In recognition of the utility of the power law hypothesis for riboswitch distribution, and in recognition of the unusual architecture of riboswitches for HMP-PP, the distinction of Breaker Laboratory “Molecule of the Year” is conferred upon these findings.

Accurate estimates for the number of riboswitch classes remaining to be discovered in bacterial species can provide useful insights into the extent of reliance modern organisms have on noncoding RNAs, and the technical demands needed to be met by researchers who seek to discover more examples. To date, projections based on the power law equation \( Y = mX^b \) (Fig. 1) make apparent several striking conclusions, including that there are many exceedingly rare riboswitch classes hidden in accumulating bacterial DNA sequence data sets.

RNA-derived coenzymes are sensed by some of the most common riboswitches, usually by elaborate and well conserved aptamer structures. Newly-validated HMP-PP riboswitches sense a coenzyme biosynthetic precursor HMP-PP, but use a surprisingly simple and compact riboswitch that embeds the aptamer almost entirely within an intrinsic terminator expression platform. Such tiny architectures might be used by other rare riboswitches.

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