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# DatLab 7: innovations

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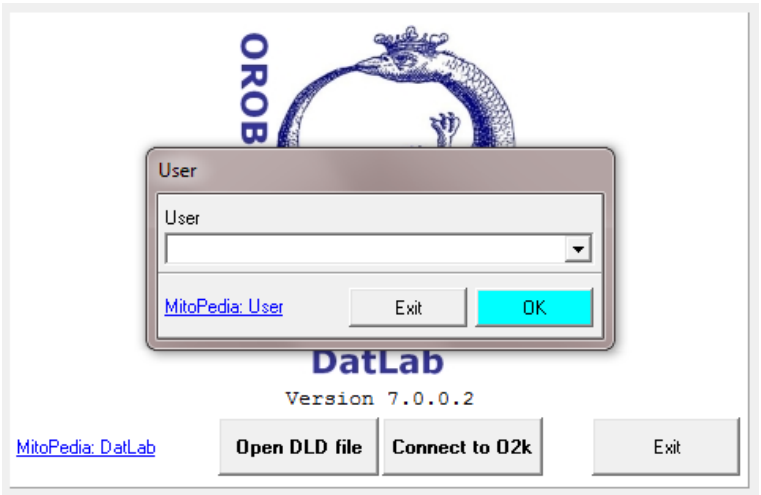
## Overview

DatLab 7 is a next step in high-resolution respirometry (HRR) incorporating user-friendly features on quality control, documentation, and traceability of measurement with the O2k (MitoFit). Conceptual unification is obtained in calibrations and flux analysis of O2k-MultiSensor channels, including normalization and baseline correction. Graphs are further improved for real-time display and publication.

## 1. General

### 1.1. User

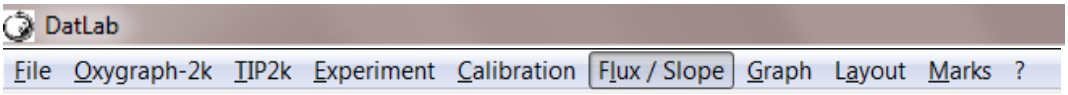



For better documentation and traceability, a user name has to be entered or selected ▾ after starting DatLab. The current user is displayed in the O2k signal line. User names are connected with personal graph layouts (see Layout menu).

**Change user:** When DatLab is connected to the O2k, the user can be changed under File \ Change user.

**Manage users:** Existing users can be renamed and deleted (with all connected graph layouts) under File \ Manage users.

### 1.2. Menus




New, user-friendly structure of menus: Flux/Slope as a separate window with new features (see Section 6).

### 1.3. Hyperlinks in DatLab windows

In many DatLab windows, a link to the OROBOROS website leads directly to context-sensitive help.

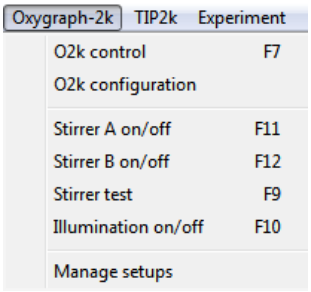
### 1.4. Event names

Event names are shown on top of the graph to avoid text overlaps with mark names.

### 1.5. Illumination

"Light" has been renamed to "Illumination" to distinguish it from the LED light introduced into the chambers in the O2k-Fluorometer.

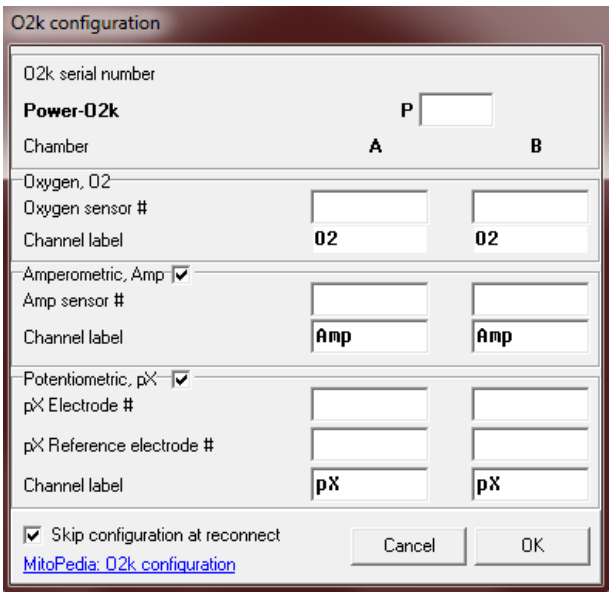
## 2. Oxygraph-2k




In the Oxygraph-2k menu, the "Show channel"-functions have been moved and an additional submenu [O2k configuration] added for a better overview.

**2.1. Data recording interval** The data recording interval can no longer be changed when the O2k is running. It has to be set when the O2k control window pops up at the beginning of an experiment.

### 2.2. O2k configuration window




In Oxygraph-2k\O2k configuration, channels (Amperometric, Amp ☑, Potentiometric, pX ☑) can be switched on/off by selecting the according tick box.

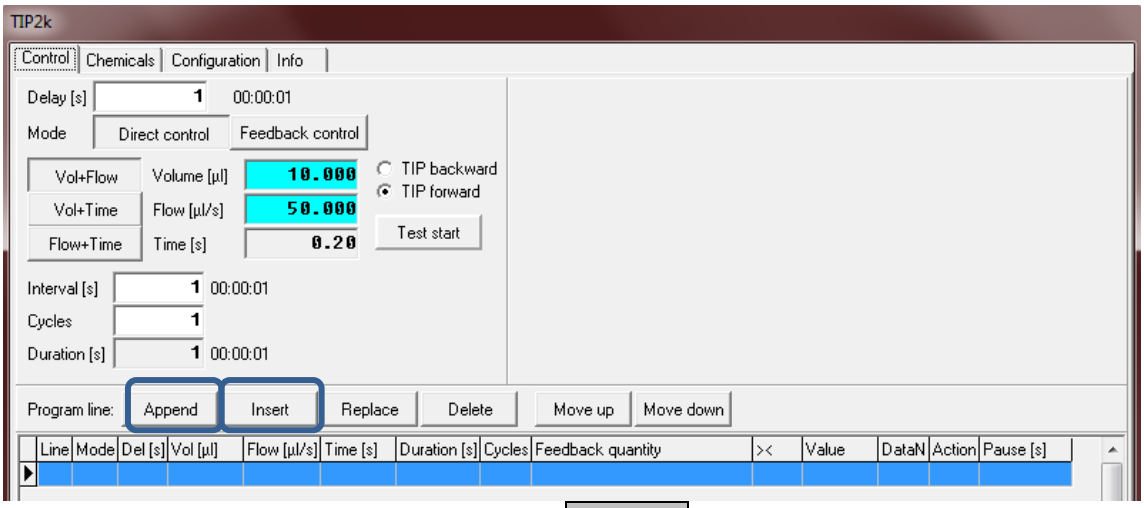
Power-O2k (P#) and numbers of Oxygen sensors, Amp sensors, pX electrodes and pX reference electrodes can be entered and edited. They are displayed in the O2k control window.

O2k configuration pops up automatically after connecting to the O2k.

☑ Skip configuration at reconnect If selected, O2k control pops up immediately when re-reconnecting to the O2k.

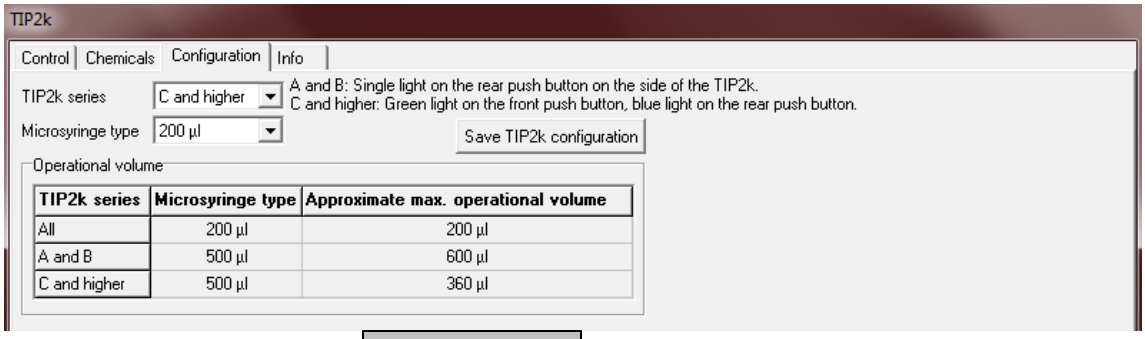
# 3. TIP2k

## 3.1. Insert/Append




A new button Append improves user-friendly programming of the TIP2k, for adding a new line at the end of the programme. Insert adds a new line at the selected position.

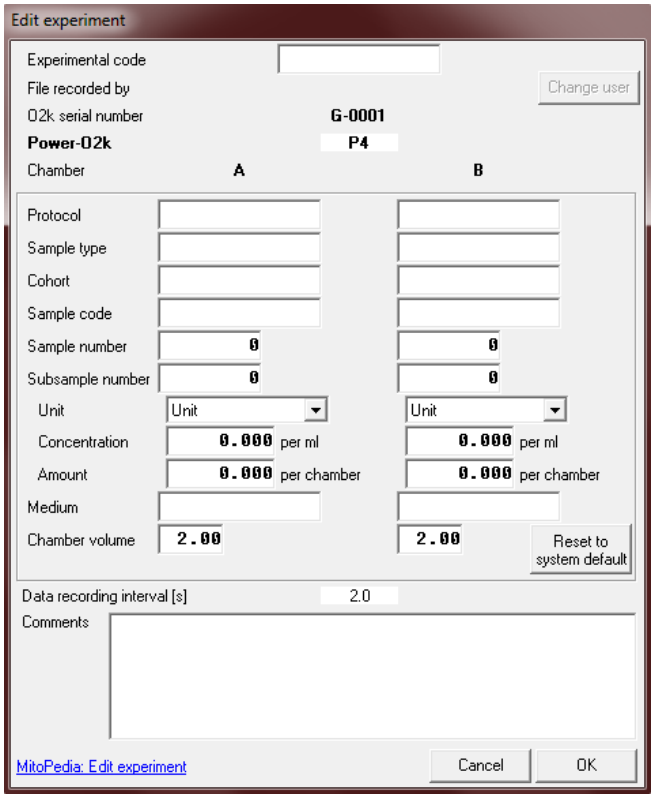
## 3.2. TIP2k configuration




The tab Configuration accommodates the TIP2k series and Microsyringe type. Based on this information, DatLab checks the total volume programmed in the Control tab and warns the user if the approximate maximum operation volume is exceeded.

# 4. Experiment

## 4.1. Edit experiment




The Edit experiment window is complemented with new entry boxes:

**File recorded by** (*automatically filled*)
**Protocol**: Protocol name
**Sample type**: former "Sample"
**Cohort**
**Sample code**
**Sample number**
**Subsample number**

Protocol and sample number are shown next to the graph (right side) above the displayed channel names.

L A double-click on Protocol name or Sample number opens the Edit experiment window.

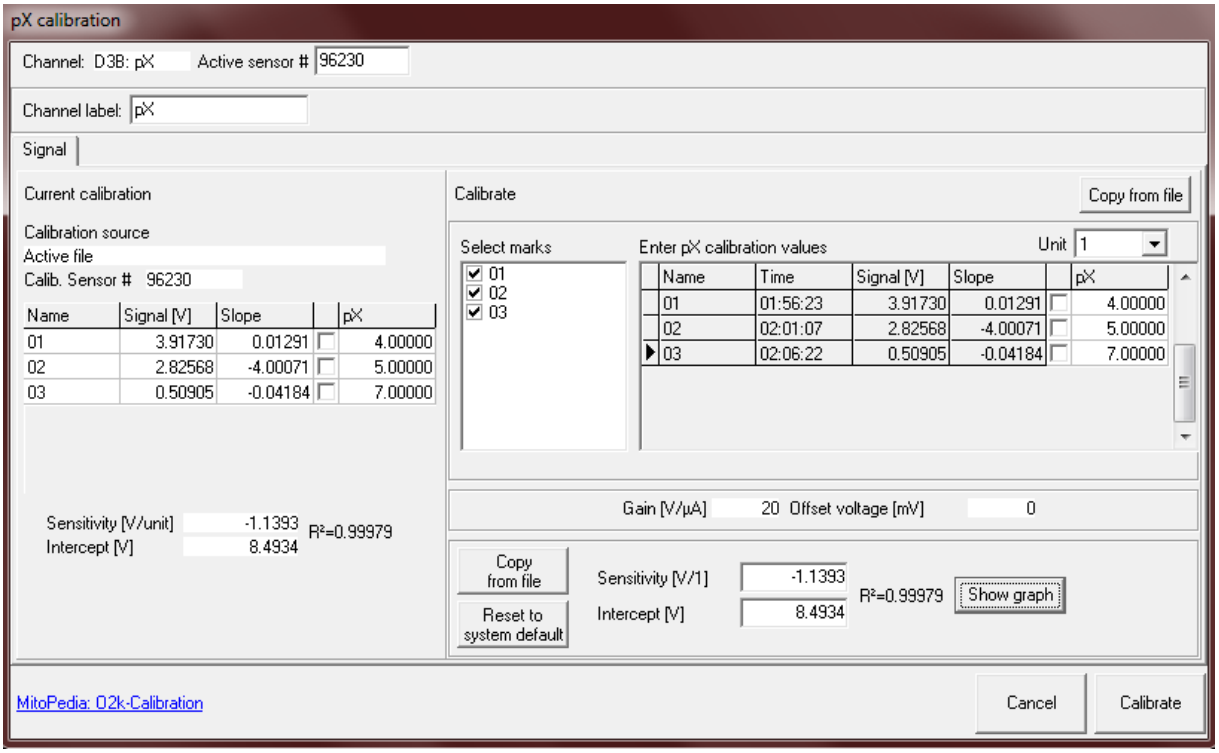

## 4.2. Experimental log

Experimental log replaces the name View protocol.

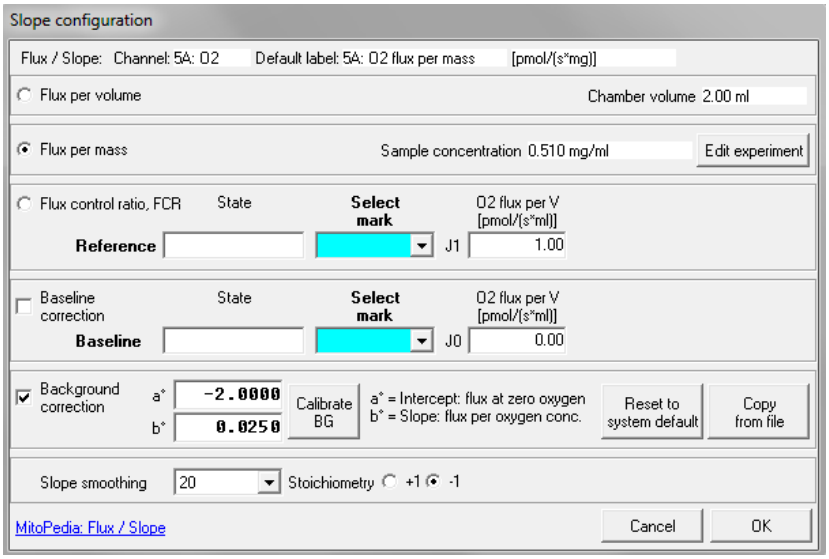
# 5. Calibration

## 5.1. Calibration of pX channel

- The new pX calibration window allows multipoint calibration, comparable to the Amp calibration window.
- Units for the calibrated pX signal and pX slope were updated, eg pH and mpH.




## 6. Flux/Slope

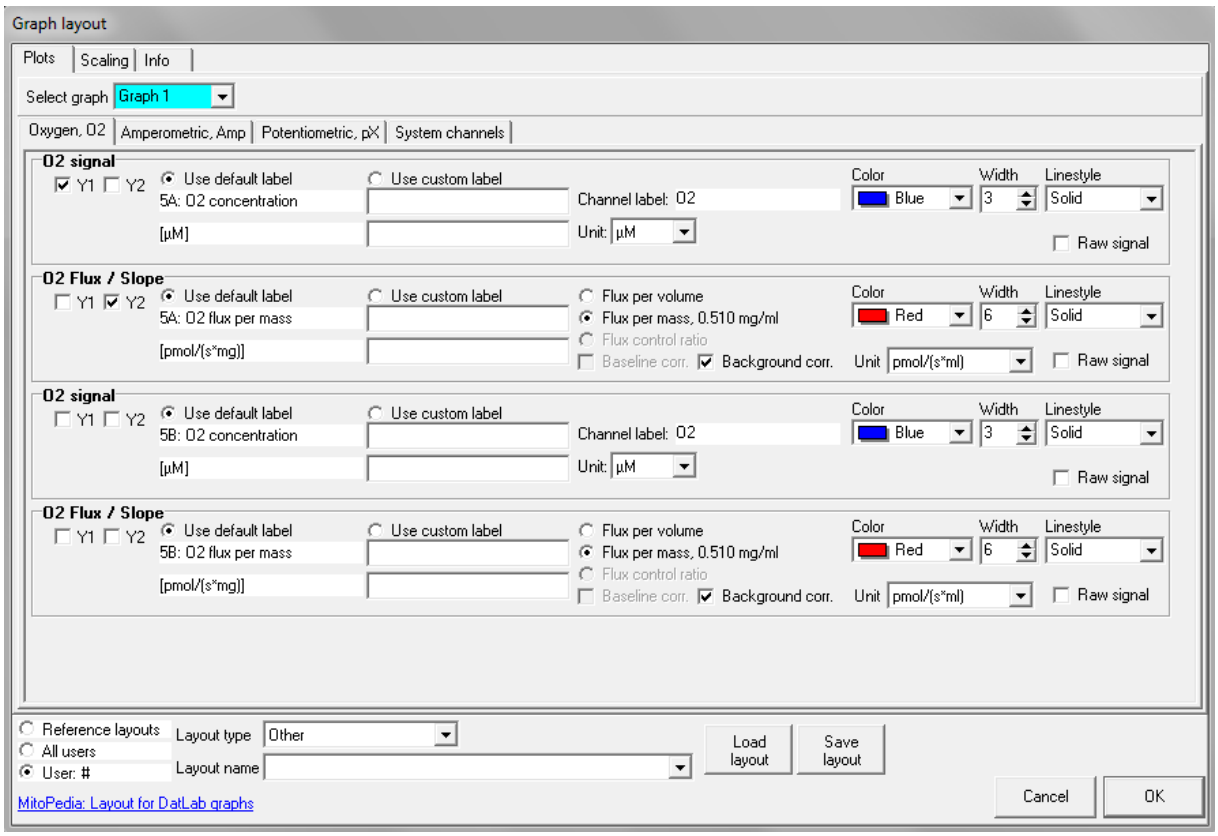



The previous tab Slope in the Calibration window has been moved to the new window Slope configuration selected for each O2k chamber and channel under the Flux/Slope menu. New features are added and selecting with the according radio button or tick box.

- ⊙ **Flux per volume**
- ⊙ **Flux per mass** or **Flow per cells**, depending on entries in the Edit experiment window, as displayed.
- ⊙ **Flux control ratio, *FCR***
- ☑ **Baseline correction** (*new*)
- ☑ **Background correction**
- ▾ **Slope smoothing**
- ⊙ **Stoichiometry** (*new*): default -1 for O2 and +1 for Amp and pX.

# 7. Graph

## 7.1. Select plots – Graph layout




The Graph \ Select plots window has been restructured and renamed as Graph layout.

In the tab Plots, channels are separated in different tabs. For each Graph, plots are selected with tick boxes for the *Y*-axes ☑ Y1 or ☑ Y2.

The axis default labels are changed automatically, according to the channel and unit. Signal units selected in Plots are independent of the units used for calibration.

To display the ☑ Raw signal, the tick box on the right side of the according channel has to be selected.

## 7.2. Custom label

In DatLab 7, users have the possibility to change the axis labels in [Graph/Select plots]. Two lines are available for entering a name and the according unit.

# 8. Layout

## 8.1. Layout structure

A new hierarchy for DatLab graph layouts is implemented by separation of the following **Layout categories:**

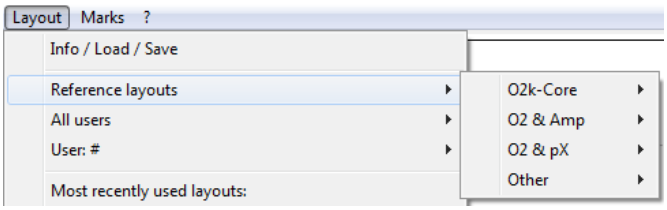
**Reference layouts** are provided with the installation package of DatLab 7. They cannot be changed or deleted, but it is possible to edit a reference layout and save it under a new name.

**All users** These layouts can be used and edited by all users.

**User: Name** These personal layouts can only be accessed and edited by the User defined upon starting DatLab.

For every layout category, the following **Layout types** are provided:

- **O2k-Core**
- **O2 & Amp**
- **O2 & pX**
- **Other**

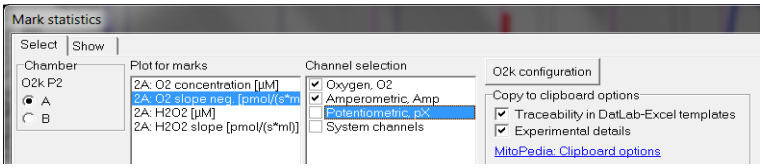



## 8.2. Most recently used layouts

The last five layouts used are displayed in the menu Layout.

# 9. Marks

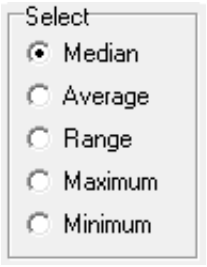
## 9.1. Mark statistics – Copy to clipboard options




☑ Experimental details are copied to clipboard as default in addition to Mark statistics information. Deselect the tick box for using older versions of DatLab-Excel templates.

☑ Traceabilit in DatLab-Excel templates is the default to show and export Flux/Slope values as uncorrected slopes (positive or negative) for traceability, where corrections and normalization are transparent on the basis of Experimental details. Deselect the tick box to show and copy the current values (e.g. flux per mass).

## 9.2. Mark statistics – Select

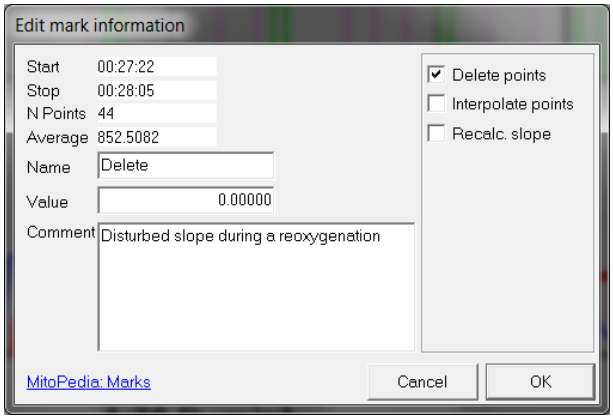



⊙ Median is exported as default (*new*) instead of the averages of values in the marks.

⊙ Range is an additional new export option.

## 9.3. Edit mark information window

The Edit mark information window (opened by a click on the mark bar) is complemented with three new functions:




☑ Delete points deletes all data points in the plot within the selected mark.

☑ Interpolate points interpolates all data points in the plot within the selected mark section from the last previous to the first following data point.

☑ Restore points reverses data deletion or interpolation in a signal plot within the marked section.

☑ Recalc slope recalculates the slope for an entire Flux/Slope plot, thus reversing all data deletions or interpolations in this plot.

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**The joy of success is the next step**

# Supplement

## A. Author contributions

[1]software security networks – ssn, Innsbruck. LG is the programmer of DatLab 7 and all previous DatLab versions and contributed to the concept of quality control in DatLab 7. External consultant of the MitoFit project.

[2]Universitätsklinik für Visceral-, Transplantations- und Thoraxchirurgie, D. Swarovski Forschungslabor, DSL, Medizinische Universität Innsbruck; [3]OROBOROS INSTRUMENTS. EG contributed to the concept of DatLab 7 and all previous DatLab versions, edited the final version of this MiPNet publication, and edited complementary websites (help) on the OROBOROS-Bioblast homepage. MitoFit project leader.

[3]OROBOROS INSTRUMENTS. OC was mainly responsible for trouble shooting of test versions from DatLab 6 to DatLab 7 and contributed to writing this MiPNet publication.

[4]Biozentrum Innsbruck - Sektion für Bioinformatik, SBI, Medizinische Universität Innsbruck. CP wrote this MiPNet publication and edited complementary websites (help) on the OROBOROS-Bioblast homepage (MitoFit project partner Univ.-Prof. Dr. Zlatko Trajanoski).

## B. Acknowledgements

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