

# DP4+ App

<https://github.com/Sarotti-Lab/DP4plus-App>

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## Instructive and general recommendations for DP4+

### Content

Overview and usage recommendations .....	1
Probability calculations: DP4+, MM-DP4+ and Custom-DP4+ .....	2
Prepare your files .....	2
Perform DP4+ calculation .....	3
Results output .....	4
HALO mode .....	5
Warnings and Input control .....	6
Gaussian calculation files .....	6
Data spreadsheet .....	7
Calculation aborted .....	7
Questionable values .....	8
Malfunctions report .....	8

### Overview and usage recommendations

The DP4+ App is a comprehensive software designed to perform parameterized DP4+ and MM-DP4+ calculations seamlessly. Additionally, it offers the capability to conduct Custom-DP4+ calculations, allowing users to parameterize any required level of theory. With its friendly graphical interface, users can easily manage multiple Gaussian calculations and automate information processing for probabilistic calculations.

To get started with the application, simply create a folder and ensure that it contains the following files:

- Well-labeled Gaussian output files: These files should include NMR calculations for all conformers of each isomeric candidate. Frequency or single point energy calculations should also be included where necessary. Make sure to label them appropriately for easy identification.
- Excel file with experimental and correlation data: This file should contain the necessary experimental data along with the correlation labels for each nucleus corresponding to the Gaussian calculations.

By providing these files, the DP4+ App can efficiently process the information and perform the desired calculations.

To ensure optimal use of the program, it is recommended to follow the guidelines below:

- Minimize the number of candidates: While the DP4+ App can handle any number of isomers, keeping the candidate count to a minimum offers several advantages. It reduces both the overall computational cost and the risk of calculated data for an incorrect isomer yielding a better fit with experimental values compared to the correct candidate.
- Conduct a thorough conformational search: It is essential to obtain an accurate depiction of the conformational landscape of the system under study. Care should be taken to avoid improper

computational work that could potentially affect the overall results. Systematic sampling is always recommended, but in the case of highly flexible molecules, stochastic searches with a reasonably large number of steps should be carried out. All conformations within a safe energy window from the corresponding global minimum should be retained to avoid missing potentially significant conformations. For this application, it is advised to use a 5 to 10 kcal/mol cutoff value, employing the MMFF force field.

- Adhere to the suggested theory levels: It is important to use the recommended theory levels since DP4+ and MM-DP4+ were optimized for these levels. If the desired theory level is not parameterized, there is the option to parametrize the desired level by following the instructions provided in the Custom-DP4+ method.
- Ensure correct assignment of NMR data: The use of unassigned or misassigned NMR data can lead to erroneous results. When dealing with equivalent nuclei that undergo fast interconversion (e.g., methyl or some equivalent methylene groups), it is necessary to average the chemical shifts. Treating each proton signal independently, such as computing different chemical shifts for the same methyl group, is incorrect. Additionally, diastereotopic methylene protons often pose challenges with arbitrary correlation. Unless additional NMR information, such as NOE or J coupling, is available to discriminate between the pro-*R* and pro-*S* signals, the most suitable approach is to treat them as interchangeable signals. Detailed instructions are provided to assist you in addressing these issues effectively.

## Probability calculations: DP4+, MM-DP4+ and Custom-DP4+

### Prepare your files

To perform correlation calculations using the DP4+ App, it is necessary to prepare the required files. The program offers a range of controls to ensure precise data entry. The following guidelines should be followed to set up the files correctly:

The Excel file (.xlsx) should include the information in the "**shifts**" sheet. This sheet will be the only one read by the program and must adhere to the structure defined in Figure 1 (refer to Warnings and Input Control). Ensure that the column headers match accordingly. For isomers with the same labels, only three columns are required. However, if isomers use different labels, each candidate should have three labeling columns (label 1 | label 2 | label 3). The name of this document does not have any specific requirements as it will be selected individually.

The following columns are intended to place the correlation labels

*if*

All candidates with the same labels  
Only 3 columns for all candidates

Candidates with different labels  
3 columns for each candidate

	Atom type		Experimental chemical shifts			Correlation labels			Correlation labels		
	index	nuclei	sp2	exp_data	exchange	label 1	label 2	label 3	label 1	label 2	label 3
1	1	C		73.7		7					
2	2	C		46.5		8					
3	3	C	1	175.5		9					
4	4	C		11.0		13					
5	5	C	1	141.5		4					
6	6	C	1	125.9		1	5				
7	7	C	1	128.1		2	3				
8	8	C	1	127.3		6					
9	9	C		60.5		11					
10	10	C		13.9		15					
11	11	H		5.09		21					
12	12	H		2.77		22					
13	13	H		1.12		26	27	28			
14	14	H	1	7.29		16	19				
15	15	H	1	7.29		17	18				
16	16	H	1	7.29		20					
17	17a	H		4.12	a	23	24				
18	17b	H		1.21	a	29	30	31			

Experimental index

sp2 nuclei must be indicated with character "1"

Interchangeable signals must be paired with letters

Sheet name: **shifts**

Figure 1. Excel sheet (experimental information and correlation labels)

NMR files have to be generated from calculations using the Gaussian software (.log or .out files) with the command line containing "#... nmr". Label these files according to the following convention, "n\_m\*\_nmr.log", where :

- "n" represents the isomer ID,
- "m" denotes the conformer number, and
- "\*" indicates a user annotation.



Figure 2. NMR Gaussian outputs

For instances where a conformational analysis based on energy calculations beyond NMR is desired, the following protocol should be adhered to. Input files must correspond to single-point energy calculations at the SCF level or frequency calculations for Gibbs free energy determinations. These files should be identically named to their associated NMR files with the sole exception of substituting "energy" for "nmr" in the filename. For example, if the NMR file is designated n\_m\_nmr.log, the corresponding energy file should be denoted n\_m\_energy.log.

To specify your input files, utilize the designated buttons situated beneath the theory-level selection panel. Each button will instantiate a navigation dialogue, facilitating the selection of your desired directories and files.

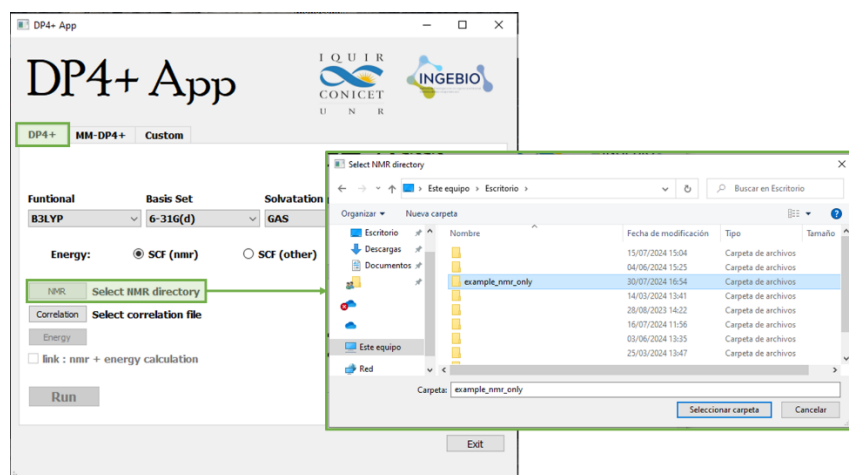


Figure 3. Folder and file selection in DP4+ Tab

## Perform DP4+ calculation

With the DP4+ App, it is possible to determine the correlation probability using 60 pre-parameterized theory levels. These levels encompass a combination of different functionals, basis sets, and solvation modes. Out of the total, 24 levels were derived from geometries optimized using quantum mechanics at the B3LYP/6-31G\* level. Below are the possible combinations:

### QM mode theory levels combinations

Functional	Basis Set		Solvation	Solvent (only for PCM)
B3L	6-31G(d)	6-31G(d,p)	GAS	CHCl <sub>3</sub> , CH <sub>2</sub> Cl <sub>2</sub> , CCl <sub>4</sub> , H <sub>2</sub> O,
mPW1PW91	6-31+G(d,p)	6-311G(d)	PCM	MeOH, MeCN, DMSO, THF,
	6-311G(d,p)	6-311+G(d,p)		Pyridine, Acetone, Benzene

If a different solvent is needed, the 'Other' option can be used for entering H<sup>1</sup> and C<sup>13</sup> TMS tensors (a popup window will allow you to enter the tensors).

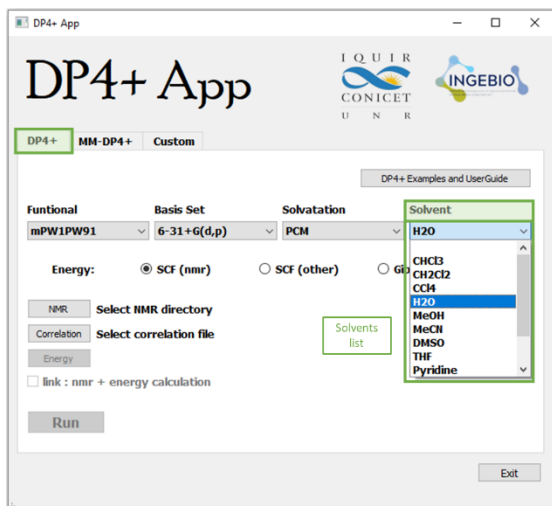


Figure 4. Solvent drop-down list

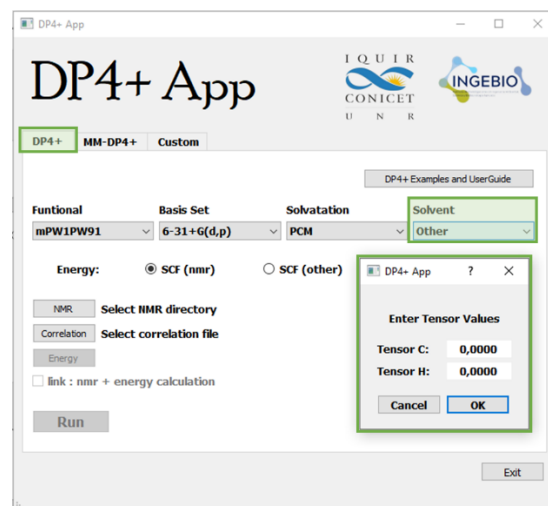


Figure 5. Pop-up window for "Other" option

To use energies different from those obtained in the NMR calculation for Boltzmann contributions, you can select the **SCF (other)** or **Gibbs (freq)** options. This will enable features to either load a separate folder containing the frequency calculations or indicate that the calculations were performed using a Gaussian link. **We recommend exploring the provided examples to familiarize yourself with the functionality of each protocol.**

Although calculations can be performed at any chosen level, the DP4+App optimizes usage by checking for consistency between the command lines in the Gaussian files and the selected theory level. When pressing the **Run** button if there is a discrepancy, a warning will be displayed, but the calculation can still proceed (see Figure 7).

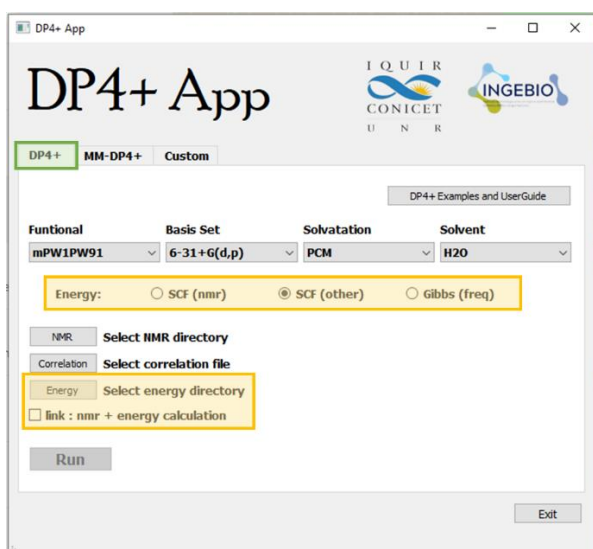


Figure 6. Energy settings

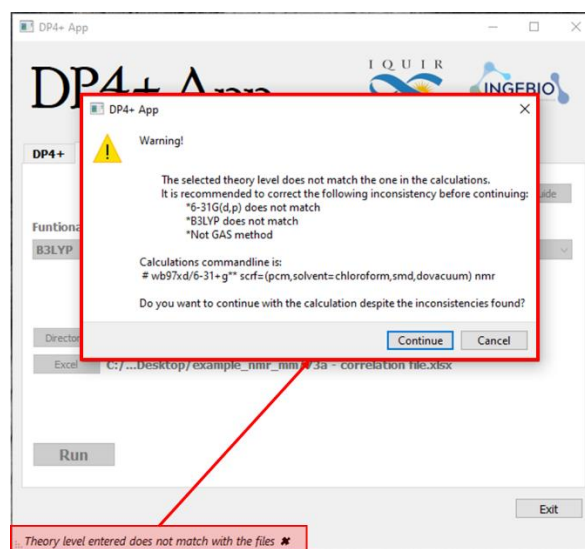


Figure 7. Example of miss matching theory level and command lines

For performing calculations at a theory level that is not mentioned, it is necessary to parameterize it first by following the instructions provided in the Custom mode (direct to the Custom tab and download the example).

## Results output

Upon successful calculation, a notification will be displayed confirming completion. Subsequently, the computed results will be exported to an Excel file entitled "DP4+plus\_results" within the designated working directory. The Excel file will contain:

- **Probability Results:** the sheet "results," provides the probabilities of the candidates categorized by their nuclei, scaling, and the full version. It also displays the selected theory level, the command line used for the Gaussian calculations, and the automatic coincidence check.
- **Tensors:** contains the Boltzmann-weighted tensors sorted according to the input labels.
- **Chemical Shifts:** two sheets display the calculated chemical shifts ("d\_sca" and "d\_uns").
- **Correlation Errors:** two sheets allocate the correlation errors. ("e\_sca" and "e\_uns").
- **Parameters:** Reports distribution parameters and reference standard for correlation calculation.

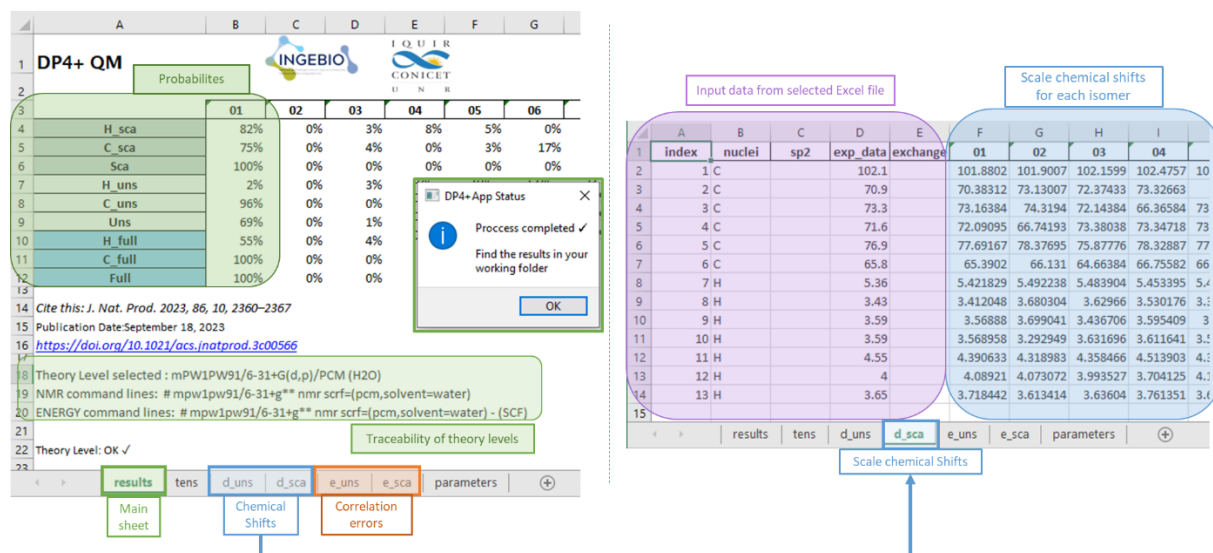


Figure 8. Output Excel file

In cases where the selected theory level does not align with the Gaussian calculation command line, a warning will be displayed, indicating any inconsistencies encountered (refer to Figure 9).

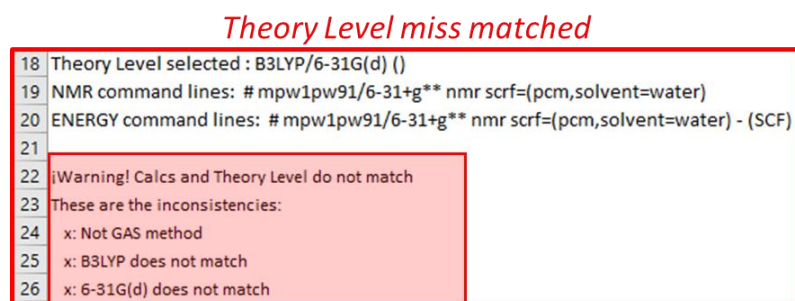


Figure 9. Examples of theory level miss selection

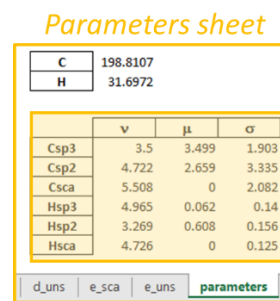


Figure 10. "Parameters" sheet view

## HALO mode

HALO mode is an advanced feature of DP4+App designed to improve chemical shift predictions in halogenated molecules, particularly those containing chlorine (Cl) or bromine (Br). When such atoms are detected in the candidate structures, the program automatically prompts the user to choose between continuing with the standard DP4+ calculation or activating HALO mode. It is generally recommended to enable HALO under these conditions. Running both modes and comparing the outcomes can provide valuable insight into halogen-related effects.

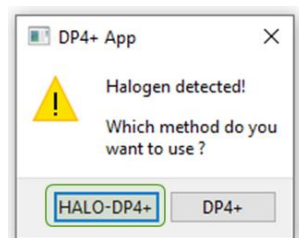


Figure 11. HALO decision pop-up

Once activated, HALO mode automatically identifies atoms directly bonded to halogens and adjusts their chemical shift referencing. Instead of using the conventional tetramethylsilane (TMS), these specific nuclei are referenced against a set of calibrated multi-reference standards that better account for the local electronic influence of halogens.

The output reflects these adjustments. The “results” sheet includes an additional column labeled “halogen,” listing atoms affected by the correction. The “parameters” sheet provides both chemical shielding tensors and predicted shifts using TMS and the HALO reference, allowing for direct comparison.

	A	B	C	D	E	F	G	H
1	index	nuclei	sp2	exp_data	exchange	halogen	01	02
2	0	C		37.62		Cl	37.14111	37.24365
3	1	C	1	131.89			133.3838	132.2603
4	2	C	1	137.83			138.0245	137.3482
5	3	C		50.44		Cl	59.58443	50.26056
6	4	C		41.32			42.02208	41.66282
7	5	C		52.7		Br	50.86219	50.96821
8	6	C		41.36			43.99031	44.30445
9	7	C		69.98		Cl	60.88516	70.46705
10	8	C		20.47 a			19.5994	20.31483
11	9	C		28.53 a			26.64704	27.30997
12	10	H		4.04 b		Cl	4.084551	4.059182
13	11	H		4.18 b		Cl	4.167639	4.1776
14	12	H	1	5.95			6.043818	6.009501
15	13	H		4.97		Cl	4.672984	4.98616
16	14	H		2.53 c			2.43916	2.516492
17	15	H		2.68 c			2.51992	2.520318
18	16	H		4.83		Br	4.749598	4.784418
19	17	H		4.38		Cl	4.771834	4.393619
20	18	H		1.01 d			1.08724	1.096847
21	19	H		1.28 d			1.313255	1.305862

	A	B	C
1	mPW1PW91.6-31+G	EXP	
2	C Cl sp2	74.8367	117.42
3	C Cl sp3	142.6926	46.91
4	C Br sp2	77.4004	104.75
5	C Br sp3	152.2521	27.89
6	H Cl sp2	25.4042	5.59
7	H Cl sp3	28.10687	3.52
8	H Br sp2	25.213	6.16
9	H Br sp3	27.839	3.427
10	C	196.6095	
11	H	31.55999	

Figure 12. Examples results spreadsheet with “halogen” column and MSTD standards

## Warnings and Input control

To enhance the user's understanding of anomalous results in DP4+ type calculations, DP4+App has implemented a comprehensive warning system. This system assists users in interpreting and identifying any unusual outcomes that may arise during the calculation process. Additionally, the application includes multiple checkpoints to validate the accuracy of data entry, ensuring reliable and consistent results.

### Gaussian calculation files

DP4+App ensures the completeness of information from Gaussian calculation files by verifying the presence of the “Normal Termination” indicator in each file. If any file lacks this indicator, it will be automatically moved to a folder labeled “fail files” within the working folder.



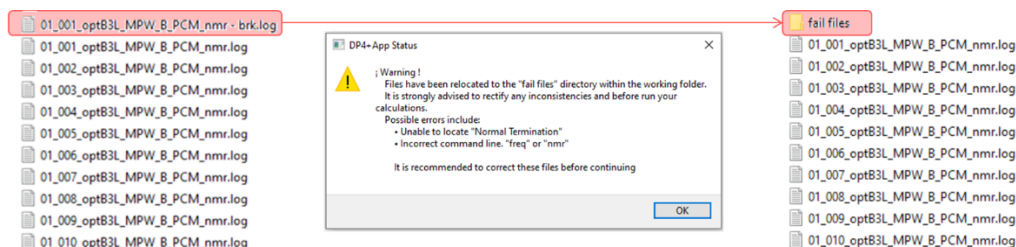


Figure 13. Example of a broken file (identified with brk) that is separated in fail folder

## Data spreadsheet

The correlation spreadsheet provided to DP4+App must follow a specific format, as illustrated in Figure

1. To ensure the accuracy of data entry, the program performs the following checks on the spreadsheet:

- Column not found: Detects missing or incorrect column headers.
- Data not found: Identifies missing data in the '*nuclei*', '*exp\_data*', or '*labels*' columns.
- Incorrect data: Checks for valid data types in specific columns
  - For the '*nuclei*' column, the data must be either 'C' or 'H'.
  - For the '*exp\_data*' column, the data must be a numerical value.
  - For the '*labels*' column, the data must be an integer number.
  - For the '*sp2*' column, the data must be 'X', 'x', or '1'.
- Mismatched diastereotopic labels: Notifies when diastereotopic labels are not paired correctly.
- Different number of candidate isomers and set of labels: Detects inconsistencies between the number of candidate isomers and the set of labels used.

The occurrence of any of these conditions will preclude the program from executing the calculation. Consequently, it is imperative to rectify all inconsistencies before proceeding.

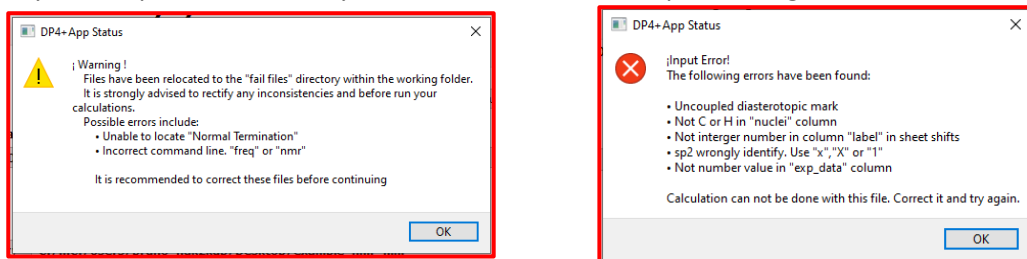


Figure 14. Examples of warning and input error

## Calculation aborted

The software includes quality control checks that are initiated at the start of each calculation. Failure of these checks will result in the calculation being terminated and an error reported. Common causes for termination include:

- Inability to match a corresponding label (columns label 1 | label 2 | label 3).
- Using Gibbs energy with a link without a prior frequency calculation.
- Link calculation broken or with more than 2 calculations

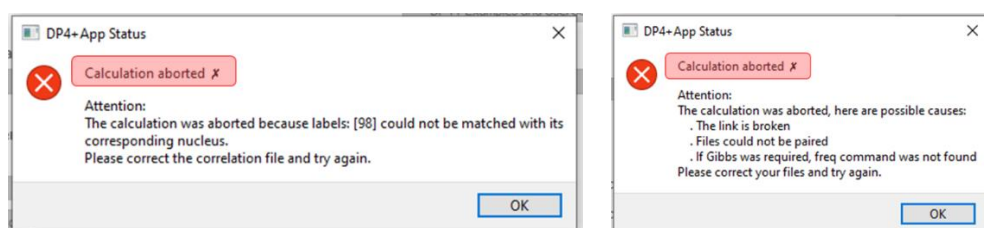


Figure 15. Example of aborted calculations

## Questionable values

DP4+ App applies specific chemical criteria to validate the results of calculations. Any values that deviate from these criteria will trigger warnings to alert the user. The following conditions are considered questionable:

- $\sigma_H > 6\text{ppm}$  and  $\sigma_C > 120\text{ ppm}$ , not marked as *sp2*
- $\sigma_H > 14\text{ppm}$ , identified as  $^{13}\text{C}$
- $e_{\text{sca-H}} > 0.7$  and  $e_{\text{sca-C}} > 10$ , related to possible miscorrelation/missed assignment

While these warnings indicate potential issues, the calculations can still proceed. The highlighted cells will draw attention to the questionable values, allowing the user to evaluate their significance. If possible, it is recommended to experiment with different paths and interpret the results to make informed decisions.

For DP4+ type calculations, the warnings will be displayed on the **e\_sca** sheet of the results.

	A	B	C	D	E	F	G	H
1	index	nuclei	sp2	exp_data	exchange	73a	73b	
2	1 C			73.7		-8.64583	-8.97892	
3	2 C			46.5		-14.5614	-14.7679	
4	3 C		1	175.5		13.15343	14.23648	
5	4 C			11		-20.9491	-18.9718	
6	5 C		1	141.5		3.750364	5.202798	
7	6 C			125.9		-1.75426	-2.99944	
8	7 C		1	128.1		-2.71407	-2.79137	
9	8 C		1	127.3		-3.90952	-4.98248	
10	9 C			60.5		-15.5238	-16.7685	
11	10 C			13.9		51.15417	50.82108	
12	11 H			5.09		-5.45829	-5.50291	
13	12 H			2.77		7.399502	7.581393	
14	13 H			1.12		-0.6099	-0.68703	
15	14 H		1	7.29		-8.33225	-8.39644	
16	15 H			7.29		-8.31415	-8.38816	
17	16 H		1	7.29		20.26961	20.40886	
18	17 H			4.12		-4.27804	-4.32062	
19	18 H			1.21		-0.67649	-0.69509	
20								

results   tens   d\_sca   **e\_sca**   d\_uns   e\_uns   parameters

Figure 16. Example of deviant values for parametrization method

## Malfunctions report

We strive to provide a reliable and efficient user experience with DP4+ App. However, if you encounter any malfunctions or issues while using the software, we appreciate your assistance in reporting them. By providing detailed information about the problem you encountered, you can contribute to the continuous improvement of DP4+ App.

Please report any faulty operations or unexpected behavior to the following email addresses:

- [brunoafranco@uca.edu.ar](mailto:brunoafranco@uca.edu.ar)
- [zanardi@inv.rosario-conicet.gov.ar](mailto:zanardi@inv.rosario-conicet.gov.ar)
- [sarotti@iquir-conicet.gov.ar](mailto:sarotti@iquir-conicet.gov.ar)