

2.2. SPECIFICATION OF THE CRYSTALLOGRAPHIC INFORMATION FILE (CIF)

(v) A **data block** is the highest-level component of a CIF, containing data items or (in the case of dictionary files only) save frames. A data block is identified by a **data-block header**, which is an isolated character string (that is, bounded by white space and not forming part of a data value) beginning with the case-insensitive reserved characters `data_`. A **block code** is the variable part of a data-block header, e.g. the string `foo` in the header `data_foo`.

(vi) A **looped list** of data is a set of data items represented as a table or matrix of values. The data names are assembled immediately following the word `loop_`, each separated by white space, and the associated data values are then listed in strict rotation. The table of values is assembled in row-major order; that is, the first occurrence of each of the data items is assembled in sequence, then the second occurrence of each item, and so forth. In a CIF, looped lists may not be nested.

2.2.3. The syntax of a CIF

The essential syntax rules for a CIF data file are discussed alongside an example (Fig. 2.2.3.1), which is an extract from a file used to exemplify the reporting of a small-molecule crystal structure to *Acta Crystallographica Section C*. The following discussion is tutorial in nature and is intended to give an overview of the syntactic features of CIF to the general reader. The special use of save frames in dictionary files is not discussed in this summary. Software developers will find the full specification at the end of the chapter. If there are any real or apparent discrepancies between the two treatments, the full specification is to be taken as definitive.

A CIF contains only ASCII characters, organized as lines of text.

Tokens (the discrete components of the file) are separated by white space; layout is not significant. Thus, in the list of atom-site coordinates in Fig. 2.2.3.1, the hydrogen-atom entries are cosmetically aligned in columns, but the non-aligned entries for the other atoms are equally valid. Indeed, there is no requirement that each cluster of looped data values be confined to a separate row; contrast the cosmetic ordering of the atom-sites loop with the loop of symmetry-equivalent positions, where entries run on the same or following lines indiscriminately.

A comment is a token introduced by a hash character # and extending to the end of the line. Comments are considered to have no portable information content and may freely be discarded by a parser. However, revision 1.1 of the CIF specification introduces a *recommendation* that a CIF begin with a comment taking the form

```
#\#CIF_1.1
```

where the 1.1 is a version identifier of the reference CIF specification. This is primarily for the benefit of general file-handling software on current operating systems (e.g. graphical file managers that associate software applications with files of specific type), and its presence or absence does not guarantee the integrity of the file with respect to any particular revision of the CIF specification.

The first non-comment token of a CIF must be a data-block header, which is a character string that does not include white space and begins with the case-insensitive characters `data_`.

The file may be partitioned into multiple data blocks by the insertion of further data-block headers. Data-block headers are case-insensitive (that is, two headers differing only in whether corresponding letter characters are upper or lower case are considered identical). Within a single data file identical data-block headers are not permitted.

```
data_99107abs

# Chemical data
_chemical_name_systematic
; 3-Benzo[b]thien-2-yl-5,6-dihydro-1,4,2-oxathiazine
  4-oxide
;
_chemical_formula_moiety          "C11 H9 N O2 S2"
_chemical_formula_weight          251.31

# Crystal data
_symmetry_cell_setting             orthorhombic
_symmetry_space_group_name_H-M    'P 21 21 21'

loop_
  _symmetry_equiv_pos_as_xyz
  'x, y, z' 'x+1/2, -y+1/2, -z' '-x, y+1/2, -z+1/2'
  '-x+1/2, -y, z+1/2'

_cell_length_a                     7.4730(11)
_cell_length_b                     8.2860(11)
_cell_length_c                     17.527(2)
_cell_angle_alpha                  90.00
_cell_angle_beta                   90.00
_cell_angle_gamma                  90.00

# Atomic coordinates and displacement parameters
loop_
  _atom_site_label
  _atom_site_type_symbol
  _atom_site_fract_x
  _atom_site_fract_y
  _atom_site_fract_z
  _atom_site_U_iso_or_equiv
S4 S 0.32163(7) 0.45232(6) 0.52011(3) 0.04532(13)
S11 S 0.39642(7) 0.67998(6) 0.29598(2) 0.04215(12)
O1 O -0.00302(17) 0.67538(16) 0.47124(8) 0.0470(3)
O4 O 0.2601(2) 0.28588(16) 0.50279(10) 0.0700(5)
N2 N 0.14371(19) 0.66863(19) 0.42309(9) 0.0402(3)
C3 C 0.2776(2) 0.57587(19) 0.43683(9) 0.0332(3)
C5 C 0.1497(3) 0.5457(3) 0.57608(11) 0.0498(5)
C6 C -0.0171(3) 0.5529(2) 0.52899(12) 0.0460(4)
C12 C 0.4215(2) 0.57488(19) 0.38139(9) 0.0344(3)
C13 C 0.5830(2) 0.4995(2) 0.38737(10) 0.0386(4)
C13A C 0.6925(2) 0.5229(2) 0.32123(10) 0.0399(4)
C14 C 0.8631(3) 0.4608(3) 0.30561(13) 0.0532(5)
C15 C 0.9423(3) 0.4948(3) 0.23709(15) 0.0644(7)
C16 C 0.8563(3) 0.5917(3) 0.18349(14) 0.0667(7)
C17 C 0.6901(3) 0.6568(3) 0.19729(12) 0.0546(5)
C17A C 0.6090(3) 0.6204(2) 0.26670(10) 0.0396(4)
H5A H 0.1284 0.4834 0.6221 0.060
H5B H 0.1861 0.6537 0.5908 0.060
H6A H -0.0374 0.4490 0.5050 0.055
H6B H -0.1186 0.5762 0.5617 0.055
H13 H 0.6182 0.4397 0.4297 0.046
H14 H 0.9218 0.3972 0.3414 0.064
H15 H 1.0548 0.4527 0.2262 0.077
H16 H 0.9127 0.6130 0.1373 0.080
H17 H 0.6340 0.7227 0.1616 0.066
```

Fig. 2.2.3.1. Typical small-molecule CIF.

Data names are character strings that begin with an underscore character `_` and do not contain white-space characters. Data names serve to index data values and are case-insensitive.

Where a data name indexes a single data value, that value follows the data name separated by white space.

Where a data name indexes a set of data values (conceptually a vector or table column), the relevant data items are preceded by the case-insensitive string `loop_` separated by white space.

The examples of Fig. 2.2.3.1 show the use of `loop_` to specify a vector or one-dimensional list of values (the symmetry-equivalent positions) and a tabular or matrix list (the atom-site positions).