

LIFE SCIENCE MASS SPECTROMETRY

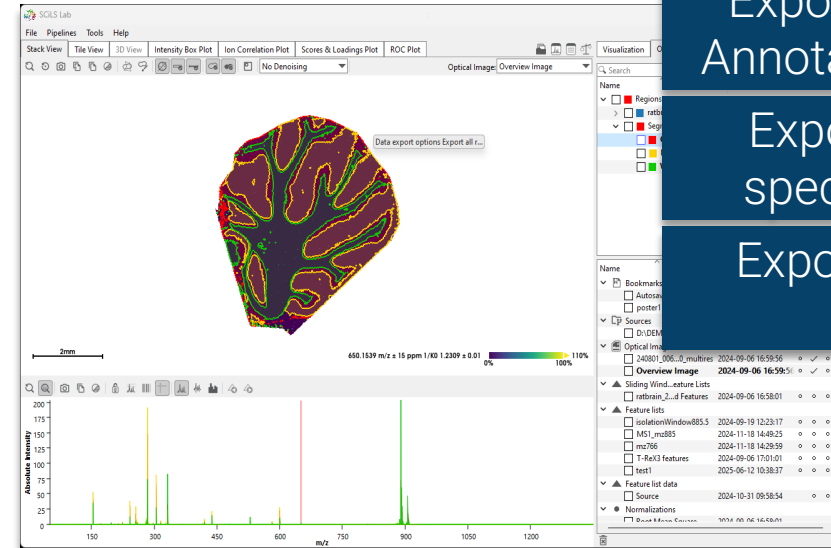
SCiLS™ Lab 2026b – What's New?

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01 *Data export options*
Molecular Annotations, MGF, Box plots

02 *T-ReX feature finding*
Performance improvements

03 *Multiple feature enhancements*
SCiLS start-up procedure, QuPath plugin



Export Molecular Annotations to CSV
Export average spectra to MGF
Export box plots to CSV



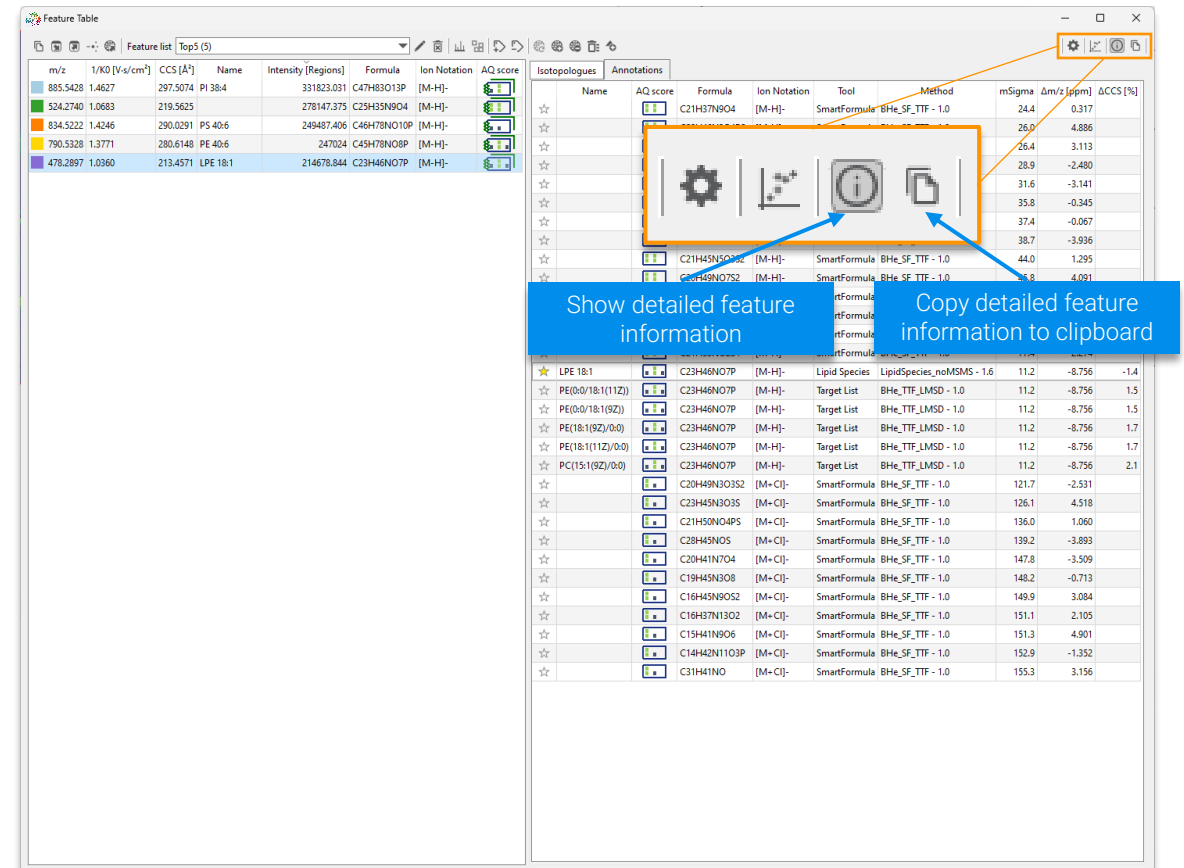
01

Data export options

Data export options

Export all results from Molecular Annotation on a Feature List

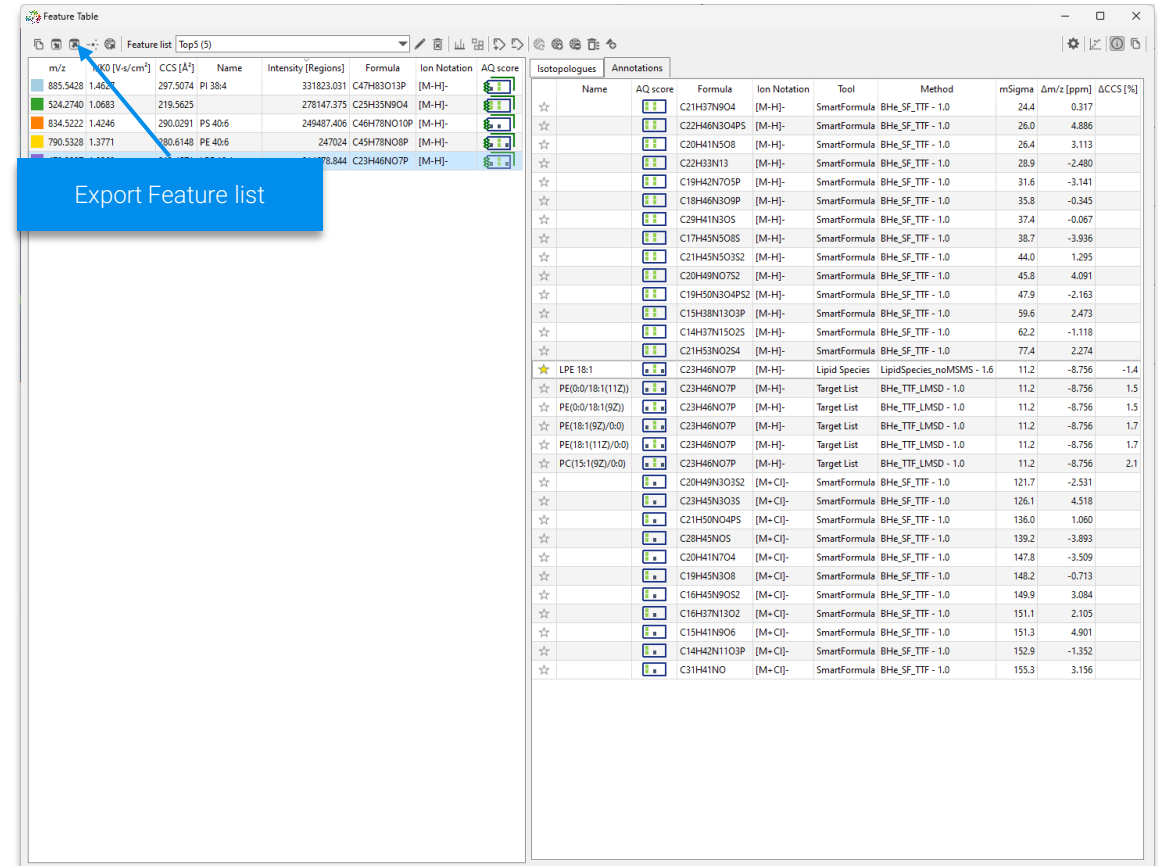
- **MetaboScape®-powered Molecular Annotation** in SCiLS Lab is a powerful workflow to annotate images with confidence.
- Use the **Target List**, **Lipid Species**, and **Smart Formula** annotation tools to annotate features in SCiLS Lab.
- **Copy the list of annotations for a single feature** from the Annotations panel.



Data export options

Export all results from Molecular Annotation on a Feature List

- **MetaboScape®-powered Molecular Annotation** in SCiLS Lab is a powerful workflow to annotate images with confidence.
- Use the **Target List**, **Lipid Species**, and **Smart Formula** annotation tools to annotate features in SCiLS Lab.
- **Copy the list of annotations for a single feature** from the Annotations panel.
- Now you can also **Export a Feature list as “Molecular Annotations CSV”**, which generates a CSV file containing all Molecular Annotation results of the selected feature list.
- **Save as type: Molecular Annotations CSV (*.csv)**



The screenshot displays the SCiLS Lab software interface. The top panel shows the 'Feature Table' with columns for m/z, X0 [V-s/cm²], CCS [Å], Name, Intensity [Regions], Formula, Ion Notation, and AQ score. A blue callout box labeled 'Export Feature list' points to a button in the top right of this panel. The bottom panel shows the 'Annotations' table with columns for Name, AQ score, Formula, Ion Notation, Tool, Method, mSigma, Δm/z [ppm], and ΔCCS [%].

Feature Table		Annotations									
m/z	X0 [V-s/cm ²]	CCS [Å]	Name	AQ score	Formula	Ion Notation	Tool	Method	mSigma	Δm/z [ppm]	ΔCCS [%]
885.5428	1.4627	297.5074	PI 38:4	331823.031	C47H83O13P	[M-H]-	SmartFormula	BHe_SF_TTF - 1.0	24.4	0.317	
524.2740	1.0683	219.5625		278147.375	C29H39N9O4	[M-H]-	SmartFormula	BHe_SF_TTF - 1.0	26.0	4.886	
834.5222	1.4246	290.0291	PS 40:6	249487.406	C46H78NO10P	[M-H]-	SmartFormula	BHe_SF_TTF - 1.0	26.4	3.113	
790.5328	1.3771	380.6148	PE 40:6	247024	C45H78NO8P	[M-H]-	SmartFormula	BHe_SF_TTF - 1.0	28.9	-2.480	
				178.844	C23H46NO7P	[M-H]-	SmartFormula	BHe_SF_TTF - 1.0	31.6	-3.141	
							SmartFormula	BHe_SF_TTF - 1.0	35.8	-0.345	
							SmartFormula	BHe_SF_TTF - 1.0	37.4	-0.067	
							SmartFormula	BHe_SF_TTF - 1.0	38.7	-3.936	
							SmartFormula	BHe_SF_TTF - 1.0	44.0	1.295	
							SmartFormula	BHe_SF_TTF - 1.0	45.8	4.091	
							SmartFormula	BHe_SF_TTF - 1.0	47.9	-2.163	
							SmartFormula	BHe_SF_TTF - 1.0	59.6	2.473	
							SmartFormula	BHe_SF_TTF - 1.0	62.2	-1.118	
							SmartFormula	BHe_SF_TTF - 1.0	77.4	2.274	
							Lipid Species	LipidSpecies_noMSMS - 1.6	11.2	-8.756	-1.4
							Target List	BHe_TTF_LMSD - 1.0	11.2	-8.756	1.5
							Target List	BHe_TTF_LMSD - 1.0	11.2	-8.756	1.5
							Target List	BHe_TTF_LMSD - 1.0	11.2	-8.756	1.7
							Target List	BHe_TTF_LMSD - 1.0	11.2	-8.756	1.7
							Target List	BHe_TTF_LMSD - 1.0	11.2	-8.756	2.1
							SmartFormula	BHe_SF_TTF - 1.0	121.7	-2.531	
							SmartFormula	BHe_SF_TTF - 1.0	126.1	4.518	
							SmartFormula	BHe_SF_TTF - 1.0	136.0	1.060	
							SmartFormula	BHe_SF_TTF - 1.0	139.2	-3.893	
							SmartFormula	BHe_SF_TTF - 1.0	147.8	-3.509	
							SmartFormula	BHe_SF_TTF - 1.0	148.2	-0.713	
							SmartFormula	BHe_SF_TTF - 1.0	149.9	3.084	
							SmartFormula	BHe_SF_TTF - 1.0	151.1	2.105	
							SmartFormula	BHe_SF_TTF - 1.0	151.3	4.901	
							SmartFormula	BHe_SF_TTF - 1.0	152.9	-1.352	
							SmartFormula	BHe_SF_TTF - 1.0	155.3	3.156	



Data export options

Export all results from Molecular Annotation on a Feature List

The Molecular Annotation CSV contains every molecular annotation result for every feature in the Feature list

Features have a feature ID for easy sorting

Manually adjusted feature names shall be written to a new line in the CSV

Features without name or annotation details are also included in the Molecular Annotations CSV

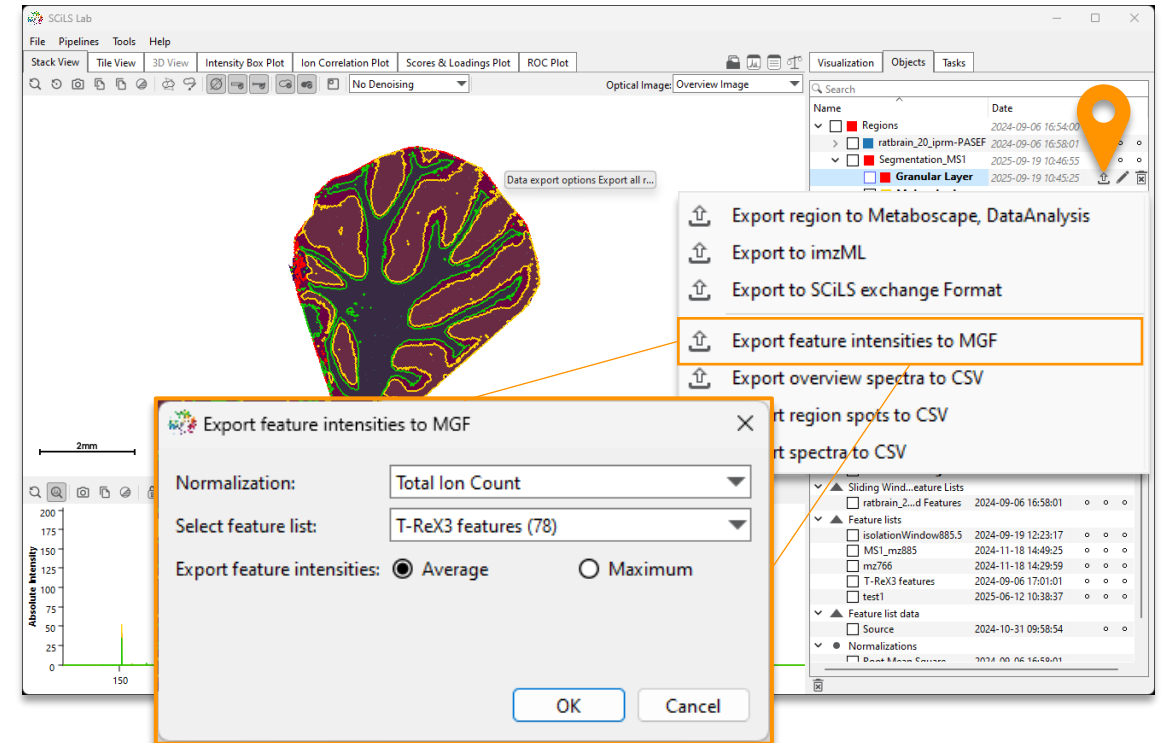
The Molecular Annotations CSV from iprm-PASEF data sets only contains annotation results for Precursor features

```
# Exported with SCILS Lab Nightly Version 14.00.17939.4493
# Export time: 2025-09-19 10:01:10
# Generated from file: E:\DEMO_data\develop\iprm-PASEF\MS1\MS1.slx
# Object Full Name: Top5
# Object ID: 8716f928-b075-4db5-89b2-409e643c00b7
# Object type: Static feature list
# Object creation time: 2025-09-19 09:02:37
#
featureID;m/z;Interval Width (+/- Da);1/E0 [V·s/cm²];1/E0 Interval Width (+/- V·s/cm²);CCS [Å²];CCS Interval Width (+/- Å²);Color;Intensity [Regions];*;Name;AQ score;Formula;Ion Notation;Tool;Method;mSigma;Δm/z;ΔCCS
[1];885.5428;0.013283142285445;1.4627;0.01;297.5074;2.0339170401639;fa6cee3;331823.03125;PI 38.4;10200;C47H83O13P;[M-H]-;Lipid Species;LipidSpecies_noMSMS - 1.6;27.3;-7.943;
[1];885.5428;0.013283142285445;1.4627;0.01;297.5074;2.0339170401639;fa6cee3;331823.03125;SODG (18:0/18:0);10200;C45H86O12S;[M+Cl]-;Target List;BHe_TTF_LMSD - 1.0;71.5;-11.949;
[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20200;C25H35N9O4;[M-H]-;SmartFormula;BHe_SF_TTF - 1.0;24.6;0.112;
[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20200;C26H44N3O4PS;[M-H]-;SmartFormula;BHe_SF_TTF - 1.0;28.0;4.281;
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[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20200;C24H39N5O8;[M-H]-;SmartFormula;BHe_SF_TTF - 1.0;30.2;2.663;
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[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20200;C16H43N7O10S;[M-H]-;SmartFormula;BHe_SF_TTF - 1.0;64.3;3.906;
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[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20100;C24H47N3O3S2;[M+Cl]-;SmartFormula;BHe_SF_TTF - 1.0;116.2;-2.486;
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[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20100;C16H43N9O6S;[M+Cl]-;SmartFormula;BHe_SF_TTF - 1.0;126.2;-2.136;
[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20100;C25H48N04PS;[M+Cl]-;SmartFormula;BHe_SF_TTF - 1.0;127.5;0.791;
[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20100;C32H43N0S;[M+Cl]-;SmartFormula;BHe_SF_TTF - 1.0;130.5;-3.728;
[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20100;C24H39N07O4;[M+Cl]-;SmartFormula;BHe_SF_TTF - 1.0;149.7;-3.378;
[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20100;C23H43N3O8;[M+Cl]-;SmartFormula;BHe_SF_TTF - 1.0;150.1;-0.827;
[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20100;C21H48N09P;[M+Cl]-;SmartFormula;BHe_SF_TTF - 1.0;151.4;-3.982;
[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20100;C20H35N13O2;[M+Cl]-;SmartFormula;BHe_SF_TTF - 1.0;152.5;1.744;
[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20100;C19H39N9O6;[M+Cl]-;SmartFormula;BHe_SF_TTF - 1.0;152.7;4.295;
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[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20100;C17H44N7O7P;[M+Cl]-;SmartFormula;BHe_SF_TTF - 1.0;154.8;1.140;
[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20100;C17H47N9O8S;[M+Cl]-;SmartFormula;BHe_SF_TTF - 1.0;154.8;-3.794;
[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20100;C20H51N5S4;[M+Cl]-;SmartFormula;BHe_SF_TTF - 1.0;155.1;3.529;
[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;;;20100;C35H39N0;[M+Cl]-;SmartFormula;BHe_SF_TTF - 1.0;157.1;2.702;
[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;PE(22:6(4Z,7Z,10Z,13Z,16Z,19Z)/0:0);10200;C27H44N07P;[M-H]-;Target List;BHe_TTF_LMSD - 1.0;15.3;-8.164;-5.2
[2];524.274;0.0078641097436503;1.0683;0.01;219.5625;2.0552932038958;#33a02c;278147.375;PE(18:2(4Z,7Z,10Z,13Z,16Z,19Z));10200;C27H44N07P;[M-H]-;Target List;BHe_TTF_LMSD - 1.0;15.3;-8.164;-5.4
[3];834.5222;0.012517833557126;1.4246;0.01;290.0291;2.0358226670617;#ff7f00;249487.40625;PS(0:0/22:6(4Z,7Z,10Z,13Z,16Z,19Z));10100;C46H78N010P;[M-H]-;Lipid Species;LipidSpecies_noMSMS - 1.6;102.8;-8.174;
[3];834.5222;0.012517833557126;1.4246;0.01;290.0291;2.0358226670617;#ff7f00;249487.40625;PS(18:2(9Z,12Z)/22:4(7Z,10Z,13Z,16Z));10100;C46H78N010P;[M-H]-;Target List;BHe_TTF_LMSD - 1.0;102.8;-8.174;-4.0
[3];834.5222;0.012517833557126;1.4246;0.01;290.0291;2.0358226670617;#ff7f00;249487.40625;PS(22:4(7Z,10Z,13Z,16Z)/18:2(9Z,12Z));10100;C46H78N010P;[M-H]-;Target List;BHe_TTF_LMSD - 1.0;102.8;-8.174;-4.0
```

Data export options

Export region average spectra to the Mascot Generic Format

- The **Mascot Generic Format (MGF)** is a common data format to share MS and MS/MS spectra between many third-party and open-source software solutions.
- **iprm-PASEF MS/MS spectrum export** for specific regions of interest, or for applications that are not supported by MetaboScape®-powered Molecular Annotation (e.g. bottom-up proteomics)
- **NOTE:** For non-iprm-PASEF data, only m/z feature export to MGF is supported





Data export options

Export region average spectra to the Mascot Generic Format

iprm-PASEF MGF file

```
# Exported with SCiLS Lab Nightly Version 14.00.17939.4493
# Export time: 2025-09-19 11:04:34
# Generated from file: E:\DEMO_data\develop\iprm-PASEF\iprm-PASEF\iprm-PASEF.slx
# Object Full Name: Regions/Segmentation_MS1/Granular Layer
# Object ID: f4ef25d7-2f84-46f0-a59e-97637285cfcb
# Object type: Region
# Object creation time: 2024-09-06 18:01:01
# Feature list: T-ReX3 features
# Normalization: Total Ion Count
# Intensity: Average
#
BEGIN IONS
TITLE=Isolation window 415.2029 m/z, 1/R0 0.95679181647464
PEPMASS=415.12051397013
CHARGE=1-
279.23191692319 563.62768554688
END IONS

BEGIN IONS
TITLE=Isolation window 437.2481 m/z, 1/R0 1.004750989919
PEPMASS=437.13376168725
CHARGE=1-
152.99540321763 2527.4045410156
153.21977364869 0.94933807849884
153.34253125716 1.1382474899292
153.59919240274 0.6656539440155
171.00581646392 140.90646362305
255.23213211603 188.58235168457
256.23545753531 321.30892944336
283.26313041072 210.87565612793
438.14623279753 3.7007949352264
END IONS

BEGIN IONS
TITLE=Isolation window 437.2481 m/z, 1/R0 1.004750989919
PEPMASS=437.26553378905
CHARGE=1-
152.99540321763 2527.4045410156
153.21977364869 0.94933807849884
153.34253125716 1.1382474899292
153.59919240274 0.6656539440155
171.00581646392 140.90646362305
255.23213211603 188.58235168457
256.23545753531 321.30892944336
283.26313041072 210.87565612793
438.14623279753 3.7007949352264
END IONS
```

Precursors are sorted in ascending order and grouped by Isolation Window

Exported (fragment) feature intensities are either the region average or the maximum intensity over the exported region

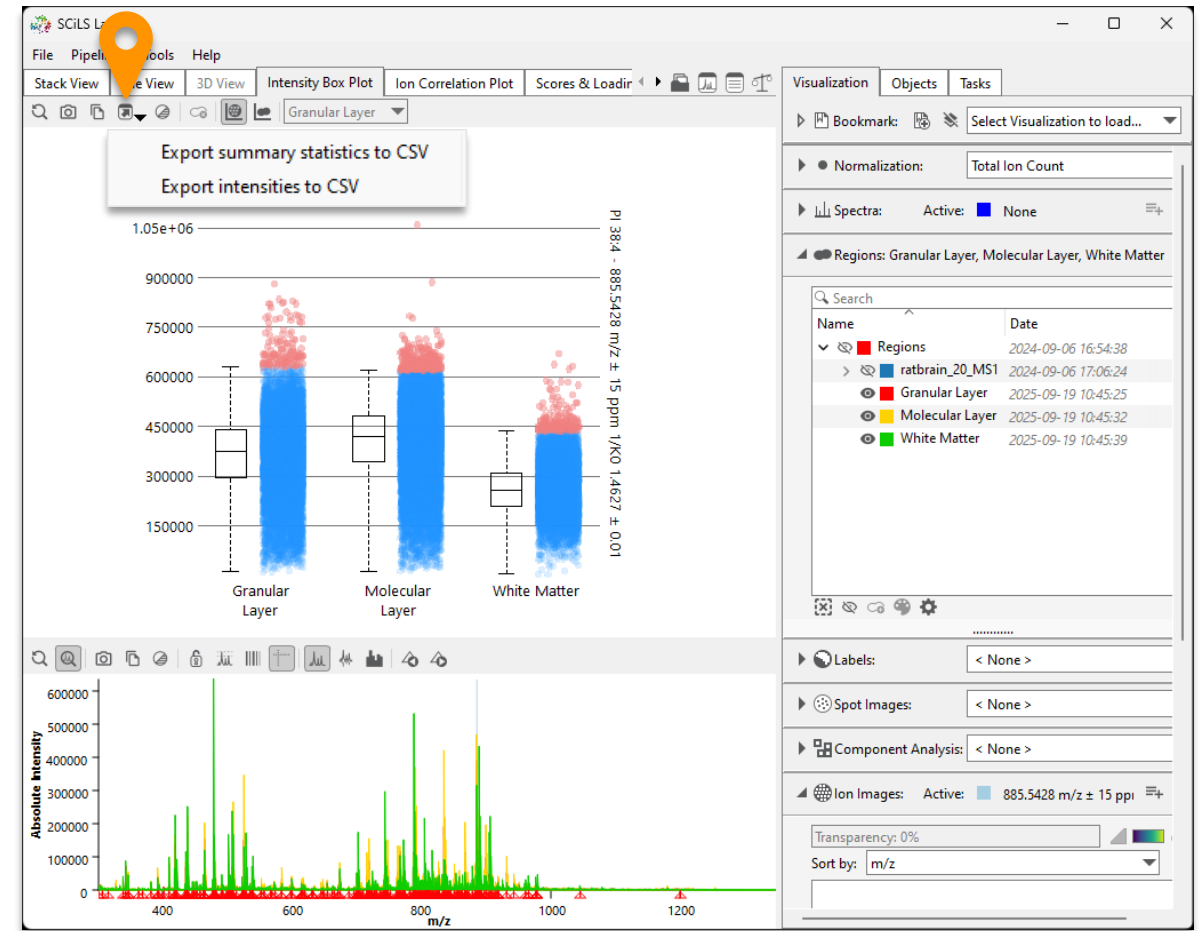
Non-iprm-PASEF MGF file

```
# Exported with SCiLS Lab Nightly Version 14.00.17939.4493
# Export time: 2025-09-19 11:15:37
# Generated from file: E:\DEMO_data\develop\iprm-PASEF\MS1\MS1.slx
# Object Full Name: Regions/Granular Layer
# Object ID: b0d0f3d3-f630-42cf-a08b-a48c6e75345d
# Object type: Region
# Object creation time: 2025-09-19 12:14:44
# Feature list: m/z_features
# Normalization: Total Ion Count
# Intensity: Average
#
# m/z int
300.0414 7520.908203125
306.0738 22051.166015625
315.0470 15549.157226562
338.1628 57001.75390625
342.1331 131930.34375
346.0536 75267.546875
347.0368 7009.8735351562
362.0585 656.1005859375
368.1926 11354.025390625
381.2023 41297.953125
391.2214 94206.7109375
391.2217 94233.625
393.2362 31053.94140625
401.0131 15807.696289062
409.2310 134262.515625
417.2366 87497.3984375
417.2375 87511.03125
419.2528 282179.71875
419.2528 282179.71875
421.2680 107149.8984375
421.2683 107134.7890625
433.2327 30035.490234375
435.2473 131326.484375
436.2795 64381.12890625
436.2799 64394.640625
437.2629 291902.6875
437.2632 291905
439.2206 27856.9140625
445.2456 1426.1507568359
447.2838 24311.703125
450.2341 42014.2421875
452.2743 24852.23046875
457.2306 27405.310546875
462.2939 67832.078125
```

Data export options

Export box plots to CSV

- The SCiLS Lab box plots provide insight into the intensity distribution of features over specific regions.
- To enhance the insight or to enable custom visualizations, **the box plots can now be exported as CSV files** containing:
 - Box plot summary statistics
 - Box plot intensities
- Functionality available for both Ion Image mode and Region mode



Data export options

Export box plots to CSV

Box plot summary statistics (ion image mode)

```
# Exported with SCiLS Lab Nightly Version 14.00.17939.4493
# Export time: 2025-09-19 12:51:50
# Generated from file: E:\DEMO_data\develop\iprm-PASEF\MS1\MS1.slx
# Export: Box Plot Ion Image Mode - summary statistics
# Feature: PI 38:4 - 885.5428 m/z ± 15 ppm 1/K0 1.4627 ± 0.01
#
# Interval processing mode: Peak Area
# Normalization: Total Ion Count
#
RegionFullName;RegionName;WhiskerTop;BoxTop;Median;BoxBottom;WhiskerBottom
Regions/Granular Layer;Granular Layer;629470.5625;440183.125;375175.84375;295634.59375;10937.458984375
Regions/Molecular Layer;Molecular Layer;619689.3125;482408.1875;419716.90625;342248.15625;11964.25
Regions/White Matter;White Matter;436487.46875;307542.15625;256858.890625;209851.265625;3027.2355957031
```

Box plot intensities (ion image mode)

```
# Exported with SCiLS Lab Nightly Version 14.00.17939.4493
# Export time: 2025-09-19 12:51:57
# Generated from file: E:\DEMO_data\develop\iprm-PASEF\MS1\MS1.slx
# Export: Box Plot Ion Image Mode - intensity values
# Feature: PI 38:4 - 885.5428 m/z ± 15 ppm 1/K0 1.4627 ± 0.01
#
# Interval processing mode: Peak Area
# Normalization: Total Ion Count
#
RegionName;spectrumIndex;Intensity;Color
Granular Layer;45686;630543.8125;#f08080
Granular Layer;22173;630776.8125;#f08080
Granular Layer;34764;630912.4375;#f08080
Granular Layer;14427;632441.6875;#f08080
Granular Layer;2578;632690.625;#f08080
Granular Layer;47023;632740.0625;#f08080
Granular Layer;28406;633411.9375;#f08080
Granular Layer;26816;634404.3125;#f08080
Granular Layer;43927;636549.9375;#f08080
Granular Layer;12079;636646.625;#f08080
Granular Layer;26851;636994.25;#f08080
Granular Layer;21291;637421.1875;#f08080
Granular Layer;45705;637448.125;#f08080
Granular Layer;2726;637875.125;#f08080
Granular Layer;48072;637952.125;#f08080
Granular Layer;22639;637979;#f08080
Granular Layer;12538;638092;#f08080
Granular Layer;45238;638217.8125;#f08080
Granular Layer;44227;638314.8125;#f08080
Granular Layer;24229;638967.75;#f08080
Granular Layer;17613;639379.125;#f08080
Granular Layer;16123;639523;#f08080
Granular Layer;46007;640608.6875;#f08080
Granular Layer;48198;640754.875;#f08080
Granular Layer;43224;641596.1875;#f08080
Granular Layer;45533;642115;#f08080
Granular Layer;1166;643744.75;#f08080
Granular Layer;45857;644457.8125;#f08080
Granular Layer;19129;645462;#f08080
Granular Layer;44060;645522.8125;#f08080
Granular Layer;43415;646657.75;#f08080
```

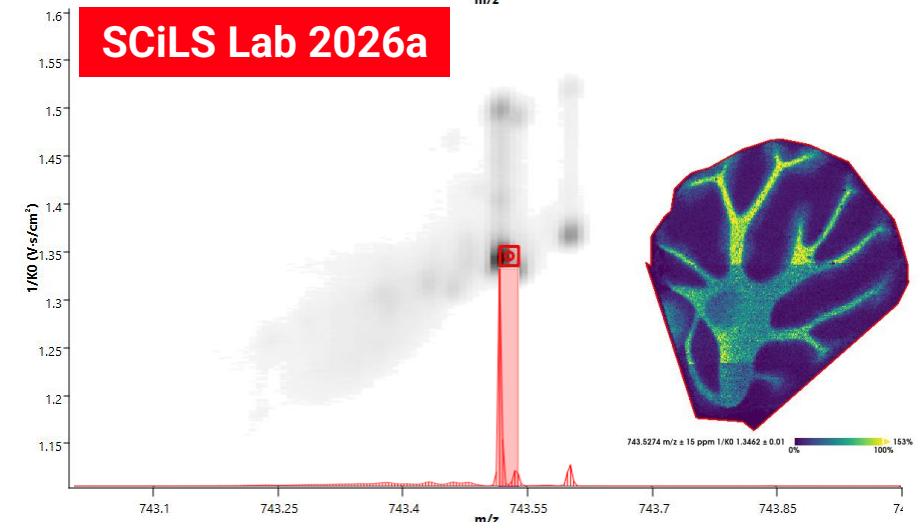
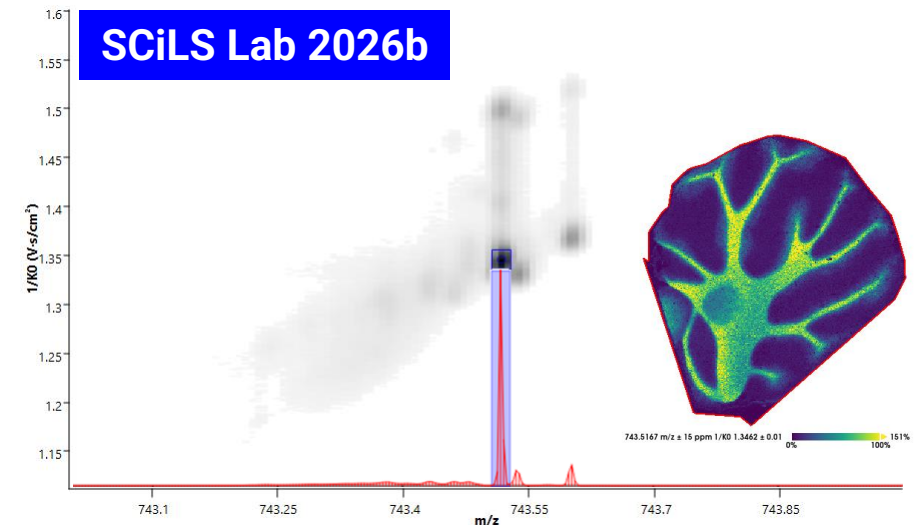
02

T-ReX feature finding

T-ReX[®] feature finding

Improved performance and result quality

- The T-ReX² and T-ReX³ **algorithms have been further enhanced**. As such, T-ReX:
 - Has an improved method for the aggregation of single-pixel centroids, which results in **more accurate m/z values** for the features (especially for T-ReX³).



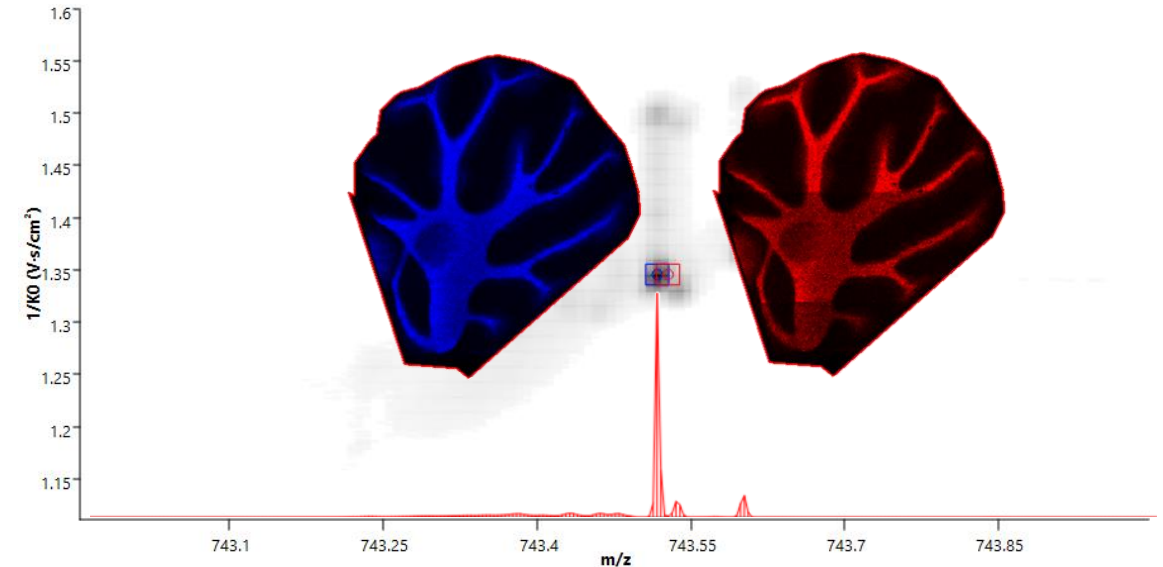
Blue features generated using SCiLS Lab 2026b
Red features generated using SCiLS Lab 2026a

T-ReX[®] feature finding

Improved performance and result quality



- The T-ReX² and T-ReX³ **algorithms have been further enhanced**. As such, T-ReX:
 - Has an improved method for the aggregation of single-pixel centroids, which results in **more accurate m/z values** for the features (especially for T-ReX³).
 - Generates **improved isotope patterns**, resulting in better (i.e. lower) mSigma scores when performing MetaboScape[®]-powered Molecular Annotation.
 - **Performs better** when SCiLS Lab files and/or source data are stored on network locations.



m/z	1/KO [V·s/cm ²]	CCS [Å ²]	Name	Intensity [Regions]	Formula	Ion Notation	Tool	mSigma
885.5428	1.4627	297.5074	PI 38:4	331823.031	C47H83O13P	[M-H] ⁻	Lipid Species	27.3
885.5427	1.4627	297.5074	PI 38:4	331826.031	C47H83O13P	[M-H] ⁻	Lipid Species	170.3
834.5222	1.4246	290.0291	PS 40:6	249487.406	C46H78NO10P	[M-H] ⁻	Lipid Species	102.8
834.5216	1.4246	290.0291	PS 40:6	249364.484	C46H78NO10P	[M-H] ⁻	Lipid Species	189.4
790.5328	1.3771	280.6148	PE 40:6	247024	C45H78NO8P	[M-H] ⁻	Lipid Species	20.9
790.5313	1.3771	280.6148	PE 40:6	246404.219	C45H78NO8P	[M-H] ⁻	Lipid Species	207.2
478.2897	1.0360	213.4571	LPE 18:1	214678.844	C23H46NO7P	[M-H] ⁻	Lipid Species	11.2
478.2894	1.0360	213.4571	LPE 18:1	214625.719	C23H46NO7P	[M-H] ⁻	Lipid Species	112.1

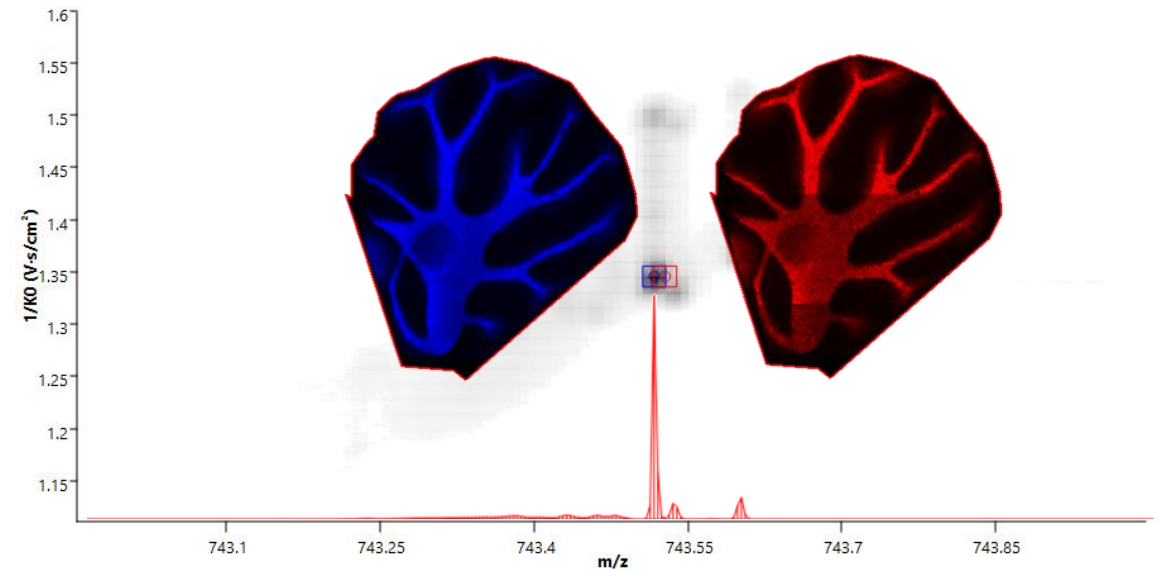
Blue features generated using SCiLS Lab 2026b
Red features generated using SCiLS Lab 2026a

T-ReX[®] feature finding

Improved performance and result quality

Disclaimers:

- T-ReX feature finding results obtained using a previous version of SCiLS Lab and opened in SCiLS Lab 2026b will not be affected by these changes.
- To benefit from these change, T-ReX feature finding needs to be repeated in SCiLS Lab 2026b or later.
- T-ReX feature finding results obtained with SCiLS Lab 2026b may be different from the results a previous version of SCiLS Lab would produce using the same data and T-ReX parameters.



m/z	1/KO [V-s/cm ²]	CCS [Å ²]	Name	Intensity [Regions]	Formula	Ion Notation	Tool	mSigma
885.5428	1.4627	297.5074	PI 38:4	331823.031	C47H83O13P	[M-H] ⁻	Lipid Species	27.3
885.5427	1.4627	297.5074	PI 38:4	331826.031	C47H83O13P	[M-H] ⁻	Lipid Species	170.3
834.5222	1.4246	290.0291	PS 40:6	249487.406	C46H78NO10P	[M-H] ⁻	Lipid Species	102.8
834.5216	1.4246	290.0291	PS 40:6	249364.484	C46H78NO10P	[M-H] ⁻	Lipid Species	189.4
790.5328	1.3771	280.6148	PE 40:6	247024	C45H78NO8P	[M-H] ⁻	Lipid Species	20.9
790.5313	1.3771	280.6148	PE 40:6	246404.219	C45H78NO8P	[M-H] ⁻	Lipid Species	207.2
478.2897	1.0360	213.4571	LPE 18:1	214678.844	C23H46NO7P	[M-H] ⁻	Lipid Species	11.2
478.2894	1.0360	213.4571	LPE 18:1	214625.719	C23H46NO7P	[M-H] ⁻	Lipid Species	112.1

Blue features generated using SCiLS Lab 2026b
 Red features generated using SCiLS Lab 2026a

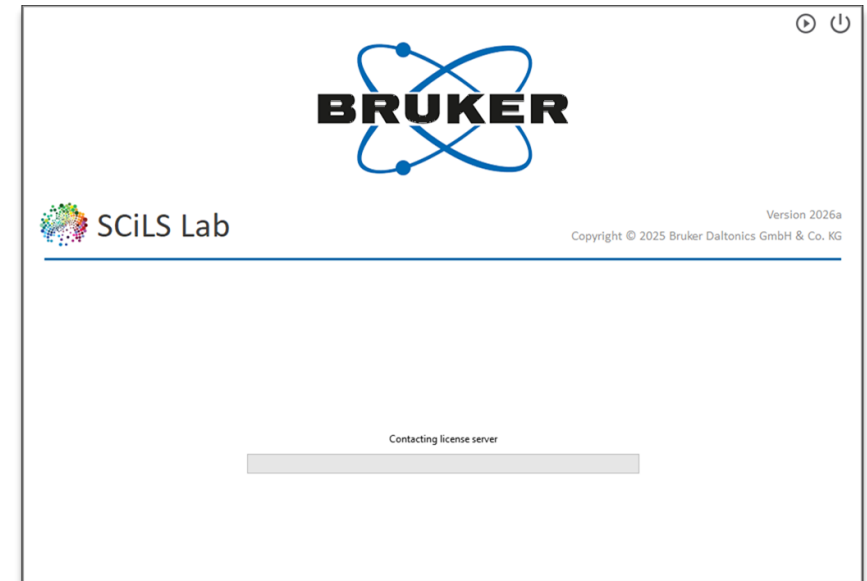
03

Multiple feature enhancements

Multiple feature enhancements

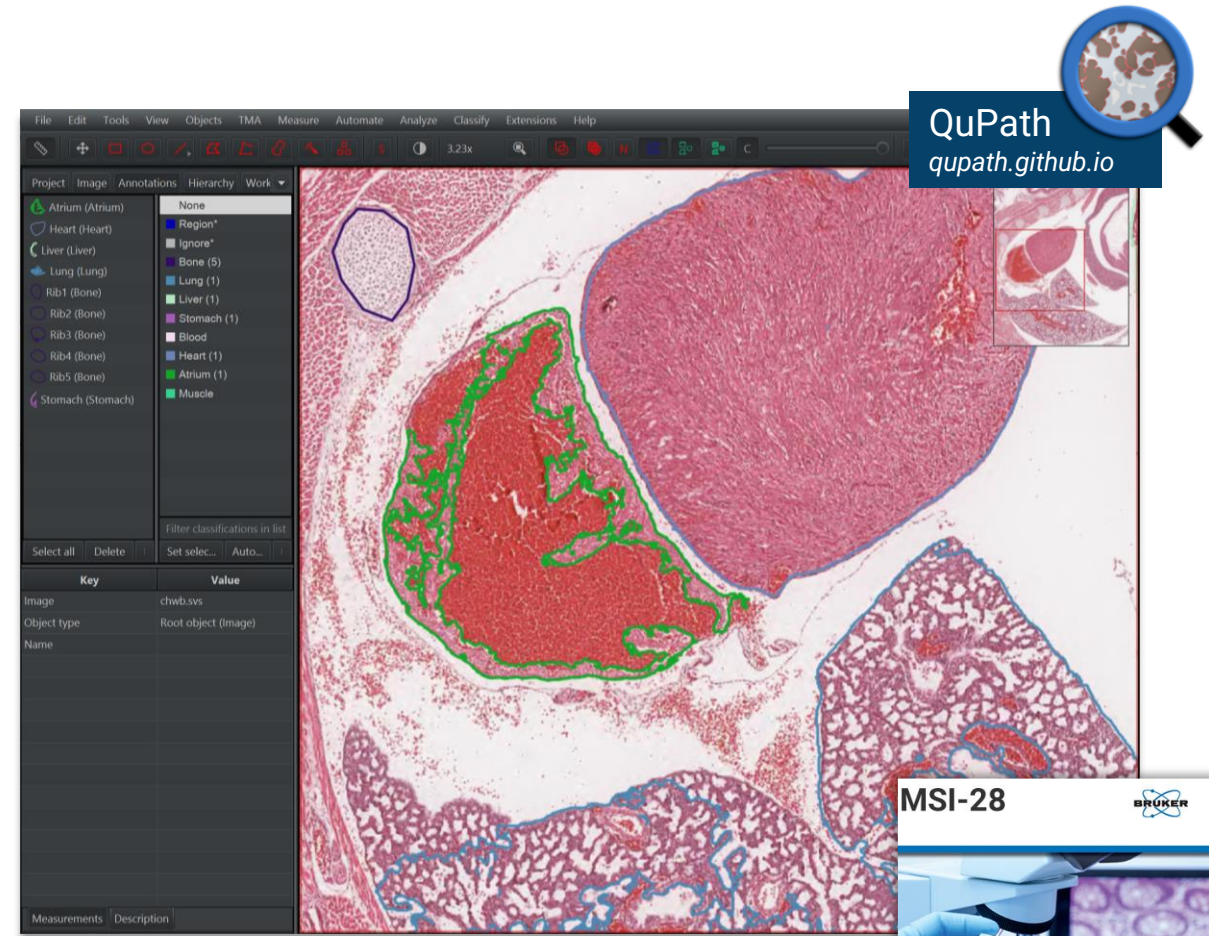
Immediate „sign of life“ during SCiLS Lab start-up procedure

- It can take some time to start up SCiLS Lab. This mostly depends on the configuration of the license server.
- There used to be no indication that SCiLS Lab was started, and all processes took place in the background.
- Now, immediately after starting an instance of SCiLS Lab, a start-up screen appears, indicating the software has started and is connecting to the license server.
- Once connected to the license sever, the license dialog, the regular start-up screen, or the SCiLS Lab main user interface appear (depending on the start up method).



Multiple feature enhancements QuPathToScilsExport plugin update

- A new version of **QuPath (v0.6.0)** was released on June 27th, 2025.
- The SCiLS Lab 2026b installation contains an **updated QuPathToSCiLS plugin (v1.5)** which is compatible with the new QuPath v0.6.0.
 - C:\Program Files\SCiLS\SCiLS Lab\QuPathPlugin



QuPath
qupath.github.io

MSI-28

QuPath integration into SCiLS Lab 4 to statistical data analysis in a fast

Abstract

04

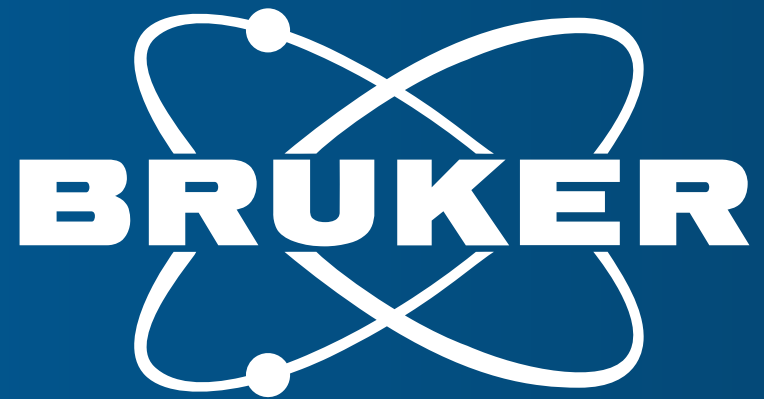
Deprecated SCiLS Lab features



Deprecated SCiLS Lab features

MetaboScape 2026 no longer supports MALDI Imaging data

- From MetaboScape® 2026 onwards, the software is no longer able to load and process MALDI Imaging data.
- In order to obtain Molecular Annotations from MetaboScape, the MetaboScape-powered Molecular Annotation workflow in SCiLS Lab is still available.
 - Details on how to use this workflow are described in the SCiLS Lab User Guide (section 3.1.6).



Innovation with Integrity