

- *Supplemental Information* –

## **PaDuA: a Python library for high-throughput (phospho)proteomic data analysis**

*Anna Ressa<sup>1‡</sup>, Martin Fitzpatrick<sup>1‡</sup>, Henk van den Toorn<sup>1</sup>, Albert J.R. Heck<sup>1</sup> & Maarten Altelaar<sup>1\*</sup>*

<sup>1</sup> Biomolecular Mass Spectrometry and Proteomics Group, Bijvoet Center for Biomolecular Research and Utrecht Institute for Pharmaceutical Science, Utrecht University, Padualaan 8, 3584 CH Utrecht, The Netherlands

<sup>‡</sup> These authors contributed equally.

\* To whom correspondence should be addressed: [m.altelaar@uu.nl](mailto:m.altelaar@uu.nl)

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## Supplementary Figure

**Figure S-1.** Example of a DataFrame generated with panda in Jupyter to combine the identification data with the quantified values from the phosphoproteomics experiment. This multi-index table contains a list of 25 quantified phosphosites with multiplicity 1 (rows) corresponding to the control samples (columns) at the timepoint 0 for 3 biological replicates and 18 technical replicates.

## Supplementary References

1. de Graaf, E. L.; Giansanti, P.; Altelaar, A. F. M.; Heck, A. J. R. Single-Step Enrichment by Ti<sup>4+</sup>- IMAC and Label-Free Quantitation Enables in-Depth Monitoring of Phosphorylation Dynamics with High Reproducibility and Temporal Resolution. *Mol. Cell. Proteomics* **2014**, *13* (9), 2426–2434.
2. Smit, M. A.; Maddalo, G.; Greig, K.; Raaijmakers, L. M.; Possik, P. A.; Van Breukelen, B.; Cappadona, S.; Heck, A. J.; Altelaar, A. M.; Peeper, D. S. ROCK1 Is a Potential Combinatorial Drug Target for BRAF Mutant Melanoma. *Mol Syst Biol* **2014**, *10*.