Webtools for Structure Elucidation and Structure Verification

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Case #1: From the ^{13}C-NMR spectrum to the structure using „Spectral Similarity Search“

Case #2: Structure proposal and ^{13}C-NMR data are known → perform verification

General rules:

- Use all pieces of secure information you have
- It is better to combine 2 (or more) „soft“ constraints than using 1 „hard“ limit

Example: You know the molecular weight of your unknown is 258 amu, halogens are absent.

Bad selection:	Only molecular weight 257.5 – 258.5
Better selection:	Molecular weight e.g. 250 – 270 and F,Cl,Br,I absent
	(Maybe deuterated / anion/ cation / labeled compound is in the database)

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Case #1: From the ^{13}C-NMR spectrum to the structure using „Spectral Similarity Search“ („Dereplication“)

Input: https://c13nmr.at/similar/eval.php
Result: Link via email – no access data necessary

Input: Peaklist – 1 value per line
Shift [Multiplicity] [Deviation]

Shift: -399 to 399ppm
Multiplicity: S D T Q O E P none (C,CH,CH_2,CH_3,C or CH_2,CH or CH_3,CH or CH_2 or CH_3)
Deviation: 1 to 5 ppm / Default = 3ppm

Make use of constraints: Range for the molecular weight
Range for number of signals in reference
Presence/Absence of elements

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615 million of predicted spectra will be searched – constraints are necessary to reduce unwanted answers („garbage“)

Worst case scenario:

No structure proposal found / Too many structure proposals found →
Constraints will be modified creating up to 14 runs = ca. 8,500,000,000 (!!) comparisons

Be patient ! Immediately the final link will be given, when you submit your request, Open link in a new Tab, final page will automatically appear here, when all jobs have finished

Check system-load: https://c13nmr.at/news/robotstatus.html

The final summary collects all structure proposals from all jobs – BUT follow the links given at the beginning to understand the details of this summary

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- **Step #1:** Enter your peaklist / one shift per line / use multiplicity when known, default setting for deviation is usually fine
- **Step #2:** Enter constraints / Range for molecular weight and number of signals in proposed structures
- **Step #3:** Select presence/absence of elements – F,P from NMR, Cl,Br – isotope ratio from MS, N – from MS
- **Step #4:** Enter your email-address, define project and sample
- **Step #5:** Submit request by clicking „Start Search“-Button

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Spectral Similarity Search with Ranking
Accessing 615,365,172 predicted ^{13}C-NMR spectra

Recall actual status and server-load from here

Server is enabled

equest submitted on 2023:05:09 at 19:33:50 from 2.56.162.76

ata successfully queued for processing
esult will be sent to: discard@univie.ac.at

ccording to the system load your request will need approximately 12 minutes

Recall the result here

Requested via:

Your request submitted on 2023:05:09 at 19:33:50

Project:	Test Workshop
Peaklist:	propionic acid, ethylester
Requested by:	discard@univie.ac.at
Requested from:	2.56.162.76
Requested via:	

Be patient, the result will appear here when finished

Your result will automatically appear here, when jobs have finished ....
Please be patient for a few minutes .....

Monitor progress and system-load - click here

Final page Incomplete at the moment

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Result from Server - 01:	Reference spectra:	74,435,185	Recall details
Result from Server - 02:	Reference spectra:	107,426,223	Recall details
Result from Server - 03:	Reference spectra:	177,099,966	Recall details
Result from Server - 04:	Reference spectra:	144,833,798	Recall details
Result from Server - 05:	Reference spectra:	111,570,000	Recall details
All Server:	Reference spectra:	615,365,172	

- Follow the links to see how the result was obtained
- When inspecting the more detailed pages you see also the variation of constraints in order to optimize the search
- You can download „zip“-files for specific runs and add them to the „Supplementary Information“ of your publication

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Structures used for linking	
Database	Structures available
PUBCHEM	150,149,731
COCONUT	407,270
LOTUS	276,518
NPASS 2.0	96,235
npatlas 2.0	33,372
NP-MRD	280,096
SuperNatural 3.0	449,008

When using reasonable constraints you are allowed to rate the result

Anonymized rating can be recalled from https://c13nmr.at/news/show_sim_rating.php

Every structure in the hitlist is linked to the PUBCHEM-collection (when available)

Every structure in the final hitlist is checked against these 6 NP-databases and in case the structure is already a known „Natural Product“ a marker is shown

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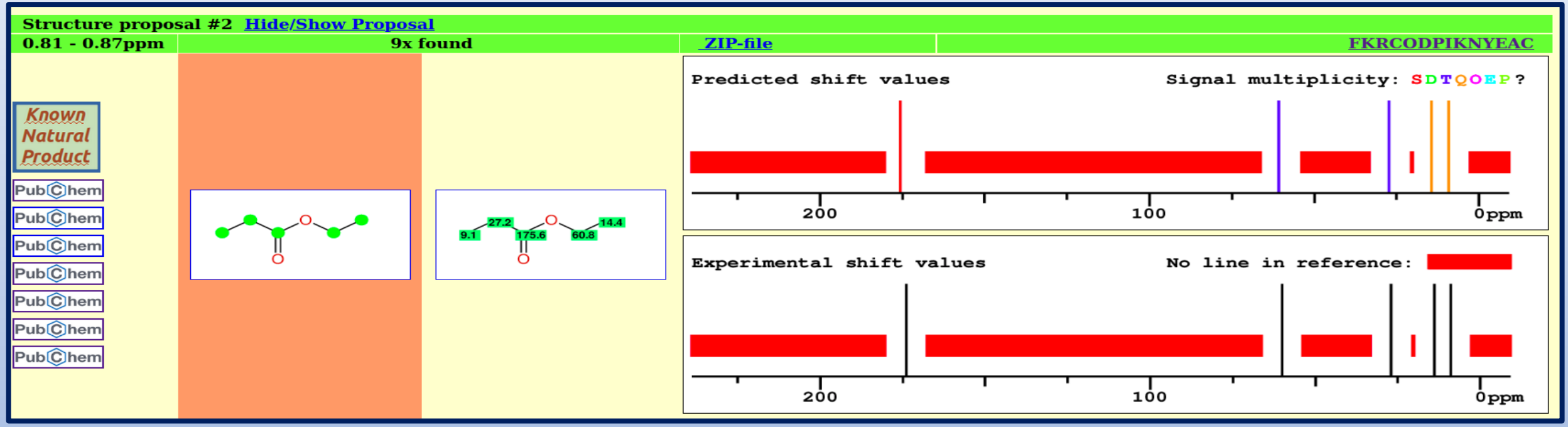
Proposals sorted by average-deviation (0.00 = perfect match)

Search Internet for this structure using „Google“ and 2D-Topology (14 chars from INCHIKEY)



Known Natural Product
Links to PUBCHEM

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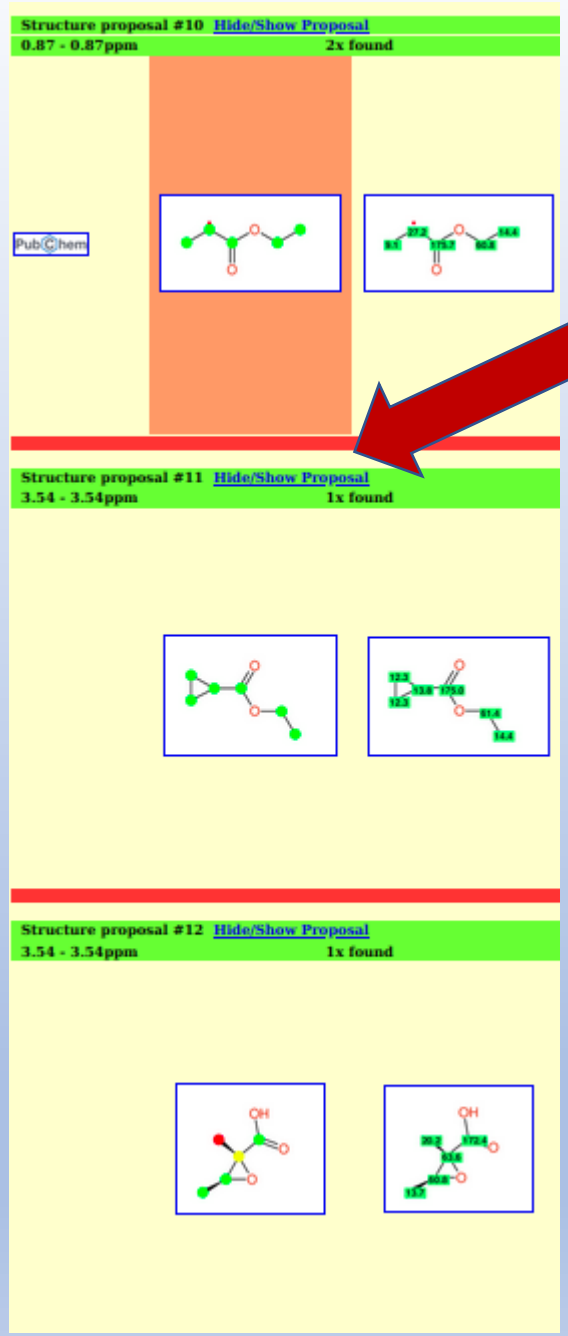
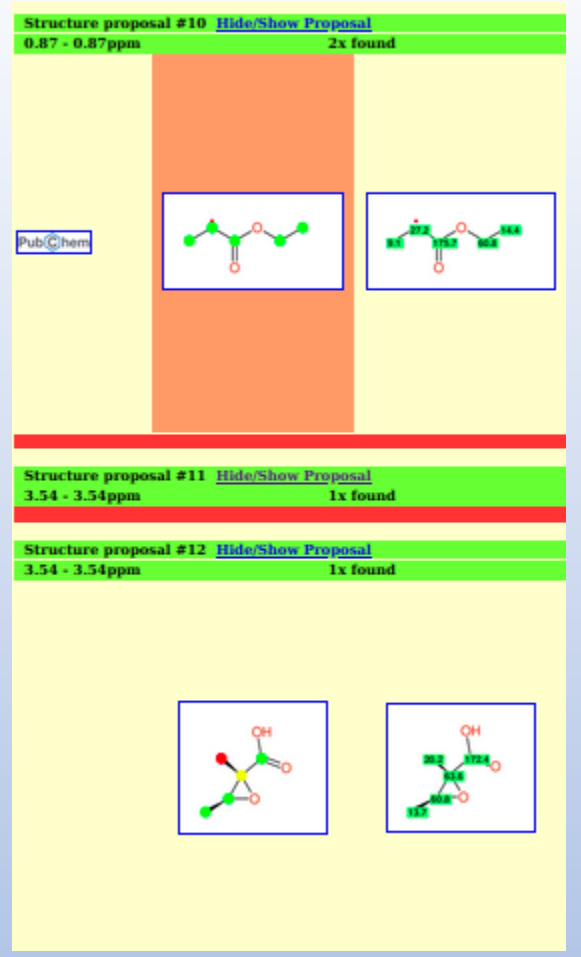
Optimize layout/content of final hitlist

This proposal does not fit e.g. the ^{1}H-NMR data



Click here



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Examples for testing the efficiency of constraints

C5 H10 O2 / MW = 102 amu
Peaklist:
9 q
14 q
27 t
60 t
174 s

Use this peaklist

with multiplicity information
without multiplicity information
no additional constraint
Use e.g. a range for the molweight 90 to 115
Allow only O, forbid all other elements
Restrict references by number of signals (e.g. 3 to 7)

Create a small table holding the number of references found, CPU-time, I/O-load on the server (can be found at the bottom of webpage) – you will learn that missing constraints increase the number of unwanted proposals („garbage“)

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Case #2: Structure proposal and ^{13}C-NMR data are known → perform verification

Input: https://c13nmr.at/c13robot/robot.php
Result: Link via email (Access data at the very end !)

Input	Result
Only structure / skip all line Input	Spectrum Prediction
Structure and Peaklist: Peaklist: unassigned/partially assigned/fully assigned	Structure verification (Accept/Minor Revision/ Major/Revision/Reject) and detailed analysis

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Rules:

- Use descriptive names for your project and your sample
- Use your own email-address
- Draw the structure with a „nice layout“
- Define stereo-centers by up-/down-bonds as usual
- Draw cis/trans-compounds in a correct and nice way
- Your drawing sequence defines the numbering of the atoms
- Automatic assignment works only when „n“ lines are given for a compound having „n“ carbons
- Enter multiplicity information when available (especially helpful for automatic assignment)
- Assign as many lines as you can
- Usage of exchange flags is allowed (similar to the presentation in the literature)

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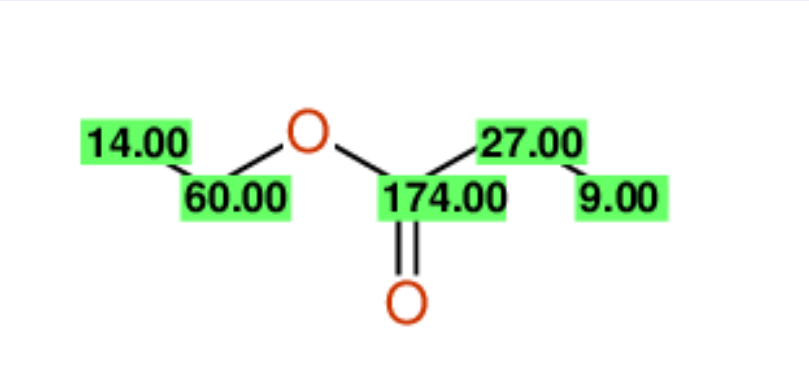
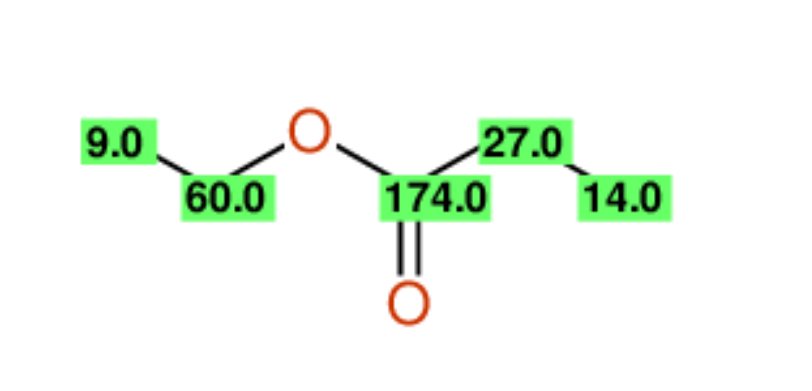
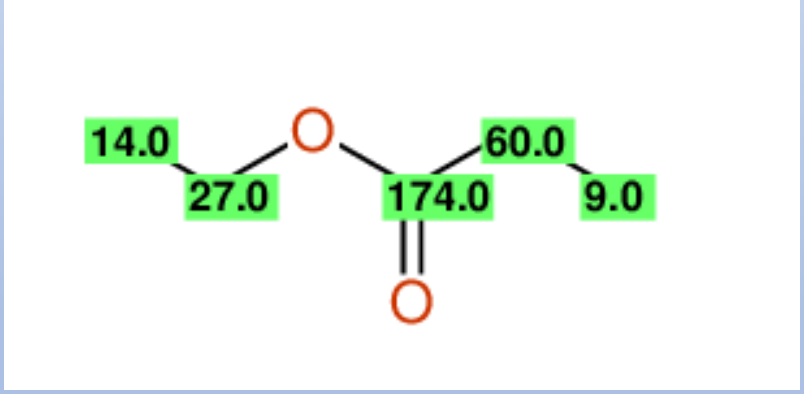
Examples: Propionic acid, ethylester (correct assignment)



Try different wrong assignments and try partially/completely unassigned





You will obtain „Accept“, „Minor Revision“ and „Major Revision“

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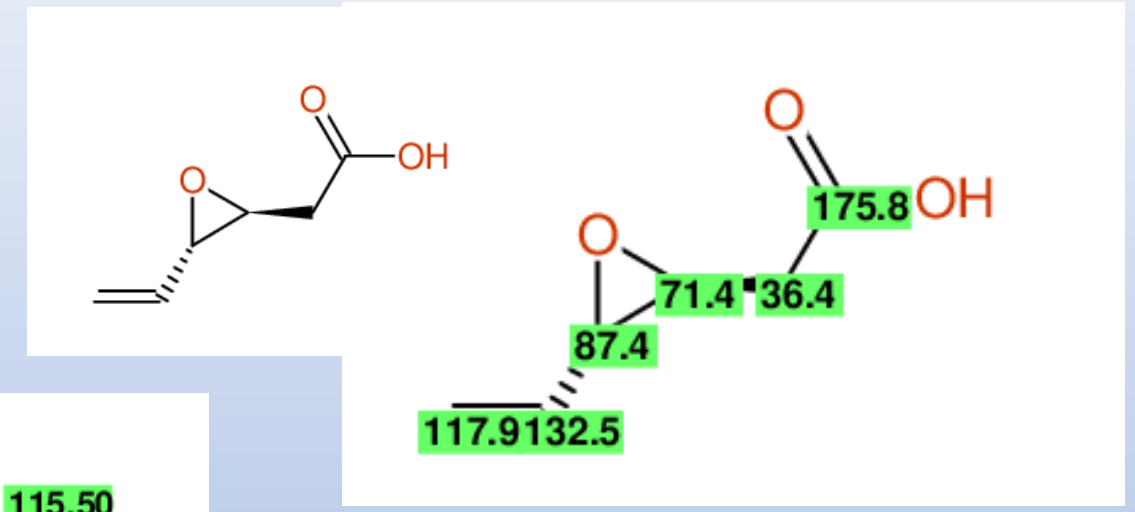
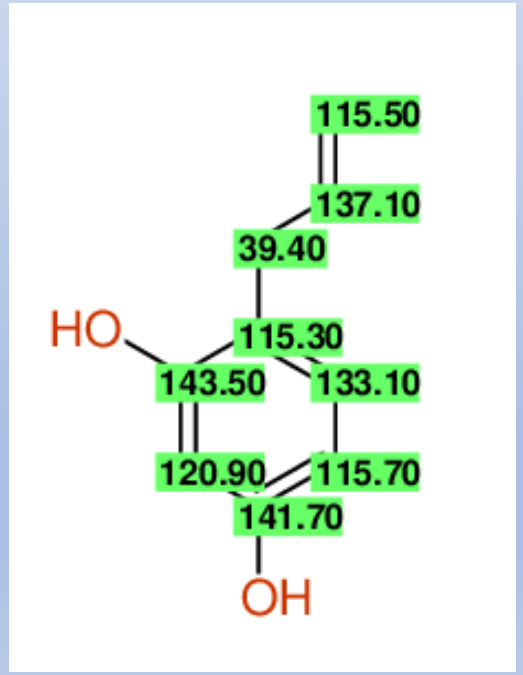
Structure proposal correct ? Data are given as published in high-quality chemistry journals
In case you think the structure proposal is wrong, create a better one !

Example #1: (from „JACS“)



Example #2: (from „Molecules“)



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Summary:

CSEARCH Spectral Similarity Search: https://c13nmr.at/similar/eval.php

CSEARCH Robot Referee: https://c13nmr.at/c13robot/robot.php

Show System-load: https://c13nmr.at/news/robotstatus.html

User-rating: https://c13nmr.at/news/show_sim_rating.php

News: https://c13nmr.at/news/news.html

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Example 1 https://c13nmr.at/DK/example_1.html
(will be online on Mon, May 15th)

Example 2 https://c13nmr.at/DK/example_2.html
(will be online on Mon, May 15th)

Further reading:

Molecules,26,11,3413(2021) https://c13nmr.at/journal/molecules/index.html

See https://c13nmr.at

- → Examples/Journal
- → Examples/Compounds
- → Literature
- → On Web

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