# In the following hours...

- Overview of the refinement process and programs used
- Step by step example of a refinement
- How to sort and number atoms
- Structure and commands in the .ins(truction)/.res(ults) file
- Description of thermal motion
- Constraints and restraints in SHELXL
- Hydrogen treatment
- Finishing the refinement

### **Structure determination**



### Programs used in a single crystal diffraction study

- Grow a crystal
- Choose and mount a single crystal
- Collect the dataset
- Determine the unit cell
- Integration of the image files and data reduction
  - Lorentz correction
  - Polarisation correction
  - Absorption correction
  - Other corrections (twinning etc.)
- Space group determination
- Structure solution
- Structure refinement
- Validation
- Preparation of tables and figures
- Data backup

SAINT SAINT  $\Rightarrow$  .raw SADABS  $\Rightarrow$  .hkl List with reflection intensities  $XPREP \Rightarrow .ins, .hkl, .pcf, .prp$ XS (SHELXS)  $\Rightarrow$  .res, .lst XL (SHELXL)  $\Rightarrow$  .res, .lst, .cif checkcif, PLATON XP, XSHELL, PLATON etc.

APEX2  $\Rightarrow$  images

APEX2  $\Rightarrow$  .p4p



### Programs used in a single crystal diffraction study



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**Difference Fourier map** 

### **Refinement organigram**







The initial solution proposes a electron density map in which the highest points of electron densities are identified (Q-peaks).



If a structure is difficult to identify, look for regular structures, such as aromatic rings etc.





For some centers of electron density an element is already proposed. You have to verify if they are correctly assigned.



Several centers of electron densities are not related to your structure.

Do not hesitate to delete them! A deleted electron density will show up again in later cycles, if it is correct.

Altea A





Q-peaks are sorted after their electronic density with Q1 being the highest electron density.

The peaks with the smallest numbers have the highest electron density and are thus fluorine atoms.



Now you have to assign correct elements to the remaining electron densities:

Carbon



Now you have to assign correct elements to the remaining electron densities:

 Carbon • Fluor



Now you have to assign correct elements to the remaining electron densities:

- Carbon
- Fluor
- Boron

At the ends no Qpeaks must be left!



### **Refinement organigram**



### Which parameters are refined?

Ins-file:

CELL 0.71073 8.1380 15.4444 15.1323 90 98.922 90

The atomic positions are given as fractions of the basis vectors. The values given are thus **not in Å** and Si1 is found at

- *x* = *u*⋅*a* = 0.16560⋅8.1380 Å = 1.3476 Å
- **y** = **v**⋅**b** = 0.14717⋅15.4444 Å = 2.2729 Å
- *z* = *w*·*c* = 0.71608·15.1323 Å = 10.836 Å

The fractional atomic positions are normally symbolized by the letters *u*, *v* and *w*. Since each atom is present in the unit cell *u*, *v* and *w* have values between 0 and 1. For practical reasons, we find sometimes < values <0 or >1, but never <-1 or >2.



### Which parameters are refined?

SI1 4 0.16560 0.14717 0.71608 11.00

11.00000 0.03452 Occupation factor

The occupation factor indicates how many atoms are occupying this position. The maximal occupation factor is 1, but in special cases, smaller numbers are possible.

### • Disorder

Ins-file:

01	3	0.12560	0.23453	0.83456	11.00000	0.02932
H1A	2	0.12864	0.23364	0.80236	10.50000	0.04732
H2A	2	0.12853	0.23923	0.85935	10.50000	0.04593





### Which parameters are refined?

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The occupation factor indicates how many atoms are occupying this position. The maximal occupation factor is 1, but in special cases, smaller numbers are possible.

- Disorder
- Special positions

An atom on a symmetry element is duplicated on its position. To avoid this, the program would have to recognize and exclude atoms on special positions from some symmetry operations.

0.03452

SI1 4 0.25000 0.14717 0.25000 10.50000 0.03452

By applying an occupation factor of <sup>1</sup>/<sub>2</sub>, the atom can be treated in the same way as all other atoms.

Occupation factor

### **Structure refinement**



### **Refinement organigram**



## **Refinement organigram**



Each atom has a label consisting out of its element symbol and a number Numbering: Two strategies

- 1. The labels of each atoms start with the number 1 : S1, B1, F1...F15, C1..C22
- One starts the first atom with 1 and continues counting regardless the element: S1, B2, F3...F17, C18..C39

#### Some remarks (in decreasing importance):

- Always use a number, even if there is only one atom present. Thus, S1, not S
- Follow the numbering of similar structures in your group.
- You can jump numbers to help understanding, but do not overdo it. Avoid numbers >100.





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- If possible, try to follow "organic" numbering rules.
- Do not use symbols such as: # \* ' \$ etc.
- The use of letters (C15A, C15B) is reserved for atoms which are identical by symmetry or disorder. Do not use them for different rings etc.





 $F_5C_6$   $C_6F_5$ 

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#### Sorting atoms:

- It is preferable to group atoms into the respective molecuels, e. g. cation, anion 1, anion 2, solvant
- Sort the elements first after their elements, then after their number, the heavy elements first. E. g. triflate : S1, F1, F2, F3, O1, O2, O3, C1

### A short detour: The res/ins file



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## A short detour: Fichier \*.res / fichier \*.ins





# **Difference Fourier map**



The refinement result does not show any new atoms.

There are no missing atoms

The remaining peaks can be attributed to:

- Thermal motion of atoms
- Hydrogen atoms

• Errors

## Thermal motion of atoms / Temperature factor

h		Atom position		Occupation factor	<b>U</b> <sub>iso</sub>
SI1 4	0.16560	0.14717	0.71608	11.00000	0.03452

### U<sub>iso</sub>?

- The distribution of the electronic density depends on the thermal motion of the atoms
- Thermal motion is not identical for all atoms
- An X-ray experiment takes significantly more time than thermal motion
- $\Rightarrow$  we obtain an averaged distribution of the electron density

#### **Isotropic motion:**

- The vibration of an atom is identical in all directions
- It is described by a Gaussian function

$$\rho(r') = \sqrt{2\pi U} e^{\frac{-r'^2}{2U}}$$

 $\rho$ : distribution of the electron density *r*': distance from the equilibrium position

### **Thermal motion of atoms**



### **Thermal motion of atoms**


## **Thermal motion of atoms**

#### **Anisotropic motion:**

- The atomic motion is not isotropic,
  - i. e. identical in all directions.

 It is described in our model by an ellipsoid (different Gaussian functions in three dimensions) or, mathematically speaking, by a symmetric tensor:  $\boldsymbol{U} = \begin{pmatrix} \left\langle \boldsymbol{x'}^2 \right\rangle & \left\langle \boldsymbol{x'} \boldsymbol{y'} \right\rangle & \left\langle \boldsymbol{x'} \boldsymbol{z'} \right\rangle \\ \left\langle \boldsymbol{x'} \boldsymbol{y'} \right\rangle & \left\langle \boldsymbol{y'}^2 \right\rangle & \left\langle \boldsymbol{y'} \boldsymbol{z'} \right\rangle \\ \left\langle \boldsymbol{x'} \boldsymbol{z'} \right\rangle & \left\langle \boldsymbol{y'} \boldsymbol{z'} \right\rangle & \left\langle \boldsymbol{z'}^2 \right\rangle \end{pmatrix}$ 

Instead of 1 parameter (U<sub>iso</sub>) we require 6 parameters for the ellipsoid (3 radii and the direction of the principal axis).

 $q(r^*) = e^{-2\pi^2(U_{11}x'^2 + U_{22}y'^2 + U_{33}z'^2 + 2U_{12}x'y' + 2U_{13}x'z' + 2U_{23}y'z')}$ 

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• Errors

## **Refinement organigram**



## **Thermal motion of atoms**

*.ins: ANIS WGHT FVAR S1 B1 F1	5 3 4	0.100000 0.71880 0.277586 0.366643 0.079477	0.724064 0.718741 11.00000 0.02858 0.625301 0.823380 11.00000 0.02507 0.474487 0.653317 11.00000 0.03965	
*.res: WGHT		0.100000		
FVAR		0.73527	0/2	
S1	5	0.277751	0.724339 0.718759 11.00000 0.03304	0.02854 =
		0.02460	0.01056 0.00663 0.01163	
B1	3	0.366302	0.625285 0.823440 11.00000 0.02772	0.02171 =
		0.02300	0.00834 0.00485 0.00625	$\cap$
F1	4	0.079086	0.473686 0.653072 11.00000 0.02849	0.03982 =
		0.04679	0.01366 0.00319 0.00667	$\smile$



 $U_{eq}$ : is the equivalent  $U_{iso}$  value giving the same volume, calculated for comparison

#### Typical U<sub>eq</sub> values:

Heavy atoms: $0.005-0.02 \text{ Å}^2$ Light atoms (H-F): $0.01-0.06 \text{ Å}^2$ Terminal atoms: $0.03-0.2 \text{ Å}^2$ 



## **Difference Fourier map**



## After anisotropic refinement:

Les pics restants peut être attribués aux:

#### Thermal motion of atoms

- Hydrogen atoms
- Errors

The 8 highest Qpeaks (Q1-Q8) correspond to hydrogen atoms!

## **Refinement organigram**



## **Constraints and restraints**

# THIS WILL TAKE A WHILE.

Å.

## **Constraints and restraints**

**Constraint:** Exact mathematical condition, which results in a **reduction of the number of parameters.** A constraint cannot be violated. Example: rigid groups and "riding" hydrogen atoms.

Restraint: Additional observations/restraints which are added to the data during refinement. Restraints can be violated to a certain degree.

$$M = \sum w_{x} (F_{o}^{2} - F_{c}^{2})^{2} + \sum w_{r} (T_{target} - T_{c})^{2}$$

Both, constraints and restraints increase the data/parameter ratio.

• Special positions (generated automatically)

These constraints, which are necessary for atoms positioned on symmetry elements, are automatically generated by the program.



- Special positions (generated automatically)
- Rigid groups (e. g. AFIX x6 ... AFIX 0)

In rigid groups the parameters for all atomic positions  $(3 \times n)$  are replaced by 3 rotations and 3 translations for the complete group. The idealized geometry of the group is fixed and the atoms cannot move independently. *AFIX* **x6**: completely rigid group; *AFIX* **x9**: group can grow and shrink keeping its relative geometry.



- Special positions (generated automatically)
- Rigid groups (e. g. AFIX x6 ... AFIX 0)
- "Riding model" for hydrogen atoms (AFIX mn)

$$xH = xC + \Delta x$$
  

$$yH = yC + \Delta y$$
  

$$zH = zC + \Delta z$$
  

$$U_{H} = 1.2 - U_{X}$$

No additional parameters are refined for the hydrogen atoms, if they are treated by a riding model!

- Special positions (generated automatically)
- Rigid groups (e. g. AFIX x6 ... AFIX 0)
- "Riding model" for hydrogen atoms (AFIX mn)
- Fixed parameters

Addition of 10 excludes a value from the refinement.

Normally occupation factors are not refined.

0.03221 С1 0.31357 0.46194 0.73087 11.00000 0.02339 =1 0.02334 0.00728 0.00820 0.00568 0.02909 =С2 0.17696 0.50000 0.65307 10.50000 0.03174 1 0.02961 0.01051 0.00909 0.00550 0.13022 0.02965 =C3 0.26106 0.57225 **11.00000** 0.03871 1 0.03073 0.00631 0.00674 -0.00625

(The program adds automatically the constraints for atoms on special positions.)

In SHELXL, each value is provided in the form of x = 10m + p. *p*: value, which is refined; *m*: refinement mode

#### m = 0: normal refinement, x = pValues fixed at 1.0000 m = 1: no refinement, x is fixed at p 0.73087 11.00000 С1 0.31357 0.46194 0.03221 1 Values 11.00000 10.035 C2 0.65307 1 0.17696 0.39844 fixed at C3 0.13022 0.26106 0.57225 11.00000 10.035 1 0.035 0.25000 0.17682 0.50000 10.50000 0.05684 CL1 2 0.50000 10.50000 0.05110 3 0.25000 0.19763 Br1 Values fixed at 0.5000

- We can exclude any value from refinement by adding 10.
- For atoms on special positions, the program does this automatically without our intervention.

C1	1	0.31357	0.46194	0.73087	11.00000	0.03221
C2	1	0.17696	0.39844	0.65307	11.00000	10.035
С3	1	0.13022	0.26106	0.57225	11.00000	10.035
CL1	2	<b>1</b> 0.25000	0.17682	<b>1</b> 0.50000	10.50000	0.05684
Br1	3	<b>1</b> 0.25000	0.19763	<b>1</b> 0.50000	10.50000	0.05110

In SHELXL, each value is provided in the form of x = 10m + p. *p*: value, which is refined; *m*: refinement mode

- m = 0: normal refinement, x = p
- m = 1: no refinement, x is fixed at p
- m > 1: x = p."free variable no. m"
- m < -1:  $x = p \cdot (1 "free variable no. m")$

The same value is refined for all three atoms

FVAR		0.73503	0.0239 0.	2365		<u>\</u>
C1	1	0.31357	0.46194	0.73087	11.00000	21.00000
C2	1	0.17696	0.39844	0.65307	11.00000	21.00000
С3	1	0.13022	0.26106	0.57225	11.00000	21.00000
CL1	2	0.25000	0.17682	0.50000	31.00000	0.05684
Br1	3	0.25000	0.19763	0.50000	-31.00000	0.05110

Using the m<-1 option, a ratio can be defined with a fixed sum of the two variables:

31.000 + -31.0000 = 130.500 + -30.5000 = 0.5 (10m)p + (-10m)p = pFree variable no. *m*, targetvalue *p* 

In SHELXL, each value is provided in the form of x = 10m + p. *p*: value, which is refined; *m*: refinement mode

- m = 0: normal refinement, x = p
- m = 1: no refinement, x is fixed at p
- m > 1: x = p."free variable no. m"
- *m* <-1: *x* = *p*-(1 "free variable no. *m*")

**FVAR** 0.73503 0.0239 0.2365

- There is no "free variable no. 1", since adding 10 is used to exclude values from refinement.
- The first position of the FVAR command is thus occupied by the "overall scale factor" (OSF).
- The OSF scales our (arbitrary) intensities, which depends on crystal size, detector sensitivity etc., to the theoretical diffraction by a single unit cell.

In SHELXL, each value is provided in the form of x = 10m + p. *p*: value, which is refined; *m*: refinement mode

- m = 0: normal refinement, x = p
- m = 1: no refinement, x is fixed at p
- m > 1: x = p."free variable no. m"
- m < -1:  $x = p \cdot (1 "free variable no. m")$

Value fixed at 1.0000

```
0.73503 0.6439 0.2365
FVAR
                                          11.00000
C1
          0.31357 0.46194
                                0.73087
                                                       0.03221
      1
                                                                   Value
C2
      1
          0.17696 0.39844 0.65307
                                          21.00000
                                                      10.035
                                                                   fixed at
C3
      1
          0.13022 0.26106 0.57225 -21.00000←
                                                      10.035
                                                                   0.035
CL1
      2
           0.25000
                     0.17682
                                0.50000 - 30.50000
                                                       0.05684
      3
Br1
           0.25000
                     0.19763
                                0.50000 -30.50000
                                                       0.05110
                                                        Value fixed at: 1.0000 x
    Value fixed at: 0.50000 x var. #3 = 0.1183
                                                        var. #2 = 0.6439
      Value fixed at: 0.50000 x (1-var. #3) = 0.3817
                                                       Value fixed at: 1.0000 x
Constraints for special positions are
                                                       (1-var. #2) = 0.2561
automatically generated by the program.
```

In contrast to constraints, which cannot be violated, restraints define only a target value for some parameters. They are associated with a standard deviation  $\sigma$ , which describes how much a violation of the target value is penalised. The smaller  $\sigma$ , the more the parameter is forced to be close to the targeted value d<sub>c</sub>. A  $\sigma$  = 0 yields a constraint.



$$M = \Sigma \ W_{\rm x} (F_{\rm o}^2 - F_{\rm c}^2)^2 + \Sigma \ 1/\sigma (d - d_{\rm c})^2$$

**Restraints in SHELX** 

DFIX, DANG, SADI, SAME: distances and angles (1,3-distances) DELU, SIMU, ISOR, RIGU: thermal motion parameters FLAT, CHIV, BUMP, NCSY, SUMP

### Using constraints and restraints: Hydrogen treatment

The position of hydrogen atoms is a challenge in X-ray diffraction studies due to their low electron density. In addition, the C-H (and OH, NH etc.) distances are determined systematically to short for two reasons:



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### Using constraints and restraints: Hydrogen treatment

The position of hydrogen atoms is a challenge in X-ray diffraction studies due to their low electron density. In addition, the C-H (and OH, NH etc.) distances are determined systematically to short for two reasons:

#### 1.«Libration»

The effect is specificially strong for hydrogen atoms (very light atoms)

2. The maximum of the electron density is located in the bond, not on the nucleus.



## Hydrogen treatment

With data of moderate quality, you can find the hydrogen atoms in the difference Fourier map... but can you refine them?



## Hydrogen treatment : 1. Free refinement

#### **1. Free refinement**

The anisotropic refinement of hydrogen atoms requires 9 parameters per hydrogen atom.

- $\Rightarrow$  We encounter problems with the data/parameter ratio
- $\Rightarrow$  The electron density of hydrogen is very low

⇒ Isotropic refinement

#### Conditions for free refinement of hydrogen atoms:

- Sufficient data quality
- The obtained distances, angles and  $U_{iso}$  must be reasonable:

rea

CH  $\approx$  1 Å ± 10% = 0.9-1.1 HCX  $\approx \angle_{ideal} \pm 10\%$  $U_{iso} < 0.2$  Å<sup>2</sup> and not too varied

### Hydrogen treatment : 1. Free refinement



.1st:  $U_{iso} = 0.033 - 0.064$ 

C20

C21

C20

C21

H19A

H20A

H21A

H22A

## Hydrogen treatment : 2. U<sub>iso</sub> constraint

**2.** Free refinement of atomic positions, but constraint  $U_{iso}$  values

⇒  $U_{iso}$  of all hydrogen atoms are restraint to the same value ⇒ One might use different values (free variables) for hydrogen atoms in CH<sub>3</sub>, C(sp<sup>2</sup>)H or (CR<sub>2</sub>H<sub>2</sub>,CR<sub>3</sub>H) groups.

FVAR		0.73503			54	8 H $\Rightarrow$ <b>32</b> paramètres
•••		0.75505				
H19A	2	0.49363	0.89888	0.80474	11.00000	0.03671
H19B	2	0.35967	0.94429	0.75075	11.00000	0.05698
H20A	2	0.54456	0.78518	0.60379	11.00000	0.04391
H20B	2	0.49706	0.91807	0.59605	11.00000	0.05058
• • •						
FVAR		0.73503	0.045			8 H $\Rightarrow$ <b>25</b> paramètres
•••						
H19A	2	0.49363	0.89888	0.80474	11.00000	21.0000
H19B	2	0.35967	0.94429	0.75075	11.00000	21.0000
H20A	2	0.54456	0.78518	0.60379	11.00000	21.0000
H20A H20B	2 2	0.54456 0.49706	0.78518 0.91807	0.60379 0.59605	11.00000 11.00000	21.0000 21.0000

### Hydrogen treatment : 2. U<sub>iso</sub> constraint



.1st:  $U_{iso} = 0.0462$ 

110.7 113.8

109.9 109.7

113.9 108.6

107.5 112.2

C20

105.0

S1

C19

S1

106.9

100.2 115.0 109.2

C20

106.0 113.5 110.8

C21

106.7 111.9 108.3

C22

109.5 112.6 109.8

C21

H19A

H20A

H21A

H22A

## 3. Restraints on distances and angles

C-H distances are restraint to equal values (*U*<sub>iso</sub> stays fixed) 1,3-distances are also restraint to be equal («angle restraints»)

SADI	С19 н19	a C19	H19b	C20 H20a	С20 Н20Ъ	C21 H21a	C21 H21b	=
	С22 Н22	2a C22	H22b					
SADI	H19a H1	9ь н20а	a H20b	H21a H21b	H22a H22b			
SADI	C19 H20	)a C19	H20b	C20 H19a	C20 H19b	C20 H21a	С20 Н21Ъ	=
	C21 H20	)a C21	H20b	C21 H22a	С21 Н22Ъ	C22 H21a	С22 Н21Ь	
SADI	S1 H19a	a S1 H	19b S	L H22a S1	н22b			
FVAR	C	0.73503	0.045					
•••								
H19A	20.	49363	0.89888	8 0.80474	11.00000	21.0000		
H19B	20.	.35967	0.94429	0.75075	11.00000	21.0000		
H20A	20.	.54456	0.78518	0.60379	11.00000	21.0000		
H20B	20.	.49706	0.91807	0.59605	11.00000	21.0000		

**28 restraints**  $\Rightarrow$  **+ 28 data** 8 H  $\Rightarrow$  25 parameters



### 3. Restraints on distances and angles



.1st:  $U_{iso} = 0.0463$ 

109.6 113.7

109.9 109.8

112.3 110.2

107.6 111.9

C20

105.0

S1

C19

S1

106.8

104.4 112.6 109.0

C20

108.7 111.3 110.3

C21

108.9 110.7 107.1

C22

108.7 112.3 111.0 C21

H19A

H20A

H21A

H22A

## 4. Constraints / Riding model

Hydrogen atoms are included as rigid groups

 $\Rightarrow$  no new parameters

**AFIX mn**: m = type of rigid group; n = treatment during refinement (see SHELXL manual)

- - 14 : X-OH (angle dièdre optimisé)
  - 15 : X<sub>4/5</sub>**BH**
  - 16 : X≡**CH**

- n = 3 : the parameters of the hydrogen atoms are derived from the parameters of the central atom and not refined.
  - 4 : same as n=3, but the C-H distance is refined.
  - 7 : Only for  $CH_3$ : same as n=3, but with rotation around Y-CH<sub>3</sub>.
  - 8 : same as n=7, but the C-H distance is also refined.

We normally use: AFIX 33, AFIX 23, AFIX 13, AFIX 43, AFIX 137, AFIX 127

## 4. Constraints / Riding model

Instead of "picking" H atoms, the command AFIX is introduced:

- manually
- using HADD in XP
- using HFIX in the .ins-file

## There are no new parameters included!

 HFIX (or		19 C20 C21 C 23 C19>C22	22 or HFIX 23	C22 <c19)< th=""></c19)<>
S1	5	0.277756	0.724342	0.718753
C19	1	0.416258	0.872768	0.732035
C20	1	0.464406	0.834804	0.604059
C21	1	0.333324	0.739317	0.500426
C22	1	0.264745	0.631186	0.545540

#### \*.res:

• • •						
C19	1 0.416148	0.872772	0.732124	11.00000	0.05241	0.02307 =
	0.03436	0.01261 0	.01026 0.0	0819 <b>1</b> idon	tique	
AFIX	23				lique	
H19A	2 0.375974	0.953289	0.750305	11.00000	-1.20000	
H19B	2 0.498548	0.894564	0.802368	11.00000	-1.20000	← = 1.2 * U <sub>iso</sub> (C19)
AFIX	0					
C20	1 0.46441	0.834821	0.604090	11.00000	0.04754	0.03455 =
	0.03890	0.01871 0	.01419 0.0	1115		
AFIX	23					
H20A	2 <b>0.54313</b>	0.788600	0.603916	11.00000	-1.20000	
H20B	2 <b>0.49919</b> 8	0.917434	0.588814	11.00000	-1.20000	
AFIX	0					
• • •						
		$= \mathbf{x(C20)} + \Delta \mathbf{x} \ (\mathbf{z})$	Ax does not cha	ange)		

## 4. Constraints / Riding model

XP: BANG C19 to C22

C19 C19 C19 C19	S1 <b>H19A H19B</b> C20	1.828 0.980 0.980 1.515	<b>110.3</b> <b>110.3</b> 107.1 S1	110.3	<b>110.3</b> H19B
C20 C20 C20 C20 C20	C19 <b>H20A</b> <b>H20B</b> C21	1.515 0.980 0.980 1.515	<b>110.4</b> <b>110.4</b> 106.8 C19	<b>108.6</b> <b>110.4</b> H20A	<b>110.4</b> H20B

C21	C20	1.515			
C21	H21A	0.980	110.2		
C21	H21B	0.980	110.2	108.5	
C21	C22	1.521	107.6	110.2	110.2
			C20	H21A	H21B

C22	S1	1.826			
C22	C21	1.521	105.0		
C22	H22A	0.980	110.8	110.8	
C22	Н22В	0.980	110.8	110.8	108.8
			S1	C21	H22A

## Comparison

	Free refinement	fixed U <sub>iso</sub>	restraints (SADI)	riding model
wR <sub>2</sub>	12.91%	12.96%	13.01%	13.14%
Residual e <sup>-</sup> dens.	0.29 e⁻/ų	0.29 e⁻/ų	0.29 e⁻/ų	0.29 e⁻/ų
C-H distances	0.95-1.02	0.94-1.02	0.95-0.99	0.98
X-C-H angles	100-115	100-115	104-114	110-111
Parameters added	32	25	25 + 28 data	0

## Which method to choose ?

### My personal view: (and obligatory for this class)

C-H distances and angles do not show much variations.

- For high quality data, there is not much difference between free refinement and the riding model with calculated hydrogen atoms.
- For low quality data, agreement factors are often better with free or semi-free refinement. But in most cases, this is only due to the additional parameters introduced in the refinement, not due to a better description of the hydrogen atoms and hydrogen positions do not agree with reality.
- $\Rightarrow$  Use the riding model for all CH and CH<sub>2</sub> groups (AFIX 13, AFIX 43, AFIX 23).
- ⇒ Use the riding model with rotation (AFIX 137) for all methyl groups. Particularly important for methyl groups connected to planar moieties.





## Which method to choose ?

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- $\Rightarrow$  Use the riding model for all CH and CH<sub>2</sub> groups (AFIX 13, AFIX 43, AFIX 23).
- ⇒ Use the riding model with rotation (AFIX 137) for all methyl groups. Particularly important for methyl groups connected to planar moieties.
- ⇒ If you observed electron densities between hydrogen atoms refined with AFIX 137, you have to use the rigid group for a disordered methyl group, AFIX 127.
- ⇒ For "special hydrogen atoms" (metal bound hydrides and all other hydrogen atoms not described above), use the semi-free refinement using appropriate restraints (SADI). If needed, constrain  $U_{iso}$  to be equal using free variables.

## **Example: A dimeric zirconium hydride**



## **Example: A dimeric zirconium hydride**



## **Example: A dimeric zirconium hydride**


We do not have a rigid group for Si<sub>2</sub>NH. We thus have to assign this hydrogen atom from the difference Fourier map (Q peaks) and refine using appropriate restraints.

XP: PICK Q9

\*.lst:

AFIX m =

d(X-H) =

.ins: DFIX 0.91 N1 H1A N2 H2A

2

0.99

1

1.00



C12

C11

Si1

N1

Si1A

C11A

C1A

H1A

C12A

#1: XP: PICK Q9

DFIX 0.91 N1 H1A N2 H2A

H1A 2 0.13770 0.25000 0.61040 10.5000 0.05

Due to the mirror plane, the Si1-N1-H1A and the Si1A-N1A-H1A angle are always identical. Thus here, we do not need to worry about the Si-N-H angles.







## **Back to our example**



## After anisotropic refinement:

Les pics restants peut être attribués aux:

#### Thermal motion of atoms

Hydrogen atoms

Errors

The 8 highest Qpeaks (Q1-Q8) correspond to hydrogen atoms!

## **Back to our original example**



After anisotropic refinement:

The remaining peaks can be attributed to:

 Thermal motion of atoms

Hydrogen atoms

• Errors

The remaining electron density  $(Q1 = 0.29 e^{-}/Å^{3})$ can be neglected.

Look at the position of the errors. Are they arbitrary?

## **Refinement organigram**



## **Refining the weighing scheme**

ist: Fc/Fc(max) 0.000	0.012	0.023	0.034	0.047	0.061	0.079	0.101	0.135	0.201	1.000
Number in group	463	423	422	475	397	439	438	433	430	439
GooF	1.406	1.493	1.414	1.317	1.076	1.029	0.813	0.734	0.633	0.453
К	1.690	1.053	1.022	1.020	1.008	1.011	1.012	0.997	1.002	0.990

Refine the weighing scheme so that the GooF is independent from the intensity.

$$w = 1/\sigma^{2}(F_{o}^{2}) + (aP)^{2} + bP \qquad P = \frac{1}{3}(F_{o}^{2} + 2F_{c}^{2})$$



## **Refinement organigram**



Prepare for publication

\*.ins:

SFAC C H N F P UNIT 56 60 16 24 4

#### Make sure that the sum formula is correct

\*.lst:

\*\* Cell contents from UNIT instruction and atom list do not agree \*\*

nrea

Unit-cell contents from UNIT instruction and atom list resp.

C 224.00 240.00 H 240.00 272.00

#### Prepare for publication

\*.ins:

SFAC C H N F P UNIT 56 60 16 24 4

L.S. 40

- Make sure that the sum formula is correct
- Let the structure converge completely

.lst:

Least-squares cycle 4 wR2 = 0.2372 before cycle 4 for 9920 data and 879 / 879 parameters GooF = S = 0.981; Restrained GooF = 0.983 for 174 restraints Weight = 1 / [ sigma^2(Fo^2) + ( 0.1609 \* P)^2 + 81.13 \* P ] where P = ( Max ( Fo^2, 0 ) + 2 \* Fc^2 ) / 3

Ν	value	esd shift	t/esd pa	rameter
1	0.29295	0.00082	0.017	OSF
2	0.51134	9.99999	0.000	FVAR 2
790	2.00000	0.49066	1.861	U22 F55A
791	0.49170	0.11402	1.331	U33 F55A
792	1.04633	0.21776	1.874	U23 F55A

Mean shift/esd = 0.042 Maximum = 1.874 for U23 F55A Max. shift = 0.011 A for F55A Max. dU = 0.205 for F55A

The max. shift has to be < 0.003 Å

#### Prepare for publication

\*.ins:

SFAC C H N F P UNIT 56 60 16 24 4

L.S. 40

ACTA

- Make sure that the sum formula is correct
- Let the structure converge completely
- Generate .cif and .fcf files

#### ACTA imposes certain conditions

- OMIT >0 is not allowed
- FMAP 2 is enforced
- LIST 4 is enforced
- You can specify a 2θ limit, e.g. ACTA 120
  - If there are missing reflections at high angle  $2\theta$
  - When you encoutered problems with the completeness of the dataset.

#### Prepare for publication

\*.ins:

SFAC C H N F P UNIT 56 60 16 24 4

L.S. 40

ACTA

BOND \$H

- Make sure that the sum formula is correct
- Let the structure converge completely
- Generate .cif and .fcf files
- Generate bond distances and angles tables

Use always BOND \$H instead of BOND! A simple BOND does not include hydrogen atoms, which causes problems when if you want to publish the structure.

#### Prepare for publication

\*.ins: ... SFAC C H N F P UNIT 56 60 16 24 4

L.S. 40

ACTA

BOND \$H

CONF

- Make sure that the sum formula is correct
- Let the structure converge completely
- Generate .cif and .fcf files
- Generate bond distances and angles tables
- Generate torsion angles table

If you want to cite a torsion angle with an error (esd), you have to include this command here. You cannot estimate errors from atomic positions later.

#### • Prepare for publication

\*.ins:

SFAC C H N F P UNIT 56 60 16 24 4

L.S. 40

ACTA

BOND \$H

CONF

#### MPLA 6 N1 C1 C2 C3 C4 C5 MPLA 3 C6 C7 C8

- Make sure that the sum formula is correct
- Let the structure converge completely
- Generate .cif and .fcf files
- Generate bond distances and angles tables
- Generate torsion angles table
- Calculate angles between planes

Again, you can obtain angles with an error (esd) only for planes refined during the refinement in the \*.ins file!

#### Prepare for publication

*.ins:		
SFAC C UNIT 56		
L.S. 40		

ACTA

BOND \$H

CONF

MPLA 6 N1 C1 C2 C3 C4 C5 MPLA 3 C6 C7 C8

- Make sure that the sum formula is correct
- Let the structure converge completely
- Generate .cif and .fcf files
- Generate bond distances and angles tables
- Generate torsion angles table
- Calculate angles between planes
- Define and calculate hydrogen bonding distances and angles

Same, same: only hydrogen distances defined by HTAB in the \*.ins file can be obtained with an error (esd).

Since hydrogen bonding is often intermolecular, you might have to find and define the correct symmetry operation.

#### • Prepare for publication

*.ins:	
 SFAC C H N UNIT 56 60 16	
L.S. 40	
ACTA	
BOND \$H	

CONF

MPLA 6 N1 C1 C2 C3 C4 C5 MPLA 3 C6 C7 C8

EQIV \$1 –x, -y, -z HTAB N1 C8\_\$1

WPDB -1

- Make sure that the sum formula is correct
- Let the structure converge completely
- Generate .cif and .fcf files
- Generate bond distances and angles tables
- Generate torsion angles table
- Calculate angles between planes
- Define and calculate hydrogen bonding distances and angles
- Generate a pdb-file with your atomic positions

This is completely facultative and not really necessary.

#### Prepare for publication

*.ins:	
 SFAC C H N UNIT 56 60 16	-
L.S. 40	
ACTA	
BOND \$H	

CONF

MPLA 6 N1 C1 C2 C3 C4 C5 MPLA 3 C6 C7 C8

EQIV \$1 -- x, -y, -z HTAB N1 C8\_\$1

WPDB -1

SIZE .15 .15 .2

- Make sure that the sum formula is correct
- Let the structure converge completely
- Generate .cif and .fcf files
- Generate bond distances and angles tables
- Generate torsion angles table
- Calculate angles between planes
- Define and calculate hydrogen bonding distances and angles
- Generate a pdb-file with your atomic positions
- Add you crystal dimensions to the CIF file.

Attention <SHELX2014: If you use SIZE, it enforces the calculation of theoretical values for the absorption  $(T_{min}, T_{max})$ , which appear in the CIF file. Those have to be replaced by the real values or deleted if no absorption correction was performed.

#### Prepare for publication

*.ins:
 SFAC C H N F P UNIT 56 60 16 24 4
L.S. 40
ACTA
BOND \$H
CONF
MPLA 6 N1 C1 C2 C3 C4 C5 MPLA 3 C6 C7 C8
EQIV \$1 –x, -y, -z HTAB N1 C8_\$1
WPDB -1

SIZE .15 .15 .2

#### **TEMP -123**

. . .

- Make sure that the sum formula is correct
- Let the structure converge completely
- Generate .cif and .fcf files
- Generate bond distances and angles tables
- Generate torsion angles table
- Calculate angles between planes
- Define and calculate hydrogen bonding distances and angles
- Generate a pdb-file with your atomic positions
- Add you crystal dimensions to the CIF file.

77631

• Include the temperature in the CIF file.

# End of Refinement

# Next thing to do: How to make sure that we did everything correctly?