

# **Mol-LLaMA: Towards General Understanding of Molecules in Large Molecular Language Model**

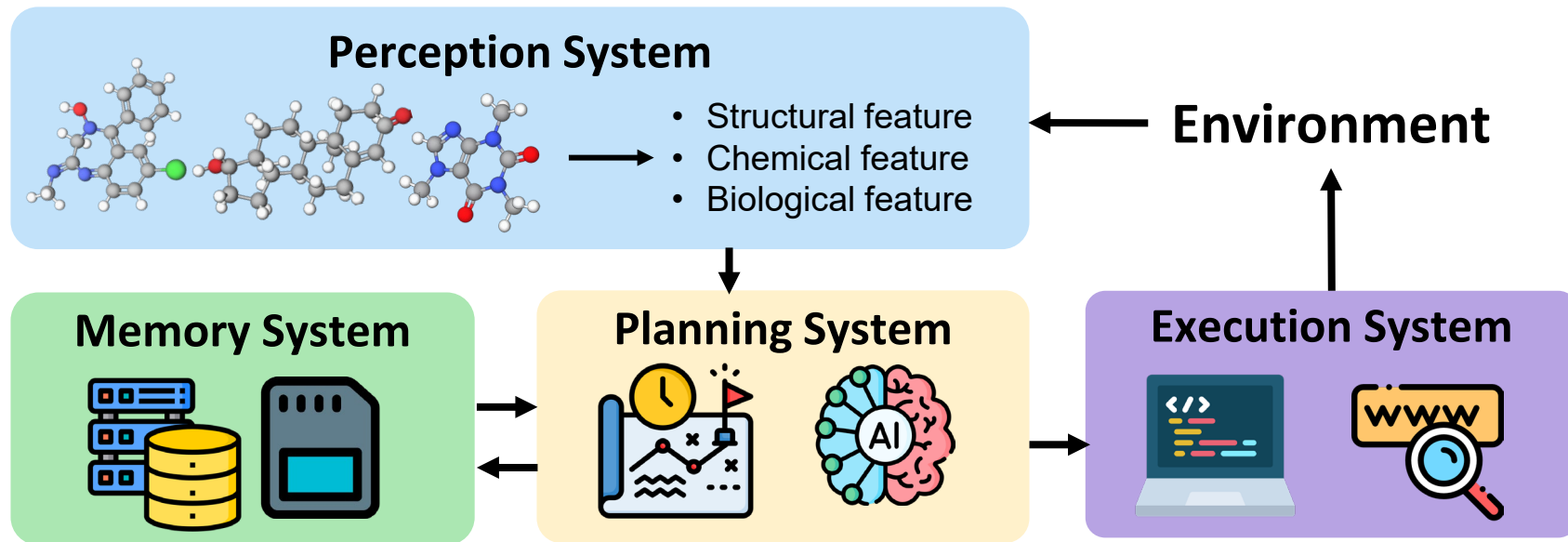
Dongki Kim<sup>1</sup>, Wonbin Lee<sup>1</sup>, Sung Ju Hwang<sup>1,2</sup>

KAIST<sup>1</sup>, DeepAuto.ai<sup>2</sup>

NeurIPS 2025

# Agent System for Scientific Discovery

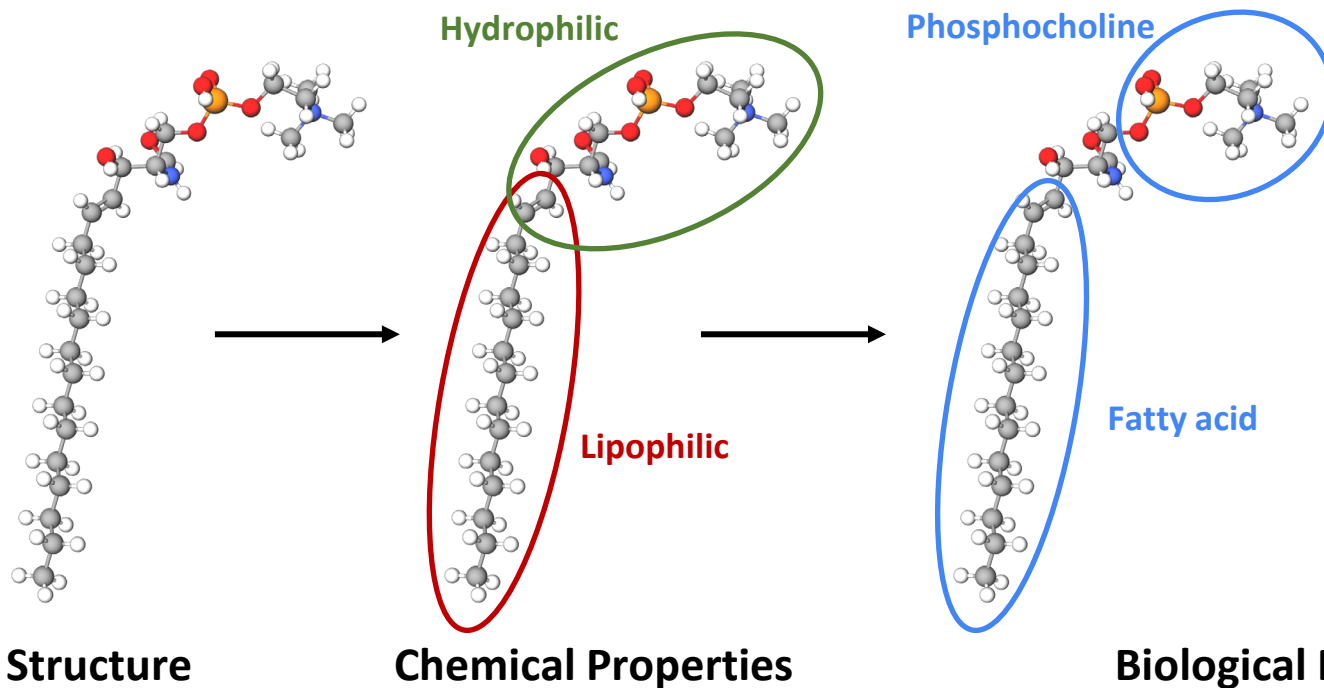
Even though the perception system takes a fundamental part in an agent system, LLMs have shortcomings to comprehend molecular structures and their properties.



To overcome this limitation, we aim to develop a molecular LLM, that can be utilized as a general-purpose assistant for molecular analysis.

# Molecular Semantics in Chemistry and Biology

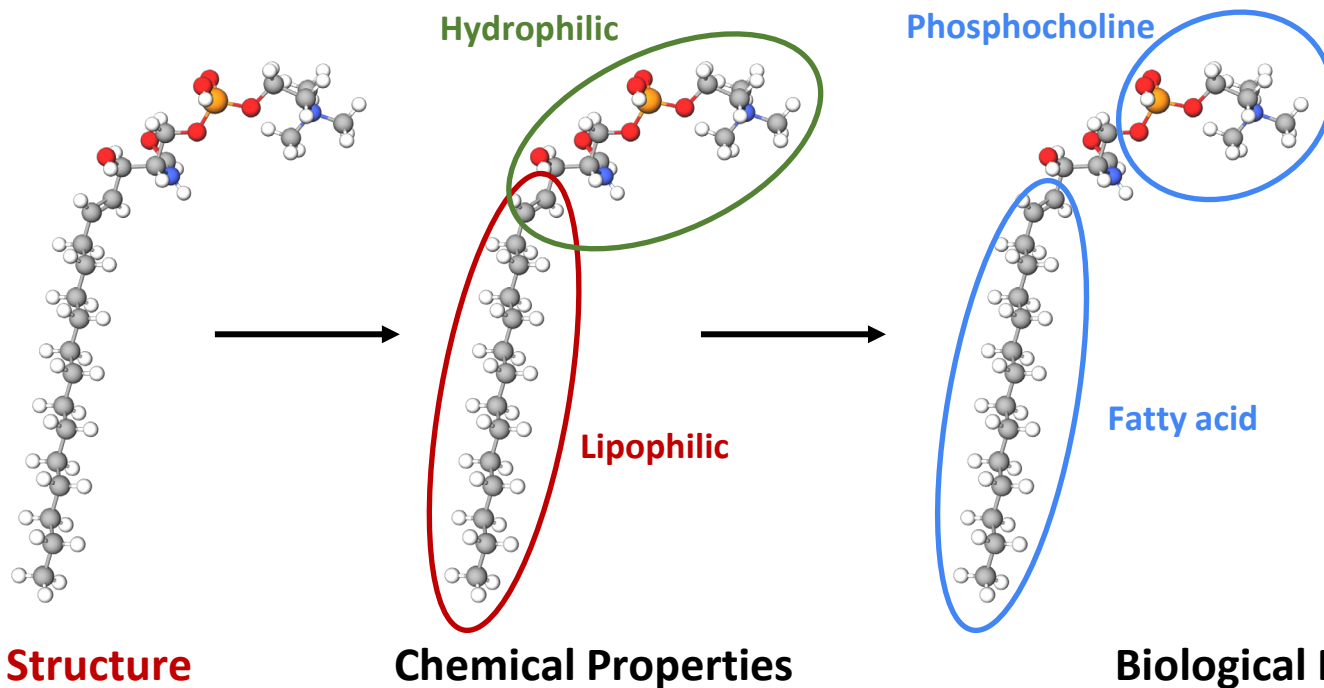
We focus on the hierarchical relationship between molecular features:  
Chemical and biological properties are determined by structural features.



- Type of **Sphingolipid**
- Found in **cell membrane**
- **Cell Signaling**
- Higher concentration in the **nerve tissue**

# Molecular Semantics in Chemistry and Biology

We focus on the hierarchical relationship between molecular features:  
Chemical and biological properties are determined by structural features.



- Type of **Sphingolipid**
- Found in **cell membrane**
- **Cell Signaling**
- Higher concentration in the **nerve tissue**

# Our Approach

To overcome the limitations of previous works, we focus on two main objectives.

- **Model Architecture:** Accurate modeling of molecular structures
  - Enhance the foundational understanding of general molecular features.
- **Instruction Dataset:** Training of general knowledge centered on molecules
  - Structures → Chemical features → Biological features

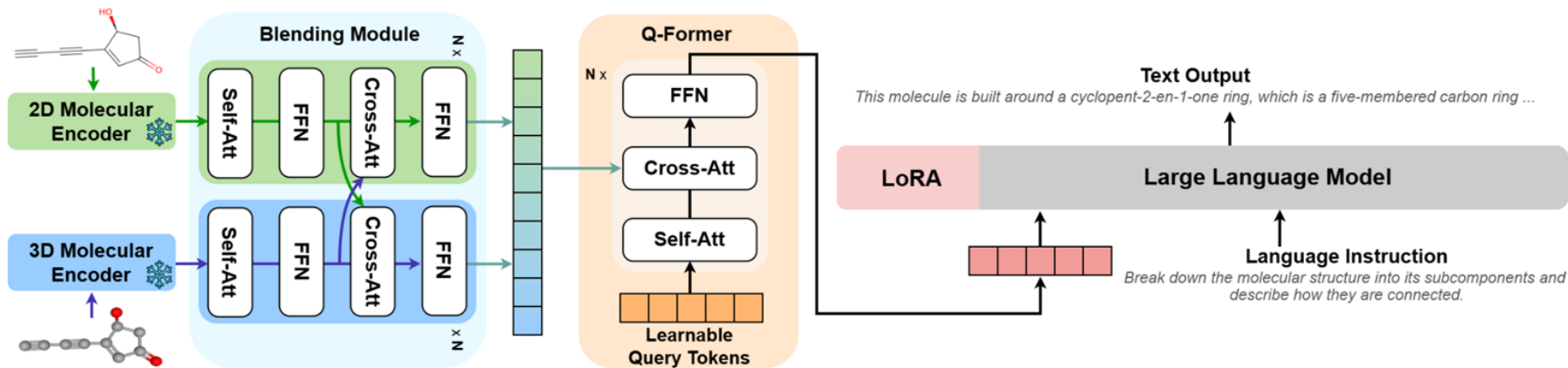
# Our Approach

To overcome the limitations of previous works, we focus on two main objectives.

- **Model Architecture:** Accurate modeling of molecular structures
  - Enhance the foundational understanding of general molecular features.
- **Instruction Dataset:** Training of general knowledge centered on molecules
  - Structures → Chemical features → Biological features

# Model Architecture

- Blending Module: We propose a blending module to fully leverage the advantages of different molecular encoder.
- Q-Former: To guarantee the permutation invariant, we leverage Q-Former architecture which performs the cross-attention.



# Our Approach

To overcome the limitations of previous works, we focus on two main objectives.

- **Model Architecture:** Accurate modeling of molecular structures
  - Enhance the foundational understanding of general molecular features.
- **Instruction Dataset:** Training of general knowledge centered on molecules
  - Structures → Chemical features → Biological features



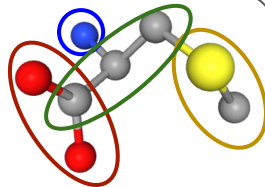
# Data Type: Detailed Structural Descriptions

To upskill the fundamental understanding of molecules and their features, we design detailed description of structures.

## Instruction to GPT -4o

Explain which substructures and functional groups are contained and how they are connected.

Input Molecule (IUPAC name): (2R)-2-amino-3-methylsulfanylpropanoic acid



The molecule provided is a **chiral amino acid** that contains several identifiable substructures.

- Amino Group:** This functional group consists of a nitrogen atom bonded to two hydrogen atoms (-NH<sub>2</sub>). It is **attached to the second carbon atom of the main carbon chain**...
  - Carboxylic Acid Group:** Represented by (-COOH), ... **It is attached to the end of the carbon chain**, characteristic of amino acids which bear a carboxylic acid group at the terminal carbon.
  - Main Carbon Chain:** The molecule has a **three-carbon chain** serving as the backbone. **The central carbon, referred to as the alpha carbon, is a chiral center**, meaning it is bonded to four different substituents: the amino group, the carboxylic acid group, a hydrogen atom, and a side chain.
  - Methylsulfanyl Group:** **Attached to the third carbon** is a side chain consisting of a sulfur atom single-bonded to a methyl group (-SCH<sub>3</sub>). This group acts as the side chain substituent and characterizes the molecule as containing a thioether linkage, ...
  - Chirality:** The molecule is chiral, with the alpha carbon being the stereocenter. Its configuration is designated as (R), indicating the spatial arrangement of its substituents ...
- Overall, this molecule is a sulfur-containing, optically active alpha amino acid ...

# Data Type: Structure-to-Feature Relationship

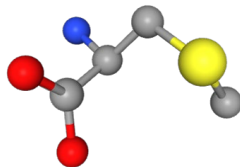
To further learn the chemical and biological features, we design S2F relationship explanations, based on our observation of the hierarchical relationship.

## Instruction to GPT -4o

Explain chemical properties by relating chemical properties to its structural information.

Input Molecule (IUPAC name): (2R)-2-amino-3-methylsulfanylpropanoic acid

Description: S-methylcysteine is a **cysteine derivative** that is L-cysteine in which the hydrogen attached to the sulfur is replaced by a methyl group. It has a role as a **human urinary metabolite** and a **plant metabolite**. It is a tautomer of a S-methylcysteine **zwitterion**.



The given molecule is a derivative of cysteine, an amino acid known for containing a thiol group. In the given molecule, this thiol group has one of its hydrogen atoms replaced by a methyl group, making it a methylthioether. ...

Firstly, the presence of the amino group (-NH<sub>2</sub>) classifies this compound as an amino acid, which [contributes to its ability to act as a zwitterion](#). ...

The sulfur atom with a methyl attachment forms a [thioether](#). [This increases the molecule's hydrophobic characteristics compared to cysteine](#), which contains a more polar thiol group. This methylsulfanyl group can also affect the molecule's reactivity and interaction with biochemical systems, ...

[As a human urinary metabolite](#), the presence of this compound in urine suggests its role in human metabolism where it might play a role in [sulfur metabolism](#) or act as a [detoxification product](#). In plants, it could partake in sulfur metabolism and possibly aid in detoxification or defense processes due to environmental stressors.

In summary, the structural modification from cysteine to include a methylthioether enhances its lipophilic properties

# Data Type: Comprehensive Conversations

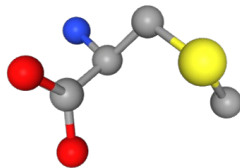
To tailor LLMs to handle diverse requests, we design comprehensive conversations that gradually deepens from structure to chemistry and biology.

## Instruction to GPT -4o

Design a sequence of pairs of questions and answers that gradually deepen the level of the conversation, from structural information and chemical properties to biological functionalities.

Input Molecule (IUPAC name): (2R)-2-amino-3-methylsulfanylpropanoic acid

Description: S-methylcysteine is a cysteine derivative that is L-cysteine in which the hydrogen attached to the sulfur is replaced by a methyl group....



-----  
User: Can you tell me about **the basic structure** of the given molecule?

Assistant: The given molecule is a derivative of **cysteine**, where the hydrogen atom attached to the sulfur group is replaced by a methyl group. ...

User: Can you tell me more about **the specific species of this compound**?

Assistant: The compound is known as **S-methylcysteine**. It is a specific derivative of cysteine with a distinctive methyl substitution on the sulfur atom, differing from the typical cysteine structure.

User: How does **the molecule's structure influence its chemical behavior**?

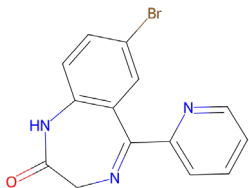
Assistant: The structure of the given molecule, particularly the presence of both amino and carboxylic acid groups, contributes to its **zwitterionic nature at physiological pH**. ...

User: What role does this molecule play **biologically**?

Assistant: Biologically, S-methylcysteine serves as a **metabolite in both humans and plants**. ...

# Qualitative Evaluation

Mol-LLaMA is able to accurately understand the molecular structures and predict the chemical and biological properties, providing detailed explanation.



Input Molecule

## Annotated Properties (Ground Truth)

It is one of the benzodiazepines that is used in the treatment of anxiety disorders. Bromazepam binds to the GABA receptor  $GABA_A$ , causing a conformational change and increasing inhibitory effects of GABA. Other neurotransmitters are not influenced.



## User

Explain the features of the given molecule that are most distinct from those of other molecules.

## Mol-LLaMA

The given molecule is a member of the benzodiazepine class, which is characterized by a fusion of a benzene ring and a seven-membered diazepine ring. This structure is crucial for its biological activity, particularly its role as a sedative and hypnotic agent.

One of the key features of the given molecule is the presence of a pyridine ring attached to the benzodiazepine core. This pyridine moiety is significant because it can influence the molecule's pharmacokinetic properties, such as its ability to cross the blood-brain barrier, which is essential for its function as a central nervous system depressant.

Additionally, the molecule contains a bromine atom attached to the benzodiazepine ring. The presence of this halogen atom can affect the molecule's lipophilicity and its binding affinity to the GABA-A receptor, which is the primary target of benzodiazepines. The bromine atom may also contribute to the molecule's metabolic stability and its duration of action.

The given molecule is also characterized by a ketone group within the diazepine ring, which is a common feature in benzodiazepines. This functional group is important for the interaction with the GABA-A receptor, as it plays a role in the formation of the benzodiazepine-receptor complex, enhancing the inhibitory effects of GABA. ...

# Molecular Property Prediction

Mol-LLaMA shows the best performance not only on the accuracy but also on the fidelity and helpfulness, implying its utility as a general-purpose assistant.

Models	Default			CoT			w/ Task Info.		
	Acc. (Ratio)	Fidel.	Help.	Acc. (Ratio)	Fidel.	Help.	Acc. (Ratio)	Fidel.	Help.
GPT-4o	48.65 (59.95)	-	-	58.23 (47.42)	-	-	47.17 (62.41)	-	-
<i>Llama2-7B-Based</i>									
Llama2-7B-Chat	57.14 (36.12)	0.517	0.508	57.53 (39.56)	0.639	0.658	84.52 (0.00)*	0.658	0.718
Mol-Instructions	49.63 (47.67)	0.277	0.210	31.16 (70.02)	0.314	0.270	38.18 (68.80)	0.331	0.256
LLaMo	<b>84.28</b> (0.74)	0.242	0.187	84.52 (0.00)*	0.246	0.191	N/A	0.226	0.185
<b>Mol-LLaMA (Ours)</b>	75.68 (11.30)	<b>0.781</b>	<b>0.820</b>	<b>79.61</b> (6.88)	<b>0.759</b>	<b>0.793</b>	<b>67.90</b> (28.75)	<b>0.757</b>	<b>0.744</b>
<i>Llama3 or Llama3.1-8B-Based</i>									
Llama3.1-8B	56.51 (45.70)	0.629	0.554	46.19 (58.48)	0.795	0.786	63.64 (34.15)	0.850	0.875
Mol-Instructions	55.91 (38.33)	0.245	0.207	33.50 (73.96)	0.299	0.247	70.47 (25.55)	0.245	0.206
3D-MoLM <sup>†</sup>	46.93 (58.72)	0.668	0.651	50.00 (51.35)	0.671	0.649	64.86 (35.87)	0.767	0.744
LLaMo <sup>†</sup>	49.25 (51.74)	0.265	0.212	<b>64.37</b> (28.50)	0.254	0.209	48.51 (53.73)	0.401	0.327
<b>Mol-LLaMA (Ours)</b>	<b>63.55</b> (36.86)	<b>0.804</b>	<b>0.829</b>	<b>64.37</b> (31.94)	<b>0.819</b>	<b>0.848</b>	<b>72.48</b> (17.44)	<b>0.927</b>	<b>0.966</b>

# Conclusion

- We present Mol-LLaMA, a large molecular language model with a general understanding of molecular features and reasoning capabilities.
- We design a model architecture that fully leverages the complementary advantages of different molecular representations.
- We construct a large instruction dataset by devising three data types, to cover the fundamental features from structural features to chemical and biological features and cultivate the explainability and reasoning capabilities.

# Thank you

## Dongki Kim



[cleverki@kaist.ac.kr](mailto:cleverki@kaist.ac.kr)



[@DongkiKim95](https://twitter.com/DongkiKim95)



<https://dongkikim95.github.io/>



<https://mol-llama.github.io>