

[Virtual Screening: An Alternative or Complement to High Throughput Screening?](#)

In the next couple of years the human genome will be fully sequenced. This will provide us with the sequence and overall function of all human genes as well as the complete genome for many micro-organisms. Subsequently it is hoped, by means of powerful bioinformatic tools, to determine the gene variants that contribute to various multifactorial diseases and genes that exist in certain infectious agents but not humans. As a consequence, this will allow us to define the most appropriate levels for drug intervention. It can be expected that the number of potential drug targets will increase, possibly by a factor of 10 or more. Nevertheless, sequencing the human genome or, for that matter, the genome of other species will only be the starting point for the understanding of their biological function. Structural genomics is a likely follow-up, combined with new techniques to validate the therapeutic relevance of such newly discovered targets. Accordingly, it can be expected that in the near future we will witness a substantial increase in novel putative targets for drugs. To address these new targets effectively, we require new approaches and innovative tools. At present, two alternative, yet complementary, techniques are employed: experimental high-throughput screening (HTS) of large compound libraries, increasingly provided by combinatorial chemistry, and computational methods for virtual screening and de novo design.

As kind of status report on the maturity of virtual screening as a technique in drug design, the first workshop on new approaches in drug design and discovery was held in March 1999, at Schloss Rauischholzhausen, near Marburg in Germany. More than 80 scientists gathered and discussed their experience with the different techniques. The speakers were invited to summarize their contributions together with their impressions on the present applicability of their approach. Several of the speakers followed this request which is summarized in this publication.

[Virtual Screening for Bioactive Molecules](#)

Recent progress in high-throughput screening, combinatorial chemistry and molecular biology has radically changed the approach to drug discovery in the pharmaceutical industry. New challenges in synthesis result in new analytical methods. At present, typically 100,000 to one million molecules have to be tested within a short period and, therefore, highly effective screening methods are necessary for today's researchers - preparing and characterizing one compound after another belongs to the past. Intelligent, computer-based search agents are needed and "virtual screening" provides solutions to many problems. Such screening comprises innovative computational techniques designed to turn raw data into valuable chemical information and to assist in extracting the relevant molecular features.

This handbook is unique in bringing together the various efforts in the field of virtual screening to provide the necessary methodological framework for more effective research. Leading experts give a thorough introduction to the state of the art along with a critical assessment of both successful applications and drawbacks. The information collated here will be indispensable for experienced scientists, as well as novices, working in medicinal chemistry and related disciplines.