Question	Answers (Time location in video - min:sec)
Can you talk more about why the data import for the MSE data needed to occur stepwise?	Live answered (Rojas - 19:08)
Very nice talk! Could you tell us more about your sample types and the endogenous peptides you have chosen for your iRT predictor?	Live answered (Rojas - 19:52)
Regarding your two peaks and issues with peak picking, did you use the ion mobility properties to improve the peak picking?	Live answered (Rojas - 19:21)
No Questions Right Now. All Compliments -Fantastic Talk -Excellent Speaker -The Speaker Needs His Own Late Night Show	Live answered (Rojas - 23:25)
These are very general background questions for Mike or anyone : -What experience do you have at moving Skyline, perhaps joined with MassLynx, into a validated environment? -I have only used MassLynx and the Waters mass spectrometers, and their chromatographic systems, within a validated environment, doing therapeutic protein and antibody characterizations. -Moving software into environments like that is highly problematic. -Does anyone have any comments on oHow they have done this, oWhere this is, oHas it done etc. This MassLynx - Skyline interface looks fantastic, but the hurdles of getting it into a validated environment could be immense,	'@Mark Winegard, MSI is designed to be used int he method development space. Once a final method has been developed, all the routine data analysis can be performed the validated MassLynx environment only.
For Mike MacCoss's question to Muluneh Fashe on detergents:	We use two detergents to extract protein, one to remove cytosolic proteins (after homogenization) and the other to solubilize the remaining membrane proteins. The enrichment/cleanup of the sample (we also clean up with solid phase extraction after digestion) is a big help in preventing blockage of the nanoLC. It also helps with electrospray efficiency (decreasing ion suppression).
On the lableled proteins and small diffierence os Retention Time: - What is the label ? Example: Deuterieum is a known bad actor	Live answered (Fashe - 07:31)
Great talk Elena! Have you been able to evaluate the ability of the method/targets to detect different species of shrimp?	Live answered (Barletta - 07:53)
Are the antibodies for tropomyosin also tissue specific, for different muscles?	Live answered (Barletta - 08:52)
How you tried other allergens like arginine kinase, sarcoplasmic CaBP beside tropomyosin?	Live answered (Barletta - 09:29)
What is the potential of this method for detecting “food counterfeiting”? Example: sale of olish horse meat in England as beef	thank you for the question. I see a great potential for PRM as we were able to distinguish tropomyosin from different species. I'll imagine that species specific peptides could be used to distinguish between the two different meat and detect counterfeiting.
Note on the last 2 talks: -Decades ago, meat production was done on a local scale. -Currently, this moved into a mass production industry, with multinational pipelines and worldwide distribution. In this new system there are rampant opportunities for either contamination, or counterfeiting. This has been an immense problem at various times. -Contamination by shellfish proteins can be deadly to certain people -Meat counterfeiting has multiple health and legal issues •Are there comments on utilizing these methods within this worldwide regulatory situation?	Thanks for the question. Of course everything that we are working on at the moment is related to cantamination of seafood in commons consumed food like meat which could induce and allergic reaction or even an anaphylactic shock. It is indeed a huge issue and hopefully with our research we will be able to address this on a regulatory point of view, mostly in the way our food is processed.
Thank you for the nice talk. Do you also add heavy peptides as internal standards for normalization in your actual samples? Do you vary the amount of heavy spike-ins to avoid extreme L/H ratios when your light analyte concentration varies across several orders of magnitude?	Live answered (Ramachandran - 24:54)
How did you calculate the recovery of your peptides ?	Recovery is calculated for the test samples we have prepared with known concentration of allergens. It is basically (concentration of allergen interpolated from calibration curve/concentration of allergen present in the test sample) *100 We calculate this with respect to each of the target peptides
Where do you list your up-coming webinars, courses, etc. ???	We post all our upcoming training to the homepage of the Skyline site ... scroll to the 'Join Us' section https://skyline.ms/Skyline.url
Skyline Batch is a great tool! Any chance you would add Python support there in addition to R?	Live answered (MacLean - 28:00)
Autointegration always need amount of time manual work, is there solution?	Live answered (MacLean - 33:07)