

The alternate assembly of retroviral integrases?

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We have determined the crystal structure of the catalytic core domain (CCD) of the avian alpha retrovirus Rous-associated virus type-1 integrase (RAV-1 IN) to 1.8 Å resolution. Data were collected on the ESRF MX and FIP beamlines. The CCD associates itself with an unexpected dimeric interface characterized by three pairs of α -helices. The protein surface exhibits a median basic groove suitable for single-stranded nucleic acid binding. The CCD of RAV-1 IN differs by a single residue from the CCD of Rous Sarcoma Virus (RSV) IN, whose crystal structure exhibits the canonical dimeric interface with two pairs of α -helices. We obtained an identical quaternary structure by mutating this divergent residue in RAV-1 IN. Our results suggest that the CCD of INs can dimerize in more than one state. Such flexibility can further explain the multifunctionality of IN, which beside integration of dsDNA is implicated in different steps of the retroviral cycle in presence of viral ssRNA.