

bound ~0.7 equivalents of ATP; we conclude that the RNA binds its ligand with a stoichiometry of unity.

Kethoxal modification<sup>6</sup> was used to assess the accessibility of guanosine residues to modification (Fig. 2d). Surprisingly, G7 and G17 within the loop, and G6 (which forms the G·C base pair on the left side of the loop), all of which are strongly protected in the absence of ATP, become highly accessible to modification by this reagent in the presence of ATP. Other guanosine residues, including G8 in the large loop, the single unpaired G opposite the loop, and Gs in the stems, are highly protected in the presence or absence of ATP. These observations suggest that the motif is highly structured both in the presence and absence of ATP, but that binding induces a conformational change in the structure of the RNA.

Much effort has been devoted to the design of abiotic synthetic receptors with specific ligand-binding properties<sup>7-15</sup>. The design of organic receptors for small molecule ligands in non-polar organic solvents has been relatively successful, but it has been more difficult to synthesize receptors that bind in aqueous solution, where hydrogen bonds are critical for specificity but contribute relatively less to binding energy. One of the major problems in small molecule receptor design is the difficulty of providing a framework that is compatible with the precise positioning of numerous functional groups that must interact with the ligand. The secondary and tertiary structures of RNAs and proteins provide a framework for the functional groups that define the ligand binding site. *In vitro* selection, by allowing the sifting of trillions of possible sequences, automatically provides not only a suitable framework but a complete binding-site structure.

As RNA is able to bind ATP with such affinity and specificity, the question arises as to whether this capability is or has been used biologically. We searched for the ATP-binding consensus sequence in structural RNAs listed in the GenBank 73 data base and identified no definitive match. Even if the ATP-binding RNA motif is not used in present day biology, its existence is consistent with theories of a much greater role for RNA in early life forms<sup>16</sup>. The frequent appearance of adenosine in enzymatic cofactors has been noted as a possible remnant of the RNA world; as the ATP-binding motif also binds adenosine it could serve to anchor such cofactors to a ribozyme<sup>17</sup>. For example, NAD<sup>+</sup> binds well to the motif, which could therefore serve as one component of a ribozyme with oxidoreductase activity. The ATP-binding motif and other RNA structures capable of binding small molecules in solution could serve as building blocks for the construction of a new set of ribozymes with a wide range of catalytic activities. □

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