# Survey comments

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**Statistics for dataComment.**

**Question: What are your main complaints (if any) about our data retrieval tools and capabilities? How can we improve them to better serve you? What data retrieval options would you like to see?**

Filter requested: None.

Total survey responders for filter: 180

Responders: 26 (14%)

Field Value to search for **Display** is not user friendly: 1 responses (4%).

clearer **layout**: 1 responses (4%).

I can get one entry from **google faster** than in the search engine of the bmrb site.: 1 responses (4%).

I would like to have a **more advanced** **(?)** way of searching the database.: 1 responses (4%).

I've had great difficulty **finding and downloading datasets** from the website in a format I can use. It would

be extremely useful if each entry gave a direct link to a **table of each type of data** available for

that entry (eg. chemical shifts, RDCs, relaxation etc.) It would also be really helpful if you could

download **single types of data as a comma- or tab-delimited text file**.: 1 responses (4%).

In general very good but I often get **many hits for the very same entry** which makes analysis of the search

results very tedious: 1 responses (4%).

In many cases there appear to be **multiple datasets for the same entry** and it is difficult to distinguish

them. The usability of the database could be increased if different **entries could be grouped** e.g. by

the publication in which they all appear.: 1 responses (4%).

It would be VERY helpful if the **search results were expanded** so that every result returned the authors,

submission date, molecules in the sample (protein and ligand names for example) and what data types

are in each entry (chemical shifts, couplings, T2, etc.) in addition to the accession number. Clicking

through each link can be painful, and some searches return many results.: 1 responses (4%).

It would be great to type in a number of **chemical shifts and then get a possible chemical to match** that

(like with the Colmar webserver).: 1 responses (4%).

It would be nice if bmrb could be **connected with actual structural data**, i.e. searching for structural

motifs etc. : 1 responses (4%).

**More annotations are needed**: 1 responses (4%).

No straight forward to **retrieve data in readable format**: 1 responses (4%).

Please make it **easier to download the entire database**, and to get a list of last (modified, file size and

file names) to aid in **periodic automatic synchronization to a local repository**.: 1 responses (4%).

Search is a problem: 1 responses (4%).

Search is simply appalling. **NMR STAR file formats are way too complex - hard to read or import into any**

**applications**.: 1 responses (4%).

Searching tool not efficient: 1 responses (4%).

Sometimes the **nmrstar format is not compatible with CARA**. It gives the weird loop error - broken loop.: 1

responses (4%).

The search engine is not user friendly at all. Often, **search results are only displayed as a long list of**

**accession numbers**, that one has to click through. Sometimes, even **though one searches for a given**

**protein name, and the name is in the dataset, the search engine turns up nothing**.: 1 responses (4%).

The search results, although accurate, merely come in a **list of BMRB ID numbers** and therefore requires a

significant amount of link to follow to find the relevant data.: 1 responses (4%).

The search tools are useless, I can even find my own deposited data. If I **search by my name data is**

**missing**. When you do find something **you are presented with a deposition number only**, you then have to

go through each number to see what it relates to. Very tiresome. : 1 responses (4%).

The search tools of the BMRB 15 years ago were better. Now I always have **difficulties to find the**

**FASTA/BLAST search**. Sometimes I **use Google to find the correct entry**. The current search tool is not

working well, some times there is **no result if I search for a name of a protein**. : 1 responses (4%).

**Web search doesn't find relevant entries**. **Not enough info** about each entry is presented **in the returned**

**list of entries**. : 1 responses (4%).

Your tools are great. It would be wonderful if a lot of **older data** (such as chemical shifts that were

published as supplements to journal articles) **could be pulled in from literature** in the preBMRB days,

to make it easier to find one place. : 1 responses (4%).

**a more modern web interface**, easier : 1 responses (4%).

better search: 1 responses (4%).

**make it more obvious how to find and download a BMRB file**.: 1 responses (4%).

**searching can be unexpectedly tricky sometimes if one does not know the BMRB ID of the data one wants** : 1

responses (4%).

sometimes I have the ***feeling*** that d**espite typing in the correct ID, search doesn't work and need to look**

**through authors or PDB etc**.: 1 responses (4%).

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**Statistics for visualComment.**

**Question: What are your main complaints (if any) about BMRB's visualization tools? How can we improve them to better serve your needs?**

Filter requested: None.

Total survey responders for filter: 180

Responders: 13 (7%)

At present D**EVise simply fails to run** on my system, giving an uninformative (to me, anyway) Java error. I

do not use DEVise frequently and only found the problem yesterday, but I saw no help in tracing or

fixing the problem: 1 responses (8%).

Dependent on the computer and Operating System Version I am using here (Linux, Windows) quite often the

**system requests a update of Java** which I am not allowed to do here. In this case I cannot use any

visualization.: 1 responses (8%).

**Hard to find tips for usage**: 1 responses (8%).

I find that the **DEVise tools frequently are blocked by modern web browsers**, sadly making them almost

useless for me. Even when I do get them to work, I find them a little frustrating. I think the RBMRB

visualisations on the website are really good, but could be improved by **reversing the axes to match**

**usual chemical shift conventions!** It would be good if there were better options to filter the chemical

shifts to particular atom types (eg. just protons, or just heavy atoms) and to set the axis limits

appropriately. This can be a real problem if you want to switch between the statistics for different

residue types, and **have to keep deselecting and rescaling each time**. **The visualisation in CCPN**

**Analysis v2.4 is pretty good, so making it more like that would be useful**!: 1 responses (8%).

I had some problems with DEVise, some things worked, but others seemed not to appear as I expected - but

then I just downloaded the data and visualized otherwise (so probably it was my fault... I never

checked): 1 responses (8%).

It seems that **DeVise does not work on all entries**: 1 responses (8%).

Java is not the best choice nowadays, many times runnig DEVise I meet problems: 1 responses (8%).

**Resolution is not great!**: 1 responses (8%).

Sometimes I've got problems to visualize the graphics: 1 responses (8%).

Soo **slow and cumbersome**. I prefer raw data, not pictures.: 1 responses (8%).

The **DEVise Tool** is great, but for me it **works only in 20% of the cases**. I always have to try on several

computers to get it running. If I am lucky, it works on one computer out of five.: 1 responses (8%).

do not use: 1 responses (8%).

don't use them mostly: 1 responses (8%).

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**Statistics for toolComment.**

**Question: What are your main complaints (if any) about BMRB's software tools and utilities? How can we improve them?**

Filter requested: None.

Total survey responders for filter: 180

Responders: 8 (4%)

**CS Rosetta lacks RDC option** : 2 responses (25%).

I do not use CS-ROSSETTA, API, a programming library, **nor do I know what API stands for.**: 1 responses

(12%).

**It wasn't clear to me that CS-Rosetta has advanced options** (eg RDCs, if I remember right) that are not

visible by default - I had to email to get a link to these. I agree it's good not to overcomplicate

the default interface, but it would be good if there was an easier way to get to these options.: 1

responses (12%).

Sometimes, ***I've got problems to visualize the graphics of the chemical shift analysis***: 1 responses (12%).

The limits off adding more complex descriptions (i.e. RDCs and oligomers are not possible) to the CS-

**Rosetta server** makes its **use very limited**.: 1 responses (12%).

**more options for Rosetta** would be useful (i.e. addition of RDCs and treatment of oligomers would be nice):

1 responses (12%).

none: 1 responses (12%).

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**Statistics for webSiteComment**.

**Question: What are your main complaints (if any) about BMRB's website? How can we improve it to better serve your needs?**

Filter requested: None.

Total survey responders for filter: 180

Responders: 25 (14%)

**finding right part of the site is cumbersome**: 1 responses (4%).

BMRB **search engine should be more easy**. Some times I have difficulty finding hits for an entry if I do not

provide accurate info like in case of acronym of protein name to fetch deposition. **Starch convertors**

**are bit problematic**, I donot recall exactly I had trouble with, but a **lot work was needed for**

**preparing files for deposition**. It would be great if **macro or scripts** are **available for Xeasy, CARA,**

**Sparky, Cyana** one click formatting/conversion for deposition. Also **pre-validation before submission**

could be another feature. : 1 responses (4%).

**Better documentation** of the files on the database ***(FTP)*** (**readme files only mention a subset of the files present**

**in each folder**). Would be **useful to know which files/folders will be continually updated**. **Better**

**description of NMR-STAR 3.0 tags/savefs/categories**. **Easier access to bulk download** of full database or

download of all entries containing RNA molecules.: 1 responses (4%).

**Can be hard to find things**: 1 responses (4%).

**Easier search and navigation** : 1 responses (4%).

I do not like the interface of <http://www.bmrb.wisc.edu/histogram/glu.shtml.> The **chemical shift ppm axis**

**should be from right to left** (commonly accepted standard NMR style). The old interface was much better

in all respects. : 1 responses (4%).

**I had to spend sometime to make the website work properly in my computer**.: 1 responses (4%).

**Improvement is search and data download is required. Compatible with standard NMR and MD softwares like**

**CARA, CCPNMR, Bruker Dynamic Center, CYANA, AMBER, CNS etc**.: 1 responses (4%).

It continues to improve and it is understandable, but **my main frustration was the mix of file formats for**

**the deposition and different analysis tools**. In addition, **the search result format** as listed above.: 1

responses (4%).

It is always good to improve websites to make them better. However, replacing websites by newer ones

sometimes makes it worst. I **never understood why the old BMRB pages with the yellow/brown layout had**

**to dissappear. They worked perfectly fine for me, and many features, which I used, are now hard to**

**find or are gone completely.** I guess I have to specify a bit which searches I did: ***e.g. download all***

***RNA or protein chemical shift data with 13C, do a FASTA search, find the chemical shift referencing***

***page, search for a protein, get a HSQC of a protein entry (DEVise).*** What I would wish for the future:

**it would be useful to have oligosaccharides in addition to the categories proteins, DNA and RNA.** It

would be great to be able to do **searches/tasks like download then all oligosaccharide data with 13C.**

Feedback for the survey: it is great that you do it. Thank you! In few cases I never used a certain

tool and had only the option to select something between dissatisfied and satisfied. When I did not

know the tool I choose 3. A N/A would have been useful in such a case. : 1 responses (4%).

**It would be useful to have printable versions of online material** e.g. amino acid chemical shift histograms,

amino acid atoms names and averaged BMRB chemical shifts. **You had some of these incredibly useful**

**printable files available years ago, but they have disappeared from the site**.: 1 responses (4%).

It's looks very **old-fashioned** (it's looked exactly the same since I started in NMR). It would be nice for

it to get an update to match the quality of the PDB, for example. Also, a **format converter would be**

**good (one that actually works though!)**.: 1 responses (4%).

It's **not always completely clear which section what I'm looking for will be located in**, but overall I've

been able to find what I need without too much trouble.: 1 responses (4%).

My main problems have been with **downloading data from particular entries in an easily usable format**, and

**being unable to use the DEVise visualisations**. B**eing able to download simple tab-delimited data**

**tables, and expanding and improving the visualisation features of RBMRB** on the website would both be

big improvements for me. I think **making the search interface for different data types easier to use**

would also help.: 1 responses (4%).

Not exactly related to the website but: I find the **NMR-Star format very complex** for my (basic) use.: 1

responses (4%).

**Search capacities could be improved**: 1 responses (4%).

**Simplicity, search, cleanliness**: 1 responses (4%).

**The search functionality**: 1 responses (4%).

The website has improved, but it is still **difficult to rapidly find one's way through**.: 1 responses (4%).

The website is pretty good. I have yet to try the CS-Rosetta server, its on my todo list.: 1 responses

(4%).

**interface is quite clunky**: 1 responses (4%).

**layout: sidebar is poor**: 1 responses (4%).

**main page is a bit busy**. Better give an overview and have the specific tools elsewhere: 1 responses (4%).

**navigation is not always intuitive**: 1 responses (4%).

**searching is not always great**, as noted above.: 1 responses (4%).

the **website seems a bit aged and outdated**: 1 responses (4%).