

Supporting Information for

CCSfind: A tool for chemically informed LC-IM-MS database building

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S1: CCSfind step-by-step

1. Before using CCSfind, convert your raw .d datafiles to mzML using ProteoWizard with default settings (note: do not select “peak picking” for centroiding).
2. Download CCSfind, Choose path of the folder for installation inside the user directory only (e.g., Desktop, Downloads, Documents). Do not choose a default Program Files location as the directory for installation as it can make access of files difficult due to administrator rights.
3. Open **CCSfind.exe**

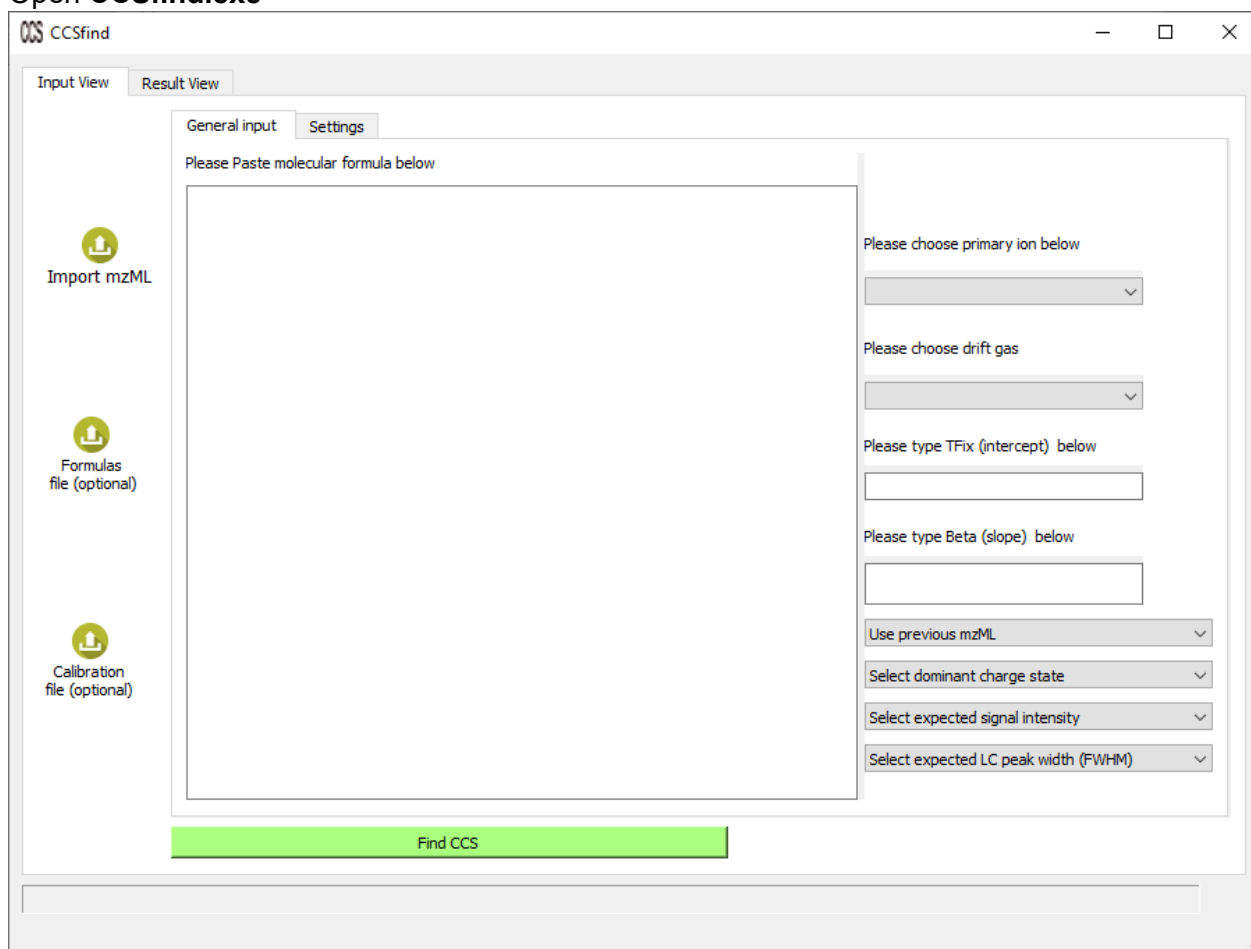


Figure S1. CCSfind start screen after opening.

4. Choose “*Import mzML*” and select your datafile.
5. Enter the appropriate settings for the file including the target molecular formulae (or use the import function), primary ion species, drift gas, single-field calibration parameters (note that these can also be imported from the raw .d file using “*OverrideImsCal.xml*” found in the *AcqData* subfolder).

CCSfind

Input View Result View

General input Settings

Please Paste molecular formula below

C8H9NO2
C7H10N4O2S
C12H14N4O4S
C19H29N3O5
C27H38N2O4
C32H41NO2
C28H37N5O7
C33H40N2O9

The uploaded :
20230310_pos_4bit_01.d.DeMP.mzML

Please choose primary ion below

[M+H]⁺

Please choose drift gas

Nitrogen

Please type TFix (intercept) below

0.289711

Please type Beta (slope) below

0.135961

Use previous mzML

Select dominant charge state

Select expected signal intensity

Select expected LC peak width (FWHM)

Find CCS

Figure S2. Exemplary general input for evaluation of positive mode LC-IM-MS measurement of a QC standard mix.

6. Additional settings (i.e., charge state, expected signal intensity, expected LC peak width) can be adjusted if the first evaluation results are not satisfactory.
7. Under the “Settings” tab, add any additional ion species of interest, or use the “*Formula to be added*” or “*Formula to be subtracted fields*” to search for related species (e.g., in-source fragments, solvent adducts). Note: it is not necessary to add the primary ion species again here as an additional adduct.

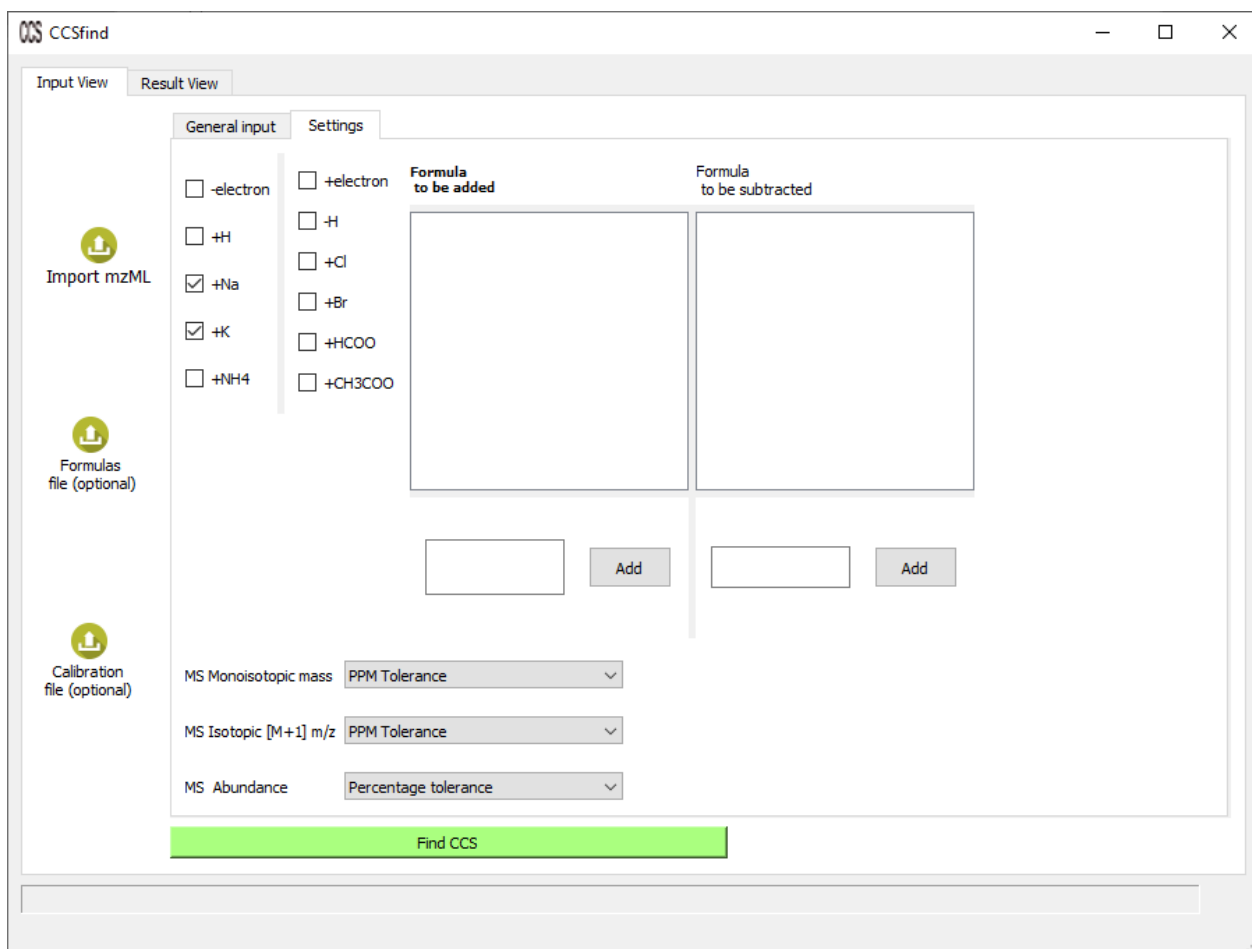


Figure S3. Exemplary settings for evaluation of positive mode LC-IM-MS measurement of a QC standard mix.

8. The “*MS Monoisotopic mass*”, “*MS Isotopic [M+1] m/z*” and “*MS Abundance*” settings can be adjusted if the first evaluation results are not satisfactory.
9. Select “*Find CCS*”.
10. After completion, close the dialog box and choose “*Result View*”.

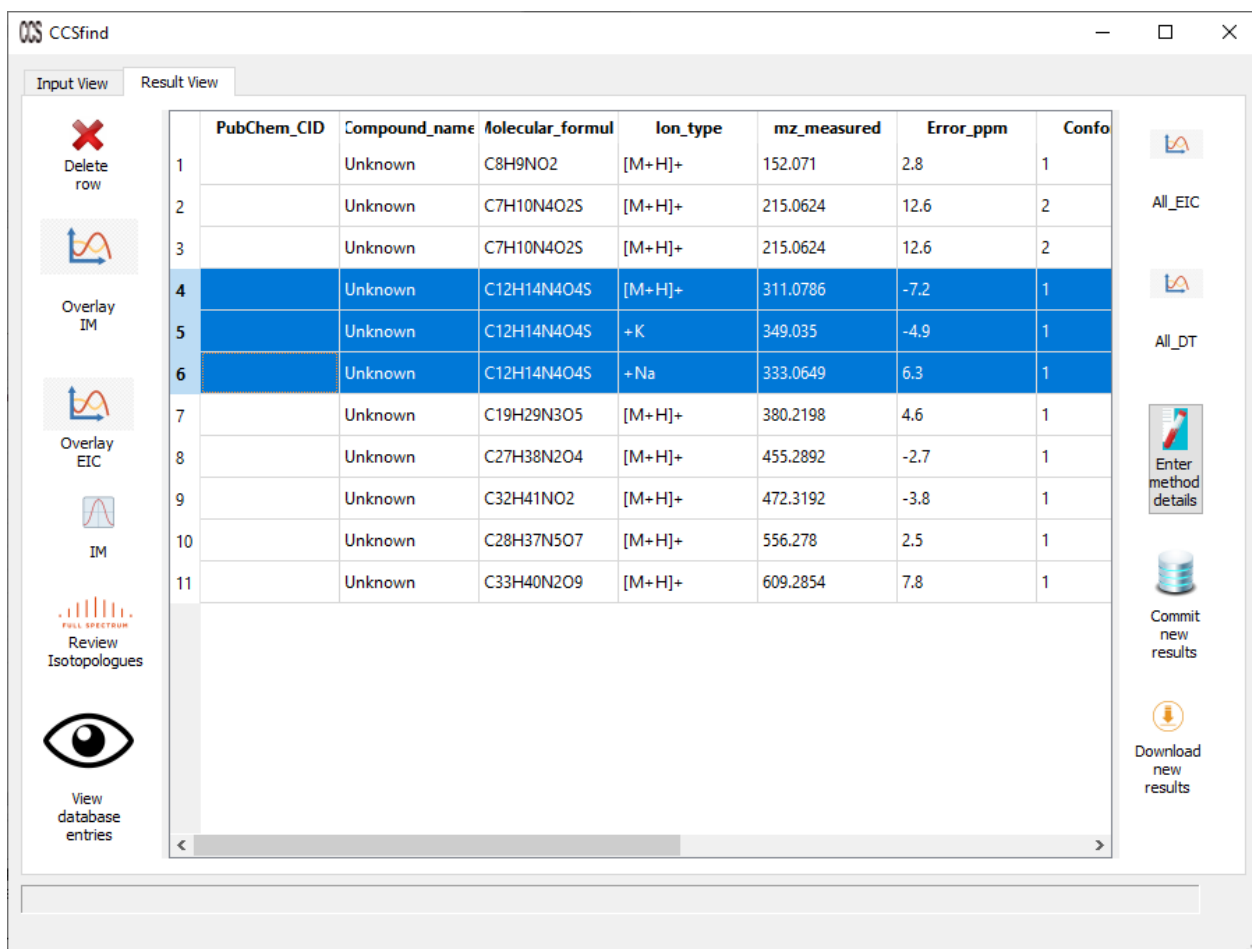


Figure S4. Exemplary results following evaluation of positive mode LC-IM-MS measurement of a QC standard mix.

11. Results of individual compounds can be reviewed with the “*Overlay*” options. EICs or IM spectra from different ion species of the same molecular formula can be compared.
12. Multi-selection of overlay IM yields a direct comparison (overlay) of results corresponding to the same target molecular formula.

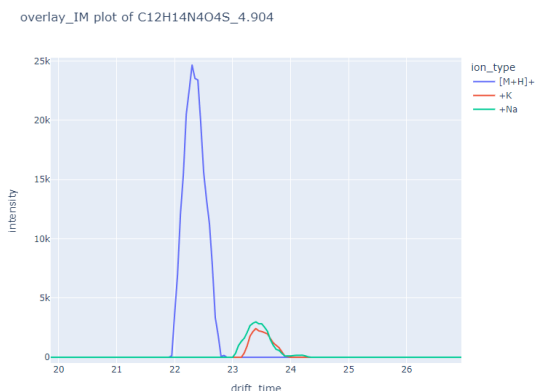


Figure S5. Overlays of IM spectra results corresponding to the input molecular formula C₁₂H₁₄N₄O₄S obtained using the “*Overlay IM*” option.

13. “Review isotopologues” can be used to check that confirming signals are detected as co-eluting LC signals for the target molecular formula and ion species.
14. Selection of “All EIC” or “All DT” yields a comparison of all results.

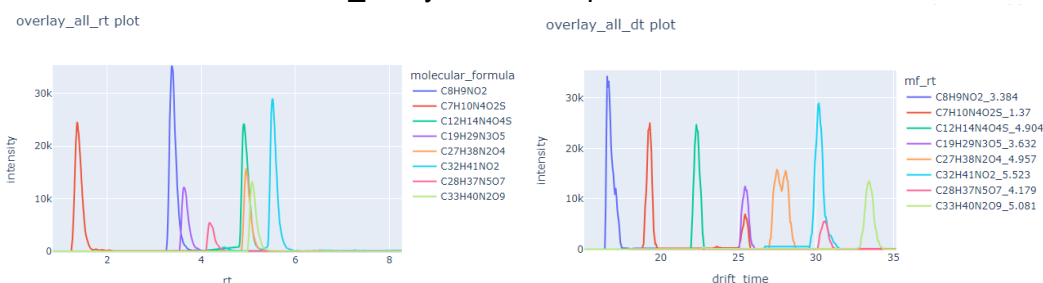


Figure S6. Results from “All EIC” and “All DT” options.

15. Incorrectly picked results can be removed with “Delete Row”.
16. If results are not satisfactory or additional formulas need to be found, the input settings can be adjusted and the option “Use previous mzML” (see **Figure S1**) set to “yes” to avoid repeating the parsing of the datafile.
17. “PubChem_CID” and “Compound_name” can be updated for the confirmed results.

	PubChem_CID	Compound_name	Molecular_formula	Ion_type	mz_measured	Error_ppm	Conformer	Arrival_time_ms	CCS_sqA	Resolving_power	RT_min
1	1983	Acetaminophen	C8H9NO2	[M+H] ⁺	152.071	2.8	1	16.71	131.42	69.63	3.384

18. Update the “Enter method details” and choose “proceed”. Note that standardization of formatting for these fields is recommended. In addition to reporting of key IM-MS reporting parameters, curation of LC methods in a separate list can also be used to compare LC results (retention order of isomers) from different database results.

Enter method details

Please add below parameters for lab information for database

Field strength (V/cm):

17.225

Drift tube pressure (Pa) :

525.8

Drift tube temperature (Kelvin):

300.15

LC method number:

BOKU_RPLC_Zorbax_1

Level of processing applied (e.g., HRdm) :

Standard 4-bit demultiplexing

Proceed

Cancel

19. Commit the results to the database “Commit new results” and then select “Download new results” to the location selected by the user.
20. Review the results using a suitable tool (e.g. SQLite Browser).

Database Structure Browse Data Edit Pragmas Execute SQL

Table: CCS_table Filter in any column

	id	PubChem_CID	Compound_name	Molecular_formula	Ion_type	mz_measured	Error_ppm	Conformer	Arrival_time_ms	CCS_sqA	Resolving_power	RT_min	Formula_RT	Time
	Filter	Filter	Filter	Filter	Filter	Filter	Filter	Filter	Filter	Filter	Filter	Filter	Filter	Filter
1	1	https://...	Acetaminophen	C8H9NO2	[M+H] ⁺	152.071	2.8	1.0	16.71	131.42	69.63	3.384	C8H9NO23.384	2024-02-06 15:15:31.917099

21. All results (EICs, IM spectra, isotopologue comparison) in HTML format can be opened directly from the results folder in a browser for viewing after downloading.