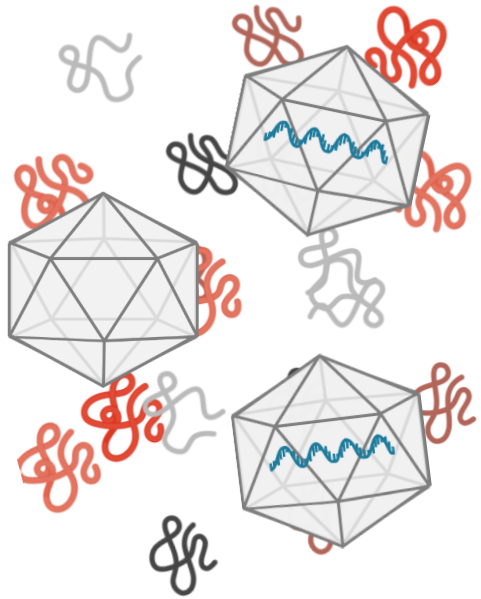
Characterising Viral Vectors for Gene Therapy using Mass Spectrometry on Different Levels

Josh Smith[1], Corentin Beaumal[1], Felipe Guapo[1], Lisa Strasser[1], Florian Füssl[1], Silvia Millán-Martín[1], Sara Carillo[1], Aaron Richardson[1], Colin Clarke[1,2] & Jonathan Bones[1,2]

[1]NIBRT, Foster Avenue, Mount Merrion, Blackrock, Co. Dublin, A94 X099, Ireland.
[2]School of Chemical and Bioprocess Engineering, University College Dublin, Belfield, Dublin 4, D04 V1W8, Ireland.

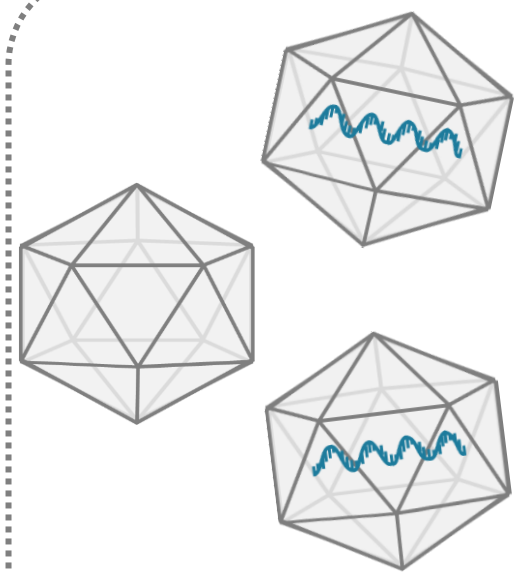
nibrt

Characterisation of AAV using Multiple Levels of Analysis



Host cell proteins:

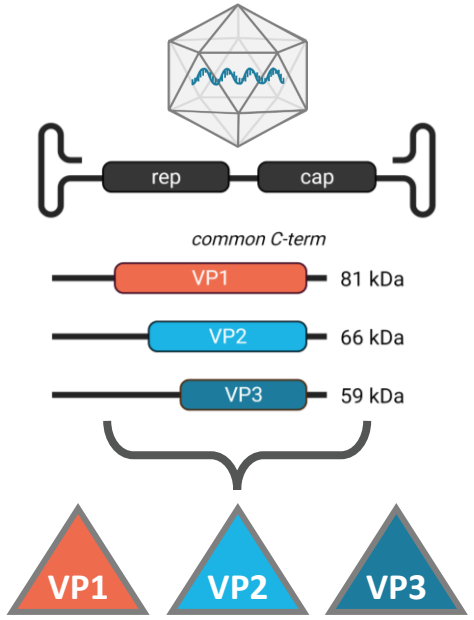
Determine and quantify residual process contaminants



Intact capsids:

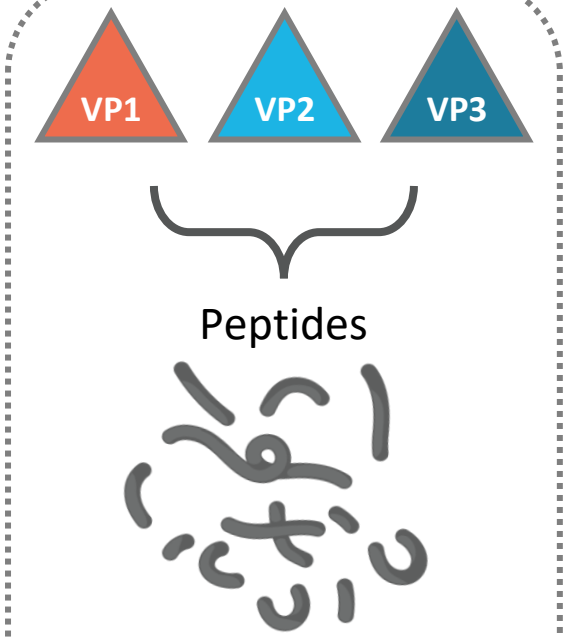
E:F ratio assessment

Determine fill state



Intact capsid proteins:

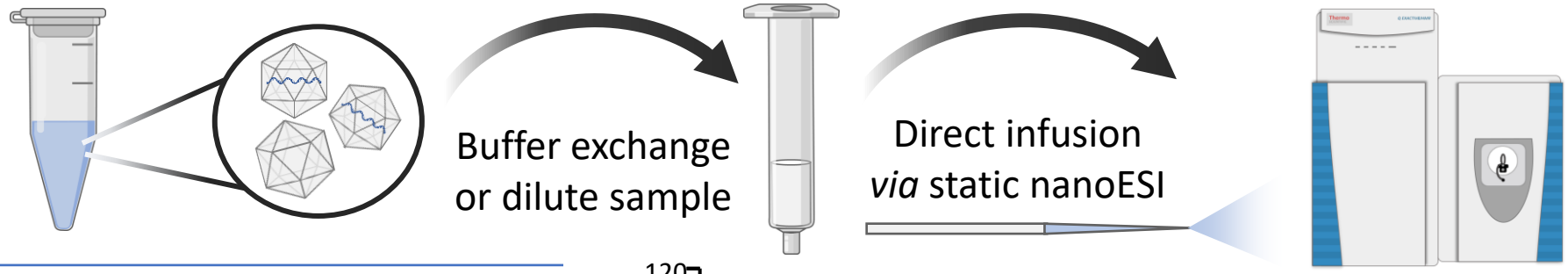
Determination of VP ratio → capsid stoichiometry



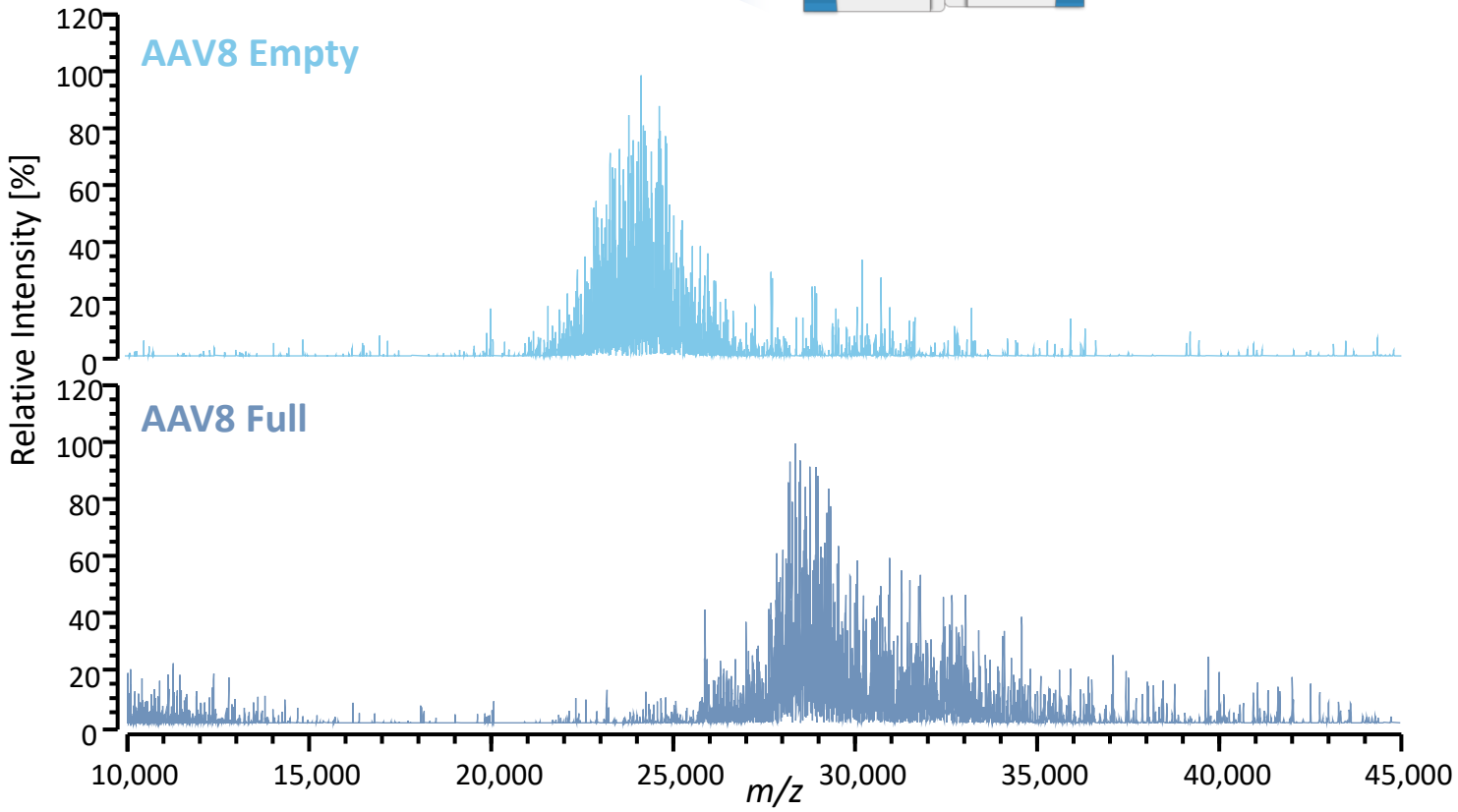
Peptide level:

Determination of AA sequence and PTM detection

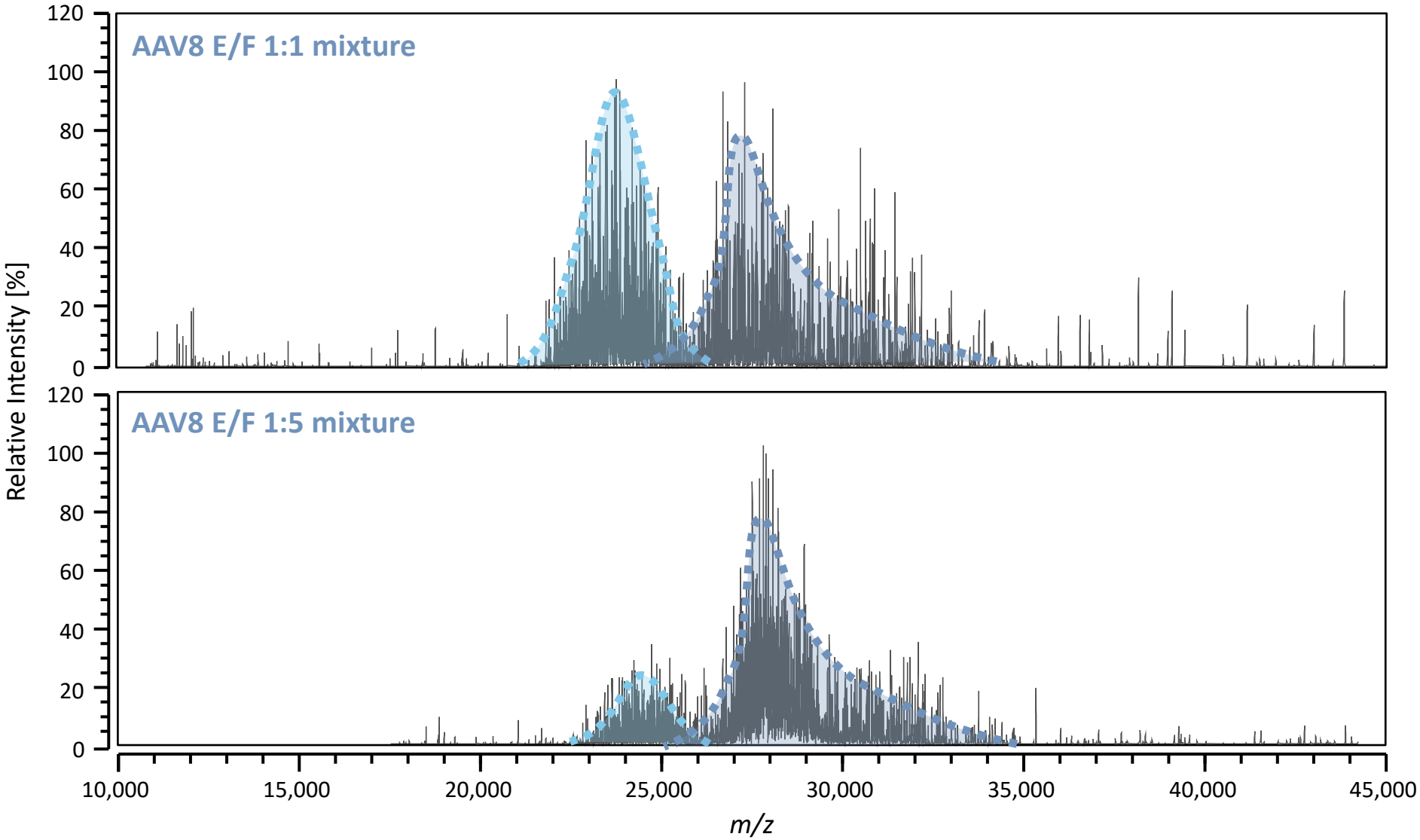
Capsid Fill State Assessment Using Native MS



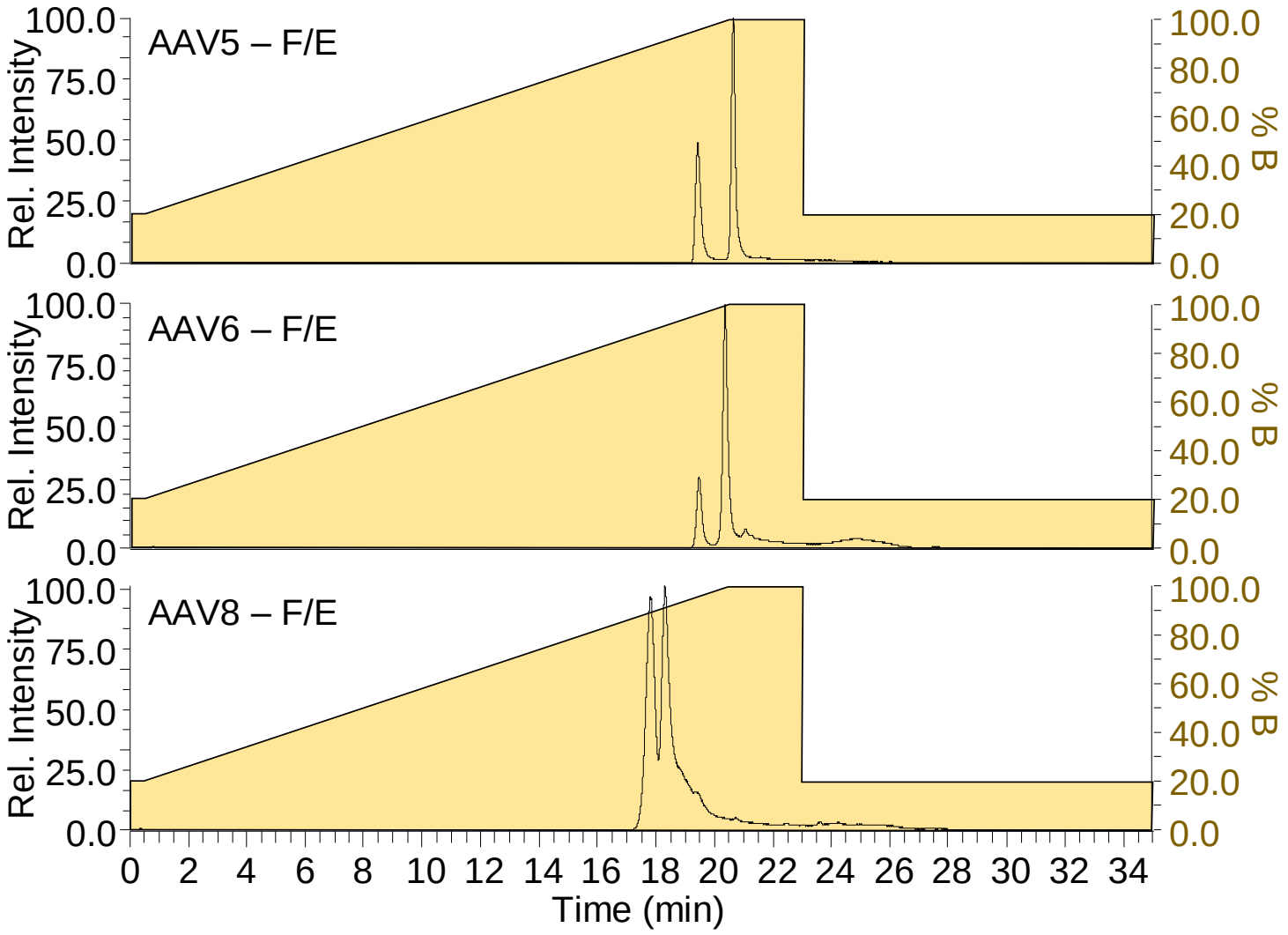
Thermo Q Exactive UHMR	Setting
Resolution	25,000 at m/z 200
Microscans	10
AGC Target	1e06
Max. IT	200 ms
In-source trapping	-100 V
Source DC offset	-50 V
Extended trapping	150 V
Trapping gas	SF_6 at 4e-10 mbar
Acquisition	5 mins with transient averaging enabled



Cluster Areas Correlate With Abundance of Capsid Species

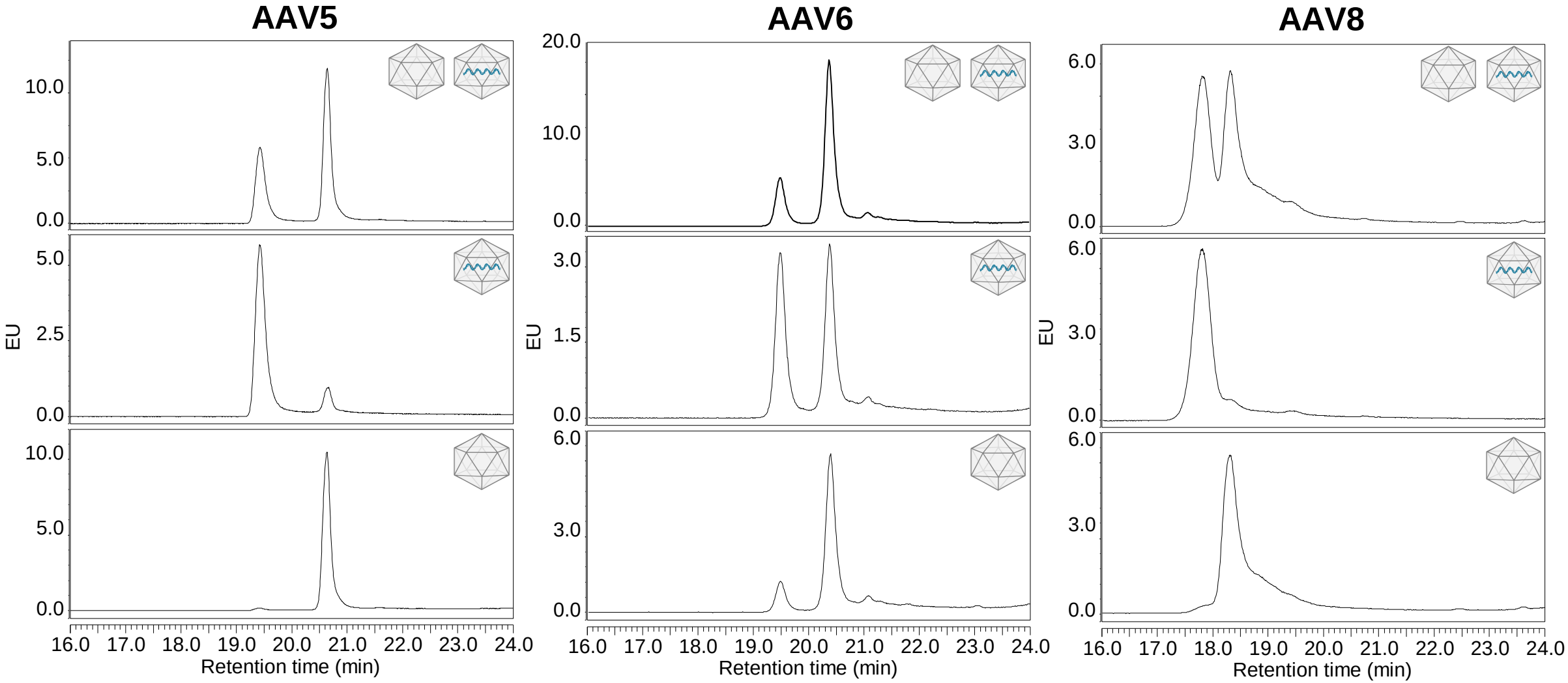


Coupling with Anion Exchange Chromatography

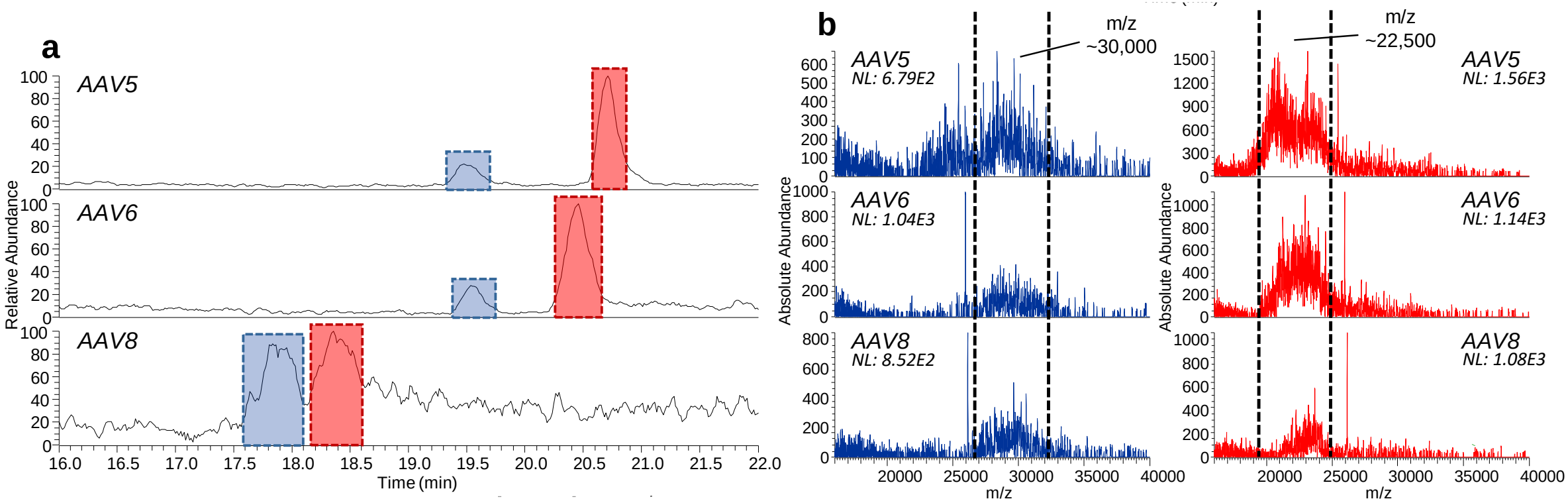


- pH gradient anion exchange separation of full and empty capsids using Thermo Scientific ProPac 3R AEX column.
- Gradient specifically designed to be generic for different serotypes and mass spectrometry compatible.
- pH gradients enable focusing effect, elution occurs when gradient pH = analyte pI, results in sharp chromatographic peaks.

Determination of Capsid Fill State Elution Order

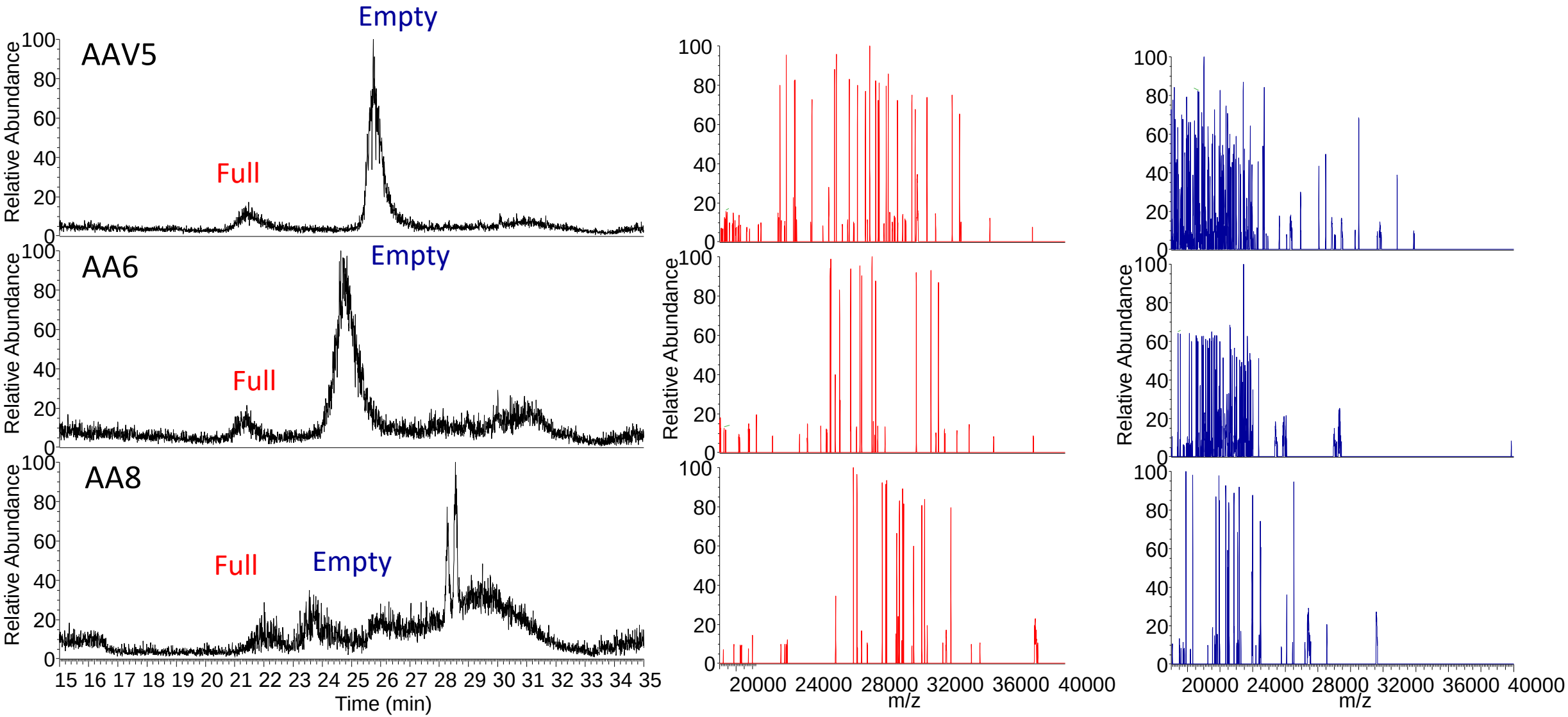


Coupling with Native MS Detection

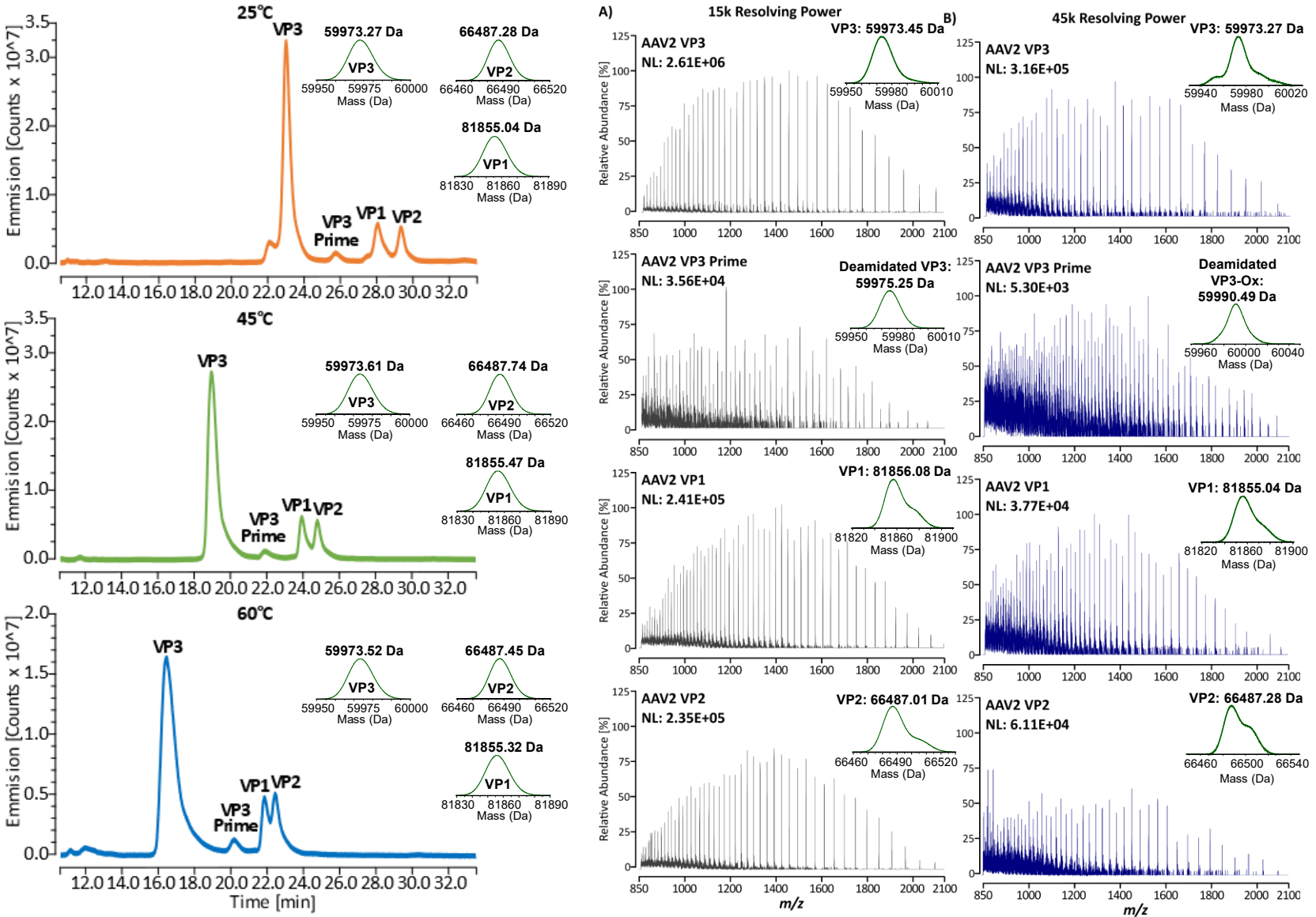


- pH gradient anion exchanged coupled directly to Thermo Scientific Q Exactive UHMR mass spectrometer for confirmation of capsid fill state species identification based on m/z.
- Assuming similar charge, earlier eluting peak contains heavier species explained by the presence of cargo DNA, additional mass of ~0.8 MDa corresponding to CMV-GFP.

Coupling CDMS with Front End F/E AEX Separation



Viral Protein Separation using LC-MS



- VP separation using hydrophilic interaction LC using an acetonitrile water gradient containing difluoro acetic acid as a mobile phase modifier.
- Fluorescence and MS detection using Thermo Scientific Orbitrap Exploris 240 MS with Biopharma Option.

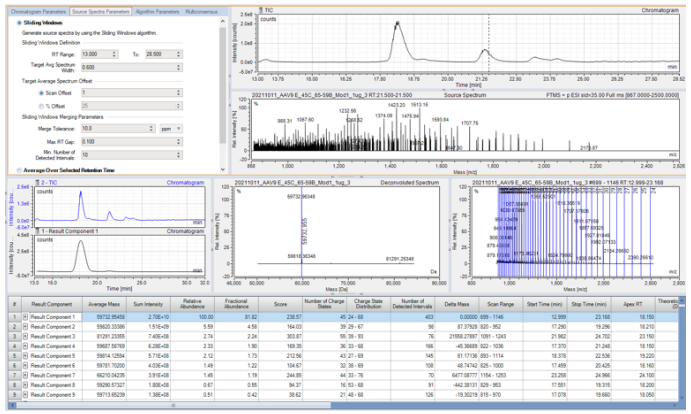
Method Translation into Rapid Identity Test

Component Identification

BioPharma Finder Software 4.1

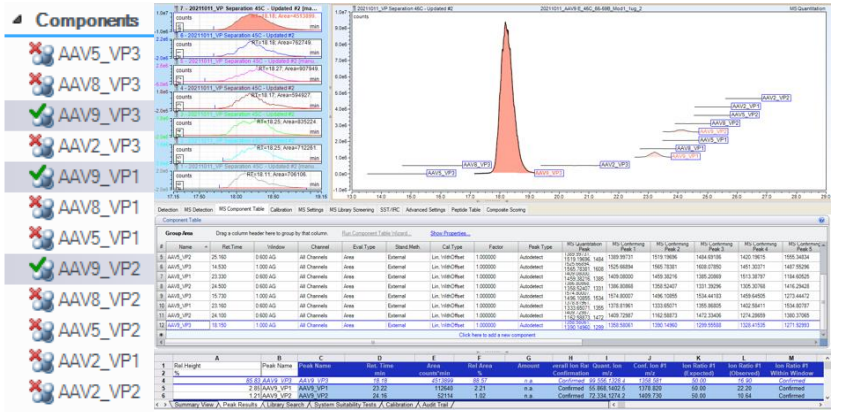
Processing Method and Component List Importation from BPF

Intact Protein Deconvolution



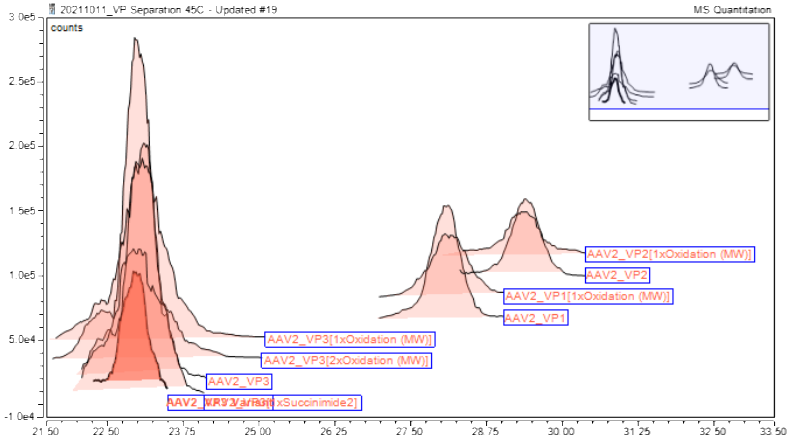
Serotype Profiling

Data Processing Parameter Optimization (Sf9 Derived AAVs)

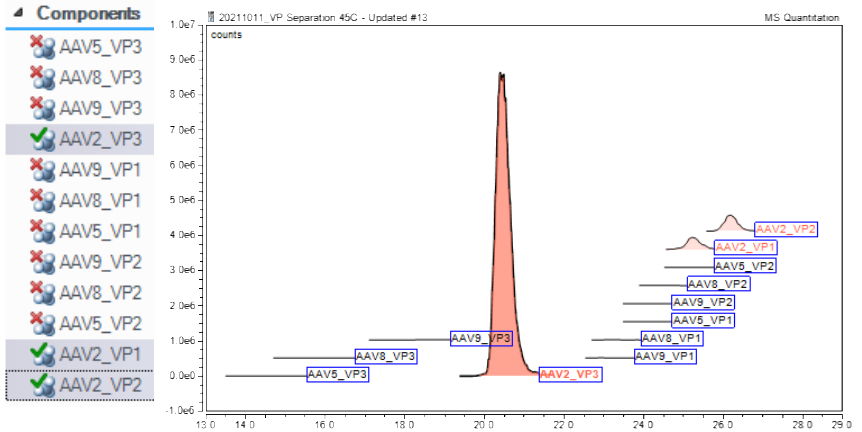


Report Generation

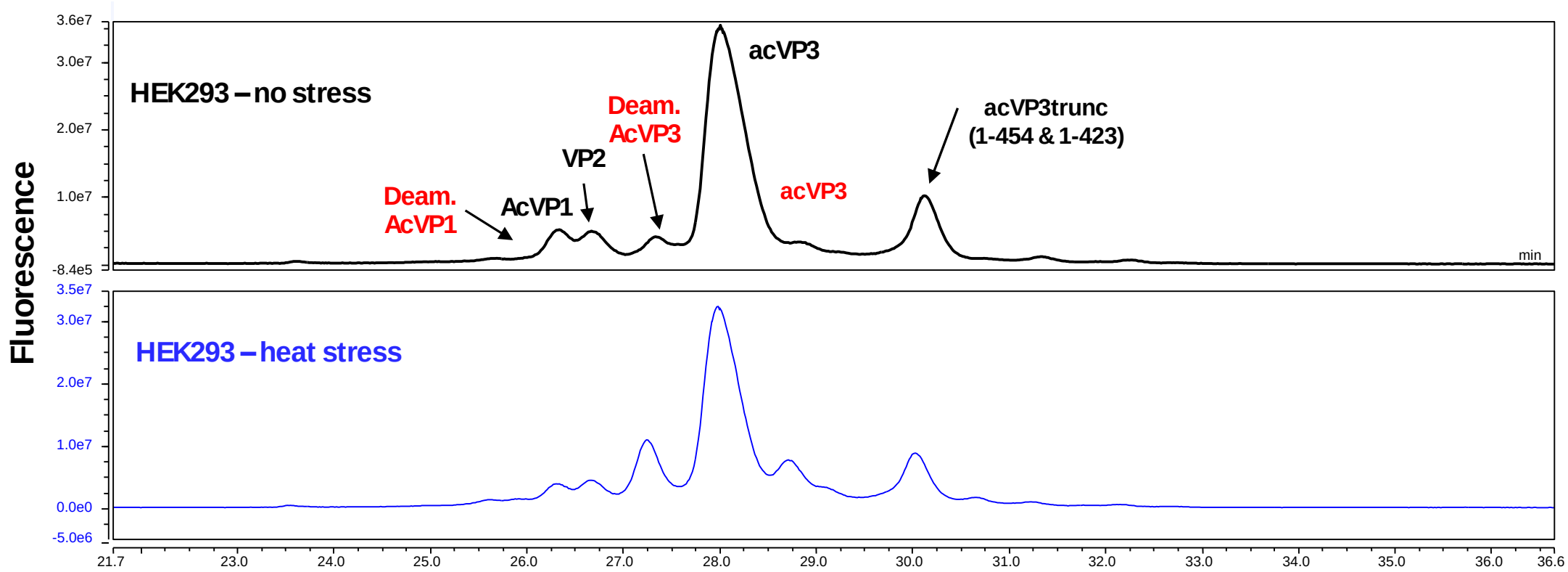
Specific Serotype PTM Monitoring



Method Validation (HEK Derived AAV)

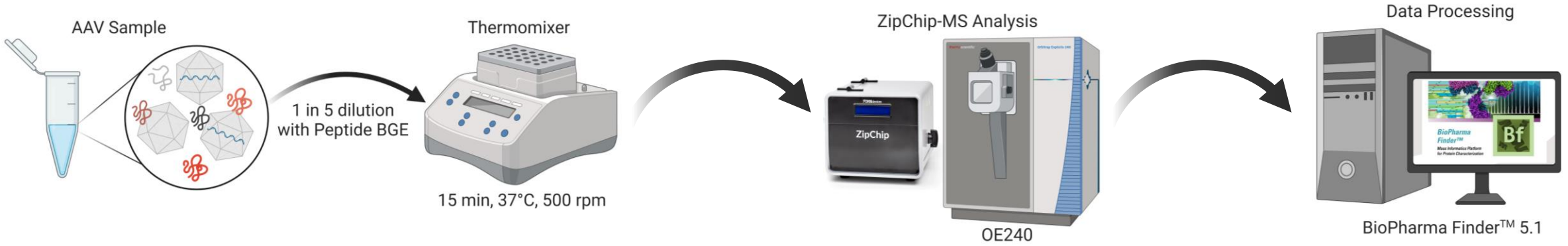


RP Separation for Detection of Deamidation Events

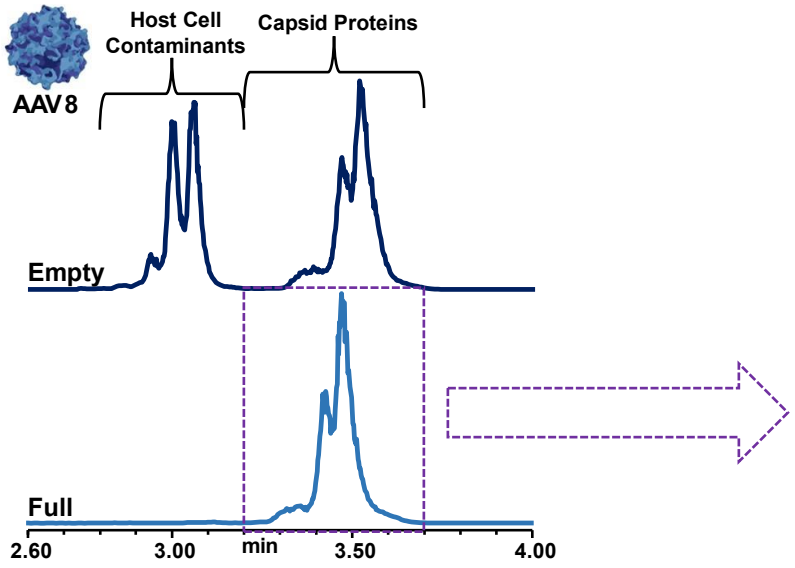


While the HILIC separation of VP's works well, for modifications such as deamidation events, HILIC does not have the necessary selectivity. Reversed-phase separation on C4 enables efficient separation of deamidated forms of the viral proteins.

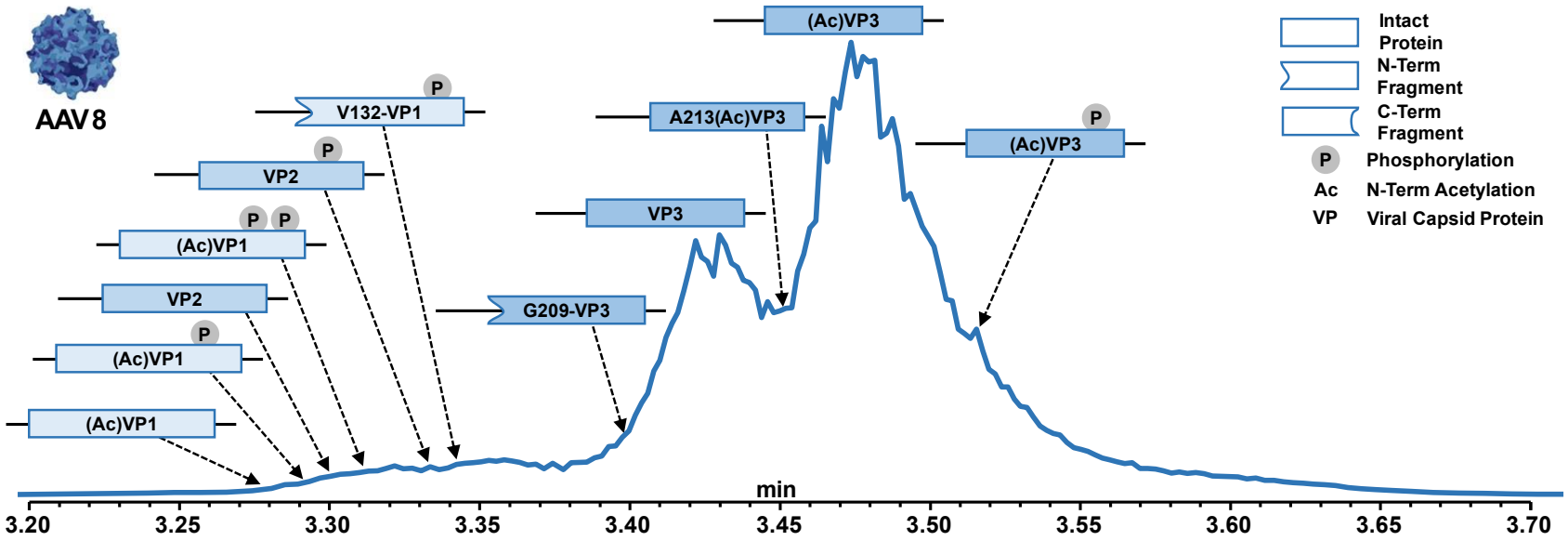
Viral Protein Separation using MCE-MS



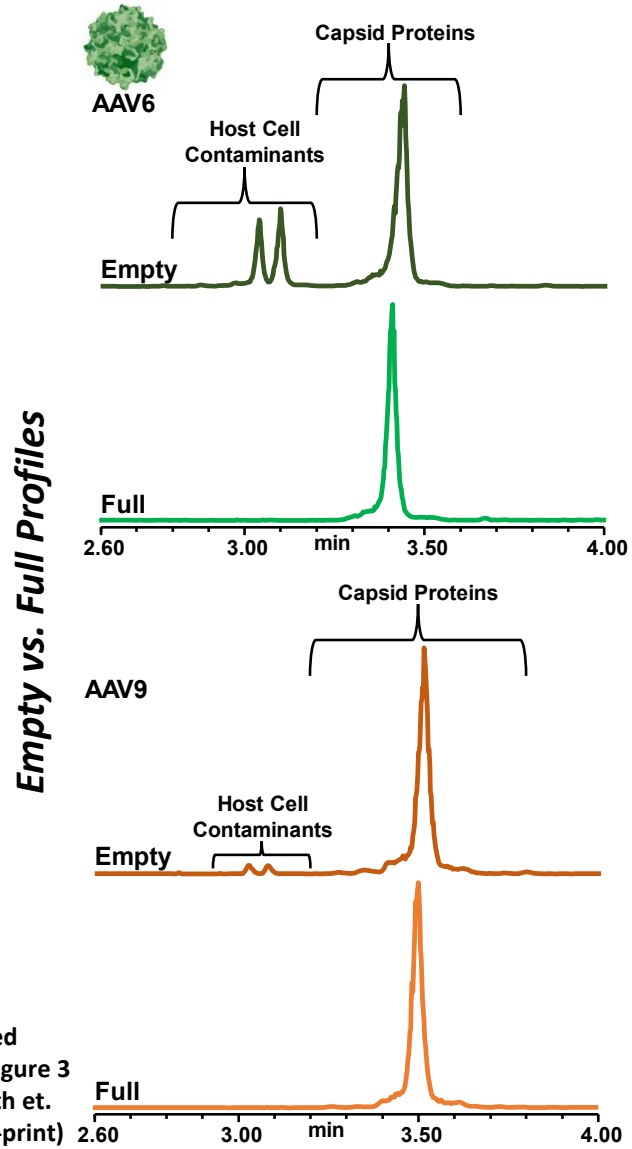
Empty vs. Full Profiles



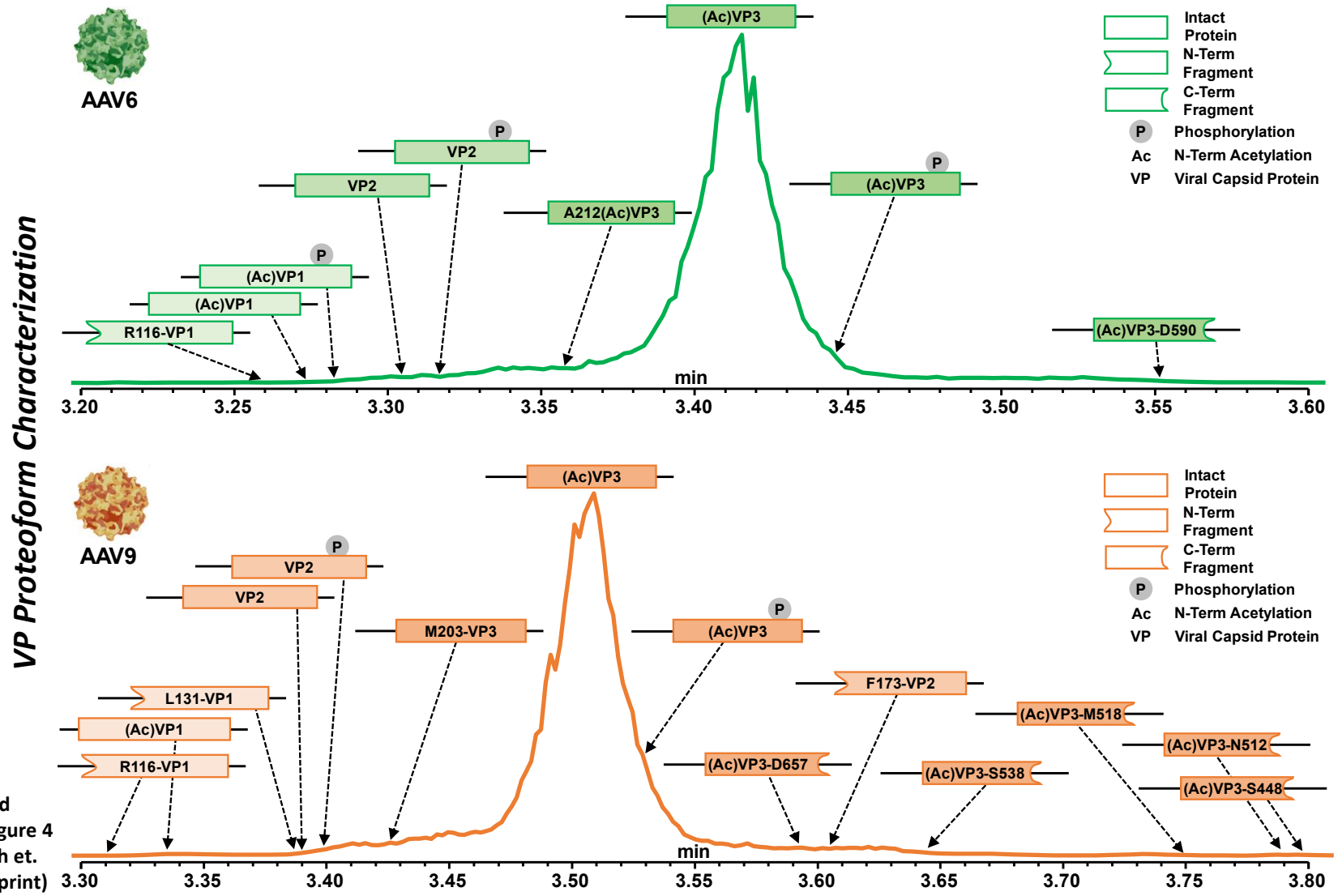
VP Proteoform Characterization



Broad Applicability of ZipChip Platform



Adapted from Figure 3 of Smith et. al (Pre-print)

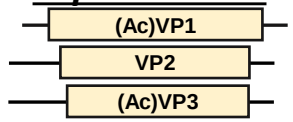


Adapted from Figure 4 of Smith et. al (Pre-print)

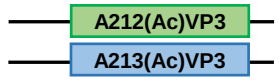
Detected VP Proteoforms and Fragments

Start of AAV Sequence

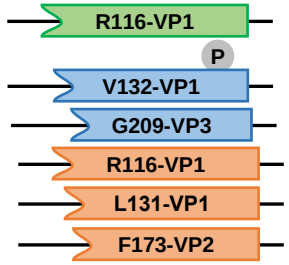
Expected VPs



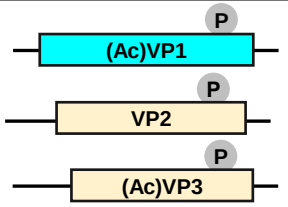
VP3 Variant



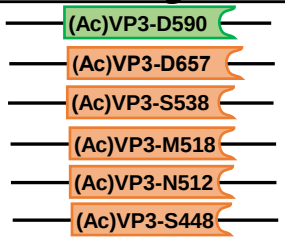
N-Term Fragments



VPs with additional PTMs



C-Term Fragments

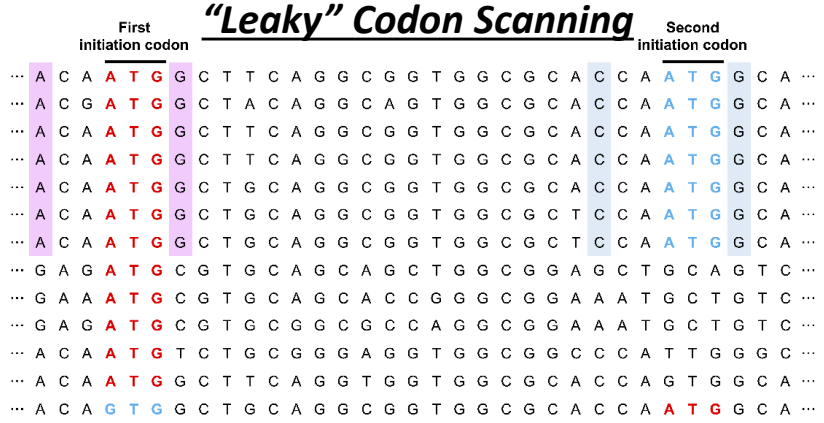


VP3 Variant Generation

Serotypes	N-terminal region (203 … 211)	DP sequence (590 591)	DG sequence (626 627)	DP sequence (656 657)
AAV1	… M A S G G G A P M A …	T D P A …	T D G H …	A N P P …
AAV2	… M A T G S G A P M A …	R Q A A …	T D G H …	A N P S …
AAV3	… M A S G G G A P M A …	T A P T …	T D G H …	A N P P …
AAV6	… M A S G G G A P M A …	T D P A …	T D G H …	A N P P …
AAV8	… M A A G G G A P M A …	T A P Q …	T D G N …	A D P P …
AAV10	… M A A G G G A P M A …	T G P I …	T D G N …	A D P P …
AAVrh10	… M A A G G G A P M A …	A A P I …	T D G N …	A D P P …
AAV4	… M R A A A G G A A V …	N L P T …	T D G H …	A N P A …
AAV11	… M R A A P G G N A V …	T A P I …	A D G H …	A N P A …
AAV12	… M R A A P G G N A V …	T A P H …	T D G H …	A N P N …
AAV5	… M S A G G G G P L G …	T A P A …	T G A H …	G N I - …
AAV9	… M A S G G G A P V A …	A Q A Q …	T D G N …	A D P P …
AAV7	… V A A G G G A P M A …	T A A Q …	T D G N …	A N P P …

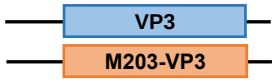
Adapted from Figure 5a of *Oyama et al. (2021)*
https://www.liebertpub.com/doi/10.1089/hum.2021.009

"Leaky" Codon Scanning



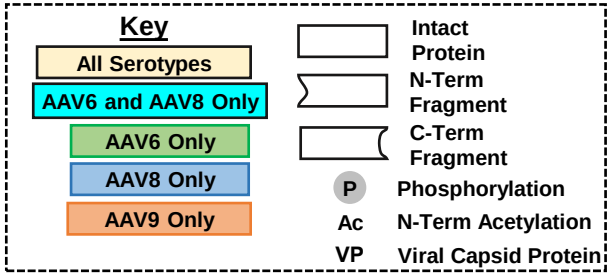
Adapted from Figure S4a of *Oyama et al. (2021)*
https://www.liebertpub.com/doi/10.1089/hum.2021.009

Unexpected VPs



Potential Causes of Fragments

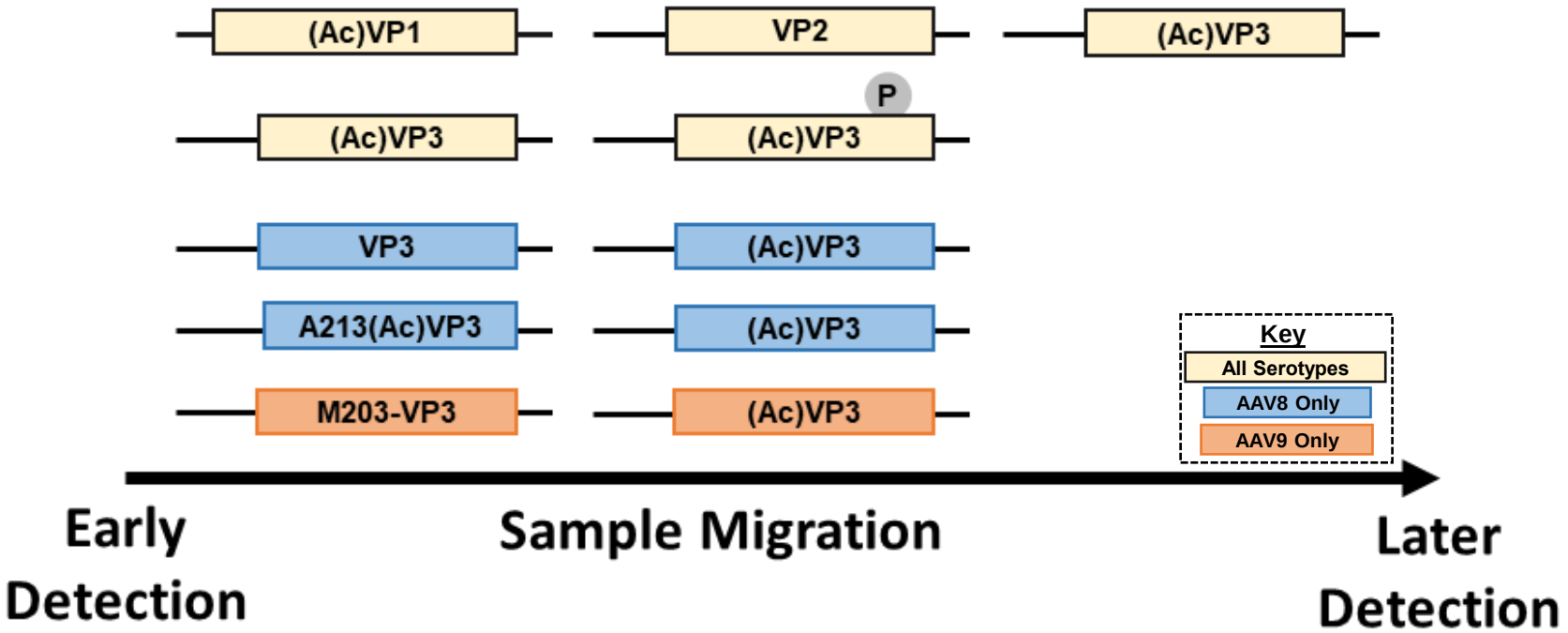
- Baculoviral cathepsin
- Immune response
- Acidic conditions



Influence of Modifications on VP Migration

Serotype	Amino Acid Sequence	Viral Protein	Capsids (Empty/Full)	Relative Abundance (%)	Migration Time (min)	Theoretical Net Charge at pH 2.4	Theoretical Charge to Mass ratio
AAV8	A2(Ac)-L738	(Ac)VP1 + 2xP	Empty Full	0.13 0.08	3.336 3.311	+73.996	9.04×10^{-4}
		(Ac)VP1 + 1xP	Empty Full	0.62 0.41	3.322 3.291	+74.937	9.17×10^{-4}
		(Ac)VP1	Empty Full	0.42 0.21	3.310 3.278	+75.878	9.29×10^{-4}
	V132-L738	V132-VP1 + 1xP Fragment	Empty Full	0.11 0.07	3.370 3.339	+59.268	8.80×10^{-4}
	A139-L738	VP2 + 1xP	Empty Full	1.27 0.89	3.374 3.332	+58.286	8.75×10^{-4}
		VP2	Empty Full	0.57 0.38	3.338 3.299	+59.226	8.90×10^{-4}
	A205(Ac)-L738	(Ac)VP3 + 1xP	Empty Full	6.64 6.85	3.546 3.511	+48.375	8.08×10^{-4}
		(Ac)VP3	Empty Full	100.00 100.00	3.521 3.485	+49.316	8.25×10^{-4}
		VP3	Empty Full	49.75 45.29	3.468 3.431	+50.316	8.42×10^{-4}
	G209-L738	G208-VP3 Fragment	Empty Full	3.40 2.61	3.441 3.402	+50.316	8.46×10^{-4}
	A213(Ac)-L738	(Ac)VP3 Variant	Empty Full	4.46 4.94	3.484 3.450	+49.316	8.33×10^{-4}

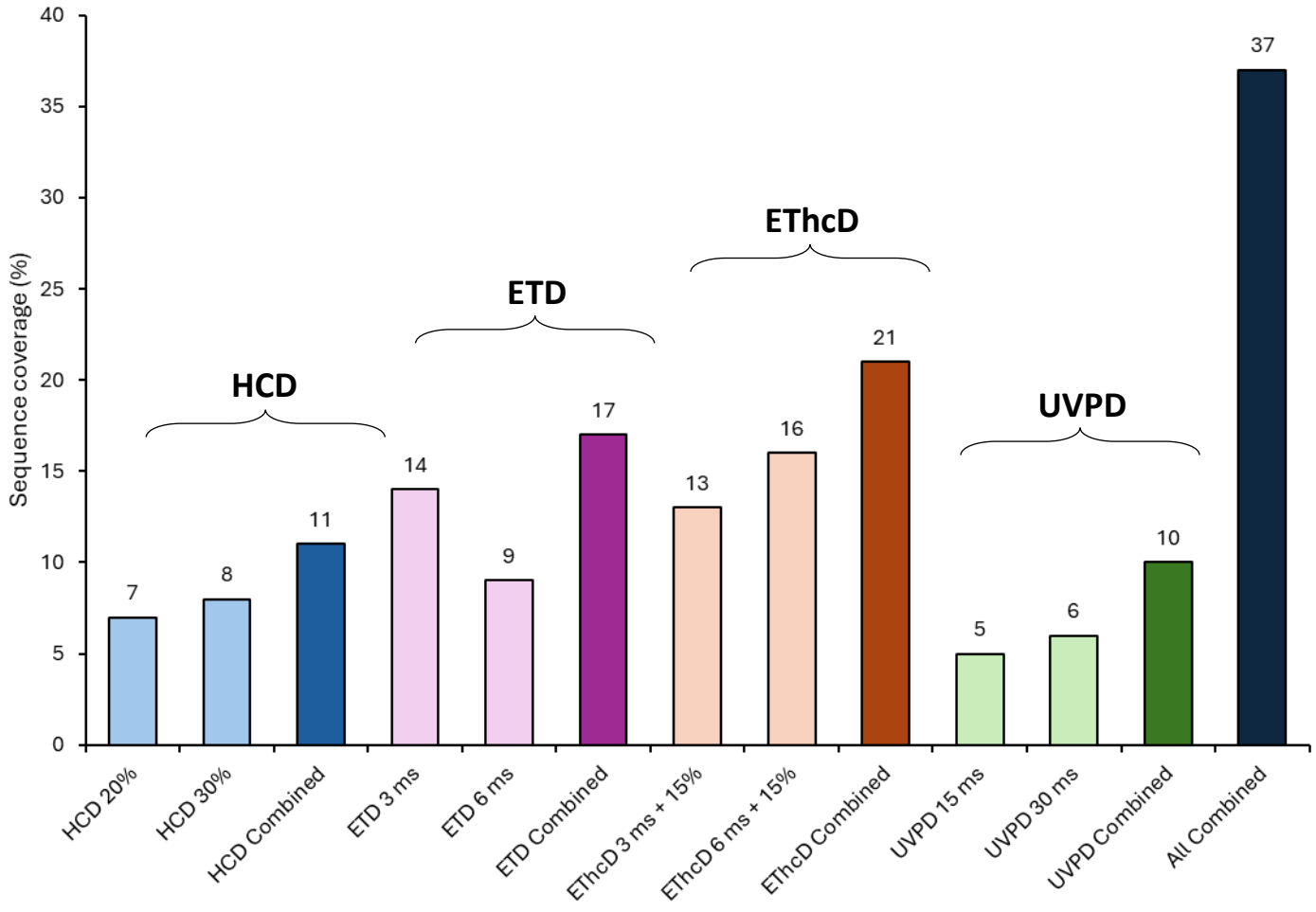
Serotype	Amino Acid Sequence	Viral Protein	Capsids (Empty/Full)	Relative Abundance (%)	Migration Time (min)	Theoretical Net Charge at pH 2.4	Theoretical Charge to Mass ratio
AAV9	A2(Ac)-L736	(Ac)VP1	Empty Full	0.11 0.02	3.328 3.335	+76.860	9.45×10^{-4}
	R116-L736	R116-VP1 Fragment 1	Empty Full	0.22 -	3.319 -	+64.161	9.33×10^{-4}
	L131-L736	L131-VP1 Fragment 2	Empty Full	0.20 0.04	3.383 3.387	+60.170	8.97×10^{-4}
	A139-L736	VP2 + 1xP	Empty Full	- 0.03	- 3.398	+58.247	8.79×10^{-4}
		VP2	Empty Full	0.67 0.33	3.389 3.390	+59.188	8.94×10^{-4}
	F173-L736	F173-VP2 Fragment	Empty Full	0.68 0.23	3.597 3.605	+52.226	8.33×10^{-4}
	M203-L736	M203-VP3	Empty Full	0.43 0.41	3.420 3.418	+52.286	8.74×10^{-4}
	A204(Ac)-L736	(Ac)VP3 + 1xP	Empty Full	7.68 9.79	3.533 3.531	+50.345	8.42×10^{-4}
		(Ac)VP3	Empty Full	100.00 100.00	3.498 3.492	+51.286	8.59×10^{-4}
	A204(Ac)-D657	(Ac)VP3-D657 Fragment	Empty Full	0.09 0.11	3.588 3.593	+42.363	8.39×10^{-4}
	A204(Ac)-S538	(Ac)VP3-S538 Fragment	Empty Full	0.37 0.42	3.645 3.647	+30.547	8.13×10^{-4}
	A204(Ac)-M518	(Ac)VP3-M518 Fragment	Empty Full	0.13 0.15	3.745 3.750	+27.594	7.80×10^{-4}
	A204(Ac)-N512	(Ac)VP3-N512 Fragment	Empty Full	0.10 0.09	3.789 3.793	+26.589	7.66×10^{-4}
	A204(Ac)-S448	(Ac)VP3-S448 Fragment	Empty Full	0.58 0.20	3.800 3.804	+21.594	7.77×10^{-4}



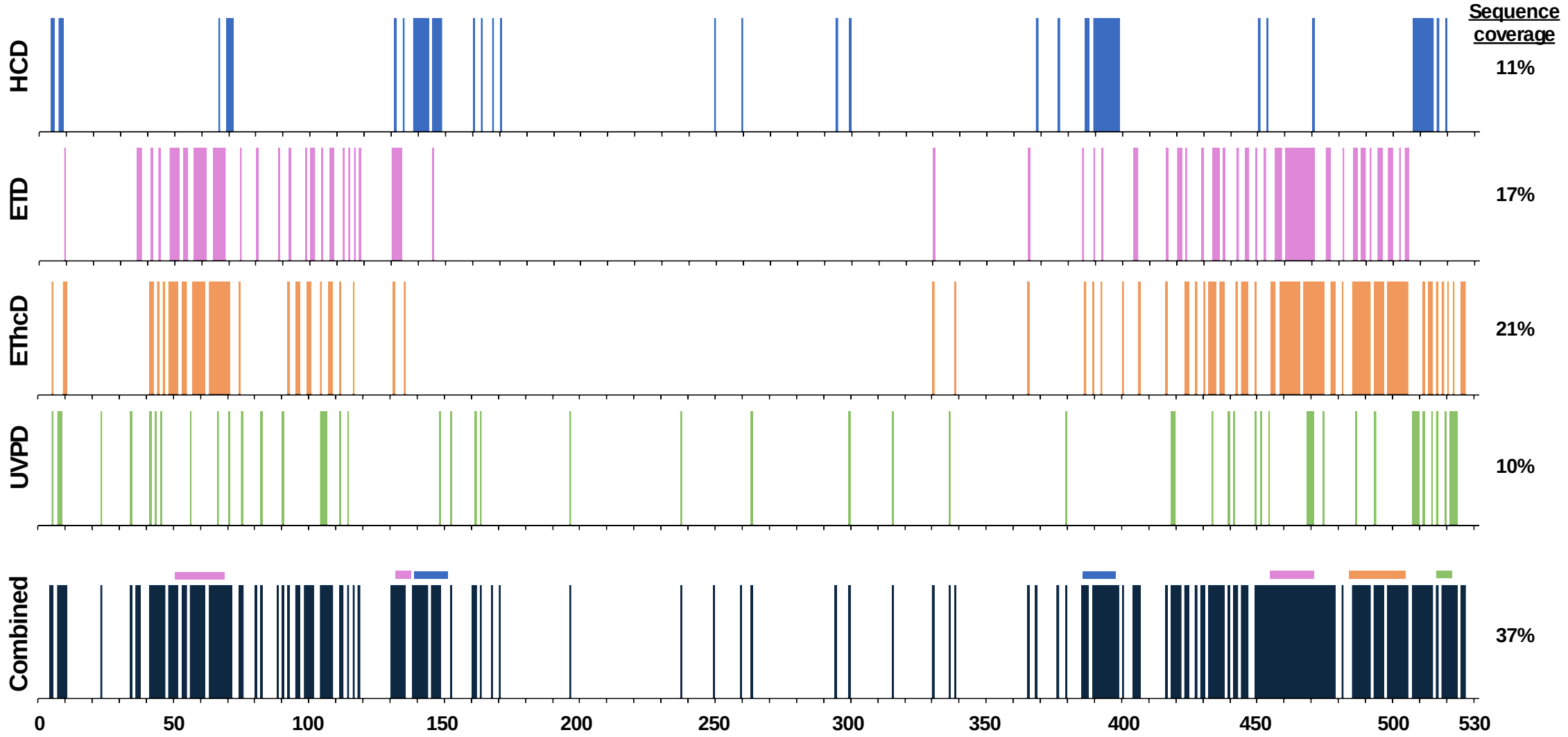
ProtPi (https://www.protpi.ch/Calculator/ProteinTool) used to calculate Theoretical Net Charge of VPs at pH 2.4 (pH of BGE)

Top-Down MS/MS Sequencing of Intact VP's – Focus on VP3

- Sequence degeneracy of VP's complicates annotation of PTMs.
- Rather than use peptide mapping, top-down MS/MS sequencing on Orbitrap Eclipse was investigated using multiple ion activation strategies.
- EThcD fragmentation resulted in highest individual coverage.
- Combining all ion activation strategies, sequence coverage resulted in nice N- and C-terminal fragmentation.

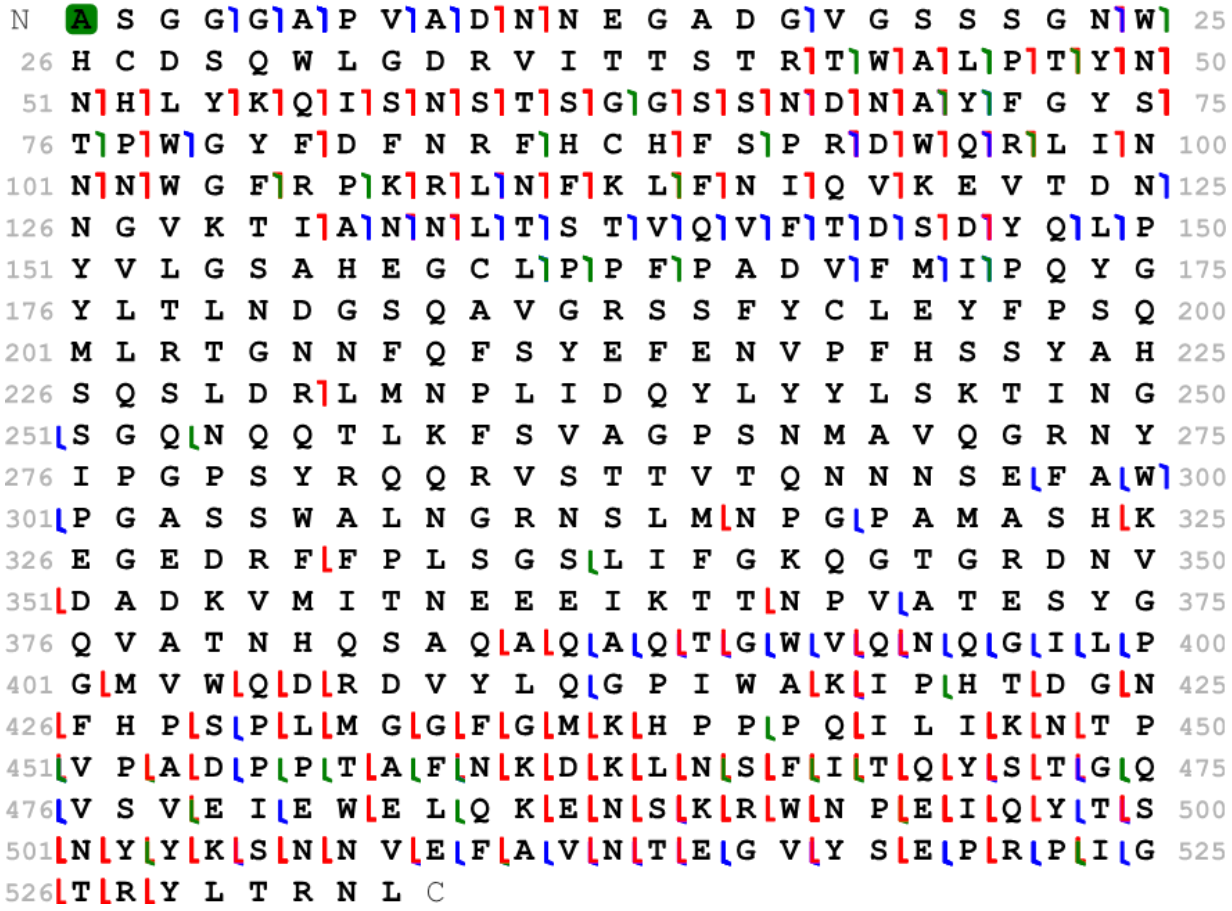


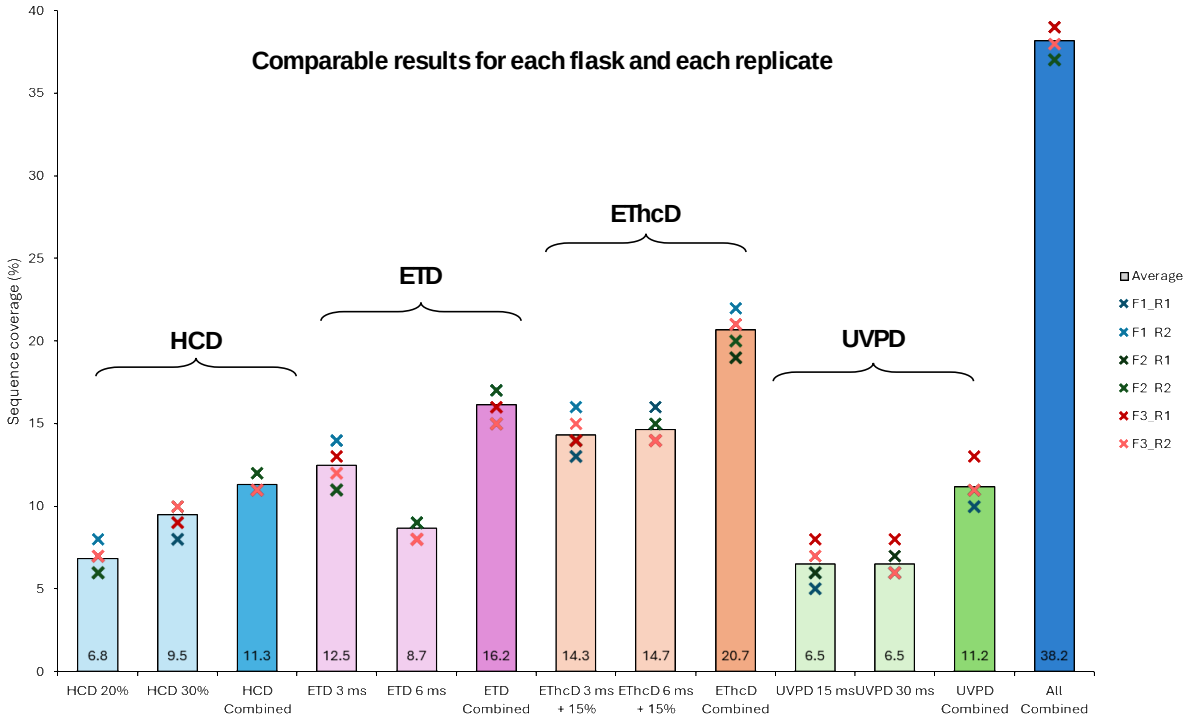
Combined Top-Down MS/MS of VP3 on Orbitrap Eclipse



Top-down MS/MS Data Sequence Map

Data from barcode plot mapped on to the sequence of VP3 demonstrating nice N- and C-terminal fragmentation.

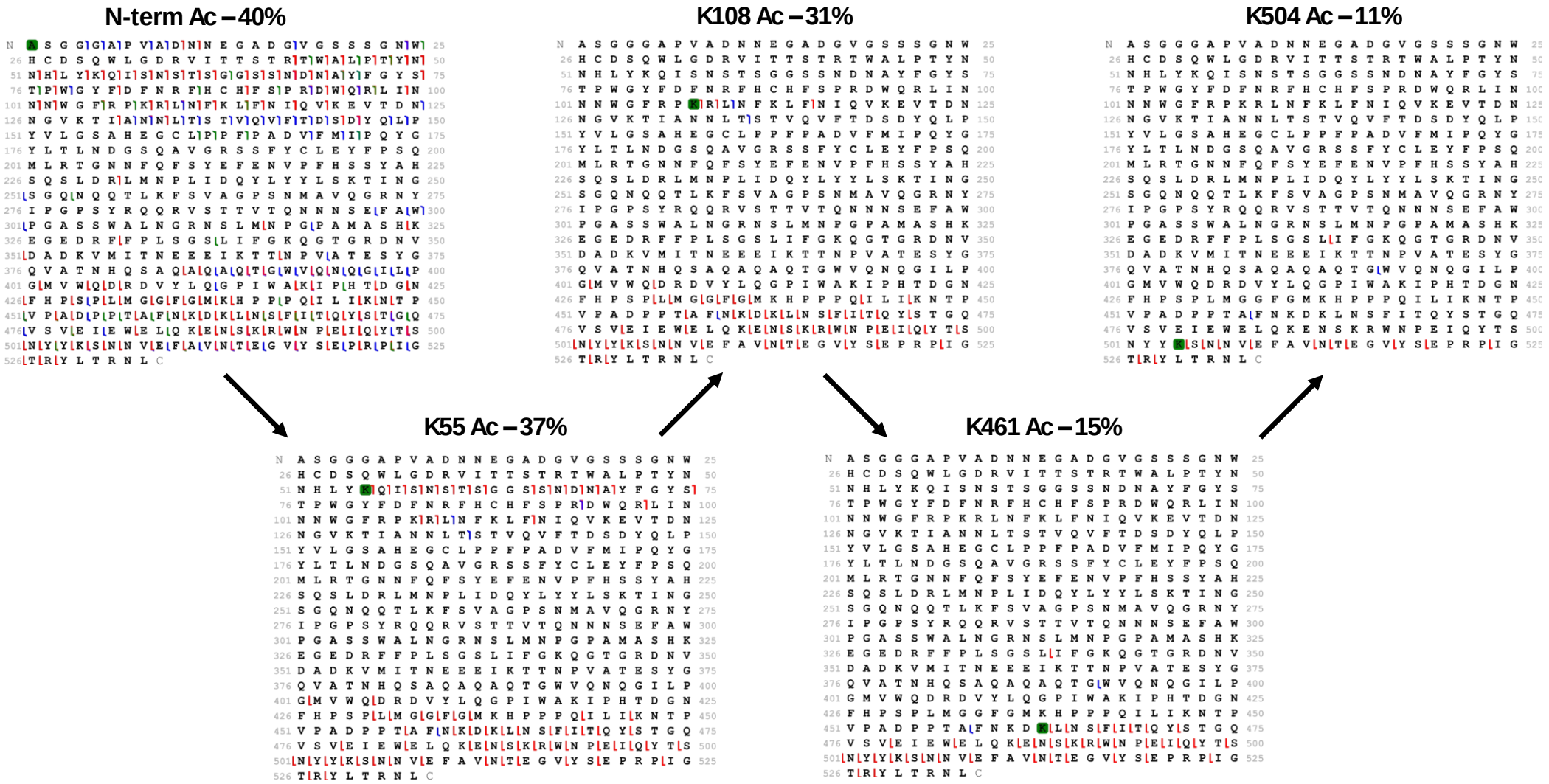




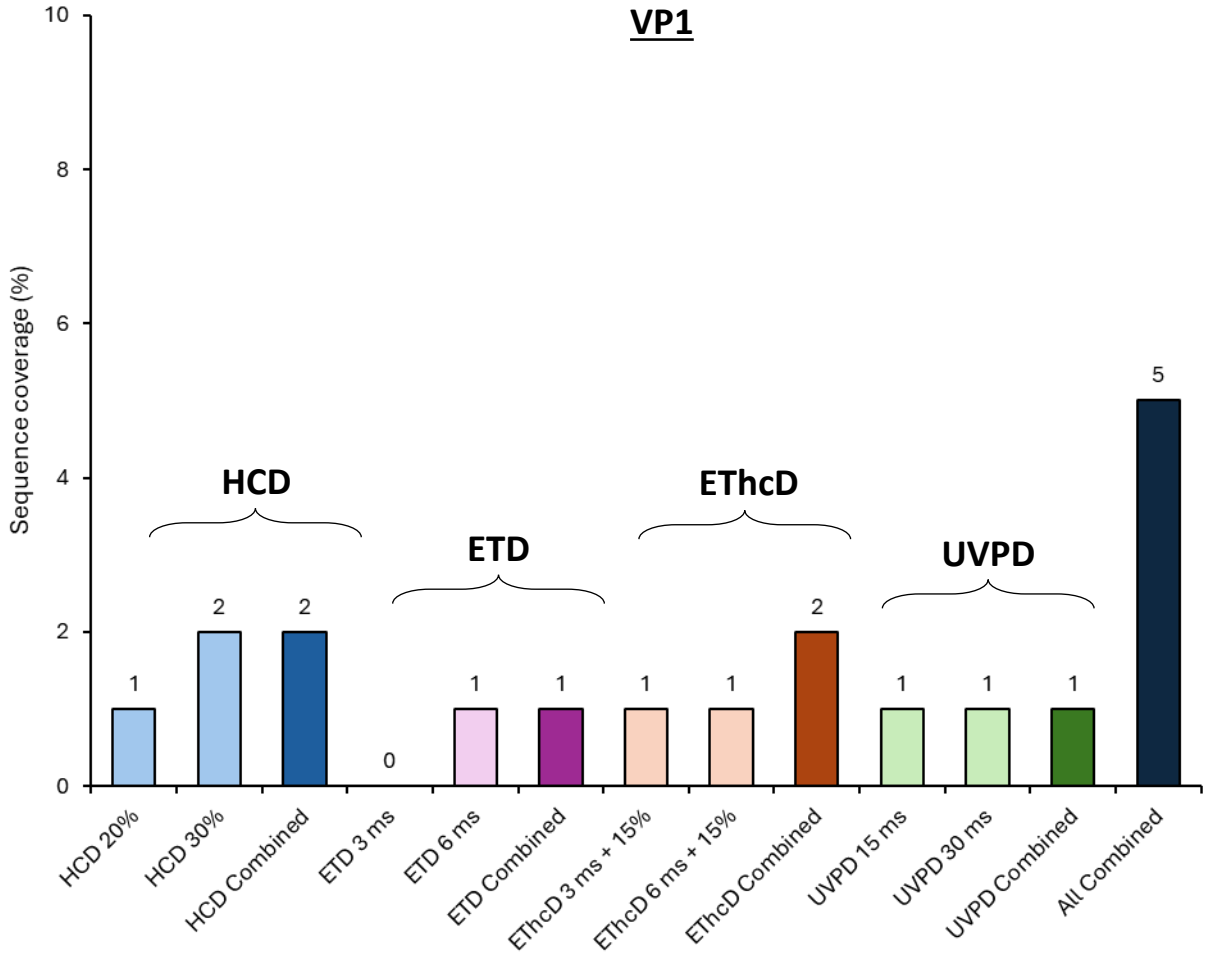
Reproducibility of fragmentation behaviour investigated using three different preparations of HEK293 derived AAV9 and replicate instrumental analysis.

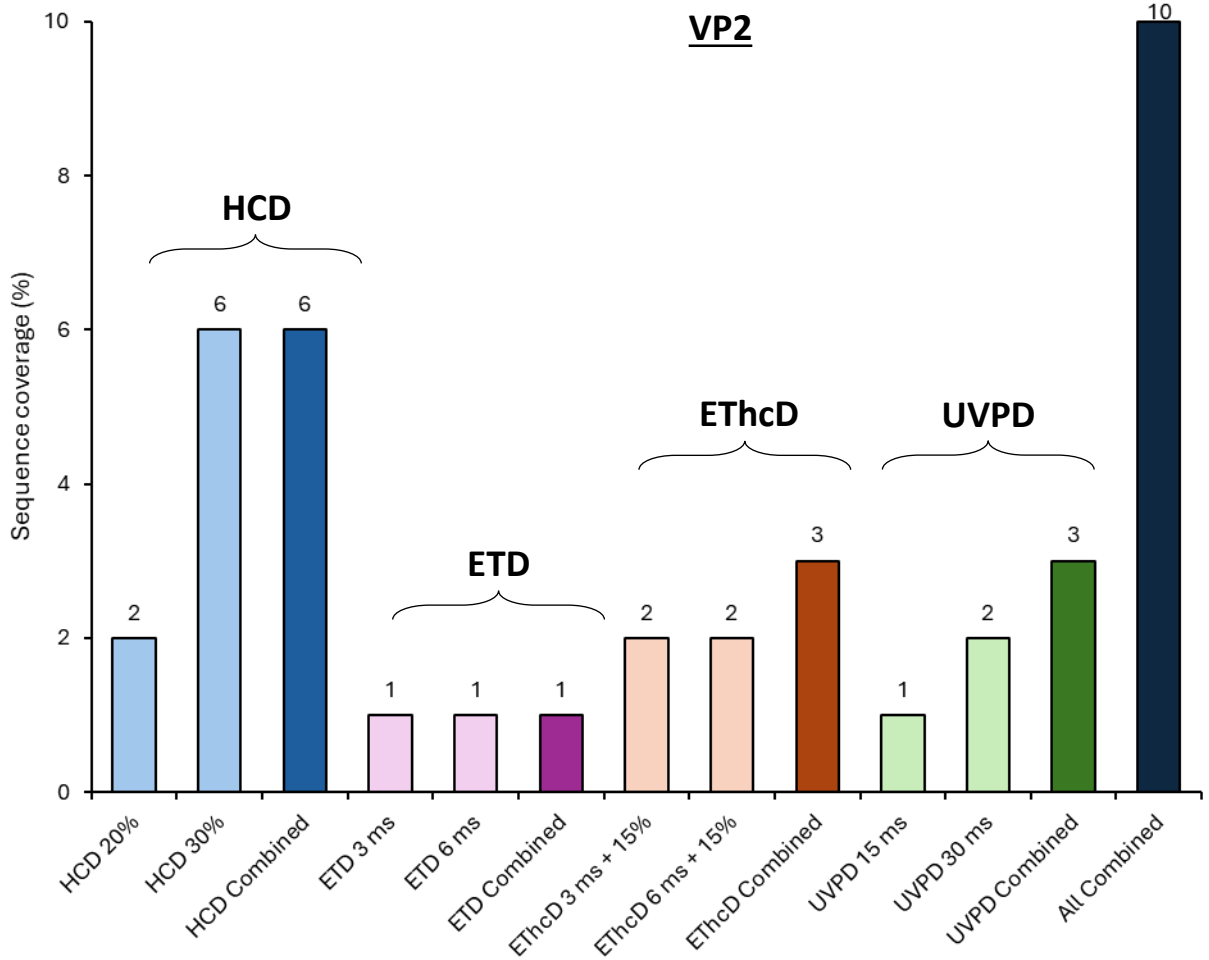
Reproducibility of fragmentation was found to be high resulting in the same pattern each time for biological and technical replicate measurements

Top-Down MS/MS Facilitated Site Specific PTM Annotation



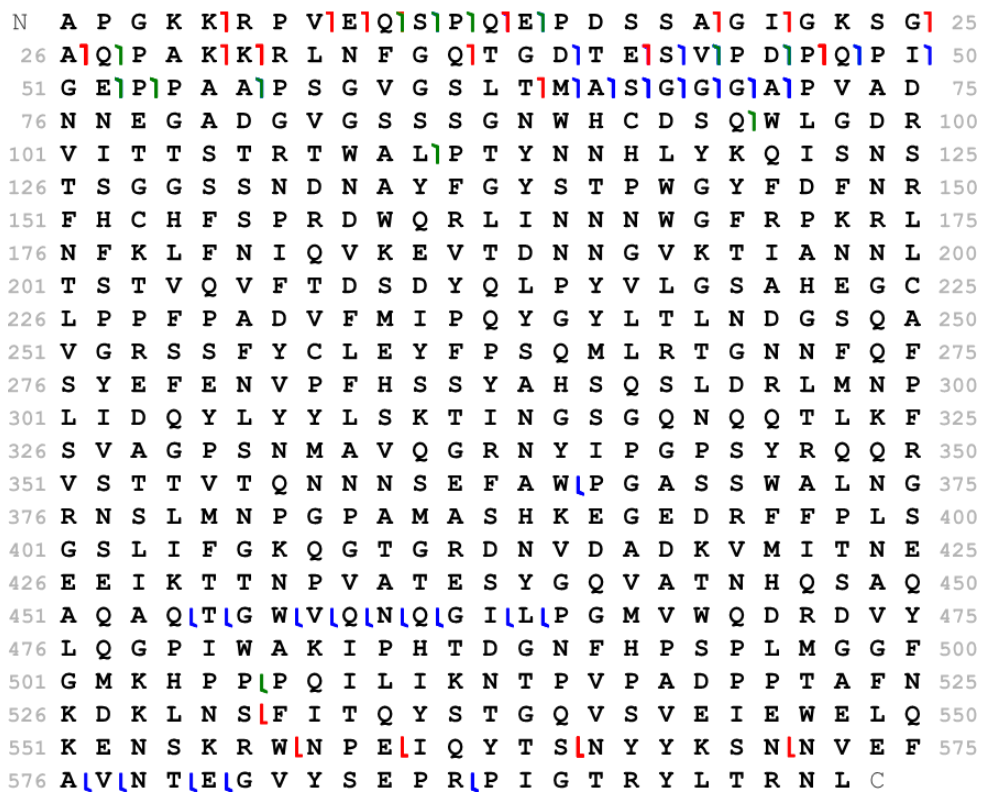
What about VP1 and VP2?





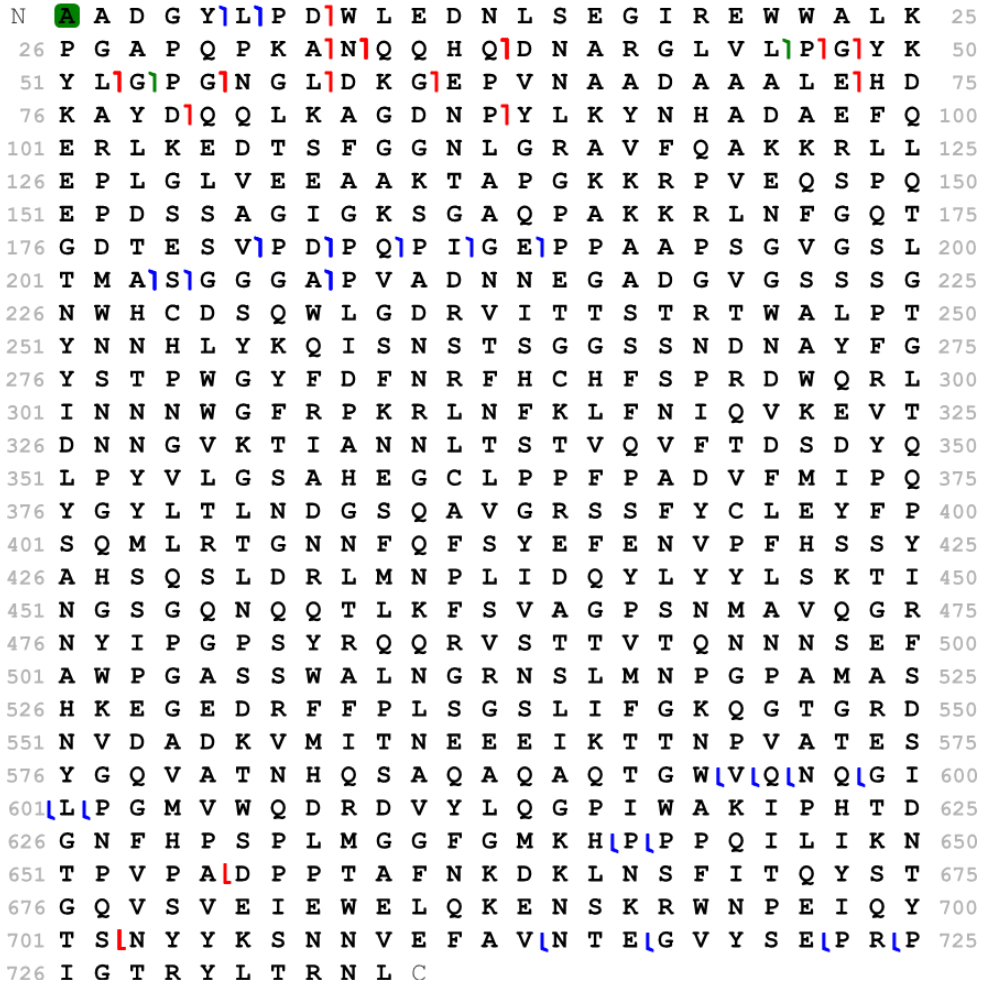
Sequence Coverage Maps

VP2 (10% sequence coverage)

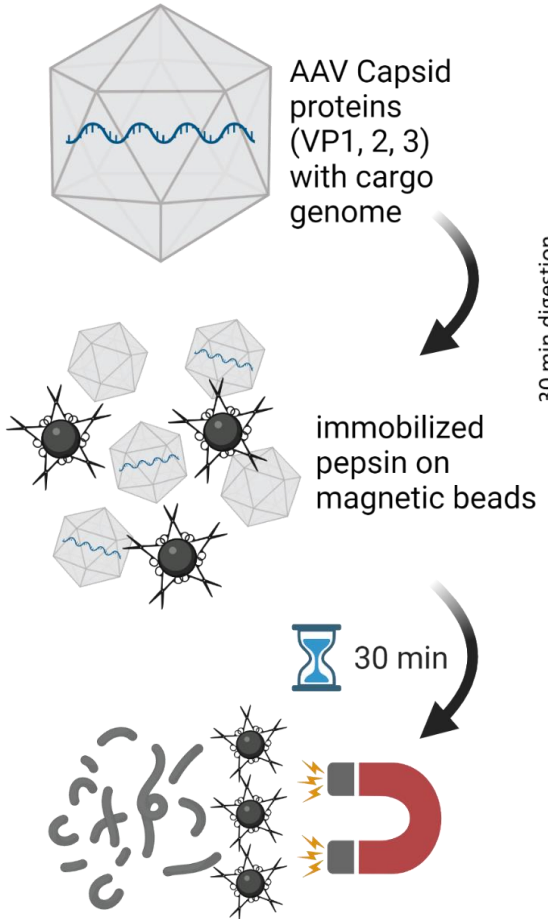


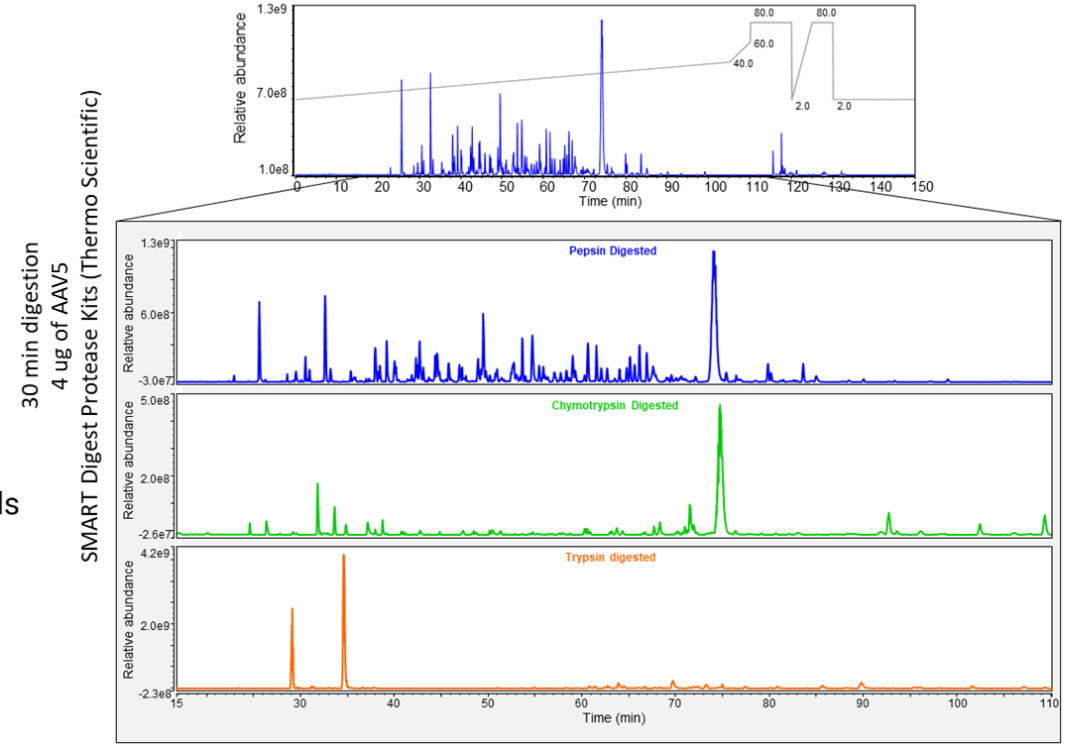
Lower abundance of VP1 and 2 resulted in lower sequence coverage. Interestingly, most fragmentation observed in the N-terminal region. Further investigation on-going.

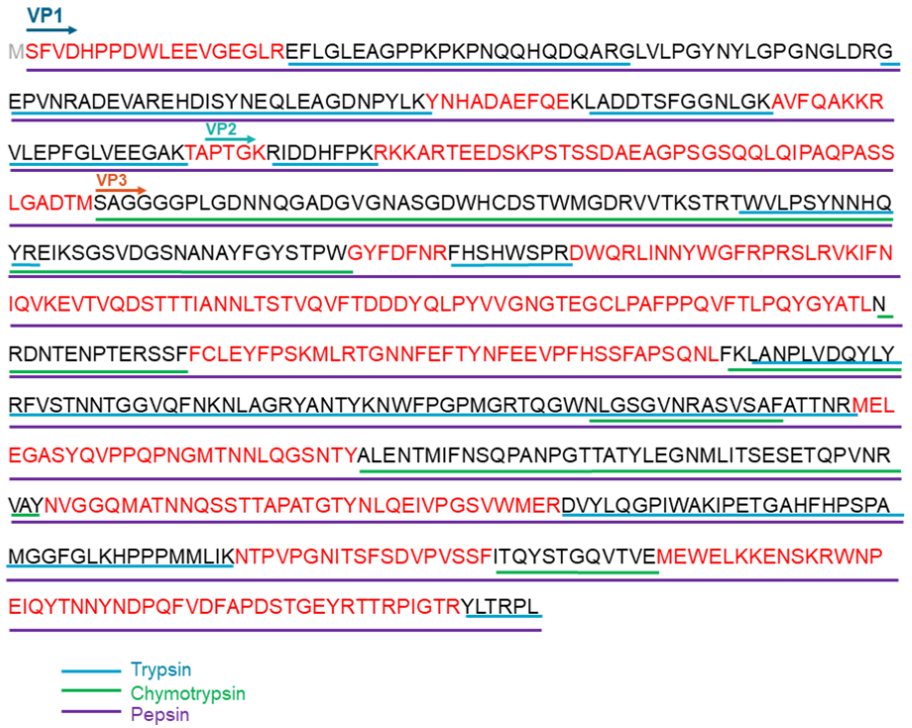
VP1 (5% sequence coverage)



AAV Peptide Mapping Workflow







Efficient digestion of AAV using pepsin. Immobilised protease on magnetic beads enabled tight time control when combined with KingFisher Duo Prime Automation Station.

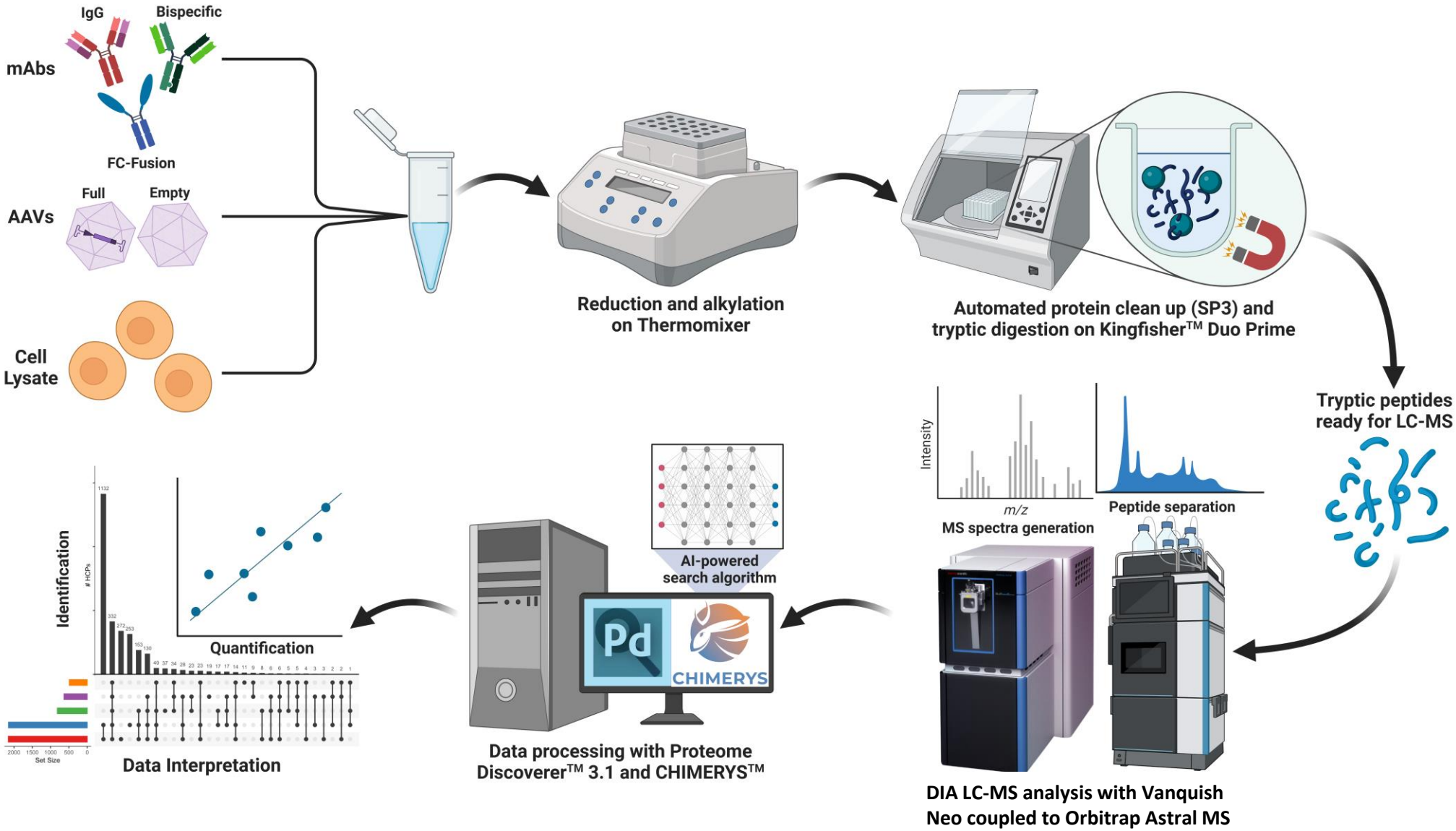
HCP Analysis Using Orbitrap Astral LC-MS

The Thermo Scientific™ Orbitrap™ Astral™ MS - Powered by the synergy of two synchronized HRAM analyzers

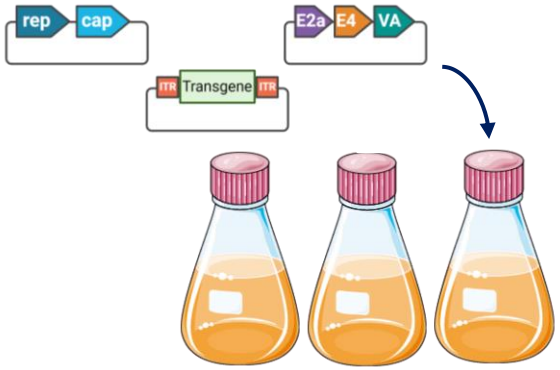
ORBITRAP ANALYZER for high dynamic range HRAM MS and MS/MS	
HRAM Scan Rate	Up to 40 Hz
Intrascan dynamic range	>5000 with single microscan
Max Resolution	480,000 at *m/z* 200
Mass Accuracy	RMS <3 ppm
Max *m/z* range	Up to *m/z* 8000 with Biopharma Option

ASTRAL ANALYZER for fast and sensitive high dynamic range HRAM SIM and MS/MS	
Sensitivity	Single ion detection
HRAM Scan Rate	Up to 200 Hz
Intrascan dynamic range	>1000 with single microscan
Resolution	80,000 at *m/z* 524
Mass Accuracy	RMS <5 ppm

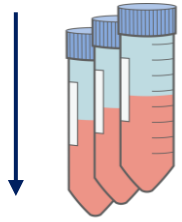
Sample Preparation Workflow



Tracking HCP Clearance using AAVX Affinity Chromatography



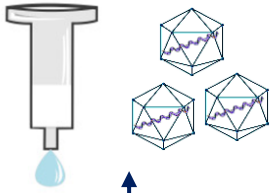
AAV produced in HEK cells using Gibco™ AAV-MAX™ platform and double transfection

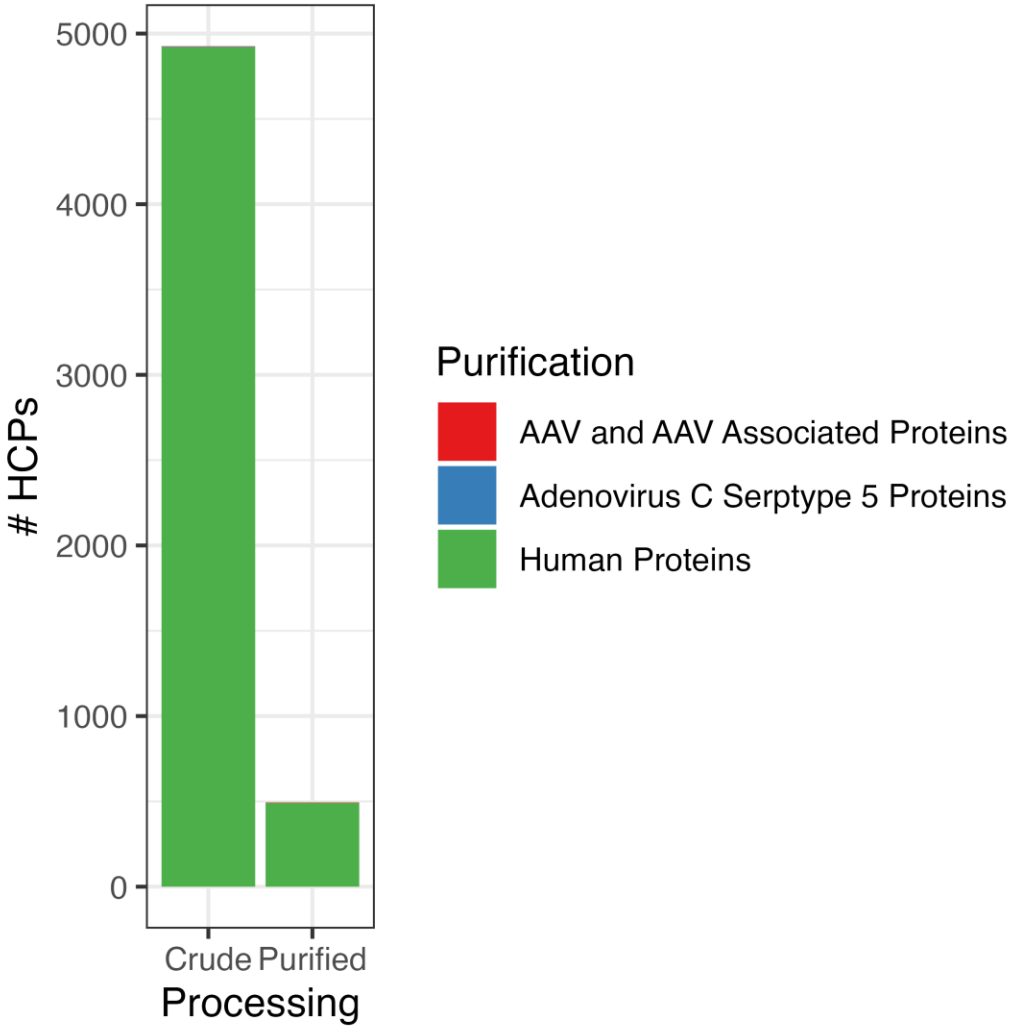


Conditioned media collected, sample retained, remainder purified using POROS™ CaptureSelect™ AAVX Affinity Resin pre-packed column

FPLC

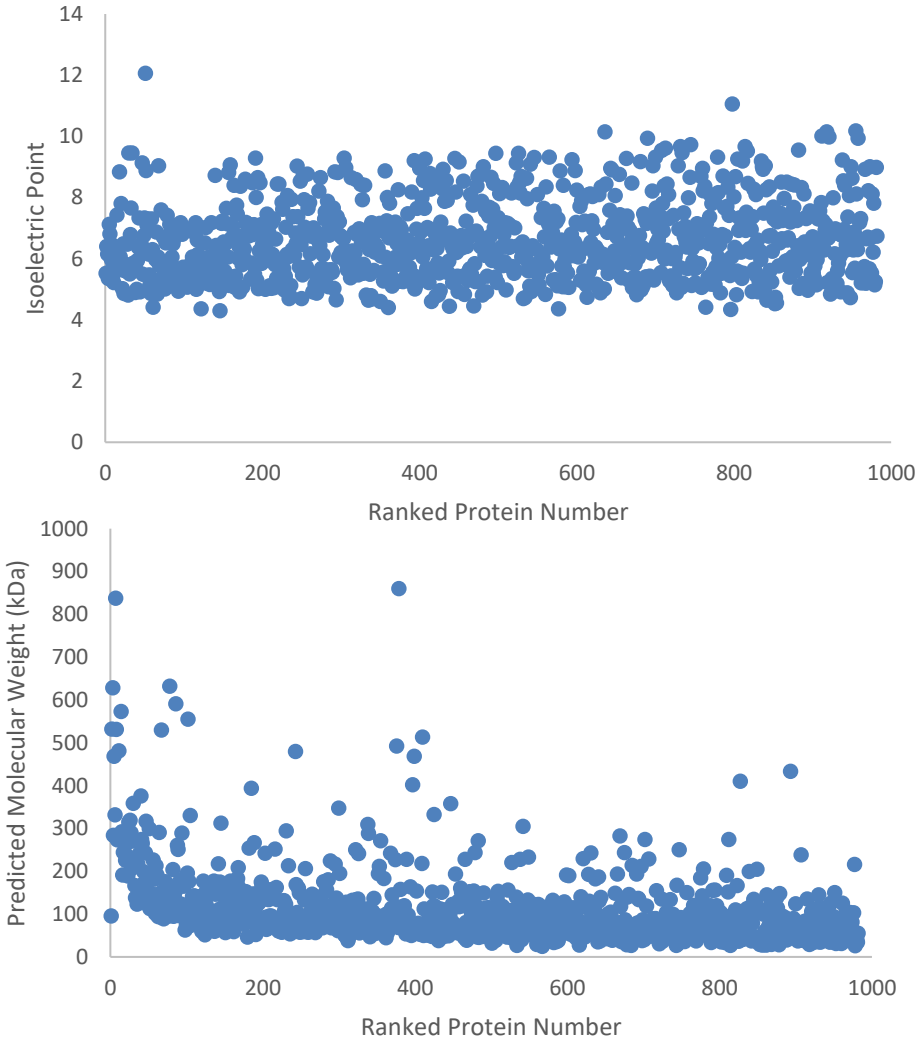
Purified AAV buffer exchanged to PBS containing 0.01% Pluronic using centrifugal filters



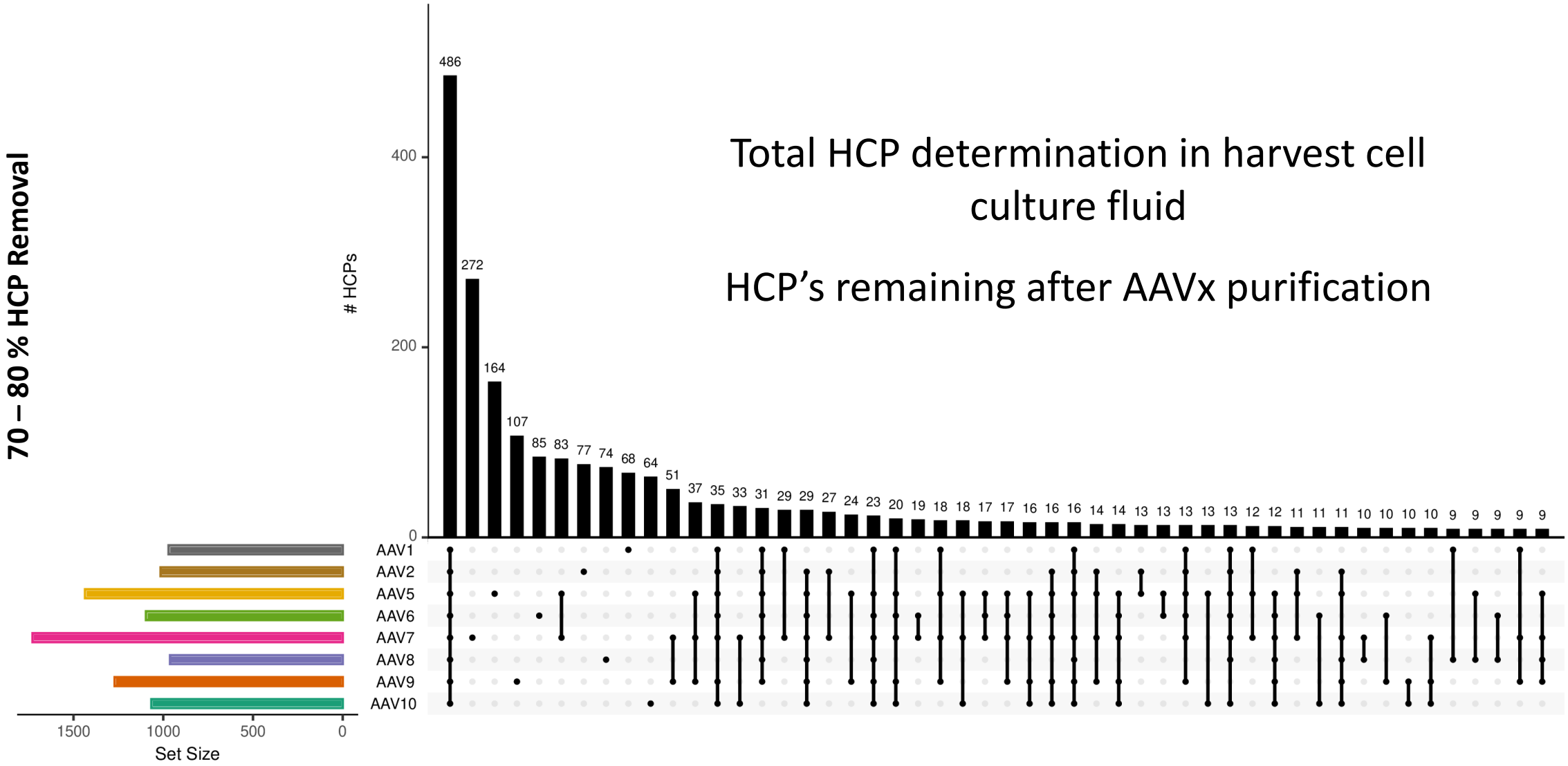


What Remained Associated with Purified CMV-GFP AAV8?

- AAVX purification resulted in ~80% reduction in the levels of HCPs present in the process stream using a simple bind and elute method.
- For proteins associated with the retained viral capsids, GO terms relating to binding, in particular protein binding (92.7% of the total set) were enriched. 97.1% were mapped as being intracellular proteins.
- Standard physiochemical parameters were explored including molecular mass, pI, hydrophobicity *etc.* However, distributions were broad and as expected, no correlation existed.



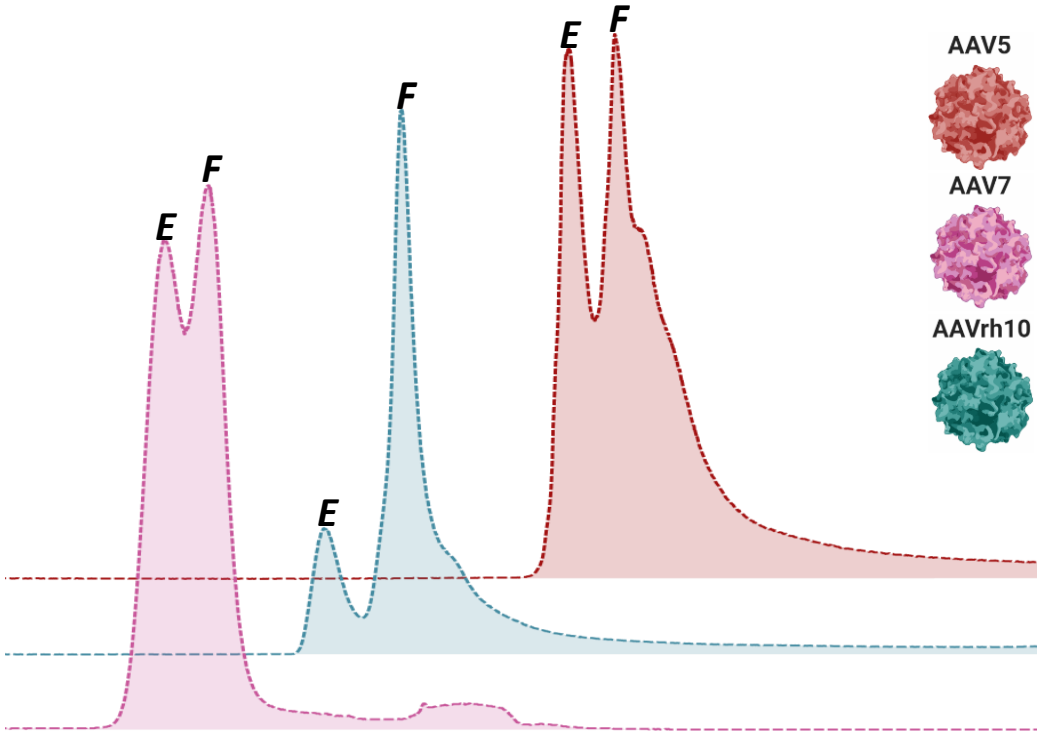
Exploring HCP Distribution Across Various AAV Serotypes

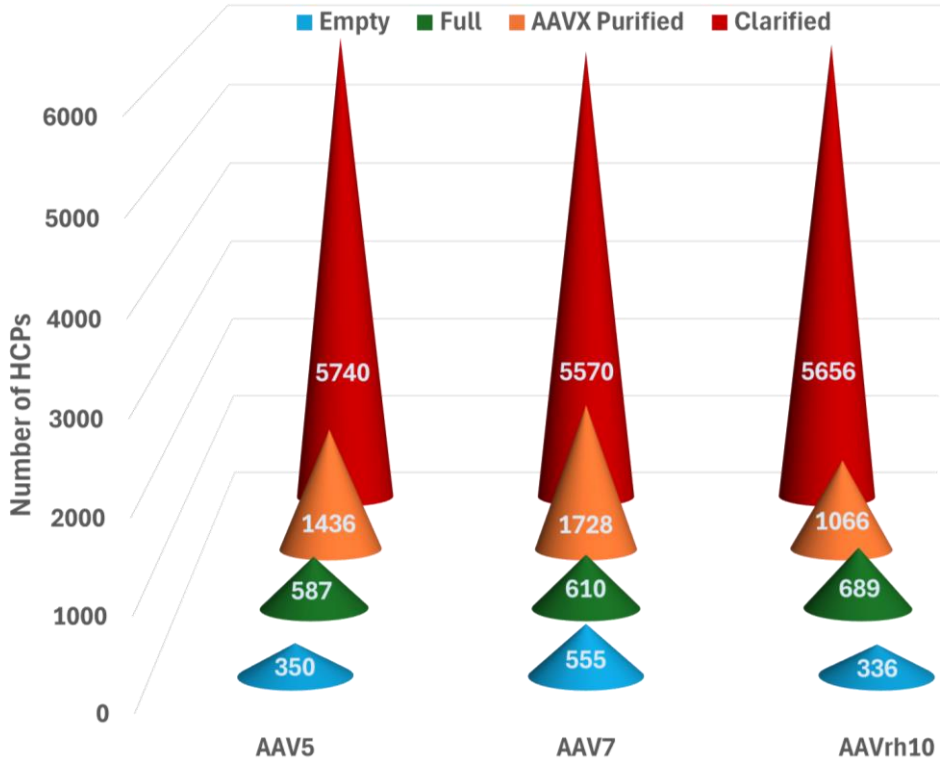


Total HCP determination in harvest cell culture fluid

HCP's remaining after AAVx purification

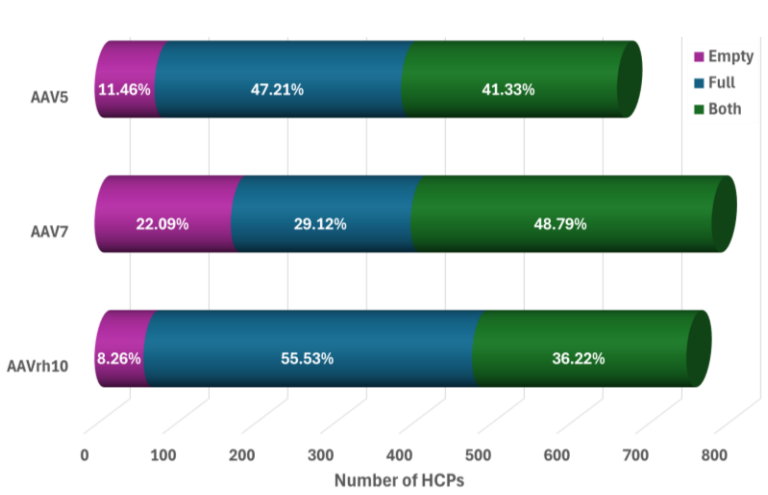
Monitoring Clearance During Downstream Processing





Post AAVx affinity purification, anion exchange separation of empty and full capsids were performed using Poros XQ. Fractions were collected and analysed by LC-MS on Orbitrap Astral to investigate clearance of the HCPs and distribution across the different capsid fill states.

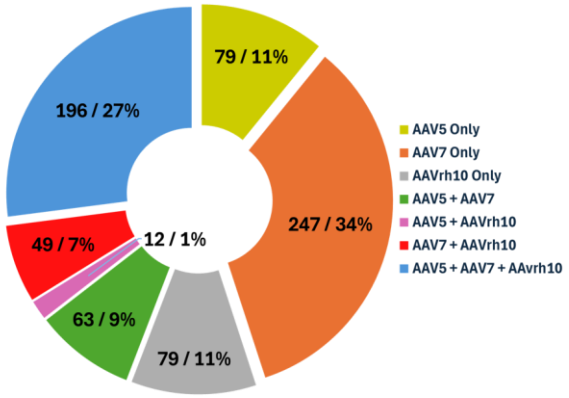
Distribution of HCP across Empty and Full Capsids



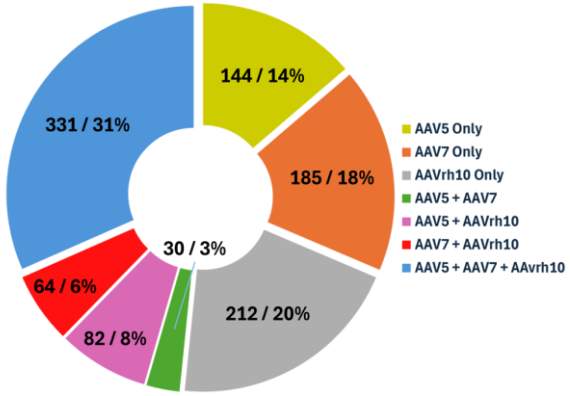
Potentially Harmful HCPs	Clarified			AAVX Purified			Empty			Full		
	AAV5	AAV7	AAVrh10	AAV5	AAV7	AAVrh10	AAV5	AAV7	AAVrh10	AAV5	AAV7	AAVrh10
Heat shock 70 kDa protein 1B	9345.64	9533.52	8595.08	23.49	38.43	15.14	4.68	3.21	2.69	3.34	1.78	2.61
Heat shock protein HSP 90-alpha	2457.25	2392.91	1184.63	7.12	7.92	0.60	0.14	0.25	0.14	0.18	0.54	0.27
Heat shock protein HSP 90-beta	1016.23	1018.65	2064.89	2.81	5.20	2.78	0.19	0.18	0.49	0.17	0.25	0.65
Heat shock cognate 71 kDa protein	736.99	705.87	629.43	3.90	2.07	0.82	0.44	0.36	0.44	0.67	0.36	0.51
60 kDa heat shock protein, mitochondrial	561.73	519.28	544.00	0.66	1.77	0.22	0.07	0.20	0.02	0.15	0.10	0.06
Pyruvate kinase PKM	383.34	381.16	334.20	3.41	6.72	2.35	0.26	0.51	0.51	0.88	0.92	1.41
DNA-binding protein	185.63	242.56	258.81	0.03	0.20	0.07		0.06				
Histone H1.4	116.54	99.24	100.20									
Histone H4	75.59	63.65	67.62	3.51	4.46	1.43	0.29	0.24	0.23	0.38	0.46	0.48
Protein disulfide-isomerase	64.42	47.73	70.53	0.09	0.14	0.01		0.03		0.02	0.09	0.05
E1B 55 kDa protein	63.24	58.20	47.12									
Annexin A2	57.37	53.66	51.90	3.66	0.38	0.80	0.70	1.56	0.92	2.08	1.18	2.23
Peroxiredoxin-2	37.52	33.10	37.38	2.96	0.30	0.27	0.63	1.51	0.25	2.36	1.56	2.28
E1B protein, small T-antigen	28.93	26.99	22.42	0.02	0.03							

10000 ppm — 50th percentile — 20 ppm | 40 ppm — 50th percentile — 0 ppm | 5 ppm — 50th percentile — 0 ppm | 5 ppm — 50th percentile — 0 ppm

***Empty* Capsids**



***Full* Capsids**



- As expected, ability to separate empty and full capsids effected the ability to differentiate HCP loads, however some specificity was observed.
- Similarly, specificity was observed for the serotypes analysed.
- ‘Problematic HCPs’ were investigated in the resulting LC-MS data to evaluate their clearance, as shown in the heatmap, the majority were cleared by AAVx affinity chromatography.

Summary

- Native MS and CDMS can be coupled with upfront anion exchange chromatography for confirmation of capsid fill state. Partial capsids not observed either by chromatography or MS, thought to be due to GOI size.
- Viral protein separation possible using various chemistries, HILIC method works well and is simple to deploy, however, reversed-phase outperforms for separation of deamidated forms.
- Top-down MS/MS showing strong potential for VP specific characterisation. Combination of different ion activation strategies on tribrid MS instrument enabled excellent N- and C-terminal fragmentation.
- HCP behaviour investigated using throughout the downstream process for HEK293 derived serotypes using Orbitrap Astral. Some specificity identified based on the serotype and capsid fill state, however, AAVx affinity chromatography enables bulk clearance.

Acknowledgements

NIBRT:
Josh Smith, Corentin Beaumal, Sara Carillo, Aaron Richardson, Felipe Guapo, Colin Clarke, Florian Füssl, Lisa Strasser, Silvia Millán-Martín

Thermo Fisher Scientific:
Eugen Damoc, Anna Pashkova, Kristina Srzentic, Tabiwang N. Arrey, Kai Scheffler, Kelly Broster, David M. Horn, Min Du, Steve G. Milian, Richard O. Snyder

908 Devices:
Erin Redman

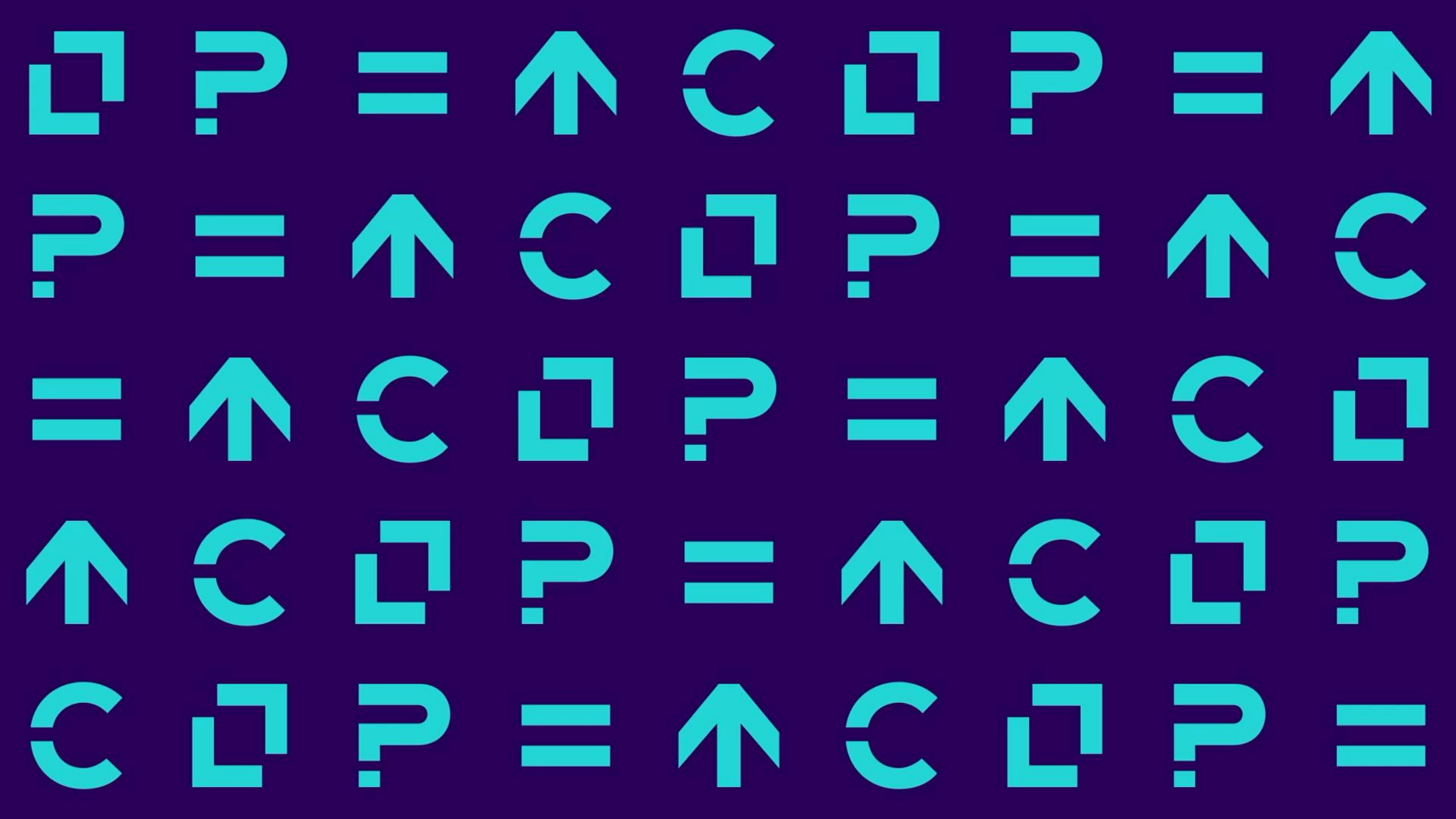
ThermoFisher SCIENTIFIC

908devices

ENTERPRISE IRELAND

Science Foundation Ireland sfi For what's next

nibrt National Institute for Bioprocessing Research and Training



CONCEPT

More info: concept-nibrt.ie