AssayMAP Bravo User Group Meeting

23 - 24 April 2026, Zagreb

Agenda

23 April - Morning session

08:30 a.m. - 09:00 a.m.	Arrival
09:00 a.m. - 09:15 a.m.	Welcome
09:15 a.m. - 12:00 p.m.	Choice of below workshops • **VWorks basic training outside workbench – write your own basic VWorks protocols** Anthony Zerlin, Agilent Technologies • **Tips and tricks on AssayMAP: Fill your own cartridges / re-use cartridges.** Steve Murphy, Agilent Technologies and Mario Cindric • **Evotip loading protocol and other field developed protocols – SP3/12 column fractionation.** Nicolas Mouton, Agilent Technologies • **Basic JavaScript in VWorks: Add in variables to your form edited protocol** Mauro Cremonini, Agilent Technologies
12:00 p.m. - 13:00 p.m.	Lunch

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23 April - Afternoon session

13:00 p.m. - 13:15 p.m.	Welcome: Anthony Zerlin, Agilent Technologies
13:15 p.m. - 13:45 p.m.	**2D micro-SPE chromatography of peptides and proteins on AssayMAP** Mario Cindric, Ruder Boskovic Institute, Zagreb
13:45 p.m. - 14:15 p.m.	**Harnessing new tools for old challenges: Optimising neat plasma proteomics with the Bravo AssayMAP** Colleen Maxwell, University of Leicester
14:15 p.m. - 14:45 p.m.	**Optimized automated workflow for BioID improves reproducibility and identification of protein–protein interactions** Emilio Cirri, Leibniz Institute on Aging – FLI, Jena
14:45 p.m. - 15:15 p.m.	Coffee break
15:15 p.m. - 15:45 p.m.	**TPTM proteomics on the AssayMAP Bravo platform, glycation and phosphorylation enrichment for low and standard input samples** Christine Schaeffer
15:45 p.m. - 16:15 p.m.	**Automated SP3 sample preparation for proteomics across diverse biological matrices on the AssayMAP Bravo** Berta Cillero Pastor
16:15 p.m. - 16:45 p.m.	**Speed up your targeted peptide MRM method development with the Agilent automation tool in Skyline** James Waddington, Agilent Technologies
16:45 p.m. - 17:00 p.m.	**Wrap up and outlook for 2027** Anthony Zerlin, Agilent Technologies

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24 April - Morning session

08:30 a.m. - 08:55 a.m.	Arrival
08:55 a.m. - 09:00 a.m.	Welcome: Anthony Zerlin, Agilent Technologies
09:00 a.m. - 09:30 a.m.	**Update AssayMAP technology tips and tricks** Steve Murphy, Agilent Technologies
09:30 a.m. - 10:00 a.m.	**nanoPhos enables ultra-sensitive and cell-type resolved phosphoproteomics** Denys Oliinyk, Max-Planck-Institute for Biochemistry, Martinsried
10:00 a.m. - 10:30 a.m.	**Deep plasma proteomics of 50,000 samples: A scalable, biologically validated workflow for population health** Vincent Albrecht, Max-Planck-Institute for Biochemistry, Martinsried
10:30 a.m. - 11:00 a.m.	Coffee break
11:00 a.m. - 11:30 a.m.	**Automation of a perchloric acid workflow for plasma proteomics using the Agilent Bravo** Dr. Dan Lane, University of Leicester
11:30 a.m. - 12:00 p.m.	**Robust semi-automated LC/MS/MS quantification using stable isotope labelled peptides** Kevin Hau, ISAS, Dortmund
12:00 p.m. - 12:30 p.m.	**Optimization of Fe-IMAC based phospho peptide enrichment workflows for platelets** Gina Piontek, ISAS, Dortmund
12:30 p.m. - 12:45 p.m.	**Wrap up and outlook for 2027** Anthony Zerlin, Agilent Technologies
13:00 p.m.	End of user group meeting 2026

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