

## MS-based 3D (MS3D) structural investigation of

## protein-nucleic acids assemblies







Initial coordinates of the components obtained from PD (NMR and X-ray), Points of contact between components and spa constraints provided by X-linking and MS detection. Simulated annealing and energy minimization by Xplor Reiterative refinement and biophysical verification

MS3I

NMR => size limitation















Initial assumption: the individual RNA secondary structures are sufficiently stable to be conserved in the global old (Yusuppy et al. "Crystal structure of the ribosome at 5.5 Å resolution". Science 2001, 292, 883-896



Top-down (SORI-CAD)





High resolution and accuracy

3C) GAC





Footprinting constraints





MC2D : ation and modeling. In ictural in



Calc. (m/z) Exp. (m/z 684.3357 684.3399 684.3721 684.3761

A = 0.0364 Da

685.0

Kellersberger et al., Anal. Chem. 2004, 76, 3930.

Crosslinking constraints

SL1

Accuracy ~ 6 ppm

Resolution 310,000 FWH

YGGFLK

YGGFLQ

olojojakojaka olojo









VPK 34 nt-seque

**FIV-PK** 



Yu, E. T.; Zhang, Q.; Fabris, D. J. Mol. Biol. 2005, 345, 69

Monomeric HIV-1 Ψ-RNA



