

Multiplex 3D MINFLUX and DNA-PAINT resolves nanoarchitecture of HIV-1 particles

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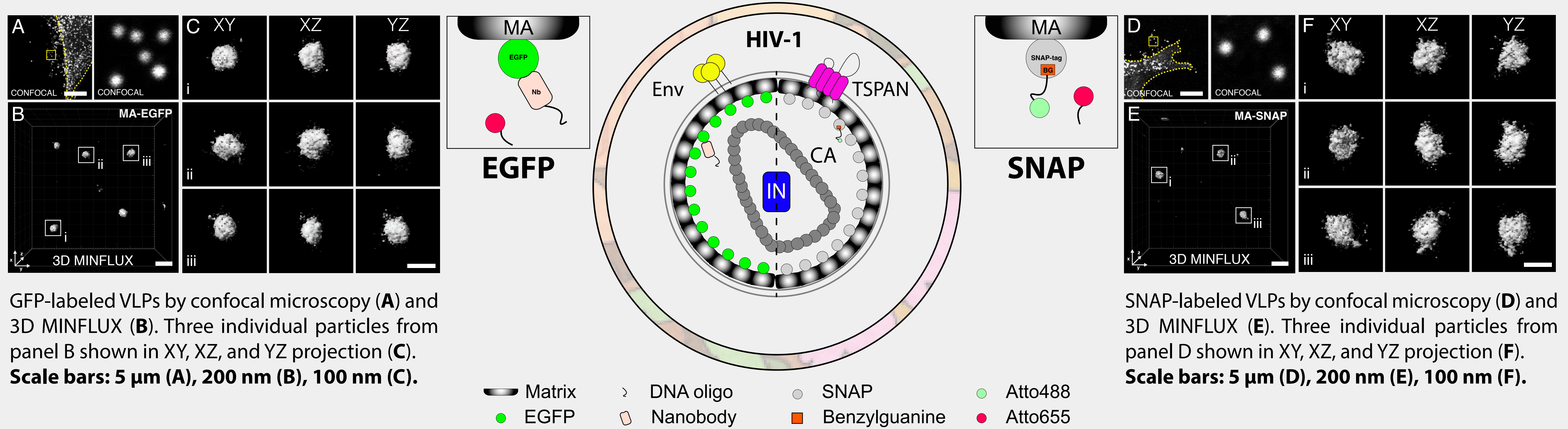
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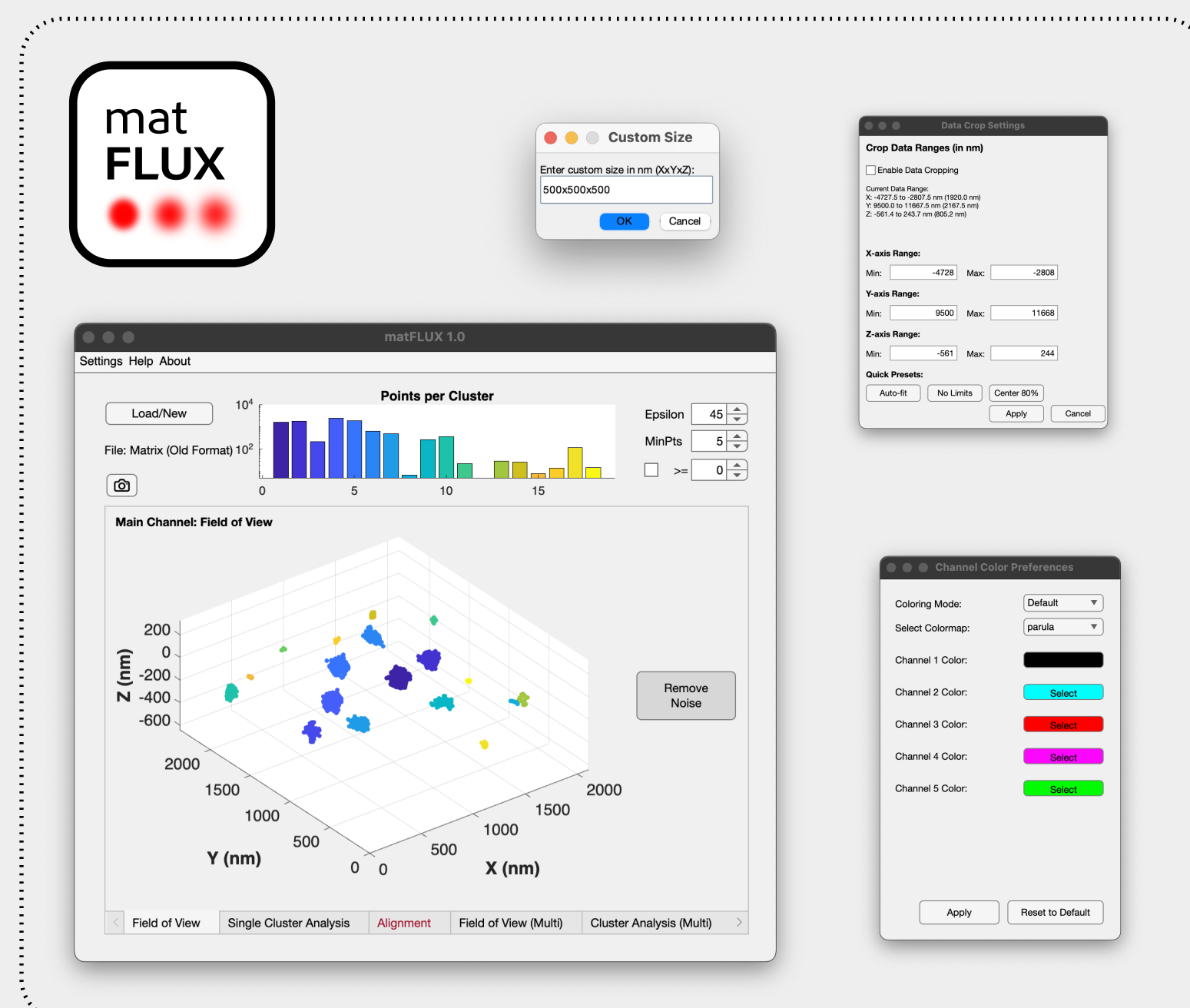
Abstract

Resolving the nanoscale organization of viral and host proteins is key to understanding HIV-1 assembly and infectivity. We present a framework for multiplexed 3D super-resolution microscopy of HIV-1 particles using MINFLUX and DNA-PAINT, achieving isotropic precision below 10 nm for up to five targets. Using the matrix protein as a reference, we quantified labeling-induced linkage errors and mapped the spatial distribution of viral and host proteins within individual particles. To support analysis, we developed matFLUX, an open-source software for quantitative visualization and alignment of multi-color MINFLUX data. This framework revealed distinct nanodomains of viral and host proteins at the HIV-1 surface, highlighting their nanoarchitecture.

DNA-PAINT Labeling Approaches for HIV-1 Particles



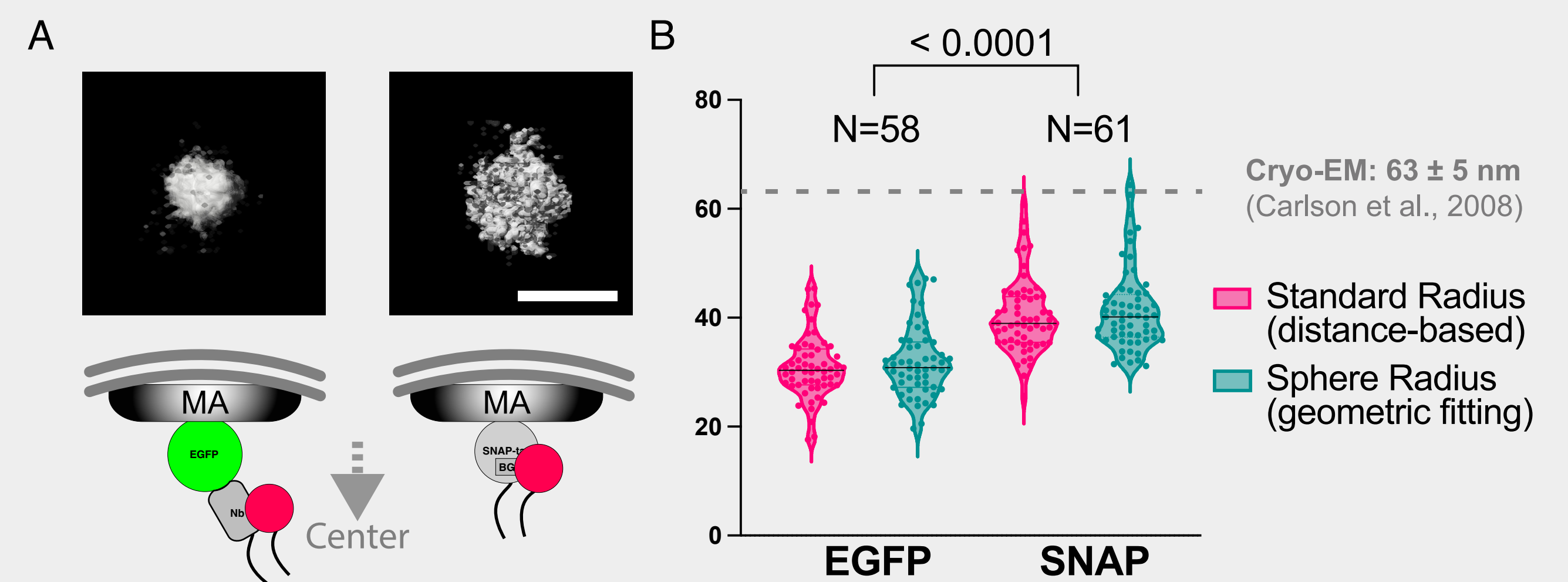
matFLUX - Particle-Centered Analysis Software



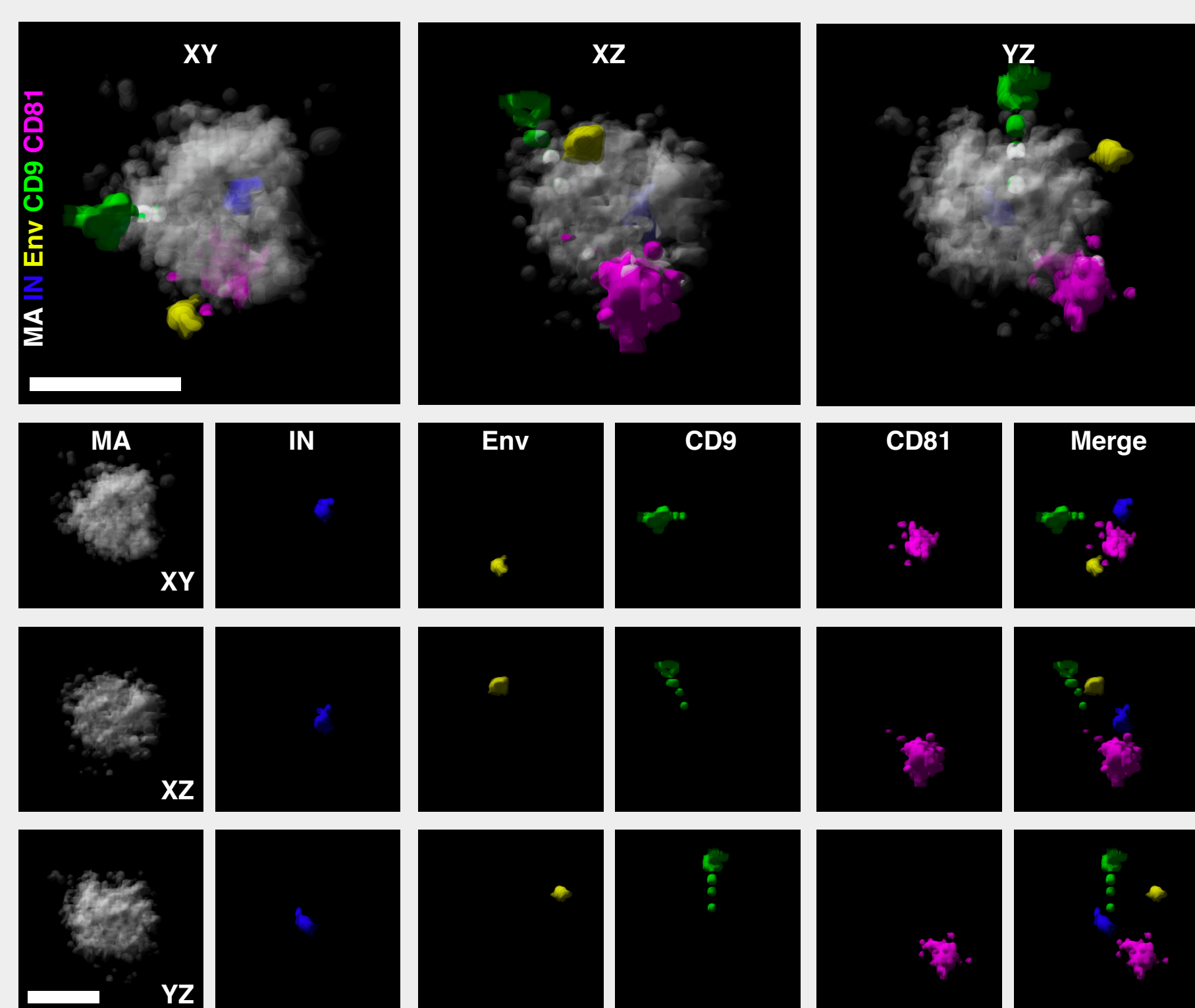
3D MINFLUX Data Processing

- Workflow-oriented
- Multi-Channel Alignment
- Single and Batch Data
- Modular
- Open Source
- All Platforms

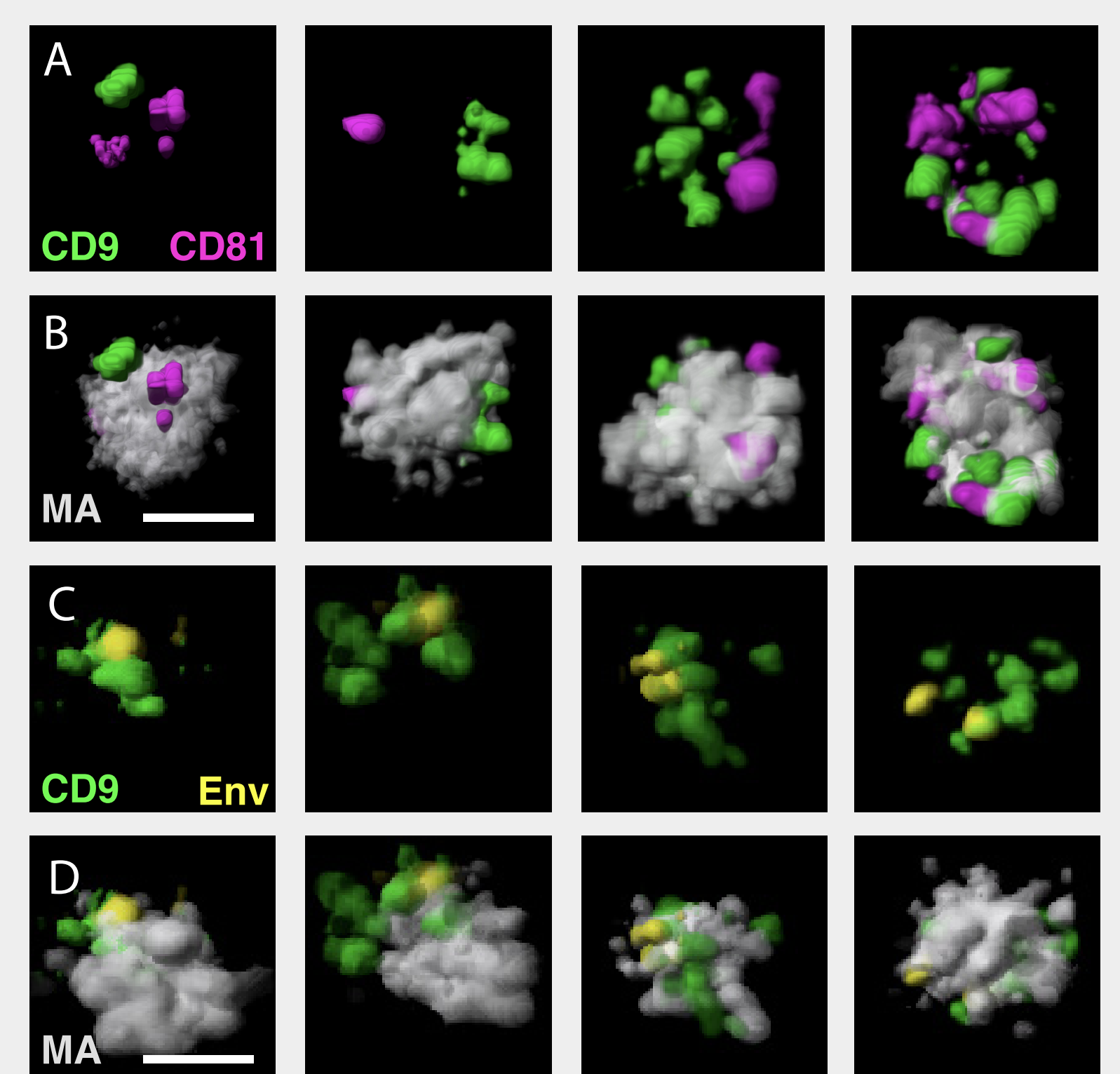
MINFLUX Reveals Linkage Error



Five-target 3D MINFLUX of a Single HIV-1 Particle



Tetraspanin Nanodomains on HIV-1 Particles



Outlook

Software: Release matFLUX as open-source software with tutorials for all platforms.

Tetraspanins: Characterize tetraspanin-enriched nanodomains in viral particles and at the plasma membrane.

HIV: Visualize HIV assembly and budding processes at the plasma membrane.

Multiplexed Viral Imaging: Apply framework to other viruses to uncover shared and unique nanoscale architectures.



Contact and Data