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_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, magnetic moments and directions, and so on.

Example 1 - based on data set TOZ of Willis, Beckwith & Tozer [(1991). Acta Cryst. 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_thermal_displace_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  ?    ?
# - - - - 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
```

Example 2 - based on data set TOZ of Willis, Beckwith & Tozer [(1991). Acta Cryst. 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
# - - - - data truncated for brevity - - - -
```

Example 3 - based on data set DPTD of Yamin, Suwandi, Fun, Sivakumar & bin Shawkataly [(1996). Acta Cryst. 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. Assembly 'M' is a disordered methyl with configurations 'A' and 'B'.

```
loop_
_atom_site_label
_atom_site_occupancy
_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_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*)

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

$$T = \exp\{-1/4 \sum_i [\sum_j (B^{ij} h_i h_j a_i^* a_j^*)]\}$$

h= the Miller indices, 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(s): _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 coordinate list and conform with the same rules described in _atom_site_label.

Appears in list as essential element of loop structure. **Must** match 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→∞. [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 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*)

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

$$T = \exp\{-2\pi^2 \sum_i [\sum_j (U^{ij} h_i h_j a_i^* a_j^*)]\}$$

h= the Miller indices, 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(s): _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 H atoms for which coordinates (measured or calculated) are given.

Appears in list containing _atom_site_label. Where no value is given, the assumed value is '0'. The permitted range is 0→8.

Example(s): '2' (water oxygen), '1' (hydroxyl oxygen), '4' (ammonium nitrogen) [atom_site]

_atom_site_B_equiv_geom_mean (*numb*)

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

$$B_{\rm equiv} = (B_i B_j B_k)^{1/3}$$

B_n = the principal components of the orthogonalised 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→∞. Related item(s): _atom_site_B_iso_or_equiv (alternate), _atom_site_U_equiv_geom_mean (conversion).
[atom_site]

_atom_site_B_iso_or_equiv (*numb*)

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

$$B_{\rm equiv} = (1/3)\sum_i [\sum_j (B^{ij} a_i^* a_j^* A_i . A_j)]$$

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

Ref: 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→∞. Related item(s): _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 if the site data 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'.

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

Appears in list containing _atom_site_label. 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*)

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. [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 data name _chemical_conn_atom_number. The permitted range is 1→∞. [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(s): '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(s): '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.

Example(s): '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 that 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 H 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.

Example(s): '1' (unique disordered site in group 1), '2' (unique disordered site in group 2), '-1' (symmetry-independent disordered site) [atom_site]

_atom_site_fract_x
_atom_site_fract_y
_atom_site_fract_z (*numb*)

Atom site coordinates as fractions of the _cell_length_ values.

Appears in list containing _atom_site_label. Where no value is given, the assumed value is '0.0'. [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 underline character. Underline separators are only used if higher-order components exist. If an intermediate component is not used it may be omitted provided the underline separators are inserted. For example the label 'C233_ _ggg' is acceptable and represents the components C, 233, '', and ggg. Each label may have a different number of components.

Appears in list as essential element of loop structure. May match subsidiary 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.

Example(s): '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 underline.

Appears in list containing _atom_site_label. [atom_site]

_atom_site_occupancy (*numb*)

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.

Appears in list containing _atom_site_label. Where no value is given, the assumed value is '1.0'. The permitted range is 0.0→1.0. [atom_site]

_atom_site_refinement_flags (*char*)

A concatenated series of single-letter codes which indicate the refinement restraints or constraints applied to this site.

.	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

Appears in list containing _atom_site_label. [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(s): 'restrained to planar ring' [atom_site]

_atom_site_symmetry_multiplicity (*numb*)

The multiplicity of a site due to the space-group symmetry as is given in *International Tables for Crystallography*, Vol. A (1987).

Appears in list containing _atom_site_label. The permitted range is 1→192. [atom_site]

_atom_site_thermal_displace_type (*char*)

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

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

Appears in list containing _atom_site_label. [atom_site]

_atom_site_type_symbol (*char*)

A code to identify the atom specie(s) 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`. May match subsidiary data name(s): `_atom_site_aniso_type_symbol`. **Must** match data name `_atom_type_symbol`.

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

_atom_site_U_equiv_geom_mean (*numb*)

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

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

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

Appears in list containing `_atom_site_label`. The permitted range is $0.0 \rightarrow \infty$. Related item(s): `_atom_site_U_iso_or_equiv` (alternate), `_atom_site_B_equiv_geom_mean` (conversion).

[atom_site]

_atom_site_U_iso_or_equiv (*numb*)

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

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

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

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

Appears in list containing `_atom_site_label`. The permitted range is $0.0 \rightarrow 10.0$. Related item(s): `_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 section of *International Tables for Crystallography*, Vol. A (1987).

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_SITES 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_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(s): 'a parallel to x; b in the plane of y & z' [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_SITES category to Cartesian coordinates. The axial alignments of this transformation are described in `_atom_sites_Cartn_transform_axes`.

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

[atom_sites]

_atom_sites_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_SITES 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_SITES 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 atomic 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 hydrogens were located.

`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

[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 [(1991). Acta Cryst. 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 $0.0 \rightarrow \infty$. [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`.

Example(s): '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 $0 \rightarrow \infty$. [atom_type]

`_atom_type_oxidation_number` (*numb*)

Formal oxidation state of this atom type in the structure.

Appears in list containing `_atom_type_symbol`. Where no value is given, the assumed value is '0'. The permitted range is $-8 \rightarrow 8$. [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 $0.0 \rightarrow 5.0$. [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. May be entered in any order.

Ref: *International Tables for X-ray Crystallography*, Vol. IV (1974) Table 2.2B, or *International Tables for Crystallography*, Vol. C (1991) 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 factors, 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_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 used for this atom type.

Appears in list containing _atom_type_symbol.

Example(s): '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 specie(s) representing this atom type. Normally this code is the element symbol. The code may be composed of any character except an underline 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 subsidiary data name(s): _atom_site_type_symbol.

Example(s): '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 [(1991). Acta Cryst. 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(s): 'TOZ_1991-03-20' [audit]

_audit_creation_date (*char*)

A date that the data block was created. The date format is *yyyy-mm-dd*.

Example(s): '1990-07-12' [audit]

_audit_creation_method (*char*)

A description of how data were entered into the data block.

Example(s): '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(s): '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(s):

```
; 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.

Example(s): 'Bleary, Percival R.', 'O'Neil, F. K.', 'Van den Bossche, G.', 'Yang, D.-L.', 'Simonov, Yu.A', 'Müller, 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       2.0
_audit_conform_dict_location
    ftp://ftp.iucr.ac.uk/pub/cif_core_2.0.dic
```

_audit_conform_dict_location (*char*)

A file name or uniform resource locator (URL) where the conformant dictionary resides.

May appear in list containing _audit_conform_dict_name.
[audit_conform]

_audit_conform_dict_name (*char*)

The string identifying the highest-level dictionary defining datanames 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 conformant dictionary.

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(s):

```
; 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 recognisable to international networks.

Example(s): 'name@host.domain.country', 'bm@iucr.ac.uk'
[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 includes the international dialing prefix, the area code in parentheses, followed by the local number with no spaces.

Example(s): '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 component, precedes the first name(s) or initial(s).

Example(s): 'Bleary, Percival R.', 'O'Neil, F. K.', 'Van den Bossche, G.', 'Yang, D.-L.', 'Simonov, Yu.A', 'Müller, 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 includes the international dialing prefix, the area code in parentheses, followed by the local number and any extension number prefixed by 'x', with no spaces.

Example(s): '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 [(1991). Acta Cryst. 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*)

Unit-cell angles in degrees of the reported structure. 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 diffraction intensities. See also `_diffrn_reflns_transf_matrix_`.

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

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 diffraction intensities. See also `_diffrn_reflns_transf_matrix_`.

The permitted range is 0.0→∞. [cell]

`_cell_measurement_pressure` (*numb*)

The pressure in kilopascals at which the unit-cell parameters were measured (not the pressure used to synthesize the sample).

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`.

Example(s): '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*)

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 in degrees of reflections used to measure the unit cell.

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_special_details` (*char*)

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

Example(s): 'pseudo-orthorhombic',
'standard setting from 45 deg rotation around c' [cell]

`_cell_volume` (*numb*)

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 determination of the crystallographic cell parameters. The _cell_measurement_refln_ data items would in general be used only for diffractometer data.

Example 1 - extracted from the CAD-4 listing of $Rb_2S_2O_6$ at room temperature (not yet published).

```
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 compounds. 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 [(1996). Acta Cryst. C52, 765–767].

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

_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.

Example(s): 'From Norilsk (USSR)',
'Extracted from the bark of Cinchona Naturalis'
[chemical]

_chemical_melting_point (*numb*)

The temperature in kelvins at which a crystalline solid changes to a liquid.

The permitted range is 0.0→∞. [chemical]

_chemical_name_common (*char*)

Trivial name by which the compound is commonly known.

Example(s): '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(s): 'chalcopyrite' [chemical]

_chemical_name_structure_type (*char*)

Commonly used structure-type name. Usually only applied to minerals or inorganic compounds.

Example(s): 'perovskite', 'sphalerite', 'A15' [chemical]

_chemical_name_systematic (*char*)

IUPAC or *Chemical Abstracts* full name of compound.

Example(s):
'1-bromoestra-1,3,5(10)-triene-3,17\b-diol' [chemical]

_chemical_conn_atom_[]

Data items in the _chemical_conn_atom_ and _chemical_conn_bond_ categories record details about the 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 [(1996). Acta Cryst. 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. Where no value is given, the assumed value is '0'. The permitted range is −6→6.

Example(s): '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 recognisable 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. If absent, values will be assigned by the journal or database staff.

Appears in list containing _chemical_conn_atom_type_symbol. The permitted range is 0.0→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→∞. [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→∞. [chemical_conn_atom]

_chemical_conn_atom_number (*numb*)

The chemical sequence number to be associated with this atom. Within an _atom_site_ list this number must match with one of the _atom_site_chemical_conn_number values.

Appears in list containing _chemical_conn_atom_type_symbol. May match subsidiary data name(s): _atom_site_chemical_conn_number, _chemical_conn_bond_atom_1, _chemical_conn_bond_atom_2. The permitted range is 1→∞. [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 recognisable 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 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 [(1996). Acta Cryst. 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 data name _chemical_conn_atom_number. The permitted range is 1→∞.

[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.

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

Appears in list containing _chemical_conn_bond_atom_. 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 parentheses. 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 or not carbon is present. 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 alphabetic 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 [(1991). Acta Cryst. C47, 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 [(1996). Acta Cryst. C52, 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 _chemical_formula_[] for rules for writing chemical formulae. Parentheses are used only for standard uncertainties (e.s.d.'s).

Example(s): '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.

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

Example(s): '[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 above _chemical_formula_[] 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 _chemical_formula_[].

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.

Example(s): '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 _chemical_formula_[] 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 data should not be included in this formula (see also _chemical_formula_analytical).

Example(s): '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 _chemical_formula_[] 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 _chemical_formula_[]. Parentheses are not normally used.

Example(s): '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→∞. [chemical_formula]

`_chemical_formula_weight_meas` (*numb*)

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

The permitted range is 1.0→∞. [chemical_formula]

`_citation_[]`

Data items in the CITATION category record details about the literature cited 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 book chapters.

Appears in list containing `_citation_id`. [citation]

`_citation_book_publisher` (*char*)

The name of the publisher of the citation; relevant for book chapters.

Appears in list containing `_citation_id`.

Example(s): 'John Wiley' [citation]

`_citation_book_publisher_city` (*char*)

The location of the publisher of the citation; relevant for book chapters.

Appears in list containing `_citation_id`.

Example(s): 'New York' [citation]

`_citation_book_title` (*char*)

The title of the book in which the citation appeared; relevant for 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'.

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

Appears in list containing `_citation_id`. [citation]

`_citation_country` (*char*)

The country of publication; relevant for both journal articles and book chapters.

Appears in list containing `_citation_id`. [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→∞.

Example(s): '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 subsidiary data name(s): `_citation_author_citation_id`, `_citation_editor_citation_id`.

Example(s): '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(s): ‘`J. Mol. Biol.`’ [`citation`]

`_citation_journal_id_ASTM` (*char*)

The American Society for the Testing of 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 Brookhaven Protein Data Bank (PDB).

Appears in list containing `_citation_id`.

Example(s): ‘`070`’ [`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_full` (*char*)

Full name of the journal cited; relevant for journal articles.

Appears in list containing `_citation_id`.

Example(s): ‘`Journal of Molecular Biology`’ [`citation`]

`_citation_journal_issue` (*char*)

Issue number of the journal cited; relevant for journal articles.

Appears in list containing `_citation_id`.

Example(s): ‘`2`’ [`citation`]

`_citation_journal_volume` (*char*)

Volume number of the journal cited; relevant for journal articles.

Appears in list containing `_citation_id`.

Example(s): ‘`174`’ [`citation`]

`_citation_language` (*char*)

Language in which the citation appears.

Appears in list containing `_citation_id`.

Example(s): ‘`german`’ [`citation`]

`_citation_page_first`
`_citation_page_last` (*char*)

The first and last pages of the citation; relevant for both journal articles and book chapters.

Appears in list containing `_citation_id`. [`citation`]

`_citation_special_details` (*char*)

A description of special aspects that describe the relationship of the contents of the data block to the literature item cited.

Appears in list containing `_citation_id`.

Example(s):

```
‘citation relates to this precise coordinate set’,
‘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 both journal articles and book chapters.

Appears in list containing `_citation_id`.

Example(s):

```
; Structure of Diferric Duck Ovotransferrin at
  2.35 \%A Resolution.
;
```
[`citation`]

`_citation_year` (*numb*)

The year of the citation; relevant for both journal articles and book chapters.

Appears in list containing `_citation_id`.

Example(s): ‘`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 data name _citation_id. [citation_author]

_citation_author_name (*char*)

Name of an author of the citation; relevant for both journal articles 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.

Example(s): 'Bleary, Percival R.', 'O'Neil, F. K.', 'Van den Bossche, G.', 'Yang, D.-L.', 'Simonov, Yu.A', 'Müller, 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. **Must** match data name _citation_id. [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 data name _citation_id. [citation_editor]

_citation_editor_name (*char*)

Names of an editor of the citation; relevant for 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.

Example(s): 'Bleary, Percival R.', 'O'Neil, F. K.', 'Van den Bossche, G.', 'Yang, D.-L.', 'Simonov, Yu.A', 'Müller, 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. **Must** match data name _citation_id. [citation_editor]

computing[]

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

Example 1 - Rodríguez-Romero, Ruiz-Pérez & Solans [(1996). Acta Cryst. 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 this data. Give the program or package name and a brief reference.

Example(s): '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 [(1991). Acta Cryst. C47, 2276–2277].

```
_database_code_CSD                'VOBYUG'
```

_database_code_CAS
_database_code_CSD
_database_code_ICSD
_database_code_MDF
_database_code_NBS
_database_code_PDF (*char*)

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

[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 [(1991). Acta Cryst. 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.

Example(s): 'He', 'vacuum', 'mother liquor' [diffrn]

`_diffrn_ambient_pressure` (*numb*)

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

The permitted range is 0.0→∞. [diffrn]

`_diffrn_ambient_temperature` (*numb*)

The mean temperature in kelvins at which the intensities were measured.

The permitted range is 0.0→∞. [diffrn]

`_diffrn_crystal_treatment` (*char*)

Remarks about how the crystal was treated prior to intensity measurement. Particularly relevant when intensities were measured at low temperature.

Example(s): 'equilibrated in hutch for 24 hours',
'flash frozen in liquid nitrogen',
'slow cooled with direct air stream' [diffrn]

`_diffrn_special_details` (*char*)

Special details of the diffraction measurement process. Should include information about source instability, crystal motion, degradation and so on.

Example(s):

```
; The results may not be entirely reliable
  as the measurement was made during a heat wave when
  the air-conditioning had failed.
;
```

[diffrn]

`_diffrn_attenuator_[]`

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

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

```
loop_
_diffrn_attenuator_code
_diffrn_attenuator_scale       1     16.976
```

`_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 subsidiary data name(s): `_diffrn_refln_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`. This scale must be multiplied by the measured intensity to convert it to the same scale as unattenuated intensities.

Appears in list containing `_diffrn_attenuator_code`. The permitted range is 1.0→∞. [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_details` (*char*)

A description of special aspects of the radiation detector.

[diffrn_detector]

`_diffrn_detector` (*char*)

The general class of the radiation detector.

Example(s): 'photographic film', 'scintillation counter', 'CCD plate', 'BF~3~ counter' [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→∞. [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.

[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 [(1991). Acta Cryst. C47, 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(s): '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.

Example(s): '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(s):

```
; 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 intensities.

Example(s): '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.

Example(s): '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 data measurement.

Example 1 - data set n-alkylation_C-4 of Hussain, Fleming, Norman & Chang [(1996). Acta Cryst. C52, 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 measurement of diffraction intensities.

Example 1 - typical output listing from 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 in degrees of a reflection used to define the orientation matrix. 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 diffraction intensities, its collimation and monochromatisation 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 [(1991). Acta Cryst. 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.

May appear in list containing `_diffrn_radiation_wavelength_id`.

Example(s): `'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.

May appear in list containing `_diffrn_radiation_wavelength_id`. The permitted range is 0.0→∞. [diffrn_radiation]

`_diffrn_radiation_inhomogeneity` (*numb*)

Half-width in millimetres of the incident beam in the direction perpendicular to the diffraction plane.

May appear in list containing `_diffrn_radiation_wavelength_id`. The permitted range is 0.0→∞. [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.

May appear in list containing `_diffrn_radiation_wavelength_id`.

Example(s): `'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 polarisation and the diffraction plane. See `_diffrn_radiation_polarisn_ratio`.

May appear in list containing `_diffrn_radiation_wavelength_id`. The permitted range is −180.0→180.0. [diffrn_radiation]

`_diffrn_radiation_polarisn_ratio` (*numb*)

Polarisation ratio of the diffraction beam incident on the crystal. It is the ratio of the perpendicularly polarised to the parallel polarised component 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).

May appear in list containing `_diffrn_radiation_wavelength_id`. The permitted range is 0.0→∞. [diffrn_radiation]

`_diffrn_radiation_probe` (*char*)

Name of the type of radiation used. It is strongly encouraged that this field be specified so that the probe radiation can be simply determined.

```
x-ray
neutron
electron
gamma
```

May appear in list containing `_diffrn_radiation_wavelength_id`. [diffrn_radiation]

`_diffrn_radiation_type` (*char*)

The nature of the radiation. This is typically a description of the X-ray wavelength in Siegbahn notation.

May appear in list containing `_diffrn_radiation_wavelength_id`.

Example(s): `'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 probe radiation.

`K-L~3~`	$K\alpha_1$ in older Siegbahn notation
`K-L~2~`	$K\alpha_2$ in older Siegbahn notation
`K-M~3~`	$K\beta_1$ in older Siegbahn notation
`K-L~2,3~`	use where $K\text{-}L_3$ and $K\text{-}L_2$ are not resolved

May appear in list containing `_diffrn_radiation_wavelength_id`. [diffrn_radiation]

`_diffrn_radiation_wavelength_[]`

Data items in the DIFFRN_RADIATION_WAVELENGTH category describe the wavelength of the radiation used in measuring 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 [(1991). Acta Cryst. 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→∞. [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 subsidiary data name(s): _diffrn_refln_wavelength_id.

Example(s): '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. Where no value is given, the assumed value is '1.0'. The permitted range is 0.0→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 of $Tl_2Cd_2(SO_4)_3$ 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
# - - - - data truncated for brevity - - - -
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 in degrees of a reflection. 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 data name _diffrn_attenuator_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_. The permitted range is 0→∞. [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 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 diffraction measurement 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 described 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`
`_diffrn_refln_intensity_sigma` (*numb*)

Net intensity and standard uncertainty (e.s.d.) 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 $0 \rightarrow \infty$. [diffrn_refln]

`_diffrn_refln_scale_group_code` (*char*)

The code identifying the scale applying to this reflection. This code must match with a specified `_diffrn_scale_group_code` value.

Appears in list containing `_diffrn_refln_index_`. **Must** match data name `_diffrn_scale_group_code`. [diffrn_refln]

`_diffrn_refln_scan_mode` (*char*)

The code identifying the mode of scanning with a diffractometer. See `_diffrn_refln_scan_width` and `_diffrn_refln_scan_mode_backgd`.

`om`	ω scan
`ot`	$\omega/2\theta$ scan
`q`	Q-scans (arbitrary reciprocal directions)

Appears in list containing `_diffrn_refln_index_`. [diffrn_refln]

`_diffrn_refln_scan_mode_backgd` (*char*)

The code identifying the mode of scanning a reflection to measure the background intensity.

`st`	stationary counter background
`mo`	moving counter background

Appears in list containing `_diffrn_refln_index_`. [diffrn_refln]

`_diffrn_refln_scan_rate` (*numb*)

The rate of scanning a reflection to measure the intensity in degrees per minute.

Appears in list containing `_diffrn_refln_index_`. [diffrn_refln]

`_diffrn_refln_scan_time_backgd` (*numb*)

The time spent measuring each background in seconds.

Appears in list containing `_diffrn_refln_index_`. [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*)

The code identifying that this reflection was measured as a standard intensity. This is the case if the code matched one of the `_diffrn_standard_refln_code` values.

Appears in list containing `_diffrn_refln_index_`. **Must** match data name `_diffrn_standard_refln_code`.

Example(s): '1', '2', '3', 's1', 's2', 's3', 'A', 'B', 'C' [diffrn_refln]

`_diffrn_refln_wavelength` (*numb*)

The mean wavelength in ångströms of radiation used to measure the intensity of this reflection. This is an important parameter for data collected 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 data name `_diffrn_radiation_wavelength_id`.

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

```
_diffrn_reflns_number              1592
_diffrn_reflns_av_R_equivalents    0
_diffrn_reflns_av_sigmaI/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 $[\sum |av\Delta(I)| / \sum |av(I)|]$ for symmetry-equivalent reflections used to calculate the average intensity $av(I)$. The $av\Delta(I)$ term is the average difference between $av(I)$ and the individual symmetry-equivalent intensities.

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

`_diffrn_reflns_av_sigmaI/netI` (*numb*)

Measure $[\sum |\sigma(I)| / \sum |net(I)|]$ for all measured reflections.

The permitted range is $0.0 \rightarrow \infty$. [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_reduction_process` (*char*)

A description of the process used to reduce the intensity data into structure-factor magnitudes.

Example(s): `'data averaged using Fisher test'`

[diffrn_reflns]

`_diffrn_reflns_theta_max`
`_diffrn_reflns_theta_min` (*numb*)

θ angle limits 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_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 subsidiary data name(s): `_diffrn_refln_scale_group_code`.

Example(s): `'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.

Example(s): `'sealed X-ray tube'`, `'nuclear reactor'`, `'spallation source'`, `'electron microscope'`, `'rotating-anode X-ray tube'`, `'synchrotron'`

[diffrn_source]

`_diffrn_source_current` (*char*)

The current in milliamperes at which the radiation source was operated.

[diffrn_source]

`_diffrn_source_details` (*char*)

A description of special aspects of the source used.

[diffrn_source]

`_diffrn_source_power` (*numb*)

The power in kilowatts at which the radiation source was operated.

[diffrn_source]

`_diffrn_source_size` (*char*)

The dimensions of the source as viewed from the sample.

Example(s): '8mm x 0.4 mm fine-focus', 'broad focus'

[diffrn_source]

`_diffrn_source_target` (*char*)

The chemical element symbol for the X-ray target (usually the anode) used for generation of X-rays. This can be used also for spallation sources.

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.

Example(s): 'NSLS beamline X8C', 'Rigaku RU200'

[diffrn_source]

`_diffrn_source_voltage` (*char*)

The voltage in kilovolts at which the radiation source was operated.

[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 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 [(1991). Acta Cryst. C47, 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 subsidiary data name(s): `_diffrn_refln_standard_code`.

Example(s): '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 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 [(1991). Acta Cryst. C47, 2276–2277].

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

`_diffrn_standards_decay_%` (*numb*)

The percentage decrease in the mean of the intensities for the set of standard reflections 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.

The permitted range is $-\infty \rightarrow 100$. [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 $0 \rightarrow \infty$. [diffrn_standards]

`_diffrn_standards_number` (*numb*)

The number of unique standard reflections used in the diffraction measurements.

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

`_diffrn_standards_scale_sigma` (*numb*)

The standard uncertainty (e.s.d.) of the individual mean standard scales applied to the intensity data.

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

`_exptl_[]`

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

Example 1 - based on a paper by Steiner [(1996). Acta Cryst. C52, 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→∞. [exptl]

`_exptl_absorpt_correction_T_max`
`_exptl_absorpt_correction_T_min` (*numb*)

The maximum and minimum transmission factors for the crystal and radiation. These factors are also referred to as the absorption correction *A* or 1/*A**.

The permitted range is 0.0→1.0. [exptl]

`_exptl_absorpt_correction_type` (*char*)

The absorption correction type and method. The value 'empirical' should *not* be used unless no more detailed information is available.

`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.

Example(s): 'Tompa analytical', 'MolEN (Fair, 1990)', '(North, Phillips & Mathews, 1968)' [exptl]

`_exptl_crystals_number` (*numb*)

The total number of crystals used in the measurement of intensities.

The permitted range is 1→∞. [exptl]

`_exptl_special_details` (*char*)

Any special information about the experimental work prior to the intensity measurement. See also `_exptl_crystal_preparation`.

[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, density, and so on.

Example 1 - based on data set TOZ of Willis, Beckwith & Tozer [(1991). Acta Cryst. 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
```

`_exptl_crystal_colour` (*char*)

The colour of the crystal.

May appear in list containing `_exptl_crystal_id`.

Example(s): 'dark green' [exptl_crystal]

`_exptl_crystal_density_diffrn` (*numb*)

Density values calculated from 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→∞. [exptl_crystal]

`_exptl_crystal_density_meas` (*numb*)

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→∞. [exptl_crystal]

`_exptl_crystal_density_meas_temp` (*numb*)

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→∞. [exptl_crystal]

`_exptl_crystal_density_method` (*char*)

The method used to measure `_exptl_crystal_density_meas`.

May appear in list containing `_exptl_crystal_id`.

Example(s): '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. Dimensional data are better placed in the `_exptl_crystal_face_` data items.

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 $F(000)$. It may contain dispersion contributions, and is calculated as

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

f_r = real part of the scattering factors at $\theta = 0$, f_i = imaginary part of the scattering factors at $\theta = 0$.

May appear in list containing `_exptl_crystal_id`. The permitted range is 0.0→∞. [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 intensity measurement and with `_refln_crystal_id` in the `_refln_` list.

Appears in list as essential element of loop structure. May match subsidiary data name(s): `_diffrn_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(s):

```
'mounted in an argon-filled quartz capillary'
```

[exptl_crystal]

_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 or a cylinder then the `*_rad` item is the radius. 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→∞. [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 [(1996). Acta Cryst. 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 diffractometer angle settings in degrees for a specific crystal face associated with `_exptl_crystal_face_perp_dist`.

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 of the face to the centre of rotation of the crystal.

Appears in list containing `_exptl_crystal_face_index_`. The permitted range is 0.0→∞. [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 contents of 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. They serve, however, the dual purpose 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 [(1996). Acta Cryst. C52, 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 contents of the ATOM, CELL, and SYMMETRY data.

Example 1 - based on data set TOZ of Willis, Beckwith & Tozer [(1991). Acta Cryst. C47, 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*)

Angle in degrees defined by the three sites `_geom_angle_atom_site_label_1`, `*_2` and `*_3`. 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 specified 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 data name `_atom_site_label`. [geom_angle]

`_geom_angle_publ_flag` (*char*)

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

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

Appears in list containing `_geom_angle_atom_site_label_`. 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 `_symmetry_equiv_pos_site_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_`.

Example(s): `'.'` (no symmetry or translation to site), `'4'` (4th symmetry operation applied), `'7_645'` (7th symm. posn.; $+a$ on x; $-b$ on y) [geom_angle]

`_geom_bond_[]`

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

Example 1 - based on data set TOZ of Willis, Beckwith & Tozer [(1991). Acta Cryst. C47, 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 - - - -
```

`_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 data name `_atom_site_label`. [geom_bond]

`_geom_bond_distance` (*numb*)

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_publ_flag` (*char*)

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

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

Appears in list containing `_geom_bond_atom_site_label_`. 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 `_symmetry_equiv_pos_site_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_bond_atom_site_label_`.

Example(s): '.' (no symmetry or translation to site), '4' (4th symmetry operation applied), '7_645' (7th symm. posn.; +*a* on *x*; −*b* on *y*) [geom_bond]

_geom_contact_[]

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

Example 1 - based on data set CLPHO6 of Ferguson, Ruhl, McKervey & Browne [(1991). Acta Cryst. C48, 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(O1) 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 data name _atom_site_label. [geom_contact]

_geom_contact_distance (*numb*)

The interatomic contact distance in ångströms.

Appears in list containing _geom_contact_atom_site_label_. The permitted range is 0.0→∞. [geom_contact]

_geom_contact_publ_flag (*char*)

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

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

Appears in list containing _geom_contact_atom_site_label_. 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 _symmetry_equiv_pos_site_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_contact_atom_site_label_.

Example(s): '.' (no symmetry or translation to site), '4' (4th symmetry operation applied), '7_645' (7th symm. posn.; +*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 contents of the ATOM, CELL, and SYMMETRY data.

Example 1 - based on $C_{14}H_{13}ClN_2O.H_2O$, reported by Palmer, Puddle & Lisgarten [(1993). Acta Cryst. C49, 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*)

Angle in degrees defined by the three sites _geom_hbond_atom_site_label_D, *_H and *_A. Site at *_D (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, 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 data name _atom_site_label. [geom_hbond]

_geom_hbond_distance_DH
_geom_hbond_distance_HA
_geom_hbond_distance_DA (*numb*)

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→∞. [geom_hbond]

_geom_hbond_publ_flag (*char*)

Signals if the hydrogen bond information is referred to in a publication or should be placed in a table of significant hydrogen-bond geometry.

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

Appears in list containing `_geom_hbond_atom_site_label_`. 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 `_symmetry_equiv_pos_site_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_hbond_atom_site_label_`.

Example(s): '`.`' (no symmetry or translation to site), '`4`' (4th symmetry operation applied), '`7_645`' (7th symm. posn.; $+a$ 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 contents of the ATOM, CELL, and SYMMETRY data.

Example 1 - based on data set CLPHO6 of Ferguson, Ruhl, McKervey & Browne [(1991). Acta Cryst. C48, 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*)

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.

Ref: 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 site2–site1 onto the projection of the vector site3–site4. Clockwise torsions are positive, anticlockwise torsions are negative.

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

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

`_geom_torsion_publ_flag` (*char*)

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

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

Appears in list containing `_geom_torsion_atom_site_label_`. 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 `_symmetry_equiv_pos_site_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_`.

Example(s): '`.`' (no symmetry or translation to site), '`4`' (4th symmetry operation applied), '`7_645`' (7th symm. posn.; $+a$ on x; $-b$ on y) [`geom_torsion`]

[journal]

journal[]

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

Example 1 - based on Acta Cryst. file for entry HL0007 [Willis, Beckwith & Tozer (1991). Acta Cryst. C47, 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_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 employed in generating the journal indexes. Normally the creator of a CIF will not specify these data items.

Example 1 - based on a paper by Zhu, Reynolds, Klein & Trudell [(1994). Acta Cryst. C50, 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 journals 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 textual content 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 data set TOZ of Willis, Beckwith & Tozer [(1991). Acta Cryst. C47, 2276–2277].

```
_publ_section_title
; trans-3-Benzoyl-2-(tert-butyl)-4-(isobutyl)-
  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 [(1996). Acta Cryst. C52, 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(s):
```
; 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(s):
```
; Department of Chemistry and Biochemistry
  University of Guelph
  Ontario
  Canada
  N1G 2W1
;
```
[publ]

_publ_contact_author_email (*char*)

Email address in a form recognisable to international networks.

Example(s): 'name@host.domain.country', 'bm@iucr.ac.uk' [publ]

_publ_contact_author_fax (*char*)

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

Example(s): '12(34)9477334', '12()349477334' [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(s): 'Professor George Ferguson' [publ]

_publ_contact_author_phone (*char*)

Telephone number of the author submitting the manuscript and data block. The recommended style includes the international dialing prefix, 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 prefixes in parentheses is no longer recommended.

Example(s): '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 wordprocessor package and computer used to create the word processed manuscript stored as _publ_manuscript_processed.

Example(s):
'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*, *only* those codes indicated for use with that journal should be used.

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*)
CO	CIF-access paper - organic (*Acta C*)
CM	CIF-access paper - metal-organic (*Acta C*)
AD	Addenda & Errata (*Acta C*)
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 process 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_figure_captions
_publ_section_table_legends (*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_* items are preferred for separating the chemical preparation and refinement 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 data set TOZ of Willis, Beckwith & Tozer [(1991). Acta Cryst. 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(s):

```
; 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.

Example(s): 'On leave from U. Western Australia', 'Also at Department of Biophysics' [publ_author]

_publ_author_name (*char*)

The name of a publication author. If there are multiple authors they 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.

Example(s): 'Bleary, Percival R.', 'O'Neil, F. K.', 'Van den Bossche, G.', 'Yang, D.-L.', 'Simonov, Yu.A', 'Müller, H. A.', 'Ross II, C. R.' [publ_author]

_publ_body_ []

Data items in the PUBL_BODY category permit labelling of different text sections within the body of a submitted 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 (1996), Acta Cryst. A52, 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 (1996), Acta Cryst. A52, 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 submitted paper.

Appears in list containing _publ_body_label. [publ_body]

_publ_body_element (*char*)

The functional role of the associated text section.

```
section
subsection
subsubsection
appendix
footnote
```

Appears in list containing _publ_body_label. [publ_body]

_publ_body_format (*char*)

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

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

Appears in list containing _publ_body_label. 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. Uniqueness of loop packet tested on _publ_body_element.

Example(s): '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 employed by 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 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 (flags are 'yes' or 'no').

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

Appears in list containing _publ_manuscript_incl_extra_item. 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 is 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 [(1991). Acta Cryst. C47, 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/(\s^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 the known chirality at C3 arising from its
  precursor l-leucine.
;
_refine_ls_abs_structure_Flack     0
_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_obs            .034
_refine_ls_wR_factor_all           .044
_refine_ls_wR_factor_obs           .042
_refine_ls_goodness_of_fit_all    1.462
_refine_ls_goodness_of_fit_obs    1.515
_refine_ls_shift/esd_max           .535
_refine_ls_shift/esd_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*)

The largest, smallest and root-mean-square-deviation, in electrons per ångström cubed, of the electron density in the final difference Fourier map. 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. For example, it may describe the Friedel pairs used.

[refine]

`_refine_ls_abs_structure_Flack` (*numb*)

The measure of absolute structure (enantiomorph or polarity) as defined by Flack. The value must be between 0. and 1. with a standard uncertainty (e.s.d.).

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

The permitted range is 0.0→1.0. [refine]

`_refine_ls_abs_structure_Rogers` (*numb*)

The measure of absolute structure (enantiomorph or polarity) as defined by Rogers.

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

[refine]

`_refine_ls_d_res_high` (*numb*)

The highest resolution in ångströms for the interplanar spacing in the reflections used in refinement. This is the smallest d value.

The permitted range is 0.0→∞. [refine]

`_refine_ls_d_res_low` (*numb*)

The lowest resolution in ångströms for the interplanar spacing in the reflections used in refinement. This is the highest d value.

The permitted range is 0.0→∞. [refine]

`_refine_ls_extinction_coef` (*numb*)

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 10000.

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

Example(s): '`3472(52)`' (Zachariasen coefficient $r* = 0.347(5) \times 10^4$) [refine]

`_refine_ls_extinction_expression` (*char*)

A description or reference of 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(s):

```
; 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 with the data item `_refine_ls_extinction_coef`. 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`.

Ref: Becker, P. J. & Coppens, P. (1974). *Acta Cryst.* A**30**, 129–153. 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`'.

Example(s): '`B-C type 2 Gaussian isotropic`', '`none`' [refine]

`_refine_ls_goodness_of_fit_all`
`_refine_ls_goodness_of_fit_obs` (*numb*)

The least-squares goodness-of-fit parameter S for all reflections, and 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. See also `_refine_ls_restrained_S_` definitions.

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

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

The permitted range is 0.0→∞. [refine]

`_refine_ls_hydrogen_treatment` (*char*)

Treatment of hydrogen atoms in the least-squares refinement.

`refall`	refined all H parameters
`refxyz`	refined H coordinates only
`refU`	refined H U only
`noref`	no refinement of H parameters

constr	H 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.

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.

Where no value is given, the assumed value is '0'. The permitted range 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→∞. [refine]

_refine_ls_number_reflns (*numb*)

The number of unique reflections contributing to the least-squares refinement calculation.

The permitted range is 0→∞. [refine]

_refine_ls_number_restraints (*numb*)

The number of restrained parameters. These are parameters which are not directly dependent on another refined parameter. Often restrained parameters 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→∞. [refine]

_refine_ls_R_factor_all
_refine_ls_R_factor_obs (*numb*)

Residual factors for all reflections, and for 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.

$$R = \frac{\sum |F(obs) - F(calc)|}{\sum |F(obs)|}$$

$F(obs)$ = the observed structure-factor amplitudes, $F(calc)$ = the calculated structure-factor amplitudes, and the sum $\sum$ is taken over the specified reflections.

The permitted range is 0.0→∞. [refine]

_refine_ls_R_Fsqd_factor (*numb*)

Residual factor $R(F^2)$ for estimated reflection intensities, calculated on the squares of the observed and calculated structure factors, for all reflections flagged 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.

$$R(F^2) = \frac{\sum |F(obs)^2 - F(calc)^2|}{\sum F(obs)^2}$$

$F(obs)^2$ = squares of the observed structure-factor amplitudes, $F(calc)^2$ = squares of the calculated structure-factor amplitudes, and the sum $\sum$ is taken over the specified reflections.

The permitted range is 0.0→∞. [refine]

_refine_ls_R_I_factor (*numb*)

Residual factor $R(I)$ for estimated reflection intensities, for all reflections flagged as observed (see _reflns_observed_criterion) and included in the refinement. This is most often calculated in Rietveld refinements of powder data, where it is referred to as R_B or R_{Bragg}.

$$R = \frac{\sum |I(obs) - I(calc)|}{\sum I(obs)}$$

$I(obs)$ = the net observed intensities, $I(calc)$ = the net calculated intensities, and the sum $\sum$ is taken over the specified reflections.

The permitted range is 0.0→∞. [refine]

_refine_ls_restrained_S_all
_refine_ls_restrained_S_obs (*numb*)

The least-squares goodness-of-fit parameter S' for all reflections, and for observed reflections, after the final cycle of least squares. This parameter explicitly includes the restraints applied in the least-squares process. See also _refine_ls_goodness_of_fit_ definitions.

$$S' = \frac{[\sum |w|Y(obs) - Y(calc)|^2| + \sum_r |w_r|P(calc) - P(targ)|^2|]^{1/2}}{N_{ref} + N_{restr} - N_{param}}$$

$Y(obs)$ = the observed coefficients (see _refine_ls_structure_factor_coef), $Y(calc)$ = the observed coefficients (see _refine_ls_structure_factor_coef) w = the least-squares reflection weight [1/square of standard uncertainty (e.s.d.)], $P(calc)$ = the calculated restraint values, $P(targ)$ = the target restraint values, w_r = the restraint weight, N_{ref} = the number of reflections used in the refinement (see _refine_ls_number_reflns), N_{restr} = the number of restraints (see _refine_ls_number_restraints), N_{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→∞. [refine]

_refine_ls_shift/esd_max
_refine_ls_shift/esd_mean (*numb*)

The largest and the average ratios of the final least-squares parameter shift divided by the final standard uncertainty (s.u., formerly described as estimated standard deviation, e.s.d.).

The permitted range is 0.0→∞. [refine]

_refine_ls_structure_factor_coef (*char*)

Structure-factor coefficient $|F|$, F^2 or I, used in the least-squares refinement process.

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 least-squares refinement. Used to describe the weighting when the value of _refine_ls_weighting_scheme is specified as 'calc'.

Example(s):

```
; 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).

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
_refine_ls_wR_factor_obs (*numb*)

Weighted residual factors for all reflections, and for reflections classified as 'observed' (see _reflns_observed_criterion) and used 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.

$$wR = \left(\frac{\sum |w|Y(obs) - Y(calc)|^2|}{\sum |wY(calc)^2|} \right)^{1/2}$$

$Y(obs)$ = the observed amplitude specified by _refine_ls_structure_factor_coef, $Y(calc)$ = the calculated amplitude specified by _refine_ls_structure_factor_coef, w = the least-squares weight, and the sum $\sum$ is taken over the specified reflections.

The permitted range is 0.0→∞. [refine]

_refine_special_details (*char*)

Description of special aspects of the refinement process.

[refine]

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 [(1993). Acta Cryst. C49, 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_observed_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. Univ. Western Australia].

```
loop_
_refln_index_h
_refln_index_k
_refln_index_l
_refln_F_meas
_refln_F_calc
_refln_F_sigma
_refln_observed_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.

$$A = |F| \cos(phase)$$

Appears in list containing _refln_index_. [refln]

_refln_B_calc
_refln_B_meas (*numb*)

The calculated and measured structure-factor component B, in electrons.

$$B = |F| \sin(phase)$$

Appears in list containing _refln_index_. [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 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.

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.

Appears in list containing _refln_index_. [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 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, in the measured units.

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_. [refln]

_refln_observed_status (*char*)

Classification of a reflection so as to indicate its status with respect to inclusion in refinement and calculation of R factors.

o	satisfies _refine_ls_d_res_high satisfies _refine_ls_d_res_low observed by _reflns_observed_criterion
<	satisfies _refine_ls_d_res_high satisfies _refine_ls_d_res_low 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

Appears in list containing _refln_index_. 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*)

The measured structure-factor phase in degrees.

Appears in list containing _refln_index_. [refln]

_refln_refinement_status (*char*)

Status of reflection in the structure refinement process.

incl	included in ls process
excl	excluded from ls process
extn	excluded due to extinction

Appears in list containing _refln_index_. 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 data name _reflns_scale_group_code.

Example(s): '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 symmetry-equivalent reflections. The equivalent reflections have the same structure-factor magnitudes because of the space-group symmetry and the Friedel relationship.

Appears in list containing _refln_index_. The permitted range is $1 \rightarrow 48$. [refln]

_refln_wavelength (*numb*)

The mean wavelength in ångströms of 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→∞. [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 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 [(1991). Acta Cryst. 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_observed          1408
_reflns_observed_criterion       'F > 6.0\s(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 interplanar spacings in the reflections. These are the smallest and largest *d* values.

The permitted range is 0.0→∞. [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 intensity measurements. These need not be the same as the `_diffrn_reflns_limit_` values.

[reflns]

`_reflns_number_total`
`_reflns_number_observed` (*numb*)

The total number of reflections, and the number of 'observed' reflections, in the `_refln_` list (not the `_diffrn_refln_` list). The observed reflections satisfy the `_reflns_observed_criterion`. They may include Friedel equivalent reflections according to the nature of the structure and the procedures used. The item `_reflns_special_details` describes the reflection data.

The permitted range is 0→∞. [reflns]

`_reflns_observed_criterion` (*char*)

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(s): `'I>2\s(I)'` [reflns]

`_reflns_special_details` (*char*)

A description of reflection data not covered by the other data names. It should include details of the Friedel pairs.

[reflns]

`_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. Univ. Western Australia]

```
loop_
_reflns_scale_group_code
_reflns_scale_meas_F
1  .895447
```

`_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 may not correspond to those in the `_diffrn_scale_` list.

Appears in list as essential element of loop structure. May match subsidiary data name(s): `_refln_scale_group_code`.

[reflns_scale]

`_reflns_scale_meas_F`
`_reflns_scale_meas_F_squared`
`_reflns_scale_meas_intensity` (*numb*)

Scales associated with `_reflns_scale_group_code`.

Appears in list containing `_reflns_scale_group_code`. The permitted range is 0.0→∞. [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_sigI_obs
_reflns_shell_number_measured_obs
_reflns_shell_number_unique_obs
_reflns_shell_percent_possible_obs
_reflns_shell_Rmerge_F_obs
31.38  3.82  69.8  9024  2540  96.8   1.98
 3.82  3.03  26.1  7413  2364  95.1   3.85
 3.03  2.65  10.5  5640  2123  86.2   6.37
 2.65  2.41   6.4  4322  1882  76.8   8.01
 2.41  2.23   4.3  3247  1714  70.4   9.86
 2.23  2.10   3.1  1140   812  33.3  13.99
```

`_reflns_shell_d_res_high` (*numb*)

The highest resolution in ångströms for the interplanar spacing in the reflections in this shell. This is the smallest *d* value.

Appears in list. The permitted range is 0.0→∞. [reflns_shell]

`_reflns_shell_d_res_low` (*numb*)

The lowest resolution in ångströms for the interplanar spacing in the reflections in this shell. This is the largest *d* value.

Appears in list. The permitted range is 0.0→∞. [reflns_shell]

`_reflns_shell_meanI_over_sigI_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. [reflns_shell]

`_reflns_shell_meanI_over_sigI_obs` (*numb*)

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_number_measured_all` (*numb*)

The total number of reflections measured for this resolution shell.

Appears in list. [reflns_shell]

`_reflns_shell_number_measured_obs` (*numb*)

The number of reflections classified as 'observed' (see `_reflns_observed_criterion`) measured for this resolution shell.

Appears in list. [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→∞. [reflns_shell]

`_reflns_shell_number_unique_all` (*numb*)

The total number of measured reflections which are symmetrically unique after merging for this resolution shell.

Appears in list. The permitted range is 0→∞. [reflns_shell]

`_reflns_shell_number_unique_obs` (*numb*)

The total number of reflections classified as 'observed' (see `_reflns_observed_criterion`) which are symmetrically unique after merging for this resolution shell.

Appears in list. The permitted range is 0→∞. [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→∞. [reflns_shell]

`_reflns_shell_percent_possible_obs` (*numb*)

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→∞. [reflns_shell]

`_reflns_shell_Rmerge_F_all` (*numb*)

The value of $R_{\rm merge}(F)$ for all reflections in a given shell.

$$R_{\rm merge}(F) = \frac{\sum_i(\sum_j |F_j - < F > |)}{\sum_i(\sum_j < F >)}$$

F_j = the amplitude of the *j*th observation of reflection *i*, $< F >$ = the mean of the amplitudes of all observations of reflection *i*, the sum $\sum_i$ is taken over all reflections, and the sum $\sum_j$ is taken over all observations of each reflection.

Appears in list. The permitted range is 0.0→∞. [reflns_shell]

`_reflns_shell_Rmerge_F_obs` (*numb*)

The value of $R_{\rm merge}(F)$ for reflections classified as 'observed' (see `_reflns_observed_criterion`) in a given shell.

$$R_{\rm merge}(F) = \frac{\sum_i(\sum_j |F_j - < F > |)}{\sum_i(\sum_j < F >)}$$

F_j = the amplitude of the *j*th observation of reflection *i*, $< F >$ = the mean of the amplitudes of all observations of reflection *i*, the sum $\sum_i$ is taken over all reflections, and the sum $\sum_j$ is taken over all observations of each reflection.

Appears in list. The permitted range is 0.0→∞. [reflns_shell]

`_reflns_shell_Rmerge_I_all` (*numb*)

The value of $R_{\rm merge}(I)$ for all reflections in a given shell.

$$R_{\rm merge}(I) = \frac{\sum_i(\sum_j |I_j - < I > |)}{\sum_i(\sum_j < I >)}$$

I_j = the intensity of the *j*th observation of reflection *i*, $< I >$ = the mean of the intensities of all observations of reflection *i*, the sum $\sum_i$ is taken over all reflections, and the sum $\sum_j$ is taken over all observations of each reflection.

Appears in list. The permitted range is 0.0→∞. [reflns_shell]

`_reflns_shell_Rmerge_I_obs` (*numb*)

The value of $R_{\rm merge}(I)$ for reflections classified as 'observed' (see `_reflns_observed_criterion`) in a given shell.

$$R_{\rm merge}(I) = \frac{\sum_i(\sum_j |I_j - < I > |)}{\sum_i(\sum_j < I >)}$$

I_j = the intensity of the *j*th observation of reflection *i*, $< I >$ = the mean of the intensities of all observations of reflection *i*, the sum $\sum_i$ is taken over all reflections, and the sum $\sum_j$ is taken over all observations of each reflection.

Appears in list. The permitted range is 0.0→∞. [reflns_shell]

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 [(1991). Acta Cryst. C47, 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*)

The cell settings for this space-group symmetry.

triclinic
monoclinic
orthorhombic
tetragonal
rhombohedral
trigonal
hexagonal
cubic [symmetry]

_symmetry_Int_Tables_number (*numb*)

Space-group number from *International Tables for Crystallography*, Vol. A (1987).

The permitted range is 1→230. [symmetry]

_symmetry_space_group_name_Hall (*char*)

Space-group symbol as described by Hall. This symbol gives the space-group setting explicitly. Leave spaces between the separate components of the symbol.

Ref: Hall, S. R. (1981). *Acta Cryst.* A**37**, 517–525.

Example(s): '-P 2ac 2n', '-R 3 2"', 'P 61 2 2 (0 0 -1)' [symmetry]

_symmetry_space_group_name_H-M (*char*)

Hermann–Mauguin space-group symbol. Note that the H–M 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 (1987) 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.

Example(s): 'P 1 21/m 1', 'P 2/n 2/n 2/n (origin at -1)', 'R -3 2/m' [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 [(1991). Acta Cryst. C47, 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 [(1991). Acta Cryst. C47, 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_site_id (*numb*)

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*'.

Appears in list containing _symmetry_equiv_pos_as_xyz. [symmetry_equiv]

_symmetry_equiv_pos_as_xyz (*char*)

Symmetry equivalent position in the '*xyz*' representation. Except for the space group *P*1, this data will be repeated in a loop. The format of the data item is as per *International Tables for Crystallography*, Vol. A. (1987). All equivalent positions should be entered, including those for lattice centring and a centre of symmetry, if present.

May appear in list.

Example(s): '-y+x,-y,1/3+z' [symmetry_equiv]