Author's Guide for Submission of Article to the 1st International Congress on Cancer and Stem Cell Biomedicine (ICCSB2024)

Number of Words:

- The number of words in the Abstract is limited to 400.
- The number of words in the entire article should not exceed 5000.

Font: Time New Romans

Abstract Format: The abstracts should include the following sections:

1) Title (Font size: 14)

2) Authors (Font size: 10)

3) Affiliations (Font size: 9)

4) Corresponding Author (The full name, affiliation, and email address)

5) Extended Abstract (Font size: 12)

- Background
- Methods
- Results
- Conclusions

6) Keywords (Font size: 12)

Full Paper Format: The full papers, in addition to abstract, should also include the following sections:

7) Introduction (Font size: 12)

8) Methods (Font size: 12)

9) Results (Font size: 12)

10) Discussion (Font size: 12)

11) Conclusion (Font size: 12)

12) Authors' Contributions (Font size: 12)

13) References (Font size: 12)

Please prepare your abstract according to the example provided in the next page.

Example Abstract:

Systems biology approach to identify biomarkers and therapeutic targets for colorectal cancer

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Background: Colorectal cancer (CRC), is the third most prevalent cancer across the globe, and is often detected at advanced stage. Late diagnosis of CRC, leave the chemotherapy and radiotherapy as the main options for the possible treatment of the disease which are associated with severe side effects. In the present study, we seek to explore CRC gene expression data using a systems biology framework to identify potential biomarkers and therapeutic targets for earlier diagnosis and treatment of the disease.

Methods: The expression data was retrieved from the gene expression omnibus (GEO). Differential gene expression analysis was conducted using R/Bioconductor package. The PPI network was reconstructed by the STRING. Cystoscope and Gephi software packages were used for visualization and centrality analysis of the PPI network. Clustering analysis of the PPI network was carried out using k-mean algorithm. Gene-set enrichment based on Gene Ontology (GO) and KEGG pathway databases was carried out to identify the biological functions and pathways associated with gene groups. Prognostic value of the selected identified hub genes was examined by survival analysis, using GEPIA.

Results: A total of 848 differentially expressed genes were identified. Centrality analysis of the PPI network resulted in identification of 99 hubs genes. Clustering analysis dissected the PPI network into seven interactive modules. While several DEGs and the central genes in each module have already reported to contribute to CRC progression, survival analysis confirmed high expression of central genes, CCNA2, CD44, and ACAN contribute to poor prognosis of CRC patients. In addition, high expression of TUBA8, AMPD3, TRPC1, ARHGAP6, JPH3, DYRK1A and ACTA1 was found to associate with decreased survival rate.

Conclusion: Our results identified several genes with high centrality in PPI network that contribute to progression of CRC. The fact that several of the identified genes have already been reported to be relevant to diagnosis and treatment of CRC, other highlighted genes with limited literature information may hold potential to be explored in the context of CRC biomarker and drug target discovery.

Keywords: Biomarker; Colorectal cancer; Hub gene; PPI network.