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Intelligent workflows for automated analysis of mass spectrometry-based proteomics data

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Citation

Güler, A. T. (2022, April 7). *Intelligent workflows for automated analysis of mass spectrometry-based proteomics data*. Retrieved from <https://hdl.handle.net/1887/3281870>

Version: Publisher's Version

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Note: To cite this publication please use the final published version (if applicable).

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ISBN: 978-94-6423-731-3

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Cover design: Arzu Tuğçe Güler

Printing: ProefschriftMaken.nl

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Proefschrift

ter verkrijging van
de graad van doctor aan de Universiteit Leiden,
op gezag van rector magnificus prof.dr.ir. H. Bijl,
volgens besluit van het college voor promoties
te verdedigen op donderdag 7 april 2022
klokke 11.15 uur

door

Arzu Tuğçe Güler
geboren te Ankara, Turkije in 1988

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Ars longa, vita brevis

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