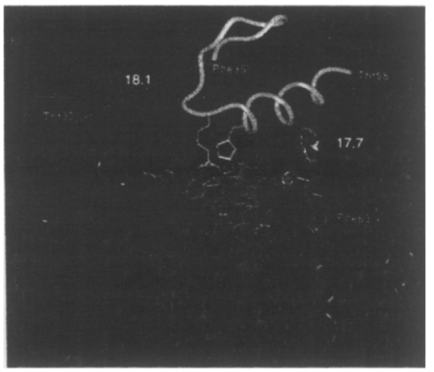
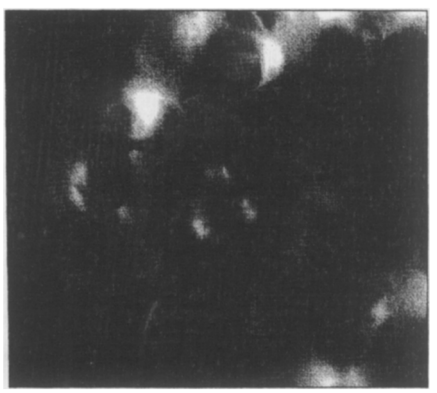
importance of the DNA conformation in the Zif268–DNA complex in recognition. Circular dichroism studies indicate that the DNA conformation changes upon complex formation; if it did not, the fingers of Zif268 would be too far apart given the linker length and the observed finger–finger contacts. The structure should provide an excellent framework for analyzing the effects of Zif268 mutations, for modeling related zinc finger–DNA complexes and for designing and selecting Zif268 variants that will recognize other DNA sites.



15 October 1996, Research Paper, *Structure*

☐ **Metal-binding sites in the major groove of a large ribozyme domain.** Jamie H Cate and Jennifer A Doudna (1996). *Structure* 4, 1221–1229.

Group I self-splicing introns catalyze sequential transesterification reactions within an RNA transcript to produce the correctly spliced product. These ribozymes are often several hundred nucleotides in size. The recently determined crystal structure of the P4–P6 domain from the *Tetrahymena thermophila* group I intron provides a detailed view of metal binding in this RNA, which is large enough to have a considerable amount of higher-order structure, including stacked RNA helices. There are three metal-binding sites in the major groove, detected by osmium hexammine. All three sites involve G and U nucleotides exclusively; two are formed by G:U wobble base pairs. Two of these sites are occupied by fully-hydrated, but weakly bound, magnesium ions. G:U wobble base pairs are often conserved in RNA structures, and may be generally important in forming metal ion binding sites. It should be possible to insert sites of this kind into other RNA structures, thus providing a general method for obtaining heavy-atom derivatives of such structures. Samarium detects a different magnesium-binding site, bridging phosphate oxygens in the A-rich bulge, a region that is essential for the folding of the entire domain.



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