

QCAL: a one stop standard for HPLC and MS

Calibration standards for MS instrumentation are typically commercially available peptides. PolyQuant has designed QCAL for use in the optimisation and standardisation of all commonly used instrumentation platforms for proteomics.

QconCATs are artificial proteins, that comprise a concatenation of proteolytic peptides (1). QCAL is a QconCAT that has been designed specifically for the calibration of the commonly used instrumentation platforms in proteomics.

Calibration of HPLC separations and MS instruments

Calibration standards for MS instrumentation are typically commercially available peptides. PolyQuant has designed a QconCAT for use in the optimisation and standardisation of all commonly used instrumentation platforms for proteomics. QCAL is a QconCAT (52.2kDa), comprising 22 unique peptides, ranging from ~ 410-3100Da. QCAL was designed to provide standards for peptide separation by reversed-phase chromatography, to facilitate the assessment and optimisation of instrument resolution and to evaluate the linearity of signal detection in different MS instruments, including MALDI-ToF, ESI MS and FTICR (2). QCAL also comprises peptides containing amino acid residues subject to modification (oxidation of methionine, deamidation of gln/asn) and modification of lysine residues by guanidination (3), allowing the routine monitoring of these processes.

Digestion of QCAL

Efficient digestion by trypsin is crucial to the use of QCAL as a calibration standard. QCAL is a protein comprising up to six repeat Q-peptide sequences, nevertheless QCAL is readily digested to completion under standard tryptic digestion conditions and since QCAL can be readily produced in large amounts QCAL can be made readily available for use in the proteomics community allowing the definition of instrument performance and data reproducibility in large studies.

References

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- 3) Brancia, F.L. et al. A combination of chemical derivatisation and improved bioinformatic tools optimises protein identification for proteomics. *Electrophoresis* 22, 552-559 (2001).

