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Discrete fracture patterns of virus shells reveal mechanical building blocks IRENA L. IVANOVSKA, Biophysical Engineering Laboratory, University of Pennsylvania, Philadelphia, PA, ROBERTO MIRANDA, JOSÉ L. CARRASCOSA, Dept. Struct. Macromol., Centro Nacional de Biotecnología, Campus Universidad Autónoma de Madrid, GIJS J.L. WUITE, Dept. Physics and Astronomy, Vrije Universiteit Amsterdam, CHRISTOPH F. SCHMIDT, Third Institute of Physics, Georg-August-Universitaet Goettingen — Viral shells are self-assembled protein nanocontainers with remarkable material properties. They combine simplicity of construction with toughness and complex functionality. To date we know little about how virus structure determines assembly pathways and shell mechanics. We have used atomic force microscopy to study structural failure of the shells of the bacteriophage $\Phi 29$. We observed rigidity patterns following the symmetry of the capsid proteins and under prolonged force exertion, we see fractures along well-defined lines of the 2D crystal lattice. We found the mechanically most stable building block of the shells was a trimer. Our approach of "reverse engineering" the virus shells thus made it possible to identify stable structural intermediates. Such stable intermediates point to a hierarchy of interactions among equal building blocks correlated with distinct next-neighbor interactions. The results also demonstrate that concepts from macroscopic materials science, such as fracture, can be usefully employed in molecular engineering.

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