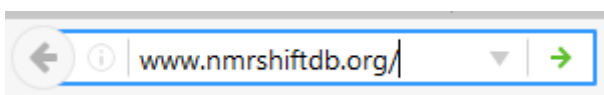




Quick Check Tutorial

An **nmrshiftdb2** account is useful, but not compulsory (registration at www.nmrshiftdb.org)

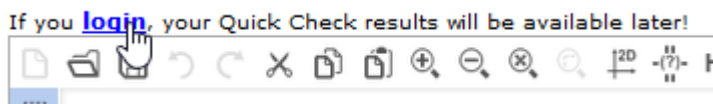
1. Visit nmrshiftdb2



Visit the public version of **nmrshiftdb2** using an internet browser of your choice at <https://www.nmrshiftdb.org> or <https://nmrshiftdb.uni-koeln.de>.

2. Login (optional)

Login is optional, but recommended to be able to recall data, and needed for a submit.



Quick Check
You are not logged in. Please do so!

Username

Password

If you login with your **user name**, you can save Quick Checks you have done and recall them later. A later submit is only possible with a login

3. Choose the Quick Check tab



Chose the **QuickCheck** using the appropriate tab.

4. Load a file or enter your molecule

The easiest way to import data into the QuickCheck is the import of a file in one of the following formats:

- NMRReDATA (imports structure and spectra)
- CMC-SE results (a zip file of the Topspin folder is needed, imports structure and all spectra)
- MNova mol or sd file (imports structure and all spectra)
- Mol file with atom labels (imports structure only)

For doing so, chose the file using „Choose File“ for the right type below the structure editor. The file name appears next to the button. Then hit „Transfer“. The data are loaded and checked. You can progress to item 14 directly.

Import from structures history

Choose an MNova mol or sd file (MNova 11 or newer) or ChemDraw mol file with labels:
 No file chosen

Choose a Topspin zip file including a CMC-SE result: cse_topspin.zip

Choose an NMRReDATA file: No file chosen

If you want to enter data manually instead of uploading a file, start with entering the structure:

IDNMR | Kurzanleitung Eingabe Zuordnung

Enter a personal ID for this Quick Check: eugenol

The screenshot displays a chemical structure editor interface. At the top, a text box contains the personal ID "eugenol". Below it is a toolbar with various editing tools. The main workspace shows the chemical structure of eugenol, a 3,4-dimethoxyphenylprop-2-ene. The atoms are numbered: 1-6 for the benzene ring, 7 for the hydroxyl group, 8 for the methoxy group, 9-11 for the propene chain, and 12 for the terminal carbon of the propene chain. A legend on the right side lists elements: H, C, N, O, S, F, P, Cl, Br, I, *, and A. A "Do Quick Check" button is visible at the bottom left of the editor window.

Draw the **structure** in the editor. Alternatively you can paste SMILES or InChI strings (or various other formats) by the Folder button or by ctrl+v. A copy & paste from ChemDraw is possible via the „copy as SMILES“ option of ChemDraw. You can enter an ID („personal ID“) for the QuickCheck here.

5. Hit „Transfer“ (optional)

Transfer

This shows the accurate number of **Shift fields**. If you are logged in and assigned a „personal ID“, the **structure is saved**.

6. Enter the chemical shifts of the structure

Atom No.	¹³C Shift	Auto reassign
1	<input type="text"/> 128.50	<input type="checkbox"/>
2	<input type="text"/> * 128.50	<input type="checkbox"/>
3	<input type="text"/> * 128.50	<input type="checkbox"/>

Enter the **¹H and ¹³C shifts** in the respective text fields. The suggested value is the result of the nmrshiftdb2 prediction, * indicates a symmetric atom (those are filled automatically if left empty). For CH₂ groups two fields are provided. If you leave the second field empty, the value from the first field is assumed for both protons.

OR

Input list: [Input format](#)

```

146.39
143.85
137.81
131.91
121.14
115.53
114.21
111.05
55.84
39.90
  
```

Enter a **shift list** in the large text field. The QuickCheck tool will suggest an assignment. Unused shifts will be shown in the text field.

7. Hit „Transfer“

Transfer

The QuickCheck tool compares your inputs with the prediction and **scores** the assignments using a traffic light system.

Atom No.	¹³ C Shift	¹³ C Shift	diff	Auto reassign
1	114.21	●●●	121.25, diff: 7.04	<input type="checkbox"/>
2	121.14	●●●	114.45, diff: 6.69	<input type="checkbox"/>
3	143.85	●●●	144.00, diff: 0.15	<input type="checkbox"/>
4	111.05	●●●	146.65, diff: 35.60	<input type="checkbox"/>
5	146.39	●●●	111.30, diff: 35.09	<input type="checkbox"/>
6	131.91	●●●	131.95, diff: 0.04	<input type="checkbox"/>
7				

Hetero atom bound protons are not scored due to low prediction reliability. Their assignment can be entered for sake of completeness, though.

¹ H Shift	¹ H Shift	diff	Auto reassign	2 nd shift for diastereotopic atoms
6.7	●●●	6.83, diff: 0.13	<input type="checkbox"/>	
6.86	●●●	6.65, diff: 0.21	<input type="checkbox"/>	
6.69	●●●	6.66, diff: 0.03	<input type="checkbox"/>	
5.52			<input type="checkbox"/>	

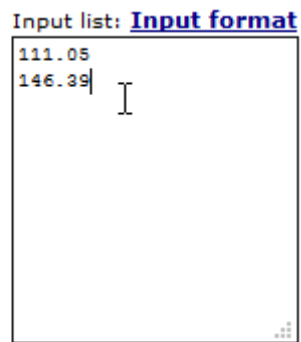
By hitting the headers of the columns you can sort by atom number or prediction value.

8. Correct individual assignments

Enter the **corrected shifts** in the respective fields and hit „Transfer“ again.

ODER

4	111.05	●●●	146.65, diff: 35.60	<input checked="" type="checkbox"/>
5	146.39	●●●	111.30, diff: 35.09	<input checked="" type="checkbox"/>
6	131.91	●●●	131.95, diff: 0.04	<input type="checkbox"/>



Enter the new shifts in the large text field und choose „**Auto reassign**“ near the positions, which should be reassigned by the Quick Check. Again, unused shifts will stay in the text field. Hit „Transfer“ again.

9. Enter 2D correlations (optional)

If you do not have 2D correlations, you can directly proceed to item 13.

Choose the tab „2D Spectra“. There are two tables for entering correlations. The expected correlations are marked in green:

1D spectra	2D spectra
------------	------------

Enter **[C]OSY**

[T]OCSY

[N]OESY

correlations here

	7 6.96	8 5.82	3 4.16	6 1.86	5 1.27
5 1.27	C <input type="checkbox"/>	C <input type="checkbox"/>	C <input checked="" type="checkbox"/>	C <input type="checkbox"/>	
6 1.86	C <input checked="" type="checkbox"/>	C <input type="checkbox"/>	C <input type="checkbox"/>		
3 4.16	C <input type="checkbox"/>	C <input type="checkbox"/>			CT
8 5.82	C <input checked="" type="checkbox"/>			T	
7 6.96		CT		CT	

Enter **H[S]QC**

Enter **H[M]BC**

correlations here

	7 6.96	8 5.82	3 4.16	6 1.86	5 1.27
5 14.21	S <input type="checkbox"/> M <input type="checkbox"/>	S <input type="checkbox"/> M <input type="checkbox"/>	S <input type="checkbox"/> M <input checked="" type="checkbox"/>	S <input type="checkbox"/> M <input type="checkbox"/>	S <input checked="" type="checkbox"/> M <input type="checkbox"/>
6 17.9	S <input type="checkbox"/> M <input checked="" type="checkbox"/>	S <input type="checkbox"/> M <input checked="" type="checkbox"/>	S <input type="checkbox"/> M <input type="checkbox"/>	S <input checked="" type="checkbox"/> M <input type="checkbox"/>	S <input type="checkbox"/> M <input type="checkbox"/>
3 60.06	S <input type="checkbox"/> M <input type="checkbox"/>	S <input type="checkbox"/> M <input type="checkbox"/>	S <input checked="" type="checkbox"/> M <input type="checkbox"/>	S <input type="checkbox"/> M <input type="checkbox"/>	S <input type="checkbox"/> M <input checked="" type="checkbox"/>
8	S <input type="checkbox"/>	S <input checked="" type="checkbox"/>	S <input type="checkbox"/>	S <input type="checkbox"/>	S <input type="checkbox"/>

10. Activate additional spectrum types

By default COSY, HSQC, and HMBC correlations can be entered. TOCSY und NOESY correlations can be added by clicking the relevant checkboxes.

1D spectra	2D spectra
------------	------------

Enter **[C]OSY**

[T]OCSY

[N]OESY

correlations here

	7 6.96	8 5.82	3 4.16	6 1.86	5 1.27
5 1.27	C <input type="checkbox"/> T <input type="checkbox"/>	C <input type="checkbox"/> T <input type="checkbox"/>	C <input checked="" type="checkbox"/> T <input checked="" type="checkbox"/>	C <input type="checkbox"/> T <input type="checkbox"/>	

11. Choose correlations from your spectra

For each spectrum type, you can selected the correlations from the spectra. On the axes of the tables the shifts of the relevant nucleus and the numbers of the assigned

atom are shown. For symmetric spectra, the symmetric correlations are added automatically.

12. Hit „Transfer“

Transfer

This evaluates the theoretical correlations and compares them to the entered ones.

13. Check the quality of the data

Ideally all shifts should be scored as **green** and for 2D spectra the green correlations should be selected. The overall score should be „accept“ for 1D and 2D spectra. The „**Show full report**“ links next to the scores link to PDF reports for the spectra. The „**Show overall report**“ link below the 1D spectra links to a report for all spectra. If you are sure that your data are correct (which may be the case with a not optimal score) you have finished the Quick Check..

14. Submit of finished inputs

If the ¹³C or the ¹H data or both are assigned, those can be written to the database. This is done via the link „Submit ¹³C/¹H“ below the shift list.

15. Recall saved Quick Checks

You can work on your data over several sessions. For this, you must be logged in and have assigned a „Personal ID“. Past QuickChecks then get **saved** and are listed below the structure editor:

2016-05-02 17:04:17.0 [eugenol](#)
2016-04-28 17:37:02.0 [3-Norbenzaldehyd](#)
2016-05-02 14:29:22.0 [indol](#)

Click on a name to recall a dataset.

QuickChecks can be deleted using the „Delete“ button next to the link.