mutations. Antiretroviral therapy suppressed HIV and cleared SARS-CoV-2 within 6-9 weeks. Increased vigilance is warranted to benefit affected individuals and prevent the emergence of novel SARS-CoV-2 variants.
Referências	MAPONGA, T. G. *et al.* Persistent SARS-CoV-2 infection with accumulation of mutations in a patient with poorly controlled HIV infection. **Clinical infectious diseases**, [United States], p. ciac548, July 6, 2022. DOI: 10.1093/cid/ciac548. Disponível em: https://doi.org/10.1093/cid/ciac548. Acesso em: 8 jul. 2022.
Fonte	https://academic.oup.com/cid/advance-article/doi/10.1093/cid/ciac548/6632801?searchresult=1

Título	Magnitude and determinants of SARS-CoV-2 household transmission: a longitudinal cohort study
Autor(es)	J Daniel Kelly, Scott Lu, Khamal Anglin, Miguel Garcia-Knight, Jesus Pineda-Ramirez, Sarah A Goldberg, Michel Tassetto, Amethyst Zhang, Kevin Donohue, Michelle C Davidson, Mariela Romero, Ruth Diaz Sanchez, Manuella Djomaleu, Sujata Mathur, Jessica Y Chen, Carrie A Forman, Venice Servellita, Rubi D Montejano, Joshua R Shak, George W Rutherford, Steven G Deeks, Glen R Abedi, (CDC), Melissa A Rolfes, (CDC), Sharon Saydah, (CDC), Melissa Briggs-Hagen, (CDC), Michael J Peluso, Charles Chiu, Claire M Midgley, (CDC), Raul Andino, Jeffrey N Martin
Resumo	Households have emerged as important venues for SARS-CoV-2 transmission. Little is known, however, regarding the magnitude and determinants of household transmission in increasingly vaccinated populations.From September 2020 to January 2022, symptomatic non-hospitalized individuals with SARS-CoV-2 infection by RNA detection were identified within 5 days of symptom onset; all individuals resided with at least one other SARS-CoV-2-uninfected household member. These infected persons (cases) and their household members (contacts) were subsequently followed with questionnaire-based measurement and serial nasal specimen collection. The primary outcome was SARS-CoV-2 infection among contacts.We evaluated 42 cases and their 74 household contacts. Among the contacts, 32 (43%) became infected, of whom 5/32 (16%) were asymptomatic; 81% of transmissions occurred by 5 days after the case's symptom onset. From 21 unvaccinated cases, 14-day cumulative incidence of SARS-CoV-2 infection among contacts was 18/40 (45%; 95% CI: 29, 62), most of whom were unvaccinated. From 21 vaccinated cases, 14-day cumulative incidence of SARS-CoV-2 infection was 14/34 (41%; 95% CI: 25, 59) among all contacts and 12/29 (41%; 95% CI: 24, 61) among vaccinated contacts. At least one co-morbid condition among cases and 10 or more days of RNA detection in cases were associated with increased risk of infection among contacts.Among households including individuals with symptomatic SARS-CoV-2 infection, both vaccinated-to-vaccinated and unvaccinated-to-unvaccinated transmission of SARS-CoV-2 to household contacts was common. Because vaccination alone did not notably reduce risk of infection, household contacts will need to employ additional interventions to avoid infection.
Referências	DANIEL KELLY, J. *et al.* Magnitude and determinants of SARS-CoV-2 household transmission: a longitudinal cohort study. **Clinical infectious diseases**, [United States], p. ciac545, July 5, 2022. DOI: 10.1093/cid/ciac545. Disponível em: https://doi.org/10.1093/cid/ciac545. Acesso em: 8 jul. 2022.
Fonte	https://academic.oup.com/cid/advance-article/doi/10.1093/cid/ciac545/6631204?searchresult=1

Título	Fifteen-Month Follow-Up of Anti-Spike Receptor-Binding Domain SARS-CoV-2 Antibodies among Healthcare Workers in Boston, MA
Autor(es)	Maura C Dodge, Manisha Cole, Elizabeth R Duffy, Martha M Werler, Yachana Kataria
Resumo	Boston Medical Center (BMC) is a safety net hospital in Boston, and from the initial wave of COVID-19 there has been an overwhelming concern about the exposure of healthcare workers (HCWs) to SARS-CoV-2.We conceived a study to follow a cohort of BMC HCWs, beginning in July 2020 and continuing for 15 months, collecting survey data and serum samples at approximately 3-month intervals. Serum samples were analyzed using the Abbott Architect i2000 for SARS-CoV-2 antibodies (anti-spike1-Receptor Binding Domain IgG and anti-nucleoprotein IgG). Positive anti-n IgG results were used, in addition to reverse transcription-PCR results, for identifying cases of infection. History of COVID-19 and vaccination status were confirmed, where possible, using electronic medical records. Participants were grouped according to vaccination and infection status in September 2021 for analysis of anti-s IgG trends.A majority of HCWs remain well above the positivity threshold for anti-spike IgG antibodies for up to 11 months post-vaccination and 15 months post-infection, regardless of combinations and permutations of vaccination and infection. Those with COVID-19 infection before vaccination had significantly higher median serum antibody concentrations in comparison to HCWs with no prior infection at each follow-up time point.These findings further support what is known regarding the decline in serum antibody concentrations following natural infection and vaccination, adding knowledge of serum antibody levels for up to 15 months post- infection and 11 months post-vaccination.
Referências	DODGE, M. C. *et al.* Fifteen-Month Follow-Up of Anti-Spike Receptor-Binding Domain SARS-CoV-2 Antibodies among Healthcare Workers in Boston, MA. **The journal of applied laboratory medicine**, [United States], p. jfac056, July 6, 2022. DOI: 10.1093/jalm/jfac056. Disponível em: https://doi.org/10.1093/jalm/jfac056. Acesso em: 8 jul. 2022.
Fonte	https://academic.oup.com/jalm/advance-article-abstract/doi/10.1093/jalm/jfac056/6632765?redirectedFrom=fulltext

Título	Breakthrough SARS-CoV-2 infections in immune mediated disease patients undergoing B cell depleting therapy: a retrospective cohort analysis
Autor(es)	Cassandra M Calabrese,Elizabeth Kirchner, Elaine M Husni, Brandon P Moss, Anthony P Fernandez, Yuxuan Jin, Leonard H Calabrese
Resumo	Objectives Patients with immune mediated inflammatory diseases (IMIDs) receiving B cell depleting therapy (BCDT) are among the most vulnerable to severe COVID-19 as well as the most likely to respond sub-optimally to SARS-CoV-2 vaccines. However, little is known about the frequency or severity of breakthrough infection in this population. We retrospectively analyzed a large group of vaccinated IMIDs patients undergoing BCDT in order to identify the presence of breakthrough COVID-19 infections and assess their outcomes. Methods In this retrospective cohort study, the pharmacy records and COVID-19 registry at the Cleveland Clinic were searched using specific ICD-10 codes to identify IMIDs patients who (1) were treated with BCDT, (2) were vaccinated against SARS-CoV-2, and (3) experienced breakthrough infections. Each EMR was reviewed to extract clinical data and outcomes. Univariate and multivariable logistic/proportional-odds regression models were used to examine the risk factors for severe outcomes. Results Of 1696 IMIDs patients on BCDT, 74 developed breakthrough COVID-19 prior to December 16th, 2021. Outcomes were severe with 29(39.2%) hospitalized, 11(14.9%) requiring critical care, and 6(8.1%) deaths. Outpatient anti-SARS-CoV-2 monoclonal antibodies were used to treat 21 with 1 hospitalization and no deaths. A comparator analysis examining 1437 unvaccinated IMIDs patients on BCDT over the same time period identified 57(3.9%) COVID-19 cases with 28(49.1%) requiring hospitalization including 7(12.3%) deaths. Conclusions IMIDs patients on BCDT regardless of vaccine status appear vulnerable to infection with SARS-CoV-2 and are frequently associated with severe outcomes. Outpatient use of anti-SARS-CoV-2 monoclonal antibody therapy appeared to be associated with enhanced clinical outcomes.
Referências	CALABRESE, C. M. *et al.* Breakthrough SARS-CoV-2 infections in immune mediated disease patients undergoing B cell depleting therapy: a retrospective cohort analysis. **Arthritis & rheumatology**, [United States], July 6, Disponível em: https://onlinelibrary.wiley.com/doi/abs/10.1002/art.42287. Acesso em: 8 jul. 2022.
Fonte	https://onlinelibrary.wiley.com/doi/epdf/10.1002/art.42287

Título	How long does SARS-CoV-2 stay in the body?
Autor(es)	Chris Stokel-Walker
Resumo	There is no definitive answer. The reality of 6.2 million deaths with covid-19 means that many people die from the effects of the virus within their body before the virus itself does, so it's difficult to know how long they would have continued to shed the virus if they'd survived. Also, different people clear viruses quicker than others, depending on underlying health conditions. For example, says Paul Hunter, professor in medicine at the University of East Anglia, "Even before covid, we've known that people who have certain immune deficiencies can struggle to clear viruses." [...]
Referências	STOKEL-WALKER, C. How long does SARS-CoV-2 stay in the body?. **BMJ**, [United Kingdom], v. 377, p. o1555, June 28, 2022. DOI: 10.1136/bmj.o1555. Disponível em: https://www.bmj.com/content/377/bmj.o1555. Acesso em: 8 jul. 2022.
Fonte	https://www.bmj.com/content/377/bmj.o1555

Título	Immune response to SARS-CoV-2 in severe disease and long COVID-19
Autor(es)	Tomonari Sumi, Kouji Harada
Resumo	COVID-19 is mild to moderate in otherwise healthy individuals but may nonetheless cause life-threatening disease and/or a wide range of persistent symptoms. The general determinant of disease severity is age mainly because the immune response declines in aging patients. Here, we developed a mathematical model of the immune response to SARSCoV-2 and revealed that typical age-related risk factors such as only a several 10 % decrease in innate immune cell activity and inhibition of type-I interferon signaling by autoantibodies drastically increased the viral load. It was reported that the numbers of certain dendritic cell subsets remained less than half those in healthy donors even seven months after infection. Hence, the inflammatory response was ongoing. Our model predicted the persistent DC reduction and showed that certain patients with severe and even mild symptoms could not effectively eliminate the virus and could potentially develop long COVID.
Referências	SUMI, T.; HARADA, K. Immune response to SARS-CoV-2 in severe disease and long COVID-19. **iScience**, [Netherlands], p. 104723, July 4, 2022. DOI: 10.1016/j.isci.2022.104723. Disponível em: https://linkinghub.elsevier.com/retrieve/pii/S2589004222009956. Acesso em: 8 jul. 2022.
Fonte	https://www.cell.com/action/showPdf?pii=S2589-0042%2822%2900995-6

Título	How different COVID-19 recovery paths affect human health, environmental sustainability, and food affordability: a modelling study
Autor(es)	Juliette Maire, Aimen Sattar, Roslyn Henry, Frances Warren, Magnus Merkle, Mark Rounsevell, Peter Alexander
Resumo	The COVID-19 pandemic arrived at a time of faltering global poverty reduction and increasing levels of diet-related diseases, both of which have a strong link to poor outcomes for those with COVID-19. Governments responded to the pandemic by placing unprecedented restrictions on internal and external movements, which have resulted in an economic contraction. In response to the economic shock, G20 governments have committed to providing US$14 trillion stimuli to support economic recovery. We aimed to assess the impact of different COVID-19 recovery paths on human health, environmental sustainability, and food sustainability.
Referências	MAIRE, J. *et al.* How different COVID-19 recovery paths affect human health, environmental sustainability, and food affordability: a modelling study. **The Lancet Planetary Health**, [United Kingdom], v. 6, n. 7, p. e565–e576, July 2022. DOI: 10.1016/S2542-5196(22)00144-9. Disponível em: https://www.thelancet.com/journals/lanplh/article/PIIS2542-5196(22)00144-9/fulltext. Acesso em: 8 jul. 2022.
Fonte	https://www.thelancet.com/action/showPdf?pii=S2542-5196%2822%2900144-9

Título	Characteristics associated with the residual risk of severe COVID-19 after a complete vaccination schedule: A cohort study of 28 million people in France
Autor(es)	Laura Semenzato, Jérémie Botton, Jérôme Drouin, Bérangère Baricault, Marion Bertrand, Marie-Joëlle Jabagi, François Cuenot, Stéphane Le Vu, Rosemary Dray-Spira, Alain Weill, Mahmoud Zureik
Resumo	Prior to the availability of vaccines, the risk factors for developing severe forms of COVID-19 were mostly older age and various comorbidities such as diabetes, cardiovascular diseases, mental disorders, transplantations, and kidney disease. Although vaccines have been shown to be highly effective in preventing severe forms of COVID-19, a residual risk may persist, despite vaccination, for certain population groups.
Referências	SEMENZATO, L. *et al.* Characteristics associated with the residual risk of severe COVID-19 after a complete vaccination schedule: A cohort study of 28 million people in France. **The Lancet regional health. Europe**, [United Kingdom], v. 19, june 30, 2022. Disponível em: https://www.thelancet.com/journals/lanepe/article/PIIS2666-7762(22)00135-1/fulltext. Acesso em: 8 jul. 2022.
Fonte	https://www.thelancet.com/journals/lanepe/article/PIIS2666-7762(22)00135-1/fulltext

Título	Risk and severity of SARS-CoV-2 reinfections during 2020–2022 in Vojvodina, Serbia: a population-level observational study
Autor(es)	Snežana Medić, Cleo Anastassopoulou, Zagorka Lozanov-Crvenković, Vladimir Vuković, Nataša Dragnić, Vladimir Petrović, Mioljub Ristić, Tatjana Pustahija, Zoran Gojković, Athanasios Tsakris, John P.A. Ioannidis
Resumo	Data on the rate and severity of SARS-CoV-2 reinfections in real-world settings are scarce and the effects of vaccine boosters on reinfection risk are unknown.
Referências	MEDIĆ, S. *et al.* Risk and severity of SARS-CoV-2 reinfections during 2020–2022 in Vojvodina, Serbia: a population-level observational study. **The Lancet regional health. Europe**, [United Kingdom], v. 20, June 30. 2022. Disponível em: https://www.thelancet.com/journals/lanepe/article/PIIS2666-7762(22)00147-8/fulltext. Acesso em: 8 jul. 2022.
Fonte	https://www.thelancet.com/journals/lanepe/article/PIIS2666-7762(22)00147-8/fulltext

Título	Severity of SARS-CoV-2 infection in pregnancy in Ontario: a matched cohort analysis
Autor(es)	Kiera R Murison, Alicia A Grima, Alison E Simmons, Ashleigh R Tuite, David N Fisman
Resumo	Pregnancy represents a physiological state associated with increased vulnerability to severe outcomes from infectious diseases, both for the pregnant person and developing infant. The SARS-CoV-2 pandemic may have important health consequences for pregnant individuals, who may also be more reluctant than non-pregnant people to accept vaccination.We sought to estimate the degree to which increased severity of SARS-CoV-2 outcomes can be attributed to pregnancy using a population-based SARS-CoV-2 case file from Ontario, Canada. Due to varying propensity to receive vaccination, and changes in dominant circulating viral strains over time, a time-matched cohort study was performed to evaluate the relative risk of severe illness in pregnant women with SARS-CoV-2 compared to other SARS-CoV-2 infected women of childbearing age (10 to 49 years old). Risk of severe SARS-CoV-2 outcomes was evaluated in pregnant women and time-matched non-pregnant controls using multivariable conditional logistic regression.Compared to the rest of the population, non-pregnant women of childbearing age had an elevated risk of infection (standardized morbidity ratio (SMR) 1.28), while risk of infection was reduced among pregnant women (SMR 0.43). After adjustment for confounding pregnant women had a markedly elevated risk of hospitalization (adjusted OR 4.96, 95% CI 3.86 to 6.37) and ICU admission (adjusted OR 6.58, 95% CI 3.29 to 13.18). The relative increase in hospitalization risk associated with pregnancy was greater in women without comorbidities than in those with comorbidities (P for heterogeneity 0.004).Given the safety of SARS-CoV-2 vaccines in pregnancy, risk-benefit calculus strongly favours SARS-CoV-2 vaccination in pregnant women.
Referências	MURISON, K. R. *et al.* Severity of SARS-CoV-2 infection in pregnancy in Ontario: a matched cohort analysis. **Clinical infectious diseases**, [United States], p. ciac544, July 6, 2022. DOI: 10.1093/cid/ciac544. Disponível em: https://doi.org/10.1093/cid/ciac544. Acesso em: 8 jul. 2022.
Fonte	https://academic.oup.com/cid/advance-article/doi/10.1093/cid/ciac544/6632524?searchresult=1

Título	Predicting progression to severe COVID-19 using the PAINT score
Autor(es)	Ming Wang, Dongbo Wu, Chang-Hai Liu, Yan Li, Jianghong Hu, Wei Wang, Wei Jiang, Qifan Zhang, Zhixin Huang, Lang Ba, Hong Tang
Resumo	One of the major challenges in treating patients with coronavirus disease 2019 (COVID-19) is predicting the severity of disease. We aimed to develop a new score for predicting progression from mild/moderate to severe COVID-19.
Referências	WANG, M. *et al.* Predicting progression to severe COVID-19 using the PAINT score. **BMC infectious diseases**, [United Kingdom], v. 22, n. 1, p. 498, 26 May, 2022. DOI: 10.1186/s12879-022-07466-4. Disponível em: https://doi.org/10.1186/s12879-022-07466-4. Acesso em: 8 jul. 2022.
Fonte	https://bmcinfectdis.biomedcentral.com/track/pdf/10.1186/s12879-022-07466-4.pdf

Título	Limited cross-variant immunity from SARS-CoV-2 Omicron without vaccination
Autor(es)	Rahul K. Suryawanshi, Irene P. Chen, Tongcui Ma, Abdullah M. Syed, Noah Brazer, Prachi Saldhi, Camille R. Simoneau, Alison Ciling, Mir M. Khalid, Bharath Sreekumar, Pei-Yi Chen, G. Renuka Kumar, Mauricio Montano, Ronne Gascon, Chia-Lin Tsou, Miguel A. Garcia-Knight, Alicia Sotomayor-Gonzalez, Venice Servellita, Amelia Gliwa, Jenny Nguyen, Ines Silva, Bilal Milbes, Noah Kojima, Victoria Hess, Maria Shacreaw, Lauren Lopez, Matthew Brobeck, Fred Turner, Frank W. Soveg, Ashley F. George, Xiaohui Fang, Mazharul Maishan, Michael Matthay, Mary Kate Morris, Debra Wadford, Carl Hanson, Warner C. Greene, Raul Andino, Lee Spraggon, Nadia R. Roan, Charles Y. Chiu, Jennifer A. Doudna, Melanie Ott
Resumo	SARS-CoV-2 Delta and Omicron are globally relevant variants of concern. Although individuals infected with Delta are at risk of developing severe lung disease, infection with Omicron often causes milder symptoms, especially in vaccinated individuals1,2. The question arises of whether widespread Omicron infections could lead to future cross-variant protection, accelerating the end of the pandemic. Here we show that without vaccination, infection with Omicron induces a limited humoral immune response in mice and humans. Sera from mice overexpressing the human ACE2 receptor and infected with Omicron neutralize only Omicron, but not other variants of concern, whereas broader cross-variant neutralization was observed after WA1 and Delta infections. Unlike WA1 and Delta, Omicron replicates to low levels in the lungs and brains of infected animals, leading to mild disease with reduced expression of pro-inflammatory cytokines and diminished activation of lung-resident T cells. Sera from individuals who were unvaccinated and infected with Omicron show the same limited neutralization of only Omicron itself. By contrast, Omicron breakthrough infections induce overall higher neutralization titres against all variants of concern. Our results demonstrate that Omicron infection enhances pre-existing immunity elicited by vaccines but, on its own, may not confer broad protection against non-Omicron variants in unvaccinated individuals.
Referências	SURYAWANSHI, R. K. *et al.* Limited cross-variant immunity from SARS-CoV-2 Omicron without vaccination. **Nature**, [United Kingdom], p. 1–5, May 18, 2022. DOI: 10.1038/s41586-022-04865-0. Disponível em: https://www.nature.com/articles/s41586-022-04865-0. Acesso em: 8 jul. 2022.
Fonte	https://www.nature.com/articles/s41586-022-04865-0.pdf

Título	Omicron BA.1 and BA.2 sub-lineages show reduced pathogenicity and transmission potential than the early SARS-CoV-2 D614G variant in Syrian hamsters
Autor(es)	Wen Su, Ka Tim Choy, Haogao Gu, Sin Fun Sia, Ka Man Cheng, Sarea Islam Nuha Nizami, Pavithra Krishnan, Yuet Mai Ng, Lydia Dai Jia Chang, Yingzhi Liu, Samuel MS Cheng, Malik Peiris, Leo LM Poon, John M Nicholls, Hui Ling Yen
Resumo	The epidemiological advantage of Omicron variant is evidenced by its rapid spread and the ability to outcompete prior variants. Among Omicron sub-lineages, early outbreaks were dominated by BA.1 while BA.2 has gained dominance since February 2022. The relative pathogenicity and transmissibility of BA.1 and BA.2 have not been fully defined.We compared viral loads and clinical signs in Syrian hamsters after infection with BA.1, BA.2, or D614G variant. A competitive transmission model and next generation sequencing were used to compare the relative transmission potential of BA.1 and BA.2.BA.1 and BA.2 caused no apparent clinical signs while D614G caused more than 10% weight loss. Higher viral loads were detected from the nasal washes, nasal turbinate and lungs of BA.1 than BA.2 inoculated hamsters. No aerosol transmission was observed for BA.1 or BA.2 under the experimental condition that D614G transmitted efficiently. BA.1 and BA.2 were able to transmit among hamsters via direct contact; however, BA.1 transmitted more efficiently than BA.2 under the competitive transmission model. No recombination was detected from direct contacts exposed simultaneously to BA.1 and BA.2.Omicron BA.1 and BA.2 demonstrated attenuated pathogenicity and reduced transmission potential in hamsters when compared to early SARS-CoV-2 strains.
Referências	SU, W. *et al.* Omicron BA.1 and BA.2 sub-lineages show reduced pathogenicity and transmission potential than the early SARS-CoV-2 D614G variant in Syrian hamsters. **The journal of infectious diseases**, [United States], p. jiac276, July 5, 2022. DOI: 10.1093/infdis/jiac276. Disponível em: https://doi.org/10.1093/infdis/jiac276. Acesso em: 8 jul. 2022.
Fonte	https://academic.oup.com/pnasnexus/advance-article/doi/10.1093/pnasnexus/pgac071/6628667?searchresult=1

Título	SARS-CoV-2 and influenza co-infection throughout the COVID-19 pandemic: An assessment of co-infection rates, cohort characteristics, and clinical outcomes
Autor(es)	Colin Pawlowski, Eli Silvert, John C O'Horo, Patrick J Lenehan, Doug Challener, Esteban Gnass, Karthik Murugadoss, Jason Ross, Leigh Speicher, Holly Geyer, A J Venkatakrishnan, Andrew D Badley, Venky Soundararajan
Resumo	Case reports of patients infected with COVID-19 and influenza virus (“flurona”) have raised questions around the prevalence and severity of co-infection. Using data from HHS Protect Public Data Hub, NCBI Virus, and CDC FluView, we analyzed trends in SARS-CoV-2 and influenza hospitalized co-infection cases and strain prevalences. We also characterized co-infection cases across the Mayo Clinic Enterprise from January 2020 to April 2022. We compared expected and observed co-infection case counts across different waves of the pandemic and assessed symptoms and outcomes of co-infection and COVID-19 mono-infection cases after propensity score matching on clinically-relevant baseline characteristics. From both Mayo Clinic and nationwide datasets, the observed co-infection rate for SARS-CoV-2 and influenza has been higher during the Omicron era (December 14, 2021 to April 2, 2022) compared to previous waves, but no higher than expected assuming infection rates are independent. At Mayo Clinic, only 120 co-infection cases were observed among 197,364 SARS-CoV-2 cases. Co-infected patients were relatively young (mean age: 26.7 years) and had fewer serious comorbidities compared to mono-infected patients. While there were no significant differences in 30-day hospitalization, ICU admission, or mortality rates between co-infected and matched COVID-19 mono-infection cases, co-infection cases reported higher rates of symptoms including congestion, cough, fever/chills, headache, myalgia/arthralgia, pharyngitis, and rhinitis. While most co-infection cases observed at Mayo Clinic occurred among relatively healthy individuals, further observation is needed to assess outcomes among subpopulations with risk factors for severe COVID-19 such as older age, obesity, and immunocompromised status.Reports of COVID-19 and influenza co-infections (“flurona”) have raised concern in recent months as both COVID-19 and influenza cases have increased to significant levels in the US. Here, we analyze trends in co-infection cases over the course of the pandemic to show that these co-infection cases are expected given the background prevalences of COVID-19 and influenza independently. In addition, from an initial analysis of these co-infection cases which have been observed at the Mayo Clinic, we find that these co-infection cases are extremely rare, have mostly been observed in relatively young, healthy patients, and do not have an increased risk of hospitalization, ICU admission, or death while they do have more emblematic viral symptoms.

Referências	PAWLOWSKI, C. et al. SARS-CoV-2 and influenza co-infection throughout the COVID-19 pandemic: An assessment of co-infection rates, cohort characteristics, and clinical outcomes. PNAS nexus, [United Kingdom], p. pgac071, July 4, 2022. DOI: 10.1093/pnasnexus/pgac071. Disponível em: https://doi.org/10.1093/pnasnexus/pgac071. Acesso em: 8 jul. 2022.
Fonte	https://academic.oup.com/pnasnexus/advance-article-pdf/doi/10.1093/pnasnexus/pgac071/44395868/pgac071.pdf

Título	Mortality and renal long-term outcome of critically ill COVID-19 patients with acute kidney failure, continuous renal replacement therapy and invasive mechanical ventilation
Autor(es)	Rosa Melero, Antonia Mijaylova, Patrocinio Rodr´ıguez-Ben´ıtez, Ana Garc´ıa-Prieto, Jamil Cedeno, Marian Goicoechea
Resumo	There are limited data describing the long-term renal outcomes of critically ill COVID-19 patients with acute kidney injury (AKI) and continuous renal replacement therapy (CRRT) and invasive mechanical ventilation. Methods: In this retrospective observational study we analyzed the long-term clinical course and outcomes of 30 critically ill patients hospitalized with COVID-19 during the peak of highest incidence in the first wave, with acute respiratory distress syndrome (ARDS) and AKI that required CRRT. Baseline features, clinical course, laboratory data, therapies and filters used in CRRT were compared between survivors and non-survivors to identify risk factors associated with in-hospital death. Renal parameters: glomerular filtration rate, proteinuria and microhematuria were collected at 6 months after discharge.Results: 19 patients (63%) died and 11 were discharged. Mean time to death was 48 days (7-206) after admission. Patients with worse baseline renal function had higher mortality (P = .009). Patients were treated with CRRT for an average of 18.4 days. Filters with adsorptive capacity (43%) did not offer survival benefits. Regarding long-term renal outcomes, survivor patients did not receive any additional dialysis, but 9 out of 11 patients had an important loss of renal function (median of eGF of 44 (13-76) ml/min/1.73 m2) after 6 months. Conclusion: Mortality among critically ill hospitalized patients diagnosed with COVID-19 on CRRT is extremely high (63%). Baseline renal function is a predictor factor of mortality. Filters with adsorption capacity did not modify survival. None survivor patients required long-term dialysis, but an important loss of renal function occurred after AKI episode related to COVID-19 infection.

Referências	MELERO, R. *et al.* Mortality and renal long-term outcome of critically ill COVID-19 patients with acute kidney failure, continuous renal replacement therapy and invasive mechanical ventilation. **Medicina clínica (English Edition)**, [Spain], July 7, 2022. DOI: 10.1016/j.medcle.2022.02.015. Disponível em: https://www.sciencedirect.com/science/article/pii/S2387020622003126. Acesso em: 8 jul. 2022.
Fonte	https://www.sciencedirect.com/science/article/pii/S2387020622003126/pdf?md5=5f61d64cc72f0ccb8ddd50a2552d1022&pid=1-s2.0-S2387020622003126-main.pdf

Título	Validity of at-home rapid antigen lateral flow assay and artificial intelligence read to detect SARS-CoV-2
Autor(es)	Shannon Richardson , Michael A. Kohn , Jenna Bollyky , Julie Parsonnet
Resumo	The gold standard for COVID-19 diagnosis–reverse-transcriptase polymerase chain reaction (RT-PCR)– is expensive and often slow to yield results whereas lateral flow tests can lack sensitivity. Methods: We tested a rapid, lateral flow antigen (LFA) assay with artificial intelligence read (LFAIR) in subjects from COVID-19 treatment trials (N=37; daily tests for five days) and from a population-based study (N=88; single test). LFAIR was compared to RT-PCR from same-day samples. Results: Using each participant's first sample, LFAIR showed 86.2% sensitivity (95% CI 73.6% - 98.8) and 94.3% specificity (88.8% - 99.7%) compared to RT-PCR. Adjusting for days since symptom onset and repeat testing, sensitivity was 97.8% (89.9% - 99.5%) on the first symptomatic day and decreased with each additional day. Sensitivity improved with artificial intelligence (AI) read (86.2%) compared to the human eye (71.4%). Conclusion: LFAIR showed improved accuracy compared to LFA alone. particularly early in infection.
Referências	RICHARDSON, S. *et al.* Validity of at-home rapid antigen lateral flow assay and artificial intelligence read to detect SARS-CoV-2. **Diagnostic microbiology and infectious disease**, [United States], p. 115763, July 7, 2022. DOI: 10.1016/j.diagmicrobio.2022.115763. Disponível em: https://www.sciencedirect.com/science/article/pii/S0732889322001298. Acesso em: 8 jul. 2022.
Fonte	https://www.sciencedirect.com/science/article/pii/S0732889322001298/pdfft?md5=7b0b4285fb7b340e67b9370f8f20b475&pid=1-s2.0-S0732889322001298-main.pdf

Título	Diabetes as a cause of death across different COVID-19 epidemic waves
Autor(es)	Ugo Fedeli, Veronica Casotto, Elena Schievano, Enzo Bonora, Giacomo Zoppini
Resumo	The aim of this study is to assess the role of diabetes as a cause of death through different epidemic waves of COVID-19. Methods: The annual percentage change in age-standardized rates (APC) was estimated for diabetes as the underlying (UCOD) and as multiple causes of death (MCOD) in 2008-2019. Diabetes-related deaths in 2020 were compared to the 2018-2019 average. SARIMA models were applied to monthly excess in mortality considering seasonality and long-term trends. Results: 2018-2019-Age-standardized mortality rates decreased, especially among females (MCOD: APC -2.49, 95%CI -3.01/-1.97%). In 2020, deaths increased by 19% (95%CI 13-25%) for UCOD, and by 27% (95%CI 24-30%) for MCOD. Diabetes and COVID-19 accounted for 74% of such excess. During the first epidemic wave, the increase in observed rates vs predicted by the model was larger in males (March +39%, April +46%) than in females (+30% and +32%). In the second wave, a huge excess of similar magnitude was observed in the two sexes; rates in December exceeded those predicted by more than 100%.Conclusions: The COVID-19 pandemic abruptly interrupted a long-term declining trend in mortality associated to diabetes. MCOD analyses are warranted to fully estimate the impact of epidemic waves on diabetes-related mortality.
Referências	FEDELI, U. *et al.* Diabetes as a cause of death across different COVID-19 epidemic waves. **Diabetes Research and Clinical Practice**, [Netherlands], p. 109984, July 6, 2022. DOI: 10.1016/j.diabres.2022.109984. Disponível em: https://www.sciencedirect.com/science/article/pii/S0168822722007987. Acesso em: 8 jul. 2022.
Fonte	https://www.sciencedirect.com/science/article/pii/S0168822722007987

Título	Clinical and epidemiological characteristics of SARS-CoV-2 Infection in Los Angeles County youth during the first year of the pandemic
Autor(es)	Tawny Saleh , Tara Kerin , Trevon Fuller , Sophia Paiola , Mary C. Cambou , Yash Motwani , Caitlin N. Newhouse , Shangxin Yang , Edwin Kamau , Omai B. Garner , Sukantha Chandrasekaran , Karin Nielsen-Saines
Resumo	Objective: To characterize SARS-CoV-2 infection patterns in Los Angeles (L.A.) County youth followed at our institution during the first pandemic year.Design and Methods: A prospective cohort of patients aged < 25 years with positive SARS-CoV-2 RT-PCR between 03/13/2020 to 03/31/2021 was evaluated at a large L.A. County health network. Demographics, age distribution and disease severity were analyzed.Results: There were 28,088 youth < 25 years of age tested for SARS-CoV-2 by RT-PCR, with 1,849 positives identified (7%). Among the positive, 475 of 11,922 (4%) were identified at the pandemic onset (03-09/2020) (Cohort 1) and 1,374 of 16,166 (9%) between 10/2020 to 03/2021 (Cohort 2), p < 0.001. When disease severity was compared across cohorts, Cohort 2 had a greater proportion of asymptomatic, and mild/moderate disease categories than Cohort 1 (98% vs. 80%,respectively); conversely, Cohort 1 had a near 10-fold higher proportion of severe disease than cohort 2 (17% vs. 1.8%). Cohort 2 was comprised by younger individuals with a mean age of 13.7 vs. 17.3 years in Cohort 1. Older age was associated with a higher percentage of infection, 63% of 19-25 year olds in cohort 1 vs. 38% in Cohort 2. Age increase was also associated with greater disease severity by linear regression modeling. (p< 0.001).Conclusions: COVID-19 disease severity in youth decreased over time in L.A. County during the first pandemic year, likely a reflection of changing demographics with younger children infected. A higher infection rate in youth did not lead to higher disease severity over time.
Referências	SALEH, T. *et al.* Clinical and epidemiological characteristics of SARS-CoV-2 Infection in Los Angeles County youth during the first year of the pandemic. **International journal of infectious diseases**, [Netherlands], July 6, 2022. DOI: 10.1016/j.ijid.2022.06.040. Disponível em: https://www.sciencedirect.com/science/article/pii/S1201971222003745. Acesso em: 8 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S1201971222003745/pdf

Título	First case of within-host co-infection of different SARS-CoV-2 variants in Ecuador
Autor(es)	Juan Carlos Fernandez-Cadena, Mateo Carvajal, Erika Muñoz, Belén Prado-Vivar, Sully Marquez, Stefanie Proaño, Rosa Bayas, Juan José Guadalupe, Mónica Becerra-Wong, Bernardo Gutierrez, Gabriel Morey-Leon, Gabriel Trueba, Michelle Grunauer, Verónica Barragán, Patricio Rojas-Silva, Derly Andrade-Molina, Paúl Cárdenas
Resumo	COVID-19 infection caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) can cause mild symptoms to severe illness and death. Co-infections of SARS-CoV-2 with other respiratory viruses has been described. However, two SARS-CoV-2 lineage co-infection have been rarely reported. Methodology: A genotyping analysis and two different types of whole genome sequencing were performed (Illumina MiniSeq and ONT MinION). When examining the phylogenetic analysis in NextClade and Pangolin webservers, and considering the genotyping findings, conflicting results were obtained. Results: The raw data of the sequencing was analyzed, and nucleotide variants were identified between different reads of the virus genome. B.1 and P.1 lineages were identified within the same sample. Conclusions: We concluded that this is a co-infection case with two SARS-CoV-2 lineages, the first one reported in Ecuador.
Referências	FERNANDEZ-CADENA, J. C. *et al.* First case of within-host co-infection of different SARS-CoV-2 variants in Ecuador. **New Microbes and New Infections**, [United Kingdom], p. 101001, July 6, 2022. DOI: 10.1016/j.nmni.2022.101001. Disponível em: https://www.sciencedirect.com/science/article/pii/S2052297522000531. Acesso em: 8 jul. 2022.
Fonte	https://www.sciencedirect.com/sdfe/reader/pii/S2052297522000531/pdf

Título	Controlling SARS-CoV-2 in schools using repetitive testing strategies
Autor(es)	Andrea Torneri, Lander Willem, Vittoria Colizza, Cécile Kremer, Christelle Meuris, Gilles Darcis, Niel Hens, Pieter JK Libin
Resumo	SARS-CoV-2 remains a worldwide emergency. While vaccines have been approved and are widely administered, there is an ongoing debate whether children should be vaccinated or prioritized for vaccination. Therefore, in order to mitigate the spread of more transmissible SARS-CoV-2 variants among children, the use of non-pharmaceutical interventions is still warranted. We investigate the impact of different testing strategies on the SARS-CoV-2 infection dynamics in a primary school environment, using an individual-based modelling approach. Specifically, we consider three testing strategies: (1) symptomatic isolation, where we test symptomatic individuals and isolate them when they test positive, (2) reactive screening, where a class is screened once one symptomatic individual was identified, and (3) repetitive screening, where the school in its entirety is screened on regular time intervals. Through this analysis, we demonstrate that repetitive testing strategies can significantly reduce the attack rate in schools, contrary to a reactive screening or a symptomatic isolation approach. However, when a repetitive testing strategy is in place, more cases will be detected and class and school closures are more easily triggered, leading to a higher number of school days lost per child. While maintaining the epidemic under control with a repetitive testing strategy, we show that absenteeism can be reduced by relaxing class and school closure thresholds.
Referências	TORNERI, A. *et al.* Controlling SARS-CoV-2 in schools using repetitive testing strategies. **eLife**, [United Kingdom], v. 11, p. e75593, July 5, 2022. DOI: 10.7554/eLife.75593. Disponível em: https://doi.org/10.7554/eLife.75593. Acesso em: 8 jul. 2022.
Fonte	https://elifesciences.org/articles/75593

Título	Effectiveness of BNT162b2 vaccine against SARS-CoV-2 infection and severe COVID-19 in children aged 5–11 years in Italy: a retrospective analysis of January–April, 2022
Autor(es)	Chiara Sacco, Martina Del Manso, Alberto Mateo-Urdiales, Maria Cristina Rota, Daniele Petrone, Flavia Riccardo, Antonino Bella, Andrea Siddu, Serena Battilomo, Valeria Proietti, Patrizia Popoli, Francesca Menniti Ippolito, Anna Teresa Palamara, Silvio Brusaferro, Giovanni Rezza, Patrizio Pezzotti, Massimo Fabiani
Resumo	By April 13, 2022, more than 4 months after the approval of BNT162b2 (Pfizer–BioNTech) for children, less than 40% of 5–11-year-olds in Italy had been vaccinated against COVID-19. Estimating how effective vaccination is in 5–11-year-olds in the current epidemiological context dominated by the omicron variant (B.1.1.529) is important to inform public health bodies in defining vaccination policies and strategies.
Referências	SACCO, C. *et al.* Effectiveness of BNT162b2 vaccine against SARS-CoV-2 infection and severe COVID-19 in children aged 5–11 years in Italy: a retrospective analysis of January–April, 2022. **Lancet**, [United Kingdom], June 30, 2022. DOI: 10.1016/S0140-6736(22)01185-0. Disponível em: https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(22)01185-0/fulltext. Acesso em: 1 jul. 2022.
Fonte	https://www.thelancet.com/action/showPdf?pii=S0140-6736%2822%2901185-0

Título	Associations of BMI with COVID-19 vaccine uptake, vaccine effectiveness, and risk of severe COVID-19 outcomes after vaccination in England: a population-based cohort study
Autor(es)	Carmen Piernas, Martina Patone, Nerys M Astbury, Min Gao, Aziz Sheikh, Kamlesh Khunti, Manu Shankar-Hari, Sharon Dixon, Carol Coupland, Paul Aveyard, Julia Hippisley-Cox, Susan A Jebb
Resumo	A high BMI has been associated with a reduced immune response to vaccination against influenza. We aimed to investigate the association between BMI and COVID-19 vaccine uptake, vaccine effectiveness, and risk of severe COVID-19 outcomes after vaccination by using a large, representative population-based cohort from England.
Referências	PIERNAS, C. *et al.* Associations of BMI with COVID-19 vaccine uptake, vaccine effectiveness, and risk of severe COVID-19 outcomes after vaccination in England: a population-based cohort study. **The Lancet. Diabetes & endocrinology**, [Netherlands], June 30, 2022. DOI: 10.1016/S2213-8587(22)00158-9. Disponível em: https://www.thelancet.com/journals/landia/article/PIIS2213-8587(22)00158-9/fulltext. Acesso em: 1 jul. 2022.
Fonte	https://www.thelancet.com/action/showPdf?pii=S2213-8587%2822%2900158-9

Título	Comparison of trends in Clostridioides difficile infections in hospitalised patients during the first and second waves of the COVID-19 pandemic: A retrospective sentinel surveillance study
Autor(es)	Karuna E.W. Vendrik, Amoe Baktash, Jelle J. Goeman, Celine Harmanus, Daan W. Notermans, Sabine C. de Greeff, Ed J. Kuijper, On behalf of the C. difficile surveillance study group
Resumo	During the COVID-19 pandemic, several factors, such as improved hand hygiene, social distancing, and restricted hospital referral, may have had an influence on the epidemiology of Clostridioides difficile infections (CDI).
Referências	VENDRIK, K. E. W. *et al.* Comparison of trends in Clostridioides difficile infections in hospitalised patients during the first and second waves of the COVID-19 pandemic: A retrospective sentinel surveillance study. **The Lancet regional health. Europe**, [United Kingdom], p. 100424, June 27, 2022. DOI: 10.1016/j.lanepe.2022.100424. Disponíve em: https://linkinghub.elsevier.com/retrieve/pii/S2666776222001181. Acesso em: 1 jul. 2022.
Fonte	https://www.thelancet.com/journals/lanepe/article/PIIS2666-7762(22)00118-1/fulltext

Título	Olfactory Dysfunction in Patients With Mild COVID-19 During Gamma, Delta, and Omicron Waves in Rio de Janeiro, Brazil
Autor(es)	Cynthia Chester Cardoso, Átila Duque Rossi, Rafael Mello Galliez, Débora Souza Faffe, Amilcar Tanuri, Terezinha Marta Pereira Pinto Castiñeiras
Resumo	Olfactory dysfunction is a common symptom of COVID-19, with reported rates as high as 70%. This symptom can be associated with mild COVID-19, mostly occurs within 5 days after symptom onset, and can persist for a few days to several months after infection resolution. The mechanism of SARS-CoV-2–related olfactory dysfunction is not completely understood.Host genetics, acute inflammation in the olfactory epithelium, local ACE2 expression, and downregulation of olfactory receptors seem to play a role; however, the viral contribution remains to be explored. We conducted a retrospective analysis of individuals with mild COVID-19 during different SARS-CoV-2 variant waves to assess the prevalence of self-reported olfactory dysfunction.
Referências	CARDOSO, C. C. *et al.* Olfactory Dysfunction in Patients With Mild COVID-19 During Gamma, Delta, and Omicron Waves in Rio de Janeiro, Brazil. **JAMA**, [United States], June 24, 2022. DOI: 10.1001/jama.2022.11006. Disponível em: https://doi.org/10.1001/jama.2022.11006. Acesso em: 1 jul. 2022.
Fonte	https://jamanetwork.com/journals/jama/fullarticle/2793811

Título	Association of receipt of the fourth BNT162b2 Dose With Omicron infection and COVID-19 hospitalizations among residents of long-term care facilities
Autor(es)	Khitam Muhsen, Boris Boltyansky, Omri Bodenheimer, Zafrira Hillel Diamant, Lea Gaon, Dani Cohen, Ron Dagan
Resumo	The administration of a fourth BNT162b2 COVID-19 vaccine dose was approved in Israel in December 2021 for individuals 60 years or older who were vaccinated with a third dose 4 months previously or earlier to control the substantial surge of the SARS-CoV-2 Omicron variant. Nonetheless, the association between receipt of the fourth dose and protection against infection remains elusive.To determine the association of the fourth BNT162b2 dose with protection against SARS-CoV-2–related infections, hospitalizations, and deaths during the Omicron surge in long-term care facility (LTCF) residents.This prospective cohort study was conducted in Israel between January 10 and March 31, 2022 and included LTCF residents 60 years or older.Vaccination with the fourth dose of BNT162b2 vs 3 doses that were administered 4 months previously or earlier.Cumulative incidences of SARS-CoV-2 infections, hospitalizations, and deaths during the Omicron surge. The follow-up was initiated more than 7 days after receipt of the fourth dose, which was matched to the follow-up initiation date of those who had received 3 doses of vaccine in each facility. We obtained hazard ratios and 95% confidence intervals from multivariable Cox regression models.The data of 43 775 residents (mean [SD] age, 80.1 [9.4] years; 29 679 women [67.8%]) were analyzed, of whom 24 088 (55.0%) and 19 687 (45.0%) received the fourth and third dose (4 months previously or earlier), respectively. The median follow-up time was 73 days (4-dose group: IQR, 6 days; 3-dose group: IQR, 56 days). More than 7 days postvaccination with the fourth dose, SARS-CoV-2 infection was detected among 4058 fourth-dose vs 4370 third-dose recipients (cumulative incidence, 17.6% vs 24.9%). The corresponding incidences of hospitalizations for mild-to-moderate COVID-19, severe illness, and mortality were 0.9% and 2.8%, 0.5% and 1.5%, and 0.2% and 0.5%, respectively. The adjusted protections were 34% (95% CI, 30%-37%), 64% (95% CI, 56%-71%), and 67% (95% CI, 57%-75%) against overall

Resumo	infection, hospitalizations for mild-to-moderate illness, and severe illness, respectively, and 72% (95% CI, 57%-83%) against related deaths.The results of this cohort study suggest that receipt of a fourth BNT162b2 dose conferred high protection against COVID-19 hospitalizations and deaths among LTCF residents during a substantial Omicron variant surge, but protection was modest against infection. These findings are relevant to the control of COVID-19 pandemic globally, especially among the population of LTCFs.
Referências	MUHSEN, K. *et al.* Association of receipt of the fourth BNT162b2 Dose With Omicron infection and COVID-19 hospitalizations among residents of long-term care facilities. **JAMA internal medicine**, [United States], June 23, 2022. DOI: 10.1001/jamainternmed.2022.2658. Disponível em: https://doi.org/10.1001/jamainternmed.2022.2658. Acesso em: 1 jul. 2022.
Fonte	https://jamanetwork.com/journals/jamainternalmedicine/fullarticle/2793699

Título	Assessment of ethnic inequities and subpopulation estimates in COVID-19 vaccination in New Zealand
Autor(es)	Andrew Anglemyer, Corina Grey, Collin Tukuitonga, Andrew Sporle, Gerard J. B. Sonder
Resumo	Introduction... COVID-19 has exposed inequities in access to care, baseline health, and economic standing.[1,2] In Aotearoa New Zealand, Pacific peoples and Māori have disproportionately experienced poor SARS-CoV-2 outcomes. To ensure prevention and care equity, the COVID-19 vaccination program targeted high-risk people first. In October 2021, the Ministry of Health (MoH) announced 90% vaccine coverage targets among eligible populations, obviating the need for future lockdowns.[3] Beginning December 2021, vaccination proof was required for everyone aged at least 12 years to access certain venues (eg, hospitality services); Pfizer-BioNTech (BNT162b2) booster vaccines were required for specific occupations (eg, health care). We highlight the outcome of different population estimate methodologies on relative gaps in vaccination between ethnic groups and the resulting population risk.
Referências	ANGLEMYER, A. *et al.* Assessment of ethnic inequities and subpopulation estimates in COVID-19 vaccination in New Zealand. **JAMA network open**, [United States], v. 5, n. 6, p. e2217653, June 21, 2022. DOI: 10.1001/jamanetworkopen.2022.17653 . Disponível em: https://doi.org/10.1001/jamanetworkopen.2022.17653. Acesso em: 01 Jul. 2022.
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Título	Modeling pandemic to endemic patterns of SARS-CoV-2 transmission using parameters estimated from animal model data
Autor(es)	Sarah Mullin, Brent Vander Wyk, Jennifer L Asher, Susan R Compton, Heather G Allore, Caroline J Zeiss
Resumo	The contours of endemic coronaviral disease in humans and other animals are shaped by the tendency of coronaviruses to generate new variants superimposed upon non-sterilizing immunity. Consequently, patterns of coronaviral reinfection in animals can inform the emerging endemic state of the SARS-CoV-2 pandemic. We generated controlled reinfection data after high and low risk natural exposure or heterologous vaccination to sialodacryoadenitis (SDAV) in rats. Using deterministic compartmental models, we utilized in vivo estimates from these experiments to model the combined effects of variable transmission rates, variable duration of immunity, successive waves of variants and vaccination on patterns of viral transmission. Using rat experiment-derived estimates, an endemic state achieved by natural infection alone occurred after a median of 724 days with approximately 41.3% of the population susceptible to reinfection. After accounting for translationally altered parameters between rat-derived data and human SARS-CoV-2 transmission, and after introducing vaccination, we arrived at a median time to endemic stability of 1437 (IQR = 749.25) days with a median 15.4% of the population remaining susceptible. We extended the models to introduce successive variants with increasing transmissibility and included the effect of varying duration of immunity. As seen with endemic coronaviral infections in other animals, transmission states are altered by introduction of new variants, even with vaccination. However, vaccination combined with natural immunity maintains a lower prevalence of infection than natural infection alone and provides greater resilience against the effects of transmissible variants.The pandemic to endemic trajectory of SARS-CoV-2 transmission will be shaped by the tendency of coronaviruses to elicit non-sterilizing immunity and generate new variants. We utilized estimates

Resumo	from controlled rat coronaviral infection in deterministic compartmental models to inform routes to endemic stability in SARS-CoV-2. We introduced translationally altered parameters to explore the effects of waning immunity, exposure to increasingly transmissible variants and successive vaccination. We arrived at an endemic state in which 15% of the population remains susceptible to reinfection. Similar to endemic coronaviral infections in other animals, transmission states are altered by introduction of new variants, even with vaccination. Accumulating and maintaining evolving immunity through vaccination and inevitable natural exposure is essential to achieving a stable endemic state.
Referências	MULLIN, S. *et al.* Modeling pandemic to endemic patterns of SARS-CoV-2 transmission using parameters estimated from animal model data. **PNAS nexus**, [United Kingdom], p. pgac096, Jul. 1, 2022. DOI: 10.1093/pnasnexus/pgac096 . Disponível em: https://doi.org/10.1093/pnasnexus/pgac096. Acesso em: 01 Jul. 2022.
Fonte	https://academic.oup.com/pnasnexus/advance-article/doi/10.1093/pnasnexus/pgac096/6625054?searchresult=1

Título	Data-driven commentary on SARS-CoV-2 infection, vaccination, and fertility
Autor(es)	Sigal Klipstein, Jodie A Dionne, Eve C Feinberg, Jennifer F Kawwass, Samantha M Pfeifer, Peter N Schlegel, Catherine Racowsky
Resumo	A recent study by Wesselink et al. (Am J Epidemiol. 2022;191(XX):XXXX–XXXX) adds to the growing body of research finding that vaccination for coronavirus disease 2019 (COVID-19) is safe for individuals either seeking pregnancy or who are pregnant. The study's authors found no effect of COVID-19 vaccination on fecundity in a population of individuals with no known infertility who were attempting conception. The finding reinforces the messaging of the American Society for Reproductive Medicine COVID-19 Task Force, the aim of which is to provide data-driven recommendations to individuals contemplating pregnancy in the face of the COVID-19 pandemic. As safe and effective COVID-19 vaccines became available, and with an increasing number of studies showing a heightened risk of severe disease during pregnancy, an important role of the Task Force is to encourage vaccination during the preconceptual window and in early pregnancy. The Task Force supports ongoing research to address gaps in knowledge about safe and effective therapies and preventive measures for individuals contemplating pregnancy and during pregnancy. Such research will help optimize care for reproductive-age individuals in the face of current and future health crises.
Referências	KLIPSTEIN, S. *et al.* Data-Driven Commentary on SARS-CoV-2 Infection, Vaccination, and Fertility. **American journal of epidemiology**, [United States], p. kwac073, 2022. DOI: 10.1093/aje/kwac073. Disponível em: https://doi.org/10.1093/aje/kwac073. Acesso em: 1 jul. 2022.
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Título	SARS-CoV-2 seroprevalence at urban and rural sites in Kaduna State, Nigeria, during October/November 2021, immediately prior to detection of the Omicron variant
Autor(es)	Gloria D Chechet, Jacob K P Kwaga, Joseph Yahaya, Harry Noyes, Annette MacLeod, Walt E Adamson
Resumo	Nigeria is Africa's most populated country. By November 2021 it had experienced three waves of SARS-CoV-2 infection. Peer-reviewed seroprevalence data assessing the proportion of the Nigerian population that have been infected were extremely limited.We conducted a serosurvey in one urban site (n = 400) and one rural site (n = 402) in Kaduna State, Nigeria between 11 October 2021 and 8 November 2021. Z-tests were used to compare seroprevalence across age groups, locations and sexes. T tests were used to determine whether age or household size are associated with seropositivity. Associations between seropositivity and recent history of common Covid-19 symptoms were tested using logistic regression.SARS-CoV-2 antibodies were detected in 42.5% an 53.5% of participants at the urban and rural sites, respectively The overall age- and sex- stratified seroprevalence was 43.7% (42.2% for unvaccinated individuals). The data indicate an infection rate in Kaduna State ≥359-fold the rate derived from polymerase chain reaction-confirmed cases. In the urban site, seroprevalence among females and participants aged <20 was lower than other groups. Reporting loss of sense of taste and/or smell was strongly associated with seropositive status. Associations with seropositivity were also found for the reporting of dry cough, fever, headache, nausea and sore throat.This study provides baseline SARS-CoV-2 seroprevalence in Kaduna State, Nigeria, immediately prior to the spread of the Omicron variant. It indicates that in October/November 2021, approximately 56% of the population did not have detectable antibodies, and population subgroups with particularly low seroprevalence remain. It highlights limitations in using PCR-confirmed cases to estimate infection rates. The data will inform public health strategies in Nigeria and other sub-Saharan African countries with

	limited SARS-CoV-2 seroprevalence data.
Referências	CHECHET, G. D. *et al.* SARS-CoV-2 seroprevalence at urban and rural sites in Kaduna State, Nigeria, during October/November 2021, immediately prior to detection of the Omicron variant. **International journal of epidemiology**, [United Kingdom], p. dyac141, June 28, 2022. DOI: 10.1093/ije/dyac141. Disponível em: https://doi.org/10.1093/ije/dyac141. Acesso em: 1 jul. 2022.
Fonte	https://academic.oup.com/ije/advance-article/doi/10.1093/ije/dyac141/6623538?searchresult=1

Título	What the harm principle says about vaccination and healthcare rationing
Autor(es)	Christopher Robertson
Resumo	Clinical ethicists hold near consensus on the view that healthcare should be provided regardless of patients' past behaviors. In classic cases, the consensus can be explained by two key rationales—a lack of acute scarcity and the intractability of the facts around those behaviors, which make discrimination on past behavior gratuitous and infeasible to do fairly. Healthcare providers have a duty to help those who can be helped. In contrast, the COVID-19 pandemic suggests the possible recurrence of a very different situation, where a foreseeable acute shortage of healthcare resources means that some cannot be helped. And that shortage is exacerbated by the discrete decision of some to decline a free, safe, and highly effective vaccine, where the facts are clear. In such a future case, if healthcare must be denied to some patients, rationers who ignore vaccination status will become complicit in externalizing the consequences of refusing vaccination onto those who did not refuse. I argue that giving the unvaccinated person healthcare resources that would have otherwise gone to other patients is to wrongfully set back the interests of, or harm, those patients. The article considers rejoinders around the voluntariness of the vaccination choice, which impinges both access and information, and how to scale this criterion proportionally with other rationing criteria that serve utility. Ultimately, the article speculates on why there will be some cognitive dissonance under this approach, while upholding a more general solidarity with and concern for all those seeking healthcare.
Referências	ROBERTSON, C. What the harm principle says about vaccination and healthcare rationing. **Journal of law and the biosciences**, [United Kingdom], v. 9, n. 1, p. lsac017, June 25, 2022. DOI: 10.1093/jlb/lsac017. Disponível em: https://doi.org/10.1093/jlb/lsac017. Acesso em: 1 jul. 2022.
Fonte	https://academic.oup.com/jlb/article/9/1/lsac017/6617804?searchresult=1

Título	Advancing precision vaccinology by molecular and genomic surveillance of SARS-CoV-2 in Germany, 2021
Autor(es)	Djin-Ye Oh, Martin Hölzer, Sofia Paraskevopoulou, Maria Trofimova, Felix Hartkopf, Matthias Budt, Marianne Wedde, Hugues Richard, Berit Haldemann, Teresa Domaszewska, Janine Reiche, Kathrin Keeren, Aleksandar Radonić, Julia Patricia Ramos Calderón, Maureen Rebecca Smith, Annika Brinkmann, Kathrin Trappe, Oliver Drechsel, Kathleen Klaper, Sascha Hein, Eberhard Hildt, Walter Haas, Sébastien Calvignac-Spencer, Torsten Semmler, Ralf Dürrwald, Andrea Thürmer, Christian Drosten, Stephan Fuchs, Stefan Kröger, Max von Kleist, Thorsten Wolff on behalf of The IMS-SC2 Laboratory Network
Resumo	Comprehensive pathogen genomic surveillance represents a powerful tool to complement and advance precision vaccinology. The emergence of the Alpha variant in December 2020 and the resulting efforts to track the spread of this and other SARS-CoV-2 variants of concern led to an expansion of genomic sequencing activities in Germany.At Robert Koch Institute (RKI), the German National Institute of Public Health, we established the "Integrated Molecular Surveillance for SARS-CoV-2" (IMS-SC2) network to perform SARS-CoV-2 genomic surveillance at the national scale, SARS-CoV-2 positive samples from laboratories distributed across Germany regularly undergo whole-genome sequencing at RKI.We report analyses of 3,623 SARS-CoV-2 genomes collected between December 2020 and December 2021, of which 3,282 were randomly sampled. All variants of concern were identified in the sequenced sample set, at ratios equivalent to those in the 100-fold larger German GISAID sequence dataset from the same time period. Phylogenetic analysis confirmed variant assignments. Multiple mutations of concern emerged during the observation period. To model vaccine effectiveness in vitro, we employed authentic-virus neutralization assays, confirming that both the Beta and Zeta variants are capable of immune evasion. The IMS-SC2 sequence dataset facilitated an estimate of the SARS-CoV-2 incidence based on genetic evolution rates. Together with modelled vaccine efficacies, Delta-specific incidence estimation indicated that the German vaccination campaign contributed substantially to a deceleration of the nascent German Delta wave.SARS-CoV-2 molecular and genomic surveillance may inform public health policies including vaccination strategies and enable a proactive approach to controlling COVID-19 spread as the virus evolves.
Referências	OH, D.-Y. *et al.* Advancing precision vaccinology by molecular and genomic surveillance of SARS-CoV-2 in Germany, 2021. **Clinical infectious diseases**, [United States], p. ciac399, June 25, 2022. DOI: 10.1093/cid/ciac399. Disponível em: https://doi.org/10.1093/cid/ciac399. Acesso em: 1 jul. 2022.
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