

Editorial

Molecular diversity evolution

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Starting from this issue, we are publishing the 10th volume of *Molecular Diversity*. Four individual issues will be published for 2006. The volume will not have any page number limit. Therefore, accepted papers will be published more rapidly.

Molecular Diversity was launched in 1995. Volumes 1–4 were edited by *Richard A. Houghten, Walter Moos, H. Mario Geysen, Mike Pavia, Stuart Kauffman and Jack Szostak*. Volumes 1 and 2 were published by ESCOM. Volumes 3–8 were published by Kluwer. Volume 5 was edited by *Richard A. Houghten and Michal Lebl*. Since volume 9, *Molecular Diversity* has been published by Springer. I have been responsible for this journal starting from Volume 6.

In this issue there are four experimental combinatorial chemistry papers and at the end, two papers of great theoretical and computational interest. The general topic of the first paper contributed by the research group of *Bernd Michael Rode* may be called *Molecular Diversity Evolution*. We plan

to publish more papers and even special issues on this topic. Only 20 amino acids are used as the building blocks of proteins and only 4 monomers labeled as G, C, A, T for genetic polymer DNA. At what early step in the biomolecular evolution of life were just these numbers of monomers already exclusively used for polymerization? Was the minimum number of different building blocks in nucleic acid polymers required for genetic material larger than 4 or less than 4 at the early stages of evolution? From the point of view of information theory, the number should be at least 2 and most probably it is 2 for genetic molecules because this kind of binary system may give high uncertainty at the early stage of evolution. However, there are large numbers of monomers available. The dilemma can be solved only by more experimental and theoretical research. I would like to invite scientists active on the related fields to contribute papers for publication in *Molecular Diversity*. Of course, contributions of papers on all other topics are also welcome.