Improving ADMET prediction with descriptor augmentation of Mol2Vec embeddings

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The accurate prediction of ADMET (Absorption, Distribution, Metabolism, Excretion, and Toxicity) properties is crucial for early-stage drug development, enabling the reduction of late-stage attrition and guiding compound prioritization. In recent years, machine learning models have emerged as powerful tools for ADMET prediction, leveraging diverse molecular representations ranging from handcrafted descriptors to graph neural networks and language model embeddings. Despite these advances, balancing predictive performance

with computational efficiency remains a key challenge, particularly for high-throughput screening scenarios. Among unsupervised embedding methods, Mol2Vec has shown promise by capturing chemical substructure context analogously to word embeddings in natural language processing. However, its performance on comprehensive ADMET benchmarks has not been systematically assessed. In this work, we reimplement Mol2Vec with an expanded training corpus and higher embedding dimensionality, and evaluate its utility across 16 ADMET prediction tasks from the Therapeutics Data Commons (TDC). We show that while Mol2Vec embeddings alone are competitive, combining them with classical molecular descriptors and applying feature selection significantly improves performance. Our final MLP models with enhanced Mol2Vec embeddings achieved top-1 results in 10 of 16 benchmarks, outperforming all previously reported models on the TDC leaderboard in this regard, demonstrating that descriptor-enriched representations, paired even with relatively simple MLPs, can rival or exceed the performance of more complex models.

Keywords: ADMET; Mol2Vec; Machine learning; Molecular embeddings; QSAR; Drug discovery

1. Introduction

Achieving favorable pharmacokinetic and toxicity profiles, collectively referred to as ADMET (Absorption, Distribution, Metabolism, Excretion, and Toxicity), remains one of the principal challenges in modern drug development. Experimental ADMET assays, while reliable, are costly and time-consuming, making them less feasible for high-throughput screening in the early phases of drug discovery. As a result, *in silico* methods, particularly those based on Quantitative Structure–Activity/Property Relationships (QSAR/QSPR), have become essential tools for the preliminary evaluation of drug-like candidates [1].

Recent advances in machine learning (ML) have led to widespread adoption of data-driven models for ADMET prediction. Trained on extensive experimental datasets, these models can estimate pharmacokinetic and toxicity properties of compounds prior to synthesis, thereby accelerating the design–make–test cycle. Given the increasing reliance on ML models, rigorous benchmarking and transparent performance evaluation are critical for assessing their real-world applicability.

The Therapeutics Data Commons (TDC) platform addresses this need by providing standardised datasets, unified data processing tools, and an active leaderboard for comparative evaluation of ADMET prediction models [2]. TDC currently includes 22 curated

datasets relevant to drug safety and pharmacokinetics, enabling systematic comparison across a broad range of modelling approaches.

A key determinant of model performance in ADMET tasks is the molecular representation used as input. Traditional approaches rely on hand-crafted descriptors such as Extended Connectivity Fingerprints (ECFP) and Mordred descriptors [3,4], which encode molecular features based on predefined structural rules. More recently, large language models have been employed to learn molecular embeddings directly from SMILES strings, as exemplified by ChemGPT in ZairaChem [5,6].

Given the graph-like nature of molecular structures, Graph Neural Networks (GNNs) have also gained popularity [7]. These models learn molecular representations by aggregating information across atomic graphs, capturing intricate topological and chemical relationships. Leading models on the TDC leaderboard leverage GNN-based encoders for end-to-end learning. However, recent findings suggest that GNN-derived embeddings can be further improved by incorporating classical descriptors. A notable example is MapLight, which integrates multiple descriptor sets, including ECFP, Avalon [8], ErG fingerprints [9], and over 200 molecular properties, with GNN-based embeddings to achieve state-of-the-art results [10,11].

Another competitive approach is DeepPurpose, a flexible deep learning framework for drug–target interaction prediction [12]. Among its various configurations, models using Morgan or RDKit2D fingerprints with a multilayer perceptron (MLP) encoder perform particularly well on TDC ADMET benchmarks and serve as strong baselines in our comparative study.

These examples illustrate that combining diverse descriptor types, both learned and handcrafted, can significantly enhance model performance. However, the large number of features can pose challenges for model training, especially in small datasets where overfitting is a concern. To address this, feature selection techniques are commonly applied, such as variance thresholding, correlation filtering, and selection based on feature importance from Random Forest models [13]. We decided to explore the application of Mol2Vec, an unsupervised embedding technique originally inspired by Word2Vec, and enrich this embedding with additional chemically relevant features [14,15]. Mol2Vec represents molecules as continuous vectors by learning substructure embeddings in analogy to words in natural language, effectively capturing chemical context while mitigating issues such as high dimensionality and bit collisions inherent in traditional fingerprints [16].

In this study, we reimplemented Mol2Vec with an expanded corpus and increased embedding dimensionality (from 300 to 512) to better capture molecular diversity. We then

evaluated the resulting embeddings on the 16 most relevant and widely used ADMET tasks from the TDC benchmark suite, using combinations of Mol2Vec with various descriptor types (e.g., physicochemical properties, ECFP, Mordred, Avalon). Through systematic feature selection and model optimisation, we demonstrate that the Mol2Vec embeddings with additional descriptors and automated feature selection achieve top ranking in 10 out of 16 tested benchmarks, the absolute best among all TCD techniques, highlighting its utility as an efficient representation for ADMET modelling. The general scheme is displayed in Figure 1.

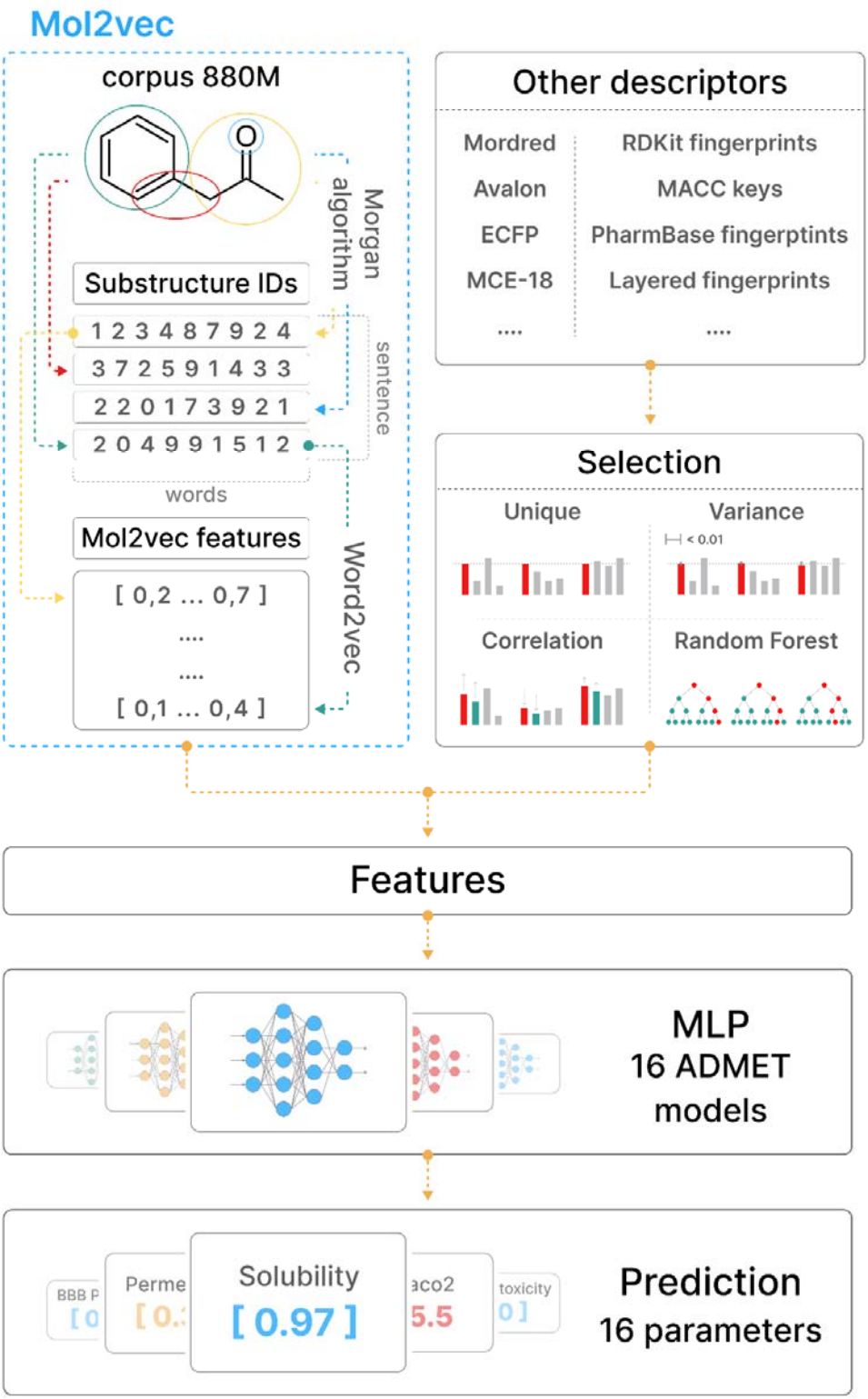

Figure 1. General Workflow for ADMET Prediction Using Mol2Vec Descriptor Augmentation. The pipeline begins with the extraction of molecular substructures using the Morgan algorithm applied

to an 880-million compound corpus from ZINC20, generating sequences of substructure IDs (analogous to "sentences") that are used to train Mol2Vec embeddings via a Word2Vec Skip-gram model. These Mol2Vec embeddings are then combined with various traditional molecular descriptors to form a comprehensive feature set. A feature selection module (using uniqueness filtering, variance thresholding, correlation pruning, and Random Forest importance scoring) reduces this high-dimensional input space. The selected features are then fed into 16 task-specific multilayer perceptron (MLP) models to predict key ADMET properties on 16 TDC benchmarks.

2. Materials and Methods

Mol2Vec is an unsupervised method for generating vector embeddings of molecular substructures, which can subsequently be used as input features for supervised learning tasks, such as ADMET prediction in our case. This section describes our Mol2Vec reimplementation, including corpus preparation and model training. We also detail the training and evaluation of ADMET models, focusing on how Mol2Vec embeddings were combined with additional molecular descriptors, the ADMET benchmark datasets used, and the overall training procedure.

2.1. Corpus preparation

To construct a robust corpus for Mol2Vec training, we leveraged the ZINC20 database [17], applying a series of filters to ensure chemical relevance and data quality. Specifically, compounds were retained if they possessed a “2D representation,” exhibited “Standard reactivity,” and were flagged as “Wait OK” in terms of commercial availability. This filtering process yielded a dataset comprising 883,897,271 small molecules.

Subsequent preprocessing steps included the removal of counterions and solvent fragments, followed by the generation of canonical SMILES strings using RDKit [18], ensuring consistency and uniqueness in molecular representation. Molecular substructures were extracted using the Morgan algorithm [4] with two radial configurations: radius 0 (capturing atomic identity) and radius 1 (incorporating immediate atomic neighbourhoods). These substructures were treated as “words”, and individual molecules were represented as “sentences” comprising sequences of such words.

The resulting corpus encompassed a vocabulary of 13,278 unique molecular “words.” To mitigate overfitting and enhance generalisation during embedding training, all substructure

tokens appearing fewer than 4 times across the entire corpus were replaced with a special “UNK” token, which is in line with standard ML practices for rare token handling.

2.2. Mol2Vec embeddings generation

To generate molecular embeddings, we employed two established architectures adapted from natural language processing: Continuous Bag of Words (CBOW) and Skip-gram [19]. The CBOW approach aims to predict a target token based on its surrounding context, whereas Skip-gram performs the inverse operation, predicting contextual tokens from a given target.

We initially evaluated both Continuous Bag of Words (CBOW) and Skip-gram architectures for generating Mol2Vec embeddings. But during the experiments, we found that the Skip-gram model, configured with a context window size of 10 and a minimum substructure occurrence threshold (unseen cut-off) of 4, yielded the most effective molecular representations. This configuration was therefore adopted for all subsequent experiments and final task-specific models training.

Molecular substructure tokens, derived from the corpus as described above, were encoded into 512-dimensional vectors using the Gensim library [20]. Each molecule was represented as a single vector by aggregating the embeddings of all its constituent substructures.

2.3. ADMET benchmark datasets

In this study, we selected a subset of 16 benchmarks from the Therapeutics Data Commons (TDC) that are highly relevant to real-world drug discovery applications. These include:

1. 4 benchmarks evaluating drug absorption: Caco-2 cell permeability [21], Human Intestinal Absorption (HIA) [22], P-glycoprotein (Pgp) inhibition [23], and Oral bioavailability [24];

2. 3 benchmarks assessing distribution properties, which describe how a drug disperses throughout the body: Blood-Brain Barrier (BBB) penetration [25,26], Plasma Protein Binding Rate (PPBR) [27], and Volume of Distribution at steady state (VDss) [28];

3. 6 metabolism-related benchmarks, which evaluate how compounds are metabolised and how this affects drug exposure and efficacy: CYP2D6, CYP3A4, and CYP2C9 inhibition, as well as CYP2D6, CYP3A4, and CYP2C9 substrate classification [29];

4. 3 toxicity benchmarks, which assess potential adverse effects: Ames mutagenicity [30], Drug-Induced Liver Injury (DILI) [31], and hERG channel inhibition [32].

Among these tasks, 3 are formulated as regression problems and 13 as binary classification tasks. The dataset sizes vary from small (e.g., HIA with 578 compounds) to large-scale (e.g., CYP2D6 inhibition with 13,130 compounds).

2.4. Featurization

To generate input features for our ADMET prediction models, we evaluated several featurization strategies:

1. Mol2Vec only – serving as a baseline representation derived from unsupervised learning of molecular substructures;

2. Mol2Vec embeddings combined with physico-chemical properties – including molecular weight, logP, number of hydrogen bond donors/acceptors, number of rotatable bonds, total polar surface area, formal charge, and other descriptors listed in the Supplementary Table 1;

3. Mol2Vec embeddings with 2D Mordred descriptors – a comprehensive set of hand-crafted molecular features capturing structural and physicochemical properties;

4. Mol2Vec embeddings enriched with a wide range of additional molecular descriptors, followed by automated feature selection procedures – this composite and optimised feature set is referred to as the “Mol2Vec Best” configuration (see Table 1 for descriptor details).

Table 1. Additional molecular descriptors used in the Mol2Vec Best.

Descriptors	**Number of descriptors**	**Descriptor parameters**
Mordred descriptors;	1613	only 2D
MCE-18 descriptor;	1	–
Morgan fingerprints;	28672	bits: [512, 1024, 2048]; radius: [1, 2, 3, 4]; branches: [True, False]
RDKit fingerprints;	25088	bits: [512, 1024, 2048]; max path: [1, 2, 3, 4, 5, 6, 7]

Layered fingerprints;	25088	bits: [512, 1024, 2048]; max path: [1, 2, 3, 4, 5, 6, 7]
Atom fingerprints;	3584	bits: [512, 1024, 2048]
Topological fingerprints;	3584	bits: [512, 1024, 2048]
Avalon fingerprints;	3584	bits: [512, 1024, 2048]
PharmBase fingerprints;	3584	–
MACCS keys.	167	–

For feature selection in the Mol2Vec Best featurization strategy, we initially considered a set of 94,729 candidate features for each ADMET task. This high-dimensional feature space was systematically reduced using a sequential four-step feature selection pipeline designed to remove redundant, non-informative, or highly correlated features:

1. Unique selector – features exhibiting a single unique value across all training samples were discarded;
2. Variance selector – features with a variance below 0.05 in the training set were excluded to eliminate those with minimal variability;
3. Correlation selector – eliminated one of any pair of features with a Pearson correlation coefficient exceeding 0.95;
4. Random Forest importance selector – retained features with an importance score greater than 0.9, as computed by a Random Forest Regressor.

These selection steps were applied sequentially to each benchmark dataset. The resulting feature subset was then concatenated with the fixed set of 512 Mol2Vec embedding features to form the final input for model training. The total number of features used for input in each final model is provided in Table 2.

Table 2. Total number of features used for input in Mol2Vec Best models after selection.

Dataset	**Selected features**	**Mol2Vec features**	**Total**
Caco2	1021	512	1533
HIA	151	512	663
Pgp Inhibition	688	512	1200
Bioavailability	1171	512	1683

BBB	1329	512	1841
PPBR	1997	512	2509
VDss	1613	512	2125
CYP2C9 Inhibition	6795	512	7307
CYP2D6 Inhibition	7588	512	8100
CYP3A4 Inhibition	7065	512	7577
CYP2C9 Substrate	1124	512	1636
CYP2D6 Substrate	7588	512	2109
CYP3A4 Substrate	7065	512	1776
hERG	794	512	1306
AMES	3130	512	3642
DILI	639	512	1151

In the following sections, we provide more detailed discussion of ADMET models trained using two specific featurization strategies: Mol2Vec only, which serves as a baseline for evaluating the utility of our reimplemented Mol2Vec approach, and the Mol2Vec Best configuration, which incorporates a broad set of additional molecular descriptors, followed by systematic feature selection. This enhanced configuration consistently achieves superior predictive performance across benchmarks. Results for models trained with other featurization strategies are not discussed, but are summarized in Supplementary Table 3.

2.5. ADMET models training

For each ADMET prediction task, a separate Multilayer Perceptron (MLP) model [33] was trained using a task-specific hyperparameter configuration. The model architecture was defined by a fixed set of candidate values for all tunable parameters, which were optimised independently for each dataset.

Hyperparameter optimisation was performed using the Optuna framework v3.3.0 [34], leveraging the Tree-structured Parzen Estimator (TPE) algorithm [35] with standard parameters. The optimisation process was conducted separately for each of the 16 TDC benchmarks, resulting in a distinct set of optimal hyperparameters for each task. Parameters subject to optimisation included:

- Number of hidden layers (ranging from 1 to 5),

- Number of hidden units per layer,
- Dropout rates (from 0.0 to 0.5),
- Activation function (chosen from ELU, ReLU, PReLU, or Leaky ReLU) [36],
- Batch size,
- Weight decay
- Learning rate (lr).

Model training for all benchmarks used the Adam optimizer [37] with the learning rate optimized by Optuna. Each model was trained for 100 epochs, and the number of trials for the tuning process was set to 200. Scaffold-based train/test splits provided by the TDC were used for training. Performance metrics for each endpoint are reported as the mean ± standard deviation, in accordance with TDC evaluation standards.

The full list of optimised hyperparameters for the Mol2Vec Best featurization strategy across all datasets is available in Supplementary Table 2.

3. Results and Discussion

Table 3 provides a comparative summary of the current state of the TDC leaderboard, highlighting several representative models that employ distinct molecular featurization strategies. These models were specifically selected for inclusion due to their diversity in encoding approaches and their relevance to our study.

In particular, MapLight, a top-performing model across multiple ADMET tasks, utilizes a combination of classical fingerprints and graph-based representations. Its enhanced variant, MapLight + GNN, further integrates graph neural network embeddings and consistently achieves top-1 rankings [38].

ZairaChem employs an ensemble of diverse molecular encoding methods, including language model-based representations, and demonstrates strong performance, although it is limited to classification tasks [6].

DeepPurpose is based on an encoder-decoder architecture that leverages Morgan fingerprints as input to a multilayer perceptron (MLP) encoder, followed by a decoder to predict biological activity. We include DeepPurpose in this comparison due to its architectural similarity to our baseline model employing Mol2Vec embeddings only [12].

Mol2Vec only models show competitive results relative to these benchmarks and surpass the model with the closest architecture – “DeepPurpose Morgan fingerprint + MLP encoder”, validating the utility of unsupervised substructure embeddings for ADMET prediction (Table

3). However, integrating additional molecular descriptors with systematic feature selection applied, as implemented in the Mol2Vec Best configuration, substantially improves predictive performance across most benchmarks. Mol2Vec Best ranks first in 10 out of 16 studied benchmarks, which is the absolute best among all TDC techniques. For Maplight+GNN this value is 8, and the other techniques only show the best ranks in 2-3 benchmarks.

Table 3. Comparison of TDC leaderboard (as of July 2025) and Mol2Vec-based ADMET models. Model ranks for each ADMET task are reported. The best models for each task are highlighted.

	Models in the TDC leaderboard				**Mol2Vec-based**	
ADMET tasks	**MapLight**	**MapLight + GNN**	**ZairaChem**	**DeepPurpose (Morgan FP)**	**Mol2Vec Only**	**Mol2Vec Best**
Caco-2	1	4	–	17	10	7
HIA	3	2	4	13	10	1
Pgp-inh	3	1	10	16	10	1
Bioavailability	3	1	2	13	8	1
BBB	1	3	5	–	2	1
PPBR	2	1	–	15	14	1
VDss	2	1	–	8	13	4
CYP2D6-inh	5	1	4	13	9	3
CYP3A4-inh	3	1	8	12	11	4
CYP2C9-inh	4	1	6	12	13	4
CYP2D6-sub	5	2	1	10	7	1
CYP3A4-sub	3	2	6	8	12	1
CYP2C9-sub	2	3	7	6	16	1
hERG	3	1	4	13	11	1
AMES	3	2	1	12	12	1
DILI	6	3	1	14	11	4
Count of first ranks	2	8	3	0	0	10

3.1. Absorption benchmarks

We achieved top-ranking positions in three out of four absorption-related classification tasks on the TDC leaderboard (Table 4). For all endpoints, excluding Caco-2 permeability, the incorporation of additional molecular descriptors combined with feature selection in the Mol2Vec Best configuration resulted in substantial performance improvements over the Mol2Vec Only baseline. These enhancements were sufficient to elevate our models to first place in the respective benchmark rankings.

In contrast, the performance gain for the Caco-2 task was minimal, with the Mol2Vec Best model reaching only 7th place. This outcome suggests that the additional descriptors do not provide substantial predictive value for this specific endpoint, possibly due to the limited relevance of the added features or inherent noise in the dataset. Notably, top-performing models in this benchmark category, such as SimGCN [39] and MapLight GNN, utilize graph neural network architectures, indicating that GNN-based encodings may better capture the molecular features relevant to a complex combination of passive and active membrane permeability.

Table 4. Performance comparison of the TDC top 1 model and Mol2Vec-based models for absorption tasks. Arrows indicate whether higher (↑) or lower (↓) values represent better performance.

			Mol2Vec Only		**Mol2vec Best**	
Task	**Metric**	**TDC Best**	**Value**	**Rank**	**Value**	**Rank**
Caco-2	MAE ↓	0.276 ± 0.005	0.377 ± 0.029	10	0.315 ± 0.017	7
HIA	ROC-AUC ↑	0.990 ± 0.002	0.961 ± 0.018	10	0.996 ± 0.001	1
Pgp-inh	ROC-AUC ↑	0.938 ± 0.002	0.899 ± 0.008	10	0.948 ± 0.004	1
Bioavailability	ROC-AUC ↑	0.748 ± 0.006	0.633 ± 0.027	8	0.776 ± 0.027	1

3.2. Distribution benchmarks

Our models achieved top-tier performance in two out of the three distribution-related tasks from the TDC benchmark suite (Table 5). Notably, the Mol2Vec-only model attained second place in the Blood-Brain Barrier (BBB) penetration task, despite the absence of additional descriptors. This strong performance indicates that the Mol2Vec embeddings alone effectively capture key structural and physicochemical features relevant to BBB permeability.

For the remaining tasks, the Mol2Vec Best configuration further enhances performance and secures leading positions on the leaderboard.

Table 5. Performance comparison of the TDC top 1 model and Mol2Vec-based models for distribution tasks. Arrows indicate whether higher (↑) or lower (↓) values represent better performance.

			Mol2Vec Only		Mol2Vec Best	
Task	**Metric**	**TDC Best**	**Value**	**Rank**	**Value**	**Rank**
BBB	ROC-AUC ↑	0.920 ± 0.003	0.916 ± 0.003	2	0.930 ± 0.004	1
PPBR	MAE ↓	7.526 ± 0.106	10.964 ± 0.248	14	7.470 ± 0.192	1
VDss	Spearman ↑	0.713 ± 0.007	0.312 ± 0.057	13	0.646 ± 0.026	4

3.3. Metabolism benchmarks

Our Mol2Vec Best models demonstrated superior performance on the majority of cytochrome P450 substrate classification tasks within the TDC benchmark suite (Table 6). While the Mol2Vec Only models underperformed relative to state-of-the-art competitors, the incorporation of additional molecular descriptors in the Mol2Vec Best configuration resulted in substantial performance gains. This enhancement enabled our models to achieve top rankings across multiple CYP-related tasks. Notably, other high-performing models on the TDC leaderboard include MapLight GNN, which excels at CYP inhibition prediction, and ZairaChem, particularly for CYP2C9 substrate classification. Overall, these results underscore the critical role of enriched molecular representations in capturing the complex biochemical determinants of drug metabolism.

Table 6. Performance comparison of the TDC top 1 model and Mol2Vec-based models for metabolism tasks. Arrows indicate whether higher (↑) or lower (↓) values represent better performance.

			Mol2Vec Only		Mol2Vec Best	
Task	**Metric**	**TDC Best**	**Value**	**Rank**	**Value**	**Rank**
CYP2D6-inh	PR-AUC ↑	0.790 ± 0.001	0.632 ± 0.016	9	0.726 ± 0.004	3
CYP3A4-inh	PR-AUC ↑	0.916 ± 0.000	0.837 ± 0.006	11	0.884 ± 0.001	4

CYP2C9-inh	PR-AUC ↑	0.859 ± 0.001	0.733 ± 0.011	13	0.800 ± 0.001	4
CYP2D6-sub	PR-AUC ↑	0.736 ± 0.024	0.678 ± 0.035	7	0.821 ± 0.008	1
CYP3A4-sub	ROC-AUC ↑	0.667 ± 0.019	0.598 ± 0.042	12	0.776 ± 0.015	1
CYP2C9-sub	PR-AUC ↑	0.441 ± 0.033	0.345 ± 0.033	16	0.556 ± 0.055	1

3.4. Toxicity benchmarks

Our Mol2Vec Best models outperformed current state-of-the-art approaches across all three TDC toxicity endpoints: hERG channel inhibition, Ames mutagenicity, and drug-induced liver injury (DILI) (Table 7). In contrast, the Mol2Vec Only models exhibited suboptimal performance, indicating that unsupervised substructure embeddings alone are insufficient to capture the complex biological signals associated with toxicity. The substantial performance gains highlight the importance of integrating diverse molecular descriptors with targeted feature selection. These improvements are particularly evident when compared to strong baseline models such as MapLight GNN (notably effective for hERG) and ZairaChem (which performs well on Ames and DILI), further validating the effectiveness of our composite feature strategy.

Table 7. Performance comparison of the TDC top 1 model and Mol2Vec-based models for toxicity tasks. Arrows indicate whether higher (↑) or lower (↓) values represent better performance.

			Mol2Vec Only		**Mol2Vec Best**	
Task	**Metric**	**TDC Best**	**Value**	**Rank**	**Value**	**Rank**
hERG	ROC-AUC ↑	0.880 ± 0.002	0.753 ± 0.03	11	0.897 ± 0.003	1
AMES	ROC-AUC ↑	0.871 ± 0.002	0.808 ± 0.004	12	0.876 ± 0.002	1
DILI	ROC-AUC ↑	0.925 ± 0.005	0.863 ± 0.034	11	0.964 ± 0.004	1

4. Conclusion

This study presents a systematic evaluation of Mol2Vec embeddings for ADMET property prediction, demonstrating that lightweight, unsupervised molecular representations can achieve strong performance when combined with classical descriptors and rigorous feature selection. By retraining Mol2Vec on an expanded chemical corpus and increasing the embedding dimensionality to 512, we significantly improved its capacity to capture structural

and physicochemical information. While Mol2Vec alone provided competitive results, outperforming certain established baselines such as DeepPurpose, its integration with descriptor sets like Mordred, Avalon, and fingerprint-based encodings yielded consistent and substantial improvements across nearly all tasks.

Our Mol2Vec Best configuration ranked first on 10 of the 16 ADMET benchmarks from the Therapeutics Data Commons and placed within the top five for nearly all others. This constitutes the highest number of top-1 benchmark results among all models reported on the TDC leaderboard. This demonstrates that descriptor-enriched embeddings, optimized through principled feature selection, can rival or even outperform more complex architectures such as GNNs and large language model-based approaches, as shown by our Mol2Vec best embedding.

5. CRediT authorship contribution statement

Roman Stratiichuk: Conceptualization, Methodology, Project administration, Data curation, Validation, Supervision, Writing – original draft. **Nazar Shevchuk:** Writing – original draft. **Roman Kyrylenko:** Writing – original draft, Writing – review & editing. **Volodymyr Vozniak:** Software, Formal analysis, Investigation, Data curation, Visualization. **Ihor Koleiev:** Methodology, Resources, Investigation, Data curation. **Taras Voitsitskyi:** Resources, Software. **Zakhar Ostrovsky:** Resources, Software. **Ivan Khropachov:** Resources, Software. **Valerii Vasylevskyi:** Data curation, Validation. **Sasha Korogodski:** Data curation, Validation. **Vladyslav Husak:** Validation, Data curation. **Serhii Starosyla:** Methodology, Project administration, Supervision. **Semen Yesylevskyy:** Methodology, Project administration, Supervision, Funding acquisition, Writing – review & editing. **Alan Nafiiev:** Conceptualization, Methodology, Project administration, Supervision.

6. Conflicts of interest

All authors but Zakhar Ostrovsky and Volodymyr Vozniak are employees of Receptor. AI INC. Serhii Starosyla, Alan Nafiiev and Semen Yesylevskyy have shares in Receptor.AI INC.

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