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Knowledge Graphs And Bayesian Networks Analyses To Elucidate Transformation Products Filiations During Wastewater Treatment: Application To Sulfamethoxazole (SMX)

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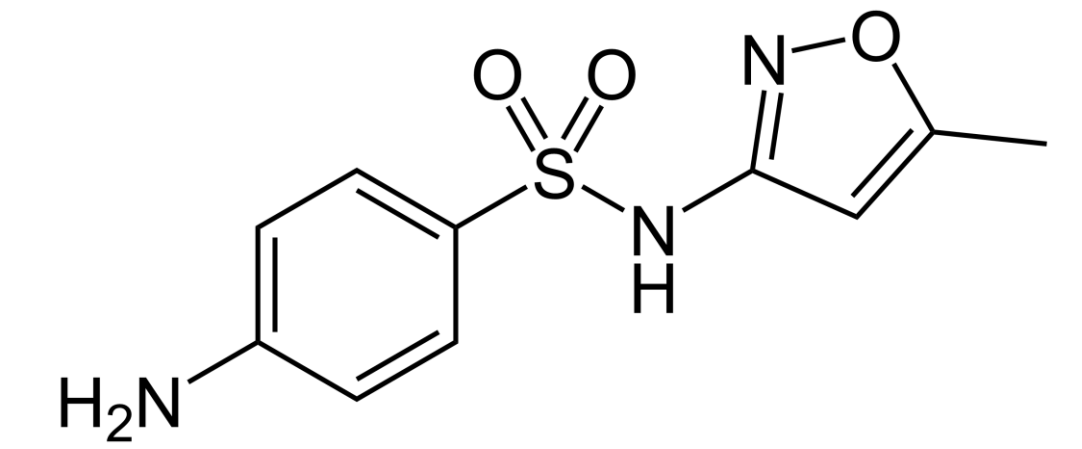
UR REVERSAAL

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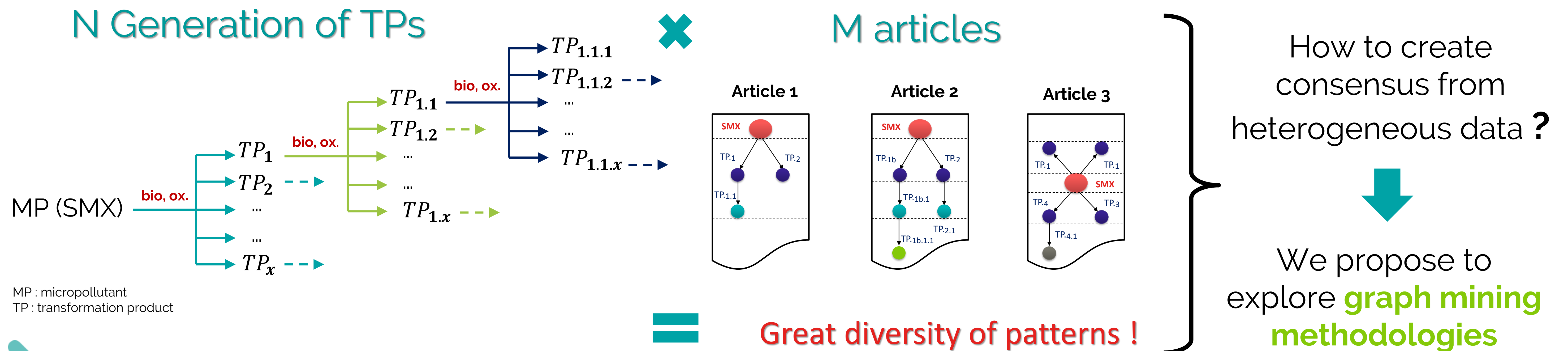
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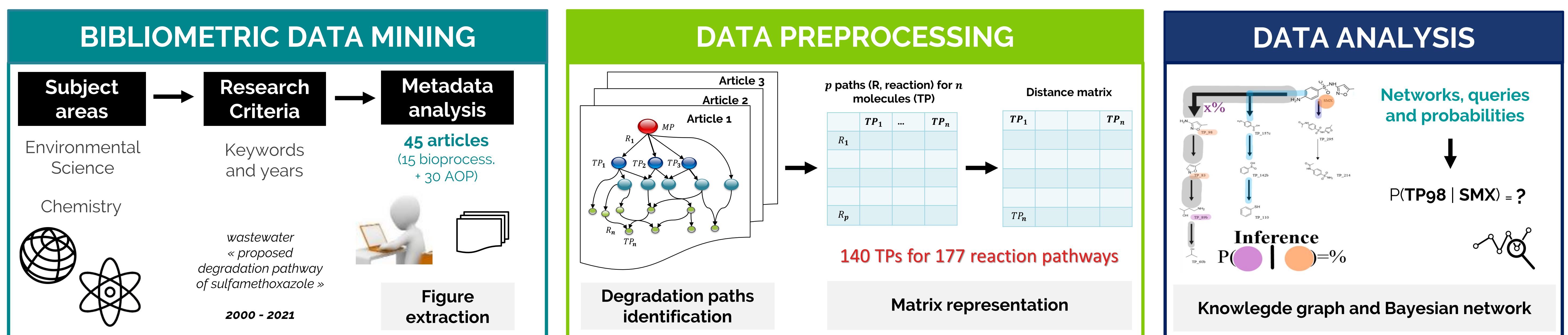
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CONTEXT AND IDEA



METHODOLOGY

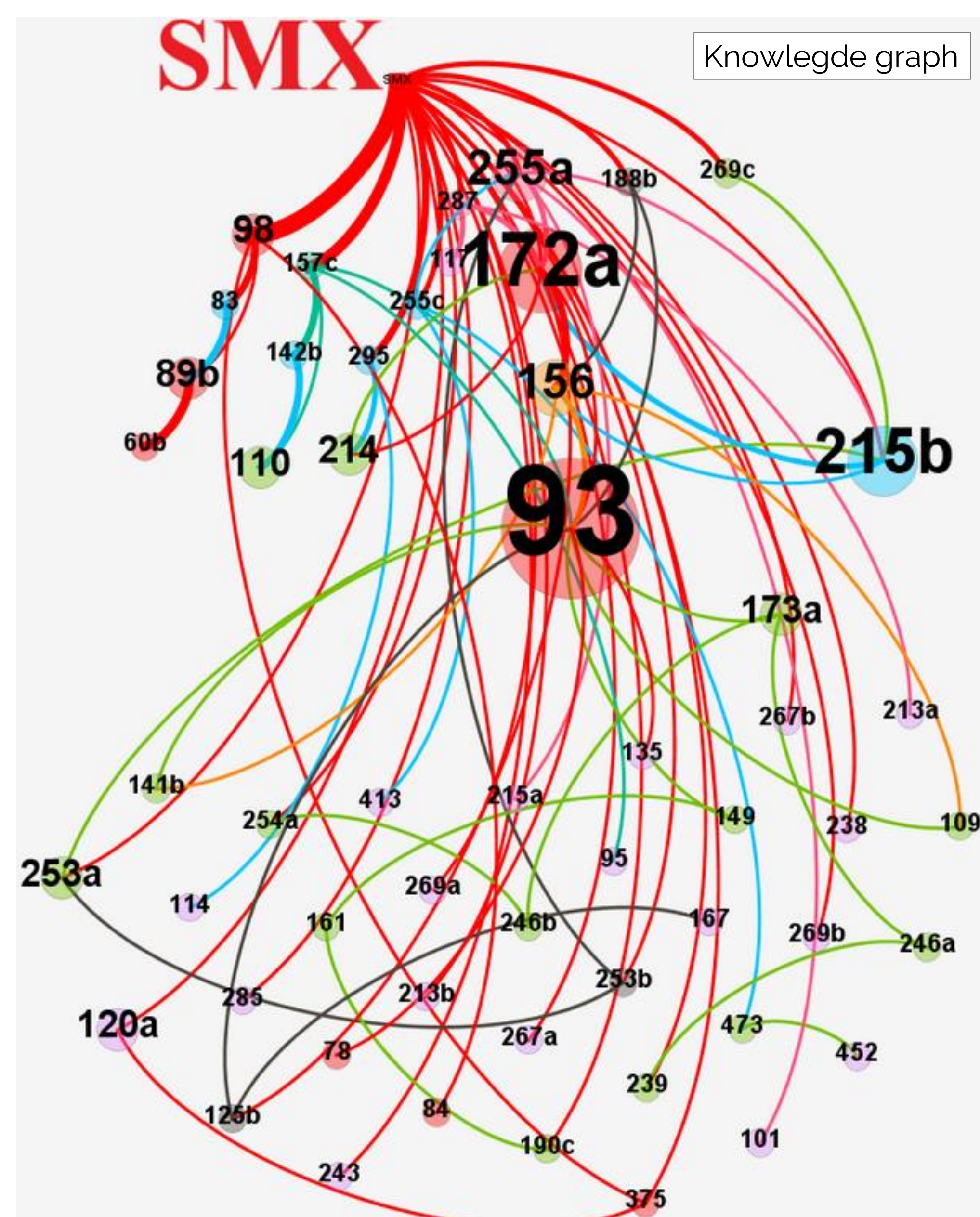


RESULTS AND PERSPECTIVES

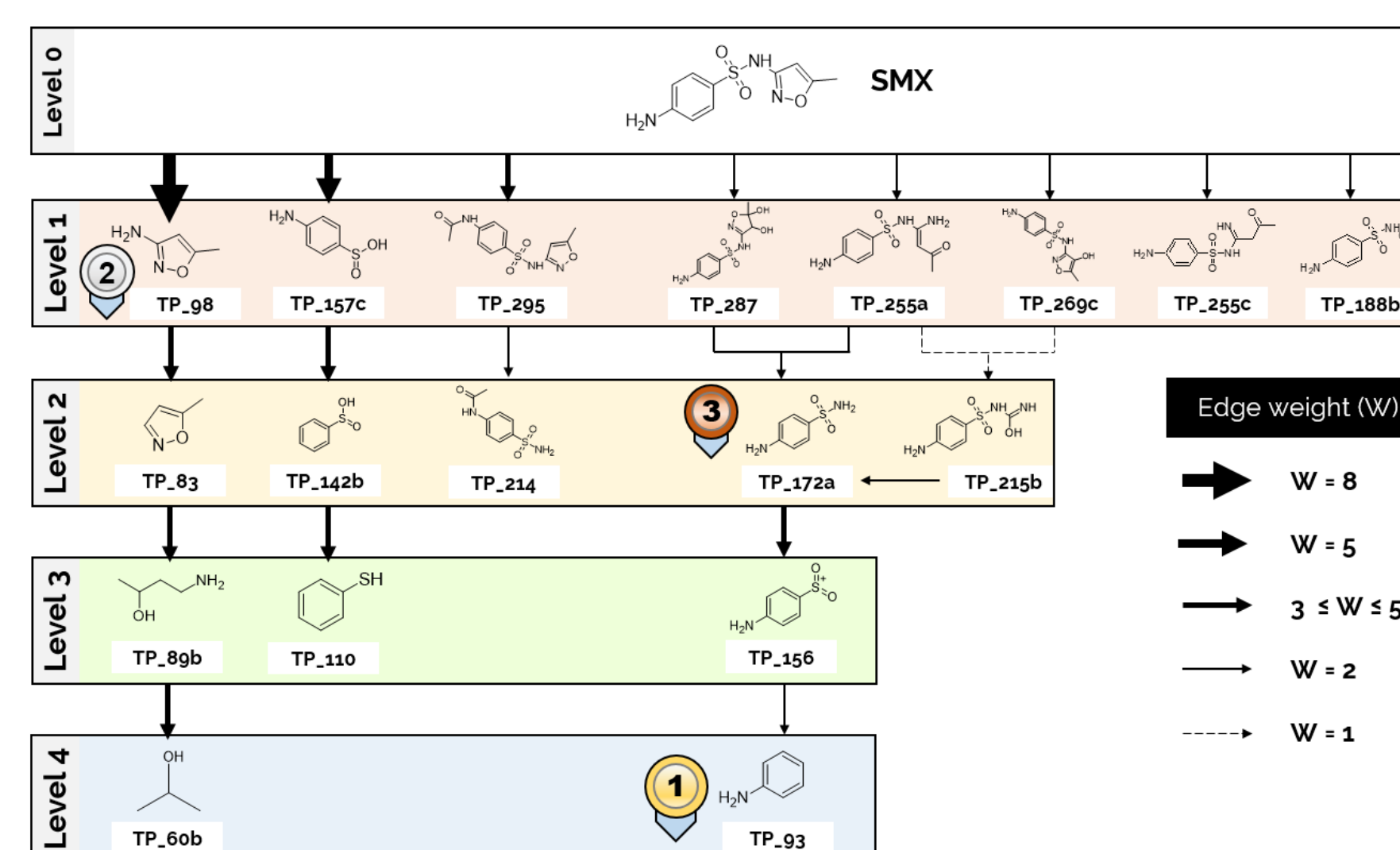
Degradation network of the SMX obtained for biological processes - based on bibliometric analysis - was plotted with Gephi software.

The size of each link (or edge) reflects the recurrence of the pathways considered, giving an indication of the **most reported reaction pathways** (SMX > TP₉₈).

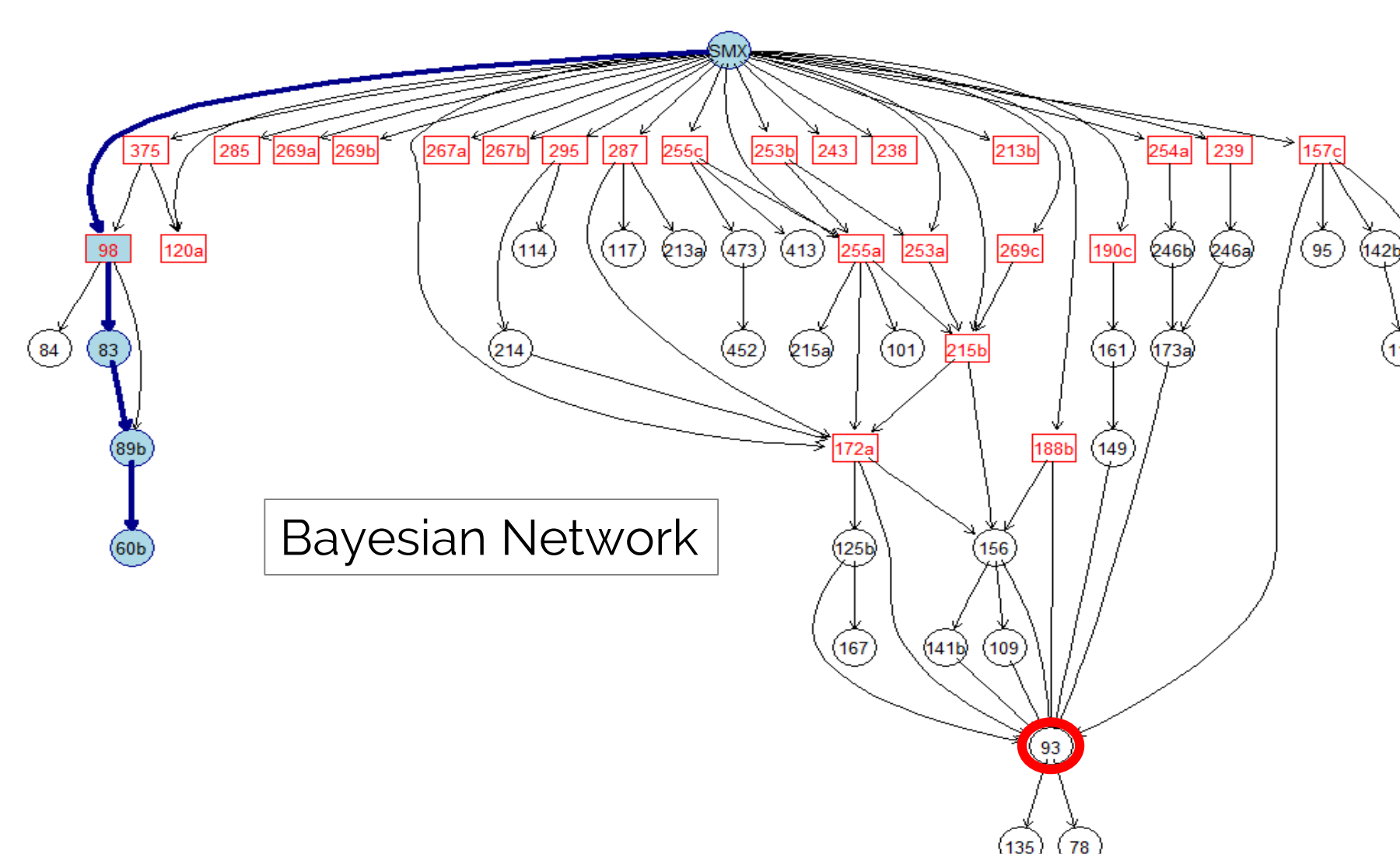
The size of the nodes represents the probability of producing a molecule from several reaction pathways (TP₉₃).



Simplified degradation scheme obtained from the knowledge graph. The three more reported TPs (TP₉₃ > TP₉₈ > TP_{172a}) are represented with medals. Edge weights are reported.



Bayesian networks (BN) were used for inference queries and to draw degradation tree after with structure initialization. Highlighted path (blue) is the most recurrent degradation way.



Queries (react. pathway)	Probability
P (TP ₉₈ SMX)	19 %
P (TP ₈₃ SMX, TP ₉₈)	37 %
P (TP _{89b} SMX, TP ₉₈)	50 %
P (TP _{60b} SMX, TP ₉₈ , TP ₈₃ , TP _{89b})	100 %

CONCLUSION

No methodology for processing and consolidating data from degradation pathways are considered in the literature.

Inspired by social networks, we proposed to explore graph methodologies and attempts to respond to this lack, to create consensus on the basis of studies where data are widely dispersed.

Graphical models shed new light on TP filiations, allowing, to visualize the degradation network, determine reactions probabilities and preferred reaction pathways.

To date, the part of the database enrichment is done manually by updating the articles and identifying new molecules and reaction pathways. The most ambitious perspective is the automation of the database enrichment phase.

