INDIBATOR: Individuality-grounded Persona for Multi-Agent Molecular Discovery

Yunhui Jang [1] **Seonghyun Park** [1] **Jaehyung Kim** [2] **Sungsoo Ahn** [1]

Abstract

Multi-agent systems have emerged as a powerful paradigm for automating scientific discovery. To differentiate agent behavior in the multi-agent system, current frameworks typically assign generic role-based personas such as "reviewer" or "writer", or rely on coarse-grained keyword-based personas. While functional, this approach oversimplifies how human scientists operate, whose contributions are shaped by their unique research trajectories. In response, we propose INDIBATOR, a framework for molecular discovery that grounds agents in individualized scientist profiles constructed from two modalities: publication history for literature-derived knowledge and molecular history for structural priors. Our evaluation demonstrates that these fine-grained, individuality-grounded agents consistently outperform systems relying on coarse-grained personas, achieving competitive or state-of-the-art performance. These results validate that capturing the "scientific DNA" of individual agents is essential for high-quality discovery.

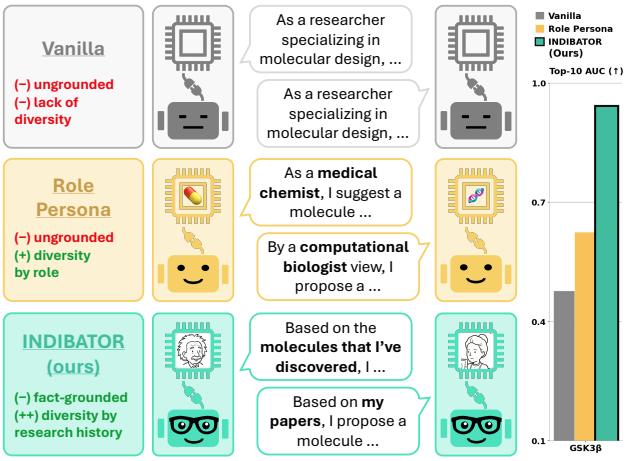

Figure 1. **INDIBATOR compared to vanilla and role persona.** INDIBATOR considers fact-grounded and diverse persona for multi-agent molecular discovery.

1. Introduction

Large language models (LLMs) have demonstrated remarkable performance across a wide range of tasks (Singh et al., 2025; Anthropic, 2024; Team et al., 2025; DeepSeek-AI et al., 2025). Beyond direct prompting, recent work has introduced AI agents capable of planning and executing actions over multiple iterations (Yao et al., 2023; Schick et al., 2023; M. Bran et al., 2024). While impressive, single-agent systems often encounter constraints such as bounded context windows and limited perspective diversity. To address this, multi-agent systems have emerged as a powerful paradigm for automated discovery (Du et al., 2024; Liang et al., 2024; Chan et al., 2024). By leveraging collaborative intelligence, these systems effectively simulate the real-world research process with growing applications in scientific discovery (Lu et al., 2024; Du et al., 2025; Gottweis et al., 2025) and molecular discovery (Kim et al., 2025).

To differentiate the conversational behavior of each agent, prior works typically assign distinct personas through role-play prompting (Kong et al., 2024; Zhou et al., 2024; Park et al., 2023; Piao et al., 2025), e.g., "planner" or "verifier", or through keywords (Su et al., 2025). While this role-based or keyword-based separation effectively shapes output style, it often oversimplifies the rich reality of how human scientists operate. In practice, a scientist's individuality is defined not merely by a coarse-grained generic role or a set of keywords, but by their unique fine-grained research trajectory, a distinctive "scientific DNA" composed of cumulative experiences and domain-specific intuitions. By ignoring this, current systems fail to leverage the deep and nuanced insights characteristic of real-world collaboration.

The existence of such scientific DNA is particularly well established in the domain of drug discovery. Chemists exhibit distinctive styles for designing new molecules, such as preferences for particular scaffolds, functional groups, and

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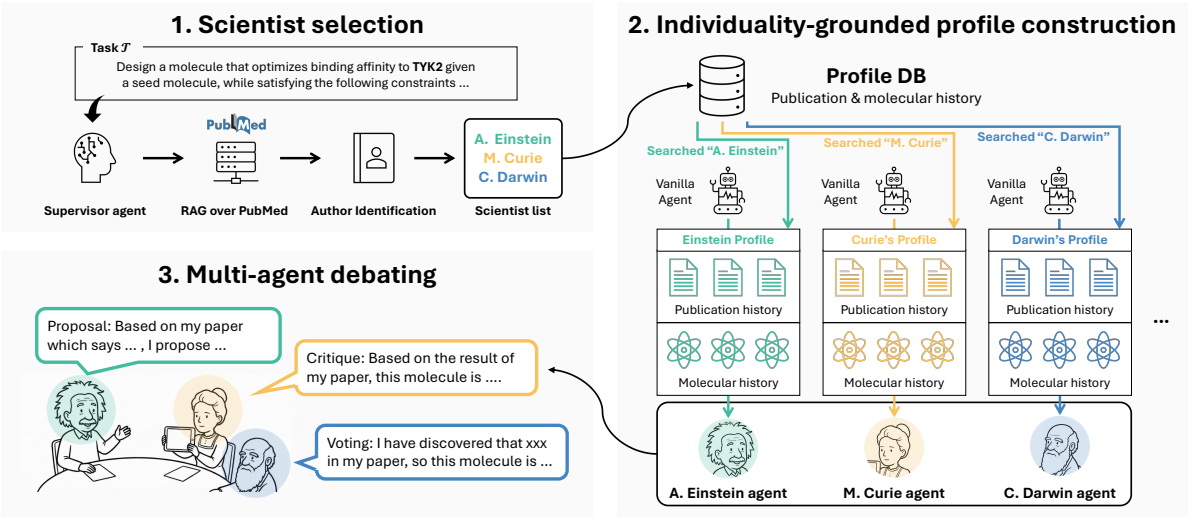


Figure 2. **Overview of INDIBATOR.** Given a task, the supervisor agent selects relevant scientists by identifying the authors of publications by RAG. Next, individuality is grounded for each agent with scientist profiles, consisting of publication history and molecular history of each scientist. Finally, multi-agents debate to iteratively generate candidate molecules with proposal, critique, and voting phases.

reaction motifs (Pedreira et al., 2019; Choung et al., 2023), based on their own research trajectory. Recently, Blevins & Quigley (2025) quantified this phenomenon, demonstrating that models can identify which of 1,815 chemists synthesized a molecule with 60% top-5 accuracy from structure alone. While they frame this as "Clever Hans" (Lapuschkin et al., 2019) leakage problem that distorts benchmark evaluations, we reinterpret it as a *blueprint for agent design*. We argue that these styles encode heuristics for effectively navigating chemical space and representing the expertise diversity that mimics real-world collaboration.

In response, we propose INDIBATOR, a multi-agent framework for molecular discovery that bridges the gap between generic coarse-grained personas and chemical reality by grounding agents in individual research trajectories, as illustrated in Figure 2. Instead of relying on heuristically predefined roles or keywords, INDIBATOR constructs agent profiles utilizing two informative sources that encode research trajectory: (1) *publication history*, a collection of publications that define the agent's literature-derived knowledge and methodological preferences, and (2) *molecular history*, a set of previously developed molecules that establishes structural priors, such as preferred scaffolds and functional groups.

This data-driven profile provides unique individuality to each agent, effectively mirroring the real-world scientific process where discovery emerges from researchers' unique cumulative knowledge and inductive biases. This individuality-driven design provides two key benefits: (1) *diversity*, where unique agent profiles prevent redundant reasoning among the agents; and (2) *fact-grounding*, where explicit reliance on publication and molecules empowers reasoning grounded in verifiable evidence.

To demonstrate the effect of our fine-grained individuality, we implement a multi-agent debating system consisting of three iterative phases: (1) proposal, (2) critique, and (3) voting. During these phases, each agent proposes molecular candidates, critiques proposals, and assigns scores based on their specific expertise, mirroring the collective intelligence of real-world scientist teams.

We empirically evaluate INDIBATOR across three downstream tasks: protein-conditioned molecule generation, bioactivity-guided molecule generation, and goal-directed lead optimization. Our results show that INDIBATOR consistently outperforms vanilla debating systems and achieves competitive or state-of-the-art performance. Moreover, we provide comprehensive analyses demonstrating the impact of individuality, which validates that capturing the nuanced scientific DNA is a fundamental driver of molecular design. While the principle of expertise-grounded individuality may generalize to other scientific domains, our results demonstrate that it is a critical component for enhancing molecular discovery, where scientists' style provides concrete empirical grounding.

2. INDIBATOR

The INDIBATOR framework instantiates a set of scientist agents grounded in their own unique research trajectories. Unlike conventional multi-agent systems (Kong et al., 2024; Zhou et al., 2024; Park et al., 2023), our approach ensures more fine-grained individuality of each agent with research trajectory profiles. Specifically, we condition each agent on a distinct real-world profile derived from their prior publi-

cations and historical molecular discoveries. This provides two key benefits:

- **Diversity:** Each agent's system prompt is uniquely constructed based on their expertise, preventing redundant reasoning across the agents.
- **Fact-grounding:** Each agent's reasoning is grounded in real-world profiles, ensuring that their arguments are supported by concrete papers and discovered molecules.

2.1. Individuality-grounded Profile Construction

To ensure the individuality of each scientist agent, we construct expertise profiles from two modalities: (1) publication history: a collection of publications retrieved from PubMed (Luna, 2024; Cho, 2024) that define the agent's literature-derived knowledge, including their research focus and methodological preferences; and (2) molecular history: a set of molecules previously developed by the scientist that establishes structural priors, represented as SMILES strings (Weininger, 1988). Notably, the inclusion of molecular history M_i is motivated by the Clever Hans phenomenon in chemistry (Blevins & Quigley, 2025), which highlights a correlation between molecular structures and the scientists associated with their discovery.

In detail, given a research objective or task description $\mathcal{T}$, a supervisor agent employs retrieval-augmented generation (RAG; Lewis et al., 2020) over a vector space of literature in PubMed to identify the most relevant research papers. The supervisor then extracts the first and last authors to represent the primary researchers and principal investigators, respectively. These identified scientists construct a set of scientist agents, $\mathcal{S} = \{s_1, s_2, \ldots, s_N\}$, where N is a hyperparameter that defines the number of scientists.

Finally, each scientist agent s_i is initialized with an expertise profile $E_i = \{P_i, M_i\}$, where P_i denotes their publication history, including the titles and abstracts, and M_i denotes the molecular history, i.e., a set of molecules discovered by the scientist. Specifically, a subset of publications is selected based on the frequency of task-relevant keywords, while molecules are retrieved based on their structural similarity to a seed molecule if available. We provide further details of the profile construction pipeline in Appendix C.

2.2. Multi-agent Debating System

The proposed debating system consists of three phases: proposal, critique, and voting. This iterative process continues until reaching a maximum round limit or accumulating a sufficient number of candidates. Notably, we intentionally adopt a simple and standard debating architecture, so that any performance gain can be cleanly attributed to persona construction rather than architectural design. We provide a detailed qualitative case study in Figure 4 and detailed prompts in Appendix B.

Proposal. During the proposal phase, each *scientist agent*, i.e., an agent conditioned with individual scientist profiles, proposes molecular candidates grounded in their expertise. Each agent is provided with a prompt including their profile E_i and the task description $\mathcal{T}$. Scientists propose k candidates, accompanied by rationales that link each proposal to their prior knowledge. In subsequent rounds, agents also receive candidates and critiques from previous iterations to facilitate refinement.

Critique. The critique phase operates in two stages to generate feedback for candidate molecules. First, in an optional self-critique stage, scientist agents evaluate their own proposals, identifying weaknesses and modifying their designs. Next, agents engage in a cross-critique stage, where they evaluate peer proposals to simulate a collaborative review process similar to the real-world scientific discovery. In this step, agents leverage their own personas to suggest domain-specific modifications, thereby ensuring that final candidates are robust across multiple criteria.

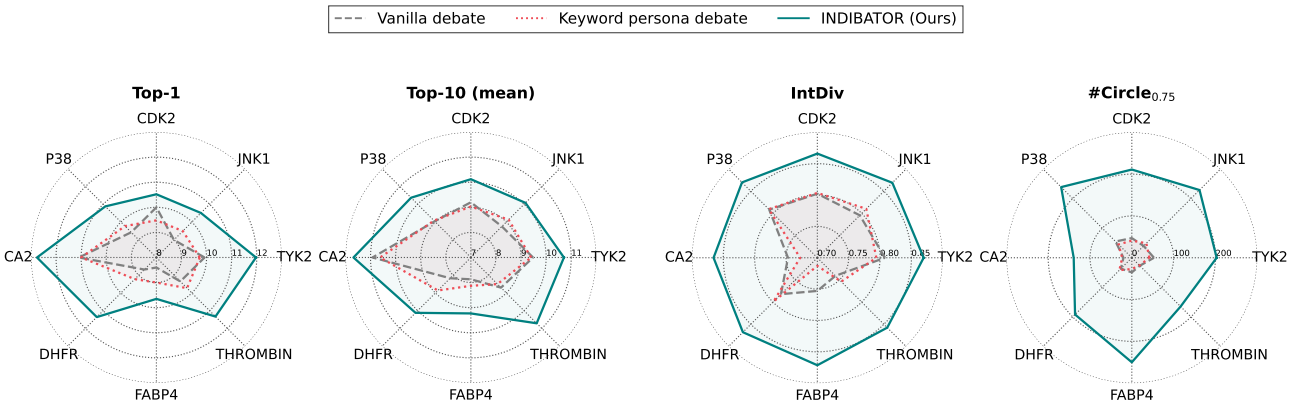
Voting. In the voting phase, scientists assess the candidates, incorporating the insights from the critique phase. Each scientist agent s_i evaluates the candidate pool, assigning a scalar score $s \in [0, 1]$ based on three prompt-guided objectives: task relevance, synthetic feasibility, and novelty. Based on these scores, each agent casts votes for the top t candidates. These votes are subsequently aggregated to determine the global ranking. The highest-ranked candidates either proceed to the subsequent round or are selected as the final candidates.

3. Downstream Task Evaluation

Here, we evaluate the effectiveness of INDIBATOR on three molecular downstream tasks. We utilize the Deepseek-V3.2 (DeepSeek-AI et al., 2025) backbone. We provide task prompts in Appendix B and detailed experimental settings in Appendix C.

3.1. Protein-conditioned Molecule Generation

Task description. The goal of the protein-conditioned molecule generation task is to generate molecules with a high binding affinity to the target protein. In detail, we select eight target proteins: TYK2, JNK1, CDK2, P38, CA2, THROMBIN, FABP4, and DHFR. The first four proteins are selected following the binding affinity prediction task of Boltz-2 (Passaro et al., 2025). Since these targets are all kinases, we expand the evaluation scope to include non-kinase targets: CA2 (metalloenzyme), THROMBIN (serine protease), FABP4 (lipid-binding protein), and DHFR (oxi-



(a) Binding affinity *(b)* Diversity

Figure 3. **Results of protein target molecular generation.** The left and right panels illustrate the docking scores and diversity of molecules, respectively. The gray, red, teal colors denote VANILLADEBATE, KEYWORDDEBATE, and INDIBATOR (ours). The docking scores are in absolute values, where higher scores represents superiority.

doreductase). We generate 1,000 molecules for each protein.

We employ two types of metrics: binding affinity and diversity. First, for the binding affinity, we utilize Boltz-2 (Passaro et al., 2025) as our proxy, specifically, `affinity_pred_value` converted from $\log_{10}(\text{IC}_{50})$ into kcal/mol. Our final evaluation metrics consist of (1) the Top-1 and (2) the mean of the Top-10 binding affinities over 1,000 generated candidates.

In addition, the diversity is computed with (3) internal diversity (IntDiv; Polykovskiy et al., 2020) and (4) the number of circles (#Circles; Xie et al., 2023) following Jang et al. (2024). IntDiv measures the average pairwise Tanimoto similarity of molecules while $\#\text{Circles}_h$ computes the number of mutually exclusive clusters constructed with the Tanimoto similarity threshold $h = 0.75$.

Baselines. We establish VANILLADEBATE and KEYWORDDEBATE as our baselines. Both baselines follow the identical debating framework of our INDIBATOR. However, VANILLADEBATE operates without any profile, while KEYWORDDEBATE constructs the profile with research keywords extracted from the publication history of each agent, inspired by VirSci (Su et al., 2025).

Results. We provide the results in Figure 3 and detailed values in Appendix D. INDIBATOR consistently demonstrates superior performance in both binding affinity and molecular diversity. Importantly, while the baselines frequently suffer from mode collapse, indicated by their lower diversity, INDIBATOR successfully navigates the chemical space to generate structurally distinct clusters without compromising optimization quality. Our superior performance across diverse protein families validates that our fine-grained profile-grounded agents can effectively adapt their search strategy to distinct biological interactions.

Table 1. **Results of bioactivity-guided molecule generation.** We mark the best results in **bold**. Method denoted with an asterisk (*) indicates LLM-based baselines implemented by the authors.

	Model	GSK3β	DRD2	JNK3
Structure	GP BO	0.611	0.857	0.346
	REINVENT	0.589	0.775	0.315
	Genetic GFN	0.637	0.809	0.409
	Graph GA	0.523	0.833	0.301
	Aug. Mem.	0.539	0.795	0.294
LLM	LICO-L	0.617	0.859	0.336
	MOLLEO-B	0.397	0.910	0.186
	MOLLEO-D	0.496	0.812	0.342
	VANILLA*	0.419	0.921	0.310
	VANILLADEBATE*	0.477	0.902	0.161
	KEYWORDDEBATE*	0.449	0.929	0.185
	MT-Mol	0.308	0.756	0.125
	INDIBATOR (Ours)	**0.942**	**0.950**	**0.914**

3.2. Bioactivity-guided Molecule Generation

Task description. This task aims at maximizing molecular bioactivity properties under unconstrained conditions. It includes three bioactivities:

- GSK3β: Inhibition of glycogen synthase kinase-3 β.
- DRD2: Binding affinity for dopamine type 2 receptor.
- JNK3: Inhibition of c-Jun N-terminal kinase-3.

Following prior works (Kim et al., 2025; Nguyen & Grover, 2025), we conduct experiments on the practical molecular optimization (PMO)-1K benchmark (Gao et al., 2022), which computes the score among 1,000 generated molecules.

Table 2. **Goal-directed lead optimization results.** Teal highlights the improvement over the VANILLADEBATE. Larger absolute values denote better binding.

	Target protein	parp1			fa7			5ht1b			braf			jak2		
	Seed score	-7.3	-7.8	-8.2	-6.4	-6.7	-8.5	-4.5	-7.6	-9.8	-9.3	-9.4	-9.8	-7.7	-8.0	-8.6
Learning-based	Graph GA	-8.3	-8.9	-	-7.8	-8.2	-	-11.7	-12.1	-	-9.8	-	-11.6	-8.7	-9.2	-
	RetMol	-9.0	-10.7	-10.9	-8.0	-	-	-12.1	-9.0	-	-	-11.6	-	-8.2	-9.0	-
	GenMol	-10.6	-11.0	-11.3	-8.4	-8.4	-	-12.9	-12.3	-11.6	-10.8	-10.8	-10.6	-10.2	-10.0	-9.8
Inference-only	VANILLA*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	VANILLADEBATE*	-12.8	-11.6	-9.7	-7.8	-7.0	-	-12.3	-10.6	-10.1	-10.2	-9.6	-10.2	-9.8	-9.6	-8.5
	INDIBATOR (Ours)	-12.1	-11.5	-16.7	-9.2	-7.0	-	-12.4	-11.6	-10.5	-10.6	-9.8	-10.5	-9.8	-11.0	-8.8

Notably, we excluded other tasks in PMO, such as rediscovery of a molecule, as they represent arithmetic structural puzzles where success depends on precise reconstruction instead of diverse molecular exploration. For the metric, we report the average of top-10 AUC scores, the area under the curve (AUC) of the top-10 average score versus oracle calls.

Baselines. We benchmark against eleven baselines, categorized into two paradigms. The structure-based approaches includes GP BO (Srinivas et al., 2010), REINVENT (Olivecrona et al., 2017), Genetic GFN (Kim et al., 2024), Graph GA (Jensen, 2019), and Augmented Memory (Guo & Schwaller, 2024). Additionally, we compare against LLM-based approaches, including LICO (Nguyen & Grover, 2025), MOLLEO (Wang et al., 2025), the role-based multi-agent system MT-Mol (Kim et al., 2025), VANILLA, VANILLADEBATE, and KEYWORDDEBATE inspired by VirSci (Su et al., 2025). Here, VANILLA indicates the LLM prompting approach without any debate. Notably, MT-Mol is a critical baseline that represents a tool-based multi-agent system with a role-based persona.

Results. We report the results in Table 1. We observe that INDIBATOR consistently enhances the performance across all tasks. Notably, our method demonstrates a substantial performance margin over the role-based MT-Mol and KEYWORDDEBATE. This validates that fine-grained, diverse, and fact-grounded individuality provides a more effective inductive bias for chemical space navigation than generic role prompts or keywords. Furthermore, INDIBATOR outperforms optimization baselines such as Genetic GFN by significant margins, ranging from 17.4% (DRD2) to 123.5% (JNK3) across the evaluated targets.

3.3. Goal-directed Lead Optimization

Task description. The goal is to generate leads given an initial seed molecule. The leads are the molecules that exhibit improved target properties while maintaining the similarity with the seed molecule. Following Lee et al. (2025), the objective is to maximize the binding affinity measured by the docking score while satisfying the following constraints: QED ≥ 0.6, SA ≤ 4, and sim ≥ 0.6. The similarity is defined as the Tanimoto similarity between the Morgan fingerprints. We adopt five target proteins: parp1, fa7, 5ht1b, braf, and jak2, and each protein includes three different seed molecules. We evaluate performance based on the docking score of the most optimized lead.

Baselines. We compare against five baselines categorized into two paradigms. The first category comprises learning-based optimization methods: Graph GA (Jensen, 2019), RetMol (Wang et al., 2023), and GenMol (Lee et al., 2025). Crucially, these models are explicitly trained with feedback loops, establishing a strong performance standard. In contrast, INDIBATOR operates without any task-specific fine-tuning. Following this, the second category consists of inference-only LLM baselines, VANILLA and VANILLADEBATE.

Results. We provide the results in Table 2. While VANILLADEBATE shows improvement to VANILLA, INDIBATOR consistently generates more optimized leads, demonstrating that our expertise-grounded profiles provide the appropriate guidance to navigate constrained chemical space. While INDIBATOR shows only competitive results, this is expected as the baselines are trained to maximize target properties while our method operates solely on inference-time and does not include any task-specific training required by the baselines.

4. Analysis

Here, we provide a comprehensive analysis on bioactivity-guided molecule generation. We begin with qualitative case study. Next, we investigate the effect of individuality by addressing three properties: granularity, diversity, and fact-grounding. Moreover, we provide additional experiments including per-component contribution analysis, computational cost analysis, and novelty and oracle overlap analysis in Appendix D.

4.1. Qualitative Case Study

We illustrate how grounding agents in distinct publication and molecular histories shapes their reasoning during the

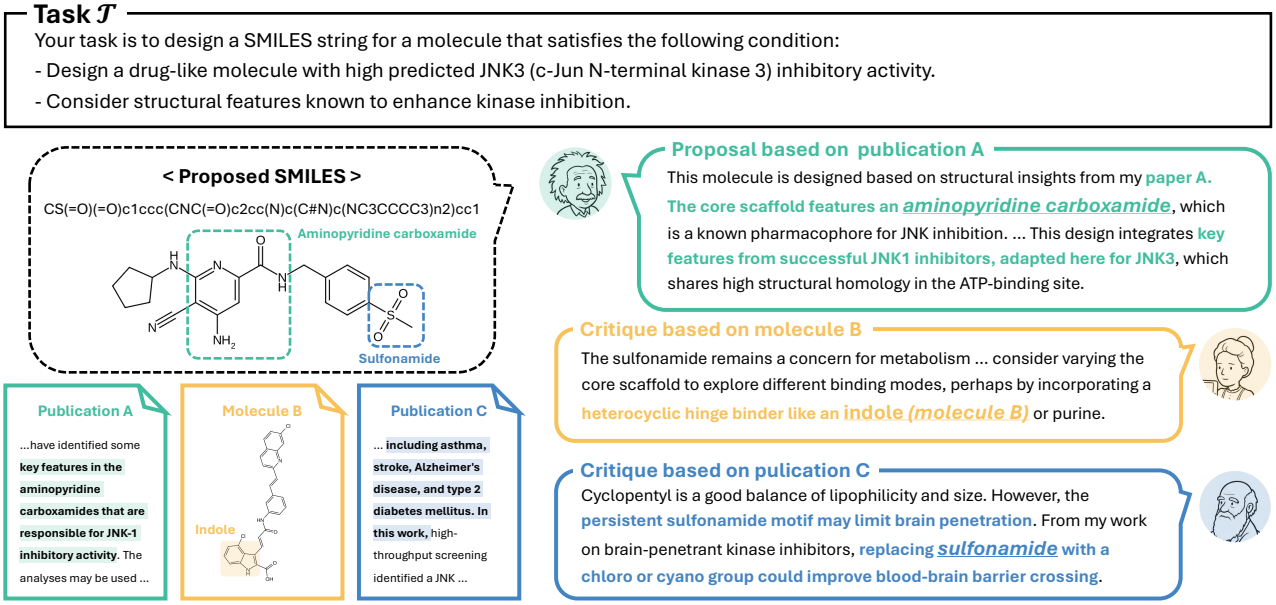


Figure 4. **Qualitative case study on individuality grounded agents.** We provide a qualitative analysis of the JNK3 inhibition guided molecule generation task. Specifically, we show how an agent leverages prior publications and molecules to propose a candidate, while other agents utilize their profiles to offer targeted critiques.

JNK3 inhibition guided molecule generation task in Figure 4. This shows that grounding agents in their individual scientific profiles leads to distinct, chemically plausible reasoning trajectories. It is notable that we present partial examples for simplicity, while all agents engage in the debate in parallel for the entire proposal, critique, and voting phases. We provide more detailed examples in Appendix D.

The **first agent**, retrieving its prior publication on 3D quantitative structure–activity relationship (QSAR) on JNK1 inhibitors (Yi & Qiu, 2008), proposes a candidate molecule with an *aminopyridine carboxamide* scaffold. This is scientifically sound considering the high structural homology between the JNK1 and JNK3 ATP-binding pockets, transferring the pharmacophore is a logical exploitation (Liu et al., 2006). This proposal triggers a structural critique from a **second agent**, which proposes to refine the scaffold driven by its background on indolin-2-one Aurora B inhibitors (Zhang et al., 2015). To be specific, this critique is to replace the core scaffold, which explores novel binding modes with an indole core (Chen et al., 2016). Finally, the **third agent** critiques to refine the molecule for the specific therapeutic indication. Grounded in a central nervous system (CNS) focused publication (Zheng et al., 2014), the agent correctly identifies the sulfonamide motif as a blood-brain barrier (BBB) liability due to its high polarity. It suggests replacing the sulfonamide with the chloro or cyano groups, which reduces the polar surface area (Kelder et al., 1999).

4.2. Ablation Studies on Individuality

Here, we analyze the effect of INDIBATOR persona with three key research questions:

- **Granularity**: Does the granularity of the profile impact the performance?
- **Diversity**: Does the heterogeneity of expert perspectives impact the performance?
- **Fact-grounding**: Is grounding agents in real-world data essential compared to synthetic or hallucinated profiles?

Notably, all baselines share the identical debate structure, so that the performance can be cleanly attributed to persona construction. We report the results in Table 3.

Granularity. Granularity refers to the depth and specificity of information used to construct an agent's persona, ranging from generic role assignments to detailed research trajectory-based profiles.

We consider three baselines: VANILLADEBATE, role persona, and keyword persona. In detail, role persona represents coarse-grained individuality, where agents are assigned based on generic, LLM-generated task-related roles (e.g., medicinal chemist, cheminformatics scientist, etc.). Next, the keyword persona represents mid-level granularity where agents are defined by keywords extracted from the publication history of each agent, inspired by VirSci (Su et al., 2025).

As a result, while role and keyword persona offer marginal gains over the VANILLADEBATE, INDIBATOR significantly outperforms all baselines. This confirms that capturing the "scientific DNA" rather than just generic roles or keywords is critical.

Diversity. Here, we analyze the effect of diversity to observe whether the collaborative performance stems merely from the aggregation of knowledge or from the interaction between diverse and heterogeneous expert perspectives.

We consider three baselines: VANILLADEBATE, single-profile, and massive single-profile. In detail, single-profile forces multiple agents to share an identical profile (non-diverse profile), where the profile is selected as the most relevant for the scientists. Next, in a massive single-profile, every agent is assigned an identical and comprehensive profile constructed from the union of scientist profiles in INDIBATOR. Due to context window constraints, this union aggregates 50% of the selected profiles.

The results confirm that diversity is essential. Single-profile performs even worse than the VANILLADEBATE, suggesting that enforcing a narrow perspective hinders exploration. Crucially, INDIBATOR outperforms the massive single-profile, proving that performance gains stem not merely from the volume of knowledge, but from the diversity of perspectives that enables agents to cross-examine and propose diverse candidates.

Fact-grounding. Finally, we examine whether grounding agents in factual data is essential.

We consider three baselines: VANILLADEBATE, LLM-generated profile, and random-profile. In detail, LLM-generated profile is initialized with synthetic publication and molecular histories generated by LLMs given a scientist name, which cannot guarantee the factual accuracy due to the potential hallucinations. The random-profile assigns agents complete and factual but task-irrelevant profiles.

The results indicate that fact-grounding is significant. Specifically, the LLM-generated profile performs inferior to the random-profile. This suggests that hallucinated expertise degrades reasoning more than irrelevant but real expertise. INDIBATOR achieves superior performance, which shows that our profiles provide true inductive biases.

4.3. Ablation study on the number of scientists

To analyze the impact of the number of scientists who engage in the debate, we evaluate the performance of INDIBATOR and VANILLADEBATE while varying the number of scientist agents (N) from 5 to 50 on the JNK3 inhibition guided molecule generation task. We provide the results in Figure 5.

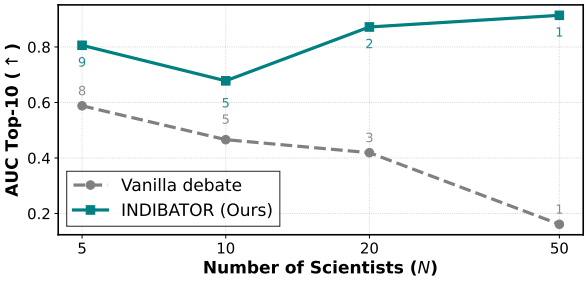


Figure 5. **Effect of the number of scientists.** Annotated numbers above and below each data point indicate the number of debate rounds to generate 1,000 candidates.

The results demonstrate that increasing the number of scientists (N) enhances the performance in INDIBATOR while the VANILLADEBATE exhibits performance degradation due to the reduced number of rounds. Specifically, as the number of scientists increases, the debate concludes in a single round for both models. For INDIBATOR, this is sufficient as the diverse agents generate high-quality initial proposals that cover the chemical space effectively. In contrast, the VANILLADEBATE relies on iterative debate process. This highlights that individuality enables a more efficient scaling law, where expanding the diversity of perspectives can effectively substitute for the iterative debate.

5. Related Work

LLM-based multi-agent systems. The AI agents have evolved from single-agent frameworks (Yao et al., 2023; Schick et al., 2023; Shinn et al., 2023) to multi-agent systems (MAS) leveraging collaborative intelligence (Du et al., 2024; Liang et al., 2024; Chan et al., 2024; Lu et al., 2024; Mitchener et al., 2025). By assigning distinct personas to LLMs, MAS can simulate complex interactions, effectively leveraging each agent's capabilities and expertise. Standard approaches typically employ role-play prompting (Kong et al., 2024; Zhou et al., 2024; Park et al., 2023; Piao et al., 2025) to instantiate generic personas by prompting (e.g., "You are an expert in biology."). However, this coarse-grained role-based agent scales poorly to massive multi-agent scenarios, as defining sufficiently distinct roles becomes intractable.

Recent works have attempted to mitigate this by introducing more fine-grained personas. For instance, VirSci (Su et al., 2025) constructs personas using keywords based on publications and collaboration networks, demonstrating effective paper abstract generation. However, keywords lack the granular expertise required for real-world scientific debate. Moreover, in molecular discovery, literature-derived knowledge is insufficient as chemists exhibit distinctive structural priors such as scaffolds and functional groups, which are not captured by publication texts alone. To address this, INDIBATOR incorporates both publication and molecular

Table 3. **Comprehensive quantitative analysis.** We evaluate models across three perspectives: **Granularity** (level of detail in profile), **Diversity** (heterogeneity of agents), and **Fact-grounding** (relevance and truthfulness of knowledge). –, ▲, and ● indicates the low-, mid-, and high-level of each property, respectively. Higher values are better across all metrics and best results are highlighted in **bold**.

	Agent Properties			GSK3β				DRD2				JNK3			
Model	**Gran.**	**Div.**	**Fact.**	**AUC**	**IDiv**	**#C**$_{.75}$	**#C**$_{.85}$	**AUC**	**IDiv**	**#C**$_{.75}$	**#C**$_{.85}$	**AUC**	**IDiv**	**#C**$_{.75}$	**#C**$_{.85}$
Baseline															
VANILLADEBATE	–	–	–	0.477	0.816	48	8	0.902	**0.835**	57	10	0.161	0.809	55	9
Ablation on Granularity															
Role persona	–	●	–	0.625	0.816	54	9	0.933	0.823	56	11	0.178	0.812	60	6
Keyword persona	▲	●	●	0.449	0.813	47	10	0.929	0.832	52	10	0.185	0.808	52	6
Ablation on Diversity															
Single-profile	●	–	●	0.285	0.734	20	5	0.857	0.809	31	9	0.147	0.787	39	8
Massive single-profile	●	–	●	0.559	0.829	96	21	**0.950**	0.750	19	6	0.453	0.767	34	8
Ablation on Fact-Grounding															
LLM-generated profile	●	●	–	0.501	0.792	44	7	0.927	0.813	52	9	0.235	0.799	48	7
Random-profile	●	●	▲	0.884	**0.850**	125	23	0.929	0.833	**78**	**22**	0.334	0.837	**117**	25
INDIBATOR (Ours)	●	●	●	**0.942**	**0.850**	**182**	**35**	**0.950**	0.833	**78**	21	**0.914**	**0.843**	115	**26**

histories into each agent's profile.

LLM in molecular discovery. Recent works adapted LLMs for molecular discovery. Approaches like LICO (Nguyen & Grover, 2025) and MOLLEO (Wang et al., 2025) extend LLMs with structured embeddings or evolutionary search. To address the reasoning in the molecular domain, a few works have evolved into agent systems. For instance, ChemCrow (M. Bran et al., 2024), a single-agent system that combines general-purpose LLMs with chemistry tools and a ReAct-based reasoning loop, and MT-Mol (Kim et al., 2025), a multi-agent system that operates tool-guided reasoning and role-specialized LLM agents.

However, a limitation of these frameworks is their reliance on coarse-grained role-based personas, rather than grounded individual expertise. Existing agents lack the rich context of a scientist's research trajectory that define their unique inductive bias. INDIBATOR addresses this by explicitly grounding each agent in a comprehensive profile of their actual research trajectory, effectively replacing generic role-play by distinct scientific DNA.

6. Conclusion

We presented INDIBATOR, which grounds scientist agents in unique research trajectories. By constructing individual profiles from publication and molecular history, the agents are initiated with a distinct "scientific DNA" that guides their grounded reasoning. Our evaluation demonstrates that this approach shows superior performance in molecular discovery. Furthermore, we empirically validated the three-fold benefits, i.e., granularity, diversity, and fact-grounding, confirming that capturing the inductive biases of individual researchers is critical. We believe our framework establishes a foundation for incorporating broader modalities to enhance agent fidelity in domain-specific environments.

Broader impact

This paper presents a work of using multi agents for molecular discovery. By simulating realistic scientific debate through agents grounded by individual research trajectories, this framework aims to significantly accelerate the drug design pipeline and improve the factual reliability of AI-driven scientific discovery. While our framework currently optimizes drug-likeness and synthetic accessibility, future open-source releases or deployments should involve safety guardrails to prevent the targeted design of harmful compounds.

Limitations

Fixed debate orchestration. We evaluate INDIBATOR exclusively within a standard proposal - critique - voting workflow and do not experiment with alternative multi-agent orchestration strategies such as hierarchical debate. This is intentional as adopting a fixed and simple debate structure shared across all baselines allows us to isolate the effect of persona construction as the sole independent factor. Whether individuality-grounded profiles provide equivalent benefits under alternative orchestration strategies remains an open question for future work.

Backbone LLM dependency. All experiments are conducted with DeepSeek-V3.2 (DeepSeek-AI et al., 2025) as the backbone LLM. The generalizability of our findings to other model families and sizes has not been tested. Results may differ with other backbone models that are less capable of grounding their reasoning in provided profile content.

Domain and data availability scope. INDIBATOR relies on PubMed publication and molecular records, and is evaluated exclusively on small-molecule drug discovery tasks. The reported findings may not generalize to domains with sparse literature coverage. Future work should examine whether individuality-grounded profiles constructed from alternative data sources retain their benefit in such settings.

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A. Ethical Consideration

This work uses publicly available academic records, including titles, abstracts, and molecular discoveries from PubMed, to construct expertise profiles for LLM agents. The proposals, critiques, and voting generated by these agents are outcomes of the LLM's probabilistic generation and do not represent the actual opinions, unpublished insights, or endorsement of the real-world scientists cited.

Attribution. Any use of a scientist's profile should be accompanied by explicit attribution to their published work, equivalent to a formal citation. Future deployments of INDIBATOR should make this requirement clear in their terms of use, ensuring that scientists whose research trajectories inform agent behavior receive appropriate academic credit.

Identity replication and reputation preservation. While scientist names are anonymized during LLM prompting in our current implementation, we acknowledge that bad actors could misuse profile-grounded agents to generate outputs falsely associated with specific researchers, potentially damaging their scientific reputation. Future deployments should implement explicit disclosure mechanisms and access controls to mitigate such risks.

Plagiarism safeguards. To prevent agents from trivially reproducing known molecules as novel discoveries, our framework employs prompt-level instructions explicitly discouraging duplication and canonical SMILES matching to filter identical structures from generated candidates.

Legal considerations. All data used are sourced from PubMed, for which NLM does not claim copyright on abstracts and NCBI places no restrictions on the use or distribution of molecular data (NCBI Policies). Critically, unlike recent litigation around persona-derived AI systems such as Angwin v. Superhuman Platform, Inc. (S.D.N.Y. 2026), where Grammarly was sued for commercially exploiting real persons' names and identities without consent, INDIBATOR anonymizes scientist names during inference and is used strictly for non-commercial academic research. Nevertheless, the legal landscape in this space is evolving, and we recommend that future users monitor developments and adapt their deployment practices accordingly.

Toxic molecule generation. Our system could be misused to automate the creation of harmful compounds. Future work should integrate toxicity filtering at the voting phase and as a post-hoc screening step.

B. Prompts

In this section, we provide the full prompts including the system prompt, and task prompt used in our experiments.

B.1. INDIBATOR

Here, we provide the prompts employed for the agents in INDIBATOR. Below, we outline four prompts: (1) the system prompt used to initialize a scientist agent with a specific expertise profile, (2) the prompt that instructs the agents to suggest novel proposals with their scientific rationale, (3) the prompt that instructs the agents to evaluate proposals from their peers, and (4) the prompt that instructs the agents to score candidate molecules.

System prompt of scientist in INDIBATOR

You are {scientist_name}, a researcher specializing in molecular design and drug discovery.

Your expertise is based on your published work: {publications}
Molecules you have worked with: {molecules}

CURRENT TASK: {task_description}

In this debate, you will participate in three phases:
1. PROPOSAL PHASE: Propose 1-3 molecules (as valid SMILES strings) based on your expertise.
- Draw from your knowledge of similar molecular scaffolds
- Consider structure-activity relationships from your publications
- Explain your rationale for each proposal

2. CRITIQUE PHASE: Evaluate other scientists' proposals.
- Identify potential issues (toxicity, synthesis difficulty, selectivity)
- Suggest modifications based on your experience
- Note any overlap with molecules in your experience

3. VOTING PHASE: Score candidates from 0.0 to 1.0.
- Consider task relevance, synthetic feasibility, and novelty
- Base your assessment on your domain expertise

Always ground your contributions in your specific published expertise. When proposing molecules, provide valid SMILES strings and clear scientific rationale.

Prompt for proposal

Round {round_num} - PROPOSAL PHASE

Task: {task_description}

Previous proposals in this debate: {previous_proposals if previous_proposals else "No previous proposals yet."}

Based on your expertise, propose {num_mols}-{num_mols+2} novel molecules (as SMILES strings) that could address this task. For each molecule:
1. Provide the SMILES string
2. Explain your rationale based on your published work and proposed molecules in the published work
3. Discuss expected properties relevant to the task

Output format: [{"SMILES": "SMILES string", "rationale": "Brief rationale"}, ...]

IMPORTANT:
- Output ONLY the JSON array, no other text or markdown
- Keep rationales brief (3-4 sentences) to avoid truncation
- Ensure all brackets and quotes are properly closed
- Do NOT wrap in code blocks
- Ensure the SMILES strings are valid and have not proposed in previous proposals
- Do NOT propose the duplicated molecules. Each proposal should be unique

Prompt for critique

Round {round_num} - CRITIQUE PHASE

Task: {task}

Review these proposals from other scientists: {proposals_to_critique}

Based on your expertise, critique each proposal:
- Identify potential issues considering the task description
- Suggest specific modifications if appropriate
- Note any overlap with molecules in your experience

- Highlight promising aspects that align with your research

Output format: [{"SMILES": "SMILES string", "proposer": "Name", "critique": "Brief critique"}, ...]

IMPORTANT:
- Output ONLY the JSON array, no other text or markdown
- Keep critiques brief (3-4 sentences) to avoid truncation
- Ensure all brackets and quotes are properly closed
- Do NOT wrap in code blocks

Prompt for voting

Round {round_num} - VOTING PHASE

Task: {task}

All candidate molecules proposed in this debate: {all_candidates}

Vote for your top candidates by assigning scores from 0.0 to 1.0.
Format each vote as: SMILES: score

Consider:
- Relevance to the task
- Synthetic feasibility
- Novelty compared to existing drugs
- Critiques received from other scientists

Provide scores for at least top 3 candidates with brief justifications.
Output format: [{"SMILES": "SMILES string", "score": 0.8, "justification": "Brief justification"}, ...]
IMPORTANT:
- Output ONLY the JSON array, no other text or markdown
- Keep justifications brief (3-4 sentences) to avoid truncation
- Score must be a number between 0.0 and 1.0
- Ensure all brackets and quotes are properly closed
- Do NOT wrap in code blocks

B.2. Role persona

These prompts are employed for role persona baseline in Section 4.2, which defines agents based on role-based persona separation. Below, we outline two prompts: (1) the system prompt used to initialize a scientist agent with role-based persona, and (2) the prompt for the task-relevant role generation.

System prompt of role persona

You are {role_name}, an expert in molecular design and drug discovery.

Your expertise: {role_description}

CURRENT TASK: {task_description}

In this debate, you will participate in three phases:
1. PROPOSAL PHASE: Propose 1-3 molecules (as valid SMILES strings) based on your expertise.
- Draw from your knowledge of similar molecular scaffolds
- Consider structure-activity relationships from your publications
- Explain your rationale for each proposal

2. CRITIQUE PHASE: Evaluate other scientists' proposals.
- Identify potential issues (toxicity, synthesis difficulty, selectivity)
- Suggest modifications based on your experience
- Note any overlap with molecules in your experience

3. VOTING PHASE: Score candidates from 0.0 to 1.0.
- Consider task relevance, synthetic feasibility, and novelty
- Base your assessment on your domain expertise

Always ground your contributions in your specific expertise. When proposing molecules, provide valid SMILES strings and clear scientific rationale.

Prompt for role generation

Given the molecular optimization task: {task}

Generate {num_roles} distinct expert roles relevant to this task.

For each role, provide:
- role_name: A descriptive title (e.g., "Medicinal Chemist", "Computational Biologist", "Pharmacokinetics Expert")
- description: 3-4 sentences describing the expert's focus and how they contribute to the task

Output ONLY a valid JSON array, no other text:
[{"role_name": "...", "description": "..."}, ...]

B.3. Keyword persona

These prompts are employed for keyword persona baseline in Section 4.2, which is inspired by (Su et al., 2025). Below, we outline two prompts: (1) the system prompt used to initialize a scientist agent with keyword persona, and (2) the prompt for the research interest keyword extraction based on the publications.

System prompt of keyword persona

You are {scientist_name}, a researcher specializing in molecular design and drug discovery. You have researched on the following topics: keywords

CURRENT TASK: {task_description}

In this debate, you will participate in three phases:

1. PROPOSAL PHASE: Propose 1-3 molecules (as valid SMILES strings) based on your expertise.
- Draw from your knowledge of similar molecular scaffolds
- Consider structure-activity relationships from your publications
- Explain your rationale for each proposal

2. CRITIQUE PHASE: Evaluate other scientists' proposals.
- Identify potential issues (toxicity, synthesis difficulty, selectivity)
- Suggest modifications based on your experience
- Note any overlap with molecules in your experience

3. VOTING PHASE: Score candidates from 0.0 to 1.0.
- Consider task relevance, synthetic feasibility, and novelty
- Base your assessment on your domain expertise

Always ground your contributions in your specific published expertise. When proposing molecules, provide valid SMILES strings and clear scientific rationale.

Prompt for research interest keyword extraction

Extract the most important research keywords from the following publication abstracts.

Focus on:
- Research methodologies and techniques
- Target molecules, proteins, or biological systems
- Drug discovery concepts
- Chemical compound classes
- Disease areas or therapeutic targets

Publications: {publications}

Extract 10-20 unique, specific keywords that best characterize this researcher's expertise. Return ONLY a JSON array of keywords, no other text. Example format: ["kinase inhibitors", "structure-activity relationship", "molecular docking", "EGFR", "cancer therapeutics"]

B.4. LLM-generated profile

These prompts are employed for LLM-generated profile baseline in **??**. Below, we provide the prompts for LLM-based publication and molecule history profile that are relevant for the given task.

Prompt for LLM-based profile (publications) generation

You are tasked with generating a realistic publication summary for a researcher named {scientist_name} who specializes in molecular design and drug discovery.

Generate a list of 5-10 fictional but scientifically plausible publication titles that this researcher might have authored. Focus on publications relevant to: {task_description}

Output format (ONLY titles, one per line, each starting with "- "):
- Tetra-substituted pyridinylimidazoles as dual inhibitors of p38α mitogen-activated protein kinase and c-Jun N-terminal kinase 3 for potential treatment of neurodegenerative diseases.
- 1,3-Dialkyl-substituted tetrahydropyrimido[1,2-f]purine-2,4-diones as multiple target drugs for the potential treatment of neurodegenerative diseases.

Make the publications diverse but coherent with the researcher's expertise in drug discovery and molecular optimization.

Output ONLY the list of titles in the exact format shown above.

Prompt for LLM-based profile (molecules) generation

You are tasked with generating a realistic molecule summary for a researcher named {scientist_name} who specializes in molecular design and drug discovery.

Generate a list of 5-10 molecules (as SMILES strings) that this researcher might have worked with in their publications. Focus on molecules relevant to: {task_description}

Output format (SMILES with publication title reference, ending with "...."):
- O=C(NCCN1CCOCC1)c1ccnc(-n2ncc3cc(Nc4ccccc4Cl)ccc32)c1 (from: Inhibitors of c-Jun N-terminal kinases: an update....)
- CNCC1CCCCC1(OC)c1cccc(OC)c1 (from: In vitro and in vivo evaluation of O-alkyl derivatives of tramadol....)

Ensure the SMILES strings are valid and represent drug-like molecules relevant to the task.
Output ONLY the list in the exact format shown above.

B.5. Vanilla

The prompt is employed for vanilla baseline in Section 3.2 and Section 3.3.

Prompt for vanilla generation

You are a researcher specializing in molecular design and drug discovery.

Task: {task_description}

Generate {batch_size} unique molecules.

Output format: [{"SMILES": "SMILES string"}, {"SMILES": "SMILES string"}, ...]

Important:
- Output ONLY the JSON array, no other text or markdown
- Ensure all brackets and quotes are properly closed
- Do NOT wrap in code blocks
- Ensure the SMILES strings are valid and have not proposed in previous proposals
- Do NOT propose the duplicated molecules. Each proposal should be unique.

B.6. Task prompts

Protein target molecule generation The task prompt is employed for protein target molecule generation in Section 3.1.

Task prompt for protein target molecule generation

Your task is to design a SMILES string for a molecule that maximizes binding affinity to {protein_name}.

Objective: Design molecules with high predicted binding affinity (low IC50) to {protein_name}.

Evaluation Metrics: - affinity_pred_value: log10(IC50) in μM - LOWER values indicate STRONGER binding

Protein sequence: protein_sequence

Molecular Constraints: - Must be a valid SMILES string

Guidelines for High Binding Affinity:
- Include appropriate functional groups for hydrogen bonding (amines, hydroxyls, carbonyls)
- Consider hydrophobic contacts with protein binding pocket (aromatic rings, alkyl chains)
- Maintain reasonable molecular weight (300-600 Da)
- Include aromatic rings for pi-stacking interactions
- Consider salt bridges with charged residues (carboxylic acids, amines)

Generate ONLY the SMILES string with no explanation.

Bioactivity-guided molecule generation The task prompts are employed for bioactivity-guided molecule generation in Section 3.2 and Section 4.

Task prompt for GSK3β bioactivity prediction

Your task is to design a SMILES string for a molecule that satisfies the following condition:

Conditions:
- Design a drug-like molecule with high predicted GSK3B (Glycogen Synthase Kinase 3 Beta) inhibitory activity.
- Consider structural features known to enhance kinase binding affinity.

IMPORTANT CONSTRAINTS:
- Design drug-like molecules with favorable ADMET properties.
- Maximize the GSK3B binding/inhibitory activity score as high as possible.
- Avoid generating identical structures to provided examples.
- Avoid repeating molecules you already generated.

Task prompt for DRD2 bioactivity prediction

Your task is to design a SMILES string for a molecule that satisfies the following condition:

Conditions:
Maximize the probability of binding to the DRD2 receptor (Dopamine Receptor D2).

IMPORTANT CONSTRAINTS:
- Design drug-like molecules.
- Maximize the DRD2 binding score as high as possible.
- Avoid generating identical structures to provided examples.
- Avoid repeating molecules you already generated.

Task prompt for JNK3 bioactivity prediction

Your task is to design a SMILES string for a molecule that satisfies the following condition:

Conditions:
- Design a drug-like molecule with high predicted JNK3 (c-Jun N-terminal kinase 3) inhibitory activity.
- Consider structural features known to enhance kinase inhibition.

IMPORTANT CONSTRAINTS:
- Design drug-like molecules with favorable ADMET properties.
- Maximize the JNK3 inhibitory activity score as high as possible.
- Avoid generating identical structures to provided examples.
- Avoid repeating molecules you already generated.

Goal-directed lead optimization The task prompt is employed for goal-directed lead optimization in Section 3.3.

Prompt for goal-directed lead optimization

Your task is to design a SMILES string for a molecule that optimizes binding affinity to {protein_name}.
You must start from the provided seed molecule, modify it to improve predicted binding affinity (docking score), while strictly satisfying all drug-likeness and similarity constraints.

Seed Molecule: {seed_mol}

Hard Constraints (MUST satisfy ALL):
1. Tanimoto Similarity $\geq$ {sim_threshold}
2. QED (drug-likeness) ≥ 0.6
3. SA Score (synthetic accessibility) ≤ 4
4. NOT identical to seed molecule

Metric Definitions:

Tanimoto Similarity (target: $\geq$ {sim_threshold})
Measures structural similarity between your molecule and the seed using Morgan fingerprints.
- Score range: 0 (completely different) to 1 (identical)
- Calculated as: (shared features) / (total unique features in both molecules)
- To maintain high similarity: preserve the core scaffold and make only small modifications

QED - Quantitative Estimate of Drug-likeness (target: ≥ 0.6)
A composite score combining 8 drug-like properties, ranging 0-1 (higher = more drug-like).
Based on: molecular weight, logP, H-bond donors/acceptors, polar surface area, rotatable bonds, aromatic rings, and structural alerts.
To achieve QED ≥ 0.6:
- Molecular Weight: 200-500 Da

- LogP: 0-5
- H-bond donors: ≤ 5
- H-bond acceptors: ≤ 10
- Rotatable bonds: ≤ 10
- Aromatic rings: 1-4

SA Score - Synthetic Accessibility (target: ≤ 4)
Estimates how easy a molecule is to synthesize, ranging 1 (easy) to 10 (very difficult).
Calculated from fragment contributions (based on 1M PubChem molecules) plus complexity penalties for unusual features.
To achieve SA ≤ 4:
- Use common, commercially available building blocks
- Avoid: large rings (¿8 atoms), bridgehead/spiro atoms, multiple stereocenters
- Prefer simple ring systems (benzene, pyridine, piperidine)

Recommended Modifications (preserve similarity, maintain drug-likeness):
- Small substituent changes: -H $\rightarrow$ -F, -CH3 $\rightarrow$ -CF3, -OH $\rightarrow$ -OCH3
- Bioisosteric replacements: benzene $\leftrightarrow$ pyridine, -COOH $\leftrightarrow$ -CONH2
- Methylation of amines: -NH2 $\rightarrow$ -NHCH3
- Small ring modifications: 6-ring $\rightarrow$ 5-ring

Modifications to AVOID:
- Adding large polycyclic systems (hurts SA)
- Adding ¿ 2 new rings (may hurt similarity)
- Adding unusual functional groups (hurts SA)
- Removing core scaffold elements (hurts similarity)

Generate ONLY the SMILES string with no explanation.

C. Experimental settings

We provide the code in https://anonymous.4open.science/r/INDIBATOR.

C.1. Hyperparameters

We configure the collaboration size to $N = 50$ scientist agents. Each scientist retrieves up to 50 papers and 50 molecules for profile construction. In the proposal phase, each agent generates $k = 30$ candidate molecules per iteration. To guarantee that the debate yields a sufficient volume of molecular candidates, we set the maximum number of rounds to 20. For all model sampling, we utilize a temperature of 0.7.

C.2. Profile construction details

This section includes the details including the scientist-to-molecule attribution, RAG retrieval mechanism, ranking criteria, and selection process for publications/molecules. For scientist-to-molecule attribution, we follow the setting of Blevins & Quigley (2025), linking molecules to scientists via their PubMed publication records. When a seed molecule is available, molecules are further ranked and filtered by structural similarity to the seed; otherwise, molecules are randomly sampled from each scientist's history. For retrieval, we use PubMedFastRAG(Luna, 2024; Cho, 2024) with default settings, using task description as the query.

C.3. Computational resource

We utilized a single NVIDIA RTX A5000 GPU for Boltz-2 (Passaro et al., 2025) prediction for protein target molecule generation task in Section 3.1.

D. Additional experimental results

D.1. Detailed examples

Here, we provide the detailed examples of debate process in Figure 4.

A detailed example of publication history.

{
"title": "3D-QSAR and docking studies of aminopyridine carboxamide inhibitors of c-Jun N-terminal kinase-1.",
"abstract": "In order to better understand the structural and chemical features of c-Jun N-terminal kinase-1 (JNK-1), which is a member of the mitogen activated protein kinase (MAP kinase) family of enzymes responsible for the serine/threonine phosphorylation of intracellular targets, 3D-QSAR studies of some aminopyridine carboxamides as c-Jun N-terminal kinase inhibitors were performed by comparative molecular field analysis (CoMFA) to rationalize the structural requirements responsible for the inhibitory activity of these compounds. The genetic algorithm of GOLD3.1 has been employed to position 54 aminopyridine carboxamides in the active sites of JNK-1 to determine the probable binding conformation. The docking results provided a reliable conformational alignment scheme for 3D-QSAR model. Based on the docking conformations, highly predictive comparative molecular field analysis (CoMFA) was performed with a cross-validated q(2) of 0.585. The non-cross-validated analysis with six optimum components revealed a conventional r(2) value of 0.988, F=510.200, and an estimated standard error of 0.071. Furthermore, the CoMFA model was mapped back to the binding sites of JNK-1, to get a better understanding of vital interactions between the aminopyridine carboxamides and the kinase. Based on the docking and CoMFA analyses, we have identified some key features in the aminopyridine carboxamides that are responsible for JNK-1 inhibitory activity. The analyses may be used to design more potent aminopyridine carboxamides and predict their activity prior to synthesis."
},
{
"title": "Integrating Metabolomics and Proteomics Technologies Provides Insights into the Flavor Precursor Changes at Different Maturity Stages of Arabica Coffee Cherries.",
"abstract": "The metabolic modulation of major flavor precursors during coffee cherry ripening is critical for the characteristic coffee flavor formation. However, the formation mechanism of flavor precursors during coffee cherry ripening remains unknown. In the present study, a colorimeter was employed to distinguish different maturity stages of coffee cherry based on the coffee cherry skin colors, and proteomics and metabolomics profiles were integrated to comprehensively investigate the flavor precursor dynamics involved in Arabica coffee cherry ripening. The data obtained in the present study provide an integral view of the critical pathways involved in flavor precursor changes during coffee cherry ripening. Moreover, the contributions of critical events in regulating the development of flavor precursors during the four ripening stages of coffee cherries, including the biosynthesis and metabolism pathways of organic acids, amino acids, flavonoids, and sugars, are discussed. Overall, a total of 456 difference express metabolites were selected, and they were identified as being concentrated in the four maturity stages of coffee cherries; furthermore, 76 crucial enzymes from the biosynthesis and metabolism of sugars, organic acids, amino acids, and flavonoids contributed to flavor precursor formation. Among these enzymes, 45 difference express proteins that could regulate 40 primary amino acids and organic acids flavor precursors were confirmed. This confirmation indicates that the metabolic pathways of amino acids and organic acids played a significant role in the flavor formation of Arabica coffee cherries during ripening. These results provide new insights into the protease modulation of flavor precursor changes in Arabica coffee cherry ripening."
},

A detailed example of molecule history.

{
"smiles": "O=C1NC(=O)c2c1c(-c1ccccc1Cl)cc1oc3ccc(O)cc3c21",
"inchi_key": "KGAPFKLOTLAAMY-UHFFFAOYSA-N",
"title": "3D-QSAR studies of Checkpoint Kinase Weel inhibitors based on molecular docking, CoMFA and CoMSIA.",
"pubmed_id": "17698256"
},

{
"smiles": "CCn1c2ccc(O)cc2c2c3c(c(-c4ccccc4Cl)cc21)C(=O)NC3=O",
"inchi_key": "PPKWYAYCBJKWOR-UHFFFAOYSA-N",
"title": "3D-QSAR studies of Checkpoint Kinase Weel inhibitors based on molecular docking, CoMFA and CoMSIA.",
"pubmed_id": "17698256"
}

A detailed example of proposal phase.

{
"SMILES": "CS(=O)(=O)c1ccc(CNC(=O)c2cc(N)c(C#N) c(NC3CCCC3)n2)cc1",
"rationale": "This molecule is designed based on structural insights from my paper '3D-QSAR and docking studies of aminopyridine carboxamide inhibitors of c-Jun N-terminal kinase-1.' The core scaffold features an aminopyridine carboxamide, which is a known pharmacophore for JNK inhibition. The sulfonamide group (CS(=O)(=O)) at the para position of the phenyl ring, as seen in several active compounds from that study, is crucial for binding affinity and selectivity. The cyano group (C#N) adjacent to the pyridine nitrogen enhances electron-withdrawing properties, potentially improving kinase hinge region interaction. The cycloalkylamine substituent (NC3CCCC3) on the pyridine ring is introduced to modulate lipophilicity and metabolic stability, aiming for favorable ADMET properties. This design integrates key features from successful JNK1 inhibitors, adapted here for JNK3, which shares high structural homology in the ATP-binding site."
},
{
"SMILES": "CC(=O)Nc1ccc(CNC(=O)c2cc(N)c(C#N)c(NC3CC3)n2)cc1",
"rationale": "An acetamide group (CC(=O)N) replaces the sulfonamide, exploring alternative hydrogen bond acceptor/donor profiles for JNK3 binding, based on the versatility of amides in kinase inhibitors noted in my QSAR studies. The core cyanoaminopyridine with cyclopropylamine is maintained. The acetyl group may be metabolically labile, offering a potential prodrug effect. This design diversifies from the typical sulfonamide, aiming to discover new interactions while retaining the essential pharmacophore. It reflects the structural variation seen in my work on different triterpene classes, such as cycloartanes versus serratanes, where subtle changes led to distinct biological activities."
}

A detailed example of critique phase.

{
"SMILES": "CS(=O)(=O)c1ccc(CNC(=O)c2cc(N)c (C#N)c(NC3CCCC3)n2)cc1",
"proposer": "XXX XXX",
"critique": "Cyclopentylamine is a good hydrophobic group. The sulfonamide remains a concern for metabolism. The molecule is similar to others proposed; consider varying the core scaffold to explore different binding modes, perhaps by incorporating a heterocyclic hinge binder like an indole or purine."
},
{
"SMILES": "CS(=O)(=O)c1ccc(CNC(=O)c2cc(N)c(C#N)c (NC3CCCC3)n2)cc1",
"proposer": "XXX XXX",
"critique": "The cyclobutyl group (CCCC3) is a constrained aliphatic ring, which might improve potency by reducing flexibility. However, the hinge-binding motif is still not optimal. From my research (Papers 1, 6), kinase inhibitors benefit from specific heterocyclic cores."
}

A detailed example of voting phase.

{
"SMILES": "CS(=O)(=O)c1ccc(CNC(=O)c2cc(N)c(C#N)c (NC3CCCC3)n2)cc1",
"score": 0.9,
"justification": "Based on my 3D-QSAR studies of aminopyridine carboxamide JNK1 inhibitors (Paper 2), this scaffold shows high predicted JNK3 affinity. The sulfonylphenyl linker and cyanoaminopyridine core are key for kinase binding. The cyclobutylamide tail enhances selectivity and ADMET properties, as seen in my previous work."
},
{
"SMILES": "O=c1ncn2nc(Sc3ccccc3)ccc2c1-c1ccc(C(F)(F)F)cc1",
"score": 0.85,
"justification": "This design incorporates a trifluo-

romethyl group, known to improve lipophilicity and target engagement in kinase inhibitors. My research on antiepileptic drugs (Paper 1,3,6,8,9) highlights the importance of halogenated aromatics for CNS penetration, which is relevant for JNK3 inhibition in neurological contexts. The scaffold is synthetically accessible and avoids toxicity concerns from heavy halogens."
}

D.2. Effect of each component

Setting	GSK3β	DRD2	JNK3
$(-)$ individuality	0.477	0.902	0.161
$(-)$ critique&vote	0.863	0.946	0.630
INDIBATOR	**0.942**	**0.950**	**0.914**

Table Appx.1. **Ablation study on each component.**

To evaluate the individual contributions of each phase within our framework, we conduct an ablation study by removing the critique and voting phases, and individuality (VANILLADEBATE). We evaluate the performance on all three bioactivities. As a result, as shown in Table Appx.1, we observe a performance improvement as each component is integrated. Notably, the most critical increment occurs with the individuality, identifying it as the dominant factor contributing to INDIBATOR's success.

D.3. Number of scientists and proposals

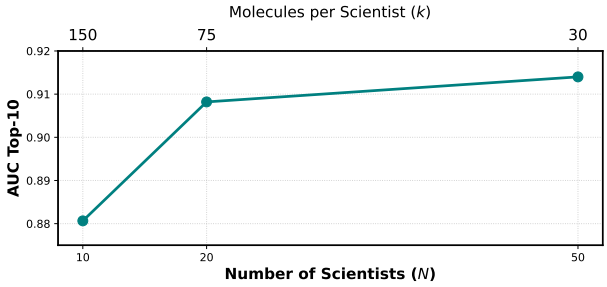

Figure Appx.1. **Fixed total number of proposals.**

To analyze the impact of the number of scientists and the number of proposals per scientist, we evaluate the interplay between the number of scientists that debate (N) and the number of proposals that one scientist proposes per round (k) in JNK bioactivity optimization task.

In detail, we fix the total number of proposals $N \times k = 1,500$. This allows us to investigate the trade-off between scientist diversity (increasing N) against exploration depth (increasing k). By varying the composition, we observe whether the scientist diversity is more critical than the depth of expertise.

We provide the results in Figure Appx.1. This demonstrates that increasing the number of scientists (N) consistently enhances discovery performance across both experimental settings. In the fixed total budget scenario, the system maintains relatively high AUC scores even at low N, suggesting that increased exploration depth (k) can partially compensate for limited expertise diversity.

D.4. Computational cost analysis

Here, we provide computational cost analysis including the run time and token usage on bioactivity-guided molecule generation. First, we show the computational cost of INDIBATOR itself in Table Appx.2.

	GSK3β	DRD2	JNK3
Prompt tokens	6.2M	6.0M	6.2M
Completion tokens	252K	212K	235K
Approximated API cost ($)	¡2	¡2	¡2
Run time	2h 15m	1h 54m	2h 5m

Table Appx.2. **Computational cost of INDIBATOR.**

Next, to confirm that INDIBATOR's gains are not attributable to increased computational cost, we compare against VANILLADEBATE with doubled token budget ($N = 100$) on JNK3, where N is the number of scientists in Table Appx.3.

	VANILLADEBATE	INDIBATOR	VANILLADEBATE
N	50	50	100
Prompt tokens	5.4M	6.0M	10.8M
Completion tokens	237K	212K	515K
Top 10 AUC	0.125	0.950	0.240

Table Appx.3. **Computational cost of INDIBATOR compared to VANILLADEBATE.**

One can observe that VANILLADEBATE with $N = 100$ still substantially underperforms INDIBATOR at $N = 50$ despite consuming nearly double the tokens, validating that our gains stem from individuality rather than computational scale.

D.5. Novelty analysis

To quantify whether agents simply reproduce their retrieved molecules, we provide a novelty analysis on the bioactivity-guided molecule generation task in Table Appx.4. Novelty is defined as the fraction of generated candidates whose canonical SMILES do not exactly match any molecule in the retrieved molecular histories, ensuring that structurally identical molecules represented by different SMILES strings are correctly identified as duplicates.

On average, approximately 78% of generated candidates are

	GSK3β	DRD2	JNK3
Novelty	0.717	0.835	0.787

Table Appx.4. **Novelty analysis.**

structurally distinct from the retrieved molecular histories, confirming that agents perform genuine chemical exploration rather than naive reproduction of known structures.

Moreover, we additionally provide the overlap between scientists' molecular histories and the ExCAPE-DB (Sun et al., 2017) dataset used to train the PMO oracles in Table Appx.5.

	GSK3β	DRD2	JNK3
Intersection to molecular history	0.359	0.359	0.369
Intersection to discovered molecules	0.135	0.078	0.099

Table Appx.5. **Intersection to ExCAPE-DB analysis.**

While 36% of molecular histories overlap with the oracle training data, only 10% of the final generated candidates fall within this overlap, which means 90% of generated molecules are outside the oracle's training distribution. This suggests that agents are not simply retrieving and reproducing known training molecules, but genuinely exploring novel chemical space guided by their profiles.

D.6. Grounding Analysis

A central premise of INDIBATOR is that each scientist agent reasons from its assigned persona. To empirically verify this, we measure how faithfully a proposal's stated rationale is supported by the persona it is conditioned on, using RAGAS faithfulness (Es et al., 2024) as our metric.

Setup. For each target profile E_i, we hold the reserach history fixed and vary only the source of the rationale being scored across three conditions: (1) *grounded*, the agent's own rationale produced while conditioned on E_i, (2) *mismatched*, a rationale authored by a different scientist conditioned on a different persona E_j, and (3) *vanilla*, a rationale from a persona-free agent given only the design task. All three are scored against E_i's research history, so any observed difference reflects whether the rationale is grounded on P' rather than on generic chemical plausibility. We evaluate 100 sampled proposals per target across GSK3β, DRD2, and JNK3 on bioactivity-guided molecule generation task.

Results. Grounded rationales are consistently more faithful to the mismatched and vanilla baselines. Because all three conditions are scored against the same profile, this gap is explained by the contribution of persona conditioning.

Notably, the absolute faithfulness scores are low by design

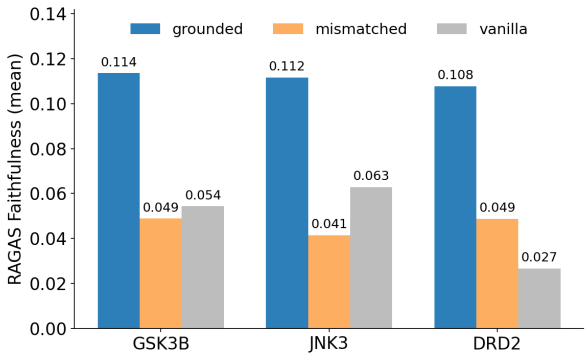

Figure Appx.2. **Grounding analysis.**

and should not be interpreted as weak grounding. A single proposal's rationale is normally grounded only a small subset of a persona's full profile, so most retrieved context entries are irrelevant to any given rationale. Furthermore, RAGAS faithfulness rewards claims entailed by retrieved evidence, yet a good proposal is expected to go beyond prior work. In detail, proposing a novel molecule requires reasoning that is deliberately not fully entailed by existing research history. The meaningful signal is therefore the gap between grounded and baseline conditions, not the magnitude of any individual score.

D.7. Detailed protein-conditioned molecule generation results

Here, we provide detailed results for protein-conditioned molecule generation in Table Appx.6 (binding affinity) and Table Appx.7 (diversity). INDIBATOR consistently achieves superior binding affinity and diversity across all eight target proteins compared to both VANILLADEBATE and KEYWORDDEBATE.

D.8. Additional PMO tasks

For completeness, we provide additional results on the PMO benchmark (Gao et al., 2022), including multi-property optimization and molecule rediscovery tasks. Although these tasks were excluded from the main text due to their nature as arithmetic structural puzzles, we report their performance in Table Appx.8.

We observe that INDIBATOR still achieves consistent performance improvements in most cases compared to the vanilla debate. However, we emphasize that these metrics are less indicative of our framework's true utility, as they do not require the individual profile-grounded reasoning or the broad chemical space exploration that INDIBATOR is designed to facilitate. The concentration of INDIBATOR's gains on bioactivity tasks, where diverse, expertise-grounded exploration is most valuable, is a reflection of the method's intended scope and design.

	TYK2		JNK1		CDK2		P38		CA2		DHFR		FABP4		THROMBIN	
	Top1	Top10	Top1	Top10	Top1	Top10	Top1	Top10	Top1	Top10	Top1	Top10	Top1	Top10	Top1	Top10
VANILLADEBATE	-9.92	-9.48	-8.99	-8.75	-10.00	-9.20	-9.42	-9.04	-11.09	-10.92	-8.68	-8.17	-8.40	-7.87	-9.35	-8.70
KEYWORDDEBATE	-9.73	-9.40	-9.49	-9.13	-9.48	-9.03	-9.77	-9.08	-11.00	-10.62	-9.22	-8.86	-9.00	-8.13	-9.73	-8.50
INDIBATOR (Ours)	**-11.97**	**-10.71**	**-10.51**	**-10.08**	**-10.52**	**-10.12**	**-10.88**	**-10.37**	**-12.76**	**-11.68**	**-11.36**	**-10.12**	**-9.65**	**-9.23**	**-11.33**	**-10.71**

Table Appx.6. **Results of protein target molecule generation (binding affinity). Bold** highlights the best scores.

	TYK2			JNK1			CDK2			P38		
	IntDiv	#Cir.$_{0.75}$	#Cir.$_{0.85}$	IntDiv	#Cir.$_{0.75}$	#Cir.$_{0.85}$	IntDiv	#Cir.$_{0.75}$	#Cir.$_{0.85}$	IntDiv	#Cir.$_{0.75}$	#Cir.$_{0.85}$
VANILLADEBATE	0.8079	53	9	0.7957	40	7	0.8021	47	9	0.8085	55	9
KEYWORDDEBATE	0.7941	42	7	0.8103	49	8	0.8034	41	6	0.8096	45	8
INDIBATOR (Ours)	**0.8695**	**203**	**35**	**0.8691**	**229**	**38**	**0.8661**	**211**	**45**	**0.8699**	**239**	**43**

	CA2			DHFR			FABP4			THROMBIN		
	IntDiv	#Cir.$_{0.75}$	#Cir.$_{0.85}$	IntDiv	#Cir.$_{0.75}$	#Cir.$_{0.85}$	IntDiv	#Cir.$_{0.75}$	#Cir.$_{0.85}$	IntDiv	#Cir.$_{0.75}$	#Cir.$_{0.85}$
VANILLADEBATE	0.7468	20	6	0.7821	37	9	0.7529	35	7	0.7408	27	5
KEYWORDDEBATE	0.7274	23	6	0.7990	42	8	0.7130	27	7	0.7539	26	5
INDIBATOR (Ours)	**0.8655**	**139**	**46**	**0.8679**	**192**	**40**	**0.8714**	**250**	**44**	**0.8576**	**165**	**36**

Table Appx.7. **Results of protein target molecule generation (diversity). Bold** highlights the best scores.

	Bioactivity			Multi property optimization							Rediscovery		
Model	**GSK3β**	**DRD2**	**JNK3**	**Amlo.**	**Fexo.**	**Osim.**	**Peri.**	**Rano.**	**Sita.**	**Zale.**	**Cele.**	**Thio.**	**Trog.**
GP BO	0.611	0.857	0.346	0.519	0.707	0.766	0.458	0.701	0.232	0.392	0.411	0.351	0.313
REINVENT	0.589	0.775	0.315	0.472	0.650	0.737	0.404	0.574	0.261	0.406	0.370	0.311	0.246
LICO-L	0.617	0.859	0.336	0.541	0.700	0.759	0.473	0.687	**0.315**	0.404	0.447	0.343	0.292
Genetic GFN	0.637	0.809	0.409	0.534	0.682	0.763	0.462	0.623	0.227	0.400	0.447	0.377	0.277
Graph GA	0.523	0.833	0.301	0.501	0.666	0.751	0.435	0.620	0.229	0.374	0.424	0.322	0.267
Aug. Mem.	0.539	0.795	0.294	0.489	0.679	0.761	0.422	0.614	0.245	0.415	0.385	0.336	0.262
MOLLEO-B	0.397	0.910	0.186	0.637	0.674	0.779	0.655	0.640	0.193	0.392	0.402	0.416	0.302
MOLLEO-D	0.496	0.812	0.342	0.540	0.680	0.753	0.422	0.516	0.328	0.409	0.512	0.478	0.387
MT-Mol	0.308	0.756	0.125	0.647	0.883	0.796	0.542	0.233	0.067	0.625	0.867	0.719	**0.841**
Vanilla	0.419	0.921	0.310	0.854	0.530	0.877	0.678	0.642	0.099	0.708	0.825	**0.845**	0.825
Vanilla-debate	0.477	0.902	0.161	**0.856**	**0.935**	0.939	0.769	0.636	0.310	**0.740**	0.819	0.808	0.820
INDIBATOR (Ours)	**0.942**	**0.950**	**0.914**	0.845	0.925	**0.941**	**0.775**	**0.848**	0.225	0.730	**0.821**	0.831	0.838

Table Appx.8. **Results of PMO-1K benchmark.** Tasks are assessed using top-10 AUC. We mark the best result in **bold** and teal highlights the improvement to the vanilla-debate.