LAUGHS: An LLM-compatible Molecular String Representation

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Abstract

Large language models (LLMs) are increasingly applied to chemistry, yet their performance depends strongly on how molecules are represented as text. IUPAC names become syntactically unwieldy for complex structures, while graph-serialized strings disperse chemically meaningful moieties across the sequence. Here, we present LAUGHS, an LLM-compatible molecular string representation that decomposes a molecule into named moieties, hierarchically organizes them into a tree structure, and linearizes the result into a natural-language-like string. Tokenization analysis reveals that LAUGHS units align near-perfectly with tokenizer spans, suggesting strong compatibility with LLMs. On site-specific editing, it substantially outperforms all baselines with a 91.4% exact match rate among valid outputs; on the property explanation task, LAUGHS matches IUPAC-level performance across all metrics. Together, our results identify the semantic mismatch between molecular representations and natural language as a key bottleneck for LLMs in chemistry, and demonstrate that the representation proposed in this work can effectively bridge this gap.

1. Introduction

Pretrained language models have advanced a wide range of natural language processing capabilities, including language understanding, representation learning (Devlin et al., 2019; Wang et al., 2018; 2019; Liu et al., 2019), and text generation (Radford et al., 2019; Brown et al., 2020). More recent instruction-following LLMs (Ouyang et al., 2022; Achiam et al., 2023; Comanici et al., 2025; Yang et al., 2025; Guo et al., 2025) now serve as general-purpose interfaces for question answering (Yue, 2025), summarization (Zhang et al., 2025), translation (Gain et al., 2026), and code generation (Li et al., 2022; Roziere et al., 2023; Jiang et al., 2026). Chemistry is highly compatible with language model architectures because molecules are routinely represented in textual form. Consequently, these architectures have been broadly adopted for molecular property prediction (Ross et al., 2022), reaction outcome prediction (Schwaller et al., 2019), retrosynthesis planning (Schwaller et al., 2020), and de novo molecular generation and optimization. (Bagal et al., 2021; He et al., 2022)

Table 1. Comparison syntactic features of representations. NL: natural language; IUPAC: IUPAC nomenclature; SMILES: Simplified Molecular Input Line Entry System (Weininger, 1988); Spaced units: space-delimited semantic units; Head-modifier: whether the main concept appears first, followed by descriptive modifiers.; Locant: position-specific substitution; Graphomorphic: units act as nodes, and their connections define the molecular structure. ✓/✗ indicate presence/absence.

	Spaced units	Head -modifier	Locant	Grapho -morphic
NL	✓	✓	✗	✗
IUPAC	✗	✗	✓	✗
SMILES	✗	✗	✗	✓
LAUGHS (ours)	✓	✓	✓	✓

LLMs receive chemical information about molecules through their textual representations. However, the most widely used molecular representations were developed primarily for systematic nomenclature or machine learning pipelines, and thus diverge considerably from the structural characteristics of natural language. Table 1 summarizes the key properties of natural language with representative molecular representations. IUPAC nomenclature provides the standard system for molecular names (Favre & Powell, 2013), but its detailed rules can make names of complex molecules difficult to understand (Fendos, 2021). SMILES (Weininger, 1988) remains the predominant molecular representation in cheminformatics owing to its compactness and pervasive integration into data pipelines. However, while its traversal syntax surfaced encodes atom- and bond-level information, higher-level chemical abstractions, such as scaffolds and attachment sites, are left implicit and must be inferred from that syntax. Although alternative encodings show that redesigning molecular encodings can improve validity (Krenn

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et al., 2019; 2022), tokenization consistency (Li & Fourches, 2021), and fragment granularity (Cheng et al., 2023), they do not directly address high-level abstractions in a format that language models can effectively leverage.

In this study, we present LAUGHS, an LLM-compatible molecular string representation designed to make chemically meaningful groups explicit. LAUGHS is constructed in three stages: decomposing the molecule into named chemical moieties, organizing them into a root-substituent hierarchy, and linearizing that tree using natural-language-like connectors and delimiter. We analyze the compatibility of LAUGHS with LLM tokenizers and evaluate its utility in downstream tasks, including localized structure editing and structure-grounded molecular property explanation.

2. Related Work

Prior work on molecular string representations has largely focused on encodings more amenable to deep learning models for property prediction(Jablonka et al., 2024) and molecular generation(Bagal et al., 2021; Chilingaryan et al., 2024; Özçelik et al., 2024). Beyond SMILES, SELFIES (Krenn et al., 2019) guarantees the validity of generated molecules through its robust syntax, and SMILES Pair Encoding (Li & Fourches, 2021) uses data-driven substructure vocabularies. Another line of work has explored fragment-level representations in which functional groups and substructures serve as building blocks for molecular generation and design (Wu et al., 2024), with related extensions marked encoding attachment patterns (Noutahi et al., 2024) and chirality (Mastrolorito et al., 2025).

Existing string encodings were carried over as inputs to language models in chemistry, spanning conventional molecular modeling tasks and agentic workflows. Early molecular language modeling centered on Transformers that were pretrained on SMILES and applied to property prediction (Ross et al., 2022) and sequence-to-sequence tasks such as reaction prediction, retrosynthesis, and molecular optimization (Irwin et al., 2022). Text2Mol and MolT5 (Edwards et al., 2021; 2022) marked an important transition by connecting molecular strings with natural language through bidirectional translation, enabling both molecule-to-text description and text-to-molecule generation. At the scale of LLMs, later work extended this framing by recasting domain tasks as instructions, including Mol-Instructions (Fang et al., 2023), a biomolecular instruction dataset, and ChemLLM (Zhang et al., 2024), an LLM for chemistry with instruction data, benchmarking, and dialogue interaction. Meanwhile, agentic systems leverage language models within tool-using workflows (M. Bran et al., 2024; Zou et al., 2025; Kim et al., 2025). Across this progression, molecular string encodings have been readily adopted by language models, but their suitability for the way LLMs process and reason over chemical information has often been overlooked.

Recent studies have shown that LLM performance in chemistry depends on how a molecule is presented to the model. In property prediction, accuracy varies across molecular representations (e.g. SMILES, DeepSMILES, SELFIES, InChI, and IUPAC names) (Baker et al., 2025). Consistency analyses likewise show that the same molecule can elicit different answers when written as SMILES or as an IUPAC name (Yan et al., 2025). In generative tasks, this sensitivity extends to validity and correction, where format choice and repair strategies affect whether generated strings correspond to valid structures (Tao et al., 2025). Taken together, these studies indicate that molecular encodings do more than specify its identity; they also shape how models behave on chemical tasks, underscoring the need for representations tailored to LLMs.

3. Method

3.1. LAUGHS Representation

LAUGHS (**LA**nguage for molec**U**lar **G**roup-aware **H**ierarchical **S**trings) represents molecules as natural-language phrases over chemical groups, where the fundamental unit of description is a named moiety and molecular structure is expressed through modifier-clause syntax. Its grammar is grounded in two design principles that mirror the structure of natural language: named chemical groups serve as the basic units of description, and the representation adopts a phrase structure analogous to natural language–comprising a head, modifier clauses, connectors, and delimiters. LAUGHS is constructed from a molecular graph through three stages: fragmentation, tree construction, and linearization.

3.1.1. Fragmentation

The first stage decomposes the input molecule into moieties. We define a vocabulary of frequently occurring named rings, functional groups, and carbon chains as the basic units, and decompose input molecules into these units. All decompositions occur exclusively at single bonds. The detailed matching and bond-cutting rules are given in Appendix A.1.

3.1.2. Hierarchical Moiety Tree Construction

The resulting moieties are then organized into a rooted hierarchy. A priority scheme selects the global root moiety (the core) and orders the attached moieties (substituents) across the molecular graph. A specialized rule set handles parent-child assignment and locant ordering within complex ring systems. Together, these rules define the moiety tree with one node per moiety and one edge for each parent-child attachment relation. Each edge records the information required to realize that relation in the final LAUGHS

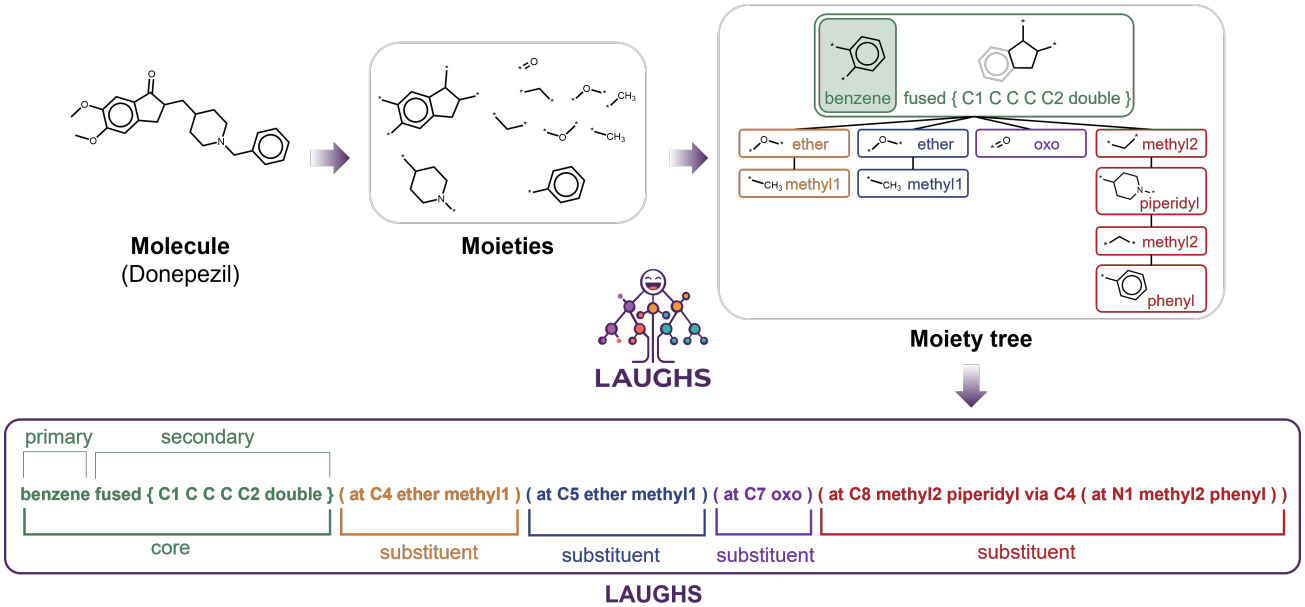

Figure 1. LAUGHS construction example for donepezil. The molecule is first decomposed into a root moiety and its substituents, organized into a rooted moiety tree, and finally rendered as a linear LAUGHS string with named groups and locants. The color coding highlights the correspondence between tree nodes and their spans in the final LAUGHS string.

string, including attachment-site locants and, when necessary, bond orders. The full hierarchy rules are detailed in Appendix A.2.

3.1.3. Linearization

Once the rooted moiety tree has been defined, the encoder converts it into a LAUGHS string. The tree is traversed via depth-first search, and based on the node and edge information, units are sorted and converting into a modifier-clause string. Its units include parent-form moieties, substituent names, locants, attachment markers such as `at` and `via`, and complex-ring topology markers such as `fused`, `spiro`, and `bridged`. All units are whitespace-delimited. Moieties that share the same name but differ in bonding valence are distinguished by a numerical suffix (e.g., a primary amine is denoted `amino1` and a tertiary amine `amino3`).

In Figure 1, the construction example traces these three stages and shows how the final string preserves the decomposition into a root moiety and its substituents. We implement this pipeline as an encoder-decoder pair, with vocabulary statistics and near-perfect round-trip reconstruction accuracy reported in Appendix A.3 and A.4.

3.2. Tokenizer Alignment

We analyzed tokenizer alignment to provide a quantitative measure of how compatible the representation is with LLMs. To distinguish tokenizer-defined units from the lexical units defined by the representation itself, we use the term "token" to refer specifically to the former. We report two tokenization statistics: token purity(Purity) and tokenization consistency (Consistency). Purity measures the fraction of tokens that correspond to exactly one unit. Consistency measures the fraction of unit occurrences that follow the most common tokenization pattern. Tokenizer Alignment (Alignment) is calculated by Purity $\times$ Consistency and reflects unit-token one-to-one mapping. Formal definitions are provided in Appendix B. For tokenizer analysis, we sampled 10,000 molecules from ChEMBL36 (Zdrazil et al., 2024), ensuring a uniform distribution across molecular weight intervals.

3.3. Structure Editing

We constructed an editing-instruction dataset from 500 seed molecules sampled from MOSES (Polykovskiy et al., 2020). The dataset covers four molecular representations (IUPAC, SMILES, SELFIES, and LAUGHS) and three edit types (elimination, substitution, and swap). For each seed molecule and edit type, we generated five instruction variants, yielding 7,500 instructions in total.

Each benchmark instance consists of an original molecule, a natural-language edit instruction, and a reference edited molecule, ensuring that the intended structural change is matched across representations. We evaluated GPT-4.1-mini on localized structure editing with this dataset, and scored Validity (the fraction of outputs that decode to valid molecules) and Exact Match (the fraction of outputs that structurally match the reference edited molecule) as a repre-

sentative metrics.

3.4. Property Explanation

The property explanation task evaluates whether the molecular representation gives LLMs enough structural evidence to produce a chemically meaningful account of a molecular property. On 500 BACE molecules from MoleculeNet (Wu et al., 2018), GPT-4.1-mini was employed to generate property-oriented explanations from four input representations: IUPAC names (abbreviated as IUPAC), SMILES, SELFIES, and LAUGHS.

The outputs are then assessed with an LLM-as-a-judge setup (Zheng et al., 2023): GPT-5.4-mini serves as the judge under the G-Eval framework (Liu et al., 2023) implemented through the DeepEval package. For Plausibility, Groundedness, Specificity, and Consistency, we use separate G-Eval rubrics and report their arithmetic mean as the overall explanation score (Overall). The generation prompt is given in Appendix C, and the judging criteria and prompt template are summarized in Appendix D.

4. Results

4.1. Tokenizer Alignment

Tokenizer alignment measures how well tokenizer-recognized spans align with the semantic units of a representation, indicating its suitability for LLM processing. As shown in Figure 2, LAUGHS attains near-perfect scores of 0.999 across all metrics, demonstrating that its grammatical structure provides LLMs with highly stable and consistent input.

Tokenizer alignment reflects the grammatical characteristics of a representation along two distinct dimensions. IUPAC achieved strong token purity (0.819), but exhibited the lowest tokenization consistency (0.703), indicating that the prefix- and suffix-based string transformation rules governing IUPAC names give rise to diverse tokenization patterns. Conversely, SELFIES reached perfect tokenization consistency (0.966), but its token purity drops (0.620), suggesting that stable segmentation alone does not guarantee chemically meaningful token boundaries. SMILES underperformed in both Purity (0.597) and Consistency (0.413), which can be attributed to its graph-traversal linearization scheme, which disperses chemical information across heterogeneous string patterns. These results were obtained with OpenAI's `o200k_base` tokenizer, with tokenizers from Mistral and Qwen showing the same trend.

4.2. Structure Editing

Structure editing evaluates whether LLMs can identify a target substructure and apply local modifications while preserving the rest of the molecule. Within Table 2, LAUGHS outperforms exact match rate (0.914), followed by IUPAC, SMILES, and SELFIES. This result suggests that LAUGHS generates more LLM-tractable tokens than IUPAC, a finding corroborated by its superior tokenizer alignment scores. SELFIES scored considerably lower than even SMILES — another atom-level representation — which can be attributed to the fact that its atomic units simultaneously carry grammatical roles, making it difficult to correctly reassign these functional units through local edits alone.

Figure 2. Tokenizer alignment scores across molecular representations. (a) Token Purity and (b) Tokenization Consistency are reported for SMILES, SELFIES, IUPAC, t-SMILES(Wu et al., 2024), and LAUGHS.

In terms of Validity, SELFIES, which was designed for syntactic robustness, attains the highest score (0.976), while LAUGHS reaches a nearly identical level (0.975). By contrast, IUPAC and SMILES exhibit lower validity despite their widespread use. Although SELFIES was designed to operate exclusively with syntactically valid units, imperfect alignment between those units and LLM tokens can still produce unsupported expressions. Nevertheless, the high validity scores of both SELFIES and LAUGHS demonstrate that principled representation design can improve the syntactic validity of LLM-generated outputs. F1-scores follow the same ordering (Appendix E).

4.3. Property Explanation

Property explanation tests whether a molecular representation gives an LLM enough structural evidence to produce a chemically meaningful account of a molecular property. In Table 2, IUPAC achieves highest score in all property explanation metrics, followed by LAUGHS. The leading performance of IUPAC may reflect both its chemically systematic structure and its likely prevalence in pretraining corpora. Notably, LAUGHS surpasses SMILES and SELFIES in this zero-shot setting, despite the complete LAUGHS syntax not being part of standard molecular representations.

Among our criteria, Groundedness is particularly revealing, as it assesses whether an explanation anchors to structural evidence such as functional groups and attachment positions. IUPAC and LAUGHS show the closest agreement on

Table 2. Comparison of molecular representations across property explanation and structure editing. Task-specific metrics are defined in the method section. Best values are shown in bold and second-best values are underlined.

Task	Metric	IUPAC	SMILES	SELFIES	LAUGHS
Structure Editing	Validity	0.906	0.832	**0.976**	0.975
	Exact Match	0.811	0.699	0.227	**0.914**
Property Explanation	Plausibility	**0.721**	0.574	0.633	0.679
	Groundedness	**0.603**	0.516	0.522	0.584
	Specificity	**0.789**	0.644	0.617	0.747
	Consistency	**0.784**	0.637	0.715	0.742

this metric (0.019), outperforming traversal-oriented strings. Such alignment suggests that LAUGHS's hierarchical and moiety-based form offers stronger support for structure-grounded answering. Furthermore, this advantage likely arises because LAUGHS leverages familiar chemical terms, which partially parallels the system in IUPAC nomenclature.

LAUGHS outperforms SMILES and SELFIES across all explanation metrics. Its Overall score surpasses these baselines by 0.095 and 0.066, respectively, which are substantial margins for this evaluation setting. When compared to SELFIES, the advantage is most notable in Specificity, where LAUGHS exceeds it by 0.130, indicating that LAUGHS generates molecule-specific responses rather than generic property descriptions. Relative to SMILES, the gains are distributed across Plausibility, Specificity, and Consistency, all three exceeding a margin of 0.10 for LAUGHS. Based on these results, the explanatory advantage of LAUGHS stems from pairing chemical named vocabulary with explicit structural relations.

5. Discussion

5.1. How representation syntax governs LLM performance

Our results show a consistent pattern across all evaluation tasks: representations that more closely mirror natural language syntax elicit stronger LLM performance. This pattern cannot be explained by chemical information alone. SMILES and SELFIES encode complete molecular graphs, yet they lag behind LAUGHS and IUPAC on explanation and editing alike. Conversely, IUPAC, the most chemically systematic representation, leads on property explanation but falls substantially behind LAUGHS on editing task. The factor that best accounts for performance differences across all tasks is how well each representation's syntactic structure aligns with the statistical regularities of natural language that LLMs internalize during pretraining.

The distribution of unit types across representations explains the observed differences in LLM performance. Figure 3 categorizes the 50 most frequent units in each representation into seven functional roles. LAUGHS has the highest

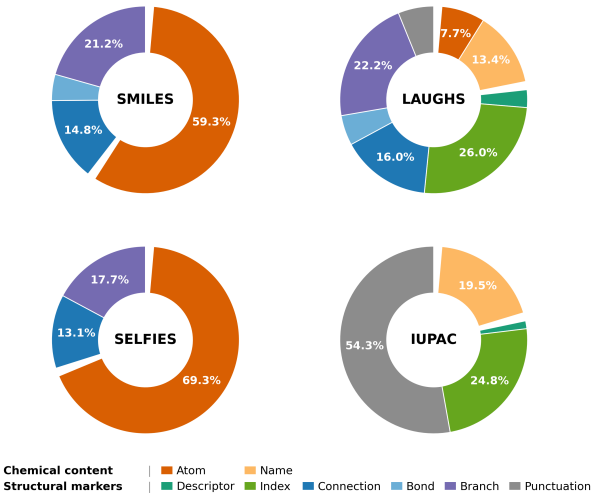

Figure 3. Functional composition of unit occurrences in 10,000 ChEMBL36 molecules sampled to balance molecular-weight ranges. Donut charts show category over all units extracted from each representation by its lexical rules. Categories are grouped into chemical content units (Atom and Name) and structural marker units (Descriptor, Index, Connection, Bond, Branch, and Punctuation). SMILES and SELFIES are dominated by atom units, IUPAC by punctuation and index units, whereas LAUGHS distributes its unit occurrences across all categories.

proportion of moiety tokens, followed by IUPAC, while IUPAC ranks first and LAUGHS second in indexing tokens. Representations rich in moiety and indexing information — namely IUPAC and LAUGHS — tend to elicit explanations that more specifically characterize substituent identity and attachment position. By contrast, SMILES and SELFIES convey chemical information only at the atomic level, which limits the recognizable structural features available to the model and consequently reduces Specificity while increasing the rate of implausible attributions. Grouping units serve to encode representational grammar; the high proportion in IUPAC reflects its rule-dense locant syntax. Paradoxically, this highly systematic framework also contributes to the difficulty of generating exact molecular strings, a challenge that has been similarly documented among human learners (Bodé et al., 2016; Fendos, 2021; Taskin & Bernholt,

2014).

5.2. Natural language structure as a design principle for LLM-facing representations

The consistent advantage of LAUGHS across evaluation tasks can be attributed to three structural features that collectively make it resemble natural language more closely than any of the baseline representations.

Lexically stable unit identities. LAUGHS assigns each structural unit a fixed lexical identity regardless of molecular context: a terminal methyl group is consistently represented as `methyl1`, and a quaternary carbon center as `methyl4`. Its syntax provides a stable token-to-meaning association, which stands in contrast to SMILES and SELFIES, where the structural role of an atom token is entirely determined by its position in the traversal sequence. The high Specificity and Groundedness scores of LAUGHS in property explanation, and its superior exact-match rate in structure editing, reflect the model's ability to identify and reason about stable unit identities without requiring contextual inference.

Explicit modifier-clause syntax for branching. LAUGHS encodes molecular branching through a post-modification syntax in which connectors such as `at` and `via` explicitly specify attachment sites, in the same way that prepositional phrases in natural language specify the relationship between modifier and its head. In contrast, SMILES parentheses and SELFIES branch tokens encode topological branching without lexical content, requiring the model to reconstruct attachment context from positional reasoning. This distinction accounts for the editing advantage of LAUGHS: targeted structural modifications correspond to local clause substitutions in LAUGHS, whereas context-dependent representations require globally consistent re-traversal of the molecular string.

Whitespace delimitation and tokenizer alignment. LLM tokenizers are optimized to segment whitespace-separated strings into stable and reusable units. This design directly addresses a known tokenization bottleneck in chemistry LLMs: general-domain tokenizers tend to fragment SMILES into semantically uninformative subtokens, whereas chemistry-specific molecular tokenizers can still suffer from incomplete coverage of the SMILES/OpenSMILES space (Kalamkar et al., 2025; Wadell et al., 2025).The whitespace-delimited architecture of LAUGHS produces near-perfect tokenizer alignment (0.999), as each LAUGHS unit maps onto tokenizer spans in the same manner as natural language words. SMILES, without delimiters, yields fragmented and inconsistent tokenization. IUPAC, though lexically familiar, compresses complex structural information into long compound tokens that segment unpredictably. SELFIES achieves consistent tokenization at the symbol level but only by sacrificing meaningful unit boundaries. LAUGHS achieves high scores on both Purity and Consistency simultaneously, because whitespace delimitation directly instantiates the segmentation assumptions underlying the tokenizer.

These three properties suggest that syntactic alignment with natural language conventions may be a productive design consideration for LLM-compatible molecular representations, independent of chemical information completeness. Chemical completeness and compact encodings are essential for cheminformatics pipelines, but do not necessarily translate to stronger LLM performance. LAUGHS offers one instantiation of how these objectives can be reconciled.

5.3. Limitations

We introduced a molecular language that marks structural features of molecules, but several limitations remain. First, because our evaluation used pretrained LLMs, the composition of the pretraining data is unknown. This may provide prior knowledge for widely used representations such as IUPAC and SMILES, while disadvantaging more recent formats such as SELFIES and LAUGHS. Second, the current implementation of LAUGHS does not cover stereochemistry. It will be addressed in future work for chemical reaction tasks. Third, we acknowledge that molecular property explanations are assessed using G-Eval scores, and future work will complement this with human expert review.

6. Conclusion

We present LAUGHS, a human-readable hierarchical molecular string representation that decomposes molecules into named moieties, organizes them as a tree, and renders the result in a natural-language-like text format. Across tokenizer alignment analysis, localized structure editing, and property explanation, our results show that surfacing chemically meaningful units with explicit delimiters helps language models interpret and manipulate molecular structure. LAUGHS achieves near-perfect alignment between tokens and chemical units, the strongest editing performance overall, and explanation quality close to IUPAC. Together, these results frame molecular representation as an interface design problem: aligning chemical abstractions with tokenization schemes can make representations serve not only as storage formats but also as communication channels between chemical knowledge and model processing.

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A. LAUGHS Construction Details

A.1. Fragmentation Rules

The encoder begins by decomposing the input molecular graph into moieties. Named rings and functional groups are matched with predefined SMARTS patterns, and the remaining non-ring sp^3 carbons are assigned to longest-path alkyl-chain motifs. Fragmentation is selective rather than bond-exhaustive: ring bonds are never cut, and cuts are introduced only when they are needed to separate distinct matched motifs or ring-system boundaries. The inter-moiety bond order is preserved at each cut site and later reused during encoding and decoding.

A.2. Hierarchy Rules

Hierarchy assignment uses two different rule sets. At the whole-molecule level, fragment-to-fragment priority first orients graph edges by connection count, heavy-atom count, and sorted atomic numbers. Root selection for the moiety tree then uses a separate criterion based on unique child-type count, heavy-atom count, atomic numbers, and neighbor-tree priority. Inside a complex ring fragment, parent-child assignment among constituent rings follows an eight-tier rule based on bridgehead count, port count, heavy-atom count, sequential atomic numbers, positional atomic numbers, double-bond count, external-fragment priority, and substituent-tree priority. Locant assignment within each ring further prioritizes bridgehead status and bridgehead traversal order before heteroatom, parent attachment, and substituent priority.

A.3. Surface Vocabulary

The supported LAUGHS surface vocabulary combines a finite set of named motifs with structural markers and generated locants. The named-motif inventory contains 278 distinct surface forms, including SMARTS-backed ring and functional-group fragments, carbon-chain fragments, and the parent-form/substituent-form variants used by the encoder and decoder. The structural inventory includes the attachment markers `at` and `via`, the range marker `-`, the explicit bond-order markers `double` and `triple`, the topology markers `ring`, `fused`, `spiro`, and `bridged`, four delimiters `(`, `)`, {, and }, and nine fold markers from `twofold` to `tenfold`. Locants are generated from element symbols and local atom indices, such as `C1` or `N2`, rather than enumerated as a fixed unit list.

A.4. Round-Trip Reconstruction

We evaluated encoder-decoder round-trip reconstruction on 2,854,705 molecules from ChEMBL36 (Zdrazil et al., 2024) after filtering invalid molecules, ionic species, and organometallics and removing chirality. Round-trip accuracy was 100% (2854705/2854815), with 110 failures due to invalid molecules. Molecules or fragments that fall outside the current LAUGHS grammar are emitted as raw-SMILES fallback blocks of the form `smiles { ... }`, which the decoder parses directly. The encoder and decoder are implemented in Python using RDKit (Greg Landrum, 2026).

B. Formal Definition of the Token-Unit Alignment Rate and Tokenization Consistency

Let r denote a representation of length L_r, and let $I_r = \{1, \ldots, L_r\}$ be its position index set. Let

$$\mathcal{T}(r) = (T_1, \ldots, T_m),$$
$$\mathcal{U}(r) = (U_1, \ldots, U_n)$$

be the ordered partitions of I_r induced by tokenizer spans and by representation-unit spans, respectively.

For a token span T, define

$$\nu_r(T) := \sum_{U \in \mathcal{U}(r)} \mathbf{1}(T \cap U \neq \varnothing),$$

the number of representation units overlapped by that token. The token-unit alignment rate is

$$A(r) := \frac{1}{|\mathcal{T}(r)|} \sum_{T \in \mathcal{T}(r)} \mathbf{1}\big(\nu_r(T) = 1\big).$$

Equivalently, $A(r)$ is the fraction of tokens that correspond to exactly one representation unit.

To characterize whether the same unit type is segmented consistently across a corpus, let $\lambda_r(U)$ denote the unit type of $U \in \mathcal{U}(r)$, and let $\pi_r(U)$ denote the ordered tokenization pattern induced on that unit. For a collection $\mathcal{R}$, define

$$N_u(p) := \sum_{r \in \mathcal{R}} \sum_{U \in \mathcal{U}(r)} \mathbf{1}\big(\lambda_r(U) = u,\ \pi_r(U) = p\big).$$

Then let

$$N_u = \sum_p N_u(p),$$
$$M_u = \max_p N_u(p),$$

and define corpus-level tokenization consistency as

$$C(\mathcal{R}) = \frac{\sum_u M_u}{\sum_u N_u}.$$

This is the fraction of representation units that follow the most frequent tokenization pattern for their unit type.

C. Property-Explanation Prompt

Property explanations were generated with a shared instruction template across representations. The system prompt was:

```
You are an expert chemist. Your task is to explain the structural basis for a given
↪  molecular property.

You will receive a molecule in a text representation, along with a property name and its
↪  observed value. Explain why this molecule exhibits that property value based on its
↪  structural features.

IMPORTANT: Do NOT mention the name or type of the molecular representation you are reading
↪  (e.g., do not say "in SMILES notation" or "the LAUGHS representation shows"). Simply
↪  describe the molecular structure and its relationship to the property directly.

Rules:
1. Return a single JSON object with one key: "explanation".
2. Identify at least 2 specific substructures or physicochemical features that contribute
↪  to the observed property value.
3. For each feature, explain the mechanistic link: how does this structural element
↪  promote or hinder the property?
4. Be concrete: name the specific functional groups, ring systems, or atom patterns you
↪  observe.
5. End with one sentence noting limitations of structure-only reasoning.
```

The user template was identical across representations except for the molecular field (`Molecule: {smiles}` or `Molecule: {laughs}`):

```
Sample ID: {id}
Molecule: {representation}
Property: {property_name}
Observed value: {property_value}

Explain the structural basis for the observed property value of this molecule.

Requirements:
- Do NOT predict or re-state the property value. Focus entirely on structural rationale.
- Do NOT mention the name or format of the representation. Just describe the structure.
- Identify specific substructures (functional groups, ring systems, chains) relevant to
↪  the property.
- For each substructure, explain the mechanism by which it contributes to the observed
↪  value.
- Discuss at least 2 distinct structural features with clear structure-to-property
↪  reasoning.
- Avoid generic statements; every claim must reference a concrete part of this molecule.
```

D. G-Eval Judge Criteria and Prompt

Property explanations were evaluated with four separate G-Eval metrics in DeepEval: Plausibility, Groundedness, Specificity, and Consistency. The Overall score reported in the main text is the arithmetic mean of these four scores rather than a fifth independently judged dimension.

The criterion strings passed to DeepEval were:

1. **Plausibility**: Evaluate whether the explanation makes chemically and structurally plausible claims. Penalize chemically implausible or structurally unjustified claims.
2. **Groundedness**: Evaluate whether the explanation is supported by the provided molecular or reaction description. Reward claims tied to explicit features in the input and penalize unsupported leaps.
3. **Specificity**: Evaluate whether the explanation is concrete and structurally specific rather than generic. Reward references to precise groups, positions, linkers, substituents, or localized features.
4. **Consistency**: Evaluate whether the explanation is internally coherent and whether its claims support one consistent structural interpretation. Penalize contradictions or mismatched causal claims.

DeepEval's default G-Eval template constructs the judge prompt in two stages. For each criterion, it first asks the judge model to generate 3-4 evaluation steps from the criterion and the evaluation parameters (`input` and `actual_output`). It then asks the judge to score the test case using those generated steps and to return a JSON object with an integer score from 0 to 10 together with a brief reason. The default template is:

Here {`parameters`} denotes DeepEval's textual placeholder for the fields supplied to the metric. In our setup, it corresponds to `input` and `actual_output`.

```
Step-generation prompt:
Given an evaluation criteria which outlines how you should judge the {parameters},
↪  generate 3-4 concise evaluation steps based on the criteria below.
Evaluation Criteria: {criteria}
Return JSON with the "steps" key as a list of strings.

Scoring prompt:
You are an evaluator.
Given the evaluation steps, assess the response below and return JSON with two fields:
- "score": an integer between 0 and 10
- "reason": a brief explanation grounded in the evaluation steps
Evaluation Steps: {evaluation_steps}
Test Case: {test_case_content}
Parameters: {parameters}
```

E. Representative Edit Operations

The editing benchmark uses functional-group-level instructions derived from MOSES seed molecules (Polykovskiy et al., 2020). For each seed, three edit families are instantiated:

- **elimination**: remove a designated functional group from the molecule,
- **substitution**: replace one functional group with another at the same local position,
- **swap**: exchange one functional group identity for another specified alternative.

Five variants are generated for each edit family, yielding 15 instructions per seed and 7,500 editing instructions in total across 500 seeds. These operations are not a full natural-language design benchmark, but they illustrate the practical advantage of LAUGHS for editing: the editable object is already surfaced as a named root moiety, group, or site.

In the main benchmark, **Validity** denotes the fraction of generated outputs that correspond to valid molecules, and **Exact Match** denotes the fraction of outputs that follow the requested edit exactly. We additionally report F1-score as a

supplementary fidelity measure, using the standard definition $F_1 = 2PR/(P + R)$, where P and R denote precision and recall. The resulting F1-scores are 0.896 for IUPAC, 0.823 for SMILES, 0.370 for SELFIES, and 0.955 for LAUGHS, following the same ordering as the main-text metrics.