



Universiteit
Leiden
The Netherlands

Multi-level approaches for the proteoform characterization of therapeutic antibodies by mass spectrometry

Grunert, I.F.K.

Citation

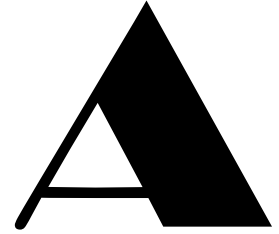
Grunert, I. F. K. (2023, May 17). *Multi-level approaches for the proteoform characterization of therapeutic antibodies by mass spectrometry*. Retrieved from <https://hdl.handle.net/1887/3618392>

Version: Publisher's Version

License: [Licence agreement concerning inclusion of doctoral thesis in the Institutional Repository of the University of Leiden](#)

Downloaded from: <https://hdl.handle.net/1887/3618392>

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



APPENDICES

LIST OF ABBREVIATIONS

μg	microgram
μL	microliter
μm	micrometer
EDTA	ethylenediamine tetraacetic acid
IdeS	immunoglobulin G-degrading enzyme of <i>Streptococcus pyogenes</i>
Thr (T)	threonine
1D/ ¹ D	first dimension
Cys (C)	cysteine
2-AB	2-aminobenzamide
2D/ ² D	second dimension
2D-LC	two-dimensional liquid chromatography
2xLC1-bsAb1	bispecific antibody 1 incorporating two times LC1 instead of LC1-LC2 (LC1-HC1/LC1-HC2)
3D/ ³ D	third dimension
4D/ ⁴ D	fourth dimension
4D-LC	four-dimensional liquid chromatography
Å	angstrom
A	acidic (charge) variant
aa	amino acid
Ab	antibody
ACN	acetonitrile
ADC	antibody-drug conjugate
ADCC	antibody-dependent cellular cytotoxicity
ADCP	antibody-dependent cellular phagocytosis
AEX	anion-exchange chromatography
AP	acidic peak
AP	alkaline phosphatase
Asn (N)	asparagine
Asp (D)	aspartate
B	basic (charge) variant
BEH	ethylene bridged hybrid
BES	N,N-bis(2-hydroxyethyl)-2-aminoethanesulfonic acid
BLA	biologics license application
BP	basic peak
bsAb	bispecific Ab
c	concentration
CDC	complement-dependent cytotoxicity
CDR	complementarity-determining region
CE	capillary electrophoresis



CEX	cation-exchange chromatography
C _H (C _{H1} , C _{H2} , C _{H3})	constant domain of heavy chain
CHO	Chinese hamster ovary
CID	collision-induced-dissociation
C _L	constant domain of light chain
cm	centimeter
CMP	cytidine-5'-monophosphate
COVID-19	coronavirus disease 2019
CpB	carboxypeptidase B
CPP	critical process parameter
CQA	critical quality attribute
CSH	charged surface hybrid
Cterm-PN	C-terminal proline amide
CTM	co-translational modification
CV	column volume
D	deuterium
d	day
D ₂ O	deuterium oxide
Da	Dalton
deam/deamid	deamidated
DNA	deoxyribonucleic acid
DoE	design of experiment
DP	drug product
DS	drug substance
DTT	dithiothreitol
ECD	electron capture dissociation
ER	endoplasmic reticulum
ESI	electrospray ionization
ETD	electron transfer dissociation
FA	formic acid
Fab	antigen binding fragment
Fc	fragment crystallizable
FcRn	neonatal Fc receptor
FcγR	Fc gamma receptor
FDA	Food and Drug Administration
Fuc	fucose
g	gram
g	gravitational force
Gal	β-galactose
GalT	β1,4-galactosyltransferase
GlcNAc	N-acetylglucosamine

Gln (Q)	glutamine
Glu (E)	glutamic acid
gly	glycated
GMP	good manufacturing practice
Gua	guanidium chloride
h	hour(s)
H ₂ O ₂	hydrogen peroxide
HC	heavy chain
HCD	higher-energy collision induced dissociation
HCP	host cell protein
HDX	hydrogen/deuterium exchange
HEK293	human embryonic kidney 293 cells
HER2	human epidermal growth factor receptor 2
HILIC	hydrophilic interaction liquid chromatography
His (H)	histidine
HMW	high-molecular weight
HPLC	high-performance liquid chromatographic
IEX	ion-exchange chromatography
Ig	immunoglobulins
IgA	immunoglobulin A
IgD	immunoglobulin D
IgE	immunoglobulin E
IgG	immunoglobulin G
IgG1	immunoglobulin G subclass 1
IgM	immunoglobulin M
IMER	immobilized enzyme reactor
iso	isomerized
isoAsp	isoaspartic acid
IT	iontrap
IVGE	<i>in vitro</i> glycoengineering
kDa	kilodalton
kg	kilogram
L	liter
LC	light chain
LC	liquid chromatography
LC-MS	liquid chromatography mass spectrometry
LC-MS/MS	liquid chromatography coupled to tandem mass spectrometric analysis
LMW	low-molecular weight
Lys (K)	lysine
M	mol/L (molar)
<i>m/z</i>	mass-to-charge ratio



mAb	monoclonal antibody
MALDI	matrix assisted laser desorption ionization
MAM	multi-attribute monitoring
Man	mannose
mAu	milli-absorbance unit
mD	multidimensional
mD-LC-MS	multidimensional liquid chromatography coupled to mass spectrometry
MES	2-(N-morpholino) ethanesulfonic acid
Met (M)	methionine
mg	milligram
MHC	multiple-heart-cutting
min	minute(s)
mL	milliliter
mM	millimolar
mm	millimeter
MP	Main Peak
mRNA	messenger ribonucleic acid
MS	mass spectrometry
MS/MS	tandem mass spectrometry
MWCO	molecular weight cutoff
NANA	N-acetylneuraminic acid (sialic acid)
nm	nanometer
nM	nanomolar
ox	oxidation
PBS	phosphate buffered saline
PDVB	polystyrene divinylbenzene
pI	isoelectric point
PK	pharmacokinetics
pmol	picomole
PNGaseF	peptide <i>N</i> -glycosidase F
ppm	parts per million
PTM	post-translational modification
pyroGlu (pyrE)	pyroglutamate
Q	quadrupole
QC	quality control
RM	reference material
RPLC	reversed-phase liquid chromatography
rpm	rounds per minute
RSV	respiratory syncytial virus
RT	room temperature
RU	resonance units

s	second(s)
S1	monosialylated
S2	disialylated
SARS-CoV-2	severe acute respiratory syndrome coronavirus 2
SB	solvent bond
SCID	severe combined immunodeficiency
SDS	sodium dodecyl-sulfate
SDS-PAGE	sodium dodecyl-sulfate polyacrylamide gel electrophoresis
SEC	size-exclusion chromatography
SPR	surface plasmon resonance
SST	system suitability test
ST6	α 2,6-sialyltransferase
suc (Asu)	succinimide
TCEP	tris(2-carboxyethyl)phosphine
TIC	total ion current
TOF	time-of-flight
Tris	tris(hydroxymethyl)aminomethane
Trp (W)	tryptophan
U	unit(s)
UDP	uridine diphosphate
UPLC	ultra-performance liquid chromatographic
UV	ultraviolet
V _H	variable domain of heavy chain
VHS	valine-histidine-serine (N-terminal signal peptide)
V _L	variable domain of light chain
WCX	weak cation-exchange chromatography
XIC	extracted ion chromatogram

