**SRMAtlas Tutorial**

Please follow along in this tutorial as we go through it in the class. If you have suggestions or bug reports, please email them to Ulrike.Kusebauch@systemsbiology.org.

Explore the SRMAtlas transition interface:

* + Access SRMAtlas at [www.srmatlas.org](http://www.srmatlas.org). Click on “Search SRM assays” under DATA ACCESS in the left navigation bar. Alternative: If you are at a page in the PeptideAtlas database, select “Query Transitions” under the “SRMAtlas” tab.
	+ Examine the query page.
	+ Select PABST Build: Complete Human SRMAtlas.
	+ Temporary: Enter your email address to access the complete human SRMAtlas build, click “Agree to terms” (not required for yeast and Mycobacterium tuberculosis builds).

Example 1:

* + Protein Accession: Type in this field P28482.
	+ Keep default settings in all other fields.
	+ Click “QUERY” at the bottom of the form.
	+ The “Results” tab will open up.
	+ Examine result page.

Q1: How many peptides and how many transitions per peptide are displayed?

* + Click on the QQQ SRM chromatogram icon as well as on the QTOF and QTRAP MS/MS icon for peptide HENIIGINDIIR, examine spectra.

Example 2

* + Click on the “Form” tab to start a new query.
	+ Select PABST Build: Complete Human SRMAtlas.
	+ Protein Accession: Type in this field P28482.
	+ Num of highest Inten Frag Ions to Keep: 3.
	+ Number of peptides per protein constraint: 8.
	+ Target Instrument: Agilent QQQ.
	+ Elution Time Type: RT\_catalogue chipcube.
	+ Keep default values in all other fields.
	+ Click “QUERY”.
	+ The “Results” tab will open up.
	+ Click on “Show more rows” at bottom of table.

Q2: How many peptides are displayed? How many peptides have transitions derived from the QQQ and how many from the QTRAP MS instrument? Were all peptides observed or are predicted peptides displayed? (A2)

Example 3

* + Click on the “Form” tab to start a new query.
	+ Select PABST Build: Complete Human SRMAtlas.
	+ Protein Accession: Type in this field P28482.
	+ Num of highest Inten Frag Ions to Keep: 3.
	+ Number of peptides per protein constraint: 3
	+ Target Instrument: Agilent QQQ.
	+ Duplicate Peptides: No Multi-mapping.
	+ Elution Time Type: RT\_catalogue chipcube.
	+ Heavy Label: Select [Lysine +8] and [Arginine +10]
	+ Labeled Transitions: Select [L&H].
	+ Click “QUERY”.
	+ The “Results” tab will open up.

Q3: Examine the results, what changed? (A3)

Answers:

* A1: Five peptides and four transitions per peptide are displayed.
* A2: Transitions for eight peptides are displayed. Transitions for seven peptides are derived from QQQ and for one peptide from QTRAP. All peptides have been observed on either QTOF, QQQ or QTRAP, no predicted transitions are among the results.
* A3: Three unlabeled (light) and three labeled (heavy) transitions are displayed for each of the three peptides. All displayed peptides are unique.