Supplementary Files

Supplementary File S1: Comparison of the data accession possibilities of the different integrated databases presented in this manuscript.

	Cytoscape plugin	Web service	Libraries	Export
BioGateway	BioGateway App	-	-	SIF, all Cytoscape export formats
OmniPath	OmniPath App	REST API	Python (pypath), R	SIF, BEL
NDEx	CyNDEx-2 App	REST API	Java, Python, R	SIF, Cytoscape CX
Pathway Commons	CyPath2 App	API	Java, Python, R	SIF, TXT, BioPAX L3, JSON-LD, GSEA
PathMe	-	Web application	Python (pathme)	BEL, GraphML, CSV, SIF, Node-link JSON, Cytoscape CX, GSEA
Bio2BEL	-	-	Python (bio2bel)	BEL, GraphML, CSV, SIF, Node-link JSON, Cytoscape CX, GSEA

Supplementary File S2: Some useful links to resources presenting the structure of the different data formats presented in this manuscript.

PSI-MITAB2.8 (GitBook with column definitions):
https://psicquic.github.io/MITAB28Format.html (accessed 29.06.2020)
BEL (official documentation): https://language.bel.bio and
https://biological-expression-language.github.io (accessed 29.06.2020)
GO-CAM (webpage): https://geneontology.cloud (accessed 29.06.2020)
SBMLqual (Level 3 specification webpage):
http://sbml.org/Documents/Specifications/SBML_Level_3/Packages/Qualitative_Models_(qual)
(accessed 29.06.2020)