

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 [1,2]	BioGateway App	-	-	SIF, all Cytoscape export formats
OmniPath [3,4]	OmniPath App	REST API	Python (pypath), R	SIF, BEL
NDEx [5]	CyNDEx-2 App	REST API	Java, Python, R	SIF, Cytoscape CX
Pathway Commons [6,7]	CyPath2 App	API	Java, Python, R	SIF, TXT, BioPAX L3, JSON-LD, GSEA
PathMe [8]	-	Web application	Python (pathme)	BEL, GraphML, CSV, SIF, Node-link JSON, Cytoscape CX, GSEA
Bio2BEL [9]	-	-	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 10.10.2020)

BEL (official documentation): <https://language.bel.bio> and

<https://biological-expression-language.github.io> (accessed 10.10.2020)

GO-CAM (webpage): <https://geneontology.cloud> (accessed 10.10.2020)

SBMLqual (Level 3 specification webpage):

[http://sbml.org/Documents/Specifications/SBML_Level_3/Packages/Qualitative_Models_\(qual\)](http://sbml.org/Documents/Specifications/SBML_Level_3/Packages/Qualitative_Models_(qual))

(accessed 10.10.2020)

References

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