



Kehan Guo, Bozhao Nan, Yujun Zhou, Taicheng Guo, Zhichun Guo, Mihir Surve Zhenwen Liang, Nitesh V. Chawla, Olaf Wiest, Xiangliang Zhang

Department of Computer Science and Engineering, University of Notre Dame, US





NSF Center for Computer Assisted Synthesis





What is Structure Elucidation?

Definition: The process of determining the molecular structure of a compound based on spectroscopic data such as Nuclear Magnetic Resonance (NMR), Infrared (IR), and Mass Spectrometry (MS).



Solving Structure Elucidation is like solving a word puzzle

Word Puzzle

Molecular Puzzle



Introduction & Motivation

For all Chemistry undergraduate students, Structure Elucidation

- is a long-standing problem and fundamental part of their curriculum.
- is a key skill learned in organic chemistry courses, allowing them to identify the structure of unknown compounds based on their spectral characteristics.

Our research goal:

- Introduce this challenging reasoning problem to the AI community: MolPuzzle, a benchmark for this problem (217 instances)
- Answer the question: Can LLMs perform better than Chemistry students on solving these puzzles?











Our MolPuzzle Benchmark

- Dataset Overview:
 - 217 instances with over 23,000 QA samples.
 - Three interlinked tasks: Molecule understanding, spectrum interpretation, molecule construction.
- Unique Aspect: Multimodal reasoning tasks incorporating IR, MASS, NMR data.

Statistic	Number
Total MolPuzzle Instances	217
Stage-1 QA samples	5,859
- Num. of molecule formula	176
- Max question length	128
- Average question length	94
Stage-2 QA samples	11,501
- Num. of spectrum images	868
- Max question length	340
- Average question length	264
Stage-3 QA samples	6,318
- Maximum Iteration	7
- Max question length	356
- Average question length	238



Figure 4: Inner ring: sample distribution in 3 stages. Outer ring: sample distribution across categories in each stage. SI: saturation identification, SDC: saturation degree calculation, FGI: functional group identification, ARI: aromatic ring identification, SA: spectrum analysis.

Figure 3: Statistic of the MolPuzzle dataset



Reasoning Tasks in MolPuzzle

- Stage 1: Molecule Understanding (e.g., functional group identification)
- Stage 2: Spectrum Interpretation (analyzing IR, H-NMR, C-NMR data)
- Stage 3: Molecule Construction (assembling based on spectra)
- Data: Derived from curated spectra, RDKit validation for molecule accuracy.







- Models Tested: GPT-40, Claude-3-opus, etc.
- Approach: Zero-shot evaluations, comparisons with human baselines.







Table 1: F1 scores ([†]) of individual QA tasks in three stages. The best LLMs results are in bold font. Tasks in stage 1 are SI-Saturation Identification, ARI-Aromatic Ring Identification, FGI-Functional Group Identification, and SDC-Saturation Degree Calculation.

Stage 1 (Molecule Understanding) Tasks					
Method	SI	ARI	FGI	SDC	
GPT-40	1.00±0.000	$0.943 {\pm} 0.016$	$0.934{\pm}0.005$	$0.667 {\pm} 0.003$	
GPT-3.5-turbo	$0.451 {\pm} 0.025$	$0.816{\pm}0.017$	$0.826{\pm}0.075$	$0.5{\pm}0.099$	
Claude-3-opus	$0.361 {\pm} 0.009$	0.988±0.015	$0.934{\pm}0.001$	$0.856{\pm}0.016$	
Galactica-30b	$0.826{\pm}0.248$	$0.347 {\pm} 0.000$	$0.467 {\pm} 0.005$	$0.000 {\pm} 0.000$	
Llama3	$0.228 {\pm} 0.043$	$0.696 {\pm} 0.051$	$0.521 {\pm} 0.003$	$0.000 {\pm} 0.000$	
Human	$1.00{\pm}0.000$	$1.000 {\pm} 0.000$	$0.890 {\pm} 0.259$	0.851 ± 0.342	
		Stage 2 (Spectrum Inter	pretation) Tasks		
Method	IR Interpretation	MASS Interpretation	H-NMR Interpretation	C-NMR Interpretation	
GPT-40	0.656±0.052	0.609±0.042	0.618±0.026	0.639±0.010	
LLava	$0.256{\pm}0.026$	$0.101 {\pm} 0.021$	$0.118 {\pm} 0.008$	$0.254{\pm}0.015$	
Human	$0.753 {\pm} 0.221$	$0.730 {\pm} 0.11$	$0.764{\pm}0.169$	0.769 ± 0.101	
		Stage-3 (Molecule Cons	struction) Tasks		
Method	H-NMR Elucidation C-NMR Elucidation				
GPT-40	0.524±0.021		0.506	±0.037	
Llama3	0.341 ± 0.015 0.352 ± 0.017		± 0.017		
Human	$0.867 {\pm} 0.230$		0.730:	± 0.220	



LLMs Evaluated

Table 2: The performance of LLMs and human baseline in solving MolPuzzle. The best LLM results are in bold font. Acc. stands for the Accuracy of Exact Match.

Method	Acc. (†)	Levenshtein (\downarrow)	Validity (†)	MACCS FTS (†)	RDK FTS (†)	Morgan FTS (†)
GPT-40	0.014±0.004	$11.653 {\pm} 0.013$	1.000 ±0.000	$0.431{\pm}0.009$	0.293±0.013	$0.232{\pm}0.007$
Claude-3-opus	6 0.013±0.008	$12.680{\pm}0.086$	1.000±0.000	$0.383{\pm}0.050$	$0.264{\pm}0.040$	0.241±0.037
Gemini-pro	0.000 ± 0.000	12.711 ± 0.196	1.000 ±0.000	$0.340{\pm}0.017$	0.208±0.002	$0.171 {\pm} 0.007$
Human	0.667±0.447	$1.332{\pm}2.111$	1.000 ± 0.000	$0.985 {\pm} 0.022$	0.795 ± 0.317	$0.810 {\pm} 0.135$

• Performance Insights:

- LLMs excel in molecule understanding but struggle with spectrum interpretation and molecule construction.
- Top LLM (GPT-4o) achieved 1.4% exact match accuracy on full tasks.
- Gap Analysis: Significant room for improvement, especially in complex reasoning tasks.



Challenges & Future Directions

• Challenges:

- Complex spectral data interpretation.
- Iterative molecule construction processes.



Figure 5: The target molecule contains four distinct non-aromatic hydrogen types, color-coded in the ground truth NMR. However, the model-derived molecule shows hydrogen counts of 3, 3, and 1, differing from the ground truth. The mismatch between the hydrogen types in the green section of the target molecule and the orange region of the predicted molecule results in incorrect fragment selection and assembly.

• Future Focus:

- Specialized LLM training for visual and chemical data.
- Advanced planning and reasoning strategies.



Thank You For Your Attention!

MolPuzzle Website: https://kehanguo2.github.io/Molpuzzle.io/

Feel free to reach out to us at kguo2@nd.edu. We welcome collaborations aimed at enhancing the reasoning capabilities of LLMs in the scientific domain.





https://kehanguo2.github.io/KehanGuo/

