



# Predicted $^{13}\text{C}$ NMR shifts and Applications in Stereochemical Assignment

SPARTAN'26 TRIAL LICENSE

Wavefunction 2026  
<https://www.wavefun.com/nmr>



## Predicted $^{13}\text{C}$ NMR shifts and Applications in Stereochemical Assignment

<https://downloads-s3.wavefun.com/training/S26NMR.pdf>

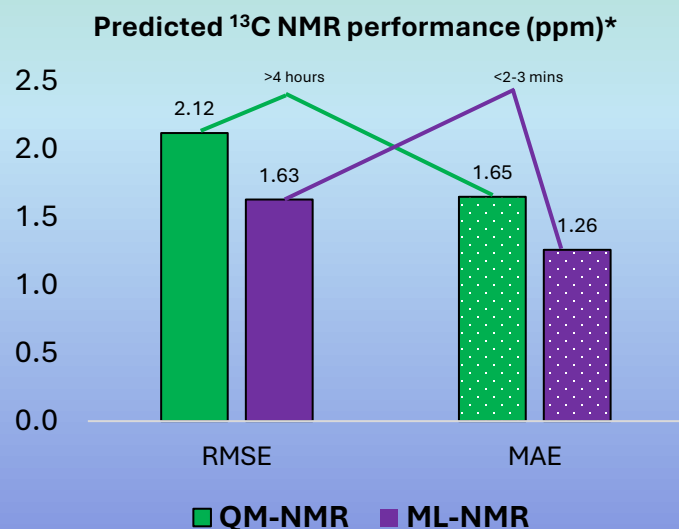


# Spartan NMR (background)

**Spartan** provides high quality  $^{13}\text{C}$  NMR shifts from **Quantum Chemical** models

## Points of difference

- In **Spartan**,  $\omega\text{B97X-D/6-31G}^*$  and  $6\text{-311G}^*$ ,  $\omega\text{B97X-V/6-31G}^*$  and  $\text{B3LYP/6-31G}^*$  models include empirical corrections for  $^{13}\text{C}$  and  $^1\text{H}$  shifts resulting in demonstrated improvements.
- Spartan** offers the **2019 QM-NMR protocol** for flexible organic molecules:  
*Multistep QM-NMR workflow:* [J. Nat. Prod. 2019, 82 \(8\), 2299–2306](#) (multi-step “Hehre” protocol: [>150 citations](#))
- QM-NMR** provides  $^{13}\text{C}$  shifts for flexible structures at  $\approx 2.0\text{--}2.5$  ppm RMSE (but often requires *hours*)



Preliminary analysis based on 100 natural products available [here](#).  
Preliminary results 1000 $^{13}\text{C}$ NP validation set available [here](#).

**Spartan** provides *very high quality*  $^{13}\text{C}$  NMR shifts from **ML** models

## Points of difference

- 2026 MLHF-NMR protocol for flexible organic molecules:**  
*Conformer Energies:* DLFF03 [J. Comp. Chem. 2025, 46 \(1\), 70016](#)  
*Boltzmann Energies:* DLXD2XV, XD2MV, XD2M2 [J. Comp. Chem. 2025, 46 \(13\), 70129](#)  
*Equilibrium Geometries:* DLFFG1 [J. Chem. Info. Mod. 2025, 65 \(5\), 2314–2321](#)  
 *$^1\text{H}$  and  $^{13}\text{C}$  shifts:* DLNMR1 network [J. Org. Chem. 2025, 90 \(32\), 11478–11485](#)  
*Multistep ML- NMR workflow:* MLHF-NMR [ChemRxiv 2026, v2](#)
- General performance** validated against **1,000** published natural products (>700 scaffolds):  
initial **MLHF**  $^{13}\text{C}$  shift average results: **RMSE 1.98 ppm** and **MAE 1.52 ppm** (avg.  $\approx 90$  sec)  
current **MLHF+P2O**  $^{13}\text{C}$  shift average results: **RMSE 1.12 ppm** and **MAE 0.86 ppm** (avg.  $\approx 90$  sec)  
[P2O neural network](#) preliminary description and training details available [here](#).

Spartan's best overall QM NMR performance comes from GIAO NMR shifts ([J. Chem. Phys. 2007, 127, 54103](#)) using either of two Martin Head-Gordon functionals for structure:  $\omega\text{B97X-D}$  ([Phys. Chem. Chem. Phys. 2008, 10, 6615–6620](#)) or  $\omega\text{B97X-V}$  ([Phys. Chem. Chem. Phys. 2014, 16, 9904–9924](#)), or the popular B3LYP functional ([J. Phys. Chem. 1994, 98, 45, 11623–11627](#)). All include integrated empirical corrections ([J. Nat. Prod. 2019, 82 \(8\), 2299–2306](#)).



# QM, MLHF<sub>i</sub>, and MLHF+P2O predicted <sup>13</sup>C shifts. Summary of Rigid Molecule Performance Assessment: 246 published Marine Natural Products (validation)

## 246 published MNP structures

Number of scaffolds: 198  
Number of carbons: 4,439  
Avg. molecular weight: 318.4 amu  
Avg. # carbons: 18  
Avg. mean absolute error: **0.66 ppm**

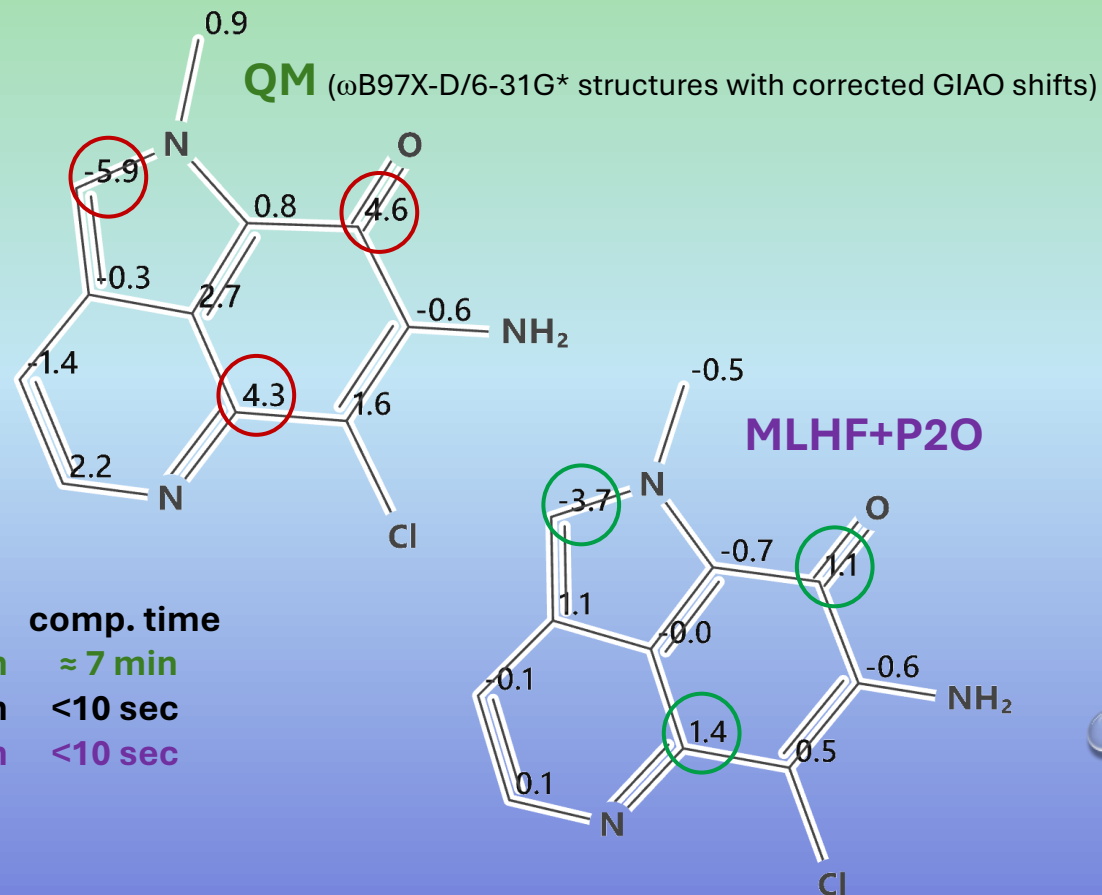
(average over 246 MNPs)

**QM** performance:

**MLHF<sub>i</sub>** (speed):

**MLHF+P2O** (accuracy):

| RMSE            | MAE             | MaxAE           | comp. time        |
|-----------------|-----------------|-----------------|-------------------|
| <b>1.80 ppm</b> | <b>1.38 ppm</b> | <b>4.30 ppm</b> | <b>≈ 7 min</b>    |
| <b>1.94 ppm</b> | <b>1.50 ppm</b> | <b>4.62 ppm</b> | <b>&lt;10 sec</b> |
| <b>0.85 ppm</b> | <b>0.66 ppm</b> | <b>1.95 ppm</b> | <b>&lt;10 sec</b> |



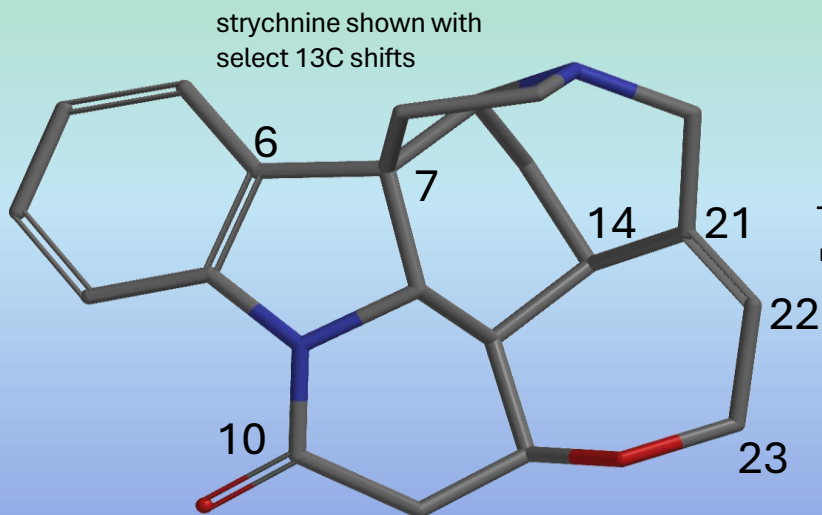


# MLHF, QM, and **MLHF+P2O** $^{13}\text{C}$ shift (validation)

## Sample Rigid Molecule Performance: strychnine

$^{13}\text{C}$  NMR Chemical Shifts: Selected Carbons in Strychnine – MLHF,  $\omega\text{B97X-D GIAO}$ , and MLHF+P2O

| position   | atom type  |                 | $\omega\text{B97X-D/6-31G}^*$ GIAO | MLHF-NMR        | <b>MLHF+P2O</b> | Expt. $^{13}\text{C}$                                                               |
|------------|------------|-----------------|------------------------------------|-----------------|-----------------|-------------------------------------------------------------------------------------|
| <b>C23</b> | sp3        | oxymethylene    | 65.0                               | 65.3            | <b>65.9</b>     | <b>64.4</b>                                                                         |
| <b>C22</b> | sp2        | methine         | 128.3                              | 128.2           | <b>127.8</b>    | <b>127.3</b>                                                                        |
| <b>C21</b> | sp2        | quaternary      | 141.8                              | 142.4           | <b>140.6</b>    | <b>140.0</b>                                                                        |
| <b>C14</b> | sp3        | allylic methine | 32.3                               | 32.2            | <b>31.7</b>     | <b>31.4</b>                                                                         |
| <b>C10</b> | sp2        | carbonyl        | 170.1                              | 170.5           | <b>169.3</b>    | <b>169.0</b>                                                                        |
| <b>C7</b>  | sp3        | quaternary      | 52.4                               | 52.9            | <b>52.5</b>     | <b>51.7</b>                                                                         |
| <b>C6</b>  | sp2        | aromatic        | 131.1                              | 130.8           | <b>133.4</b>    | <b>132.4</b>                                                                        |
| molecule   | <b>RMS</b> | across all      | <b>1.03 ppm</b>                    | <b>1.11 ppm</b> | <b>0.96 ppm</b> |  |



**strychnine** NMR assignments:

*J. Nat. Prod.* **1998**, 61, 8, 2299-2306

strychnine – Pub Chem ID: 441071

Against the **gold standard DELTA50** benchmark **MLHF+P2O** performance:

Avg. **RMSE** of **0.62 ppm**

Avg. **MAE** of **0.54 ppm**

Avg. **Max error** of **0.94 ppm**

To our knowledge, this is best **DELTA50** validation performance from a widely available molecular modeling application (*Spartan*'26).

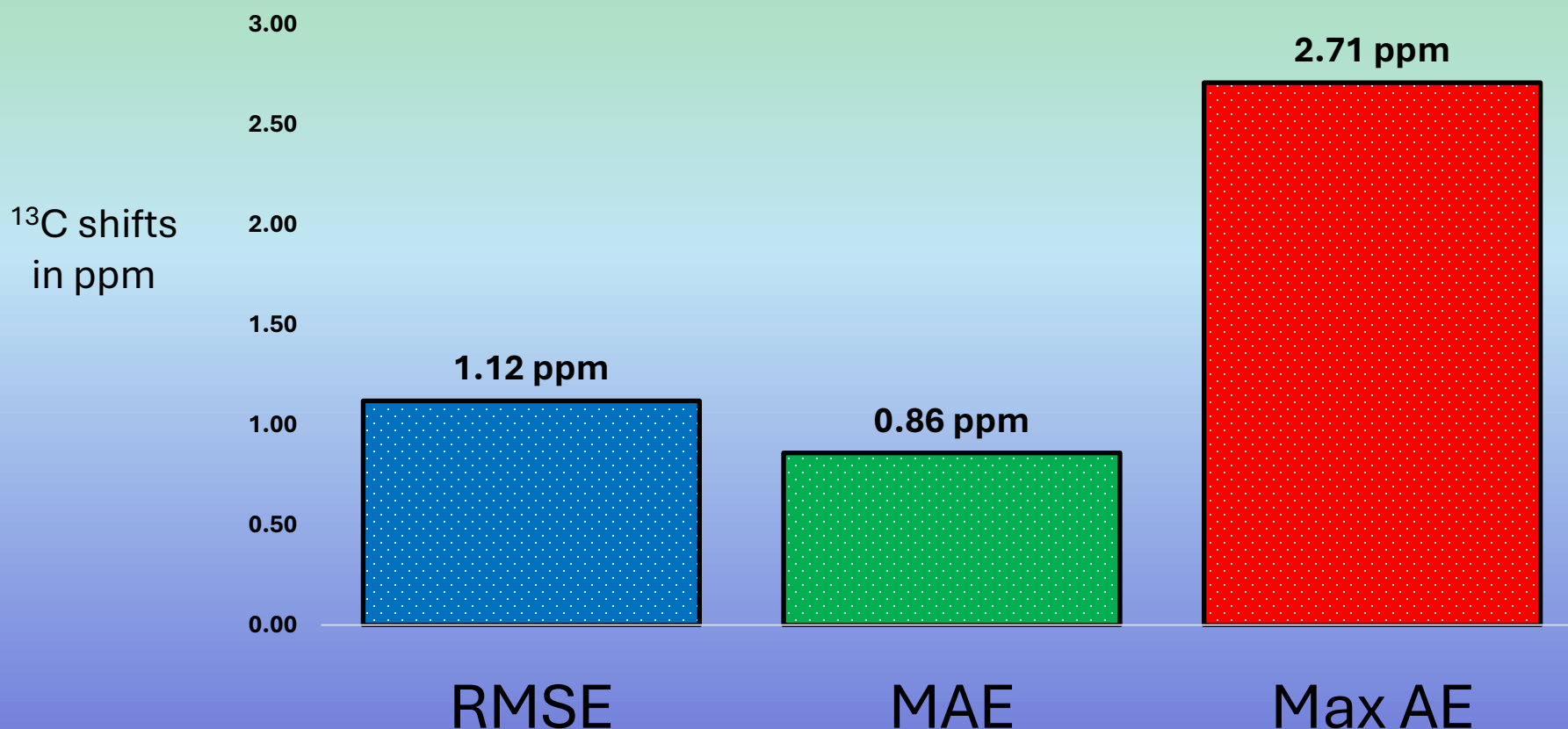
[DELTA50 validation collection download](#)



## Spartan **MLNMR** assessed over 1,000 diverse and predominantly flexible natural products (validation)

preliminary data

Average **MLHF+P2O** predicted  $^{13}\text{C}$  shifts across 1,000 natural products (comprising 20,016 carbons)



The **1000 $^{13}\text{C}$** NP validation set consists of the **420 $^{13}\text{C}$** NP collection, includes **577** NPs with X-ray crystal structure verification (from the [2026 CSD](#) – Cambridge Structure Database) and **15** structures from the NMR Database of Lignin and Cell Wall Model Compounds [LCW-NMR-DB](#).

1000 $^{13}\text{C}$ NP validation set

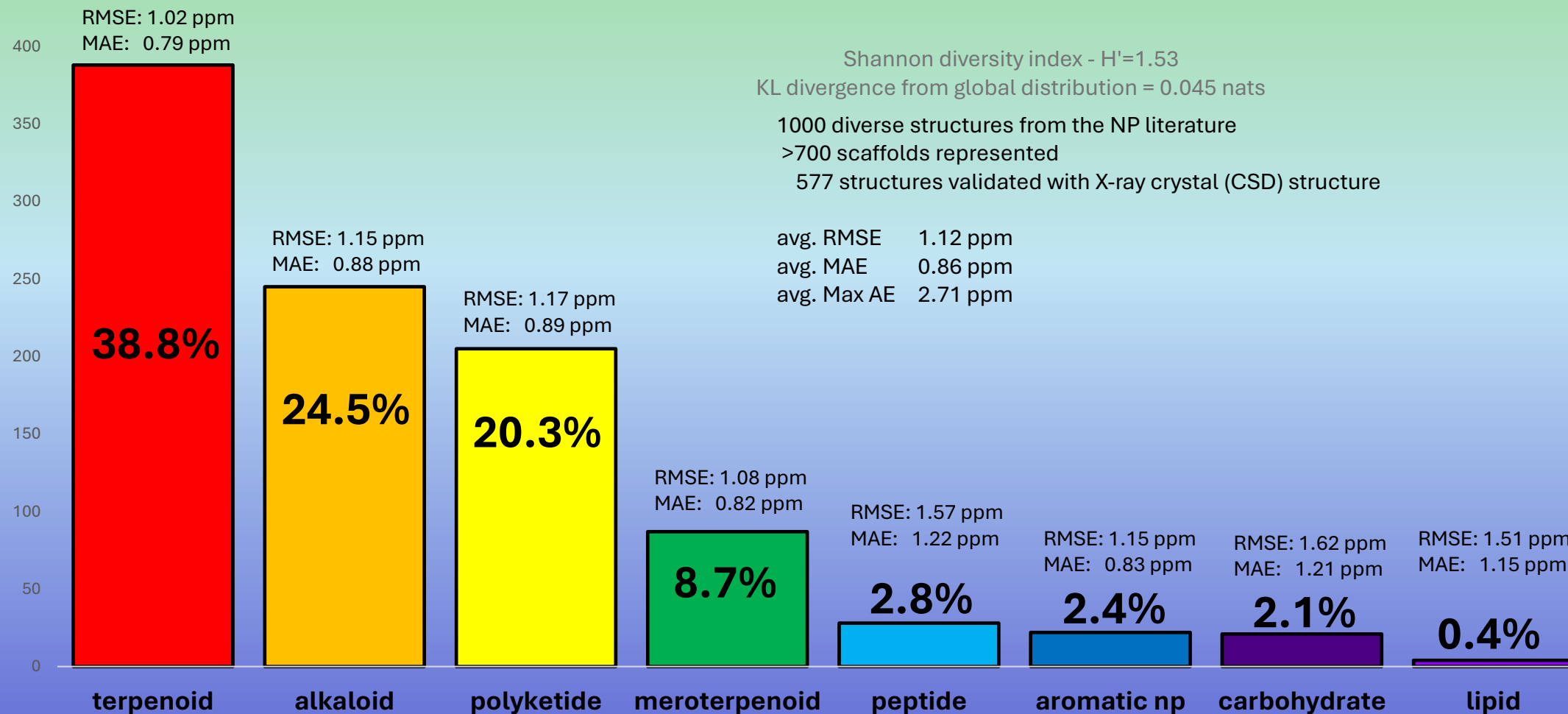
### \*1000 $^{13}\text{C}$ NP flexibility:

|                     |                            |
|---------------------|----------------------------|
| mean # confs        | 3.48 M                     |
| median # conformers | <b>243 (3<sup>5</sup>)</b> |
| # with >10k         | 181                        |
| # with < 27         | 259                        |



preliminary data

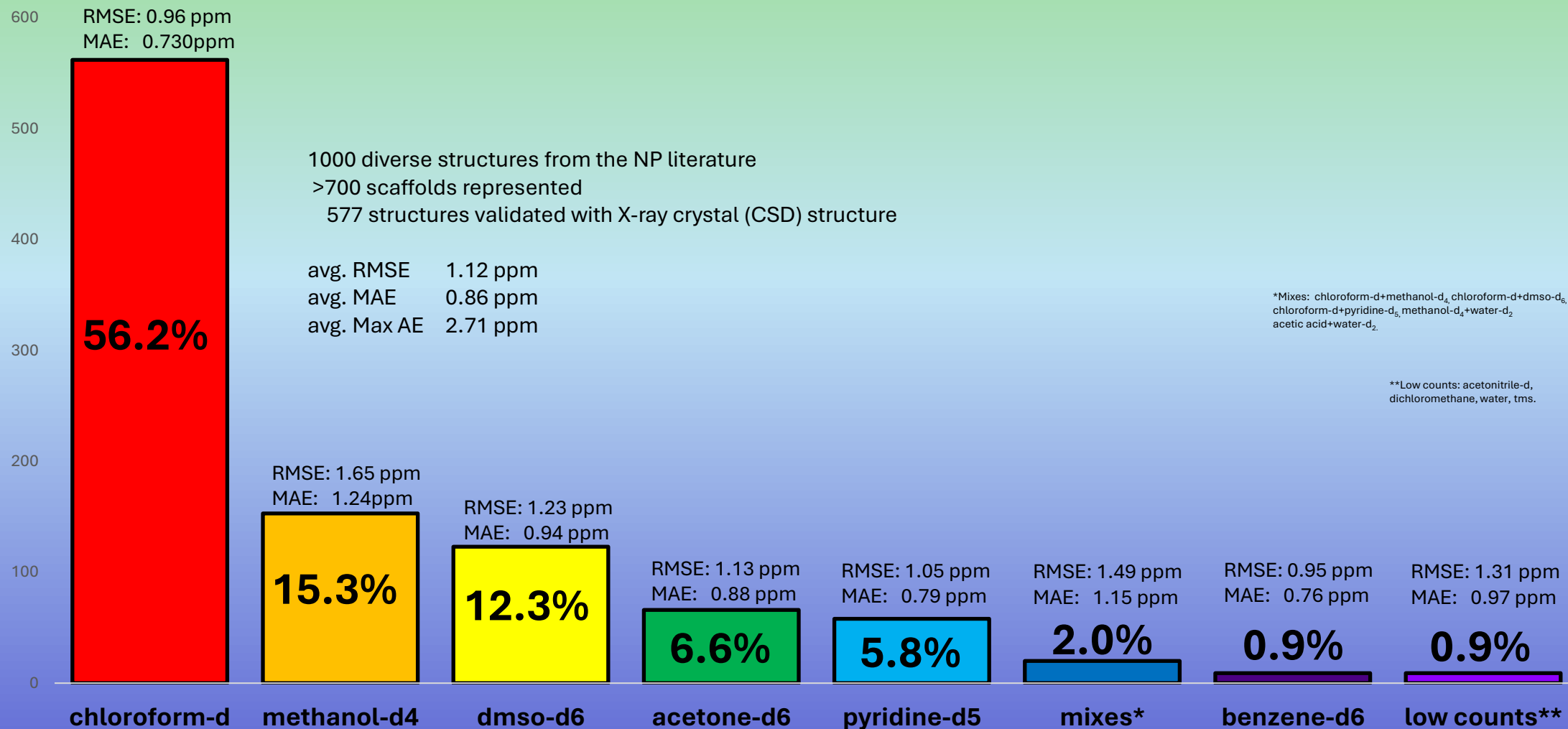
# 1000<sup>13</sup>CNP diversity and performance by NP category for 20,016 carbons (validation/diversity)





preliminary data

## 1000<sup>13</sup>CNP diversity and performance by solvent for 20,016 carbons (validation/performance by solvent)





# STEREOCHEMISTRY (application/validation):

Predicted NMR shifts can be used to confirm or refute complete stereochemistry assignment via statistical comparison of **DP4** probability (%), **RMSE**, **MAE**, **Max AE**, and **errors** at key carbons.

**100** published natural products with **X-ray diffraction** confirmation and **CSD** entries and between **2–11 chiral centers** were reviewed. The **correct** diastereomer was **confirmed\*** in **94%** of cases. The remaining **6%** were scored as **avored\*** (and averaged **>70% DP4** probability score with average **RMSE** of **0.72 ppm**). Mean computational time required was less than **2 minutes** per diastereomer on reasonable hardware.

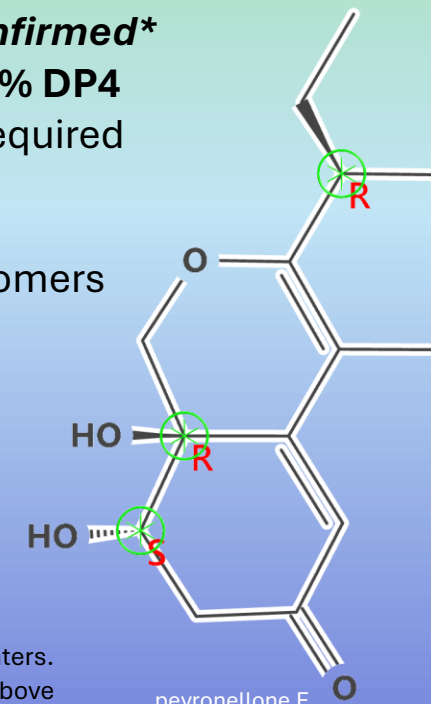


**Spartan's Generate Isomer** tool allows for easy/rapid enumeration of diastereomers based on selection of stereocenters.

\*In evaluation of identifying the correct diastereomers (P2O+MLHF), the following metrics\* were used:

- C = Confirms** with a **DP4** score of **85% or higher** and an RMSE of 2.0 ppm or lower
- F = Favors** with a **DP4** score of **50–85%** and RMSE of 1.5 ppm or lower
- S = Suggests** with a **DP4** score of **15–50%** and an RMSE of 1.0 ppm or lower
- R = Refutes** with a **DP4** score of **0–15%** irrespective of RMSE

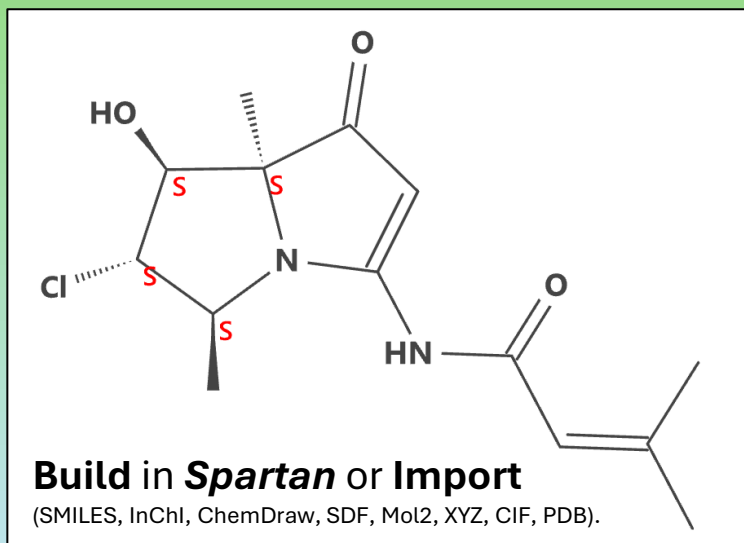
\*Metrics for stereochemistry: DP4, RMSE, additionally reviewed: MAE, and max errors at chiral and adjacent centers. For QM or MLHF<sub>i</sub> (without the P2O network), suggested RMSE performance thresholds are 0.5 ppm higher than above (2.5 ppm or better for confirming, 2.0 ppm or better for favoring, and 1.5 ppm or better for suggesting).



peyronellone F  
*J. Nat. Prod* **2018**, 91 (5), 1148-1153

# Diastereomer Analysis Workflow (application)

1



2

Review/confirm  
imported structure

then **import/assign**  
expt.  $^{13}\text{C}$  shifts.

Edit Experimental Chemical Shifts

Experimental Chemical Shifts:

|    | C  | $^{13}\text{C}$ | $^1\text{H}\alpha$ | $^1\text{H}\beta$ | Calculated $^{13}\text{C}$ |
|----|----|-----------------|--------------------|-------------------|----------------------------|
| 1  | 1  | 200.8           |                    |                   | 203.0                      |
| 2  | 2  | 94.9            |                    |                   | 95.3                       |
| 3  | 3  | 166.8           |                    |                   | 167.6                      |
| 4  | 4  | 63.8            |                    |                   | 63.1                       |
| 5  | 5  | 70.9            |                    |                   | 70.5                       |
| 6  | 6  | 78.9            |                    |                   | 80.2                       |
| 7  | 7  | 76.9            |                    |                   | 76.6                       |
| 8  | 8  | 24.4            |                    |                   | 23.0                       |
| 9  | 9  | 17.0            |                    |                   | 17.1                       |
| 11 | 11 | 163.8           |                    |                   | 165.0                      |
| 12 | 12 | 117.5           |                    |                   | 117.1                      |
| 13 | 13 | 156.6           |                    |                   | 158.2                      |
| 14 | 14 | 27.3            |                    |                   | 27.2                       |
| 15 | 15 | 20.0            |                    |                   | 20.8                       |

Scratch Pad:

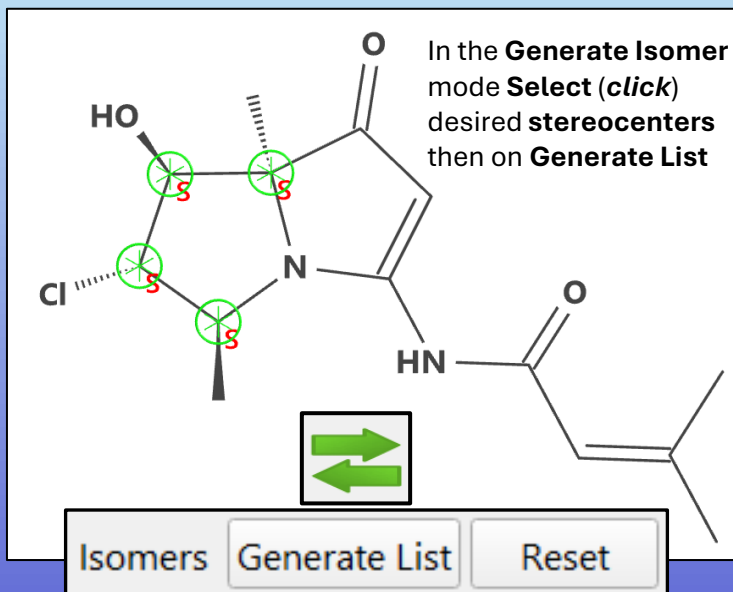
|    | 1  | 2     |
|----|----|-------|
| 1  | 1  | 200.8 |
| 2  | 2  | 94.9  |
| 3  | 3  | 166.8 |
| 4  | 4  | 63.8  |
| 5  | 5  | 70.9  |
| 6  | 6  | 78.9  |
| 7  | 7  | 76.9  |
| 8  | 8  | 24.4  |
| 9  | 9  | 17.0  |
| 10 | 11 | 163.8 |
| 11 | 12 | 117.5 |
| 12 | 13 | 156.6 |
| 13 | 14 | 27.3  |
| 14 | 15 | 20.0  |

Import CSV Tabular Data... Delete All

☐ Use Keypads

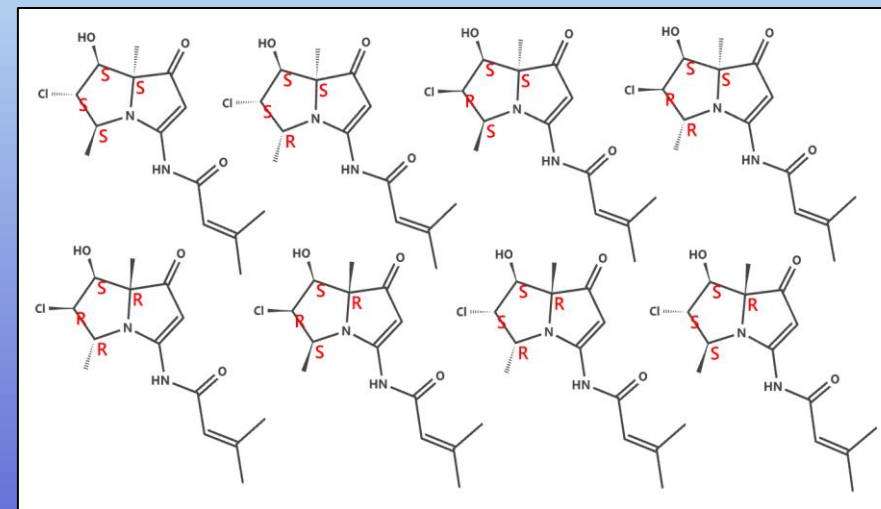
Hide

3



4

**Submit** the generated  
diastereomer list (with  
included expt.  $^{13}\text{C}$  shifts)  
to the **MLHF** Protocol.



5-chlorobohemamine C  
*J. Nat. Prod.* **2006**, 69 (11): 1626–1628.



## *Spartan* Flexible Molecule NMR Calculation Setup: Choose from a drop down of 4 workflows (application)

Calculations

Calculate: NMR Protocol with **2026 MLHF** →

2026 MLHF  
2025 MLXD  
2024 QM  
2019 QM

Total Charge: Neutral (0)  
Unpaired Electrons: 0

☐ Use Custom Structure List. Coupling Constants: Empirical Start With At Most: 1500 Conformers ☒ Keep Wavefunction

Details:

| Step                                          | Theoretical Approach    | Level                   | Keep ≤    | At Most        | Options           |
|-----------------------------------------------|-------------------------|-------------------------|-----------|----------------|-------------------|
| <input checked="" type="checkbox"/> Geometry: | Molecular Mechanics     | MMFF                    | 40 kJ/mol | 200 Conformers | CONF2EXAMINE=1500 |
| <input checked="" type="checkbox"/> Energy:   | Molecular Mechanics     | DLFF03 (Corrected MMFF) | 20 kJ/mol | 100 Conformers |                   |
| <input checked="" type="checkbox"/> Geometry: | Est. Density Functional | DLFFG1                  | 25 kJ/mol | 50 Conformers  | TWOSTEPOPT        |
| <input checked="" type="checkbox"/> Energy:   | Hartree-Fock            | 3-21G(*)                | 99 kJ/mol | 50 Conformers  |                   |
| <input checked="" type="checkbox"/> Energy:   | Est. Density Functional | DLHF2XD                 | 10 kJ/mol | 30 Conformers  |                   |
| <input checked="" type="checkbox"/> Energy:   | Est. Density Functional | DLXD2XV                 | 10 kJ/mol | 30 Conformers  |                   |
| <input checked="" type="checkbox"/> Energy:   | Est. Density Functional | DLNMR1                  |           |                | CESTNMR=1         |

☐ Options ☒ Edit Global Calculations ☒ OK **Submit**

Items in tan are ML models. There are 2 default ML options and 2 default QM options.

Customization is possible (although in most cases, not necessary).



## ***Spartan* Flexible Molecule MLHF-NMR workflow accounts for conformation, structure, energy, and proton and $^{13}\text{C}$ NMR (background)**

The current **MLHF** protocol utilizes the following  
hybrid method workflow<sup>1</sup>:

- (initial) conformer searching: MM<sup>2</sup> and ML (neural network)<sup>3</sup>
- structure (geometry opt.): ML (neural network)<sup>4</sup>
- Boltzmann energy and weighting: QM<sup>5,6</sup> and ML (neural networks)<sup>7</sup>
- proton and  $^{13}\text{C}$  NMR shifts: ML (neural networks)<sup>8</sup>

MMFF molecular mechanics for initial conformational searching with neural network energy improvements (DLFF03), a neural network model for structure (geometry) optimization (DLFFG1), quantum mechanics, a single calibrating HF/3-21G(\*), and neural networks trained to reproduce good DFT approaches for Boltzmann energy and weights: DLHF2XD, then DLXD2XV, DLXD2MV, or DLXD2M(2), and finally neural networks trained to reproduce QM NMR results for proton and  $^{13}\text{C}$  NMR shifts (DLNMR1) and to correct DLNMR1 results to experiment for  $^{13}\text{C}$  NMR shifts (P2O).

A seamless customizable workflow.

1. *ChemRxiv* **2026**, (preprint) v2. [🔗](#)
2. *J. Comput. Chem.* **1996**, 33, 490. [🔗](#)
3. *J. Comp. Chem.* **2025**, 46 (1), 70016. [🔗](#)
4. *J. Chem. Info. Mod.* **2025**, 65 (5), 2314–2321. [🔗](#)
5. *J. Am Chem. Soc.* **1980**, 102, 939–947. [🔗](#)
6. *J. Am Chem. Soc.* **1982**, 104 (10), 2797–2803. [🔗](#)
7. *J. Comp. Chem.* **2025**, 46 (13), 70129. [🔗](#)
8. *J. Org. Chem.* **2025**, 90 (32), 11478–11485. [🔗](#)

At present the **MLHF** parameterization includes H, C, N, O, F, S, Cl, and Br, neutral and closed shell systems (only). P, I, Si, B, and Se centers are all potential training targets.

All elements H-Kr are supported via *Spartan*'s 2019 QM protocol.



## Spartan MLNMR Diastereomer Analysis:

**100** natural products: 10 each with 2 to 11 total chiral centers.  
**All** members with structure/stereochemistry **CSD**-confirmation.  
 (validation)

P2O-diastereomer-analysis-assessment-MLpool-2-to-11-chiral-centers:psidial A

| Label                                                   | RMSE | DP4   | Max E. | MAE  | P2O+MLHF confirms diastereomer |
|---------------------------------------------------------|------|-------|--------|------|--------------------------------|
| <input type="checkbox"/> phomanoxide                    | 0.70 | 99.4  | 1.52   | 0.57 | C                              |
| <input checked="" type="checkbox"/> psidial A           | 1.10 | 100.0 | 4.49   | 0.77 | C                              |
| <input type="checkbox"/> sodwanone G                    | 0.82 | 94.7  | 3.65   | 0.49 | C                              |
| <input type="checkbox"/> tomentodione A                 | 0.69 | 100.0 | 1.85   | 0.55 | C                              |
| <input type="checkbox"/> alstonoxine E                  | 0.46 | 99.1  | 1.02   | 0.35 | C                              |
| <input type="checkbox"/> alstonoxine F                  | 0.56 | 95.2  | 1.28   | 0.43 | C                              |
| <input type="checkbox"/> 13,14-dibromolabdane-8,15-diol | 0.46 | 92.9  | 1.09   | 0.34 | C                              |
| <input type="checkbox"/> dongtingnoid F                 | 0.72 | 79.2  | 1.82   | 0.56 | F 79%/21% dp4 .72/.80 rmse     |
| <input type="checkbox"/> fischericin E                  | 0.61 | 100.0 | 1.41   | 0.48 | C                              |
| <input type="checkbox"/> leoleorin D                    | 0.54 | 99.8  | 1.11   | 0.46 | C                              |
| <input type="checkbox"/> pseudovillosine                | 0.66 | 100.0 | 1.06   | 0.57 | C                              |
| <input type="checkbox"/> sinulariolone                  | 0.87 | 99.9  | 1.54   | 0.71 | C                              |
| <input type="checkbox"/> uasdlabdane A                  | 0.57 | 99.9  | 1.38   | 0.46 | C                              |
| <input type="checkbox"/> uprolide H                     | 0.58 | 99.5  | 1.38   | 0.48 | C                              |
| <input type="checkbox"/> neolaxiflorin E                | 0.47 | 100.0 | 1.22   | 0.37 | C                              |
| <input type="checkbox"/> mitchellene F                  | 0.71 | 99.9  | 1.58   | 0.57 | C                              |
| <input type="checkbox"/> prevezol C1                    | 0.74 | 100.0 | 1.63   | 0.58 | C                              |
| <input type="checkbox"/> psiguadial C                   | 0.58 | 100.0 | 1.36   | 0.46 | C                              |

f(x) Add Delete Sort Formulas Find: Previous Next Match Case Scroll to Focus

### summary of results:

Avg. RMSE **0.77 ppm**

Avg. DP4 **97.1%**

Avg. MAE **0.61 ppm**

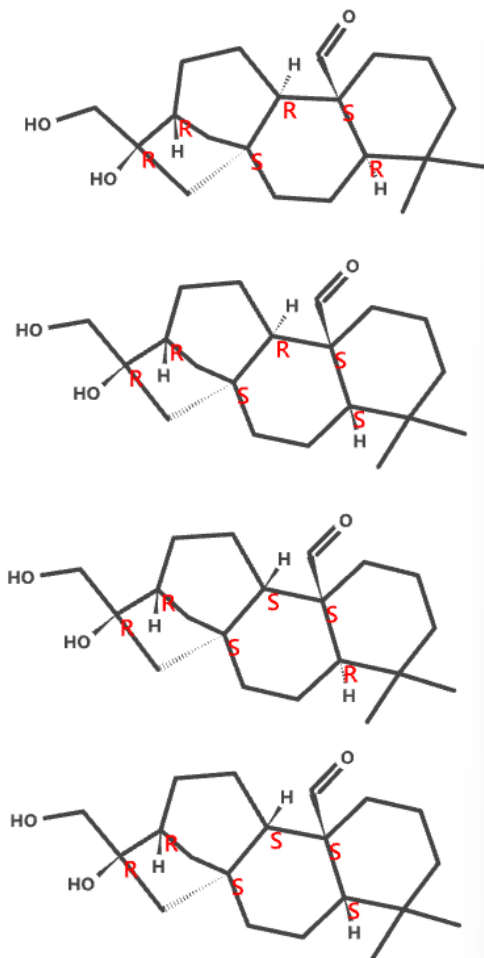
Correct Diastereomer **94-100%**



# Spartan ML-NMR Diastereomer Analysis

## Fischericin E (application/interpreting results)

fischericins A-F - *J. Nat. Prod.* **2017**, 80, 2263-2268.



fischericin E6:fischericin E

fischericin E

| Label                                             | RMS  | DP4 (%) | Max Absolute | Mean Absolute | *                                   |
|---------------------------------------------------|------|---------|--------------|---------------|-------------------------------------|
| <input checked="" type="checkbox"/> fischericin E | 0.61 | 100.0   | 1.41         | 0.48          | C25=R,C28=S,C29=R,C30=S,C33=R,C36=R |
| <input checked="" type="checkbox"/> M0002         | 3.85 | 0.0     | 10.28        |               |                                     |
| <input checked="" type="checkbox"/> M0003         | 4.24 | 0.0     | 10.00        |               |                                     |
| <input checked="" type="checkbox"/> M0004         | 5.36 | 0.0     | 13.58        |               |                                     |
| <input type="checkbox"/> M0005                    | 5.44 | 0.0     | 15.43        |               |                                     |
| <input type="checkbox"/> M0006                    | 5.82 | 0.0     | 17.89        |               |                                     |
| <input type="checkbox"/> M0007                    | 4.97 | 0.0     | 14.33        |               |                                     |
| <input type="checkbox"/> M0008                    | 4.30 | 0.0     | 10.81        |               |                                     |
| <input type="checkbox"/> M0009                    | 1.62 | 0.0     | 4.65         |               |                                     |
| <input type="checkbox"/> M0010                    | 4.02 | 0.0     | 10.39        |               |                                     |
| <input type="checkbox"/> M0011                    | 4.50 | 0.0     | 9.83         |               |                                     |
| <input type="checkbox"/> M0012                    | 5.45 | 0.0     | 13.40        |               |                                     |
| <input type="checkbox"/> M0013                    | 5.32 | 0.0     | 15.00        | 3.74          | C25=R,C28=S,C29=R,C30=R,C33=R,C36=S |
| <input type="checkbox"/> M0014                    | 5.91 | 0.0     | 17.30        | 4.15          | C25=S,C28=S,C29=R,C30=R,C33=R,C36=S |
| <input type="checkbox"/> M0015                    | 5.65 | 0.0     | 16.16        | 4.10          | C25=R,C28=S,C29=S,C30=R,C33=R,C36=S |
| <input type="checkbox"/> M0016                    | 4.48 | 0.0     | 10.83        | 2.84          | C25=S,C28=S,C29=S,C30=R,C33=R,C36=S |

f(x) Add Delete Sort Formulas Find: Previous Next Match Case Scroll to Focus

The **correct** diastereomer scores **100% DP4** probability and predicts  $^{13}\text{C}$  shifts with **RMSE of 0.61 ppm** **MAE of 0.48 ppm** **Max E of 1.41 ppm** Nothing else comes close.

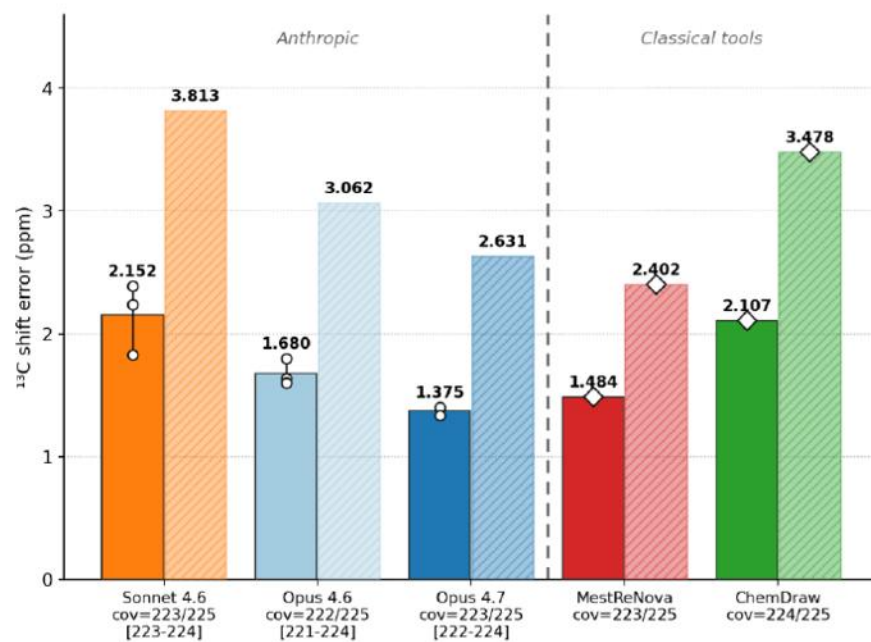


# Spartan $MLHF_i$ and $MLHF+P2O$ vs. Anthropic models, MestReNova, and ChemDraw ( $^{13}C$ NMR prediction comparison)

**Per-tool MAE/RMSE summary across 20 compounds (4 papers)**

LLM bars show mean across 3 prediction replicates with min-max whisker and overlaid replicate dots; classical tools shown as single point

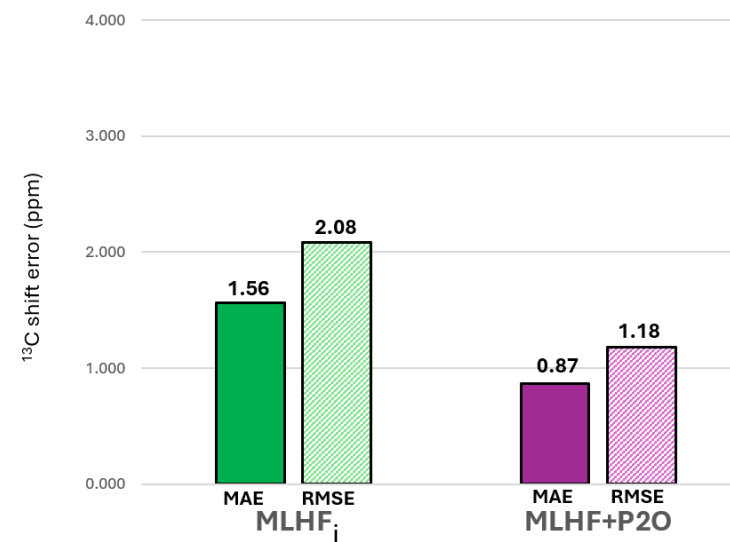
■ MAE ■ RMSE ○ Individual LLM replicate (N=3) ◇ Classical tool (single point) — Min-max range across 3 LLM replicates



Data above from [Anthropic/Claude 2026 writeup](#) (D. Kamber):  
Assessing Claude/Opus 4.7 against ChemDraw 25.0 (and MestReNova 17.0)

Per tool MAE/RMSE summary across P1, P2, and P3 scaffolds from the Anthropic writeup

Spartan ML-NMR v. Anthropic dataset (15/20 compounds)



$MLHF_i$  and  $MLHF+P2O$  [results available](#) (.spartan, Excel, and .sdf).

Data above available from [WAVEFUNCTION/SPARTAN:](#)  
([MLHF+P2O-results](#) – in .spartan, Excel, and .sdf)

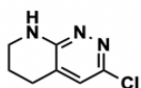


# Spartan MLHF+P2O comparison covers P1-P3 (15 of 20 compounds/performance comparison)

Four scaffold classes covered by the forward-prediction benchmark — each probes a different category of NMR challenge

**P1**

Chloropyridazines

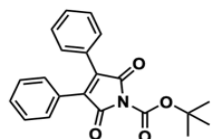


Slow-exchange NH  
on aminopyridazine

DMSO-d<sub>6</sub> · n = 5

**P2**

maleimides

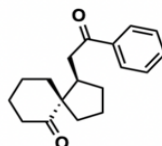


Symmetrical maleimide

CDCl<sub>3</sub> · n = 5

**P3**

Spiroketones

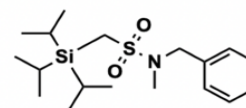


Spirobicyclic ketone  
with pendant phenacyl

CDCl<sub>3</sub> · n = 5

**P4** ❌

α-Silyl methane-  
sulfonamides



Shielded α-silyl

CDCl<sub>3</sub> · n = 5

At present the **MLHF** parameterization includes H, C, N, O, F, S, Cl, and Br, neutral and closed shell systems. (P, I, Si, B, and Se centers are all potential training targets).

All elements H-Kr are supported via *Spartan's* 2019 QM protocol.

Analysis data available from **WAVEFUNCTION**:  
(MLHF+P2O-results – in .spartan, Excel, and .sdf)

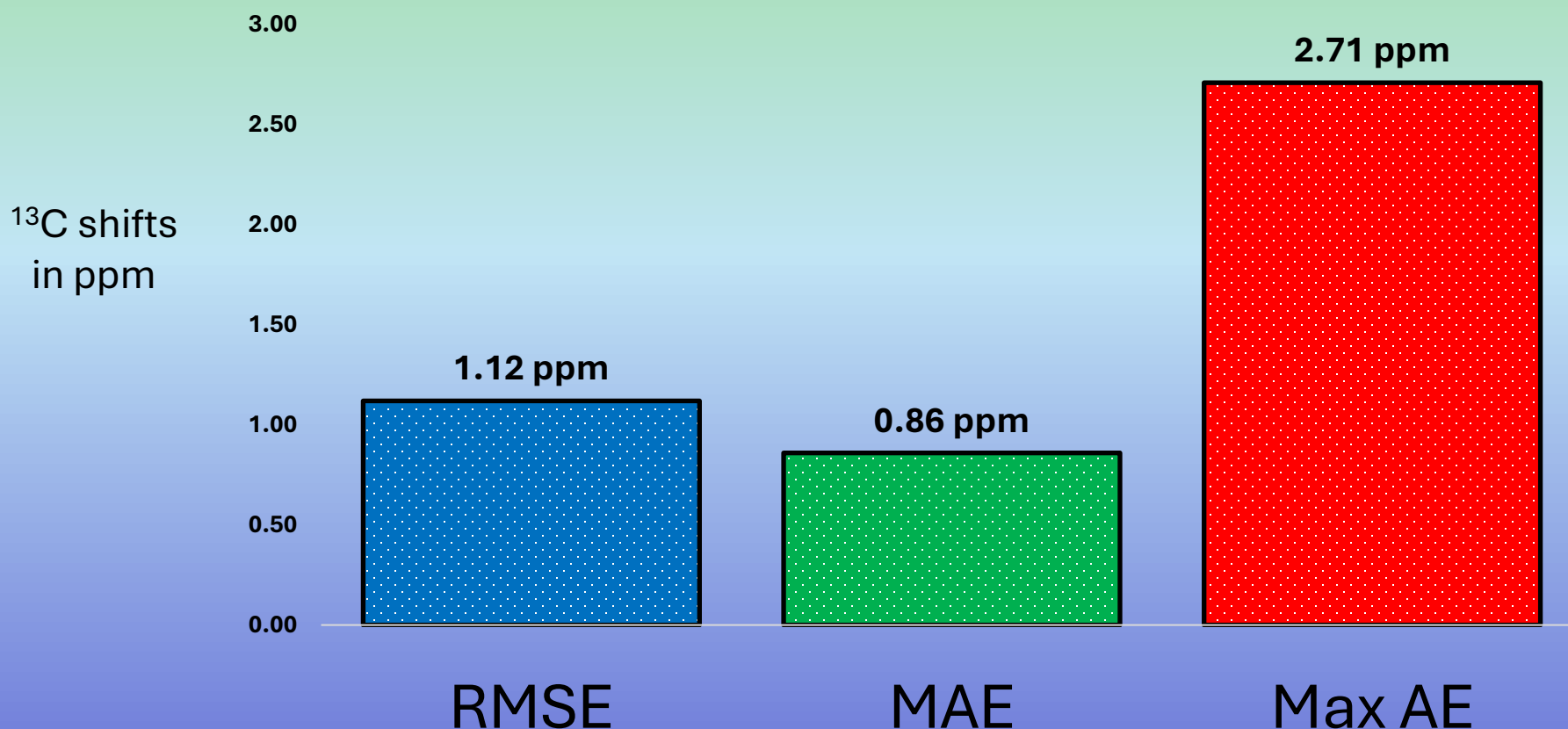
| P3-8a-spiro:R,R diastereomer                         |         |      |            | P3-8b-spiro:S,S diastereomer                         |         |      |            | P3-8c-spiro:S,R diastereomer                         |         |      |            | P3-8d-spiro:S,R diastereomer                         |         |      |            | P3-8e-spiro:R,R diastereomer                    |      |         |            |
|------------------------------------------------------|---------|------|------------|------------------------------------------------------|---------|------|------------|------------------------------------------------------|---------|------|------------|------------------------------------------------------|---------|------|------------|-------------------------------------------------|------|---------|------------|
| Label                                                | DP4 (%) | RMS  | Conformers | Label                                                | DP4 (%) | RMS  | Conformers | Label                                                | DP4 (%) | RMS  | Conformers | Label                                                | DP4 (%) | RMS  | Conformers | Label                                           | RMS  | DP4 (%) | Conformers |
| <input type="checkbox"/> P3-8a-spiro                 | 100.0   | 0.79 | 36         | <input type="checkbox"/> P3-8b-spiro                 | 100.0   | 1.16 | 36         | <input type="checkbox"/> P3-8c-spiro                 | 99.9    | 1.36 | 18         | <input type="checkbox"/> P3-8d-spiro                 | 100.0   | 1.28 | 18         | <input checked="" type="checkbox"/> P3-8e-spiro | 1.07 | 98.7    | 4374       |
| <input checked="" type="checkbox"/> R,R diastereomer | 0.0     | 2.51 | 36         | <input checked="" type="checkbox"/> S,S diastereomer | 0.0     | 2.92 | 36         | <input checked="" type="checkbox"/> S,R diastereomer | 0.1     | 2.51 | 9          | <input checked="" type="checkbox"/> S,R diastereomer | 0.0     | 3.44 | 18         | <input type="checkbox"/> R,R diastereomer       | 1.76 | 1.3     | 4374       |



# Spartan **MLNMR** assessed over 1,000 diverse and predominantly flexible natural products (validation)

preliminary data

Average **MLHF+P2O** predicted  $^{13}\text{C}$  shifts across 1,000 natural products (comprising 20,016 carbons)



The **1000 $^{13}\text{C}$** NP validation set consists of the **420 $^{13}\text{C}$** NP collection, includes **577** NPs with X-ray crystal structure verification (from the [2026 CSD](#) – Cambridge Structure Database) and **15** structures from the NMR Database of Lignin and Cell Wall Model Compounds [LCW-NMR-DB](#).

1000 $^{13}\text{C}$ NP validation set

**\*1000 $^{13}\text{C}$ NP flexibility:**

|                     |                            |
|---------------------|----------------------------|
| mean # confs        | 3.48 M                     |
| median # conformers | <b>243 (3<sup>5</sup>)</b> |
| # with >10k         | 181                        |
| # with < 27         | 259                        |



# Spartan **MLNMR** sample results from 1,000 diverse natural products

## 1,000 published NP structures

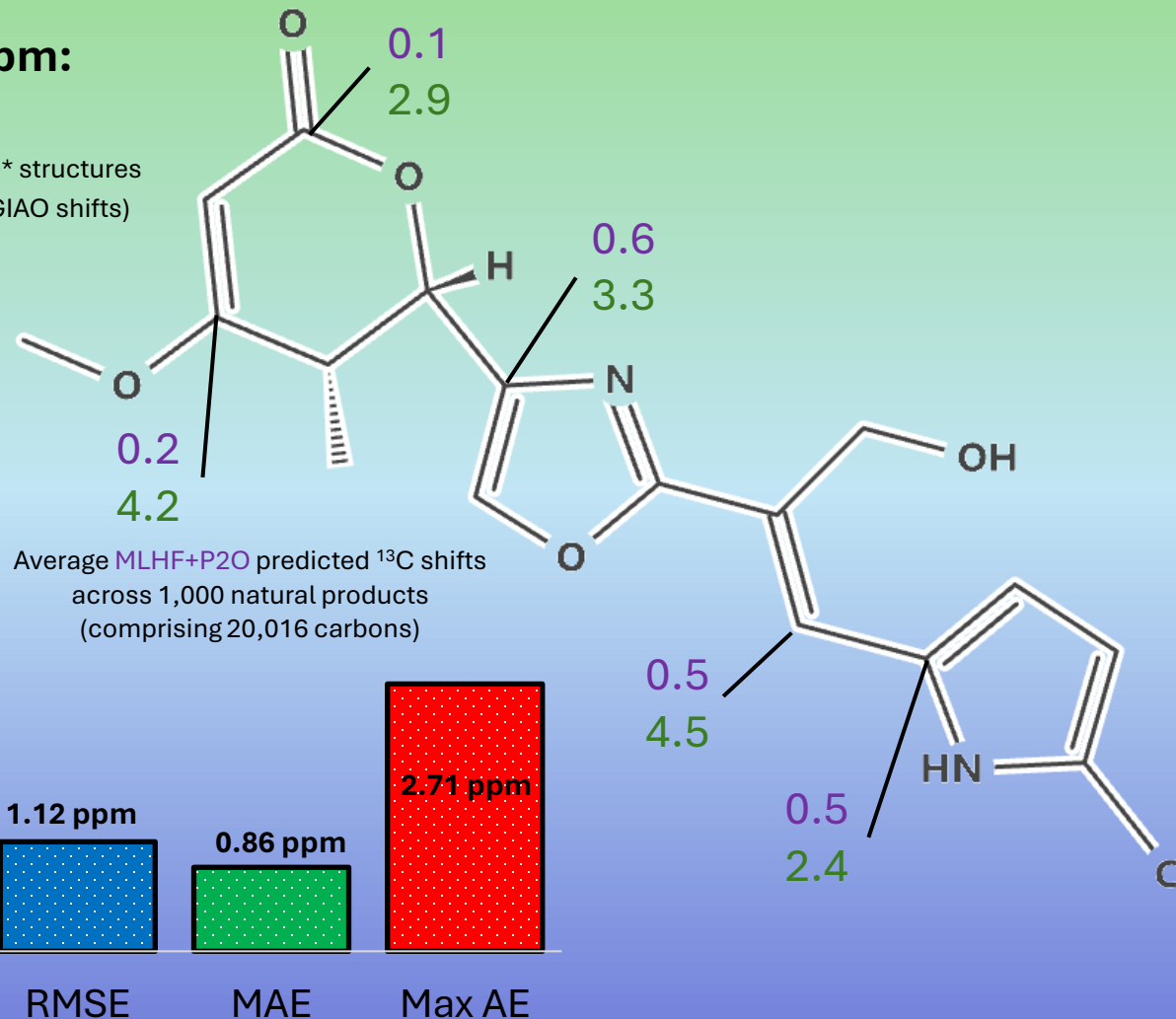
|                            |                 |
|----------------------------|-----------------|
| Number of carbons:         | 20,016          |
| Number of scaffolds:       | 736             |
| Number confirmed via CSD:  | 577             |
| Avg. molecular weight:     | 362.5 amu       |
| Avg. and median # carbons: | 20              |
| Avg. mean absolute error:  | <b>0.86 ppm</b> |

**Spartan'26 1.1** includes the latest MLNMR workflow with the integrated **MLHF+P2O** prediction for  $^{13}\text{C}$  shifts. High quality  $^{13}\text{C}$  results with sub ppm error are routinely available for flexible organic structures within minutes. This allows for diastereomer analysis in conjunction (or In advance) of  $^{13}\text{C}$  NMR experiments, providing near perfect confirmation of complete stereochemistry (between **94-100%**).

$^{13}\text{C}$  shift error in ppm:

**MLHF+P2O**

**QM** ( $\omega\text{B97X-D/6-31G}^*$  structures with corrected GIAO shifts)



pyrronazol A – *J. Nat. Prod.* **2014**, 77 (2), 320-326.



## Wavefunction/*Spartan* Contact Information/Resources:

Sales/Trial Licensing:

[sales@wavefun.com](mailto:sales@wavefun.com)

Technical Support:

[support@wavefun.com](mailto:support@wavefun.com)

Research Citations:

[spartan in research](#)

Education Citations:

[spartan/odyssey in education](#)

MLNMR workflow description

[mlhf-nmr](#) (speed)

[p2o](#) (accuracy)

NMR Resources:

[nmr.wavefun.com](http://nmr.wavefun.com)

[mlnmr.wavefun.com](http://mlnmr.wavefun.com)

Natural Products Resources:

[naproc<sup>13</sup> disambiguation database](#)

CSD Resources:

[cambridge crystallographic data centre](#)

***Spartan'26***  
***For Windows, Macintosh and Linux***



presentation available:

<https://downloads-s3.wavefun.com/training/S26NMR.pdf>