Example 3.6.6.12. *Part of the reflection list for an HIV-1 protease structure (PDB 5HVP) described with data items in the* REFLN *category.*

```
loop_
_refln.index_h
_refln.index_k
_refln.index_l
_refln.F_squared_calc
_refln.F_squared_meas
_refln.F_squared_sigma
_refln.status
   2   0   0       85.57       58.90      1.45 o
   3   0   0    15718.18    15631.06     30.40 o
   4   0   0    55613.11    49840.09     61.86 o
   5   0   0      246.85      241.86     10.02 o
   6   0   0       82.16       69.97      1.93 o
   7   0   0     1133.62      947.79     11.78 o
   8   0   0     2558.04     2453.33     20.44 o
   9   0   0      283.88      393.66      7.79 o
  10   0   0      283.70      171.98      4.26 o
```

```
  _refln.wavelength_id
        →  _diffrn_radiation.wavelength_id
```

(*b*) REFLN_SYS_ABS

```
• _refln_sys_abs.index_h
• _refln_sys_abs.index_k
• _refln_sys_abs.index_l
  _refln_sys_abs.I
  _refln_sys_abs.I_over_sigmaI
  _refln_sys_abs.sigmaI
```

The bullet (•) *indicates a category key. Where multiple items within a category are marked with a bullet, they must be taken together to form a compound key. The arrow* (→) *is a reference to a parent data item. Items in italics have aliases in the core CIF dictionary formed by changing the full stop* (.) *to an underscore* (_) *except where indicated by the* ∼ *symbol.*

Data items in the REFLN category are used in the same way in the mmCIF and core CIF dictionaries, and Section 3.2.3.2.1 can be consulted for details. However, in macromolecular crystallography it is not usual for reflection intensities to be given in units of electrons (the units specified by the core CIF dictionary). Thus it was necessary to introduce in the mmCIF dictionary data items for the magnitudes of structure factors and their *A* and *B* components in arbitrary units (Example 3.6.6.12). A figure of merit (`_refln.fom`) can also be included for reflections that were phased using experimental methods.

The REFLN_SYS_ABS category allows the intensities of the reflections that should be systematically absent to be tabulated. The ratio of the intensity to its standard uncertainty, given in the data item `_refln_sys_abs.I_over_sigmaI`, can be used to assess whether the reflection is indeed absent. The decision as to whether it is absent is left to the user of the mmCIF and is not recorded in the mmCIF.

3.6.6.3.2. *Groups of reflections*

The data items in these categories are as follows:

(*a*) REFLNS

```
• _reflns.entry_id
        → _entry.id
  _reflns.B_iso_Wilson_estimate
  _reflns.data_reduction_details
  _reflns.data_reduction_method
  _reflns.d_resolution_high
  _reflns.d_resolution_low
  _reflns.details (∼ _reflns_special_details)
  _reflns.Friedel_coverage
  _reflns.limit_h_max
  _reflns.limit_h_min
  _reflns.limit_k_max
  _reflns.limit_k_min
  _reflns.limit_l_max
  _reflns.limit_l_min
  _reflns.number_all (∼ _reflns_number_total)
  _reflns.number_gt
  _reflns.number_obs (∼ _reflns_number_observed)
  _reflns.observed_criterion
  _reflns.observed_criterion_F_max
  _reflns.observed_criterion_F_min
  _reflns.observed_criterion_I_max
  _reflns.observed_criterion_I_min
  _reflns.observed_criterion_sigma_F
  _reflns.observed_criterion_sigma_I
  _reflns.percent_possible_obs
  _reflns.R_free_details
  _reflns.Rmerge_F_all
  _reflns.Rmerge_F_obs
  _reflns.threshold_expression
```

(*b*) REFLNS_SCALE

```
• _reflns_scale.group_code
  _reflns_scale.meas_F
  _reflns_scale.meas_F_squared
  _reflns_scale.meas_intensity
```

(*c*) REFLNS_SHELL

```
• _reflns_shell.d_res_high
• _reflns_shell.d_res_low
  _reflns_shell.meanI_over_sigI_all
  _reflns_shell.meanI_over_sigI_gt
  _reflns_shell.meanI_over_sigI_obs
  _reflns_shell.meanI_over_uI_all
  _reflns_shell.meanI_over_uI_gt
  _reflns_shell.number_measured_all
  _reflns_shell.number_measured_gt
  _reflns_shell.number_measured_obs
  _reflns_shell.number_possible
  _reflns_shell.number_unique_all
  _reflns_shell.number_unique_gt
  _reflns_shell.number_unique_obs
  _reflns_shell.percent_possible_all
  _reflns_shell.percent_possible_gt
  _reflns_shell.percent_possible_obs
  _reflns_shell.Rmerge_F_all
  _reflns_shell.Rmerge_F_gt
  _reflns_shell.Rmerge_F_obs
  _reflns_shell.Rmerge_I_all
  _reflns_shell.Rmerge_I_gt
  _reflns_shell.Rmerge_I_obs
```

(*d*) REFLNS_CLASS

```
• _reflns_class.code
  _reflns_class.d_res_high
  _reflns_class.d_res_low
  _reflns_class.description
  _reflns_class.number_gt
  _reflns_class.number_total
  _reflns_class.R_factor_all
  _reflns_class.R_factor_gt
  _reflns_class.R_Fsqd_factor
  _reflns_class.R_I_factor
  _reflns_class.wR_factor_all
```

The bullet (•) *indicates a category key. Where multiple items within a category are marked with a bullet, they must be taken together to form a compound key. The arrow* (→) *is a reference to a parent data item. Items in italics have aliases in the core CIF dictionary formed by changing the full stop* (.) *to an underscore* (_) *except where indicated by the* ∼ *symbol.*

Data items in the REFLNS category of the core CIF dictionary can be used to summarize the properties or attributes of the complete set of reflections used in refinement (Section 3.2.3.2.2). The mmCIF dictionary adds a number of data items to this category, including the formal category key required by the DDL2 data model. There are also data items for describing the data-reduction method and recording any relevant details about data reduction, and for giving an estimate of the overall Wilson *B* factor for the data set.

A number of the new data items relate to the issue of how reflections are flagged as being observed and are thus used in the refinement. In the core CIF dictionary, the criteria used to consider

Example 3.6.6.13. *The data set used in the refinement of an HIV-1 protease structure (PDB 5HVP) described using data items in the* REFLNS *and* REFLNS_SHELL *categories.*

```
_reflns.entry_id                         '5HVP'
_reflns.data_reduction_method
; Xengen program scalei. Anomalous pairs were merged.
  Scaling proceeded in several passes, beginning with
  1-parameter fit and ending with 3-parameter fit.
;
_reflns.data_reduction_details
; Merging and scaling based on only those reflections
  with I > sigma(I).
;

_reflns.d_resolution_high                2.00
_reflns.d_resolution_low                 8.00

_reflns.limit_h_max                      22
_reflns.limit_h_min                      0
_reflns.limit_k_max                      46
_reflns.limit_k_min                      0
_reflns.limit_l_max                      57
_reflns.limit_l_min                      0

_reflns.number_obs                       7228
_reflns.observed_criterion_sigma_I       1.0
_reflns.details                          none

loop_
_reflns_shell.d_res_high
_reflns_shell.d_res_low
_reflns_shell.meanI_over_sigI_obs
_reflns_shell.number_measured_obs
_reflns_shell.number_unique_obs
_reflns_shell.percent_possible_obs
_reflns_shell.Rmerge_F_obs
   31.38   3.82   69.8   9024   2540   96.8    1.98
    3.82   3.03   26.1   7413   2364   95.1    3.85
    3.03   2.65   10.5   5640   2123   86.2    6.37
    2.65   2.41    6.4   4322   1882   76.8    8.01
    2.41   2.23    4.3   3247   1714   70.4    9.86
    2.23   2.10    3.1   1140    812   33.3   13.99
```

a reflection as being observed are given using the data item `_reflns.observed_criterion`. This is a free-text field so is not automatically parsable. Therefore it is supplemented in the mmCIF dictionary by data items that can be used to stipulate the criterion in terms of the values of F, I or the uncertainties in these quantities (Example 3.6.6.13). The percentage of the total number of reflections that meet the criterion can be recorded.

Data items are also provided for describing the selection of the reflections used to calculate the free R factor, and for giving the $R_{\rm merge}$ values for all reflections and for the subset of 'observed' reflections. Data items in the REFLNS_SCALE and REFLNS_SHELL categories are used in the same way in the mmCIF and core CIF dictionaries, and Section 3.2.3.2.2 can be consulted for details.

As with the related categories DIFFRN_REFLNS_CLASS and REFINE_LS_CLASS, the core dictionary category REFLNS_CLASS was introduced after the release of the first version of the mmCIF dictionary. It provides a more general way of describing the treatment of particular subsets of the observations, but it is not expected to be used in macromolecular structural studies, where partition by shells of resolution is traditional.

3.6.7. Atomicity, chemistry and structure

The basic concepts of the mmCIF model for describing a macromolecular structure were outlined in Section 3.6.3. The present section describes the components of the model in more detail. The category groups used to describe the molecular chemistry and structure are: the ATOM group describing atom positions (Section 3.6.7.1); the CHEMICAL, CHEM_COMP and CHEM_LINK groups describing molecular chemistry (Section 3.6.7.2); the ENTITY group describing distinct chemical species (Section 3.6.7.3); the GEOM group describing molecular or packing geometry (Section 3.6.7.4); the STRUCT group describing the large-scale features of molecular structure (Section 3.6.7.5); and the SYMMETRY group describing the symmetry and space group (Section 3.6.7.6).

The CHEMICAL category group itself is not generally used in an mmCIF. The purpose of this category group in the core CIF dictionary is to specify the chemical identity and connectivity of the relatively simple molecular or ionic species in a small-molecule or inorganic crystal. In principle, a macromolecular structure determined to atomic resolution could be represented as a coherent chemical entity with a complete connectivity graph. However, in practice, biological macromolecules are built from units from a library of models of standard amino acids, nucleotides and sugars. Data items in the CHEM_COMP and CHEM_LINK category groups of the mmCIF dictionary describe the internal connectivity and standard bonding processes between these units.

Molecular or packing geometry is also rarely tabulated for large macromolecular complexes, so the GEOM category group is rarely used in an mmCIF.

3.6.7.1. Atom sites

The categories describing atom sites are as follows:

ATOM group
Individual atom sites (§3.6.7.1.1)
  ATOM_SITE
  ATOM_SITE_ANISOTROP
Collections of atom sites (§3.6.7.1.2)
  ATOM_SITES
  ATOM_SITES_FOOTNOTE
Atom types (§3.6.7.1.3)
  ATOM_TYPE
Alternative conformations (§3.6.7.1.4)
  ATOM_SITES_ALT
  ATOM_SITES_ALT_ENS
  ATOM_SITES_ALT_GEN

The ATOM category group represents a compromise between the representation of a small-molecule structure as an annotated list of atomic coordinates and the need in macromolecular crystallography to present a more structured view organized around residues, chains, sheets, turns, helices *etc.* The locations of individual atoms and other information about the atom sites are given using data items in this category group. The categories within the group may be classified as shown in the summary above.

The ATOM_SITE, ATOM_SITES and ATOM_TYPE categories have many data items that are aliases of equivalent data items in the same categories in the core CIF dictionary, but the conventions for the labelling of the atom sites are different.

The ATOM_SITE_ANISOTROP and ATOM_SITES_FOOTNOTE categories are new to the mmCIF dictionary, as are the categories related to alternative conformations: ATOM_SITES_ALT, ATOM_SITES_ALT_ENS and ATOM_SITES_ALT_GEN.

3.6.7.1.1. *Individual atom sites*

The data items in these categories are as follows:

(*a*) ATOM_SITE

• **_atom_site.id** (∼ ***_atom_site_label***)
  _atom_site.adp_type
\+ **_atom_site.aniso_B[1][1]**
  ⇌ ***_atom_site_anisotrop.B[1][1]***