

Menagerie of Viruses: Diverse Chemical Sequences or Simple Electrostatics?

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The genome packing in hundreds of viruses is investigated by analyzing the chemical sequences of the genomes and the corresponding capsid proteins, in combination with experimental facts on the structures of the packaged genomes. A universal model, based simply on non-specific electrostatic interactions, is able to predict the essential aspects of genome packing in diversely different viruses, such as the genome size and its density distribution. Our result is in contrast to the long-held view that specific interactions between the sequenced amino acid residues and the nucleotides of the genome control the genome packing. Key issues related to the stability of assembled virus structures and the kinetics of their formation will be addressed theoretically.