

## 3. CIF DATA DEFINITION AND CLASSIFICATION

Table 3.6.4.1. Major category groups defined in the mmCIF dictionary

The groups are listed in the order in which they are described in this chapter. There is also an INCLUSIVE category group, which serves as a formal higher-order container group to which all other category groups belong.

Section	Category group	Subject covered
<i>(a) Experimental measurements</i>		
3.6.5.1	CELL	Unit cell
3.6.5.2	DIFFRN	Diffraction experiment
3.6.5.3	EXPTL	Experimental conditions
<i>(b) Analysis</i>		
3.6.6.1	PHASING	Phasing techniques
3.6.6.2	REFINE	Refinement procedures
3.6.6.3	REFLN	Reflection measurements
<i>(c) Atomicity, chemistry and structure</i>		
3.6.7.1	ATOM	Atom sites
3.6.7.2	CHEMICAL	Chemical properties and nomenclature
3.6.7.3	ENTITY	Chemical entities
3.6.7.4	GEOM	Geometry of atom sites
3.6.7.5	STRUCT	Crystallographic structure
3.6.7.6	SYMMETRY	Symmetry information
3.6.7.7	VALENCE	Bond-valence information
<i>(d) Publication</i>		
3.6.8.1	CITATION	Bibliographic references
3.6.8.2	COMPUTING	Computational details of the experiment
3.6.8.3	DATABASE	Database information
3.6.8.4	IUCR	Journal housekeeping and the contents of a published article
<i>(e) File metadata</i>		
3.6.9.1	AUDIT	Dictionary maintenance and identification
3.6.9.2	ENTRY	Links between data blocks
3.6.9.3	COMPLIANCE	Compliance with previous dictionaries

attribute `_type_conditions_esd` and allows the standard uncertainty of the value to be placed in parentheses after the numerical value, as in

```
_cell_length_a      58.39(5)
```

This is also permitted in mmCIF, but it is preferable to use a separate data item to record the standard uncertainty, as in

```
_cell_length_a      58.39
_cell_length_a_esd   0.05
```

There are many of these kinds of data names in the mmCIF dictionary. The name of each is derived by adding `_esd` to the data name for the value. They are indicated by a + symbol in the category summaries in this chapter.

### 3.6.5. Experimental measurements

The CELL, DIFFRN and EXPTL category groups are used to describe the crystallographic experiment. The data items used for this purpose in mmCIF are for the most part identical to those in the core CIF dictionary. A complete discussion of the data names in each category may be found in Section 3.2.2.

mmCIF also contains the new categories EXPTL\_CRYSTAL\_GROW and EXPTL\_CRYSTAL\_GROW\_COMP (Section 3.6.5.3.2), which are used to provide a more structured description of crystallization than is available in the core CIF dictionary.

#### 3.6.5.1. Crystal cell parameters and measurement conditions

The categories describing the crystal unit cell and its determination are as follows:

CELL group  
CELL  
CELL\_MEASUREMENT  
CELL\_MEASUREMENT\_REFLN

The mmCIF dictionary differs from the core CIF dictionary in assigning separate categories to data names that define the crystal unit-cell parameters and to data names relating to the experimental determination of the unit cell. Details of the unit-cell parameters are given in the CELL category and data items in the distinct CELL\_MEASUREMENT category are used to describe how the unit-cell parameters were measured. The category CELL\_MEASUREMENT\_REFLN, which is used to list the reflections used in the unit-cell determination, is common to the core and mmCIF dictionaries.

The data items in these categories are as follows:

*(a) CELL*

- `_cell.entry_id`  
→ `_entry.id`
- + `_cell.angle_alpha`
- + `_cell.angle_beta`
- + `_cell.angle_gamma`
- `_cell.details` (~ `_cell.special_details`)
- `_cell.formula_units_Z`
- + `_cell.length_a`
- + `_cell.length_b`
- + `_cell.length_c`
- + `_cell.reciprocal_angle_alpha`
- + `_cell.reciprocal_angle_beta`
- + `_cell.reciprocal_angle_gamma`
- + `_cell.reciprocal_length_a`
- + `_cell.reciprocal_length_b`
- + `_cell.reciprocal_length_c`
- + `_cell.volume`
- `_cell.Z_PDB`

*(b) CELL\_MEASUREMENT*

- `_cell_measurement.entry_id`  
→ `_entry.id`
- + `_cell_measurement.pressure`
- `_cell_measurement.radiation`
- `_cell_measurement.reflns_used`
- + `_cell_measurement.temp`  
(~ `_cell_measurement.temperature`)
- `_cell_measurement.theta_max`
- `_cell_measurement.theta_min`
- `_cell_measurement.wavelength`

*(c) CELL\_MEASUREMENT\_REFLN*

- `_cell_measurement_refl.index_h`
- `_cell_measurement_refl.index_k`
- `_cell_measurement_refl.index_l`
- `_cell_measurement_refl.theta`

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. 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 marked with a plus (+) have companion data names for the standard uncertainty in the reported value, formed by appending the string `_esd` to the data name listed.

The summary above includes the formal category keys that have been introduced in mmCIF because the corresponding core categories do not expect looped data, and therefore do not require the specification of a unique identifier. In the relational model of DDL2, all categories are considered to be tables and therefore each category must have a unique identifier. Where core CIF categories have one or more data names that fulfil the role of table-row identifiers, these have generally been carried over as category keys in the mmCIF dictionary (for example, the data items that correspond to the *h*, *k*, and *l* Miller indices of a reflection in the CELL\_MEASUREMENT\_REFLN category).

### 3.6. CLASSIFICATION AND USE OF MACROMOLECULAR DATA

Example 3.6.5.1. *Cell constants and their measurement for an HIV-1 protease crystal (PDB 5HVP) described with data items in the CELL and CELL\_MEASUREMENT categories (Fitzgerald et al., 1990).*

```

_cell.entry_id          '5HVP'
_cell.length_a         58.39
_cell.length_a_esd     0.05
_cell.length_b         86.70
_cell.length_b_esd     0.12
_cell.length_c         46.27
_cell.length_c_esd     0.06
_cell.angle_alpha      90.00
_cell.angle_beta       90.00
_cell.angle_gamma      90.00
_cell.volume           234237
_cell.details
; The cell parameters were refined every twenty
frames during data integration. The cell lengths
given are the mean of 55 such refinements; the
esds given are the root-mean-square deviations
of these 55 observations from that mean.
;
_cell_measurement.entry_id      '5HVP'
_cell_measurement.temp         293
_cell_measurement.temp_esd     3
_cell_measurement.theta_min    11
_cell_measurement.theta_max    31
_cell_measurement.wavelength   1.54

```

Example 3.6.5.1 shows how data items from these categories are used in practice and shows the use of separate data items to record standard uncertainties of measurable quantities.

#### 3.6.5.2. Data collection

The categories describing data collection are as follows:

DIFFRN group

```

DIFFRN
DIFFRN_ATTENUATOR
DIFFRN_DETECTOR
DIFFRN_MEASUREMENT
DIFFRN_ORIENT_MATRIX
DIFFRN_ORIENT_REFLN
DIFFRN_RADIATION
DIFFRN_RADIATION_WAVELENGTH
DIFFRN_REFLN
DIFFRN_REFLNS
DIFFRN_REFLNS_CLASS
DIFFRN_SCALE
DIFFRN_SOURCE
DIFFRN_STANDARD_REFLN
DIFFRN_STANDARDS

```

The categories in the DIFFRN category group describe the diffraction experiment. Data items in the DIFFRN category itself can be used to give overall information about the experiment, such as the temperature and pressure. Examples of the other categories are DIFFRN\_DETECTOR, which is used for describing the detector used for data collection, and DIFFRN\_SOURCE, which is used to give details of the source of the radiation used in the experiment. Data items in the DIFFRN\_REFLN category can be used to give information about the raw data and data items in the DIFFRN\_REFLNS category can be used to give information about all the reflection data collectively.

The data items in the categories in the DIFFRN group are as follows:

(a) DIFFRN

```

• _diffrn.id
  _diffrn.ambient_environment
+ _diffrn.ambient_pressure
  _diffrn.ambient_pressure_gt
  _diffrn.ambient_pressure_lt

```

```

+ _diffrn.ambient_temp (~ _diffrn_ambient_temperature)
  _diffrn.ambient_temp_details
  _diffrn.ambient_temp_gt
  _diffrn.ambient_temp_lt
  _diffrn.crystal_id (~ _diffrn_reflnt_crystal_id)
  _diffrn.crystal_support
  _diffrn.crystal_treatment
  _diffrn.details (~ _diffrn_special_details)

```

(b) DIFFRN\_ATTENUATOR

```

• _diffrn_attenuator.code
  _diffrn_attenuator.material
  _diffrn_attenuator.scale

```

(c) DIFFRN\_DETECTOR

```

• _diffrn_detector.diffrn_id
  → _diffrn.id
  _diffrn_detector.area_resol_mean
  _diffrn_detector.details
  _diffrn_detector.detector (~ _diffrn_detector)
  _diffrn_detector.dtime
  _diffrn_detector.type

```

(d) DIFFRN\_MEASUREMENT

```

• _diffrn_measurement.diffrn_id
  → _diffrn.id
  _diffrn_measurement.details
  _diffrn_measurement.device
  _diffrn_measurement.device_details
  _diffrn_measurement.device_type
  _diffrn_measurement.method
  _diffrn_measurement.specimen_support

```

(e) DIFFRN\_ORIENT\_MATRIX

```

• _diffrn_orient_matrix.diffrn_id
  → _diffrn.id
  _diffrn_orient_matrix.type
  _diffrn_orient_matrix.UB[1] [1]
  (~ _diffrn_orient_matrix_UB_11)
  _diffrn_orient_matrix.UB[1] [2]
  (~ _diffrn_orient_matrix_UB_12)
  _diffrn_orient_matrix.UB[1] [3]
  (~ _diffrn_orient_matrix_UB_13)
  _diffrn_orient_matrix.UB[2] [1]
  (~ _diffrn_orient_matrix_UB_21)
  _diffrn_orient_matrix.UB[2] [2]
  (~ _diffrn_orient_matrix_UB_22)
  _diffrn_orient_matrix.UB[2] [3]
  (~ _diffrn_orient_matrix_UB_23)
  _diffrn_orient_matrix.UB[3] [1]
  (~ _diffrn_orient_matrix_UB_31)
  _diffrn_orient_matrix.UB[3] [2]
  (~ _diffrn_orient_matrix_UB_32)
  _diffrn_orient_matrix.UB[3] [3]
  (~ _diffrn_orient_matrix_UB_33)

```

(f) DIFFRN\_ORIENT\_REFLN

```

• _diffrn_orient_reflnt.diffrn_id
  → _diffrn.id
• _diffrn_orient_reflnt.index_h
• _diffrn_orient_reflnt.index_k
• _diffrn_orient_reflnt.index_l
  _diffrn_orient_reflnt.angle_chi
  _diffrn_orient_reflnt.angle_kappa
  _diffrn_orient_reflnt.angle_omega
  _diffrn_orient_reflnt.angle_phi
  _diffrn_orient_reflnt.angle_psi
  _diffrn_orient_reflnt.angle_theta

```

(g) DIFFRN\_RADIATION

```

• _diffrn_radiation.diffrn_id
  → _diffrn.id
  _diffrn_radiation.collimation
  _diffrn_radiation.filter_edge
  _diffrn_radiation.inhomogeneity
  _diffrn_radiation.monochromator
  _diffrn_radiation.polarisn_norm
  _diffrn_radiation.polarisn_ratio
  _diffrn_radiation.probe
  _diffrn_radiation.type

```

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- `_diffrn_radiation.wavelength_id`  
→ `_diffrn_radiation.wavelength_id`
  - `_diffrn_radiation.xray_symbol`
- (h) DIFFRN\_RADIATION\_WAVELENGTH
- `_diffrn_radiation.wavelength_id`
  - `_diffrn_radiation.wavelength.wavelength`  
(~ `_diffrn_radiation.wavelength.wavelength`)
  - `_diffrn_radiation.wavelength.wt`
- (i) DIFFRN\_REFLN
- `_diffrn_refl.diffrn_id`  
→ `_diffrn_id`
  - `_diffrn_refl.id`  
`_diffrn_refl.angle_chi`  
`_diffrn_refl.angle_kappa`  
`_diffrn_refl.angle_omega`  
`_diffrn_refl.angle_phi`  
`_diffrn_refl.angle_psi`  
`_diffrn_refl.angle_theta`  
`_diffrn_refl.attenuator_code`  
→ `_diffrn_attenuator.code`  
`_diffrn_refl.class_code`  
`_diffrn_refl.counts_bg_1`  
`_diffrn_refl.counts_bg_2`  
`_diffrn_refl.counts_net`  
`_diffrn_refl.counts_peak`  
`_diffrn_refl.counts_total`  
`_diffrn_refl.detect_slit_horiz`  
`_diffrn_refl.detect_slit_vert`  
`_diffrn_refl.elapsed_time`  
`_diffrn_refl.index_h`  
`_diffrn_refl.index_k`  
`_diffrn_refl.index_l`  
`_diffrn_refl.intensity_net`  
`_diffrn_refl.intensity_sigma`  
`_diffrn_refl.intensity_u`  
`_diffrn_refl.scale_group_code`  
→ `_diffrn_scale_group.code`  
`_diffrn_refl.scan_mode`  
`_diffrn_refl.scan_mode_backgd`  
`_diffrn_refl.scan_rate`  
`_diffrn_refl.scan_time_backgd`  
`_diffrn_refl.scan_width`  
`_diffrn_refl.sint_over_lambda`  
(~ `_diffrn_refl.sint/lambda`)  
`_diffrn_refl.standard_code`  
→ `_diffrn_standard_refl.code`  
`_diffrn_refl.wavelength`  
`_diffrn_refl.wavelength_id`  
→ `_diffrn_radiation.wavelength_id`
- (j) DIFFRN\_REFLNS
- `_diffrn_reflns.diffrn_id`  
→ `_diffrn_id`  
`_diffrn_reflns.av_R_equivalents`  
`_diffrn_reflns.av_sigmaI_over_netI`  
`_diffrn_reflns.av_unetI/netI`  
`_diffrn_reflns.limit_h_max`  
`_diffrn_reflns.limit_h_min`  
`_diffrn_reflns.limit_k_max`  
`_diffrn_reflns.limit_k_min`  
`_diffrn_reflns.limit_l_max`  
`_diffrn_reflns.limit_l_min`  
`_diffrn_reflns.number`  
`_diffrn_reflns.reduction_process`  
`_diffrn_reflns.theta_max`  
`_diffrn_reflns.theta_min`  
`_diffrn_reflns.transf_matrix[1][1]`  
(~ `_diffrn_reflns.transf_matrix_11`)  
`_diffrn_reflns.transf_matrix[1][2]`  
(~ `_diffrn_reflns.transf_matrix_12`)  
`_diffrn_reflns.transf_matrix[1][3]`  
(~ `_diffrn_reflns.transf_matrix_13`)  
`_diffrn_reflns.transf_matrix[2][1]`  
(~ `_diffrn_reflns.transf_matrix_21`)  
`_diffrn_reflns.transf_matrix[2][2]`  
(~ `_diffrn_reflns.transf_matrix_22`)  
`_diffrn_reflns.transf_matrix[2][3]`  
(~ `_diffrn_reflns.transf_matrix_23`)  
`_diffrn_reflns.transf_matrix[3][1]`  
(~ `_diffrn_reflns.transf_matrix_31`)
- `_diffrn_reflns.transf_matrix[3][2]`  
(~ `_diffrn_reflns.transf_matrix_32`)
  - `_diffrn_reflns.transf_matrix[3][3]`  
(~ `_diffrn_reflns.transf_matrix_33`)
- (k) DIFFRN\_REFLNS\_CLASS
- `_diffrn_reflns.class.code`  
`_diffrn_reflns.class.av_R_eq`  
`_diffrn_reflns.class.av_sgI/I`  
`_diffrn_reflns.class.av_uI/I`  
`_diffrn_reflns.class.d_res_high`  
`_diffrn_reflns.class.d_res_low`  
`_diffrn_reflns.class.description`  
`_diffrn_reflns.class.number`
- (l) DIFFRN\_SCALE\_GROUP
- `_diffrn_scale_group.code`  
`_diffrn_scale_group.I_net`
- (m) DIFFRN\_SOURCE
- `_diffrn_source.diffrn_id`  
→ `_diffrn_id`  
`_diffrn_source.current`  
`_diffrn_source.details`  
`_diffrn_source.power`  
`_diffrn_source.size`  
`_diffrn_source.source` (~ `_diffrn_source`)  
`_diffrn_source.take-off_angle`  
`_diffrn_source.target`  
`_diffrn_source.type`  
`_diffrn_source.voltage`
- (n) DIFFRN\_STANDARD\_REFLN
- `_diffrn_standard_refl.code`
  - `_diffrn_standard_refl.diffrn_id`  
→ `_diffrn_id`  
`_diffrn_standard_refl.index_h`  
`_diffrn_standard_refl.index_k`  
`_diffrn_standard_refl.index_l`
- (o) DIFFRN\_STANDARDS
- `_diffrn_standards.diffrn_id`  
→ `_diffrn_id`  
`_diffrn_standards.decay_%`  
`_diffrn_standards.interval_count`  
`_diffrn_standards.interval_time`  
`_diffrn_standards.number`  
`_diffrn_standards.scale_sigma`  
`_diffrn_standards.scale_u`

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 marked with a plus (+) have companion data names for the standard uncertainty in the reported value, formed by appending the string `_esd` to the data name listed.

To a very great extent, data items in the DIFFRN category group are used in the same way in the mmCIF and core CIF dictionaries, and Section 3.2.2.2 can be consulted for details. Example 3.6.5.2 shows how these categories are used to describe the data collection for a macromolecule.

There is, however, one important difference. An mmCIF may describe several separate diffraction experiments that were conducted with a common purpose; each such experiment would be given a unique value of `_diffrn.id`, the key for the DIFFRN category. Descriptions of features of that experiment in related categories would be given a matching identifier with the same value (e.g. `_diffrn_detector.diffrn_id`). The use of the suffix `*.diffrn_id` for the key data names in each related category emphasizes the connection to the parent experiment.

As a consequence, there are differences between the mmCIF and core CIF dictionaries in the definition of the category keys for

Example 3.6.5.2. *Data collection for an HIV-1 protease crystal (PDB 5HVP) described with data items in the DIFFRN and related categories.*

```

_diffrn.id                'set1'
_diffrn.crystal_id        1
_diffrn.ambient_temp      293(3)
_diffrn.ambient_environment
; Mother liquor from the reservoir of the vapor
  diffusion experiment, mounted in room air
;
_diffrn.crystal_support
; 0.7 mm glass capillary, sealed with dental wax
;
_diffrn.crystal_treatment
; Equilibrated in rotating anode radiation enclosure
  for 18 hours prior to beginning of data collection.
;
_diffrn_detector.diffrn_id  'set1'
_diffrn_detector.detector  'multiwire'
_diffrn_detector.type      'Siemens'

_diffrn_measurement.diffrn_id  'd1'
_diffrn_measurement.device    '3-circle camera'
_diffrn_measurement.device_type  'Supper model x'
_diffrn_measurement.device_details  'none'
_diffrn_measurement.method    'omega scan'
_diffrn_measurement.details
; 440 frames, 0.20 degrees, 150 sec, detector
  distance 12 cm, detector angle 22.5 degrees
;
_diffrn_radiation.diffrn_id  'set1'
_diffrn_radiation.collimation
  '0.3 mm double pinhole'
_diffrn_radiation.monochromator  'graphite'
_diffrn_radiation.type          'Cu Kalpha'
_diffrn_radiation.wavelength_id  1
_diffrn_radiation_wavelength_id  1
_diffrn_radiation_wavelength_wavelength  1.54
_diffrn_radiation_wavelength_wt  1.0
_diffrn_source.diffrn_id      'set1'
_diffrn_source.source         'rotating anode'
_diffrn_source.type           'Rigaku RU-200'
_diffrn_source.power          50
_diffrn_source.current        180
_diffrn_source.target         '8mm x 0.4 mm broad-focus'

```

the DIFFRN categories. These differences were introduced in order to accommodate data from more than one experiment in the same table. For example, in the core CIF dictionary, the Miller indices `_diffrn_refl_index_h`, `*_k` and `*_l` play the role of the category key for the DIFFRN\_REFLN category. In the mmCIF dictionary, the category key is formed by the data items `_diffrn_refl_id` and `_diffrn_refl.diffrn_id`.

### 3.6.5.3. Growth, description and analysis of the crystal

The categories describing the crystal properties and growth are as follows:

EXPTL group

*Crystal properties* (§3.6.5.3.1)

EXPTL

EXPTL\_CRYSTAL

EXPTL\_CRYSTAL\_FACE

*Crystal growth* (§3.6.5.3.2)

EXPTL\_CRYSTAL\_GROW

EXPTL\_CRYSTAL\_GROW\_COMP

Categories in the EXPTL category group are used to describe experimental measurements on the crystal (e.g. of its shape, size and density) and the growth of the crystal. Data items in the EXPTL category are used to describe the gross properties of the crystal or crystals used in the experiment. Data items in the EXPTL\_CRYSTAL

category are used to describe the crystal properties in detail and allow for cases where multiple crystals are used. The data items in the EXPTL\_CRYSTAL\_FACE category are used to describe the crystal faces.

Data items for describing crystal growth are given in two categories that are not found in the current version of the core CIF dictionary. Data items in the EXPTL\_CRYSTAL\_GROW category are used to describe the conditions and methods used to grow the crystals, and data items in the EXPTL\_CRYSTAL\_GROW\_COMP category can be used to list the components of the solutions in which the crystals were grown.

#### 3.6.5.3.1. Crystal properties

The data items in these categories are as follows:

##### (a) EXPTL

- `_exptl_entry_id`
  - `_entry_id`
  - `_exptl_absorpt_coefficient_mu`
  - `_exptl_absorpt_correction_T_max`
  - `_exptl_absorpt_correction_T_min`
  - `_exptl_absorpt_correction_type`
  - `_exptl_absorpt_process_details`
  - `_exptl_crystals_number`
  - `_exptl_details` (~ `_exptl_special_details`)
  - `_exptl_method`
  - `_exptl_method_details`

##### (b) EXPTL\_CRYSTAL

- `_exptl_crystal_id`
  - `_exptl_crystal_colour`
  - `_exptl_crystal_colour_lustre`
  - `_exptl_crystal_colour_modifier`
  - `_exptl_crystal_colour_primary`
  - `_exptl_crystal_density_diffrn`
  - `_exptl_crystal_density_Matthews`
  - + `_exptl_crystal_density_meas`
  - `_exptl_crystal_density_meas_gt`
  - `_exptl_crystal_density_meas_lt`
  - + `_exptl_crystal_density_meas_temp`
  - `_exptl_crystal_density_meas_temp_gt`
  - `_exptl_crystal_density_meas_temp_lt`
  - `_exptl_crystal_density_method`
  - `_exptl_crystal_density_percent_sol`
  - `_exptl_crystal_description`
  - `_exptl_crystal_F_000`
  - `_exptl_crystal_preparation`
  - `_exptl_crystal_size_max`
  - `_exptl_crystal_size_mid`
  - `_exptl_crystal_size_min`
  - `_exptl_crystal_size_rad`

##### (c) EXPTL\_CRYSTAL\_FACE

- `_exptl_crystal_face_crystal_id`
  - `_exptl_crystal_id`
  - `_exptl_crystal_face_index_h`
  - `_exptl_crystal_face_index_k`
  - `_exptl_crystal_face_index_l`
  - `_exptl_crystal_face_diffraction_chi`
  - `_exptl_crystal_face_diffraction_kappa`
  - `_exptl_crystal_face_diffraction_phi`
  - `_exptl_crystal_face_diffraction_psi`
  - `_exptl_crystal_face_perp_dist`

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 marked with a plus (+) have companion data names for the standard uncertainty in the reported value, formed by appending the string `_esd` to the data name listed.

Data items in these categories are used in the same way in the mmCIF and core CIF dictionaries, and Section 3.2.2.3 can be consulted for details (see Example 3.6.5.3). Identifiers have been introduced to the categories to provide the formal category keys required by the DDL2 data model.

Example 3.6.5.3. *The crystal used in the determination of an HIV-1 protease structure (PDB 5HVP) described using data items in the EXPTL and EXPTL\_CRYSTAL categories.*

```
_exptl.entry_id          '5HVP'
_exptl.crystals_number   1
_exptl.method            'single-crystal x-ray diffraction'
_exptl.method_details
; graphite monochromatized Cu K(alpha) fixed tube
  and Siemens multiwire detector used
;
_exptl_crystal.id        1
_exptl_crystal.colour    'colorless'
_exptl_crystal.density_percent_sol 0.57
_exptl_crystal.description 'rectangular plate'
_exptl_crystal.size_max  0.30
_exptl_crystal.size_mid  0.20
_exptl_crystal.size_min  0.05
```

### 3.6.5.3.2. Crystal growth

The data items in these categories are as follows:

#### (a) EXPTL\_CRYSTAL\_GROW

- `_exptl_crystal_grow.crystal_id`  
→ `_exptl_crystal.id`
- `_exptl_crystal_grow.apparatus`
- `_exptl_crystal_grow.atmosphere`
- `_exptl_crystal_grow.details`
- `_exptl_crystal_grow.method`
- `_exptl_crystal_grow.method_ref`
- `_exptl_crystal_grow.pH`
- + `_exptl_crystal_grow.pressure`
- `_exptl_crystal_grow.seeding`
- `_exptl_crystal_grow.seeding_ref`
- + `_exptl_crystal_grow.temp`
- `_exptl_crystal_grow.temp_details`
- `_exptl_crystal_grow.time`

#### (b) EXPTL\_CRYSTAL\_GROW\_COMP

- `_exptl_crystal_grow_comp.crystal_id`  
→ `_exptl_crystal.id`
- `_exptl_crystal_grow_comp.id`
- `_exptl_crystal_grow_comp.conc`
- `_exptl_crystal_grow_comp.details`
- `_exptl_crystal_grow_comp.name`
- `_exptl_crystal_grow_comp.sol_id`
- `_exptl_crystal_grow_comp.volume`

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. Data items marked with a plus (+) have companion data names for the standard uncertainty in the reported value, formed by appending the string `_esd` to the data name listed.

Crystallization strategies and protocols are very varied and may not lend themselves to a formal tabulation. Common or well defined techniques may be indicated using the data item `_exptl_crystal_grow.method`, and a literature reference, where appropriate, may be given using `_exptl_crystal_grow.method_ref`. Frequently, however, a detailed description of methodology is required; this can be given in `_exptl_crystal_grow.details`. Example 3.6.5.4 shows how information about strategies that were attempted and proved unsuccessful can be recorded. In circumstances such as this, the data item `_exptl_crystal_grow.pH` would record the final pH.

Where the crystallization protocol is well defined, it is useful to list the individual components of the solution in the category `EXPTL_CRYSTAL_GROW_COMP`. Example 3.6.5.4 labels the solutions used as 1 and 2, in accordance with the convention that solution 1 contains the molecule to be crystallized and solution 2 (and if necessary additional solutions) contains the precipitant. However, it is permissible and may be preferable to use more explicit labels such as 'well solution' in the `_exptl_crystal_grow_comp.sol_id` field.

Example 3.6.5.4. *The growth of HIV-1 protease crystals (PDB 5HVP) described with data items in the EXPTL\_CRYST\_GROW and EXPTL\_CRYSTAL\_GROW\_COMP categories.*

```
_exptl_crystal_grow.crystal_id 1
_exptl_crystal_grow.method      'hanging drop'
_exptl_crystal_grow.apparatus   'Linbro plates'
_exptl_crystal_grow.atmosphere  'room air'
_exptl_crystal_grow.pH          4.7
_exptl_crystal_grow.temp        18(3)
_exptl_crystal_grow.time        'approximately 2 days'
_exptl_crystal_grow.details
; The dependence on pH for successful crystal growth
  is very sharp. At pH 7.4 only showers of tiny
  crystals grew, at pH 7.5 well formed single
  crystals grew, at pH 7.6 no crystallization
  occurred at all.
;
loop_
_exptl_crystal_grow_comp.crystal_id
_exptl_crystal_grow_comp.id
_exptl_crystal_grow_comp.sol_id
_exptl_crystal_grow_comp.name
_exptl_crystal_grow_comp.volume
_exptl_crystal_grow_comp.conc
_exptl_crystal_grow_comp.details
1 1 1 'HIV-1 protease' '0.002 ml' '6 mg/ml'
; The protein solution was in a buffer containing
  25 mM NaCl, 100 mM NaMES/MES buffer, pH 7.5,
  3 mM NaAzide
;
1 2 2 'NaCl' '0.200 ml' '4 M'
  'in 3 mM NaAzide'
1 3 2 'Acetic Acid' '0.047 ml' '100 mM'
  'in 3 mM NaAzide'
1 4 2 'Na Acetate' '0.053 ml' '100 mM'
; in 3 mM NaAzide. Buffer components were mixed
  to produce a pH of 4.7 according to a ratio
  calculated from the pKa. The actual pH of
  solution 2 was not measured.
;
1 5 2 'water' '0.700 ml' 'neat'
  'in 3 mM NaAzide'
```

## 3.6.6. Analysis

The mmCIF dictionary contributes several new categories and data items to the REFINE and REFLN category groups. These reflect common practices in macromolecular crystallography in refinement and in the handling of experimental observations.

A new category group, the PHASING group, has been introduced to provide a structured description of phasing strategies, as macromolecular crystallography differs strongly from small-molecule crystallography in how phases are determined. The data model for phasing in the current version of the mmCIF dictionary cannot describe all approaches to phasing yet. Additions and revisions to the data items in the PHASING group of categories are anticipated in future versions of the dictionary.

### 3.6.6.1. Phasing

The categories describing phasing are as follows:

PHASING group

*Overall description of phasing* (§3.6.6.1.1)

PHASING

*Phasing via molecular averaging* (§3.6.6.1.2)

PHASING\_AVERAGING

*Phasing via isomorphous replacement* (§3.6.6.1.3)

PHASING\_ISOMORPHOUS

*Phasing via multiple-wavelength anomalous dispersion*  
(§3.6.6.1.4)

PHASING\_MAD

PHASING\_MAD\_CLUST