

Welcome to mzmine ×

Tasks ×

Feature Table
Aligned feature list 13C peak gaps d... ×

Feature row specific columns

Sample specific columns

Checkbox to automatically show the selected feature list

Aligned feature list 13C peak gaps dup corr PEARSON r greq 0.85 dp greq 5

ID	m/z	RT	Area	Height	Fragment scans	Shapes	Height box plot	Ion identity		Spectral match			Height	Height
								IIN ID	Ion identity	Spectral match	Similarity	Structure		
1188	217.1546	0.65	3.3E7	1.3E9	31			66	[M+H]+	AKOS011963716 (0.800)	0.800		1.6E7	1.2E7
2681	265.1545	1.20	3.6E7	1.2E9	29			177	[M+H]+	CID 6993119 (0.954)	0.954		4.3E6	3.9E6
3695	342.2386	1.57	3.1E7	1.0E9	32			253	[M+H]+	diprotin A (0.846)	0.846		7.3E7	6.9E7
302	182.0811	0.41	2.2E7	7.8E8	42			20	[M+NH4]+	L-tyrosine (0.971)	0.971		7.0E7	5.5E7
123	150.0583	0.34	2.2E7	7.7E8	45			6	[M+H]+	L-methionine (0.960)	0.960		1.2E8	1.1E8

Filters for row ID, m/z, RT, and more complex queries like formula, substructures, or lipids

Q ID=

1,5-6

m/z=

120.1 - 1430.9

RT=

0.3 - 7.9

SMARTS

<

>

[NX3,NX4+][CX4H][(*)][CX3](=[OX1])[O,N]

Save filter presets

Quick column selection

Documentation

Configuration