

Identification and Quantitation of Host Cell Protein Impurities in Peptide Therapeutics Using Liquid Chromatography-Mass Spectrometry

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This presentation reflects the views of the author and should not be construed to represent FDA's views or policies

Outline

□ Introduction

- Overview of mass spectrometry (MS) usage in FDA approved peptide therapeutic NDAs
- Guidelines and methods for host cell protein (HCP) analysis

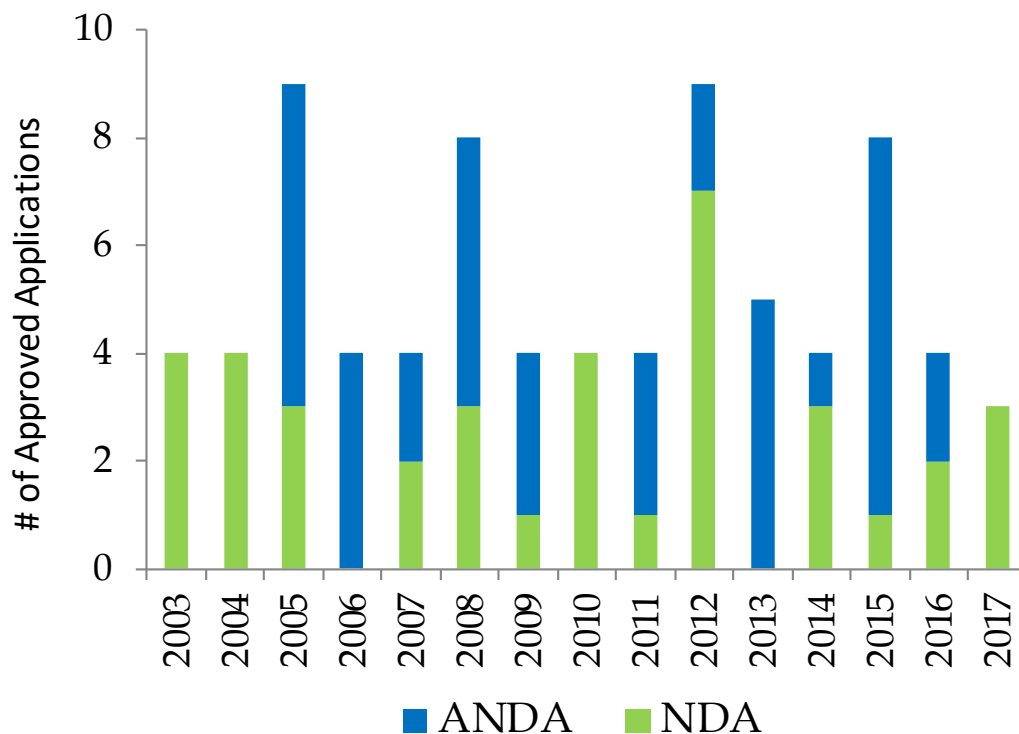
□ Results

- LC-MS/MS workflow for HCP characterization
- Identification and quantitation of HCP from teriparatide RLD

□ Conclusions and future work

Peptide Application Approvals

- 38 peptide NDAs and 40 peptide ANDAs have been approved by FDA since 2003.
- 10% were recombinant peptide products.
- 20 Type 1 NDAs (NME) were analyzed for MS usage.
- All NDAs used MS for characterization.



Manufacturing method	Percentage of Type 1 NDAs
SPPS alone	65%
SPPS and LPPS	15%
LPPS alone	10%
Recombinant	10%

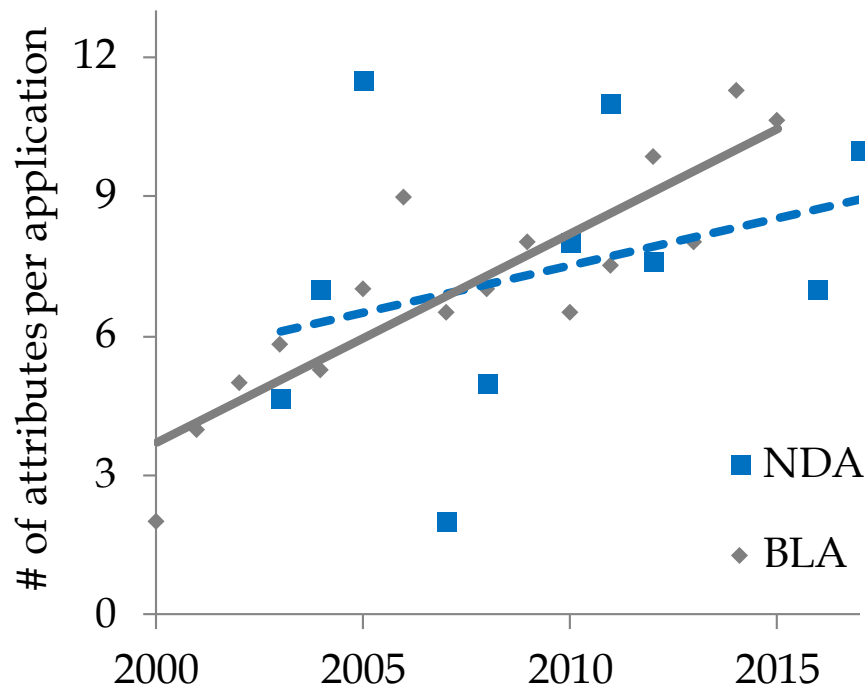
MS in Peptide Characterization

- 28 product quality attributes (PQAs) were monitored by MS.

MS Attribute	% of MS NME NDAs	MS Attribute	% of MS NME NDAs
Molecular weight	100%	Disulfide bonds	20%
Amino acid sequence	85%	Incomplete deprotection	20%
Amino acids deletion/insertion	60%	Dehydration	15%
Terminus modification	55%	Aggregation	10%
Racemisation/diastereomer	50%	Side chain modification caused by solvent	10%
Amino acid enantiomeric purity by GC-MS	45%	Cyclization	10%
Oxidation	45%	Residue solvent by GC-MS	10%
Metals	40%	Thioether	5%
Deamidation	40%	Free thiol	5%
Fragmentation/truncation	35%	Trisulfide	5%
Dimerization/trimerization	30%	PEGylation	5%
Succinimidation/Asu	30%	Palmitoyl	5%
Iso-Asp/beta-Asp	30%	Glycosylation	5%
Acetylation	25%	Mutation	5%

MS PQA Analysis

- A weak correlation was obtained for peptide NDAs ($R^2 = 0.10$), which is lower than that from protein BLA data ($R^2 = 0.77$).
- Similar mean numbers of MS attributes per NDA by manufacturing methods and peptide lengths.

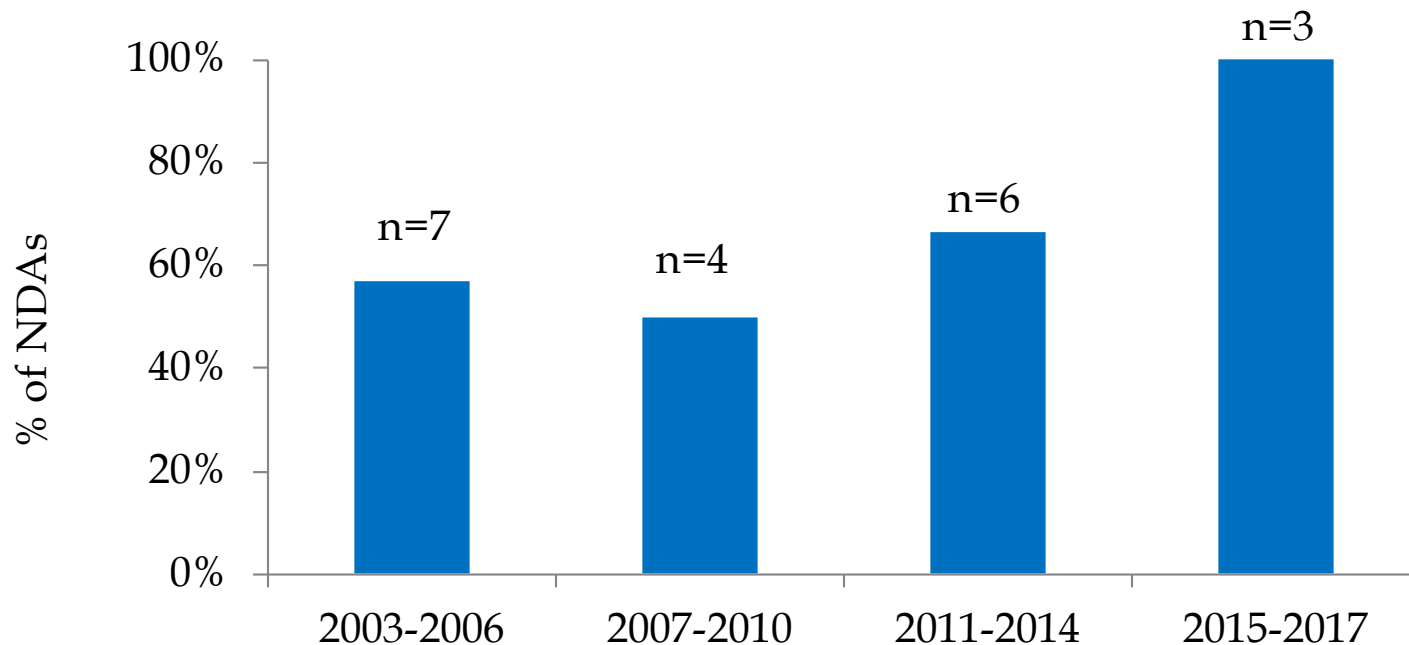


Manufacturing method	# of NDAs	MS attributes per NDA
SPPS alone	13	8.3
SPPS and LPPS	3	6.0
LPPS alone	2	6.0
Recombinant	2	6.5

Peptide length	# of NDAs	MS attributes per NDA
2 aa to 14 aa	8	7.5
15 aa to 29 aa	4	6.8
30 aa to 44 aa	8	8.0

MS in Peptide Quality Control

- MS is commonly used for peptide therapeutics in lot release.
- 65% of the 20 Type 1 peptide NDAs used MS as a release assay for molecular weight measurement.
- MS usage in QC is increasing over time.



HCP in Drug Development

- HCPs are process related impurities produced by the host organisms used to produce recombinant drug products.
- HCP are considered as critical quality attributes (CQAs), HCP associated risks may include:
 - Safety and efficacy of the drug product.
 - Immunogenicity
 - Specific biological activity
 - Product stability issues
- HCP are removed to the lowest feasible extent and HCP levels must be monitored in process and at release.
- Low ppm-level HCPs are typically present in DS/DP following purification processes.

Regulations on HCP



Regulators classify residual host cell proteins (HCPs) as “process-related impurities.” (US 21 CFR 610.13)

Whenever possible, contaminants introduced by recovery and purification process should be below detectable levels using a highly sensitive analytical methods.

- FDA CBER. Points to consider in the manufacture and Testing of Monoclonal Products for Human Use, Docket No. 94D-0259, Feb 28, 1997



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The ability of the purification process to remove other specific contaminants such as host-cell proteins ... should also be demonstrated...

... for HCP, whatever the product or production system, residual HCPs have to be tested for on a routine basis... Results from batch to batch should be consistent and meet specification limits.

-EMA guideline:CPMP/BWP/382/97



Regulator guidelines are in place globally (ICH Q6B 2.1.4, 4.1.3, 6.2.1)

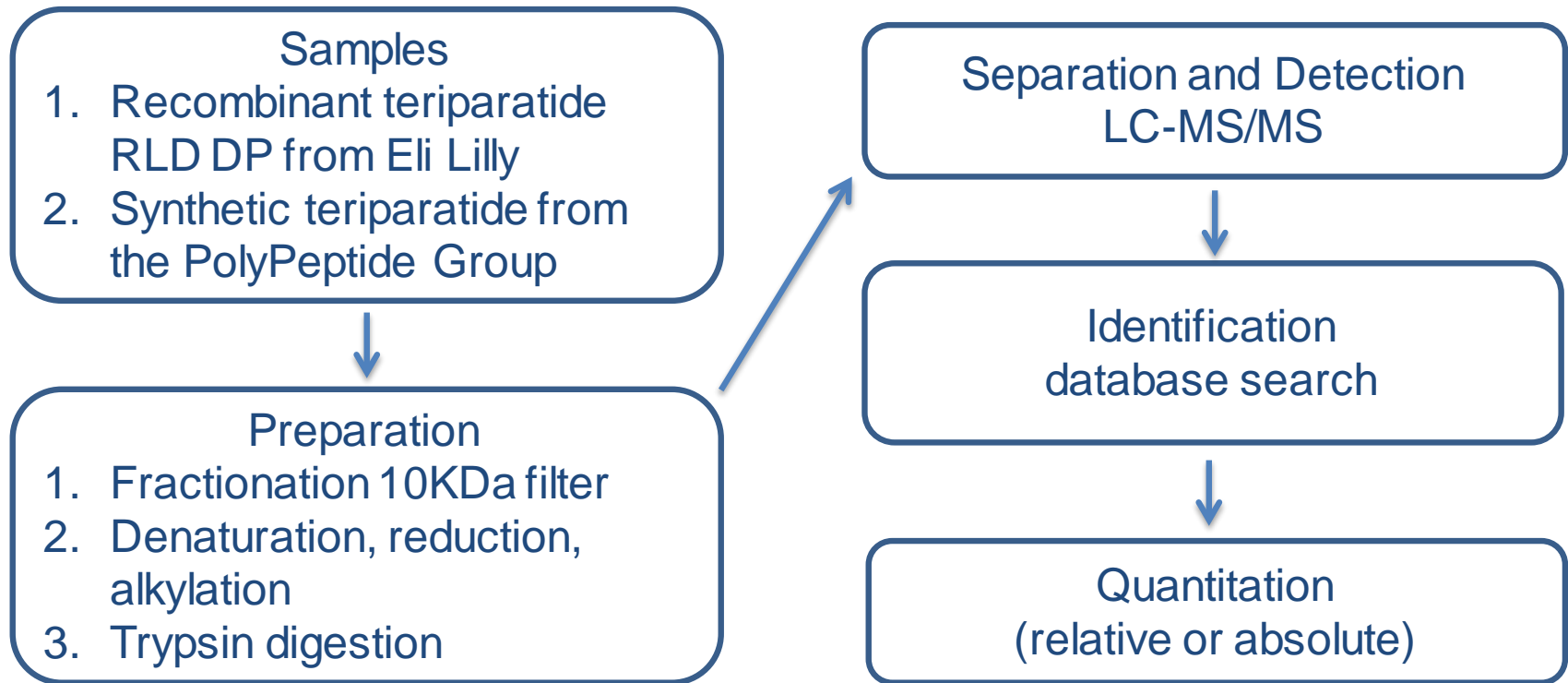
For host cell proteins, a sensitive assay – e.g. immunoassay – capable of detecting a wide range of protein impurities is generally utilized.

- ICH Q6B

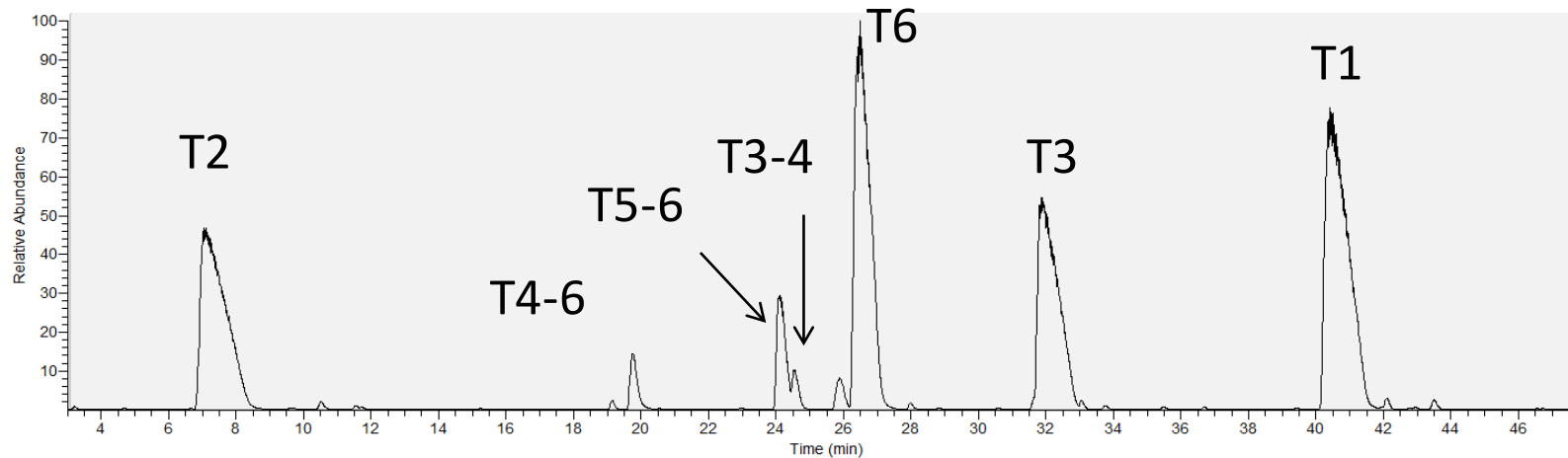
HCP Characterization Methods

Method	Strength	Weakness
SDS-PAGE /Silver stain	<ul style="list-style-type: none"> ➤ Good sensitivity (100pg/band) ➤ Resolves multiple components 	<ul style="list-style-type: none"> ➤ Subjective interpretation ➤ Not quantitative ➤ Technique-dependent
HPLC /UV- fluorescent	<ul style="list-style-type: none"> ➤ High resolution ➤ Quantitative 	<ul style="list-style-type: none"> ➤ Subjective interpretation ➤ Low sensitivity ➤ Non-specific
Western blot	<ul style="list-style-type: none"> ➤ High sensitivity (0.1-1ng/band) ➤ Semi-quantitative ➤ Immunological identity ➤ Resolves multiple components 	<ul style="list-style-type: none"> ➤ Antibody may fail to detect some contaminants ➤ Technique-dependent
ELISA (gold standard)	<ul style="list-style-type: none"> ➤ High sensitivity (1ppm) ➤ Semi-quantitative ➤ Easy to perform 	<ul style="list-style-type: none"> ➤ Objective endpoint ➤ Summed value ➤ Bias toward only immunoreactive species ➤ Not transferable (process related)
LC-MS/MS	<ul style="list-style-type: none"> ➤ Identification of individual HCPs ➤ High sensitivity (1ppm) ➤ Quantitative ➤ Process transferable ➤ Useful info for risk assessment 	<ul style="list-style-type: none"> ➤ Potential bias towards high abundant species ➤ Technique dependent ➤ Instrument high maintenance

LC-MS/MS Workflow for HCP Characterization



Peptide Map of Teriparatide



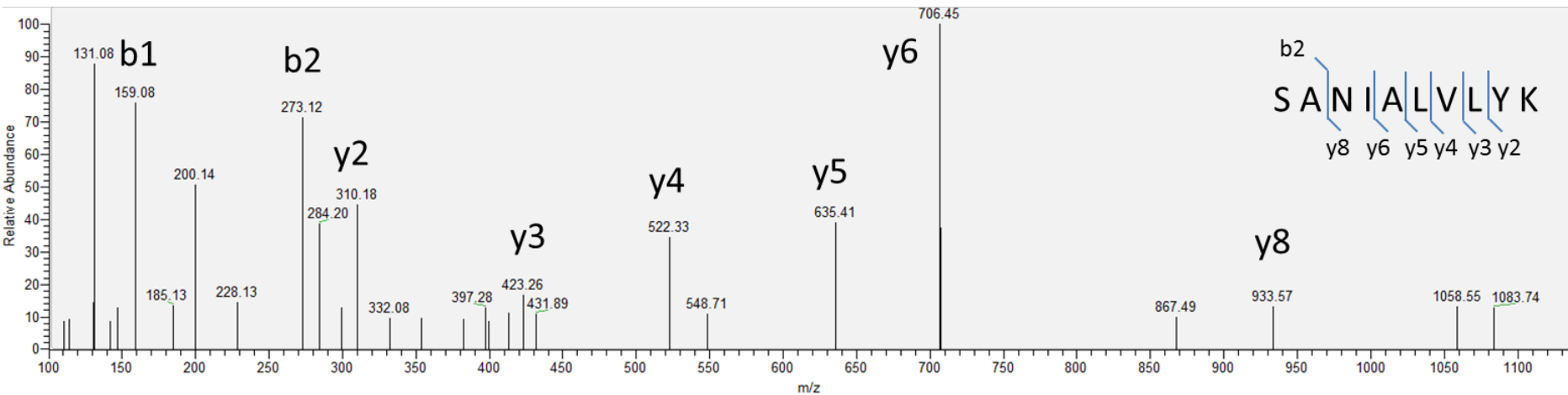
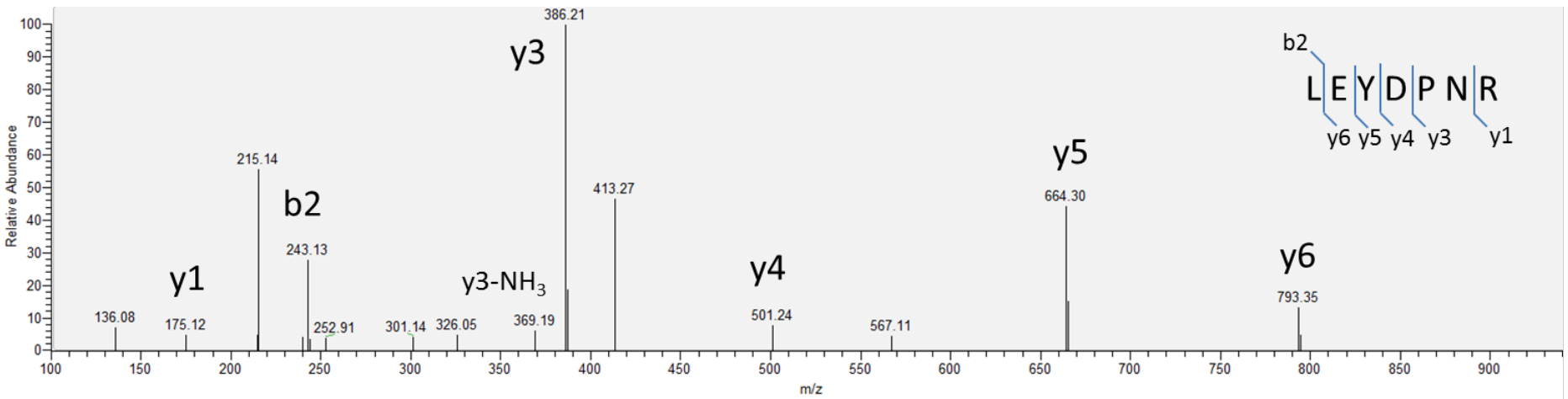
Name	Sequence	Start	End	Theoretical Mass MH+ (Da)	ΔM (ppm)
T1	SVSEQLMHNLGK	1	13	1455.7641	1.10
T2	HLNSMER	14	20	866.4236	4.03
T3	VEWLR	21	25	702.3923	-1.50
T6	LQDVHNF	28	34	872.4275	1.55
T5-6	KLQDVHNF	27	34	1000.5218	0.67
T4-6	KKLQDVHNF	26	34	1128.6181	1.80
T3-4	VEWLK	21	26	830.4889	0.65

HCPs in Teriparatide RLD

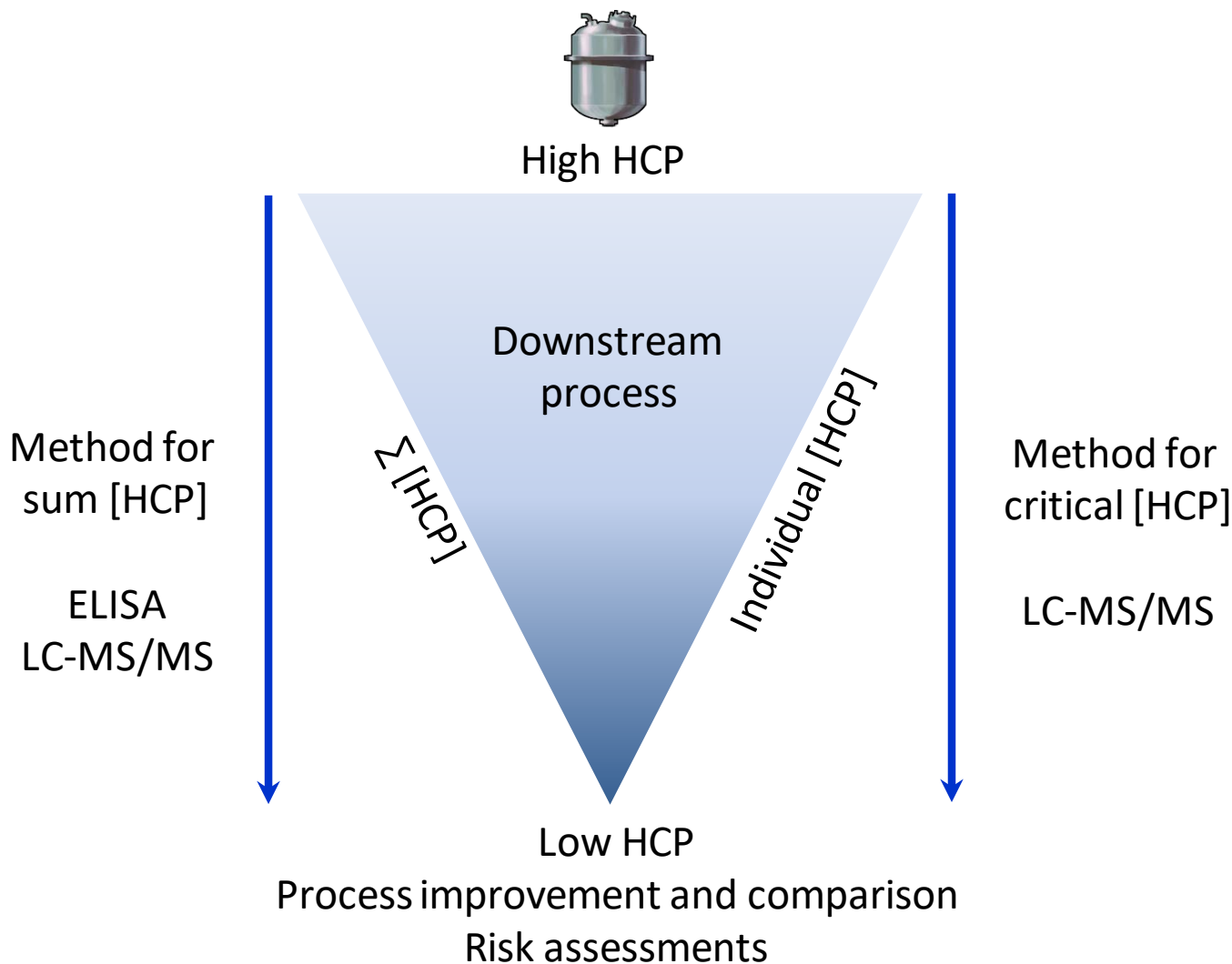
Accession	Description	Unique peptide sequence	PTM	MH+ (Da)	ΔM (ppm)	Rel Ratio (ppm)	
						RLD	Synthetic teriparatide
P60422	50S ribosomal protein L2	SANIALVLYK	N/A	1091.6480	1.86	27	0
		LEYDPNR	N/A	906.4328	1.31		
		NKDGIPAVVER	N/A	1197.6604	1.46		
P0A7M9	50S ribosomal protein L31	STVGHDLNLDVcSK	C12(IAM)	1544.7428	3.50	8	0
		YEEITAScScGNVMK	C8(IAM) C10(IAM)	1748.7253	-2.00		

- HCP fractionation (10KDa filter) and concentration increased the chance of low abundant HCP being identified by LC-MS method.
- Two E. Coli HCPs were identified with at least two unique peptides each in the concentrated HCP fraction of RLD teriparatide.
- Relative ratios of individual HCPs were quantitated.
- Those peptides were not present in commercial available synthetic teriparatide.
- MS/MS b y ion assignments to major peaks according to the sequences.

MS/MS Spectra of Peptides from 50S Ribosomal Protein L2



Future of HCP Characterization



Conclusions and Future Work

- Mass spectrometry is critical for peptide therapeutic characterization and quality control.
- HCP fractionation and concentration increased the identification of low abundant HCPs through LC-MS/MS.
- Two *E. Coli* HCPs were identified with at least two unique peptides each in the concentrated HCP fraction of the RLD teriparatide.
- Relative ratios of individual HCP were quantitated.
- Absolution quantitation and method validation are ongoing.
- This LC-MS/MS method will be applied to other recombinant peptide drug products for HCP characterization.

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