## **Supplementary Material**

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## 1 **1** Training details

<sup>2</sup> For both experiments, toxicity estimation of PFAS molecules [1] <sup>1</sup> and biodegradability of general

<sup>3</sup> molecules [2], we divided the datasets into: 60% for training purposes, 20% for validation purposes,

<sup>4</sup> and 20% for testing purposes. In both cases, the divisions have been made following the original

5 papers in order to have a fair comparison with the state-of-the-art algorithms.

<sup>6</sup> Table 1 refers to the hyper-parameters considered for the toxicity estimation task.

Table 1: MULTIMODAL-MOLFORMER hyper-parameters for toxicity prediction considering the LDToxDB dataset.

Hyper-parameter	Value
Device	cuda
GPU	1
Batch Size	32
Number of heads	12
Number of embeddings	768
Dropout	0.1
Learning rate	3e-5
Number of workers	8
Number of epochs	2000
Dimension of the Feed-Forward network	[797 797 797 1]

7 Table 2 refers to the hyper-parameters considered for biodegradability classification..

Table 2: MULTIMODAL-MOLFORMER hyper-parameters for biodegradability prediction.

Hyper-parameter	Value
Device	cuda
GPU	1
Batch Size	32
Number of heads	12
Number of layers	12
Number of embeddings	768
Dropout	0.1
Learning rate	3e-5
Number of workers	8
Number of epochs	2000
Dimension of the Feed-Forward network	[773 773 773 1]

8 Both experiments have been conducted in the IBM computing cluster with 32 GB of RAM memory

- 9 and a Nvidia V100 GPU.
- <sup>10</sup> The experiments conducted in this research are based on the recently introduced MOLFORMER

approach which can be accessed through this link (https://github.com/IBM/molformer).

<sup>1</sup>AI4PFAS project https://github.com/AI4PFAS/AI4PFAS.

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- 12 To extract the physico-chemical features based on the Mordred descriptors we used the library avail-
- able at http://mordred-descriptor.github.io/documentation/v0.1.0/introduction.
- 14 html [3]. To build the Markov-Blanket causal feature selection blocks we used the library available
- 15 at https://github.com/atif-hassan/PyImpetus [4]. The default parameters were used for
- the physico-chemical extraction from SMILES and to build the Markov-Blanket causal graphs.

## **17 References**

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