

Transcriptome Analysis Console (TAC) Software 3.1 Release Notes

(For research use only. Not for use in diagnostic procedures.)

Transcriptome Analysis Console Software 3.1 includes the following changes and enhancements:

1. Filter the miRNA and mRNA interactions network by validated vs. predicted interactions
2. Visualize multiple RNA samples (exon level) in 3D bar chart graph
3. Run two Way Balanced ANOVA
4. Provide pathway p-values in Wikipathways
5. Provide gene level p-value for Splicing analysis
6. Provide Venn Diagram and Gene List interaction

Software and Hardware Requirements:

Transcriptome Analysis 3.1 is only supported on 64-bit systems.

- Windows 7 Professional SP1 (64-bit)
- Windows 10 Professional (64-bit)

Memory and CPU Recommended Requirements

- Quad Core System, 2.83 GHz
- 64-bit stations: 8GB RAM, recommended 16GB RAM

The following are the known issues/differences that exist in Transcriptome Analysis Console Software 3.1:

1. In the Interactive miRNA and mRNA graph, if the nodes have been moved to new locations in the graph, using the navigational “back” and “forward” buttons will not preserve the new node locations. The nodes will appear in their original location when navigating.
2. Opening a TAC 3.0 result file in TAC 3.1 will convert the result file to TAC 3.1 format. This conversion cannot be undone.