# Analysing growth curves and other user-defined plates in opm

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#### Abstract

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Keywords: Growth Kinetics.

### 1. Introduction

## 2. Preparation

```
R> if ("package:opm" %in% search())
         detach("package:opm", unload = TRUE)
R> library("opm")
```

## 3. growth curve data input

In the following we will use the growth-measurements data set from Vaas, Marheine, Sikorski, Göker, and Schumacher (2013) as exemplar.

The **opm** package contains a number of functions suitable for accessing precomputed information on entire plates and on the substrates within certain wells.

Currently substrate layouts of various plates are available within **opm**. An overview of the plate types available in the respective version of **opm** is obtained by entering

```
R> plate_type(full = TRUE)
```

The resulting vector of names does not only include OmniLog® plates; see the manual and the main tutorial for further details. Using other values for full, or additional arguments, distinct spelling variants of the plate names can be obtained.

### 4. visualisation

- 4.0.1. Finding substrates within pathways
- 4.0.2. Visualisation of differences of group means in pathway maps

## 5. Finding the pathways of interest

## 6. Acknowledgements

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#### References

Vaas LAI, Marheine M, Sikorski J, Göker M, Schumacher HM (2013). "Impacts of pr-10a Overexpression at the Molecular and the Phenotypic Level." *International Journal of Molecular Sciences*, 14, 15141–15166. doi:10.3390/ijms140715141. URL http://www.mdpi.com/1422-0067/14/7/15141.

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