

## Instructions for use of result files (Confirmatory methods)

You will receive a separate e-mail with two individual files (xxxx.LAB and xxxx.LA2) for the submission of your results to the EURL.

These so-called “RingDat” files are provided by QuoData as a reliable module for interlaboratory-test participants to enter their data. This application makes it possible to transmit laboratory results as files to the proficiency test organisers.

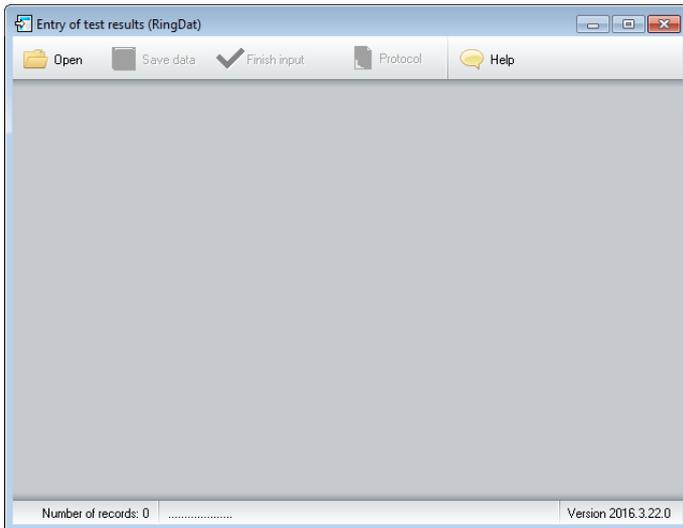
The proficiency test organiser sends the data files xxxx.LAB and xxxx.LA2 to the labs, who then enter their data and send them back. These files are then directly evaluated with PROLab™, thereby simplifying communication between participants and organisers.

You require the programme “RingDat4.exe” to open your laboratory file for data input. It is not necessary to install the Windows software “RingDat”. You can launch the file from any directory or from a USB stick.

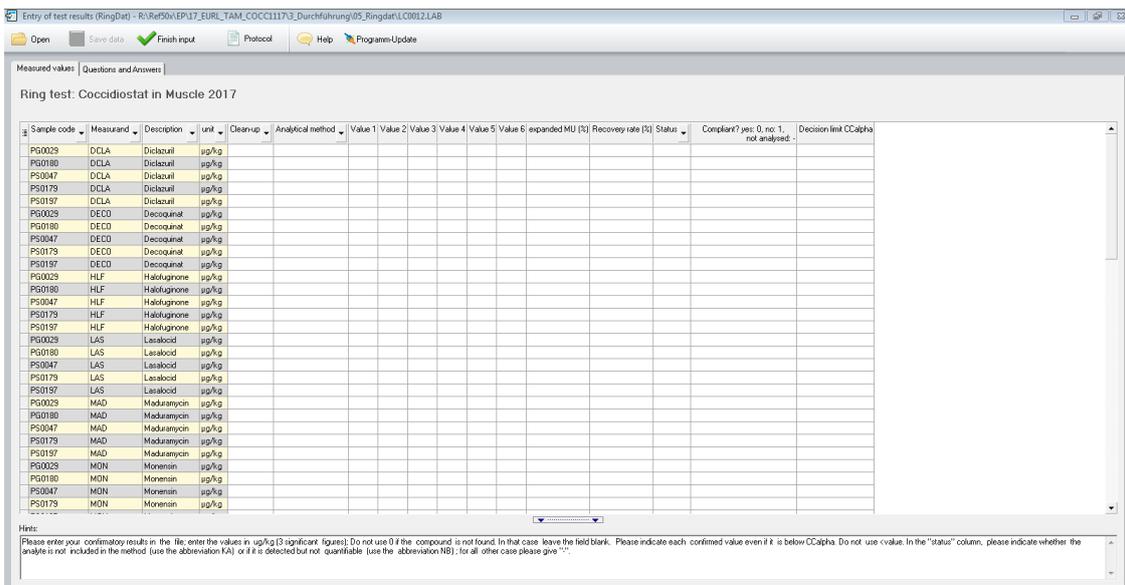
**Since this file cannot be sent by e-mail, please download it from the FIS-VL or find it at:**

**[https://quodata.de/fileadmin/RingDat/ringdat4\\_en.exe](https://quodata.de/fileadmin/RingDat/ringdat4_en.exe).**

When executing the file “RingDat4.exe”, the following window will open:



By clicking on “open” you can open your **\*\*\*.LAB** file.



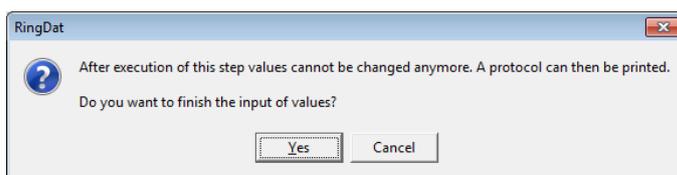
On the “measured values” page please enter your data. On the “questions and answers” page additional information on your method is requested.

| No. | Cue                          | Question   | Answer   |
|-----|------------------------------|--|--|
| 1   | Sample amount                | Please indicate the sample amount per reconstituted sample   | <input type="checkbox"/> < 2 g<br><input type="checkbox"/> 2 g<br><input type="checkbox"/> 2 to 4 g<br><input type="checkbox"/> 4 to 6 g<br><input type="checkbox"/> total amount<br><input type="checkbox"/> No<br><input type="checkbox"/> Yes   |
| 2   | Hydrolysis                   | Hydrolysis   | <input type="checkbox"/> Protease<br><input type="checkbox"/> Glucuronidase<br><input type="checkbox"/> Glucuronidase/arylsulfatase<br><input type="checkbox"/> mineralic acid<br><input type="checkbox"/> other   |
| 3   | If Hydrolysis ?              | If Hydrolysis ?  | <input type="checkbox"/> Ultrasonic bath<br><input type="checkbox"/> Shaker<br><input type="checkbox"/> Vortex<br><input type="checkbox"/> Medialash homogenizer<br><input type="checkbox"/> Other   |
| 4   | Extraction method            | which extraction method was used ?   | <input type="checkbox"/> organic solvent<br><input type="checkbox"/> aqueous solvent<br><input type="checkbox"/> acetonitril<br><input type="checkbox"/> methanol<br><input type="checkbox"/> water<br><input type="checkbox"/> ethylacetate<br><input type="checkbox"/> buffer<br><input type="checkbox"/> addition of acid<br><input type="checkbox"/> other |
| 5   | Extraction solution          | Which extraction solution did you use ?  |  |
| 6   | Duration of extraction       | How long did you extract the sample ?  | <input type="radio"/> 1<br><input type="radio"/> 2<br><input type="radio"/> > 2  |
| 7   | Number of extractions        | How often did you extract your sample ?  |  |
| 8   | Extraction solution 2        | Which solvent did you use for the second (or more) extraction ? Please only answer, if you use a second (or more) extraction |  |
| 9   | Duration of the extraction 2 | How long did you extract the sample ? Please only answer, if a second (or more) extraction was carry out                     |  |
| 10  | Clean-up                     | Which clean-up did you use ? Please give detailed listing of the steps   | <input type="checkbox"/> No clean up<br><input type="checkbox"/> SPE<br><input type="checkbox"/> Dissipative SPE<br><input type="checkbox"/> LLE<br><input type="checkbox"/> defatting<br><input type="checkbox"/> Low temperature<br><input type="checkbox"/> other   |
| 11  | Kind of calibration          | Kind of calibration ?  | <input type="checkbox"/> standard calibration (solvent)<br><input type="checkbox"/> matrix calibration<br><input type="checkbox"/> matrix matched calibration<br><input type="checkbox"/> standard addition<br><input type="checkbox"/> use of internal standard   |

### **Please note:**

- If you did not detect a compound, leave the field blank.
- Enter the values in  $\mu\text{g}/\text{kg}$  (3 significant figures). Use “.” as a decimal separator.
- Please enter each confirmed result, even if it is below  $\text{CC}\alpha$ . If you detected an analyte, but could not confirm it, you can enter the result as “<value of  $\text{CC}\alpha$ ”. If you do not wish to report the result, leave the field blank.
- The field “ $\text{CC}\alpha$ ” is mandatory for all minimum required and recommended analytes. In case any of those analytes are not included in your method, please enter “<0”.
- **Take care to also respond to the questions in the “Questions and Answers” Tab!**

After your data have been entered, you can save the data and preview the protocol. If the data are correct, click “finish input” and the data are fixed.



**Please print out the protocol as pdf-file, sign it and send it together with your two RingDat files (**\*.LA2 and \*.LAB**) to [eurlvetdrug@bvl.bund.de](mailto:eurlvetdrug@bvl.bund.de) (i.e. **3 files altogether**).**

**For screening results you will receive a separate paper form.**

If you have any questions or difficulties, please do not hesitate to contact us!