Using DIA to inform the development of Cerebrospinal Fluid triple quad assays

Webinar #22: Using DIA Data To Create SRM Methods

Deanna L. Plubell MS PhD Candidate, MacCoss Lab, University of Washington



Strategies for building a new targeted triple quad assay:

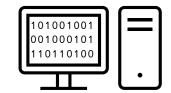
• Analysis of recombinant target proteins

• Search for proteins in existing data

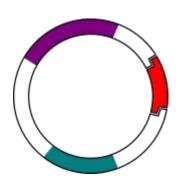
• Use prediction algorithms for selecting peptides





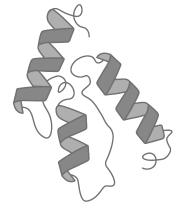


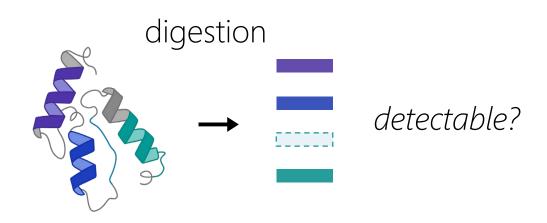
Using recombinant proteins to select peptides



Expand, Purify, In Vitro & Sequence Transcription cDNA clone and Translation

Enrichment





Measurement in a background matrix is important!

Strategies for building a new targeted triple quad assay:

• Analysis of recombinant target proteins

• Search for proteins in existing data

• Use prediction algorithms for selecting peptides

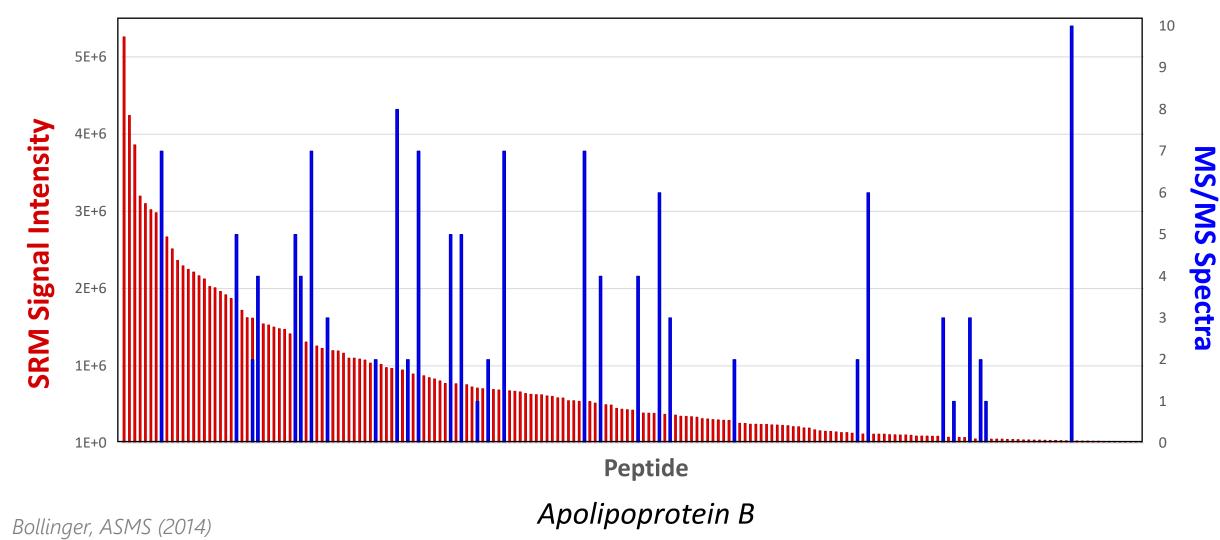






DDA is a poor indicator of SRM peptide performance

SRM DDA



Strategies for building a new targeted triple quad assay:

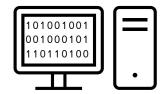
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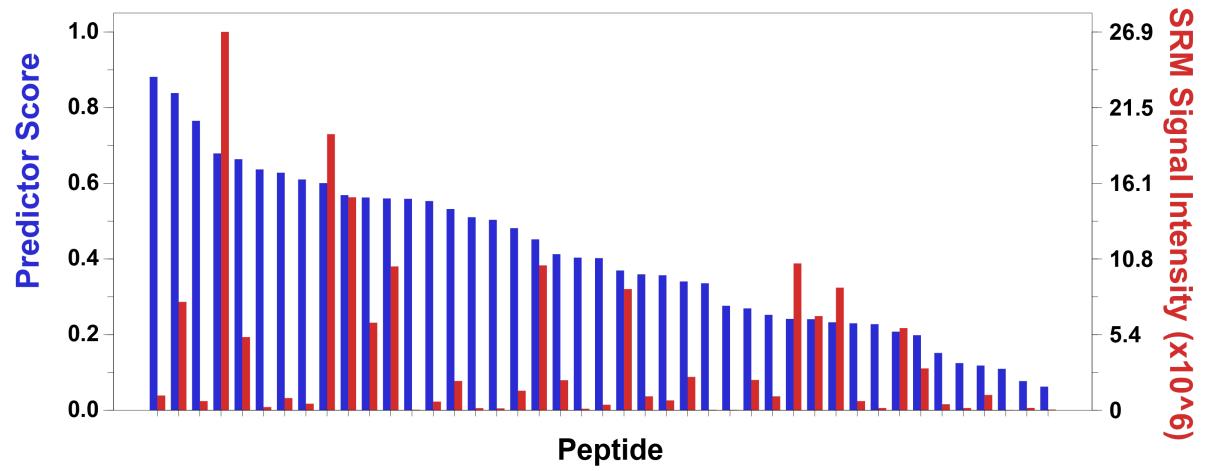






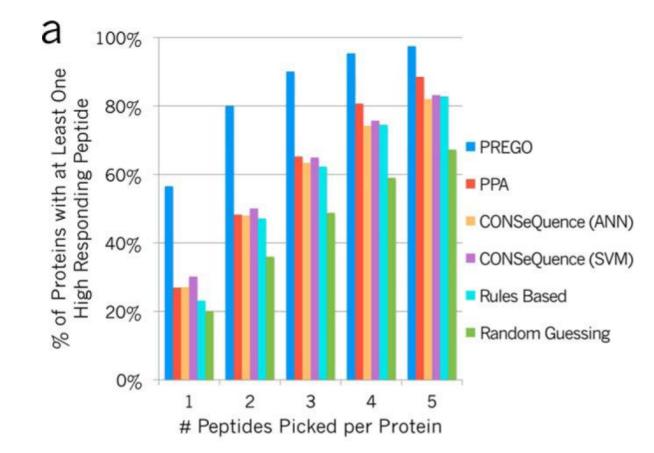
DDA is a poor predictor of SRM peptide performance

NFKB1



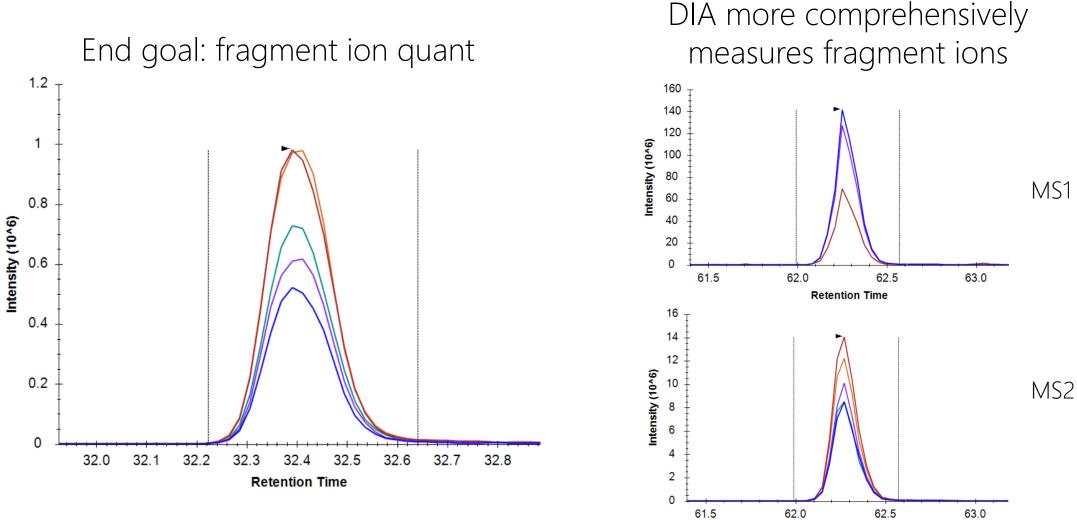
Stergachis et al., Nature Methods (2011)

DIA is a better predictor of SRM peptide performance



Searle et al., Mol. Cell. Proteomics (2015)

DIA provides evidence useful for SRM peptide selection



Retention Time

Strategies for building a new targeted triple quad assay:

• Analysis of recombinant target proteins

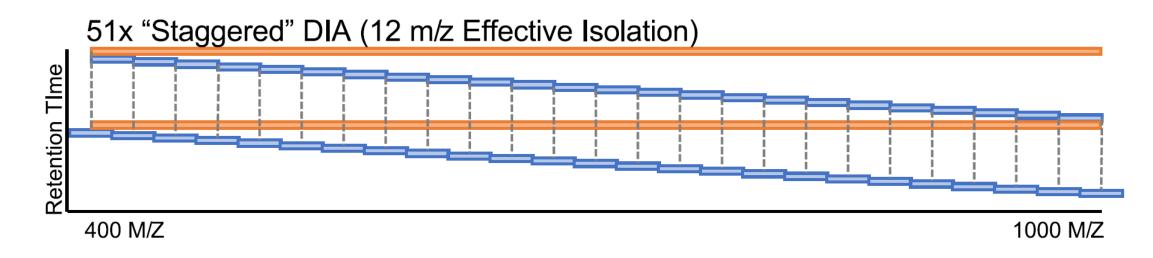
• Search for proteins in existing data ... now with DIA data

• Use prediction algorithms for selecting peptides

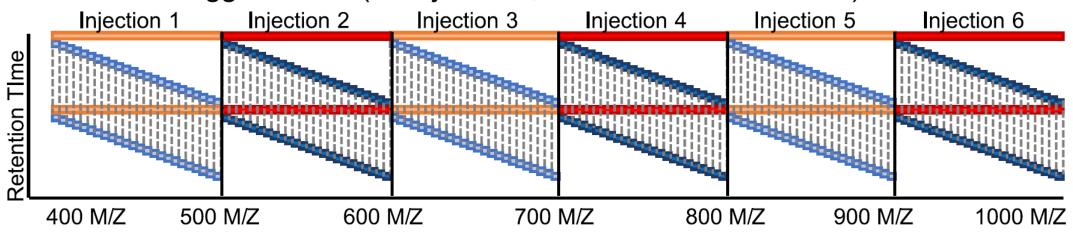




Gas-phase fractionated DIA: narrow isolation

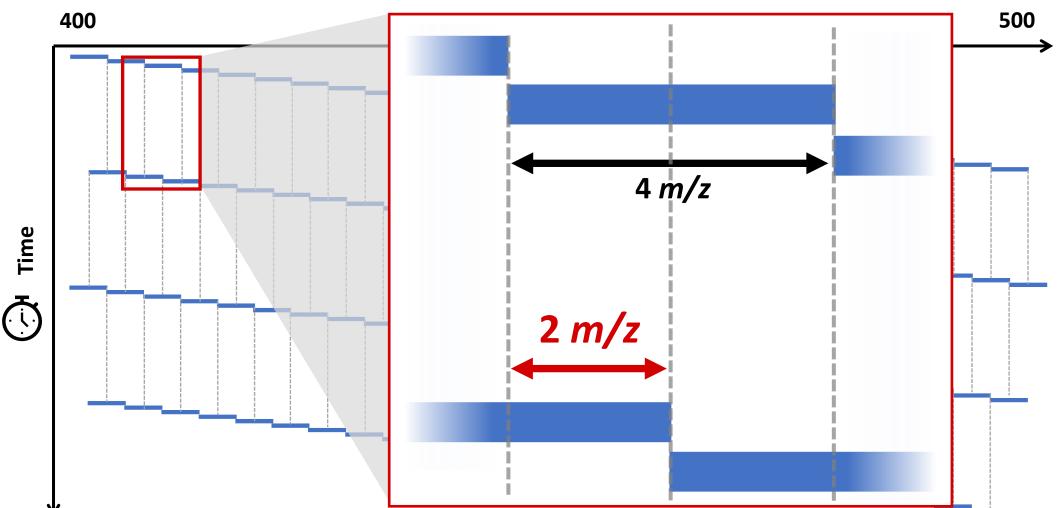


GPF 51x Staggered DIA (x6 Injections, 2 m/z Effective Isolation)



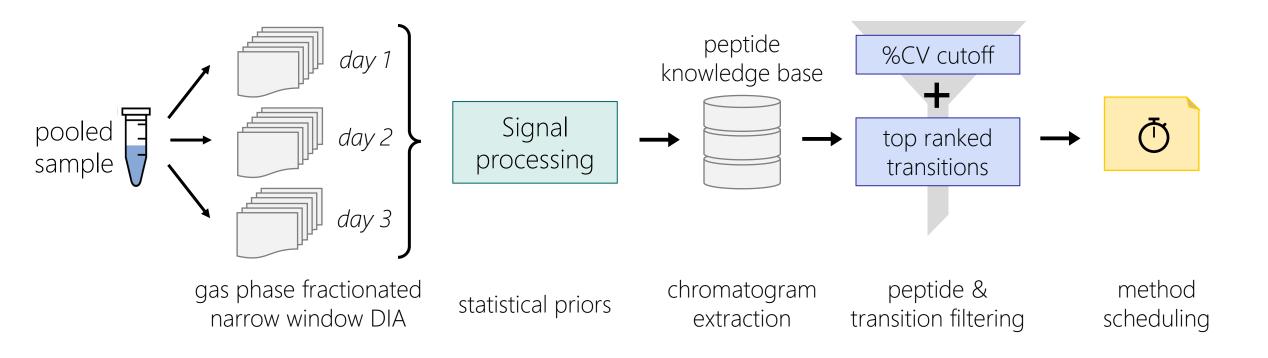
Pino L, et al., Mol. Cell. Prot. (2020)

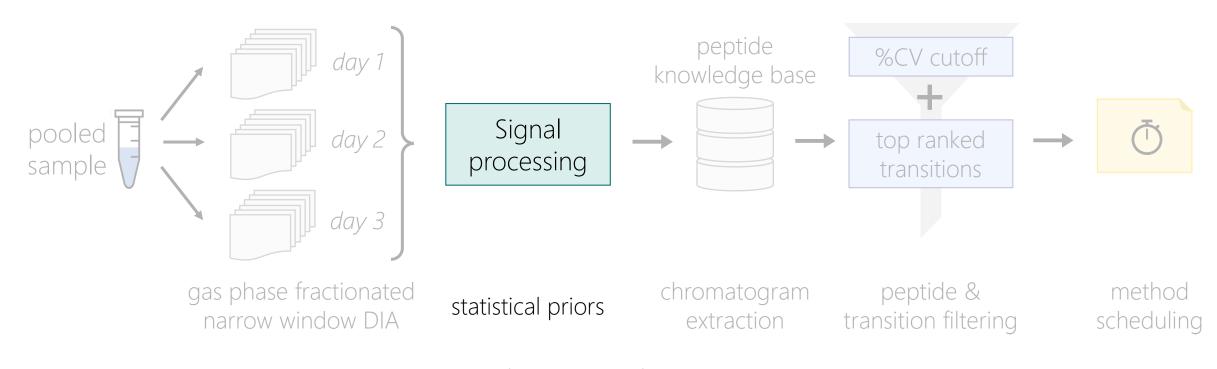
Gas-phase fractionated DIA: narrow isolation



52 4 *m/z-overlapping narrow* windows

Panchaud, A, et al., Anal. Chem. (2009); Ting, Y, et al., Nat. Meth., (2017); Searle, B, et al., Nat. Comm., (2019)

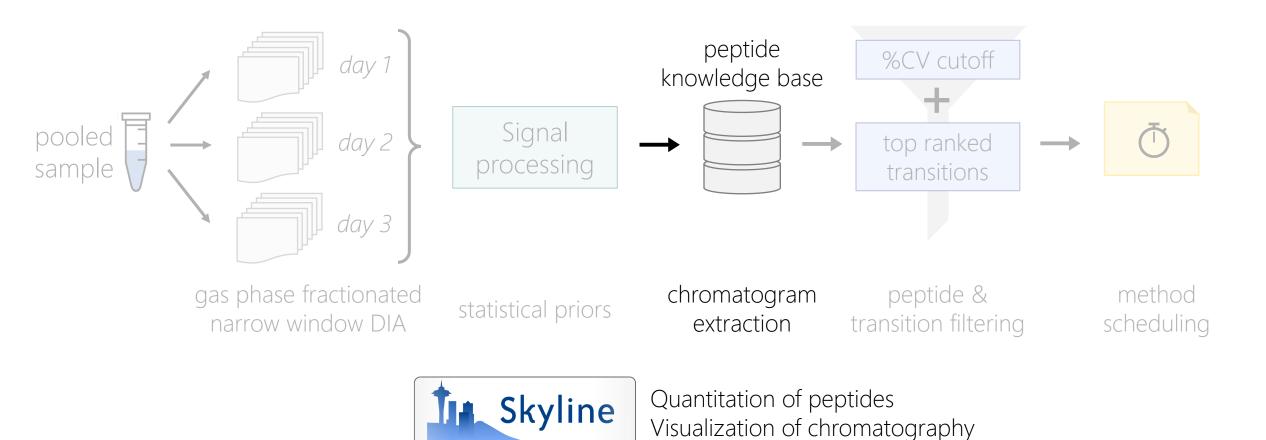


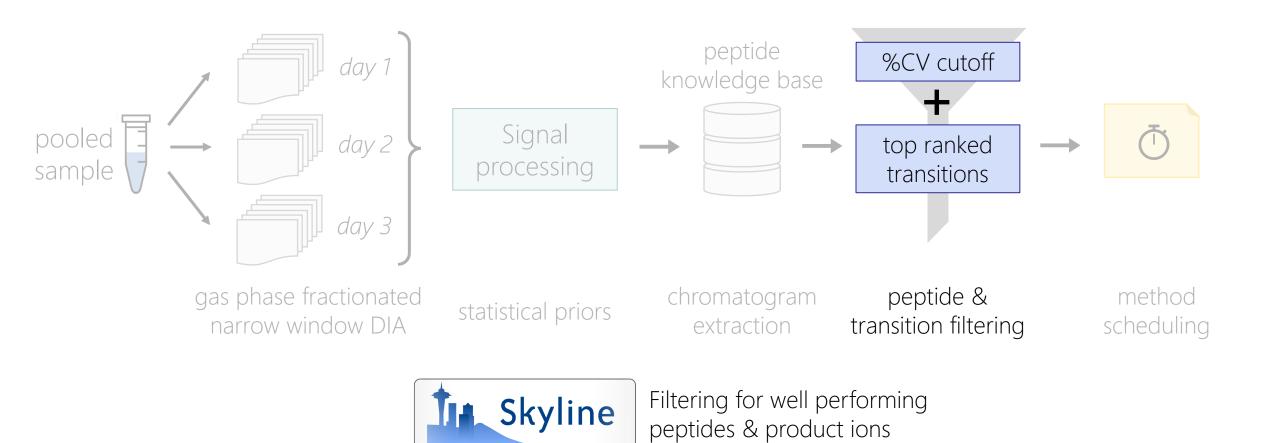


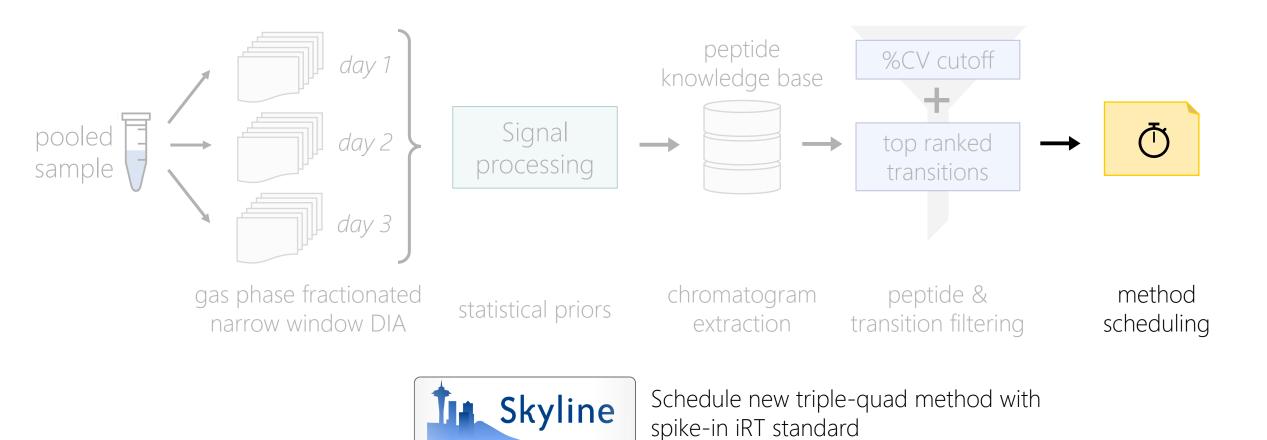


Precursor-product ion pair detection relative retention time Co-elution

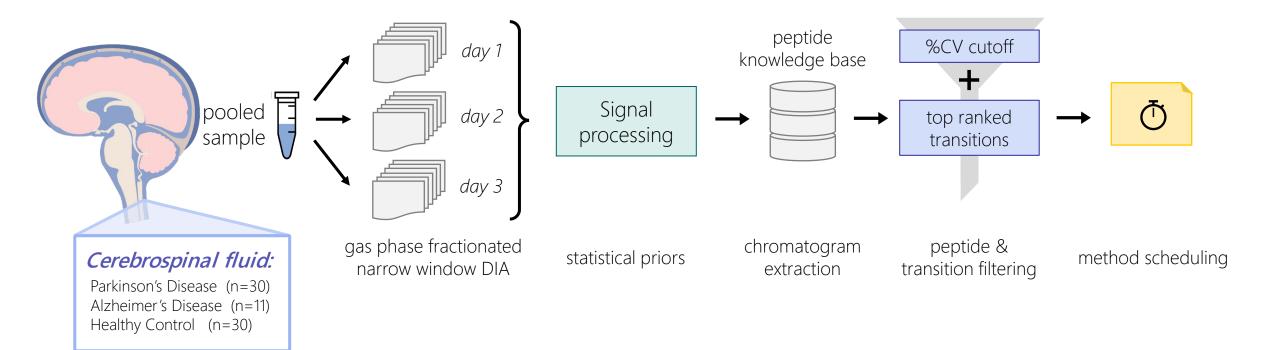
Searle et al., Nat. Comm (2018)



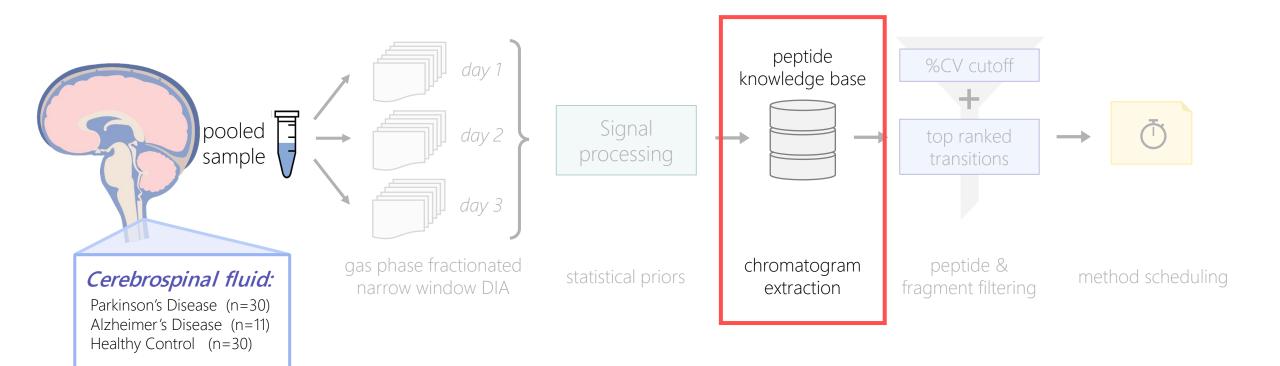




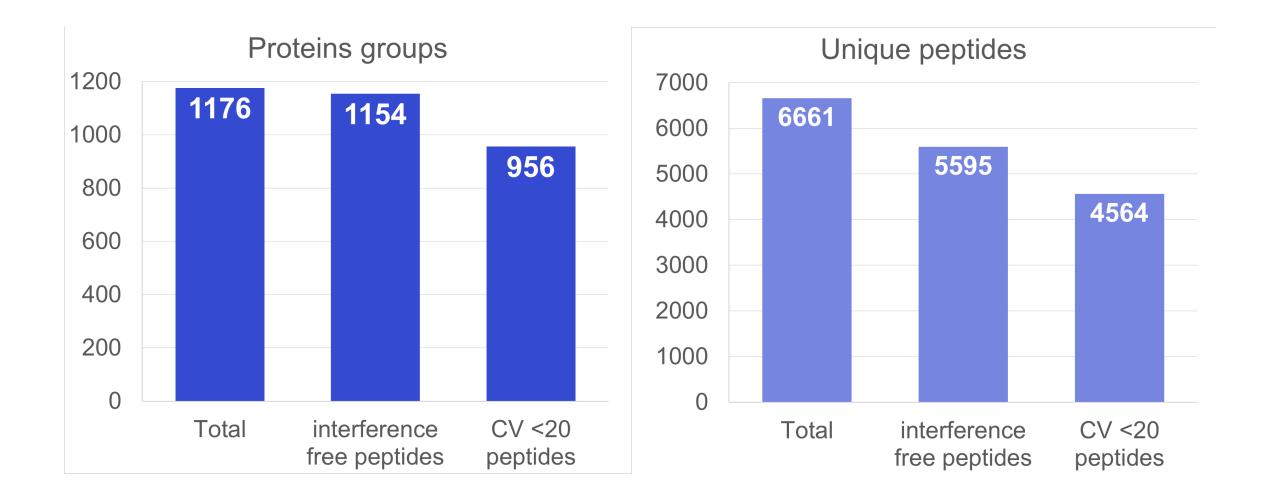
Application to Alzheimer's disease proteins in CSF



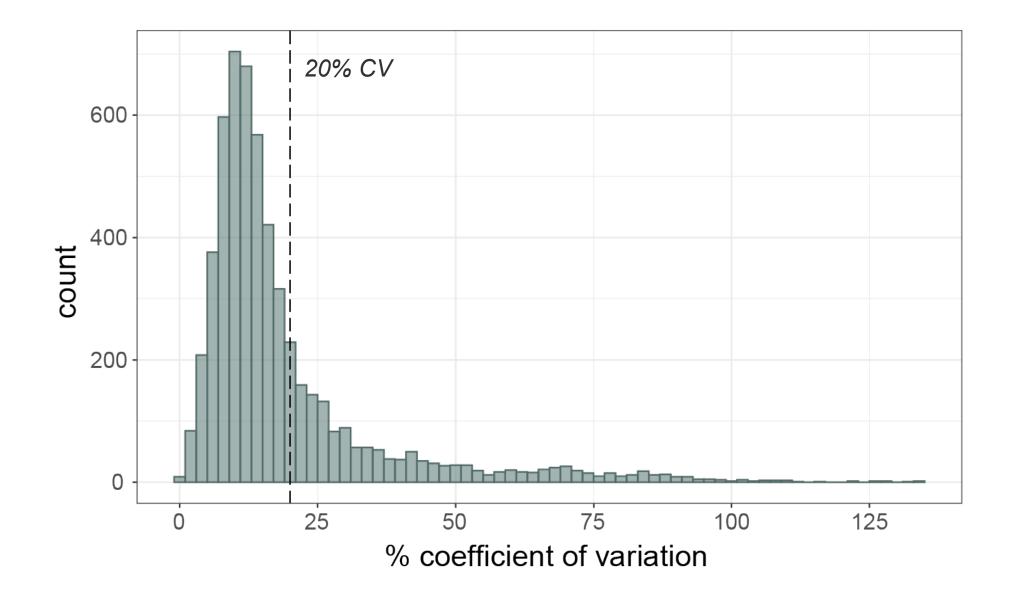
Application to Alzheimer's disease proteins in CSF



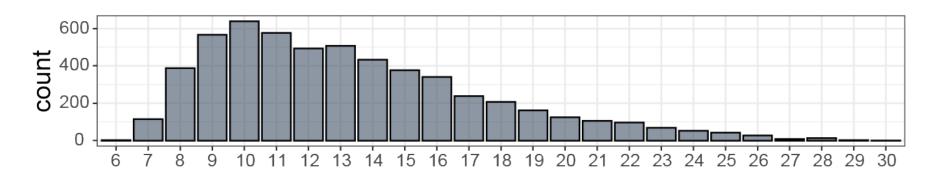
Not all proteins and peptides measured are reproducible

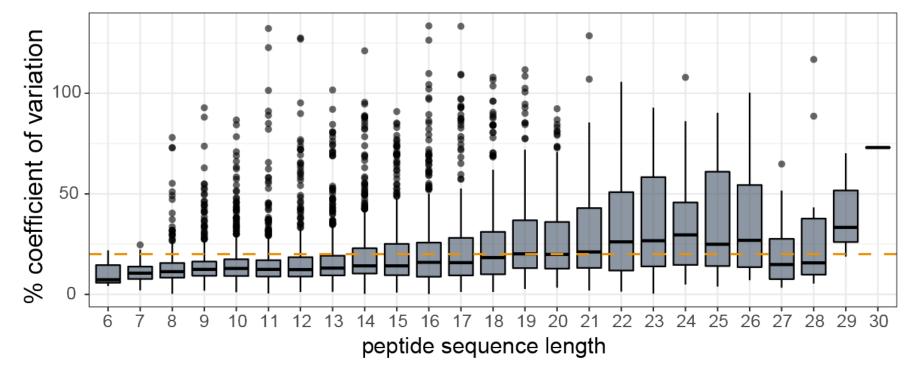


In our DIA a majority of peptides have less than 20% CV

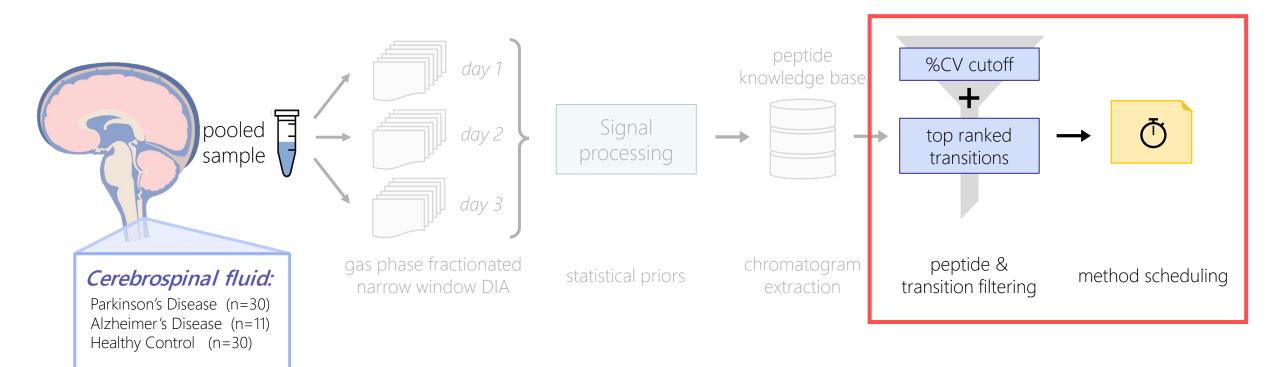


Reproducibility of peptides decreases with increasing sequence length.

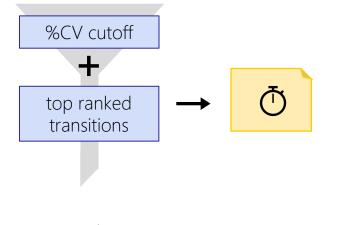




Application to Alzheimer's disease proteins in CSF



Building an assay for Alzheimer's disease proteins in CSF



peptide &	
transition filtering	J

method scheduling

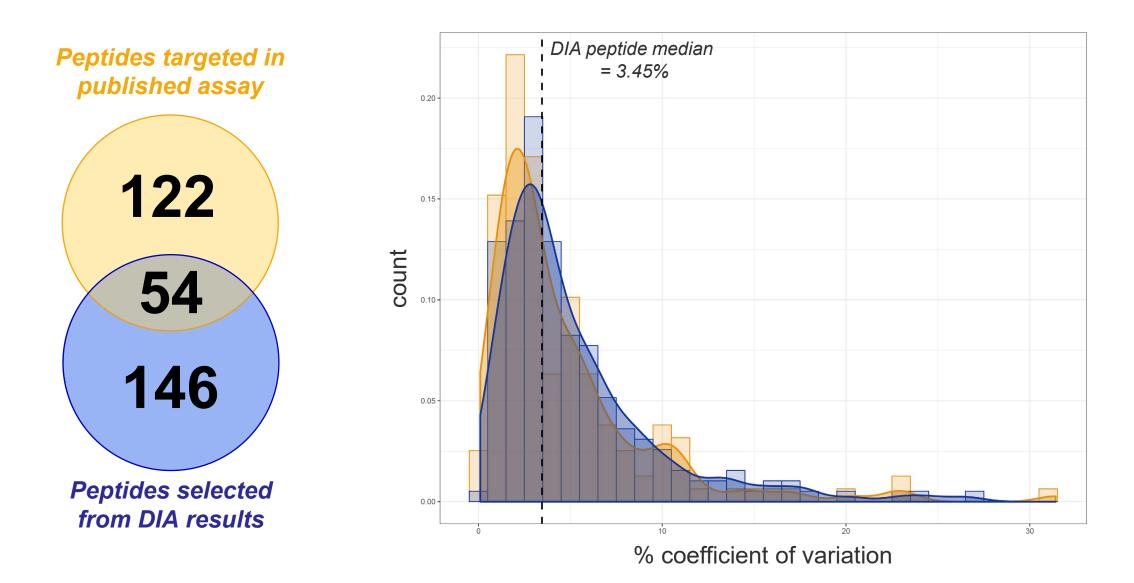
Proteins of interest: 100 from previous Alzheimer's assay (Spellman et al., Proteomics Clin. Appl. 2016)

Peptide filtering criteria for 2 peptides/protein of interest:

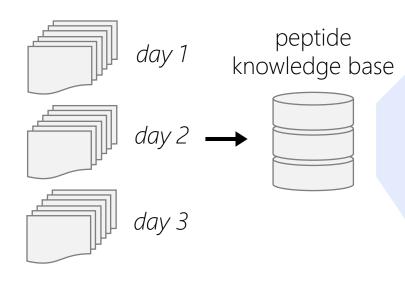
- 5 interference-free product ions (top ranked intensity)
- <20 %CV
- Rank 1-2 based on total product intensity

Peptides from both previous assay and selected from DIA experiment measured in triplicate by SRM on Thermo Altis

Peptides selected from narrow window DIA results perform similarly to previously characterized Alzheimer's disease assay peptide selections



DIA provides useful information for expediting development of multiple triple quadrupole assays



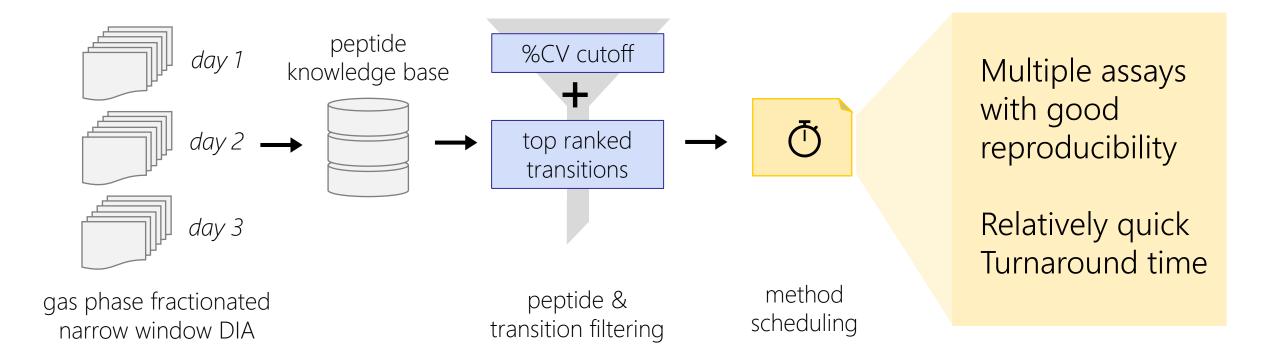
gas phase fractionated narrow window DIA For precursor & product ion pairs:

- Detectable in background
- Retention time
- Reproducibility





DIA provides useful information for expediting development of multiple triple quadrupole assays



We can mine the same data for different targets

The human CSF pain proteome

Payam Emami Khoonsari^{a,c,1}, Elena Ossipova^{b,1}, Johan Lengqvist^b, Camilla I. Svensson^c, Eva Kosek^d, Diana Kadetoff^d, Per-Johan Jakobsson^b, Kim Kultima^{a,2}, Jon Lampa^{b,*,2}

^a Department of Medical Sciences, Clinical Chemistry, Uppsala University, Sweden
^b Unit of Rheumatology, Department of Medicine, Rheumatology Clinic, Karolinska Institute, Karolinska University Hospital, Stockholm, Sweden
^c Department of Physiology and Pharmacology, Karolinska Institute, Stockholm, Sweden
^d Department of Clinical Neuroscience, Karolinska Institute, Stockholm, Sweden

New assay: with 3.06 median %CV!

Acknowledgements

MacCoss Lab Mike MacCoss Eric Huang Gennifer Merrihew Christine Wu Julia Robbins

Skyline/Panorama

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Stanford

Tom Montine Kathleen Poston

<u>UW</u> C. Dirk Keene Andy Hoofnagle



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Overview of our Skyline walk-through:

- 1. Importing GPF DIA search results into Skyline
- 2. Filtering peptides based on %CV
- 3. Filtering target proteins then filtering peptides based on intensity
- 4. Scheduling & exporting transition lists for SRM methods