**Crystal Structure of a Disintegrin Heterodimer from *Echis carinatus* at 1.9 Å resolution**

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Disintegrins are a family of small proteins that bind to integrins specifically. Their binding site is characterized by the presence of Arg-Gly-Asp motif which indicates an RGD-dependant mode of interaction with integrins. The disintegrins interfere with the functions of integrins as antagonists. Disintegrin was isolated from the venom of *Echis carinatus* and crystallized in the tetragonal space group $P4_32_12$ with a=b=90.7Å and c=55.5Å. It exits as a heterodimer unlike the low resolution structure which existed as a homodimer with its two subunits related by a two fold crystallographic symmetry. It is interlinked by two disulfide bonds at the N-terminal region and contains 64 amino acid residues in each chain. Each monomer contains three pairs of six antiparallel β-strands and is stabilized by four disulphide bridges. It has been refined to an R-factor of 0.212 and $R_{free}$ of 0.251 for all the data. The two chains of the dimer are anchored at N-terminal but diverge away at their C-termini exposing the Arg-Gly-Asp motif onto opposite directions, thus enhancing their binding efficiency. This is one of its unique features. The structural studies of disintegrins can provide a useful framework for the design of potent antagonists of integrins.

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