

The Virus World Database: An Invaluable Resource for Public Health and Healthcare

Dr Vijay Reddy

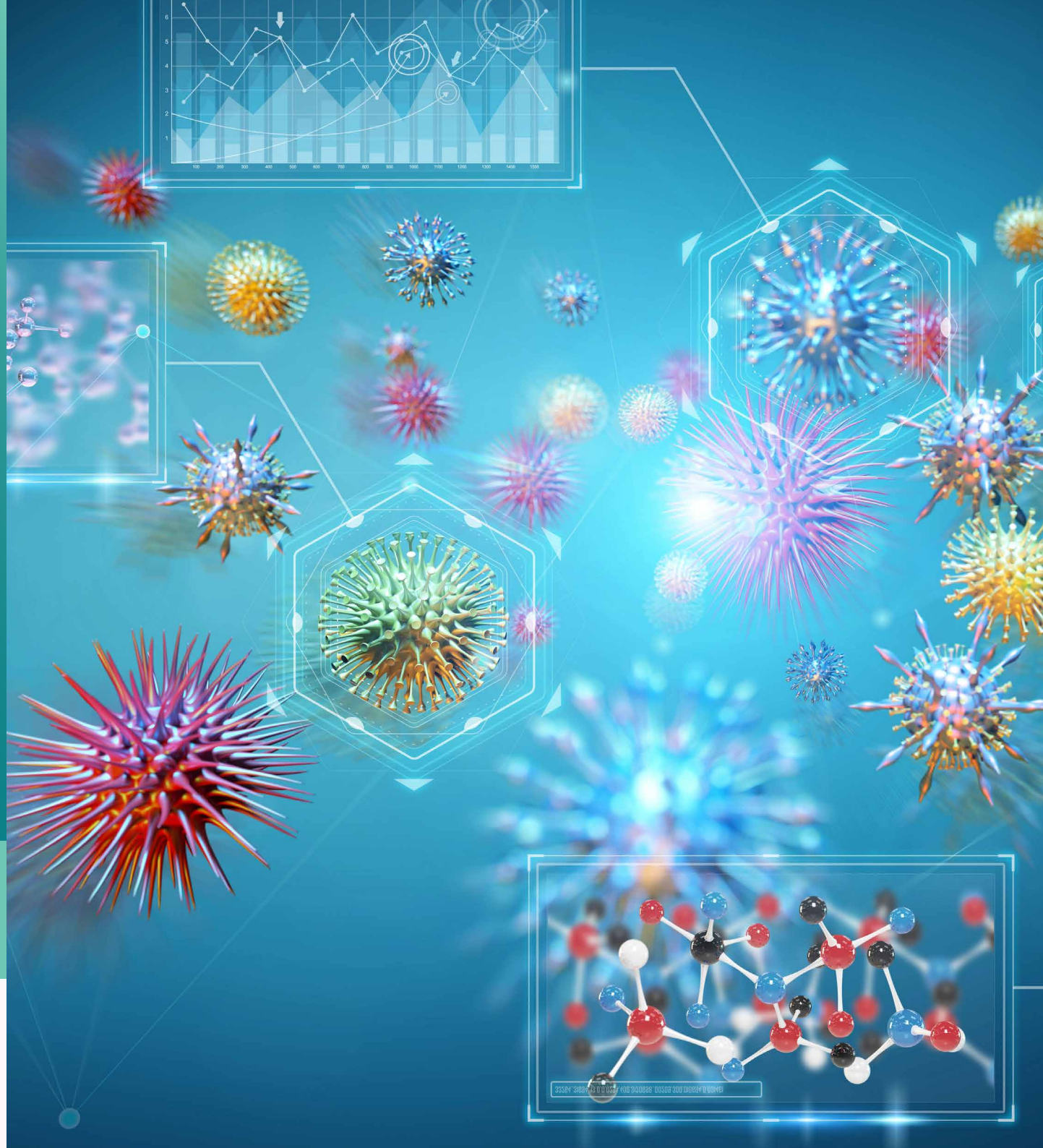
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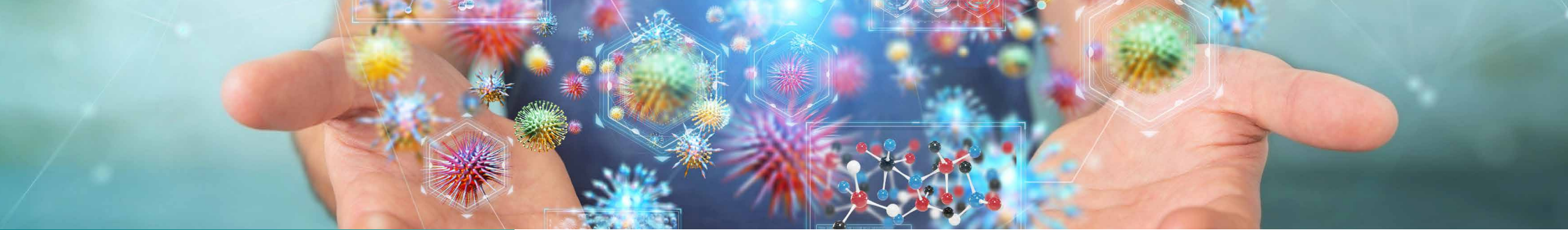
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Severe viral disease presents an ongoing challenge to the health of humankind. While unparalleled developments in science and technology are improving our understanding of such viruses, this information needs to be readily accessible to researchers to ensure continued progress in public health and healthcare. **Dr Vijay Reddy** and his colleagues at the Hormel Institute (University of Minnesota) developed the [Virus World database](#), an invaluable resource that details the genome, structure, and host of practically every discovered virus to date.

Viruses and Public Health

Viruses are the most abundant organisms on Earth. There are millions of viruses in every millilitre of seawater, and roughly half the human genome comes from ancient viruses. Despite being the smallest and, in some respects, the simplest type of microorganism in the world, viral biochemistry and replication mechanisms are much more varied than those found in bacteria, animals, and plants.

Scientific advances allow us to discover new viruses at an increasing rate while, at the same time, we are learning more and more about the genetics, structure, and lifecycle of previously discovered viruses. In the case of potential pathogens, this information is crucial to public health as it informs the development of diagnostic tests and control mechanisms, such as vaccines or treatments.

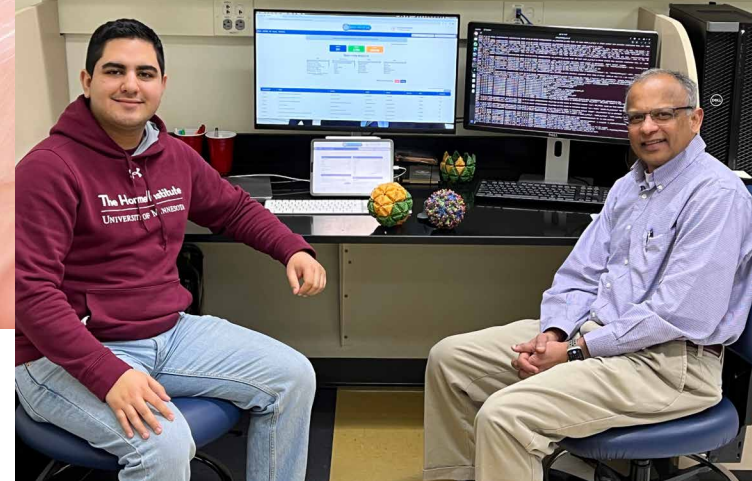
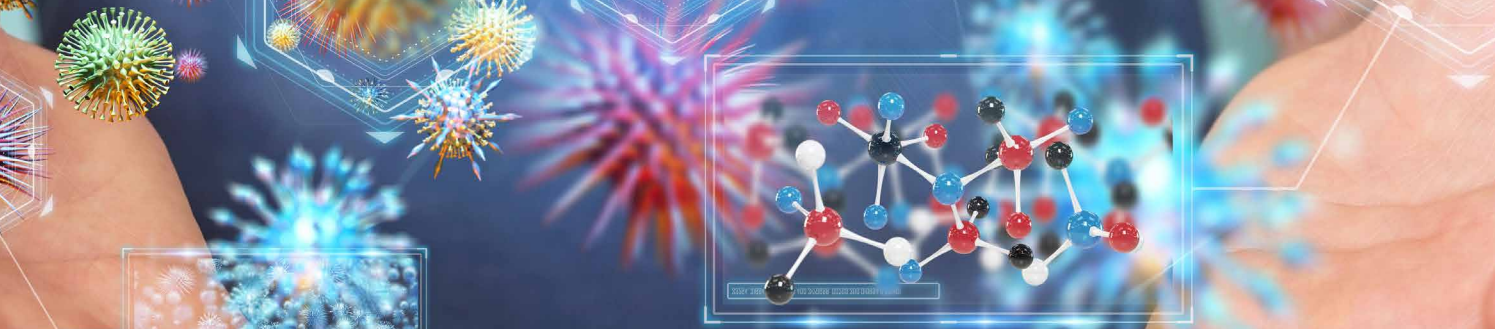
Dr Vijay Reddy and a team of virologists and computer scientists at the Hormel Institute (part of the University of Minnesota) designed and developed the [Virus World database](#) to help researchers meet the public health demands of viral diseases. This is the largest and most comprehensive repository of viral information ever created, and allows scientists around the world to access information about the genome, structures, and hosts of currently 245,590 different viruses. This information is updated on a biweekly basis.

Categorising Viruses

While nearly all the organisms on Earth are thought to share a common ancestor, viruses are so diverse and different from other lifeforms that they likely evolved independently multiple times throughout history. This means that viruses aren't classified in the same way as other organisms. Viruses can be classified by the way they produce mRNA (the molecule that tells cells how to make proteins from DNA instructions), by the way they look, their host organism, the type of disease they cause, or their genetic relationships to each other.

The International Committee of Taxonomy of Viruses (ICTV) is the organisation responsible for naming and classifying viruses. ICTV classification is based on genetic relatedness and groups viruses into families, genera, and species based on shared genes and morphological characteristics.

The Baltimore classification system classifies viruses by their genome type (double or single-stranded DNA or RNA) and replication strategy. There are seven viral groups under this system. This system is widely taught and used by virologists around the world. It focuses on replication strategies and highlights the mechanisms underlying viral replication that can provide targets for antiviral vaccines and therapies. This system can also help researchers predict certain characteristics of newly discovered viruses based on their genome, such as potential hosts, mode of transmission, and clinical effects.



A specific and unique feature of the Virus World database is that users can view and search using either or both classification systems, maximising the accessibility and versatility of the information it contains.

The Virus World database also allows users to search and filter by host. Viruses can infect a broad range of hosts, including animals, plants, bacteria, and even other viruses. Some viruses have narrow host ranges limited to a single species, whereas others have very wide host ranges, such as the rabies virus, which is able to infect any mammal. Viral host range has important public health implications, as highlighted by viruses such as SARS-CoV-2 and Ebola, which are readily able to move from animal to human hosts.

Viruses are made up of a nucleic acid (DNA or RNA) within a protein coat, and beyond this, can have a range of different shapes and structures. Viruses can be divided into enveloped and nonenveloped, whereby some viruses have a lipid layer taken from the host cell membrane covering their protein coat (i.e., enveloped). Viruses may also have structures extending from their main body to help them attach to and infect their host cells. Wherever possible, the Virus World database contains details and images of key structures and links to other viral structure resources.

Virus World Database

Dr Reddy and his team realised that new viruses were being discovered and that the details of known viruses were being updated faster than existing resources could take on board. A detailed understanding of the biology of viruses is key to many aspects of public health, technology, agriculture, and ecology.

However, specific details of individual viruses are traditionally only available within academic textbooks. To address this and better aid scientists, students, and clinical researchers, the team developed the Virus World database. This is the only resource where integrated information on viral taxonomy, host range, genome type, and structural details is freely accessible in an easy-to-understand and use fashion.

The team developed Virus World by extracting and compiling information from multiple other online databases and resources. Importantly, they also added useful information and resources as well as an easy-to-use search function. Viruses belonging to certain families or fitting certain searchable criteria are listed in a table and can be downloaded into Excel or JSON formats. The database creates an information page for each virus containing key information, links to other resources, and, where available, structural illustrations. Dr Reddy and the team have also provided an application programming interface (API) to enable users to access the Virus World metadata programmatically, allowing further data exchange and analysis.

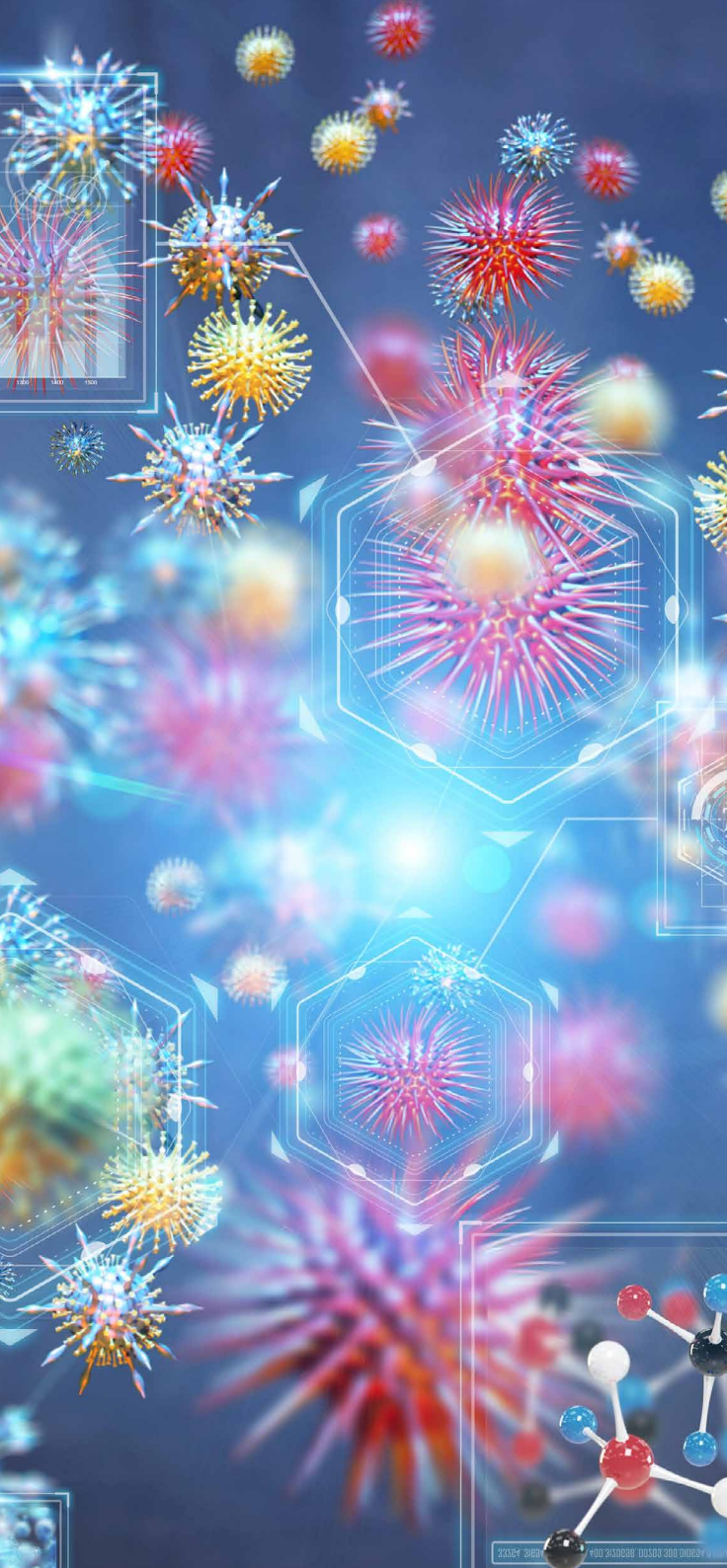
The Virus World database is a valuable resource for students, scientists, healthcare practitioners, and public health officials as it provides a comprehensive overview of the key features of every known virus – offering a vital role in the research, surveillance, and management of viral diseases. In the current era of rapid artificial intelligence, the Virus World database also promises to be a key resource for the training of machine learning and artificial intelligence technologies. The wealth of information contained within the database could potentially be used to train algorithms designed to predict viral structures and behaviour to inform health interventions.



Picture of Oscar Rojas Labra, the computer scientist instrumental in developing the Virus World database along with Dr Reddy.



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MEET THE RESEARCHER

Dr Vijay Reddy, The Hormel Institute, University of Minnesota Medical Research Center, Austin, MN, USA

Dr Vijay Reddy is an Associate Professor in Structural Virology, Informatics, and Customized Vaccine Design at the prestigious Hormel Institute, an independent biomedical research department within the University of Minnesota. He leads a team conducting research into the imaging and understanding of viral structures using cutting-edge technologies, as well as the use of simple viral particles as customisable vaccines. Before joining the Hormel Institute, he received his PhD in Molecular Biophysics from the Indian Institute of Science in Bangalore, India. His postdoctoral research included positions at Scripps Research (previously known as the Scripps Research Institute) and Purdue University. Alongside his research responsibilities, he provides teaching and mentoring to postgraduate students. Dr Reddy also serves on the Editorial Board of several academic journals.

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FURTHER READING

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