

DAjust

with
AJUST & SGAid

Jordi Rius, Oriol Vallcorba, Inma Peral, Carlos Frontera, Carles Miravittles



DAjust software

Pattern matching, space group determination and
intensity extraction from powder diffraction data

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CELLS - ALBA
Synchrotron Light Facility



The screenshot shows the DAjust software interface. On the left, the text 'DAjust' is displayed in a large, stylized font, with 'with AJUST & SGAid' below it. To the right, a powder diffraction pattern is shown with several sharp peaks. Text to the right of the pattern lists capabilities: 'Powder Diffraction', 'whole-pattern matching', 'space group determination', and 'intensity extraction'. At the bottom left, it says 'v. 1209'. Below the pattern, it lists the 'Principal author' as 'Jordi Rius' and 'Collaborators' as 'Oriol Vallcorba, Inma Peral, Carlos Frontera, Carles Miravittles'. At the bottom right, it says '© J.Rius 2011' and 'Institut de Ciència de Materials de Barcelona (CSIC)'. A '(click to continue)' prompt is at the bottom left.

DAjust
with AJUST & SGAid

v. 1209

Principal author *Jordi Rius*
Collaborators *Oriol Vallcorba, Inma Peral, Carlos Frontera, Carles Miravittles*

(click to continue)

Powder Diffraction
whole-pattern matching
space group determination
intensity extraction

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AJUST: whole-pattern matching

Cell parameters refinement
Profile fitting
Intensity extraction

SGAID: ranked list of most probable space groups

Iterative intensity refinement

Based on Le Bail *et al.* (1988) method

$$M = \sum_i w_i \left[y_{\text{obs},i} - \left(y_{\text{bkg},i} + \sum_k j_k I_k \Omega_{k,i} \right) \right]^2$$

$$I_{k,\text{new}} = I_{k,\text{old}} + c_k \sum_i w_i \Omega_{k,i} (y_{\text{obs},i} - y_{\text{calc},i})$$

$$y_{\text{calc},i} = y_{\text{bkg},i} + \sum_k j_k I_k \Omega_{k,i}$$

$$c_k = \frac{1}{\sum_i w_i \Omega_{k,i}^2}$$

Profile parameters

pseudo-Voigt (TCH, 1987)

Pearson-VII

Criterion of fit

$$\chi = R_{\text{wp}}/R_{\text{exp}}$$

$$R_{\text{wp}} = \left[\frac{\sum_i w_i (y_{\text{obs},i} - y_{\text{calc},i})^2}{\sum_i w_i (y_{\text{obs},i} - y_{\text{bkg},i})^2} \right]^{1/2}$$

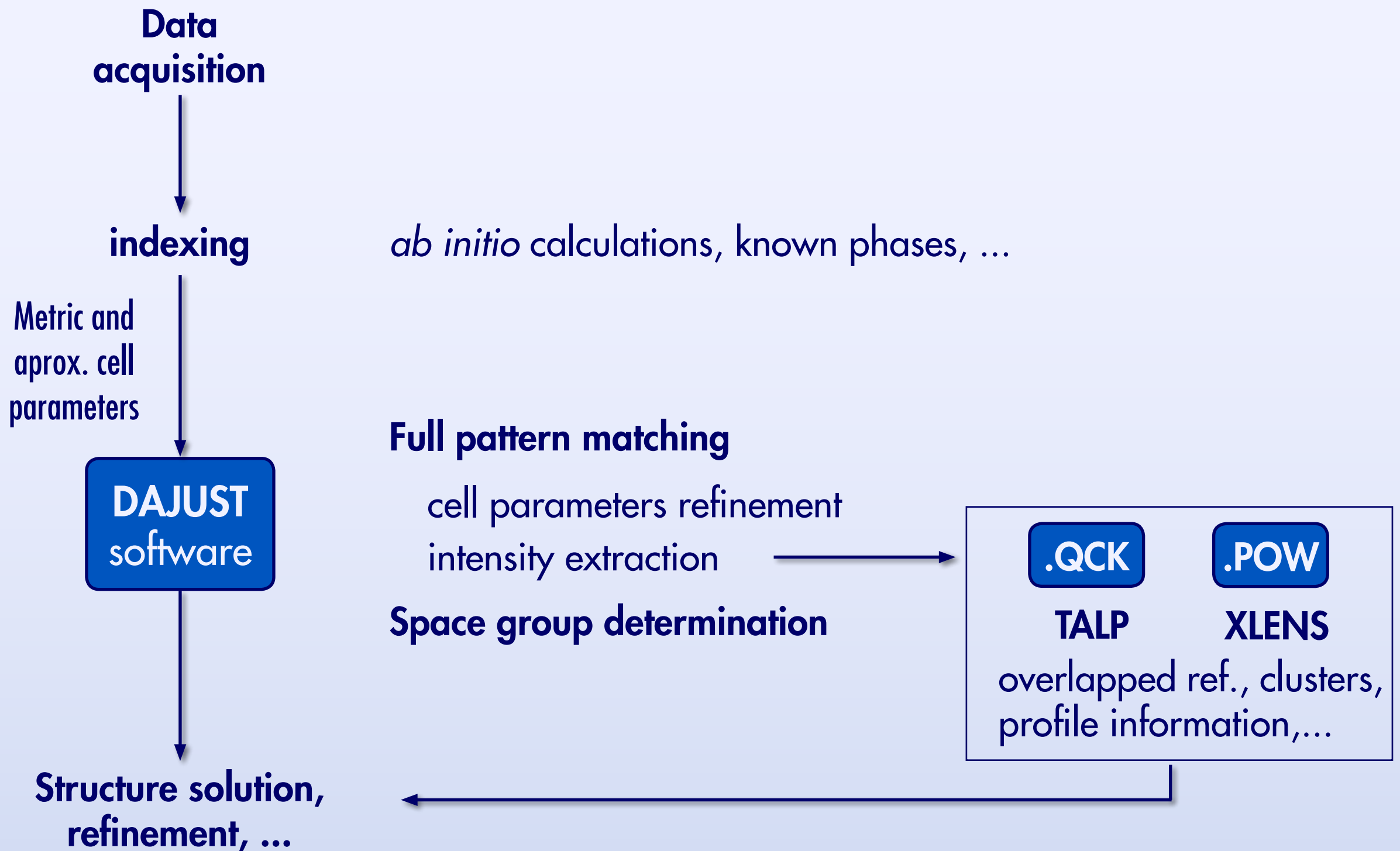
$$R_{\text{exp}} = \left[\frac{N - P}{\sum_i w_i (y_{\text{obs},i} - y_{\text{bkg},i})^2} \right]^{1/2}$$

$$w_i = \frac{1}{\sum_i (y_{\text{obs},i} - y_{\text{bkg},i})}$$

Options

Automated background, asymmetry correction, absorption, variable divergence,...

Overall procedure

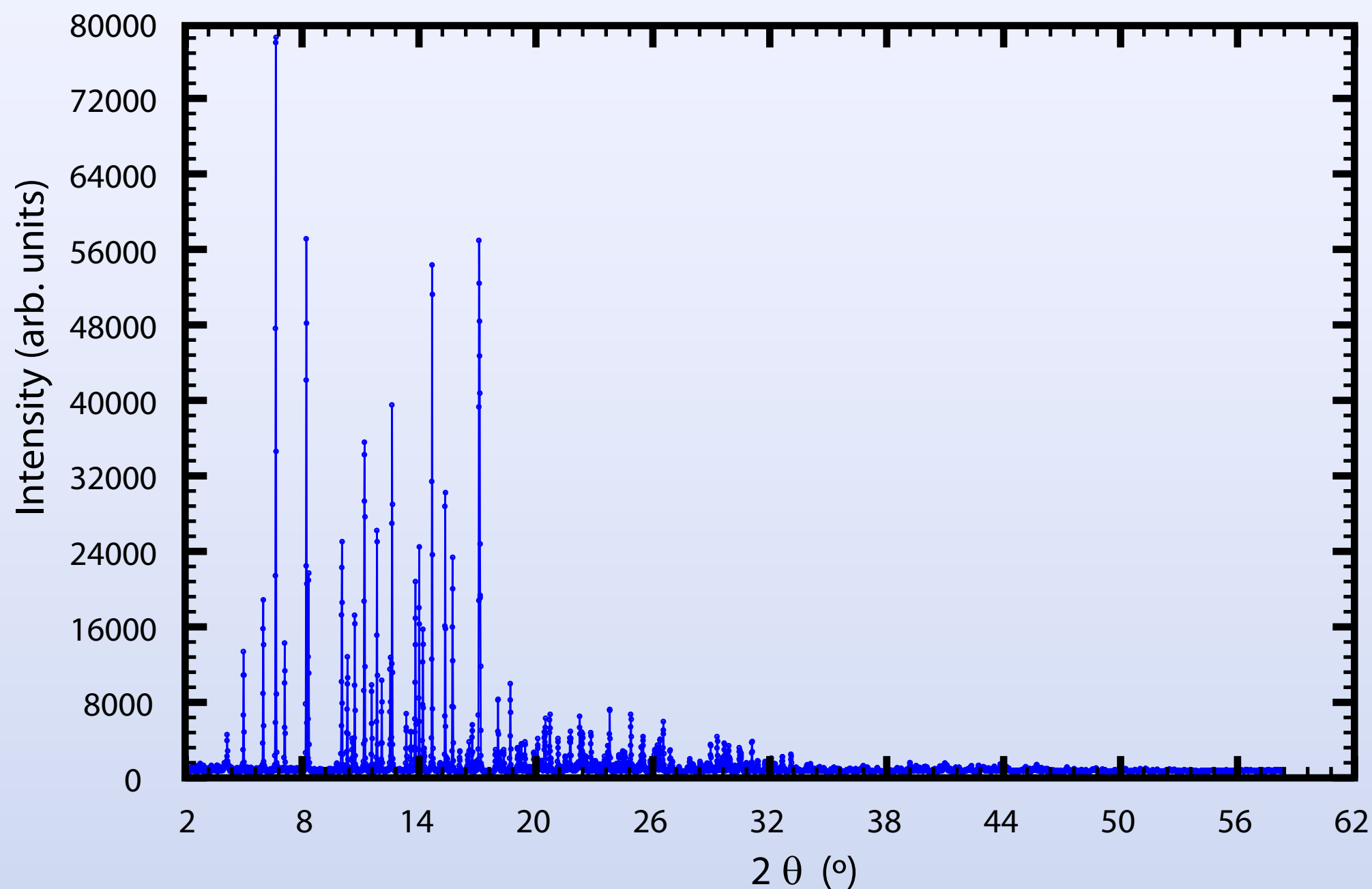
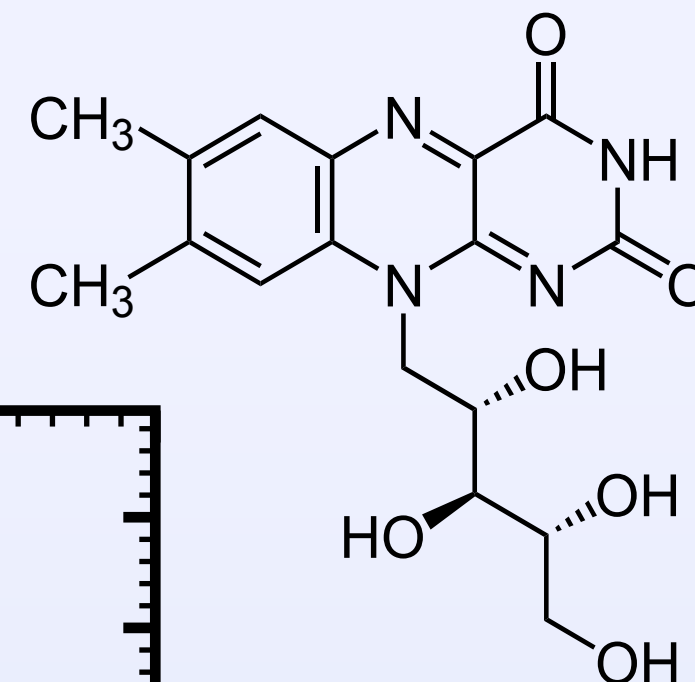


DAjust/SGAid example

Powder diffraction data from MYTHEN II detector
organic compound

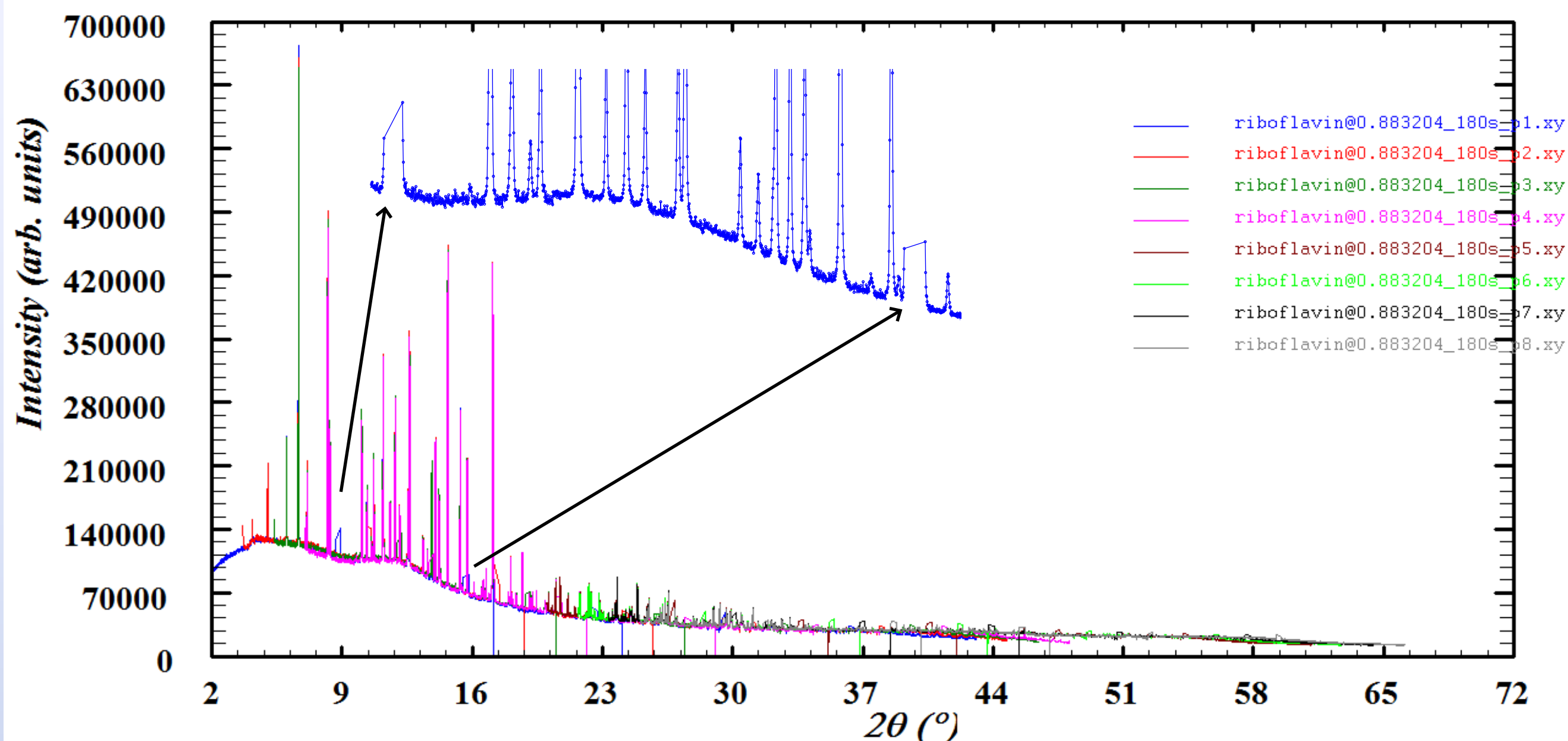
Powder data of (–)-Riboflavin

- Capillary Synchrotron data (MYTHEN II)
- $\lambda = 0.88320 \text{ \AA}$
- $\text{C}_{17}\text{H}_{20}\text{N}_4\text{O}_6$



Powder data of (–)-Riboflavin - Data preparation

- MERGE and BACKGROUND subtraction
- Manual/automatic (programs)



Powder data of (–)-Riboflavin - Data preparation

- **DMerge** COMBINATION OF POWDER PATTERNS FOR LINEAR MULTISTRIP DETECTORS

Merge control: param.txt

```
! === MYTHENII PARAMETERS ===
```

```
! DETECTOR SETTINGS:
```

```
! Sample-Detector distance (mm)
```

```
552.464
```

```
! Number of modules, channels/module and channel size (mm)
```

```
5 1280 0.05
```

```
! EXCLUDED ZONES AND EXPERIMENTAL DATA:
```

```
! 2T min
```

```
2.00353
```

```
! EXCLUDED ZONES
```

```
2.06
```

```
8.56 8.95
```

```
14.47 15.85
```

```
22.40 22.76
```

```
29.31 29.64
```

```
36.16
```

```
! DEAD PIXELS (module pixel)
```

```
0
```

```
! Wavelength (Å)
```

```
0.88320395
```

```
! OUTPUT PARAMETERS
```

```
! step size (°)
```

```
0.010
```

```
! t2ini t2fin
```

```
2.0 58.33
```

- **DMerge file1.xy file2.xy ... fileN.xy**

- **Output: file1-merged.xy**

- e.g. DICVOL

(...)

THE SOLUTION IS NOW USED TO TRY TO INDEX ALL INPUT 56 LINES :

=====

DIRECT PARAMETERS : A= 20.17036 B= 15.17811 C= 5.35121 VOLUME= 1638.26

STANDARD DEVIATIONS : .00034 .00029 .00010

REFINED ZERO-POINT SHIFT : 0.0181 deg. 2-theta

H	K	L	DOBS	DCAL	DOBS-DCAL	2TH.OBS	2TH.CAL	DIF.2TH.
1	1	0	12.17640	12.18077	-0.00438	4.157	4.155	0.001
2	0	0	10.12641	10.12167	0.00473	4.999	5.001	-0.002
2	1	0	8.42660	8.42523	0.00137	6.008	6.009	-0.001
0	2	0	7.61019	7.60968	0.00051	6.653	6.654	0.000

(...)

* NUMBER OF LINES

.- LINES INPUT = 56

.- LINES INDEXED = 56

.- LINES CALCULATED = 224

* AVERAGE 2-Theta DIFFERENCE FOR INDEXED LINES = -0.0007

* MEAN ABSOLUTE DISCREPANCIES

<Q> = 0.2522E-04

<DELTA(2-THETA)> = 0.1880E-02

MAX. ERROR ACCEPTED (DEG. 2-THETA) = 0.4500E-01

* FIGURES OF MERIT

1.- M(20) = 82.2

2.- F(20) = 345.4(0.0016, 36)

3.- F(56) = 133.0(0.0019, 224)

DAjust requires the previous indexing of the pattern to obtain the approximate cell parameters:

a 20.17 Å α 90°
b 15.18 Å β 90°
c 5.35 Å γ 90°
V 1638 Å³

Orthorhombic

Z=4 Z'=1

DAjust_UI_v1209

File Options Help

General

Name

Formula

Z

Cycles

Cell parameters

a α 90.000
b β 90.000
c γ 90.000
Metric cubic
☐ Fix cell param.
☐ Use existing LAT file

Symmetry

SG.Num:Symbol : set Lattice P
☐ Centrosimetric
☐ No centrosimetric
Highest symmetry
Symmetry matrices unlock

Instrumental & Data parameters

Pattern type 2 (2T Yobs)
Rad. source Synchrotron
Intensity Extraction
Sample ☐ Flat ☒ Capillary
Primary monochromator
☐ Yes ☒ No
Divergence correction
☐ Yes ☒ No
Absorption correction
☐ Yes ☒ No

nYline 1
 λ 1
NFWHM 20
tolerance 0.5
cos 2 θ 1.000
Fixed slit
Variable slit
slit-w ($^\circ$) 0.000
sample size 0.000
armlenght 0.000
2 θ sup 65.000
 λ 2
2 θ inf
2 θ sup
2Tinf
2Tsup
2 θ RefInt 0.000
Transmi. 0.000

Profile Function

Type Pseudo-Voigt T...
Lorentzian coef. X 0.001
Gaussian coef. W 0.000
Pref. Orientation: March-coef 1.000
direction (h k l) 0 0 1

zero 0.001
exp 1.000
Y 0.001
V 0.000
U 0.000

Excluded zones

2 θ inf Add
2 θ sup Del.
2Tinf
2Tsup

Background

type Calcula...
<back> 60.000
FWHM 0.150
Iterations 20
2 θ
bg-value
2T
bg-value

Asymmetry correction

coef. Add
2 θ sup Del.
coef
2Tsup

Ghost peaks

value 2 θ width
 η asym
value 2T width nu asym

Run AJUST Stop run open PRF Output window

Run SGAid Update fields SGAid window

Work file: no file
Data file: no file

DAjust UI - Cell parameters and symmetry

- (-)-Riboflavin
- $C_{17}H_{20}N_4O_6$

General

Name

Formula

Z

Cycles

a 20.17 Å α 90°
b 15.18 Å β 90°
c 5.35 Å γ 90°

Cell parameters

a α Metric

b β ☐ Fix cell param.

c γ ☐ Use existing LAT file

Orthorhombic

V 1650 Å³

Z=4 Z'=1

Symmetry

SG.Num:Symbol : Lattice

☒ Centrosimetric Symmetry matrices

☐ No centrosimetric

PXRD data format

The .DAT (or .NET) file has the following structure:

- LINE 1: Title line beginning with !
- LINE 2: 2 θ min(deg.) step(deg.) 2 θ max(deg.)
- NEXT LINES (free format): Intensity data. Three different options are supported. The choice is indicated in DAjust_UI (Pattern type option):
 1. Only intensity data. Yobs Yobs2 Yobs3 ...
The number of Yobs values per line must be specified in the nYline field of DAjust_UI.
 2. 2 θ Yobs
 3. 2 θ Yobs sigma(Yobs)

```
! Riboflavin ALBA-MYTHENII
2.060000      0.010000      58.320000
10           0          295          26           0          14          91           0          263          68
196          110         27          145         154         200         20          314         361         151
244           96           0          269         340         147         444         307         273         150
...
```

Pattern type = 1

(NYLINE=10)

2 θ_{sup} = 55°

Synchrotron (λ =0.88320Å)

Instrumental & Data parameters

Pattern type	<input type="text" value="1 (Yobs)"/>	nYline	<input type="text" value="10"/>	2 θ sup	<input type="text" value="55"/>
Rad. source	<input type="text" value="Synchrotron"/>	λ 1	<input type="text" value="0.88320"/>	λ 2	<input type="text" value=""/>
Intensity Extraction		NFWHM	<input type="text" value="20"/>	tolerance	<input type="text" value="0.5"/>
Sample	<input type="radio"/> Flat <input checked="" type="radio"/> Capillary				
Primary monochromator	<input type="radio"/> Yes <input checked="" type="radio"/> No $\cos 2\theta$ <input type="text" value="1.000"/>				
Divergence correction	<input type="radio"/> Yes <input checked="" type="radio"/> No <input type="radio"/> Fixed slit <input type="radio"/> Variable slit				
	slit-w (°)	<input type="text" value="0.000"/>	sample size	<input type="text" value="0.000"/>	armlenght <input type="text" value="0.000"/>
Absorption correction	<input type="radio"/> Yes <input checked="" type="radio"/> No				
	R*mu	<input type="text" value="0.000"/>	2 θ RefInt	<input type="text" value="0.000"/>	Transmi. <input type="text" value="0.000"/>

Profile Function

Pseudo-Voigt (TCH)

- Zero
- Lorentzian coef. X,Y

Background

Removed (.NET)

Excluded Zones

Asymmetry correction

Profile Function									
Type	Pseudo-Voigt T...		zero	0.001	<input checked="" type="checkbox"/>	exp	1.000	<input type="checkbox"/>	
Lorentzian coef.			X	0.001	<input checked="" type="checkbox"/>	Y	0.001	<input checked="" type="checkbox"/>	
Gaussian coef.			W	0.000	<input type="checkbox"/>	V	0.000	<input type="checkbox"/>	U 0.000 <input type="checkbox"/>
Pref. Orientation:		March-coef		1.000		direction (h k l)		0 0 1	

Excluded zones				Background					
2 θ inf	<input type="text"/>	Add		type	Removed	2 θ	<input type="text"/>	+	-
2 θ sup	<input type="text"/>	Del.		<back>	60.000	bg-value	<input type="text"/>	File	
2Tinf	<input type="text"/>	2Tsup	<input type="text"/>	FWHM	0.150	2T	<input type="text"/>	bg-value	<input type="text"/>
				Iterations	20				

Asymmetry correction				Ghost peaks					
coef.	<input type="text"/>	Add		value	<input type="text"/>	2 θ	<input type="text"/>	width	<input type="text"/>
2 θ sup	<input type="text"/>	Del.		η	<input type="text"/>	asym	<input type="text"/>	+	-
coef	<input type="text"/>	2Tsup	<input type="text"/>	value	<input type="text"/>	2T	<input type="text"/>	width	<input type="text"/>
				nu	<input type="text"/>	asym	<input type="text"/>		

DAjust UI - Save JST and run DAjust

DAjust_UI_v1209

File Options Help

General
Name: (-)-Riboflavin
Formula: C17 H20 N4 O6
Z: 4
Cycles: 20

Cell parameters
a: 20.20 α : 90.000
b: 15.21 β : 90.000
c: 5.37 γ : 90.000
Metric: orthorombic
☐ Fix cell param.
☐ Use existing LAT file

Symmetry
SG.Num:Symbol: P m m m set Lattice: P
☒ Centrosimetric
☐ No centrosimetric
Symmetry matrices: -X, -Y, Z
X, -Y, -Z
-X, Y, -Z
Highest symmetry

Instrumental & Data parameters
Pattern type: 1 (Yobs)
Rad. source: Synchrotron
Intensity Extraction: NFWHM: 20 tolerance: 0.5
Sample: ☐ Flat ☒ Capillary
Primary monochromator: ☐ Yes ☒ No cos 2 θ : 1.000
Divergence correction: ☐ Yes ☒ No ☐ Fixed slit ☐ Variable slit
slit-w ($^\circ$): 0.000 sample size: 0.000 armlenght: 0.000
Absorption correction: ☐ Yes ☒ No
R*mu: 0.000 2 θ RefInt: 0.000 Transmi.: 0.000

Profile Function
Type: Pseudo-Voigt T... zero: 0.001 ☒ exp: 1.000 ☐
Lorentzian coef. X: 0.001 ☒ Y: 0.001 ☒
Gaussian coef. W: 0.000 ☐ V: 0.000 ☐ U: 0.000 ☐
Pref. Orientation: March-coef: 1.000 direction (h k l): 0 0 1

Excluded zones
2 θ inf: Add
2 θ sup: Del.

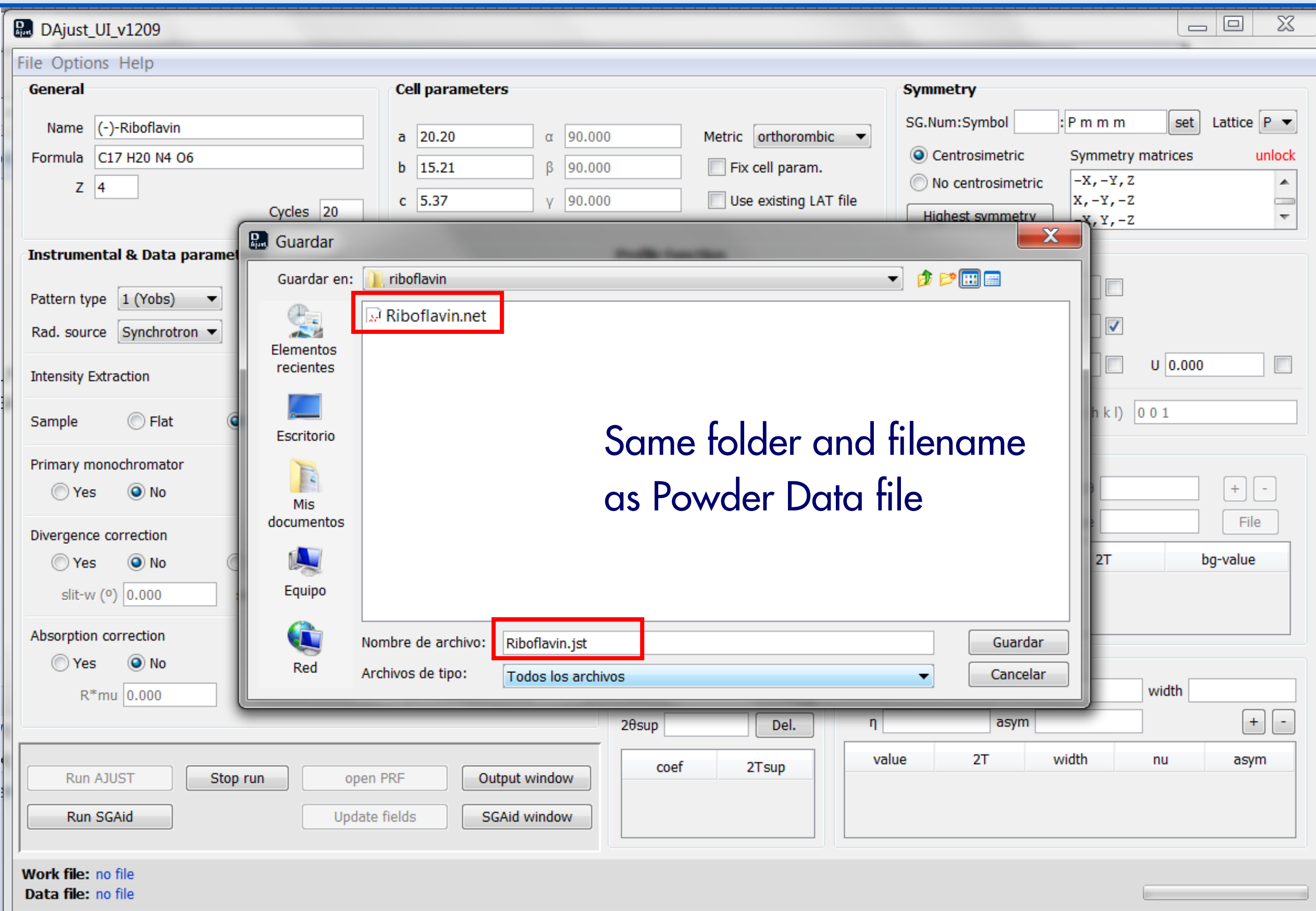
Background
type: Removed 2 θ : + -
<back> 60.000 bg-value: File

Buttons
Run AJUST Stop run open PRF Output window
Run SGAid Update fields SGAid window

Work file: no file
Data file: no file

DAjust_UI Output
Font Size: + - on top
DAjust Software - version 1209
Report of errors to the authors will be appreciated.
[08:58] bin directory: C:\ovallcorba\UIs\WEB dajust-xlens\DAjust_1209\bin\

DAjust UI - Save JST and run DAjust



Same folder and filename
as Powder Data file

DAjust UI - Check DAjust result

```

DAjust_UI Output
Font Size: + - on top
[10:49] file saved: O:\ovallcorba\riboflavin\dajust\riboflavin.jst
[10:49] PDD file found: O:\ovallcorba\riboflavin\dajust\riboflavin.net

[10:49] *****
[10:49] ***** AJUST OUTPUT: *****
[10:49] *****
[10:49] 2.060000 9.9999998E-03 58.32000
[10:49] 2.060000 9.9999998E-03 55.00000
[10:49] NUM.REFLEXS < T2MAX= 1205
[10:49] 0 0.4275E+01 0.1497E+01 0.1322E+01 0.1214E+03
[10:49] 1 0.1018E+01 0.8890E+00 0.1007E+01 0.2889E+02
[10:49] 2 0.1567E+01 0.9504E+00 0.9611E+00 0.4448E+02
[10:49] 3 0.1799E+01 0.1022E+01 0.1229E+01 0.5108E+02
[10:49] 4 0.1463E+01 0.9440E+00 0.1056E+01 0.4154E+02
[10:49] 5 0.8848E+00 0.7936E+00 0.9234E+00 0.2512E+02
[10:49] 6 0.1069E+01 0.8336E+00 0.1011E+01 0.3036E+02
[10:49] 7 0.8727E+00 0.7605E+00 0.9015E+00 0.2478E+02
[10:49] 8 0.8086E+00 0.7308E+00 0.9036E+00 0.2296E+02
[10:49] 9 0.7899E+00 0.6941E+00 0.8543E+00 0.2242E+02
[10:49] 10 0.7255E+00 0.6464E+00 0.8064E+00 0.2060E+02
[10:49] 11 0.6781E+00 0.5973E+00 0.7567E+00 0.1925E+02
[10:49] 12 0.6381E+00 0.5530E+00 0.6970E+00 0.1811E+02
[10:49] 13 0.6046E+00 0.5187E+00 0.6302E+00 0.1716E+02
[10:49] 14 0.5671E+00 0.4780E+00 0.5612E+00 0.1610E+02
[10:49] 15 0.5295E+00 0.4349E+00 0.4851E+00 0.1503E+02
[10:49] 16 0.4950E+00 0.3951E+00 0.4170E+00 0.1405E+02
[10:49] 17 0.4599E+00 0.3593E+00 0.3697E+00 0.1306E+02
[10:49] 18 0.4261E+00 0.3228E+00 0.3134E+00 0.1210E+02
[10:49] 19 0.3931E+00 0.2914E+00 0.2677E+00 0.1116E+02
[10:49] 20 0.3716E+00 0.2674E+00 0.2259E+00 0.1055E+02
[10:49]
[10:49] ZERO-SHIFT:
[10:49] -0.01587 0.00021
[10:49] FINAL LATTICE PARAMETERS:
[10:49] 20.16345 15.17621 5.35084 90.0000 90.0000 90.0000
[10:49]
[10:49] Volume= 1637.383
[10:49]
[10:49] ST. DEVS. OF LATTICE PARAMETERS:
[10:49] 1 0.00046
[10:49] 2 0.00031
[10:49] 3 0.00010
[10:49] PEAK WIDTH PARAMETERS:
[10:49] 0.540E-01 0.328E-02 -0.339E-03
[10:49] 0.111E-01 0.411E-03 -0.671E-03
[10:49] SCALA FACTOR:
[10:49] 0.1009E+01 0.6427E-02 0.9414E-02
[10:49] -----
[10:49] Cycle Rwp Rp RB Chi(planes) Chi(dist) Chi(I)
[10:49] 20 0.3716E+00 0.2674E+00 0.2259E+00 0.1055E+02
[10:49]
[10:49] New  $\chi = 10.55$  (no previous run to compare with)
[10:49] Better  $\chi$ , fields updated. To recover old values click on reload JST.
[10:49] file read: O:\ovallcorba\riboflavin\dajust\riboflavin.new
[10:49] dAjust finished
  
```

more cycles
needed

$\chi=10.55$

DAjust_UI_v1209

File Options Help

General
Name: (-)-Riboflavin
Formula: C17 H20 N4 O6
Z: 4
Cycles: 20

Cell parameters
a: 20.16345 α : 90.000
b: 15.17621 β : 90.000
c: 5.35084 γ : 90.000
Metric: orthorhombic
Fix cell param.
Use existing LAT file

Symmetry
SG.Num:Symbol: P m m m set Lattice P
Centrosimetric
No centrosimetric
Highest symmetry
Symmetry matrices: -X, -Y, Z
X, -Y, -Z

Instrumental & Data parameters
Pattern type: 1 (Yobs)
Rad. source: Synchrotron
Intensity Extraction: NFWHM
Sample: Flat Capillary
Primary monochromator: Yes No cos 2 θ : 1.0000
Divergence correction: Yes No Fixed slit Variable slit
Absorption correction: Yes No R μ : 0.0000 2 θ RefInt: 0.0000 Transm.: 0.0000

Profile Function
Type: Pseudo-Voigt T... zero: -0.015873 exp: 1.0000
Lorentzian coef. X: 0.540E-01 Y: 0.111E-01
Gaussian coef. W: 0.000E+00 V: 0.000E+00 U: 0.000E+00
Pref. Orientation: March-coef: 1.000 direction (h k l): 0 0 1

Excluded zones
2 θ inf: 2 θ sup: 2Tinf: 2Tsup

Background
type: Removed
<back>: 60.00000 bg-value: FWHM: 0.15000 Iterations: 20

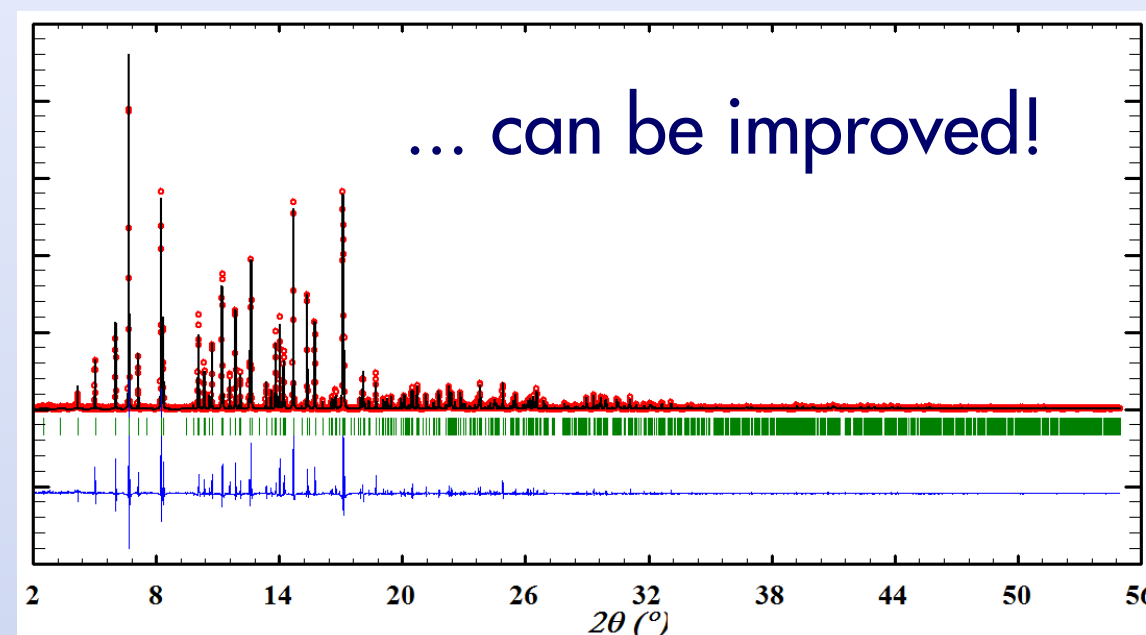
Asymmetry correction
coef: 2 θ sup: 2Tsup

Ghost peaks
value: 2 θ width: η asym

Run AJUST Stop run open PRF Output window
Run SGaid Reload JST SGaid window

Work file: O:\ovallcorba\riboflavin\dajust\riboflavin.jst
Data file: O:\ovallcorba\riboflavin\dajust\riboflavin.net

Fields updated



DAjust UI - Run DAjust (#2)

- 20 extra cycles with new parameters
- 1 Gaussian parameter (W)

DAjust_UI_v1209

File Options Help

General

Name: (-)-Riboflavin
Formula: C17 H20 N4 O6
Z: 4
Cycles: 20

Cell parameters

a: 20.16345 α : 90.000
b: 15.17621 β : 90.000
c: 5.35084 γ : 90.000
Metric: orthorhombic
☐ Fix cell param.
☐ Use existing LAT file

Symmetry

SG.Num:Symbol: P m m m set Lattice: P
☒ Centrosimetric
☐ No centrosimetric
Symmetry matrices: -X, -Y, Z
X, -Y, -Z
Highest symmetry

Profile Function

Type: Pseudo-Voigt T... zero: -0.015873 ☒ exp: 1.0000 ☐
Lorentzian coef. X: 0.540E-01 ☒ Y: 0.111E-01 ☒
Gaussian coef. W: 0.001 ☒ V: 0.000E+00 ☐ U: 0.000E+00 ☐

DAjust_UI Output

Font Size: + - on top

```
[10:55] 16 0.1897E+00 0.1012E+00 0.5403E-01 0.5385E+01
[10:55] 17 0.1896E+00 0.1012E+00 0.5414E-01 0.5382E+01
[10:55] 18 0.1895E+00 0.1012E+00 0.5426E-01 0.5381E+01
[10:55] 19 0.1895E+00 0.1011E+00 0.5434E-01 0.5379E+01
[10:55] 20 0.1894E+00 0.1011E+00 0.5447E-01 0.5379E+01
[10:55] ZERO-SHIFT:
[10:55] -0.01853 0.00011
[10:55] FINAL LATTICE PARAMETERS:
[10:55] 20.17025 15.17809 5.35091 90.0000 90.0000 90.0000
[10:55] Volume= 1638.159
[10:55] ST. DEVS. OF LATTICE PARAMETERS:
[10:55] 1 0.00022
[10:55] 2 0.00016
[10:55] 3 0.00005
[10:55] PEAK WIDTH PARAMETERS:
[10:55] 0.272E-01 0.138E-02 -0.628E-04
[10:55] 0.239E-02 0.179E-03 0.510E-05
[10:55] 0.793E-03 0.809E-05 0.112E-07
[10:55] SCALA FACTOR:
[10:55] 0.9997E+00 0.2850E-02 -0.2533E-03
[10:55] -----
[10:55] Cycle Rwp Rp RB Chi(planes) Chi(dist) Chi(I)
[10:55] 20 0.1894E+00 0.1011E+00 0.5447E-01 0.5379E+01
[10:55] New  $\chi$  = 5.379 (previous  $\chi$  = 10.55)
[10:55] Better  $\chi$  fields updated. To recover old values click on reload JST.
[10:55] file read: O:\ovallcorba\riboflavin\dajust\riboflavin.new
[10:55] dAjust finished
```

$\chi=5.38$

much better!

- Space group determination

The screenshot displays the DAjust UI v1209 interface. The 'Run SGAid' button is highlighted with a red rectangle. A 'Guardar' (Save) dialog box is open, showing the file 'Riboflavin.NEW' selected. A 'Save confirmation' dialog box is also open, asking 'File .NEW will be saved' with 'OK' and 'Cancel' buttons. The background interface includes sections for General, Cell parameters, Symmetry, and Instrumental & Data parameters.

General

Name: (-)-Riboflavin
Formula: C17 H20 N4 O6
Z: 4
Cycles: 20

Cell parameters

a: 20.17025 α : 90.000
b: 15.17809 β : 90.000
c: 5.35091 γ : 90.000
Metric: orthorombic
☐ Fix cell param.
☐ Use existing LAT file

Symmetry

SG.Num:Symbol: P m m m set Lattice P
☒ Centrosimetric
☐ No centrosimetric
Symmetry matrices: -X, -Y, Z; X, -Y, -Z
Highest symmetry

Instrumental & Data parameters

Pattern type: 1 (Yobs) nYline: 10
Rad. source: Synchrotron λ : 0.88320
Intensity Extraction: NFWHM: 20
Sample: ☐ Flat ☒ Capillary
Primary monochromator: ☐ Yes ☒ No $\cos 2\theta$: 1.00000
Divergence correction: ☐ Yes ☒ No slit-w ($^\circ$): 0.00
Absorption correction: ☐ Yes ☒ No R*mu: 0.00

Guardar

Guardar en: riboflavin
Riboflavin.jst
Riboflavin.NEW

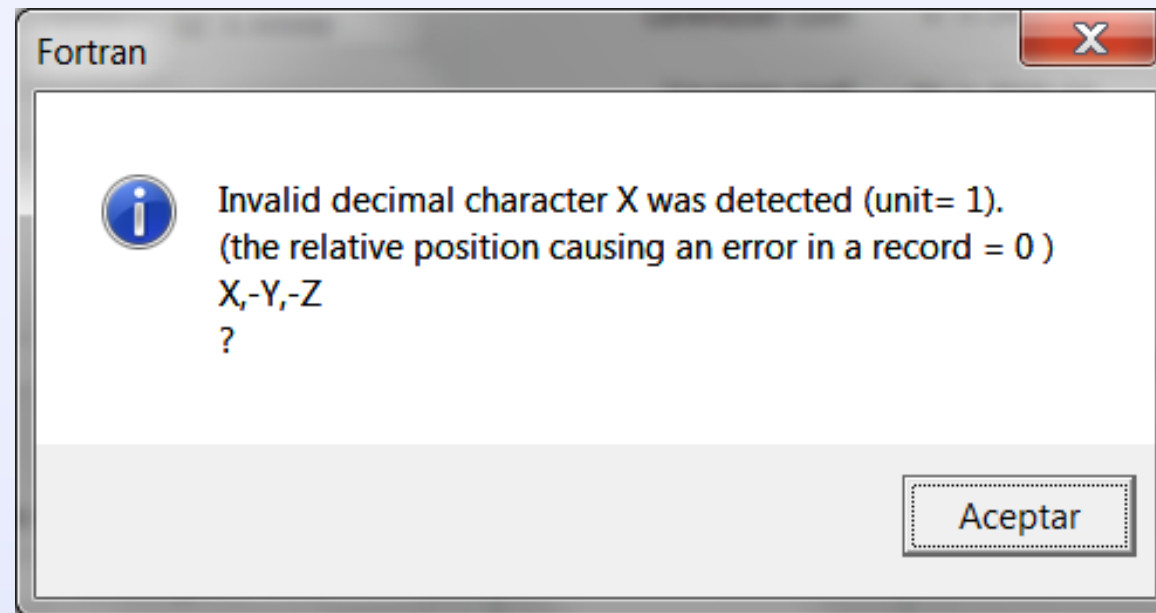
Save confirmation

? File .NEW will be saved
OK Cancel

Run SGAid

Work file: O:\ovallcorba\riboflavin\dajust\riboflavin.jst
Data file: O:\ovallcorba\riboflavin\dajust\riboflavin.net

(Maybe a Fortran error in some systems)



Just wait a moment and click
again **run SGAid!**

SGAid Output

Click on a row to load symmetry matrices for the S.G into main window ☐ on top

SGNum	H-M symbol	RW (%)	NREF	Setti...
25	Pmm2	19,02	1205	abc
47	Pmmm	19,02	1205	abc
16	P222	19,02	1205	abc
17	P222(1)	19,03	1197	acb
18	P2(1)2(1)2	19,05	1194	bca
19	P2(1)2(1)2(1)	19,12	1183	abc
26	Pmc2(1)	19,45	1165	cab
51	Pmma	19,45	1165	bca
28	Pma2	19,45	1165	bac
31	Pmn2(1)	22,05	1165	bac
59	Pmmn	22,05	1165	bca
32	Pba2	22,55	1113	abc
55	Pbam	22,55	1113	abc
62	Pnma	23,73	1112	bca
33	Pna2(1)	23,73	1112	bac
57	Pbcm	25,13	1115	bac
29	Pca2(1)	25,13	1115	abc
58	Pnnm	25,59	1115	abc
34	Pnn2	25,59	1115	abc
53	Pmna	26,15	1117	cba
30	Pnc2	26,15	1117	bac
27	Pcc2	27,60	1121	abc
49	Pccm	27,60	1121	abc
50	Pban	33,57	991	abc

a=20.1702 b=15.178 c=5.3509 α=90.0 β=90.0 γ=90.0

Ranked list of possible Space Groups

- Rw(%) in bold are the most probable
- Lowest NREF

(–)-Riboflavin is P2₁2₁2₁

in this case the three SGs with Rw=19.38 considered as probable are not correct (can be tested clicking and running DAjust)

DAjust UI - Final DAjust run

DAjust_UI_v1209

File Options Help

General
Name: (-)-Riboflavin
Formula: C17 H20 N4 O6
Z: 4
Cycles: 20

Cell parameters
a: 20.1702 α : 90.000
b: 15.178 β : 90.0
c: 5.3509 γ : 90.000
Metric: orthorhombic
☐ Fix cell param.
☐ Use existing LAT file

Symmetry
SG.Num:Symbol 19 : P 21 21 21 set Lattice P
☐ Centrosimetric
☒ No centrosimetric
Symmetry matrices: X+1/2, -Y+1/2, -Z
-X, Y+1/2, -Z+1/2
-X+1/2, -Y, Z+1/2
Highest symmetry unlock

Instrumental & Data parameters
Pattern type: 1 (Yobs)
Rad. source: Synchrotron
Intensity Extraction: NFWHM: 20 tolerance: 0.5000
Sample: ☐ Flat ☒ Capillary
Primary monochromator: ☐ Yes ☒ No cos 2 θ : 1.00000
Divergence correction: ☐ Yes ☒ No ☒ Fixed slit ☐ Variable slit
slit-w ($^\circ$): 0.0000 sample size: 0.0000 armlenght: 0.0000
Absorption correction: ☐ Yes ☒ No
R*mu: 0.0000 2 θ RefInt: 0.0000 Transmi.: 0.0000

Profile Function
Type: Pseudo-Voigt T... zero: -0.018528 ☒ exp: 1.0000 ☐
Lorentzian coef. X: 0.272E-01 ☒ Y: 0.239E-02 ☒
Gaussian coef. W: 0.793E-03 ☒ V: 0.000E+00 ☐ U: 0.000E+00 ☐
Pref. Orientation: March-coef: 1.000 direction (h k l): 0 0 1

Excluded zones
2 θ inf: Add
2 θ sup: Del.
2Tinf: 2Tsup:

Background
type: Removed 2 θ : + -
<back>: 60.00000 bg-value: File
FWHM: 0.15000
Iterations: 20
2T: bg-value

Asymmetry correction
coef.: Add
2 θ sup: Del.
coef: 2Tsup:

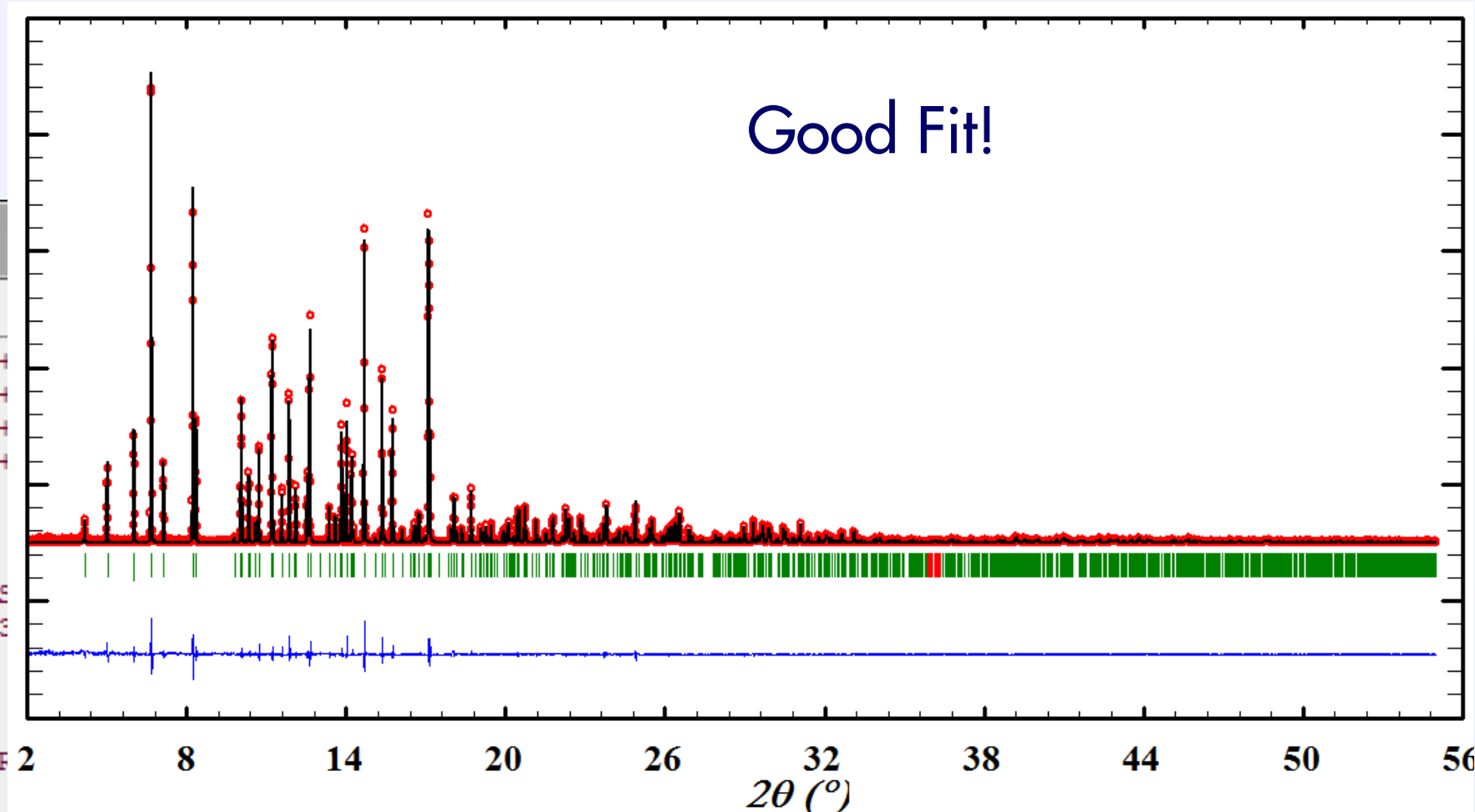
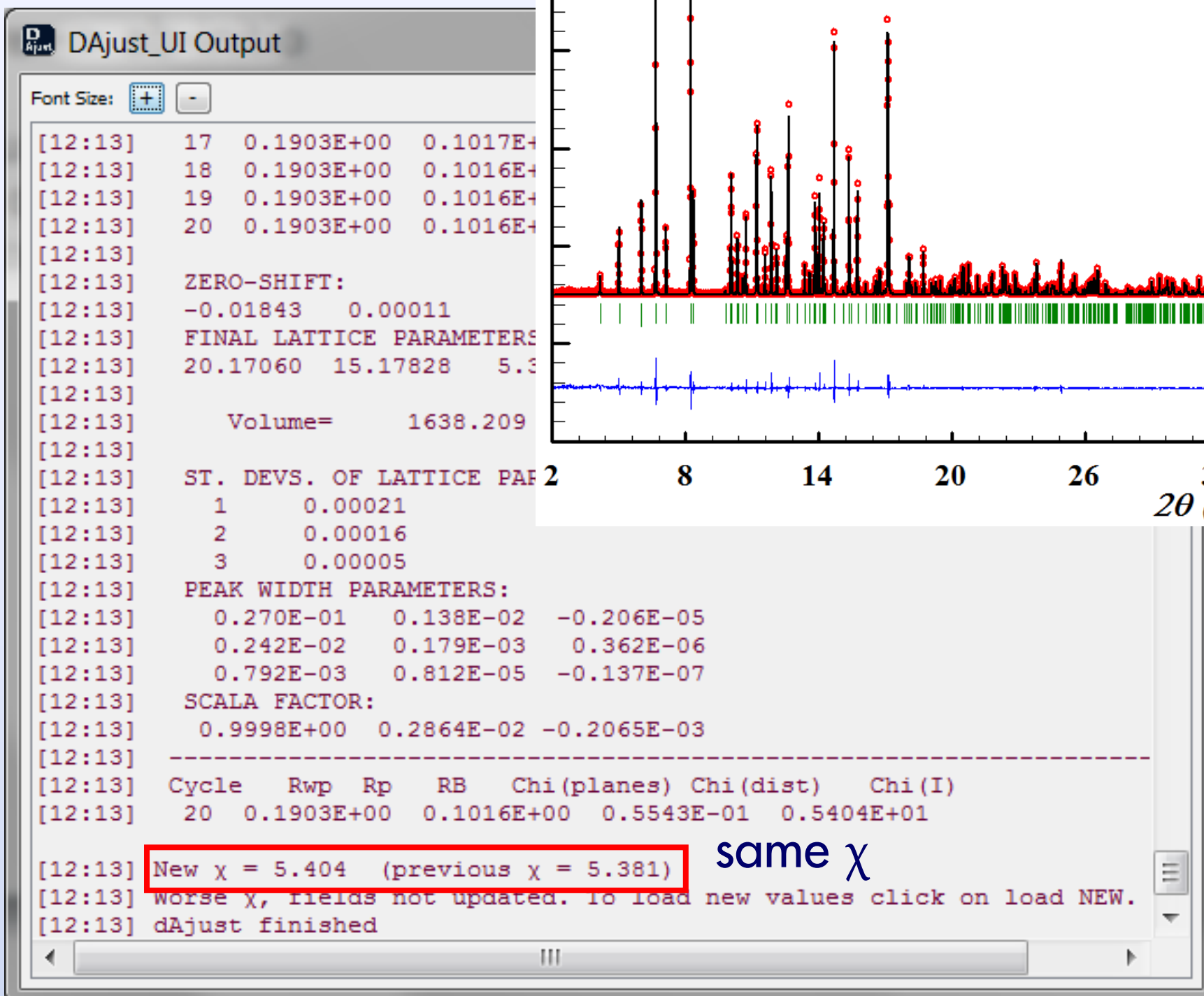
Ghost peaks
value: 2 θ : width: + -
 η : asym: + -
value: 2T: width: nu: asym:

Buttons
Run AJUST Stop run open PRF Output window
Run SGAid Reload JST SGAid window

Work file: O:\ovallcorba\riboflavin\dajust\riboflavin.jst
Data file: O:\ovallcorba\riboflavin\dajust\riboflavin.net

Updated!

DAjust UI - DAjust Result



same χ

DAjust UI - Output Files and possibilities

.LST

Relevant information
on the refinement.

RIETVELD REFINEMENT OUTPUT:

ZERO-SHIFT:

-0.01843 0.00011

FINAL LATTICE PARAMETERS:

20.17060 15.17828 5.35091 90.0000 90.0000
90.0000

Volume= 1638.209

ST. DEVS. OF LATTICE PARAMETERS:

1 0.00021
2 0.00016
3 0.00005

PEAK WIDTH PARAMETERS:

0.270E-01 0.138E-02 -0.206E-05
0.242E-02 0.179E-03 0.362E-06
0.792E-03 0.812E-05 -0.137E-07

SCALA FACTOR:

0.9998E+00 0.2864E-02 -0.2065E-03

Cycle Rwp Rp RB Chi(I)
20 0.1903E+00 0.1016E+00 0.5543E-01 0.5404E+01

.NEW

Updated JST file

Structure Solution (tomorrow talks)

.QCK

Input data file for TALP
(Structure solution by
Direct-Space Methods)
[Vallcorba *et al.* 2012]

.POW

Input data file for XLENS
(Structure solution by
Direct Methods)
[Rius, 2011]

.PRF

For visual inspection with
WinPLOT
[Roisnel & Rodriguez-
Carvajal, 2010]

**.LTN, .NOT,
.CAL, .OBS,
.DIF, .FON**

(see DAjust publication or
program manual)

DAjust

with
AJUST & SGAid

Jordi Rius, Oriol Vallcorba, Inma Peral, Carlos Frontera, Carles Miravittles



www.icmab.es/crystallography/software

Vallcorba, O., Rius, J., Frontera, C., Peral, I. & Miravittles, C. (2012). "DAJUST: a suite of computer programs for pattern matching, space-group determination and intensity extraction from powder diffraction data", *J. Appl. Cryst.*, **45**, 844–848

THANK YOU FOR YOUR ATTENTION!!



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