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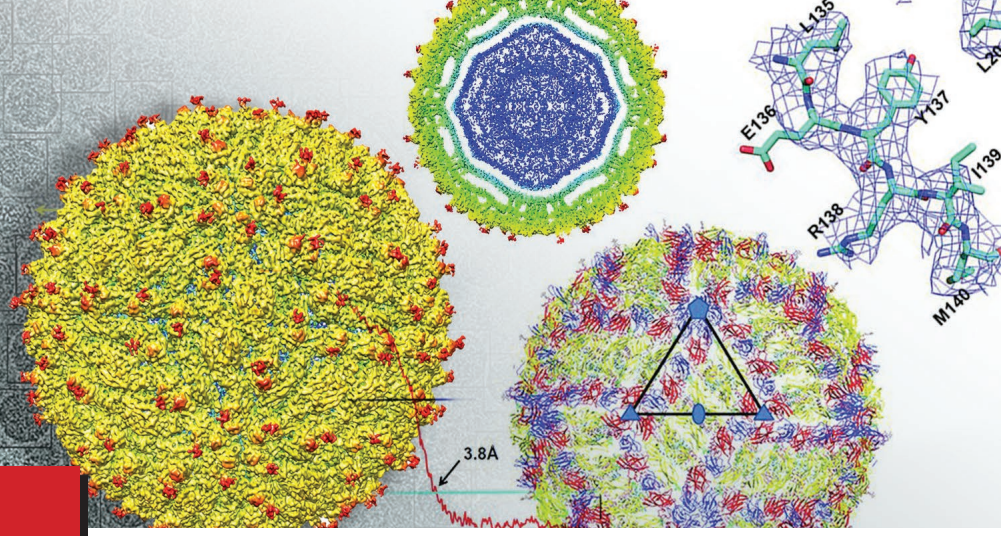

Special Seminar

Images from: The 3.8 Å resolution cryo-EM structure of Zika virus (2016)
D. Sirohi, Z. Chen, L. Sun, T. Klose, T. C. Pierson, M. G. Rossmann, R. J. Kuhn. *Science* **352**(6284): 467-470.

Hui-Ting Chou, Ph.D.

Harvard Medical School

Molecular Architecture of Membrane Trafficking Machineries Revealed by Single Particle Electron Microscopy

Monday, February 27, 2017 • 3:00 PM

Proteomics, Room 120

In membrane trafficking pathways, multisubunit tethering complexes (MTCs) are recruited to the organelles through Rab GTPasees and orchestrate the events from the vesicle recognition to membrane fusion with a number of proteins. Here we characterized the molecular architecture of three tethering complexes, Golgi-associated retrograde protein (GARP) complex, conserved oligomeric Golgi (COG) complex, and homotypic fusion and vacuole protein sorting (HOPS) complex using single particle electron microscopy. GARP promotes fusion of endosome-derived vesicles to the trans-Golgi network and COG is required for vesicle docking to and within the Golgi apparatus. Our analysis showed that GARP and COG subcomplex, Cog1-4, share the same subunit organization, even though the subunits have very low sequence similarity. We also found the overall structures of COG complex, Cog1-8, and subcomplex, Cog5-8, and identified the subunit arrangement of Cog5-8. HOPS is associated to the lysosome acting in the endolysosomal pathway and belongs to different MTC subfamily. Our electron microscopy class averages revealed that the HOPS particles containing flexible rod-like extensions were markedly different from the more globular and rigid particles in previous report. The class averages of full and sub-complexes showed HOPS forms a core composed of Vps16, Vps33 and Vps41, and three flexible legs including Vps11, Vps18 and Vps39. Our data suggested that the HOPS, COG and GARP complexes are similarly multilegged and share a common building plan, reflecting their analogous functions.

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