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CORRIGENDUM

IPAVS: Integrated Pathway Resources, Analysis and Visualization System

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The Authors would like to apologize for not citing manuscripts describing software libraries that were used in development of IPAVS input/output loaders.

KEGGtranslator (1) and JSBML (2) software packages are used by IPAVS input loader for generating SBML files from KEGG pathway data (KGML files). BiNoM (3) software package is used by IPAVS output converter to generate downloadable BioPAX and XGGML output files from the CellDesigner XML files. Paxtools (www.biopax.org/paxtools.php) software package is used to generate SIF files from BioPAX files.

This correction does not influence the validity of the results and the conclusions of this article.

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