Dear editorial board,

Please find attached our manuscript „ *R*obi*NA*: A user-friendly, integrated software solution for RNA-Seq based transcriptomics” which we would like to be considered for publication in the stand-alone program section of the Nucleic Acids Research 2012 web server issue. It describes a new integrated application providing a user-friendly workflow for high-throughput RNA sequencing based analysis of differential gene expression (RNA-Seq). The workflow comprises all steps of RNA-Seq analysis, starting with raw data import, quality checking and filtering, mapping to a reference and statistical analysis of differential gene expression. In order to make it a valuable tool for both novices and experts, we tried to offer as much flexibility as possible while maintaining a clear and intuitive user interface that guides inexperienced users and provides in-line help texts.

The application is freely available and can be downloaded from our website <http://mapman.gabipd.org/web/guest/robin> together with a demonstration data set and a manual in PDF format.

With best regards,

Marc Lohse