Here is a selection of the latest papers by BMSS members:-

A proteomic investigation into mechanisms underpinning corticosteroid effects on neural stem cells

Al-Mayyahia, R.S, Sterioc.L.D., Connolly, J.B., Adams, C.F., Al-Tumah W.A. , Jon Sen, Emes R.D., , Hart, S.R., Chari D.M. doi.org/10.1016/j.mcn.2017.11.006

This paper describes the characterisation of the impact of corticosteroid treatment on the pluripotency of neural stem cells.

Complementary Imaging of Silver Nanoparticle Interactions with Green Algae: Dark-Field Microscopy, Electron Microscopy and Nanoscale Secondary-Ion Mass Spectrometry

Sekine, R., Moore, K., Matzke, M., Vallotton, P., Jiang, H., Hughes, G. M., Kirby, J. K., Grovenor, C. R. M., Svendsen, C. & Lombi, E. ACS Nano. 11, 10894-10902 (2017)

Increasing use of engineered nanomaterials means we must understand their impact on the environment and living organisms. Currently, no individual technique can provide all the necessary information in complex biological systems, so complementary imaging approaches are needed to understand "bio-nano" interactions. Here a multimodal imaging approach was used incorporating dark-field light microscopy, high resolution electron microscopy and nanoscale secondary ion mass spectrometry (NanoSIMS).

Identification of a novel site of interaction between ataxin-3 and the amyloid aggregation inhibitor polyglutamine binding peptide

1, P. D. Knight, T. K. Karamanos, Radford S. E., Ashcroft, A. E. Eur. J. Mass Spectrom. 24, (1), 129–140 (2018) doi rg/10.1177/1469066717729298

The neurodegenerative condition Machado–Joseph disease is characterised by self-aggregation of the protein ataxin-3. Ataxin-3 contains a globular N-terminal Josephin domain, which can aggregate into protofibrils, and a disordered C-terminal domain including a polyglutamine stretch. Upon expansion of the polyglutamine region above 50 residues, ataxin-3 undergoes a second stage of aggregation in which long, straight amyloid fibrils form. Here, inhibition of ataxin-3 fibril formation using a peptide is demonstrated.

Determination of the Biocide Econea® in Artificial Seawater by Solid Phase Extraction and High Performance Liquid Chromatography Mass Spectrometry

Downs R.A., Dean J.R., Downer A. and Perry J.J. Separations 4, 34 (2017) doi:10.3390/separations4040034 http://www.mdpi.com/data/covers/separations/big_cover-separations-v4-i4.png

Econea®, or 4-bromo-2-(4-chlorophenyl)-5-(trifluoromethyl)-1H-pyrrole-3-carbonitrile, is an environmentally friendly anti-fouling compound used in the immersed coatings of commercial sea-going vessels. This paper reports the development of a new analytical method to directly detect it in an artificial sea water matrix using LCMS, and to then investigate the biocide's release from painted surfaces immersed in artificial sea water over a 45-day period.

Connecting color with assembly in the fluorescent B-phycoerythrin protein complex.

A.C. Leney, A. Tschanz, A.J.R. Heck. The FEBS Journal. 285 (1), 178-187 (2018,).

B-phycoerythrin is the most

fluorescent naturally occurring protein known to date. Here, we investigate the species that contribute to B-phycoerythrin's colour and the factors that give B-phycoerythrin its highly fluorescent properties using a combination of high-resolution native MS and fluorescence spectroscopy. Together, the data provide structural insights into the structural properties of B-phycoerythrin which is beneficial for its use within the biotechnology industry.

Characterization of the Proteome of Theobroma cacao Beans by Nano-UHPLC-ESI MS/MS

Scollo, E., Neville, D., Oruna-Concha, M.J., Trotin, M., Cramer, R. Proteomics. 27. (2017) doi: 10.1002/pmic.201700339. [Epub ahead of print]

This work is the first attempt to characterize the whole cocoa bean proteome by nano-UHPLC-ESI MS/MS analysis using tryptic digests of cocoa bean protein extracts. The results of this analysis show that >1000 proteins could be identified using a species-specific Theobroma cacao database. A comparison of MS/MS data searches carried out against larger non-specific databases confirmed that using a species-specific database can increase the number of identified proteins, and at the same time reduce the number of false positives.

Historical mystery solved: A multi-analytical approach to the identification of a key marker for the historical use of brazilwood (Caesalpinia spp.) in paintings and textiles

Peggie, D., Kirby, J., Poulin, J., Genuit, W., Romanuka, J., Wills, D.F., De Simone, A., Hulme, A.N., Analytical Methods 10, 617–623 (2018) doi.org/10.1039/C7AY02626A

Using a combination of synthesis, UPLC-ESI-MS/MS, HPLC, NMR and GC-MS, we have confirmed that the benzochromenone, urolithin C, is the marker component used to detect brazilwood-based colourants in historical objects. The paper shows that it is a reliable reference compound across a range of analytical techniques employed in the cultural heritage sector and will enable the future development of non-destructive techniques for its identification on high-status objects.

Peptide Selection for the Quantification of P-III-NP in Human Serum by Mass Spectrometry.

Moncrieffe D, Parkin MC and Cowan D. doi: 10.1002/rcm.8066.

Recognising the need for a MS method to analyse P-III-NP, a biomarker for growth hormone used in doping control tests, we have initiated the development of a quantitative bioassay. Through partial characterisation of the tryptic digest protein, suitable peptides were selected and used to develop nano- and micro-flow LC-MS methods capable of analysing human P-III-NP at basal serum levels.

Collision-induced dissociation of doubly-charged barium-cationized lipids generated from liquid samples by atmospheric pressure matrix-assisted laser desorption/ionization provides structurally diagnostic product ions

Hale O. J., Cramer R. Bioanal. Anal. Chem. 410, 1435-1444 (2018) doi:10.1007/s00216-007-0788-6

Doubly charged metal-cationised phospholipids were generated from liquid samples, using a custom atmospheric pressure matrix-assisted desorption/ionisation (AP-MALDI) source. The source was attached to a Waters Synapt G2-Si mass spectrometer. The ability to obtain enhanced structural information by collision-induced dissociation (CID), in-source decay (ISD) and ion mobility-enabled time-aligned parallel (TAP) fragmentation is demonstrated.

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