Feedback to Reasoning: LLM-Assisted Molecular Optimization with Domain Feedback and Historical Reasoning

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Abstract

The success of large language models (LLMs) across domains highlights their potential in scientific tasks, with molecular optimization being a promising frontier. Traditionally, this optimization relies on iterative expert feedback to refine molecules toward desired properties, a process well aligned with LLMs' strengths. **As an experience-driven task, molecular optimization depends critically on the domain feedback and accumulation of historical knowledge. However, none of the existing methods fully leverages such feedback and historical knowledge with reasoning traces and chemical insights.** In this work, we propose **F2R**: Feedback to Reasoning, a conversational molecular optimization pipeline that enables LLMs to accumulate and retrieve past actions, rationales, and feedback. Like humans, LLMs can generate imperfect reasoning; F2R is the first framework to use detailed domain feedback to critique and improve this reasoning. This transforms LLMs from passive text generators into agentic experts that learn both actions and reasoning from experience. Consequently, F2R shows remarkable performance.

1 Introduction

Large language models (LLMs) have recently attracted significant interest for scientific applications such as molecular optimization (Zheng et al., 2024; Zhang et al., 2025; Qu et al., 2025). Molecular optimization is a complex, iterative process that depends on expert input and continual refinement. Given a molecule[1] and a target property, experts propose structural modifications based on domain knowledge. These changes are applied, and the resulting analogue is tested in vitro (e.g., enzyme assays) or in silico to evaluate improvements. If the modified molecule meets the target criteria, the process ends; otherwise, experts review the results and suggest further refinements (Jorgensen, 2009; Cao et al., 2023; Liu et al., 2024). This iterative workflow aligns naturally with LLMs' strengths in interactive dialogue and feedback incorporation, enabling LLM-assisted conversational molecular optimization where the model proposes modifications. However, despite strong generative and reasoning abilities, LLMs still often perform suboptimally in this setting because they lack mechanisms to accumulate and reuse historical knowledge and feedback from past tasks (Wang et al., 2023; Edge et al., 2025; Packer et al., 2024).

To better leverage the broad chemistry knowledge of LLMs, recent work proposes integrating them with specialized external guidance modules (agents) that offer optimization suggestions. These agent-assisted approaches aim to bridge the gap between an LLM's general chemical intuition and the specialized, context-dependent reasoning required for practical molecular optimization. In a typical optimization pipeline, each generated candidate is evaluated for desirability, and human experts accumulate historical knowledge from this feedback, which includes information such as molecular validity and property values. Crucially, experts reflect on why specific structural modifications succeed or fail, developing reasoning and domain expertise that informs future optimization. This process of reflection and reasoning is crucial for domain experts, and it is equally important for LLMs to perform effective molecular optimization. However, current guidance agents either do not incorporate any form of historical knowledge accumulation (Liu et al., 2024; Sprueill et al., 2024) or provide only static, one-step suggestions from a limited action space without leveraging reasoning traces or implicit chemical knowledge (Liu et al., 2025b).

In this work, we propose F2R, a conversational molecular optimization pipeline that allows LLMs to dynamically accumulate and retrieve the rich historical knowledge about prior actions, rationales,

[1] Including both small molecules and larger macromolecules such as peptides and proteins.

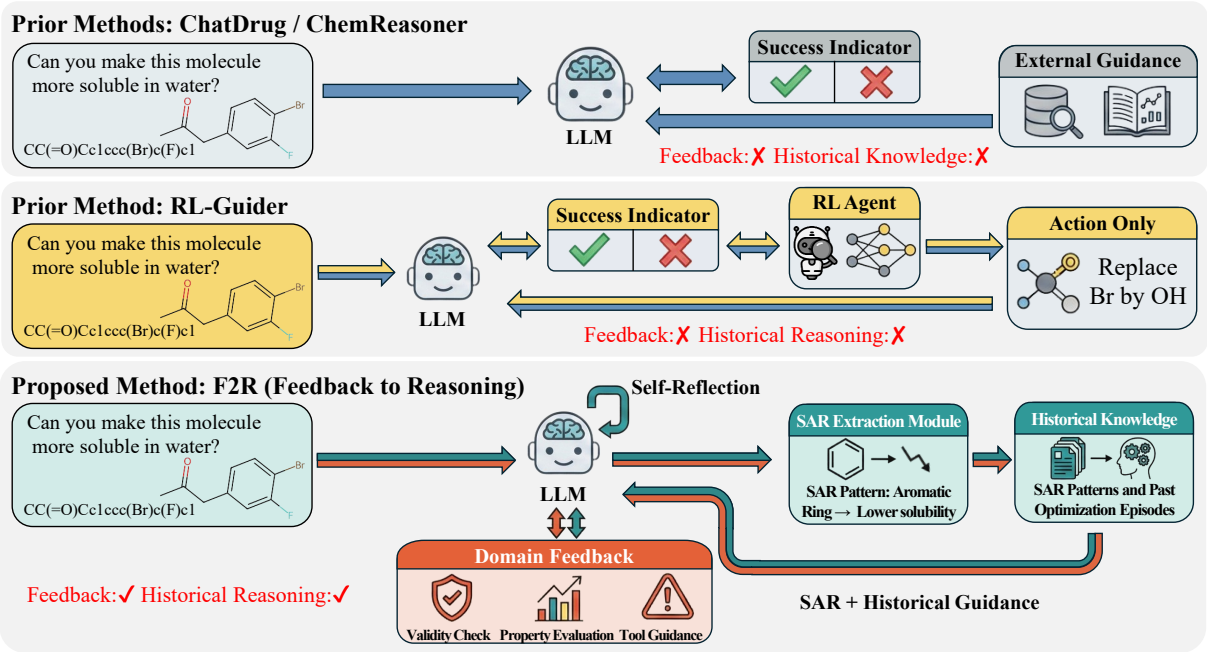


Figure 1: An overview of guidance pipelines for LLM-assisted molecule optimization. Prior methods do not use domain feedback as guidance; they only check whether an optimized molecule meets the objective (success indicator). They also either ignore historical experience (ChatDrug, ChemReasoner) or use it only to guide actions without capturing the underlying reasoning (RL-Guider). In contrast, F2R incorporates detailed domain feedback, allowing the LLM to self-reflect and refine its decisions. F2R also summarizes SAR patterns (see Sec. 4.2), accumulates and retrieves relevant past experiences to guide both actions and the reasoning behind them.

and feedback while fully leveraging LLMs' broad general chemical knowledge and reasoning capabilities. An overview of F2R is provided in Fig. 1. **Overall, we summarize our contribution as follows:** ① We highlight the importance of enabling LLMs to learn from feedback, why past actions succeed or fail in each individual task, to better guide future actions (guided self-reflection). ② We propose F2R, a molecular optimization pipeline that enables guided self-reflection and dynamical historical reasoning for LLMs. ③ F2R does not rely on a predefined external knowledge base or a predefined action space. ④ Experiments demonstrate the superiority of F2R not only in quantitative evaluation metrics but also in transparent knowledge accumulation.

2 Related Work

Over recent years, machine learning has achieved strong success in molecular modeling (Schütt et al., 2017; Chen et al., 2019; Jin et al., 2019; Duval et al., 2024; Chen et al., 2025; Peng, 2024). At the same time, LLMs (Team et al., 2023; Achiam et al., 2023; Bi et al., 2024; Grattafiori et al., 2024) have demonstrated impressive capability across diverse tasks. These advances have motivated growing interest in applying LLMs to molecular tasks (Flam-Shepherd et al., 2022), including early efforts to fine-tune language models for drug discovery (Cao et al., 2023; Liang et al., 2023). Molecular optimization (lead optimization, drug editing[2]) is a crucial subtask in drug discovery, yet LLM-assisted molecular optimization remains underexplored. There are a few existing works. ChatDrug (Liu et al., 2024) employs a domain-specific database to retrieve similar known molecules that satisfy the desired properties as guidance. ChemReasoner (Sprueill et al., 2024) utilizes trained models with predefined domain knowledge to provide optimization suggestions. RL-Guider (Liu et al., 2025b) trains a reinforcement learning (RL) agent on past results to offer guidance on which substructures to modify.

Relations with Prior Works. As noted in Liu et al. (2025b), both ChatDrug and ChemReasoner depend on a predefined knowledge base, which introduces bias by pushing optimized molecules to resemble those already in that knowledge base. To address this limitation, RL-Guider (Liu et al., 2025b) uses historical successes and failures to train an RL-agent whose action space is restricted to a fixed set of atom types and functional groups. However, this fixed action space limits exploration

[2]Drug editing is a specific type of molecular optimization focused on therapeutics; since this work also includes structural optimization tasks such as peptide and protein optimization, we use the broader term molecular optimization.

Pipeline	Utilization of Historical Knowledge	Free of Predefined Knowledge	Unconstrained Exploration Space	Guided Self-Reflection
Plain LLM	✗	✓	✓	✗
ChatDrug	✗	✗	✓♣	✗
ChemReasoner	✗	✗	✓	✗
RL-Guider	✓◇	✓◇	✗	✗
F2R (ours)	✓	✓	✓	✓

♣ ChatDrug uses a limited external dataset as guidance; the space is constrained by the dataset size.
◇ RL-Guider does not use past reasoning and relies on a fixed set of predefined actions.

Table 1: A comparison of existing conversational molecular optimization pipelines.

and constrains the reasoning capabilities of LLMs. Moreover, RL-Guider is trained on, and provides, only discrete actions (e.g., replacing a hydroxyl group with an amino group). We argue that action-level learning alone is insufficient: **LLMs must also understand why certain modifications succeed or fail so they can absorb historical experience and make full use of their broader chemical knowledge and reasoning abilities.** Therefore, we propose F2R, a feedback-and-reasoning-enhanced pipeline that fully leverages rich evaluation information, self-reflects on failed attempts, and enables experience-driven, reasoning-aware LLM-assisted molecular optimization. A comparison between F2R and prior methods is shown in Table 1.

3 Background

Molecular optimization describes the task of transforming a given molecule into another that retains structural similarity while achieving a desired property. Formally, given an input molecule x_{in} represented as a string and a textual task x_{t} describing the optimization objective, molecular optimization can be formulated as a conditional generation problem (Liu et al., 2024) with the goal of producing an optimized molecule $x_{\text{out}} \sim P\left(x \mid x_{\text{in}}, x_{\text{t}}\right)$. In the context of LLM-assisted molecular optimization, this sampling from distribution P is realized by a large language model that generates $x_{\text{out}} = \text{LLM}\left(x_{\text{in}}, x_{\text{t}}\right)$. In contrast to traditional deep generative models that are explicitly trained on domain-specific datasets, LLMs primarily rely on their general chemistry knowledge to reason about molecular structures and properties, enabling them to infer appropriate edits. As a result, LLMs are highly sensitive to the quality of the guidance they receive in the form of prompts, which shape their ability to reason effectively. In addition to their broad knowledge and reasoning capabilities, the conversational abilities (Bubeck et al., 2023) of LLMs are particularly valuable, making it natural for iterative tasks such as molecular optimization. When an edit is not successful, the user can provide feedback to the LLM and prompt it to refine its result. Formally, this is described as

$$x_i = \text{LLM}\left(x_{\text{in}}, x_{\text{t}}, x_{\text{g}}^i\right) \text{ for } i = 0, 1, \ldots, K, \quad (1)$$

where x_{g}^i denotes the guidance provided to the LLM at iteration i, K is the maximum number of iterations, and the final output is x_i for the smallest i such that x_i satisfies the target condition or once the maximum number of iterations is reached. The guidance can be as simple as informing the LLM that the generated molecule does not meet the requirements, or as complex as providing detailed instructions on how to adjust its reasoning. Existing work in this line of research aims to develop more effective forms of guidance for the LLM. A table of notations used in this work is provided in Appendix A.

4 F2R: Feedback to Reasoning

In this section, we introduce F2R, a novel conversational molecular optimization framework with historical knowledge and reasoning enhanced by feedback. While there exist general frameworks for memory and feedback mechanisms (Lu et al., 2025; Chhikara et al., 2025; Xu et al., 2025), F2R is designed specifically for LLM-assisted molecular optimization. It incorporates **domain-specific** similarity metrics for retrieval, summarizes **domain-specific** SAR patterns, and leverages **domain tools** to provide meaningful molecular feedback.

4.1 Molecular Optimization with Feedback and Reasoning

Given an input molecule x_{in} and a textual prompt x_{t} describing the target, F2R proceeds in rounds:

$$\begin{aligned} x_0, r_0 &= \text{LLM}\left(x_{\text{in}}, x_{\text{t}}, x_{\text{g}}^0 \| P_{\text{edit}}\right), \\ \gamma_{i-1}, x_i, r_i &= \text{LLM}\left(x_{\text{in}}, x_{\text{t}}, x_{\text{g}}^i, f_{i-1} \| P_{\text{edit}}\right), \end{aligned} \quad (2)$$

where $i = 1, 2, \ldots, K$, f_i is the feedback on the optimized molecule x_i from the i-th iteration, P_{edit} is a carefully designed prompt template that requires the LLM to return not only the optimized

molecule, but also the reasoning r_i behind this particular edit, and γ_{i-1} is the self-reflection on the last failed result x_{i-1} based on the feedback f_{i-1}. This feedback can also be seen as a form of guidance that encourages the LLM to reason more critically. Here, Eq. (2) differs from Eq. (1) in two key aspects: ① the optimization and reasoning are explicitly required and structured in the output; and ② domain feedback (e.g., the optimize molecule failing to improve the desired property) is incorporated into subsequent iterations, enabling the model to self-reflect on its reasoning and refine future edits.

Autonomous Domain Feedback. While domain feedback can come from various sources, such as in vitro experiments (e.g., enzyme assays) or in silico predictions (computational models), our work focuses on a fully autonomous pipeline. This pipeline integrates computational software tools and rule-based algorithms to operate without human intervention. This process is described in Algorithm 1 in Appendix B.1. Specifically, for optimized molecules, we first evaluate validity: if a molecule is invalid, the LLM receives detailed feedback on why it is invalid, which is done by combining computational tools and carefully designed prompt templates; if valid, its chemical properties are further analyzed and compared with those of the input molecule with respect to the optimization objective x_{t}. These evaluation feedback from computational tools are translated into natural language using carefully designed templates to ensure interpretability for LLMs. Once the optimized molecule meets the objective, the iterative process terminates. For property values, we use computational software tools, including `RDKit` (Landrum et al., 2013) for small molecules, MHCflurry2.0 (O'Donnell et al., 2020) for peptides, and deep learning models such as ProteinDT (Liu et al., 2025a) for proteins. For validity, we use `RDKit` for small molecules and rule-based algorithms for others; more details are described in Appendix B.2. An example of feedback obtained from interacting with `RDKit` is provided below:

> ***Example Feedback.*** *The generated molecule "CCCCn1nc(C(=O)Nc2ccc(N3CCOCC3) nc2)c1O" is checked and it is NOT valid because alternating single and double bonds cannot be assigned to the aromatic atoms while keeping all valences valid.*

4.2 Agentic Awareness of Structure–Activity Relationship

Structure–Activity Relationships (SARs) describe how the chemical structure of a molecule relates to its biological or pharmacological activity (e.g., solubility in water). Chemists design and synthesize related compounds, test their activities, and analyze how specific structural modifications affect performance. Overtime, SARs that chemists learn from past experience help them make informed decisions about which edits are likely to improve a molecule's properties. After an optimization task j is finished, we further request the LLM to extract key SAR insights:

$$p, c = \text{LLM}\left(m || P_{\text{SAR}}\right), \tag{3}$$

where m is the messages (interactions between the user and the LLM) in all the iterative rounds, p denotes the extracted structural pattern or transformation (e.g., replace hydroxyl with amino), c describes the conditions under which this pattern holds (e.g., only valid for aromatic rings), and P_{SAR} is a carefully designed prompt template for the extraction of SAR patterns. All the prompts for F2R are provided in Appendix C.

4.3 Leveraging Historical Experience

Knowledge Accumulation Module. To accumulate historical experience, we store optimization histories in a structured way. Specifically, for an individual optimization task, we store a knowledge entry $e_j = \{x_{\text{in}}, x_{\text{t}}, p, c, (x_i, r_i, f_i, \gamma_i)\forall_i\}$. Overall, we will maintain a collection of knowledge entries $\mathcal{E} = \{e_1, e_2, \ldots, e_N\}$ as the historical knowledge base. For each optimization task performed by the LLM, a new entry is autonomously added to this growing knowledge base. As more edits are conducted across different molecules and targets, the accumulated knowledge collection $\mathcal{E}$ continues to expand over time.

Historical Knowledge Retrieval Module. As the historical knowledge base $\mathcal{E}$ expands over time, an important aspect of F2R is to effectively retrieve the most relevant pieces of accumulated knowledge to guide new optimization tasks. Given a new optimization task specified by $(x_{\text{in}}, x_{\text{t}})$, we identify a subset of historical knowledge entries that share the same target $\mathcal{E}_{x_{\text{t}}} = \{e_j \in \mathcal{E} \mid e_j[x_{\text{t}}] = x_{\text{t}}\}$, where $[\,\cdot\,]$ denotes accessing a specific field in the knowledge entry. Within $\mathcal{E}_{x_{\text{t}}}$, we further retrieve a set R^* of $k_{\text{retrieval}}$ knowledge entries that are most relevant

to the optimization task. Formally,

$$R^* = \underset{R \subseteq \mathcal{E}_{x_t}, |R| = k_{\text{retrieval}}}{\arg\max} \sum_{e \in R} \text{sim}\left(x_{\text{in}}, e[x_{\text{in}}]\right), \quad (4)$$

where $\text{sim}(\cdot, \cdot)$ is a similarity function that measures how similar the two molecules are. In practice, string representations of molecules (e.g., SMILES strings, protein sequences) are in discrete metric spaces. Standard similarity functions, such as cosine similarity, are no longer applicable. Tanimoto similarity is adopted for small molecules, and Levenshtein distance is adopted for peptides and proteins. More details about these similarity metrics are provided in Appendix B.3. Note that we only provide this guidance in the first round; in subsequent rounds, only feedback will be given. The SAR patterns in the retrieval knowledge entries R^* will be used in the guidance x_g^i in Eq. (2).

4.4 Why F2R? Feedback-driven Reasoning and Knowledge Accumulation

Feedback-driven Reasoning. In molecular optimization, each generated molecule is evaluated to determine whether it meets the target properties. Even when a molecule fails, the evaluation provides rich feedback, such as validity, structural similarity, property values, and domain tool feedback, that helps human experts refine their decisions and propose more effective modifications. However, none of the existing approaches (Liu et al., 2024, 2025b)[3] incorporate this feedback into the LLM-assisted iterative process. F2R explicitly treats feedback as a core driver of reasoning. By learning from evaluation signals, it corrects prior mistakes and avoids repeating them in later iterations. As shown in Sec. 5, guidance approaches that emphasize reasoning (ChemReasoner and F2R) outperform action-focused methods (RL-Guider and ChatDrug), and F2R further surpasses ChemReasoner due to its feedback-driven reasoning mechanism.

Knowledge Accumulation. Chemists often build intuition by recognizing recurring structural patterns: similar molecules tend to behave similarly. To mirror this intuition, F2R stores optimization trajectories and extracts transferable SAR patterns. Unlike prior methods that use such information only to propose a single action (Liu et al., 2025b) or retrieve a similar molecule (Liu et al., 2024), F2R uses these patterns to provide higher-level guidance, encouraging the LLM to reason about why a transformation may work and how it can be adapted to a new context. Thus, accumulated SAR knowledge becomes a source of reasoning rather than imitation. Because LLMs may generate misleading or incorrect reasoning, these historical experiences and SAR-derived insights are continually self-reflected against domain feedback, providing a more reliable and grounded basis for future reasoning.

[3] RL-Guider (Liu et al., 2025b) uses feedback only as an RL reward; the LLM itself does not receive feedback on the molecules it generates.

5 Experiments

In this section, we evaluate the effectiveness of F2R through experiments on diverse molecular types, including small molecules, peptides, and proteins, following (Liu et al., 2024). Additional task details are provided in Appendix D.

Setup. We compare F2R with a raw LLM without guidance (Base LLM), ChatDrug, ChemReasoner, RL-Guider, and F2R itself. Like RL-Guider, F2R requires historical optimization results to evaluate knowledge accumulation. To obtain these, we construct a greedy coreset of small molecules, peptides, and proteins from the remaining dataset (excluding the test set), with the coreset size matching the test set. Molecular optimization is first performed on this coreset to generate initial historical trajectories. For peptides and proteins, we omit RL-Guider since it is not implemented for these tasks due to infeasible action space construction. All methods, including F2R, are LLM-agnostic; we use GPT-4.1 and Gemini-2.5-Flash as backbone models. **We follow exactly the test dataset of Liu et al. (2024).** We follow the experimental setup of Liu et al. (2024): the maximum number of iterations is $K = 2$. In the first round ($k = 0$), no guidance is provided. If the output is unsatisfactory, a second round is run with suggestions for all methods; if still unsatisfactory, a third round follows. Baseline prompts are taken directly from Liu et al. (2024, 2025b), and we additionally enforce output-format compliance using `Structured Outputs` with a JSON schema.

Evaluation Metric. We evaluate performance using the success ratio, defined as the proportion of generated molecules that are both valid and satisfy the target property, relative to the total number of optimization tasks. This differs from the hit ratio used in Liu et al. (2024), which computes the proportion of successful outcomes only among valid molecules. Success ratio is a stricter metric, also adopted in Liu et al. (2025b).

Task	Δ	ChatGPT-4.1					Gemini-2.5-Flash				
		Base LLM	Chat Drug	Chem Reasoner	RL-Guider	F2R	Base LLM	Chat Drug	Chem Reasoner	RL-Guider	F2R
More soluble in water	0	81.00	83.50	83.50	85.50	99.00	85.00	81.00	84.00	82.50	99.00
	0.5	84.00	81.50	84.00	83.50	96.00	80.50	81.50	76.50	79.50	96.00
Less soluble in water	0	85.00	85.50	84.50	85.50	99.00	95.50	97.00	98.00	91.50	99.00
	0.5	72.00	56.00	76.50	63.50	81.50	87.50	87.00	88.50	87.00	95.50
More like a drug	0	46.00	61.50	73.50	47.50	69.00	79.00	77.50	79.50	73.50	83.50
	0.5	6.00	20.00	18.00	8.50	21.00	16.50	27.00	22.50	19.50	30.50
Less like a drug	0	68.50	61.50	72.50	65.00	89.00	70.50	68.50	85.50	69.50	78.50
	0.1	16.50	28.50	52.00	24.50	63.50	44.00	43.00	67.00	53.50	65.00
Higher permeability	0	31.50	53.50	81.50	47.50	94.50	92.50	91.00	91.00	93.00	97.00
	10	19.50	36.50	62.50	34.00	74.00	52.50	62.00	63.00	61.50	79.00
Lower permeability	0	87.00	85.50	88.00	86.50	99.00	86.00	86.50	83.50	84.50	99.00
	10	87.00	83.50	88.50	86.50	97.50	85.00	81.50	82.00	84.50	98.50
More hydro-bond acceptors	0	74.00	69.00	76.50	77.50	97.00	80.50	82.50	78.50	74.50	99.00
	1	19.00	23.00	34.00	20.50	42.50	44.00	44.00	57.00	44.50	68.50
More hydro-bond donors	0	80.00	78.00	85.50	81.00	97.50	74.50	70.50	75.00	70.50	98.00
	1	13.00	26.50	19.50	22.50	41.50	16.50	15.00	47.00	15.50	52.50

Table 2: Results on 16 single-objective small molecule optimization tasks. The best and second-best results are highlighted in red and blue, respectively. F2R consistently achieves the highest success ratios in 15 out of 16 tasks with ChatGPT-4.1 and 14 out of 16 tasks with Gemini-2.5-Flash. **These results demonstrate the effectiveness of feedback-driven reasoning and knowledge accumulation.**

5.1 Small Molecules

We evaluate the performance of F2R against baseline methods on small molecules. 200 test molecules are drawn from the ZINC dataset.

Evaluation. An edited molecule is deemed successful if its property value improves by at least Δ compared to the original molecule. For instance, if $\Delta = 0.1$ and the goal is to increase solubility, then the solubility of the modified molecule must exceed that of the original by at least 0.1 unit to be counted as a success. We evaluate under two settings: (1) *Single-objective optimization*, where the goal is to improve a single property value, and (2) *Multi-objective optimization*, where the goal is to improve two property values simultaneously.

Results and Discussion. We report single-objective optimization results in Table 2 and multi-objective results in Table 9 in Appendix E.1. A visualization of an optimization task, along with the historical knowledge retrieved by F2R, is shown in Table 3, illustrating how historical trajectories provide strong guidance. In a case study in Appendix E.2, we further show that feedback-driven reasoning enables the LLL to correct its own mistakes through self-reflection. Across tasks, F2R consistently outperforms all baselines. It achieves the highest success ratio in 15 of 16 single-objective tasks with ChatGPT-4.1 and in 14 of 16 tasks with Gemini-2.5-Flash. For multi-objective optimization, F2R attains the highest success ratio across all tasks for both models. We also observe that Gemini-2.5-Flash slightly outperforms ChatGPT-4.1 despite being smaller and faster, likely due to its built-in chain-of-thought reasoning, highlighting the importance of reasoning for molecular optimization.

The performance of ChatDrug and RL-Guider does not show any consistent improvement over even the base LLM. We suspect that recent advanced LLMs possess sufficient chemical knowledge and reasoning capabilities such that external guidance on actions does not enhance reasoning; instead, it may mislead the model and even constrain its reasoning ability as the action is given. In contrast, ChemReasoner achieves the second best success ratio in most of the tasks because it leverages LLMs to reason and plan to achieve the optimization objective, thereby enabling guidance on explicit reasoning. This emphasizes the importance of guiding LLMs to better reasoning rather than providing static guidance on actions to take.

5.2 Immunogenic Binding Peptides

We evaluate the performance of F2R against baseline methods on immunogenic binding peptides. The test examples are from the experimental dataset of peptide-MHC binding affinities (O'Donnell et al., 2020), which contains 149 human MHC Class I proteins (alleles) and 309 thousand peptides. The test data contains 500 target-source pairs from 30 common MHC proteins (alleles).

Evaluation. The actual bindings require wet-lab experiments, which are expensive and prohibited for large-scale evaluation. MHCflurry2.0 (O'Donnell et al., 2020) is used as a pseudo-oracle to predict the peptide-MHC binding affinity. The success of peptide optimization must meet two criteria: (1) the resulting peptide

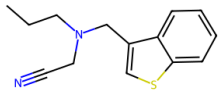
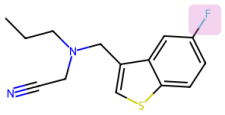
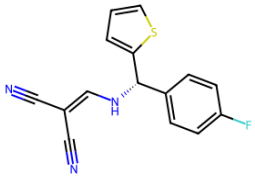
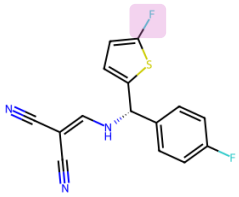
	Input Molecule	Output Molecule	Reasoning
Historical Knowledge	 CCCN(CC#N) Cc1csc2ccccc12	 CCCN(CC#N) Cc1csc2ccc(F)cc12	SAR: 1. Addition of a second fluorine enhances metabolic stability and drug-likeness; 2. Chlorine substitution does not enhance drug-like.....
Current Optimization Task	 N#CC(C#N)=CN[C@@H] (c1ccc(F)cc1)c1cccs1	 N#CC(C#N)=CN[C@@H] (c1ccc(F)cc1)c1ccc(F)s1	Reasoning: Based on the history and SAR feedback, introducing a fluorine to the aromatic system is a proven strategy to enhance drug-likeness.....

Table 3: Visualization of an optimization task to make the input molecule *more like a drug* and the relevant SAR patterns from historical knowledge. **Clearly, leveraging historical knowledge provides substantial guidance in accomplishing this task.** We only show part of the SAR and reasoning due to length limits.

Task	ChatGPT-4.1				Gemini-2.5-Flash			
	Base LLM	Chat Drug	Chem Reasoner	F2R	Base LLM	Chat Drug	Chem Reasoner	F2R
301	3.40	62.80	84.80	95.60	93.80	94.60	96.20	98.20
302	46.60	40.60	51.60	55.80	60.20	51.00	64.00	72.20
303	2.60	52.80	61.80	66.80	77.80	85.40	90.20	87.20
304	53.80	35.80	59.60	64.00	43.20	40.00	45.20	56.40
305	47.00	34.80	56.20	63.80	50.40	43.80	50.40	67.80
306	25.20	61.60	80.60	78.20	79.60	87.20	90.00	95.40
401	28.20	15.40	27.60	34.40	19.80	14.60	15.60	26.80
402	10.40	12.00	11.80	13.80	16.00	10.80	13.80	17.60

Table 4: Results on 8 peptide optimization tasks. The task descriptions corresponding to task IDs are provided in Appendix D. The best and second-best results are highlighted in red and blue, respectively. F2R consistently achieves the highest success ratios in 7 out of 8 tasks, **demonstrating the generalizability of F2R to peptide tasks.**

should exhibit a higher binding affinity to the target allele than the original peptide; and (2) the binding affinity between the edited peptide and the target allele must exceed a specified threshold. Following Liu et al. (2024), we set this threshold to be one-half of the average binding affinity observed in experimental data for the target allele. There are both single-objective and multi-objective tasks; single-objective tasks only require the peptide to bind to one target allele type, whereas multi-objective tasks require the peptide to bind to two target allele types. The detailed tasks are provided in Appendix D.

Results and Discussion. Similar to the case of small molecules, Gemini-2.5-Flash generally outperforms ChatGPT-4.1, underscoring the importance of reasoning. Across the benchmarks, F2R consistently achieves the best performance in 7 out of 8 tasks for both ChatGPT-4.1 and Gemini-2.5-Flash, while being a second in the remaining task. Although not as strong as F2R, ChemReasoner also demonstrates competitive results. Overall, these findings highlight the critical role of providing explicit reasoning guidance, thereby reinforcing the effectiveness of our method. A case study illustrating the optimization process for a peptide-optimization task is provided in Appendix E.2 to clarify the procedure.

5.3 Protein Secondary Structures

We evaluate the performance of F2R against baseline methods on protein secondary structures. TAPE (Rao et al., 2019) is a benchmark for protein sequence property prediction, including the secondary structure prediction task. We use the test set of TAPE as our testing examples following Liu et al. (2024) exactly.

Evaluation. We use a pretrained secondary structure prediction model, ProteinCLAP-EBM-NCE from ProteinDT (Liu et al., 2025a), to evaluate the edited proteins. An edit is considered successful if the output protein sequences have more secondary structures than the input sequences.

Task	ChatGPT-4.1				Gemini-2.5-Flash			
	Base LLM	Chat Drug	Chem Reasoner	F2R	Base LLM	Chat Drug	Chem Reasoner	F2R
More helix structures	72.58	74.42	78.34	86.18	69.59	72.81	76.50	82.72
More strand structures	53.23	47.24	64.98	74.19	58.29	55.76	61.06	66.82

Table 5: Results on 2 protein optimization tasks. The best and second-best results are highlighted in red and blue, respectively. F2R performs the best in both tasks, **demonstrating the generalizability of F2R to protein tasks.**

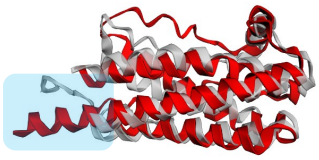
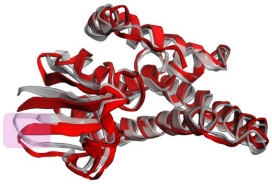
Task	Input&Output Proteins	Reasoning
More helix structures		Based on the feedback from history, successful edits specifically increase helix content by targeting loop and coil regions (rich in glycine, proline, or serine) and strategically introducing helix-promoting residues such as alanine (A), leucine (L),.....
More strand structures		Based on prior feedback and structure-activity relationships, I specifically replaced or inserted multiple strand-favoring residues (V, I, F, Y, W, T) at positions not already dominated by these amino acids, particularly in regions.....

Table 6: Visualization of two optimization tasks aimed at producing *more helix structures* and *more strand structures*, respectively. The input protein is shown in light grey, and the final optimized protein is shown in red. **In these examples, the LLM leverages relevant historical knowledge and learns from prior patterns to guide the optimization toward the desired secondary-structure enrichment.**

Results and Discussion. The results are presented in Table 5. F2R consistently outperforms all baseline methods, further highlighting its generalizability to proteins. Consistent with the results on small molecules and peptides, ChemReasoner achieves the second-best performance, underscoring the importance of explicit guidance for reasoning. In Table 6, we also provide visualization of two optimization tasks alongside the LLM's reasoning, where retrieved historical knowledge offers substantial guidance in completing the tasks.

5.4 Additional Results and Visualization

We provide several case studies in Appendix E.2 that illustrate how feedback-driven reasoning and historical knowledge enable the LLM to make correct decisions. We conduct **ablation studies** to demonstrate that: ① Both feedback-driven reasoning and knowledge accumulation are crucial components of LLM-assisted molecular optimization pipelines; and ② As the knowledge base grows, the guidance it provides becomes more effective, leading to higher success rates. The results are provided in Appendix E.3. We provide failure analysis for all methods in Appendix E.4. We also provide additional general visualization for all three types of optimization tasks (small molecules, immunogenic binding peptides, and protein secondary structures) in Appendix E.5.

6 Conclusion and Future Work

In this work, we introduce F2R, a novel framework that employs a multi-agent system to autonomously accumulate, distill, and reuse historical knowledge and reasoning traces for more efficient and effective LLM-assisted molecular optimization. Specifically, F2R is the first to explicitly learn from detailed optimized outcomes, capturing not only actions but also the rationales behind successes and failures. By combining a dynamic historical knowledge base with an agentic SAR memory, F2R progressively refines its optimization strategies through experience-driven counterfactual replay, addressing key limitations of existing predefined guidance approaches. Experimental results across small molecules, peptides, and proteins demonstrate F2R's superior performance and transparent reasoning compared to strong baselines, validating the benefits of experience accumulation and agentic memory systems in complex molecular optimization tasks.

As future work, the proposed feedback mechanism and historical records could serve as a natural foundation for reinforcement learning fine-tuning (RLFT), enabling LLMs to iteratively improve their reasoning capabilities and domain adaptation.

7 Limitations

As a fully autonomous system built on LLMs, the effectiveness of F2R is inherently constrained by the reasoning accuracy and domain knowledge of the underlying language models. Improving the capabilities of the backbone LLMs remains an open limitation of this work. In addition, the extracted reasoning and SAR patterns are learned from observed optimization trajectories and feedback, which may reflect correlations rather than true causal structure–property relationships. As a result, the system may overgeneralize patterns that work in specific contexts but fail under distributional shifts or more complex constraints.

8 Ethical Considerations

This work advances LLM-assisted molecular optimization through a novel feedback-to-reasoning framework. Although large language models may raise general ethical considerations, the scope of this work is methodological and scientific in nature. We do not identify any specific societal or ethical risks introduced by our approach beyond those commonly associated with the use of LLMs.

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A Table of Notations

We summarize notations used throughout this paper in Table 7.

Notation	Description
x_{in}	Input molecule (SMILES strings, peptide and protein sequences).
x_{t}	Textual task or optimization objective.
x_{out}	Final optimized molecule produced by the LLM.
K	Maximum number of allowed optimization iterations.
x_i	Optimized molecule at iteration i.
x_{g}^i	Guidance (feedback, SAR knowledge, etc.) provided to the LLM at iteration i.
r_i	Reasoning provided by the LLM at iteration i (why the action was taken).
f_i	Domain feedback on the optimized molecule x_i (validity, property change, etc.).
γ_i	Self-reflection of the LLM at iteration i, based on f_i.
P_{edit}	Structured prompt template requiring reasoning output.
p	Extracted structural pattern (e.g., hydroxyl $\rightarrow$ amino substitution).
c	Condition under which a structural pattern p holds (e.g., for aromatic rings).
m	All iterative messages (dialogue history) between user and LLM in an optimization task.
e_j	Knowledge entry for optimization task j: $\{x_{\text{in}}, x_{\text{t}}, p, c, (x_i, a_i, r_i, f_i, \gamma_i)_{\forall i}\}$.
$\mathcal{E}$	Historical knowledge base of all accumulated entries.
$\mathcal{E}_{x_{\text{t}}}$	Subset of $\mathcal{E}$ containing tasks with the same target x_{t}.
$k_{\text{retrieval}}$	Number of historical entries retrieved.
R^*	Retrieved subset of $k_{\text{retrieval}}$ most relevant entries for a new task.
$\text{sim}(\cdot, \cdot)$	Similarity function (Tanimoto similarity for small molecules, Levenshtein distance for peptides/proteins).
p_{in}	Property values of the input molecule.
p_i	Property values of the optimized molecule x_i.

Table 7: Summary of Notations.

B Additional Details for F2R

B.1 Autonomous Domain Feedback Algorithm

We present the autonomous domain feedback process in Algorithm 1. In the algorithm, `ExplainInvalidity` is the detailed feedback on why it is invalid, and `ParseToNaturalLanguage` translates the feedback from computational tools into natural language using carefully designed templates to ensure interpretability for LLMs.

Algorithm 1 Autonomous Domain Feedback

Require: Relevant property values of the input molecule p_{in}, optimization objective x_{t}, current optimized molecule x_i

if `IsValid`(x_i) = **false then**
  $f_i \leftarrow$ `ExplainInvalidity`(x_i)
  return f_i, ContinueIteration
end if
$p_i \leftarrow$ `ComputeProperties`(x_i)
EvaluationFeedback$\leftarrow$ `ParseToNaturalLanguage`($p_i, p_{\text{in}}, x_{\text{t}}$)
if `MeetsObjective`(p_i, x_t) **then**
  $f_i \leftarrow$ "The optimized molecule is valid." + EvaluationFeedback
  return f_i, StopIteration
else
  $f_i \leftarrow$ "The optimized molecule is valid." + EvaluationFeedback
  return f_i, ContinueIteration
end if=0

ContinueIteration and StopIteration are Boolean indicators to continue and stop the optimization iterations, respectively.

B.2 Validity and Feedback

Small Molecules. For small molecules, we use the `Chem.MolFromSmiles()` method from `RDKit`. First of all, we detect if there are characters that are not possible to appear in a SMILES string by regular expression (rule-based). Then, if the SMILES string contains only valid characters, we use RDKit to test for validity. In particular, there are several common reasons for it to fail. ① Kekulization failures: There are aromatic atoms that can't be assigned alternating single/double bonds. ② Valence errors: Atom exceeds its allowed valence. ③ Caromaticity assignment: Mixing aromatic and non-aromatic atoms in a ring inconsistently. ④ Ring problems: Missing ring closure digits (unclosed rings). We carefully design templates to convert the error messages into natural language for LLM feedback. It is rare, but there are other potential errors; we directly use the error message as the feedback in such case.

Peptides and Proteins. Peptides and proteins are represented as sequences of amino acids using the standard one-letter code. Among the 26 English alphabets, 20 correspond to the canonical amino acids, 2 (U and O) represent rare amino acids, and 4 (B, Z, J, X) are reserved for ambiguous or unknown residues. In principle, any combination of these letters forms a syntactically valid sequence, although not all combinations correspond to chemically plausible or biologically functional proteins. For validation, we detect invalid characters using regular expressions. If only valid letters are present, the sequence is accepted as a valid peptide/protein string. Depending on the task, we can restrict to only the canonical amino acids or unambiguous residues. Additional biological plausibility checks (e.g., domain detection or similarity search) may also be applied depending on the downstream task.

B.3 Tanimoto Similarity and Levenshtein Distance

Small Molecules. For small molecules represented in SMILES, Tanimoto similarity measures the similarity between two molecules based on their chemical structures. First, SMILES strings are converted into molecular fingerprints (binary) by RDKit. Then, the Tanimoto similarity coefficient is defined as:

$$S(A, B) = \frac{|A \cap B|}{|A \cup B|} \in [0, 1],$$

where A and B are two binary fingerprint vectors, $|A \cap B|$ is the number of common bits set to 1 in both fingerprints, $|A \cup B|$ is the number of bits to 1 in either fingerprint.

Peptides and Proteins. For peptide and protein sequences, the Levenshtein distance provides a way to measure sequence similarity by counting the minimum number of edit operations required to transform one amino acid sequence into another. The Levenshtein distance between two amino acid sequences a and b (of lengths $|a|$ and $|b|$ respectively) is defined as $\text{lev}(a, b)$:

$$\text{lev}(a,b) = \begin{cases} |a|, & |b| = 0, \\ |b|, & |a| = 0, \\ \text{lev}(\text{tail}(a), \text{tail}(b)), & \text{head}(a) = \text{head}(b), \\ 1 + \min\{X_1, X_2, X_3\}, & \text{otherwise}, \end{cases}$$

where

$$X_1 = \mathrm{lev}(\mathrm{tail}(a), b),$$
$$X_2 = \mathrm{lev}(a, \mathrm{tail}(b)),$$
$$X_3 = \mathrm{lev}(\mathrm{tail}(a), \mathrm{tail}(b)).$$

Here, $\mathrm{head}(x)$ denotes the first character of the sequence x (i.e., the first amino acid), and $\mathrm{tail}(x)$ is the remainder of the sequence after removing the first character. The recurrence relation captures three types of edit operations: (1) Deletion: removing an amino acid from a to align with b; (2) Insertion: adding an amino acid into a to align with b; (3) Substitution: replacing one amino acid in a with another to match b. Thus, the Levenshtein distance $\mathrm{lev}(a, b)$ corresponds to the minimum number of insertions, deletions, and substitutions needed to transform sequence a into sequence b.

C Prompts

We give an example of conversation messages for F2R for a complete optimization round. We have the following system prompt following prior work

System Prompt

You are a helpful chemistry expert with extensive knowledge of drug design.

In the first round, we ask the LLM to generate 5 edited candidates following the exact setup as in Liu et al. (2024), and the first that does not contain invalid characters will be taken as the optimized molecule. Note that we now require the reasoning traces and optimized molecules to be structured as a json object through *Structured Outputs* with a JSON schema. All baselines adopt this strategy to ensure that the optimized molecules are structured.

First Round Task Prompt

<task_prompt>. The output <molecule_type> should be similar to the input molecule. Give me 5 <molecule_type> in string representation only.
Give me a short reasoning first, and then a list of <molecule_type> under the key "optimized_molecules".
Return the result as a json object in the following format:
{{"reasoning": <reasoning>, "optimized_molecules": [<string1>, <string2>, <string3>, <string4>, <string5>] }}

The task prompts are given in details in Appendix D below. If the optimized molecule in the first round is not valid or does not satisfy the property requirements:

Iterative Round Task Prompt

The optimized molecule <optimized_molecule> is evaluated: <autonomous_domain_feedback>. Here is the history and feedback from the most similar molecule for the same task:
- The original molecule is: <input_molecule> - The optimized molecule is: <optimized_molecule> - The feedback on the attempt from evaluation: <autonomous_domain_feedback>
- Potential structure-activity relationship summarized from the same task: <SAR_patterns> However, you should remember that it does not always apply to your task.
Can you give me a new <molecule_type>? This time, return only one <molecule_type> in string format.
Return the result as a json object in the following format:
{{ "reasoning": <reasoning>, "optimized_molecule": [<string1>] }}

After the task in completed or the maximum number of iterations is reached, the LLM is asked to summarize the conversation and identify transferable SAR patterns:

SAR Task Prompt

1. Summarize in concise sentences why these edits were successful or not. This should also include certain reasoning and how to improve. Be explicit and relatively short.
2. If you see any clear structure–activity relationship (SAR) trend across different molecules, state in precise and very short phrases. If you do not see any obvious SAR pattern, just return an empty string.
Return ONLY the following JSON object:
{{ "summary": <concise bullet or sentence per peptide, keep in a single string>, "sar": [<very short SAR statement or empty string>] }}

D Task Description and Task Prompts

Small Molecules. For small molecules, the task is to edit the SMILES string to satisfy the task requirements listed in Table 2 and Table 9, respectively (e.g. "more soluble in water"). The task prompt is:

> **Task Prompt for Small Molecules**
>
> Can you make the molecule <input_smiles_string> <task_requirements>?

Peptides. For peptides, the task is to modify a peptide that binds to a source allele type so that it can bind to given target allele type(s), which is a common task in peptide design and immunology research. The task prompt is:

> **Task Prompt for Peptides**
>
> We want a peptide that binds to <target_allele_types>. We have a peptide <input_peptide> that binds to <source_allele_type>, can you help modify it?

The task IDs and their corresponding source and target allele types are given in Table 8.

Task ID	Source Allele Type	Target Allele Type(s)
301	HLA-C*16:01	HLA-B*44:02
302	HLA-B*08:01	HLA-C*03:03
303	HLA-C*12:02	HLA-B*40:01
304	HLA-A*11:01	HLA-B*08:01
305	HLA-A*24:02	HLA-B*08:01
306	HLA-C*12:02	HLA-B*40:02
401	HLA-A*29:02	HLA-B*08:01 and HLA-C*15:02
402	HLA-A*03:01	HLA-B*40:02 and HLA-C*14:02

Table 8: Target allele type(s) and source allele type for peptide optimization.

Proteins. For proteins, the task is to modify a protein sequence so that more amino acids adopt desired secondary structures, specifically α-helix (more helix structure) or β-strand (more strand structure) conformations. The task prompt is:

> **Task Prompt for Small Molecules**
>
> We have a protein <input_protein_sequence>. Can you modify it by making more amino acids into the <desired_secondary_structure_type> (secondary structure)?

E Additional Experimental Results and Discussion

E.1 Results on Multi-objective Small Molecule Optimization Tasks.

We provide the results on 12 multi-objective small molecule optimization tasks in Table 9.

E.2 Case Studies: Feedback Driven Self-reflection and Historical Knowledge

We provide several case studies to showcase instances where feedback-driven reasoning and historical knowledge lead to successful optimization, whereas without them, the LLM struggles to produce a satisfying molecule. One case study is provided for each type of molecule (small molecules, peptides, and proteins), using either feedback-driven reasoning or historical knowledge to illustrate the optimization process. However, we note that for all molecule types, both feedback-driven reasoning and historical knowledge significantly aid the LLM in performing these tasks. **In all examples below, the sentences after "Note: " are not LLM outputs; they are added to help readers better understand the results.**

E.2.1 Feedback-Driven Reasoning

We first provide a case study that showcases instances where the LLM initially produces an invalid molecule, and we then provide detailed feedback to the LLM. We also perform the same experiment without detailed feedback from domain tools, using only a success indicator as done in prior works. To do this, we reuse the same messages until feedback so that the input molecule and the optimized molecule from the first iteration are the same. In this case, the LLM makes the same mistake of producing an invalid molecule.

With Feedback:

- **Input Molecule:**

  Cn1ccc(C(=O)Nc2sc3c(c2C#N)CCC3)cc1=O

- **Task:** *More soluble in water*

Task	Δ	ChatGPT-4.1					Gemini-2.5-Flash				
		Base LLM	Chat Drug	Chem Reasoner	RL-Guider	F2R	Base LLM	Chat Drug	Chem Reasoner	RL-Guider	F2R
More soluble in water	0, 0	79.50	74.50	82.50	83.50	96.00	76.00	78.00	78.50	77.50	93.00
More hydro-bond acceptors	0.5, 1	20.00	26.50	39.00	28.50	40.50	38.50	31.00	44.00	36.50	59.50
Less soluble in water	0, 0	17.00	16.50	23.00	17.50	50.00	63.50	61.00	61.50	57.50	77.50
More hydro-bond acceptors	0.5, 1	0.00	4.00	0.50	1.00	4.50	13.50	13.00	14.00	13.00	25.00
More soluble in water	0, 0	86.00	84.00	86.00	88.50	98.50	73.00	72.00	70.00	70.50	96.50
More hydro-bond donors	0.5, 1	57.50	42.50	48.00	38.50	63.00	33.50	30.50	60.00	41.50	71.50
Less soluble in water	0, 0	4.00	16.50	28.00	21.00	54.50	64.00	64.00	65.50	64.50	78.50
More hydro-bond donors	0.5, 1	0.00	1.00	1.50	1.50	3.00	8.50	10.00	9.50	10.50	16.00
More soluble in water	0, 0	8.00	16.50	11.00	12.50	25.50	5.50	4.50	3.50	5.00	8.50
Higher permeability	0.5, 10	0.00	3.00	3.00	2.50	4.50	0.50	1.00	0.50	0.50	1.00
More soluble in water	0, 0	86.00	85.50	85.50	84.50	98.50	83.00	80.00	81.00	83.50	98.00
Lower permeability	0.5, 10	86.50	80.00	81.00	84.50	95.50	82.00	79.50	79.00	83.50	95.00

Table 9: Results on 12 multi-objective small molecule optimization tasks. The best and second-best results are highlighted in red and blue, respectively. F2R achieves the highest success ratios for all tasks. It should be noted that certain tasks are sufficiently challenging that all methods yield very low success ratios; however, F2R still demonstrates improvements on such a limited search space.

- **Optimized Molecule (1st iteration):**

  HOCH2c1cc(Sc2cc3ccccc3[nH]2)ccc1C=O (Note: This is an invalid molecule due to a syntax error in the methylene group)

- **Feedback:**

  The optimized molecule HOCH2c1cc(Sc2cc3ccccc3[nH]2)ccc1C=O is checked by experts and it is NOT valid because of RDKit error: "syntax error while parsing; check for mistakes around position 1; failed to parse SMILES."

- **Reasoning:**
  The previous SMILES HOCH2c1cc(...) was syntactically incorrect for a hydroxymethyl group. The corrected SMILES replaces the methyl group with a hydroxymethyl group (CH2OH) by explicitly defining the bond from the ring carbon to the new carbon, which is then bonded to oxygen, thereby increasing water solubility through the addition of a hydroxyl group.

- **Optimized Molecule (2nd iteration):**

  c1(CO)cc(Sc2cc3ccccc3[nH]2)ccc1C=O (Note: This is a valid molecule that is more soluble in water)

Without Feedback:

- **Input Molecule:**

  Cn1ccc(C(=O)Nc2sc3c(c2C#N)CCC3)cc1=O

- **Task:** *More soluble in water*

- **Optimized Molecule (1st iteration):**

  HOCH2c1cc(Sc2cc3ccccc3[nH]2)ccc1C=O (Note: This is an invalid molecule due to a syntax error in the methylene group)

- **Feedback:**

  Your provided sequence HOCH2c1cc(Sc2cc3ccccc3[nH]2)ccc1C=O is not correct.

- **Reasoning:**

  A small polar modification near the aromatic core can improve water solubility while retaining overall scaffold similarity. Introducing a hydroxyl-bearing substituent increases hydrogen-bonding capacity without drastically changing the molecule's shape.

- **Optimized Molecule (2nd iteration):**

  OCH2Cc1cc(Sc2cc3ccccc3[nH]2)ccc1C=O (Note: This is still an invalid molecule due to a syntax error in the methylene group)

Clearly, in this example, the LLM is able to identify and correct its own mistake once explicit structural feedback is provided. With guidance, the model transitions from producing an invalid SMILES string to generating a syntactically valid molecule that reflects the intended functional modification. In contrast, without feedback, the LLM repeats the same mistake, the syntax error in the methylene group remains uncorrected. This demonstrates the effectiveness of feedback-driven reasoning in guiding the model toward correct outputs.

E.2.2 Historical Knowledge

We present two cases showing the role of historical knowledge in optimization: an example where the model benefits from prior successes, and another

example where it learns from past failures to avoid repeating the same errors.

Learning from Past Success:

- **Input Peptide:** *ITAPTVRQY*
- **Task:** *We want a peptide that binds to HLA-B*44:02. We have a peptide ITAPTVRQY that binds to HLA-C*16:01, can you help modify it?*
- **Optimized Peptide (1st iteration):**

  IPAPTVRQY (Note: This is a valid peptide; however, it does not bind to HLA-B*44:02)
- **Historical Knowledge:**

  *Original Peptide: AEAGVRLLSY; Optimized Peptide:AEAGVRLLSW; Summary: Substitution to W at the C-terminus enhanced binding to HLA-B*44:02*
- **SAR:**
  *C-terminal tryptophan (W) substitution improves HLA-B*44:02 binding*
- **Reasoning:**

  *The feedback from "History 2" indicated that substituting the C-terminal Tyrosine (Y) with Tryptophan (W) significantly enhanced binding to HLA-B*44:02 (AEAGVRLLSY → AEAGVRLLSW). Given that the current peptide ITAPTVRQY also has a Tyrosine at its C-terminus, replacing it with Tryptophan is a direct application of a previously successful modification to improve HLA-B*44:02 binding.*
- **Optimized Peptide (2nd iteration):**

  ITAPTVRQW (This is a valid peptide, and it binds to HLA-B*44:02)

Learning from Past Failure:

- **Input Protein:** *MRGSHHHH.....* (Lengthy protein Sequence)
- **Task:** *Making more amino acids into the strand structure (secondary structure)*
- **Optimized Protein (1st iteration):** *DQVGKSPN.....* (Note: It does not have more amino acids in the strand structure)
- **Historical Knowledge:**
  Edits 1, 2, and 5 failed to increase strand-forming amino acids likely due to minor side-chain substitutions or loop/helix-preserving changes.....
- **SAR:**
  Fluorine substitution and heteroaromatic ring incorporation improve drug-likeness
- **Reasoning:**
  Based on prior feedback and histories, simply substituting residues one by one is not always sufficient to promote additional strand (beta-sheet) structure. To improve strand (beta-sheet) propensity based on the feedback, I applied more extensive and targeted substitutions in predicted loop/coil regions and at the edges of existing beta sheets, using amino acids with a strong tendency to promote beta-strand conformation (V, I, F, Y, T, Q, E, D, A, G). I emphasized patchwise replacement rather than single-residue changes, aligning stretches of V, I, F, Y for extended backbone and avoiding substitutions in core (likely functionally essential) regions.
- **Optimized Protein (2nd iteration):**

  DQVGKSPN..... (Note: It has more amino acids in the strand structure)

E.3 Ablation Study

1. Separating Feedback-Driven Knowledge and Historical Knowledge. We conduct an ablation study to disentangle the effects of feedback-driven reasoning and historical knowledge from knowledge accumulation. Specifically, we use only the feedback (F2R-Feedback) as guidance and only the historical knowledge entries (F2R-Hist.) as guidance, respectively. We select the last four single-objective small molecule optimization tasks where F2R significantly outperforms the base LLM, allowing us to clearly attribute the observed performance gains. The results are presented in Table 10. Clearly, both contribute to the superior performance of F2R; feedback accounts for more substantial performance gains, but historical knowledge also plays a critical role that further improves performance.

2. Size and Retrieval Count of Historical Knowledge. In this ablation study, we investigate how the size of the historical knowledge database and the number of retrieved entries influence the

Task	Δ	Base LLM	F2R-Hist.	F2R-Feedback	F2R
More hydro-bond acceptors	0	80.50	86.50	94.00	99.00
	1	44.00	50.50	58.50	68.50
More hydro-bond donors	0	74.50	78.50	91.50	98.00
	1	16.50	39.00	45.50	52.50

Table 10: Ablation study on 4 single-objective small molecule optimization tasks with Gemini-Flash-2.5. Clearly, both feedback driven reasoning and historical knowledge accumulation are important to the superior performance of F2R.

model's performance. Given the cost of extensive experimentation, we perform this ablation study on only the first task introduced above (More hydro-bond acceptors with $\Delta = 0$). We test with 3 different historical knowledge sizes 100, 200, and 500 (200 is used for all small molecule optimization tasks in the main paper), and 3 different retrieval counts 1, 3, and 5 (3 is used for all small molecule optimization tasks in the main paper). In addition, we do not provide domain feedback in this experiment; only historical knowledge is used to control the variable. The results are provided in Table 11. These results indicate that enlarging the historical knowledge dataset leads to clear improvements in success rate. However, increasing the retrieval count does not reliably enhance performance, especially when the available historical knowledge remains limited. This is likely because when the database is small, it contains relatively few relevant historical examples, and retrieving unrelated entries may introduce distracting or misleading information, ultimately limiting the benefit of larger retrieval counts.

$k_{\text{retrieval}}$ \N	100	200	500
1	80.50	82.50	83.00
3	84.50	86.50	86.50
5	84.00	86.00	87.50

Table 11: Ablation study on the impact of size of the historical knowledge database (N) and the number of retrieved entries ($k_{\text{retrieval}}$) for the small-molecule optimization task "More hydro-bond acceptors" with $\Delta = 0$, using Gemini-Flash-2.5.

E.4 Failure Analysis

We provide the reasons for failure for each method to offer another perspective on the sources of improvement achieved by F2R. For peptides and proteins, the primary source of failure comes from not meeting the task requirements (e.g., the optimized peptide does not bind to the target allele type, or the optimized protein does not contain more amino acids in the desired secondary structures). There are almost no cases in which an invalid peptide or protein is produced. Therefore, the main benefit of feedback and memory in F2R is to guide the LLM toward satisfying the task requirements. For small molecule optimization, we find that LLMs often make invalid SMILES strings, which can be seen in the failure count of each method in Table 12. Clearly, methods incorporating reasoning (F2R and ChemReasoner) demonstrate strong performance in meeting property requirements. However, ChemReasoner does not reduce SMILES syntax errors. In contrast, F2R achieves both satisfactory property values and significantly fewer syntax errors, thanks to the use of feedback and memory. Note that ChemReasoner appears to have fewer failures due to not satisfying property requirements; however, this should be interpreted with caution, as it also produces a large number of syntax errors. These syntax errors may arise in difficult tasks where the model attempts extreme edits that ultimately violate SMILES grammar.

E.5 Additional Visualization of Results

We provide additional visualization for all three types of optimization tasks—small molecules, immunogenic binding peptides, and protein secondary structures—to offer a clearer qualitative and visual understanding of the results of LLM-assisted molecular optimization. Specifically, the visualization of input and optimized small molecules are shown in Table 13. For peptides, we provide the visualization using position weight matrices (PWMs) in Fig. 2. PWMs have been widely used for the visualization of protein motifs (patterns), and they plot the distribution of each amino acid at the corresponding position. Thus, more important motifs with higher probabilities will be marked with higher letters. The visualization of input and optimized proteins are shown in Table 14.

Task	F2R	BaseLLM	ChatDrug	ChemReasoner	RL-Guider
More soluble in water	198 / 1 / 1	162 / 2 / 36	167 / 3 / 30	167 / 0 / 33	171 / 1 / 28
Less soluble in water	198 / 0 / 2	170 / 1 / 29	171 / 4 / 25	169 / 0 / 31	171 / 1 / 28
More like a drug	138 / 51 / 11	92 / 73 / 35	123 / 49 / 28	147 / 24 / 29	95 / 71 / 34
Less like a drug	178 / 16 / 6	137 / 22 / 41	123 / 32 / 45	145 / 14 / 41	130 / 24 / 46
Higher permeability	189 / 6 / 5	63 / 86 / 51	107 / 50 / 43	163 / 7 / 30	95 / 56 / 49
Lower permeability	198 / 0 / 2	174 / 0 / 26	171 / 5 / 24	176 / 0 / 24	173 / 8 / 19
More hydro-bond acceptors	194 / 2 / 4	148 / 2 / 50	138 / 7 / 55	153 / 0 / 47	155 / 4 / 41
More hydro-bond donors	195 / 2 / 3	160 / 2 / 38	156 / 8 / 36	171 / 0 / 29	162 / 14 / 24
Total	**1488 / 78 / 34**	**1106 / 188 / 306**	**1156 / 158 / 286**	**1291 / 45 / 264**	**1152 / 179 / 269**

Table 12: Failure analysis of all methods for small-molecule optimization with $\Delta = 0$ using ChatGPT-4.1. The numbers are reported in the format S/P/I, where S denotes the number of successes, P denotes the number of failures due to not satisfying property requirements, and I denotes the number of failures caused by invalid SMILES strings. Clearly, methods incorporating reasoning (F2R and ChemReasoner) demonstrate strong performance in meeting property requirements. However, ChemReasoner does not reduce SMILES syntax errors. In contrast, F2R achieves both satisfactory property values and significantly fewer syntax errors, thanks to the use of feedback and memory.

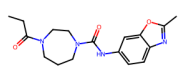
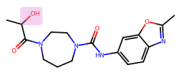
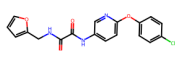
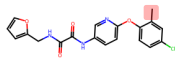
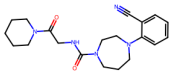
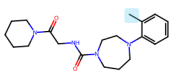
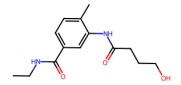
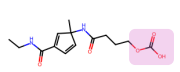
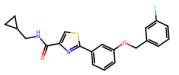
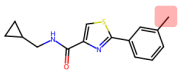
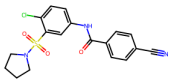
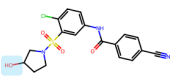
(a) Task: More soluble in water		(b) Task: Less soluble in water		(c) Task: More like a drug	
Input Molecule	Optimized Molecule	Input Molecule	Optimized Molecule	Input Molecule	Optimized Molecule
					
CCC(=O)N1CCCN(C(=O)Nc2ccc3nc(C)oc3c2)CC1	CC(O)C(=O)N1CCCN(C(=O)Nc2ccc3nc(C)oc3c2)CC1	O=C(NCc1ccco1)C(=O)Nc1ccc(Oc2ccc(Cl)cc2)nc1	O=C(NCc1ccco1)C(=O)Nc1ccc(Oc2ccc(Cl)cc2C)nc1	N#Cc1ccccc1N1CCCN(C(=O)NCC(=O)N2CCCCC2)CC1	Cc1ccccc1N1CCCN(C(=O)NCC(=O)N2CCCCC2)CC1
(d) Task: Less like a drug		(e) Task: Higher permeability		(f) Task: Lower permeability	
Input Molecule	Optimized Molecule	Input Molecule	Optimized Molecule	Input Molecule	Optimized Molecule
					
CCNC(=O)c1ccc(C)c(NC(=O)CCCO)c1	CCNC(=O)c1ccc(C)(NC(=O)CCCOC(=O)O)c1	O=C(NCC1CC1)c1csc(-c2cccc(OCc3cccc(F)c3)c2)n1	O=C(NCC1CC1)c1csc(-c2cccc(C)c2)n1	N#Cc1ccc(C(=O)Nc2ccc(Cl)c(S(=O)(=O)N3CCCC3)c2)ccc1	N#Cc1ccc(C(=O)Nc2ccc(Cl)c(S(=O)(=O)N3CCC(O)C3)c2)ccc1

Table 13: Visualization of six small molecule optimization tasks.

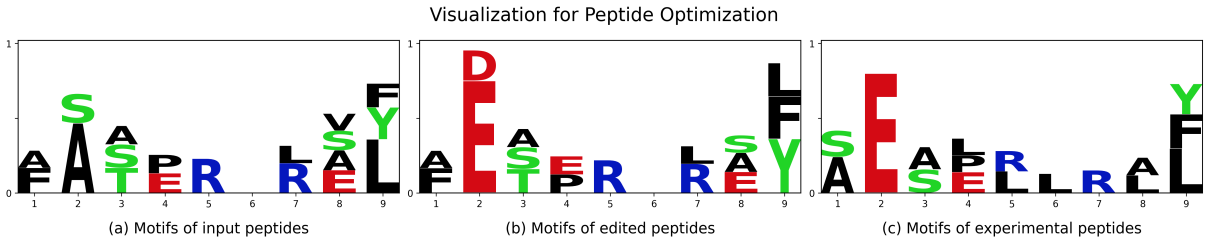


Figure 2: Visualization of peptide optimization with ChatGPT-4.1 for the task of optimizing peptides that bind to HLA-C16:01 into peptides that bind to HLA-B44:02. We provide the visualization using position weight matrices (PWMs). PWMs have been widely used for the visualization of protein motifs (patterns), and they plot the distribution of each amino acid at the corresponding position. Thus, more important motifs with higher probabilities will be marked with higher letters.

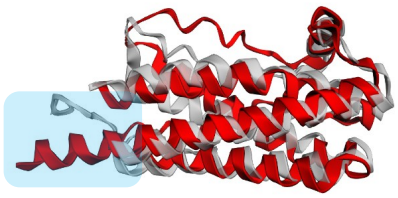
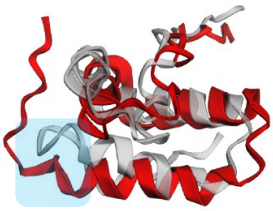
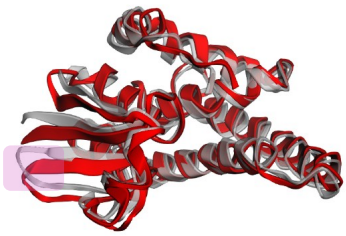
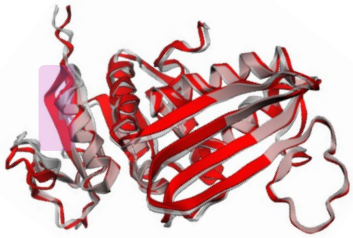
Task	Input&Output Proteins	Input&Output Proteins
More helix structures		
More strand structures		

Table 14: Visualization of four protein optimization tasks. The input protein is shown in light grey, and the final optimized protein is shown in red.