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| 13 Coronavirus as a possible cause of severe acute respiratory syndrome https://www.sciencedirect.com/science/article/pii/S0140673603130772 Background An outbreak of severe acute respiratory syndrome (SARS) has been reported in Hong Kong. We investigated the viral cause and clinical presentation among 50 patients. Methods We analysed case notes and microbiological findings for 50 patients with SARS¬†‚Ä¶ |
| 20 [HTML][HTML] Hospital outbreak of Middle East respiratory syndrome coronavirus [https://www.nejm.org/doi/pdf/10.1056/NEJMoa1306742 Background In September 2012](https://www.nejm.org/doi/pdf/10.1056/NEJMoa1306742%20Background%20In%20September%202012) |
| 25 A contemporary view of coronavirus transcription https://jvi.asm.org/content/81/1/20.short Coronaviruses are a family of enveloped |
| 35 Identification of a novel coronavirus in bats https://jvi.asm.org/content/79/4/2001.short Exotic wildlife can act as reservoirs of diseases that are endemic in the area or can be the source of new emerging diseases through interspecies transmission. The recent emergence of severe acute respiratory syndrome-associated coronavirus (SARS-CoV) highlights the¬†‚Ä¶ |
| 65 An enteric coronavirus infection of cats and its relationship to feline infectious peritonitis. https://europepmc.org/abstract/med/6267960 An enteric coronavirus that is antigenically closely related to feline infectious peritonitis virus (FIPV) is ubiquitous in the cat population. This virus has been designated feline enteric coronavirus to differentiate it from FIPV. The virus is shed in the feces by many seropositive¬†‚Ä¶ |
| 72 Coronavirus genomics and bioinformatics analysis https://www.mdpi.com/1999-4915/2/8/1804 The drastic increase in the number of coronaviruses discovered and coronavirus genomes being sequenced have given us an unprecedented opportunity to perform genomics and bioinformatics analysis on this family of viruses. Coronaviruses possess the largest¬†‚Ä¶ |
| 78 Bovine respiratory coronavirus https://www.vetfood.theclinics.com/article/S0749-0720(10)00011-3/abstract Bovine coronaviruses (BCoVs) cause respiratory and enteric infections in cattle and wild ruminants. 1‚Äì3 BCoVs belong to the family Coronaviridae in the order Nidovirales and are members of subgroup 2a along with swine hemagglutinating encephalomyelitis virus (HEV)¬†‚Ä¶ |
| 87 Coronavirus minus-strand RNA synthesis and effect of cycloheximide on coronavirus RNA synthesis. https://jvi.asm.org/content/57/1/328.short The temporal sequence of coronavirus plus-strand and minus-strand RNA synthesis was determined in 17CL1 cells infected with the A59 strain of mouse hepatitis virus (MHV). MHV-induced fusion was prevented by keeping the pH of the medium below pH 6.8. This had no¬†‚Ä¶ |
| 88 Isolation of coronavirus envelope glycoproteins and interaction with the viral nucleocapsid. https://jvi.asm.org/content/33/1/449.short The two envelope glycoproteins and the viral nucleocapsid of the coronavirus A59 were isolated by solubilization of the viral membrane with Nonidet P-40 at 4 degrees C followed by sucrose density gradient sedimentation. Isolated E2 consisted of rosettes of peplomers¬†‚Ä¶ |
| 90 [PDF][PDF] Design of wide-spectrum inhibitors targeting coronavirus main proteases https://journals.plos.org/plosbiology/article/file?type=printable&id=10.1371/journal.pbio.0030324 The genus Coronavirus belongs to the plus-strand RNA virus family of the Coronaviridae and currently contains about 25 species that are classified into three groups according to their genetic and serological relationships [1‚Äì4]. Coronaviruses (CoVs) infect humans and¬†‚Ä¶ |
| 93 Human coronavirus NL63 infection and other coronavirus infections in children hospitalized with acute respiratory disease in Hong Kong |
| 97 Reverse genetics system for the avian coronavirus infectious bronchitis virus https://jvi.asm.org/content/75/24/12359.short Major advances in the study of the molecular biology of RNA viruses have resulted from the ability to generate and manipulate full-length genomic cDNAs of the viral genomes with the subsequent synthesis of infectious RNA for the generation of recombinant viruses¬†‚Ä¶ |