**ABSTRACT PREPARATION INSTRUCTIONS**

Authors must create a personal account in the BCADD-2023 Registration System. More than one abstract can be submitted from one account.

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* The results and accomplishments and their significance.

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Page size: A4.

Margins: top, bottom and left - 2.0 cm, right - 1.5 cm.

Line spacing: single (1.0).

Alignment of the text of abstracts: in width.

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Title of abstract: Times New Roman, 14 pt, capital letters, bold.

Authors: Times New Roman, 12 pt, italic, bold. The surname of the author who will represent the work is underlined. The initials are put before the surnames. If the authors represent different organizations, the names are followed by superscript numbers, which are deciphered below when listing the organizations. If the authors work in the same organization, no indexes are added. Organization: Times New Roman, 12 pt, italics.

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**Sample of the abstract is provided here.**

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**GENOME ENHANCER: NON-CODING GENOME GIVES CLUES TO ANTICANCER DRUG TREATMENT**

***D. Stelmashenko1,2, O. Kel-Margoulis1, S. Aplako3, A. Kel1,2,4***

*1geneXplain GmbH, Wolfenbüttel, Germany;
2biosoft.ru, Novosibirsk, Russia;
3City Hospital no.40, St. Petersburg, Russia;
4Institute of Chemical Biology and Fundamental Medicine, Novosibirsk, Russia*

The development of omics technologies and emerging of targeted therapies have opened a new era in the medicine of 21st century - the era of personalized medicine based on identification of the precise molecular mechanism of a certain pathology in a concrete patient. Personalized medicine and targeted therapy play a very special role in cancer diseases as it has been widely shown in multiple studies that the same types of cancer in two different patients can appear to be very different in their origins and mechanisms and therefore responding differently to the same treatment. Development of personalized drug target identification algorithm based on the patient omics data analysis would solve this problem of optimal therapy selection and would bring the cancer treatment strategy to a completely new level. Our work aims to introduce an algorithm for reconstruction of the molecular mechanism of a certain pathology and selection of effective therapies based on the personalized model of the disease. The drug target identification algorithm introduced in this work can be applied for various types of omics data. For illustrating the algorithm in the current study, we will show its application example on the basis of RNA-seq data of colorectal cancer tumor sequencing. We analyzed RNA-seq data of the patients with the good and pure response to standard therapy and revealed differentially expressed genes (DEGs) in the tumor compared to normal surrounding tissue. We applied *Upstream Analysis* algorithm [1] for identification of key master-regulators responsible for pathologic gene regulation in cancer cells of the studied cases. The analysis comprised of three main steps: 1) AI-based algorithm to scan promoters of DEGs using TRANSFAC database and to identify complexes of transcription factors (TF), which regulate DEGs; 2) a graph search algorithm using TRANSPATH database to identify common regulators of the TFs selected on the previous step as potential drug targets; 3) effective treatments are then selected for the identified drug targets, on the basis of HumanPSD database, containing the information about the approved drugs, as well as the therapies under development, and their targets. This algorithm is available at the Genome Enhancer web site (ge.genexplain.com).

The performed analysis revealed that the studied patient cases had rather different mechanism of carcinogenesis that involve fairly different although partially overlapping sets of master regulators in the molecular circuits that control activity of the gene expression in these tumors. Based on the revealed master regulators our algorithm proposed highly tuned personalized prospective drug treatment for the different patients with various cancer progression. The target-oriented approach towards treatment prescription accelerates the off-label drug usage and enables effective treatment selection for clinically complicated cases with no obvious treatment options.

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1. Kel, A., Boyarskikh, U., Stegmaier, P. et al. (2019) *BMC Bioinformatics*, 20, 119.