EUPA OPEN PROTEOMICS

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DESCRIPTION

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INTRODUCTION
EuPA Open Proteomics is published by Elsevier on behalf of the European Proteomics Association (EuPA) and is aimed at both European and international protein scientists.

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**Additional information**

**Standard abbreviations**

Standard abbreviations allowed to be used without explanation or definition.

A absorbance
ACES 2-[(2-amino-2-oxoethyl)amino] ethanesulphonic acid
CAN acetonitrile
A/D analog to digital converter
AEBSF 4-(2-aminoethyl)benzenesulphonyl fluoride
amu atomic mass unit
ANOVA analysis of variance
API atmospheric pressure ionization
AUC area under curve
Bis N,N'-methylenedisacrylamide
bp base pairs
BSA bovine serum albumin
%C cross-linking agent (g/100 mL)/%T
CAPS 3-(cyclohexylamino)-1-propanesulphonic acid
CBB Coomassie Brilliant Blue
CCD charge-coupled device
CD circular dicroism
CE capillary electrophoresis
CEC capillary electrochromatography
CFE continuous flow electrophoresis
CHAPS 3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulphonate
CHCA 2-cyano-4-hydroxycinnamic acid
CHES 2-(N-cyclohexylamino)ethanesulphonic acid
CID collision-induced dissociation
CIEF capillary isoelectric focusing
CMC critical micelle concentration
Con A Concanavalin A
IT ion trap
iTRAQ isobaric tag for relative and absolute quantitation
kbp kilobase pairs
kDa kilodalton (molecular mass)
LC liquid chromatography
LED light-emitting diode
LOD limit of detection
LOQ limit of quantitation
mAb monoclonal antibody
MALDI-MS matrix-assisted laser-desorption ionization-mass spectrometry
Mbp megabase
MEKC micellar electrokinetic capillary chromatography
MES 2-(N-morpholino)ethanesulphonic acid
MHC major histocompatibility complex
MOPS 3-(N-morpholino)propanesulphonic acid
Mr relative molecular mass (dimensionless)
MS mass spectrometry
MS/MS tandem mass spectrometry

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