Less for More: Enhanced Feedback-aligned Mixed LLMs for Molecule Caption Generation and Fine-Grained NLI Evaluation

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Abstract

Scientific language models drive research innovation but require extensive fine-tuning on large datasets. This work enhances such models by improving their inference and evaluation capabilities with minimal or no additional training. Focusing on molecule caption generation, we explore synergies between alignment fine-tuning and model merging in a cross-modal setup. We reveal intriguing insights into the behaviour and suitability of such methods while significantly surpassing state-of-the-art models. Moreover, we propose a novel atomic-level evaluation method leveraging off-the-shelf Natural Language Inference (NLI) models for use in the unseen chemical domain. Our experiments demonstrate that our evaluation operates at the right level of granularity, effectively handling multiple content units and subsentence reasoning, while widely adopted NLI methods consistently misalign with assessment criteria.

1 Introduction

AI in Chemistry is essential for developing scalable and cost-effective scientific solutions, such as pioneering drugs (Ferguson and Gray, 2018), advanced materials (Kippelen and Brédas, 2009), and improved chemical processes (Zhong et al., 2023). The vast search spaces in which these solutions reside make chemical language models crucial for accelerating scientific discovery (AI4Science and Quantum, 2023; Zhang et al., 2023). Recent trends have led to the use of multimodal models to learn molecular and linguistic representations, either in separate but coordinated spaces (Edwards et al., 2021, 2022; Liu et al., 2023a), in a common space (Liu et al., 2023b), or through dual approaches (Luo et al., 2023; Christofidellis et al., 2023). These models often rely heavily on extensive supervised fine-tuning. However, merely increasing model size and data does not guarantee improvement (Tirumala et al., 2022; Xu et al., 2023). Thus we propose focusing on novel training methods to improve molecule language models.

Here we enhance molecule language models using minimal training by leveraging synergies between alignment fine-tuning (Ouyang et al., 2022) and model merging (Yang et al., 2024) in a cross-modal setup. Specifically, we focus on molecule-language translation, using as little as 10% of the training data (Edwards et al., 2024). Figure 1 illustrates our proposed three-step process.

Model merging, a technique for fusing models fine-tuned on different tasks, builds a versatile model without needing the original training data or expensive computation. This method has been quickly adopted in foundation models and Large Language Models (LLMs) (Yang et al., 2024). We extend this concept to a crossmodal setting by merging per-task pretrained molecule language models (step 1 in Fig. 1), deploying both weight- and subspace-based techniques to obtain universal models (§ 3.2.1).

For fine-tuning alignment, we focus on Reinforcement Learning from Human Feedback (RLHF)(Stiennon et al., 2020) to align the universal models. Although alignment has typically been used to calibrate LLM behaviour (Askell et al., 2021), we hypothesise that it can also accelerate learning in crossmodal spaces by rewarding preferred over dispreferred outputs, thus improv-

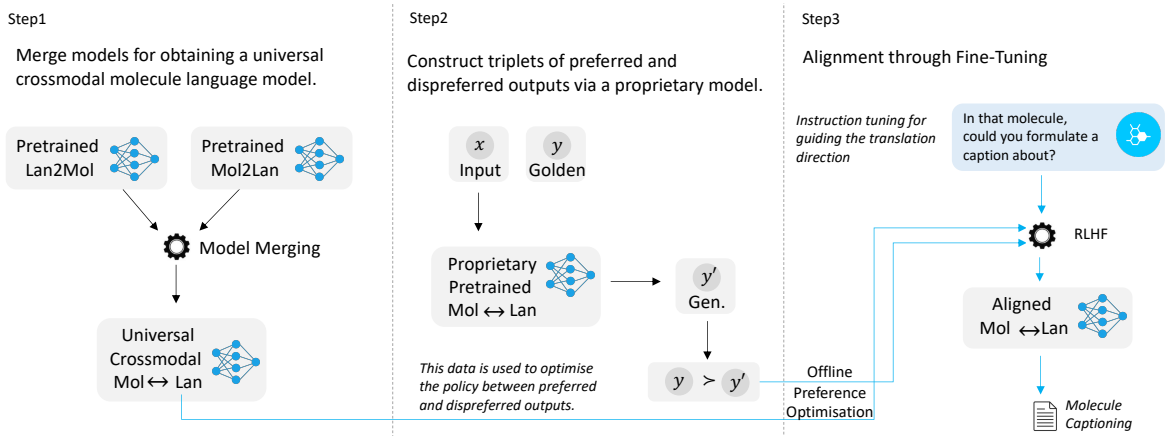

Figure 1: A diagram illustrating the three-step process to enhance molecule language models with minimal training. Black arrows indicate that no training data is required to operate the models, while blue arrows show that only a minimal amount of training data (10%) is used.

ing inference with minimal training data. We focus on optimisation algorithms using closed-form losses on offline preferences, such as Direct Preference Optimisation (DPO) (Rafailov et al., 2024), Contrastive Preference Optimisation (CPO) (Xu et al., 2024), and Kahneman-Tversky Optimisation (KTO) (Ethayarajh et al., 2024). We incorporate golden data as human preferences and dispreferred synthetic outputs generated by proprietary models into the reward signal (Step2 in Fig. 1).

We evaluate our models on out-of-distribution data using established statistical-based metrics (Sets, 2022; Edwards et al., 2022). Additionally, we use Natural Language Inference (NLI) models to assess generated text within the chemical domain. However, we argue that off-the-shelf NLI models are suboptimal for several reasons: a) they are trained on relatively short texts (Williams et al., 2018), while generated text may aggregate multiple content units that partially overlap with different sentences in the reference text (Nenkova et al., 2007); b) they are limited by the data they were trained on, making them unreliable for unseen domains (McIntosh et al., 2024); and c) they lack subsentence inference, hindering their ability to handle reordered content in generated text (see Fig. 3). Thus we propose a novel atomic-level cross-NLI approach that addresses these issues. By decomposing reference and generated texts into atomic premises and hypotheses using an LLM, we calculate probability distributions of contradiction and entailment via an NLI model and finally apply row-wise operations to obtain novel hallucination and coverage metrics (§3.3). Our findings and contributions are as follows:

- **Extensive training doesn't guarantee better models.** Models trained on large benchmark datasets exhibit memorisation effects, with performance dropping by 50% to 100% on out-of-distribution data (§ 4.2.1).
- **Alignment fine-tuning is not a panacea.** Our experiments reveal that not all fine-tuning approaches applicable to heavily trained models are effective with minimal training (§ 4.2.1).
- **Effective alignment methods balance structured learning and generalisation.** Of the alignment fine-tuning methods, only CPO managed both crossmodal agnostic and minimal training effectively (§ 4.2.1).
- **Model merging addresses inherent limitations in alignment fine-tuning**. It improves performance with minimal training, reduces dependence on human-labeled data, and provides a scalable, cost-effective alignment method for LLMs. (§ 4.2.2).
- **Our novel atomic-level cross-NLI evaluation reveals intriguing insights about performance interpretability and effectively handles multiple content units in text.** By contrast, widely adopted NLI methods consistently

misalign with assessment criteria (§ 4.2.3).

2 Related Work

2.1 LLMs for Chemistry

Existing approaches for LLMs in the chemical domain typically depend on costly pretraining with large unimodal datasets for reaction prediction and retrosynthesis (Schwaller et al., 2019; Vaucher et al., 2020), or task-specific fine-tuning for language-molecule learning (Edwards et al., 2021, 2022, 2024) and molecule editing (Liu et al., 2023a; Fang et al., 2023). Other initiatives focus on multitask learning, which involves resource-intensive pretraining and large multitask datasets (Lu and Zhang, 2022; Ross et al., 2022; Christofidellis et al., 2023; Zhang et al., 2024). By contrast, we investigate synergies between fine-tuning alignment and model merging to enhance molecule language models with minimal training.

2.2 Model Merging

Existing model merging techniques can be broadly categorised into weight-based, subspace-based, and routing-based approaches. Advanced weight-based methods typically utilise optimisation algorithms (Yang et al., 2023; Akiba et al., 2024) or geometric interpolations (Zhou et al., 2024; Goddard et al., 2024) to determine optimal task vector coefficients while preserving the capabilities of independent models. Subspace-based methods involve pruning (Yadav et al., 2023; Yu et al., 2024) or masking (Wang et al., 2024) to eliminate insignificant parameters before merging sparse models in the parameter subspace, thereby reducing task interference. By contrast, routing-based methods adaptively combine models during inference, adjusting the merge dynamically per the specific input (Muqeeth et al., 2023; Tang et al., 2024). We experiment with weight- and subspace-based merging in a crossmodal context.

2.3 Aligning LLMs

LLM alignment methods can be divided into two categories: test-time and fine-tuning. Test-time alignment techniques, such as prompt engineering and guided decoding (Khanov et al., 2024; Huang et al., 2024), adjust LLMs without altering their weights, although performance relies on the original model. Fine-tuning methods, such as RLHF (Stiennon et al., 2020; Ouyang et al., 2022), are effective but complex, requiring model training and continuous sampling. DPO (Rafailov et al., 2024) simplifies RLHF by focusing on a direct optimisation objective from PPO (Schulman et al., 2017), thereby streamlining the process to the training of supervised policy models. CPO (Xu et al., 2024) enhances efficiency by utilising a uniform reference model, which reduces memory demands. Other methods employ SFT to optimise the management of the RLHF model and parameter tuning (Ethayarajh et al., 2024; Meng et al., 2024). Here, we explore alignment fine-tuning in a crossmodal setup.

2.4 NLI-based Evaluation

NLI models are trained to determine the relationship between a *premise* and a *hypothesis*. Existing approaches either identify a sentence in the reference text as the premise (sentence-level NLI) (Nie et al., 2019b; Laban et al., 2022), or measure entailment using the entire reference as the premise (Dziri et al., 2022; Honovich et al., 2022). However, a single sentence may lack sufficient content, and using the entire reference is inefficient for long texts (Schuster et al., 2022). Context-level NLI addresses this by retrieving relevant sentences to create a short context for NLI (Nie et al., 2019a; Schuster et al., 2022; Kamoi et al., 2023), although it still does not operate at a sufficiently detailed or precise level of granularity (Nenkova et al., 2007). Here, we propose a novel atomic-level NLI evaluation for the chemical domain to tackle such limitations.

3 Methodology

3.1 Task Definition

Let (x, y) represent a pair of source and target sequences mapped to the X and Y spaces, respectively. We cast molecule caption generation (MoCG) as a crossmodal alignment task that operates on offline preference data $\mathcal{D} = \{x^{(i)}, y_w^{(i)}, y_l^{(i)}\}_{i=1}^{N}$, where x is the input, and y_w

and y_l are the preferred and dispreferred outputs, respectively, with N being the total number of pairs in $\mathcal{D}$. The goal is to learn an optimal function $f : X \leftrightarrow Y$ via a model π_θ parameterised by θ. We coordinate the molecule and caption generation tasks via instruction modelling [1].

3.2 Aligned Mixed Molecule Language Models

This section elaborates on how we obtain aligned universal molecule language models.

3.2.1 Universal Models via Model Merging

Let τ_1 and τ_2 represent task vectors [2] from pretrained molecule and caption generation models. Our goal is to obtain a multitasking cross-modal model $\Theta^{(merge)}$ without accessing training data by exploring weight-based and subspace-based merging techniques. Fig. 2 illustrates the process.

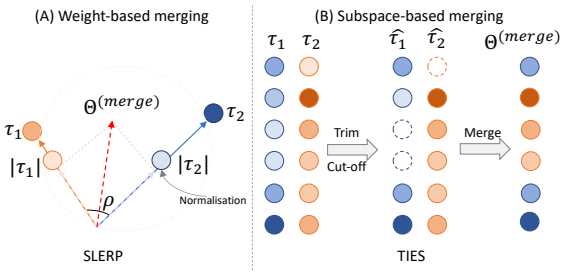

Figure 2: Model merging techniques for obtaining universal models. (A) Weight-based merging via spherical interpolation. (B) Subspace-based merging by pruning and merging parameter magnitudes. τ_1 and τ_2 are task vectors obtained from pretrained molecule and caption generation models, respectively.

Weight-based model merging: We experiment with SLERP (Goddard et al., 2024), which applies spherical interpolation to fuse model parameters. The goal is to find optimal coefficients λ_1 and λ_2 so that the merged model $\Theta^{(merge)} = \lambda_1\tau_1 + \lambda_2\tau_2$ retains the capabilities of the independent models. The coefficients are given by $\frac{\sin((1-\lambda)\cdot\rho)}{\sin(\rho)}$ and $\frac{\sin(\lambda\cdot\rho)}{\sin(\rho)}$, respectively, where $\rho = \arccos\left(\frac{\tau_1\cdot\tau_2}{|\tau_1|\cdot|\tau_2|}\right)$ is the angle between the task vectors, and λ is the merging coefficient.

Subspace-based model merging: We utilise TIES (Yadav et al., 2023) to prune the task vectors τ_1 and τ_2, retaining the top 20% parameters, resulting in refined vectors $\hat{\tau}_1$ and $\hat{\tau}_2$ (see Fig. 2 (B)). We then fuse the vectors via Task Arithmetic (Ilharco et al., 2022) to obtain the merged model as $\Theta^{(merge)} = \frac{1}{2}\sum_{i=1}^{2}\hat{\tau}_i$. During the merging process, conflicts arising from differing signs in the parameters p are resolved by aligning the pruned vectors as follows:

$$\text{Align}(\hat{\tau}_1^p, \hat{\tau}_2^p) = \begin{cases} \hat{\tau}_1^p & \text{if } |\hat{\tau}_1^p| > |\hat{\tau}_2^p| \\ \hat{\tau}_2^p & \text{if } |\hat{\tau}_2^p| \geq |\hat{\tau}_1^p| \end{cases} \quad (1)$$

3.2.2 Crossmodal Alignment Fine-tuning

Let π_{ref} be the reference policy (i.e., the universal model from model merging), π_θ the policy model being trained, parameterised by θ, and $\mathcal{D} = \{x^{(i)}, y_w^{(i)}, y_l^{(i)}\}$ the offline preference data. Our goal is to learn effective crossmodals for the MoCG task with minimal training via alignment fine-tuning. Table 1 provides an overview of the optimisation methods employed in this process.

- **SFT** minimises the difference between generated output z and target y_w by optimising model π_θ through negative log-likelihood (Eq. 2).
- **DPO** (Rafailov et al., 2024) enhances crossmodal translations using an offline preference dataset $\mathcal{D}$. It aligns model π_θ by maximising the likelihood of preference data, with reference model π_{ref}, Sigmoid function σ, and hyperparameter β (Eq. 3).
- **CPO** (Xu et al., 2024) reduces reliance on high-quality data by avoiding suboptimal translations. It modifies Eq. 3 using a uniform reference model, ensuring equal likelihood for all outputs. A behaviour cloning (BC) regulariser is injected to reflect uniform output matching, with an additional SFT term in the final loss (Eq. 4).
- **KTO** (Ethayarajh et al., 2024) utilises non-paired preference data $\mathcal{D} = \{x^{(i)}, y^{(i)}, \lambda^{(i)}\}$ where λ denotes the desirability of y. The loss is computed from the generated output z in relation to a reference z_{ref} and λ (Eq. 5).

[1] Instructions can be found in Appx. D.

[2] A task vector τ represents the model's parameters $\Theta^{(t)}$ fine-tuned for task t (Ilharco et al., 2022).

Method	Optimisation Objective
SFT	$$\min_{\theta} -\log \pi_\theta(y_w\|x) \quad (2)$$
DPO	$$\log \sigma\Big(\beta \log \frac{\pi_\theta(y_w\|x)}{\pi_{\text{ref}}(y_w\|x)} - \beta \log \frac{\pi_\theta(y_l\|x)}{\pi_{\text{ref}}(y_l\|x)}\Big) \quad (3)$$
CPO	$$\min_{\theta} \log \sigma\Big(\beta \log \pi_\theta(y_w\|x) - \beta \log \pi_\theta(y_l\|x)\Big) - \log \pi_\theta(y_w\|x) \quad \text{s.t.} \quad \mathbb{E}_{(x,y_w)\sim D}\Big[\mathbb{KL}(\pi_w(y_w\|x)\|\pi_\theta(y_w\|x))\Big] < \epsilon \quad (4)$$
KTO	$$-\lambda_w \sigma\left(\beta \log \frac{\pi_\theta(y_w\|x)}{\pi_{\text{ref}}(y_w\|x)} - z_{ref}\right) + \lambda_l \sigma\left(z_{ref} - \beta \log \frac{\pi_\theta(y_l\|x)}{\pi_{\text{ref}}(y_l\|x)}\right) \quad \text{where } z_{\text{ref}} = \mathbb{E}_{(x,y)\sim D}\left[\beta \mathbb{KL}(\pi_\theta(y\|x)\|\pi_{\text{ref}}(y\|x))\right] \quad (5)$$

Table 1: Alignment fine-tuning algorithms for the MoCG task given preference data $\mathcal{D} = \{x, y_w, y_l\}$.

3.3 Atomic-level Cross-NLI Evaluation

Our aim is to develop a method that operates at the right level of granularity, precisely capturing small distinctions and subtle nuances in captions, ensuring reliable evaluation. Atomic-level cross-NLI evaluation uses a LLM and an NLI model to assess relationships between generated and reference captions. The process begins with an LLM (Touvron et al., 2023) decomposing a (reference, generated) pair into atomic premises $\{P_i\}_{i=1}^{N}$ and hypotheses $\{H_j\}_{j=1}^{L}$, where each atomic unit conveys a single piece of information (see Appx. C). An NLI model (He et al., 2020) then constructs probabilistic distributions of entailment and contradiction by considering all possible combinations of premises and hypotheses. Finally, pooling operators match atomic hypotheses and premises in terms of both factual correctness, i.e., *hallucination*, and completeness, i.e., *coverage*. Fig. 3 illustrates this process.

Hallucination we define here as the introduction of information not present in the reference text. Given $\{(P_i, H_j)\}$, the NLI model constructs a contradiction probability distribution for each atomic hypothesis against all premises, such as $p_{j,i} = (C_{j,i}|P_i, H_j)$. This results in an $M_{L\times N}$ matrix of contradiction probabilities $C_{j,i}$ (see Fig. 3). To measure hallucination, we apply min row-wise pooling and average the matching probabilities to compute the score by the formula:

$$Hallucination = \frac{1}{L}\sum_{j=1}^{L} \min_{i} C_{j,i} \quad (6)$$

Coverage we define as atomic unit recall, representing how much reference information is present in the generated text. Unlike hallucination, here generated text forms the atomic premises (P_j) and the reference text the hypotheses (H_i). The NLI model constructs an entailment probability distribution for each H_i against all P_j, such that $p_{i,j} = (E_{i,j}|P_j, H_i)$, resulting in an $M_{N\times L}$ matrix of entailment probabilities $E_{i,j}$. To measure coverage, we apply max row-wise pooling and average the matching probabilities to compute the score given by the formula:

$$Coverage = \frac{1}{N}\sum_{i=1}^{N} \max_{j} E_{i,j} \quad (7)$$

4 Experiments

4.1 Experimental Setup

We conduct experiments training Meditron(Chen et al., 2023) on the benchmark L+M-24 (Edwards et al., 2024) dataset, using only 10% of the data for training, and evaluate on out-of-distribution data (see Appx. B for details). For alignment fine-tuning, we create synthetic dispreferred outputs generated by MolT5 (Edwards et al., 2022). Our training, validation, and test sets contain approximately 12.7k, 3.4k, and 3k samples, respectively. For evaluation, we use established statistical metrics (see Appx. E), along with our atomic-level cross-NLI evaluation method (§ 3.3).

We compare our models thus obtained against established ones trained on extensive data. *TxtChem-T5* (Christofidellis et al., 2023) is a $T5_{XL}$ multitask model trained on linguistic and molecule modalities across multiple datasets, including CheBI-20, akin to L+M-24. *ChemLLM* (Zhang et al., 2024), an InternLM2-Base-7B model, is trained on large chemical knowledge

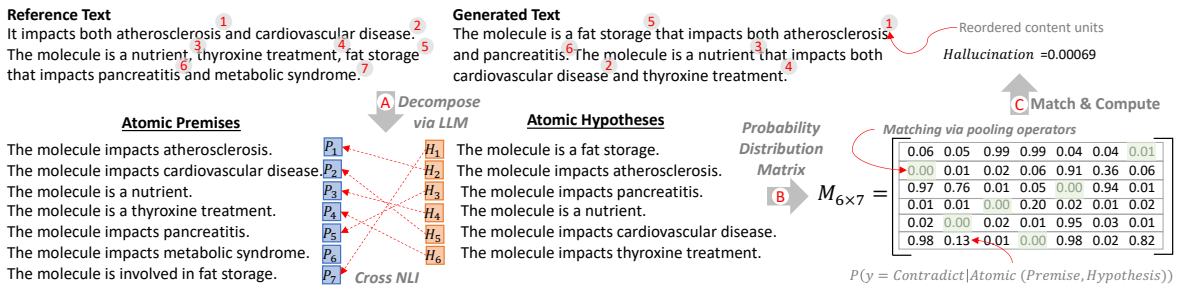

Figure 3: The process of atomic-level cross-NLI evaluation when measuring the level of hallucination.

databases using DPO, achieving GPT-4-level results. *Meditron* (Chen et al., 2023), a 7B model, is fine-tuned on the entire L+M-24 dataset. Lastly, we fine-tune Meditron with *SFT* using only 10% of the training data. We leave all the implementation details in Appx. G.

4.2 Experimental Results

4.2.1 Aligning Molecule-Language Modals with Minimal Training

We first present results for molecule language models with minimal alignment fine-tuning, initialising pretrained weights from molecule generation rather than deploying model merging (see Appx. G for details). Tables 2 and 3 summarise experimental results. Generally, benchmarking models trained on extensive data with SFT exhibit memorisation effects, with performance dropping by 50% to 100% compared to reported results, when evaluated on out-of-distribution data.

Our experiments show that not all alignment optimisations are effective in the minimal training setting. Both DPO and KTO show zero performance in caption generation when models are initialised with crossmodal weights unrelated to the task (see Table 2). However, performance improves significantly when the crossmodals are known (see Table 3). In molecule generation, DPO achieves up to 42% better performance than Meditron, trained on the full dataset, while KTO still performs poorly, likely due to overfitting (see Appx. F).

By contrast, CPO effectively handles both the crossmodal agnostic and minimal training settings, outperforming Meditron by up to 20% in caption generation and 42% in molecule generation. This is likely due to its inherent ability to balance structured learning and generalisation. It aligns with preferred data through behaviour cloning and SFT, which encourage the model to mimic expert behaviour, while reducing bias and suboptimal outcomes via a uniform reference model that assigns equal likelihood to all possible outputs.

4.2.2 Synergies Between Model Merging and Alignment Fine-tuning

Tables 4 and 5 summarise the experimental results when we incorporate model merging in alignment fine-tuning while keeping the training data the same. Combining DPO with molecule and caption crossmodals via TIES improves caption generation (see $\Delta_{DPO\text{vs}TIES+DPO}$ in Table 4) but leads to significant performance loss in molecule generation (see $\Delta_{DPO\text{vs}TIES+DPO}$ in Table 4). Conversely, fusing CPO with crossmodals via SLERP significantly boosts performance in caption generation (see $\Delta_{CPO\text{vs}SLERP+CPO}$ in Table 4) while having minimal impact on molecule generation (see $\Delta_{CPO\text{vs}SLERP+CPO}$ in Table 5), demonstrating overall gains compared to Meditron trained on the full dataset.

Overall, our experiments show that model merging can effectively address key limitations in alignment fine-tuning. By fusing pretrained models, one can enhance performance with minimal training, reducing reliance on human-labelled data, lowering training costs, minimising human bias, and improving generalisation. Examples of caption and molecule generation are provided in Appx. H.

Method	Blue-2 ↑	Blue-4 ↑	Rouge-1 ↑	Rouge-2 ↑	Rouge-L ↑	METEOR ↑
TxtChem-T5 (Christofidellis et al., 2023)	0.08	0.09	0.19	0.06	0.17	0.16
Chem-LLM (Zhang et al., 2024)	0.03	0.00	0.11	0.02	0.09	0.14
Meditron (Chen et al., 2023)	0.42	0.30	0.63	0.47	**0.49**	0.54
SFT §4.1	0.37	0.26	0.55	0.40	0.39	0.61
DPO (Rafailov et al., 2024)	0.00	0.00	0.00	0.00	0.00	0.00
CPO (Xu et al., 2024)	**0.62**	**0.45**	**0.68**	**0.50**	0.48	**0.62**
KTO (Ethayarajh et al., 2024)	0.00	0.00	0.00	0.00	0.00	0.00
$\Delta_{CPO\text{vs}MED}$	+20%	+19%	+5%	+3%	-1%	+8%

Table 2: Alignment fine-tuning results for caption generation on 3k unseen pairs. Arrows next to metrics denote value increase with performance gains. Best results are in bold. $\Delta_{CPO\text{vs}MED}$ is the performance gain of our best model, trained on 10% of the data, compared to Meditron trained on the entire dataset.

Method	BLEU ↑	Levenshtein ↓	MACCS FTS ↑	RDK FTS ↑	Morgan FTS ↑	FCD ↓	Validity ↑
TxtChem-T5	0.18	133.29	0.21	0.10	0.03	37.67	0.58
Chem-LLM	0.04	732.74	0.00	0.00	0.00	59.44	0.19
Meditron	0.43	66.16	0.35	0.29	0.19	13.64	0.57
SFT	0.30	186.99	0.70	0.62	0.41	11.14	0.98
DPO	**0.72**	**42.40**	**0.77**	0.69	**0.49**	10.47	0.99
CPO	0.71	42.65	**0.77**	**0.70**	0.48	**4.19**	**1.00**
KTO	0.23	294.63	0.03	0.03	0.02	32.64	0.06
$\Delta_{CPO\text{vs}MED}$	+29%	-23.76%	+42%	+41%	+30%	-9.45%	+41%

Table 3: Alignment fine-tuning results for molecule generation on 3k unseen pairs. Arrows next to metrics indicate whether higher or lower values denote better performance. Best results are highlighted in bold. $\Delta_{CPO\text{vs}MED}$ represents the performance gain of our best model compared to Meditron trained on the entire dataset.

4.2.3 Atomic-level Cross-NLI Evaluation

Atomic-level NLI revealed intriguing insights regarding performance interpretation. Fig. 4 shows assessment score distributions from our proposed evaluation method, comparing our top models against Meditron trained on the entire dataset. All models exhibit low hallucination, likely due to the narrow, well-defined topics that enable factually correct captions without unrelated information. However, our models excel in coverage, generating more comprehensive captions, with performance increasing to 69% compared to Meditron's 51% (Fig. 4 (B)). Examples of insights captured by our proposed evaluation are in Appx. I.

We compare our atomic-level NLI method against established approaches, including *full NLI*, which treats entire premises and hypotheses as single units, and *sentence-level NLI* (Laban et al., 2022)), which evaluates smaller parts. Using outputs from our top-performing model, CPO+SLERP, as preferred captions and those

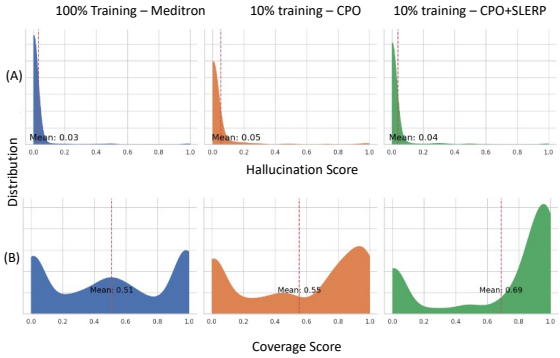

Figure 4: Score distributions from our atomic-level cross-NLI evaluation comparing (A) hallucination and (B) coverage between our top models and Meditron.

from Meditron as dispreferred ones, we measure the relative entropy in coverage score distributions. The results indicate that both full and sentence-level NLI methods misclassify preferred captions as non-entailment and dispreferred ones as entailment (Fig. 5 (B)-(D)). By con-

Fusion	Method	Blue-2 ↑	Blue-4 ↑	Rouge-1 ↑	Rouge-2 ↑	Rouge-L ↑	METEOR ↑
TIES (Yadav et al., 2023)	DPO	0.74	0.53	0.74	0.54	0.51	0.70
	CPO	0.74	0.54	0.76	0.57	0.53	0.72
SLERP (Goddard et al., 2024)	DPO	0.00	0.00	0.02	0.01	0.00	0.00
	CPO	0.73	0.53	0.76	0.56	0.53	0.71
$\Delta_{DPO vs TIES+DPO}$		+74%	+53%	+74%	+54%	+51%	+70%
$\Delta_{CPO vs SLERP+CPO}$		+11%	+8%	+8%	+6%	+5%	+9%
$\Delta_{MED vs SLERP+CPO}$		+31%	+28%	+13%	+9%	+4%	+17%

Table 4: Model merging and alignment fine-tuning results for caption generation. $\Delta_{DPO vs TIES+DPO}$, $\Delta_{CPO vs SLERP+CPO}$, and $\Delta_{MED vs SLERP+CPO}$ measure performance gains of the best-combined approaches compared to the vanilla crossmodal setting of *DPO*, *CPO*, and the benchmark *Meditron*, as reported in Table 2.

Fusion	Method	BLEU ↑	Levenshtein ↓	MACCS FTS ↑	RDK FTS ↑	Morgan FTS ↑	FCD ↓	Validity ↑
TIES	DPO	0.32	93.18	0.31	0.22	0.19	19.80	0.42
	CPO	0.68	46.91	0.72	0.65	0.45	24.50	0.94
SLERP	DPO	0.72	43.85	0.77	0.70	0.51	10.35	0.98
	CPO	0.71	44.01	0.73	0.66	0.45	11.22	0.95
$\Delta_{DPO vs TIES+DPO}$		-40%	+51%	-46%	-47%	-30%	+7.33%	+58%
$\Delta_{CPO vs SLERP+CPO}$		0%	+1.36%	-4%	-4%	-3%	+5%	-4%
$\Delta_{MED vs SLERP+CPO}$		+29%	-22.40%	+38%	+37%	+27%	-4.45%	+37%

Table 5: Model merging and alignment fine-tuning results for molecule generation. $\Delta_{DPO vs TIES+DPO}$, $\Delta_{CPO vs SLERP+CPO}$, and $\Delta_{MED vs SLERP+CPO}$ measure performance gains of the best-combined approaches from the vanilla crossmodal setting of *DPO*, *CPO*, and the benchmark *Meditron*, as reported in Table 2.

trast, atomic-level cross-NLI accurately favours preferred captions, assigning higher scores to certain cases (Fig. 5 (A)). Additionally, Kullback–Leibler divergence shows that atomic-level NLI offers better discrimination, achieving a divergence score of 0.54 compared to 0.12–0.17 for other methods, demonstrating its effectiveness in distinguishing the quality of generated captions.

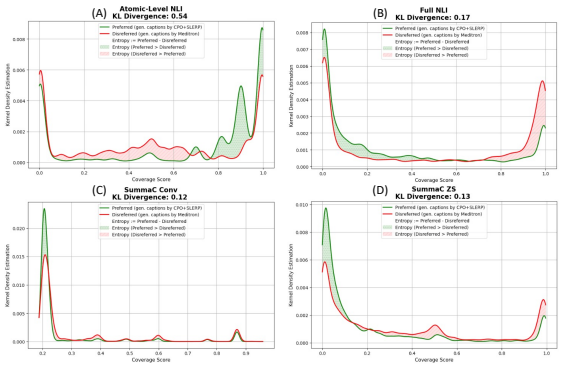

Figure 5: Relative entropy in coverage scores for preferred vs. dispreferred generated captions across atomic-level (A), full (B), and sentence-level (C & D) NLI approaches.

5 Conclusion

In this work, we address limitations of scientific language models that rely on extensive training. Focusing on molecule caption generation, we propose synergies between model merging and alignment fine-tuning with minimal training to enhance chemical language models. Our experiments show that while alignment fine-tuning performs poorly, incorporating model merging significantly outperforms extensively trained models on out-of-distribution data, offering a cost-effective approach that relies less on human-labelled data. Furthermore, we propose an atomic-level cross-NLI evaluation to overcome limitations of widely used NLI evaluation methods, which lack appropriate granularity. Our method provides valuable insight into performance interpretability and effectively handles multiple content units, where existing NLI methods consistently misalign with assessment criteria.

Limitations

In this work, we employ weight-based and subspace-based merging methods to create universal models for the MoCG task, facilitating alignment fine-tuning in a training setting with minimal data. However, both are static merging methods. This means that the merged model remain the same for all samples or tasks. Given that there are differences between input samples/tasks, the models' ability may vary when processing different samples/tasks. In the future, we aim to investigate dynamically merging models (or subsets of layers) based on the samples/tasks during the inference phase (Kang et al., 2024).

We also propose an atomic-level NLI evaluation method that successfully handles multiple content units, offering valuable insights into performance interpretability for caption generation, where widely adopted NLI methods consistently misalign with assessment criteria. However, decomposing text into atomic units can be challenging for other tasks involving complex or lengthy text. While this method captures nuanced content, there is a risk of over-fragmentation, which may lead to a loss of context or coherence in evaluation. Additionally, the effectiveness of this approach relies heavily on the LLM for decomposition and the NLI model for entailment and contradiction assessment. If either model struggles with domain-specific content (e.g., highly technical language), the evaluation could yield inaccurate or biased results. Furthermore, if generated texts introduce valid but creative or non-standard content, this approach may penalise them by classifying such deviations as contradictions or hallucinations, even when they provide accurate information. Future work will need to address these limitations across various domains.

Finally, the proposed methods in this work are tailored specifically for the chemical domain, focusing on tasks like molecule caption generation. While these techniques—such as model merging and alignment fine-tuning—show promising results within this context, their ability to generalise to other domains or scientific fields is uncertain. Different domains may have distinct data structures, tasks, and requirements, which might not align well with the crossmodal setup used here. For instance, a method optimised for chemical language and molecular structures may not work as effectively in domains like physics or biology, where the types of entities and relationships differ significantly. This potential lack of generalisation highlights the need for future research to explore the applicability of the proposed approaches in diverse scientific domains beyond chemistry, aiming to adapt and validate the methods for varying data structures and task requirements.

Ethical Considerations

The potential for generating misleading or incorrect information poses significant ethical considerations in this work, particularly given the scientific context in which the language models are applied. If the models produce inaccurate captions or misrepresent molecular characteristics, it could lead to erroneous conclusions in research and applications that rely on these outputs. This risk is particularly critical in fields like chemistry, where precise data interpretation is vital for safety, compliance, and advancing scientific knowledge. Furthermore, the reliance on automated evaluations may not adequately catch nuanced errors that human experts would recognise, potentially allowing flawed outputs to go unchecked. Therefore, ensuring that the models maintain a high standard of accuracy and reliability is essential to prevent the dissemination of misinformation, which could undermine trust in automated systems and hinder scientific progress. Addressing these ethical concerns requires implementing robust validation mechanisms and continuously involving domain experts in the evaluation process to ensure the integrity of the generated content.

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A Foundations in Alignment with RLHF

Feedback-aligned LLMs traditionally undergo fine-tuning with RLHF, where human preferences serve as a reward signal in optimisation (Stiennon et al., 2020; Ouyang et al., 2022). To train a LLM with RLHF, a reinforcement learning optimisation algorithm such as PPO (Schulman et al., 2017) is typically deployed on offline preference data, commonly involving three steps:

- **Model Training:** Typically, a model π is trained for auto-regressive language generation on a large generic corpus. This training operates under the premise that the probability distribution of a sequence of words can be broken down into the product of conditional distributions for the next word (Radford et al., 2019).
- **Reward Model Training:** A reference model π_{ref} is employed to optimise π for a downstream task. Typically, the π_{ref} model undergoes fine-tuning with an auto-regressive objective, using data pertinent to the downstream task. This often involves instruction tuning π_{ref} to regulate the generated outputs.
- **Reinforcement Learning:** The optimisation of π with respect to π_{ref} operates on a triple dataset $\mathcal{D} = \{x, y_w, y_l\}$, where x represents the input, and y_w and y_l denote preferred and dispreferred outputs, respectively, such that $y_w \succ y_l$ for x. In the Bradley–Terry model (Bradley and Terry, 1952), the probability of y_w being preferred over y_l in pairwise comparisons can be formulated as follows:

$$p^*(y_w \succ y_l|x) = \sigma(r^*(x, y_w) - r^*(x, y_l)) \tag{8}$$

Here, σ represents the logistic function, and r^* denotes the "true" reward function that underlies the preferences. As obtaining the true reward directly from a human would be prohibitively expensive, a reward model r_ϕ is trained to act as a surrogate. This is achieved by minimising the negative log-likelihood in human preference data;

$$\mathcal{L}(r_\phi) = -\mathbb{E}_{(x,y_w,y_l)\sim\mathcal{D}}[\log \sigma(r_\phi(x, y_w) - r_\phi(x, y_l))] \tag{9}$$

Additionally, the Kullback-Leibler (KL) divergence between the outputs generated by π_{ref} and the parameterised π_θ models serves as an additional reward signal, ensuring that the generated responses closely align with the reference model. Consequently, an optimal model π_θ is one that maximises;

$$\mathbb{E}_{(x\in\mathcal{D},y\in\pi_\theta)}[r_\phi(x, y)] - \beta\mathcal{D}_{\text{KL}}(\pi_\theta(y \mid x) \,||\, \pi_{\text{ref}}(y \mid x)) \tag{10}$$

where β is parameter typically $\in [0.1, 0.5]$.

Human-aware Loss Functions (HALOs):

Definition 1 (HALOs) *Let $x \in X$ and $y \in Y$ denote an input and output respectively. An $f : (x, y) \to \mathbb{R}$ is considered a human-aware loss function if it satisfies*

$$f(x, y; \theta) = t\Big(v_f(r_\theta(x, y) - \mathbb{E}_{x'\sim Q', y'\sim Q'}[r_\theta(x', y')])\Big) \tag{11}$$

with a parameterised reward function r_θ such that $\forall (x_1, y_1), (x_2, y_2) \in X \times Y$, $r_\theta(x_1, y_1) > r_\theta(x_2, y_2) \Leftrightarrow (x_1, y_1) \succ_{r_\theta} (x_2, y_2)$, reference point distributions $Q_x(X')$ and $Q_y(Y'|X')$, a value function $v_f : \mathbb{R} \to \mathbb{R}$ that is monotonic non-decreasing and concave in $(0, \infty)$, and a negative affine function t.

RLHF can present challenges due to inherent slowness and instability, especially in the case of highly varied outputs (Zheng et al., 2024). Recently, there has been a shift towards using closed-form losses in RLHF to align LLMs with human preferences. These losses are predominantly HALOs that model human biases, as discussed in (Tversky and Kahneman, 1992), aiming to maximise the margin between preferred and dispreferred generated outputs. This approach offers a mathematical equivalence with RLHF, while effectively addressing inherent limitations.

B Data

Experiments are conducted on the benchmark *L+M-24*, which integrates molecular and linguistic modalities in four key categories: biomedical; light and electricity; human interaction and

organoleptics; and agriculture and industry (Edwards et al., 2024). The dataset was created by extracting SMILES (Simplified Molecular-Input Line-Entry System) strings and their chemical properties from databases. The properties were transformed into natural language using GPT-4 templates. The training and validation subsets contain around 127k and 34k language-molecule pairs, with only 10% used for our experiments.

For evaluation, we randomly selected 3k unseen pairs from a separate dataset provided by the L+M-24 research group. The samples were drawn from 635k molecule-caption pairs included in the supplementary data for the Language + Molecules @ ACL2024 workshop [3].

C LLM Instruction for Decomposing Text into Atomic Context Units

User:
Please breakdown the following text into independent facts:
{It impacts both atherosclerosis and cardiovascular disease. The molecule is a nutrient, thyroxine treatment, fat storage that impacts pancreatitis and metabolic syndrome.}

**
IMPORTANT: No words or explanation is needed.
Only include truths that are factual.
You should NOT include any prior knowledge, and take the text at face value when extracting facts.
**
Assistant:
- The molecule impacts atherosclerosis. - The molecule impacts cardiovascular disease. - The molecule is a nutrient. - The molecule is a thyroxine treatment. - The molecule impacts pancreatitis. - The molecule impacts metabolic syndrome. - The molecule is involved in fat storage.

Figure 6: Instruction for decomposing text into atomic content units conveying one piece of information.

D Instructions for Molecule Language Translation

Below is an instruction that describes a task, paired with an input that provides further context.
Write a response that appropriately completes the request.

Instruction: You are a researcher. You can come up captions based on your existing knowledge.
Captions are given against the following input. You should be as detailed as possible.

Input: Molecule: {source molecule}
In that molecule, could you formulate a caption about?

Response:{target caption}

Instruction for caption generation, i.e., $M \rightarrow L$

Below is an instruction that describes a task, paired with an input that provides further context.
Write a response that appropriately completes the request.

Instruction: You are a researcher. You can come up molecule smile strings based on your existing knowledge.
Molecule smile strings are given against the following input. You should be as detailed as possible.

Input: Caption: {source caption}
In that caption, could you generate a molecule smile string?

Response: {target molecule}

Instruction for molecule generation, i.e., $L \rightarrow M$

E Evaluation Metrics

For performance evaluation, we employ established metrics from the literature (Sets, 2022; Edwards et al., 2022). In translation from molecule to language, we assess using BLEU-2, BLEU-4, ROUGE-1, ROUGE-2, ROUGE-L, and METEOR metrics. For translation from molecule to language, evaluation metrics include BLEU, Levenshtein distance, fingerprint metrics (MACCS, RDK, and Morgan), Fréchet ChemNet Distance (FCD), and molecule validity metrics. The anno-

[3] https://github.com/language-plus-molecules/LPM-24-Dataset

tations in the result tables indicate whether higher or lower values indicate superior performance.

F Training Efficiency

Figure 7: Training efficiency across alignment fine-tuning methods

G Implementation Details

All implementations used Meditron (Chen et al., 2023) as the backbone model, known for its performance on L+M-24. For alignment fine-tuning experiments, we initialised Meditron crossmodals, trained for molecule generation [4]. For the model merging experiments, we combined Meditron weights trained on MoCG tasks in a 19:1 ratio. This ratio aimed to preserve the balance of information between the linguistic and molecule modalities. All models were fine-tuned using QLoRA (Dettmers et al., 2024).

For the atomic-level NLI evaluation method, we instruct Meta-Llama-3-8B (Touvron et al., 2023) to break down (reference, generated) pairs into a series of atomic premises and hypotheses. We then use DeBERTa [5] to measure hallucination and coverage by performing NLI across all the atomic premises and hypotheses.

[4]Crossmodal initialisation was based on the most challenging task reported in (Edwards et al., 2024).

[5]https://huggingface.co/MoritzLaurer/DeBERTa-v3-large-mnli-fever-anli-ling-wanli

```
# Training Configurations
args = TrainingArguments(
output_dir=save_path,
overwrite_output_dir=True,
load_best_model_at_end=True,
num_train_epochs=3,
per_device_train_batch_size=1
per_device_eval_batch_size=1
gradient_accumulation_steps=64
gradient_checkpointing=False
optim="adamw_torch_fused",
learning_rate=5e-5,
max_grad_norm=0.3,
warmup_ratio=0.1,
lr_scheduler_type="cosine",

)


# Quantisation Configurations
(
load_in_4bit=True,
bnb_4bit_use_double_quant=True,
bnb_4bit_quant_type=nf64,
bnb_4bit_compute_dtype=torch.bfloat16
)


# LoRA Configurations
(
lora_alpha=16,
r = 64,
lora_dropout=0.1,
task_type="CAUSAL_LM",
bias=False,
target_modules= "all-linear"
)
```

Figure 8: Training configurations

H Examples of generated molecules and captions.

Fig. 9 and 10 illustrate examples of molecules and captions generated by our top-performing models compared to Meditron, respectively.

I Examples of Atomic-level Cross-NLI evaluation

Table 6 presents examples of assessing hallucination and coverage in generated captions using our atomic-level cross-NLI evaluation method.

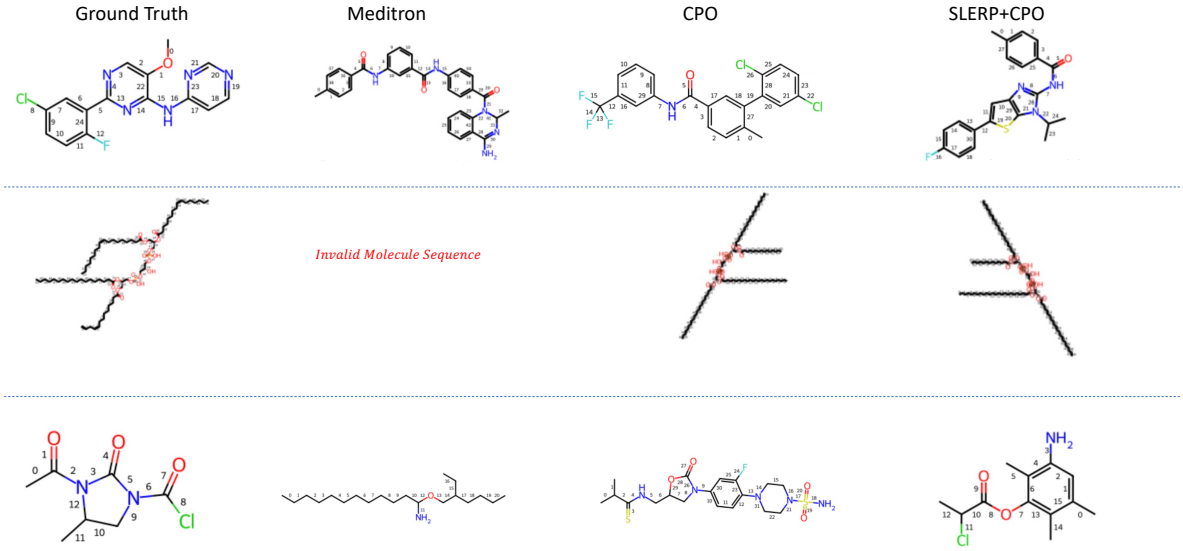

Figure 9: Examples of molecules generated by our top-performing models compared to Meditron, the best benchmark model trained on the entire dataset.

Ground Truth	Meditron	CPO	SLERP+CPO
The molecule is a stabilizing cytochrome oxidase, cholesterol translocation, proton trap for oxidative phosphorylation, apoptosis that impacts non-alcoholic fatty liver disease. The molecule is a stabilizing mitochondrial structure that impacts diabetic heart disease, aging, barth syndrome, and tangier disease	The molecule is a stabilizing cytochrome oxidase, a cholesterol translocation, and a energy source, and it impacts tangier disease. The molecule is a membrane stabilizer, a proton trap for oxidative phosphorylation, and a food additive	The molecule is a cholesterol translocation and a stabilizing cytochrome oxidase that impacts barth syndrome, non-alcoholic fatty liver disease, and aging. The molecule is a stabilizing mitochondrial structure, proton trap for oxidative phosphorylation, apoptosis that impacts tangier disease and diabetic heart disease.	The molecule is a stabilizing cytochrome oxidase and a stabilizing mitochondrial structure that impacts non-alcoholic fatty liver disease, aging, and diabetic heart disease. The molecule is a cholesterol translocation, proton trap for oxidative phosphorylation, apoptosis that impacts barth syndrome and tangier disease.
It impacts non-alcoholic fatty liver disease. The molecule is a nutrient that impacts Parkinson's disease, Alzheimer's disease, and diabetes mellitus type 2.	It impacts cardiovascular disease, Alzheimer's disease, seizure, and diabetes mellitus.	The molecule is a nutrient that impacts non-alcoholic fatty liver disease, diabetes mellitus type 2, Alzheimer's disease, and Parkinson's disease	The molecule is a nutrient that impacts non-alcoholic fatty liver disease, diabetes mellitus type 2, and Alzheimer's disease.
The molecule is a stabilizing mitochondrial structure, a stabilizing cytochrome oxidase, and a apoptosis, and it impacts diabetic heart disease. The molecule is a proton trap for oxidative phosphorylation and a cholesterol translocation, impacting both tangier disease and non-alcoholic fatty liver disease. It impacts both aging and barth syndrome.	The molecule is a stabilizing mitochondrial structure, apoptosis, and stabilizing cytochrome oxidase.	The molecule is a cholesterol translocation, stabilizing cytochrome oxidase, proton trap for oxidative phosphorylation that impacts barth syndrome and non-alcoholic fatty liver disease. The molecule is a stabilizing mitochondrial structure and a apoptosis that impacts tangier disease, aging, and diabetic heart disease.	The molecule is a stabilizing cytochrome oxidase and a stabilizing mitochondrial structure that impacts non-alcoholic fatty liver disease, aging, and diabetic heart disease. The molecule is a cholesterol translocation, proton trap for oxidative phosphorylation, apoptosis that impacts barth syndrome and tangier disease.

Figure 10: Examples of captions generated by our top-performing models compared to Meditron, the best benchmark model trained on the entire dataset.

Reference Text	Atomic Premises	Generated Text	Atomic Hypothesis	Hallucination	Coverage
It impacts pancreatitis. The molecule is a fat storage and nutrient, belonging to the thyroxine treatment class of molecules, and impacts metabolic syndrome, atherosclerosis, and cardiovascular disease.	- The molecule impacts pancreatitis. -The molecule is a fat storage molecule. -The molecule is a nutrient. - The molecule belongs to the thyroxine treatment class of molecules. - The molecule impacts metabolic syndrome. - The molecule impacts atherosclerosis. - The molecule impacts cardiovascular disease.	The molecule is a nutrient.	- The molecule is a nutrient.	0.00	0.14
The molecule is a energy storage and is floral. The molecule is a emulsifier, nutrient, surfactant, energy source, membrane stabilizer, and rose.	- The molecule is a floral energy storage. - The molecule is an emulsifier. - The molecule is a nutrient. - The molecule is a surfactant. - The molecule is an energy source. - The molecule is a membrane stabilizer. - The molecule is rose.	The molecule is a energy storage, a membrane stabilizer, and a energy source. The molecule is a surfactant, a emulsifier, and a nutrient.	- The molecule is an energy storage. - The molecule is a membrane stabilizer. - The molecule is an energy source. - The molecule is a surfactant. - The molecule is an emulsifier. - The molecule is a nutrient.	0.00	0.75
The molecule is a orexin receptor antagonist.	- The molecule is an orexin receptor antagonist.	The molecule is a anti viral.	- The molecule is an anti-viral.	0.75	0.00
The molecule is a stabilizing cytochrome oxidase, apoptosis, stabilizing mitochondrial structure that impacts non-alcoholic fatty liver disease and tangier disease. The molecule is a cholesterol translocation and a proton trap for oxidative phosphorylation that impacts aging, barth syndrome, and diabetic heart disease.	- The molecule is a cytochrome oxidase. - The molecule is a stabilizer of apoptosis. - The molecule is a stabilizer of mitochondrial structure. - The molecule impacts non-alcoholic fatty liver disease. - The molecule impacts Tangier disease. - The molecule is a cholesterol translocation. - The molecule is a proton trap. - The molecule impacts oxidative phosphorylation. - The molecule impacts aging. - The molecule impacts Barth syndrome. - The molecule impacts diabetic heart disease.	The molecule is a cholesterol translocation, a apoptosis, and a stabilizing cytochrome oxidase, and it impacts tangier disease. The molecule is a stabilizing mitochondrial structure and a proton trap for oxidative phosphorylation that impacts barth syndrome, aging, and non-alcoholic fatty liver disease. It impacts diabetic heart disease.	- The molecule is a cholesterol translocation. - The molecule is involved in apoptosis. - The molecule is a stabilizing cytochrome oxidase. - The molecule impacts Tangier disease. - The molecule is a stabilizing mitochondrial structure. - The molecule is a proton trap for oxidative phosphorylation. - The molecule impacts Barth syndrome. - The molecule impacts aging. - The molecule impacts non-alcoholic fatty liver disease. - The molecule impacts diabetic heart disease.	0.00	0.91
The molecule is a anti microbial member of the anti fungal class.	- The molecule is anti-microbial. - The molecule is a member of the anti-fungal class.	It belongs to the anti viral class of molecules. The molecule is both a hepatitis c treatment and a hcv inhibitor.	- The molecule belongs to the anti-viral class of molecules. - The molecule is a hepatitis C treatment. - The molecule is an HCV inhibitor.	0.02	0.10

Table 6: Cases showcasing insights captured by our atomic-level cross-NLI in assessing the level of hallucination and coverage in generated captions. Red highlights indicate missing information in atomic premises or invalid information in atomic hypotheses. Hallucination refers to the introduction of information absent from the reference, while coverage assesses the recall of atomic units (refer to § 3.3).