DISORDER

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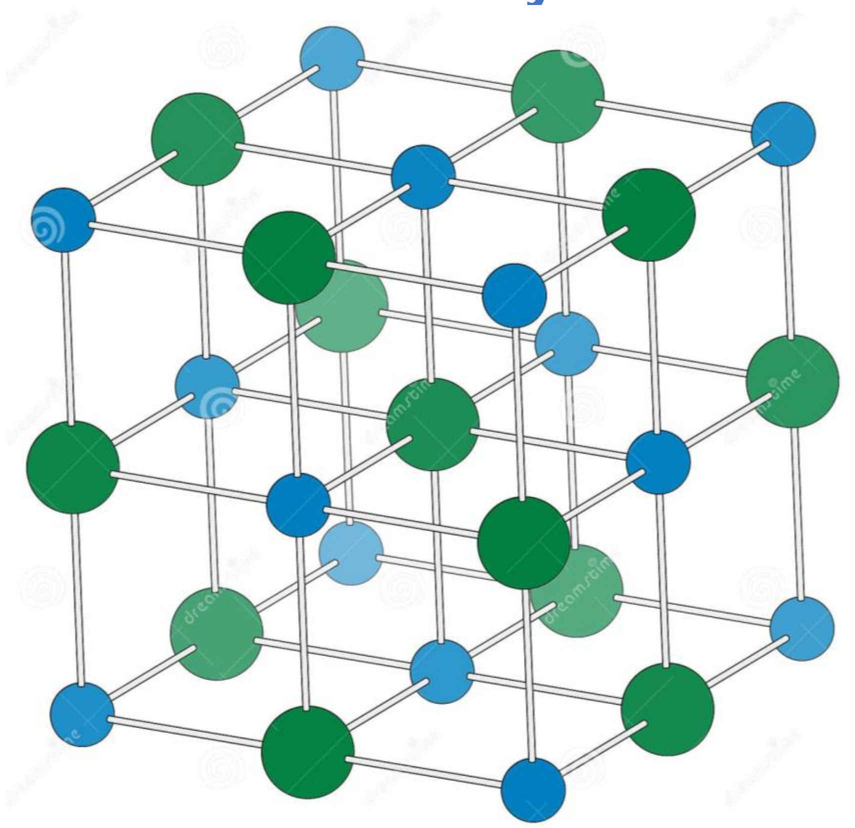
Disorder

- Not all crystals are perfectly ordered
- Crystal structure sees the average occupancy

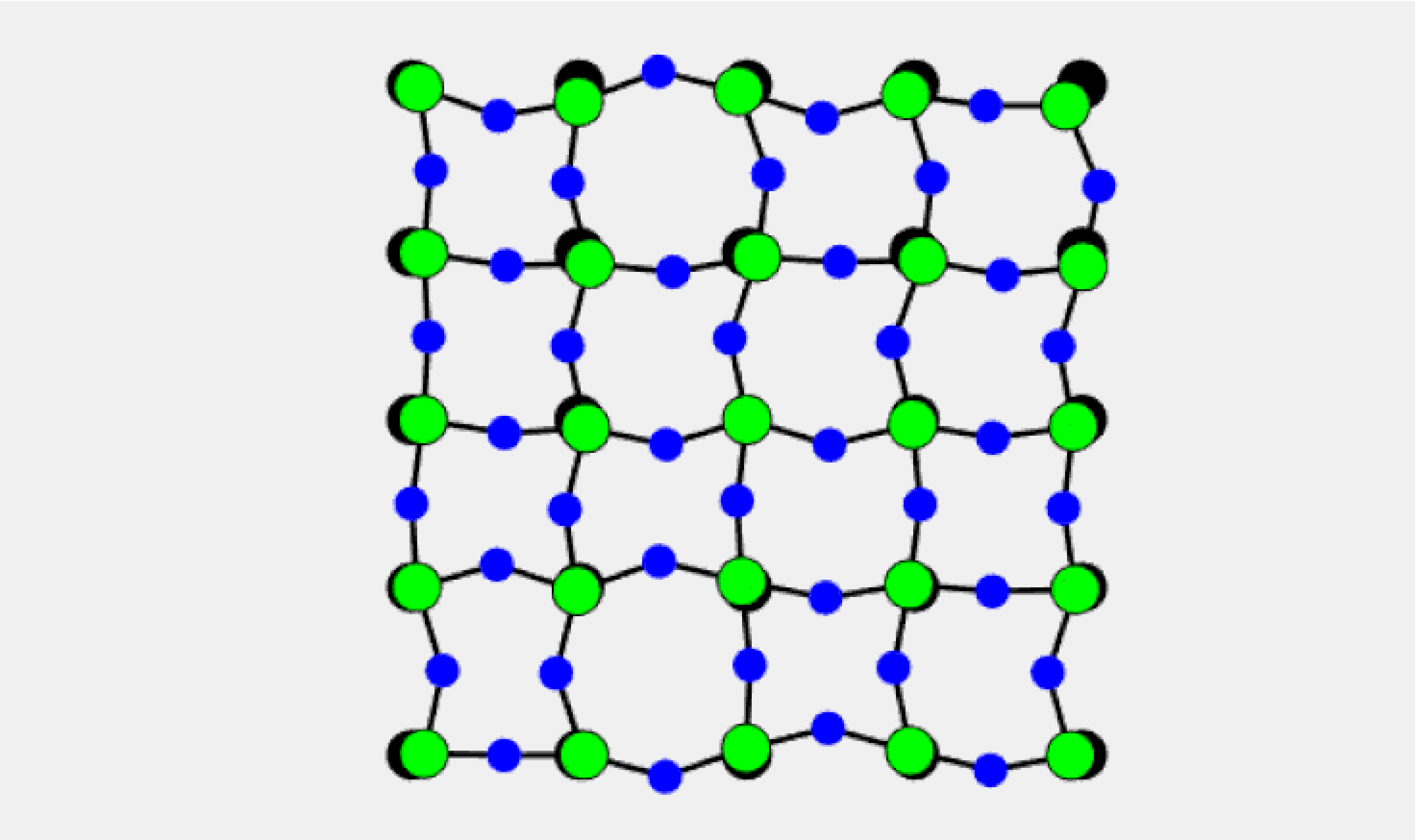
Disorder

Thermal motion in crystals

Atoms vibrate around equilibrium positions

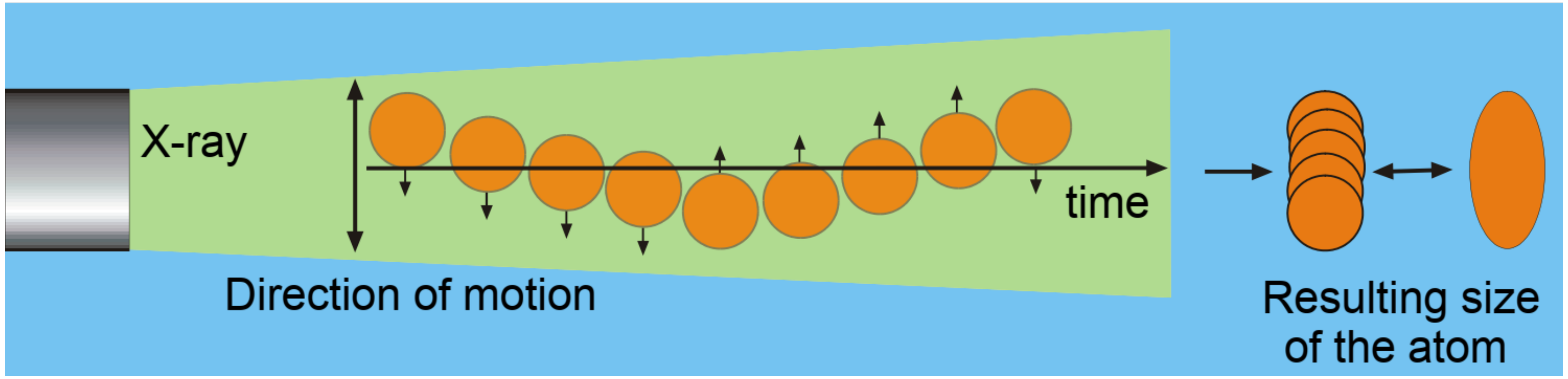


Crystal of NaCl



What happens when the data are collected along the time?

Single crystal structure analysis only an average electron distribution (atomic position) is determined

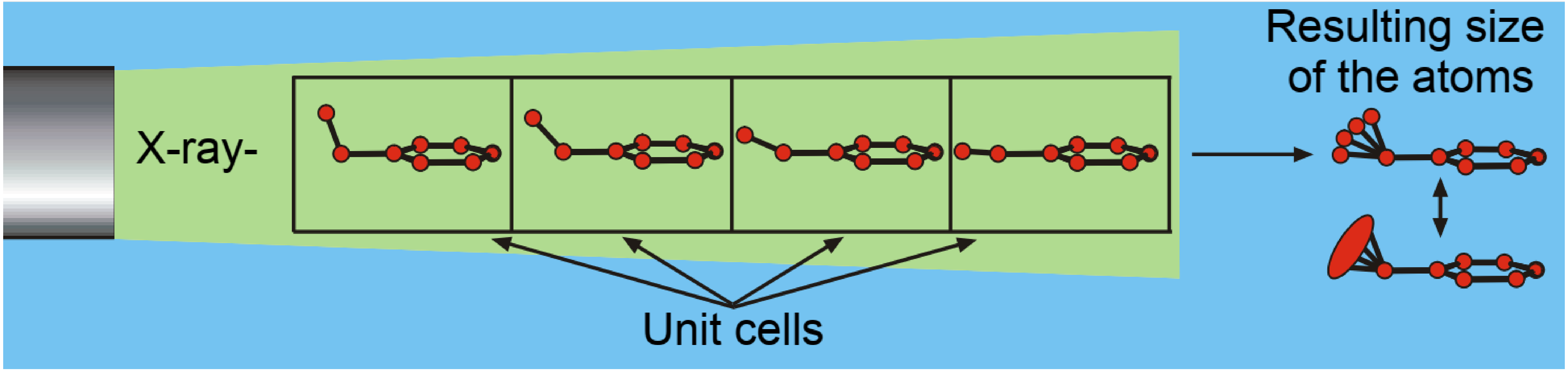


A crystal contains about 10^{18} unit cells

The structure, e. g. the conformation of a molecule can be different in the different unit cells leading to

DISORDER

Disorder



Disorder can originate from:

- different conformation of side-chains in molecules
- different orientation of molecules
- existence of topologically similar but different molecules in a crystal
- alternative hydrogen bonds

DISORDER TYPES

Perfect order: Each atom is located on one certain site

Substitutional disorder: A crystallographic position is occupied by more than one type of atom

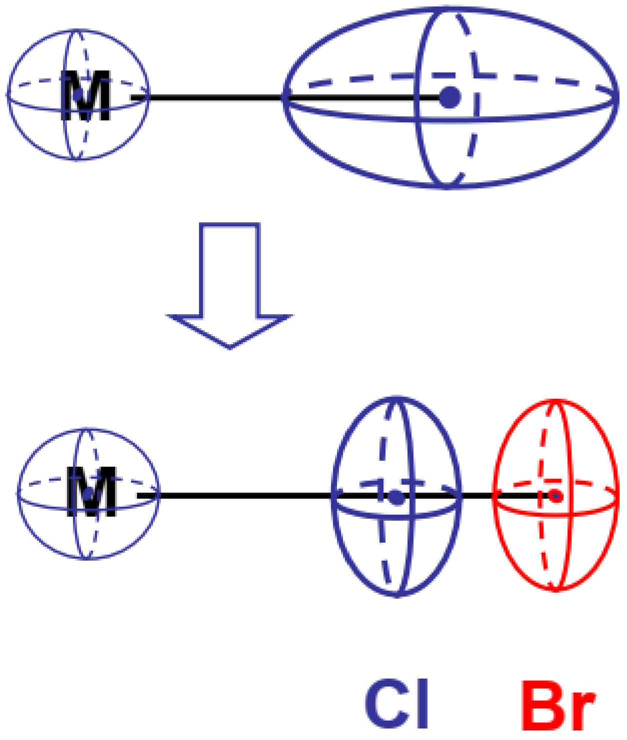
Positional disorder: One atom moves between different sites

Mixture from static and dynamic disorder: One atom jumps from one site onto another

Warning signs of disorder:

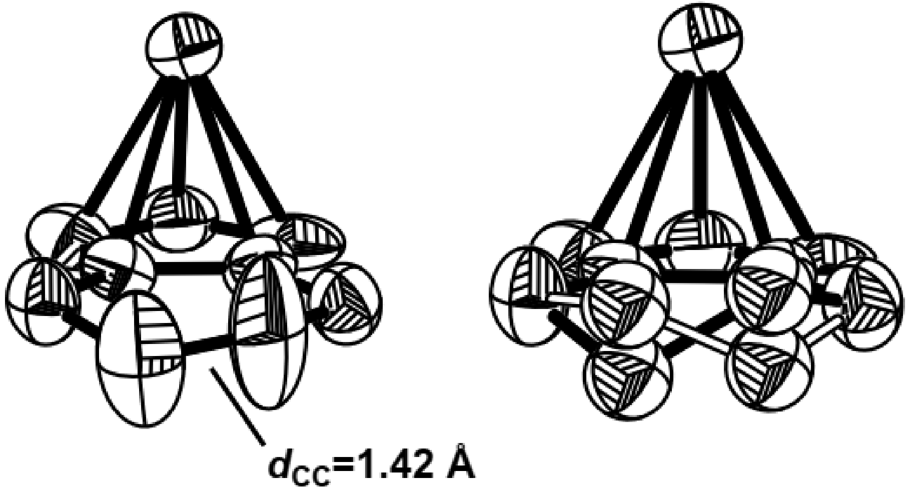
1. Substitutional disorder

• a thermal factor too big or too small
• orientation of the ellipsoid parallel to a bond, and/or
• an incorrect bond distance
• CHECKCIF: Hirshfeld test violation

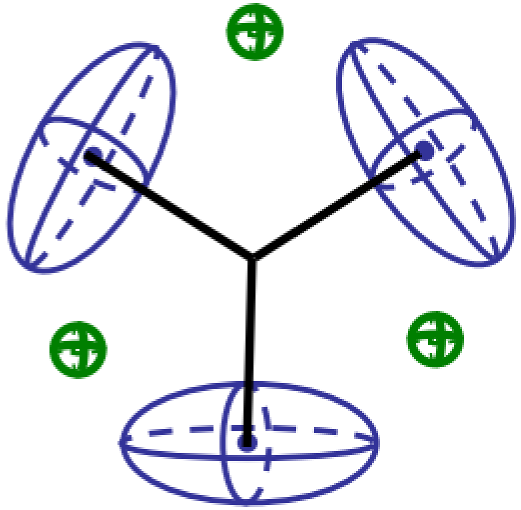


Warning signs of disorder:

Pseudorotational disorder
• Increase (compared to neighbours) thermal ellipsoids
• Shortened C-C distances
• Flattened saturated carbocycles



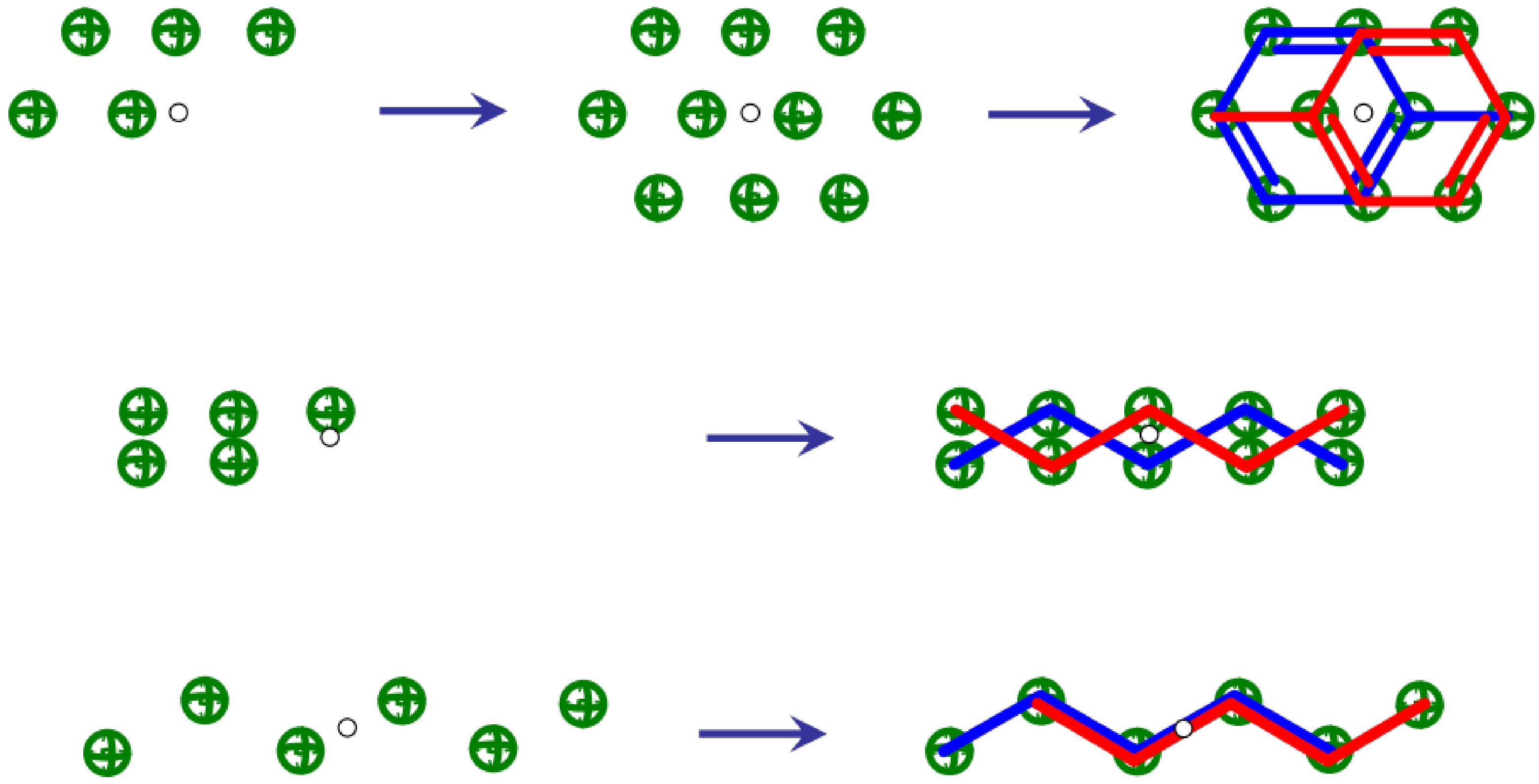
Rotational disorder
• Increased thermal ellipsoids
• Electron density present between the refined atom positions



Warning signs of disorder:

Whole molecule disorder of solvent

Symmetric distribution of electron density around a symmetry element



Refinement disorder

In most real life cases it is sufficient to describe a disorder by formulating two different positions per disordered atom.

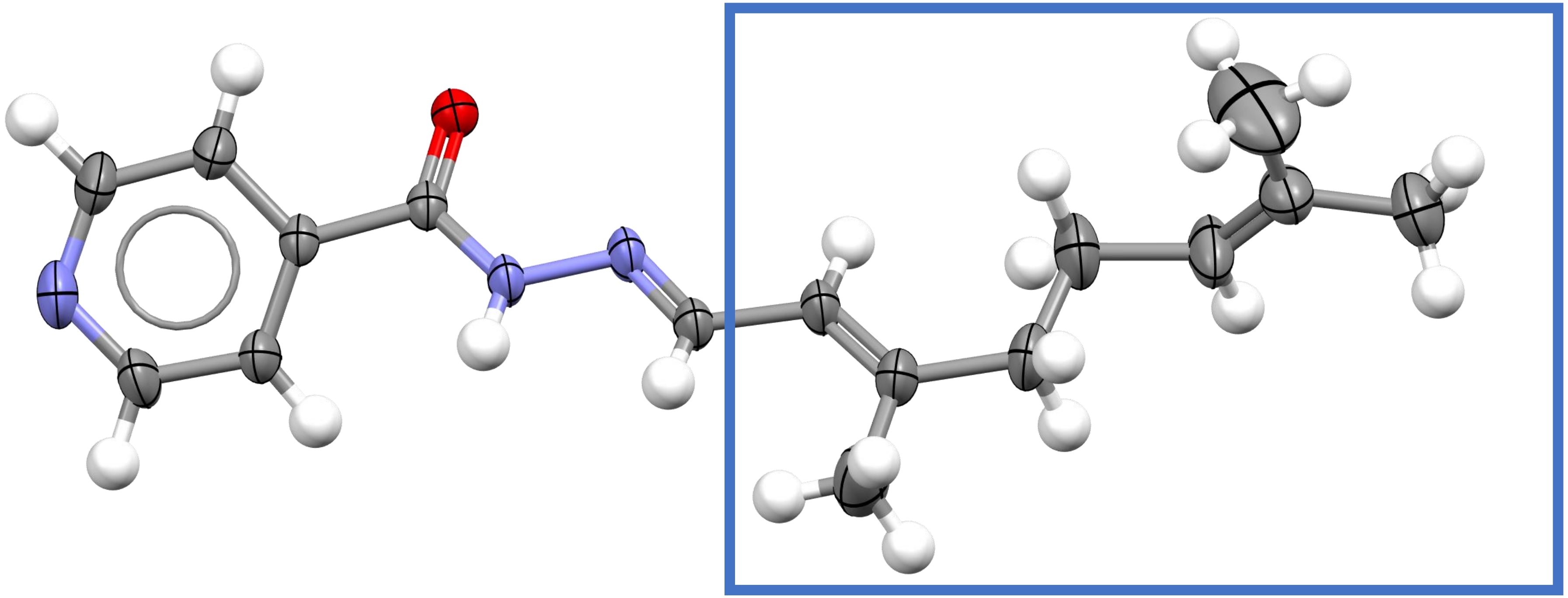
principle of disorder refinement

program needs to know the two sets of coordinates (i.e. positions) for each atom together with the relative occupancies (i.e. the ratio)

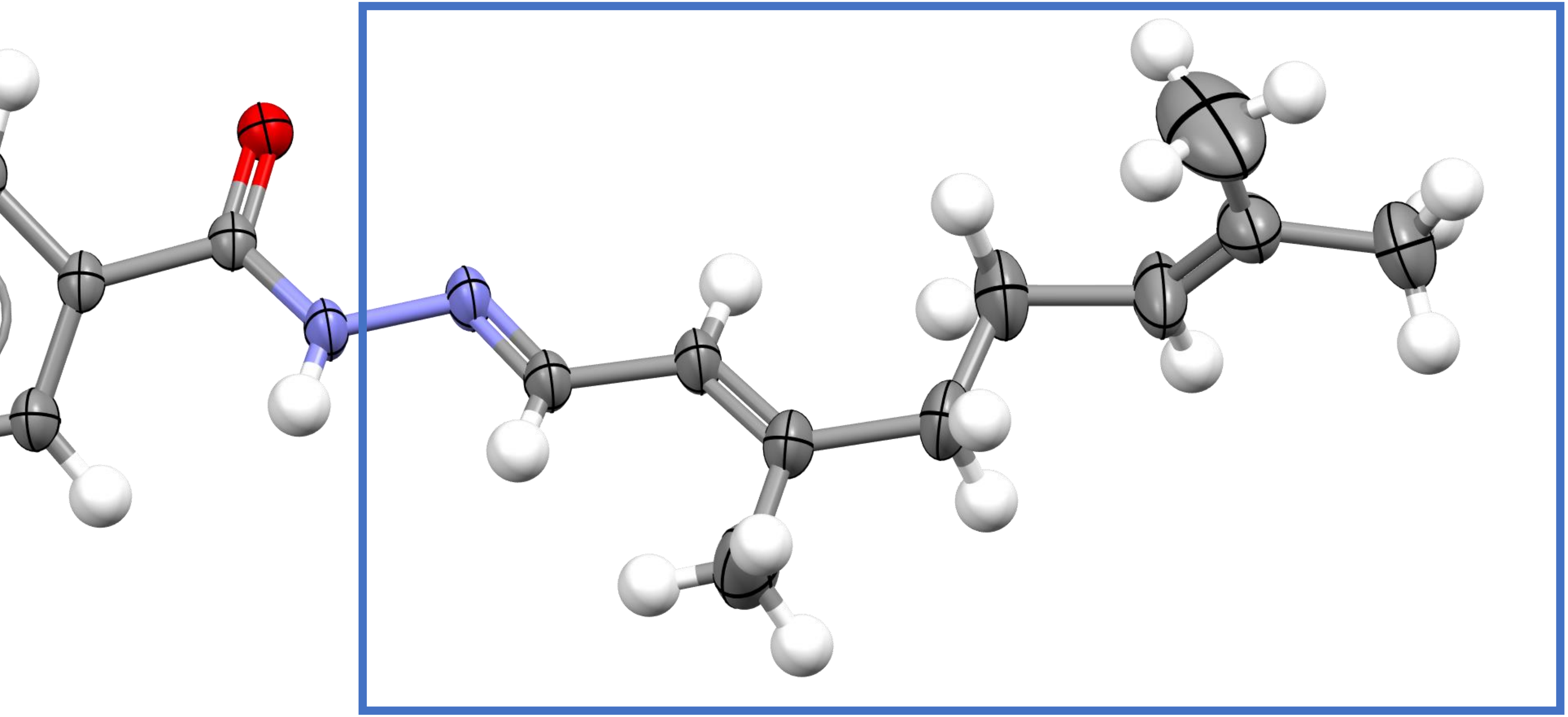
relative occupancies can either be given or refined.

refine disorders at first isotropically, to be easily to find additional positions

Refinement disorder



Refinement disorder



Refinement of disorder with SHELXL

Difficult part: How to find the second site

3 methods:

1. ADPs of an atom behaves strongly anisotropically

   SHELXL writes a suggestion for the two possible sites of this atom into the .lst file.

2. Positions of the disordered atoms are too far from each other to allow one ellipsoid to cover both sites

   Use the coordinates of residual electron density peaks for the second site, or sometimes for both sites → found at the very bottom of the .res file

3. No residual electron density near an atom and the ADPs are elongated but not anisotropic enough.

   Use the same initial coordinates for both sites of a split atom; SHELXL separates them during the refinement. Slightly "move" one of the two sites to prevent mathematical singularity

Refinement of disorder with SHELXL

Open SHELX.LST

Principal mean square atomic displacements U

```
  0.1065   0.0875   0.0326   N3
  0.0755   0.0538   0.0268   N1
  0.0695   0.0472   0.0253   N2
  0.0618   0.0494   0.0413   O1
  0.1256   0.0775   0.0319   C13
  0.0901   0.0581   0.0352   C14
  0.0529   0.0442   0.0296   C10
  0.0789   0.0545   0.0326   C11
  0.1057   0.0690   0.0319   C12
  0.0489   0.0418   0.0315   C16
  0.0714   0.0503   0.0296   C8
  0.0959   0.0557   0.0288   C9
  0.1111   0.0639   0.0348   C7
  0.1538   0.0885   0.0325   C6B
  0.1555   0.1090   0.0362   C5
  0.1584   0.0804   0.0366   C4
  0.1042   0.0663   0.0543   C2
  0.1516   0.1167   0.0456   C1
  0.3061   0.1297   0.0711   C3
  0.2267   0.0770   0.0476   C20    may be split into  0.4314  0.0469  0.1435  and  0.4412  0.0228  0.1724

** Warning:     1  atoms may be split and     0  atoms NPD **
```

Refinement of disorder with SHELXL

SHELXL refines disorder by dividing the disordered atoms into groups of components of disorder.

Occupancies of disordered groups are refined freely

PART instruction

In the .ins file

- write **PART 1** before the first atom disordered
- Follow with all the atoms of the first component
- before the atoms of the second component one writes **`PART 2`**
- After all the disordered atoms have been put in the file, write
  PART 0

Both parts the atoms should be in the same order to simplify the use of other instructions and also to be more enlightening.

Refinement of disorder with SHELXL

```
PART 1
C6B    1    0.33610    0.0661     0.33260    21.00000    0.04467    0.08404 =
          0.10134   -0.01693    0.02147   -0.02415
AFIX 23
H6A    2    0.33240   -0.0110     0.34100    21.00000   -1.20000
H6B    2    0.29620    0.0852     0.22700    21.00000   -1.20000
AFIX 0
C5     1    0.30717    0.1203     0.47830    21.00000    0.04914    0.10204 =
          0.10644   -0.00942    0.03320   -0.02179
H5A    2    0.309000    0.200000    0.469000    21.00000   -1.20000
H5B    2    0.342400    0.116000    0.585000    21.00000   -1.20000
C4     1    0.228150    0.079970    0.494800    21.00000    0.04605    0.06910 =
          0.11367    0.01928    0.02926   -0.00478
H4A    2    0.231000    0.013000    0.560000    21.00000   -1.20000
C2     1    0.159800    0.123800    0.440600    21.00000    0.06278    0.06791 =
          0.08230    0.01373    0.02796    0.00580
C1     1    0.085570    0.065800    0.463600    21.00000    0.05051    0.10182 =
          0.12493    0.00907    0.02941   -0.00305
AFIX  33
H1A    2    0.098800    0.000400    0.533200    21.00000   -1.20000
H1B    2    0.055700    0.114900    0.520800    21.00000   -1.20000
H1C    2    0.055400    0.045500    0.351500    21.00000   -1.20000
AFIX   0
C3     1    0.144000    0.233340    0.359000    21.00000    0.14233    0.11480 =
          0.25154    0.09752    0.09420    0.03617
```

o be

Refinement of disorder with SHELXL

```
PART 2
C6A   1    0.347000    0.050100    0.426000   -21.00000    0.04460    0.06051 =
         0.10186    0.01256    0.02554   -0.02100
AFIX 23
H6C   2    0.363000    0.027000    0.605000   -21.00000   -1.20000
H6D   2    0.342000   -0.023000    0.440000   -21.00000   -1.20000
AFIX 0
C5A   1    0.277300    0.108000    0.320000   -21.00000    0.04914    0.10204 =
         0.10644   -0.00942    0.03320   -0.02179
H5C   2    0.285000    0.193000    0.362000   -21.00000   -1.20000
H5D   2    0.279000    0.130000    0.174000   -21.00000   -1.20000
C4A   1    0.206700    0.064200    0.360000   -21.00000    0.04605    0.06910 =
         0.11367    0.01928    0.02926   -0.00478
H4B   2    0.216000   -0.011000    0.439000   -21.00000   -1.20000
C2A   1    0.154800    0.135000    0.388000   -21.00000    0.06278    0.06791 =
         0.08230    0.01373    0.02796    0.00580
C1A   1    0.085700    0.104300    0.408000   -21.00000    0.05051    0.10182 =
         0.12493    0.00907    0.02941   -0.00305
```

Refinement of disorder with SHELXL

```
C1A   1   0.085700   0.104300   0.408000  -21.00000   0.05051   0.10182 =
          0.12493   0.00907   0.02941  -0.00305
AFIX  33
H1D   2   0.070100   0.038900   0.340100  -21.00000  -1.20000
H1E   2   0.087500   0.088600   0.528900  -21.00000  -1.20000
H1F   2   0.048900   0.162600   0.370200  -21.00000  -1.20000
AFIX   0
C3A   1   0.181200   0.264000   0.373500  -21.00000   0.14233   0.11480 =
          0.25154   0.09752   0.09420   0.03617
AFIX  33
H3D   2   0.236400   0.267400   0.373500  -21.00000  -1.20000
H3E   2   0.154100   0.293600   0.255860  -21.00000  -1.20000
H3F   2   0.168700   0.307900   0.461400  -21.00000  -1.20000
AFIX   0
PART 0
```

Refinement of disorder with SHELXL

The second free variable

the occupancies of both components are allowed to possess any ratio

the site occupancy factors (*sof*) sum up to exactly one

the occupancy is refined with the help of a free variable

In the .ins file

FVAR instruction

- contains the overall scale factor (***osf***), also known as first free variable.
- line which directly precedes the first atom
- ***osf*** should be followed by a second free variable whose value is between 0 and 1, describing the fraction of unit cells with the conformation in **PART 1.**

the second free variable is equivalent to the occupancy of the atoms in component one
free variables are refined and a plausible starting value for this variable is 0.5

Refinement of disorder with SHELXL

OPEN .INS FILE

```
WGHT    0.100000
FVAR      5.85876   0.84909
N3   3   0.93908   0.37305   0.45560   11.00000   0.04028   0.09078 =
         0.10466  -0.00763   0.02483  -0.01637
N1   3   0.59012   0.23876   0.50981   11.00000   0.03743   0.06527 =
         0.06282  -0.01026   0.02297  -0.01339
N2   3   0.66332   0.25578   0.47211   11.00000   0.03404   0.06048 =
         0.05473  -0.00958   0.01896  -0.01067
AFIX  43
```

Refinement of disorder with SHELXL

site occupancy factor (*sof*)

In the .ins file

changing the value of the *sof* instruction from `11.0000` to `21.0000` for the atoms in **`PART 1`**

changing the value of the *sof* instruction from **11.0000** to **-21.0000** for the **PART 2** atoms

an atom lies on a special position

its occupancy for the ordered case has to be reduced to 0.5 or 0.25 and the sof instruction should be **20.5000** or **20.2500** for disordered atoms

Refinement of disorder with SHELXL

```
PART 1
C6B    1    0.33610    0.0661     0.33260     21.00000    0.04467    0.08404 =
          0.10134   -0.01693    0.02147    -0.02415
AFIX 23
H6A    2    0.33240   -0.0110     0.34100     21.00000   -1.20000
H6B    2    0.29620    0.0852     0.22700     21.00000   -1.20000
AFIX 0
C5     1    0.30717    0.1203     0.47830     21.00000    0.04914    0.10204 =
          0.10644   -0.00942    0.03320    -0.02179
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C4     1    0.228150    0.079970    0.494800    21.00000    0.04605    0.06910 =
          0.11367    0.01928    0.02926    -0.00478
H4A    2    0.231000    0.013000    0.560000    21.00000   -1.20000
C2     1    0.159800    0.123800    0.440600    21.00000    0.06278    0.06791 =
          0.08230    0.01373    0.02796    0.00580
C1     1    0.085570    0.065800    0.463600    21.00000    0.05051    0.10182 =
          0.12493    0.00907    0.02941    -0.00305
AFIX  33
H1A    2    0.098800    0.000400    0.533200    21.00000   -1.20000
H1B    2    0.055700    0.114900    0.520800    21.00000   -1.20000
H1C    2    0.055400    0.045500    0.351500    21.00000   -1.20000
AFIX   0
C3     1    0.144000    0.233340    0.359000    21.00000    0.14233    0.11480 =
          0.25154    0.09752    0.09420    0.03617
```
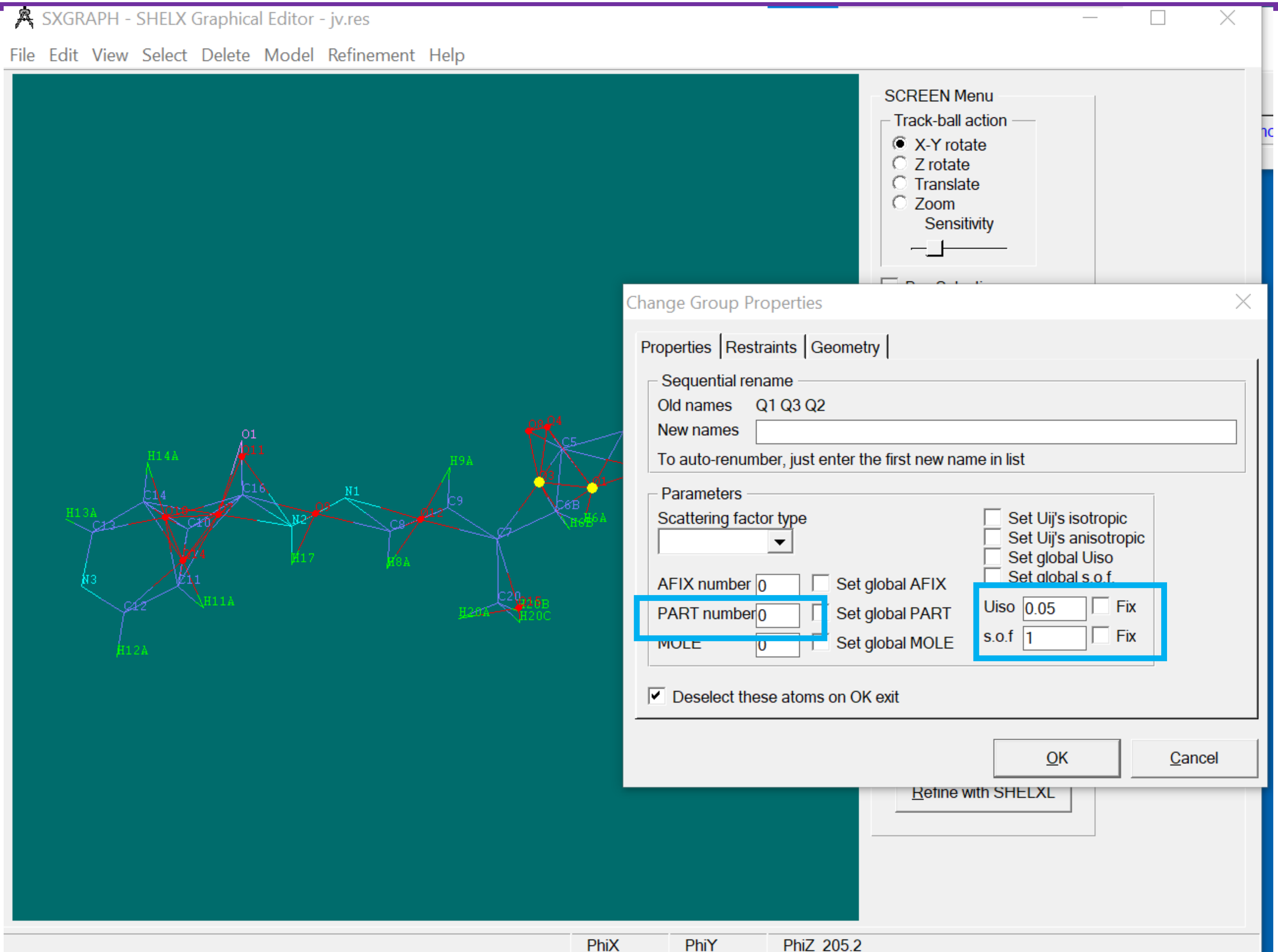

to be

Refinement of disorder with SHELXL

```
PART 2
C6A   1   0.347000   0.050100   0.426000   -21.00000   0.04460   0.06051 =
        0.10186   0.01256   0.02554   -0.02100
AFIX 23
H6C   2   0.363000   0.027000   0.605000   -21.00000   -1.20000
H6D   2   0.342000   -0.023000   0.440000   -21.00000   -1.20000
AFIX 0
C5A   1   0.277300   0.108000   0.320000   -21.00000   0.04914   0.10204 =
        0.10644   -0.00942   0.03320   -0.02179
H5C   2   0.285000   0.193000   0.362000   -21.00000   -1.20000
H5D   2   0.279000   0.130000   0.174000   -21.00000   -1.20000
C4A   1   0.206700   0.064200   0.360000   -21.00000   0.04605   0.06910 =
        0.11367   0.01928   0.02926   -0.00478
H4B   2   0.216000   -0.011000   0.439000   -21.00000   -1.20000
C2A   1   0.154800   0.135000   0.388000   -21.00000   0.06278   0.06791 =
        0.08230   0.01373   0.02796   0.00580
C1A   1   0.085700   0.104300   0.408000   -21.00000   0.05051   0.10182 =
        0.12493   0.00907   0.02941   -0.00305
```

Refinement of disorder with SHELXL



Refinement of disorder with SHELXL

Disorder and Restraints

Disorder increase the number of refined parameters → the refinement of disorders should always include restraints

Similarity Restraints

EADP instruction

The same isotropic or anisotropic displacement parameters are used for all the named atoms. The displacement parameters (and possibly free variable references) are taken from the first atom in the atom list that is linked to other atoms by EADP.

```
TITL jv in P2(1)/c
CELL  0.71073  17.5360  12.0610   7.8390   90.000  101.851   90.000
ZERR    4.00   0.0005   0.0004   0.0003    0.000    0.003    0.000
LATT   1
SYMM  - X, 1/2 + Y, 1/2 - Z
SFAC  C    H    N    O
UNIT  64   84  12   4
MERG   2
FMAP   2
PLAN   1
ACTA 1
L.S.  500
EADP C1 C1A
EADP C3 C3A
EADP C2 C2A
EADP C4 C4A
EADP C5 C5A
EADP C6 C6A
WGHT    0.100000
FVAR       5.85876   0.84909
N3    3    0.93908    0.37305    0.45560    11.00000    0.04028    0.09078 =
```

Refinement of disorder with SHELXL

Disorder and Restraints   See SHELX_instructions.pdf

Disorder increase the number of refined parameters → the refinement of disorders should always include restraints

Similarity Restraints

SAME instruction
Equivalent bond lengths and angles in the two (or more) components of a disorder are assumed to be equal

```
FVAR   ....   0.6
(...)
PART 1
SAME O1B C1B C2B C3B C4B
SAME O1A C4A C3A C2A C1A
O1A   4   ....   ....   ....    21.000
C1A   1   ....   ....   ....    21.000
C2A   1   ....   ....   ....    21.000
C3A   1   ....   ....   ....    21.000
C4A   1   ....   ....   ....    21.000
PART 2
O1B   4   ....   ....   ....   -21.000
C1B   1   ....   ....   ....   -21.000
C2B   1   ....   ....   ....   -21.000
C3B   1   ....   ....   ....   -21.000
C4B   1   ....   ....   ....   -21.000
PART 0
```

Refinement of disorder with SHELXL

Disorder and Restraints

Disorder increase the number of refined parameters → the refinement of disorders should always include restraints

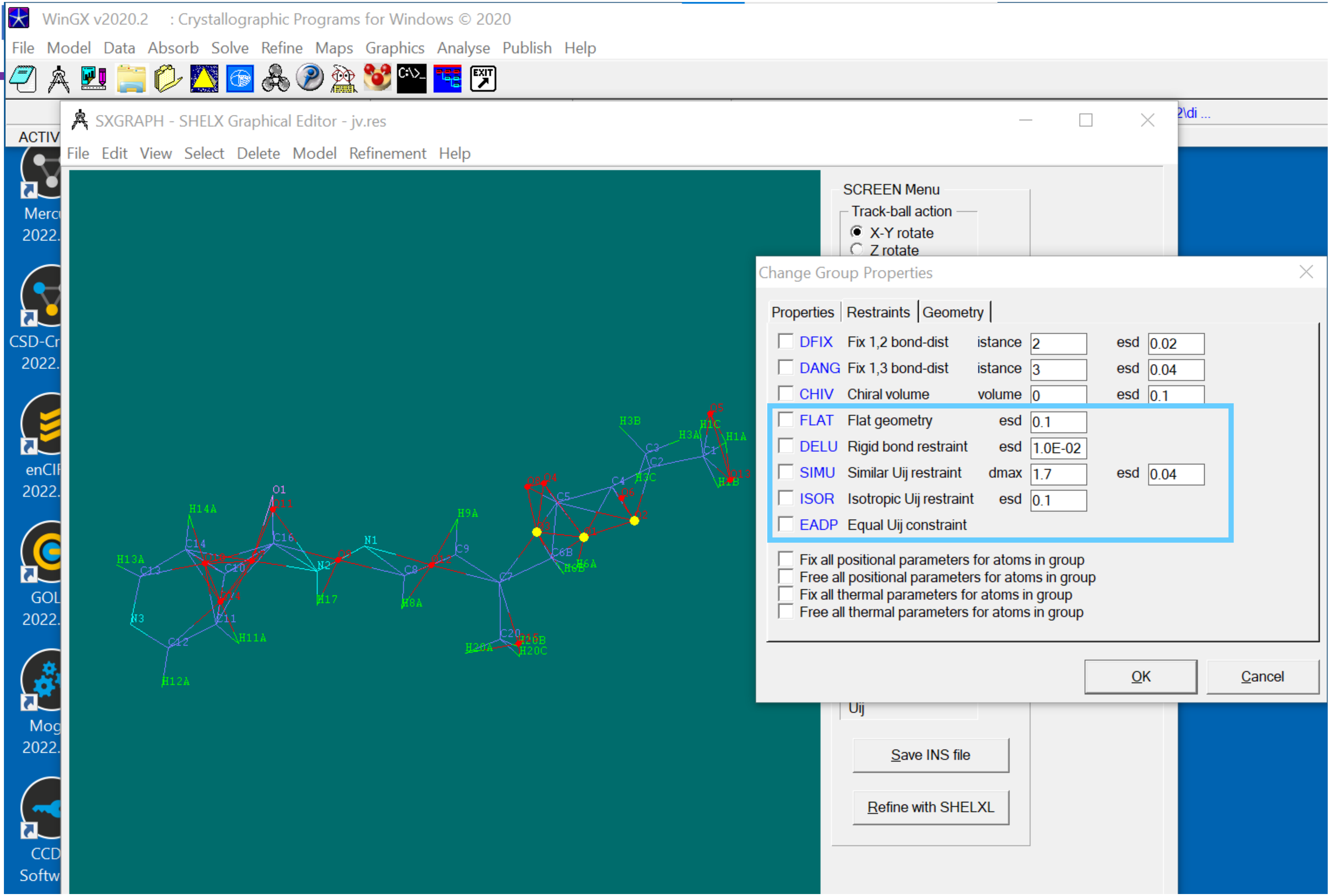
Similarity Restraints

SAME instruction
Equivalent bond lengths and angles in the two (or more) components of a disorder are assumed to be equal

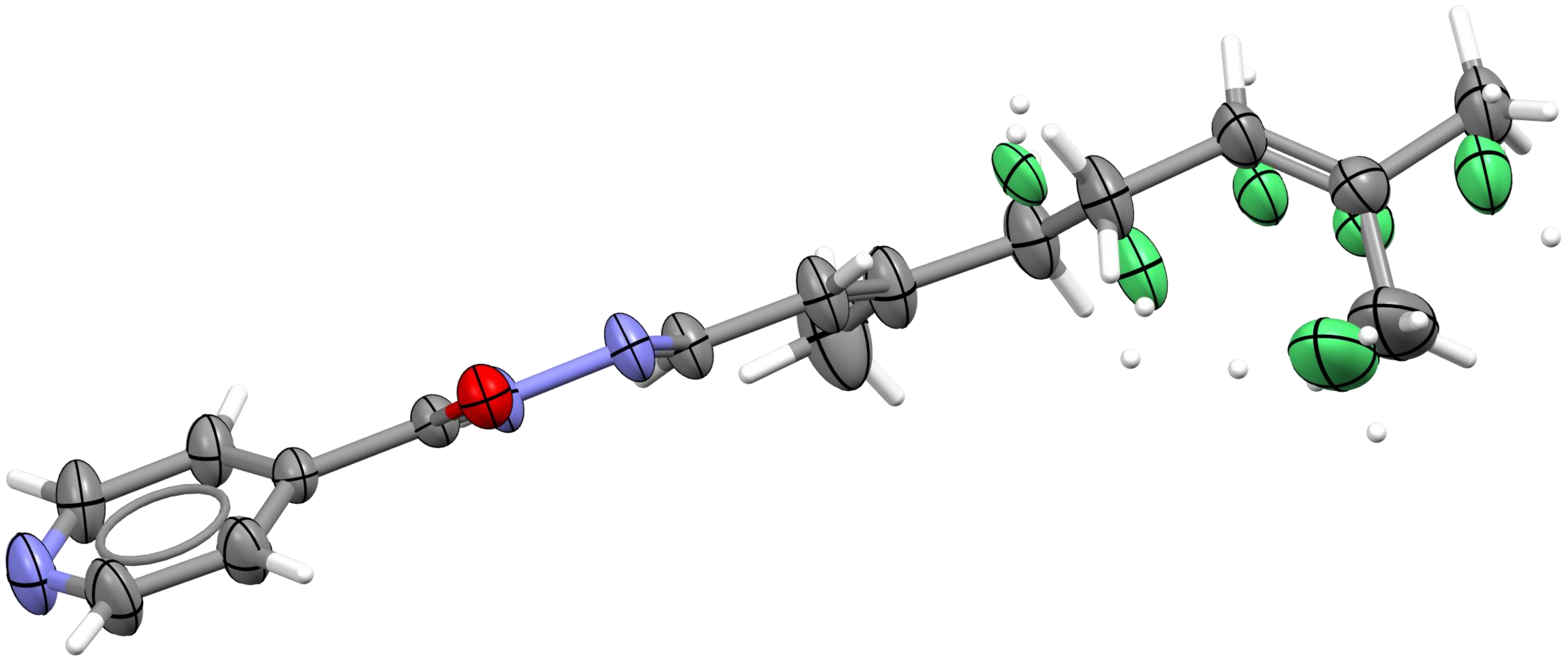
SADI instruction
Distances between arbitrary atom pairs can be restrained to possess the same value

```
SADI O1A C1A O1A C4A O1B C1B O1B C4B
SADI C1A C2A C3A C4A C1B C2B C3B C4B
SADI C2A C3A C2B C3B
SADI 0.04 O1A C2A O1A C3A O1B C1B O1B C3B
SADI 0.04 C1A C3A C2A C4A C1B C3B C2B C4B
SADI 0.04 C1A C4A C1B C4B
```

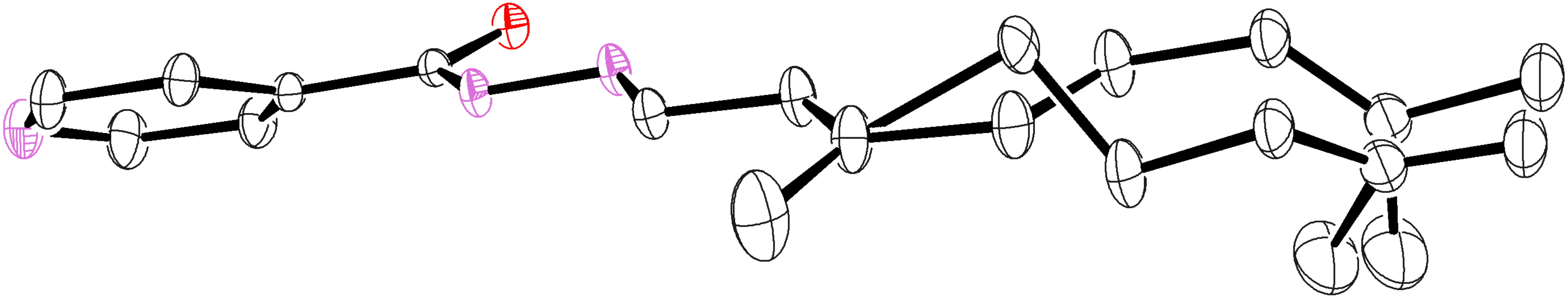
```
FVAR  ....   0.6
(...)
PART 1
SAME O1B C1B C2B C3B C4B
SAME O1A C4A C3A C2A C1A
O1A   4   ....   ....   ....    21.000
C1A   1   ....   ....   ....    21.000
C2A   1   ....   ....   ....    21.000
C3A   1   ....   ....   ....    21.000
C4A   1   ....   ....   ....    21.000
PART 2
O1B   4   ....   ....   ....   -21.000
C1B   1   ....   ....   ....   -21.000
C2B   1   ....   ....   ....   -21.000
C3B   1   ....   ....   ....   -21.000
C4B   1   ....   ....   ....   -21.000
PART 0
```


WinGX v2020.2 : Crystallographic Programs for Windows © 2020
File Model Data Absorb Solve Refine Maps Graphics Analyse Publish Help
SXGRAPH - SHELX Graphical Editor - jv.res
File Edit View Select Delete Model Refinement Help
SCREEN Menu
Track-ball action
X-Y rotate
Z rotate
Change Group Properties
Properties Restraints Geometry
DFIX Fix 1,2 bond-dist istance 2 esd 0.02
DANG Fix 1,3 bond-dist istance 3 esd 0.04
CHIV Chiral volume volume 0 esd 0.1
FLAT Flat geometry esd 0.1
DELU Rigid bond restraint esd 1.0E-02
SIMU Similar Uij restraint dmax 1.7 esd 0.04
ISOR Isotropic Uij restraint esd 0.1
EADP Equal Uij constraint
Fix all positional parameters for atoms in group
Free all positional parameters for atoms in group
Fix all thermal parameters for atoms in group
Free all thermal parameters for atoms in group
OK
Cancel
Uij
Save INS file
Refine with SHELXL

Refinement of disorder with SHELXL



Refinement of disorder with SHELXL



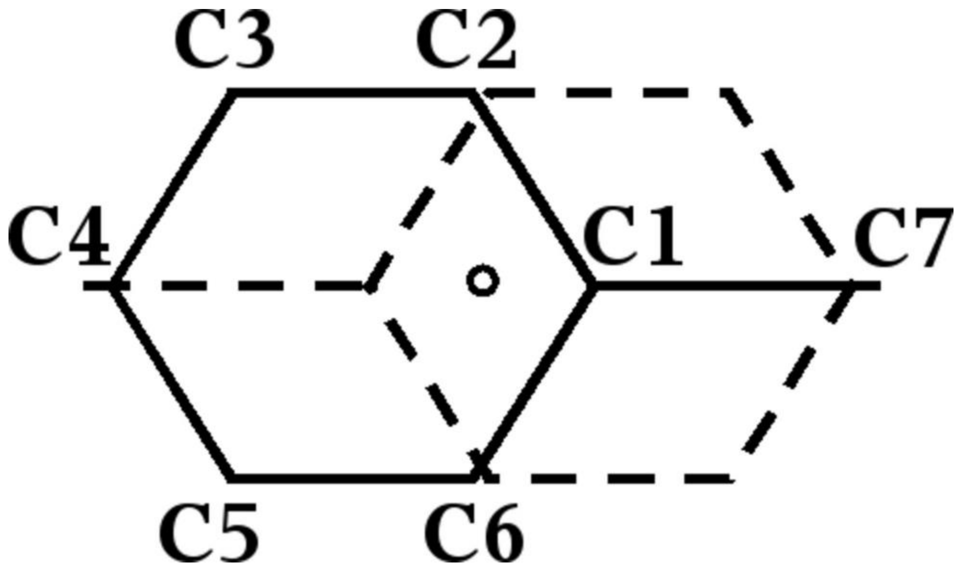
Disorder about special positions

1. Molecule lies on a special position of higher symmetry than the molecule can possess

   - changes the space group to one of lower symmetry without this particular special position

2. assumes a disorder of the molecule about this particular special position.

Example: toluene molecule on an inversion center

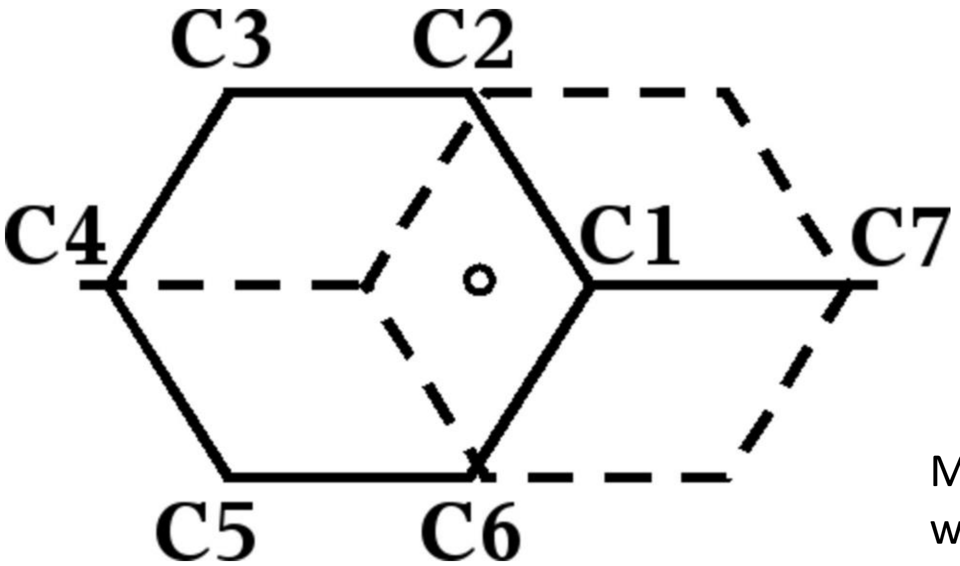


the second site of each atom can be calculated directly from the positions of the atoms of the first component *via* the symmetry operator of the special position

Refinement of disorder with SHELXL

Disorder about special positions

Example: toluene molecule on an inversion center



1. set all seven occupancies to 10.5
2. put a **PART −1** instruction before the first atom and **PART 0** after the last. The negative part number suppresses the generation of special position constraints, and bonds to symmetry-related atoms are excluded from the connectivity table

Molecules located very close to special positions, so that the symmetry would lead to chemically unreasonable arrangements, are treated the same way.

SPEC instruction is used for generate all appropriate special position constraints for the specified atoms.