

Use of carbon-13 NMR to identify known natural products by querying a nuclear magnetic resonance database—An assessment

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Abstract

The quick identification of known organic low molecular weight compounds, also known as structural dereplication, is a highly important task in the chemical profiling of natural resource extracts. To that end, a method that relies on carbon-13 nuclear magnetic resonance (NMR) spectroscopy, elaborated in earlier works of the author's research group, requires the availability of a dedicated database that establishes relationships between chemical structures, biological and chemical taxonomy, and spectroscopy. The construction of such a database, called *acd_lotus*, was reported earlier, and its usefulness was illustrated by only three examples. This article presents the results of structure searches carried out starting from 58 carbon-13 NMR data sets recorded on compounds selected in the metabolomics section of the biological magnetic resonance bank (BMRB). Two compound retrieval methods were employed. The first one involves searching in the *acd_lotus* database using commercial software. The second one operates through the freely accessible web interface of the *nmrshiftdb2* database, which includes the compounds present in *acd_lotus* and many others. The two structural dereplication methods have proved to be efficient and can be used together in a complementary way.

KEYWORDS

¹³C, databases, dereplication, natural products, NMR

1 | INTRODUCTION

Natural products (NPs) chemistry and metabolomics share almost the same tools, including those for the identification of chemical compounds within complex mixtures.¹ The topic of NP structure identification is extremely important and appeals nowadays to two main analytical methods, nuclear magnetic resonance (NMR) spectroscopy and liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS) either considered separately or in association.^{2,3} A recent preprint provides a stunning overview of what can be achieved

through the LC-MS/MS approach.⁴ NMR is well suited to the identification of known compounds and to the elucidation of unknown structures.^{5,6} ¹³C NMR alone has been reported as an efficient method for the identification of known compounds of small molecular weight such as NPs when the available sample amount is not limiting. Resorting on ¹H NMR is an obvious option, but its practical adoption is limited by (i) the difficulty of spectrum analysis caused by the multiplet structure of resonance peaks resulting from ¹H-¹H scalar couplings, (ii) the high dependence of experimental spectra on sample temperature, pH, salt effect, and

concentration, and (iii) the low quality of chemical shift prediction.

Avoiding duplication of NP identification work for already reported compounds is known as structural dereplication.^{7,8} Collecting and associating NP molecular structures, chemical or biological taxonomic information, and spectroscopic data are necessary to build databases for structural dereplication.⁹ The creation of exhaustive catalogs of NP structures was undertaken only recently and lead to the COLleCtion of Open Natural ProdUCts (COCONUT)^{10,11} and to the natural prOducTs occUrrences databaSe (LOTUS).¹² LOTUS collects publicly accessible structures and natively includes the related chemical and biological taxonomy data. The spectroscopic pillar of dereplication was given to LOTUS by the adjunction of predicted NMR chemical shift values. Choosing predicted values instead of experimental ones¹³ is the result of the relatively scarce availability of the latter data.¹⁴ The *acd_lotus* database was created using LOTUS structural and taxonomic data and the Advanced Chemistry Development, Inc. (ACD/Labs) ¹³C NMR chemical shift validation tool for prediction.¹⁵ The process that led to the creation of *acd_lotus* was presented in a recent article.⁷ It contains 218,478 structures. Its use was illustrated by the retrieval of only three structures from published sets of experimental chemical shift values.⁷ The present article reports an assessment of the same method through the attempted retrieval of 58 structures of metabolites.

2 | MATERIAL AND METHODS

All calculations were carried out on a DELL Precision 3530 laptop computer with 16 GB of RAM memory and an Intel® Core™ i5-8400H CPU @ 2.5 GHz running Windows 10 Education version 20H2. The ACD/C+H NMR Predictors and DB 2021.1.0 software was purchased from ACD/Labs (Toronto, Ontario, Canada).

The metabolites involved in the present assessment task were selected from the Biological Magnetic Resonance Bank (BMRB).¹⁶ The home page of its website proclaims: “BMRB collects, annotates, archives, and disseminates spectral and quantitative data derived from NMR spectroscopic investigations of biological macromolecules and metabolites.” A dedicated web page leads to a list of “biologically relevant small molecules in the BMRB.”¹⁷ This page contains hypertext links that quickly lead investigators to chemical structures and to the corresponding NMR data. Structures, NMR spectra, and related metadata are available in the Self-defining Text Archival and Retrieval (STAR) format as NMR-STAR files.¹⁸ The simplicity of fetching structures and

experimental NMR data of small molecules at BMRB motivated the focus on this data source in view of the planned evaluation work. The metabolites subset in BMRB include the primary and secondary ones, as well as xenobiotics. A selection of 58 secondary metabolites belonging to diverse chemical classes was arbitrarily constituted to assess the structural dereplication process based on *acd_lotus*. Two structure retrieval assays were conducted for each experimental chemical shift set drawn from BMRB, one using the ACD/Labs software and the other one with nmrshiftdb2.^{19,20}

The *acd_lotus* database built from LOTUS version 9 is provided in Structure-Data File (SDF) format²¹ and as an NMRUDB ACD/Labs database file that can be downloaded from zenodo.org.²² Querying this database was achieved by copying the targeted ¹³C NMR chemical shift values in the dedicated text entry area, selecting by default a tolerance for a ± 4 ppm difference, and searching for at least as many carbon atoms as there are resonances to find. Duplicate experimental chemical shift values, occurring either by accident or through symmetry, were left duplicated in the list of queried values. The search options “Search through Unambiguous Assignment” and “Do not Match One Chemical Shift for Several Shift Queries” were left inactive. Results were sorted according to “HQI Based on Minimal Distances.” Each search produces a list of structure proposals whose length, or number of hits, is noted. A structure in LOTUS and in *acd_lotus* is associated to a Wikidata reference, or Q-Id, so that the validity of a query result can be easily checked.²³ Wikidata is a wide scope knowledge graph that contains nodes for many chemical compounds, including those present in LOTUS. Validity of a query result was defined by identity of compound names and InChI keys.²⁴ A query may fail, as indicated by the retrieval of structures in which carbon atoms were not associated to ¹³C NMR resonances. Finding the expected structure can then be achieved by enlarging the chemical shift tolerance for the match between queried and predicted values. Each compound selected in BMRB was associated with a list of queries to *acd_lotus*, often containing only a single element and characterized by the tolerance value. A query was identified by a minimal number of queried chemical shifts, a tolerance value, a number of hits, and a list of results. A result was characterized by a Boolean (true or false value) for compound matching success, a rank in the list of proposals, a link to Wikidata for the proposed structures, the InChI and the InChI key identifiers from Wikidata, and a remark as free text.

The structures and predicted NMR data in *acd_lotus* were made available for compound searching in the nmrshiftdb2 website.⁷ The lists of chemical shifts drawn

from BMRB that were used for searches in *acd_lotus*v9. NMRUDB were also submitted for searches in *nmrshiftdb2*. The latter operates completely unsupervised, meaning that no number of expected chemical shift matchings and no tolerance value has to be provided. Each search result from *nmrshiftdb2* was characterized by a spectrum similarity index as a percentage value, a rank in the list of proposals, a Boolean value indicating compound matching success, a link to Wikidata, the InChI and the InChI key identifiers from Wikidata, and a remark as free text. The *nmrshiftdb2* website contains structures that originate from many sources, not only from *acd_lotus*. The ^{13}C NMR data associated to these structures may be experimental or predicted. The experimental ones were drawn from literature and from spectra deposited by the maintainer of the website and by the registered users. As a consequence, *nmrshiftdb2* can provide structures that are not present in the LOTUS database.

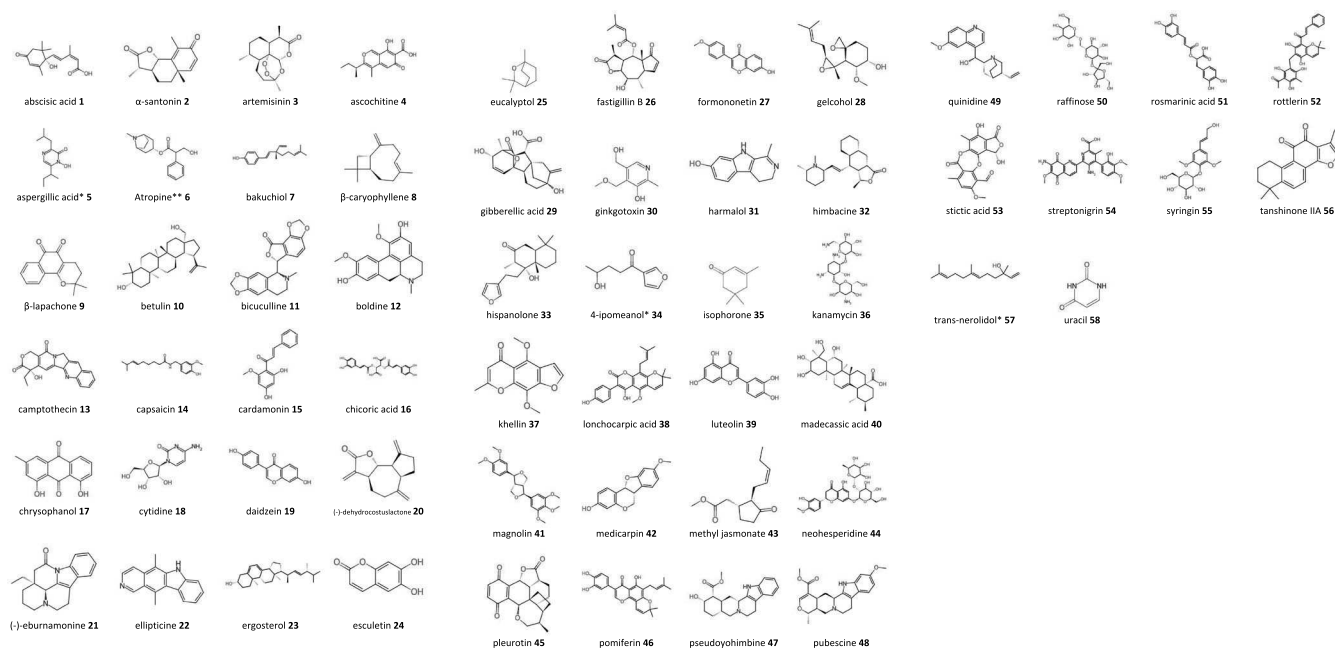
Each compound selected in BMRB was characterized in a formal way by its name, its Chemical Abstract Service Registry Number (CAS RN), its SMILES, InChI, and InChIKey identifiers, the link to the associated NMR-STAR file, the list of its ^{13}C NMR chemical shift values, the sample supplier, the compound reference by the supplier, and the characteristics, as stated here above, of the queries submitted to *acd_lotus* through the ACD/Labs software and to *nmrshiftdb2* as well as the outcome of these queries.

Results encoding was achieved in practice by means of the formalism brought by the JavaScript Object Notation (JSON).²⁵ The adoption of JSON for data representation was motivated by its simplicity of being read and written by humans and computers. Extensible markup language (XML) was found less practical than JSON for this purpose.²⁶

The structures of all compounds were collected in a single SDF file in which the 2D atomic coordinates were calculated from SMILES chains using the RDKit library of cheminformatic functions.²⁷ Structure depictions in the portable network graphics (PNG) format of all compounds were also created by means of RDKit and reported in Scheme 1.

3 | RESULTS

Scheme 1 shows the structures, names, and numbers of all the compounds selected for the assessment of *acd_lotus* as a tool for structural dereplication. Table 1 reports the results of the tests carried out on these compounds, presented as the ranking of the targeted compound in the list of the proposals returned by the compound search tools in ACD/Labs and *nmrshiftdb2*. More details on compounds, queries, and answers to queries are available as supplementary material from zenodo.org. Among the 58 tested structures, 37 were placed in first position by the compound search tool of



SCHEME 1 Structure diagram, trivial name, and structure number of the compounds from BMRB involved in the assessment of the dereplication procedure based on *acd_lotus*. * indicates names of compounds without determined absolute configuration. ** indicates names of compounds analyzed in racemic form.

TABLE 1 Results of compound retrieval from experimental ¹³C NMR chemical shifts.

Compound name	Rank ACD/Labs	Rank nmrshiftdb2
Abscisic acid 1	1 ^a	1
Alpha-santonin 2	1	1
Artemisinin 3	1	1
Ascochitine 4	2 ^b	6
Aspergillic acid 5	1	1
Atropine 6	1	4
Bakuchiol 7	1	1
Beta-caryophyllene 8	2	3
Beta-lapachone 9	1 ^a	1
Betulin 10	3	12
Bicuculline 11	1	1
Boldine 12	2	2
Camptothecin 13	1	2
Capsaicin 14	2	2
Cardamonin 15	6	4
Chicoric acid 16	2	2
Chrysophanol 17	1	1
Cytidine 18	—	—
Daidzein 19	1	1
(–)-Dehydrocostuslactone 20	1	1
(–)-Eburnamonine 21	1	1
Ellipticine 22	1	1
Ergosterol 23	2	10
Esculetin 24	1	1
Eucalyptol 25	1	1
Fastigillin B 26	1 ^a	3
Formononetin 27	1	1
Gelcohol 28	1	1
Gibberellic acid 29	1 ^a	13
Ginkgotoxin 30	1	1
Harmalol 31	1 ^b	4
Himbacine 32	1 ^a	6
Hispanolone 33	2	2
4-Ipomeanol 34	—	—
Isophorone 35	1	1
Kanamycin 36	5 ^a	10
Khellin 37	1	1
Lonchocarpic acid 38	1	1
Luteolin 39	1	1
Madecassic acid 40	3	3
Magnolol 41	10	4

(Continues)

TABLE 1 (Continued)

Compound name	Rank ACD/Labs	Rank nmrshiftdb2
Medicarpin 42	3	5
Methyl jasmonate 43	1	2
Neohesperidine 44	4	15
Pleurotin 45	1	11
Pomiferin 46	1	1
Pseudoyohimbine 47	1	1
Pubescine 48	1 ^a	4
Quinidine 49	2	1
Raffinose 50	21	1
Rosmarinic acid 51	1	1
Rottlerin 52	1	1
Stictic acid 53	1	1
Streptonigrin 54	1 ^b	1
Syringin 55	3	1
Tanshinone IIA 56	1	1
Trans-nerolidol 57	2	1
Uracil 58	— ^b	2

Note: The — sign indicates that the compound search was unsuccessful.

^aChemical shift tolerance was set to 6 ppm.

^bChemical shift tolerance was set to 8 ppm.

the ACD/Labs software operating on *acd_lotus* on the basis of chemical shift list similarity. Furthermore, in eight cases, an increase of the chemical shift tolerance either to 6 or to 8 ppm was required to obtain this result. Compound search in nmrshiftdb2 leads to 32 rankings of the targeted compounds in first position. Target ranking in first position by the two search tools simultaneously occurred 28 times.

Structural dereplication was considered to have failed in the three following cases. 4-Ipomeanol **34** is the only compound among the 58 selected ones from BMRB that is present neither in *acd_lotus* nor in nmrshiftdb2. Cytidine, **18**, is present in these databases only as a tautomeric form originating from the improper decoding of an InChI string from LOTUS, a form that is not considered as a correct answer to the compound identification queries. The same decoding problem arose for uracil, **58**. However, the nmrshiftdb2 database contains a structure of uracil that is not related to LOTUS and for which NMR experimental NMR data are available, thus allowing for proper structural dereplication. Notable cases that were encountered during the present study are discussed in more detail hereafter. Information about compound structures were searched in public sources Wikidata²³ and PubChem²⁸ as well as in SciFinder^{n, 29}.

Abscissic acid, **1**, was analyzed by BMRB using a sample of natural (+)-abscissic acid. The structure contains a single asymmetric carbon atom and two double carbon-carbon bonds. The first proposal from ACD/Labs, obtained with a chemical shift tolerance of 6 ppm, has no defined configuration of the asymmetric center and correct configurations of the double bonds. This proposal is considered as correct because NMR is unable to distinguish between enantiomers in standard spectrum recording conditions. Structures completely lacking an asymmetric center configuration data are present in *acd_lotus* and are referred to as a flat structure. The second proposal is a single enantiomer, but the geometry of one of the double bonds is left unspecified. Such a structure is not considered as a valid answer to the query. The third proposal is as valid as the first because all of the elements of the 3D geometry are properly defined. nmrshiftdb2 provides an answer to the query that is similar to the one by the ACD/Labs software.

(-)-Alpha-santonin, **2**, was retrieved by the ACD/Labs search tool at first rank. Its Wikidata Q-Id, Q413166, according to *acd_lotus*, leads to a compound simply named santonin in Wikidata but with (-)-alpha-santonin as synonym. nmrshiftdb2 ranks at the first place Q105328952, the enantiomer of Q413166 named alpha-Santonin in Wikidata, and Q413166 in the second place. The structures of the two enantiomers are considered valid for dereplication purposes. The presence of the two enantiomers in LOTUS and in Wikidata is apparently surprising, as the natural occurrence of only one of the two enantiomers is the most likely hypothesis. The only santonin known to SciFinderⁿ is Q413166, in which the four asymmetric centers exhibit the (*S*) stereoconfiguration. Compound naming in Wikidata can possibly be misleading in some cases.

The case of ascochitine, **4**, illustrates the confusion in compound identification brought about by the existence of tautomeric forms. The molecular structure of ascochitine contains a single asymmetric center and a series of conjugated double bonds. The first proposal from the ACD/Labs software is a tautomer, Q110168575 in Wikidata, of the structure declared by BMRB and confirmed by SciFinderⁿ on the basis of the trivial name ascochitine. The second proposal, Q77573394, has its single and double bonds at the expected positions and would have been the correct proposal if its asymmetric center configuration was defined. This proposal was accepted because the corresponding ¹³C NMR spectrum matches that of the enantiomerically pure ascochitine. The expected structure is neither present in *acd_lotus* nor in nmrshiftdb2, but it is referenced Q27275562 in Wikidata. Even though the InChI code was created in order to solve compound identification issues, it does not create

different identifiers for compounds related by non-trivial tautomerism such as Q27275562 and Q110168575. Retrieving a tautomer is not considered in this study as a valid result for dereplication.

Aspergillic acid, **5**, derives from two amino acid residues, leucine and isoleucine. SciFinderⁿ indicates that the absolute configuration of the asymmetric center in the side-chain of isoleucine is not defined, even though it reports a non-zero optical rotation. Interestingly, this database contains two entries, one for aspergillic acid with a Registry Number (RN) 490-02-8, drawn with an explicit pentavalent nitrogen atom and one for aspergillic acid, DL- of RN 22810-67-9. PubChem and the NCI catalog³⁰ do not indicate a defined chirality either, as found for Q4807880 in Wikidata. Moreover, the data sheet of aspergillic acid in BMRB reports a defined configuration that corresponds to the one of Q105120934, retrieved and ranked first by the ACD/Labs software and nmrshiftdb2, even though the process by which this configuration was defined is not clear. A hypothesis can be proposed for the spontaneous apparition of a new chiral center: a flat 2D structure as the one derived from a non-isomeric SMILES chain can be transformed into a 3D structure by means of a cheminformatic toolkit so that an asymmetric center is created with a randomly assigned absolute configuration. Transforming the 3D structure into textual chemical descriptors initiates the propagation of “fake” information.

Atropine, **6**, is another case in which configuration information plays an important role. The sample analyzed by BMRB is (+/-)-atropine, also named (+/-)-hyoscyamine in Wikidata and ranked first as such by the ACD/Labs compound search tool. The structure of atropine contains four asymmetric carbons, but the planar symmetry of the non-aromatic tropine part makes a configuration inversion at the position close to the aromatic ring sufficient to create enantiomers. In BMRB and PubChem, the geometry of the tropine part is incorrect, being reported in the *exo* (or β) form instead of the *endo* (or α) form. Moreover, BMRB fully defines the configuration of all the asymmetric center, in contradiction with the data sheet provided by the sample supplier. The identification of atropine is further complicated by the fact that it is a scalemic natural compound, possibly occurring neither in enantiopure nor in racemic form.

Betulin, **10**, in its flat form was ranked first by the ACD/Labs and nmrshiftdb2 search tools. The exact structure was ranked at the third place by ACD/Labs and at the 12th by nmrshiftdb2, but the fact that many stereoisomers were reported for this molecule renders the ranking non-significant.

Bicuculline is the name in Wikidata for bicuculline, **12**, and for its flat form. Two enantiomers of the molecule

are present in Wikidata, but SciFinderⁿ contains only one.

Cytidine, **18**, is not present in *acd_lotus* in the appropriate di-amide tautomeric form. The ¹³C NMR chemical shifts predicted from the di-iminol tautomer are too far off to allow for structure retrieval from experimental chemical shifts. The experimental and *acd_lotus*-predicted chemical shifts differ by 16.6 ppm for the carbon atom of the carbonyl group. The nmrshiftdb2 search tool is not constrained by a user-supplied chemical shift tolerance and finds the cytidine di-iminol tautomer at rank 87. In that particular case, prediction was carried out using the HOSE code approach, as explained in Kuhn and Nuzillard.⁷

Eburnamonine, **21**, was isolated in its two enantiomeric forms, depending on the nature of the investigated plant. (–)-Eburnamonine is strangely written (∼)-eburnamonine in the BMRB website, and it is designated as vinburnine in Wikidata. Its enantiomer is also present in Wikidata, and it is named eburnamonin. The two compound search tools ranked at first place one or the other enantiomer.

nmrshiftdb2 ranked ergosterol, **23**, at position 10, but compounds ranked from position 1 to position 10 bear the same similarity index to targeted chemical shifts, thus making ranking meaningless.

The InChI code of eucalyptol, **25**, in BMRB erroneously indicates the presence of two asymmetric centers. The correct identifiers were substituted to the proposed ones and reported in the JSON file. InChI and SMILES for fastigillin B, **26**, (possibly also written fastigilin) are wrong in BMRB but match together; they were replaced by the correct ones from PubChem. SMILES in BMRB is wrong for harmalol, **31**, and replaced in the JSON file by the one in PubChem. The InChI, InChI Key, and SMILES in BMRB are wrong for himbacine, **32**, and were replaced in the JSON file by the ones in PubChem.

4-Ipomeanol, **34**, is present in neither LOTUS nor nmrshiftdb2 and was therefore not retrieved in this study. The absolute configuration of the asymmetric center is defined as being (*R*) in BMRB only and nowhere else. The exact configuration might have never been determined, as suggested by SciFinderⁿ. Flat 4-ipomeanol is present in Wikidata as Q27291230.

The InChI of methyl jasmonate, **43**, in BMRB is wrong, with a *trans* double bond, but the InChI key is correct. The SMILES in BMRB does not include the double bond geometry. The SMILES, InChI, and InChI key from Pubchem, identical to those in Wikidata, were copied in the JSON file.

nmrshiftdb2 ranked raffinose, **50**, at the first place because it contains experimental NMR data for this compound that match well with those reported by BMRB.

However, the InChI key associated with the retrieved compound does not match that of raffinose. The origin of this mismatch lies in the structural drawing of the molecule that contains sugar rings in chair form, thus preventing a correct automatic interpretation of the structure from 2D atomic coordinates. Sugar rings are best drawn as regular hexagons for database storage purpose, even though this results in ring conformation data loss.³¹

Rosmarinic acid, **51**, is ranked first by nmrshiftdb2 on the basis of experimental data. The configurations of the asymmetric centers are not defined in the retrieved structure, but the correct compound name is provided.

BMRB analyzed *trans*-nerolidol, **57**, is a compound for which the absolute configuration of its asymmetric center was not determined. The SMILES, InChI, and InChI key identifiers proposed by BMRB were replaced by those from PubChem derived from the flat structure with a correct geometry of the double bonds.

The correct di-amide tautomer of uracil, **58**, is not present in *acd_lotus*, which contains only the di-iminol form. The correct tautomer was found in nmrshiftdb2, ranked at the second place behind a non-natural boronic acid derivative, because the uracil data it contains do not originate from *acd_lotus*. Uracil in its di-amide form is Q182990 in Wikidata and the corresponding InChI is unexpectedly decoded by RDKit into the di-amide tautomer, even though a warning message is issued during decoding. “Unexpectedly,” as stated in the previous sentence, refers to the usual InChI software behavior that produces iminol structures instead of amides. So, two different InChI strings may be converted into two different tautomers that in turn are back converted to the same InChI string. Using PerkinElmer ChemDraw or ACD/Labs ChemSketch interactive structure drawing software to carry out structure-to-InChI and InChI-to-structure conversions produces the same result as the one obtained with RDKit.

4 | CONCLUSION

The structures of the compounds arbitrarily selected by the author from the BMRB website for ¹³C NMR-based structural dereplication were on average satisfactorily identified. Compound identification by means of the nmrshiftdb2 database only required having access to a web browser. This approach allows any investigator to refine searches by assigning a number of directly bound hydrogen atoms to each targeted chemical shift value, a possibility that has been purposely ignored in the present study in order to maintain some degree of fairness in the comparison with the ACD/Labs compound search tool. Moreover, nmrshiftdb2 contains compounds that do not

result from *acd_lotus* data importation and for which experimental NMR data are available, thus enhancing its identification capability. Resorting on the *acd_lotus* database through the ACD/Labs compound search tool results often in a better ranking of the expected structures among the set of proposals, even though the reason for this cannot be easily investigated. This slight supplement in ranking quality takes place at the price of purchasing the necessary software.

DATA AVAILABILITY STATEMENT

The JSON files, the structures, the structure descriptors, and the structure depictions of all compounds were deposited at <https://zenodo.org/record/8186827>.

The *acd_lotus* database files in SDF and in ACD/Labs format are available from <https://zenodo.org/record/8175939>.

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How to cite this article: J.-M. Nuzillard, *Magn Reson Chem* **2023**, *1*. <https://doi.org/10.1002/mrc.5386>