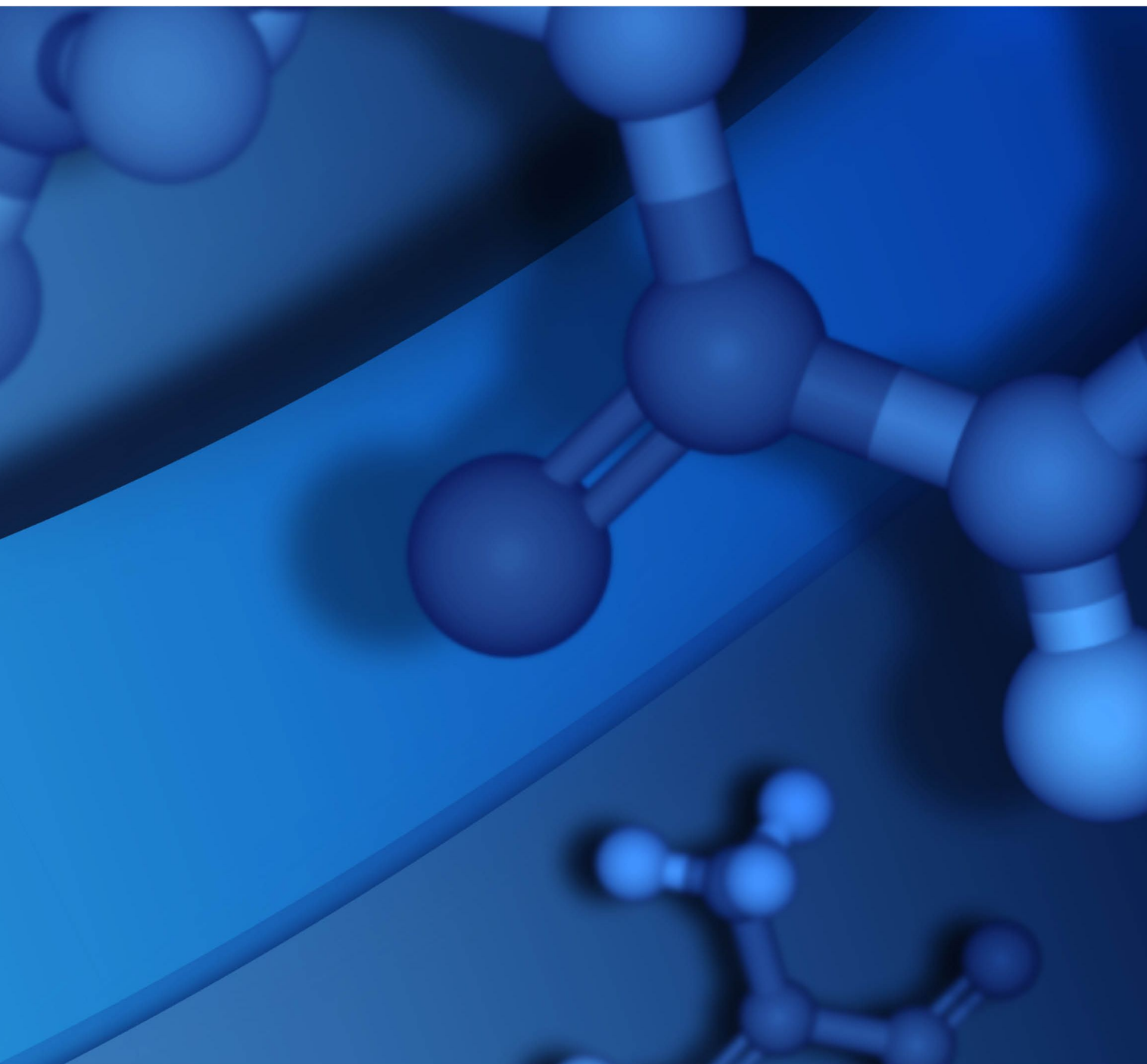


# CTFILE FORMATS

BIOVIA DATABASES 2017



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## About BIOVIA CTfile formats

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BIOVIA applications support various formats of chemical table files formats (CTfile formats) for representing and communicating chemical information. To find out which file formats a specific BIOVIA product supports, see the documentation for that product.

The intended audience for this document is any software programmer who is coding an application that parses files written in one or more of the CTfile formats.

### Overview

A connection table (Ctab) contains information describing the structural relationships and properties of a collection of atoms. The atoms can be wholly or partially connected by bonds. An atom can also be an unconnected fragment. Such collections might, for example, describe molecules, molecular fragments, substructures, substituent groups, polymers, alloys, formulations, mixtures, and unconnected atoms.

The connection table is fundamental to all BIOVIA CTfile formats. The Ctab is included in a molfile, and multiple Ctabs can be included in an rxnfile, RGfile, RDfile, or SDfile.

This chapter provides an overview of the connection table (CTAB) for the preferred V3000 format. For information on the legacy format, see [V2000 Connection Table \[CTAB\]](#).

### Advantages of V3000 Format

The V3000 format is intended to be the primary means for communication of future enhancements to BIOVIA chemical representation features. The preferred molfile format (V3000) offers advantages over the legacy V2000 format:

- Provides better support for new chemical properties or objects, and supports enhanced stereochemistry.
- Removes fixed field widths to support large structures. The fixed limits and distributed property information in the V2000 format make V2000 less than ideal for enhancing chemical representation.
- Supports the use of templates in a template block, which is useful for representing large structures, such as biological molecules. See “Template block” on page 31. Consolidates property information for chemical objects.
- Uses free format and tagging of information for easier parsing.
- Provides better backward compatibility through BEGIN/END blocks.

### Automatic V3000 Output

Current BIOVIA products support reading and writing of both V2000 and V3000 formats. These products continue to default to writing V2000 molfiles to maximize interoperability with third party applications. Future product versions might default to output of the preferred V3000 format.

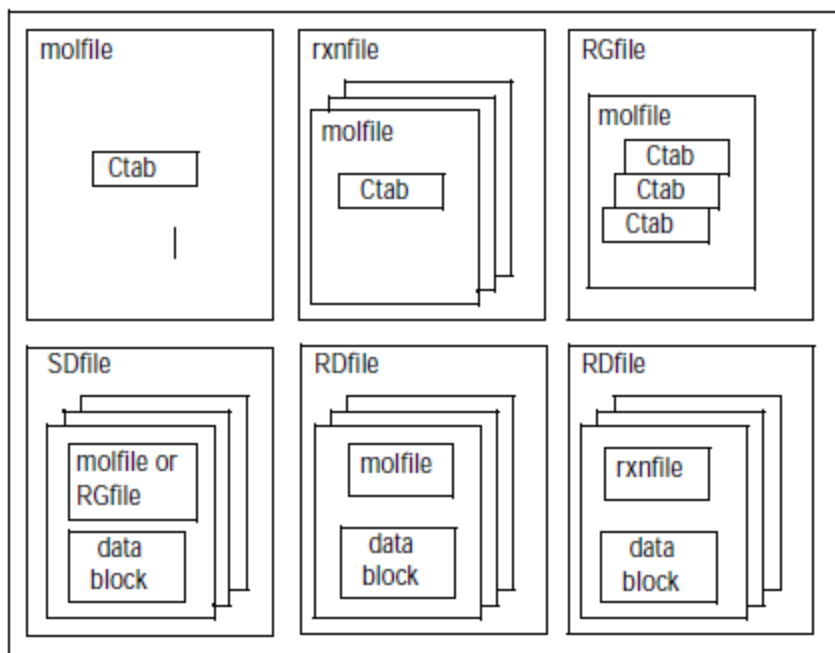
Because of the limitations imposed by the V2000 format, there are situations when the V3000 format must be used:

- Structure highlighting - The V3000 format is required for molecule or collection highlighting. For information about structure highlighting, see the [Collection Block](#).

- Enhanced stereochemistry features - The V3000 format is required when using the enhanced stereochemical representations. See the [Collection Block](#). For a complete discussion of BIOVIA enhanced chemical representation, see BIOVIA Chemical Representation.
- Long fields - If any of the fields with fixed widths for any connection table properties are exceeded, the V3000 format is used. For example, if the number of atoms (or bonds) exceeds 999. This is because the number of atoms (or bonds) on the V2000 counts line cannot exceed 3 columns (see [The Counts Line](#)). For more details about the fixed field widths in the V2000 format, see [V2000 Connection Table \[CTAB\]](#).
- Template block - useful for representing large structures, such as biological molecules. See [Template block](#).
- New properties supported only in V3000 format - such as atom CLASS and SEQID. See [Meaning of Values in the Atom Block](#).

## CTfiles - Summary of Each Format

The following diagram illustrates the relationship between the various file formats. See [Description of the formats](#).



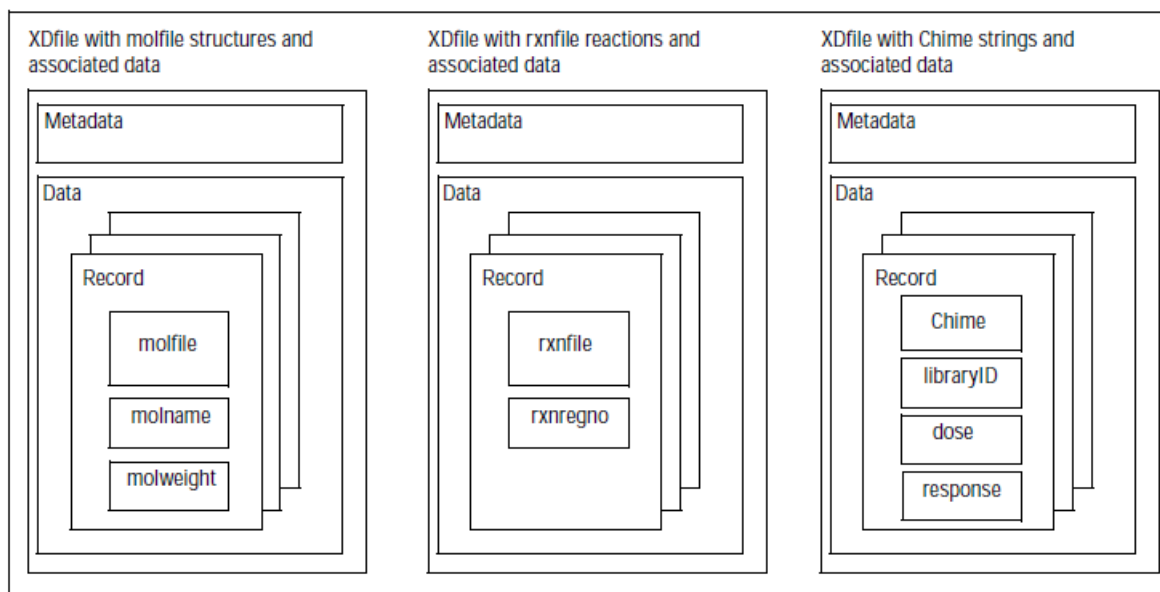
## Description of the Formats

- molfiles** Molecule files: Each molfile describes a single molecular structure which can contain disjoint fragments. See [Molfile](#).
- 
- RGfiles** Rgroup files: An RGfile describes a single molecular query with Rgroups. Each RGfile is a combination of Ctabs defining the root molecule and each member of each Rgroup in the query. See [RGfiles \(Rgroup file\)](#).
-

<b>rxnfiles</b>	Reaction files: Each rxnfile contains the structural information for the reactants and products of a single reaction. See <a href="#">Rxnfile</a> .
<b>SDfiles</b>	Structure-data files: An SDfile contains structures and data for any number of molecules. Together with RFiles, SDfiles are the primary format for large-scale data transfer between BIOVIA databases.
<b>RFiles</b>	Reaction-data files: Similar to SDfiles in concept, the RFile is a more general format that can include reactions as well as molecules, together with their associated data.
<b>XDfiles</b>	<p>XML-data files: XML-based data format for transferring recordsets of structure or reaction information with associated data. An XDfile can contain structures or reactions that use any of the CTfile formats, Chime strings, or SMILES strings.</p> <p>Chime is a compressed, encrypted format used to render structures and reactions on a Web page.</p> <p>SMILES (Simplified Molecule Input Line Entry System) is a line notation format that uses character strings and SMILES syntax to represent a structure.</p> <p>For detailed documentation of this file format, see the XML Reference of Isentris Developer Documentation.</p>

## XDfile Types

The following diagram illustrates three examples of XDfiles:



## Properties Supported by CTfile Types

Some of the structural and query properties described in this document are generic in their applicability, while others are peculiar to certain CTfile types. The applicability of each property is identified in subsequent chapters by the bracketed terms shown in the following table.

Property	molfile	RGfile	SDfile	rxnfile	RFile	XDfile
[Generic]	+	+	–	+	+	+(mol/rxn)

Property	molfile	RGfile	SDfile	rxnfile	RDfile	XDfile
[Sgroup]	+	+	+	[+]	+	+ (mol[rxn])
[Rgroup]	+	+	+			+ (mol)
[3D]	+	+	+			+ (mol)
[Reaction]				+	+	+ (rxn)
[Query]	+	+	+	+	+	+ (mol/rxn)

**Note:** The XDfile inherits the functionality of the format of the embedded structure or reaction. In addition to the molfile and rxnfile formats, the XDfile supports Chime and SMILES strings.

## Conventions

The format conventions used in this document are as follows:

<b>UPPERCASE</b>	Literal text, to be entered as shown. Only the position of "M V30 " is significant. White space can be added anywhere else to improve readability. Both lower- and uppercase characters, or any combination of them, are acceptable for literals. They are shown here in uppercase for readability.
<b>lowercase</b>	A token, which is defined elsewhere.
[ ]	An optional item. Do not include the brackets.
[ ]*	An optional item, where there can be zero, one, two, or more of the item.
	Separates two or more options, only one of which is valid.
/	Separates two or more items. Either or both can appear in any order.
{ }	Braces are used for grouping. They indicate indefinite or definite repeat.



## Connection Table [CTAB]

A connection table (Ctab) contains information describing the structural relationships and properties of a collection of atoms. The atoms can be wholly or partially connected by bonds. An atom can also be an unconnected fragment. Such collections might, for example, describe molecules, molecular fragments, substructures, substituent groups, polymers, alloys, formulations, mixtures, and unconnected atoms.

The connection table is fundamental to all of BIOVIA' file formats.

This chapter describes the legacy V2000 format. The current V3000 format supports more features. See [Connection Table \[CTAB\]](#).

### Ctab Block Format

The format for a Ctab block is:

<b>Counts line:</b>	Specifies the number of atoms, bonds, Sgroups, 3D constituents, as well as the chiral flag setting, and the regno. For details, see <a href="#">Counts Line</a> .
<b>Atom block:</b>	Specifies the atomic symbol and any mass difference, charge, stereochemistry, and associated hydrogens for each atom. For details, see <a href="#">Atom Block</a> .
<b>Bond block:</b>	Specifies the two atoms connected by the bond, the bond type, and any bond stereochemistry and topology (chain or ring properties) for each bond. For details, see <a href="#">Bond Block</a> .
<b>Link atom line:</b>	Supports the representation of certain kinds of Sgroups with repeating units, such as link nodes. For details about Sgroups, see <i>BIOVIA Chemical Representation</i> . See <a href="#">Link Atom Line</a> .
<b>Sgroup block:</b>	Sgroup block. For details about Groups, see <i>BIOVIA Chemical Representation</i> .
<b>Collection block:</b>	A collection block specifies all collection information for objects in the current connection table context. See <a href="#">Collection Block</a> .
<b>3D block:</b>	Contains values for x, y, and z dimensions, and supports three-dimensional concepts, such as plane and exclusion sphere. See <a href="#">3D Block</a> .

<b>Rgroup block:</b>	Supports Markush representation. See <a href="#">Rgroup Logic Lines</a> . For details about Markush structures (Rgroups), see <i>BIOVIA Chemical Representation</i> .
<b>Template block</b>	Supports the representation of large molecules, such as biologics. See <a href="#">Template Block</a> .

## General Syntax of Entries

The general syntax of an entry is:

```
M  V30 key posval posval ... [keyword=value] [keyword=value] ...
```

or

```
M  V30 BEGIN key [blockname]
M  V30 posval posval ... keyword=value keyword=value ...
...
M  V30 END key
```

Each line must begin with "M V30 " with the two blank spaces after M and one blank space after 30. Following this is a list of zero or more required positional values (*posval*). Optional values can follow that use a 'KEYWORD=va<sub>l</sub>ue' format. Items are separated by white space. There can also be white space preceding the first item. Trailing white space is ignored.

The value of a keyword can be a list containing two or more values:

```
KEYWORD=(N val1 val2 ... valN)
```

where N specifies the number of values that follow.

Values (*posval*, *va<sub>l</sub>ue*, or *va<sub>l</sub>1*, and so forth) can be strings. Strings that contain blank spaces or start with left parenthesis or double quote, must be surrounded by double quotes. A double quote can be entered literally by doubling it.

Each entry is one line of no more than 80 characters. To allow continuation when the 80-character line is too short, use a dash (-) as the last character. When read, the line is concatenated with the next line by removing the dash and stripping the initial "M V30" from the following line. For example:

```
M  V30 10 20 30 "abc-
M  V30 def"
```

is read as:

```
M  V30 10 20 30 "abcdef"
```

Generally, each section of the molfile is enclosed in a block that consists of lines such as:

```
M  V30 BEGIN key [blockname]
...
M  V30 END key
```

The 'key' value defines the kind of block, for example, CTAB, ATOM, or BOND. Depending upon the type of block, there might or might not be values on the BEGIN line.

## The Connection Table

The connection table contains core information used in all the CTfile types.

### CTAB Block

A Ctab block defines the basic connection table:

```
M V30 BEGIN CTAB [ctabname]
counts-line
atom-block
[bond-block]
[Sgroup-block]
[3d-block]
[link-line]*
[collection-block]
M V30 END CTAB
[collection-block]
[Rgroup-block]*
[template-block]
```

The atom block and counts line are required. The counts line, atom block, and bond block must appear in the order indicated. The Sgroup block, 3D block, and link lines can occur in any order after the atom and bond blocks.

### Counts Line

A counts line is required, and must be first. It specifies the number of atoms, bonds, 3D objects, and Sgroups. It also specifies whether or not the CHIRAL flag is set. Optionally, the counts line can specify a regno (a number that could be used for molecule registration). The regno specification on the counts line is only used when the regno exceeds 999999 (the limit of the format in the molfile header line). The format of the counts line is:

```
M V30 COUNTS na nb nsg n3d chiral [REGNO=regno]
```

where:

<b>na</b>	number of atoms
<b>nb</b>	number of bonds
<b>nsg</b>	number of Sgroups
<b>n3d</b>	number of 3D constraints
<b>chiral</b>	1 if molecule is chiral, 0 if not
<b>regno</b>	molecule or model regno

### Atom Block

An atom block specifies all node information for the connection table. It must precede the bond block. It has the following format:

```
M V30 BEGIN ATOM
M V30 index type x y z aamap -
M V30 [CHG=val] [RAD=val] [CFG=val] [MASS=val] - MV30 [VAL=val] -
```

```

M V30 [HCOUNT=val] [STBOX=val] [INVRET=val] [EXACHG=val] - MV30
[SUBST=val] [UNSAT=val] [RBCNT=val] -
M V30 [ATTCHPT=val] -
M V30 [Rgroups=(nvals val [val ...])] -
M V30 [ATTCHORD=(nvals nbr1 val1 [nbr2 val2 ...])] - MV30
[CLASS=template_class] -
M V30 [SEQID=sequence_id] -
. . .
M V30 END ATOM

```

## Meaning of values in the atom block

Field	Meaning	Values	Notes
<b>index</b>	Atom index	Integer > 0	Identifies atoms. The actual value of the index does not matter as long as each index is unique to each atom.
<b>type</b>	Atom type	Type = reserved atom or atom or [NOT] ['atom, atom,...'] where reserved atom = R# = Rgroup A = "any" atom Q = any atom but C or H * = "star" atom Atom = character string (for example, 'C' or 'Cl')	A character string. If the string contains white space, it must be quoted. It can be a single atom or an atom list enclosed in square brackets with an optional preceding NOT.
<b>x y z</b>	Atom coordinates		
<b>aamap</b>	Atom-atom mapping	0 = no mapping > 0 = mapped atom	Reaction property
<b>CHG</b>	Atom charge	Integer 0 = none (default)	-15 to +15. Default of 0 = uncharged atom.
<b>RAD</b>	Atom radical	0 = none (default) 1 = singlet 2 = doublet 3 = triplet	
<b>CFG</b>	Stereo configuration	0 = none (default) 1 = odd parity 2 = even parity 3 = either parity	
<b>MASS</b>	Atomic weight	Default = natural abundance	A specified value indicates the absolute atomic weight of the designated atom.
<b>VAL</b>	Valence	Integer > 0 or 0 = none (default) -1 = zero	Abnormal valence, -1, 0, 1-14

Field	Meaning	Values	Notes
<b>HCOUNT</b>	Query hydrogen count	Integer >= -1 0 = not specified (default) -1 = zero	-1 = H0, 0 = not specified (default), 1 = H1, 2 = H2, 3=H3, 4 = H4 [Query] H0 means no H atoms allowed unless explicitly drawn. Hn means atom must have n or more H's in excess of explicit H's.
<b>STBOX</b>	Stereo box	0 = ignore the configuration of this double bond atom (default) 1 = consider the stereo configuration of this double bond atom	Both atoms of a double bond must be marked to search double bond stereochemistry. Alternatively, the STBOX bond property can be used.
<b>INVRET</b>	Configuration inversion	0 = none (default) 1 = configuration inverts 2 = configuration retained	Reaction property
<b>EXACHG</b>	Exact change	0 = property not applied (default) 1 = exact change as displayed in the reaction	Reaction property
<b>SUBST</b>	Query substitution count	Integer > 0 or 0 = not specified (default) -1 = none	Number of substitutions allowed: default of 0 = off, -1 = no substitution (s0), -2 = as drawn (s*); 1, 2, 3, 4, 5 = (s1) through (s5), 6 or more = (s6).
<b>UNSAT</b>	Query unsaturation flag	0 = not specified (default) 1 = unsaturated	
<b>RBCNT</b>	Query ring bond count	Integer > 0 or 0 = not specified (default) -1 = none	Number of ring bonds allowed: default of 0 = off, -1 = no ring bonds (r0), -2 = as drawn (r*); 2 = (r2), 3 = (r3), 4 or more = (r4).
<b>ATTCHPT</b>	Rgroup member attachment points	Attachment points on member: -1 = first and second site 1 = first site only 2 = second site only	
<b>Rgroups</b>	nvals is the number of Rgroups that comprise this R# atom. val is the Rgroup number.	Integer > 0	

Field	Meaning	Values	Notes
<b>ATTCHORD</b>	nvals is the number of values that follow on the ATTCHORD line nbr1 is atom neighbor index #1, nbr2 is index #2 val1 is the attachment order for the nbr1 attachment.	Integer > 0	A list of atom neighbor index and atom neighbor value pairs that identify the attachment order information at an R# atom or template atom.  This property allows textual attachment ids. Only Rgroup atoms and collapsed template atoms may provide ATTACHORD information. It is an error to provide this information on explicit atom types. Rgroup atoms support only integer ATTACHORD values. Collapsed template atoms support text values (for example, Al,Br). See <a href="#">Example of a V3000 molfile</a> for the hybrid representation for sequences (template representation of residues).
<b>CLASS</b>	This property provides the class information for a collapsed template atom.		Example: for a collapsed alanine template atom (AA/Ala), its type=Ala and CLASS=AA
<b>SEQID</b>	This property supports a positive integer value to capture residue sequence id information.		This property supports a positive integer value to capture residue sequence id information for a template.

## Bond Block

A bond block specifies all edge information for the connection table. It must precede the Sgroup or 3D blocks. Its format is:

```

M V30 BEGIN BOND
M V30 index type atom1 atom2 -
M V30 [CFG=val] -
M V30 [TOPO=val] -
M V30 [RXCTR=val] -
M V30 [STBOX=val] -
M V30 [ATTACH=[ALL|ANY] -
M V30 [ENDPTS]=(natoms atom1 atoms2 [atom3 ...])]
M V30 [DISP=[HBOND1|HBOND2|COORD|DATIVE]] -
...
M V30 END BOND

```

## Meaning of values in the bond block

Field	Meaning	Values	Notes
<b>index</b>	Bond index	Integer > 0	The actual value of the index does not matter as long as all are unique.
<b>type</b>	Bond type	Integer: 1 = single 2 = double 3 = triple 4 = aromatic 5 = single or double 6 = single or aromatic 7 = double or aromatic 8 = any 9 = coordination 10 = hydrogen	Types 4 through 8 are for queries only. Type 9 has display options for dipolar bonds: COORD or DATIVE COORD for coordinative bonds used in metal complexes DATIVE for dative bonds used in molecules such as Lewis acids and bases Type 10 has display options: HBOND1 or HBOND2
<b>atom1,atom2</b>	Atom indexes	Integer > 0	Atom1 and Atom2 are bond end points.
<b>CFG</b>	Bond configuration	0 = none (default) 1 = up 2 = either 3 = down	
<b>TOPO</b>	Query property	0 = not specified (default) 1 = ring 2 = chain	
<b>RXCTR</b>	Reacting center status	0 = unmarked (default) -1 = not a reacting center 1 = generic reacting center Additional: 2 = no change 4 = bond made or broken 8 = bond order changes 12 = (4 + 8) bond made or broken and change 5 = (4 + 1), 9 = (8 + 1), and 13 = (12 + 1) are also possible	
<b>STBOX</b>	Stereo box	0 = ignore the configuration of this double bond (default) 1 = consider the stereo configuration of this double bond	A double bond must be marked to search double bond stereochemistry.
<b>ENDPTS</b>	multiple endpoint	ALL or ANY	One-to-all for organometallics or one-to-any for generics. For example, ENDPTS=(5 1 2 3 4 5) ATTACH=ALL

## Link Atom Line

One link atom line exists for each link atom in the Ctab. A link atom line has the format:

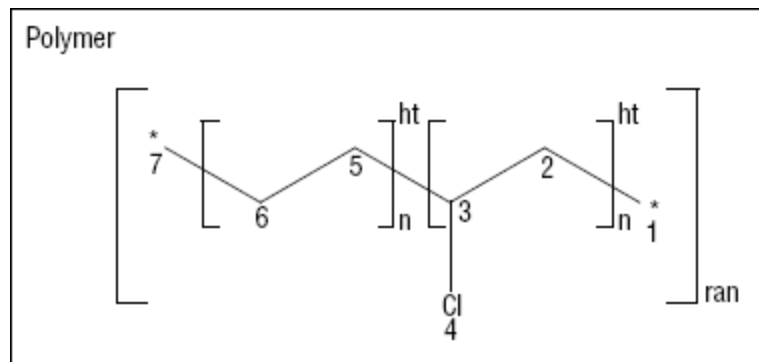
M V30 LINKNODE minrep maxrep nbonds inatom outatom [inatom outatom...]

## Meaning of values in link lines

Field	Meaning	Values	Notes
<b>minrep</b>	Minimum number of group repetitions.	1	For future expansion. Not currently used.
<b>maxrep</b>	Maximum number of group repetitions.	Integer > 0	
<b>nbonds</b>	Number of directed bonds defining the group.	nbonds = # of pairs of inatom-outatom tuples	The number of tuples is usually two (a pair), but can be one for link nodes with an attachment point.
<b>inatom</b>	Atom index of atom in the repeating group.	Integer > 0	
<b>outatom</b>	Atom index of atom bonded to inatom, but outside of repeating group.	Integer > 0	

## Sgroup Block

The Sgroup block contains general Sgroup information and information on each Sgroup structure as shown here. For the V2000 version, see [V2000 Molfile](#).





## Connection Table Organization of an Sgroup Structure

Connection Table (Ctab)	Header	Polymer
	Block	07189510252D 10.003740.000000
	Comment Line	Figure 5, J. Chem. Inf. Comput. Sci., Vol 32, No. 3., 1992
		00000999 V3000
	Counts Line	M V30 BEGIN CTAB
		M V30 COUNTS 7 6 3 0 0
	Atom Block	M V30 BEGIN ATOM
		M V30 4 Cl 0.2789 -1.1911 0 0
		M V30 5 C -1.0548 1.119 0 0
		M V30 6 C -2.3885 0.349 0 0
		M V30 7 * -3.9246 1.147 0 0
	Bond Block	M V30 END ATOM
		M V30 BEGIN BOND
		M V30 1 1 1 2
		M V30 2 1 2 3
		M V30 3 1 3 4
		M V30 4 1 5 6
		M V30 5 1 5 3
	SGroup Block	MV30 6 1 7 6
		M V30 END BOND
		M V30 BEGIN SGROUP
		M V30 1 SRU 5 ATOMS=(2 5 6) XBONDS=(2 5 6) BRKXYZ=(9 -0.6103
		1.2969 0 -0.6103
		M V30 0.171 0 0 0 0) BRKXYZ=(9 -3.1565 0.185 0 -3.1565 1.311
		0 0 0 0)
		M V30 CONNECT=HT
		M V30 2 SRU 6 ATOMS=(3 2 3 4) XBONDS=(2 1 5) BRKXYZ=(9
		2.2794 1.2969 0 2.2794
		M V30 0.1709 0 0 0 0) BRKXYZ=(9 -0.1657 0.171 0 -0.1657
		1.2969 0 0 0 0)
		M V30 CONNECT=HT
		M V30 3 COP 7 ATOMS=(7 1 2 3 4 5 6 7) BRKXYZ=(9 3.6382
		1.6391 0 3.6382 -
		M V30 -1.7685 0 0 0 0) BRKXYZ=(9 -4.707 -1.7685 0 -4.707
		1.6391 0 0 0 0)
		M V30 SUBTYPE=RAN
		M V30 END SGROUP
		M V30 END CTAB
		M END

For information on the comment line, see [V3000 Header](#).

An Sgroup block defines all Sgroups in the molecule, including any abbreviation Sgroup (formerly called abbrev or superatom). The format of the Sgroup block is:

```

M V30 BEGIN Sgroup
[M V30 DEFAULT [CLASS=class] -]
M V30 index type extindex -
M V30 [ATOMS=(natoms atom [atom ...])] -
M V30 [XBONDS=(nxbonds xbond [xbond ...])] -
M V30 [CBONDS=(ncbonds cbond [cbond ...])] -
M V30 [PATOMS=(npatoms patom [patom ...])] -
M V30 [SUBTYPE=subtype] [MULT=mult] -
M V30 [CONNECT=connect] [PARENT=parent] [COMPNO=compno] -
M V30 [XBHEAD=(nxbonds xbond [xbond ...])] -
M V30 [XBCORR=(nxbpairs xb1 xb2 [xb1 xb2 ...])] -
M V30 [LABEL=label] -
M V30 [BRKXYZ=(9 bx1 by1 bz1 bx2 by2 bz2 bx3 by3 bz3)]* -
M V30 [ESTATE=estate] [CSTATE=(4 xbond cbvx cbvy cbvz)]* -
M V30 [FIELDNAME=fieldname] [FIELDINFO=fieldinfo] -

```

```

M V30 [FIELDISP=fielddisp] -
M V30 [QUERYTYPE=querytype] [QUERYOP=queryop] -
M V30 [FIELDATA=fielddata] ... -
M V30 [CLASS=class] -
M V30 [SAP=(3 aidx lvidx id)]* -
M V30 [BRKTYP=bracketType] -
...
M V30 [SEQID=sequence_id] -
M V30 [NATREPLACE=[class]/name/[altname]] -
M V30 END Sgroup

```

The DEFAULT field provides a way to specify default values for keyword options. The same keyword options and values as defined in the following table.

### Meaning of values in the Sgroup block

Field	Meaning	Values	Notes
<b>index</b>	Sgroup index	Integer > 0	The actual value of the index does not matter as long as all indexes are unique.
<b>type</b>	Sgroup type	String. Only first 3 letters are significant: SUPERatom MULTiple SRU MONomer COPolymer CROSSlink MODification GRAft COMponent MIXture FORMulation DATa ANY GENeric	superatoms are now called abbreviation Sgroups
<b>extindex</b>	External index value	Integer => 0: If 0, positive integer assigned	Use 0 to autogenerate a number.
<b>ATOMS</b>	natoms is the number of atoms that define the Sgroup. atom is the atom index.	Integer > 0	
<b>XBONDS</b>	nxbonds is the number of crossing bonds. xbond is the crossing-bond index.	Integer > 0	

Field	Meaning	Values	Notes
<b>CBONDS</b>	ncbonds is the number of containment bonds. cbond is the containment-bond index.	Integer > 0	Only used for data Sgroups.
<b>PATOMS</b>	npatom is the number of paradigmatic repeating unit atoms. patom is the atom index of an atom in the paradigmatic repeating unit for a multiple group.	Integer > 0	
<b>SUBTYPE</b>	subtype is the Sgroup subtype.	String. Only the first 3 letters are significant: ALTErnate RANdom BLOck	
<b>MULT</b>	mult is the multiple group multiplier.	Integer > 0	
<b>CONNECT</b>	connect is the connectivity.	String values are as follows: EU (default) HH HT	The default, if missing, is EU.
<b>PARENT</b>	parent is the parent Sgroup index.	Integer > 0	
<b>COMPNO</b>	compno is the component order number.	Integer > 0	
<b>XBHEAD</b>	nxbonds is the number of crossing bonds that cross the "head" bracket.	Integer > 0	
	xbond is the crossing-bond index.	Integer > 0	If XBHEAD is missing, no bonds are paired as the head or tail of the repeating unit
<b>XBCORR</b>	nxbpairs	2 x the number of pairs of crossing-bond correspondence, that is, the number of values in list.	
	xb1 - xb2 is the pairs of crossing-bond correspondence, that is, xb1 connects to xb2.	Integer > 0	

Field	Meaning	Values	Notes
<b>LABEL</b>	label is the display label for this Sgroup.	String	For example, the abbreviation Sgroup name
<b>BRKXYZ</b>	bx1 - bz3 are the double (X,Y,Z) display coordinates in each bracket.	Angstroms	By specifying 3 triples, the format allows a 3D display. However, only the first two (X, Y) coordinates are currently used. The Z value and last (X, Y) coordinates are currently ignored and should be set to zero.
<b>ESTATE</b>	estate is the expanded display state information for abbreviation Sgroups.	String E = expanded abbreviation Sgroup or multiple group	Only abbreviation Sgroups and multiple groups (shortcuts) in an expanded internal state are supported. This field defines whether a abbreviation Sgroup or multiple group is displayed as expanded or contracted.
<b>CSTATE</b>	xbond is the crossing bond of the expanded abbreviation Sgroup.	Integer > 0	Display vector information for the contracted abbreviation Sgroup.
	cbvx - cvbz is the vector to contracted abbreviation Sgroup.	Angstroms	Only present for expanded abbreviation Sgroups. One CSTATE entry per crossing bond.
<b>FIELDNAME</b>	fieldname is the name of data field for Data Sgroup.	String	BIOVIA internal namespace - do not use: data Sgroups having a fieldname that starts with SMMX: (case insensitive). Denotes data that does not differentiate structures.
	<p>Example for FIELDNAME, FIELDDISP, and FIELDDDATA to describe a sequence chain:</p> <pre>MV30 1 DAT 1 ATOMS=(2 1 2) FIELDNAME=SMMX:CHAIN:type;name;color - MV30 FIELDDISP="0.00000.0000DAALL15" - MV30 FIELDDDATA="active site;myPeptide;Green"</pre> <p>where active site, myPeptide, and Green correspond to type, name, and color.</p>		
<b>FIELDDISP</b>	fielddisp is the Data Sgroup field display information.	Free-format string	This string is interpreted by V3000 as identical to V2000 appendix for Data Sgroup display ('M SDD') except for the index value.

Field	Meaning	Values	Notes
<b>FIELDATA</b>	fielddata is the query or field data.	Free-format string	Only one entry per query, but can be more than one for actual data. The order of the entries is important.
<b>FIELDINFO</b>	fieldinfo is the program-specific field information.	Free-format string	Example: “ <type><units/format>”
<b>QUERYTYPE</b>	querytype is the type of query or no query if missing.	String ‘’ = not a query (default) ‘MQ’ = legacy ‘IQ’ = ISIS query <p>Q’ = <program> query	
<b>QUERYOP</b>	queryop is the query operator.	String. query operator	Example: “=” or “LIKE”
<b>FIELDATA</b>	fielddata is the query or field data.	Free-format string	Only one entry per query, but can be more than one for actual data. The order of the entries is important.
<b>CLASS</b>	class is the character string for abbreviation Sgroup class.	String	Example: PEPTIDE
<b>SAP</b>	aidx is the index of attachment point or potential attachment point atom.	Integer > 0	
	lidx is the index of leaving atom.	Allowed integers are: 0 = none or implied H ‘aidx’ = atom index number of attachment point atom > 0 = atom index number of atom bonded to ‘aidx’	
	id is the attachment identifier.	String (two chars in V2000)	There must be multiple entries if the abbreviation Sgroup has more than one attachment point. The order of the entries defines the order of the attachment points. SAP entries might or might not include the actual attachment points, depending on the particular abbreviation Sgroup and its representation.

Field	Meaning	Values	Notes
<b>BRKTYP</b>	bracketType is the displayed bracket style.	Allowed values for this string are: BRACKET (default) PAREN	
<b>SEQID</b>	This property supports a positive integer value to capture residue sequence id information.	* SEQID	
<b>NATREPLAC E</b>	Specifies the natural residue replacement for modified templates.	A string: [class]/name/[altname]	The class of the natural replacement is optional. If not defined, it is assumed to be the same class as the template.

## Collection Block

A collection block specifies all collection information for objects in the current connection table context. Collection blocks must be provided after the blocks that define the objects included in the collection to minimize the amount of forward object references that must be maintained by the file reader.

```

M  V30 BEGIN COLLECTION
    [M  V30 DEFAULT -]
M  V30 name/subname -
M  V30 [ATOMS=(natoms atom [atom ...])] -
M  V30 [BONDS=(nbonds bond [bond ...])] -
M  V30 [Sgroups=(nSgroups sgrp [sgrp ...])] -
M  V30 [OBJ3DS=(nobj3ds obj3d [obj3d ...])] -
M  V30 [MEMBERS=(nmembers member [member ...])] -
M  V30 [Rgroups=(nRgroups Rgroup [Rgroup ...])] -
...
M  V30 END COLLECTION

```

## Meaning of values in the collection block

Field	Meaning	Value	Notes
<b>name/subname</b>	Collection id	Nonblank string	
<b>ATOMS</b>	natoms is the number of atoms included in the collection	Integer > 0	
	atom is the atom index	Integer > 0	
<b>BONDS</b>	nbonds is the number of bonds included in the collection	Integer > 0	
	bond is the bond index	Integer > 0	

Field	Meaning	Value	Notes
<b>Sgroups</b>	nSgroups is the number of Sgroups included in the collection	Integer > 0	
	sgrp is the Sgroup index	Integer > 0	
<b>OBJ3DS</b>	nobj3ds is the number of 3D features included in the collection	Integer > 0	
	obj3d is the 3D feature index	Integer > 0	
<b>MEMBERS</b>	nmembers is the number of members included in the collection	Integer > 0	
	member is the member identifier	ROOT or RrMm	r > 0, m > 0
<b>Rgroups</b>	nRgroups is the number of Rgroups included in the collection	Integer > 0	
	Rgroup is the Rgroup identifier	Rr	r > 0

Collections naming must meet the following criteria:

- A two-part name (name and subname) is supported for collections on import and export. The subname designation is required. The name is the unique identifier for the collection contents.
- All collections of the same name are presumed to indicate various pieces of the same collection, which can be provided in one or more COLLECTION block entries provided within various subblocks of the full connection table.
- Collection names and subnames are not case sensitive, contain only printable characters, and begin with an alphabetic character. The start of the name cannot be MDL (case insensitive).
- Collection objects are presumed to be unordered, and no preservation of input order is necessary or required on subsequent file writes.
- Future enhancements to the collection block information will provide ordered collection support.

The default delimiter for the collection name is the forward-slash (/) character. For example:

surfactiveAgent/agent001

where the name is surfactiveAgent and the subname is agent001

A non-default delimiter is specified by using a non-alphabet character before the name. The following example specifies hyphen (-) as the delimiter and uses that delimiter for both name and subname:

-surfactiveAgent-agent001-

If the first character is a quotation mark ("), it is presumed that the string that represents the collection name is within quotation marks due to the presence of spaces. For example, "surfactive agent".

The name MDLV30 is a reserved name used to designate internal collections.

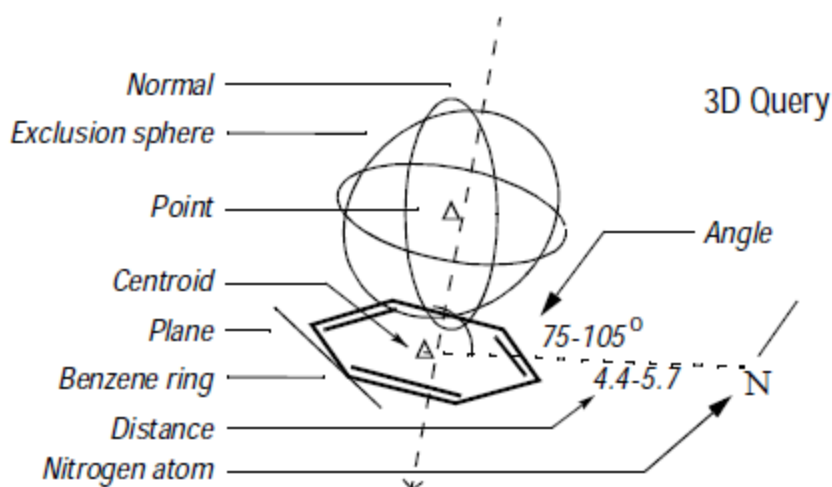
User-specified collections can use any other arbitrary naming conventions. The default action for all V3000 readers and writers provided by BIOVIA is to preserve persistent collections and internal collections for CTfile import/export operations. Internal collections can also be preserved if their contents have been validated as correct input for the specified internal representation. There is no implied validation for user collections other than requiring the collection to refer to valid objects. Collections cannot contain other collections in their definition.

The default action on registration is to strip user collection information without error, but possibly with status or warning messages being issued. The internal collection types are:

<b>MDLV30/HILITE</b>	Highlighting collection. Default action for renderers is to provide a "highlighted" display of the specified objects. All object types are allowed in this collection: atoms, bonds, Sgroups, 3Dfeatures, Rgroups, members, and components.
<b>MDLV30/STEABS</b>	Absolute stereochemistry collection. This collection defines the set of stereocenters in the structure that have absolute configurations. This is an atom collection.
<b>MDLV30/STERAC<math>n</math></b>	"Racemic" stereochemistry collection ( $n > 0$ ). This collection defines a set of stereogenic centers whose relative configuration is known. A mixture of the two enantiomeric relative configurations is present. This is an atom collection.
<b>MDLV30/STEREL<math>n</math></b>	Relative stereochemistry collection ( $n > 0$ ) that is non-tetrahedral. This collection defines a set of stereogenic centers whose relative configuration is known. Only one of the two enantiomeric relative configurations is present. There is no assumption about which of the two configurations is present. This is an atom collection.

### 3D Block

The 3D block contains the three-dimensional information as shown below.





## Connection Table Organization of an 3D Structure

	Header Block		3D Query
	Comment Line		07189510253D 11.000000.000000 Figure 5, J. Chem. Inf. Comput. Sci., Vol 32, No. 3., 1992 00000999 V3000
	Counts Line		M V30 BEGIN CTAB
			M V30 COUNTS 8 7 0 7 0
	Atom Block		M V30 BEGIN ATOM
			M V30 1 Cl 0.2892 1.1122 0 M V30 2 C -0.4562 0.6578 1.13156 0 M V30 3 C -1.4813 0.3687 0.2033 0 M V30 4 C -1.0252 0.2892 -1.1122 0 M V30 5 C 1.4562 -0.6578 -1.3156 0 M V30 6 C 1.4813 -0.3687 -0.2033 0 M V30 7 N 4.1401 -0.1989 1.3456 0 M V30 8 C 4.6453 0.5081 1.17417 0 M V30 END ATOM
	Bond Block		M V30 BEGIN BOND
			M V30 1 1 1 2 M V30 2 2 2 3 M V30 3 1 3 4 M V30 4 2 4 5 M V30 5 1 5 6 M V30 6 2 6 1 M V30 7 1 7 8 M V30 END BOND
	3D Object Block		M V30 BEGIN OBJ3D
			M V30 1 -7 6 "" 0 0 BASIS=(3 6 4 2) M V30 2 -5 13 "" 0 0 BASIS=(6 1 2 3 4 5 6) MV30 3 -8 7 "" 0 0 BASIS=(2 03D.1 03D.2) MV30 4 -3 6 "" -2 0 BASIS=(2 03D.1 03D.3) PNTDIR=1 MV30 5 -16 12 "" 1.5 0 BASIS=(1 03D.4) UNCONNOK=1 MV30 6 -12 10 "" 75 105 BASIS=(3 03D.4 03D.1 7) MV30 7 -9 3 "" 4.4 5.7 BASIS=(2 7 03D.1) MV30 END OBJ3D M V30 END CTAB M END

A 3D block specifies information for all 3D objects in the connection table. It must follow the atom and bond blocks. As in V2000 molfiles, there can be only one fixed-atom constraint.

The format of the 3D block is as follows:

```

M V30 BEGIN OBJ3D
M V30 index type color name value1 value2
M V30 BASIS=(nbvals bval [bval ...])
M V30 [ALLOW=(nbvals val [val ...])] [PNTDIR=val] [ANGDIR=val]
M V30 [UNCONNOK=val] [DATA=strval]
M V30 [COMMENT=comment]
...
M V30 END OBJ3D

```

## Meaning of values in the 3D block

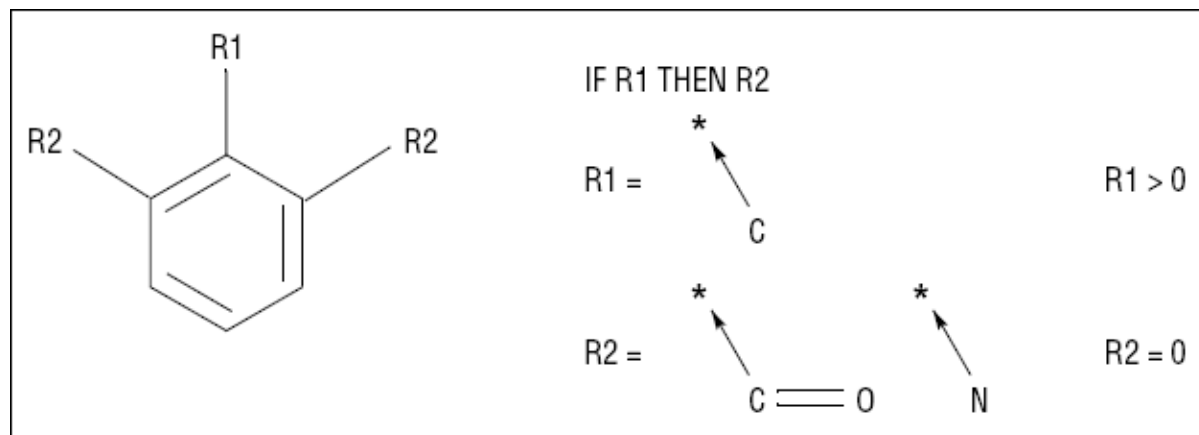
Field	Meaning	Values	Notes
<b>index</b>	3D object index	Integer > 0	The actual value of the index does not matter as long as all indexes are unique. However, extremely large numbers used as indexes can cause the program to fail to allocate memory for the correspondence array.
<b>type</b>	Object type	Integer < 0 for geometric constraints and for data constraints Integer > 0 are field IDs	
<b>color</b>	Color value	Integer > 0	
<b>name</b>	Object name or, for data query, the field name.	String	
<b>value1</b>	Distance, radius, deviation, or minimum value.	Floating point, value1 = 0 if constraint has no floating values	
<b>value2</b>	Maximum value for range constraints.	Floating point, value2 = 0 if not a range constraint	

Field	Meaning	Values	Notes
<b>BASIS</b>	nbvals is the number of objects in basis.	Integer > 0	
	bval is the atom number or 3D object index	Integer or O3D.integer	For objects where order is important, for example, in an angle constructed from three points, the order must be the same as in V2000 molfiles. See <a href="#">V2000 Connection Table [CTAB]</a> .
<b>ALLOW</b>	nvals is the number of atoms allowed in an exclusion sphere.	Integer > 0	
	val is the atom number.	Integer > 0	
<b>PNTDIR</b>		0 = point has no direction  1 = point has direction	
<b>ANGDIR</b>		0 = dihedral angle has no direction  1 = dihedral angle has direction	
<b>UNCONNO K</b>		0 = unconnected atoms are not OK  1 = unconnected atoms are OK	
<b>DATA</b>	strval is the data query string	String	
<b>COMMENT</b>	string comment	String	0 - 32 characters

## The Rgroup

### Rgroup Block

The Rgroup query shown below corresponds to the Rgroup file that follows it.



## Connection table organization of an Rgroup query

Header Block			0 7189510252D 1 0.00353 0.00000 0 0 0 0 0 0 9 9 9 V3000
Ctab for Rgroup Root	Counts Line	Atom Block for Root	M V30 BEGIN CTAB
			M V30 COUNTS 9 9 0 0 0
	Bond Block for Root		M V30 BEGIN ATOM
			M V30 1 C 1.3337 0.77 0 0
			M V30 2 C 0 1.54 0 0
			M V30 3 C -1.3337 0.77 0 0
			M V30 4 C -1.3337 -0.77 0 0
			M V30 5 C 0 -1.54 0 0
			M V30 6 C 1.3337 -0.77 0 0
			M V30 7 R# 0 3.08 0 0 RGROUPS=(1 1)
			M V30 8 R# 2.6674 1.54 0 0 RGROUPS=(1 2)
			M V30 9 R# -2.6674 1.54 0 0 RGROUPS=(1 2)
			M V30 END ATOM
	M V30 BEGIN BOND MV30 1 1 1 2		
	M V30 2 2 2 3		
	M V30 3 1 3 4		
	M V30 4 2 4 5		
	M V30 5 1 5 6		
	M V30 6 2 6 1		
	M V30 7 1 1 8		
	M V30 8 1 2 7		
	M V30 9 1 3 9		
	M V30 END BOND		
	M V30 END CTAB		
Rgroup Logic Line			M V30 BEGIN RGROUP 1
Block for Rgroup 1	Ctab for Rgroup 1 Member 1	Counts Line	M V30 RLOGIC 2 0 ""
		Atom Block	M V30 BEGIN CTAB
	Atom Block	Counts Line	M V30 COUNTS 1 0 0 0 0
		Atom Block	M V30 BEGIN ATOM
		Atom Block	M V30 1 C 12.21 14.3903 0 0 ATTCHPT=1
			M V30 END ATOM
			M V30 END CTAB
			M V30 END RGROUP
Rgroup Logic Line			M V30 BEGIN RGROUP 2
Block for Rgroup 2	Ctab for Rgroup 2 member1	Counts Line	M V30 RLOGIC 0 0 0
		Atom Block	M V30 BEGIN CTAB
	Atom Block	Counts Line	M V30 COUNTS 2 1 0 0 0
		Atom Block	M V30 BEGIN ATOM
		Atom Block	M V30 1 C -1.4969 0.0508 0 0 ATTCHPT=1
		Atom Block	M V30 2 O 0.0431 0.0508 0 0
		Atom Block	M V30 END ATOM
	Bond Block	Bond Block	M V30 BEGIN BOND
		Bond Block	M V30 1 2 1 2
		Bond Block	M V30 END BOND
		Bond Block	M V30 END CTAB
	Ctab for Rgroup 2 Member 2	Counts Line	M V30 BEGIN CTAB
		Atom Block	M V30 COUNTS 1 0 0 0 0
		Atom Block	M V30 BEGIN ATOM
	Atom Block	M V30 1 N 12.21 14.3903 0 0 ATTCHPT=1	
	Atom Block	M V30 END ATOM	
			M V30 END RGROUP
			M END

For information on the comment line, see [V3000 Header](#).

An Rgroup block defines one Rgroup. Each Ctab block specifies one member.

```
M V30 BEGIN Rgroup Rgroup-number
  [Rgroup-logic-line]
  ctab-block
  [ctab-block]*
  [collection-block]
M V30 END Rgroup
```

### Meaning of values in the Rgroup block

Field	Meaning	Values
<b>Rgroup-number</b>	Index of this Rgroup	Integer > 0

### Rgroup Logic Lines

There is zero or one Rgroup logic line for each Rgroup in the molecule. If present, the Rgroup logic line specifies if-then logic between Rgroups, the convention about unfilled valence sites, and the Rgroup occurrence information. Its format is:

```
M V30 RLOGIC thenR RestH Occur
```

### Meaning of values in Rgroup logic line

Field	Meaning	Values	Notes
<b>thenR</b>	Number of a "then" Rgroup	0 = none (default)	
<b>RestH</b>	Attachment(s) at Rgroup position	0 = off, that is, any molecule fragment at any unsatisfied Rgroup location (default) 1 = only hydrogen or a member of Rgroup is allowed	
<b>Occur</b>	String specifying number (range) of Rgroup occurrence sites that need to be satisfied.	String '> 0' = default	Examples: 1,3,5,7 1,2-6,8 >0

### Template Block

A Template block can be used to represent large biomolecules by defining one or more template definitions.

```
M V30 BEGIN TEMPLATE
  [template-definition]*
M V30 END TEMPLATE
```

where \* means 1 or many template definitions.

A template definition begins with a line that defines template properties, followed immediately with a single ctab block to provide the ctab definition:

```
M V30 TEMPLATE index [ name | class/name[/alternate_name1[...]] ]
  [NATREPLACE=[class]/name/[altname]] [ COMMENT=template_comment ]
M V30 BEGIN CTAB
...
```

M V30 END CTAB

Template definitions can be present only at the root ctabs of a CTfile, not within Rgroup blocks or within any other multi-ctabs blocks. The optional NATREPLACE keyword specifies the natural residue replacement for modified templates. The class of the natural replacement is optional. If not defined, it is assumed to be the same class as the template.

### Example of a V3000 molfile for Hybrid Representation for Sequences

The hybrid representation uses templates to represent residues, which allows for significant compression of the structure stored in the database and transmitted in molfile format between different programs. This hybrid representation is formally known as Self-Contained Sequence Representation (SCSR). One advantage of the hybrid representation for biologic sequences is that repetition is represented in a compact manner.

<sup>1</sup>A G meS A G

ACCLDraw03281611052D

```
0 0 0 0 0 999 V3000
M V30 BEGIN CTAB
M V30 COUNTS 5 4 1 0 1
M V30 BEGIN ATOM
M V30 1 A1a 1.5563 -9.2328 0 0 CLASS=AA ATTCHORD=(2 2 Br) SEQID=1
M V30 2 Gly 2.7137 -9.23 0 0 CLASS=AA ATTCHORD=(4 3 Br 1 A1) SEQID=2
M V30 3 meS 3.8712 -9.23 0 0 CLASS=AA ATTCHORD=(4 4 Br 2 A1) SEQID=3
M V30 4 A1a 5.4539 -9.23 0 0 CLASS=AA ATTCHORD=(4 3 A1 5 Br) SEQID=4
M V30 5 Gly 6.6114 -9.23 0 0 CLASS=AA ATTCHORD=(2 4 A1) SEQID=5
M V30 END ATOM
M V30 BEGIN BOND
M V30 1 1 2 1
M V30 2 1 3 2
M V30 3 1 4 3
M V30 4 1 5 4
M V30 END BOND
M V30 BEGIN SGROUP
M V30 1 DAT 1 ATOMS=(1 1) FIELDNAME="SMMX:sequence position data" -
M V30 FIELDDISP=" 1.5563 -9.2328 DA ALL 1 "
M V30 END SGROUP
M V30 END CTAB
M V30 BEGIN TEMPLATE
M V30 TEMPLATE 1 AA/A1a/A/
M V30 BEGIN CTAB
M V30 COUNTS 7 6 3 0 1
M V30 BEGIN ATOM
M V30 1 O 6.6266 -2.0662 0 0
M V30 2 H 5.0016 -2.0876 0 0
M V30 3 N 5.1358 -2.0784 0 0 CFG=3
M V30 4 C 5.7844 -1.5983 0 0 CFG=2
M V30 5 C 6.4753 -2.0653 0 0
M V30 6 O 6.4753 -2.8977 0 0
M V30 7 C 5.7844 -0.7662 0 0
M V30 END ATOM
M V30 BEGIN BOND
M V30 1 1 3 4
M V30 2 1 4 5
```

```

M V30 3 2 5 6
M V30 4 1 4 7 CFG=1
M V30 5 1 3 2
M V30 6 1 5 1
M V30 END BOND
M V30 BEGIN SGROUP
M V30 1 SUP 1 ATOMS=(1 1) XBONDS=(1 6) BRKXYZ=(9 7.02 -2.26 0 7.02 -
1.85 0 -
M V30 0 0 0) CSTATE=(4 6 -0.82 -0.01 0) LABEL=OH CLASS=LGRP
M V30 2 SUP 2 ATOMS=(1 2) XBONDS=(1 5) BRKXYZ=(9 4.58 -1.87 0 4.6 -
2.28 0 -
M V30 0 0 0) CSTATE=(4 5 0.8 0.02 0) LABEL=H CLASS=LGRP
M V30 3 SUP 3 ATOMS=(5 3 4 5 6 7) XBONDS=(2 5 6) BRKXYZ=(9 3.95 -3.33
0 3.95 -
M V30 -0.38 0 0 0 0) CSTATE=(4 5 -0.8 -0.02 0) CSTATE=(4 6 0.82 0.01
-
M V30 0) LABEL=A CLASS=AA SAP=(3 3 2 A1) SAP=(3 5 1 Br)
M V30 END SGROUP
M V30 BEGIN COLLECTION
M V30 MDLV30/STEABS ATOMS=(1 4)
M V30 END COLLECTION
M V30 END CTAB
M V30 TEMPLATE 2 AA/Gly/G/
M V30 BEGIN CTAB
M V30 COUNTS 6 5 3 0 0
M V30 BEGIN ATOM
M V30 1 N 3.676 -12.5274 0 0 CFG=3
M V30 2 C 4.2675 -12.095 0 0
M V30 3 O 4.8932 -13.2691 0 0
M V30 4 C 4.8904 -12.5161 0 0
M V30 5 O 5.1042 -12.5167 0 0
M V30 6 H 3.4542 -12.5125 0 0
M V30 END ATOM
M V30 BEGIN BOND
M V30 1 1 1 2
M V30 2 1 2 4
M V30 3 2 4 3
M V30 4 1 4 5
M V30 5 1 1 6
M V30 END BOND
M V30 BEGIN SGROUP
M V30 1 SUP 1 ATOMS=(1 5) XBONDS=(1 4) CSTATE=(4 4 -0.82 -0.01 0)
LABEL=OH -
M V30 CLASS=LGRP
M V30 2 SUP 2 ATOMS=(4 1 2 3 4) XBONDS=(2 4 5) CSTATE=(4 4 0.82 0.01
0) -
M V30 CSTATE=(4 5 -0.83 0.01 0) LABEL=G CLASS=AA SAP=(3 4 5 Br) -
M V30 SAP=(3 1 6 A1)
M V30 3 SUP 3 ATOMS=(1 6) XBONDS=(1 5) CSTATE=(4 5 0.83 -0.01 0)
LABEL=H -
M V30 CLASS=LGRP
M V30 END SGROUP
M V30 END CTAB

```



```

M V30 TEMPLATE 3 AA/meS/meS/ NATREPLACE=AA/S
M V30 BEGIN CTAB
M V30 COUNTS 9 8 3 0 1
M V30 BEGIN ATOM
M V30 1 C 9.9525 -5.6641 0 0
M V30 2 O 9.9451 -6.8641 0 0
M V30 3 N 7.3518 -5.6442 0 0 CFG=3
M V30 4 C 8.6579 -4.9049 0 0 CFG=1
M V30 5 C 8.6671 -3.4041 0 0
M V30 6 O 7.6319 -2.7971 0 0
M V30 7 C 6.3173 -5.0361 0 0
M V30 8 O 10.8217 -5.1697 0 0
M V30 9 H 7.3436 -6.6442 0 0
M V30 END ATOM
M V30 BEGIN BOND
M V30 1 2 2 1
M V30 2 1 1 4
M V30 3 1 4 3
M V30 4 1 4 5 CFG=1
M V30 5 1 5 6
M V30 6 1 3 7
M V30 7 1 1 8
M V30 8 1 3 9
M V30 END BOND
M V30 BEGIN SGROUP
M V30 1 SUP 1 ATOMS=(7 1 2 3 4 5 6 7) XBONDS=(2 7 8) CSTATE=(4 7 2.17
0.48 -
M V30 0) CSTATE=(4 8 -1.31 -0.99 0) LABEL=meS CLASS=AA SAP=(3 1 8 Br)
-
M V30 SAP=(3 3 9 A1) NATREPLACE=AA/S
M V30 2 SUP 2 ATOMS=(1 8) XBONDS=(1 7) CSTATE=(4 7 -2.17 -0.48 0)
LABEL=OH -
M V30 CLASS=LGRP
M V30 3 SUP 3 ATOMS=(1 9) XBONDS=(1 8) CSTATE=(4 8 1.31 0.99 0)
LABEL=H -
M V30 CLASS=LGRP
M V30 END SGROUP
M V30 BEGIN COLLECTION
M V30 MDLV30/STEABS ATOMS=(1 4)
M V30 END COLLECTION
M V30 END CTAB
M V30 END TEMPLATE
M END

```

## Molfile

The V3000 molfile and V3000 rxnfile formats support the latest features of BIOVIA chemical representation. See [Molfile in V3000 Format - Advantages Over V2000](#). V3000 is both a superset of V2000 but a different format. For information on the earlier V2000 format, see [V2000 Connection Table \[CTAB\]](#).

### A no-structure

- Is a placeholder structure that has no contents, represented by a counts line with many zeros.
- Can be flagged with the V3000 or the V2000 version stamp.

```
1 [name or blank]
2          06031011012D 1    1.00000    0.00000    0
3 [comment or blank]
4    0 0 0    0 0          999 V2000
5 M  END
```

```
1 [name or blank]
2          06031011022D 1    1.00000    0.00000    0
3 [comment or blank]
4    0 0 0    0 0          999 V3000
5 M  V30 BEGIN CTAB
6 M  V30 COUNTS 0 0 0 0 0
7 M  V30 END CTAB
8 M  END
```

## Example of molfile - Alanine

ACCLDraw12161507522D

```
    0 0 0    0 0          999 V3000
M  V30 BEGIN CTAB
M  V30 COUNTS 5 4 0 0 1
M  V30 BEGIN ATOM
M  V30 1 N 16.998 -17.4463 0 0
M  V30 2 C 16.998 -16.2972 0 0 CFG=1
M  V30 3 C 18.1179 -15.9033 0 0
M  V30 4 O 18.1179 -14.7224 0 0
M  V30 5 C 16.0183 -15.6308 0 0
M  V30 END ATOM
M  V30 BEGIN BOND
M  V30 1 1 2 5 CFG=3
M  V30 2 2 3 4
M  V30 3 1 2 3
M  V30 4 1 1 2
M  V30 END BOND
M  V30 BEGIN COLLECTION
M  V30 MDLV30/STEABS ATOMS=(1 2)
M  V30 END COLLECTION
M  V30 END CTAB
M  END
```

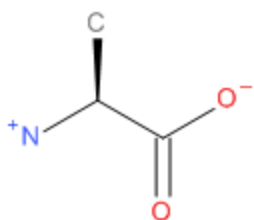
The structure of the molfile is:

Feature	Line(s)
Header Block	1 - 4
Comment Line	3
Connection Table (ctab)	5 - 26
Counts Line	6
Atom Block	7 - 14
Bond Block	15 - 25

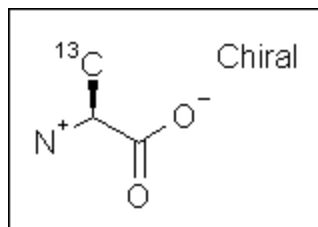
**Note:** This example does not have the following Ctab blocks: Sgroup, Rgroup, 3D, Template.

Different applications might render the same chemical structure with some superficial differences.

BIOVIA Draw version of alanine:



ISIS/Draw Version of alanine:



See also

[V3000 Header](#)

## V3000 Header

Line 1:	<p>Molecule name. This line is unformatted, but like all other lines in a molfile cannot extend beyond column 80. If no name is available, a blank line must be present.</p> <p><b>Caution:</b> This line must not contain any of the reserved tags that identify any of the other CTAB file types such as \$MDL (RGfile), \$\$\$\$ (SDfile record separator), \$RXN (rxnfile), or \$RDFILE (RDfile headers).</p>
---------	---

Line 2:	<p>This line has the format:</p> <pre>IIPPPPPPPMDDYYHHmddSSSSSSSSSSSEEEEEEEEEERRRRRR A2&lt;--A8--&gt;&lt;---A10--&gt;A2I2&lt;--F10.5--&gt;&lt;---F12.5--&gt;&lt;-I6-&gt; )</pre> <p>User's first and last initials (I), program name (P), date/time (M/D/Y,H:m), dimensional codes (d) such as 2D or 3D, scaling factors (S, s), energy (E) if modeling program input, internal registry number (R)</p> <p>The “dimensional code” is maintained explicitly. Thus “3D” really means 3D, although “2D” will be interpreted as 3D if any non-zero Z-coordinates are found.</p> <p><b>Note:</b> A blank line can be substituted for line 2.</p>
Line 3:	A line for comments. If no comment is available, a blank line must be present.
Line 4:	<p>This line contains the version number, V3000</p> <p>The number of appendix lines is always written as 999, regardless of how many there actually are. See <a href="#">Counts Line</a>.</p> <p>(For V2000, Line 4 is the no-structure counts line. See <a href="#">The Counts Line</a>)</p>

#### Notes:

- The first 3 lines are for compatibility with legacy V2000 molfile readers.
- Unlike the V2000 molfile, the V3000 extended Rgroup molfile has the same header format as a non-Rgroup molfile.
- Do not create a molfile with a pre-V3000 Rgroup header (" \$MDL", and so forth) but with V3000 Ctab blocks. A pre-V3000 Rgroup molfile can only have embedded molfiles that are also pre-V3000 versions, for example, the version is either "V2000" or "".

## RGfiles (Rgroup file)

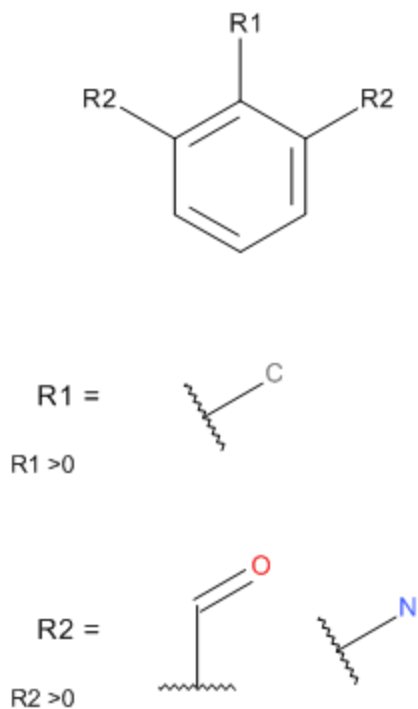
The format of an RGfile (Rgroup file) is shown below. Rgroups are also known as Markush structures.

In addition to the primary connection table (Ctab block) for the root structure, a Ctab block defines each member within each Rgroup. For an example of the header, see [Connection Table Organization of an Rgroup Query](#). For a description of the Rgroup, see [The Rgroup](#).

[Example of an RGfile \(Rgroup file\)](#) ..... 33

### Example of an RGfile (Rgroup file)

Rendering in BIOVIA Draw.



The following is the RGfile corresponding to the rendering above. The structure of the RGfile is:

Feature	Lines
RGfile header Block	1 - 4
Ctab for Rgroup root	5 - 29
Block for Rgroup R1	30 - 38
Block for Rgroup R2	39 - 57

```
1
2   ACCLDraw12231508522D
3
4   0  0  0      0  0          999 v3000
5   M  V30 BEGIN CTAB
6   M  V30 COUNTS 9 9 0 0 0
```

```

7 M V30 BEGIN ATOM
8 M V30 1 C 3.509 -8.7214 0 0
9 M V30 2 C 5.5513 -8.7208 0 0
10 M V30 3 C 4.5321 -8.1311 0 0
11 M V30 4 C 5.5513 -9.9023 0 0
12 M V30 5 C 3.509 -9.9076 0 0
13 M V30 6 C 4.5347 -10.4918 0 0
14 M V30 7 R# 2.4858 -8.1307 0 0 RGROUPS=(1 2)
15 M V30 8 R# 4.5321 -6.9496 0 0 RGROUPS=(1 1)
16 M V30 9 R# 6.5745 -8.1301 0 0 RGROUPS=(1 2)
17 M V30 END ATOM
18 M V30 BEGIN BOND
19 M V30 1 1 6 4
20 M V30 2 2 5 6
21 M V30 3 1 2 3
22 M V30 4 1 1 5
23 M V30 5 2 4 2
24 M V30 6 2 3 1
25 M V30 7 1 1 7
26 M V30 8 1 3 8
27 M V30 9 1 2 9
28 M V30 END BOND
29 M V30 END CTAB
30 M V30 BEGIN RGROUP 1
31 M V30 RLOGIC 0 0 >0
32 M V30 BEGIN CTAB
33 M V30 COUNTS 1 0 0 0 0
34 M V30 BEGIN ATOM
35 M V30 1 C 5.0898 -12.4244 0 0 ATTCHPT=1
36 M V30 END ATOM
37 M V30 END CTAB
38 M V30 END RGROUP
39 M V30 BEGIN RGROUP 2
40 M V30 RLOGIC 0 0 >0
41 M V30 BEGIN CTAB
42 M V30 COUNTS 2 1 0 0 0
43 M V30 BEGIN ATOM
44 M V30 1 C 3.8627 -16.0165 0 0 ATTCHPT=1
45 M V30 2 O 4.8856 -15.426 0 0
46 M V30 END ATOM
47 M V30 BEGIN BOND
48 M V30 1 2 1 2
49 M V30 END BOND
50 M V30 END CTAB
51 M V30 BEGIN CTAB
52 M V30 COUNTS 1 0 0 0 0
53 M V30 BEGIN ATOM
54 M V30 1 N 7.1764 -16.0755 0 0 ATTCHPT=1
55 M V30 END ATOM
56 M V30 END CTAB
57 M V30 END RGROUP
58 M END

```

## Rxnfile

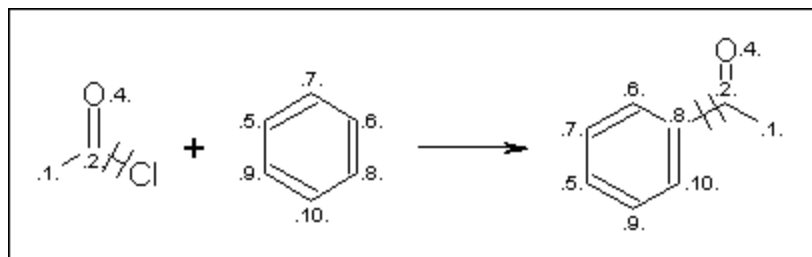
Rxnfiles contain structural data for the reactants and products of a reaction. This section covers the preferred V3000 reaction file format. For the V2000 version of this reaction file format, see [V2000 Rxnfile Overview](#).

### Header Block

<b>Line 1:</b>	\$RXN in the first position on this line identifies the file as a reaction file. After one blank space, V3000 follows.
<b>Line 2:</b>	A line for the reaction name. If no name is available, a blank line must be present.
<b>Line 3:</b>	User's initials (I), program name and version (P), date/time (M/D/Y,H:m), and reaction registry number (R). This line has the format:  IIIIIIIPPPPPPPPMDDYYYYHHmmRRRRRRR <-A6-><---A9--><---A12-----><--I7-> )  A blank line can be substituted for line 3.  If the internal registry number is more than 7 digits long, it is stored in an "MREG" line (see <a href="#">Large REGNO</a> ).
<b>Line 4:</b>	A line for comments. If no comment is entered, a blank line must be present.

### Counts line

**Line 5:** The counts line specifies the number of reactants and products. Two reactants and one product are indicated in line 5 of [Example V3000 Rxnfile for the acylation of benzene](#).



## Example V3000 Rxnfile for the Acylation of Benzene



Header Block			\$RXN V3000 05030217387439
Counts Line			M V30 COUNTS 2 1
Reactant block	Ctab for first reactant		M V30 BEGIN REACTANT
			M V30 BEGIN CTAB
		Counts Line	M V30 COUNTS 4 3 0 0 0
			M V30 BEGIN ATOM
		Atom Block	M V30 1 C 0.323 -0.2377 0 1
			M V30 2 C -1.0362 -0.9618 0 2
			M V30 3 O 0.323 1.4154 0 3
			M V30 4 Cl 1.6423 -1.0307 0 0
			M V30 END ATOM
		Bond Block	M V30 BEGIN BOND
			M V30 1 1 1 2 RXCTR=2
			M V30 2 2 1 3 RXCTR=2
			M V30 3 1 1 4 RXCTR=4
			M V30 END BOND
			M V30 END CTAB
		Ctab for second reactant	
	Counts Line		M V30 COUNTS 6 6 0 0 0
			M V30 BEGIN ATOM
	Atom Block		M V30 1 C 1.3331 -0.7694 0 5
			M V30 2 C 1.3331 0.7694 0 6
			M V30 3 C 0 -1.5417 0 7
			M V30 4 C 0 1.5417 0 8
			M V30 5 C -1.3331 -0.7694 0 9
			M V30 6 C -1.3331 0.7694 0 10
			M V30 END ATOM
	Bond Block		M V30 BEGIN BOND
			M V30 1 1 1 2 RXCTR=2
		M V30 2 2 1 3 RXCTR=2	
M V30 3 2 2 4 RXCTR=2			
M V30 4 1 3 5 RXCTR=2			
M V30 5 1 4 6 RXCTR=2			
	M V30 6 2 5 6 RXCTR=2		
	M V30 END BOND		
	M V30 END CTAB		
Product block	Ctab for product		M V30 END REACTANT
			M V30 BEGIN PRODUCT
			M V30 BEGIN CTAB
		Counts Line	M V30 COUNTS 9 9 0 0 0
			M V30 BEGIN ATOM
		Atom Block	M V30 1 C -0.5331 -0.1358 0 5
			M V30 2 C -1.8606 0.633 0 6
			M V30 3 C -0.5331 -1.6992 0 7
			M V30 4 C 0.8201 0.6305 0 1
			M V30 5 C -3.2189 -0.1358 0 8
			M V30 6 C -1.8811 -2.4731 0 9
			M V30 7 C 2.1297 -0.1128 0 2
			M V30 8 O 0.8534 2.2297 0 3
			M V30 9 C -3.2292 -1.6863 0 10
			M V30 END ATOM
		Bond Block	M V30 BEGIN BOND
	M V30 1 1 1 2 RXCTR=2		
	M V30 2 2 1 3 RXCTR=2		
	M V30 3 1 1 4 RXCTR=		
	M V30 4 2 2 5 RXCTR=2		
	M V30 5 1 3 6 RXCTR=2		
		M V30 6 1 4 7 RXCTR=2	
		M V30 7 2 4 8 RXCTR=2	
		M V30 8 1 5 9 RXCTR=2	
		M V30 9 2 6 9 RXCTR=2	
		M V30 END BOND M	
		V30 END CTAB	
		M V30 END PRODUCT	
	M END		

## V2000 Connection Table [CTAB]

A connection table (Ctab) contains information describing the structural relationships and properties of a collection of atoms. The atoms can be wholly or partially connected by bonds. (An atom can also be an unconnected fragment.) Such collections might, for example, describe molecules, molecular fragments, substructures, substituent groups, polymers, alloys, formulations, mixtures, and unconnected atoms.

The connection table is fundamental to all of BIOVIA's file formats.

This chapter describes the legacy V2000 format. The current V3000 format supports more features. See [Connection Table \[CTAB\]](#).

### Ctab Block Format for V2000

The format for a Ctab block is:

<b>Counts line:</b>	Important specifications here relate to the number of atoms, bonds, and atom lists, the chiral flag setting, and the Ctab version.
<b>Atom block:</b>	Specifies the atomic symbol and any mass difference, charge, stereochemistry, and associated hydrogens for each atom.
<b>Bond block:</b>	Specifies the two atoms connected by the bond, the bond type, and any bond stereochemistry and topology (chain or ring properties) for each bond.
<b>Atom list block:</b>	Identifies the atom (number) of the list and the atoms in the list.
<b>Stext (structural text descriptor) block:</b>	Used by ISIS/Desktop programs.
<b>Properties block:</b>	Provides for future expandability of Ctab features, while maintaining compatibility with earlier Ctab configurations.

The detailed format for each block outlined above follows:

#### Notes:

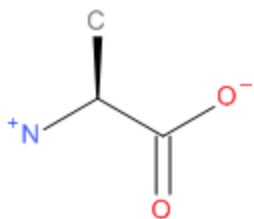
A blank numerical entry on any line should be read as "0" (zero). Spaces are significant and correspond to one or more of the following:

- Absence of an entry
- Empty character positions within an entry
- Spaces between entries; single unless specifically noted otherwise

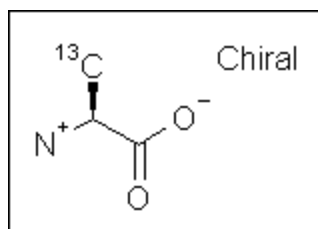
### Example: Alanine in V2000 format

Different applications might render the same chemical structure with some superficial differences.

BIOVIA Draw version of alanine:



ISIS/Draw version of alanine:



The connection table of alanine:

```

1
2  ACCLDraw12231509452D
3
4      6  5  0  0  1  0  0  0  0  0999 v2000
5      3.5938 -8.5438 0.0000 N 0 3 0 0 0 0 0 0 0 0 0 0
5      4.6169 -7.9530 0.0000 C 0 0 2 0 0 0 0 0 0 0 0 0
7      5.6401 -8.5438 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0
8      6.6633 -7.9530 0.0000 O 0 5 0 0 0 0 0 0 0 0 0 0
9      5.6401 -9.7252 0.0000 O 0 0 0 0 0 0 0 0 0 0 0 0
10     4.6169 -6.7716 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0
11    1  2  1  0  0  0  0
12    2  3  1  0  0  0  0
13    3  4  1  0  0  0  0
14    3  5  2  0  0  0  0
15    2  6  1  1  0  0  0
16 M  CHG  2  1  1  4  -1
17 M  END
18

```

The structure of the molfile is:

Feature	Line(s)
Header Block	1 - 3
Comment Line	3
Connection Table (ctab)	4 - 18
Counts Line	4
Atom Block	5 - 10
Bond Block	11- 15
Properties Block	16 - 18

This example does not have the following Ctab blocks: Atom List, Stext.

## The Counts Line

aaabbb111ffcccsssxxrrrrpppiiimmvvvvvv

Where:

<b>aaa</b>	= number of atoms (current max 255)*	[Generic]
<b>bbb</b>	= number of bonds (current max 255)*	[Generic]
<b>lll</b>	= number of atom lists (max 30)*	[Query]
<b>fff</b>	= (obsolete)	
<b>ccc</b>	= chiral flag: 0=not chiral, 1=chiral	[Generic]
<b>sss</b>	= number of stext entries	[ISIS/Desktop]
<b>xxx</b>	= (obsolete)	
<b>rrr</b>	= (obsolete)	
<b>ppp</b>	= (obsolete)	
<b>iii</b>	= (obsolete)	
<b>mmm</b>	= number of lines of additional properties, including the MEND line. No longer supported, the default is set to 999.	[Generic]

\* These limits apply to the ISIS/Host Reaction Gateway, but not to the ISIS/Host Molecule Gateway or ISIS/Desktop.

For example, the counts line in the Ctab shown above has six atoms, five bonds, the CHIRAL flag on, and three lines in the properties block:

6 5 0 0 1 0 3 v2000

A V2000 no-structure might have a counts line (line 4) as follows:

0 0 0 0 0 0 0 0 0 0999 v2000

## The Atom Block

The Atom Block is made up of atom lines, one line per atom with the following format:

xxxxx.xxxxxyyyy.yyyyzzzz.zzzz aaaddcccssshhbbbvvhHrrriiimmnnneee

where the values are described in the following table:

Field	Meaning	Values	Notes
<b>x y z</b>	atom coordinates		[Generic]
<b>aaa</b>	atom symbol	entry in periodic table or L for atom list, A, Q, * for unspecified atom, and LP for lone pair, or R# for Rgroup label	[Generic, Query, 3D, Rgroup]

Field	Meaning	Values	Notes
<b>dd</b>	mass difference	-3, -2, -1, 0, 1, 2, 3, 4 (0 if value beyond these limits)	<b>[Generic]</b> Difference from mass in periodic table. Wider range of values allowed by M ISO line, below. Retained for compatibility with older Ctabs, M ISO takes precedence.
<b>ccc</b>	charge	0, 1, 2, 3, 4, 5, 6, 7 (0 if uncharged; 1, 2, 3 if positive charges where 1 = +3, 2 = +2, 3 = +1; 4 if doublet radical; 5, 6, 7 if negative charges where 5 = -1, 6 = -2, 7 = -3)	<b>[Generic]</b> Wider range of values in M CHG and M RAD lines below. Retained for compatibility with older Ctabs, M CHG and M RAD lines take precedence.
<b>sss</b>	atom stereo parity	0 = not stereo, 1 = odd, 2 = even, 3 = either or unmarked stereo center	<b>[Generic]</b> Ignored when read.
<b>hhh</b>	hydrogen count + 1	1 = H0, 2 = H1, 3 = H2, 4 = H3, 5 = H4	<b>[Query]</b> H0 means no H atoms allowed unless explicitly drawn. Hn means atom must have n or more H's in excess of explicit H's.

Field	Meaning	Values	Notes
<b>bbb</b>	stereo care box	0 = ignore stereo configuration of this double bond atom 1 = stereo configuration of double bond atom must match	<b>[Query]</b> Double bond stereochemistry is considered during SSS only if both ends of the bond are marked with stereo care boxes.
<b>vvv</b>	valence	0 = no marking (default) (1 to 14) = (1 to 14) 15 = zero valence	<b>[Generic]</b> Shows number of bonds to this atom, including bonds to implied H's.
<b>HHH</b>	H0 designator	0 = not specified (default) 1 = no H atoms allowed	<b>[ISIS/Desktop]</b> Redundant with hydrogen count information. Might be unsupported in future releases of BIOVIA software.
<b>rrr</b>	Not used		
<b>iii</b>	Not used		
<b>mmm</b>	atom-atom mapping number	1 - number of atoms	<b>[Reaction]</b>
<b>nnn</b>	inversion/retention flag	0 = property not applied 1 = configuration is inverted, 2 = configuration is retained	<b>[Reaction]</b>
<b>eee</b>	exact change flag	0 = property not applied, 1 = change on atom must be exactly as shown	<b>[Reaction, Query]</b>

With Ctab version V2000, the **dd** and **ccc** fields have been superseded by the **M ISO**, **M CHG**, and **M RAD** lines in the properties block, described below. For compatibility, all releases since ISIS 1.0:

- Write appropriate values in both places if the values are in the old range.
- Use the atom block fields if there are no **M ISO**, **M CHG**, or **M RAD** lines in the properties block.

Support for these atom block fields might be removed in future releases of BIOVIA software.

## The Bond Block

The Bond Block is made up of bond lines, one line per bond, with the following format:

111222tttssssxxxrrrccc

The values are described below.

### Meaning of values in the bond block

Field	Meaning	Values	Notes
<b>111</b>	first atom number	1 - number of atoms	<b>[Generic]</b>
<b>222</b>	second atom number	1 - number of atoms	<b>[Generic]</b>
<b>ttt</b>	bond type	1 = Single, 2 = Double, 3 = Triple, 4 = Aromatic, 5 = Single or Double, 6 = Single or Aromatic, 7 = Double or Aromatic, 8 = Any	<b>[Query]</b> Values 4 through 8 are for SSS queries only.
<b>sss</b>	bond stereo	Single bonds: 0 = not stereo, 1 = Up, 4 = Either, 6 = Down, Double bonds: 0 = Use x-, y-, z-coords from atom block to determine cis or trans, 3 = Cis or trans (either) double bond	<b>[Generic]</b> The wedge (pointed) end of the stereo bond is at the first atom (Field 111 above)
<b>xxx</b>	not used		
<b>rrr</b>	bond topology	0 = Either, 1 = Ring, 2 = Chain	<b>[Query]</b> SSS queries only.
<b>ccc</b>	reacting center status	0 = unmarked, 1 = a center, -1 = not a center Additional: 2 = no change, 4 = bond made/broken, 8 = bond order changes 12 = 4+8 (both made/broken and changes); Also possible: 5 = (4 + 1), 9 = (8 + 1), and 13 = (12 + 1)	<b>[Reaction, Query]</b>

### The Atom List Block[Query]

**Note:** Current BIOVIA applications use the M ALS item in the properties block in place of the atom list block. The atom list block is retained for compatibility, but information in an M ALS item supersedes atom list block information.

Made up of atom list lines, one line per list, with the following format:

aaa kSSSSn 111 222 333 444 555

where:

Field	Meaning
aaa	= number of atom (L) where list is attached
k	= T = [NOT] list, = F = normal list
n	= number of entries in list; maximum is 5
111...555	= atomic number of each atom on the list
S	= space

## The Stext Block [ISIS/Desktop - not used in current products]

The Stext Block is made up of two-line entries with the following format:

```
xxxxx . xxxxyyyyy . yyyy  
TTTT . . .
```

where:

Field	Meaning
x y	= stext coordinate
T	= stext text

## The Properties Block

The Properties Block is made up of mmm lines of additional properties, where mmm is the number in the counts line described above. If a version stamp is present, mmm is ignored and the file is read until an "M END" line is encountered.

**Note:** mmm is no longer supported and is set to 999 as the default.

Most lines in the properties block are identified by a prefix of the form MXXX where two spaces separate the M and XXX. Exceptions are:

- A aaa, V aaa vvvvvv, and G aaappp, which indicate the following ISIS/Desktop properties: atom alias, atom value, and group abbreviation (called residue in ISIS), respectively.
- S SKPnnn which causes the next nnn lines to be ignored.

The prefix: M END terminates the properties block.

Variables in the formats can change properties but keep the same letter designation. For example, on the Charge, Radical, or Isotope lines, the "uniformity" of the vvv designates a general property identifier. On Sgroup property lines, the sss uniformity is used as an Sgroup index identifier.

All lines that are not understood by the program are ignored.

The descriptions below use the following conventions for values in field widths of 3:

```
n15    number of entries on line; value = 1 to 15  
nn8    number of entries on line; value = 1 to 8  
nn6    number of entries on line; value = 1 to 6  
nn4    number of entries on line; value = 1 to 4  
nn2    number of entries on line; value = 1 or 2
```



nn1      number of entries on line; value = 1  
aaa      atom number; value = (1 to number of atoms)

The format for the properties included in this block are described in what follows. The format shows one entry and ellipses (. . .) indicate additional entries.

### Atom Alias [ISIS/Desktop - not used in current products]

A aaa  
x . . .

aaa: Atom number  
x:    Alias text

### Atom Value [ISIS/Desktop - not used in current products]

V aaa  
v . . .

aaa: Atom number  
v:    Value text

### Group Abbreviation [ISIS/Desktop - not used in current products]

G aaappp  
x . . .

aaa: Atom number  
ppp: Atom number  
x:    Abbreviation label

Abbreviation is required for compatibility with previous versions of ISIS/Desktop, which allowed abbreviations with only one attachment. The attachment is denoted by two atom numbers, aaa and ppp. All of the atoms on the aaa side of the bond formed by aaa-ppp are abbreviated. The coordinates of the abbreviation are the coordinates of aaa. The text of the abbreviation is on the following line (x...). In current versions of ISIS, abbreviations can have any number of attachments and are written out using the Sgroup appendixes. However, any ISIS abbreviations that do have one attachment are also written out in the old style, again for compatibility with older ISIS versions, but this behavior might not be supported in future versions.

### Charge [Generic]

M CHGnn8 aaa vvv . . .

vvv:      15 to +15. Default of 0 = uncharged atom. When present, this property supersedes all charge and radical values in the atom block, forcing a 0 charge on all atoms not listed in an M CHG or M RAD line.

## Radical [Generic]

M RADnn8 aaa vvv ...

vvv: Default of 0 = no radical, 1 = singlet (:), 2 = doublet ( . or ^), 3 = triplet (^^). When present, this property supersedes all charge and radical values in the atom block, forcing a 0 (zero) charge and radical on all atoms not listed in an MCHG or MRAD line.

## Isotope [Generic]

M ISOnn8 aaa vvv ...

vvv: Absolute mass of the atom isotope as a positive integer. When present, this property supersedes all isotope values in the atom block. Default (no entry) means natural abundance. The difference between this absolute mass value and the natural abundance value specified in the PTABLE.DAT file must be within the range of -18 to +12.

## Ring Bond Count [Query]

M RBCnn8 aaa vvv ...

vvv: Number of ring bonds allowed: default of 0 = off, -1 = no ring bonds (r0), -2 = as drawn (r\*); 2 = (r2), 3 = (r3), 4 or more = (r4).

## Substitution Count [Query]

M SUBnn8 aaa vvv ...

vvv: Number of substitutions allowed: default of 0 = off, -1 = no substitution (s0), -2 = as drawn (s\*); 1, 2, 3, 4, 5 = (s1) through (s5), 6 or more = (s6).

## Unsaturated Count [Query]

M UNSnn8 aaa vvv ...

vvv: At least one multiple bond: default of 0 = off, 1 = on.

## Link Atom [Query]

M LINnn4 aaa vvv bbb ccc

vvv, bbb, ccc: Link atom (aaa) and its substituents, other than bbb and ccc, can be repeated 1 to vvv times, (vvv >= 2). The bbb and ccc parameters can be 0 (zero) for link nodes on atoms with attachment point information.

## Atom List [Query]

M ALS aaannn e 11112222333344445555...

aaa: Atom number, value  
nnn: number of entries on line (16 maximum)  
e: Exclusion, value is T if a 'NOT' list, F if a normal list.  
1111: Atom symbol of list entry in field of width 4

**Note:** This line contains the atom symbol rather than the atom number used in the atom list block, and is independent of the Ptable. (For information about the Ptable, see *BIOVIA Chemical Representation*.). Any data found in this item supersedes data from the atom list block. The number of entries can exceed the fixed limit of 5 in the atom list block entry.

## Attachment Point [Rgroup]

M APOnn2 aaa vvv ...

Indicates whether atom aaa of the Rgroup member is the first attachment point (vvv = 1), second attachment point (vvv = 2), both attachment points (vvv = 3); default of 0 = no attachment.

## Atom Attachment Order [Rgroup]

M AAL aaann2 111 v1v 222 v2v ...

aaa:	Atom index of the Rgroup usage atom
nn2:	Number of pairs of entries that follow on the line
111:	Atom index of a neighbor of aaa
v1v	Attachment order for the aaa-111 bond
222	Atom index of a neighbor of aaa
v2v	Attachment order for the aaa-222 bond

### Notes:

v1v and v2v are either 1 or 2 for the simple doubly attached Rgroup member.

The atom neighbor value information identifies the atom neighbor index as the nth attachment. The implied ordering in V2000 molfiles is by atom index order for the neighbors of Rgroup usage atoms. If atom index order conflicts with the desired neighbor ordering at the R# atom, this appendix allows you to override to this default order.

If v1v=1 and v2v=2, ISIS/Host only writes this appendix if 111 is greater than 222. Note, however, that the attachment values can be written in any order.

## Rgroup Label Location [Rgroup]

M RGPnn8 aaa rrr ...

rrr: Rgroup number, value from 1 to 32 \*, labels position of Rgroup on root.

\* ISIS/Desktop limit

## Rgroup Logic, Unsatisfied Sites, Range of Occurrence [Rgroup]

M LOGnn1 rrr iii hhh ooo...

rrr: Rgroup number, value from 1 to 32 \*

iii: Number of another Rgroup which must only be satisfied if rrr is satisfied (IF rrr THEN iii)

hhh: RestH property of Rgroup rrr; default is 0 = off, 1 = on. If this property is applied (on), sites labeled with Rgroup rrr can only be substituted with a member of the Rgroup or with H

Range of Rgroup occurrence required: n = exactly n, n - m = n through m, > n = greater than n, < n = fewer than n, default (blank) is > 0. Any non-contradictory combination of the preceding values is also allowed; for example:

1, 3-7, 9, >11.

\* ISIS/Desktop limit

## Sgroup Type [Sgroup]

M STYnn8 sss ttt ...

sss: Sgroup number

Sgroup type: SUP = abbreviation Sgroup (formerly called superatom), MUL = multiple group, SRU = SRU type, MON = monomer, MER = Mer type, COP = copolymer, CRO = crosslink, MOD = modification, GRA = graft, COM = component, MIX = mixture, FOR = formulation, DAT = data Sgroup, ANY = any polymer, GEN = generic.

**Note:** For a given Sgroup, an STY line giving its type must appear before any other line that supplies information about it. For a data Sgroup, an SDT line must describe the data field before the SCD and SED lines that contain the data (see Data Sgroup Data below). When a data Sgroup is linked to another Sgroup, the Sgroup must already have been defined.

Sgroups can be in any order on the Sgroup Type line. Brackets are drawn around Sgroups with the M SDI lines defining the coordinates.

## Sgroup Subtype [Sgroup]

M SSTnn8 sss ttt ...

ttt: Polymer Sgroup subtypes: ALT = alternating, RAN = random, BLO = block

## Sgroup Labels [Sgroup]

M SLBnn8 sss vvv ...

vvv: Unique Sgroup identifier

## Sgroup Connectivity [Sgroup]

M SCNnn8 sss ttt ...

ttt: HH = head-to-head, HT = head-to-tail, EU = either unknown. Left justified.

## Sgroup Expansion [Sgroup]

M SDS EXPn15 sss ...

sss: Sgroup index of expanded abbreviation Sgroups

## Sgroup Atom List [Sgroup]

M SAL sssn15 aaa ...

aaa: Atoms in Sgroup sss



**Note:** To ensure that all current molfile readers consistently interpret chemical structures, multiple groups are written in their fully expanded state to the molfile. The M SPA atom list is a subset of the full atom list that is defined by the Sgroup Atom List M SAL entry.

## Sgroup Subscript [Sgroup]

M SMT sss m...

m...: Text of subscript Sgroup sss. (For multiple groups, m... is the text representation of the multiple group multiplier. For abbreviation Sgroups, m... is the text of the abbreviation Sgroup label.)

## Sgroup Correspondence [Sgroup]

M CRS sssnn6 bb1 bb2 bb3

bb1, bb2: Crossing bonds that share a common bracket

bb3: Crossing bond in repeating unit that connect to bond bb1

## Sgroup Display Information [Sgroup]

M SDI sssnn4 x1 y1 x2 y2

x1,y1, x2,y2: Coordinates of bracket endpoints

## Abbreviation Sgroup Bond and Vector Information [Sgroup]

M SBV sss bb1 x1 y1

bb1: Bond connecting to contracted abbreviation Sgroup

x1,y1: Vector for bond bb1 connecting to contracted abbreviation Sgroup sss

## Data Sgroup Field Description [Sgroup]

M SDT sss fff...fffgghhh...hhhijjj...

sss: Index of data Sgroup

fff...fff: 30 character field name - no blanks, commas, or hyphens for MACCS-II gg:Field type - F = formatted, N = numeric, T = text (ignored) hhh...hhh20-character field units or format

ii: Nonblank if data line is a query rather than Sgroup data, MQ= MACCS-II query, IQ= ISIS query, PQ = program name code query

jjj...: Data query operator

## Data Sgroup Display Information [Sgroup]

M SDD sss xxxxx.xxxxxyyyy.yyyy eeefgh i jjjkkk ll m noo

sss: Index of data Sgroup

x,y: Coordinates (2F10.4)

eee: (Reserved for future use)

f: Data display, A = attached, D = detached

g: Absolute, relative placement, A = absolute, R = relative

h: Display units, blank = no units displayed, U = display units

i: (Reserved for future use)

jjj: Number of characters to display (1...999 or ALL)  
 kkk: Number of lines to display (unused, always 1)  
 ll: (Reserved for future use)  
 m: Tag character for tagged detached display (if non-blank)  
 n: Data display DASP position (1...9). (MACCS-II only)  
 oo: (Reserved for future use)

## Data Sgroup Data [Sgroup]

MSCD sss d...

MSED sss d...

d...: Line of data for data Sgroup sss (69 chars per line, columns 12-80)

A line of data is entered as text in 69-character substrings. Each SCD line adds 69 characters to a text buffer (starting with successive SCDs at character positions 1, 70, and 139). Following zero or more SCDs must be an SED, which can supply a final 69 characters. The SED initiates processing of the buffered line of text: trailing blanks are removed and right truncation to 200 characters is performed, numeric and formatted data are validated, and the line of data is added to data Sgroup sss. Left justification is not performed.

A data Sgroup can have more than one line of data, so more than one set of SCD and SED lines can be present for the same data Sgroup. The lines are added in the same order that they are encountered.

If 69 or fewer characters are to be entered on a line, they can be entered with a single SED not preceded by an SCD. On the other hand, a line can be entered to a maximum of 3 SCDs followed by a blank SED that terminates the line. The set of SCD and SED lines describing one line of data for a given data Sgroup must appear together, with no intervening lines for other data Sgroups' data.

## Sgroup Hierarchy Information [Sgroup]

M SPLnn8 ccc ppp ...

ccc: Sgroup index of the child Sgroup

ppp: Sgroup index of the parent Sgroup (ccc and ppp must already be defined via an STY line prior to encountering this line)

## Sgroup Component Numbers [Sgroup]

M SNCnn8 sss 000 ...

sss: Index of component Sgroup

000: Integer component order (1...256). This limit applies only to MACCS-II

## 3D Feature Properties [3D]

M \$3Dnnn

M \$3D...: See [The Properties Block for 3D Features](#) for information on the properties block of a 3D molfile. These lines must all be contiguous

## Phantom Extra Atom

The format for phantom extra atom information is as follows:

M PXA aaaxxxxx.xxxxxyyyyy.yyyyzzzzz.zzzz H e...

where:

aaa: Index of (real) atom for attachment

xyz: Coordinates for the added atom

H: Atom symbol

e...: Additional text string (for example, the abbreviation Sgroup label)

The bond to the added phantom atom is added as a crossing bond to the outermost Sgroup that contains atom aaa. Note this appendix supplies coordinates and up to 35 characters of 'label' that can be used for the ISIS/Desktop abbreviation Sgroup conversion mechanism. ISIS/Desktop uses this appendix to register hydrogen-only abbreviation Sgroups, which are often used as abbreviation Sgroup leaving groups on the desktop, but which cannot be directly registered into ISIS/Host databases. The hydrogen-only leaving groups are converted to PXA appendices for registration, and converted back when ISIS/Desktop reads the structure.

The following are limitations on phantom extra atom:

- Abbreviation Sgroup nesting cases
- No bonded phantom atom-phantom atom support

## Abbreviation Sgroup Attachment Point

The format for abbreviation Sgroup attachment point is as follows:

```
M SAP sssnn6 iii ooo cc
```

where:

sss: Index of abbreviation Sgroup attachment point

nn6: Number of iii,ooo,cc entries on the line (6 maximum)

iii: Index of the attachment point atom

ooo: Index of atom in sss that leaves when iii is substituted

cc: 2 character attachment identifier (for example, H or T for head/tail). No validation of any kind is performed, and ' ' is allowed. ISIS/Desktop uses the first character as the ID of the leaving group to attach if the bond between ooo and iii is deleted, and uses the second character to indicate the sequence polarity: l for left, r for right, and x for none (a crosslink).

The bond iii-ooo is either a sequence bond, a sequence crosslink bond, or a bond to a leaving group that terminates a sequence or caps a crosslink bond. This bond might have been deleted by the user to perform a substructure search. In this case, ooo will be 0. If the leaving group attached to iii consists of only a hydrogen, the leaving group will be replaced by a Phantom Extra Atom, as previously described. In this case, iii is set equal to ooo as a signal to ISIS/Desktop that a hydrogen-only leaving group must be reattached to iii.

An attachment point entry is one iii,ooo,cc triad.

Multiple M SAP lines are permitted for each abbreviation Sgroup to the maximum of the atom attachment limit. The order of the attachment entries is significant because the first iii,ooo,c becomes the first connection made when drawing to the collapsed abbreviation Sgroup, and so forth.

## Abbreviation Sgroup Class

The format for abbreviation Sgroup class is as follows:

```
M SCL sss d...
```

where:



sss:	Index of abbreviation Sgroup
d...:	Text string (for example, PEPTIDE, ...) 69 characters maximum

## Large REGNO

The format for the regno appendix is as follows:

```
M REG r...
```

where:

rrr: Free format integer regno

This appendix supports overflow of the I6 regno field in the molfile header. If this appendix is present, the value of the regno in the molfile header is superceded.

## Sgroup Bracket Style

The format for the Sgroup bracket style is as follows:

```
M SBTnn8 sss ttt ...
```

where:

sss: Index of Sgroup

ttt: Bracket display style: 0 = default, 1 = curved (parenthetic) brackets

This appendix supports altering the display style of the Sgroup brackets.

## End of Block

```
M END
```

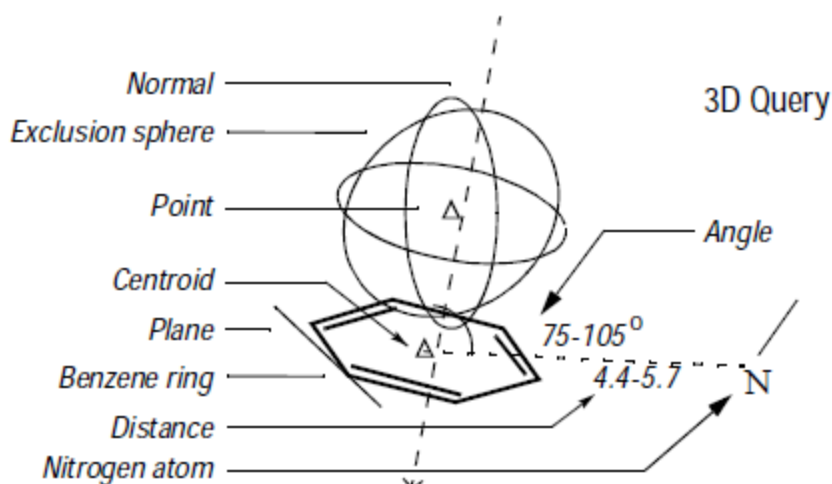
This entry goes at the end of the properties block and is required for molfiles which contain a version stamp in the counts line.

## The Properties Block for 3D Features [3D]

For each 3D feature, the properties block includes:

- One 3D features count line
- One or more 3D features detail lines

The characters M \$3D appear at the beginning of each line describing a 3D feature. The information for 3D features starts in column 7.



Ctab organization of a 3D query

		3D Query
Header Block		10179109553D1 1.00000 0.00000 0
Counts Line		8 7 0 0 0 0 18V2000
Ctab Block	Atom Block	1.0252 0.2892 1.1122C 00 00 00
		-0.4562 0.6578 1.3156C 00 00 00
		-1.4813 0.3687 0.2033C 00 00 00
		-1.0252 -0.2892 -1.1122C 00 00 00
		0.4562 -0.6578 -1.3156C 00 00 00
		1.4813 -0.3687 -0.2033C 00 00 00
		4.1401 -0.1989 1.3456N 00 00 00
		4.6453 0.5081 1.7417C 00 00 00
	Bond Block	1 2 1 0 0 0
		2 3 2 0 0 0
		3 4 1 0 0 0
		4 5 2 0 0 0
		5 6 1 0 0 0
		6 1 2 0 0 0
		7 8 1 0 0 0
	Atom List Block Stext Block	
	3D Features Count	
	Properties Block	M \$3D 7
		M \$3D -7 6
		M \$3D 3
		M \$3D 6 4 2
		M \$3D -5 13
		M \$3D 6 0.0000
		M \$3D 1 2 3 4 5 6
		M \$3D -8 7
		M \$3D 9 10
		M \$3D -3 6
		M \$3D 9 11 -2.0000
		M \$3D -16 12
		M \$3D 12 1 0 1.5000
		M \$3D -12 10
		M \$3D 12 9 7 75.0000 105.0000
		M \$3D -9 3
		M \$3D 7 9 4.4000 5.7000
		M END

## 3D Features Count Line

The first line in the properties block is the 3D features count line and has the following format:

M \$3Dnnn

where nnn is the number of 3D features on a model.

## 3D Features Detail Lines

The lines following the 3D features count line describe each 3D feature on a model. Each 3D feature description consists of an identification line and one or more data lines:

- The identification line is the first line and contains the 3D feature's type identifier, color, and name.
- Each data line describes the construction of the 3D feature.

## Identification Line

The 3D feature identification line has the following format:

M \$3Dfffccc aaa...aaa ttt...ttt

where the variables represent:

fff: 3D feature type

ccc: Color number (an internal number which is terminal dependent)

aaa...aaa: 3D feature name (up to 32 characters)

ttt...ttt: Text comments (up to 32 characters) used by BIOVIA programs (see "3D data constraints [3D, Query]" )

## 3D Feature Type Identifiers

Identifier	Meaning
-1	Point defined by two points and a distance (in Angstroms)
-2	Point defined by two points and a percentage
-3	Point defined by a point, a normal line, and a distance
-4	Line defined by two or more points (a best fit line if more than two points)
-5	Plane defined by three or more points (a best fit plane if more than three points)
-6	Plane defined by a point and a line
-7	Centroid defined by points
-8	Normal line defined by a point and a plane
-9	Distance defined by two points and a range (in Angstroms)
-10	Distance defined by a point, line, and a range (in Angstroms)
-11	Distance defined by a point, plane, and a range (in Angstroms)
-12	Angle defined by three points and a range (in degrees)
-13	Angle defined by two intersecting lines and a range (in degrees)
-14	Angle defined by two intersecting planes and a range (in degrees)
-15	Dihedral angle defined by 4 points and a range (in degrees)
-16	Exclusion sphere defined by a point and a distance (in Angstroms)
-17	Fixed atoms in the model
nnn	A positive integer indicates atom or atom-pair data constraints

## Data Line

The 3D feature defines the data line format. Each 3D object is treated as a pseudoatom and identified in the connection table by a number. The 3D object numbers are assigned sequentially, starting with the next number greater than the number of atoms. The data line formats for the 3D feature types are:

### 3D feature type identifiers

Type	Description of Data Line
-1	<p>The data line for a point defined by two points and a distance (Å) has the following format:</p> <pre>M \$3Diii jjj d d d d d . d d d d</pre> <p>where the variables represent:</p> <p>iii: ID number of a point</p> <p>jjj: ID number of a second point</p> <p>d d d d d . d d d d: Distance from first point in direction of second point (Å), 0 if not used</p> <p>The following example shows POINT_1 created from the atoms 1 and 3 with a constraint distance of 2Å. The first line is the identification line. The second line is the data line.</p> <pre>M \$3D -14 POINT_1 M \$3D132.0000</pre>
-2	<p>The data line for a point defined by two points and a percentage has the format:</p> <pre>M \$3Diii jjj d d d d d . d d d d d</pre> <p>where the variables represent:</p> <p>iii: ID number of a point</p> <p>jjj: ID number of a second point</p> <p>d d d d d . d d d d: Distance (fractional) relative to distance between first and second points, 0 if not used</p>
-3	<p>The data line for a point defined by a point, a normal line, and a distance (Å) has the format:</p> <pre>M \$3Diii l l l d d d d d . d d d d</pre> <p>where the variables represent:</p> <p>iii: ID number of a point</p> <p>l l l: ID number of a normal line</p> <p>d d d d d . d d d d: Distance (Å), 0 if not used</p> <p><b>Note:</b> For chiral models, the distance value is signed to specify the same or opposite direction of the normal.</p>

Type	Description of Data Line
-4	<p>The data lines for a best fit line defined by two or more points have the following format:</p> <pre> M \$3Dpppttttt.tttt M \$3Diii jjj...zzz . . . </pre> <p>where the variables represent:</p> <p>ppp: Number of points defining the line</p> <p>ttttt.tttt: Deviation (Å), 0 if not used.</p> <p>iii: Each iii, jjj, and zzz is the ID number jjj of an item in the model that defines the line</p> <p>jjj</p> <p>...</p> <p>zzz: (to maximum of 20 items per data line)</p> <p>The following line is defined by the four points 1, 14, 15, and 19 and has a deviation of 1.2Å. The first line is the identification line. The second and third lines are the data lines.</p> <pre> M \$3D -42 N_TO_AROM M \$3D41.2000 M \$3D1 14 15 19 </pre>
-5	<p>The data lines for a plane defined by three or more points (a best fit plane if more than three points) have the following format:</p> <pre> M \$3Dpppttttt.tttt M \$3Diii jjj...zzz ... </pre> <p>where the variables represent:</p> <p>ppp: Number of points defining the line</p> <p>ttttt.tttt: Deviation (Å), 0 if not used.</p> <p>iii: Each iii, jjj, and zzz is the ID number jjj of an item in the model that defines the plane</p> <p>jjj</p> <p>...</p> <p>zzz: (to maximum of 20 items per data line)</p> <p>The following plane is defined by the three points 1, 5, and 14. The first line is the identification line. The second and third lines are the data lines.</p> <pre> M \$3D -54 PLANE_2 M \$3D30.0000 M \$3D1 5 14 </pre>

Type	Description of Data Line
-6	<p>The data line for a plane defined by a point and a line has the following format:</p> <pre>M \$3Diii111</pre> <p>where the variables represent:</p> <p>iii: ID number of a point</p> <p>111: ID number of a line</p> <p>The following plane is defined by the point 1 and the plane 16. The first line is the identification line. The second line is the data line.</p> <pre>M \$3D -63 PLANE_1 M \$3D1 16</pre>
-7	<p>The data lines of a centroid defined by points have the following format:</p> <pre>M \$3Dppp M\$3Diiijjj...zzz ...</pre> <p>where the variables represent:</p> <p>ppp: Number of points defining the centroid</p> <p>iii: Each iii, jjj, and zzz is the ID number jjj of an item in the model that defines the centroid</p> <p>jjj</p> <p>...</p> <p>zzz: (maximum of 20 items per data line).</p> <p>The following centroid, ARO_CENTER, is defined by 3 items: 6, 8, and 10. The first line is the identification line. The second and third lines are the data lines.</p> <pre>M \$3D -71 ARO_CENTER M\$3D3 M \$3D68 10</pre>
-8	<p>The data line for a normal line defined by a point and a plane has the following format:</p> <pre>M \$3Diiijjj</pre> <p>where the variables represent:</p> <p>iii: ID number of a point</p> <p>jjj: ID number of a plane</p> <p>The following normal line, ARO_NORMAL, is defined by the point 14 and the plane 15. The first line is the identification line. The second line is the data line.</p> <pre>M \$3D -81 ARO_NORMAL M\$3D 14 15</pre>

Type	Description of Data Line
-9	<p>The data line for a distance defined by two points and a range (Å) has the following format:</p> <pre>M \$3Diii jjj dddd dddd zzzz . zzzz</pre> <p>where the variables represent:</p> <p>iii: ID number of a point</p> <p>jjj: ID number of a second point</p> <p>dddd . dddd: Minimum distance (Å)</p> <p>zzzz . zzzz: Maximum distance (Å)</p> <p>The following distance, L, is between items 1 and 14 and has a minimum distance of 4.9Å and a maximum distance of 6.0Å. The first line is the identification line. The second line is the data line.</p> <pre>M \$3D -96 L M \$3D1 144 .90006 .0000</pre>
-10	<p>The data line for a distance defined by a point, line, and a range (Å) has the format:</p> <pre>M \$3Diii lll dddd dddd zzzz . zzzz</pre> <p>where the variables represent:</p> <p>iii: ID number of a point</p> <p>lll ID number of a line</p> <p>dddd . dddd: Minimum distance (Å)</p> <p>zzzz . zzzz: Maximum distance (Å)</p>
-11	<p>The data line for a distance defined by a point, plane, and a range (Å) has the format:</p> <pre>M \$3Diii jjj dddd dddd zzzz . zzzz</pre> <p>where the variables represent:</p> <p>iii: ID number of a point</p> <p>jjj: ID number of a plane</p> <p>dddd . dddd: Minimum distance (Å)</p> <p>zzzz . zzzz: Maximum distance (Å)</p>

Type	Description of Data Line
-12	<p>The data line for an angle defined by three points and a range (in degrees) has the following format:</p> <pre>M \$3Diii jjj kkk dddd. ddddzzzz. zzzz</pre> <p>where the variables represent:</p> <p>iii: ID number of a point</p> <p>jjj: ID number of a second point</p> <p>kkk: ID number of a third point</p> <p>dddd. dddd: Minimum degrees</p> <p>zzzz. zzzz: Maximum degrees</p> <p>The following angle, THETA1, is defined by the three points: 5, 17, and 16. The minimum angle is 80° and the maximum is 105°. The first line is the identification line. The second line is the data line.</p> <pre>M \$3D-125 THETA1 M \$3D5 17 1680.0000105.0000</pre>
-13	<p>The data line for an angle defined by two lines and a range (in degrees) has the following format:</p> <pre>M \$3D111 mmm dddd. ddddzzzz. zzzz</pre> <p>where the variables represent:</p> <p>111: ID number of a line</p> <p>mmm: ID number of a second line</p> <p>dddd. dddd: Minimum degrees</p> <p>zzzz. zzzz: Maximum degrees</p> <p>THETA2 is defined by the lines 27 and 26 with maximum and minimum angles of 45° and 80°. The first line is the identification line. The second line is the data line.</p> <pre>M \$3D-135 THETA2 M \$3D 27 2645.000080.0000</pre>
-14	<p>The data line for an angle defined by two planes and a range (in degrees) has the following format:</p> <pre>M \$3Diii jjj dddd. ddddzzzz. zzzz</pre> <p>where the variables represent:</p> <p>iii: ID number of a plane</p> <p>jjj: ID numbers of a second plane</p> <p>dddd. dddd: Minimum degrees</p> <p>zzzz. zzzz: Maximum degrees</p>



Type	Description of Data Line
-15	<p>The data line for a dihedral angle defined by four points and a range (in degrees) has the following format:</p> <pre>M \$3Diii jjj kkk lll dddd . dddd zzzz . zzzz</pre> <p>where the variables represent:</p> <p>iii: ID number of a point  jjj: ID number of a second point  kkk: ID number of a third point  lll: ID number of a fourth point  dddd . dddd: Minimum degrees  zzzz . zzzz: Maximum degrees</p> <p>DIHED1 is defined by the items 7, 6, 4, and 8 with minimum and maximum angles of 45° and 80°, respectively. The first line is the identification line. The second line is the data line.</p> <pre>M \$3D-155 DIHED1 M \$3D764845 . 000080 . 0000</pre>
-16	<p>The data lines for an exclusion sphere defined by a point and a distance (Å) have the following format:</p> <pre>M \$3Diii uuu aa dddd . dddd M \$3Dbbb ccc . . . zzz . . .</pre> <p>where the variables represent:</p> <p>iii: ID number of the center of the sphere  uuu: 1 or 0. 1 means unconnected atoms are ignored within the exclusion sphere during a search; 0 otherwise  aaa: Number of allowed atoms  dddd . dddd: Radius of sphere (Å)  bbb: Each bbb, ccc, and zzz is an ID number of an allowed atom  ccc  . . .  zzz: (to maximum of 20 items per data line)</p> <p>The following exclusion sphere is centered on point 24, has a radius of 5, and allows atom 9 within the sphere. The first line is the identification line. The second and third lines are the data lines.</p> <pre>M \$3D-167 EXCL_SPHERE M \$3D 24015 . 0000 M \$3D9</pre>

Type	Description of Data Line
-17	<p>The data lines of the fixed atoms have the following format:</p> <pre> M \$3Dppp M \$3Diijjj...zzz ... </pre> <p>where the variables represent:</p> <p>ppp: Number of fixed points</p> <p>iii: Each iii, jjj, and zzz is an ID number of a fixed atom</p> <p>jjj</p> <p>zzz: (to maximum of 20 items per data line)</p> <p>The following examples shows 4 fixed atoms. The first line is the identification line. The second and third lines are the data lines.</p> <pre> M \$3D-17 M \$3D4 M \$3D37 12 29 </pre>

### 3D Data Constraints [3D, Query]

A positive integer is used as a type identifier to indicate an atom or atom-pair data constraint. Two lines are used to describe a data constraint.

The lines have the following format:

```

M $3Dnncccaa...aaabbbbbbbppppppppss...sss
M $3Diijjjddd...ddd

```

where the variables represent:

nnn: Database-field number

ccc: Color

aaa...aaa: Database-field name (up to 30 characters)

bbbbbbbb: /BOX = box-number (source of data) (up to 8 characters)

pppppppp /DASP = n1, n2 where n1 and n2 are digits from 1-9 (data size and position) (up to 9 characters)

sss...sss: /DISP = 3DN (name), 3DV (value), 3DQ (query), NOT (no text). First three in any combination to maximum total of 15 characters

iii: ID number of an atom

jjj: ID number of a second atom for atom-pair data, 0 if data is atom data

ddd...ddd: Data constraint (based on format from database) (up to 64 characters)

**Note:** The ISIS data query requires a search operator, a blank space, then one or more operands. For more information on ISIS data query syntax, see the ISIS Help system entries on SBF (Search By Form) or QB (Query Builder) for entering text in a query.

The following example shows a numeric data constraint for the field CNDO.CHARGE on atom 12. The first line is the identification line. The second line is the data line.

```

M $3D 7 0 CNDO.CHARGE
M $3D 12 0 -0.3300 -0.1300

```

The following example shows a numeric data constraint for the field BOND.LENGTH on the atom pair 1 and 4. The first line is the identification line. The second line is the data line.

```
M    $3D 9 0 BOND.LENGTH
M    $3D 1 4      2.0500      1.8200
```

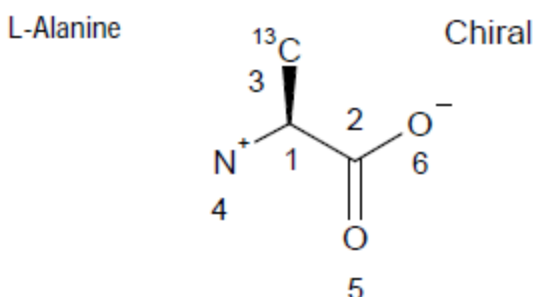
The following example shows a data constraint allowing any charge value for the field CHARGE on all the atoms. The first line is the identification line. The second line is the data line.

```
M    $3D 120 CHARGE M$3D9990 @
```

## V2000 Molfile

### V2000 Molfile Overview

A molfile consists of a header block and a connection table. The following shows a V2000 molfile for alanine corresponding to the following structure:



Molfile organization illustrated using alanine

Connection Table (Ctab)	Header Block	L-Alanine (13C) 10169115362D 1 0.00366 0.00000 0									
	Counts Line	6	5	0	0	1	0	3	V2000		
	Atom Block	-0.6622	0.5342	0.0000	C	0	0	2	0	0	0
		0.6622	-0.3000	0.0000	C	0	0	0	0	0	0
		-0.7207	2.0817	0.0000	C	1	0	0	0	0	0
		-1.8622	-0.3695	0.0000	N	0	3	0	0	0	0
		0.6220	-1.8037	0.0000	O	0	0	0	0	0	0
		1.9464	0.4244	0.0000	O	0	5	0	0	0	0
	Bond Block	1	2	1	0	0	0				
		1	3	1	1	0	0				
		1	4	1	0	0	0				
		2	5	2	0	0	0				
		2	6	1	0	0	0				
	Properties Block	M	CHG	2	4	1	6	-1			
		M	ISO	1	3	13					
		M	END								

The format for a molfile is:

<b>Header Block:</b>	Identifies the molfile: molecule name, user's name, program, date, and other miscellaneous information and comments
<b>Ctab Block:</b>	Connection table

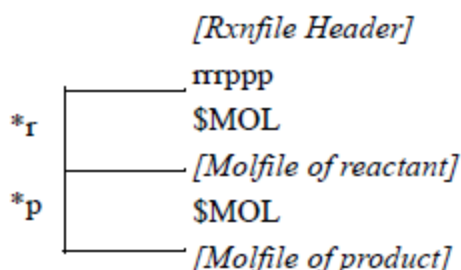
## Header Block for V2000 Molfile

<b>Line 1:</b>	<p>Molecule name. This line is unformatted, but like all other lines in a molfile cannot extend beyond column 80. If no name is available, a blank line must be present.</p> <p><b>Caution:</b> This line must not contain any of the reserved tags that identify any of the other CTAB file types such as \$MDL (RGfile), \$\$\$\$ (SDfile record separator), \$RXN (rxnfile), or \$RDFILE (RDfile headers).</p>
<b>Line 2:</b>	<p>This line has the format:</p> <pre> IIPPPPPPPMDDYYHHmddSSSSSSSSSSSEEEEEEEEEERRRRRR A2&lt;--A8--&gt;&lt;---A10--&gt;A2I2&lt;--F10.5-&gt;&lt;---F12.5--&gt;&lt;-I6-&gt; ) </pre> <p>User's first and last initials (I), program name (P), date/time (M/D/Y, H:m), dimensional codes (d), scaling factors (S, s), energy (E) if modeling program input, internal registry number (R) if input through MDL form.</p> <p>A blank line can be substituted for line 2.</p> <p>If the internal registry number is more than 6 digits long, it is stored in an M REG line (see "<a href="#">Large REGNO</a>").</p>
<b>Line 3:</b>	<p>A line for comments. If no comment is entered, a blank line must be present.</p>

## V2000Rxnfile

### V2000 Rxnfile Overview

Rxnfiles contain structural data for the reactants and products of a reaction. See the example "[V2000 Rxnfile for the acylation of benzene](#)". The format is:



where:

`*r` is repeated for each reactant

`*p` is repeated for each product

### Header Block

Line 1:	\$RXN in the first position on this line identifies the file as a reaction file.
Line 2:	A line for the reaction name. If no name is available, a blank line must be present.
Line 3:	User's initials (I), program name and version (P), date/time (M/D/Y, H:m), and reaction registry number (R). This line has the format: <code>IIIIII PPPPPPPPPMDDYYYYHHmmRRRRRRRR</code> <code>&lt;-A6-&gt;&lt;---A9--&gt;&lt;---A12-----&gt;&lt;--I7-&gt; )</code> A blank line can be substituted for line 3. If the internal registry number is more than 7 digits long, it is stored in an "M REG" line (see <a href="#">Large REGNO</a> ). <b>Note:</b> In rxnfiles produced by earlier versions of ISIS/Host, the year occupied two digits instead of four. There are corresponding minor changes in the adjacent fields. The format of the line is: <code>IIIIII PPPPPPPPPMDDYYHHmmRRRRRRRR</code> <code>&lt;-A6-&gt;&lt;---A10--&gt;&lt;---A10--&gt;&lt;--I8--&gt; )</code>
	A line for comments. If no comment is entered, a blank line must be present.

### Reactants/Products

A line identifying the number of reactants and products, in that order. The format is:

`rrrppp`

where the variables represent:

rrr                      Number of reactants\*

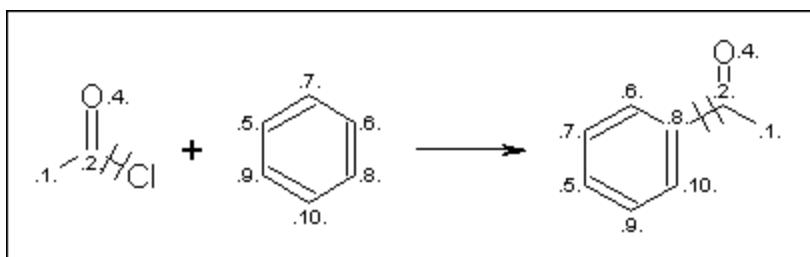
ppp                      Number of products\*

\* ISIS/Host has a limit of 8 reactants and 8 products. BIOVIA Direct does not impose any limits.

## Molfile Blocks

A series of blocks, each starting with \$MOL as a delimiter, giving the molfile for each reactant and product in turn. The molfile blocks are always in the same order as the molecules in the reaction; reactants first and products second.

The rxnfile in "[V2000 Rxnfile for the acylation of benzene](#)" corresponds to the following reaction which includes atom-atom mapping:



## V2000 Rxnfile for the Acylation of Benzene

<i>Header Block</i>	\$RXN
	1017911041 7439
#Reactants & #Products	2 1
Molfile delimiter	\$MOL
<i>Molfile for 1st reactant</i>	REACCS8110179110412D 1 0.00380 0.00000 315
	4 3 0 0 0 01 V2000
	0.3929 -0.2577 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0
	-1.0590 -0.7710 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 2 0 0
	0.3929 1.2823 0.0000 O 0 0 0 0 0 0 0 0 0 0 0 0 3 0 0
	1.6503 -1.1468 0.0000 Cl 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	1 2 1 0 0 0 2
	1 3 2 0 0 0 2
	1 4 1 0 0 0 4
	M END
	\$MOL
<i>Molfile for 2nd reactant</i>	10179110412D 1 0.00371 0.00000 8
	6 6 0 0 0 01 V2000
	1.3335 -0.7689 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 5 0 0
	1.3335 0.7689 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 6 0 0
	0.0000 -1.5415 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 7 0 0
	0.0000 1.5415 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 8 0 0
	-1.3335 -0.7689 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 9 0 0
	-1.3335 0.7689 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 10 0 0
	1 2 1 0 0 0 2
	1 3 2 0 0 0 2
	2 4 2 0 0 0 2
	3 5 1 0 0 0 2
	4 6 1 0 0 0 2
	5 6 2 0 0 0 2
	M END
	\$MOL
<i>Molfile for product</i>	10179110412D 1 0.00374 0.00000 255
	9 9 0 0 0 01 V2000
	-0.5311 -0.1384 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 5 0 0
	-1.8626 0.6321 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 6 0 0
	-0.5311 -1.6943 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 7 0 0
	0.8191 0.6284 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0
	-3.2278 -0.1346 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 8 0 0
	-1.8813 -2.4723 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 9 0 0
	2.1282 -0.1085 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 2 0 0
	0.8191 2.2292 0.0000 O 0 0 0 0 0 0 0 0 0 0 0 0 3 0 0
	-3.2278 -1.6831 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0 10 0 0
	1 2 1 0 0 0 2
	1 3 2 0 0 0 2
	1 4 1 0 0 0 4
	2 5 2 0 0 0 2
	3 6 1 0 0 0 2
	4 7 1 0 0 0 2
	4 8 2 0 0 0 2
	5 9 1 0 0 0 2
	6 9 2 0 0 0 2
	M END



## V2000 RGfiles (Rgroup file)

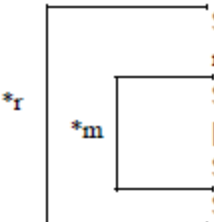
### RGfile Overview

The format of an RGfile (Rgroup file) is shown below. Lines beginning with \$ define the overall structure of the Rgroup query. The molfile header block is embedded in the Rgroup header block.

In addition to the primary connection table (Ctab block) for the root structure, a Ctab block defines each member (\*m) within each Rgroup (\*r).

```

$MDL REV 1 date/time
$MOL
$HDR
[Molfile Header Block = name, pgm info, comment]
$END HDR
$CTAB
[Ctab Block = count + atoms + bonds + lists + props]
$END CTAB
$RGP
rrr [where rrr = Rgroup number]
$CTAB
[Ctab Block]
$END CTAB
$END RGP
$END MOL
```

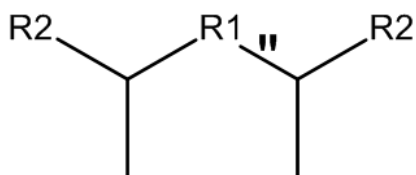


where:

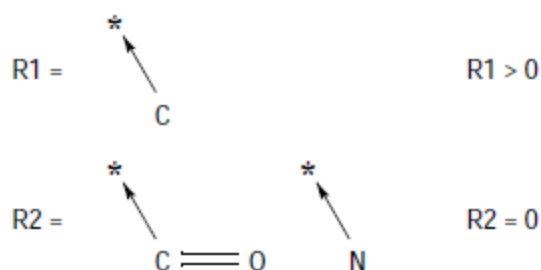
\*r (Rgroup) is repeated. ISIS/Desktop has an internal limit of 32 Rgroups.

\*m (member) is repeated.

The "[Example of an RGfile \(Rgroup query file\)](#)" corresponds to the following Rgroup query:



IF R1 THEN R2



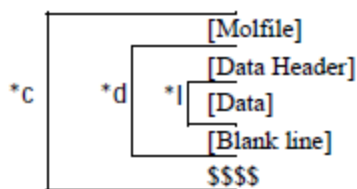
## Example of an RGfile

<b>RGfile header block</b>		\$MDL REV 1 16OCT91 15:40
<b>Molfile header block</b>		\$MOL
		\$HDR
		10169115402D 1 0.00353 0.00000 0
		\$END HDR
<b>ctab for Rgroup root</b>	<b>Counts Line</b>	\$CTAB
		9 9 0 0 0 04 V2000
		1.3337 0.7700 0.0000 C 0 0 0 0 0 0
	<b>Atom block of root</b>	1.3337 -0.7700 0.0000 C 0 0 0 0 0 0
		0.0000 3.0800 0.0000 R# 0 0 0 0 0 0
<b>Bond block of root</b>		2.6674 1.5400 0.0000 R# 0 0 0 0 0 0
		-2.6674 1.5400 0.0000 R# 0 0 0 0 0 0
	<b>#of entries on line</b>	1 2 1 0 0 0
	<b>RGroup Label Location</b>	3 9 1 0 0 0
	<b>And Rgroup number</b>	M RGP 3 7 1 8 2 9 2
<b>Properties block of root</b>		M LOG 1 1 2 0
		M LOG 1 2 0 0 0
		M END
	<b>If/then, RestH, Occurrence</b>	\$END CTAB
		\$RGP
<b>Block for Rgroup R1</b>		1
	<b>ctab for Rgroup 1 Member 1</b>	\$CTAB
		1 0 0 0 0 02 V2000
		12.2100 14.3903 0.0000 C 0 0 0 0 0 0
		M APO 1 1 1
<b>Block for Rgroup R2</b>		M END
		\$END CTAB
		\$RGP
	<b>ctab for Rgroup 2 Member 1</b>	2
		\$CTAB
<b>Block for Rgroup R2</b>		2 1 0 0 0 02 V2000
		-1.4969 0.0508 0.0000 C 0 0 0 0 0 0
		0.0431 0.0508 0.0000 O 0 0 0 0 0 0
		1 2 2 0 0 0
		M APO 1 1 1
<b>Block for Rgroup R2</b>		M END
		\$END CTAB
		\$CTAB
	<b>ctab for Rgroup 2 Member 2</b>	1 0 0 0 0 02 V2000
		12.2100 14.3903 0.0000 N 0 0 0 0 0 0
<b>Block for Rgroup R2</b>		M APO 1 1 1
		M END
		\$END CTAB
		\$END RGP
		\$END MOL

## SDfiles (multiple structures and optional data)

An SDfile (structure-data file) contains the structural information and associated data items for one or more compounds, which can be V3000, V2000, or a combination of both.

The format is:



where:

\*l is repeated for each line of data

\*d is repeated for each data item

\*c is repeated for each compound

A [Molfile] block has the molfile format.

A [Data Header] (one line) precedes each item of data, starts with a *greater than* (>) sign, and contains at least one of the following:

- The field name enclosed in angle brackets. For example: <melting\_point>
- The field number, DTn , where n represents the number assigned to the field in a MACCS-II database

**Note:** The > sign is a reserved character. A field name cannot contain hyphen (-), period (.), less than (<), greater than (>), equal sign (=), percent sign (%) or blank space (.). Field names must begin with an alpha character and can contain alpha and numeric characters after that, including underscore.

Optional information for the data header includes:

- The compound's external and internal registry numbers. External registry numbers must be enclosed in parentheses.
- Any combination of information

The following are examples of valid data headers:

```
> <MELTING_POINT>
> 55 (MD-08974) <BOILING_POINT> DT12
> DT1255
> (MD-0894) <BOILING_POINT> FROM ARCHIVES
```

## Example of an SDfile

Compound	Molfile	Header block	1,2 CYCLO-C6 DI-COOH TRANS,L 06039016292D 1 0.00339 0.00000 25
		Connection table	12 12 0 0 1 01 V2000 -0.0238 -0.7702 0.0000 C 0 0 1 0 0 0 .. 2.6974 0.7634 0.0000 O 0 0 0 0 0 0 1 2 1 0 0 0 .. 7 10 1 0 0 0 M END
	Non-structural data	Data item	> 25 <MELTING_POINT> 179.0 - 183.0
		Data header	
		Data	
Compound	Molfile	Blank Line	
		Data items	>25 <DESCRIPTION> PW(W)  >25 <ALTERNATE_NAMES> 1,2 CYCLOHEXANE-DICARBOXYLIC ACID TRANS,L HEXAHYDROPHthalic ACID TRANS,L  > 25 <DATE> 01-10-1980  > 25 <CRC_NUMBER> C-0710Dat
	Non- structural Data	Delimiter	\$\$\$\$
		Header Block	2-METHYL FURAN MACCS-II06039016302D 1 0.00186 0.00000 29
		Connection Table	6 6 0 0 0 01 V2000 0.5343 0.3006 0.0000 C 0 0 0 0 0 0 .. -2.0038 0.2857 0.0000 C 0 0 0 0 0 0 1 2 2 0 0 0 .. 5 6 2 0 0 0 M END
Compound	Non- structural Data	Data header	> 29 <DENSITY> 0.9132 - 20.0
		Data	> 29 <BOILING_POINT> 63.0 (737 MM) 79.0 (42 MM)
		Blank Line	
	Non- structural Data	Data items	> 29 <ALTERNATE_NAMES> SYLVAN  > 29 <DATE> 09-23-1980  > 29 <CRC_NUMBER> F-0213
		Delimiter	\$\$\$\$

A *[Data]* value can extend over multiple lines containing up to 200 characters each. A blank line terminates each data item.

A line beginning with four dollar signs (\$\$\$\$) terminates each complete data block describing a compound.

A datfile (data file) is effectively an SDfile with no *[Molfile]* descriptions or \$\$\$ delimiters. The *[Data Header]* in a datfile must include either an external or internal registry number in addition to a field name or number.

### Notes about using blank lines:

- Only one blank line should terminate a data item.
- There should only be one blank line between the last data item and the \$\$\$\$ delimiter line.
- If the SDfile only contains structures, there can be no blank line between the last "M END" and the \$\$\$\$ delimiter line.

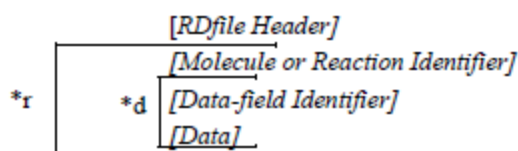
## RDfiles

### RDfile Overview

An RDfile (reaction-data file) consists of a set of editable “records.”, which can be which can be V3000, V2000, or a combination of both.

Each record defines a molecule or reaction, and its associated data. See “[Example of a reaction RDfile](#)”).

The format for an RDfile is:



where:

\*d is repeated for each data item

\*r is repeated for each reaction or molecule

Each logical line in an RDfile starts with a keyword in column 1 of a physical line. One or more blanks separate the first argument (if any) from the keyword. The blanks are ignored when the line is read. After the first argument, blanks are significant.

An argument longer than 80 characters breaks at column 80 and continues in column 1 of the next line. (The argument can continue on additional lines up to the physical limits on text length imposed by the database.)

**Note:** For data lines, a line break between portions of text items is interpreted as a newline character in the text unless column 81 contains a + mark.

The RDfile must not contain any blank lines except as part of embedded molfiles, rxnfiles, or data. An identifier separates records.

### RDfile Header

<b>Line 1:</b>	\$RDFILE 1: The [RDfile Header] must occur at the beginning of the physical file and identifies the file as an RDfile. The version stamp “1” is intended for future expansion of the format.
<b>Line 2:</b>	\$DATM: Date/time (M/D/Y, c) stamp. This line is treated as a comment and ignored when the program is read.

### Molecule and Reaction Identifiers

A *[Molecule or Reaction Identifier]* defines the start of each complete record in an RDfile. The form of a *molecule* identifier must be one of the following:

```
$MFMT [$MIREG internal-regno embedded molfile
$MFMT [$MREG external-regno]] embedded molfile
```

\$MIREG internal-regno  
\$MEREg external-regno

where:

- \$MFMT defines a molecule by specifying its connection table as a molfile
- \$MIREG internal-regno is the internal registry number (sequence number in the database) of the molecule
- \$MEREg external-regno is the external registry number of the molecule (any uniquely identifying character string known to the database, for example, CAS number)
- Square brackets ( [ ] ) enclose optional parameters
- An embedded molfile follows immediately after the \$MFMT line

The forms of a reaction identifier closely parallel that of a molecule:

```
$RFMT [$RIREG internal-regno] embedded rxnfile  
$RFMT [$REREg external-regno] embedded rxnfile  
$RIREG internal-regno  
$REREg external-regno
```

where:

- \$RFMT defines a reaction by specifying its description as a rxnfile
- \$RIREG internal-regno is the internal registry number (sequence number in the database) of the reaction
- \$REREg external-regno is the external registry number of the reaction (any uniquely identifying character string known to the database)
- Square brackets ( [ ] ) enclose optional parameters
- An embedded rxnfile follows immediately after the \$RFMT line

**Note:** Host and Isentris allow a reaction or molecule to be identified by internal or external regno but not both types of regno.

## Data-field Identifier

The [Data-field Identifier] specifies the name of a data field in the database. The format is:

```
$DTYPE field name
```

## Data

Data associated with a field follows the field name on the next line and has the form:

```
$DATUM datum
```

The format of datum depends upon the data type of the field as defined in the database. For example: integer, real number, real range, text, molecule regno.

For fields whose data type is "molecule regno," the *datum* must specify a molecule and, with the exception noted below, use one of the formats defined above for a molecular identifier. For example:

```
$DATUM $MFMT embedded molfile  
$DATUM $MEREg external-regno  
$DATUM $MIREG internal-regno
```

In addition, the following special format is accepted:

```
$DATUM molecule-identifier
```

Here, molecule-identifier acts in the same way as external-regno in that it can be any text string known to the database that uniquely identifies a molecule. (It is usually associated with a data field different from the external-regno.)

## Example of a reaction RDfile

<i>RD Header</i>		\$RDFILE 1
		\$DATM 10/17/91 10:41
		\$RFMT \$RIREG 7439
		\$RXN
<i>First Rxn Record</i>	<i>Rxn file header</i>	1017911041 7439
	<i>#Reactants/ #products</i>	2 1
		\$MOL
	<i>Molfile for 1<sup>st</sup> reactant</i>	10179110412D 1 0.00380 0.00000 315
		4 3 0 0 0 0 0 0 0 0 0
		. . .
		1 4 1 0 0 0 4
		\$MOL
	<i>Molfile for 2nd reactant</i>	10179110412D 1 0.00371 0.00000 8
		6 6 0 0 0 0 0 0 0 0 0
<i>Data Block for record</i>		. . .
		5 6 2 0 0 0 2
		\$MOL
	<i>Molfile for product</i>	10179110412D 1 0.00374 0.00000 255
		9 9 0 0 0 0 0 0 0 0 0
		. . .
		6 9 2 0 0 0 2
		\$DTYPE rxn:VARIATION(1):rxnTEXT(1)
		\$DATUM CrCl3
		\$DTYPE rxn:VARIATION(1):LITTEXT(1)
<i>Start of next rxn record</i>		\$DATUM A G Repin, Y Y Makarov-Zemlyanskii, Zur Russ Fiz-Chim, 44, p.2360, 1974
		. . .
		\$DTYPE rxn:VARIATION(1):CATALYST(1):REGNO
		\$DATUM \$MFMT \$MIREG 688
		10179110412D 1 0.00371 0.00000 0
		4 3 0 0 0 0 0 0 0 0 0
		. . .
		1 4 1 0 0 0 0
		\$DTYPE rxn:VARIATION(1):PRODUCT(1):YIELD
		\$DATUM 70.0
		. . .
		\$RFMT \$RIREG 8410
		\$RXN
		1017911041 8410
		2 1
		\$MOL
		. . .

## XDfiles

### Overview

An XDfile (XML-data file) uses a standard set of XML elements that represent records of data.



The XFile format also provides:

- Metadata or information about the origin of the data. Unlike the other CTfile formats such as the SFile or RFile, the XFile enables the consumer of the data to correctly interpret it.
- The ability to handle generalized data models, such as multiple structures and nonstructure fields per record, multiple reactions per record, multiline data, and binary data. None of the other CTfile formats such as SFiles or RFiles have this ability.
- Very few restrictions on data formatting within the actual content. Data formatting is based on XML, which does not have restrictions on line length or blank lines. See [Data Formatting](#).
- Fast and easy parsing by using any XML parser. The XML data can be validated by using a DTD (Document Type Definition) or an XML schema that defines primitive rules which the data must follow.

**Note:** Due to limitations in the capabilities of DTDs and XML schemas, an XFile that is validated by the DTD and XML schema is not guaranteed to be correct. For example, it is possible to create a record with duplicate field values. The DTD and XML schema only provide a low level of validation. Applications which process XFiles must provide high level checks on the consistency of the data.

- Flexibility in creating application-specific XML tags. Note, however, that it is the responsibility of the client application to interpret these custom tags.

**Note:** Although it is possible to convert SFiles and RFiles to XFiles, there are risks involved in converting an XFile to the original format. The backward conversion will lose the metadata which is not supported in the other CTfile formats.

See also

[Hierarchy of Elements](#)

[Alphabetic List of Elements](#)

## Data Formatting

XML puts little or no restrictions on data formatting within the actual content. Data that is sensitive to white space, molfiles and rxnfiles in particular, must be enclosed in a CDATA section. You must set the xml:space attribute to preserve. The following example is a Field element that contains a molfile:

```
<Field name="Mol" xml:space="preserve"><![CDATA[
-ISIS- 03190310282D
1 0 0 0 0 0 0 0 0 0 0999 v2000
-2.1000 -0.1208 0.0000 C 0 0 0 0 0 0 0 0 0 0 0 0
M END
]]></Field>
```

Note that for data outside a CDATA

section, certain characters must be escaped as described in the following table:

Character	Representation
<	&lt;
>	&gt;

Character	Representation
"	&quot;
'	&apos;
&	&amp;

For example, **mp < 100** becomes **mp &lt; 100**.

## XML Processing Instructions

The XDfile uses the following instructions as XML file headers:

[XML Declaration](#)

[Java-Locale](#)

### XML Declaration

The first line in the XDfile specifies the XML version and the character encoding used in the document. The following example shows that the XDfile conforms to the 1.0 specification of XML and uses the UTF-8 Unicode character set.

```
<?xml version="1.0" encoding="UTF-8"?>
```

### Java-Locale

The second line in the XDfile specifies the java-locale processing instruction:

```
<?java-locale value="en_US"?>
```

The value consists of the ISO language and country codes. The language code is a lower-case, two-letter code defined by ISO-639; the country code is an upper-case, two-letter code defined by ISO-3166. Applications can read this processing instruction using an XML parser.

The

The following example shows how to get the locale value using a parser called XMLPullParser:

```
try {
    // XMLPullParser is a sample XML parser.
    XMLPullParser node = new XMLPullParser();
    // myexport_data.xml is an output XDfile from Core Interface.
    if (node.createXMLParse("c:\\home\\myexport_data.xml")) {
        int jj = node._xmlReader.next();
        jj = node._xmlReader.next();
        if (jj ==
javax.xml.stream.XMLStreamReader.PROCESSING_INSTRUCTION) {
            // This returns "java-locale"
            String target = node._xmlReader.getPITarget();
            // This returns " value=\"en_US\""
            String data = node._xmlReader.getPIData();
        }
    }
} catch (Exception e) {
    System.out.println("Got an exception -- " + e.getMessage());
}
```

## Hierarchy of Elements

The following shows the hierarchy of elements within an XDfile. The attributes of the elements are not shown in order to more clearly show the structure of the XML:

```
<XDfile>
  <Dataset>
    <Source>
      <DataSource/>
      <ProgramSource/>
      <CreatorName/>
      <CreateDate/>
      <CreateTime/>
      <Description/>
      <Copyright/>
    </Source>
    <Metadata>
      <FieldDef/>
      <ParentDef>
        <FieldDef/>
      </ParentDef>
    </Metadata>
    <Data>
      <Record>
        <Field>
        </Field>
        <Parent>
          <Record>
            <Field>
            </Field>
          </Record>
        </Parent>
      </Record>
    </Data>
  </Dataset>
</XDfile>
```

## Alphabetical List of Elements

Element	Parent	Description
<a href="#">Copyright</a>	Source	A copyright for the attached data
<a href="#">CreateDate</a>	Source	The date the data was created

Element	Parent	Description
<a href="#">CreateTime</a>	Source	The time the data was created
<a href="#">CreatorName</a>	Source	The person who created the data
<a href="#">Data</a>	Dataset	Contains records of data
<a href="#">Dataset</a>	XDfile	Contains a collection of data
<a href="#">DataSource</a>	Source	The source of the data
<a href="#">Description</a>	Source	A description or comment about the data
<a href="#">Field</a>	Record	The value of a field in a record
<a href="#">FieldDef</a>	Metadata ParentDef	The definition of a field in a record
<a href="#">XDfile</a>		The root element
<a href="#">Metadata</a>	Dataset	Contains definitions of fields in the data
<a href="#">Parent</a>	Record	Contains subrecords of data
<a href="#">ParentDef</a>	Metadata	The definition of a parent field in the data
<a href="#">ProgramSource</a>	Source	The program that created the data
<a href="#">Record</a>	Data Parent	The unit of data; contains a set of field values
<a href="#">Source</a>	Dataset	Contains information about the source of the data

## Copyright

A copyright notice for the data.

### Attributes

None

### Parent Element

[Source](#)

### Child Elements

None

### Example

```
<Copyright>Copyright 2003 by Acme Corporation </Copyright>
```

### See also

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

## CreateDate

The date the actual data was created.

## Attributes

The data type of all attributes is CDATA.

Attribute	Required	Description
dateOrder	No	The format for the date in < CreateDate >. The separator character is specified as part of the format. The valid formats are: M-D-Y D-M-Y Y-M-D Y-D-M The default format is M-D-Y

## Parent Element

[Source](#)

## Child Elements

None

## Example

```
<CreateDate dateOrder="M/D/Y">7/22/99</CreateDate>
```

## See also

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

## CreateTime

The time the actual data was created.

## Attributes

The data type of all attributes is CDATA.

Attribute	Required	Description
timeFormat	No	The format for time in < CreateTime >. The valid formats are: 24 12 The default format is 24.

## Parent Element

[Source](#)

## Child Elements

None

## Example

```
<CreateTime>24:15</CreateTime>
```

## See also

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

## CreatorName

The name of the person who created the data.

### Attributes

None

### Parent Element

[Source](#)

### Child Elements

None

### Example

```
<CreatorName>John Doe</CreatorName>
```

### See also

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

## Data

Contains a collection of `Record` child elements that contain the actual data. Each `Record` element contains a collection of `Parent` and `Field` elements whose hierarchical structure must match the hierarchy in the `Metadata` element. The `Data` element can be empty if there is no data or only the metadata is to be transferred.

### Attributes

The data type of all attributes is CDATA.

Attribute	Required	Description
<code>totalRecords</code>	No	The total number of root-level records in the data.

### Parent Element

[Dataset](#)

### Child Elements

Element	Required	Description
<a href="#">Record</a>	Yes	A record of data

### Example

```
<Data totalRecords="2">
  <Record>
    <Field name="Molstructure" xml:space="preserve">
      <![CDATA[7YALen$Ak1$QPbas35quasdfsdf38...]]></Field>
    <Field name="Reaction Vessel ID">SAR6077R-01A02</Field>
    <Field name="Library ID">SAR6077R</Field>
    <Field name="Tag Id">yes</Field>
    <Parent name="XYZ Test Results" totalRecords="2">
      <Record>
        <Field name="Dose">1.0</Field>
        <Field name="Response">99.0</Field>
      </Record>
    </Parent>
  </Record>
</Data>
```

```

    </Record>
    <Record>
      <Field name="Dose">2.0</Field>
      <Field name="Response">999.0</Field>
    </Record>
  </Parent>
</Record>
<Record>
  <Field name="Molstructure" xml:space="preserve">
    <![CDATA[7YALen$Ak1$QPbas35quasdfsdf38...]]></Field>
  <Field name="Reaction Vessel ID">SAR6077R-01A03</Field>
  <Field name="Library ID">SAR6077R</Field>
  <Field name="Tag Id">no</Field>
</Record>
</Data>

```

#### See also

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

## Dataset

Dataset is a self-contained, single collection of data.

#### Attributes

The data type of all attributes is CDATA.

Attribute	Required	Description
name	Yes, if multiple datasets	The name of the dataset. If <a href="#">XDfile</a> contains only one dataset, name is optional. If XDfile contains multiple datasets, name is required in order to identify each dataset.

#### Parent Element

[XDfile](#)

#### Child Elements

Element	Required	Description
<a href="#">Source</a>	No	Describes the source of the data
<a href="#">Metadata</a>	No	Describes the individual fields in the data
<a href="#">Data</a>	Yes	The actual data

#### Example

```

<Dataset>
  <Metadata>
    <FieldDef name="CTAB" type="Structure" molFormat="Chime"/>
    <FieldDef name="Regno" type="Integer" isPrimaryKey="true"/>
    <FieldDef name="Molname" type="FixedText"/>
    <FieldDef name="Date" type="Date"/>
    <FieldDef name="DoubleValue" type="Double"/>
  </Metadata>

```

```
<Data totalRecords="1">
  <Record>
    <Field name="CTAB">40Aieg6Mprlczdb^fg37JiOh</Field>
    <Field name="Regno">1</Field>
    <Field name="Molname">Test Structure</Field>
    <Field name="Date">05/10/2002</Field>
  </Record>
</Data>
</Dataset>
```

#### See also

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

## DataSource

The source of the data.

#### Attributes

None

#### Parent Element

[Source](#)

#### Child Elements

None

#### Example

```
<DataSource>ACD99.1 Hview</DataSource>
```

#### See also

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

## Description

A description or comment about the data.

#### Attributes

None

#### Parent Element

[Source](#)

#### Child Elements

None

#### Example

```
<Description>This is test data.</Description>
```

#### See also

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)



## Field

Contains data for a single field in a record. Note that the `molFormat`, `molVersion`, and `rxnFormat` attributes can be used on individual `Field` elements to override the format specified in the `Metadata` element.

### Attributes

The data type of all attributes is CDATA.

Attribute	Required	Description
<code>name</code>	Yes	The name of the parent field.
<code>molFormat</code>	No	The format for the structure, if the field contains structures. This value overrides the <code>molFormat</code> specified in the <code>Metadata</code> element. The valid values are: <code>Molfile</code> <code>Chime</code> <code>Smiles</code> The default value is <code>Molfile</code> .
<code>rxnFormat</code>	No	The format for the reaction, if the field contains reactions. This value overrides the <code>rxnFormat</code> specified in the <code>Metadata</code> element. The valid values are: <code>Rxnfile</code> <code>Chime</code> The default value is <code>Rxnfile</code> .
<code>molVersion</code>	No	The version of the data format. <code>molVersion</code> is currently only applicable to structures. The absence of this attribute implies a pre-V2000 molfile. This value overrides the <code>molVersion</code> specified in the <code>Metadata</code> element. The valid values are: <code>v2000</code> <code>v3000</code>

### Parent Element

[Record](#)

### Child Elements

None

### Example

```
<Field name="Dose">1.0</Field>
```

### See also

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

## FieldDef

Contains information about a single field within the data.

## Attributes

The data type of all attributes is CDATA.

Attribute	Required	Description
name	Yes	The name of the parent field. This is a simple name because the context of the field in the hierarchy is implied by the XML structure.
type	Yes	The type of data in the field. Applications can define their own type, but it will be the responsibility of client applications to interpret these. The valid values are: Reaction Structure Integer Double FixedText VariableText Date Time DateTime Binary
isKey	No	true if the field is a key. The valid values are true or false. The default value is false.
isPrimaryKey	No	true if the field is a primary key. The valid values are true or false. The default value is false.
nativeName	No	The name of the field specific to the source from which it is derived. For example, a native name for an Oracle database is schema.table.column.
encoding	No	The encoding set used by the data. Sample values are: binhex rot64
charset	No	The character set used by the text. A sample value is ISO-8859-1.
decimalSeparator	No	The decimal separator used for floating point numbers. The valid values are: Period Comma The default value is Period.
maxLength	No	The maximum length of the data in this field. For binary fields in a relational data source (such as CLOB and BLOB fields), the maximum length varies depending on the version of the Oracle JDBC driver.

Attribute	Required	Description
molFormat	No	The format for the structure, if the field contains structures. The valid values are: Molfile Chime Smiles The default value is Molfile.
rxnFormat	No	The format for the reaction, if the field contains reactions. The valid values are: Rxnfile Chime The default value is Rxnfile.
molVersion	No	The version of the data format. molVersion is currently only applicable to structures. The absence of this attribute implies a pre-V2000 molfile. The valid values are: v2000 v3000
dateOrder	No	The order and format of a date field. The value specifies the separator character. Dates must be specified using numbers only; do not use month names. The valid orders are: M-D-Y D-M-Y Y-M-D Y-D-M The default value is M-D-Y.
timeOrder	No	The order of a date field. The value specifies the separator character. The valid orders are: h:m m:h The default value is h:m.
timeFormat	No	The format of a time field. The valid values are: 24 12 The default value is 24.
precision	No	The precision for a real number field. This is the total number of digits.
scale	No	The scale for a real number field. This is the number of digits to the right of the decimal point.

Attribute	Required	Description
nullable	No	true if the field can contain nulls. The valid values are true or false. The default value is false.
indexed	No	true if the field is indexed. The valid values are true or false. The default value is false.
hidden	No	true if the field is hidden. The valid values are true or false. The default value is false.
units	No	The units of measurement associated with the field.
javaFormat	No	The Java format to use when the field value is parsed. This is the Java output format used by the NumberFormat or DecimalFormat class.

#### Parent Element

[Metadata](#)

[ParentDef](#)

#### Child Elements

None

#### Example

```
<FieldDef name="Molstructure"
type="Structure"
molFormat="Chime"/>
<FieldDef name="Reaction Vessel ID"
type="FixedText"
maxLength="15" />
```

#### See also

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

## Parent

Contains child records of data. A Parent can contain other Parent elements, thus, creating a sub-hierarchy of data.

#### Attributes

The data type of all attributes is CDATA.

Attribute	Required	Description
name	Yes	The name of the field.
totalRecords	No	The total number of root-level records in the data.

#### Parent Element

Record

## Child Elements

Element	Required	Description
<a href="#">Record</a>	Yes	A record of data

### Example

```
<Parent name="XYZ Test Results" ID="100">
  <Record>
    <Field name="Dose">1.0</Field>
    <Field name="Response">99.0</Field>
  </Record>
  <Record>
    <Field name="Dose">2.0</Field>
    <Field name="Response">999.0</Field>
  </Record>
</Parent>
```

### See also

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

## ParentDef

Contains information about a single parent field within the data.

Do not create unnecessary parent fields at the root. Parent fields should only be used when there is an actual hierarchical structure to the data. For example, an SDFFile would not have `ParentDef` elements, but would only have multiple `FieldDef` elements directly under the `Metadata` element. The actual data in the SDFFile follows this format by having multiple `Record` elements directly under the `Data` element.

### Attributes

The data type of all attributes is CDATA.

Attribute	Required	Description
name	Yes	The name of the parent field. This is a simple name because the context of the parent in the hierarchy is implied by the XML structure.

### Parent Element

[Metadata](#)

`ParentDef`

### Child Elements

Element	Required	Description
<a href="#">FieldDef</a>	Yes	Contains information about a single field within the data
<code>ParentDef</code>	No	Contains information about a single parent within the data. A parent within a parent creates a hierarchy.

### Example

```
<?xml version="1.0"?>
<XDfile version="1.2" xmlns="http://www.mdl.com/XDfile/NS">
  <Dataset
    name="MySource">
    <Source>
      <DataSource>ACD99.1 Hview</DataSource>
      <ProgramSource>GCS 1.0</ProgramSource>
      <CreatorName>John Doe</CreatorName>
      <CreateDate dateOrder="M/D/Y">7/22/99</CreateDate>
      <CreateTime timeFormat="24">13:45</CreateTime>
    </Source>
    <Metadata>
      <FieldDef name="Molstructure" type="Structure"
        molFormat="Chime"/>
      <FieldDef name="Reaction Vessel ID" type="FixedText"
        maxLength="15"/>
      <FieldDef name="Library ID" type="FixedText"
        maxLength="8"/>
      <FieldDef name="Tag Id" type="fixedText"
        maxLength="3"/>
      <ParentDef name="XYZ Test Results">
        <FieldDef name="Dose" type="Double"/>
        <FieldDef name="Response" type="Double"/>
      </ParentDef>
    </Metadata>
    <Data>
      <Record>
        <Field name="Molstructure" xml:space="preserve">
          <![CDATA[7YALen$Ak1$QPbas35quasdfsdf38...]]></Field>
        <Field name="Reaction Vessel ID">SAR6077R-01A02</Field>
        <Field name="Library ID">SAR6077R</Field>
        <Field name="Tag Id">yes</Field>
        <Parent name="XYZ Test Results" totalRecords="2">
          <Record>
            <Field name="Dose">1.0</Field>
            <Field name="Response">99.0</Field>
          </Record>
          <Record>
            <Field name="Dose">2.0</Field>
            <Field name="Response">999.0</Field>
          </Record>
        </Parent>
      </Record>
      <Record>
        <Field name="Molstructure" xml:space="preserve">
          <![CDATA[7YALen$Ak1$QPbas35quasdfsdf38...]]></Field>
        <Field name="Reaction Vessel ID">SAR6077R-01A03</Field>
        <Field name="Library ID">SAR6077R</Field>
        <Field name="Tag Id">no</Field>
      </Record>
    </Data>
  </Dataset>
</XDfile>
```

```
</Dataset>
</XDfile>
```

#### See also

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

## Metadata

Contains information that describes the fields in the data. Applications can use this information to allow automatic creation of database tables or better formatting of data. The hierarchical structure of the Metadata element must match the data model contained in the Data element.

#### Attributes

None

#### Parent Element

[Dataset](#)

#### Child Elements

Element	Required	Description
<a href="#">ParentDef</a>	No	Contains information about a single parent within the data
<a href="#">FieldDef</a>	No	Contains information about a single field within the data

#### Example

```
<Metadata>
  <FieldDef name="Molstructure"
    type="Structure"
    molFormat="Chime"/>
  <FieldDef name="Reaction Vessel ID"
    type="FixedText"
    maxLength="15"/>
  <FieldDef name="Library ID"
    type="FixedText"
    maxLength="8"/>
  <FieldDef name="Tag Id"
    type="FixedText"/>
  <ParentDef name="XYZ Test Results">
    <FieldDef name="Dose"
      type="Double"/>
    <FieldDef name="Response"
      type="Double"/>
  </ParentDef>
</Metadata>
```

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

## ProgramSource

The program that created the data.

**Attributes**

None

**Parent Element**

[Source](#)

**Child Elements**

None

**Example**

```
<ProgramSource>MDL Core Interface 1.0</ProgramSource>
```

**See also**

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

**Record**

A record of data, and contains a set of `Field` elements.

**Attributes**

None

**Parent Element**

[Data](#)

[Parent](#)

**Child Elements**

Element	Required	Description
<a href="#">Field</a>	No	A single field of data
<a href="#">Parent</a>	No	Contains subrecords of data. A parent within a record creates a hierarchy.

**Example**

```
<Record>  
  <Field name="Dose">1.0</Field>  
  <Field name="Response">99.0</Field>  
</Record>
```

**See also**

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

**Source**

Contains information that describes the source of the data. Note that although each child element is optional, the order of the child elements is fixed. If a child element does not follow the order specified below, the element is discarded.

**Attributes**

None



## Parent Element

[Dataset](#)

## Child Elements

Element	Required	Description
<a href="#">DataSource</a>	No	The source of the data
<a href="#">ProgramSource</a>	No	The program that created the data
<a href="#">CreatorName</a>	No	The person who created the data
<a href="#">CreateDate</a>	No	The date the data was created. The default format is M-D-Y.
<a href="#">CreateTime</a>	No	The time the data was created. The default format is 24-hour
<a href="#">Description</a>	No	A description or comments about the data
<a href="#">Copyright</a>	No	A copyright notice for the data

## Example

```
<Source>
  <DataSource>ACD99.1 Hview</DataSource>
  <ProgramSource>Core Interface 1.1</ProgramSource>
  <CreatorName>John Doe</CreatorName>
  <CreateDate dateOrder="M/D/Y">7/22/99</CreateDate>
  <CreateTime timeFormat="24">13:45</CreateTime>
</Source>
```

## See also

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

## XDfile

XDfile is the root element. XML data that uses the XDfile format must begin with <XDfile> and end with </XDfile>. It contains one or more Dataset elements.

## Attributes

The data type of all attributes is CDATA.

Attribute	Required	Description
xmlns	Yes	The default namespace for elements in the XDfile. The default is http://www.mdl.com/XDfile/NS
version	Yes	The version number of the XDfile data.

## Parent Element

None

## Child Elements

Element	Required	Description
<a href="#">Dataset</a>	Yes	A single collection of data

### Example

```
<?xml version="1.0"?>
<XDfile version="1.2" xmlns="http://www.mdl.com/XDfile/NS">
  <Dataset
    name="MySource">
    <Source>
      <DataSource>ACD99.1 Hview</DataSource>
      <ProgramSource>GCS 1.0</ProgramSource>
      <CreatorName>John Doe</CreatorName>
      <CreateDate dateOrder="M/D/Y">7/22/99</CreateDate>
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**See also**

[Hierarchy of Elements](#)

[Alphabetical List of Elements](#)

## Stereo Notes

Parity values can appear in the atom blocks of CTFiles. See CFG (for stereo configuration) and and sss (atom stereo parity) in the table for "[Atom Block](#)".

Parity is illustrated as follows:

Mark a bond attached at a stereo center Up or Down to define the configuration.

Number the atoms surrounding the stereo center with 1, 2, 3, and 4 in order of increasing atom number (position in the atom block) (a hydrogen atom should be considered the highest numbered atom, in this case atom 4). View the center from a position such that the bond connecting the highest-numbered atom (4) projects behind the plane formed by atoms 1, 2, and 3.

**Note:** In Figure 1, atoms 1, 2, and 4 are all in the plane of the paper, and atom 3 is above the plane.

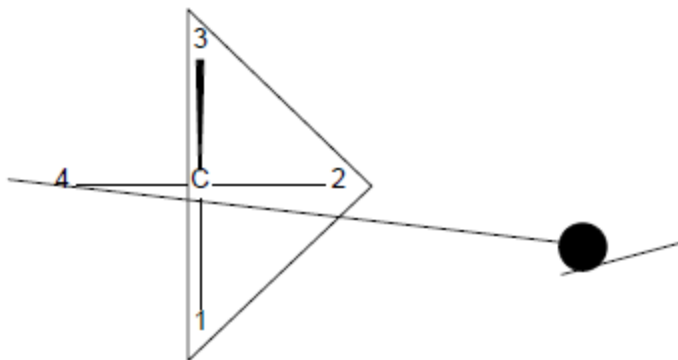


Figure 1

Sighting towards atom number 4 through the plane (123), you see that the three remaining atoms can be arranged in either a clockwise or counterclockwise direction in ascending numerical order.

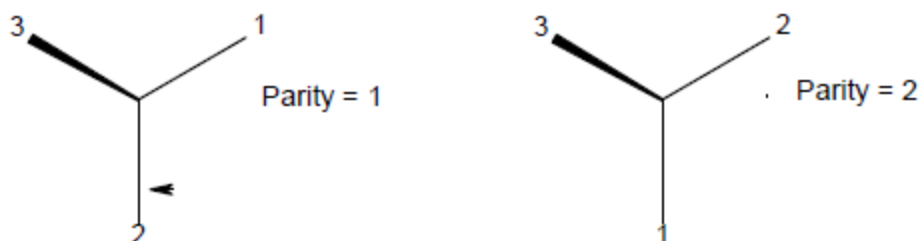


Figure 2

**Note:** The Ctab lists a parity value of 1 for a clockwise arrangement at the stereo center and 2 for counterclockwise. A center with an Either bond has a parity value of 3. An unmarked stereo center is also assigned a value of 3. The first example in Figure 2 has a parity value of 2.

For additional information about BIOVIA stereochemistry, see *BIOVIA Chemical Representation*, which has an appendix entitled 'Representation of Stereochemistry in BIOVIA Databases.'