



VESID – Viral Entry Structural Integrity Disruptor

The core of VESID research the right molecules for use in antiviral action and in formulating such active chemical agents in a manner that is practical, safe and conducive for use by large and open-ended populations. This entails, necessarily:

- Developing a comprehensive theoretical model of viral information processing that is expressed in and can be understood in terms of topological orders, efficiencies of energy transfer and conformational changes, and in the context of viral interactions with receptors and host-cell membrane interfaces, thereby providing a broader understanding of how viruses interact with, enter, infect, and use host cells for their replicative processes.
- Developing, upon the above foundations, a general model for how to disable viruses in ways that may be different from the conventional strategies and tactics that are focused upon blocking particular receptors and making use of antibodies and the immune system through both vaccines and other specific antiviral medicinal substances.

A significant component of VESID is the

TDM -- Topological Dynamics Modeler (aka VDM - Viral Dynamics Modeler)

TDM is intended as a methodology, not as a specific and certainly not as a new stand-alone software engine. (TDM software operates within the ROSETTA molecular biology modeling and simulation environment.)

Its purpose is to enable: identification of structural locations within viruses that can be affected by external agents such as drug molecules to create disruptions in the viral structure that will prevent the virus from completing its “normal process” of entry into a host cell and triggering replication.

TDM is based upon the underlying fundamental principles of topological ordering within viral structures, involving the envelopes and other structures such as spikes and any protruding variations that are employed, integrally, in receptor and entry functions

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