

# Novel developments in SBGN-ED and applications

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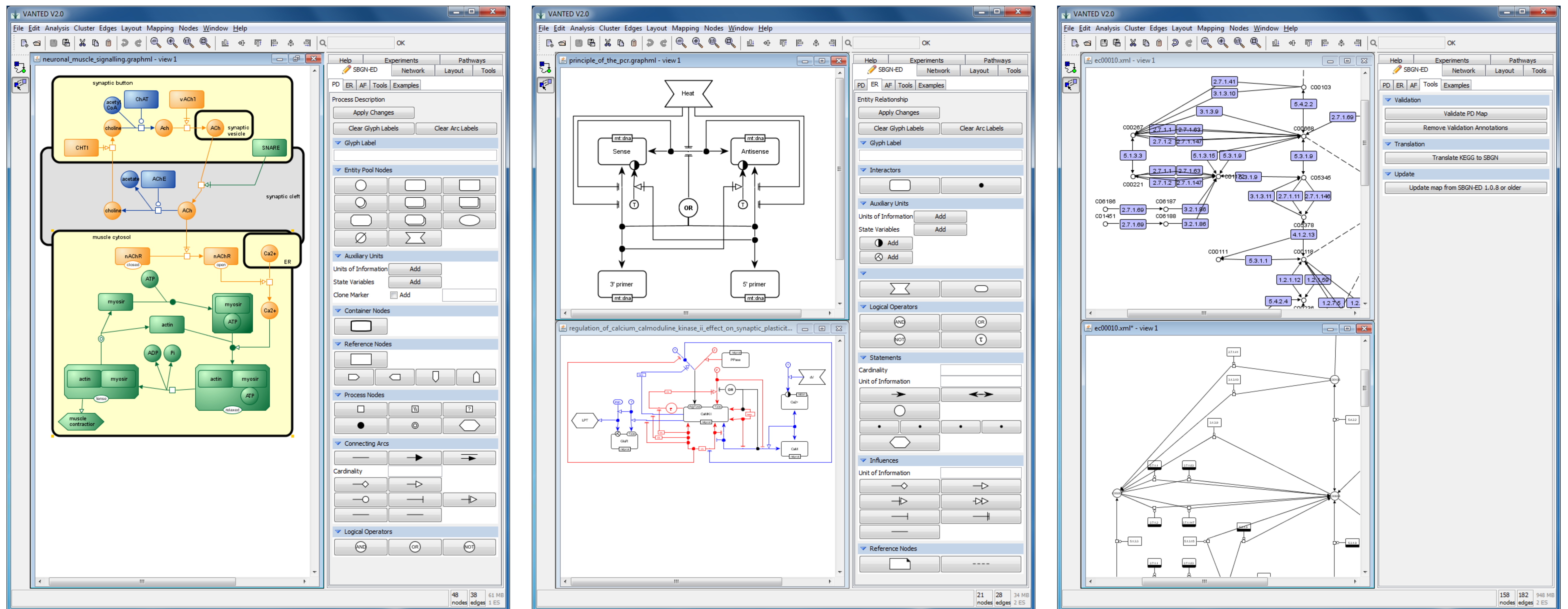
## SBGN

The Systems Biology Graphical Notation (SBGN, www.sbgn.org) [1] is an emerging standard for graphical representations of biochemical and cellular processes studied in systems biology. Three different views (Process Description, Entity Relationship, and Activity Flow) cover several aspects of the represented processes in different levels of detail. SBGN helps to communicate biological knowledge more efficient and accurate between different research communities in the life sciences. However, to support SBGN, methods and tools for editing, validating, and translating of SBGN maps are necessary.

## SBGN-ED

SBGN-ED (www.sbgn-ed.org) [2] was developed as an add-on for VANTED (www.vanted.org) [3] to provide a tool for creating and editing all three types of SBGN maps. Furthermore the syntactical and semantical correctness of created or edited maps can be validated. Already existing non-SBGN diagrams from the KEGG database can be translated automatically into SBGN.

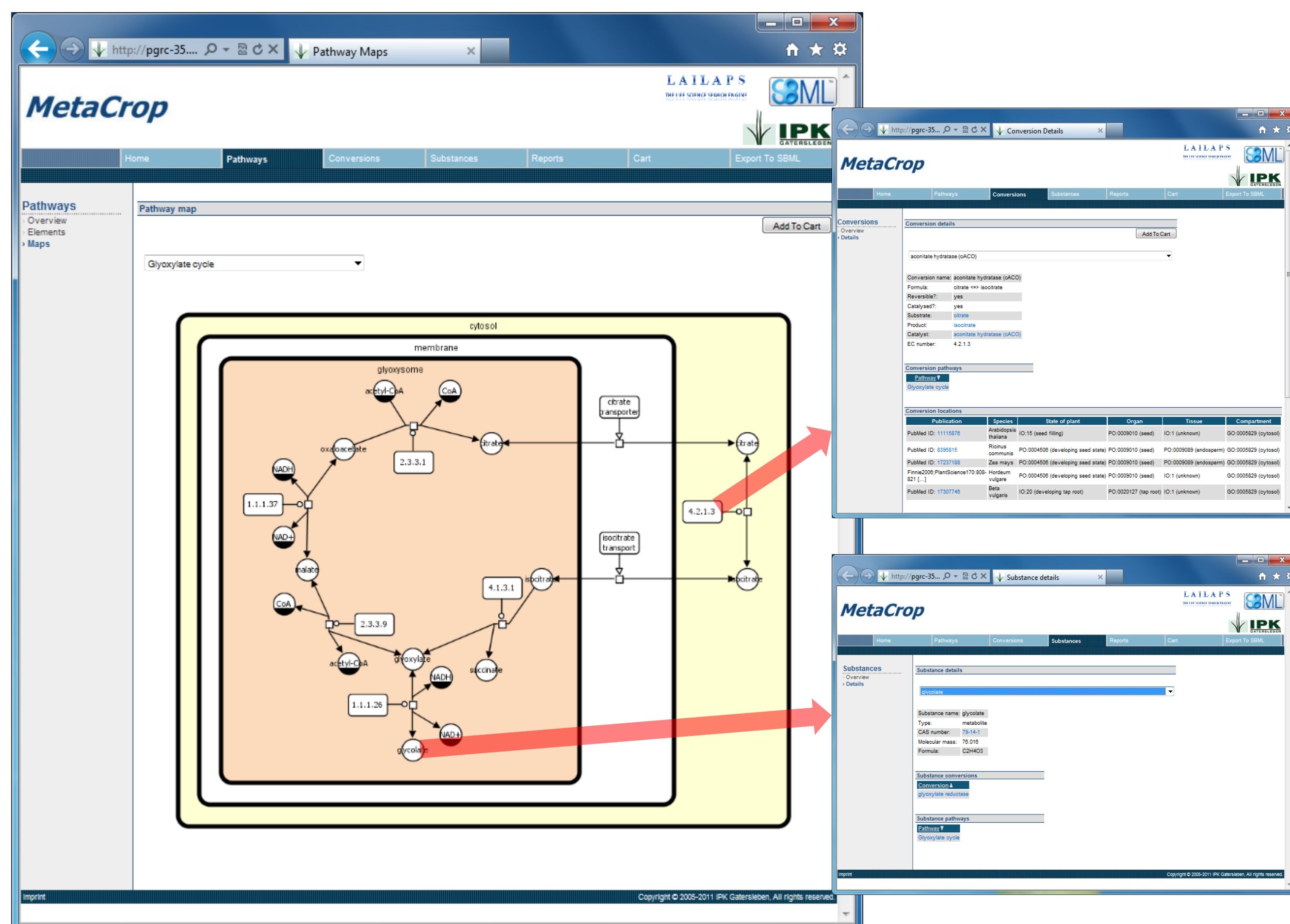
In the latest version the user interface has been improved for easier handling of SBGN features and the validation of maps has been extended. Additionally SBGN-ED now supports the import and export of SBGN Process Description maps in the SBGN-ML file format (LibSBGN, libsbgn.sourceforge.net).



The SBGN-ED add-on is implemented as a side panel with five subpanels in VANTED. Left: Subpanel for Process Description and an example map. Middle: Subpanel for Entity Relationship and two example maps. Right: Tools subpanel and Glycolysis / Gluconeogenesis pathway from the KEGG database (top) and after translation into SBGN (bottom).

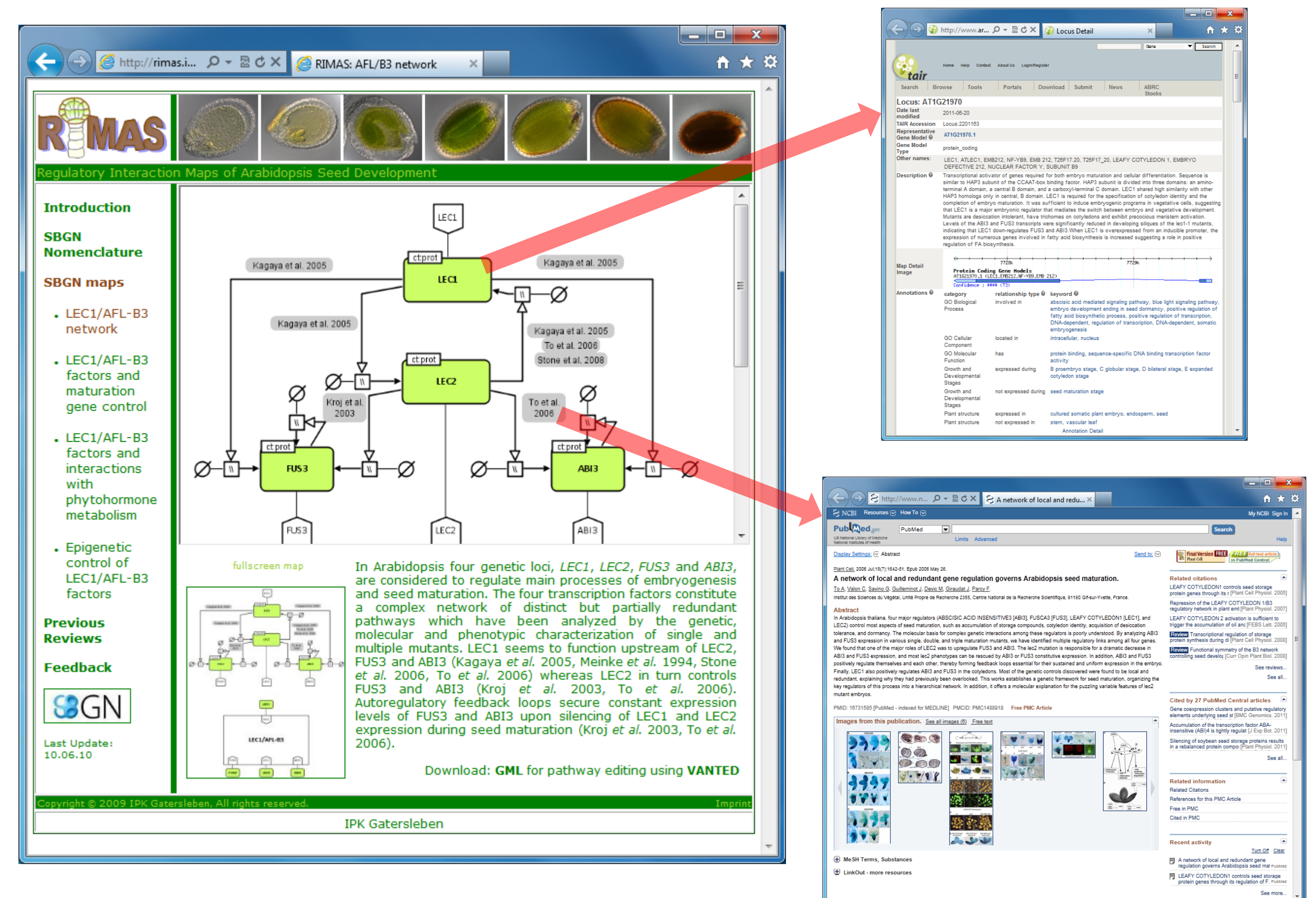
## MetaCrop

MetaCrop is a database that summarizes manually curated information (such as reactions, locations, transport processes, reaction kinetics, literature references) about metabolic pathways in crop plants (metacrop.ipk-gatersleben.de) [4]. The pathways have been drawn with SBGN-ED and the entire SBGN maps are available in MetaCrop as clickable image maps for online exploration and as SBGN-ML files for download and usage in other LibSBGN supporting tools. The clickable SBGN maps are linked to entries in the database, thereby allowing easy access to additional information.



## RIMAS

As one of the first applications of SBGN, the RIMAS (Regulatory Interaction Maps of Arabidopsis Seed Development) web-based information portal provides a comprehensive overview of regulatory pathways and genetic interactions during Arabidopsis embryo and seed development (rimas.ipk-gatersleben.de) [5]. The regulatory interaction maps have been drawn and validated using SBGN-ED and exported to websites with clickable image-maps. The RIMAS service provides access to these clickable SBGN maps which are linked to literature and other databases.



## References

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- [2] T. Czauderna, C. Klukas, F. Schreiber: Editing, Validating, and Translating of SBGN Maps. *Bioinformatics*, 26(18):2340-2341 (2010).
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- [4] E. Grafahrend-Belau, S. Weise, D. Koschützki, U. Scholz, B. H. Junker, F. Schreiber: MetaCrop - A detailed database of crop plant metabolism. *Nucleic Acids Research*, 36:D954-D958 (2008).
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