4.1. Core dictionary (coreCIF)

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This is version 2.4 of the core CIF dictionary (coreCIF). A commentary on the use of this dictionary may be found in Chapter 3.2.

The data names defined here are central to the description and reporting of any crystal structure determination, and this dictionary collects the natural set of descriptors for small-unit-cell structures (typically inorganic or small-molecular organic and metal-organic compounds) determined in single-crystal experiments. These data items may be supplemented by additional items designed for use in powder-diffraction experiments (Chapter 3.3), modulated and composite structures (Chapter 3.4), or electron-density studies (Chapter 3.5).

The data items in this dictionary also form a suitable basis for the description of biological macromolecular structures, but the complexity of such structures requires a more extensive dictionary using a rigorously relational data model that expresses dependencies and inheritances between individual items. The macromolecular CIF (mmCIF) dictionary described in Chapter 3.6 and given in Chapter 4.5 provides a complete set of data items within this model, including the content of the core CIF dictionary in a modified formalism.

Categories are described in alphabetic order; data items are arranged alphabetically within each category.

ATOM_SITE

Data items in the ATOM_SITE category record details about the atom sites in a crystal structure, such as the positional coordinates, atomic displacement parameters, and magnetic moments and directions.

Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C47, 2276–2277].

```
loop_
_atom_site_label
_atom_site_fract_x
_atom_site_fract_y
_atom_site_fract_z
_atom_site_U_iso_or_equiv
_atom_site_adp_type
_atom_site_calc_flag
_atom_site_calc_attached_atom
  O1   .4154(4)  .5699(1)  .3026(0)  .060(1)  Uani  ?    ?
  C2   .5630(5)  .5087(2)  .3246(1)  .060(2)  Uani  ?    ?
  C3   .5350(5)  .4920(2)  .3997(1)  .048(1)  Uani  ?    ?
  N4   .3570(3)  .5558(1)  .4167(0)  .039(1)  Uani  ?    ?
  C5   .3000(5)  .6122(2)  .3581(1)  .045(1)  Uani  ?    ?
  O21  .6958(5)  .4738(2)  .2874(1)  .090(2)  Uani  ?    ?
  C31  .4869(6)  .3929(2)  .4143(2)  .059(2)  Uani  ?    ?
 # - - - - data truncated for brevity - - - -
  H321C  .04(1)  .318(3)   .320(2)   .14000   Uiso  ?    ?
  H322A  .25(1)  .272(4)   .475(3)   .19000   Uiso  ?    ?
  H322B  .34976  .22118    .40954    .19000   Uiso  calc C322
  H322C  .08(1)  .234(4)   .397(3)   .19000   Uiso  ?    ?
```

Example 2 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C47, 2276–2277].

```
loop_
_atom_site_aniso_label
_atom_site_aniso_B_11
_atom_site_aniso_B_22
_atom_site_aniso_B_33
_atom_site_aniso_B_12
_atom_site_aniso_B_13
_atom_site_aniso_B_23
_atom_site_aniso_type_symbol
 O1   .071(1) .076(1) .0342(9) .008(1)   .0051(9) -.0030(9) O
 C2   .060(2) .072(2) .047(1)  .002(2)   .013(1)  -.009(1)  C
 C3   .038(1) .060(2) .044(1)  .007(1)   .001(1)  -.005(1)  C
 N4   .037(1) .048(1) .0325(9) .0025(9)  .0011(9) -.0011(9) N
 C5   .043(1) .060(1) .032(1)  .001(1)  -.001(1)   .001(1)  C
 # - - - - data truncated for brevity - - - -
 O21  .094(2) .109(2) .068(1)  .023(2)   .038(1)  -.010(1)  O
 C51  .048(2) .059(2) .049(1)  .002(1)  -.000(1)   .007(1)  C
 C511 .048(2) .071(2) .097(3) -.008(2)  -.003(2)   .010(2)  C
 C512 .078(2) .083(2) .075(2)  .009(2)  -.005(2)   .033(2)  C
 C513 .074(2) .055(2) .075(2)  .004(2)   .001(2)  -.010(2)  C
 # - - - - data truncated for brevity - - - -
```

Example 3 – based on data set DPTD of Yamin, Suwandi, Fun, Sivakumar & bin Shawkataly [Acta Cryst. (1996), C52, 951–953].

```
loop_
_atom_site_label
_atom_site_chemical_conn_number
_atom_site_fract_x
_atom_site_fract_y
_atom_site_fract_z
_atom_site_U_iso_or_equiv
 S1  1  0.74799(9)  -0.12482(11)  0.27574(9)  0.0742(3)
 S2  2  1.08535(10)  0.16131(9)   0.34061(9)  0.0741(3)
 N1  3  1.0650(2)   -0.1390(2)    0.2918(2)   0.0500(5)
 C1  4  0.9619(3)   -0.0522(3)    0.3009(2)   0.0509(6)
 # - - - - data truncated for brevity - - - -
```

Example 4 – hypothetical example to illustrate the description of a disordered methyl group.

```
 loop_
  _atom_site_label     # *_assembly M is a disordered methyl
  _atom_site_occupancy # with configurations 'A' and 'B':
  _atom_site_disorder_assembly #
  _atom_site_disorder_group    #    H11B    H11A      H13B
                               #      .       |       .
   C1     1      .       .     #        .     |     .
   H11A   .5     M       A     #          .   |   .
   H12A   .5     M       A     #              C1 --------C2---
   H13A   .5     M       A     #            / .  \
   H11B   .5     M       B     #          /   .    \
   H12B   .5     M       B     #        /     .      \
   H13B   .5     M       B     #    H12A    H12B    H13A
```

_atom_site_adp_type (*char*)

A standard code used to describe the type of atomic displacement parameters used for the site.

Appears in list containing **_atom_site_label**.

Related item: **_atom_site_thermal_displace_type** (alternate).

The data value must be one of the following:

Uani	anisotropic U^{ij}
Uiso	isotropic U
Uovl	overall U
Umpe	multipole expansion U
Bani	anisotropic B^{ij}
Biso	isotropic B
Bovl	overall B

[atom_site]

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_atom_site_aniso_B_11
_atom_site_aniso_B_12
_atom_site_aniso_B_13
_atom_site_aniso_B_22
_atom_site_aniso_B_23
_atom_site_aniso_B_33 (*numb, su*)

These are the standard anisotropic atomic displacement components in ångströms squared which appear in the structure-factor term

$$T = \exp\Big\{-(1/4)\sum_i\Big[\sum_j(B^{ij}h_ih_ja_i^*a_j^*)\Big]\Big\},$$

where h = the Miller indices and a^* = the reciprocal-space cell lengths.

The unique elements of the real symmetric matrix are entered by row. The IUCr Commission on Nomenclature recommends against the use of **B** for reporting atomic displacement parameters. **U**, being directly proportional to **B**, is preferred.

Appears in list containing **_atom_site_aniso_label**.

Related item: **_atom_site_aniso_U_** (conversion). **[atom_site]**

_atom_site_aniso_label (*char*)

Anisotropic atomic displacement parameters are usually looped in a separate list. If this is the case, this code must match the **_atom_site_label** of the associated atom in the atom coordinate list and conform with the same rules described in **_atom_site_label**.

Appears in list. **Must** match parent data name **_atom_site_label**. **[atom_site]**

_atom_site_aniso_ratio (*numb*)

Ratio of the maximum to minimum principal axes of displacement (thermal) ellipsoids.

Appears in list containing **_atom_site_aniso_label**.

The permitted range is $1.0 \rightarrow \infty$. **[atom_site]**

_atom_site_aniso_type_symbol (*char*)

This **_atom_type_symbol** code links the anisotropic atom parameters to the atom-type data associated with this site and must match one of the **_atom_type_symbol** codes in this list.

Appears in list containing **_atom_site_aniso_label**. **Must** match parent data name **_atom_site_type_symbol**. **[atom_site]**

_atom_site_aniso_U_11
_atom_site_aniso_U_12
_atom_site_aniso_U_13
_atom_site_aniso_U_22
_atom_site_aniso_U_23
_atom_site_aniso_U_33 (*numb, su*)

These are the standard anisotropic atomic displacement components in ångströms squared which appear in the structure-factor term

$$T = \exp\Big\{-2\pi^2\sum_i\Big[\sum_j(U^{ij}h_ih_ja_i^*a_j^*)\Big]\Big\},$$

where h = the Miller indices and a^* = the reciprocal-space cell lengths.

The unique elements of the real symmetric matrix are entered by row.

Appears in list containing **_atom_site_aniso_label**.

Related item: **_atom_site_aniso_B_** (conversion). **[atom_site]**

_atom_site_attached_hydrogens (*numb*)

The number of hydrogen atoms attached to the atom at this site excluding any hydrogen atoms for which coordinates (measured or calculated) are given.

Appears in list containing **_atom_site_label**.

The permitted range is $0 \rightarrow 8$. Where no value is given, the assumed value is '0'.

Examples: '2' (water oxygen), '1' (hydroxyl oxygen), '4' (ammonium nitrogen).

[atom_site]

_atom_site_B_equiv_geom_mean (*numb, su*)

Equivalent isotropic atomic displacement parameter, $B_{\rm equiv}$, in ångströms squared, calculated as the geometric mean of the anisotropic atomic displacement parameters.

$$B_{\rm equiv} = (B_iB_jB_k)^{1/3},$$

where B_n = the principal components of the orthogonalized B^{ij}.

The IUCr Commission on Nomenclature recommends against the use of **B** for reporting atomic displacement parameters. **U**, being directly proportional to **B**, is preferred.

Appears in list containing **_atom_site_label**.

The permitted range is $0.0 \rightarrow \infty$.

Related items:

_atom_site_B_iso_or_equiv (alternate),
_atom_site_U_equiv_geom_mean (conversion). **[atom_site]**

_atom_site_B_iso_or_equiv (*numb, su*)

Isotropic atomic displacement parameter, or equivalent isotropic atomic displacement parameter, $B_{\rm equiv}$, in ångströms squared, calculated from anisotropic displacement components.

$$B_{\rm equiv} = (1/3)\sum_i\Big[\sum_j(B^{ij}A_iA_ja_i^*a_j^*)\Big],$$

where A = the real-space cell lengths and a^* = the reciprocal-space cell lengths; $B^{ij} = 8\pi^2U^{ij}$.

Reference: Fischer, R. X. & Tillmanns, E. (1988). *Acta Cryst.* C**44**, 775–776.

The IUCr Commission on Nomenclature recommends against the use of **B** for reporting atomic displacement parameters. **U**, being directly proportional to **B**, is preferred.

Appears in list containing **_atom_site_label**.

The permitted range is $0.0 \rightarrow \infty$.

Related items:

_atom_site_B_equiv_geom_mean (alternate),
_atom_site_U_iso_or_equiv (conversion). **[atom_site]**

_atom_site_calc_attached_atom (*char*)

The **_atom_site_label** of the atom site to which the 'geometry-calculated' atom site is attached.

Appears in list containing **_atom_site_label**. Where no value is given, the assumed value is '.'. **[atom_site]**

_atom_site_calc_flag (*char*)

A standard code to signal whether the site coordinates have been determined from the intensities or calculated from the geometry of surrounding sites, or have been assigned dummy coordinates. The abbreviation 'c' may be used in place of 'calc'.

Appears in list containing **_atom_site_label**.

The data value must be one of the following:

d	determined from diffraction measurements
calc	calculated from molecular geometry
c	abbreviation for 'calc'
dum	dummy site with meaningless coordinates

Where no value is given, the assumed value is 'd'. **[atom_site]**

_atom_site_Cartn_x
_atom_site_Cartn_y
_atom_site_Cartn_z (*numb, su*)

The atom-site coordinates in ångströms specified according to a set of orthogonal Cartesian axes related to the cell axes as specified by the **_atom_sites_Cartn_transform_axes** description.

Appears in list containing **_atom_site_label**.

Related item: **_atom_site_fract_** (alternate). **[atom_site]**

_atom_site_chemical_conn_number (*numb*)

This number links an atom site to the chemical connectivity list. It must match a number specified by **_chemical_conn_atom_number**.

Appears in list containing **_atom_site_label**. **Must** match parent data name **_chemical_conn_atom_number**.

The permitted range is $1 \rightarrow \infty$. **[atom_site]**

_atom_site_constraints (*char*)

A description of the constraints applied to parameters at this site during refinement. See also **_atom_site_refinement_flags** and **_refine_ls_number_constraints**.

Appears in list containing **_atom_site_label**. Where no value is given, the assumed value is '.'.

Example: 'pop=1.0-pop(Zn3)'. **[atom_site]**

_atom_site_description (*char*)

A description of special aspects of this site. See also **_atom_site_refinement_flags**.

Appears in list containing **_atom_site_label**.

Example: 'Ag/Si disordered'. **[atom_site]**

_atom_site_disorder_assembly (*char*)

A code which identifies a cluster of atoms that show long-range positional disorder but are locally ordered. Within each such cluster of atoms, **_atom_site_disorder_group** is used to identify the sites that are simultaneously occupied. This field is only needed if there is more than one cluster of disordered atoms showing independent local order.

Appears in list containing **_atom_site_label**.

Examples: 'A' (disordered methyl assembly with groups 1 and 2), 'B' (disordered sites related by a mirror), 'S' (disordered sites independent of symmetry). **[atom_site]**

_atom_site_disorder_group (*char*)

A code which identifies a group of positionally disordered atom sites that are locally simultaneously occupied. Atoms that are positionally disordered over two or more sites (*e.g.* the hydrogen atoms of a methyl group that exists in two orientations) can be assigned to two or more groups. Sites belonging to the same group are simultaneously occupied, but those belonging to different groups are not. A minus prefix (*e.g.* '-1') is used to indicate sites disordered about a special position.

Appears in list containing **_atom_site_label**.

Examples: '1' (unique disordered site in group 1), '2' (unique disordered site in group 2), '-1' (symmetry-independent disordered site). **[atom_site]**

_atom_site_distributed_density_id (*char*)

An identifier that links the atom defined by **_atom_site_label** with the distributed density of this atom defined in the DISTRIBUTED_DENSITY category. Note that all the atoms that give rise to a particular distributed density, *e.g.* a ring, should be included in the ATOM_SITE list, even when they, or the centroid of the distribution, lie on a special position. That is, the crystallographic site symmetry of the distribution is not used to generate the full distributed density shape from the crystallographic asymmetric portion. The value of **_atom_site_symmetry_multiplicity** should be chosen so that for each of the atoms in the ATOM_SITE list (**_atom_site_occupancy**)* (**_atom_site_symmetry_multiplicity**) is equal to its contribution to (**_chemical_formula_sum**)* (**_cell_formula_units_Z**).

Appears in list. containing **_atom_site_label**. **Must** match parent data name **_distributed_density_id**.

Example: 'an1' (see example in category DISTRIBUTED_DENSITY). **[atom_site]**

_atom_site_fract_x
_atom_site_fract_y
_atom_site_fract_z (*numb, su*)

Atom-site coordinates as fractions of the **_cell_length_** values.

Appears in list containing **_atom_site_label**.

Related item: **_atom_site_Cartn_** (alternate). **[atom_site]**

_atom_site_label (*char*)

The **_atom_site_label** is a unique identifier for a particular site in the crystal. This code is made up of a sequence of up to seven components, **_atom_site_label_component_0** to ***_6**, which may be specified as separate data items. Component 0 usually matches one of the specified **_atom_type_symbol** codes. This is not mandatory if an **_atom_site_type_symbol** item is included in the atom-site list. The **_atom_site_type_symbol** always takes precedence over an **_atom_site_label** in the identification of the atom type. The label components 1 to 6 are optional, and normally only components 0 and 1 are used. Note that components 0 and 1 are concatenated, while all other components, if specified, are separated by an underscore. Underscore separators are only used if higher-order components exist. If an intermediate component is not used, it may be omitted provided the underscore separators are inserted. For example, the label 'C233__ggg' is acceptable and represents the components C, 233, '' and ggg. Different labels may have a different number of components.

Appears in list as essential element of loop structure. May match child data name(s):
_atom_site_aniso_label, **_geom_angle_atom_site_label_1**, **_geom_angle_atom_site_label_2**, **_geom_angle_atom_site_label_3**, **_geom_bond_atom_site_label_1**, **_geom_bond_atom_site_label_2**, **_geom_contact_atom_site_label_1**, **_geom_contact_atom_site_label_2**, **_geom_hbond_atom_site_label_D**, **_geom_hbond_atom_site_label_H**, **_geom_hbond_atom_site_label_A**, **_geom_torsion_atom_site_label_1**, **_geom_torsion_atom_site_label_2**, **_geom_torsion_atom_site_label_3**, **_geom_torsion_atom_site_label_4**.

Examples: 'C12', 'Ca3g28', 'Fe3+17', 'H*251', 'boron2a', 'C_a_phe_83_a_0', 'Zn_Zn_301_A_0'. **[atom_site]**

_atom_site_label_component_0
_atom_site_label_component_1
_atom_site_label_component_2
_atom_site_label_component_3
_atom_site_label_component_4
_atom_site_label_component_5
_atom_site_label_component_6 (*char*)

Component 0 is normally a code which matches identically with one of the **_atom_type_symbol** codes. If this is the case, then the rules governing the **_atom_type_symbol** code apply. If, however, the data item **_atom_site_type_symbol** is also specified in the atom-site list, component 0 need not match this symbol or adhere to any of the **_atom_type_symbol** rules. Component 1 is referred to as the 'atom number'. When component 0 is the atom-type code, it is used to number the sites with the same atom type. This component code must start with at least one digit which is not followed by a + or - sign (to distinguish it from the component 0 rules). Components 2 to 6 contain the identifier, residue, sequence, asymmetry identifier and alternate codes, respectively. These codes may be composed of any characters except an underscore.

Appears in list containing **_atom_site_label**. **[atom_site]**

_atom_site_occupancy (*numb, su*)

The fraction of the atom type present at this site. The sum of the occupancies of all the atom types at this site may not significantly exceed 1.0 unless it is a dummy site. The value must lie in the 99.97% Gaussian confidence interval $-3u \leq x \leq 1 + 3u$. The **_enumeration_range** of $0.0 \rightarrow 1.0$ is thus correctly interpreted as meaning $(0.0 - 3u) \leq x \leq (1.0 + 3u)$.

Appears in list containing **_atom_site_label**.

The permitted range is $0.0 \rightarrow 1.0$. Where no value is given, the assumed value is '1.0'. **[atom_site]**

_atom_site_refinement_flags (*char*)

This definition has been superseded and is retained here only for archival purposes. Use instead _atom_site_refinement_flags_posn, _atom_site_refinement_flags_adp, _atom_site_refinement_flags_occupancy.

*A concatenated series of single-letter codes which indicate the refinement restraints or constraints applied to this site. This item should not be used. It has been replaced by _atom_site_refinement_flags_posn, *_adp and *_occupancy. It is retained in this dictionary only to provide compatibility with legacy CIFs.*

Appears in list containing _atom_site_label.

The data value must be one of the following:

.	*no refinement constraints*
S	*special-position constraint on site*
G	*rigid-group refinement of site*
R	*riding-atom site attached to non-riding atom*
D	*distance or angle restraint on site*
T	*thermal displacement constraints*
U	U_{iso} *or* U^{ij} *restraint (rigid bond)*
P	*partial occupancy constraint*

[atom_site]

_atom_site_refinement_flags_adp (*char*)

A code which indicates the refinement restraints or constraints applied to the atomic displacement parameters of this site.

Appears in list containing **_atom_site_label**.

Related item: **_atom_site_refinement_flags** (alternate).

The data value must be one of the following:

.	no constraints on atomic displacement parameters
T	special-position constraints on atomic displacement parameters
U	U_{iso} or U^{ij} restraint (rigid bond)
TU	both constraints applied

[atom_site]

_atom_site_refinement_flags_occupancy (*char*)

A code which indicates that refinement restraints or constraints were applied to the occupancy of this site.

Appears in list containing **_atom_site_label**.

Related item: **_atom_site_refinement_flags** (alternate).

The data value must be one of the following:

.	no constraints on site-occupancy parameters
P	site-occupancy constraint

[atom_site]

_atom_site_refinement_flags_posn (*char*)

A code which indicates the refinement restraints or constraints applied to the positional coordinates of this site.

Appears in list containing **_atom_site_label**.

Related item: **_atom_site_refinement_flags** (alternate).

The data value must be one of the following:

.	no constraints on positional coordinates
D	distance or angle restraint on positional coordinates
G	rigid-group refinement of positional coordinates
R	riding-atom site attached to non-riding atom
S	special-position constraint on positional coordinates
DG	combination of the above constraints
DR	combination of the above constraints
DS	combination of the above constraints
GR	combination of the above constraints
GS	combination of the above constraints
RS	combination of the above constraints
DGR	combination of the above constraints
DGS	combination of the above constraints
DRS	combination of the above constraints
GRS	combination of the above constraints
DGRS	combination of the above constraints

[atom_site]

_atom_site_restraints (*char*)

A description of restraints applied to specific parameters at this site during refinement. See also **_atom_site_refinement_flags** and **_refine_ls_number_restraints**.

Appears in list containing **_atom_site_label**.

Example: 'restrained to planar ring'. **[atom_site]**

_atom_site_symmetry_multiplicity (*numb*)

The multiplicity of a site due to the space-group symmetry as given in *International Tables for Crystallography* Vol. A (2002).

Appears in list containing **_atom_site_label**.

The permitted range is 1 → 192. **[atom_site]**

_atom_site_thermal_displace_type (*char*)

This definition has been superseded and is retained here only for archival purposes. Use instead _atom_site_adp_type.

A standard code used to describe the type of atomic displacement parameters used for the site.

Appears in list containing _atom_site_label.

The data value must be one of the following:

Uani	*anisotropic* U^{ij}
Uiso	*isotropic U*
Uovl	*overall U*
Umpe	*multipole expansion U*
Bani	*anisotropic* B^{ij}
Biso	*isotropic B*
Bovl	*overall B*

[atom_site]

_atom_site_type_symbol (*char*)

A code to identify the atom species (singular or plural) occupying this site. This code must match a corresponding **_atom_type_symbol**. The specification of this code is optional if component 0 of the **_atom_site_label** is used for this purpose. See **_atom_type_symbol**.

Appears in list containing **_atom_site_label**. **Must** match parent data name **_atom_type_symbol**. May match child data name(s): **_atom_site_aniso_type_symbol**.

Examples: 'Cu', 'Cu2+', 'dummy', 'Fe3+Ni2+', 'S-', 'H*', 'H(SDS)'. **[atom_site]**

_atom_site_U_equiv_geom_mean (*numb, su*)

Equivalent isotropic atomic displacement parameter, U_{equiv}, in ångströms squared, calculated as the geometric mean of the anisotropic atomic displacement parameters.

$$U_{equiv} = (U_i U_j U_k)^{1/3},$$

where U_n = the principal components of the orthogonalized U^{ij}.

Appears in list containing **_atom_site_label**.

The permitted range is 0.0 → ∞.

Related items:

_atom_site_U_iso_or_equiv (alternate),
_atom_site_B_equiv_geom_mean (conversion). **[atom_site]**

_atom_site_U_iso_or_equiv (*numb, su*)

Isotropic atomic displacement parameter, or equivalent isotropic atomic displacement parameter, U_{equiv}, in ångströms squared, calculated from anisotropic atomic displacement parameters.

$$U_{equiv} = (1/3) \sum_i \left[\sum_j (U^{ij} A_i A_j a_i^* a_j^*) \right],$$

where A = the real-space cell lengths and a^* = the reciprocal-space cell lengths.

Reference: Fischer, R. X. & Tillmanns, E. (1988). *Acta Cryst.* C**44**, 775–776.

Appears in list containing **_atom_site_label**.

The permitted range is 0.0 → ∞.

Related items:

_atom_site_U_equiv_geom_mean (alternate),
_atom_site_B_iso_or_equiv (conversion). **[atom_site]**

_atom_site_Wyckoff_symbol (*char*)

The Wyckoff symbol (letter) as listed in the space-group tables of *International Tables for Crystallography* Vol. A (2002).

Appears in list containing **_atom_site_label**. **[atom_site]**

ATOM_SITES

Data items in the ATOM_SITES category record details about the crystallographic cell and cell transformations, which are common to all atom sites.

Example 1 – based on PDB entry 5HVP and laboratory records for the structure corresponding to PDB entry 5HVP.

```
_atom_sites_Cartn_transform_axes
      'c along z, astar along x, b along y'

_atom_sites_Cartn_tran_matrix_11    58.39
_atom_sites_Cartn_tran_matrix_12     0.00
_atom_sites_Cartn_tran_matrix_13     0.00
_atom_sites_Cartn_tran_matrix_21     0.00
_atom_sites_Cartn_tran_matrix_22    86.70
_atom_sites_Cartn_tran_matrix_23     0.00
_atom_sites_Cartn_tran_matrix_31     0.00
_atom_sites_Cartn_tran_matrix_32     0.00
_atom_sites_Cartn_tran_matrix_33    46.27
```

_atom_sites_Cartn_tran_matrix_11
_atom_sites_Cartn_tran_matrix_12
_atom_sites_Cartn_tran_matrix_13
_atom_sites_Cartn_tran_matrix_21
_atom_sites_Cartn_tran_matrix_22
_atom_sites_Cartn_tran_matrix_23
_atom_sites_Cartn_tran_matrix_31
_atom_sites_Cartn_tran_matrix_32
_atom_sites_Cartn_tran_matrix_33 (*numb*)

Matrix elements used to transform fractional coordinates in the ATOM_SITE category to Cartesian coordinates. The axial alignments of this transformation are described in **_atom_sites_Cartn_transform_axes**. The 3 × 1 translation is defined in **_atom_sites_Cartn_tran_vector_**.

$$\begin{pmatrix} x' \\ y' \\ z' \end{pmatrix}_{\text{Cartesian}} = \begin{pmatrix} 11 & 12 & 13 \\ 21 & 22 & 23 \\ 31 & 32 & 33 \end{pmatrix} \begin{pmatrix} x \\ y \\ z \end{pmatrix}_{\text{fractional}} + \begin{pmatrix} 1 \\ 2 \\ 3 \end{pmatrix}.$$

[atom_sites]

_atom_sites_Cartn_tran_vector_1
_atom_sites_Cartn_tran_vector_2
_atom_sites_Cartn_tran_vector_3 (*numb*)

Elements of a 3 × 1 translation vector used in the transformation of fractional coordinates in the ATOM_SITE category to Cartesian coordinates. The axial alignments of this transformation are described in **_atom_sites_Cartn_transform_axes**.

$$\begin{pmatrix} x' \\ y' \\ z' \end{pmatrix}_{\text{fractional}} = \begin{pmatrix} 11 & 12 & 13 \\ 21 & 22 & 23 \\ 31 & 32 & 33 \end{pmatrix} \begin{pmatrix} x \\ y \\ z \end{pmatrix}_{\text{Cartesian}} + \begin{pmatrix} 1 \\ 2 \\ 3 \end{pmatrix}.$$

[atom_sites]

_atom_sites_Cartn_transform_axes (*char*)

A description of the relative alignment of the crystal cell axes to the Cartesian orthogonal axes as applied in the transformation matrix **_atom_sites_Cartn_tran_matrix_**.

Example: 'a parallel to x; b in the plane of y and z'.

[atom_sites]

_atom_sites_fract_tran_matrix_11
_atom_sites_fract_tran_matrix_12
_atom_sites_fract_tran_matrix_13
_atom_sites_fract_tran_matrix_21
_atom_sites_fract_tran_matrix_22
_atom_sites_fract_tran_matrix_23
_atom_sites_fract_tran_matrix_31
_atom_sites_fract_tran_matrix_32
_atom_sites_fract_tran_matrix_33 (*numb*)

Matrix elements used to transform Cartesian coordinates in the ATOM_SITE category to fractional coordinates. The axial alignments of this transformation are described in **_atom_sites_Cartn_transform_axes**. The 3 × 1 translation is defined in **_atom_sites_fract_tran_vector_**.

$$\begin{pmatrix} x' \\ y' \\ z' \end{pmatrix}_{\text{fractional}} = \begin{pmatrix} 11 & 12 & 13 \\ 21 & 22 & 23 \\ 31 & 32 & 33 \end{pmatrix} \begin{pmatrix} x \\ y \\ z \end{pmatrix}_{\text{Cartesian}} + \begin{pmatrix} 1 \\ 2 \\ 3 \end{pmatrix}.$$

[atom_sites]

_atom_sites_fract_tran_vector_1
_atom_sites_fract_tran_vector_2
_atom_sites_fract_tran_vector_3 (*numb*)

Elements of a 3 × 1 translation vector used in the transformation of Cartesian coordinates in the ATOM_SITE category to fractional coordinates. The axial alignments of this transformation are described in **_atom_sites_Cartn_transform_axes**.

$$\begin{pmatrix} x' \\ y' \\ z' \end{pmatrix}_{\text{fractional}} = \begin{pmatrix} 11 & 12 & 13 \\ 21 & 22 & 23 \\ 31 & 32 & 33 \end{pmatrix} \begin{pmatrix} x \\ y \\ z \end{pmatrix}_{\text{Cartesian}} + \begin{pmatrix} 1 \\ 2 \\ 3 \end{pmatrix}.$$

[atom_sites]

_atom_sites_solution_primary
_atom_sites_solution_secondary
_atom_sites_solution_hydrogens (*char*)

Codes which identify the methods used to locate the initial atom sites. The ***_primary** code identifies how the first atom sites were determined; the ***_secondary** code identifies how the remaining non-hydrogen sites were located; and the ***_hydrogens** code identifies how the hydrogen sites were located.

Reference: Sheldrick, G. M., Hauptman, H. A., Weeks, C. M., Miller, R. and Usón, I. (2001). Ab initio phasing. In *International Tables for Crystallography*, Vol. F. *Crystallography of biological macromolecules*, edited by M. G. Rossmann and E. Arnold, ch. 16.1. Dordrecht: Kluwer Academic Publishers.

The data value must be one of the following:

`difmap`	difference Fourier map
`vecmap`	real-space vector search
`heavy`	heavy-atom method
`direct`	structure-invariant direct methods
`geom`	inferred from neighbouring sites
`disper`	anomalous-dispersion techniques
`isomor`	isomorphous structure methods
`notdet`	coordinates were not determined
`dual`	dual-space method (Sheldrick et al., 2001)
`other`	a method not included elsewhere in this list

[atom_sites]

_atom_sites_special_details (*char*)

Additional information about the atomic coordinates not coded elsewhere in the CIF.

[atom_sites]

ATOM_TYPE

Data items in the ATOM_TYPE category record details about properties of the atoms that occupy the atom sites, such as the atomic scattering factors.

Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C47, 2276–2277].

```
loop_
_atom_type_symbol
_atom_type_oxidation_number
_atom_type_number_in_cell
_atom_type_scat_dispersion_real
_atom_type_scat_dispersion_imag
_atom_type_scat_source
  C 0 72  .017  .009  International_Tables_Vol_IV_Table_2.2B
  H 0 100  0     0    International_Tables_Vol_IV_Table_2.2B
  O 0 12  .047  .032  International_Tables_Vol_IV_Table_2.2B
  N 0 4   .029  .018  International_Tables_Vol_IV_Table_2.2B
```

_atom_type_analytical_mass_% (*numb*)
Mass percentage of this atom type derived from chemical analysis.
Appears in list containing **_atom_type_symbol**.
The permitted range is 0.0 → 100.0. **[atom_type]**

_atom_type_description (*char*)
A description of the atom(s) designated by this atom type. In most cases, this will be the element name and oxidation state of a single atom species. For disordered or nonstoichiometric structures it will describe a combination of atom species.
Appears in list containing **_atom_type_symbol**.
Examples: 'deuterium', '0.34Fe+0.66Ni'. **[atom_type]**

_atom_type_number_in_cell (*numb*)
Total number of atoms of this atom type in the unit cell.
Appears in list containing **_atom_type_symbol**.
The permitted range is 0 → ∞. **[atom_type]**

_atom_type_oxidation_number (*numb*)
Formal oxidation state of this atom type in the structure.
Appears in list containing **_atom_type_symbol**.
The permitted range is −8 → 8. Where no value is given, the assumed value is '0'.
[atom_type]

_atom_type_radius_bond
_atom_type_radius_contact (*numb*)
The effective intra- and intermolecular bonding radii in ångströms of this atom type.
Appears in list containing **_atom_type_symbol**.
The permitted range is 0.0 → 5.0. **[atom_type]**

_atom_type_scat_Cromer_Mann_a1
_atom_type_scat_Cromer_Mann_a2
_atom_type_scat_Cromer_Mann_a3
_atom_type_scat_Cromer_Mann_a4
_atom_type_scat_Cromer_Mann_b1
_atom_type_scat_Cromer_Mann_b2
_atom_type_scat_Cromer_Mann_b3
_atom_type_scat_Cromer_Mann_b4
_atom_type_scat_Cromer_Mann_c (*numb*)
The Cromer–Mann scattering-factor coefficients used to calculate the scattering factors for this atom type.

References: *International Tables for X-ray Crystallography* (1974). Vol. IV, Table 2.2B; *International Tables for Crystallography* (2004). Vol. C, Tables 6.1.1.4 and 6.1.1.5.
Appears in list containing **_atom_type_symbol**. **[atom_type]**

_atom_type_scat_dispersion_imag
_atom_type_scat_dispersion_real (*numb*)
The imaginary and real components of the anomalous-dispersion scattering factor, f'' and f', in electrons for this atom type and the radiation given in **_diffrn_radiation_wavelength**.
Appears in list containing **_atom_type_symbol**. Where no value is given, the assumed value is '0.0'. **[atom_type]**

_atom_type_scat_dispersion_source (*char*)
Reference to source of real and imaginary dispersion corrections for scattering factors used for this atom type.
Appears in list containing **_atom_type_symbol**.
Example: 'International Tables Vol. IV Table 2.3.1'. **[atom_type]**

_atom_type_scat_length_neutron (*numb*)
The bound coherent scattering length in femtometres for the atom type at the isotopic composition used for the diffraction experiment.
Appears in list containing **_atom_type_symbol**. Where no value is given, the assumed value is '0.0'. **[atom_type]**

_atom_type_scat_source (*char*)
Reference to source of scattering factors or scattering lengths used for this atom type.
Appears in list containing **_atom_type_symbol**.
Example: 'International Tables Vol. IV Table 2.4.6B'. **[atom_type]**

_atom_type_scat_versus_stol_list (*char*)
A table of scattering factors as a function of $(\sin\theta)/\lambda$. This table should be well commented to indicate the items present. Regularly formatted lists are strongly recommended.
Appears in list containing **_atom_type_symbol**. **[atom_type]**

_atom_type_symbol (*char*)
The code used to identify the atom species (singular or plural) representing this atom type. Normally this code is the element symbol. The code may be composed of any character except an underscore with the additional proviso that digits designate an oxidation state and must be followed by a + or - character.
Appears in list as essential element of loop structure. May match child data name(s): **_atom_site_type_symbol**.
Examples: 'C', 'Cu2+', 'H(SDS)', 'dummy', 'FeNi'. **[atom_type]**

AUDIT

Data items in the AUDIT category record details about the creation and subsequent updating of the data block.

Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C47, 2276–2277].

```
_audit_block_code                 TOZ_1991-03-20

_audit_creation_date              1991-03-20
_audit_creation_method   from_xtal_archive_file_using_CIFIO
_audit_update_record
; 1991-04-09     text and data added by Tony Willis.
  1991-04-15     rec'd by co-editor as manuscript HL0007.
  1991-04-17     adjustments based on first referee report.
  1991-04-18     adjustments based on second referee report.
;
```

_audit_block_code (*char*)
A code intended to identify uniquely the current data block.
Example: 'TOZ_1991-03-20'. **[audit]**

_audit_creation_date (*char*)
The date that the data block was created. The date format is *yyyy-mm-dd*.
Example: '1990-07-12'. **[audit]**

_audit_creation_method (*char*)
A description of how data were entered into the data block.
Example: 'spawned by the program QBEE'. **[audit]**

_audit_update_record (*char*)
A record of any changes to the data block. The update format is a date (*yyyy-mm-dd*) followed by a description of the changes. The latest update entry is added to the bottom of this record.
Example: '1990-07-15 Updated by the Co-editor'. **[audit]**

AUDIT_AUTHOR

Data items in the AUDIT_AUTHOR category record details about the author(s) of the data block.

Example 1 – based on PDB entry 5HVP and laboratory records for the structure corresponding to PDB entry 5HVP.

```
loop_
_audit_author_name
_audit_author_address
    'Fitzgerald, Paula M. D.'
;  Department of Biophysical Chemistry
   Merck Research Laboratories
   PO Box 2000, Ry80M203
   Rahway
   New Jersey 07065
   USA
;
    'Van Middlesworth, J. F.'
;  Department of Biophysical Chemistry
   Merck Research Laboratories
   PO Box 2000, Ry80M203
   Rahway
   New Jersey 07065
   USA
;
```

_audit_author_address (*char*)
The address of an author of this data block. If there are multiple authors, **_audit_author_address** is looped with **_audit_author_name**.
Appears in list containing **_audit_author_name**.
Example:

```
; Department
  Institute
  Street
  City and postcode
  COUNTRY
;
```

[audit_author]

_audit_author_name (*char*)
The name of an author of this data block. If there are multiple authors, **_audit_author_name** is looped with **_audit_author_address**. The family name(s), followed by a comma and including any dynastic components, precedes the first name(s) or initial(s).
Appears in list as essential element of loop structure.
Examples: 'Bleary, Percival R.', 'O'Neil, F.K.', 'Van den Bossche, G.', 'Yang, D.-L.', 'Simonov, Yu.A.', 'M\"uller, H.A.', 'Ross II, C.R.'.
[audit_author]

AUDIT_CONFORM

Data items in the AUDIT_CONFORM category describe the dictionary versions against which the data names appearing in the current data block are conformant.

Example 1 – any file conforming to the current CIF core dictionary.

```
_audit_conform_dict_name          cif_core.dic
_audit_conform_dict_version       2.3.1
_audit_conform_dict_location
      ftp://ftp.iucr.org/pub/cif_core.2.3.1.dic
```

_audit_conform_dict_location (*char*)
A file name or uniform resource locator (URL) for the dictionary to which the current data block conforms.
May appear in list containing **_audit_conform_dict_name**. **[audit_conform]**

_audit_conform_dict_name (*char*)
The string identifying the highest-level dictionary defining data names used in this file.
May appear in list as essential element of loop structure. **[audit_conform]**

_audit_conform_dict_version (*char*)
The version number of the dictionary to which the current data block conforms.
May appear in list containing **_audit_conform_dict_name**. **[audit_conform]**

AUDIT_CONTACT_AUTHOR

Data items in the AUDIT_CONTACT_AUTHOR category record details about the name and address of the author to be contacted concerning the contents of this data block.

Example 1 – based on PDB entry 5HVP and laboratory records for the structure corresponding to PDB entry 5HVP.

```
loop_
_audit_contact_author_name
_audit_contact_author_address
_audit_contact_author_email
_audit_contact_author_fax
_audit_contact_author_phone
    'Fitzgerald, Paula M. D.'
;  Department of Biophysical Chemistry
   Merck Research Laboratories
   PO Box 2000, Ry80M203
   Rahway
   New Jersey 07065
   USA
;
    'paula_fitzgerald@merck.com'
    '1(908)5945510'
    '1(908)5945510'
```

_audit_contact_author_address (*char*)
The mailing address of the author of the data block to whom correspondence should be addressed.
Example:

```
; Department
  Institute
  Street
  City and postcode
  COUNTRY
;
```

[audit_contact_author]

_audit_contact_author_email (*char*)
The electronic mail address of the author of the data block to whom correspondence should be addressed, in a form recognizable to international networks. The format of e-mail addresses is given in Section 3.4, *Address Specification*, of *Internet Message Format*, RFC 2822, P. Resnick (Editor), Network Standards Group, April 2001.
Examples: 'name@host.domain.country', 'bm@iucr.org'.
[audit_contact_author]

_audit_contact_author_fax (*char*)
The facsimile telephone number of the author of the data block to whom correspondence should be addressed. The recommended style starts with the international dialing prefix, followed by the area code in parentheses, followed by the local number with no spaces.
Examples: '12(34)9477334', '12()349477334'. **[audit_contact_author]**

_audit_contact_author_name (*char*)
The name of the author of the data block to whom correspondence should be addressed. The family name(s), followed by a comma and including any dynastic components, precedes the first name(s) or initial(s).
Examples: 'Bleary, Percival R.', 'O'Neil, F.K.', 'Van den Bossche, G.', 'Yang, D.-L.', 'Simonov, Yu.A.', 'M\"uller, H.A.', 'Ross II, C.R.'.
[audit_contact_author]

_audit_contact_author_phone (*char*)
The telephone number of the author of the data block to whom correspondence should be addressed. The recommended style starts with the international dialing prefix, followed by the area code in parentheses, followed by the local number and any extension number prefixed by 'x', with no spaces.
Examples: '12(34)9477330', '12()349477330', '12(34)9477330x5543'.
[audit_contact_author]

AUDIT_LINK

Data items in the AUDIT_LINK category record details about the relationships between data blocks in the current CIF.

Example 1 – multiple structure paper, as illustrated in A Guide to CIF for Authors (1995). IUCr: Chester.

```
loop_
_audit_link_block_code
_audit_link_block_description
   .         'discursive text of paper with two structures'
   morA_(1)  'structure 1 of 2'
   morA_(2)  'structure 2 of 2'
```

Example 2 – example file for the one-dimensional incommensurately modulated structure of K_2SeO_4.

```
loop_
_audit_link_block_code
_audit_link_block_description
  .       'publication details'
  KSE_COM 'experimental data common to ref./mod. structures'
  KSE_REF 'reference structure'
  KSE_MOD 'modulated structure'
```

_audit_link_block_code (*char*)
The value of **_audit_block_code** associated with a data block in the current file related to the current data block. The special value '.' may be used to refer to the current data block for completeness.
Appears in list as essential element of loop structure. **[audit_link]**

_audit_link_block_description (*char*)
A textual description of the relationship of the referenced data block to the current one.
Appears in list containing **_audit_link_block_code**. **[audit_link]**

CELL

Data items in the CELL category record details about the crystallographic cell parameters and their measurement.

Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C47, 2276–2277].

```
_cell_length_a                    5.959(1)
_cell_length_b                    14.956(1)
_cell_length_c                    19.737(3)
_cell_angle_alpha                 90
_cell_angle_beta                  90
_cell_angle_gamma                 90
_cell_volume                      1759.0(3)

_cell_measurement_temperature     293
_cell_measurement_reflns_used     25
_cell_measurement_theta_min       25
_cell_measurement_theta_max       31
```

_cell_angle_alpha
_cell_angle_beta
_cell_angle_gamma (*numb, su*)
Unit-cell angles of the reported structure in degrees. The values of **_refln_index_h**, ***_k**, ***_l** must correspond to the cell defined by these values and **_cell_length_a**, ***_b** and ***_c**. The values of **_diffrn_refln_index_h**, ***_k**, ***_l** may not correspond to these values if a cell transformation took place following the measurement of the diffraction intensities. See also **_diffrn_reflns_transf_matrix_**.
The permitted range is 0.0 → 180.0. Where no value is given, the assumed value is '90.0'.
[cell]

_cell_formula_units_Z (*numb*)
The number of the formula units in the unit cell as specified by **_chemical_formula_structural**, **_chemical_formula_moiety** or **_chemical_formula_sum**.
The permitted range is 1 → ∞. **[cell]**

_cell_length_a
_cell_length_b
_cell_length_c (*numb, su*)
Unit-cell lengths in ångströms corresponding to the structure reported. The values of **_refln_index_h**, ***_k**, ***_l** must correspond to the cell defined by these values and **_cell_angle_** values. The values of **_diffrn_refln_index_h**, ***_k**, ***_l** may not correspond to these values if a cell transformation took place following the measurement of the diffraction intensities. See also **_diffrn_reflns_transf_matrix_**.
The permitted range is 0.0 → ∞. **[cell]**

_cell_measurement_pressure (*numb, su*)
The pressure in kilopascals at which the unit-cell parameters were measured (not the pressure at which the sample was synthesized).
The permitted range is 0.0 → ∞. **[cell]**

_cell_measurement_radiation (*char*)
Description of the radiation used to measure the unit-cell data. See also **_cell_measurement_wavelength**.
Examples: 'neutron', 'Cu K\a', 'synchrotron'. **[cell]**

_cell_measurement_reflns_used (*numb*)
The total number of reflections used to determine the unit cell. These reflections may be specified as **_cell_measurement_refln_** data items.
[cell]

_cell_measurement_temperature (*numb, su*)
The temperature in kelvins at which the unit-cell parameters were measured (not the temperature of synthesis).
The permitted range is 0.0 → ∞. **[cell]**

_cell_measurement_theta_max
_cell_measurement_theta_min (*numb*)
The maximum and minimum θ angles of reflections used to measure the unit cell in degrees.
The permitted range is 0.0 → 90.0. **[cell]**

_cell_measurement_wavelength (*numb*)
The wavelength in ångströms of the radiation used to measure the unit cell. If this is not specified, the wavelength is assumed to be the same as that given in **_diffrn_radiation_wavelength**.
The permitted range is 0.0 → ∞. **[cell]**

_cell_reciprocal_angle_alpha
_cell_reciprocal_angle_beta
_cell_reciprocal_angle_gamma (*numb, su*)

The angles defining the reciprocal cell in degrees. These are related to those in the real cell by

$$\cos\alpha^* = (\cos\beta\cos\gamma - \cos\alpha)/(\sin\beta\sin\gamma),$$
$$\cos\beta^* = (\cos\gamma\cos\alpha - \cos\beta)/(\sin\gamma\sin\alpha),$$
$$\cos\gamma^* = (\cos\alpha\cos\beta - \cos\gamma)/(\sin\alpha\sin\beta).$$

Reference: Buerger, M. J. (1942). *X-ray Crystallography*, p. 360. New York: John Wiley & Sons Inc.

The permitted range is 0.0 → 180.0. Where no value is given, the assumed value is '90.0'.
[cell]

_cell_reciprocal_length_a
_cell_reciprocal_length_b
_cell_reciprocal_length_c (*numb, su*)

The reciprocal-cell lengths in inverse ångströms. These are related to the real cell by

$$a^* = bc\sin\alpha/V,$$
$$b^* = ca\sin\beta/V,$$
$$c^* = ab\sin\gamma/V,$$

where V is the cell volume.

Reference: Buerger, M. J. (1942). *X-ray Crystallography*, p. 360. New York: John Wiley & Sons Inc.

The permitted range is 0.0 → ∞. **[cell]**

_cell_special_details (*char*)

A description of special aspects of the cell choice, noting possible alternative settings.

Examples: 'pseudo-orthorhombic',
'standard setting from 45 deg rotation around c'. **[cell]**

_cell_volume (*numb, su*)

Cell volume V in ångströms cubed.

$$V = abc(1 - \cos^2\alpha - \cos^2\beta - \cos^2\gamma + 2\cos\alpha\cos\beta\cos\gamma)^{1/2},$$

where a = **_cell_length_a**, b = **_cell_length_b**, c = **_cell_length_c**, α = **_cell_angle_alpha**, β = **_cell_angle_beta** and γ = **_cell_angle_gamma**.

The permitted range is 0.0 → ∞. **[cell]**

CELL_MEASUREMENT_REFLN

Data items in the CELL_MEASUREMENT_REFLN category record details about the reflections used in the determination of the crystallographic cell parameters. The **_cell_measurement_refln_** data items would in general be used only for diffractometer measurements.

Example 1 – extracted from the CAD-4 listing for $Rb_2S_2O_6$ at room temperature (unpublished).

```
loop_
 _cell_measurement_refln_index_h
 _cell_measurement_refln_index_k
 _cell_measurement_refln_index_l
 _cell_measurement_refln_theta
   -2    4    1          8.67
    0    3    2          9.45
    3    0    2          9.46
   -3    4    1          8.93
   -2    1   -2          7.53
   10    0    0         23.77
    0   10    0         23.78
   -5    4    1         11.14
  # - - - - data truncated for brevity - - - -
```

_cell_measurement_refln_index_h
_cell_measurement_refln_index_k
_cell_measurement_refln_index_l (*numb*)

Miller indices of a reflection used for measurement of the unit cell.

Appears in list as essential element of loop structure. **[cell_measurement_refln]**

_cell_measurement_refln_theta (*numb*)

θ angle in degrees for the reflection used for measurement of the unit cell with the indices **_cell_measurement_refln_index_**.

Appears in list containing **_cell_measurement_refln_index_**.

The permitted range is 0.0 → 90.0. **[cell_measurement_refln]**

CHEMICAL

Data items in the CHEMICAL category record details about the composition and chemical properties of the compound. The formula data items must agree with those that specify the density, unit-cell and Z values.

Example 1 – based on data set 9597gaus of Alyea, Ferguson & Kannan [Acta Cryst. (1996), C52, 765–767].

```
_chemical_name_systematic
  trans-bis(tricyclohexylphosphine)tetracarbonylmolybdenum(0)
```

_chemical_absolute_configuration (*char*)

Necessary conditions for the assignment of **_chemical_absolute_configuration** are given by H. D. Flack and G. Bernardinelli (1999, 2000).

References: Flack, H. D. & Bernardinelli, G. (1999). *Acta Cryst.* A**55**, 908–915; Flack, H. D. & Bernardinelli, G. (2000). *J. Appl. Cryst.* **33**, 1143–1148.

The data value must be one of the following:

rm	Absolute configuration established by the structure determination of a compound containing a chiral reference molecule of known absolute configuration.
ad	Absolute configuration established by anomalous-dispersion effects in diffraction measurements on the crystal.
rmad	Absolute configuration established by the structure determination of a compound containing a chiral reference molecule of known absolute configuration and confirmed by anomalous-dispersion effects in diffraction measurements on the crystal.
syn	Absolute configuration has not been established by anomalous-dispersion effects in diffraction measurements on the crystal. The enantiomer has been assigned by reference to an unchanging chiral centre in the synthetic procedure.
unk	Absolute configuration is unknown, there being no firm chemical evidence for its assignment to hand and it having not been established by anomalous-dispersion effects in diffraction measurements on the crystal. An arbitrary choice of enantiomer has been made.
.	Inapplicable.

[chemical]

_chemical_compound_source (*char*)

Description of the source of the compound under study, or of the parent molecule if a simple derivative is studied. This includes the place of discovery for minerals or the actual source of a natural product.

Examples: 'From Norilsk (USSR)',
'Extracted from the bark of Cinchona Naturalis'. **[chemical]**

_chemical_enantioexcess_bulk (*numb, su*)

The enantioexcess of the bulk material from which the crystals were grown. A value of 0.0 indicates the racemate. A value of 1.0 indicates that the compound is enantiomerically pure. Enantioexcess is defined in the IUPAC Recommendations (1996). The composition of the crystal and bulk must be the same.

Reference: Moss G.P. *et al.* (1996). Basic Terminology of Stereochemistry. *Pure Appl. Chem.* **68**, 2193–2222. http://www.chem.qmul.ac.uk/iupac/stereo/index.html

The permitted range is 0.0 → 1.0. **[chemical]**

_chemical_enantioexcess_bulk_technique (*char*)
The experimental technique used to determine the enantioexcess of the bulk compound.
The data value must be one of the following:

OA	Enantioexcess determined by measurement of the specific rotation of the optical activity of the bulk compound in solution.
CD	Enantioexcess determined by measurement of the visible/near UV circular dichroism spectrum of the bulk compound in solution.
EC	Enantioexcess determined by enantioselective chromatography of the bulk compound in solution.
other	Enantioexcess determined by a technique not described in the enumeration list.

[chemical]

_chemical_enantioexcess_crystal (*numb, su*)
The enantioexcess of the crystal used for the diffraction study. A value of 0.0 indicates the racemate. A value of 1.0 indicates that the crystal is enantiomerically pure. Enantioexcess is defined in the IUPAC Recommendations (1996).

Reference: Moss G.P. *et al.* (1996). Basic Terminology of Stereochemistry. *Pure Appl. Chem.* **68**, 2193–2222. http://www.chem.qmul.ac.uk/iupac/stereo/index.html
The permitted range is 0.0 → 1.0. **[chemical]**

_chemical_enantioexcess_crystal_technique (*char*)
The experimental technique used to determine the enantioexcess of the crystal.
The data value must be one of the following:

CD	Enantioexcess determined by measurement of the visible/near UV circular dichroism spectrum of the crystal taken into solution.
EC	Enantioexcess determined by enantioselective chromatography of the crystal taken into solution.
other	Enantioexcess determined by a technique not described in the enumeration list.

[chemical]

_chemical_melting_point (*numb, su*)
The temperature in kelvins at which the crystalline solid changes to a liquid.
The permitted range is 0.0 → ∞. **[chemical]**

_chemical_melting_point_gt
_chemical_melting_point_lt (*numb*)
A temperature in kelvins below which (*_lt) or above which (*_gt) the melting point (the temperature at which the crystalline solid changes to a liquid) lies. These items allow a range of temperatures to be given. **_chemical_melting_point** should always be used in preference to these items whenever possible.
The permitted range is 0.0 → ∞.
Related item: **_chemical_melting_point** (alternate). **[chemical]**

_chemical_name_common (*char*)
Trivial name by which the compound is commonly known.
Example: '1-bromoestradiol'. **[chemical]**

_chemical_name_mineral (*char*)
Mineral name accepted by the International Mineralogical Association. Use only for natural minerals. See also **_chemical_compound_source**.
Example: 'chalcopyrite'. **[chemical]**

_chemical_name_structure_type (*char*)
Commonly used structure-type name. Usually only applied to minerals or inorganic compounds.
Examples: 'perovskite', 'sphalerite', 'A15'. **[chemical]**

_chemical_name_systematic (*char*)
IUPAC or *Chemical Abstracts* full name of the compound.
Example: '1-bromoestra-1,3,5(10)-triene-3,17\b-diol'. **[chemical]**

_chemical_optical_rotation (*char*)
The optical rotation in solution of the compound is specified in the following format:

$$[\alpha]^{\mathrm{TEMP}}_{\mathrm{WAVE}} = \mathrm{SORT} \quad (c = \mathrm{CONC},\ \mathrm{SOLV}),$$

where TEMP is the temperature of the measurement in degrees Celsius, WAVE is an indication of the wavelength of the light used for the measurement, CONC is the concentration of the solution given as the mass of the substance in g per 100 ml of solution, SORT is the signed value (preceded by a + or a - sign) of $100\alpha/(lc)$, where α is the signed optical rotation in degrees measured in a cell of length l in dm and c is the value of *CONC* as defined above, and SOLV is the chemical formula of the solvent.
Example: '[\a]^25^~D~ = +108 (c = 3.42, CHCl~3~)'. **[chemical]**

_chemical_properties_biological (*char*)
A free-text description of the biological properties of the material.
Examples:

```
; diverse biological activities including use as a
  laxative and strong antibacterial activity against
  S. aureus and weak activity against
  cyclooxygenase-1 (COX-1)
;
; antibiotic activity against Bacillus subtilis
  (ATCC 6051) but no significant activity against
  Candida albicans (ATCC 14053), Aspergillus flavus
  (NRRL 6541) and Fusarium verticillioides (NRRL
  25457)
;
; weakly potent lipoxygenase nonredox inhibitor
;
; no influenza A virus sialidase inhibitory and
  plaque reduction activities
;
; low toxicity against Drosophila melanogaster
;
```

[chemical]

_chemical_properties_physical (*char*)
A free-text description of the physical properties of the material.
Examples: 'air-sensitive', 'moisture-sensitive', 'hygroscopic', 'deliquescent', 'oxygen-sensitive', 'photo-sensitive', 'pyrophoric', 'semiconductor', 'ferromagnetic at low temperature', 'paramagnetic and thermochromic'. **[chemical]**

_chemical_temperature_decomposition (*numb, su*)
The temperature in kelvins at which the solid decomposes.
The permitted range is 0.0 → ∞.
Example: '350'. **[chemical]**

_chemical_temperature_decomposition_gt
_chemical_temperature_decomposition_lt (*numb*)
A temperature in kelvins below which (*_lt) or above which (*_gt) the solid is known to decompose. These items allow a range of temperatures to be given. **_chemical_temperature_decomposition** should always be used in preference to these items whenever possible.
The permitted range is 0.0 → ∞.
Related item: **_chemical_temperature_decomposition** (alternate).
Example: '350'. **[chemical]**

_chemical_temperature_sublimation (*numb, su*)
The temperature in kelvins at which the solid sublimes.
The permitted range is 0.0 → ∞.
Example: '350'. **[chemical]**

_chemical_temperature_sublimation_gt
_chemical_temperature_sublimation_lt (*numb*)

A temperature in kelvins below which (*_lt) or above which (*_gt) the solid is known to sublime. These items allow a range of temperatures to be given. _chemical_temperature_sublimation should always be used in preference to these items whenever possible.

The permitted range is $0.0 \rightarrow \infty$.

Related item: _chemical_temperature_sublimation (alternate).

Example: '350'. [chemical]

CHEMICAL_CONN_ATOM

Data items in the _chemical_conn_atom_ and _chemical_conn_bond_ categories record details about the two-dimensional (2D) chemical structure of the molecular species. They allow a 2D chemical diagram to be reconstructed for use in a publication or in a database search for structural and substructural relationships. The _chemical_conn_atom_ data items provide information about the chemical properties of the atoms in the structure. In cases where crystallographic and molecular symmetry elements coincide, they must also contain symmetry-generated atoms, so that the _chemical_conn_atom_ and _chemical_conn_bond_ data items will always describe a complete chemical entity.

Example 1 – based on data set DPTD of Yamin, Suwandi, Fun, Sivakumar & bin Shawkataly [Acta Cryst. (1996), C52, 951–953].

```
loop_
_chemical_conn_atom_number
_chemical_conn_atom_type_symbol
_chemical_conn_atom_display_x
_chemical_conn_atom_display_y
_chemical_conn_atom_NCA
_chemical_conn_atom_NH
    1   S    .39  .81   1   0
    2   S    .39  .96   2   0
    3   N    .14  .88   3   0
    4   C    .33  .88   3   0
    5   C    .11  .96   2   2
    6   C    .03  .96   2   2
    7   C    .03  .80   2   2
    8   C    .11  .80   2   2
    9   S    .54  .81   1   0
    10  S    .54  .96   2   0
    11  N    .80  .88   3   0
    12  C    .60  .88   3   0
    13  C    .84  .96   2   2
    14  C    .91  .96   2   2
    15  C    .91  .80   2   2
    16  C    .84  .80   2   2
```

_chemical_conn_atom_charge (*numb*)

The net integer charge assigned to this atom. This is the formal charge assignment normally found in chemical diagrams.

Appears in list containing _chemical_conn_atom_type_symbol.

The permitted range is $-6 \rightarrow 6$. Where no value is given, the assumed value is '0'.

Examples: '1' (for an ammonium nitrogen), '-1' (for a chloride ion).

[chemical_conn_atom]

_chemical_conn_atom_display_x
_chemical_conn_atom_display_y (*numb*)

The 2D Cartesian coordinates (x, y) of the position of this atom in a recognizable chemical diagram. The coordinate origin is at the lower left corner, the x axis is horizontal and the y axis is vertical. The coordinates must lie in the range 0.0 to 1.0. These coordinates can be obtained from projections of a suitable uncluttered view of the molecular structure.

Appears in list containing _chemical_conn_atom_type_symbol.

The permitted range is $0.0 \rightarrow 1.0$. [chemical_conn_atom]

_chemical_conn_atom_NCA (*numb*)

The number of connected atoms excluding terminal hydrogen atoms.

Appears in list containing _chemical_conn_atom_type_symbol.

The permitted range is $0 \rightarrow \infty$. [chemical_conn_atom]

_chemical_conn_atom_NH (*numb*)

The total number of hydrogen atoms attached to this atom, regardless of whether they are included in the refinement or the _atom_site_ list. This number will be the same as _atom_site_attached_hydrogens only if none of the hydrogen atoms appear in the _atom_site_ list.

Appears in list containing _chemical_conn_atom_type_symbol.

The permitted range is $0 \rightarrow \infty$. [chemical_conn_atom]

_chemical_conn_atom_number (*numb*)

The chemical sequence number to be associated with this atom.

Appears in list containing _chemical_conn_atom_type_symbol. May match child data name(s): _atom_site_chemical_conn_number, _chemical_conn_bond_atom_1, _chemical_conn_bond_atom_2.

The permitted range is $1 \rightarrow \infty$. [chemical_conn_atom]

_chemical_conn_atom_type_symbol (*char*)

A code identifying the atom type. This code must match an _atom_type_symbol code in the _atom_type_ list or be a recognizable element symbol.

Appears in list as essential element of loop structure. [chemical_conn_atom]

CHEMICAL_CONN_BOND

Data items in the _chemical_conn_atom_ and _chemical_conn_bond_ categories record details about the two-dimensional (2D) chemical structure of the molecular species. They allow a 2D chemical diagram to be reconstructed for use in a publication or in a database search for structural and substructural relationships. The _chemical_conn_bond_ data items specify the connections between the atoms in the _chemical_conn_atom_ list and the nature of the chemical bond between these atoms.

Example 1 – based on data set DPTD of Yamin, Suwandi, Fun, Sivakumar & bin Shawkataly [Acta Cryst. (1996), C52, 951–953].

```
loop_
_chemical_conn_bond_atom_1
_chemical_conn_bond_atom_2
_chemical_conn_bond_type
   4     1     doub     4     3     sing
   4     2     sing     5     3     sing
   6     5     sing     7     6     sing
   8     7     sing     8     3     sing
   10    2     sing     12    9     doub
   12    11    sing     12    10    sing
   13    11    sing     14    13    sing
   15    14    sing     16    15    sing
   16    11    sing     17    5     sing
   18    5     sing     19    6     sing
   20    6     sing     21    7     sing
   22    7     sing     23    8     sing
   24    8     sing     25    13    sing
   26    13    sing     27    14    sing
   28    14    sing     29    15    sing
   30    15    sing     31    16    sing
   32    16    sing
```

_chemical_conn_bond_atom_1
_chemical_conn_bond_atom_2 (*numb*)

Atom numbers which must match with chemical sequence numbers specified as _chemical_conn_atom_number values. These link the bond connection to the chemical numbering and atom sites.

Appears in list. **Must** match parent data name _chemical_conn_atom_number.

The permitted range is $1 \rightarrow \infty$. [chemical_conn_bond]

_chemical_conn_bond_type (*char*)

The chemical bond type associated with the connection between the two sites **_chemical_conn_bond_atom_1** and ***_2**.

Appears in list containing **_chemical_conn_bond_atom_**.

The data value must be one of the following:

sing	single bond
doub	double bond
trip	triple bond
quad	quadruple bond
arom	aromatic bond
poly	polymeric bond
delo	delocalized double bond
pi	π bond

Where no value is given, the assumed value is 'sing'. **[chemical_conn_bond]**

CHEMICAL_FORMULA

_chemical_formula_ items specify the composition and chemical properties of the compound. The formula data items must agree with those that specify the density, unit-cell and *Z* values. The following rules apply to the construction of the data items **_chemical_formula_analytical**, ***_structural** and ***_sum**. For the data item ***_moiety**, the formula construction is broken up into residues or moieties, *i.e.* groups of atoms that form a molecular unit or molecular ion. The rules given below apply within each moiety but different requirements apply to the way that moieties are connected (see **_chemical_formula_moiety**). (1) Only recognized element symbols may be used. (2) Each element symbol is followed by a 'count' number. A count of '1' may be omitted. (3) A space or parenthesis must separate each cluster of (element symbol + count). (4) Where a group of elements is enclosed in parentheses, the multiplier for the group must follow the closing parenthesis. That is, all element and group multipliers are assumed to be printed as subscripted numbers. (An exception to this rule exists for ***_moiety** formulae where pre- and post-multipliers are permitted for molecular units.) (5) Unless the elements are ordered in a manner that corresponds to their chemical structure, as in **_chemical_formula_structural**, the order of the elements within any group or moiety depends on whether carbon is present or not. If carbon is present, the order should be: C, then H, then the other elements in alphabetical order of their symbol. If carbon is not present, the elements are listed purely in alphabetical order of their symbol. This is the 'Hill' system used by *Chemical Abstracts*. This ordering is used in **_chemical_formula_moiety** and **_chemical_formula_sum**.

*Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C**47**, 2276–2277].*

```
_chemical_formula_moiety            'C18 H25 N O3'
_chemical_formula_sum               'C18 H25 N O3'
_chemical_formula_weight            303.40
```

*Example 2 – based on data set 9597gaus of Alyea, Ferguson & Kannan [Acta Cryst. (1996), C**52**, 765–767].*

```
_chemical_formula_iupac      '[Mo (C O)4 (C18 H33 P)2]'
_chemical_formula_moiety     'C40 H66 Mo O4 P2'
_chemical_formula_structural '((C O)4 (P (C6 H11)3)2)Mo'
_chemical_formula_sum         'C40 H66 Mo O4 P2'
_chemical_formula_weight      768.81
```

_chemical_formula_analytical (*char*)

Formula determined by standard chemical analysis including trace elements. See the CHEMICAL_FORMULA category description for rules for writing chemical formulae. Parentheses are used only for standard uncertainties (e.s.d.'s).

Example: 'Fe2.45(2) Ni1.60(3) S4'. **[chemical_formula]**

_chemical_formula_iupac (*char*)

Formula expressed in conformance with IUPAC rules for inorganic and metal-organic compounds where these conflict with the rules for any other **_chemical_formula_** entries. Typically used for formatting a formula in accordance with journal rules. This should appear in the data block in addition to the most appropriate of the other **_chemical_formula_** data names.

Reference: IUPAC (1990). *Nomenclature of Inorganic Chemistry*. Oxford: Blackwell Scientific Publications.

Example: '[Co Re (C12 H22 P)2 (C O)6].0.5C H3 O H'. **[chemical_formula]**

_chemical_formula_moiety (*char*)

Formula with each discrete bonded residue or ion shown as a separate moiety. See the CHEMICAL_FORMULA category description for rules for writing chemical formulae. In addition to the general formulae requirements, the following rules apply: (1) Moieties are separated by commas ','. (2) The order of elements within a moiety follows general rule (5) in the CHEMICAL_FORMULA category description. (3) Parentheses are not used within moieties but may surround a moiety. Parentheses may not be nested. (4) Charges should be placed at the end of the moiety. The charge '+' or '-' may be preceded by a numerical multiplier and should be separated from the last (element symbol + count) by a space. Pre- or post-multipliers may be used for individual moieties.

Examples: 'C7 H4 Cl Hg N O3 S', 'C12 H17 N4 O S 1+, C6 H2 N3 O7 1-', 'C12 H16 N2 O6, 5(H2 O1)', '(Cd 2+)3, (C6 N6 Cr 3-)2, 2(H2 O)'. **[chemical_formula]**

_chemical_formula_structural (*char*)

See the CHEMICAL_FORMULA category description for the rules for writing chemical formulae for inorganics, organometallics, metal complexes *etc.*, in which bonded groups are preserved as discrete entities within parentheses, with post-multipliers as required. The order of the elements should give as much information as possible about the chemical structure. Parentheses may be used and nested as required. This formula should correspond to the structure as actually reported, *i.e.* trace elements not included in atom-type and atom-site lists should not be included in this formula (see also **_chemical_formula_analytical**).

Examples: 'Ca ((Cl O3)2 O)2 (H2 O)6', '(Pt (N H3)2 (C5 H7 N3 O)2) (Cl O4)2'. **[chemical_formula]**

_chemical_formula_sum (*char*)

See the CHEMICAL_FORMULA category description for the rules for writing chemical formulae in which all discrete bonded residues and ions are summed over the constituent elements, following the ordering given in general rule (5) in the CHEMICAL_FORMULA category description. Parentheses are not normally used.

Example: 'C18 H19 N7 O8 S'. **[chemical_formula]**

_chemical_formula_weight (*numb*)

Formula mass in daltons. This mass should correspond to the formulae given under **_chemical_formula_structural**, ***_iupac**, ***_moiety** or ***_sum** and, together with the *Z* value and cell parameters, should yield the density given as **_exptl_crystal_density_diffrn**.

The permitted range is $1.0 \rightarrow \infty$. **[chemical_formula]**

_chemical_formula_weight_meas (*numb*)

Formula mass in daltons measured by a non-diffraction experiment.

The permitted range is $1.0 \rightarrow \infty$. **[chemical_formula]**

CITATION

Data items in the CITATION category record details about the literature cited as being relevant to the contents of the data block.

Example 1 – based on PDB entry 5HVP and laboratory records for the structure corresponding to PDB entry 5HVP.

```
loop_
_citation_id
_citation_coordinate_linkage
_citation_title
_citation_country
_citation_page_first
_citation_page_last
_citation_year
_citation_journal_abbrev
_citation_journal_volume
_citation_journal_issue
_citation_journal_id_ASTM
_citation_journal_id_ISSN
_citation_book_title
_citation_book_publisher
_citation_book_id_ISBN
_citation_special_details
  primary  yes
; Crystallographic analysis of a complex between human
  immunodeficiency virus type 1 protease and
  acetyl-pepstatin at 2.0-Angstroms resolution.
;
  US  14209  14219  1990  'J. Biol. Chem.'  265  .
  HBCHA3  0021-9258  .  .  .
; The publication that directly relates to this coordinate
  set.
;
  2  no
; Three-dimensional structure of aspartyl-protease from
  human immunodeficiency virus HIV-1.
;
  UK  615  619  1989  'Nature'  337  .
  NATUAS  0028-0836  .  .  .
; Determination of the structure of the unliganded enzyme.
;
  3 no
; Crystallization of the aspartylprotease from human
  immunodeficiency virus, HIV-1.
;
  US  1919  1921  1989  'J. Biol. Chem.'  264  .
  HBCHA3  0021-9258  .  .  .
; Crystallization of the unliganded enzyme.
;
```

_citation_abstract (*char*)
Abstract for the citation. This is used most when the citation is extracted from a bibliographic database that contains full text or abstract information.
Appears in list containing **_citation_id**. **[citation]**

_citation_abstract_id_CAS (*char*)
The *Chemical Abstracts* Service (CAS) abstract identifier; relevant for journal articles.
Appears in list containing **_citation_id**. **[citation]**

_citation_book_id_ISBN (*char*)
The International Standard Book Number (ISBN) code assigned to the book cited; relevant for books or book chapters.
Appears in list containing **_citation_id**. **[citation]**

_citation_book_publisher (*char*)
The name of the publisher of the citation; relevant for books or book chapters.
Appears in list containing **_citation_id**.
Example: 'John Wiley'. **[citation]**

_citation_book_publisher_city (*char*)
The location of the publisher of the citation; relevant for books or book chapters.
Appears in list containing **_citation_id**.
Example: 'New York'. **[citation]**

_citation_book_title (*char*)
The title of the book in which the citation appeared; relevant for books or book chapters.
Appears in list containing **_citation_id**. **[citation]**

_citation_coordinate_linkage (*char*)
_citation_coordinate_linkage states whether or not this citation is concerned with precisely the set of coordinates given in the data block. If, for instance, the publication described the same structure, but the coordinates had undergone further refinement prior to creation of the data block, the value of this data item would be 'no'.
Appears in list containing **_citation_id**.
The data value must be one of the following:

no	citation unrelated to current coordinates
n	abbreviation for 'no'
yes	citation related to current coordinates
y	abbreviation for 'yes'

[citation]

_citation_country (*char*)
The country of publication; relevant for books and book chapters.
Appears in list containing **_citation_id**. **[citation]**

_citation_database_id_CSD (*char*)
Identifier ('refcode') of the database record in the Cambridge Structural Database that contains details of the cited structure.
Appears in list containing **_citation_id**.
Example: 'LEKKUH'. **[citation]**

_citation_database_id_Medline (*numb*)
Accession number used by Medline to categorize a specific bibliographic entry.
Appears in list containing **_citation_id**.
The permitted range is $1 \rightarrow \infty$.
Example: '89064067'. **[citation]**

_citation_id (*char*)
The value of **_citation_id** must uniquely identify a record in the **_citation_** list. The **_citation_id** 'primary' should be used to indicate the citation that the author(s) consider to be the most pertinent to the contents of the data block. Note that this item need not be a number; it can be any unique identifier.
Appears in list as essential element of loop structure. May match child data name(s):
_citation_author_citation_id, **_citation_editor_citation_id**.
Examples: 'primary', '1', '2', '3'. **[citation]**

_citation_journal_abbrev (*char*)
Abbreviated name of the journal cited as given in the *Chemical Abstracts* Service *Source Index*.
Appears in list containing **_citation_id**.
Example: 'J. Mol. Biol.'. **[citation]**

_citation_journal_full (*char*)
Full name of the journal cited; relevant for journal articles.
Appears in list containing **_citation_id**.
Example: 'Journal of Molecular Biology'. **[citation]**

_citation_journal_id_ASTM (*char*)
The American Society for Testing and Materials (ASTM) code assigned to the journal cited (also referred to as the CODEN designator of the *Chemical Abstracts* Service); relevant for journal articles.
Appears in list containing **_citation_id**. **[citation]**

_citation_journal_id_CSD (*char*)
The Cambridge Structural Database (CSD) code assigned to the journal cited; relevant for journal articles. This is also the system used at the Protein Data Bank (PDB).
Appears in list containing **_citation_id**.
Example: '0070'. **[citation]**

_citation_journal_id_ISSN (*char*)
The International Standard Serial Number (ISSN) code assigned to the journal cited; relevant for journal articles.
Appears in list containing **_citation_id**. **[citation]**

_citation_journal_issue (*char*)
Issue number of the journal cited; relevant for journal articles.
Appears in list containing **_citation_id**.
Example: '2'. **[citation]**

_citation_journal_volume (*char*)
Volume number of the journal cited; relevant for journal articles.
Appears in list containing **_citation_id**.
Example: '174'. **[citation]**

_citation_language (*char*)
Language in which the cited article is written.
Appears in list containing **_citation_id**.
Example: 'German'. **[citation]**

_citation_page_first
_citation_page_last (*char*)
The first and last pages of the citation; relevant for journal articles, books and book chapters.
Appears in list containing **_citation_id**. **[citation]**

_citation_special_details (*char*)
A description of special aspects of the relationship of the contents of the data block to the literature item cited.
Appears in list containing **_citation_id**.
Examples:
```
; citation relates to this precise coordinate set
;
; citation relates to earlier low-resolution structure
;
; citation relates to further refinement of structure
  reported in citation 2
;
```
[citation]

_citation_title (*char*)
The title of the citation; relevant for journal articles, books and book chapters.
Appears in list containing **_citation_id**.
Example:
```
; Structure of diferric duck ovotransferrin at 2.35 \%A
  resolution.
;
```
[citation]

_citation_year (*numb*)
The year of the citation; relevant for journal articles, books and book chapters.
Appears in list containing **_citation_id**.
Example: '1984'. **[citation]**

CITATION_AUTHOR

Data items in the CITATION_AUTHOR category record details about the authors associated with the citations in the **_citation_** list.

Example 1 – based on PDB entry 5HVP and laboratory records for the structure corresponding to PDB entry 5HVP.

```
loop_
_citation_author_citation_id
_citation_author_name
  primary  'Fitzgerald, P.M.D.'
  primary  'McKeever, B.M.'
  primary  'Van Middlesworth, J.F.'
  primary  'Springer, J.P.'
  primary  'Heimbach, J.C.'
  primary  'Leu, C.-T.'
  primary  'Herber, W.K.'
  primary  'Dixon, R.A.F.'
  primary  'Darke, P.L.'
  2        'Navia, M.A.'
  2        'Fitzgerald, P.M.D.'
  2        'McKeever, B.M.'
  2        'Leu, C.-T.'
  2        'Heimbach, J.C.'
  2        'Herber, W.K.'
  2        'Sigal, I.S.'
  2        'Darke, P.L.'
  2        'Springer, J.P.'
  3        'McKeever, B.M.'
  3        'Navia, M.A.'
  3        'Fitzgerald, P.M.D.'
  3        'Springer, J.P.'
  3        'Leu, C.-T.'
  3        'Heimbach, J.C.'
  3        'Herber, W.K.'
  3        'Sigal, I.S.'
  3        'Darke, P.L.'
```

_citation_author_citation_id (*char*)
The value of **_citation_author_citation_id** must match an identifier specified by **_citation_id** in the **_citation_** list.
Appears in list as essential element of loop structure. **Must** match parent data name **_citation_id**. **[citation_author]**

_citation_author_name (*char*)
Name of an author of the citation; relevant for journal articles, books and book chapters. The family name(s), followed by a comma and including any dynastic components, precedes the first name(s) or initial(s).
Appears in list as essential element of loop structure.
Examples: 'Bleary, Percival R.', 'O'Neil, F.K.', 'Van den Bossche, G.', 'Yang, D.-L.', 'Simonov, Yu.A.', 'M\"uller, H.A.', 'Ross II, C.R.'.
[citation_author]

_citation_author_ordinal (*char*)
This data name defines the order of the author's name in the list of authors of a citation.
Appears in list. **[citation_author]**

CITATION_EDITOR

Data items in the CITATION_EDITOR category record details about the editor associated with the book or book chapter citations in the **_citation_** list.

Example 1 – hypothetical example.

```
loop_
_citation_editor_citation_id
_citation_editor_name
  5        'McKeever, B.M.'
  5        'Navia, M.A.'
  5        'Fitzgerald, P.M.D.'
  5        'Springer, J.P.'
```

_citation_editor_citation_id (*char*)

The value of _citation_editor_citation_id must match an identifier specified by _citation_id in the _citation_ list.

Appears in list as essential element of loop structure. **Must** match parent data name _citation_id. **[citation_editor]**

_citation_editor_name (*char*)

Name of an editor of the citation; relevant for books and book chapters. The family name(s), followed by a comma and including any dynastic components, precedes the first name(s) or initial(s).

Appears in list as essential element of loop structure.

Examples: 'Bleary, Percival R.', 'O'Neil, F.K.', 'Van den Bossche, G.', 'Yang, D.-L.', 'Simonov, Yu.A.', 'M\"uller, H.A.', 'Ross II, C.R.'. **[citation_editor]**

_citation_editor_ordinal (*char*)

This data name defines the order of the editor's name in the list of editors of a citation.

Appears in list. **[citation_editor]**

COMPUTING

Data items in the COMPUTING category record details about the computer programs used in the crystal structure analysis.

Example 1 – Rodrìguez-Romero, Ruiz-Pérez & Solans [Acta Cryst. (1996), C52, 1415–1417].

```
_computing_data_collection       'CAD-4 (Enraf-Nonius, 1989)'
_computing_cell_refinement       'CAD-4 (Enraf-Nonius, 1989)'
_computing_data_reduction        'CFEO (Solans, 1978)'
_computing_structure_solution    'SHELXS86 (Sheldrick, 1990)'
_computing_structure_refinement  'SHELXL93 (Sheldrick, 1993)'
_computing_molecular_graphics    'ORTEPII (Johnson, 1976)'
_computing_publication_material  'PARST (Nardelli, 1983)'
```

_computing_cell_refinement
_computing_data_collection
_computing_data_reduction
_computing_molecular_graphics
_computing_publication_material
_computing_structure_refinement
_computing_structure_solution (*char*)

Software used in the processing of the data. Give the program or package name and a brief reference.

Examples: 'CAD-4 (Enraf-Nonius, 1989)', 'DIFDAT, SORTRF, ADDREF (Hall & Stewart, 1990)', 'FRODO (Jones, 1986), ORTEP (Johnson, 1965)', 'CRYSTALS (Watkin, 1988)', 'SHELX85 (Sheldrick, 1985)'. **[computing]**

DATABASE

Data items in the DATABASE category record details about the database identifiers of the data block. These data items are assigned by database managers and should only appear in a CIF if they originate from that source.

Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C47, 2276–2277].

```
_database_code_CSD                'VOBYUG'
```

_database_code_CAS
_database_code_CSD
_database_code_ICSD
_database_code_MDF
_database_code_NBS
_database_code_PDB
_database_code_PDF (*char*)

The codes are assigned by databases: *Chemical Abstracts*; Cambridge Structural Database (organic and metal-organic compounds); Inorganic Crystal Structure Database; Metals Data File (metal structures); NBS (NIST) Crystal Data Database (lattice parameters); Protein Data Bank; and the Powder Diffraction File (JCPDS/ICDD). **[database]**

_database_code_depnum_ccdc_archive (*char*)

Deposition numbers assigned by the Cambridge Crystallographic Data Centre (CCDC) to files containing structural information archived by the CCDC. **[database]**

_database_code_depnum_ccdc_fiz (*char*)

Deposition numbers assigned by the Fachinformationszentrum Karlsruhe (FIZ) to files containing structural information archived by the Cambridge Crystallographic Data Centre (CCDC). **[database]**

_database_code_depnum_ccdc_journal (*char*)

Deposition numbers assigned by various journals to files containing structural information archived by the Cambridge Crystallographic Data Centre (CCDC). **[database]**

_database_CSD_history (*char*)

A history of changes made by the Cambridge Crystallographic Data Centre and incorporated into the Cambridge Structural Database (CSD). **[database]**

_database_journal_ASTM
_database_journal_CSD (*char*)

The ASTM CODEN designator for a journal as given in the *Chemical Source List* maintained by the *Chemical Abstracts* Service, and the journal code used in the Cambridge Structural Database. **[database]**

DIFFRN

Data items in the DIFFRN category record details about the intensity measurements.

Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C47, 2276–2277].

```
_diffrn_special_details
; \q scan width (1.0 + 0.14tan\q)\%, \q scan rate
  1.2\% min^-1^. Background counts for 5 s on each side
  every scan.
;

_diffrn_ambient_temperature         293
```

_diffrn_ambient_environment (*char*)

The gas or liquid surrounding the sample, if not air.

Examples: 'He', 'vacuum', 'mother liquor'. **[diffrn]**

_diffrn_ambient_pressure (*numb, su*)

The mean hydrostatic pressure in kilopascals at which the intensities were measured.

The permitted range is $0.0 \rightarrow \infty$. **[diffrn]**

_diffrn_ambient_pressure_gt
_diffrn_ambient_pressure_lt (*numb*)
The mean hydrostatic pressure in kilopascals above which (*_gt) or below which (*_lt) the intensities were measured. These items allow for a pressure range to be given. **_diffrn_ambient_pressure** should always be used in preference to these items whenever possible.
The permitted range is $0.0 \rightarrow \infty$.
Related item: **_diffrn_ambient_pressure** (alternate). **[diffrn]**

_diffrn_ambient_temperature (*numb, su*)
The mean temperature in kelvins at which the intensities were measured.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn]**

_diffrn_ambient_temperature_gt
_diffrn_ambient_temperature_lt (*numb*)
The mean temperature in kelvins above which (*_gt) or below which (*_lt) the intensities were measured. These items allow a range of temperatures to be given. **_diffrn_ambient_temperature** should always be used in preference to these items whenever possible.
The permitted range is $0.0 \rightarrow \infty$.
Related item: **_diffrn_ambient_temperature** (alternate). **[diffrn]**

_diffrn_crystal_treatment (*char*)
Remarks about how the crystal was treated prior to the intensity measurements. Particularly relevant when intensities were measured at low temperature.
Examples: 'equilibrated in hutch for 24 hours',
'flash frozen in liquid nitrogen',
'slow cooled with direct air stream'. **[diffrn]**

_diffrn_measured_fraction_theta_full (*numb*)
Fraction of unique (symmetry-independent) reflections measured out to **_diffrn_reflns_theta_full**.
The permitted range is $0 \rightarrow 1.0$. **[diffrn]**

_diffrn_measured_fraction_theta_max (*numb*)
Fraction of unique (symmetry-independent) reflections measured out to **_diffrn_reflns_theta_max**.
The permitted range is $0 \rightarrow 1.0$. **[diffrn]**

_diffrn_special_details (*char*)
Special details of the intensity-measurement process. Should include information about source instability, crystal motion, degradation and so on.
Example:
```
; The results may not be entirely reliable
  as the measurement was made during a heat
  wave when the air-conditioning had failed.
;
```
[diffrn]

_diffrn_symmetry_description (*char*)
Observed diffraction point symmetry, systematic absences and possible space group(s) or superspace group(s) compatible with these.
[diffrn]

DIFFRN_ATTENUATOR

Data items in the DIFFRN_ATTENUATOR category record details about the diffraction attenuator scales employed.

Example 1 – hypothetical example.

```
loop_
  _diffrn_attenuator_code
  _diffrn_attenuator_scale
      0         1.00
      1        16.97
      2        33.89
```

_diffrn_attenuator_code (*char*)
A code associated with a particular attenuator setting. This code is referenced by the **_diffrn_refln_attenuator_code** which is stored with the intensities. See **_diffrn_attenuator_scale**.
Appears in list as essential element of loop structure. May match child data name(s):
_diffrn_refln_attenuator_code. **[diffrn_attenuator]**

_diffrn_attenuator_material (*char*)
Material from which the attenuator is made.
Appears in list containing **_diffrn_attenuator_code**. **[diffrn_attenuator]**

_diffrn_attenuator_scale (*numb*)
The scale factor applied when an intensity measurement is reduced by an attenuator identified by **_diffrn_attenuator_code**. The measured intensity must be multiplied by this scale to convert it to the same scale as unattenuated intensities.
Appears in list containing **_diffrn_attenuator_code**.
The permitted range is $1.0 \rightarrow \infty$. **[diffrn_attenuator]**

DIFFRN_DETECTOR

Data items in the DIFFRN_DETECTOR category describe the detector used to measure the scattered radiation, including any analyser and post-sample collimation.

Example 1 – based on PDB entry 5HVP and laboratory records for the structure corresponding to PDB entry 5HVP.

```
_diffrn_detector                'multiwire'
_diffrn_detector_type           'Siemens'
```

_diffrn_detector (*char*)
The general class of the radiation detector.
Related item: **_diffrn_radiation_detector** (alternate).
Examples: 'photographic film', 'scintillation counter', 'CCD plate',
'BF~3~ counter'. **[diffrn_detector]**

_diffrn_detector_area_resol_mean (*numb*)
The resolution of an area detector, in pixels mm^{-1}.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_detector]**

_diffrn_detector_details (*char*)
A description of special aspects of the radiation detector.
[diffrn_detector]

_diffrn_detector_dtime (*numb*)
The deadtime in microseconds of the detector used to measure the diffraction intensities.
The permitted range is $0.0 \rightarrow \infty$.
Related item: **_diffrn_radiation_detector_dtime** (alternate).
[diffrn_detector]

_diffrn_detector_type (*char*)
The make, model or name of the detector device used.
[diffrn_detector]

_diffrn_radiation_detector (*char*)
This definition has been superseded and is retained here only for archival purposes. Use instead _diffrn_detector.
The detector used to measure the diffraction intensities.
[diffrn_detector]

_diffrn_radiation_detector_dtime (*numb*)

This definition has been superseded and is retained here only for archival purposes. Use instead _diffrn_detector_dtime.

The deadtime in microseconds of the detector used to measure the diffraction intensities.

The permitted range is 0.0 → ∞. **[diffrn_detector]**

DIFFRN_MEASUREMENT

Data items in the DIFFRN_MEASUREMENT category refer to the mounting of the sample and to the goniometer on which it is mounted.

*Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C**47**, 2276–2277].*

```
_diffrn_measurement_device_type
          'Philips PW1100/20 diffractometer'
_diffrn_measurement_method          \q/2\q
```

_diffrn_measurement_details (*char*)

A description of special aspects of the intensity measurement.

Example: '440 frames of 0.25\%'. **[diffrn_measurement]**

_diffrn_measurement_device (*char*)

The general class of goniometer or device used to support and orient the specimen.

Examples: 'three-circle diffractometer', 'four-circle diffractometer', '\k-geometry diffractometer', 'oscillation camera', 'precession camera'. **[diffrn_measurement]**

_diffrn_measurement_device_details (*char*)

A description of special aspects of the device used to measure the diffraction intensities.

Example:

```
; commercial goniometer modified locally to
  allow for 90\% \t arc
;
```

[diffrn_measurement]

_diffrn_measurement_device_type (*char*)

The make, model or name of the measurement device (goniometer) used.

[diffrn_measurement]

_diffrn_measurement_method (*char*)

Method used to measure the intensities.

Example: 'profile data from \q/2\q scans'. **[diffrn_measurement]**

_diffrn_measurement_specimen_support (*char*)

The physical device used to support the crystal during data collection.

Examples: 'glass capillary', 'quartz capillary', 'fiber', 'metal loop'.

[diffrn_measurement]

DIFFRN_ORIENT_MATRIX

Data items in the DIFFRN_ORIENT_MATRIX category record details about the orientation matrix used in the measurement of the diffraction intensities.

*Example 1 – data set n-alkylation_C-4 of Hussain, Fleming, Norman & Chang [Acta Cryst. (1996), C**52**, 1010–1012].*

```
_diffrn_orient_matrix_UB_11          -0.04170
_diffrn_orient_matrix_UB_12          -0.01429
_diffrn_orient_matrix_UB_13          -0.02226
_diffrn_orient_matrix_UB_21          -0.00380
_diffrn_orient_matrix_UB_22          -0.05578
_diffrn_orient_matrix_UB_23          -0.05048
_diffrn_orient_matrix_UB_31           0.00587
_diffrn_orient_matrix_UB_32          -0.13766
_diffrn_orient_matrix_UB_33           0.02277

_diffrn_orient_matrix_type 'TEXSAN convention (MSC, 1989)'
```

_diffrn_orient_matrix_type (*char*)

A description of the orientation matrix type and how it should be applied to define the orientation of the crystal precisely with respect to the diffractometer axes.

[diffrn_orient_matrix]

_diffrn_orient_matrix_UB_11
_diffrn_orient_matrix_UB_12
_diffrn_orient_matrix_UB_13
_diffrn_orient_matrix_UB_21
_diffrn_orient_matrix_UB_22
_diffrn_orient_matrix_UB_23
_diffrn_orient_matrix_UB_31
_diffrn_orient_matrix_UB_32
_diffrn_orient_matrix_UB_33 (*numb*)

The elements of the diffractometer orientation matrix. These define the dimensions of the reciprocal cell and its orientation to the local diffractometer axes. See **_diffrn_orient_matrix_type**.

[diffrn_orient_matrix]

DIFFRN_ORIENT_REFLN

Data items in the DIFFRN_ORIENT_REFLN category record details about the reflections that define the orientation matrix used in the measurement of the diffraction intensities.

Example 1 – typical output listing from an Enraf-Nonius CAD-4 diffractometer.

```
loop_
_diffrn_orient_refln_index_h
_diffrn_orient_refln_index_k
_diffrn_orient_refln_index_l
_diffrn_orient_refln_angle_theta
_diffrn_orient_refln_angle_phi
_diffrn_orient_refln_angle_omega
_diffrn_orient_refln_angle_kappa
  -3   2   3    7.35   44.74   2.62    17.53
  -4   1   0    9.26   83.27   8.06     5.79
   0   0   6    5.85  -43.93 -25.36    86.20
   2   1   3    7.36  -57.87   6.26     5.42
   0   0  -6    5.85 -161.59  36.96   -86.79
  -3   1   0    6.74   80.28   5.87     2.60
   2   0   3    5.86  -76.86  -0.17    21.34
   0   0  12   11.78  -44.02 -19.51    86.41
   0   0 -12   11.78 -161.67  42.81   -86.61
  -5   1   0   11.75   86.24   9.16     7.44
   0   4   6   11.82  -19.82  10.45     4.19
   5   0   6   14.13  -77.28  10.17    15.34
   8   0   0   20.79  -77.08  25.30   -13.96
```

_diffrn_orient_refln_angle_chi
_diffrn_orient_refln_angle_kappa
_diffrn_orient_refln_angle_omega
_diffrn_orient_refln_angle_phi
_diffrn_orient_refln_angle_psi
_diffrn_orient_refln_angle_theta (*numb*)

Diffractometer angles of a reflection used to define the orientation matrix in degrees. See **_diffrn_orient_matrix_UB_** and **_diffrn_orient_refln_index_h**, *_k and *_l.

Appears in list containing **_diffrn_orient_refln_index_**.

[diffrn_orient_refln]

_diffrn_orient_refln_index_h
_diffrn_orient_refln_index_k
_diffrn_orient_refln_index_l (*numb*)
The indices of a reflection used to define the orientation matrix. See **_diffrn_orient_matrix_**.
Appears in list as essential element of loop structure. **[diffrn_orient_refln]**

DIFFRN_RADIATION

Data items in the DIFFRN_RADIATION category describe the radiation used in measuring the diffraction intensities, its collimation and monochromatization before the sample. Post-sample treatment of the beam is described by data items in the DIFFRN_DETECTOR category.

Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C47, 2276–2277].

```
_diffrn_radiation_type             'Cu K\a'
_diffrn_radiation_monochromator    'graphite'
```

_diffrn_radiation_collimation (*char*)
The collimation or focusing applied to the radiation.
Examples: '0.3 mm double-pinhole', '0.5 mm', 'focusing mirrors'.
[diffrn_radiation]

_diffrn_radiation_filter_edge (*numb*)
Absorption edge in ångströms of the radiation filter used.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_radiation]**

_diffrn_radiation_inhomogeneity (*numb*)
Half-width in millimetres of the incident beam in the direction perpendicular to the diffraction plane.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_radiation]**

_diffrn_radiation_monochromator (*char*)
The method used to obtain monochromatic radiation. If a monochromator crystal is used, the material and the indices of the Bragg reflection are specified.
Examples: 'Zr filter', 'Ge 220', 'none', 'equatorial mounted graphite'.
[diffrn_radiation]

_diffrn_radiation_polarisn_norm (*numb*)
The angle in degrees, as viewed from the specimen, between the perpendicular component of the polarization and the diffraction plane. See **_diffrn_radiation_polarisn_ratio**.
The permitted range is $-180.0 \rightarrow 180.0$. **[diffrn_radiation]**

_diffrn_radiation_polarisn_ratio (*numb*)
Polarization ratio of the diffraction beam incident on the crystal. It is the ratio of the perpendicularly polarized to the parallel polarized components of the radiation. The perpendicular component forms an angle of **_diffrn_radiation_polarisn_norm** to the normal to the diffraction plane of the sample (*i.e.* the plane containing the incident and reflected beams).
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_radiation]**

_diffrn_radiation_probe (*char*)
The nature of the radiation used (*i.e.* the name of the subatomic particle or the region of the electromagnetic spectrum). It is strongly recommended that this information be given, so that the probe radiation can be simply determined.
The data value must be one of the following:

x-ray	
neutron	
electron	
gamma	**[diffrn_radiation]**

_diffrn_radiation_type (*char*)
The type of the radiation. This is used to give a more detailed description than **_diffrn_radiation_probe** and is typically a description of the X-ray wavelength in Siegbahn notation.
Examples: 'Cu K\a', 'Cu K\a~1~', 'Cu K-L~2,3~', 'white-beam'.
[diffrn_radiation]

_diffrn_radiation_xray_symbol (*char*)
The IUPAC symbol for the X-ray wavelength for the probe radiation.
The data value must be one of the following:

K-L~3~	$K\alpha_1$ in older Siegbahn notation
K-L~2~	$K\alpha_2$ in older Siegbahn notation
K-M~3~	$K\beta$ in older Siegbahn notation
K-L~2,3~	use where K-L_3 and K-L_2 are not resolved

[diffrn_radiation]

DIFFRN_RADIATION_WAVELENGTH

Data items in the DIFFRN_RADIATION_WAVELENGTH category describe the wavelength of the radiation used in measuring the diffraction intensities. Items may be looped to identify and assign weights to distinct wavelength components from a polychromatic beam.

Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C47, 2276–2277].

```
_diffrn_radiation_wavelength       1.5418
```

_diffrn_radiation_wavelength (*numb*)
The radiation wavelength in ångströms.
May appear in list containing **_diffrn_radiation_wavelength_id**.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_radiation_wavelength]**

_diffrn_radiation_wavelength_id (*char*)
An arbitrary code identifying each value of **_diffrn_radiation_wavelength**. Items in the DIFFRN_RADIATION category are looped when multiple wavelengths are used. This code is used to link with the **_diffrn_refln_** list. It must match with one of the **_diffrn_refln_wavelength_id** codes.
Appears in list as essential element of loop structure. May match child data name(s): **_diffrn_refln_wavelength_id**.
Examples: 'x1', 'x2', 'neut'. **[diffrn_radiation_wavelength]**

_diffrn_radiation_wavelength_wt (*numb*)
The relative weight of a wavelength identified by the code **_diffrn_radiation_wavelength_id** in the list of wavelengths.
Appears in list containing **_diffrn_radiation_wavelength_id**.
The permitted range is $0.0 \rightarrow 1.0$. Where no value is given, the assumed value is '1.0'.
[diffrn_radiation_wavelength]

DIFFRN_REFLN

Data items in the DIFFRN_REFLN category record details about the intensities measured in the diffraction experiment. The DIFFRN_REFLN data items refer to individual intensity measurements and must be included in looped lists. (The DIFFRN_REFLNS data items specify the parameters that apply to all intensity measurements. The DIFFRN_REFLNS data items are not looped.)

Example 1 – extracted from the CAD-4 listing for $Tl_2Cd_2(SO_4)_3$ at 85 K (unpublished).

```
loop_
    _diffrn_refln_index_h
    _diffrn_refln_index_k
    _diffrn_refln_index_l
    _diffrn_refln_angle_chi
    _diffrn_refln_scan_rate
    _diffrn_refln_counts_bg_1
    _diffrn_refln_counts_total
    _diffrn_refln_counts_bg_2
    _diffrn_refln_angle_theta
    _diffrn_refln_angle_phi
    _diffrn_refln_angle_omega
    _diffrn_refln_angle_kappa
    _diffrn_refln_scan_width
    _diffrn_refln_elapsed_time

 0  0 -16  0. 4.12  28 127  36  33.157  -75.846  16.404
50.170  1.516 19.43
 0  0 -15  0. 4.12  38 143  28  30.847  -75.846  14.094
50.170  1.516 19.82
 0  0 -14  0. 1.03 142 742 130  28.592  -75.846  11.839
50.170  1.516 21.32
 0  0 -13  0. 4.12  26 120  37  26.384  -75.846   9.631
50.170  1.450 21.68
 0  0 -12  0. 0.97 129 618 153  24.218  -75.846   7.464
50.170  1.450 23.20
 0  0 -11  0. 4.12  33 107  38  22.087  -75.846   5.334
50.170  1.384 23.55
 0  0 -10  0. 4.12  37 146  33  19.989  -75.846   3.235
50.170  1.384 23.90
 0  0  -9  0. 4.12  50 179  49  17.918  -75.846   1.164
50.170  1.384 24.25
# - - - - data truncated for brevity - - - -
 3  4  -4  0. 1.03  69 459  73  30.726  -53.744  46.543
-47.552  1.516 2082.58
 3  4  -5  0. 1.03  91 465  75  31.407  -54.811  45.519
-42.705  1.516 2084.07
 3 14  -6  0. 1.03  84 560  79  32.228  -55.841  44.745
-38.092  1.516 2085.57
# - - - - data truncated for brevity - - - -
```

_diffrn_refln_angle_chi
_diffrn_refln_angle_kappa
_diffrn_refln_angle_omega
_diffrn_refln_angle_phi
_diffrn_refln_angle_psi
_diffrn_refln_angle_theta (*numb*)

The diffractometer angles of a reflection in degrees. These correspond to the specified orientation matrix and the original measured cell before any subsequent cell transformations.

Appears in list containing **_diffrn_refln_index_**. **[diffrn_refln]**

_diffrn_refln_attenuator_code (*char*)

The code identifying the attenuator setting for this reflection. This code must match one of the **_diffrn_attenuator_code** values.

Appears in list containing **_diffrn_refln_index_**. **Must** match parent data name **_diffrn_attenuator_code**. **[diffrn_refln]**

_diffrn_refln_class_code (*char*)

The code identifying the class to which this reflection has been assigned. This code must match a value of **_diffrn_reflns_class_code**. Reflections may be grouped into classes for a variety of purposes. For example, for modulated structures each reflection class may be defined by the number $m = \sum |m_i|$, where the m_i are the integer coefficients that, in addition to h, k, l, index the corresponding diffraction vector in the basis defined for the reciprocal cell.

Appears in list containing **_diffrn_refln_index_**. **Must** match parent data name **_diffrn_reflns_class_code**. **[diffrn_refln]**

_diffrn_refln_counts_bg_1
_diffrn_refln_counts_bg_2
_diffrn_refln_counts_net
_diffrn_refln_counts_peak
_diffrn_refln_counts_total (*numb*)

The diffractometer counts for the measurements: background before the peak, background after the peak, net counts after background removed, counts for peak scan or position, and the total counts (background plus peak).

Appears in list containing **_diffrn_refln_index_**. **[diffrn_refln]**

_diffrn_refln_crystal_id (*char*)

Code identifying each crystal if multiple crystals are used. Is used to link with **_exptl_crystal_id** in the **_exptl_crystal_** list.

Appears in list containing **_diffrn_refln_index_**. **Must** match parent data name **_exptl_crystal_id**. **[diffrn_refln]**

_diffrn_refln_detect_slit_horiz
_diffrn_refln_detect_slit_vert (*numb*)

Total slit apertures in degrees in the diffraction plane (*_**horiz**) and perpendicular to the diffraction plane (*_**vert**).

Appears in list containing **_diffrn_refln_index_**.
The permitted range is 0.0 → 90.0. **[diffrn_refln]**

_diffrn_refln_elapsed_time (*numb*)

Elapsed time in minutes from the start of the diffraction experiment to the measurement of this intensity.

Appears in list containing **_diffrn_refln_index_**.
The permitted range is 0.0 → ∞. **[diffrn_refln]**

_diffrn_refln_index_h
_diffrn_refln_index_k
_diffrn_refln_index_l (*numb*)

Miller indices of a measured reflection. These need not match the **_refln_index_h**, *_**k**, *_**l** values if a transformation of the original measured cell has taken place. Details of the cell transformation are given in **_diffrn_reflns_reduction_process**. See also **_diffrn_reflns_transf_matrix_**.

Appears in list as essential element of loop structure. **[diffrn_refln]**

_diffrn_refln_intensity_net (*numb*)

Net intensity calculated from the diffraction counts after the attenuator and standard scales have been applied.

Appears in list containing **_diffrn_refln_index_**.
The permitted range is 0 → ∞. **[diffrn_refln]**

_diffrn_refln_intensity_sigma (*numb*)

This definition has been superseded and is retained here only for archival purposes. Use instead _diffrn_refln_intensity_u.

Standard uncertainty (e.s.d.) of the net intensity calculated from the diffraction counts after the attenuator and standard scales have been applied.

*Appears in list containing **_diffrn_refln_index_**.*
The permitted range is 0 → ∞. ***[diffrn_refln]***

_diffrn_refln_intensity_u (*numb*)

Standard uncertainty of the net intensity calculated from the diffraction counts after the attenuator and standard scales have been applied.

Appears in list containing **_diffrn_refln_index_**.
The permitted range is 0 → ∞.
Related item: **_diffrn_refln_intensity_sigma** (alternate). **[diffrn_refln]**

_diffrn_refln_scale_group_code (*char*)
The code identifying the scale applicable to this reflection. This code must match with a specified **_diffrn_scale_group_code** value.
Appears in list containing **_diffrn_refln_index_**. **Must** match parent data name **_diffrn_scale_group_code**. **[diffrn_refln]**

_diffrn_refln_scan_mode (*char*)
The code identifying the mode of scanning for measurements using a diffractometer. See **_diffrn_refln_scan_width** and **_diffrn_refln_scan_mode_backgd**.
Appears in list containing **_diffrn_refln_index_**.
The data value must be one of the following:
om ω scan
ot $\omega/2\theta$ scan
q Q scans (arbitrary reciprocal directions)
[diffrn_refln]

_diffrn_refln_scan_mode_backgd (*char*)
The code identifying the mode of scanning a reflection to measure the background intensity.
Appears in list containing **_diffrn_refln_index_**.
The data value must be one of the following:
st stationary counter background
mo moving counter background
[diffrn_refln]

_diffrn_refln_scan_rate (*numb*)
The rate of scanning a reflection in degrees per minute to measure the intensity.
Appears in list containing **_diffrn_refln_index_**.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_refln]**

_diffrn_refln_scan_time_backgd (*numb*)
The time spent measuring each background in seconds.
Appears in list containing **_diffrn_refln_index_**.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_refln]**

_diffrn_refln_scan_width (*numb*)
The scan width in degrees of the scan mode defined by the code **_diffrn_refln_scan_mode**.
Appears in list containing **_diffrn_refln_index_**.
The permitted range is $0.0 \rightarrow 90.0$. **[diffrn_refln]**

_diffrn_refln_sint/lambda (*numb*)
The $(\sin\theta)/\lambda$ value in reciprocal ångströms for this reflection.
Appears in list containing **_diffrn_refln_index_**.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_refln]**

_diffrn_refln_standard_code (*char*)
A code indicating that this reflection was measured as a standard reflection. The value must be '.' or match one of the **_diffrn_standard_refln_code** values.
Appears in list containing **_diffrn_refln_index_**. **Must** match parent data name **_diffrn_standard_refln_code**.
Examples: '1', '2', '3', 's1', 's2', 's3', 'A', 'B', 'C'. **[diffrn_refln]**

_diffrn_refln_wavelength (*numb*)
The mean wavelength in ångströms of the radiation used to measure the intensity of this reflection. This is an important parameter for reflections measured using energy-dispersive detectors or the Laue method.
Appears in list containing **_diffrn_refln_index_**.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_refln]**

_diffrn_refln_wavelength_id (*char*)
Code identifying the wavelength in the **_diffrn_radiation_** list.
Appears in list containing **_diffrn_refln_index_**. **Must** match parent data name **_diffrn_radiation_wavelength_id**.
Examples: 'x1', 'x2', 'neut'. **[diffrn_refln]**

DIFFRN_REFLNS

Data items in the DIFFRN_REFLNS category record details about the set of intensities measured in the diffraction experiment. The DIFFRN_REFLNS data items specify the parameters that apply to all intensity measurements. The DIFFRN_REFLNS data items are not looped. (The DIFFRN_REFLN data items refer to individual intensity measurements and must be included in looped lists.)

*Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C**47**, 2276–2277].*

```
_diffrn_reflns_number              1592
_diffrn_reflns_av_R_equivalents    0
_diffrn_reflns_av_unetI/netI       .027
_diffrn_reflns_limit_h_min         0
_diffrn_reflns_limit_h_max         6
_diffrn_reflns_limit_k_min        -17
_diffrn_reflns_limit_k_max         0
_diffrn_reflns_limit_l_min         0
_diffrn_reflns_limit_l_max         22
_diffrn_reflns_theta_min           3.71
_diffrn_reflns_theta_max           61.97
```

_diffrn_reflns_av_R_equivalents (*numb*)
The residual $[\sum \mathrm{av}|\Delta(I)| / \sum |\mathrm{av}(I)|]$ for symmetry-equivalent reflections used to calculate the average intensity $\mathrm{av}(I)$. The $\mathrm{av}|\Delta(I)|$ term is the average absolute difference between $\mathrm{av}(I)$ and the individual symmetry-equivalent intensities.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_reflns]**

_diffrn_reflns_av_sigmaI/netI (*numb*)
This definition has been superseded and is retained here only for archival purposes. Use instead _diffrn_reflns_av_unetI/netI.
Measure $[\sum |u(\mathrm{net}I)| / \sum |\mathrm{net}I|]$ *for all measured reflections.*
The permitted range is $0.0 \rightarrow \infty$. ***[diffrn_reflns]***

_diffrn_reflns_av_unetI/netI (*numb*)
Measure $[\sum |u(\mathrm{net}I)| / \sum |\mathrm{net}I|]$ for all measured reflections.
The permitted range is $0.0 \rightarrow \infty$.
Related item: **_diffrn_reflns_av_sigmaI/netI** (alternate). **[diffrn_reflns]**

_diffrn_reflns_Laue_measured_fraction_full (*numb*)
Fraction of Laue unique reflections (symmetry-independent in the Laue group) measured out to the resolution given in **_diffrn_reflns_resolution_full** or **_diffrn_reflns_theta_full**. The Laue group always contains a centre of symmetry so that the reflection h, k, l is always equivalent to the reflection $-h, -k, -l$ even in space groups without a centre of symmetry. This number should not be less than 0.95, since it represents the fraction of reflections measured in the part of the diffraction pattern that is essentially complete.
The permitted range is $0.95 \rightarrow 1.0$.
Related item: **_diffrn_measured_fraction_theta_full** (alternate).
[diffrn_reflns]

_diffrn_reflns_Laue_measured_fraction_max (*numb*)
Fraction of Laue unique reflections (symmetry-independent in the Laue group) measured out to the resolution given in **_diffrn_reflns_resolution_max** or **_diffrn_reflns_theta_max**. The Laue group always contains a centre of symmetry so that the reflection h, k, l is always equivalent to the reflection $-h, -k, -l$ even in space groups without a centre of symmetry.
The permitted range is $0 \rightarrow 1.0$.
Related item: **_diffrn_measured_fraction_theta_max** (alternate).
[diffrn_reflns]

_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 (*numb*)
The limits on the Miller indices of the intensities specified by **_diffrn_refln_index_h**, ***_k**, ***_l**.
[diffrn_reflns]

_diffrn_reflns_number (*numb*)
The total number of measured intensities, excluding reflections that are classed as systematically absent arising from translational symmetry in the crystal unit cell.
The permitted range is $0 \rightarrow \infty$. **[diffrn_reflns]**

_diffrn_reflns_point_group_measured_fraction_full (*numb*)
Fraction of crystal point-group unique reflections (*i.e.* symmetry-independent in the crystal point group) measured out to the resolution given in **_diffrn_reflns_resolution_full** or **_diffrn_reflns_theta_full**. For space groups that do not contain a centre of symmetry the reflections h, k, l and $-h, -k, -l$ are independent. This number should not be less than 0.95, since it represents the fraction of reflections measured in the part of the diffraction pattern that is essentially complete.
The permitted range is $0.95 \rightarrow 1.0$.
Related item: **_diffrn_measured_fraction_theta_full** (alternate).
[diffrn_reflns]

_diffrn_reflns_point_group_measured_fraction_max (*numb*)
Fraction of crystal point-group unique reflections (*i.e.* symmetry-independent in the crystal point group) measured out to the resolution given in **_diffrn_reflns_resolution_max** or **_diffrn_reflns_theta_max**. For space groups that do not contain a centre of symmetry the reflections h, k, l and $-h, -k, -l$ are independent.
The permitted range is $0 \rightarrow 1.0$.
Related item: **_diffrn_measured_fraction_theta_max** (alternate).
[diffrn_reflns]

_diffrn_reflns_reduction_process (*char*)
A description of the process used to reduce the intensities into structure-factor magnitudes.
Example: 'data averaged using Fisher test'. **[diffrn_reflns]**

_diffrn_reflns_resolution_full (*numb*)
The resolution in reciprocal ångströms at which the measured reflection count is close to complete. The fraction of unique reflections measured out to this angle is given by **_diffrn_measured_fraction_theta_full**.
The permitted range is $0.0 \rightarrow \infty$.
Related item: **_diffrn_reflns_theta_full** (alternate). **[diffrn_reflns]**

_diffrn_reflns_resolution_max (*numb*)
Maximum resolution in reciprocal ångströms of the measured diffraction pattern. The fraction of unique reflections measured out to this angle is given by **_diffrn_measured_fraction_theta_max**
The permitted range is $0.0 \rightarrow \infty$.
Related item: **_diffrn_reflns_theta_max** (alternate). **[diffrn_reflns]**

_diffrn_reflns_theta_full (*numb*)
The θ angle (in degrees) at which the measured reflection count is close to complete. The fraction of unique reflections measured out to this angle is given by **_diffrn_measured_fraction_theta_full**.
The permitted range is $0.0 \rightarrow 90.0$. **[diffrn_reflns]**

_diffrn_reflns_theta_max (*numb*)
Maximum θ angle in degrees for the measured intensities. The fraction of unique reflections measured out to this angle is given by **_diffrn_measured_fraction_theta_max**
The permitted range is $0.0 \rightarrow 90.0$. **[diffrn_reflns]**

_diffrn_reflns_theta_min (*numb*)
Minimum θ angle in degrees for the measured intensities.
The permitted range is $0.0 \rightarrow 90.0$. **[diffrn_reflns]**

_diffrn_reflns_transf_matrix_11
_diffrn_reflns_transf_matrix_12
_diffrn_reflns_transf_matrix_13
_diffrn_reflns_transf_matrix_21
_diffrn_reflns_transf_matrix_22
_diffrn_reflns_transf_matrix_23
_diffrn_reflns_transf_matrix_31
_diffrn_reflns_transf_matrix_32
_diffrn_reflns_transf_matrix_33 (*numb*)
Elements of the matrix used to transform the diffraction reflection indices **_diffrn_refln_index_h**, ***_k**, ***_l** into the **_refln_index_h**, ***_k**, ***_l** indices.

$$(\,h \quad k \quad l\,)_{\text{diffraction}} \begin{pmatrix} 11 & 12 & 13 \\ 21 & 22 & 23 \\ 31 & 32 & 33 \end{pmatrix} = (\,h' \quad k' \quad l'\,)\,.$$

[diffrn_reflns]

DIFFRN_REFLNS_CLASS

Data items in the DIFFRN_REFLNS_CLASS category record details about the classes of reflections measured in the diffraction experiment.

Example 1 – example corresponding to the one-dimensional incommensurately modulated structure of K_2SeO_4.

Each reflection class is defined by the number $m = \sum |m_i|$, where the m_i are the integer coefficients that, in addition to h, k, l, index the corresponding diffraction vector in the basis defined for the reciprocal lattice.

```
loop_
    _diffrn_reflns_class_number
    _diffrn_reflns_class_d_res_high
    _diffrn_reflns_class_d_res_low
    _diffrn_reflns_class_av_R_eq
    _diffrn_reflns_class_code
    _diffrn_reflns_class_description
        1580 0.551 6.136 0.015 'Main'
                                'm=0; main reflections'
        1045 0.551 6.136 0.010
                    'Sat1' 'm=1; first-order satellites'
```

_diffrn_reflns_class_av_R_eq (*numb*)
For each reflection class, the residual $[\sum \mathrm{av}|\Delta(I)| / \sum |\mathrm{av}(I)|]$ for symmetry-equivalent reflections used to calculate the average intensity $\mathrm{av}(I)$. The $\mathrm{av}|\Delta(I)|$ term is the average absolute difference between $\mathrm{av}(I)$ and the individual symmetry-equivalent intensities.
Appears in list containing **_diffrn_reflns_class_code**.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_reflns_class]**

_diffrn_reflns_class_av_sgI/I (*numb*)
This definition has been superseded and is retained here only for archival purposes. Use instead _diffrn_reflns_class_av_uI/I.
Measure $[\sum |u(\mathrm{net}I)| / \sum |\mathrm{net}I|]$ *for all measured intensities in a reflection class.*
Appears in list containing ***_diffrn_reflns_class_code***.
The permitted range is $0.0 \rightarrow \infty$. ***[diffrn_reflns_class]***

_diffrn_reflns_class_av_uI/I (*numb*)
Measure $[\sum |u(\mathrm{net}I)| / \sum |\mathrm{net}I|]$ for all measured intensities in a reflection class.
Appears in list containing **_diffrn_reflns_class_code**.
The permitted range is $0.0 \rightarrow \infty$.
Related item: **_diffrn_reflns_class_av_sgI/I** (alternate).
[diffrn_reflns_class]

_diffrn_reflns_class_code (*char*)
The code identifying a certain reflection class.
Appears in list as essential element of loop structure. May match child data name(s): **_diffrn_refln_class_code**.
Examples: '1', 'm1', 's2'. **[diffrn_reflns_class]**

_diffrn_reflns_class_d_res_high (*numb*)
The smallest value in ångströms of the interplanar spacings of the reflections in each reflection class. This is called the highest resolution for this reflection class.
Appears in list containing **_diffrn_reflns_class_code**.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_reflns_class]**

_diffrn_reflns_class_d_res_low (*numb*)
The highest value in ångströms of the interplanar spacings of the reflections in each reflection class. This is called the lowest resolution for this reflection class.
Appears in list containing **_diffrn_reflns_class_code**.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_reflns_class]**

_diffrn_reflns_class_description (*char*)
Description of each reflection class.
Appears in list containing **_diffrn_reflns_class_code**.
Examples: 'm=1 first order satellites',
'H0L0 common projection reflections'. **[diffrn_reflns_class]**

_diffrn_reflns_class_number (*numb*)
The total number of measured intensities for each reflection class, excluding the systematic absences arising from centring translations.
Appears in list containing **_diffrn_reflns_class_code**.
The permitted range is $0 \rightarrow \infty$. **[diffrn_reflns_class]**

DIFFRN_SCALE_GROUP

Data items in the DIFFRN_SCALE_GROUP category record details of the scaling factors applied to place all intensities in the reflection lists on a common scale. Scaling groups might, for instance, correspond to each film in a multi-film data set or each crystal in a multi-crystal data set.

Example 1 – hypothetical example.

```
loop_
_diffrn_scale_group_code
_diffrn_scale_group_I_net
  1    .86473
  2   1.0654
```

_diffrn_scale_group_code (*char*)
The code identifying a specific measurement group (*e.g.* for multi-film or multi-crystal data). The code must match a **_diffrn_refln_scale_group_code** in the reflection list.
Appears in list as essential element of loop structure. May match child data name(s): **_diffrn_refln_scale_group_code**.
Examples: '1', '2', '3', 's1', 'A', 'B', 'c1', 'c2', 'c3'. **[diffrn_scale_group]**

_diffrn_scale_group_I_net (*numb*)
The scale for a specific measurement group which is to be multiplied with the net intensity to place all intensities in the **_diffrn_refln_** or **_refln_** list on a common scale.
Appears in list containing **_diffrn_scale_group_code**.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_scale_group]**

DIFFRN_SOURCE

Data items in the DIFFRN_SOURCE category record details of the source of radiation used in the diffraction experiment.

Example 1 – based on PDB entry 5HVP and laboratory records for the structure corresponding to PDB entry 5HVP.

```
_diffrn_source                'rotating anode X-ray tube'
_diffrn_source_type           'Rigaku RU-200'
_diffrn_source_power          50
_diffrn_source_current        180
_diffrn_source_size           '8 mm x 0.4 mm broad focus'
```

_diffrn_radiation_source (*char*)
This definition has been superseded and is retained here only for archival purposes. Use instead _diffrn_source.
The source of radiation.
[diffrn_source]

_diffrn_source (*char*)
The general class of the source of radiation.
Related item: **_diffrn_radiation_source** (alternate).
Examples: 'sealed X-ray tube', 'nuclear reactor', 'spallation source', 'electron microscope', 'rotating-anode X-ray tube', 'synchrotron'.
[diffrn_source]

_diffrn_source_current (*numb*)
The current in milliamperes at which the radiation source was operated.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_source]**

_diffrn_source_details (*char*)
A description of special aspects of the source.
[diffrn_source]

_diffrn_source_power (*numb*)
The power in kilowatts at which the radiation source was operated.
The permitted range is $0.0 \rightarrow \infty$. **[diffrn_source]**

_diffrn_source_size (*char*)
The dimensions of the source as viewed from the sample.
Examples: '8mm x 0.4 mm fine-focus', 'broad focus'. **[diffrn_source]**

_diffrn_source_take-off_angle (*numb*)
The complement of the angle in degrees between the normal to the surface of the X-ray tube target and the primary X-ray beam for beams generated by traditional X-ray tubes.
The permitted range is 0 → 90.
Example: '1.53'. **[diffrn_source]**

_diffrn_source_target (*char*)
The chemical element symbol for the X-ray target (usually the anode) used to generate X-rays. This can also be used for spallation sources.
The data value must be one of the following:

```
H  He Li Be B  C  N  O  F  Ne Na Mg Al Si P
S  Cl Ar K  Ca Sc Ti V  Cr Mn Fe Co Ni Cu Zn
Ga Ge As Se Br Kr Rb Sr Y  Zr Nb Mo Tc Ru Rh
Pd Ag Cd In Sn Sb Te I  Xe Cs Ba La Ce Pr Nd
Pm Sm Eu Gd Tb Dy Ho Er Tm Yb Lu Hf Ta W  Re
Os Ir Pt Au Hg Tl Pb Bi Po At Rn Fr Ra Ac Th
Pa U  Np Pu Am Cm Bk Cf Es Fm Md No Lr
```

[diffrn_source]

_diffrn_source_type (*char*)
The make, model or name of the source of radiation.
Examples: 'NSLS beamline X8C', 'Rigaku RU200'. **[diffrn_source]**

_diffrn_source_voltage (*numb*)
The voltage in kilovolts at which the radiation source was operated.
The permitted range is 0.0 → ∞. **[diffrn_source]**

DIFFRN_STANDARD_REFLN

Data items in the DIFFRN_STANDARD_REFLN category record details about the reflections treated as standards during the measurement of the diffraction intensities. Note that these are the individual standard reflections, not the results of the analysis of the standard reflections.

*Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C**47**, 2276–2277].*

```
loop_
_diffrn_standard_refln_index_h
_diffrn_standard_refln_index_k
_diffrn_standard_refln_index_l
3 2 4    1 9 1    3 0 10
```

_diffrn_standard_refln_code (*char*)
The code identifying a reflection measured as a standard reflection with the indices **_diffrn_standard_refln_index_**. This is the same code as the **_diffrn_refln_standard_code** in the **_diffrn_refln_** list.
Appears in list containing **_diffrn_standard_refln_index_**. May match child data name(s): **_diffrn_refln_standard_code**.
Examples: '1', '2', '3', 's1', 'A', 'B'. **[diffrn_standard_refln]**

_diffrn_standard_refln_index_h
_diffrn_standard_refln_index_k
_diffrn_standard_refln_index_l (*numb*)
Miller indices of standard reflections used in the diffraction measurement process.
Appears in list as essential element of loop structure. **[diffrn_standard_refln]**

DIFFRN_STANDARDS

Data items in the DIFFRN_STANDARDS category record details about the set of standard reflections used to monitor intensity stability during the measurement of diffraction intensities. Note that these records describe properties common to the set of standard reflections, not the standard reflections themselves.

*Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C**47**, 2276–2277].*

```
_diffrn_standards_number            3
_diffrn_standards_interval_time     120
_diffrn_standards_decay_%           0
```

_diffrn_standards_decay_% (*numb, su*)
The percentage decrease in the mean intensity of the set of standard reflections measured at the start of the measurement process and at the finish. This value usually affords a measure of the overall decay in crystal quality during the diffraction measurement process. Negative values are used in exceptional instances where the final intensities are greater than the initial ones. If no measurable decay has occurred, the standard uncertainty should be quoted to indicate the maximum possible value the decay might have. A range of 3 standard uncertainties is considered possible. Thus 0.0(1) would indicate a decay of less than 0.3% or an enhancement of less than 0.3%.
The permitted range is −∞ → 100.
Examples: '0.5(1)' (represents a decay between 0.2% and 0.8%), '-1(1)' (the change in the standards lies between a decay of 2% and an increase of 4%), '0.0(2)' (the change in the standards lies between a decay of 0.6% and an increase of 0.6%.).
[diffrn_standards]

_diffrn_standards_interval_count
_diffrn_standards_interval_time (*numb*)
The number of reflection intensities, or the time in minutes, between the measurement of standard reflection intensities.
The permitted range is 0 → ∞. **[diffrn_standards]**

_diffrn_standards_number (*numb*)
The number of unique standard reflections used during the measurement of the diffraction intensities.
The permitted range is 0 → ∞. **[diffrn_standards]**

_diffrn_standards_scale_sigma (*numb*)
This definition has been superseded and is retained here only for archival purposes. Use instead _diffrn_standards_scale_u.
The standard uncertainty (e.s.d.) of the individual mean standard scales applied to the intensity data.
The permitted range is 0.0 → ∞. ***[diffrn_standards]***

_diffrn_standards_scale_u (*numb*)
The standard uncertainty of the individual mean standard scales applied to the intensity data.
The permitted range is 0.0 → ∞.
Related item: **_diffrn_standards_scale_sigma** (alternate).
[diffrn_standards]

DISTRIBUTED_DENSITY

Data items in the DISTRIBUTED_DENSITY category describe the geometric arrangement of an atom or atoms when they are distributed uniformly over a line or surface such as a ring, cylindrical shell or spherical shell, the line or surface being given a thickness through the application of an atomic displacement parameter.

Example 1 – This example is fictitious (and chemically implausible) but it is designed to illustrate how a complex system of distributed density can be recorded. In this example pentamethyl cyclopentadiene (Cp) and borazole occupy the same location in the crystal in the ratio 5:1. The atoms of the borazole ring are fixed as are three quarters of the atoms in the Cp* ring, but the remaining quarter of the Cp* molecules are freely rotating around the cylindrical Cp* axis. The rotating Cp* molecules give rise to two concentric rings of density, one from the atoms in the ring and the other from the methyl groups (hydrogen atoms are ignored). On top of these rings lie the atoms of the fixed Cp* molecules. The atoms of the borazole molecule also lie over the inner Cp* ring. Full details of the chemical composition are given in the ATOM_SITE loop together with the positions of the fixed atoms. The coordinates of the atoms that give rise to the distributed ring of density are set to '.', meaning that they have no significance as the atoms are dummy atoms. They are included to give the correct composition when* **_atom_site_occupancy** *and* **_atom_site_symmetry_multiplicity** *are given. The composition defined in the ATOM_SITE loop is linked to the DISTRIBUTED_DENSITY loop through the parent-child identifiers, 'an1' and 'an2' (for annulus 1 and 2). The one quarter of the Cp* molecules that are rotating have the occupation number of 0.208 = 2/24 = 5/6 (the total occupancy of the Cp*) x 1/4 (the portion rotating). The three quarters that are in fixed positions have the occupation number of 0.625 = 15/24 = 5/6 x 3/4.*

```
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
_atom_site_occupancy
_atom_site_symmetry_multiplicity
_atom_site_adp_type
_atom_site_distributed_density_id
_atom_site_calc_flag
 # Inner ring of cyclopentadiene carbon atoms and borazole
 C1   C -0.1362(8) -0.0974(8) -0.3116(10) 0.0662(18) 0.625(1) 4 Uiso .   d
 C2   C -0.1060(8) -0.2165(8) -0.1837(10) 0.071(2)   0.625(1) 4 Uiso .   d
 C3   C -0.1774(9) -0.1939(9) -0.0820(11) 0.082(2)   0.625(1) 4 Uiso .   d
 C4   C -0.2529(9) -0.0561(9) -0.1479(12) 0.084(2)   0.625(1) 4 Uiso .   d
 C5   C -0.2261(8) -0.0002(8) -0.2891(10) 0.072(2)   0.625(1) 4 Uiso .   d
 C1a  C   .          .          .          .         0.208(1) 4 .    an1 dum
 C2a  C   .          .          .          .         0.208(1) 4 .    an1 dum
 C3a  C   .          .          .          .         0.208(1) 4 .    an1 dum
 C4a  C   .          .          .          .         0.208(1) 4 .    an1 dum
 C5a  C   .          .          .          .         0.208(1) 4 .    an1 dum
 N1   N -0.1375(8) -0.0968(8) -0.3201(10) 0.065(2)   0.167(1) 4 Uiso .   d
 B1   B -0.1002(8) -0.2265(8) -0.1728(10) 0.071(2)   0.167(1) 4 Uiso .   d
 N2   N -0.1402(8) -0.1034(8) -0.0765(10) 0.076(2)   0.167(1) 4 Uiso .   d
 B2   B -0.2370(9) -0.0364(9) -0.1832(10) 0.085(2)   0.167(1) 4 Uiso .   d
 N3   N -0.2893(8)  0.0034(8) -0.3621(10) 0.062(2)   0.167(1) 4 Uiso .   d
 B3   B -0.2246(9) -0.0452(9) -0.3004(11) 0.073(2)   0.167(1) 4 Uiso .   d
 # Outer ring of methyl groups
 C11  C -0.0951    -0.0733    -0.4330     0.1901     0.625(1) 4 Uani .   d
 C12  C -0.0272    -0.3236    -0.1750     0.1990     0.625(1) 4 Uani .   d
 C13  C -0.1719    -0.2833     0.0404     0.2483     0.625(1) 4 Uani .   d
 C14  C -0.3291    -0.0080    -0.0844     0.2450     0.625(1) 4 Uani .   d
 C15  C -0.2817     0.1218    -0.3770     0.2219     0.625(1) 4 Uani .   d
 C11a C   .          .          .          .         0.208(1) 4 .    an2 dum
 C12a C   .          .          .          .         0.208(1) 4 .    an2 dum
 C13a C   .          .          .          .         0.208(1) 4 .    an2 dum
 C14a C   .          .          .          .         0.208(1) 4 .    an2 dum
 C15a C   .          .          .          .         0.208(1) 4 .    an2 dum


# Details of the two rings of distributed density are given
# in the following loop
loop_
_distributed_density_id
_distributed_density_shape
_distributed_density_position_x
_distributed_density_position_y
_distributed_density_position_z
_distributed_density_radius
_distributed_density_direction_h
_distributed_density_direction_k
_distributed_density_direction_l
_distributed_density_Uiso
_distributed_density_symmetry_multiplicity
an1 ring -0.1810(8)  -0.1133(8)  -0.2058(8)
          1.198(6)    1.35(2) 0.07(2) -0.45(2)   0.052(2)   4
an2 ring -0.1873(14) -0.1156(14) -0.2210(2)
          2.626(6)    1.30(2) 0.10(2) -0.40(2)   0.131(3)   4
```

_distributed_density_details (*char*)

Information about the distribution of density not given in other items.

May appear in list containing **_distributed_density_id**.

Example:

```
; The distribution was modelled using a disk of
  density of the given radius.
;
```

[distributed_density]

_distributed_density_direction_h
_distributed_density_direction_k
_distributed_density_direction_l (*numb, su*)

The (covariant) components on a reciprocal-lattice basis of a vector of arbitrary length used to indicate the direction of the unique axis of the distribution, *e.g.* the axis of a cylindrical shell or the normal to the plane of a ring.

May appear in list containing **_distributed_density_id**.

[distributed_density]

_distributed_density_id (*char*)

An identifier that links the atom defined by **_atom_site_label** with a distributed density defined in the DISTRIBUTED_DENSITY category.

May appear in list as essential element of loop structure. May match child data name(s): **_atom_site_distributed_density_id**.

[distributed_density]

_distributed_density_length (*numb, su*)

The length of the line or cylindrical shell of distributed density in Ångström units.

May appear in list containing **_distributed_density_id**.

The permitted range is $0.0 \rightarrow \infty$.

[distributed_density]

_distributed_density_position_x
_distributed_density_position_y
_distributed_density_position_z (*numb, su*)

The position of the centroid of the distributed density in fractions of the unit cell values.

May appear in list containing **_distributed_density_id**.

[distributed_density]

_distributed_density_radius (*numb, su*)

The radius of the ring, or of the cylindrical or spherical shell, of distributed density in Ångström units.

May appear in list containing **_distributed_density_id**.

The permitted range is $0.0 \rightarrow \infty$.

[distributed_density]

_distributed_density_shape (*char*)

A flag that indicates the shape of the distributed density. The lines and ring are one-dimensional distributions of atoms and the cylindrical shell and spherical shell are two-dimensional distributions. In each case the root-mean-square thickness of the distribution is given by the atomic displacement parameter defined in **_distributed_density_Uiso**.

May appear in list containing **_distributed_density_id**.

The data value must be one of the following:

line	line segment
infline	infinite line running through the crystal
ring	circular ring
cylshell	cylindrical shell of finite length
infcylshell	cylindrical shell running through the crystal
sphereshell	spherical shell
other	give details in **_distributed_density_details**

[distributed_density]

_distributed_density_symmetry_multiplicity (*numb*)
The number of images of the centroid of the distributed density that the space group symmetry generates in the unit cell reported in the CELL category. It is the number that appears in *International Tables for Crystallography* Vol. A (2002) for the Wyckoff position occupied by the centroid. In this treatment the symmetry of the distribution itself is ignored, including any operations of its point group that are part of the crystallographic site symmetry of the centroid. All the atoms that give rise to the distributed density should therefore be listed in the ATOM_SITE category even if they, or the centroid of the distribution, lie on crystallographic special positions. For example, if the distribution is a ring and the centroid of the ring lies on a crystallographic mirror plane, all the atoms in the ring are listed if the ring lies either in or perpendicular to the mirror plane since the mirror image of the ring lies over the ring itself. If the ring is at some arbitrary angle to the mirror plane, the mirror generates a second ring and both rings should be described independently. However, because both rings cannot be simultaneously occupied, the occupation numbers given in the ATOM_SITE category must have a value equal to or less than 0.5.
May appear in list containing **_distributed_density_id**.
The permitted range is $1 \rightarrow 192$. **[distributed_density]**

_distributed_density_Uiso (*numb, su*)
The factor $\exp(-Ux^{-2})$ is applied to all parts of the distribution, where U = **_distributed_density_Uiso** and x is the distance from the ideal one- or two-dimensional shape. This emulates the effects of thermal motion or static displacement from the ideal positions described in this category and has the effect of converting the simple one- or two-dimensional geometric shapes into three-dimensional objects of mean square thickness U.
May appear in list containing **_distributed_density_id**.
The permitted range is $0.0 \rightarrow \infty$.
Example: '`0.018(3)`'. **[distributed_density]**

EXPTL

Data items in the EXPTL category record details about the experimental work prior to the intensity measurements and details about the absorption-correction technique employed.

*Example 1 – based on a paper by Steiner [Acta Cryst. (1996), C**52**, 2554–2556].*

```
_exptl_absorpt_coefficient_mu     0.962
_exptl_absorpt_correction_type    psi-scan
_exptl_absorpt_process_details
        'North, Phillips & Mathews (1968)'
_exptl_absorpt_correction_T_min   0.929
_exptl_absorpt_correction_T_max   0.997
```

_exptl_absorpt_coefficient_mu (*numb*)
The absorption coefficient μ in reciprocal millimetres calculated from the atomic content of the cell, the density and the radiation wavelength.
The permitted range is $0.0 \rightarrow \infty$. **[exptl]**

_exptl_absorpt_correction_T_max
_exptl_absorpt_correction_T_min (*numb*)
The maximum and minimum transmission factors applied to the diffraction pattern measured in this experiment. These factors are also referred to as the absorption correction A or $1/A*$. As this value is the one that is applied to the measured intensities, it includes the correction for absorption by the specimen mount and diffractometer as well as by the specimen itself.
The permitted range is $0.0 \rightarrow 1.0$. **[exptl]**

_exptl_absorpt_correction_type (*char*)
The absorption-correction type and method. The value 'empirical' should *not* be used unless more detailed information is not available.
The data value must be one of the following:

`analytical`	analytical from crystal shape
`cylinder`	cylindrical
`empirical`	empirical from intensities
`gaussian`	Gaussian from crystal shape
`integration`	integration from crystal shape
`multi-scan`	symmetry-related measurements
`none`	no absorption correction applied
`numerical`	numerical from crystal shape
`psi-scan`	ψ-scan corrections
`refdelf`	refined from ΔF
`sphere`	spherical

[exptl]

_exptl_absorpt_process_details (*char*)
Description of the absorption process applied to the intensities. A literature reference should be supplied for ψ-scan techniques.
Examples: '`Tompa analytical`', '`MolEN (Fair, 1990)`', '`(North, Phillips & Mathews, 1968)`'. **[exptl]**

_exptl_crystals_number (*numb*)
The total number of crystals used for the measurement of intensities.
The permitted range is $1 \rightarrow \infty$. **[exptl]**

_exptl_special_details (*char*)
Any special information about the experimental work prior to the intensity measurements. See also **_exptl_crystal_preparation**.
[exptl]

_exptl_transmission_factor_max (*numb, su*)
The calculated maximum value of the transmission factor for the specimen. Its value does not include the effects of absorption in the specimen mount. The presence of this item does not imply that the structure factors have been corrected for absorption. The applied correction should be given by **_exptl_absorpt_correction_T_max**.
The permitted range is $0.0 \rightarrow 1.0$. **[exptl]**

_exptl_transmission_factor_min (*numb, su*)
The calculated minimum value of the transmission factor for the specimen. Its value does not include the effects of absorption in the specimen mount. The presence of this item does not imply that the structure factors have been corrected for absorption. The applied correction should be given by **_exptl_absorpt_correction_T_min**.
The permitted range is $0.0 \rightarrow 1.0$. **[exptl]**

EXPTL_CRYSTAL

Data items in the EXPTL_CRYSTAL category record details about experimental measurements on the crystal or crystals used, such as shape, size or density.

Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C47, 2276–2277].

```
_exptl_crystal_description          prism
_exptl_crystal_colour               colourless
_exptl_crystal_size_max             0.32
_exptl_crystal_size_mid             0.27
_exptl_crystal_size_min             0.10
_exptl_crystal_density_diffrn       1.146
_exptl_crystal_density_meas         ?
_exptl_crystal_density_method       'not measured'
_exptl_crystal_F_000                656
```

Example 2 – using separate items to define upper and lower limits for a value.

```
_exptl_crystal_density_meas_gt       2.5
_exptl_crystal_density_meas_lt       5.0
```

Example 3 – here the density was measured at some unspecified temperature below room temperature.

```
_exptl_crystal_density_meas_temp_lt    300
```

_exptl_crystal_colour (*char*)

The colour of the crystal.

May appear in list containing **_exptl_crystal_id**.

Related items:

_exptl_crystal_colour_lustre (alternate),
_exptl_crystal_colour_modifier (alternate),
_exptl_crystal_colour_primary (alternate).

Example: 'dark green'. **[exptl_crystal]**

_exptl_crystal_colour_lustre (*char*)

The enumeration list of standardized names developed for the International Centre for Diffraction Data. The colour of a crystal is given by the combination of **_exptl_crystal_colour_modifier** with **_exptl_crystal_colour_primary**, as in 'dark-green' or 'bluish-violet', if necessary combined with **_exptl_crystal_colour_lustre**, as in 'metallic-green'.

May appear in list containing **_exptl_crystal_id**.

Related item: **_exptl_crystal_colour** (alternate).

The data value must be one of the following:

- metallic
- dull
- clear

[exptl_crystal]

_exptl_crystal_colour_modifier (*char*)

The enumeration list of standardized names developed for the International Centre for Diffraction Data. The colour of a crystal is given by the combination of **_exptl_crystal_colour_modifier** with **_exptl_crystal_colour_primary**, as in 'dark-green' or 'bluish-violet', if necessary combined with **_exptl_crystal_colour_lustre**, as in 'metallic-green'.

May appear in list containing **_exptl_crystal_id**.

Related item: **_exptl_crystal_colour** (alternate).

The data value must be one of the following:

- light
- dark
- whitish
- blackish
- grayish
- brownish
- reddish
- pinkish
- orangish
- yellowish
- greenish
- bluish

[exptl_crystal]

_exptl_crystal_colour_primary (*char*)

The enumeration list of standardized names developed for the International Centre for Diffraction Data. The colour of a crystal is given by the combination of **_exptl_crystal_colour_modifier** with **_exptl_crystal_colour_primary**, as in 'dark-green' or 'bluish-violet', if necessary combined with **_exptl_crystal_colour_lustre**, as in 'metallic-green'.

May appear in list containing **_exptl_crystal_id**.

Related item: **_exptl_crystal_colour** (alternate).

The data value must be one of the following:

- colourless
- white
- black
- gray
- brown
- red
- pink
- orange
- yellow
- green
- blue
- violet

[exptl_crystal]

_exptl_crystal_density_diffrn (*numb*)

Density values calculated from the crystal cell and contents. The units are megagrams per cubic metre (grams per cubic centimetre).

May appear in list containing **_exptl_crystal_id**.

The permitted range is $0.0 \rightarrow \infty$. **[exptl_crystal]**

_exptl_crystal_density_meas (*numb, su*)

Density values measured using standard chemical and physical methods. The units are megagrams per cubic metre (grams per cubic centimetre).

May appear in list containing **_exptl_crystal_id**.

The permitted range is $0.0 \rightarrow \infty$. **[exptl_crystal]**

_exptl_crystal_density_meas_gt (*numb*)

The value above which the density measured using standard chemical and physical methods lies. The units are megagrams per cubic metre (grams per cubic centimetre). **_exptl_crystal_density_meas_gt** and **_exptl_crystal_density_meas_lt** should not be used to report new experimental work, for which **_exptl_crystal_density_meas** should be used. These items are intended for use in reporting information in existing databases and archives which would be misleading if reported under **_exptl_crystal_density_meas**.

May appear in list containing **_exptl_crystal_id**.

The permitted range is $0.0 \rightarrow \infty$.

Related item: **_exptl_crystal_density_meas** (alternate).

Example: '2.5' (lower limit for the density (only the range within which the density lies was given in the original paper)). **[exptl_crystal]**

_exptl_crystal_density_meas_lt (*numb*)

The value below which the density measured using standard chemical and physical methods lies. The units are megagrams per cubic metre (grams per cubic centimetre). **_exptl_crystal_density_meas_gt** and **_exptl_crystal_density_meas_lt** should not be used to report new experimental work, for which **_exptl_crystal_density_meas** should be used. These items are intended for use in reporting information in existing databases and archives which would be misleading if reported under **_exptl_crystal_density_meas**.

May appear in list containing **_exptl_crystal_id**.

The permitted range is $0.0 \rightarrow \infty$.

Related item: **_exptl_crystal_density_meas** (alternate).

Examples: '1.0' (specimen floats in water), '5.0' (upper limit for the density (only the range within which the density lies was given in the original paper)). **[exptl_crystal]**

_exptl_crystal_density_meas_temp (*numb, su*)

Temperature in kelvins at which **_exptl_crystal_density_meas** was determined.

May appear in list containing **_exptl_crystal_id**.

The permitted range is $0.0 \rightarrow \infty$. **[exptl_crystal]**

_exptl_crystal_density_meas_temp_gt (*numb*)
Temperature in kelvins above which **_exptl_crystal_density_meas** was determined. **_exptl_crystal_density_meas_temp_gt** and **_exptl_crystal_density_meas_temp_lt** should not be used for reporting new work, for which the correct temperature of measurement should be given. These items are intended for use in reporting information stored in databases or archives which would be misleading if reported under **_exptl_crystal_density_meas_temp.**
May appear in list containing **_exptl_crystal_id**.
The permitted range is $0.0 \rightarrow \infty$.
Related item: **_exptl_crystal_density_meas_temp** (alternate).
[exptl_crystal]

_exptl_crystal_density_meas_temp_lt (*numb*)
Temperature in kelvins below which **_exptl_crystal_density_meas** was determined. **_exptl_crystal_density_meas_temp_gt** and **_exptl_crystal_density_meas_temp_lt** should not be used for reporting new work, for which the correct temperature of measurement should be given. These items are intended for use in reporting information stored in databases or archives which would be misleading if reported under **_exptl_crystal_density_meas_temp.**
May appear in list containing **_exptl_crystal_id**.
The permitted range is $0.0 \rightarrow \infty$.
Related item: **_exptl_crystal_density_meas_temp** (alternate).
Example: '300' (The density was measured at some unspecified temperature below room temperature.). **[exptl_crystal]**

_exptl_crystal_density_method (*char*)
The method used to measure **_exptl_crystal_density_meas.**
May appear in list containing **_exptl_crystal_id**.
Examples: 'flotation in aqueous KI', 'not measured', 'Berman density torsion balance'. **[exptl_crystal]**

_exptl_crystal_description (*char*)
A description of the quality and habit of the crystal. The crystal dimensions should not normally be reported here; use instead **_exptl_crystal_size_** for the gross dimensions of the crystal and **_exptl_crystal_face_** to describe the relationship between individual faces.
May appear in list containing **_exptl_crystal_id**. **[exptl_crystal]**

_exptl_crystal_F_000 (*numb*)
The effective number of electrons in the crystal unit cell contributing to $F(000)$. This may contain dispersion contributions and is calculated as

$$F(000) = \left[\left(\sum f_r\right)^2 + \left(\sum f_i\right)^2\right]^{1/2},$$

where f_r = real part of the scattering factors at $\theta = 0°$, f_i = imaginary part of the scattering factors at $\theta = 0°$ and the sum is taken over each atom in the unit cell.
May appear in list containing **_exptl_crystal_id**.
The permitted range is $0.0 \rightarrow \infty$. **[exptl_crystal]**

_exptl_crystal_id (*char*)
Code identifying each crystal if multiple crystals are used. It is used to link with **_diffrn_refln_crystal_id** in the intensity measurements and with **_refln_crystal_id** in the **_refln_** list.
Appears in list as essential element of loop structure. May match child data name(s): **_diffrn_refln_crystal_id**, **_refln_crystal_id**. **[exptl_crystal]**

_exptl_crystal_preparation (*char*)
Details of crystal growth and preparation of the crystal (*e.g.* mounting) prior to the intensity measurements.
May appear in list containing **_exptl_crystal_id**.
Example: 'mounted in an argon-filled quartz capillary'.
[exptl_crystal]

_exptl_crystal_pressure_history (*char*)
Relevant details concerning the pressure history of the sample.
May appear in list containing **_exptl_crystal_id**. **[exptl_crystal]**

_exptl_crystal_recrystallization_method (*char*)
Describes the method used to recrystallize the sample. Sufficient details should be given for the procedure to be repeated. The temperature or temperatures should be given as well as details of the solvent, flux or carrier gas with concentrations or pressures and ambient atmosphere.
[exptl_crystal]

_exptl_crystal_size_length
_exptl_crystal_size_max
_exptl_crystal_size_mid
_exptl_crystal_size_min
_exptl_crystal_size_rad (*numb*)
The maximum, medial and minimum dimensions in millimetres of the crystal. If the crystal is a sphere, then the ***_rad** item is its radius. If the crystal is a cylinder, then the ***_rad** item is its radius and the ***_length** item is its length. These may appear in a list with **_exptl_crystal_id** if multiple crystals are used in the experiment.
May appear in list containing **_exptl_crystal_id**.
The permitted range is $0.0 \rightarrow \infty$. **[exptl_crystal]**

_exptl_crystal_thermal_history (*char*)
Relevant details concerning the thermal history of the sample.
May appear in list containing **_exptl_crystal_id**. **[exptl_crystal]**

EXPTL_CRYSTAL_FACE

Data items in the EXPTL_CRYSTAL_FACE category record details of the crystal faces.

Example 1 – based on structure PAWD2 of Vittal & Dean [Acta Cryst. (1996), C52, 1180–1182].

```
loop_
_exptl_crystal_face_index_h
_exptl_crystal_face_index_k
_exptl_crystal_face_index_l
_exptl_crystal_face_perp_dist
     0   -1   -2    .18274
     1    0   -2    .17571
    -1    1   -2    .17845
    -2    1    0    .21010
    -1    0    2    .18849
     1   -1    2    .20605
     2   -1    0    .24680
    -1    2    0    .19688
     0    1    2    .15206
```

_exptl_crystal_face_diffr_chi
_exptl_crystal_face_diffr_kappa
_exptl_crystal_face_diffr_phi
_exptl_crystal_face_diffr_psi (*numb*)
The goniometer angle settings in degrees when the perpendicular to the specified crystal face is aligned along a specified direction (*e.g.* the bisector of the incident and reflected beams in an optical goniometer).
Appears in list containing **_exptl_crystal_face_index_**.
[exptl_crystal_face]

_exptl_crystal_face_index_h
_exptl_crystal_face_index_k
_exptl_crystal_face_index_l (*numb*)
Miller indices of the crystal face associated with the value **_exptl_crystal_face_perp_dist.**
Appears in list as essential element of loop structure. **[exptl_crystal_face]**

_exptl_crystal_face_perp_dist (*numb*)
The perpendicular distance in millimetres from the face to the centre of rotation of the crystal.
Appears in list containing **_exptl_crystal_face_index_**.
The permitted range is $0.0 \rightarrow \infty$. **[exptl_crystal_face]**

GEOM

Data items in the GEOM and related (GEOM_ANGLE, GEOM_BOND, GEOM_CONTACT, GEOM_HBOND and GEOM_TORSION) categories record details about the molecular and crystal geometry as calculated from the ATOM, CELL and SYMMETRY data. Geometry data are usually redundant, in that they can be calculated from other more fundamental quantities in the data block. However, they serve the dual purposes of providing a check on the correctness of both sets of data and of enabling the most important geometric data to be identified for publication by setting the appropriate publication flag.

*Example 1 – based on data set bagan of Yamane & DiSalvo [Acta Cryst. (1996), C**52**, 760–761].*

```
    _geom_special_details
;  All esds (except the esd in the dihedral angle between
   two l.s. planes) are estimated using the full covariance
   matrix. The cell esds are taken into account individually
   in the estimation of esds in distances, angles and
   torsion angles; correlations between esds in cell
   parameters are only used when they are defined by crystal
   symmetry. An approximate (isotropic) treatment of cell
   esds is used for estimating esds involving l.s. planes.
;
```

_geom_special_details (*char*)
The description of geometrical information not covered by the existing data names in the geometry categories, such as least-squares planes.

[geom]

GEOM_ANGLE

Data items in the GEOM_ANGLE category record details about the bond angles as calculated from the ATOM, CELL and SYMMETRY data.

*Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C**47**, 2276–2277].*

```
loop_
_geom_angle_atom_site_label_1
_geom_angle_atom_site_label_2
_geom_angle_atom_site_label_3
_geom_angle
_geom_angle_site_symmetry_1
_geom_angle_site_symmetry_2
_geom_angle_site_symmetry_3
_geom_angle_publ_flag
 C2  O1  C5   111.6(2)  1_555  1_555  1_555  yes
 O1  C2  C3   110.9(2)  1_555  1_555  1_555  yes
 O1  C2  O21  122.2(3)  1_555  1_555  1_555  yes
 C3  C2  O21  127.0(3)  1_555  1_555  1_555  yes
 C2  C3  N4   101.3(2)  1_555  1_555  1_555  yes
 C2  C3  C31  111.3(2)  1_555  1_555  1_555  yes
 C2  C3  H3   107(1)    1_555  1_555  1_555  no
 N4  C3  C31  116.7(2)  1_555  1_555  1_555  yes
# - - - - data truncated for brevity - - - -
```

_geom_angle (*numb, su*)
Angle in degrees defined by the three sites **_geom_angle_atom_site_label_1**, ***_2** and ***_3**. The site at ***_2** is at the apex of the angle.
Appears in list containing **_geom_angle_atom_site_label_**. **[geom_angle]**

_geom_angle_atom_site_label_1
_geom_angle_atom_site_label_2
_geom_angle_atom_site_label_3 (*char*)
The labels of the three atom sites which define the angle given by **_geom_angle**. These must match labels specified as **_atom_site_label** in the atom list. Label 2 identifies the site at the apex of the angle.
Appears in list as essential element of loop structure. **Must** match parent data name **_atom_site_label**. **[geom_angle]**

_geom_angle_publ_flag (*char*)
This code signals whether the angle is referred to in a publication or should be placed in a table of significant angles.
Appears in list containing **_geom_angle_atom_site_label_**.
The data value must be one of the following:

no	do not include angle in special list
n	abbreviation for 'no'
yes	do include angle in special list
y	abbreviation for 'yes'

Where no value is given, the assumed value is 'no'. **[geom_angle]**

_geom_angle_site_symmetry_1
_geom_angle_site_symmetry_2
_geom_angle_site_symmetry_3 (*char*)
The symmetry code of each atom site as the symmetry-equivalent position number '*n*' and the cell translation number '*klm*'. These numbers are combined to form the code '*n klm*' or *n_klm*. The character string *n_klm* is composed as follows: *n* refers to the symmetry operation that is applied to the coordinates stored in **_atom_site_fract_x**, **_atom_site_fract_y** and **_atom_site_fract_z**. It must match a number given in **_space_group_symop_id**. k, l and m refer to the translations that are subsequently applied to the symmetry-transformed coordinates to generate the atom used in calculating the angle. These translations (x, y, z) are related to (k, l, m) by the relations $k = 5 + x$, $l = 5 + y$, $m = 5 + z$. By adding 5 to the translations, the use of negative numbers is avoided.
Appears in list containing **_geom_angle_atom_site_label_**.
Examples: '.' (no symmetry or translation to site), '4' (4th symmetry operation applied), '7_645' (7th symmetry position: $+a$ on x, $-b$ on y). **[geom_angle]**

GEOM_BOND

Data items in the GEOM_BOND category record details about bonds as calculated from the ATOM, CELL and SYMMETRY data.

*Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C**47**, 2276–2277].*

```
loop_
_geom_bond_atom_site_label_1
_geom_bond_atom_site_label_2
_geom_bond_distance
_geom_bond_site_symmetry_1
_geom_bond_site_symmetry_2
_geom_bond_publ_flag
  O1  C2   1.342(4)  1_555  1_555  yes
  O1  C5   1.439(3)  1_555  1_555  yes
  C2  C3   1.512(4)  1_555  1_555  yes
  C2  O21  1.199(4)  1_555  1_555  yes
  C3  N4   1.465(3)  1_555  1_555  yes
  C3  C31  1.537(4)  1_555  1_555  yes
  C3  H3   1.00(3)   1_555  1_555  no
  N4  C5   1.472(3)  1_555  1_555  yes
# - - - - data truncated for brevity - - - -
```

Example 2 – An example showing a listing of only symmetry unique bonds. In high-symmetry structures when many bonds are related by symmetry, it may not be necessary or desirable to list all the bonds in the environment of the first named atom. Some users may wish to give only the symmetry independent distances and supply a multiplicity to indicate how many such bonds are found in the atomic environment.

```
loop_
_geom_bond_atom_site_label_1
_geom_bond_atom_site_label_2
_geom_bond_distance
_geom_bond_multiplicity
Ca1   F1   2.495(9)    1
Ca1   F2   2.291(10)   2
Ca1   F2   2.391(11)   2
Ca1   F3   2.214(11)   2
Cr1   F1   1.940(11)   2
Cr1   F2   1.918(9)    2
Cr1   F3   1.848(10)   2
```

Example 3 – The same structure as in Example 2, but where the multiplicity is given with a full bond list. Note the use of a value of 0 for ***_geom_bond_multiplicity*** *in such a case.*

```
loop_
_geom_bond_atom_site_label_1
_geom_bond_atom_site_label_2
_geom_bond_site_symmetry_2
_geom_bond_distance
_geom_bond_multiplicity
Ca1   F1   1_555  2.495(9)    1
Ca1   F2   1_555  2.291(10)   2
Ca1   F2   2_555  2.291(10)   0
Ca1   F2   3_565  2.391(11)   2
Ca1   F2   4_555  2.391(11)   0
Ca1   F3   2_545  2.214(11)   2
Ca1   F3   5_555  2.214(11)   0
Cr1   F1   1_555  1.940(11)   2
Cr1   F1   2_555  1.940(11)   0
Cr1   F2   1_555  1.918(9)    2
Cr1   F2   2_555  1.918(9)    0
Cr1   F3   1_555  1.848(10)   2
Cr1   F3   2_555  1.848(10)   0
```

_geom_bond_atom_site_label_1
_geom_bond_atom_site_label_2 (*char*)

The labels of two atom sites that form a bond. These must match labels specified as **_atom_site_label** in the atom list.

Appears in list as essential element of loop structure. **Must** match parent data name **_atom_site_label**. **[geom_bond]**

_geom_bond_distance (*numb, su*)

The intramolecular bond distance in ångströms.

Appears in list containing **_geom_bond_atom_site_label_**.

The permitted range is $0.0 \rightarrow \infty$. **[geom_bond]**

_geom_bond_multiplicity (*numb*)

The number of times the given bond appears in the environment of the atoms labelled **_geom_bond_atom_site_label_1**. In cases where the full list of bonds is given, one of the series of equivalent bonds may be assigned the appropriate multiplicity while the others are assigned a value of 0.

Appears in list containing **_geom_bond_atom_site_label_**.

The permitted range is $0 \rightarrow \infty$. Where no value is given, the assumed value is '1'. **[geom_bond]**

_geom_bond_publ_flag (*char*)

This code signals whether the bond distance is referred to in a publication or should be placed in a list of significant bond distances.

Appears in list containing **_geom_bond_atom_site_label_**.

The data value must be one of the following:

no	do not include bond in special list
n	abbreviation for 'no'
yes	do include bond in special list
y	abbreviation for 'yes'

Where no value is given, the assumed value is 'no'. **[geom_bond]**

_geom_bond_site_symmetry_1
_geom_bond_site_symmetry_2 (*char*)

The symmetry code of each atom site as the symmetry-equivalent position number '*n*' and the cell translation number '*klm*'. These numbers are combined to form the code '*n klm*' or *n_klm*. The character string *n_klm* is composed as follows: *n* refers to the symmetry operation that is applied to the coordinates stored in **_atom_site_fract_x**, **_atom_site_fract_y** and **_atom_site_fract_z**. It must match a number given in **_space_group_symop_id**. *k*, *l* and *m* refer to the translations that are subsequently applied to the symmetry-transformed coordinates to generate the atom used in calculating the bond. These translations (x, y, z) are related to (k, l, m) by the relations $k = 5 + x$, $l = 5 + y$, $m = 5 + z$. By adding 5 to the translations, the use of negative numbers is avoided.

Appears in list containing **_geom_bond_atom_site_label_**.

Examples: '.' (no symmetry or translation to site), '4' (4th symmetry operation applied), '7_645' (7th symmetry position: $+a$ on x, $-b$ on y). **[geom_bond]**

_geom_bond_valence (*numb*)

The bond valence calculated from **_geom_bond_distance**.

Appears in list containing **_geom_bond_atom_site_label_**. **[geom_bond]**

GEOM_CONTACT

Data items in the GEOM_CONTACT category record details about interatomic contacts as calculated from the ATOM, CELL and SYMMETRY data.

*Example 1 – based on data set CLPHO6 of Ferguson, Ruhl, McKervey & Browne [Acta Cryst. (1992), C**48**, 2262–2264].*

```
loop_
 _geom_contact_atom_site_label_1
 _geom_contact_atom_site_label_2
 _geom_contact_distance
 _geom_contact_site_symmetry_1
 _geom_contact_site_symmetry_2
 _geom_contact_publ_flag
 O(1)  O(2)     2.735(3)  .  .  yes
 H(01) O(2)     1.82      .  .  no
```

_geom_contact_atom_site_label_1
_geom_contact_atom_site_label_2 (*char*)

The labels of two atom sites that are within contact distance. The labels must match **_atom_site_label** codes in the atom list.

Appears in list as essential element of loop structure. **Must** match parent data name **_atom_site_label**. **[geom_contact]**

_geom_contact_distance (*numb, su*)

The interatomic contact distance in ångströms.

Appears in list containing **_geom_contact_atom_site_label_**.

The permitted range is $0.0 \rightarrow \infty$. **[geom_contact]**

_geom_contact_publ_flag (*char*)

This code signals whether the contact distance is referred to in a publication or should be placed in a list of significant contact distances.

Appears in list containing **_geom_contact_atom_site_label_**.

The data value must be one of the following:

no	do not include distance in special list
n	abbreviation for 'no'
yes	do include distance in special list
y	abbreviation for 'yes'

Where no value is given, the assumed value is 'no'. **[geom_contact]**

_geom_contact_site_symmetry_1
_geom_contact_site_symmetry_2 (*char*)

The symmetry code of each atom site as the symmetry-equivalent position number '*n*' and the cell translation number '*klm*'. These numbers are combined to form the code '*n klm*' or *n_klm*. The character string *n_klm* is composed as follows: *n* refers to the symmetry operation that is applied to the coordinates stored in **_atom_site_fract_x**, **_atom_site_fract_y** and **_atom_site_fract_z**. It must match a number given in **_space_group_symop_id**. *k*, *l* and *m* refer to the translations that are subsequently applied to the symmetry-transformed coordinates to generate the atom used in calculating the contact. These translations (x, y, z) are related to (k, l, m) by the relations $k = 5 + x$, $l = 5 + y$, $m = 5 + z$. By adding 5 to the translations, the use of negative numbers is avoided.

Appears in list containing **_geom_contact_atom_site_label_**.

Examples: '`.`' (no symmetry or translation to site), '`4`' (4th symmetry operation applied), '`7_645`' (7th symmetry position: $+a$ on x, $-b$ on y). **[geom_contact]**

GEOM_HBOND

Data items in the GEOM_HBOND category record details about hydrogen bonds as calculated from the ATOM, CELL and SYMMETRY data.

*Example 1 – based on $C_{14}H_{13}ClN_2O.H_2O$, reported by Palmer, Puddle & Lisgarten [Acta Cryst. (1993), C**49**, 1777–1779].*

```
loop_
_geom_hbond_atom_site_label_D
_geom_hbond_atom_site_label_H
_geom_hbond_atom_site_label_A
_geom_hbond_distance_DH
_geom_hbond_distance_HA
_geom_hbond_distance_DA
_geom_hbond_angle_DHA
_geom_hbond_publ_flag

N6   HN6  OW   0.888(8)  1.921(12)  2.801(8)  169.6(8)  yes
OW   HO2  O7   0.917(6)  1.923(12)  2.793(8)  153.5(8)  yes
OW   HO1  N10  0.894(8)  1.886(11)  2.842(8)  179.7(9)  yes
```

_geom_hbond_angle_DHA (*numb, su*)

Angle in degrees defined by the three sites **_geom_hbond_atom_site_label_D**, ***_H** and ***_A**. The site at ***_H** (the hydrogen atom participating in the interaction) is at the apex of the angle.

Appears in list containing **_geom_hbond_atom_site_label_**. **[geom_hbond]**

_geom_hbond_atom_site_label_D
_geom_hbond_atom_site_label_H
_geom_hbond_atom_site_label_A (*char*)

The labels of three atom sites (respectively, the donor atom, hydrogen atom and acceptor atom) participating in a hydrogen bond. These must match labels specified as **_atom_site_label** in the atom list.

Appears in list as essential element of loop structure. **Must** match parent data name **_atom_site_label**. **[geom_hbond]**

_geom_hbond_distance_DH
_geom_hbond_distance_HA
_geom_hbond_distance_DA (*numb, su*)

Distances in ångströms between the donor and hydrogen (***_DH**), hydrogen and acceptor (***_HA**) and donor and acceptor (***_DA**) sites in a hydrogen bond.

Appears in list containing **_geom_hbond_atom_site_label_**.

The permitted range is $0.0 \rightarrow \infty$. **[geom_hbond]**

_geom_hbond_publ_flag (*char*)

This code signals whether the hydrogen-bond information is referred to in a publication or should be placed in a table of significant hydrogen-bond geometry.

Appears in list containing **_geom_hbond_atom_site_label_**.

The data value must be one of the following:

`no`	do not include bond in special list
`n`	abbreviation for 'no'
`yes`	do include bond in special list
`y`	abbreviation for 'yes'

Where no value is given, the assumed value is '`no`'. **[geom_hbond]**

_geom_hbond_site_symmetry_D
_geom_hbond_site_symmetry_H
_geom_hbond_site_symmetry_A (*char*)

The symmetry code of each atom site as the symmetry-equivalent position number '*n*' and the cell translation number '*klm*'. These numbers are combined to form the code '*n klm*' or *n_klm*. The character string *n_klm* is composed as follows: *n* refers to the symmetry operation that is applied to the coordinates stored in **_atom_site_fract_x**, **_atom_site_fract_y** and **_atom_site_fract_z**. It must match a number given in **_space_group_symop_id**. *k*, *l* and *m* refer to the translations that are subsequently applied to the symmetry-transformed coordinates to generate the atom used in calculating the hydrogen bond. These translations (x, y, z) are related to (k, l, m) by the relations $k = 5 + x$, $l = 5 + y$, $m = 5 + z$. By adding 5 to the translations, the use of negative numbers is avoided.

Appears in list containing **_geom_hbond_atom_site_label_**.

Examples: '`.`' (no symmetry or translation to site), '`4`' (4th symmetry operation applied), '`7_645`' (7th symmetry position: $+a$ on x, $-b$ on y). **[geom_hbond]**

GEOM_TORSION

Data items in the GEOM_TORSION category record details about interatomic torsion angles as calculated from the ATOM, CELL and SYMMETRY data.

*Example 1 – based on data set CLPHO6 of Ferguson, Ruhl, McKervey & Browne [Acta Cryst. (1992), C**48**, 2262–2264].*

```
loop_
 _geom_torsion_atom_site_label_1
 _geom_torsion_atom_site_label_2
 _geom_torsion_atom_site_label_3
 _geom_torsion_atom_site_label_4
 _geom_torsion
 _geom_torsion_site_symmetry_1
 _geom_torsion_site_symmetry_2
 _geom_torsion_site_symmetry_3
 _geom_torsion_site_symmetry_4
 _geom_torsion_publ_flag
 C(9)  O(2)  C(7)   C(2)    71.8(2)  .  .  .  .      yes
 C(7)  O(2)  C(9)   C(10) -168.0(3)  .  .  .  2_666  yes
 C(10) O(3)  C(8)   C(6)  -167.7(3)  .  .  .  .      yes
 C(8)  O(3)  C(10)  C(9)   -69.7(2)  .  .  .  2_666  yes
 O(1)  C(1)  C(2)   C(3)  -179.5(4)  .  .  .  .      no
 O(1)  C(1)  C(2)   C(7)    -0.6(1)  .  .  .  .      no
```

_geom_torsion (*numb, su*)

The torsion angle in degrees bounded by the four atom sites identified by the **_geom_torsion_atom_site_label_** codes. These must match labels specified as **_atom_site_label** in the atom list. The torsion-angle definition should be that of Klyne and Prelog.

Reference: Klyne, W. & Prelog, V. (1960). *Experientia*, **16**, 521–523.

Appears in list containing **_geom_torsion_atom_site_label_**. **[geom_torsion]**

_geom_torsion_atom_site_label_1
_geom_torsion_atom_site_label_2
_geom_torsion_atom_site_label_3
_geom_torsion_atom_site_label_4 (*char*)

The labels of the four atom sites which define the torsion angle specified by **_geom_torsion**. These must match codes specified as **_atom_site_label** in the atom list. The torsion-angle definition should be that of Klyne and Prelog. The vector direction *_label_2 to *_label_3 is the viewing direction, and the torsion angle is the angle of twist required to superimpose the projection of the vector between site 2 and site 1 onto the projection of the vector between site 3 and site 4. Clockwise torsions are positive, anticlockwise torsions are negative.

Reference: Klyne, W. & Prelog, V. (1960). *Experientia*, **16**, 521–523.

Appears in list as essential element of loop structure. **Must** match parent data name **_atom_site_label**. **[geom_torsion]**

_geom_torsion_publ_flag (*char*)

This code signals whether the torsion angle is referred to in a publication or should be placed in a table of significant torsion angles.

Appears in list containing **_geom_torsion_atom_site_label_**.

The data value must be one of the following:

no	do not include angle in special list
n	abbreviation for 'no'
yes	do include angle in special list
y	abbreviation for 'yes'

Where no value is given, the assumed value is 'no'. **[geom_torsion]**

_geom_torsion_site_symmetry_1
_geom_torsion_site_symmetry_2
_geom_torsion_site_symmetry_3
_geom_torsion_site_symmetry_4 (*char*)

The symmetry code of each atom site as the symmetry-equivalent position number '*n*' and the cell translation number '*klm*'. These numbers are combined to form the code '*n klm*' or *n_klm*. The character string *n_klm* is composed as follows: *n* refers to the symmetry operation that is applied to the coordinates stored in **_atom_site_fract_x**, **_atom_site_fract_y** and **_atom_site_fract_z**. It must match a number given in **_space_group_symop_id**. k, l and m refer to the translations that are subsequently applied to the symmetry-transformed coordinates to generate the atom used in calculating the angle. These translations (x, y, z) are related to (k, l, m) by the relations $k = 5 + x$, $l = 5 + y$, $m = 5 + z$. By adding 5 to the translations, the use of negative numbers is avoided.

Appears in list containing **_geom_torsion_atom_site_label_**.

Examples: '.' (no symmetry or translation to site), '4' (4th symmetry operation applied), '7_645' (7th symmetry position: $+a$ on x, $-b$ on y). **[geom_torsion]**

*Example 1 – based on Acta Cryst. file for entry HL0007 [Willis, Beckwith & Tozer (1991). Acta Cryst. C**47**, 2276–2277].*

```
_journal_date_recd_electronic     91-04-15
_journal_date_from_coeditor       91-04-18
_journal_date_accepted            91-04-18
_journal_date_printers_first      91-08-07
_journal_date_proofs_out          91-08-07
_journal_coeditor_code            HL0007
_journal_techeditor_code          C910963
_journal_coden_ASTM               ACSCEE
_journal_name_full        'Acta Crystallographica Section C'
_journal_year                     1991
_journal_volume                   47
_journal_issue                    NOV91
_journal_page_first               2276
_journal_page_last                2277
```

JOURNAL

Data items in the JOURNAL category record details about the book-keeping by the journal staff when processing a CIF submitted for publication. The creator of a CIF will not normally specify these data items. The data names are not defined in the dictionary because they are for journal use only.

_journal_coden_ASTM
_journal_coden_Cambridge
_journal_coeditor_address
_journal_coeditor_code
_journal_coeditor_email
_journal_coeditor_fax
_journal_coeditor_name
_journal_coeditor_notes
_journal_coeditor_phone
_journal_data_validation_number
_journal_date_accepted
_journal_date_from_coeditor
_journal_date_to_coeditor
_journal_date_printers_final
_journal_date_printers_first
_journal_date_proofs_in
_journal_date_proofs_out
_journal_date_recd_copyright
_journal_date_recd_electronic
_journal_date_recd_hard_copy
_journal_issue
_journal_language
_journal_name_full
_journal_page_first
_journal_page_last
_journal_paper_category
_journal_suppl_publ_number
_journal_suppl_publ_pages
_journal_techeditor_address
_journal_techeditor_code
_journal_techeditor_email
_journal_techeditor_fax
_journal_techeditor_name
_journal_techeditor_notes
_journal_techeditor_phone
_journal_volume
_journal_year (*char*)

Data items specified by the journal staff.

[journal]

JOURNAL_INDEX

Data items in the JOURNAL_INDEX category are used to list terms used to generate the journal indexes. The creator of a CIF will not normally specify these data items.

*Example 1 – based on a paper by Zhu, Reynolds, Klein & Trudell [Acta Cryst. (1994), C**50**, 2067–2069].*

```
loop_
_journal_index_type
_journal_index_term
_journal_index_subterm
  O   C16H19NO4            .
  S   alkaloids           (-)-norcocaine
  S   (-)-norcocaine       .
  S
;  [2R,3S-(2\b,3\b)]-methyl
   3-(benzoyloxy)-8-azabicyclo[3.2.1]octane-2-carboxylate
;                          .
```

_journal_index_subterm
_journal_index_term
_journal_index_type (*char*)
Indexing terms supplied by the journal staff.

[journal_index]

PUBL

Data items in the PUBL category are used when submitting a manuscript for publication. They refer either to the paper as a whole, or to specific named elements within a paper (such as the title and abstract, or the *Comment* and *Experimental* sections of *Acta Crystallographica Section C*). The data items in the PUBL_BODY category should be used for the text of other submissions. Typically, each journal will supply a list of the specific items it requires in its *Notes for Authors*.

*Example 1 – based on Willis, Beckwith & Tozer [Acta Cryst. (1991), C**47**, 2276–2277].*

```
_publ_section_title
;  trans-3-Benzoyl-2-(tert-butyl)-4-(iso-butyl)-
   1,3-oxazolidin-5-one
;

_publ_section_abstract
;  The oxazolidinone ring is a shallow envelope
   conformation with the tert-butyl and iso-butyl groups
   occupying trans-positions with respect to the ring. The
   angles at the N atom sum to 356.2\%, indicating a very
   small degree of pyramidalization at this atom. This is
   consistent with electron delocalization between the N
   atom and the carbonyl centre [N-C=O = 1.374(3)\%A].
;
```

*Example 2 – based on $C_{31}H_{48}N_4O_4$, reported by Coleman, Patrick, Andersen & Rettig [Acta Cryst. (1996), C**52**, 1525–1527].*

```
_publ_section_title
;  Hemiasterlin methyl ester
;

_publ_section_title_footnote
;  IUPAC name: methyl 2,5-dimethyl-4-2-[3-methyl-
   2-methylamino-3-(N-methylbenzo[b]pyrrol-
   3-yl)butanamido]-3,3-dimethyl-N-methyl-
   butanamido-2-hexenoate.
;
```

_publ_contact_author (*char*)
The name and address of the author submitting the manuscript and data block. This is the person contacted by the journal editorial staff. It is preferable to use the separate data items **_publ_contact_author_name** and **_publ_contact_author_address**.

Example:
```
; Professor George Ferguson
  Department of Chemistry and Biochemistry
  University of Guelph
  Ontario
  Canada
  N1G 2W1
;
```
[publ]

_publ_contact_author_address (*char*)
The address of the author submitting the manuscript and data block. This is the person contacted by the journal editorial staff.

Example:
```
; Department of Chemistry and Biochemistry
  University of Guelph
  Ontario
  Canada
  N1G 2W1
;
```
[publ]

_publ_contact_author_email (*char*)
E-mail address in a form recognizable to international networks. The format of e-mail addresses is given in Section 3.4, *Address Specification*, of *Internet Message Format*, RFC 2822, P. Resnick (Editor), Network Standards Group, April 2001.

Examples: '`name@host.domain.country`', '`bm@iucr.org`'. **[publ]**

_publ_contact_author_fax (*char*)
Facsimile telephone number of the author submitting the manuscript and data block. The recommended style is the international dialing prefix, followed by the area code in parentheses, followed by the local number with no spaces. The earlier convention of including the international dialing prefix in parentheses is no longer recommended.

Examples: '`12(34)9477334`', '`12()349477334`'. **[publ]**

_publ_contact_author_id_iucr (*char*)
Identifier in the IUCr contact database of the author submitting the manuscript and data block. This identifier may be available from the *World Directory of Crystallographers* (http://wdc.iucr.org).

Example: '`2985`'. **[publ]**

_publ_contact_author_name (*char*)
The name of the author submitting the manuscript and data block. This is the person contacted by the journal editorial staff.

Example: '`Professor George Ferguson`'. **[publ]**

_publ_contact_author_phone (*char*)
Telephone number of the author submitting the manuscript and data block. The recommended style is the international dialing prefix, followed by the area code in parentheses, followed by the local number and any extension number prefixed by 'x', with no spaces. The earlier convention of including the international dialing prefix in parentheses is no longer recommended.

Examples: '`12(34)9477330`', '`12()349477330`', '`12(34)9477330x5543`'.
[publ]

_publ_contact_letter (*char*)
A letter submitted to the journal editor by the contact author.

[publ]

_publ_manuscript_creation (*char*)
A description of the word-processor package and computer used to create the word-processed manuscript stored as **_publ_manuscript_processed**.

Example: '`Tex file created by FrameMaker on a Sun 3/280`'. **[publ]**

_publ_manuscript_processed (*char*)
The full manuscript of a paper (excluding possibly the figures and the tables) output in ASCII characters from a word processor. Information about the generation of this data item must be specified in the data item **_publ_manuscript_creation**.

[publ]

_publ_manuscript_text (*char*)
The full manuscript of a paper (excluding figures and possibly the tables) output as standard ASCII text.

[publ]

_publ_requested_category (*char*)
The category of paper submitted. For submission to *Acta Crystallographica Section C* or *Acta Crystallographica Section E*, *only* the codes indicated for use with these journals should be used.

The data value must be one of the following:

FA	Full article
FI	Full submission – inorganic (*Acta C*)
FO	Full submission – organic (*Acta C*)
FM	Full submission – metal-organic (*Acta C*)
CI	CIF-access paper – inorganic (*Acta C*) (no longer in use)
CO	CIF-access paper – organic (*Acta C*) (not longer in use)
CM	CIF-access paper – metal-organic (*Acta C*) (no longer in use)
EI	Electronic submission – inorganic (*Acta E*)
EO	Electronic submission – organic (*Acta E*)
EM	Electronic submission – metal-organic (*Acta E*)
QI	Inorganic compounds (*Acta E*)
QO	Organic compounds (*Acta E*)
QM	Metal-organic compounds (*Acta E*)
AD	Addenda and Errata (*Acta C*, *Acta E*)
SC	Short communication

Where no value is given, the assumed value is 'FA'. **[publ]**

_publ_requested_coeditor_name (*char*)
The name of the co-editor whom the authors would like to handle the submitted manuscript.

[publ]

_publ_requested_journal (*char*)
The name of the journal to which the manuscript is being submitted.

[publ]

_publ_section_title
_publ_section_title_footnote
_publ_section_synopsis
_publ_section_abstract
_publ_section_comment
_publ_section_introduction
_publ_section_experimental
_publ_section_exptl_prep
_publ_section_exptl_refinement
_publ_section_exptl_solution
_publ_section_discussion
_publ_section_acknowledgements
_publ_section_references
_publ_section_related_literature
_publ_section_figure_captions
_publ_section_table_legends
_publ_section_keywords (*char*)
The sections of a manuscript if submitted in parts. As an alternative, see **_publ_manuscript_text** and **_publ_manuscript_processed**. The **_publ_section_exptl_prep**, **_publ_section_exptl_refinement** and **_publ_section_exptl_solution** items are preferred for separating the chemical preparation, refinement and structure solution aspects of the experimental description.

[publ]

PUBL_AUTHOR

Data items in the PUBL_AUTHOR category record details of the authors of a manuscript submitted for publication.

Example 1 – based on Willis, Beckwith & Tozer [Acta Cryst. (1991), C47, 2276–2277].

```
loop_
_publ_author_name
_publ_author_address

     'Willis, Anthony C.'
;    Research School of Chemistry
     Australian National University
     GPO Box 4
     Canberra, ACT
     Australia    2601
;
```

_publ_author_address (*char*)
The address of a publication author. If there is more than one author, this will be looped with **_publ_author_name**.

May appear in list containing **_publ_author_name**.

Example:

```
; Department
  Institute
  Street
  City and postcode
  COUNTRY
;
```

[publ_author]

_publ_author_footnote (*char*)
A footnote accompanying an author's name in the list of authors of a paper. Typically indicates sabbatical address, additional affiliations or date of decease.

May appear in list containing **_publ_author_name**.

Examples: 'On leave from U. Western Australia', 'Also at Department of Biophysics'. **[publ_author]**

_publ_author_email (*char*)
The e-mail address of a publication author. If there is more than one author, this will be looped with **_publ_author_name**. The format of e-mail addresses is given in Section 3.4, Address Specification, of Internet Message Format, RFC 2822, P. Resnick (Editor), Network Standards Group, April 2001.

May appear in list containing **_publ_author_name**.

Examples: 'name@host.domain.country', 'bm@iucr.org'. **[publ_author]**

_publ_author_id_iucr (*char*)
Identifier in the IUCr contact database of a publication author. This identifier may be available from the *World Directory of Crystallographers* (http://wdc.iucr.org).

May appear in list.

Example: '2985'. **[publ_author]**

_publ_author_name (*char*)
The name of a publication author. If there are multiple authors, this will be looped with **_publ_author_address**. The family name(s), followed by a comma and including any dynastic components, precedes the first names or initials.

May appear in list as essential element of loop structure.

Examples: 'Bleary, Percival R.', 'O'Neil, F.K.', 'Van den Bossche, G.', 'Yang, D.-L.', 'Simonov, Yu.A.', 'M\"uller, H.A.', 'Ross II, C.R.'.

[publ_author]

PUBL_BODY

Data items in the PUBL_BODY category permit the labelling of different text sections within the body of a paper. Note that these should not be used in a paper which has a standard format with sections tagged by specific data names (such as in *Acta Crystallographica Section C*). Typically, each journal will supply a list of the specific items it requires in its *Notes for Authors*.

*Example 1 – based on a paper by R. Restori & D. Schwarzenbach [Acta Cryst. (1996), A**52**, 369–378].*

```
loop_
_publ_body_element
_publ_body_label
_publ_body_title
_publ_body_format
_publ_body_contents

     section   1         Introduction                    cif
; X-ray diffraction from a crystalline material provides
  information on the thermally and spatially averaged
  electron density in the crystal...
;
     section   2         Theory                          tex
; In the rigid-atom approximation, the dynamic electron
  density of an atom is described by the convolution
  product of the static atomic density and a probability
  density function,
  $\rho_dyn(\bf r) = \rho_stat(\bf r) * P(\bf r). \eqno(1)$
;
```

*Example 2 – based on a paper by R. J. Papoular, Y. Vekhter & P. Coppens [Acta Cryst. (1996), A**52**, 397–407].*

```
loop_
_publ_body_element
_publ_body_label
_publ_body_title
_publ_body_contents

     section     3
; The two-channel method for retrieval of the deformation
  electron density
;
     .
     subsection  3.1  'The two-channel entropy S[\D\r(r)]'
; As the wide dynamic range involved in the total electron
  density...
;
     subsection  3.2
'Uniform vs informative prior model densities'        .
     subsubsection  3.2.1  'Use of uniform models'
; Straightforward algebra leads to expressions analogous
  to...
;
```

_publ_body_contents (*char*)

A text section of a paper.

Appears in list containing **_publ_body_label**. **[publ_body]**

_publ_body_element (*char*)

The functional role of the associated text section.

Appears in list containing **_publ_body_label**.

The data value must be one of the following:

- `section`
- `subsection`
- `subsubsection`
- `appendix`
- `footnote`

[publ_body]

_publ_body_format (*char*)

Code indicating the appropriate typesetting conventions for accented characters and special symbols in the text section.

Appears in list containing **_publ_body_label**.

The data value must be one of the following:

`ascii`	no coding for special symbols
`cif`	CIF convention
`latex`	LaTeX
`rtf`	Rich Text Format
`sgml`	SGML (ISO 8879)
`tex`	TeX
`troff`	troff or nroff

Where no value is given, the assumed value is '`cif`'. **[publ_body]**

_publ_body_label (*char*)

Code identifying the section of text. The combination of this with **_publ_body_element** must be unique.

Appears in list as essential element of loop structure.

Examples: '`1`', '`1.1`', '`2.1.3`'. **[publ_body]**

_publ_body_title (*char*)

Title of the associated section of text.

Appears in list containing **_publ_body_label**. **[publ_body]**

PUBL_MANUSCRIPT_INCL

Data items in the PUBL_MANUSCRIPT_INCL category allow the authors of a manuscript submitted for publication to list data names that should be added to the standard request list used by the journal printing software. Although these fields are primarily intended to identify CIF data items that the author wishes to include in a published paper, they can also be used to identify data names created so that non-CIF items can be included in the publication. Note that ***_item** names *must* be enclosed in single quotes.

Example 1 – directive to include a hydrogen-bonding table, including cosmetic headings in comments.

```
loop_
_publ_manuscript_incl_extra_item
_publ_manuscript_incl_extra_info
_publ_manuscript_incl_extra_defn
#
# Include Hydrogen Bonding Geometry Description
# =============================================
# Name                              explanation    standard?
# ----                              -----------    ---------
  '_geom_hbond_atom_site_label_D'  'H-bond donor'     yes
  '_geom_hbond_atom_site_label_H'  'H-bond hydrogen'  yes
  '_geom_hbond_atom_site_label_A'  'H-bond acceptor'  yes
  '_geom_hbond_distance_DH'        'H-bond D-H'       yes
  '_geom_hbond_distance_HA'        'H-bond H...A'     yes
  '_geom_hbond_distance_DA'        'H-bond D...A'     yes
  '_geom_hbond_angle_DHA'          'H-bond D-H...A'   yes
```

Example 2 – hypothetical example including both standard CIF data items and a non-CIF quantity which the author wishes to list.

```
loop_
_publ_manuscript_incl_extra_item
_publ_manuscript_incl_extra_info
_publ_manuscript_incl_extra_defn
  '_atom_site_symmetry_multiplicity'
      'to emphasise special sites'       yes
  '_chemical_compound_source'
      'rare material, unusual source'    yes
  '_reflns_d_resolution_high'
      'limited data is a problem here'   yes
  '_crystal_magnetic_permeability'
      'unusual value for this material'  no
```

_publ_manuscript_incl_extra_defn (*char*)

Flags whether the corresponding data item marked for inclusion in a journal request list is a standard CIF definition or not.

Appears in list containing **_publ_manuscript_incl_extra_item**.

The data value must be one of the following:

`no`	not a standard CIF data name
`n`	abbreviation for 'no'
`yes`	a standard CIF data name
`y`	abbreviation for 'yes'

Where no value is given, the assumed value is '`yes`'. **[publ_manuscript_incl]**

_publ_manuscript_incl_extra_info (*char*)

A short note indicating the reason why the author wishes the corresponding data item marked for inclusion in the journal request list to be published.

Appears in list containing **_publ_manuscript_incl_extra_item**.

[publ_manuscript_incl]

_publ_manuscript_incl_extra_item (*char*)

Specifies the inclusion of specific data into a manuscript which are not normally requested by the journal. The values of this item are the extra data names (which *must* be enclosed in single quotes) that will be added to the journal request list.

Appears in list as essential element of loop structure. **[publ_manuscript_incl]**

REFINE

Data items in the REFINE category record details about the structure-refinement parameters.

*Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C**47**, 2276–2277].*

```
_refine_special_details     sfls:_F_calc_weight_full_matrix

_refine_ls_structure_factor_coef   F
_refine_ls_matrix_type             full
_refine_ls_weighting_scheme        calc
_refine_ls_weighting_details      'w=1/(u^2^(F)+0.0004F^2^)'
_refine_ls_hydrogen_treatment      refxyz
_refine_ls_extinction_method       Zachariasen
_refine_ls_extinction_coef         3514(42)
_refine_ls_extinction_expression
; Larson, A. C. (1970). "Crystallographic Computing", edited
  by F. R. Ahmed. Eq. (22) p. 292. Copenhagen: Munksgaard.
;
_refine_ls_abs_structure_details
; The absolute configuration was assigned to agree with that
  of its precursor l-leucine at the chiral centre C3.
;
_refine_ls_number_reflns           1408
_refine_ls_number_parameters       272
_refine_ls_number_restraints       0
_refine_ls_number_constraints      0
_refine_ls_R_factor_all            .038
_refine_ls_R_factor_gt             .034
_refine_ls_wR_factor_all           .044
_refine_ls_wR_factor_gt            .042
_refine_ls_goodness_of_fit_all    1.462
_refine_ls_goodness_of_fit_gt     1.515
_refine_ls_shift/su_max            .535
_refine_ls_shift/su_mean           .044
_refine_diff_density_min          -.108
_refine_diff_density_max           .131
```

_refine_diff_density_max
_refine_diff_density_min
_refine_diff_density_rms (*numb, su*)

The largest and smallest values and the root-mean-square deviation, in electrons per ångström cubed, of the final difference electron density. The *_**rms** value is measured with respect to the arithmetic mean density and is derived from summations over each grid point in the asymmetric unit of the cell. This quantity is useful for assessing the significance of *_**min** and *_**max** values, and also for defining suitable contour levels.

[refine]

_refine_ls_abs_structure_details (*char*)

The nature of the absolute structure and how it was determined.

[refine]

_refine_ls_abs_structure_Flack (*numb, su*)

The measure of absolute structure as defined by Flack (1983). For centrosymmetric structures, the only permitted value, if the data name is present, is 'inapplicable', represented by '.' . For noncentrosymmetric structures, the value must lie in the 99.97% Gaussian confidence interval $-3u \leq x \leq 1+3u$ and a standard uncertainty (e.s.d.) u must be supplied. The **_enumeration_range** of $0.0 \rightarrow 1.0$ is correctly interpreted as meaning $(0.0-3u) \leq x \leq (1.0+3u)$.

Reference: Flack, H. D. (1983). *Acta Cryst.* A**39**, 876–881.

The permitted range is $0.0 \rightarrow 1.0$. **[refine]**

_refine_ls_abs_structure_Rogers (*numb, su*)

The measure of absolute structure as defined by Rogers (1981). The value must lie in the 99.97% Gaussian confidence interval $-1-3u \leq \eta \leq 1+3u$ and a standard uncertainty (e.s.d.) u must be supplied. The **_enumeration_range** of $-1.0 \rightarrow 1.0$ is correctly interpreted as meaning $(-1.0-3u) \leq \eta \leq (1.0+3u)$.

Reference: Rogers, D. (1981). *Acta Cryst.* A**37**, 734–741.

The permitted range is $-1.0 \rightarrow 1.0$. **[refine]**

_refine_ls_d_res_high (*numb*)

The smallest value in ångströms of the interplanar spacings of the reflections used in the refinement. This is called the highest resolution.

The permitted range is $0.0 \rightarrow \infty$. **[refine]**

_refine_ls_d_res_low (*numb*)

The largest value in ångströms of the interplanar spacings of the reflections used in the refinement. This is called the lowest resolution.

The permitted range is $0.0 \rightarrow \infty$. **[refine]**

_refine_ls_extinction_coef (*numb, su*)

The extinction coefficient used to calculate the correction factor applied to the structure-factor data. The nature of the extinction coefficient is given in the definitions of **_refine_ls_extinction_expression** and **_refine_ls_extinction_method**. For the 'Zachariasen' method it is the r^* value; for the 'Becker–Coppens type 1 isotropic' method it is the 'g' value and for 'Becker–Coppens type 2 isotropic' corrections it is the 'ρ' value. Note that the magnitude of these values is usually of the order of 10 000.

References: Becker, P. J. & Coppens, P. (1974). *Acta Cryst.* A**30**, 129–147, 148–153. Zachariasen, W. H. (1967). *Acta Cryst.* **23**, 558–564. Larson, A. C. (1967). *Acta Cryst.* **23**, 664–665.

Example: '3472(52)' (Zachariasen coefficient r^* = 0.347(5) E04). **[refine]**

_refine_ls_extinction_expression (*char*)

A description of or reference to the extinction-correction equation used to apply the data item **_refine_ls_extinction_coef**. This information must be sufficient to reproduce the extinction-correction factors applied to the structure factors.

Example:

```
; Larson, A. C. (1970). "Crystallographic Computing",
  edited by F. R. Ahmed. Eq. (22), p. 292.
  Copenhagen: Munksgaard.
;
```

[refine]

_refine_ls_extinction_method (*char*)
A description of the extinction-correction method applied. This description should include information about the correction method, either 'Becker–Coppens' or 'Zachariasen'. The latter is sometimes referred to as the 'Larson' method even though it employs Zachariasen's formula. The Becker–Coppens procedure is referred to as 'type 1' when correcting secondary extinction dominated by the mosaic spread; as 'type 2' when secondary extinction is dominated by particle size and includes a primary extinction component; and as 'mixed' when there is a mixture of types 1 and 2. For the Becker–Coppens method, it is also necessary to set the mosaic distribution as either 'Gaussian' or 'Lorentzian' and the nature of the extinction as 'isotropic' or 'anisotropic'. Note that if either the 'mixed' or 'anisotropic' corrections are applied, the multiple coefficients cannot be contained in *_extinction_coef and must be listed in _refine_special_details.

References: Becker, P. J. & Coppens, P. (1974). *Acta Cryst*. A**30**, 129–147, 148–153. Zachariasen, W. H. (1967). *Acta Cryst*. **23**, 558–564. Larson, A. C. (1967). *Acta Cryst*. **23**, 664–665.

Where no value is given, the assumed value is 'Zachariasen'.

Examples: 'B-C type 2 Gaussian isotropic', 'none'. **[refine]**

_refine_ls_F_calc_details (*char*)
Details concerning the evaluation of the structure factors using the expression given in _refine_ls_F_calc_formula.

Examples: 'Gaussian integration using 16 points',
; Bessel functions expansion up to 5th order.
Bessel functions estimated accuracy: better
than 0.001 electrons.
; . **[refine]**

_refine_ls_F_calc_formula (*char*)
Analytical expression used to calculate the structure factors.

[refine]

_refine_ls_F_calc_precision (*numb*)
This item gives an estimate of the precision resulting from the numerical approximations made during the evaluation of the structure factors using the expression given in _refine_ls_F_calc_formula following the method outlined in _refine_ls_F_calc_details. For X-ray diffraction the result is given in electrons.

The permitted range is $0.0 \rightarrow \infty$. **[refine]**

_refine_ls_goodness_of_fit_all (*numb, su*)
The least-squares goodness-of-fit parameter S for all reflections after the final cycle of refinement. Ideally, account should be taken of parameters restrained in the least-squares refinement. See also _refine_ls_restrained_S_ definitions.

$$S = \left(\frac{\sum \left| w |Y_{\rm obs} - Y_{\rm calc}|^2 \right|}{N_{\rm ref} - N_{\rm param}} \right)^{1/2},$$

where $Y_{\rm obs}$ = the observed coefficients (see _refine_ls_structure_factor_coef), $Y_{\rm calc}$ = the calculated coefficients (see _refine_ls_structure_factor_coef), w = the least-squares reflection weight $(1/u^2)$, u = the standard uncertainty, $N_{\rm ref}$ = the number of reflections used in the refinement, $N_{\rm param}$ = the number of refined parameters and the sum is taken over the specified reflections.

The permitted range is $0.0 \rightarrow \infty$. **[refine]**

_refine_ls_goodness_of_fit_gt (*numb, su*)
The least-squares goodness-of-fit parameter S for significantly intense reflections (see _reflns_threshold_expression) after the final cycle of refinement. Ideally, account should be taken of parameters restrained in the least-squares refinement. See also _refine_ls_restrained_S_ definitions.

$$S = \left(\frac{\sum \left| w |Y_{\rm obs} - Y_{\rm calc}|^2 \right|}{N_{\rm ref} - N_{\rm param}} \right)^{1/2},$$

where $Y_{\rm obs}$ = the observed coefficients (see _refine_ls_structure_factor_coef), $Y_{\rm calc}$ = the calculated coefficients (see _refine_ls_structure_factor_coef), w = the least-squares reflection weight $(1/u^2)$, u = the standard uncertainty, $N_{\rm ref}$ = the number of reflections used in the refinement, $N_{\rm param}$ = the number of refined parameters; the sum is taken over the specified reflections.

The permitted range is $0.0 \rightarrow \infty$.

Related item: _refine_ls_goodness_of_fit_obs (alternate). **[refine]**

_refine_ls_goodness_of_fit_obs (*numb, su*)
This definition has been superseded and is retained here only for archival purposes. Use instead _refine_ls_goodness_of_fit_gt.
The least-squares goodness-of-fit parameter S for observed reflections (see _reflns_observed_criterion) after the final cycle of refinement. Ideally, account should be taken of parameters restrained in the least-squares refinement. See also _refine_ls_restrained_S_ definitions.

$$S = \left(\frac{\sum \left| w |Y_{\rm obs} - Y_{\rm calc}|^2 \right|}{N_{\rm ref} - N_{\rm param}} \right)^{1/2},$$

where $Y_{\rm obs}$ = the observed coefficients (see _refine_ls_structure_factor_coef), $Y_{\rm calc}$ = the calculated coefficients (see _refine_ls_structure_factor_coef), w = the least-squares reflection weight $(1/u^2)$, u = the standard uncertainty, $N_{\rm ref}$ = the number of reflections used in the refinement, $N_{\rm param}$ = the number of refined parameters; the sum is taken over the specified reflections.

The permitted range is $0.0 \rightarrow \infty$. ***[refine]***

_refine_ls_goodness_of_fit_ref (*numb, su*)
The least-squares goodness-of-fit parameter S for all reflections included in the refinement after the final cycle of refinement. Ideally, account should be taken of parameters restrained in the least-squares refinement. See also _refine_ls_restrained_S_ definitions.

$$S = \left(\frac{\sum \left| w |Y_{\rm obs} - Y_{\rm calc}|^2 \right|}{N_{\rm ref} - N_{\rm param}} \right)^{1/2},$$

where $Y_{\rm obs}$ = the observed coefficients (see _refine_ls_structure_factor_coef), $Y_{\rm calc}$ = the calculated coefficients (see _refine_ls_structure_factor_coef), w = the least-squares reflection weight $(1/u^2)$, u = the standard uncertainty, $N_{\rm ref}$ = the number of reflections used in the refinement, $N_{\rm param}$ = the number of refined parameters; the sum is taken over the specified reflections.

The permitted range is $0.0 \rightarrow \infty$. **[refine]**

_refine_ls_hydrogen_treatment (*char*)
Treatment of hydrogen atoms in the least-squares refinement.

The data value must be one of the following:

refall	refined all H-atom parameters
refxyz	refined H-atom coordinates only
refU	refined H-atom U's only
noref	no refinement of H-atom parameters
constr	H-atom parameters constrained
mixed	some constrained, some independent
undef	H-atom parameters not defined

Where no value is given, the assumed value is 'undef'. **[refine]**

_refine_ls_matrix_type (*char*)
Type of matrix used to accumulate the least-squares derivatives.
The data value must be one of the following:

full	full
fullcycle	full with fixed elements per cycle
atomblock	block diagonal per atom
userblock	user-defined blocks
diagonal	diagonal elements only
sparse	selected elements only

Where no value is given, the assumed value is '**full**'. **[refine]**

_refine_ls_number_constraints (*numb*)
The number of constrained (non-refined or dependent) parameters in the least-squares process. These may be due to symmetry or any other constraint process (*e.g.* rigid-body refinement). See also **_atom_site_constraints** and **_atom_site_refinement_flags**. A general description of constraints may appear in **_refine_special_details**.
The permitted range is $0 \rightarrow \infty$. Where no value is given, the assumed value is '**0**'.
[refine]

_refine_ls_number_parameters (*numb*)
The number of parameters refined in the least-squares process. If possible, this number should include some contribution from the restrained parameters. The restrained parameters are distinct from the constrained parameters (where one or more parameters are linearly dependent on the refined value of another). Least-squares restraints often depend on geometry or energy considerations and this makes their direct contribution to this number, and to the goodness-of-fit calculation, difficult to assess.
The permitted range is $0 \rightarrow \infty$. **[refine]**

_refine_ls_number_reflns (*numb*)
The number of unique reflections contributing to the least-squares refinement calculation.
The permitted range is $0 \rightarrow \infty$. **[refine]**

_refine_ls_number_restraints (*numb*)
The number of restrained parameters. These are parameters which are not directly dependent on another refined parameter. Restrained parameters often involve geometry or energy dependencies. See also **_atom_site_constraints** and **_atom_site_refinement_flags**. A general description of refinement constraints may appear in **_refine_special_details**.
The permitted range is $0 \rightarrow \infty$. **[refine]**

_refine_ls_R_factor_all (*numb*)
Residual factor for all reflections satisfying the resolution limits established by **_refine_ls_d_res_high** and **_refine_ls_d_res_low**. This is the conventional *R* factor. See also **_refine_ls_wR_factor_** definitions.

$$R = \frac{\sum |F_{\rm obs} - F_{\rm calc}|}{\sum |F_{\rm obs}|},$$

where $F_{\rm obs}$ = the observed structure-factor amplitudes, $F_{\rm calc}$ = the calculated structure-factor amplitudes and the sum is taken over the specified reflections.
The permitted range is $0.0 \rightarrow \infty$. **[refine]**

_refine_ls_R_factor_gt (*numb*)
Residual factor for the reflections (with number given by **_reflns_number_gt**) judged significantly intense (*i.e.* satisfying the threshold specified by **_reflns_threshold_expression**) and included in the refinement. The reflections also satisfy the resolution limits established by **_refine_ls_d_res_high** and **_refine_ls_d_res_low**. This is the conventional *R* factor. See also **_refine_ls_wR_factor_** definitions.

$$R = \frac{\sum |F_{\rm obs} - F_{\rm calc}|}{\sum |F_{\rm obs}|},$$

where $F_{\rm obs}$ = the observed structure-factor amplitudes, $F_{\rm calc}$ = the calculated structure-factor amplitudes and the sum is taken over the specified reflections.
The permitted range is $0.0 \rightarrow \infty$.
Related item: **_refine_ls_R_factor_obs** (alternate). **[refine]**

_refine_ls_R_factor_obs (*numb*)
This definition has been superseded and is retained here only for archival purposes. Use instead _refine_ls_R_factor_gt.
*Residual factor for the reflections classified as 'observed' (see **_reflns_observed_criterion**) and included in the refinement. The reflections also satisfy the resolution limits established by **_refine_ls_d_res_high** and **_refine_ls_d_res_low**. This is the conventional R factor. See also **_refine_ls_wR_factor_** definitions.*

$$R = \frac{\sum |F_{\rm obs} - F_{\rm calc}|}{\sum |F_{\rm obs}|},$$

where $F_{\rm obs}$ = the observed structure-factor amplitudes, $F_{\rm calc}$ = the calculated structure-factor amplitudes and the sum is taken over the specified reflections.
The permitted range is $0.0 \rightarrow \infty$. ***[refine]***

_refine_ls_R_Fsqd_factor (*numb*)
Residual factor $R(F^2)$, calculated on the squared amplitudes of the observed and calculated structure factors, for significantly intense reflections (satisfying **_reflns_threshold_expression**) and included in the refinement. The reflections also satisfy the resolution limits established by **_refine_ls_d_res_high** and **_refine_ls_d_res_low**.

$$R(F^2) = \frac{\sum |F^2_{\rm obs} - F^2_{\rm calc}|}{\sum |F^2_{\rm obs}|},$$

where $F^2_{\rm obs}$ = squares of the observed structure-factor amplitudes, $F^2_{\rm calc}$ = squares of the calculated structure-factor amplitudes and the sum is taken over the specified reflections.
The permitted range is $0.0 \rightarrow \infty$. **[refine]**

_refine_ls_R_I_factor (*numb*)
Residual factor $R(I)$ for significantly intense reflections (satisfying **_reflns_threshold_expression**) and included in the refinement. This is most often calculated in Rietveld refinements against powder data, where it is referred to as R_B or $R_{\rm Bragg}$.

$$R(I) = \frac{\sum |I_{\rm obs} - I_{\rm calc}|}{\sum |I_{\rm obs}|},$$

where $I_{\rm obs}$ = the net observed intensities, $I_{\rm calc}$ = the net calculated intensities and the sum is taken over the specified reflections.
The permitted range is $0.0 \rightarrow \infty$. **[refine]**

_refine_ls_restrained_S_all (*numb*)

The least-squares goodness-of-fit parameter S' for all reflections after the final cycle of least-squares refinement. This parameter explicitly includes the restraints applied in the least-squares process. See also **_refine_ls_goodness_of_fit_** definitions.

$$S' = \left(\frac{\sum \left| w|Y_{\rm obs} - Y_{\rm calc}|^2 \right| + \sum_r \left| w_r|P_{\rm calc} - P_{\rm targ}|^2 \right|}{N_{\rm ref} + N_{\rm restr} - N_{\rm param}} \right)^{1/2},$$

where $Y_{\rm obs}$ = the observed coefficients (see **_refine_ls_structure_factor_coef**), $Y_{\rm calc}$ = the calculated coefficients (see **_refine_ls_structure_factor_coef**), w = the least-squares reflection weight [1/square of standard uncertainty (e.s.d.)], $P_{\rm calc}$ = the calculated restraint values, $P_{\rm targ}$ = the target restraint values, w_r = the restraint weight, $N_{\rm ref}$ = the number of reflections used in the refinement (see **_refine_ls_number_reflns_obs**), $N_{\rm restr}$ = the number of restraints (see **_refine_ls_number_restraints**) and $N_{\rm param}$ = the number of refined parameters (see **_refine_ls_number_parameters**); the sum $\sum$ is taken over the specified reflections and the sum $\sum_r$ is taken over the restraints.

The permitted range is $0.0 \rightarrow \infty$. **[refine]**

_refine_ls_restrained_S_gt (*numb*)

The least-squares goodness-of-fit parameter S' for significantly intense reflections (satisfying **_reflns_threshold_expression**) after the final cycle of least-squares refinement. This parameter explicitly includes the restraints applied in the least-squares process. See also **_refine_ls_goodness_of_fit_** definitions.

$$S' = \left(\frac{\sum \left| w|Y_{\rm obs} - Y_{\rm calc}|^2 \right| + \sum_r \left| w_r|P_{\rm calc} - P_{\rm targ}|^2 \right|}{N_{\rm ref} + N_{\rm restr} - N_{\rm param}} \right)^{1/2},$$

where $Y_{\rm obs}$ = the observed coefficients (see **_refine_ls_structure_factor_coef**), $Y_{\rm calc}$ = the calculated coefficients (see **_refine_ls_structure_factor_coef**), w = the least-squares reflection weight [1/square of standard uncertainty (e.s.d.)], $P_{\rm calc}$ = the calculated restraint values, $P_{\rm targ}$ = the target restraint values, w_r = the restraint weight, $N_{\rm ref}$ = the number of reflections used in the refinement (see **_refine_ls_number_reflns_obs**), $N_{\rm restr}$ = the number of restraints (see **_refine_ls_number_restraints**) and $N_{\rm param}$ = the number of refined parameters (see **_refine_ls_number_parameters**); the sum $\sum$ is taken over the specified reflections and the sum $\sum_r$ is taken over the restraints.

The permitted range is $0.0 \rightarrow \infty$.

Related item: **_refine_ls_restrained_S_obs** (alternate). **[refine]**

_refine_ls_restrained_S_obs (*numb*)

This definition has been superseded and is retained here only for archival purposes. Use instead _refine_ls_restrained_S_gt.

*The least-squares goodness-of-fit parameter S' for observed reflections after the final cycle of least-squares refinement. This parameter explicitly includes the restraints applied in the least-squares process. See also **_refine_ls_goodness_of_fit_** definitions.*

$$S' = \left(\frac{\sum \left| w|Y_{\rm obs} - Y_{\rm calc}|^2 \right| + \sum_r \left| w_r|P_{\rm calc} - P_{\rm targ}|^2 \right|}{N_{\rm ref} + N_{\rm restr} - N_{\rm param}} \right)^{1/2},$$

*where $Y_{\rm obs}$ = the observed coefficients (see **_refine_ls_structure_factor_coef**), $Y_{\rm calc}$ = the calculated coefficients (see **_refine_ls_structure_factor_coef**), w = the least-squares reflection weight [1/square of standard uncertainty (e.s.d.)], $P_{\rm calc}$ = the calculated restraint values, $P_{\rm targ}$ = the target restraint values, w_r = the restraint weight, $N_{\rm ref}$ = the number of reflections used in the refinement (see **_refine_ls_number_reflns_obs**), $N_{\rm restr}$ = the number of restraints (see **_refine_ls_number_restraints**) and $N_{\rm param}$ = the number of refined parameters (see **_refine_ls_number_parameters**); the sum $\sum$ is taken over the specified reflections and the sum $\sum_r$ is taken over the restraints.*

The permitted range is $0.0 \rightarrow \infty$. ***[refine]***

_refine_ls_shift/esd_max (*numb*)

This definition has been superseded and is retained here only for archival purposes. Use instead _refine_ls_shift/su_max.

The largest ratio of the final least-squares parameter shift to the final standard uncertainty (s.u., formerly described as estimated standard deviation, e.s.d.).

The permitted range is $0.0 \rightarrow \infty$. ***[refine]***

_refine_ls_shift/esd_mean (*numb*)

This definition has been superseded and is retained here only for archival purposes. Use instead _refine_ls_shift/su_mean.

The average ratio of the final least-squares parameter shift to the final standard uncertainty (s.u., formerly described as estimated standard deviation, e.s.d.).

The permitted range is $0.0 \rightarrow \infty$. ***[refine]***

_refine_ls_shift/su_max (*numb*)

The largest ratio of the final least-squares parameter shift to the final standard uncertainty.

The permitted range is $0.0 \rightarrow \infty$.

Related item: **_refine_ls_shift/esd_max** (alternate). **[refine]**

_refine_ls_shift/su_max_lt (*numb*)

An upper limit for the largest ratio of the final least-squares parameter shift to the final standard uncertainty. This item is used when the largest value of the shift divided by the final standard uncertainty is too small to measure.

The permitted range is $0.0 \rightarrow \infty$.

Related item: **_refine_ls_shift/su_max** (alternate). **[refine]**

_refine_ls_shift/su_mean (*numb*)

The average ratio of the final least-squares parameter shift to the final standard uncertainty.

The permitted range is $0.0 \rightarrow \infty$.

Related item: **_refine_ls_shift/esd_mean** (alternate). **[refine]**

_refine_ls_shift/su_mean_lt (*numb*)

An upper limit for the average ratio of the final least-squares parameter shift to the final standard uncertainty. This item is used when the average value of the shift divided by the final standard uncertainty is too small to measure.

The permitted range is $0.0 \rightarrow \infty$.

Related item: **_refine_ls_shift/su_mean** (alternate). **[refine]**

_refine_ls_structure_factor_coef (*char*)

Structure-factor coefficient $|F|$, F^2 or I used in the least-squares refinement process.

The data value must be one of the following:

F	structure-factor magnitude
Fsqd	structure factor squared
Inet	net intensity

Where no value is given, the assumed value is '**F**'. **[refine]**

_refine_ls_weighting_details (*char*)

A description of special aspects of the weighting scheme used in the least-squares refinement. Used to describe the weighting when the value of **_refine_ls_weighting_scheme** is specified as 'calc'.

Example:

```
; Sigdel model of Konnert-Hendrickson:
  Sigdel = Afsig +  Bfsig*(sin(\q)/\l - 1/6)
  Afsig = 22.0, Bfsig = 150.0 at the beginning of refinement.
  Afsig = 16.0, Bfsig =  60.0 at the end of refinement.
;
```

[refine]

_refine_ls_weighting_scheme (*char*)
The weighting scheme applied in the least-squares process. The standard code may be followed by a description of the weight (but see **_refine_ls_weighting_details** for a preferred approach).
The data value must be one of the following:

sigma	based on measured s.u.'s
unit	unit or no weights applied
calc	calculated weights applied

Where no value is given, the assumed value is 'sigma'. **[refine]**

_refine_ls_wR_factor_all (*numb*)
Weighted residual factors for all reflections. The reflections also satisfy the resolution limits established by **_refine_ls_d_res_high** and **_refine_ls_d_res_low**. See also the **_refine_ls_R_factor_** definitions.

$$wR = \left(\frac{\sum \left| w|Y_{\rm obs} - Y_{\rm calc}|^2 \right|}{\sum |wY_{\rm obs}^2|} \right)^{1/2},$$

where $Y_{\rm obs}$ = the observed amplitude specified by **_refine_ls_structure_factor_coef**, $Y_{\rm calc}$ = the calculated amplitude specified by **_refine_ls_structure_factor_coef**, w = the least-squares weight and the sum is taken over the specified reflections.
The permitted range is $0.0 \rightarrow \infty$. **[refine]**

_refine_ls_wR_factor_gt (*numb*)
Weighted residual factors for significantly intense reflections (satisfying **_reflns_threshold_expression**) included in the refinement. The reflections also satisfy the resolution limits established by **_refine_ls_d_res_high** and **_refine_ls_d_res_low**. See also the **_refine_ls_R_factor_** definitions.

$$wR = \left(\frac{\sum \left| w|Y_{\rm obs} - Y_{\rm calc}|^2 \right|}{\sum |wY_{\rm obs}^2|} \right)^{1/2},$$

where $Y_{\rm obs}$ = the observed amplitude specified by **_refine_ls_structure_factor_coef**, $Y_{\rm calc}$ = the calculated amplitude specified by **_refine_ls_structure_factor_coef**, w = the least-squares weight and the sum is taken over the specified reflections.
The permitted range is $0.0 \rightarrow \infty$.
Related item: **_refine_ls_wR_factor_obs** (alternate). **[refine]**

_refine_ls_wR_factor_obs (*numb*)
This definition has been superseded and is retained here only for archival purposes. Use instead _refine_ls_wR_factor_gt.
*Weighted residual factors for the reflections classified as 'observed' (see **_reflns_observed_criterion**) and included in the refinement. The reflections also satisfy the resolution limits established by **_refine_ls_d_res_high** and **_refine_ls_d_res_low**. See also the **_refine_ls_R_factor_** definitions.*

$$wR = \left(\frac{\sum \left| w|Y_{\rm obs} - Y_{\rm calc}|^2 \right|}{\sum |wY_{\rm obs}^2|} \right)^{1/2},$$

*where $Y_{\rm obs}$ = the observed amplitude specified by **_refine_ls_structure_factor_coef**, $Y_{\rm calc}$ = the calculated amplitude specified by **_refine_ls_structure_factor_coef**, w = the least-squares weight and the sum is taken over the specified reflections.*
The permitted range is $0.0 \rightarrow \infty$. ***[refine]***

_refine_ls_wR_factor_ref (*numb*)
Weighted residual factors for all reflections included in the refinement. The reflections also satisfy the resolution limits established by **_refine_ls_d_res_high** and **_refine_ls_d_res_low**. See also the **_refine_ls_R_factor_** definitions.

$$wR = \left(\frac{\sum \left| w|Y_{\rm obs} - Y_{\rm calc}|^2 \right|}{\sum |wY_{\rm obs}^2|} \right)^{1/2},$$

where $Y_{\rm obs}$ = the observed amplitude specified by **_refine_ls_structure_factor_coef**, $Y_{\rm calc}$ = the calculated amplitude specified by **_refine_ls_structure_factor_coef**, w = the least-squares weight and the sum is taken over the specified reflections.
The permitted range is $0.0 \rightarrow \infty$. **[refine]**

_refine_special_details (*char*)
Description of special aspects of the refinement process.
[refine]

REFINE_LS_CLASS

Data items in the REFINE_LS_CLASS category record details (for each reflection class separately) about the reflections used for the structure refinement.

*Example 1 – example for a modulated structure extracted from van Smaalen [J. Phys. Condens. Matter (1991), **3**, 1247–1263.]*

```
loop_
    _refine_ls_class_R_factor_gt
    _refine_ls_class_code
        0.057    'Main'
        0.074    'Com'
        0.064    'NbRefls'
        0.046    'LaRefls'
        0.112    'Sat1'
        0.177    'Sat2'
```

_refine_ls_class_code (*char*)
The code identifying a certain reflection class. This code must match a **_reflns_class_code**.
Appears in list. **Must** match parent data name **_reflns_class_code**.
Examples: '1', 'm1', 's2'. **[refine_ls_class]**

_refine_ls_class_d_res_high (*numb*)
For each reflection class, the highest resolution in ångströms for the reflections used in the refinement. This is the lowest d value in a reflection class.
Appears in list containing **_refine_ls_class_code**.
The permitted range is $0.0 \rightarrow \infty$. **[refine_ls_class]**

_refine_ls_class_d_res_low (*numb*)
For each reflection class, the lowest resolution in ångströms for the reflections used in the refinement. This is the highest d value in a reflection class.
Appears in list containing **_refine_ls_class_code**.
The permitted range is $0.0 \rightarrow \infty$. **[refine_ls_class]**

_refine_ls_class_R_factor_all
_refine_ls_class_R_factor_gt (*numb*)

For each reflection class, the residual factors for all reflections, and for significantly intense reflections (see **_reflns_threshold_expression**), included in the refinement. The reflections also satisfy the resolution limits established by **_refine_ls_class_d_res_high** and **_refine_ls_class_d_res_low**. This is the conventional *R* factor.

$$R = \frac{\sum |F_{\rm obs} - F_{\rm calc}|}{\sum |F_{\rm obs}|},$$

where $F_{\rm obs}$ = the observed structure-factor amplitudes, $F_{\rm calc}$ = the calculated structure-factor amplitudes and the sum is taken over the specified reflections. See also **_refine_ls_class_wR_factor_all** definitions.

Appears in list containing **_refine_ls_class_code**.

The permitted range is $0.0 \rightarrow \infty$. **[refine_ls_class]**

_refine_ls_class_R_Fsqd_factor (*numb*)

For each reflection class, the residual factor $R(F^2)$ calculated on the squared amplitudes of the observed and calculated structure factors for the reflections judged significantly intense (*i.e.* satisfying the threshold specified by **_reflns_threshold_expression**) and included in the refinement. The reflections also satisfy the resolution limits established by **_refine_ls_class_d_res_high** and **_refine_ls_class_d_res_low**.

$$R(F^2) = \frac{\sum |F^2_{\rm obs} - F^2_{\rm calc}|}{\sum |F^2_{\rm obs}|},$$

where $F^2_{\rm obs}$ = squares of the observed structure-factor amplitudes, $F^2_{\rm calc}$ = squares of the calculated structure-factor amplitudes and the sum is taken over the specified reflections.

Appears in list containing **_refine_ls_class_code**.

The permitted range is $0.0 \rightarrow \infty$. **[refine_ls_class]**

_refine_ls_class_R_I_factor (*numb*)

For each reflection class, the residual factor $R(I)$ for the reflections judged significantly intense (*i.e.* satisfying the threshold specified by **_reflns_threshold_expression**) and included in the refinement. This is most often calculated in Rietveld refinements against powder data, where it is referred to as R_B or $R_{\rm Bragg}$.

$$R(I) = \frac{\sum |I_{\rm obs} - I_{\rm calc}|}{\sum |I_{\rm obs}|},$$

where $I_{\rm obs}$ = the net observed intensities, $I_{\rm calc}$ = the net calculated intensities and the sum is taken over the specified reflections.

Appears in list containing **_refine_ls_class_code**.

The permitted range is $0.0 \rightarrow \infty$. **[refine_ls_class]**

_refine_ls_class_wR_factor_all (*numb*)

For each reflection class, the weighted residual factors for all reflections included in the refinement. The reflections also satisfy the resolution limits established by **_refine_ls_class_d_res_high** and **_refine_ls_class_d_res_low**.

$$wR = \left(\frac{\sum \left| w|Y_{\rm obs} - Y_{\rm calc}|^2 \right|}{\sum |wY^2_{\rm obs}|} \right)^{1/2},$$

where $Y_{\rm obs}$ = the observed amplitudes specified by **_refine_ls_structure_factor_coef**, $Y_{\rm calc}$ = the calculated amplitudes specified by **_refine_ls_structure_factor_coef**, w = the least-squares weights and the sum is taken over the reflections of this class. See also **_refine_ls_class_R_factor_** definitions.

Appears in list containing **_refine_ls_class_code**.

The permitted range is $0.0 \rightarrow \infty$. **[refine_ls_class]**

REFLN

Data items in the REFLN category record details about the reflections used to determine the ATOM_SITE data items. The REFLN data items refer to individual reflections and must be included in looped lists. The REFLNS data items specify the parameters that apply to all reflections. The REFLNS data items are not looped.

*Example 1 – based on data set fetod of Todres, Yanovsky, Ermekov & Struchkov [Acta Cryst. (1993), C**49**, 1352–1354].*

```
loop_
 _refln_index_h
 _refln_index_k
 _refln_index_l
 _refln_F_squared_calc
 _refln_F_squared_meas
 _refln_F_squared_sigma
 _refln_include_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
```

Example 2 – based on standard test data set p6122 of the Xtal distribution [Hall, King & Stewart (1995). Xtal3.4 User's Manual. University of Western Australia].

```
loop_
_refln_index_h
_refln_index_k
_refln_index_l
_refln_F_meas
_refln_F_calc
_refln_F_sigma
_refln_include_status
_refln_scale_group_code
    0   0   6  34.935  36.034   3.143  o  1
    0   0  12  42.599  40.855   2.131  o  1
    0   1   0  42.500  42.507   4.719  o  1
    0   1   1  59.172  57.976   4.719  o  1
    0   1   2  89.694  94.741   4.325  o  1
    0   1   3  51.743  52.241   3.850  o  1
    0   1   4   9.294  10.318   2.346  o  1
    0   1   5  41.160  39.951   3.313  o  1
    0   1   6   6.755   7.102    .895  <  1
    0   1   7  30.693  31.171   2.668  o  1
    0   1   8  12.324  12.085   2.391  o  1
    0   1   9  15.348  15.122   2.239  o  1
    0   1  10  17.622  19.605   1.997  o  1
```

_refln_A_calc
_refln_A_meas (*numb*)

The calculated and measured structure-factor component *A* (in electrons for X-ray diffraction).

$$A = |F| \cos(\text{phase}).$$

Appears in list containing **_refln_index_**. **[refln]**

_refln_B_calc
_refln_B_meas (*numb*)

The calculated and measured structure-factor component *B* (in electrons for X-ray diffraction).

$$B = |F| \sin(\text{phase}).$$

Appears in list containing **_refln_index_**. **[refln]**

_refln_class_code (*char*)

The code identifying the class to which this reflection has been assigned. This code must match a value of **_reflns_class_code**. Reflections may be grouped into classes for a variety of purposes. For example, for modulated structures each reflection class may be defined by the number $m = \sum |m_i|$, where the m_i are the integer coefficients that, in addition to h, k, l, index the corresponding diffraction vector in the basis defined for the reciprocal lattice.

Appears in list containing **_refln_index_**. **Must** match parent data name **_reflns_class_code**. **[refln]**

_refln_d_spacing (*numb*)

The d spacing in ångströms for this reflection. This is related to the $(\sin\theta)/\lambda$ value by the expression **_refln_d_spacing** = 2/(**_refln_sint/lambda**).

Appears in list containing **_refln_index_**.

The permitted range is $0.0 \rightarrow \infty$. **[refln]**

_refln_crystal_id (*char*)

Code identifying each crystal if multiple crystals are used. Is used to link with **_exptl_crystal_id** in the **_exptl_crystal_** list.

Appears in list containing **_refln_index_**. **Must** match parent data name **_exptl_crystal_id**. **[refln]**

_refln_F_calc
_refln_F_meas
_refln_F_sigma (*numb*)

The calculated, measured and standard uncertainty (derived from measurement) of the structure factors (in electrons for X-ray diffraction).

Appears in list containing **_refln_index_**. **[refln]**

_refln_F_squared_calc
_refln_F_squared_meas
_refln_F_squared_sigma (*numb*)

Calculated, measured and estimated standard uncertainty (derived from measurement) of the squared structure factors (in electrons squared for X-ray diffraction).

Appears in list containing **_refln_index_**. **[refln]**

_refln_include_status (*char*)

Classification of a reflection indicating its status with respect to inclusion in the refinement and the calculation of *R* factors.

Appears in list containing **_refln_index_**.

Related item: **_refln_observed_status** (alternate).

The data value must be one of the following:

o	(lower-case letter o for 'observed') satisfies **_refine_ls_d_res_high**, satisfies **_refine_ls_d_res_low** and exceeds **_reflns_threshold_expression**
<	satisfies **_refine_ls_d_res_high**, satisfies **_refine_ls_d_res_low** and does not exceed **_reflns_threshold_expression**
-	systematically absent reflection
x	unreliable measurement – not used
h	does not satisfy **_refine_ls_d_res_high**
l	does not satisfy **_refine_ls_d_res_low**

Where no value is given, the assumed value is 'o'. **[refln]**

_refln_index_h
_refln_index_k
_refln_index_l (*numb*)

Miller indices of the reflection. The values of the Miller indices in the REFLN category must correspond to the cell defined by the cell lengths and cell angles in the CELL category.

Appears in list as essential element of loop structure. **[refln]**

_refln_intensity_calc
_refln_intensity_meas
_refln_intensity_sigma (*numb*)

The calculated, measured and standard uncertainty (derived from measurement) of the intensity, all in the same arbitrary units as **_refln_intensity_meas**.

Appears in list containing **_refln_index_**. **[refln]**

_refln_mean_path_length_tbar (*numb*)

Mean path length in millimetres through the crystal for this reflection.

Appears in list containing **_refln_index_**.

The permitted range is $0.0 \rightarrow \infty$. **[refln]**

_refln_observed_status (*char*)

This definition has been superseded and is retained here only for archival purposes. Use instead _refln_include_status.

Classification of a reflection indicating its status with respect to inclusion in the refinement and the calculation of R factors.

*Appears in list containing **_refln_index_**.*

The data value must be one of the following:

o	*satisfies **_refine_ls_d_res_high**, satisfies **_refine_ls_d_res_low** and observed by **_reflns_observed_criterion***
<	*satisfies **_refine_ls_d_res_high**, satisfies **_refine_ls_d_res_low** and unobserved by **_reflns_observed_criterion***
-	*systematically absent reflection*
x	*unreliable measurement – not used*
h	*does not satisfy **_refine_ls_d_res_high***
l	*does not satisfy **_refine_ls_d_res_low***

Where no value is given, the assumed value is 'o'. ***[refln]***

_refln_phase_calc (*numb*)

The calculated structure-factor phase in degrees.

Appears in list containing **_refln_index_**. **[refln]**

_refln_phase_meas (*numb, su*)

The measured structure-factor phase in degrees.

Appears in list containing **_refln_index_**. **[refln]**

_refln_refinement_status (*char*)

Status of a reflection in the structure-refinement process.

Appears in list containing **_refln_index_**.

The data value must be one of the following:

incl	included in least-squares process
excl	excluded from least-squares process
extn	excluded due to extinction

Where no value is given, the assumed value is 'incl'. **[refln]**

_refln_scale_group_code (*char*)

Code identifying the structure-factor scale. This code must correspond to one of the **_reflns_scale_group_code** values.

Appears in list containing **_refln_index_**. **Must** match parent data name **_reflns_scale_group_code**.

Examples: '1', '2', '3', 's1', 'A', 'B', 'c1', 'c2', 'c3'. **[refln]**

_refln_sint/lambda (*numb*)

The $(\sin\theta)/\lambda$ value in reciprocal ångströms for this reflection.

Appears in list containing **_refln_index_**.

The permitted range is $0.0 \rightarrow \infty$. **[refln]**

_refln_symmetry_epsilon (*numb*)

The symmetry reinforcement factor corresponding to the number of times the reflection indices are generated identically from the space-group symmetry operations.

Appears in list containing **_refln_index_**.

The permitted range is $1 \rightarrow 48$. **[refln]**

_refln_symmetry_multiplicity (*numb*)
The number of reflections symmetry-equivalent under the Laue symmetry to the present reflection. In the Laue symmetry, Friedel opposites (*hkl* and $-h\ -k\ -l$) are equivalent. Tables of symmetry-equivalent reflections are available in *International Tables for Crystallography* Volume A (2002), Chapter 10.1.
Appears in list containing **_refln_index_**.
The permitted range is $1 \rightarrow 48$. **[refln]**

_refln_wavelength (*numb*)
The mean wavelength in ångströms of the radiation used to measure this reflection. This is an important parameter for data collected using energy-dispersive detectors or the Laue method.
Appears in list containing **_refln_index_**.
The permitted range is $0.0 \rightarrow \infty$. **[refln]**

_refln_wavelength_id (*char*)
Code identifying the wavelength in the **_diffrn_radiation_** list. See **_diffrn_radiation_wavelength_id**.
Appears in list containing **_refln_index_**. **Must** match parent data name **_diffrn_radiation_wavelength_id**. **[refln]**

REFLNS

Data items in the REFLNS category record details about the reflections used to determine the ATOM_SITE data items. The REFLN data items refer to individual reflections and must be included in looped lists. The REFLNS data items specify the parameters that apply to all reflections. The REFLNS data items are not looped.

Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C47, 2276–2277].

```
_reflns_limit_h_min              0
_reflns_limit_h_max              6
_reflns_limit_k_min              0
_reflns_limit_k_max              17
_reflns_limit_l_min              0
_reflns_limit_l_max              22
_reflns_number_total             1592
_reflns_number_gt                1408
_reflns_threshold_expression     'F > 6.0u(F)'
_reflns_d_resolution_high        0.8733
_reflns_d_resolution_low         11.9202
```

_reflns_d_resolution_high
_reflns_d_resolution_low (*numb*)
The highest and lowest resolution in ångströms for the reflections. These are the smallest and largest d values.
The permitted range is $0.0 \rightarrow \infty$. **[reflns]**

_reflns_Friedel_coverage (*numb*)
The proportion of Friedel-related reflections present in the number of 'independent' reflections specified by the item **_reflns_number_total**. This proportion is calculated as the ratio

$$\frac{[N(\text{crystal class}) - N(\text{Laue symmetry})]}{N(\text{Laue symmetry})},$$

where, working from the **_diffrn_refln_** list, N(crystal class) is the number of reflections obtained on averaging under the symmetry of the crystal class and N(Laue symmetry) is the number of reflections obtained on averaging under the Laue symmetry.

Examples: (*a*) For centrosymmetric structures, **_reflns_Friedel_coverage** is necessarily equal to 0.0 as the crystal class is identical to the Laue symmetry. (*b*) For whole-sphere data for a crystal in the space group $P1$, **_reflns_Friedel_coverage** is equal to 1.0, as no reflection *hkl* is equivalent to $-h\ -k\ -l$ in the crystal class and all Friedel pairs $\{hkl;\ -h\ -k\ -l\}$ have been measured. (*c*) For whole-sphere data in space group *Pmm*2, **_reflns_Friedel_coverage** will be < 1.0 because although reflections *hkl* and $-h\ -k\ -l$ are not equivalent when *hkl* indices are nonzero, they are when $l = 0$. (*d*) For a crystal in the space group *Pmm*2, measurements of the two inequivalent octants $h \geq 0, k \geq 0, l$ lead to the same value as in (*c*), whereas measurements of the two equivalent octants $h \geq 0, k, l \geq 0$ will lead to a value of zero for **_reflns_Friedel_coverage**.
The permitted range is $0.0 \rightarrow 1.0$. **[reflns]**

_reflns_limit_h_max
_reflns_limit_h_min
_reflns_limit_k_max
_reflns_limit_k_min
_reflns_limit_l_max
_reflns_limit_l_min (*numb*)
Miller indices limits for the reported reflections. These need not be the same as the **_diffrn_reflns_limit_** values.
[reflns]

_reflns_number_gt (*numb*)
The number of reflections in the **_refln_** list (not the **_diffrn_refln_** list) that are significantly intense, satisfying the criterion specified by **_reflns_threshold_expression**. This may include Friedel-equivalent reflections (*i.e.* those which are symmetry-equivalent under the Laue symmetry but inequivalent under the crystal class) according to the nature of the structure and the procedures used. Special characteristics of the reflections included in the **_refln_** list should be given in the item **_reflns_special_details**.
The permitted range is $0 \rightarrow \infty$.
Related item: **_reflns_number_observed** (alternate). **[reflns]**

_reflns_number_observed (*numb*)
This definition has been superseded and is retained here only for archival purposes. Use instead _reflns_number_gt.
*The number of 'observed' reflections in the **_refln_** list (not the **_diffrn_refln_** list). The observed reflections satisfy the threshold criterion specified by **_reflns_threshold_expression** (or the deprecated item **_reflns_observed_criterion**). They may include Friedel-equivalent reflections according to the nature of the structure and the procedures used. Special characteristics of the reflections included in the **_refln_** list should be given in the item **_reflns_special_details**.*
The permitted range is $0 \rightarrow \infty$. ***[reflns]***

_reflns_number_total (*numb*)
The total number of reflections in the **_refln_** list (not the **_diffrn_refln_** list). This may include Friedel-equivalent reflections (*i.e.* those which are symmetry-equivalent under the Laue symmetry but inequivalent under the crystal class) according to the nature of the structure and the procedures used. Special characteristics of the reflections included in the **_refln_** list should be given in the item **_reflns_special_details**.
The permitted range is $0 \rightarrow \infty$. **[reflns]**

_reflns_observed_criterion (*char*)
This definition has been superseded and is retained here only for archival purposes. Use instead _reflns_threshold_expression.
The criterion used to classify a reflection as 'observed'. This criterion is usually expressed in terms of a $\sigma(I)$ *or* $\sigma(F)$ *threshold.*
Example: 'I>2u(I)'. ***[reflns]***

_reflns_special_details (*char*)
Description of the properties of the reported reflection list that are not given in other data items. In particular, this should include information about the averaging (or not) of symmetry-equivalent reflections including Friedel pairs.
[reflns]

_reflns_threshold_expression (*char*)
The threshold, usually based on multiples of $u(I)$, $u(F^2)$ or $u(F)$, that serves to identify significantly intense reflections, the number of which is given by **_reflns_number_gt**. These reflections are used in the calculation of **_refine_ls_R_factor_gt**.
Related item: **_reflns_observed_criterion** (alternate).
Example: 'I>2u(I)'. **[reflns]**

REFLNS_CLASS

Data items in the REFLNS_CLASS category record details, for each reflection class, about the reflections used to determine the structural parameters.

Example 1 – corresponding to the one-dimensional incommensurately modulated structure of K_2SeO_4.

```
loop_
    _reflns_class_number_gt
    _reflns_class_code
        584     'Main'
        226     'Sat1'
        50      'Sat2'
```

_reflns_class_code (*char*)
The code identifying a certain reflection class.
Appears in list. May match child data name(s): **_refln_class_code**, **_refine_ls_class_code**.
Examples: '1', 'm1', 's2'. **[reflns_class]**

_reflns_class_d_res_high (*numb*)
For each reflection class, the highest resolution in ångströms for the reflections used in the refinement. This is the smallest d value.
Appears in list containing **_reflns_class_code**.
The permitted range is $0.0 \rightarrow \infty$. **[reflns_class]**

_reflns_class_d_res_low (*numb*)
For each reflection class, the lowest resolution in ångströms for the reflections used in the refinement. This is the largest d value.
Appears in list containing **_reflns_class_code**.
The permitted range is $0.0 \rightarrow \infty$. **[reflns_class]**

_reflns_class_description (*char*)
Description of each reflection class.
Appears in list containing **_reflns_class_code**.
Examples: 'm=1 first order satellites', 'H0L0 common projection reflections'. **[reflns_class]**

_reflns_class_number_gt (*numb*)
For each reflection class, the number of significantly intense reflections (see **_reflns_threshold_expression**) in the **_refln_** list (not the **_diffrn_refln_** list). This may include Friedel-equivalent reflections (*i.e.* those which are symmetry-equivalent under the Laue symmetry but inequivalent under the crystal class) according to the nature of the structure and the procedures used. Special characteristics of the reflections included in the **_refln_** list should be given in the item **_reflns_special_details**.
Appears in list containing **_reflns_class_code**.
The permitted range is $0.0 \rightarrow \infty$. **[reflns_class]**

_reflns_class_number_total (*numb*)
For each reflection class, the total number of reflections in the **_refln_** list (not the **_diffrn_refln_** list). This may include Friedel-equivalent reflections (*i.e.* those which are symmetry-equivalent under the Laue symmetry but inequivalent under the crystal class) according to the nature of the structure and the procedures used. Special characteristics of the reflections included in the **_refln_** list should be given in the item **_reflns_special_details**.
Appears in list containing **_reflns_class_code**.
The permitted range is $0.0 \rightarrow \infty$. **[reflns_class]**

_reflns_class_R_factor_all
_reflns_class_R_factor_gt (*numb*)
For each reflection class, the residual factors for all reflections, and for significantly intense reflections (see **_reflns_threshold_expression**), included in the refinement. The reflections also satisfy the resolution limits established by **_reflns_class_d_res_high** and **_reflns_class_d_res_low**. This is the conventional R factor.

$$R = \frac{\sum |F_{\rm obs} - F_{\rm calc}|}{\sum |F_{\rm obs}|},$$

where $F_{\rm obs}$ = the observed structure-factor amplitudes, $F_{\rm calc}$ = the calculated structure-factor amplitudes and the sum is taken over the reflections of this class. See also **_reflns_class_wR_factor_all** definitions.
Appears in list containing **_reflns_class_code**.
The permitted range is $0.0 \rightarrow \infty$. **[reflns_class]**

_reflns_class_R_Fsqd_factor (*numb*)
For each reflection class, the residual factor $R(F^2)$ calculated on the squared amplitudes of the observed and calculated structure factors, for the reflections judged significantly intense (*i.e.* satisfying the threshold specified by **_reflns_threshold_expression**) and included in the refinement. The reflections also satisfy the resolution limits established by **_reflns_class_d_res_high** and **_reflns_class_d_res_low**.

$$R(F^2) = \frac{\sum |F^2_{\rm obs} - F^2_{\rm calc}|}{\sum |F^2_{\rm obs}|},$$

where $F^2_{\rm obs}$ = squares of the observed structure-factor amplitudes, $F^2_{\rm calc}$ = squares of the calculated structure-factor amplitudes and the sum is taken over the reflections of this class.
Appears in list containing **_reflns_class_code**.
The permitted range is $0.0 \rightarrow \infty$. **[reflns_class]**

_reflns_class_R_I_factor (*numb*)
For each reflection class, the residual factor $R(I)$ for the reflections judged significantly intense (*i.e.* satisfying the threshold specified by **_reflns_threshold_expression**) and included in the refinement. This is most often calculated in Rietveld refinements against powder data, where it is referred to as R_B or $R_{\rm Bragg}$.

$$R(I) = \frac{\sum |I_{\rm obs} - I_{\rm calc}|}{\sum |I_{\rm obs}|},$$

where $I_{\rm obs}$ = the net observed intensities, $I_{\rm calc}$ = the net calculated intensities and the sum is taken over the reflections of this class.
Appears in list containing **_reflns_class_code**.
The permitted range is $0.0 \rightarrow \infty$. **[reflns_class]**

_reflns_class_wR_factor_all (*numb*)
For each reflection class, the weighted residual factors for all reflections included in the refinement. The reflections also satisfy the resolution limits established by **_reflns_class_d_res_high** and **_reflns_class_d_res_low**.

$$wR = \left(\frac{\sum \left| w |Y_{\rm obs} - Y_{\rm calc}|^2 \right|}{\sum |wY^2_{\rm obs}|} \right)^{1/2},$$

where $Y_{\rm obs}$ = the observed amplitudes specified by **_refine_ls_structure_factor_coef**, $Y_{\rm calc}$ = the calculated amplitudes specified by **_refine_ls_structure_factor_coef**, w = the least-squares weights and the sum is taken over the reflections of this class. See also **_reflns_class_R_factor_** definitions.
Appears in list containing **_reflns_class_code**.
The permitted range is $0.0 \rightarrow \infty$. **[reflns_class]**

REFLNS_SCALE

Data items in the REFLNS_SCALE category record details about the structure-factor scales. They are referenced from within the REFLN list through **_refln_scale_group_code**.

Example 1 – based on standard test data set p6122 of the Xtal distribution [Hall, King & Stewart (1995). Xtal3.4 User's Manual. University of Western Australia].

```
loop_
_reflns_scale_group_code
_reflns_scale_meas_F
  1  .895447
  2  .912743
```

_reflns_scale_group_code (*char*)
The code identifying a scale **_reflns_scale_meas_**. These are linked to the **_refln_** list by the **_refln_scale_group_code**. These codes need not correspond to those in the **_diffrn_scale_** list.
Appears in list as essential element of loop structure. May match child data name(s):
_refln_scale_group_code. **[reflns_scale]**

_reflns_scale_meas_F
_reflns_scale_meas_F_squared
_reflns_scale_meas_intensity (*numb, su*)
Scales associated with **_reflns_scale_group_code**.
Appears in list containing **_reflns_scale_group_code**.
The permitted range is $0.0 \rightarrow \infty$. **[reflns_scale]**

REFLNS_SHELL

Data items in the REFLNS_SHELL category record details about the reflections used to determine the ATOM_SITE data items, as broken down by shells of resolution.

Example 1 – based on PDB entry 5HVP and laboratory records for the structure corresponding to PDB entry 5HVP.

```
loop_
_reflns_shell_d_res_high
_reflns_shell_d_res_low
_reflns_shell_meanI_over_uI_gt
_reflns_shell_number_measured_gt
_reflns_shell_number_unique_gt
_reflns_shell_percent_possible_gt
_reflns_shell_Rmerge_F_gt
  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
```

_reflns_shell_d_res_high (*numb*)
The highest resolution in ångströms for the reflections in this shell. This is the smallest *d* value.
Appears in list.
The permitted range is $0.0 \rightarrow \infty$. **[reflns_shell]**

_reflns_shell_d_res_low (*numb*)
The lowest resolution in ångströms for the reflections in this shell. This is the largest *d* value.
Appears in list.
The permitted range is $0.0 \rightarrow \infty$. **[reflns_shell]**

_reflns_shell_meanI_over_sigI_all (*numb*)
This definition has been superseded and is retained here only for archival purposes. Use instead _reflns_shell_meanI_over_uI_all.
The ratio of the mean of the intensities of all reflections in this shell to the mean of the standard uncertainties of the intensities of all reflections in the resolution shell.
Appears in list. ***[reflns_shell]***

_reflns_shell_meanI_over_sigI_gt (*numb*)
This definition has been superseded and is retained here only for archival purposes. Use instead _reflns_shell_meanI_over_uI_gt.
*The ratio of the mean of the intensities of the significantly intense reflections (see **_reflns_threshold_expression**) in this shell to the mean of the standard uncertainties of the intensities of the significantly intense reflections in the resolution shell.*
Appears in list. ***[reflns_shell]***

_reflns_shell_meanI_over_sigI_obs (*numb*)
This definition has been superseded and is retained here only for archival purposes. Use instead _reflns_shell_meanI_over_sigI_gt.
*The ratio of the mean of the intensities of the reflections classified as 'observed' (see **_reflns_observed_criterion**) in this shell to the mean of the standard uncertainties of the intensities of the 'observed' reflections in the resolution shell.*
Appears in list. ***[reflns_shell]***

_reflns_shell_meanI_over_uI_all (*numb*)
The ratio of the mean of the intensities of all reflections in this shell to the mean of the standard uncertainties of the intensities of all reflections in the resolution shell.
Appears in list.
Related item: **_reflns_shell_meanI_over_sigI_all** (alternate).
[reflns_shell]

_reflns_shell_meanI_over_uI_gt (*numb*)
The ratio of the mean of the intensities of the significantly intense reflections (see **_reflns_threshold_expression**) in this shell to the mean of the standard uncertainties of the intensities of the significantly intense reflections in the resolution shell.
Appears in list.
Related items:
_reflns_shell_meanI_over_sigI_gt (alternate),
_reflns_shell_meanI_over_sigI_obs (alternate). **[reflns_shell]**

_reflns_shell_number_measured_all (*numb*)
The total number of reflections measured for this resolution shell.
Appears in list.
The permitted range is $0.0 \rightarrow \infty$. **[reflns_shell]**

_reflns_shell_number_measured_gt (*numb*)
The number of significantly intense reflections (see **_reflns_threshold_expression**) measured for this resolution shell.
Appears in list.
The permitted range is $0.0 \rightarrow \infty$.
Related item: **_reflns_shell_number_measured_obs** (alternate).
[reflns_shell]

_reflns_shell_number_measured_obs (*numb*)
This definition has been superseded and is retained here only for archival purposes. Use instead _reflns_shell_number_measured_gt.
*The number of reflections classified as 'observed' (see **_reflns_observed_criterion**) measured for this resolution shell.*
Appears in list.
The permitted range is $0.0 \rightarrow \infty$. ***[reflns_shell]***

_reflns_shell_number_possible (*numb*)
The number of unique reflections it is possible to measure in this reflection shell.
Appears in list.
The permitted range is $0 \rightarrow \infty$. **[reflns_shell]**

_reflns_shell_number_unique_all (*numb*)
The total number of measured reflections resulting from merging measured symmetry-equivalent reflections for this resolution shell.
Appears in list.
The permitted range is $0 \rightarrow \infty$. **[reflns_shell]**

_reflns_shell_number_unique_gt (*numb*)
The total number of significantly intense reflections (see **_reflns_threshold_expression**) resulting from merging measured symmetry-equivalent reflections for this resolution shell.
Appears in list.
The permitted range is $0 \rightarrow \infty$.
Related item: **_reflns_shell_number_unique_obs** (alternate). **[reflns_shell]**

_reflns_shell_number_unique_obs (*numb*)
This definition has been superseded and is retained here only for archival purposes. Use instead _reflns_shell_number_unique_gt.
*The total number of reflections classified as 'observed' (see **_reflns_observed_criterion**) resulting from merging measured symmetry-equivalent reflections for this resolution shell.*
Appears in list.
The permitted range is $0 \rightarrow \infty$. ***[reflns_shell]***

_reflns_shell_percent_possible_all (*numb*)
The percentage of geometrically possible reflections represented by all reflections measured for this resolution shell.
Appears in list.
The permitted range is $0.0 \rightarrow 100.0$. **[reflns_shell]**

_reflns_shell_percent_possible_gt (*numb*)
The percentage of geometrically possible reflections represented by significantly intense reflections (see **_reflns_threshold_expression**) measured for this resolution shell.
Appears in list.
The permitted range is $0.0 \rightarrow 100.0$.
Related item: **_reflns_shell_percent_possible_obs** (alternate).
[reflns_shell]

_reflns_shell_percent_possible_obs (*numb*)
This definition has been superseded and is retained here only for archival purposes. Use instead _reflns_shell_percent_possible_gt.
*The percentage of geometrically possible reflections represented by reflections classified as 'observed' (see **_reflns_observed_criterion**) measured for this resolution shell.*
Appears in list.
The permitted range is $0.0 \rightarrow 100.0$. ***[reflns_shell]***

_reflns_shell_Rmerge_F_all (*numb*)
The value of $R_{\rm merge}(F)$ for all reflections in a given shell.

$$R_{\rm merge} = \frac{\sum_i(\sum_j |F_j - \langle F\rangle|)}{\sum_i(\sum_j \langle F\rangle)},$$

where F_j = the amplitude of the jth observation of reflection i, $\langle F\rangle$ = the mean of the amplitudes of all observations of reflection i, $\sum_i$ is taken over all reflections and $\sum_j$ is taken over all observations of each reflection.
Appears in list.
The permitted range is $0.0 \rightarrow \infty$. **[reflns_shell]**

_reflns_shell_Rmerge_F_gt (*numb*)
The value of $R_{\rm merge}(F)$ for significantly intense reflections (see **_reflns_threshold_expression**) in a given shell.

$$R_{\rm merge} = \frac{\sum_i(\sum_j |F_j - \langle F\rangle|)}{\sum_i(\sum_j \langle F\rangle)},$$

where F_j = the amplitude of the jth observation of reflection i, $\langle F\rangle$ = the mean of the amplitudes of all observations of reflection i, $\sum_i$ is taken over all reflections and $\sum_j$ is taken over all observations of each reflection.
Appears in list.
The permitted range is $0.0 \rightarrow \infty$.
Related item: **_reflns_shell_Rmerge_F_obs** (alternate). **[reflns_shell]**

_reflns_shell_Rmerge_F_obs (*numb*)
This definition has been superseded and is retained here only for archival purposes. Use instead _reflns_shell_Rmerge_F_gt.
The value of $R_{\rm merge}(F)$ *for reflections classified as 'observed' (see **_reflns_observed_criterion**) in a given shell.*

$$R_{\rm merge} = \frac{\sum_i(\sum_j |F_j - \langle F\rangle|)}{\sum_i(\sum_j \langle F\rangle)},$$

where F_j *= the amplitude of the* j*th observation of reflection* i*,* $\langle F\rangle$ *= the mean of the amplitudes of all observations of reflection* i*,* $\sum_i$ *is taken over all reflections and* $\sum_j$ *is taken over all observations of each reflection.*
Appears in list.
The permitted range is $0.0 \rightarrow \infty$. ***[reflns_shell]***

_reflns_shell_Rmerge_I_all (*numb*)
The value of $R_{\rm merge}(I)$ for all reflections in a given shell.

$$R_{\rm merge}(I) = \frac{\sum_i(\sum_j |I_j - \langle I\rangle|)}{\sum_i(\sum_j \langle I\rangle)},$$

where I_j = the intensity of the jth observation of reflection i, $\langle I\rangle$ = the mean of the intensities of all observations of reflection i, $\sum_i$ is taken over all reflections and $\sum_j$ is taken over all observations of each reflection.
Appears in list.
The permitted range is $0.0 \rightarrow \infty$. **[reflns_shell]**

_reflns_shell_Rmerge_I_gt (*numb*)
The value of $R_{\rm merge}(I)$ for significantly intense reflections (see **_reflns_threshold_expression**) in a given shell.

$$R_{\rm merge}(I) = \frac{\sum_i(\sum_j |I_j - \langle I\rangle|)}{\sum_i(\sum_j \langle I\rangle)},$$

where I_j = the intensity of the jth observation of reflection i, $\langle I\rangle$ = the mean of the intensities of all observations of reflection i, $\sum_i$ is taken over all reflections and $\sum_j$ is taken over all observations of each reflection.
Appears in list.
The permitted range is $0.0 \rightarrow \infty$.
Related item: **_reflns_shell_Rmerge_I_obs** (alternate). **[reflns_shell]**

_reflns_shell_Rmerge_I_obs (*numb*)
This definition has been superseded and is retained here only for archival purposes. Use instead _reflns_shell_Rmerge_I_gt.
The value of $R_{\rm merge}(I)$ *for reflections classified as 'observed' (see **_reflns_observed_criterion**) in a given shell.*

$$R_{\rm merge}(I) = \frac{\sum_i(\sum_j |I_j - \langle I\rangle|)}{\sum_i(\sum_j \langle I\rangle)},$$

where I_j *= the intensity of the* j*th observation of reflection* i*,* $\langle I\rangle$ *= the mean of the intensities of all observations of reflection* i*,* $\sum_i$ *is taken over all reflections and* $\sum_j$ *is taken over all observations of each reflection.*
Appears in list.
The permitted range is $0.0 \rightarrow \infty$. ***[reflns_shell]***

SPACE_GROUP

Contains all the data items that refer to the space group as a whole, such as its name or crystal system. They may be looped, for example, in a list of space groups and their properties. Only a subset of the SPACE_GROUP category items appear in the core dictionary. The remainder are found in the symmetry CIF dictionary. Space-group types are identified by their number as given in *International Tables for Crystallography* Vol. A. Specific settings of the space groups can be identified either by their Hall symbol or by specifying their symmetry operations. The commonly used Hermann–Mauguin symbol determines the space-group type uniquely but several different Hermann–Mauguin symbols may refer to the same space-group type. A Hermann–Mauguin symbol contains information on the choice of the basis, but not on the choice of origin. Different formats for the Hermann–Mauguin symbol are found in the symmetry CIF dictionary.

Example 1 – the monoclinic space group No. 15 with unique axis b.

```
_space_group_id                 1
_space_group_name_H-M_alt       'C 2/c'
_space_group_IT_number          15
_space_group_name_Hall          '-C 2yc'
_space_group_crystal_system     monoclinic
```

_space_group_crystal_system (*char*)

The name of the system of geometric crystal classes of space groups (crystal system) to which the space group belongs. Note that rhombohedral space groups belong to the trigonal system.

May appear in list containing **_space_group_id**.

Related item: **_symmetry_cell_setting** (alternate).

The data value must be one of the following:

triclinic
monoclinic
orthorhombic
tetragonal
trigonal
hexagonal
cubic

[space_group]

_space_group_id (*char*)

This is an identifier needed if **_space_group_** items are looped.

Appears in list as essential element of loop structure. May match child data name(s): **_space_group_symop_sg_id**.

[space_group]

_space_group_IT_number (*numb*)

The number as assigned in *International Tables for Crystallography* Vol. A, specifying the proper affine class (*i.e.* the orientation-preserving affine class) of space groups (crystallographic space-group type) to which the space group belongs. This number defines the space-group type but not the coordinate system in which it is expressed.

May appear in list containing **_space_group_id**.

The permitted range is $1 \rightarrow 230$.

Related item: **_symmetry_Int_Tables_number** (alternate).

[space_group]

_space_group_name_H-M_alt (*char*)

_space_group_name_H-M_alt allows any Hermann–Mauguin symbol to be given. The way in which this item is used is determined by the user and in general is not intended to be interpreted by computer. It may, for example, be used to give one of the extended Hermann–Mauguin symbols given in Table 4.3.2.1 of *International Tables for Crystallography* Vol. A (2002) or a Hermann–Mauguin symbol for a conventional or unconventional setting. Each component of the space-group name is separated by a space or an underscore. The use of a space is strongly recommended. The underscore is only retained because it was used in older files. It should not be used in new CIFs. Subscripts should appear without special symbols. Bars should be given as negative signs before the numbers to which they apply. The commonly used Hermann–Mauguin symbol determines the space-group type uniquely but a given space-group type may be described by more than one Hermann–Mauguin symbol. The space-group type is best described using **_space_group_IT_number**. The Hermann–Mauguin symbol may contain information on the choice of basis, but not on the choice of origin. To define the setting uniquely, use **_space_group_name_Hall** or list the symmetry operations.

May appear in list containing **_space_group_id**.

Related item: **_symmetry_space_group_name_H-M** (alternate).

Example:

```
; loop_
  _space_group_id
  _space_group_name_H-M_alt
  1    'C m c m'
  2    'C 2/c 2/m 21/m'
  3    'A m a m'
;  (three examples for space group No. 63)
```

[space_group]

_space_group_name_Hall (*char*)

Space-group symbol defined by Hall. Each component of the space-group name is separated by a space or an underscore. The use of a space is strongly recommended. The underscore is only retained because it was used in older files. It should not be used in new CIFs. **_space_group_name_Hall** uniquely defines the space group and its reference to a particular coordinate system.

References: Hall, S. R. (1981). *Acta Cryst.* A**37**, 517–525; erratum (1981), A**37**, 921. [See also *International Tables for Crystallography*, Vol. B (2001), Chapter 1.4, Appendix 1.4.2].

May appear in list containing **_space_group_id**.

Related item: **_symmetry_space_group_name_Hall** (alternate).

Examples: '`P 2c -2ac`' (equivalent to $Pca2_1$), '`-I 4bd 2ab 3`' (equivalent to $Ia\bar{3}d$).

[space_group]

SPACE_GROUP_SYMOP

Contains information about the symmetry operations of the space group.

Example 1 – the symmetry operations for the space group $P2_1/c$.

```
loop_
_space_group_symop_id
_space_group_symop_operation_xyz
  1    x,y,z
  2   -x,-y,-z
  3   -x,1/2+y,1/2-z
  4    x,1/2-y,1/2+z
```

_space_group_symop_id (*char*)

An arbitrary identifier that uniquely labels each symmetry operation in the list. In order for the defaults to work correctly, the identity operation should have **_space_group_symop_id** or **_symmetry_equiv_pos_site_id** set to 1, and **_space_group_symop_operation_xyz** or **_symmetry_equiv_pos_as_xyz** set to x, y, z; *i.e.* the operation labelled 1 should be the identity operation.

Appears in list as essential element of loop structure.

Related item: **_symmetry_equiv_pos_site_id** (alternate). Where no value is given, the assumed value is '`1`'.

[space_group_symop]

_space_group_symop_operation_xyz (*char*)

A parsable string giving one of the symmetry operations of the space group in algebraic form. If W is a matrix representation of the rotational part of the symmetry operation defined by the positions and signs of x, y and z, and $\mathbf{w}$ is a column of translations defined by fractions, an equivalent position $\boldsymbol{x}'$ is generated from a given position $\boldsymbol{x}$ by

$$\boldsymbol{x}' = W\boldsymbol{x} + \mathbf{w}.$$

When a list of symmetry operations is given, it must contain a complete set of coordinate representatives which generates all the operations of the space group by the addition of all primitive translations of the space group. Such representatives are to be found as the coordinates of the general-equivalent position in *International Tables for Crystallography* Vol. A (2002), to which it is necessary to add any centring translations shown above the general-equivalent position. That is to say, it is necessary to list explicitly all the symmetry operations required to generate all the atoms in the unit cell defined by the setting used. In order for the defaults to work correctly, the identity operation should have **_space_group_symop_id** or **_symmetry_equiv_pos_site_id** set to 1, and **_space_group_symop_operation_xyz** or **_symmetry_equiv_pos_as_xyz** set to x, y, z; *i.e.* the operation labelled 1 should be the identity operation.

May appear in list containing **_space_group_symop_id**.

Related item: **_symmetry_equiv_pos_as_xyz** (alternate). Where no value is given, the assumed value is '`x,y,z`'.

Example: '`x,1/2-y,1/2+z`' (glide reflection through the plane (x, 1/4, z), with glide vector (1/2)**c**). **[space_group_symop]**

_space_group_symop_sg_id (*numb*)

This must match a particular value of **_space_group_id**, allowing the symmetry operation to be identified with a particular space group.

May appear in list. containing **_space_group_symop_id**. **Must** match parent data name **_space_group_id**. **[space_group_symop]**

SYMMETRY

Data items in the SYMMETRY category record details about the space-group symmetry.

*Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C**47**, 2276–2277].*

```
_symmetry_cell_setting              orthorhombic
_symmetry_space_group_name_H-M      'P 21 21 21'
_symmetry_space_group_name_Hall     'P 2ac 2ab'
```

_symmetry_cell_setting (*char*)

This definition has been superseded and is retained here only for archival purposes. Use instead _space_group_crystal_system.

The cell settings for this space-group symmetry.

The data value must be one of the following:

`triclinic`
`monoclinic`
`orthorhombic`
`tetragonal`
`rhombohedral`
`trigonal`
`hexagonal`
`cubic` **[symmetry]**

_symmetry_Int_Tables_number (*numb*)

This definition has been superseded and is retained here only for archival purposes. Use instead _space_group_IT_number.

Space-group number from International Tables for Crystallography Vol. A (2002).

The permitted range is 1 → 230. **[symmetry]**

_symmetry_space_group_name_H-M (*char*)

This definition has been superseded and is retained here only for archival purposes. Use instead _space_group_name_H-M_alt.

Hermann–Mauguin space-group symbol. Note that the Hermann–Mauguin symbol does not necessarily contain complete information about the symmetry and the space-group origin. If used, always supply the full *symbol from International Tables for Crystallography Vol. A (2002) and indicate the origin and the setting if it is not implicit. If there is any doubt that the equivalent positions can be uniquely deduced from this symbol, specify the **_symmetry_equiv_pos_as_xyz** or *__Hall** *data items as well. Leave spaces between symbols referring to different axes.*

Examples: '`P 1 21/m 1`', '`P 2/n 2/n 2/n (origin at -1)`', '`R -3 2/m`'. **[symmetry]**

_symmetry_space_group_name_Hall (*char*)

This definition has been superseded and is retained here only for archival purposes. Use instead _space_group_name_Hall.

Space-group symbol as described by Hall. This symbol gives the space-group setting explicitly. Leave spaces between the separate components of the symbol.

*Reference: Hall, S. R. (1981). Acta Cryst. A**37**, 517–525; erratum (1981), A**37**, 921.*

Examples: '`-P 2ac 2n`', '`-R 3 2"`', '`P 61 2 2 (0 0 -1)`'. **[symmetry]**

SYMMETRY_EQUIV

Data items in the SYMMETRY_EQUIV category list the symmetry-equivalent positions for the space group.

*Example 1 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C**47**, 2276–2277].*

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

*Example 2 – based on data set TOZ of Willis, Beckwith & Tozer [Acta Cryst. (1991), C**47**, 2276–2277].*

Formally, the value of **_symmetry_equiv_pos_site_id** can be any unique character string; it is recommended that it be assigned the sequence number of the list of equivalent positions for compatibility with older files in which it did not appear.

```
loop_
_symmetry_equiv_pos_site_id
_symmetry_equiv_pos_as_xyz
    1     x,y,z
    2     1/2-x,-y,1/2+z
    3     1/2+x,1/2-y,-z
    4     -x,1/2+y,1/2-z
```

_symmetry_equiv_pos_as_xyz (*char*)

This definition has been superseded and is retained here only for archival purposes. Use instead _space_group_symop_operation_xyz.

*Symmetry-equivalent position in the 'xyz' representation. Except for the space group P*1*, these data will be repeated in a loop. The format of the data item is as per International Tables for Crystallography Vol. A. (2002). All equivalent positions should be entered, including those for lattice centring and a centre of symmetry, if present. In order for the defaults to work correctly, the identity operation should have **_space_group_symop_id** or **_symmetry_equiv_pos_site_id** set to 1, and **_space_group_symop_operation_xyz** or **_symmetry_equiv_pos_as_xyz** set to x, y, z; i.e. the operation labelled 1 should be the identity operation.*

May appear in list. Where no value is given, the assumed value is '`x,y,z`'.

Example: '`-y+x,-y,1/3+z`'. **[symmetry_equiv]**

_symmetry_equiv_pos_site_id (*numb*)

This definition has been superseded and is retained here only for archival purposes. Use instead _space_group_symop_id.

*A code identifying each entry in the **_symmetry_equiv_pos_as_xyz** list. It is normally the sequence number of the entry in that list, and should be identified with the code 'n' in **_geom_*_symmetry_** codes of the form 'n_klm'. In order for the defaults to work correctly, the identity operation should have **_space_group_symop_id** or **_symmetry_equiv_pos_site_id** set to 1, and **_space_group_symop_operation_xyz** or **_symmetry_equiv_pos_as_xyz** set to x, y, z; i.e. the operation labelled 1 should be the identity operation.*

*Appears in list containing **_symmetry_equiv_pos_as_xyz**. Where no value is given, the assumed value is '1'.* **[symmetry_equiv]**

VALENCE_PARAM

Data items in the VALENCE_PARAM category define the parameters used for calculating bond valences from bond lengths. In addition to the parameters, a pointer is given to the reference (in VALENCE_REF) from which the bond-valence parameters were taken.

Example 1 – a bond-valence parameter list with accompanying references.

```
loop_
_valence_param_id
_valence_param_atom_1
_valence_param_atom_1_valence
_valence_param_atom_2
_valence_param_atom_2_valence
_valence_param_Ro
_valence_param_B
_valence_param_ref_id
_valence_param_details
  1   Cu 2 O -2 1.679 0.37 a .
  2   Cu 2 O -2 1.649 0.37 j .
  3   Cu 2 N -3 1.64  0.37 m '2-coordinate N'
  4   Cu 2 N -3 1.76  0.37 m '3-coordinate N'
loop_
_valence_ref_id
_valence_ref_reference
  a  'Brown & Altermatt (1985), Acta Cryst. B41, 244-247'
  j  'Liu & Thorp (1993), Inorg. Chem. 32, 4102-4205'
  m  'See, Krause & Strub (1998), Inorg. Chem. 37, 5369-5375'
```

_valence_param_atom_1 (*char*)

The element symbol of the first atom forming the bond whose bond-valence parameters are given in this category.

Appears in list containing **_valence_param_id**. **[valence_param]**

_valence_param_atom_1_valence (*numb*)

The valence (formal charge) of the first atom whose bond-valence parameters are given in this category.

Appears in list containing **_valence_param_id**. **[valence_param]**

_valence_param_atom_2 (*char*)

The element symbol of the second atom forming the bond whose bond-valence parameters are given in this category.

Appears in list containing **_valence_param_id**. **[valence_param]**

_valence_param_atom_2_valence (*numb*)

The valence (formal charge) of the second atom whose bond-valence parameters are given in this category.

Appears in list containing **_valence_param_id**. **[valence_param]**

_valence_param_B (*numb*)

The bond-valence parameter B used in the expression

$$s = \exp[(R_o - R)/B],$$

where s is the valence of a bond of length R.

Appears in list containing **_valence_param_id**. **[valence_param]**

_valence_param_details (*char*)

Details of or comments on the bond-valence parameters.

Appears in list containing **_valence_param_id**. **[valence_param]**

_valence_param_id (*char*)

An identifier for the valence parameters of a bond between the given atoms.

Appears in list. **[valence_param]**

_valence_param_ref_id (*char*)

An identifier which links to the reference to the source from which the bond-valence parameters are taken. A child of **_valence_ref_id**, which it must match.

Appears in list containing **_valence_param_id**. **Must** match parent data name **_valence_ref_id**. **[valence_param]**

_valence_param_Ro (*numb*)

The bond-valence parameter R_o used in the expression

$$s = \exp[(R_o - R)/B],$$

where s is the valence of a bond of length R.

Appears in list containing **_valence_param_id**. **[valence_param]**

VALENCE_REF

Data items in the VALENCE_REF category list the references from which the bond-valence parameters have been taken.

_valence_ref_id (*char*)

An identifier for items in this category. Parent of **_valence_param_ref_id**, which must have the same value.

Appears in list containing **_valence_ref_id**. May match child data name(s): **_valence_param_ref_id**. **[valence_ref]**

_valence_ref_reference (*char*)

Literature reference from which the valence parameters identified by **_valence_param_id** were taken.

Appears in list containing **_valence_ref_id**. **[valence_ref]**