

Agilent ChemVista Library Manager

An innovative tool for confident identification

Introduction

Despite advances in structure elucidation tools, empirical high-resolution MS/MS (and full scan) spectra remain the standard to confidently identify unknowns via targeted screening and nontargeted analysis workflows. Generating spectral libraries, however, is a costly and time-consuming process. Even when complete, these libraries are often siloed and not in easily accessible formats, limiting the scope and identifiable chemical space of screening workflows. Integrating spectra from multiple sources into an identification workflow is necessary for expanding the capabilities of confident identification. Agilent ChemVista software is a standalone software application that can integrate compound, retention time, and spectral information from multiple sources to facilitate identification workflows within Agilent MassHunter data analysis applications and beyond. Efficient library management is accomplished through list organization, intuitive searching, and filtering options throughout a streamlined user interface. Optionally included with the software are extensive, curated libraries for the metabolomics, food safety, environmental, material, and forensic toxicology markets. This technical overview describes the use of ChemVista software to improve the efficiency and productivity of high-resolution mass spectrometry (HRMS) spectral management.

Extending data access with ChemVista

Import

Integrating compound and spectral data from internal and third-party sources is critical to expanding identification capabilities. As a standalone application, ChemVista supports the import of data from the Agilent Personal Compound Database and Library (PCDL) format, MassBank EU, MassBank of North America (MoNA), and the U.S. EPA CompTox Chemicals Dashboard. Details and access links are presented in Table 1.

Table 1. Formats supported by Agilent ChemVista.

Format	Supported File Type	Access Links
Agilent PCDL	.cdb	
CSV	.csv	
MassBank EU	.txt	https://massbank.eu/MassBank/ https://github.com/MassBank/MassBank-data
MassBank of North America (MoNA)	.sdf	https://massbank.us/ https://mona.fiehnlab.ucdavis.edu/downloads
EPA CompTox Chemicals Dashboard	.sdf	https://comptox.epa.gov/dashboard/ https://comptox.epa.gov/dashboard/chemical-lists

Consolidation

On import to ChemVista, data is parsed according to source format specifications and stored in an accessible and flexible manner. Consolidation of data occurs first at the chemical structure and compound level, with a chemical structure identifier generation (e.g., SMILES, InChI, MOL) and merging protocol. The result of this background process is a compound-centric organizational structure, where identifiers are used to consolidate data corresponding to the same compound and structure under one chemical substance record within the system. If properly matched, a compound will only exist once within the system, but will include all stored information from imports. This allows for a consistent organizational structure and representation despite disparate organizational structures in third-party repositories (for example, MassBank and MoNA are spectral-centric repositories). Certain settings are configurable to support varied data use cases, such as the classification process entirely and whether stereochemistry errors should be ignored in incoming data.

ChemVista Library Manager

File Home Search Import Jobs Lists System

History Pages

Search Results

Search... Export Browse methods Add to list Create substance Merge Break Delete Edit columns

Loaded 976 of 976 substances

Substance Name	Formula	CAS	Mass	InChIKey	Agilent ID	Spectra Count	ChemSpider	PubChem
Hexaconazole(l)	C14H17Cl2N2	79983-71-4	313.07487	STMIIPIFODD	990	6	59839	
Osetamivir-carboxylate	C14H24N2O4	187227-45-8	284.17361	NENPYTRHICK	9158	5	395929	449381
Isotioate	C7H17O2PS3	86614-38-7	260.01283	SPCNPOWOBZ	20568	0	34393	
Benzododecinium (Ajatin)	C21H38N	10328-35-5	304.30043	CYDRKTMKUD	6896	3	8424	
Oxymorphone	C17H19NO4	76-41-5	301.13141	UGGNKQICZOF	2282	3	4447650	
Dimethachlor	C13H18ClNO2	55353-08-7	255.10261	SCCDDNKYDZ	592	8	36319	39722
Alachlor ESA	C14H21NO5S	142368-53-9	315.11404	UTCJUGUQCHW	9244	3	103108	
Fenamiphos	C13H22NO3PS	22224-92-6	303.1058	ZCJOPBZHLU	920	3	28827	
Trimethoprim	C14H18N4O2	738-70-5	290.13789	IEDVJHCIMCR	1600	3	5376	
Lorazepam	C15H10Cl2N2	846-49-1	320.01193	DIWRORZWF1	403	5	3821	
N-Bisdesmethyl Tramadol	C14H21NO2	931115-27-4	235.15723	QNPPIKMBJCL	5	2317896	3056578	
N-Acetyl-Sulfamethoxazole	C12H13N3O4S	21312-10-7	295.06268	GXPILUNZCALH	7844	5	58771	65280
Metolachlor-OXA	C15H21NO4	152019-73-3	279.14706	LNOOSYCKMK	20043	6	21170688	15842092
Metazachlor-ESA	C14H17N3O4S	172960-62-2	323.09398	IPVCSECEVHK	9372	5	28290254	86290102
2,7-Naphthalene disulfonic acid (Ebert-N)	C10H8O6S2	92-41-1	287.97623	VILFVXKHYVY	9345	0	60073	
Pyridate	C19H23ClN2O	55512-93-9	378.11688	JTZCTMAVMWHI	1359	6	37851	
17 α -Estradiol (Alfatradiol)	C18H24O2	57-91-0	272.17763	VOXZDWNPUJ	7571	3	61840	
Oribfloxacin	C19H20F3N3O	113617-63-3	395.14568	QJPDASLPWJW	7335	3	54631	
PCP / Phenacyclidine	C17H25N	77-10-1	243.1987	JTJMJGVQZDZ	2791	3	6224	
Nuarimol	C17H12ClF2N2	63284-71-9	314.06222	SAPGTCDSBGI	2563	3	82786	
Promazine	C17H20N2S	58-40-2	284.13472	ZGUGUWULJS	2695	3	4757	
Ribavirin	C8H12N4O5	36791-04-5	244.08077	IWUCXVSUMC	6316	3	34439	
Isocarboxiphos	C11H16NO4PS	24353-61-5	289.05377	YFVOKLXJBJQI	1650	3	81690	
Nevasstatin	C23H34O5	73573-88-3	390.34062	AJLFOPRYVGI	4821	3	58262	
Dimethenamid-OXA	C12H17NO4S	380412-59-9	271.08783	HOYCASTVMC	9371	5	28290255	86290064
Propiconazole(l)	C15H17Cl2N3	60207-90-1	341.06978	STJLVHWMYQ	1746	9	39402	
Acetylsulfadiazine (N4-Acetylsulfadiazin	C12H12N4O3S	127-74-2	292.06301	NJZLWVGIMK	7840	6	58478	
Ciomipramine	C19H23ClN2	303-49-1	314.15498	GDLGKIOYRN	3387	3	2699	
Benzoylcegonine	C16H19NO4	519-09-5	289.13141	GVGYEFKHJTI	2361	3	395095	
Hydrocodone	C18H21NO3	125-29-1	299.15214	LLPOLZWFYMI	3017	3	4447623	
PFBA / Perfluorobutanoic acid (Heptafluor	C4HF7O2	375-22-4	213.98648	YFJUNDFVDDI	9363	2	9394	
Trichlorfon (Dylox) (DEP)	C4H8Cl3O4P	52-68-6	255.92258	NFAGZMKEDP	595	3	5644	
Pymetrozine	C10H11N5O	123312-89-0	217.09636	QHMTXANGCG	339	3	7850487	
Bensulidide	C14H24NO4PS	741-58-2	397.06051	RRNZKPKKND	1795	3	12397	
Fenbutazone	C19H17ClN4	114369-43-6	336.11417	RQDIADAKJFF	1159	3	77712	
Donepezil	C24H29NO3	120014-06-4	379.21474	ADEBP85SDYV	7037	3	3040	
Acetisulfanilamide	C8H10N2O3S	121-61-9	214.04121	PKDFBDHYTM	6259	0	8169	

Metolachlor-OXA

CAS: 152019-73-3
 Formula: C15H21NO4
 InChI: InChI=1S/C15H21NO4/C1-5-12-8-6-7-10(2)13(12)16(11)13(9)-20-4(14)17(15)18(19)/h6-8,11H,5,9H2,1-4H3,(H,18,1)
 InChIKey: LNOOSYCKMKZOB-UHFFFAOYSA-N
 Mass: 279.14706
 SMILES: CC(C=CC(C)=N(C(C)COC)C(=O)O)C(=O)O
 Synonyms: 2-[2-ethyl-N-(1-methoxypropan-2-yl)-6-methylanilino]-2-oxoacetic acid; Metolachlor OXA [Metolachlor C

View full compound data
 Edit View spectra Add to list Export substance

Tags: Herbicide degradate, Pesticide degradate, Environmental contaminant, Polar metabolite, LCMS Amenable, Forensic and Toxicology Drug, Pesticide, EPA 535

Number of spectra 8
 LC | ESI | QTOF: 5 spectra
 POSITIVE: 8 spectra
 ESI | QTOF: 3 spectra

Latest Retention Times

Current user: MCEACHRAN,ANDREW (Agilent USA), Active project: Default

Figure 1. Spectral and compound data consolidated from multiple sources to compile a Pesticides for Targeted Screening list. Using the default classification and merging protocols results in streamlined data instead of many entries for the same compound. Data here contains Agilent IDs, spectra from MassBank and PCDLs, and synonyms from multiple sources.

Using ChemVista for library management

Organize, manage, and edit compounds

Establishing a flexible means to organize data is critical when managing library data from multiple sources without reliance on single files on disk. Lists are introduced in ChemVista to keep compounds organized. Lists can be (A) created on import, (B) created or appended from any compound view, (C) merged, and (D) removed. Lists are organizational tools and do not affect the underlying data. A compound can exist in multiple lists but is still just a single record, and a compound can be removed from a list but will not be deleted from the application.

Tailoring compound and chemical structure data may be necessary to achieve the desired set of targets for screening. Editing compound and chemical structure information is achievable when viewing compounds in a list view. Compound metadata is not overwritten by default; rather, when new data is added, the prior value is moved to the background of that data field. On commit of chemical structure information for a compound, new identifiers and a new structural image are generated automatically using the embedded EPAM Indigo toolkit¹ when possible. If needed, edits can be reverted to restore data to the state before the changes.

Enhanced cheminformatics features with the Indigo toolkit result in fully populated structure-identifier sets to support downstream workflows, but also enable support for structural skeleton searching using the first block of the InChIKey and quick identification of missing structures using the empty InChI designations (empty InChI: InChI=1S//, empty InChIKey: MOSFIJXAXDLOML-UHFFFAOYSA-N).

View, edit, and create spectra

In line with the compound-centric data model in ChemVista, spectral and method data are organized underneath chemical substance records, regardless of the data structure from the source format (i.e., when spectral-centric records are imported from MassBank, they are parsed and stored according to the ChemVista data model). Spectral and method data are processed in a manner that allows for consistent display and filter of pertinent information, including display of the separation type, ionization type, mass analyzer type, and collision energy. Further, SPLASH identifiers are generated for all spectra in the system and then deduplicated using this SPLASH, to prevent identical spectra from being stored under the same chemical substance.²

Browsing spectra is helpful for understanding data availability and fragmentation patterns, and further interrogating individual spectral data can elucidate method parameters for method development. Spectra can be created manually within ChemVista, and spectra can be edited via the Clone operation. Cloning spectral records copies all existing spectral details to a new record that can then be edited, preserving the original spectral record while allowing a user-manipulated spectral record to co-exist. Again, if needed, changes can be reverted to restore data to the state before the changes.

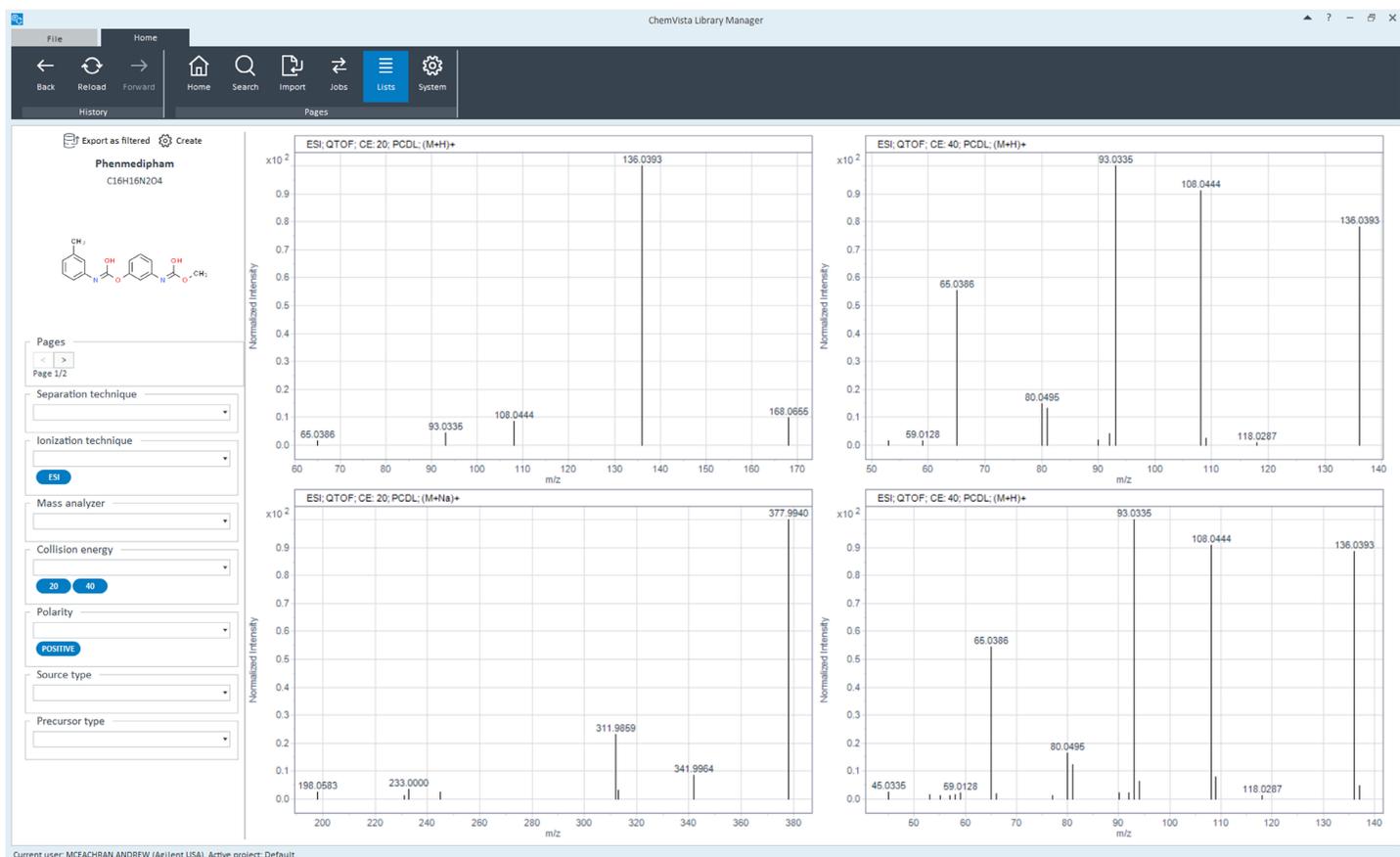


Figure 2. Spectral view with filter options on the left. Clicking a spectral plot opens extra details.

Organize, manage, and edit retention times and indices

Identification confidence is bolstered by inclusion of retention times (RTs) and indices (RIs). ChemVista supports organization of RTs and RIs by method information and customizable method labels, allowing many RTs and RIs to be stored per compound. Interactive browsing of RT/RI information by method and method label supports user interrogation and ultimate selection of RT/RI sets for export and inclusion in data analysis and identification workflows.

Editing RTs/RIs and creation of new method labels is achievable in the Browse Methods page. Further, a complete matrix of all method data (including RTs, RIs) for the compounds in view can be downloaded as a Microsoft Excel-compatible XML file. This organizes pertinent RT/RI and chemical structure data for more in-depth analysis outside ChemVista (for RT prediction, for example).

The screenshot shows the ChemVista Library Manager interface. The top navigation bar includes 'File', 'Home', and 'System' menus. The main content area is titled 'Select method label or parameters' and shows a list of 255 substances. The 'Umiconazole-P(I)' entry is selected, and its details are shown on the right. The details include the method label 'HPLC C18 Method 1 March 2023', total method RTs (1), total method RIs (0), and a table of historical RT values.

Date and Time	Retention Time	Retention Index	Source type
3/10/2023 4:17:14 PM	12.226	-	User

Figure 3. The Browse Methods page allows for RT and RI organization, and supports many RTs/RIs per compound. In this page, the user can toggle between existing methods to determine the best method to include RTs from an export for downstream analysis.

Search underlying data

Searching the underlying data in the application enhances list creation and target-screening subsetting. Data can be searched from the ChemVista home page in a single-entry manner using a name/synonym, CAS, or formula. Advanced and batch searches can be conducted via the Search page. Single-field searches can be conducted by entering search terms in the user-entry field. Identifiers (name, CAS, InChIKey, and SMILES) and formulas can be searched in batch mode by entering many search terms in new lines, and can be searched in part or as an exact match. Identifier searches can also be conducted against nonprimary data, meaning those identifiers that exist in the background set of data stored for a chemical substance (for example, an alternative name/synonym or alternate CAS). Other query options include searching by mass (range or mass \pm error), tag, and presence in defined lists.

Combined searches built using the Search Builder tool are initiated from the basic controls when search terms are added as sets to the builder. If more than one set is added, only chemical substances that are common between sets will be returned. Searches built in the Search Builder tool can be saved and reloaded later to conduct the same query.

Complex searches against any data field in the system can be generated using regular expression queries via the Pattern Search. Here, the field of interest (i.e., AgilentID) is selected first and then the selected field is searched against using a regular expression (i.e., $^(?:[1-9][0-9]{3})|[1-9][0-9]{2}|[1-9][0-9]|[1-9])\$$ to conduct a search for all Agilent IDs between 1-9999). Pattern Searches can also be added to search sets to construct complex search combinations.

Multuser configurations

When desirable, ChemVista can be set up for multiuser access in a client/server configuration. The backend server can be installed on a local-networked PC, and multiple clients can be installed on other PCs connected to the same network. In this fashion, multiple users can access the same backend data store from multiple PCs to utilize the same library data.

Exporting data to support workflows

Data can be exported from ChemVista into multiple file formats to support downstream workflows (see Table 2). Exports can be initiated from the List, Search Results, Browse Methods, and Spectral views. On initiation to the export page, filters and export options can be selected to fine-tune the make up of the export. For example, users can select **Only compounds with spectra**, or the spectra could be filtered to only include spectra with a positive polarity (Figure 4). To produce deposition-ready MassBank .txt files, export details can be edited to provide all required information.³

Table 2. ChemVista export formats.

Export Format	File Type	Downstream Support
PCDL	.cdb	Agilent MassHunter Qualitative Analysis software, MassHunter Quantitative Analysis software, MassHunter Mass Profiler software, etc.
MassBank	.txt	MassBank EU contribution
SDF	.sdf	Agilent MassHunter Molecular Structure Correlator software NIST Library format (via Lib2NIST conversion)

Export Options

Export as: PCDL (*.cdb)

Only compounds with spectra
 Only most recent spectra for substance/method
 Only compounds with unequivocally defined formula/mass
 Exclude spectra
 Exclude compound-level RTs

Spectral Filters

Separation technique: []
 Ionization technique: ESI
 Mass analyzer: []
 Collision energy: []
 Polarity: POSITIVE
 Source type: []
 MS level: 2
 Method label: HPLC C18 Method 1 March 2023

Summary

Substances	1402
Substances with spectra	962
Substances with RTs	180
Substances with method data	1078
Spectra	3681

Start export

Figure 4. Export data to the desired format to fit your downstream workflow. Filter the spectra that are included by making selections from the Spectral Filters options.

Conclusion

Agilent ChemVista software enables users to merge compound, spectral, and retention time data from multiple sources into one location. In doing so, ChemVista software enables users to screen against spectra that have been previously inaccessible, enhancing the compound identification possibilities.

References

1. EPAM Life Sciences. <https://lifescience.opensource.epam.com/indigo/>
2. Wohlgemuth, G. *et al.* SPLASH, A Hashed Identifier for Mass Spectra. *Nat. Biotechnol.*, **2016**. 34, 1099–1101. DOI: <https://doi.org/10.1038/nbt.3689>
3. MassBank Record Format. <https://github.com/MassBank/MassBank-web/blob/main/Documentation/MassBankRecordFormat.md>