

Bilbao Crystallographic Server and Fullprof refinement of $\text{Cs}_2\text{Fe}_2(\text{MoO}_4)_3$ data

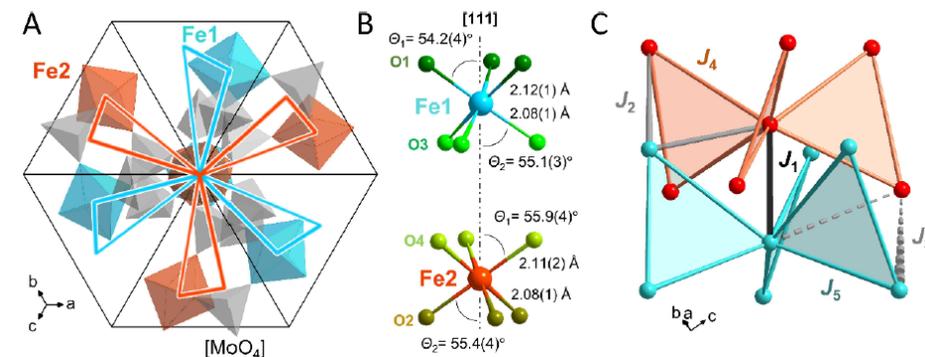
Stuart Calder, ORNL

MagStr 2024 at Kennesaw State University

ORNL is managed by UT-Battelle, LLC for the US Department of Energy

Cs₂Fe₂(MoO₄)₃: Background

- Highly frustrated with same space group as FeSi Skymion.
- Fe is magnetic ion.
 - Two different Fe sites
 - Indications of distinct ordering of Fe
- Long range order expected below 1 K, with short range order above >20 K

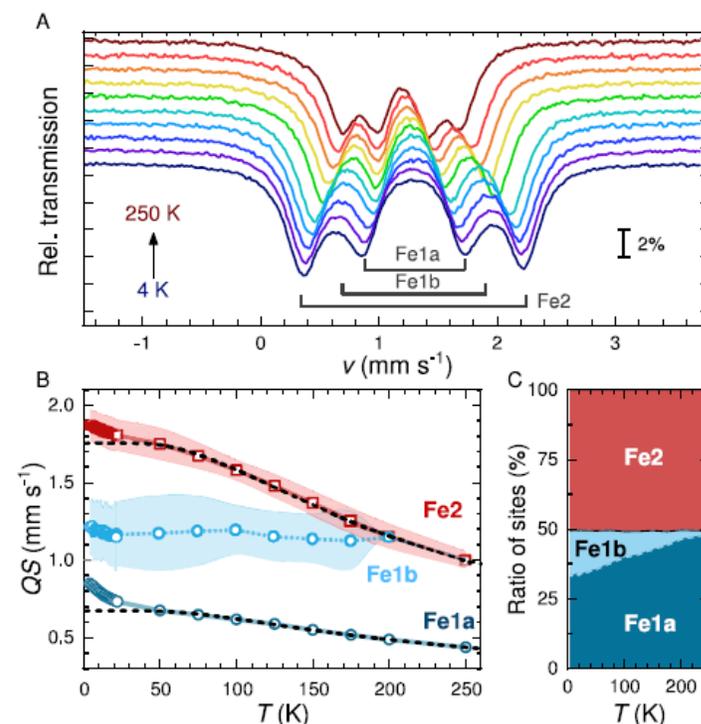


Non-centrosymmetric cubic space group $P2_13$ (198)

a	b	c	alpha	beta	gamma
10.91610	10.91610	10.91610	90.0000	90.0000	90.0000

Structure parameters

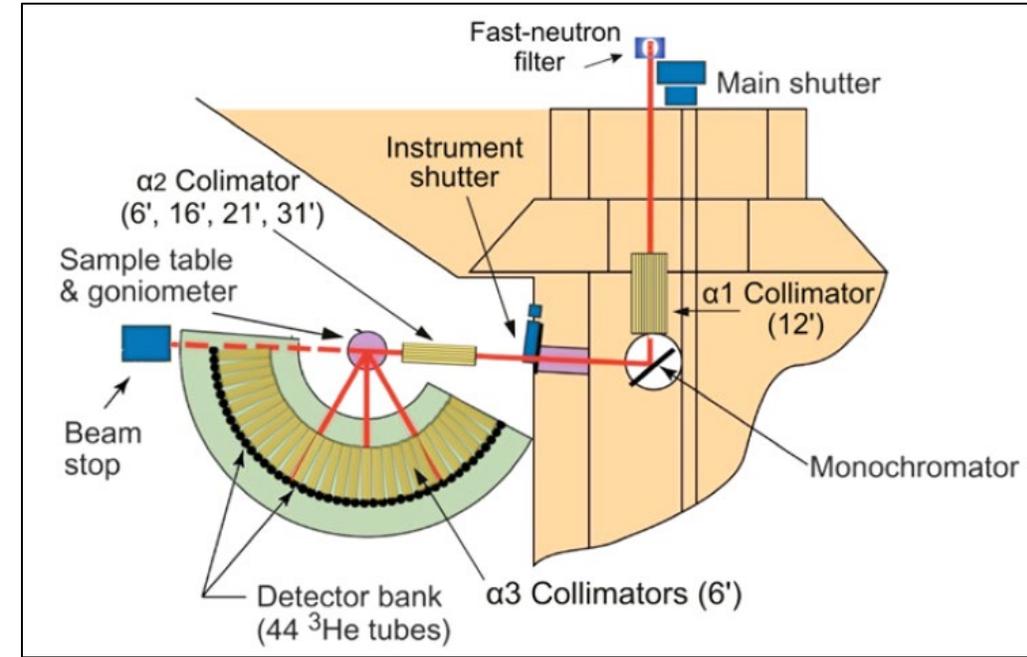
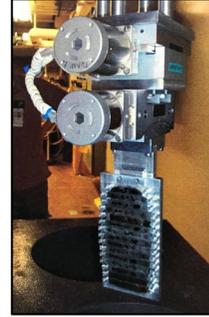
	x	y	z	Occ.	Site
Cs1	0.17938	0.32062	0.67938	1.000	4a
Mo1	0.30061	0.62363	0.52597	1.000	12b
Fe1	0.33737	0.33737	0.33737	1.000	4a
O1	0.27587	0.48544	0.44750	1.000	12b
Cs2	0.45761	0.95761	0.54239	1.000	4a
Fe2	0.61246	0.61246	0.61246	1.000	4a
O2	0.45432	0.67110	0.51709	1.000	12b
O3	0.25187	0.60297	0.67761	1.000	12b
O4	0.21150	0.73545	0.45198	1.000	12b



Goal: Use neutron data to determine the magnetic structure

$\text{Cs}_2\text{Fe}_2(\text{MoO}_4)_3$: Neutron measurements on HB-2A, HFIR.

- Constant wavelength
- Germanium monochromator
 - $\sim 90^\circ$ take off angle for medium-high resolution
 - Variety of complex sample environments: 50mK, 6 Tesla, 2GPa pressure...
- Current detector is an array of 44 individual ^3He tubes
 - Low background
 - Covers ~ 2 - 150° in 2θ by scanning detector
 - **MIDAS detector upgrade coming soon!**



Ge(hkl)	λ (Å)	d_{max} (Å)	Q (Å ⁻¹)	Flux (n/cm ² s)
(113)	2.41	27.6	0.2-5.1	5×10^6
(115)	1.54	17.6	0.35-7.9	1×10^7
(117)	1.12	12.8	0.5-10.9	4×10^6



<https://neutrons.ornl.gov/powder>



HB-2A instrument resolution and peak shape

MYRESOL.irf

This file is read only when `Res`≠0. The name of the file is stored in the character variable `FILERES= MYRESOL.irf`. All items are read in free format.

This options works, at present, only for constant wavelength type of data. The profile is assumed to be a Voigt function (`Npr=7`). 12 parameters or a table determine the resolution function. The parameters are $U_i, V_i, W_i, X_i, Y_i, Z_i$ ($i=1,2$ for λ_1 and λ_2)

The different types of functions are:

$$\text{Res}=1 \quad H_G^2 = (U_i \tan \theta + V_i) \tan \theta + W_i$$

$$H_L = X_i \tan \theta + \frac{Y_i}{\cos \theta} + Z_i$$

- Caglioti function describes reactor based diffractometers.
- U,V,W parameters in Fullprof.
- See paper by Hewat for definitions of U,V,W

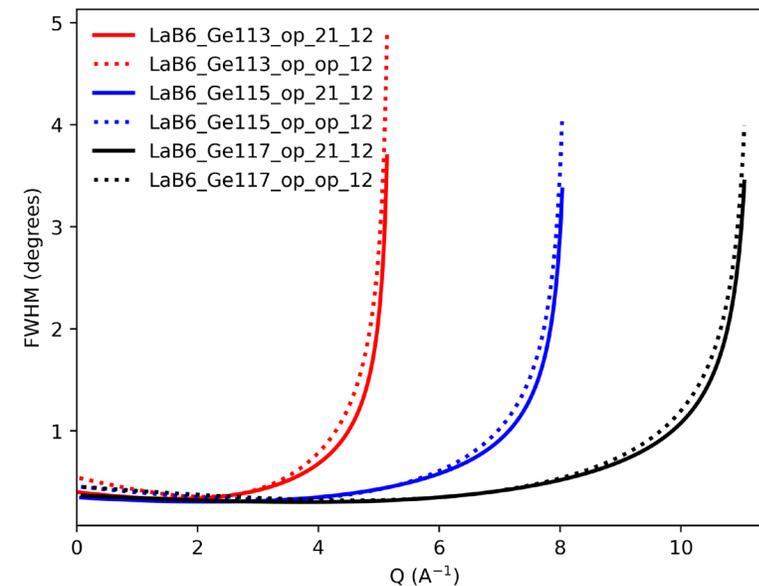
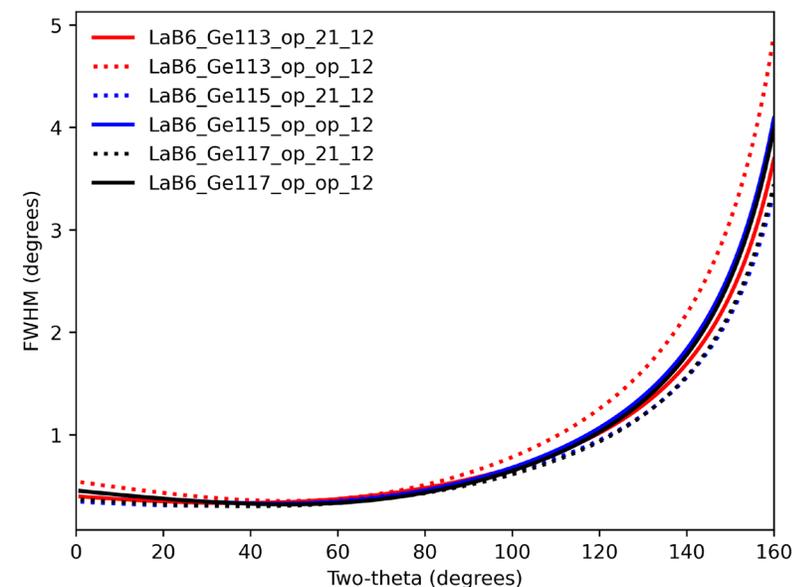
NUCLEAR INSTRUMENTS AND METHODS 127 (1975) 361-370; © NORTH-HOLLAND PUBLISHING CO.

DESIGN FOR A CONVENTIONAL HIGH-RESOLUTION NEUTRON POWDER DIFFRACTOMETER

A. W. HEWAT

Institut Laue-Langevin, B.P. N° 156, 38042-Grenoble Cédex, France

Received 14 April 1975



$\text{Cs}_2\text{Fe}_2(\text{MoO}_4)_3$: Low temperature measurements at HB-2A

- Transition temperature of 1 K requires ultra-low temperatures (ULT) sample environments.
- A unique “push-button” ^3He sample changer was used that can measure **up to 10 samples** down to millikelvin temperatures of 0.28 K.
- The $\text{Cs}_2\text{Fe}_2(\text{MoO}_4)_3$ powder was contained in an Al can with Cu lid.
 - An overpressure of 10 atm. of helium was added to the can to ensure thermal conduction to millikelvin temperatures.
 - Aluminium has a low background, but adds additional reflections to the diffraction pattern.



$\text{Cs}_2\text{Fe}_2(\text{MoO}_4)_3$: Files for the example



CFMO_10K



CFMO_300mK



hb2a_resolution_Ge113_op_op_12



ICSD_CollCode422752

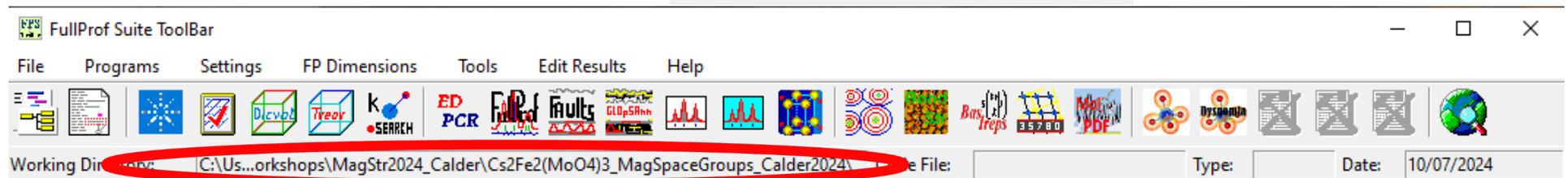
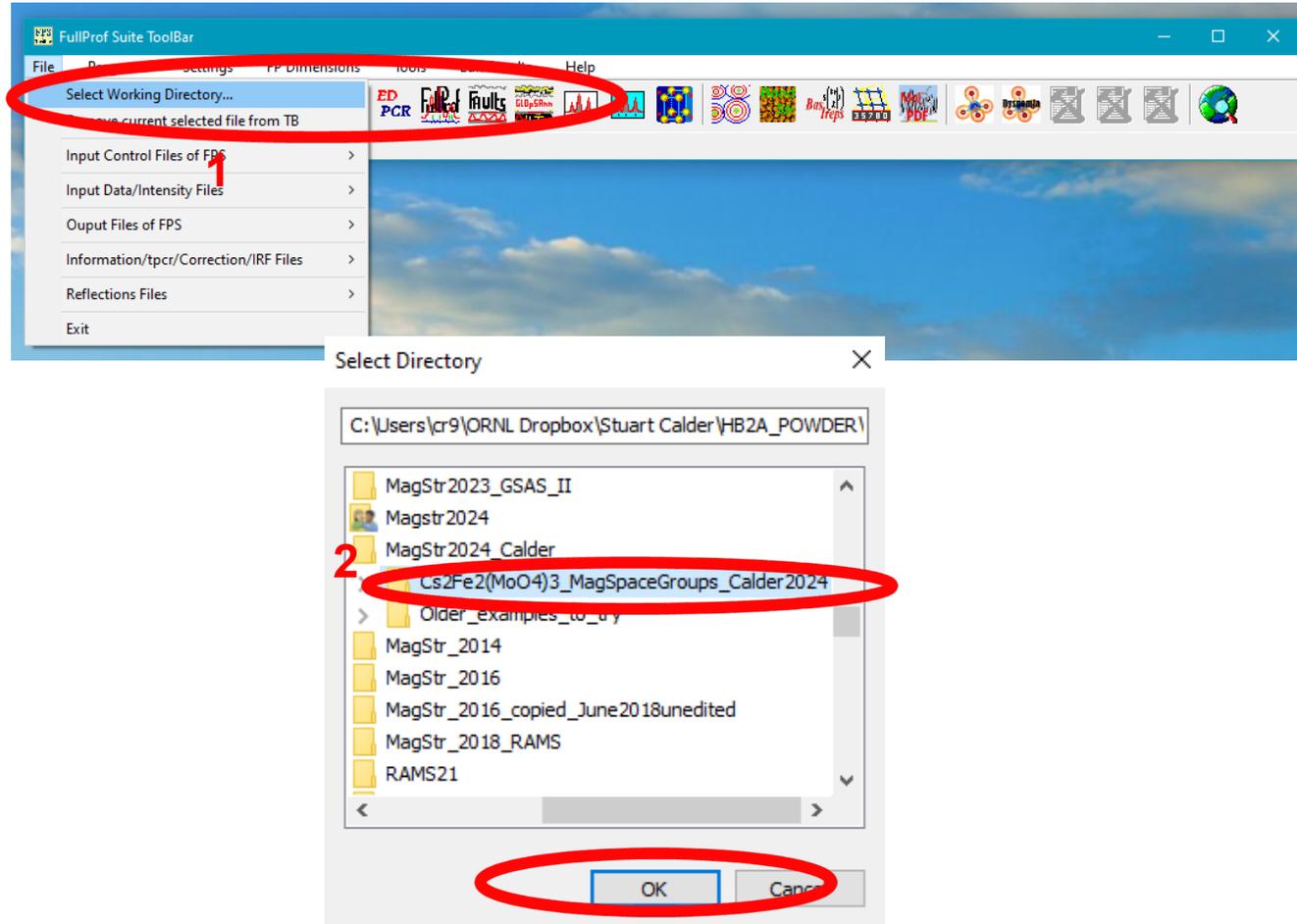
- Files are in folder
“**Cs2Fe2(MoO4)3_MagSpaceGroups_Calder2024**”

Filename	Description
CFMO_10K.dat CFMO_300mK.dat	Neutron data from HB2A. Columns are two-theta, intensity, error
ICSD_CollCode422752.cif	Crystal structure information. File obtained from ICSD https://icsd.fiz-karlsruhe.de/search/basic.xhtml
HB2A_Ge113.irf	Instrument parameter file. Instrument specific, download at https://neutrons.ornl.gov/powder/users

- Goal of this exercise is to obtain the magnetic structure at 300 mK for $\text{Cs}_2\text{Fe}_2(\text{MoO}_4)_3$.

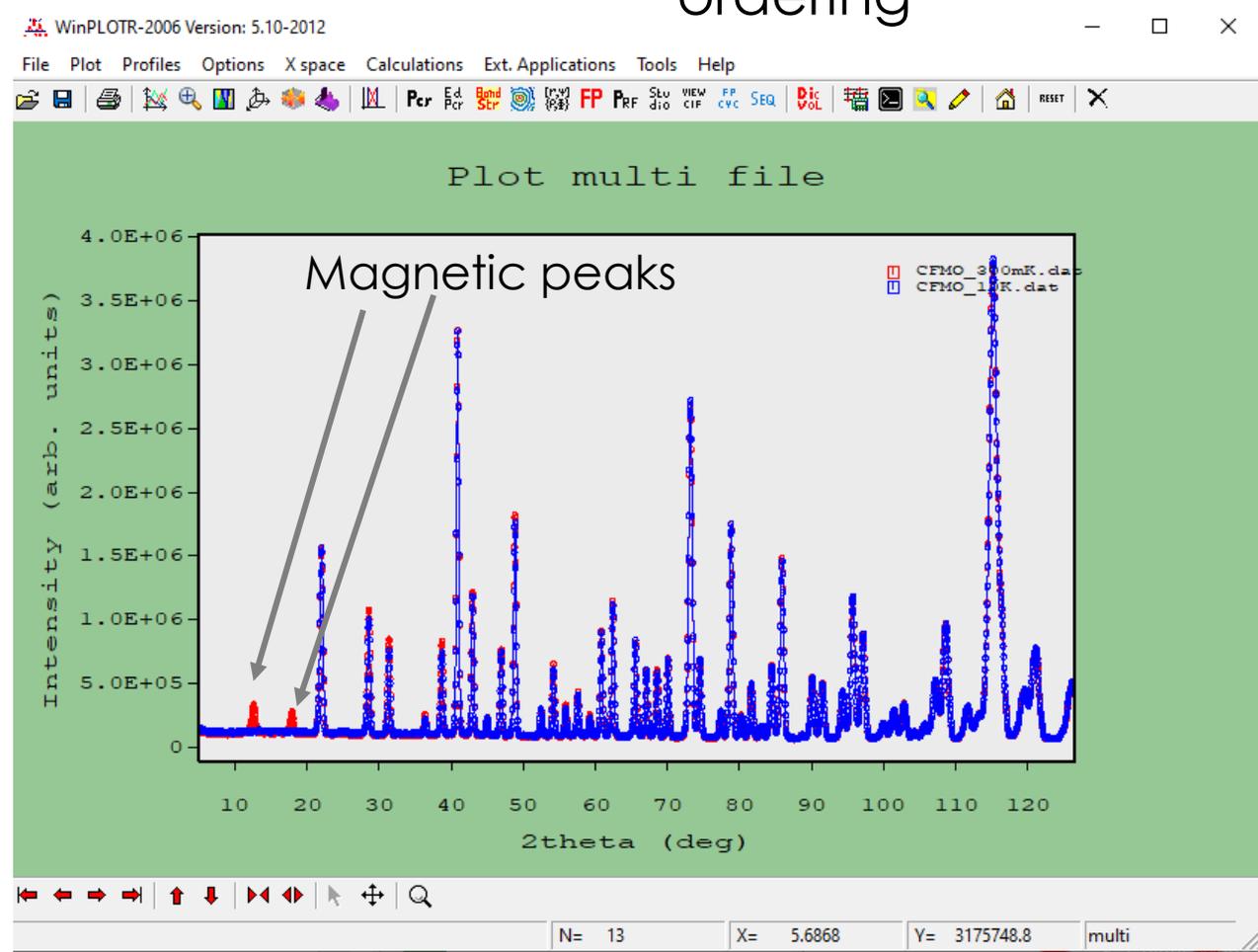
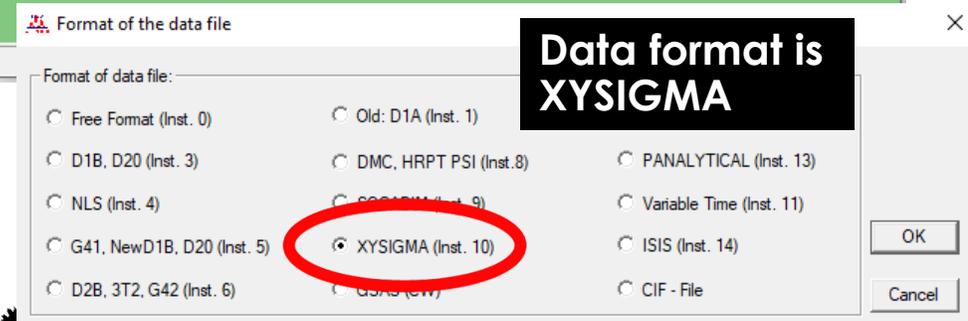
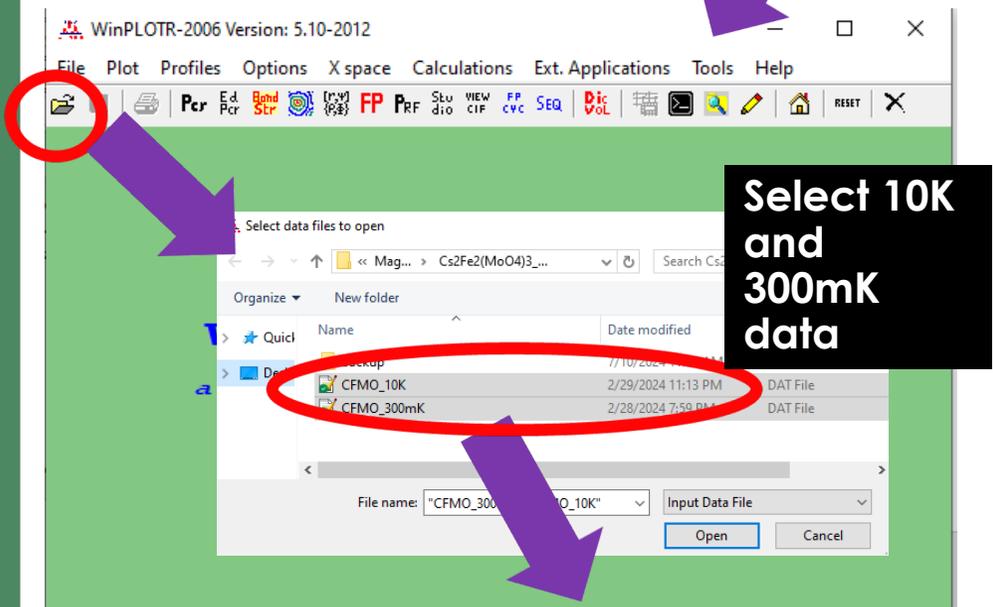
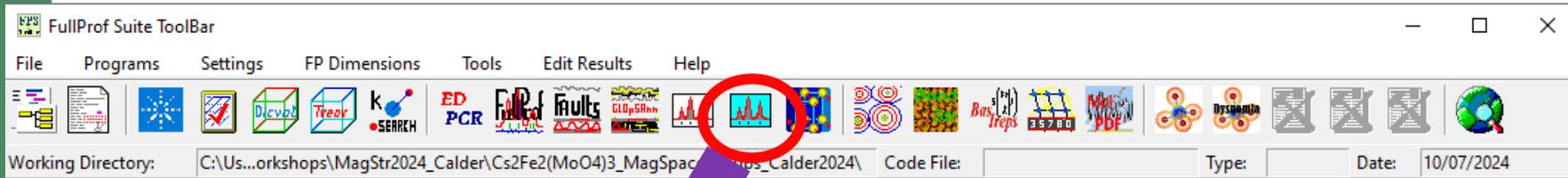
$\text{Cs}_2\text{Fe}_2(\text{MoO}_4)_3$: Set-up Fullprof Suite Toolbar

- Open Fullprof Suite toolbar.
 - **1.** Select working directory with data
“File>Select Working directory...”
 - **2.** Browse to wherever your folder
“Cs2Fe2(MoO4)3_MagSpaceGroups_Calder2024” is located on your computer and select “ok”
 - **3.** Path on FP studio toolbar should now be updated. This helps with interacting with other features of Fullprof



Cs₂Fe₂(MoO₄)₃: View Data

- After downloading files open the data with WinPLOTR-2006
- Extra peaks at 300 mK indicate magnetic ordering



$\text{Cs}_2\text{Fe}_2(\text{MoO}_4)_3$: Refinement Strategy

- This example will use the Bilbao Crystallographic Server (<http://www.cryst.ehu.es/>) and follow these steps:
 - Step 1: Refine the crystal structure using FullProf
 - Step 2: Determine the k-vector by indexing the magnetic reflections using k-search
 - Step 3: Create test magnetic space groups using MAXMAGN on the Bilbao Crystallographic Server. Save these as mcif files.
 - Step 4: Convert the mcif file into a .pcr file using mCIF2PCR.
 - Step 5: Use the created .pcr file to fit the nuclear and magnetic neutron data using Fullprof to determined the magnetic structure.

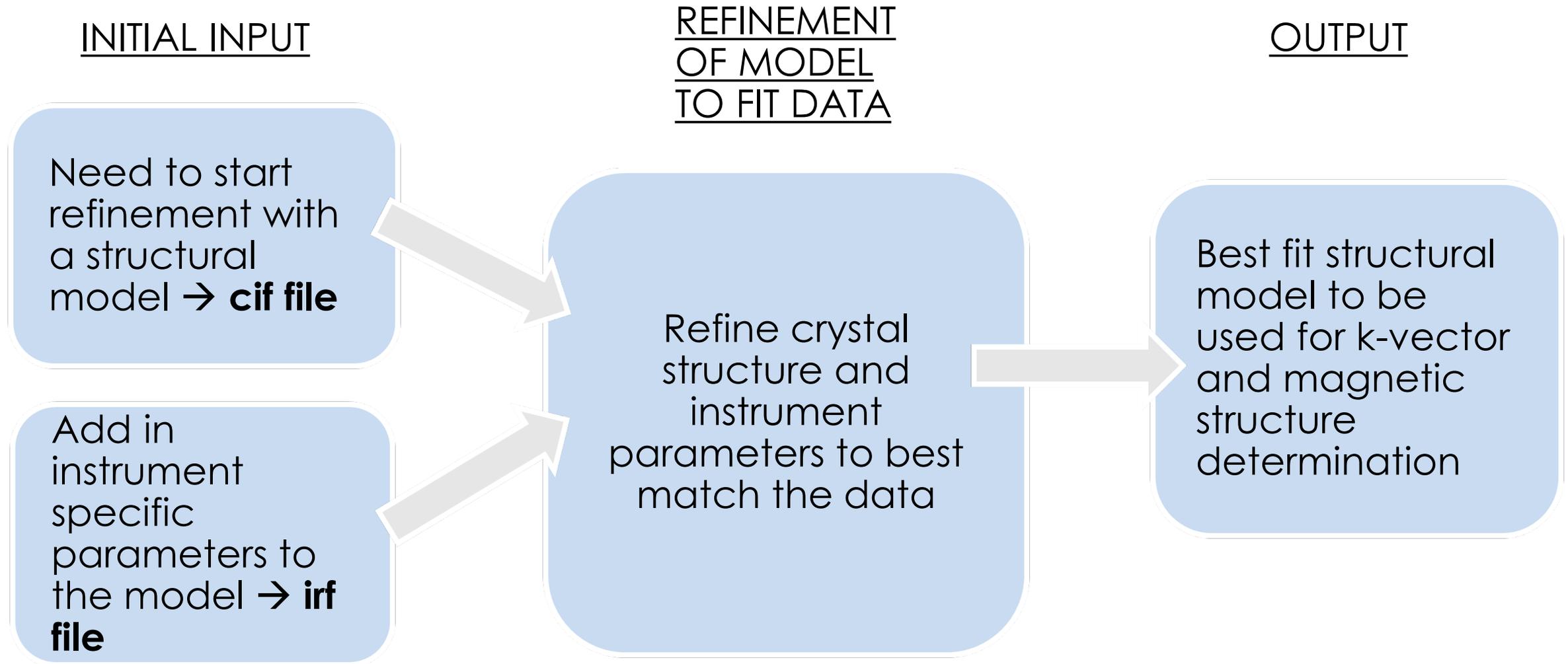
$\text{Cs}_2\text{Fe}_2(\text{MoO}_4)_3$: Refinement Strategy

- This example will use the Bilbao Crystallographic Server (<http://www.cryst.ehu.es/>) and follow these steps:
 - **Step 1: Refine the crystal structure using FullProf**
 - Step 2: Determine the k-vector by indexing the magnetic reflections using k-search
 - Step 3: Create test magnetic space groups using MAXMAGN on the Bilbao Crystallographic Server. Save these as mcif files.
 - Step 4: Convert the mcif file into a .pcr file using mCIF2PCR.
 - Step 5: Use the created .pcr file to fit the nuclear and magnetic neutron data using Fullprof to determined the magnetic structure.

Step 1: Refining the crystal structure using Fullprof

- Need to start refinement with a structural model → **cif file**
- Add in instrument specific parameters to the model → **irf file**
- Then refine this model.

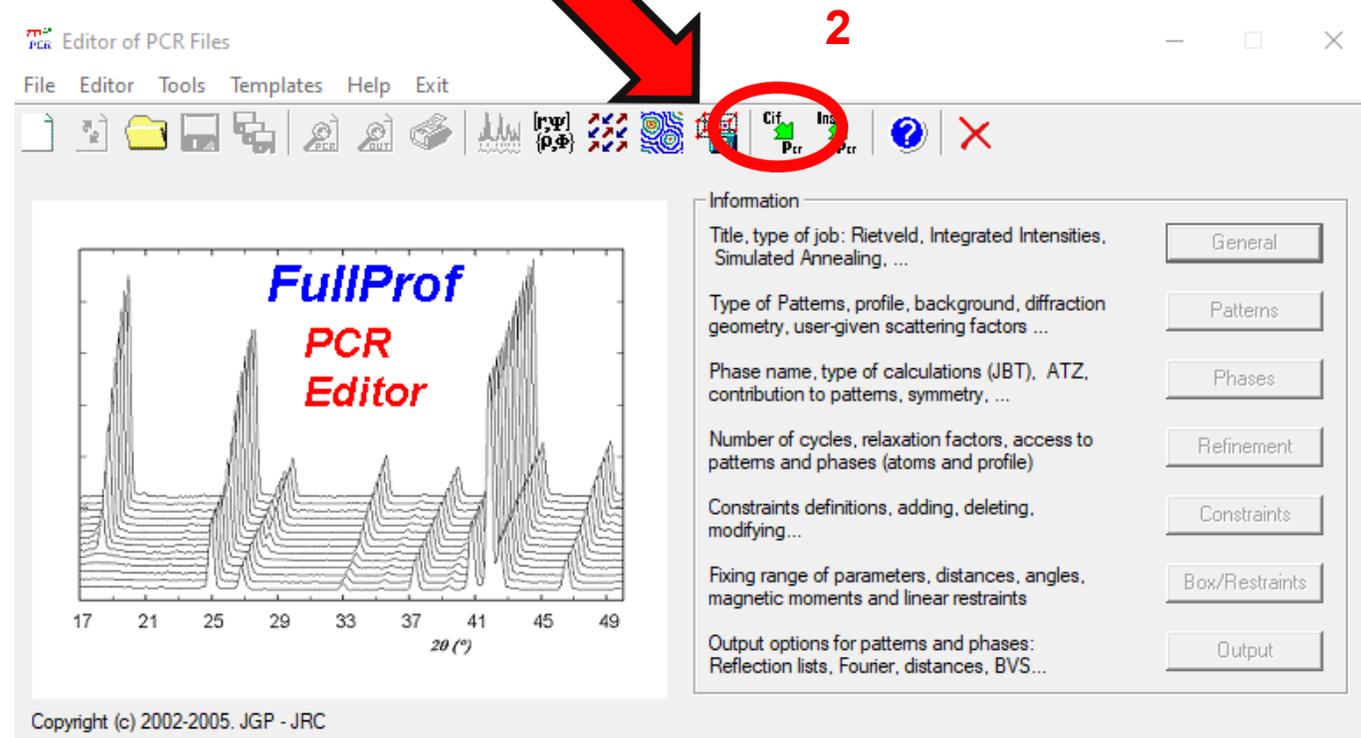
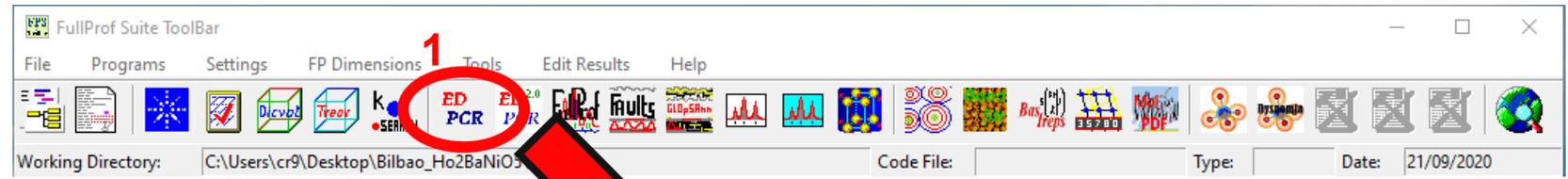
Step 1: Refining the crystal structure using Fullprof



Step 1: Refining the crystal structure using Fullprof

Start by putting crystal model into Fullprof

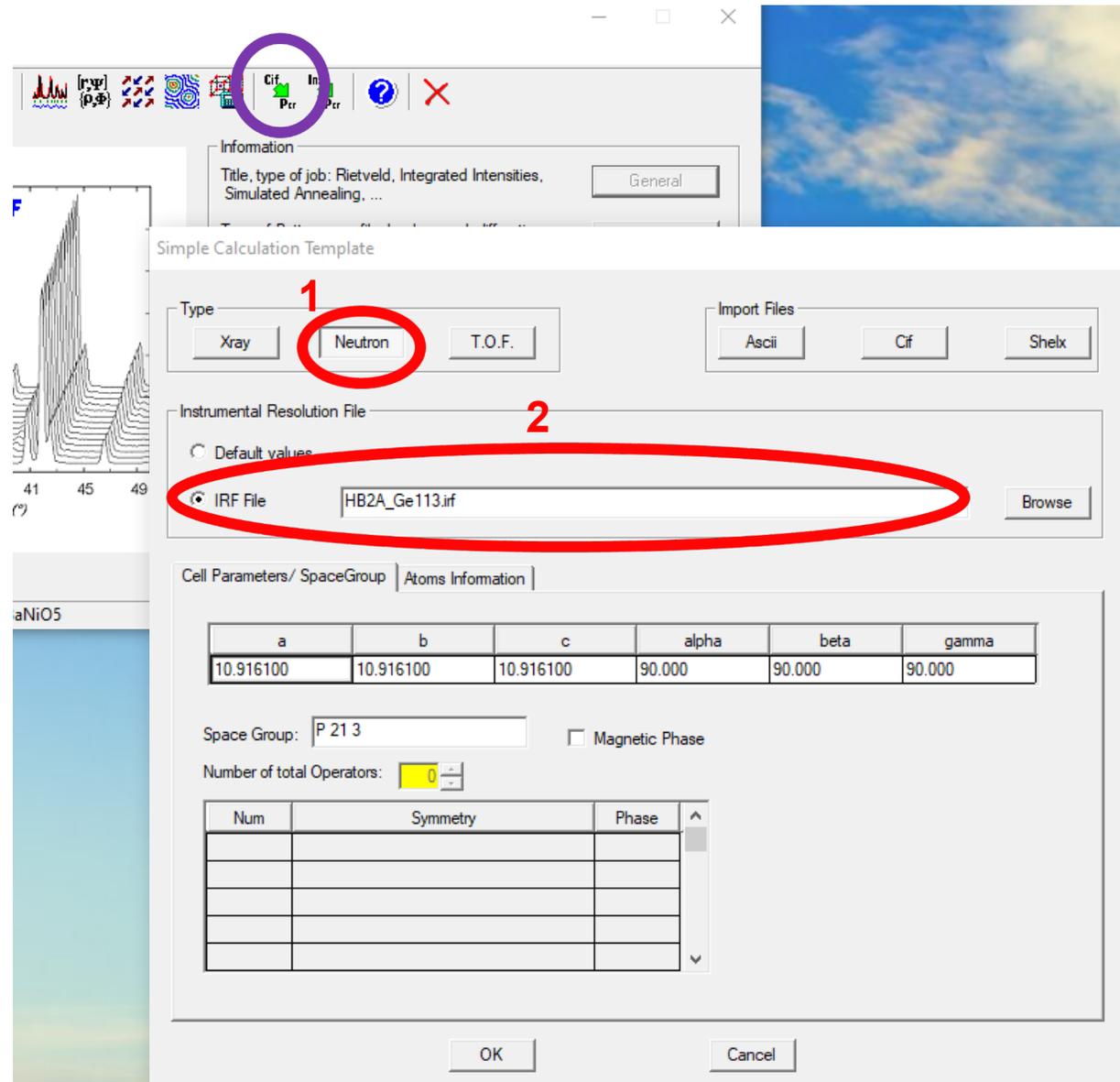
- 1. From FullProf Suite Toolbar open EdPCR.
- 2. Import crystallographic information file by clicking on "CIF→PCR"
- 3. Select the file "ICSD_CollCode422752.cif" when prompted.



Step 1: Refine the crystal structure using FullProf

Cif→PCR opens a window to input instrument parameters and shows structural info.

- **1.** Change “Type” to “Neutron” for constant wavelength
- **2.** Load the instrument resolution file “HB2A_Ge113.irf” (click circle and browse to file).
 - *NOTE: remove the full path to just keep “HB2A_Ge113.irf”. If you don’t it could create problems later if you share file or change folders....*
- Starting **Cell Parameters, Space Group** and **Atomic Information** are now loaded.



Step 1: Refine the crystal structure using FullProf

Simple Calculation Template

- Look in the tab “Atoms Information”
 - Fullprof treats occupancies (Occ) in a particular way related to multiplicities.
 - For example the Cs1 site with Occ=0.333 does not mean that site is deficient or doped. In VESTA, GSAS-II etc this would just say “1”.
 - **occ = site multip./general multip.**
Always check this has been correctly calculated after importing the .cif file.
- Hit “OK” to close the window

Type: Xray Neutron T.O.F.

Import Files: Ascii Cif Shelx

Instrumental Resolution File:
 Default values
 IRF File: HB2A_Ge113.irf

Cell Parameters/ SpaceGroup: **Atoms Information**

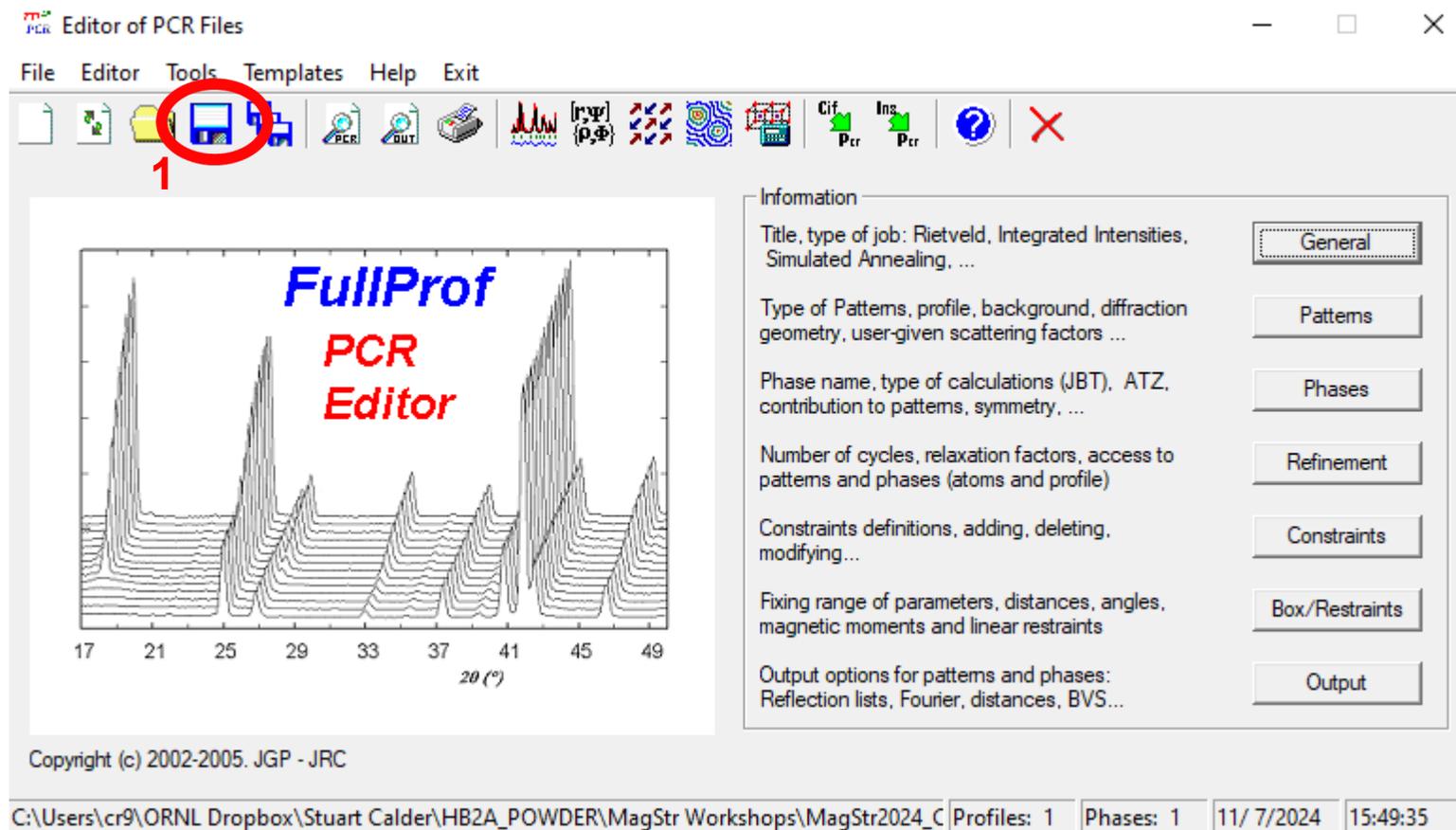
	Name	Type	X	Y	Z	B	Occ
Atom #1	Cs1	Cs	0.17938	0.32062	0.67938	0.00000	0.33333
Atom #2	Mo1	Mo	0.30061	0.62363	0.52597	0.00000	1.00000
Atom #3	Fe1	Fe	0.33737	0.33737	0.33737	0.84168	0.33333
Atom #4	O1	O	0.27587	0.48544	0.44750	1.96603	1.00000
Atom #5	Cs2	Cs	0.45761	0.95761	0.54239	2.33317	0.33333

	Rx	Ry	Rz	lx	ly	lz	MPPhase
Atom #1							
Atom #2							
Atom #3							
Atom #4							

When finished, hit OK

Step 1: Refine the crystal structure using FullProf

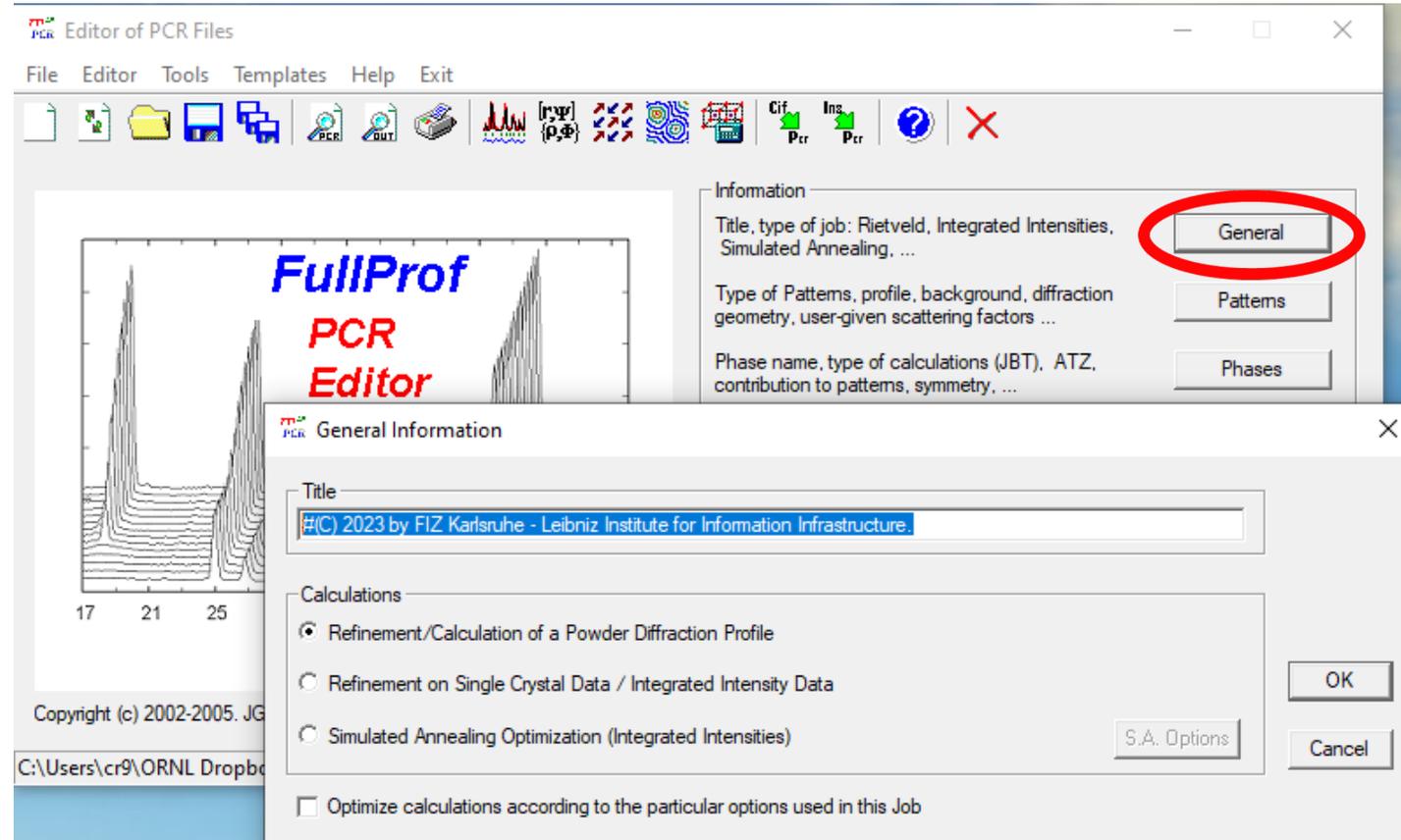
- **1.** Save the changes.
- This should be done whenever changes are made in the GUI.



Step 1: Refine the crystal structure using FullProf

- “**General**” tab has refinement of powder data as default. This is what we’ll do in this example.
- Can edit title as wanted.

For powder refinements there is no need to edit this tab

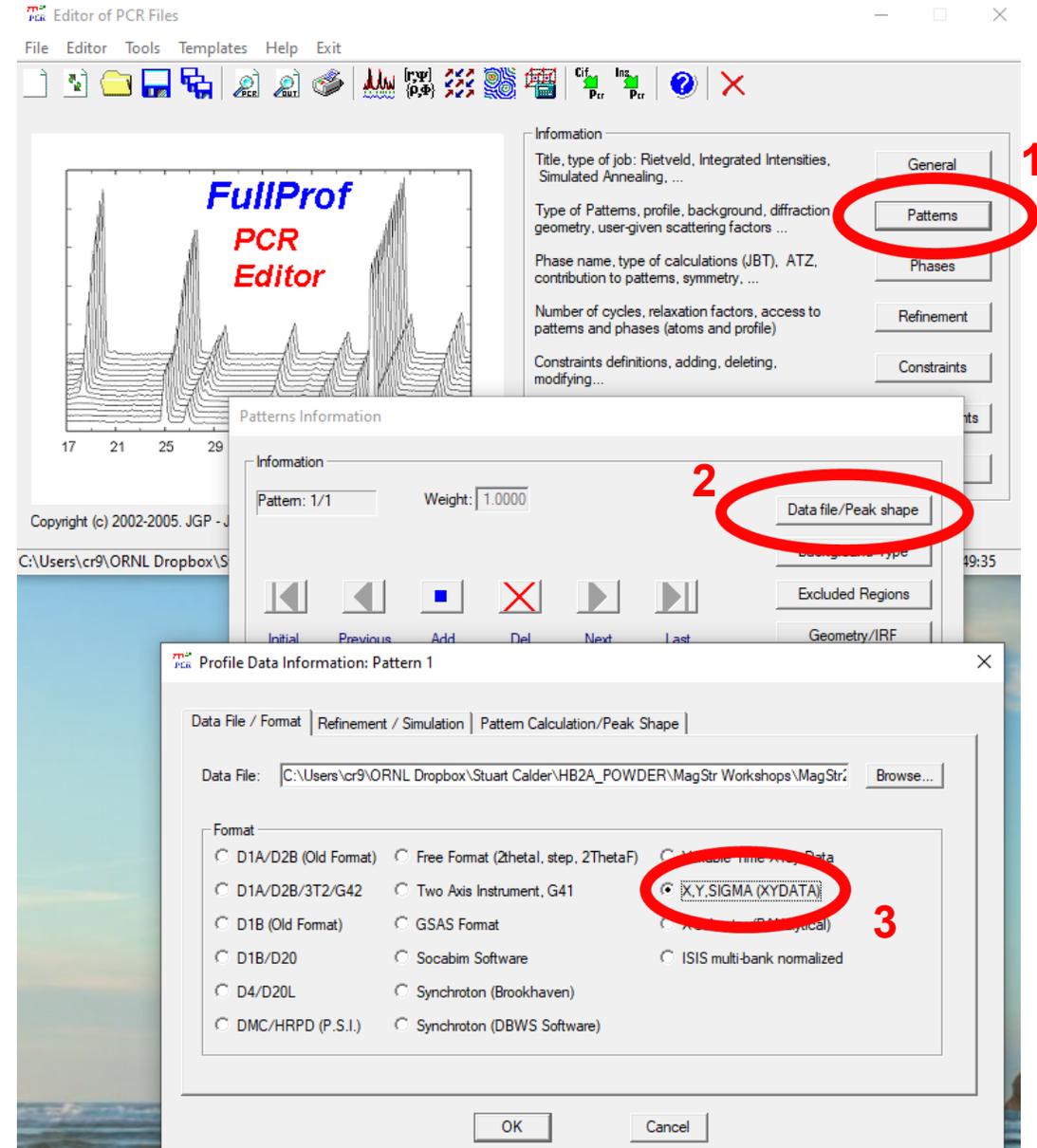


Step 1: Refine the crystal structure using FullProf

1. "Patterns" tab

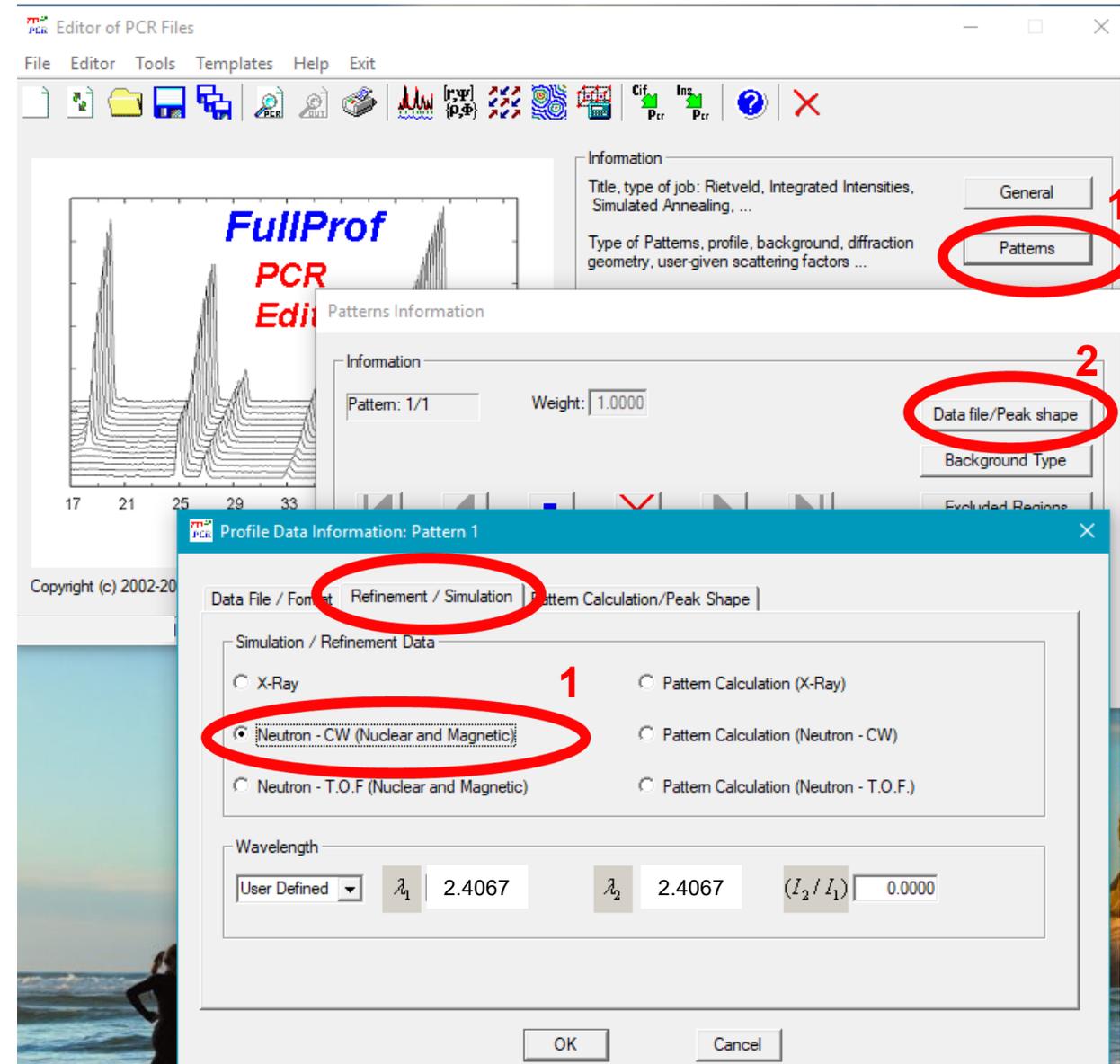
- 2. Select the format of the data file Fullprof should refine.
- 3. Patterns → Data file/Peak Shape → X,Y,SIGMA (XYDATA)

Data format from HB-2A is simply three columns with two-theta, Intensity, Intensity Error



Step 1: Refine the crystal structure using FullProf

- Patterns → Data file/Peak Shape → Refinement/Simulation
- **[1]** Select Neutron – CW
- Wavelength is already set by irf file, 2.4067 in this example.



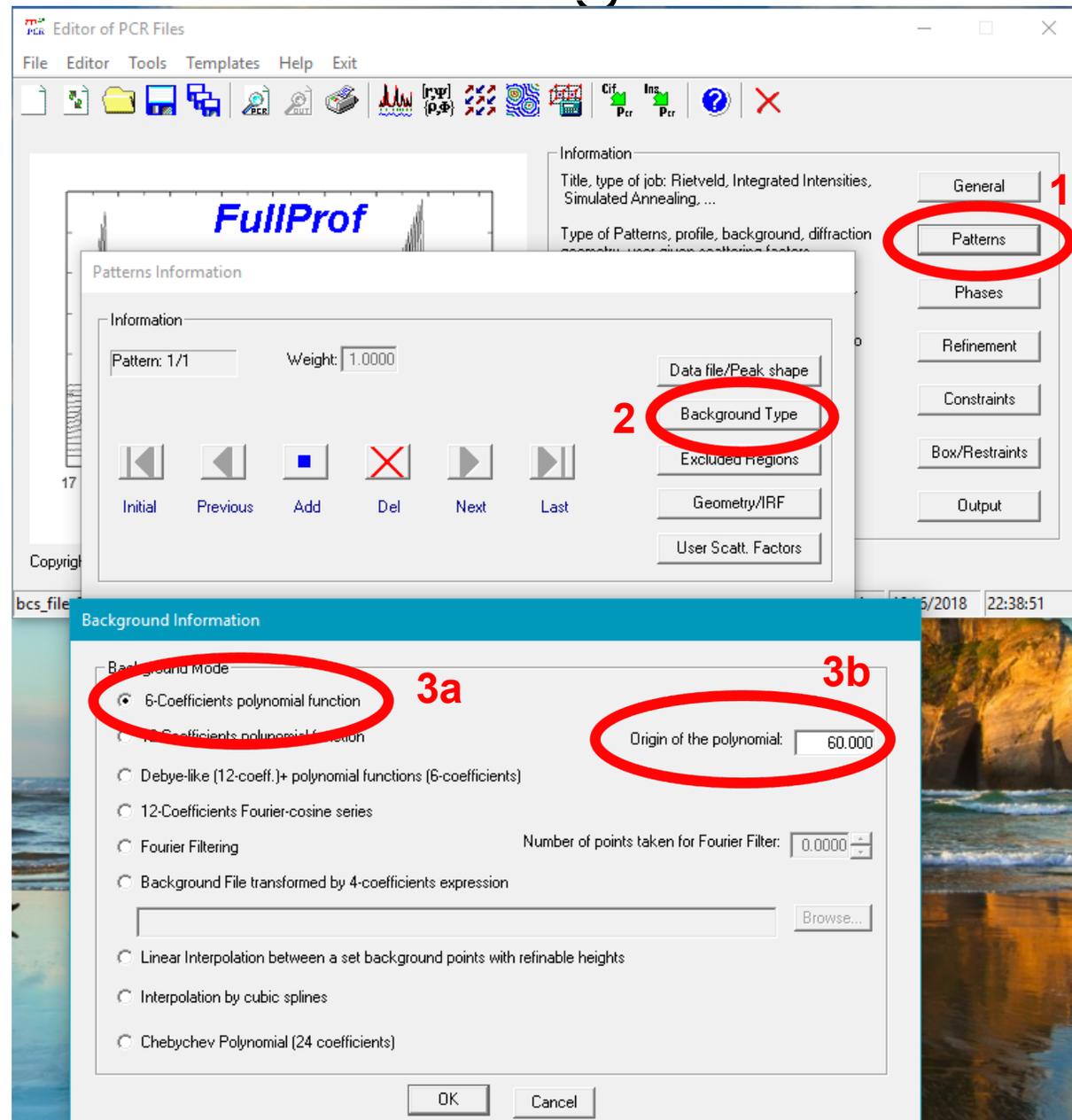
Step 1: Refine the crystal structure using FullProf

- Check final tab:
- Patterns → Data file/Peak Shape → Pattern Calculation/Peak Shape
- Peak shape is already loaded correctly from irf file.

The screenshot displays the FullProf software interface. The main window shows a plot of diffraction patterns with the text 'FullProf PCR Editor' overlaid. A 'Patterns Information' dialog box is open, showing 'Pattern: 1/1' and 'Weight: 1.0000'. The 'Data file/Peak shape' button is circled in red and labeled '2'. A 'Profile Data Information: Pattern 1' dialog box is also open, showing the 'Pattern Calculation/Peak Shape' tab selected. The 'Peak Shape' dropdown menu is set to 'Thompson-Cox-Hastings pseudo-Voigt * Axial divergence asymmetry'. The 'Scattering Variable' is set to '2Theta'. The 'Range' section shows 'Theta_min: 0.0000', 'Theta_max: 155.0000', and 'Step: 0.0300'. The 'Range of calculation of a single reflection in units of FWHM' is set to '8.0000' and the 'Incident beam angle at sample surface (°)' is set to '0.000'. The 'OK' and 'Cancel' buttons are visible at the bottom of the dialog box.

Step 1: Refine the crystal structure using FullProf

- Move to next tab down to select background type
- Patterns → Background Type
Check “6-coefficient”
- Put origin of polynomial at 60 for this example.

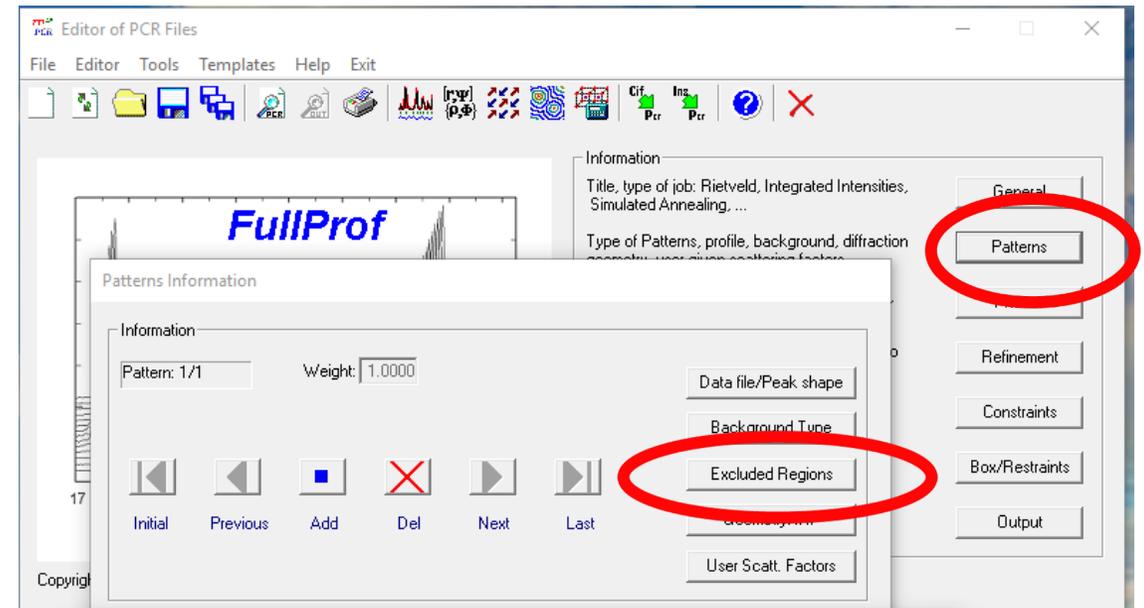


Background on HB-2A typically low and featureless so can be captured by simple polynomial function. But multiple background choices exist in Fullprof.

Step 1: Refine the crystal structure using FullProf

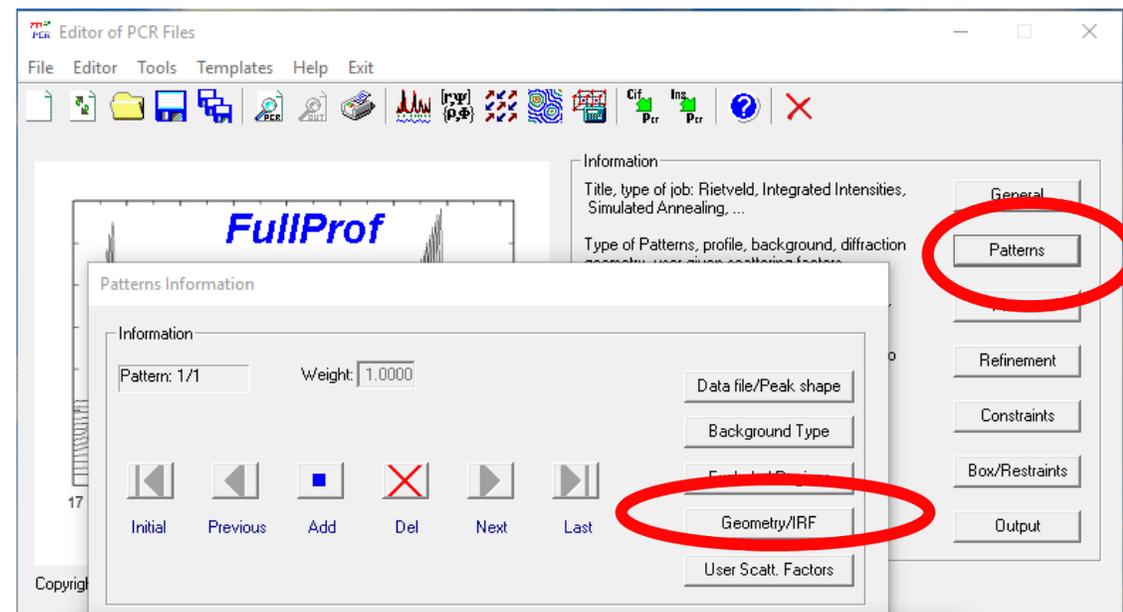
Exclude regions in the data?

- For now we will not exclude any regions of the data
- Use with care, but can cut out background.
- Can allow focus of refinement on different regions, e.g. only low Q
- Quick way to remove peaks from sample holder or can → but should try to fit these if possible!

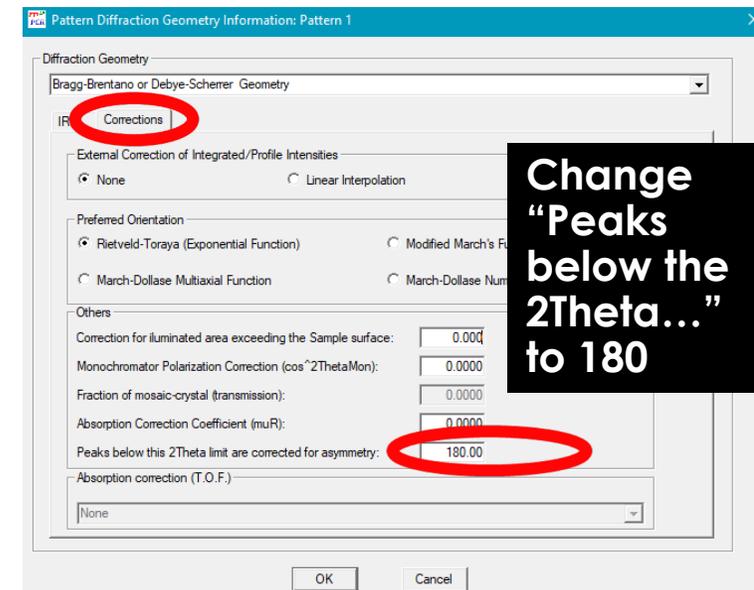
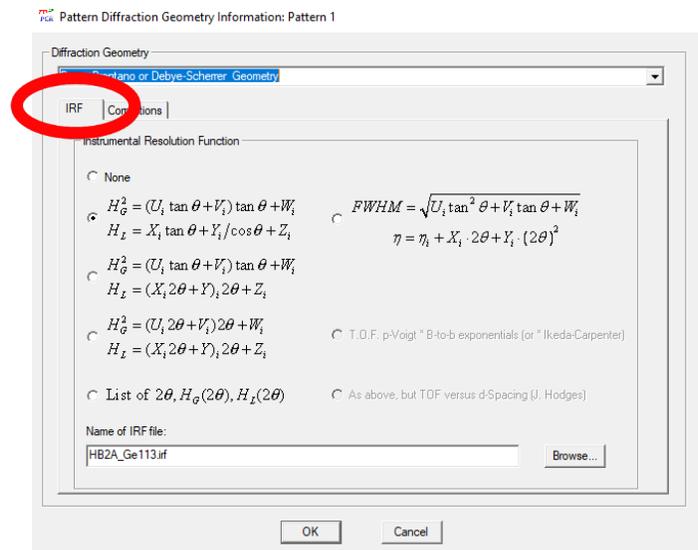


Step 1: Refine the crystal structure using FullProf

- Geometry/IRF
Populated by irf file.
- Corrections: the instrument layout gives asymmetric peaks, particularly at low angle. These can be corrected. Change "Peaks below this 2Theta limit are corrected for asymmetry" to 180. Forgetting to do this, then refining the asymmetry parameters is a common error!

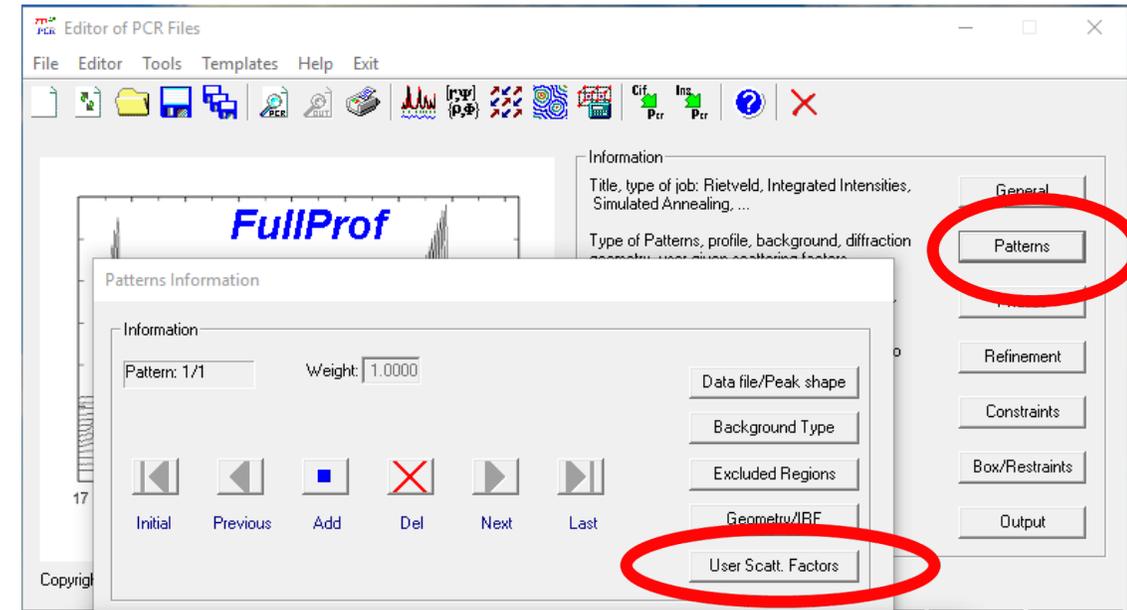


- Can correct for absorption if needed. "muR" is mu (absorption) multiplied by sample radius. Can find mu at NIST website <https://www.ncnr.nist.gov/resources/activation/>



Step 1: Refine the crystal structure using FullProf

- No further editing should be needed of the remaining “Patterns” tab “User Scatt. Factors”
 - This can be used to add e.g. a form factor that isn’t tabulated



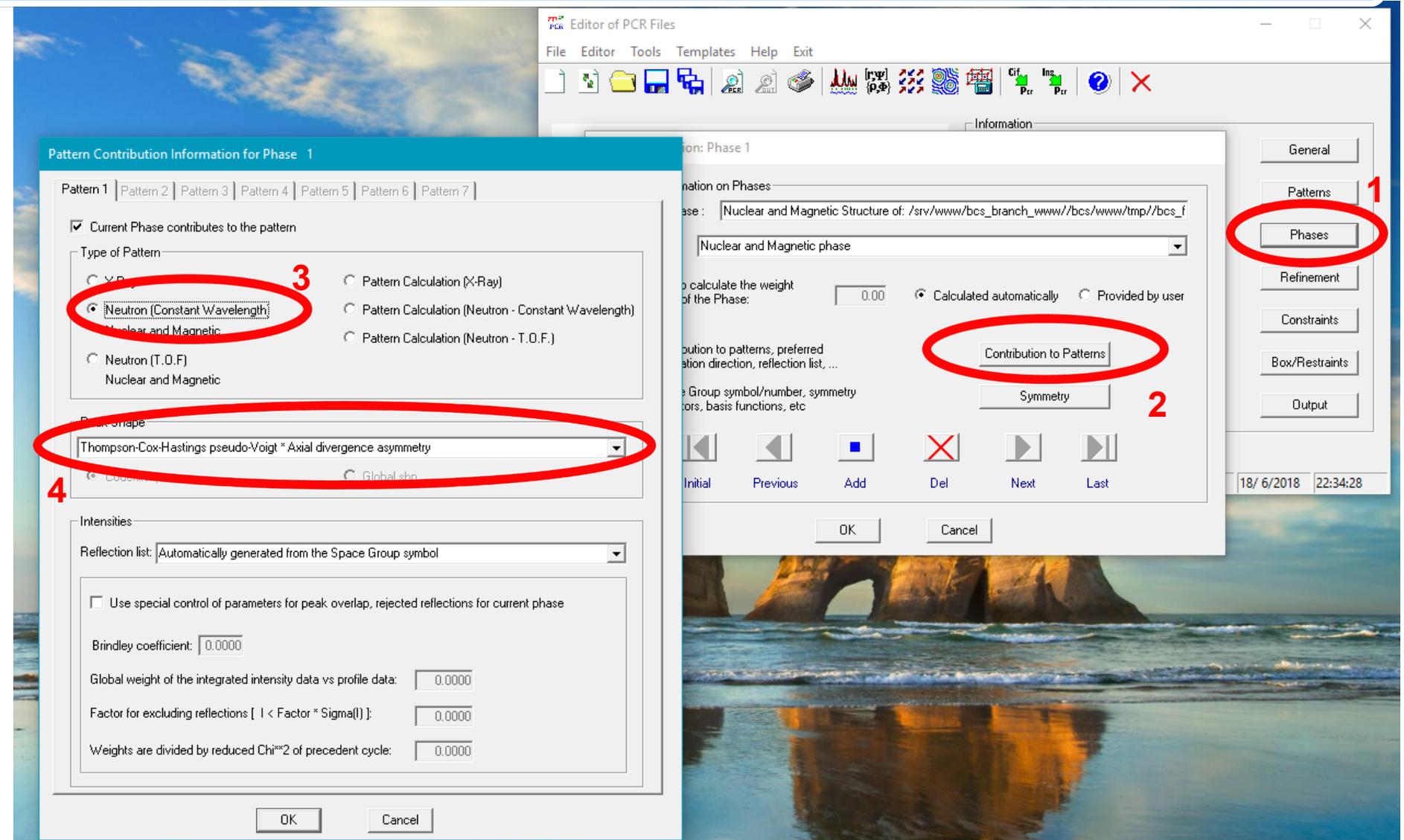
If the magnetic ion does not have form factor tables tabulated, or you want to test a non-standard form factor, this can be added here. One example would be for 5d ions, such as Ir, Os, etc.

Step 1: Refine the crystal structure using FullProf

PHASES tab

Can do a simulation or refinement with data. Select which one here.

- Make phase contribute to refinement.
- **[1]** Phases → **[2]** Contribution to Patterns → **[3]** Neutron (constant wavelength)
- Set peak shape to **“Thompson-Cox-Hastings pseudo-Voigt”**



Step 1: Refine the crystal structure using FullProf

REFINEMENT tab:

- Setting starting values for refinements
- Starting background value of 100000 (check data)

The screenshot shows the FullProf software interface. The main window is titled "Editor of PCR Files" and displays the "Refinement Information" dialog box. The "Refinement" tab is selected in the right-hand menu, indicated by a red circle and the number 1. The "Refinement Information" dialog box shows the following settings:

- Cycles of Refinement: 1
- Stop Criterium of Coverage: Forced Termination when shifts < 0.02 x E.S.D.
- Others: None
- Relaxation Factors for Shifts: Atomic 1.00, Anisotropic 1.00, Profile 1.00, Global 1.00
- Reflections ordering: Only at the first cycle (selected)
- Refinement weighting model: Background (selected, circled with a red circle and the number 2)

The "Background" dialog box is open, showing a table of coefficients for a 6 Coefficients Polynomial Background. The coefficient d_0 is set to 100000, which is circled with a red circle and the number 3. The other coefficients (d_1 to d_23) are set to 0.0000.

	d_0	d_1	d_2	d_3	d_4	d_5
Coefficients	100000	0.0000	0.0000	0.0000	0.0000	0.0000
Coefficients	d_6	d_7	d_8	d_9	d_10	d_11
Coefficients	d_12	d_13	d_14	d_15	d_16	d_17
Coefficients	d_18	d_19	d_20	d_21	d_22	d_23

In the bottom left corner, there is a plot of Intensity (arb. units) versus 2theta (deg). The plot shows a series of sharp peaks on a background. A black box with white text says "Select initial background by looking at data".

Step 1: Refine the crystal structure using FullProf

- Select “Refinement” tab again.
- Update “Cycle of Refinement” to 10
- From “Refinement” tab select: Refinement>Profile
- Change scale to 100.
 - Note – it is often best to run a refinement without anything refining and then adjusting scale manually until it is close.

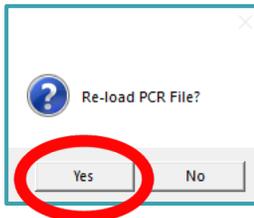
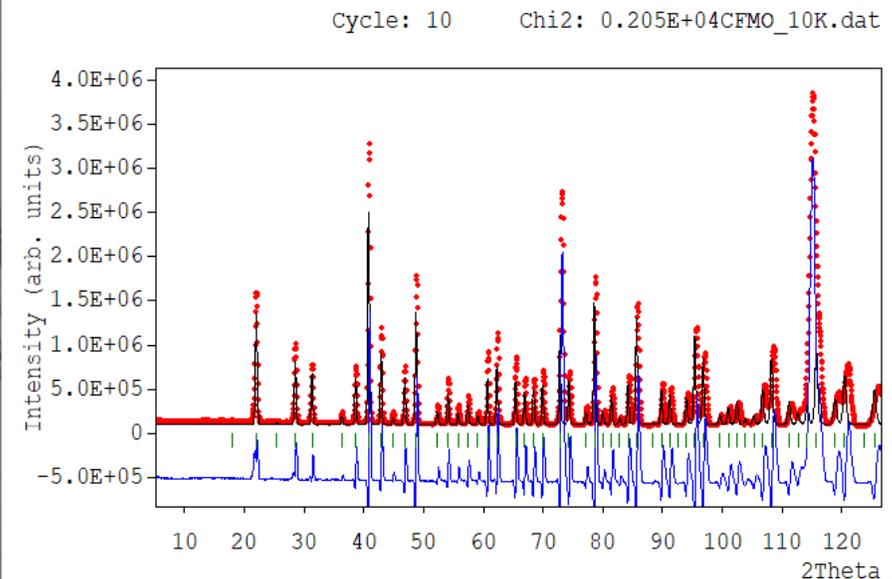
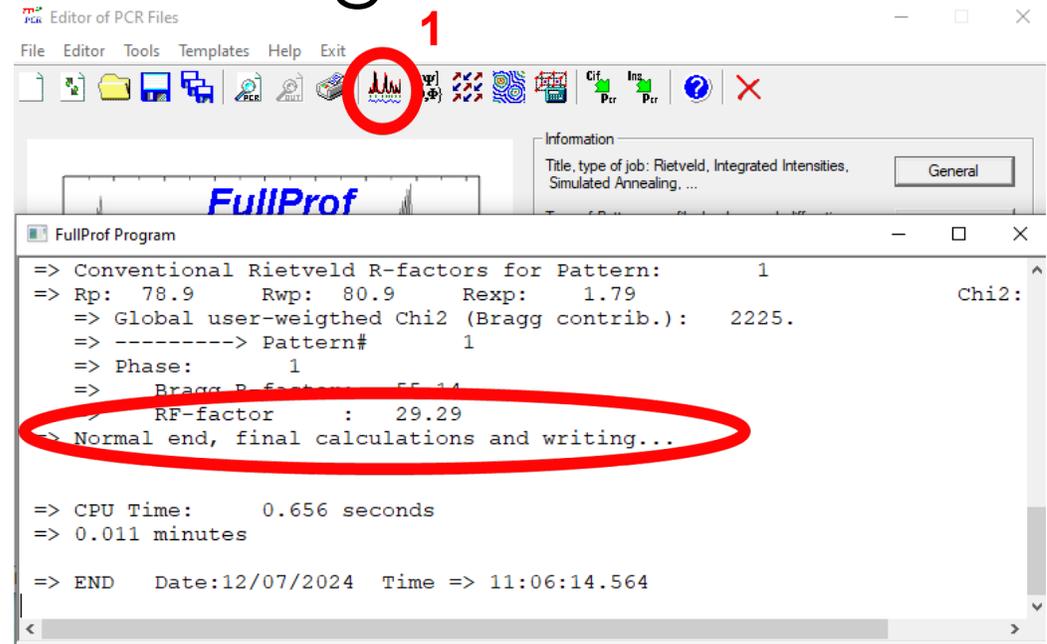
The screenshot displays the FullProf software interface. The main window is titled "FullProf PCR Editor" and shows a plot of intensity versus 2θ (degrees) with several peaks. The "Refinement" tab is selected in the "Information" panel, indicated by a red circle and the number 1. Below this, the "Profile Parameters: Phase 1 Pattern 1" dialog box is open. In this dialog, the "Scale" parameter is set to 100, circled in red with the number 3. The "Cell Parameters" table is visible, showing values for a, b, c, alpha, beta, and gamma. The "FWHM / Shape Parameters" section is also visible. In the "Refinement Information" panel, the "Cycles of Refinement" is set to 10, circled in red. The "Refinement weighting model" is set to "Least Squares". The "Profile" button is circled in red with the number 2. The "HKL Shifts" button is also visible.

Crystal structure has been added.
Instrument parameters added. We have checked background.
BEFORE setting anything to vary, run the refinement with nothing refining.
This lets you see how close you are and if things have to be manually changed or if it is close enough to try a refinement

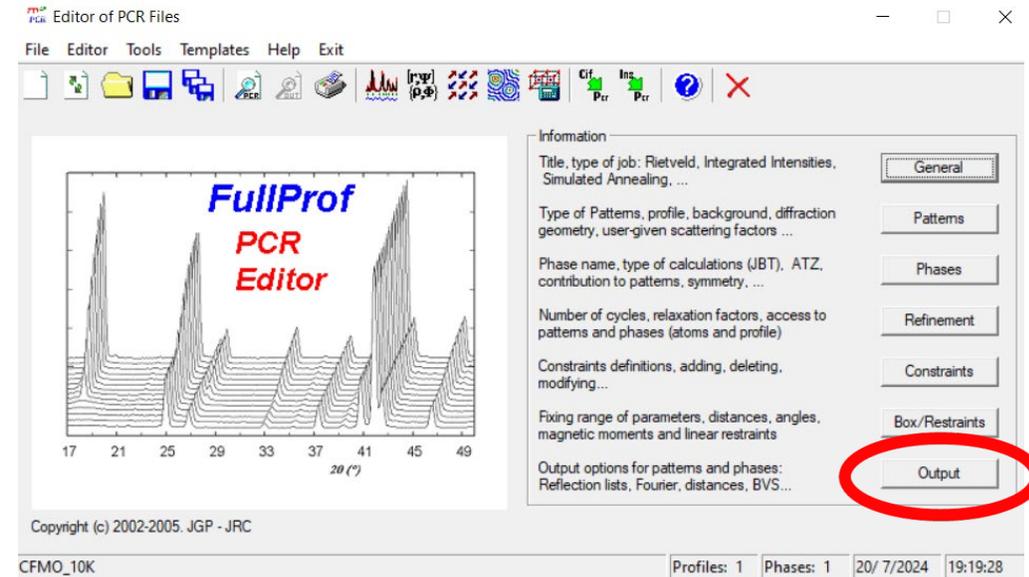
Step 1: Refine the crystal structure using FullProf

- 1. Run the refinement
Select the “CFMO_10K.dat” data
- 2. Refinement runs for the number of cycles or until converged. Since we’re not yet refining anything it just runs for ne cycle. You can repeat this by pushing run until “Normal end, final calculation and writing...” shows rather than “Convergence not reached”

The residual (blue) shows lots of differences between data (red) and model (black). But scale is close, background is close. Looks mainly like the position of the Bragg peaks are slightly off. We used a cif file from a database, likely different temperature.



When you first run a refinement several files are created in the same folder as the pcr file. Some by default and others than can be turned on/off using the output tab.



Now we can turn of parameters to refine
to try to get he model and data to match

Step 1: Refine the crystal structure using FullProf

- Now allow the following to refine to fit the nuclear crystal:
 - Scale factor (*Refinement>Profile*)
 - Lattice parameters (*Refinement>Profile*)
 - Background (*Refinement>Background*)
 - 2theta zero. (*Refinement>Instrumental*)
Zero corrects for any offset between two-theta in data and actual two-theta, should be small.
- Can also try to refine atomic parameters (but in this case data may not have enough reflections to be stable):
Refinement → Phase tab → Atoms

Profile Parameters: Phase 1 Pattern 1

Factors		
	Scale	Overall B-factor
Coefficients	100.00 <input checked="" type="checkbox"/>	0.0000 <input type="checkbox"/>

Cell Parameters						
	a	b	c	alpha	beta	gamma
Coefficients	10.916100 <input checked="" type="checkbox"/>	10.916100 <input checked="" type="checkbox"/>	10.916100 <input checked="" type="checkbox"/>	90.000 <input type="checkbox"/>	90.000 <input type="checkbox"/>	90.000 <input type="checkbox"/>

FWHM / Shape Parameters Asymmetry Parameters Preferred Orientation

FWHM Parameters				
	U	V	W	IG
Coefficients	0.000000 <input type="checkbox"/>	0.000000 <input type="checkbox"/>	0.000000 <input type="checkbox"/>	0.000000 <input type="checkbox"/>

Refine All Fix All

6 Coefficients Polynomial Background: Pattern 1

6 Coefficients Polynomial Background: Pattern 1						
	d_0	d_1	d_2	d_3	d_4	d_5
Coefficients	0.10000E+06 <input checked="" type="checkbox"/>	0.0000 <input type="checkbox"/>	0.0000 <input type="checkbox"/>			
	d_6	d_7	d_8	d_9	d_10	d_11
Coefficients	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Refine All Fix All

Instrumental Parameters Refinement: Pattern 1

2_Theta				
	Zero	Displacement	Transparency	Wavelength
Coefficients	0.000000 <input checked="" type="checkbox"/>	0.000000 <input type="checkbox"/>	0.000000 <input type="checkbox"/>	0.000000 <input type="checkbox"/>

Refine All Fix All
Cancel OK

List of Atoms

Number of Atoms:

	Label	Ntyp	X	Y	Z	B	Occ	Them. Fact.
Atom # 1	Ho1	Ho	0.50000 <input type="checkbox"/>	0.00000 <input type="checkbox"/>	0.20250 <input checked="" type="checkbox"/>	0.00000 <input type="checkbox"/>	0.25000 <input type="checkbox"/>	Isotropic
Atom # 2	Ba1	Ba	0.50000 <input type="checkbox"/>	0.50000 <input type="checkbox"/>	0.00000 <input type="checkbox"/>	0.00000 <input type="checkbox"/>	0.12500 <input type="checkbox"/>	Isotropic
Atom # 3	Ni1	Ni	0.00000 <input type="checkbox"/>	0.00000 <input type="checkbox"/>	0.00000 <input type="checkbox"/>	0.00000 <input type="checkbox"/>	0.12500 <input type="checkbox"/>	Isotropic
Atom # 4	O1	O	0.00000 <input type="checkbox"/>	0.24140 <input checked="" type="checkbox"/>	0.14950 <input checked="" type="checkbox"/>	0.00000 <input type="checkbox"/>	0.50000 <input type="checkbox"/>	Isotropic

Refinement parameters in Fullprof

Checking the box turns the number **blue** to show they are set to refine.

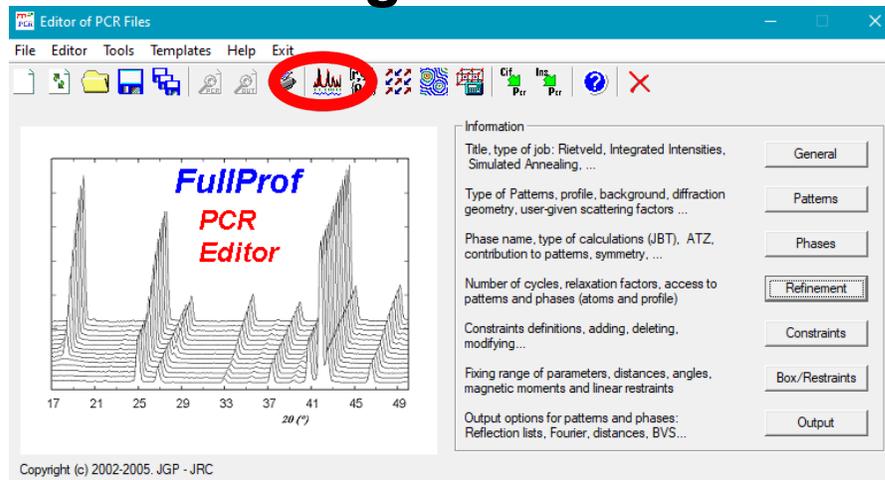
If they are **red** then they are constrained to refine with another parameter.

Looking in the text of the pcr file shows refined parameters by codes ending in 1.

Those constrained have the same code e.g. 11 and 11 or 511 and 511.

Step 1: Refine the crystal structure using FullProf

Run refinement again



FullProf Program

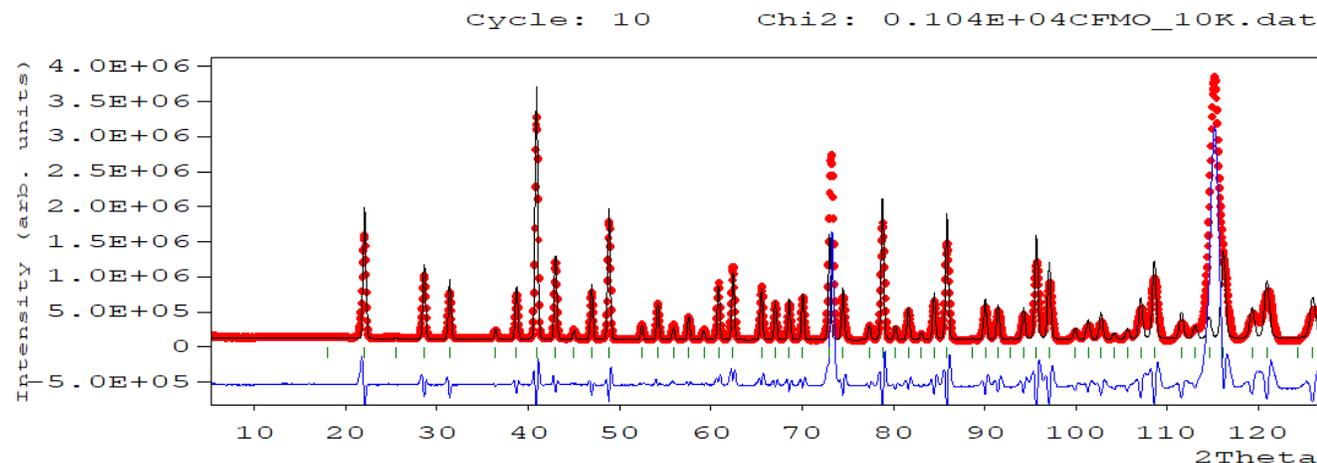
```
=====>>> CYCLE:      10
=> Control file *.pcr: ICSD_CollCode422752
=> Pattern: 1 CFMO_10K
=> Calculation of Yi for all points + Normal Matrix & Vector...
=> Calculation for pattern: 1
=> Solving L.S. equations...
=> Writing results for cycle      10
=> R-Factors: 30.4      42.5      Chi2: 0.104E+04 DW-Stat.: 0.0325      Patt#: 1
=> Expected :          1.32                      1.8795
=> Conventional Rietveld R-factors for Pattern: 1
=> Rp: 49.5      Rwp: 58.4      Rexp: 1.81                      Chi2: 0.104E+04
=> Global user-weighted Chi2 (Bragg contrib.): 1132.
=> -----> Pattern# 1
=> Phase: 1
=> Bragg R-factor: 33.09
=> RF-factor : 16.45
=> Conv. not yet reached -> [Max] Shift(Cell_A_ph1_pat1)/(eps*Sigma)= 14.71 abs> 1
=> Normal end, final calculations and writing...

=> CPU Time: 2.232 seconds
=> 0.037 minutes

=> END Date:12/07/2024 Time => 11:25:26.900
```

- Refinement is getting close.
- Peak positions look better. But the peak shape isn't matching
 - Refine peak profiles next

Peak profiles should only be run after the refinement and peak positions are close, others refinement will blow-up



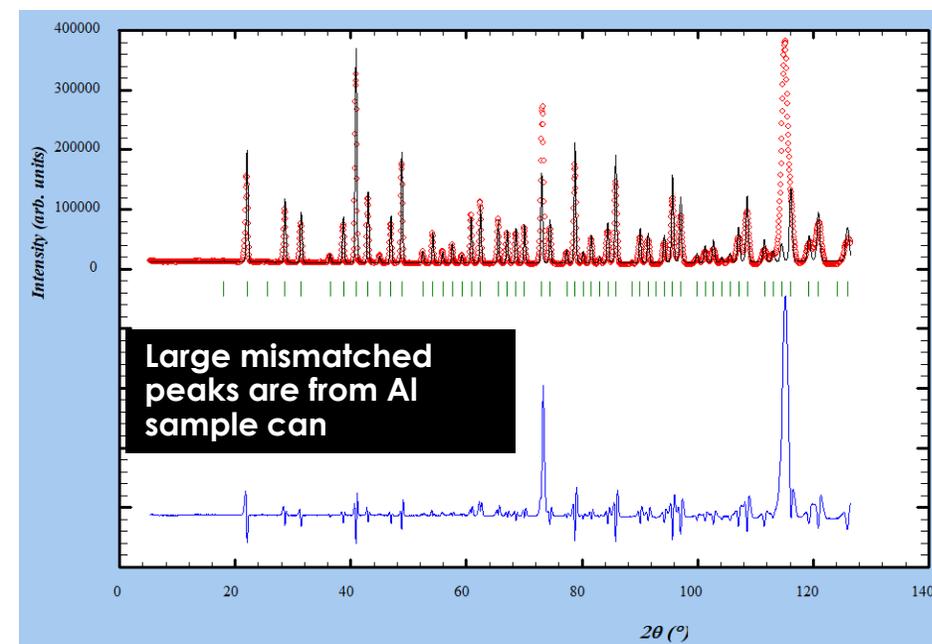
Step 1: Refine the crystal structure using FullProf

Run refinement again

Can be easier to look at fit in WINPLOTR which opens the created .prf file.

Name	Date modified		
backup	7/11/2024 10:41 AM		
CFMO_10K	2/29/2024 11:13 PM		
CFMO_300mK	2/28/2024 7:59 PM		
edpqr.set	7/12/2024 11:06 AM		
fullprof.dir	7/12/2024 11:31 AM		
HB2A_Ge113	7/11/2024 5:08 PM		
ICSD_CollCode422752	2/29/2024 2:36 PM		
ICSD_CollCode422752.out	7/12/2024 11:25 AM	OUT File	117 KB
ICSD_CollCode422752	7/12/2024 11:31 AM	PCR File	5 KB
ICSD_CollCode422752	7/12/2024 11:25 AM	PRF File	129 KB
ICSD_CollCode422752	7/12/2024 11:25 AM	SUM File	8 KB
ICSD_CollCode4227521	7/12/2024 11:25 AM	FST File	1 KB
ICSD_CollCode4227521.mic	7/12/2024 11:25 AM	MIC File	17 KB
Published_paper_Cs2Fe2(MoO4)3	7/10/2024 10:50 AM	Adobe Acrobat D...	5,506 KB
tfp.set	7/11/2024 11:24 AM	SET File	1 KB
winplotr.mlf	7/11/2024 11:25 AM	MLF File	1 KB

Set WINPLOTR to always open .prf files. Then don't need to rely on toolbar (which doesn't always work)



Step 1: Refine the crystal structure using FullProf

Run refinement again (10 K data)

- Refinement getting close.
- Refine peak positions:
- Refinement>profile
- Refine U,V,W.
- These are the Caglioti parameters that define peak shape for reactor based instruments.

Profile Parameters: Phase 1 Pattern 1

Factors	
Scale	149.28 <input checked="" type="checkbox"/>
Overall B-factor	0.0000 <input type="checkbox"/>

Cell Parameters						
	a	b	c	alpha	beta	gamma
Coefficients	10.890513 <input checked="" type="checkbox"/>	10.890513 <input checked="" type="checkbox"/>	10.890513 <input checked="" type="checkbox"/>	90.000 <input type="checkbox"/>	90.000 <input type="checkbox"/>	90.000 <input type="checkbox"/>

FWHM / Shape Parameters Asymmetry Parameters Preferred Orientation

FWHM Parameters				
	U	V	W	IG
Coefficients	0.000 <input checked="" type="checkbox"/>	0.000 <input checked="" type="checkbox"/>	0.000 <input checked="" type="checkbox"/>	0.000000 <input type="checkbox"/>

Shape Parameters			
	X	Y	SZ
Coefficients	0.000 <input type="checkbox"/>	0.000000 <input type="checkbox"/>	0.000000 <input type="checkbox"/>

Refine FWHM for second wavelength

	U2	V2	W2
Coefficients	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Refine All
Fix All
Cancel
OK

These are zero here BUT reading the values from the .irf file. So refining them will add on to the values. This is a way to see how much peak broadening comes from sample. For detailed refinements could use strain, grain size, etc. We don't need this for magnetism

Step 1: Refine the crystal structure using FullProf

Run refinement again (10 K data)

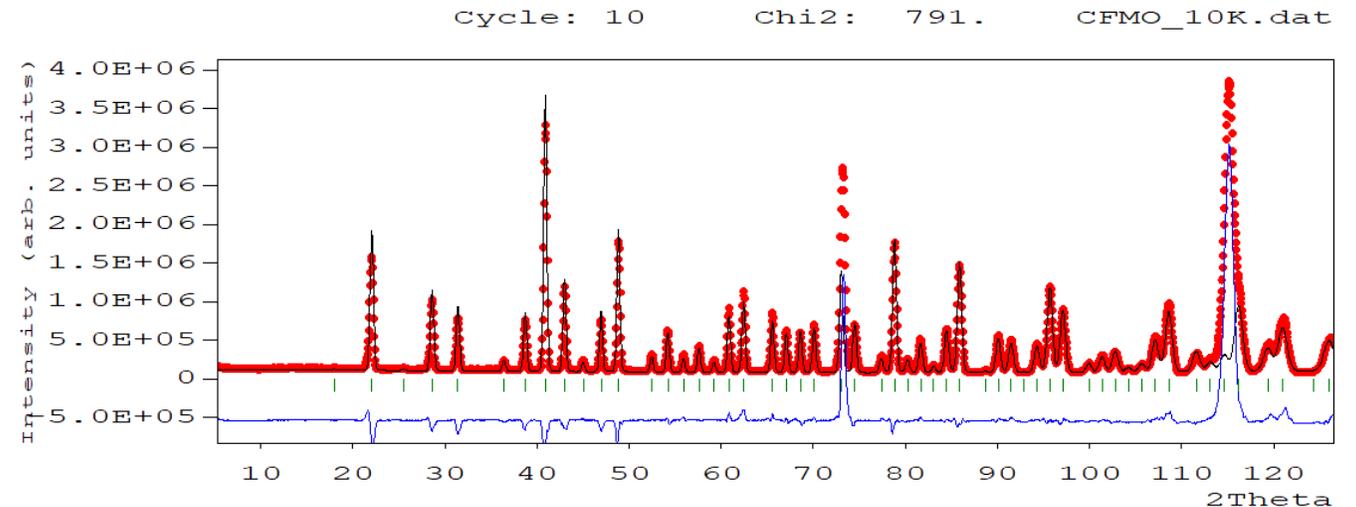
- Now much closer.
 - Do not focus on the chi or other fit values, visually see how close the fit is and what needs improved.
- Two peaks are not fit. These are at 2theta positions consistent with the Al sample can.
 - To save time we will simple exclude the regions around the Al can. But these can and should be fit in final published refinement. But cannot just add an Al phase due to texture. Need to use profile matching to fit each peak separately.

```
FullProf Program
=> Expected : 1.32 1.8820
=> Conventional Rietveld R-factors for Pattern: 1
=> Rp: 33.7 Rwp: 49.2 Rexp: 1.75 Chi2: 791.
=> Global user-weighted Chi2 (Bragg contrib.): 859.5
=> -----> Pattern# 1
=> Phase: 1
=> Bragg R-factor: 29.69
=> RF-factor : 12.84

=> Convergence reached at this CYCLE !!!!: CYCLE No. 7
=> R-Factors: 22.5 37.0 Chi2: 791. DW-Stat.: 0.0126 Patt#: 1
=> Expected : 1.32 1.8820
=> Conventional Rietveld R-factors for Pattern: 1
=> Rp: 33.7 Rwp: 49.2 Rexp: 1.75 Chi2: 791.
=> Global user-weighted Chi2 (Bragg contrib.): 860.1
=> -----> Pattern# 1
=> Phase: 1
=> Bragg R-factor: 29.69
=> RF-factor : 12.84
=> Normal end, final calculations and writing...

=> CPU Time: 2.207 seconds
=> 0.037 minutes

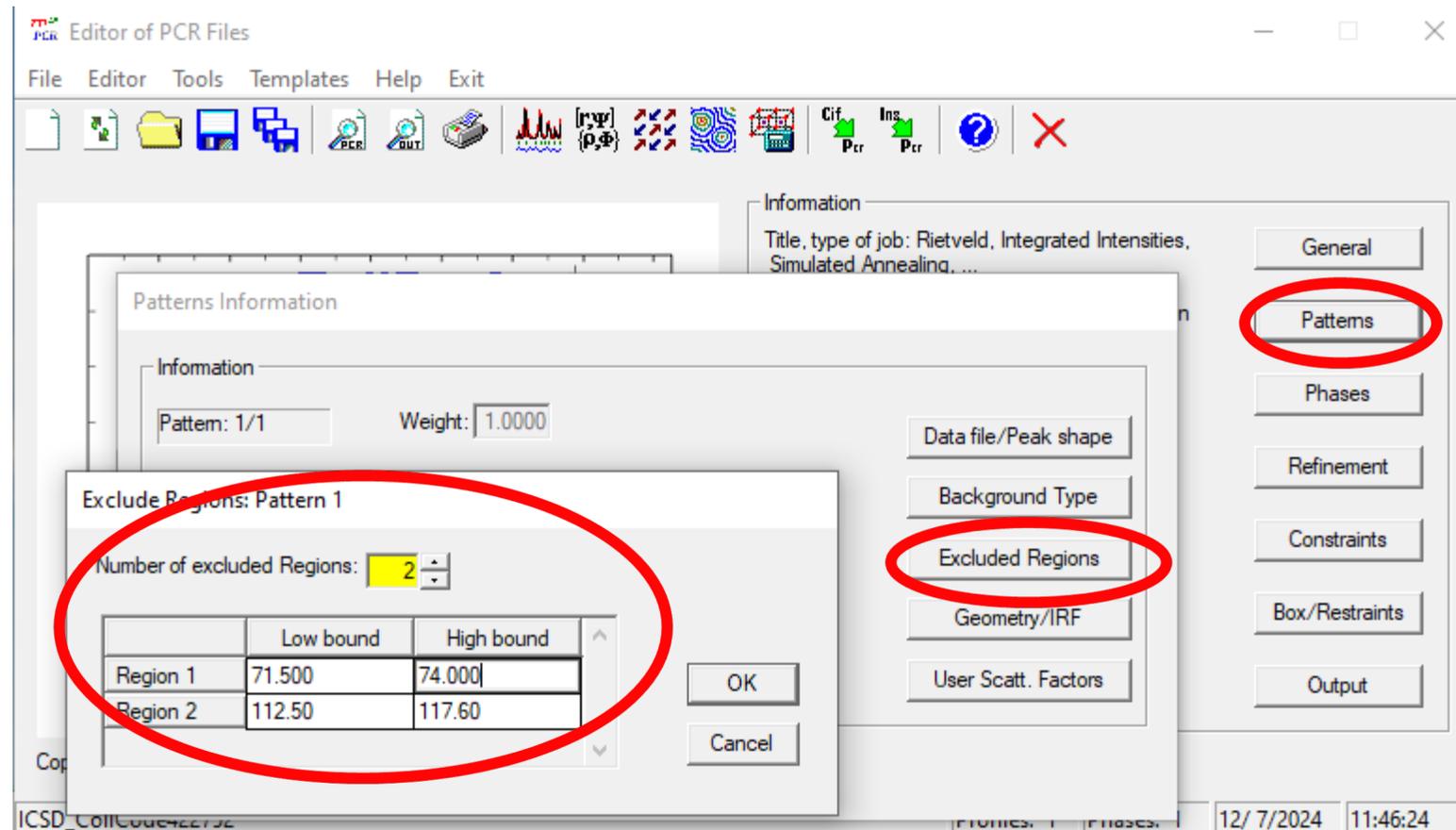
=> END Date:12/07/2024 Time => 11:40:46.599
```



Step 1: Refine the crystal structure using FullProf

Exclude the Al sample holder. This cannot be fit by adding a standard Al phase since it is highly textured, to fit this would need to do profile matching and fit each peak separately.

- Look at data and fit to choose which regions to cut out.
- Patterns>Excluded Regions



Step 1: Refine the crystal structure using FullProf

- Can also try to refine atomic parameters (but in this case data may not have enough reflections to be stable): Refinement → Phase tab → Atoms
- Click “Refine Positions”

Atoms Information: Phase 1

The screenshot shows the 'List of Atoms' table in the FullProf software. The table has columns for Label, Ntyp, X, Y, Z, B, Occ, and Therm. Fact. The 'B' column is circled in red, and the 'Therm. Fact.' column is also circled in red. The 'Refine Positions' button is circled in red on the right side of the interface.

	Label	Ntyp	X	Y	Z	B	Occ	Therm. Fact.
Atom # 1	Cs1	Cs	0.17938	0.32062	0.67938	0.30000	0.33333	Isotropic
Atom # 2	Mo1	Mo	0.30061	0.62363	0.52597	0.30000	1.00000	Isotropic
Atom # 3	Fe1	Fe	0.33737	0.33737	0.33737	0.30000	0.33333	Isotropic
Atom # 4	O1	O	0.27587	0.48544	0.44750	0.30000	1.00000	Isotropic

Below the table is the 'Anisotropic Thermal Factors / Form Factors' section, which is currently empty.

- Change all thermal parameters (B) to Isotropic in the “Therm. Fact.” column.
- Then make all B values 0.3. The maximum Q here is ~4 Å. So it is not high enough to refine thermal parameters.
- NOTE: do this for all 9 atoms, use scroll bar.

Step 1: Refine the crystal structure using FullProf

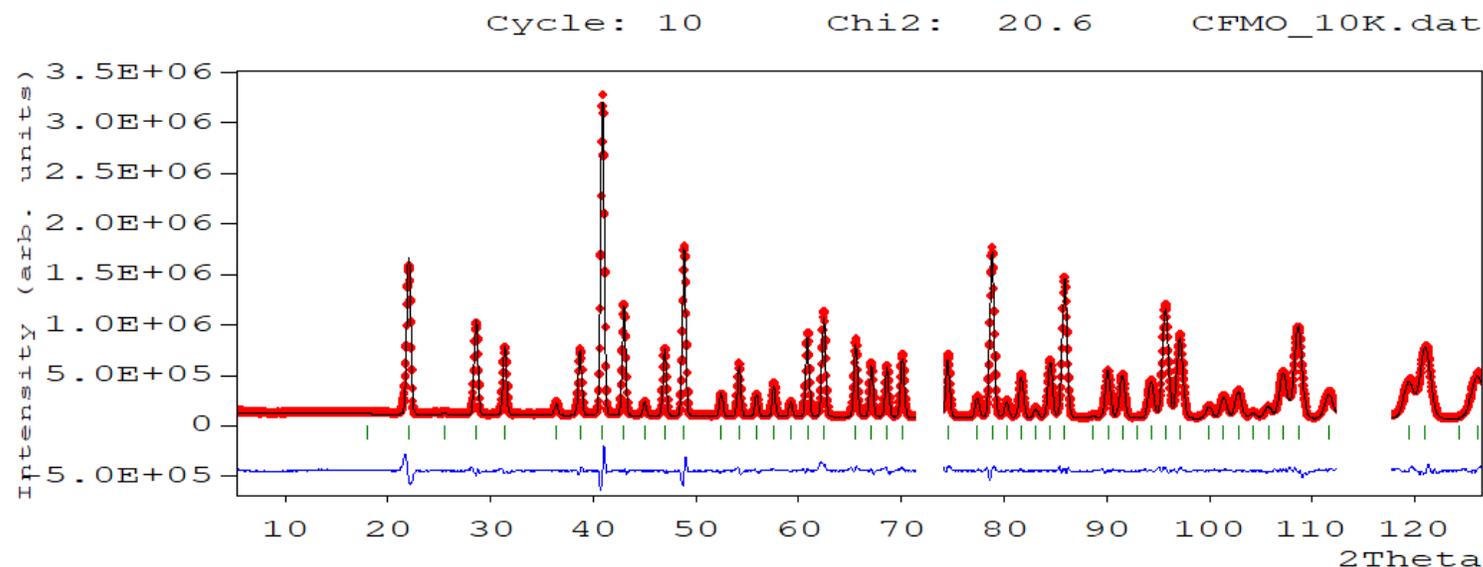
- Fit is now very close to the 10 K data.

```
FullProf Program
=> Bragg R-factor: 2.363
=> RF-factor : 1.397

=> Convergence reached at this CYCLE !!!!: CYCLE No. 10
=> R-Factors: 4.58 6.59 Chi2: 20.6 DW-Stat.: 0.1909 Patt#: 1
=> Expected : 1.45 1.8953
=> Conventional Rietveld R-factors for Pattern: 1
=> Rp: 7.48 Rwp: 9.33 Rexp: 2.05 Chi2: 20.6
=> Global user-weighted Chi2 (Bragg contrib.): 22.43
=> -----> Pattern# 1
=> Phase: 1
=> Bragg R-factor: 2.363
=> RF-factor : 1.397
=> Normal end, final calculations and writing...

=> CPU Time: 2.590 seconds
=> 0.043 minutes

=> END Date:12/07/2024 Time => 11:56:46.106
```



Step 1: Refine the crystal structure using FullProf

- Can try to refine the asymmetry further.

Profile Parameters: Phase 1 Pattern 1

Factors

	Scale		Overall B-factor	
Coefficients	152.24	<input checked="" type="checkbox"/>	0.0000	<input type="checkbox"/>

Cell Parameters

	a		b		c		alpha		beta		gamma	
Coefficients	10.885204	<input checked="" type="checkbox"/>	10.885204	<input checked="" type="checkbox"/>	10.885204	<input checked="" type="checkbox"/>	90.000	<input type="checkbox"/>	90.000	<input type="checkbox"/>	90.000	<input type="checkbox"/>

FWHM / Shape Parameters | **Asymmetry Parameters** | Preferred Orientation

	S_L		D_L	
Coefficients	0.000000	<input type="checkbox"/>	0.000000	<input type="checkbox"/>

	Asym 1		Asym 2		Asym 3		Asym 4	
Coefficients	0.000000	<input checked="" type="checkbox"/>						

	P5		P6		P7		P8	
Coefficients		<input type="checkbox"/>		<input type="checkbox"/>		<input type="checkbox"/>		<input type="checkbox"/>

Refine All
Fix All
Cancel
OK

Step 1: Refine the crystal structure using FullProf

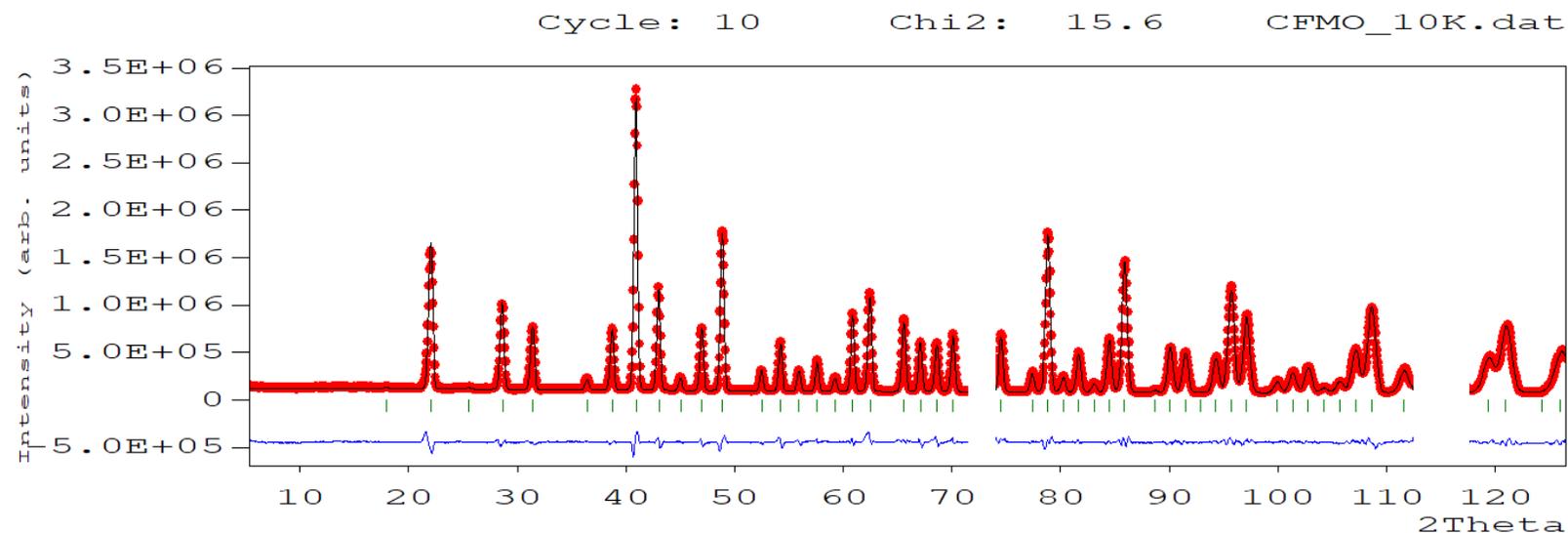
- Fit to the 10 K data is now good enough to move on to refine the 0.3 K data and try to determine the magnetic structure.
- Some mismatch could be from short range order that is expected in this material at 10 K.

```
FullProf Program
=> Expected : 1.45 1.9008
=> Conventional Rietveld R-factors for Pattern: 1
=> Rp: 6.85 Rwp: 8.14 Rexp: 2.06 Chi2: 15.6
=> Global user-weighted Chi2 (Bragg contrib.): 16.47
=> -----> Pattern# 1
=> Phase: 1
=> Bragg R-factor: 2.230
=> RF-factor : 1.588

=> Convergence reached at this CYCLE !!!!: CYCLE No. 6
=> R-Factors: 4.16 5.72 Chi2: 15.6 DW-Stat.: 0.2463 Patt#: 1
=> Expected : 1.45 1.9008
=> Conventional Rietveld R-factors for Pattern: 1
=> Rp: 6.85 Rwp: 8.14 Rexp: 2.06 Chi2: 15.6
=> Global user-weighted Chi2 (Bragg contrib.): 16.94
=> -----> Pattern# 1
=> Phase: 1
=> Bragg R-factor: 2.230
=> RF-factor : 1.588
=> Normal end, final calculations and writing...

=> CPU Time: 1.936 seconds
=> 0.032 minutes

=> END Date:12/07/2024 Time => 12:00:40.582
```



Now refine the 0.3 K
data using this model.
Before doing this TURN
OFF ALL PARAMATERS.

Step 1: Refine the crystal structure using FullProf

- Check everything is turned off in the text file.

```
External EdPCR Text Editor - [C:\Users\cr9\ORNL Dropbox\Stuart Calder\HB2A_POWDER\MagStr Workshops\MagStr2024_Calder\Cs2Fe2(...)
```

```
File Edit Search
```

```
COMM # (C) 2023 by FIZ Karlsruhe - Leibniz Institute for Information Infrastructure.
! Files => DAT-file: , PCR-file: ICSD_CollCode422752
! Job Npr Nph Nba Nex Nsc Nor Dum Iwg Ilo Ias Res Ste Nre Cry Uni Cor Opt Aut
1 7 1 0 2 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 1
!
! Resolution file for Pattern# 1
HB2A_Ge113.irf
! Ipr Ppl Ioc Mat Pcr Ls1 Ls2 Ls3 NLI Prf Ins Rpa Sym Hk1 Fou Sho Ana
0 0 1 0 1 0 4 0 0 3 10 0 0 0 0 0 0 0
!
! Lambda1 Lambda2 Ratio Bkpos wdt Cthm muR AsyLim Rpolarz 2nd-muR -> Patt# 1
2.406700 2.406700 0.00000 40.000 8.000 0.0000 0.0000 180.00 0.0000 0.0000
!
! NCY Eps R_at R_an R_pr R_gl Thmin Step Thmax PSD Sent0
10 0.10 1.00 1.00 1.00 1.00 -0.0200 0.030000 155.0000 0.000 0.000
!
! Excluded regions (LOWT HighT) for Pattern# 1
71.50 74.00
112.50 117.60
!
! 0 !Number of refined parameters
!
! Zero Code SyCos Code SySin Code Lambda Code MORE -> Patt# 1
0.03802 0.0 0.00000 0.0 0.00000 0.0 0.000000 0.00 0
!
! Background coefficients/codes for Pattern# 1 (Polynomial of 6th degree)
101536.125 -33252.898 12622.551 7347.125 -14217.325 4698.028
0.00 0.00 0.00 0.00 0.00 0.00
!
-----
! Data for PHASE number: 1 ==> Current R_Bragg for Pattern# 1: 0.0000
-----
# (C) 2023 by FIZ Karlsruhe - Leibniz Institute for Information Infrastructure. All rights reserved.
! Nat Dis Ang Pr1 Pr2 Pr3 Jbt Irf Isy Str Furth ATZ Nvk Npr More
9 0 0 0.0 0.0 1.0 0 0 0 0 0 3429.220 0 7 0
!
!
P 21 3 <--Space group symbol
! Atom Typ X Y Z Basis Occ In Fin N_t Spc /Codes
Cs1 Cs 0.17935 0.32065 0.67935 0.30000 0.33333 0 0 0 0
0.00 0.00 0.00 0.00 0.00
Mo1 Mo 0.29978 0.62310 0.52710 0.30000 1.00000 0 0 0 0
0.00 0.00 0.00 0.00 0.00
Fe1 Fe 0.33726 0.33726 0.33726 0.30000 0.33333 0 0 0 0
0.00 0.00 0.00 0.00 0.00
O1 O 0.27437 0.48199 0.45051 0.30000 1.00000 0 0 0 0
0.00 0.00 0.00 0.00 0.00
Cs2 Cs 0.45806 0.95806 0.54194 0.30000 0.33333 0 0 0 0
0.00 0.00 0.00 0.00 0.00
Fe2 Fe 0.61176 0.61176 0.61176 0.30000 0.33333 0 0 0 0
0.00 0.00 0.00 0.00 0.00
O2 O 0.45457 0.67094 0.51574 0.30000 1.00000 0 0 0 0
0.00 0.00 0.00 0.00 0.00
O3 O 0.25546 0.60404 0.68066 0.30000 1.00000 0 0 0 0
0.00 0.00 0.00 0.00 0.00
O4 O 0.20847 0.73550 0.45177 0.30000 1.00000 0 0 0 0
0.00 0.00 0.00 0.00 0.00
!
! -----> Profile Parameters for Pattern # 1 -----> Phase # 1
! Scale Shape1 Bov Str1 Str2 Str3 Strain-Model
152.4438 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0
0.00000 0.000 0.000 0.000 0.000 0.000
!
! U V W X Y Gausiz LorSiz Size-Model
0.574767 -0.547859 0.173882 0.000000 0.000000 0.000000 0.000000 0.000000 0
0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00
!
! a b c alpha beta gamma # Cell Info
10.892169 10.892169 10.892169 90.000000 90.000000 90.000000
0.00000 0.00000 0.00000 0.00000 0.00000 0.00000
!
! Pref1 Pref2 Asy1 Asy2 Asy3 Asy4 S_L D_L
0.00000 0.00000 0.07494 0.05829 0.27161 -0.02522 0.00000 0.00000
0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00
!
! 2Th1/TOF1 2Th2/TOF2 Pattern to plot
5.325 126.525 1
```

Step 1: Refine the crystal structure using FullProf

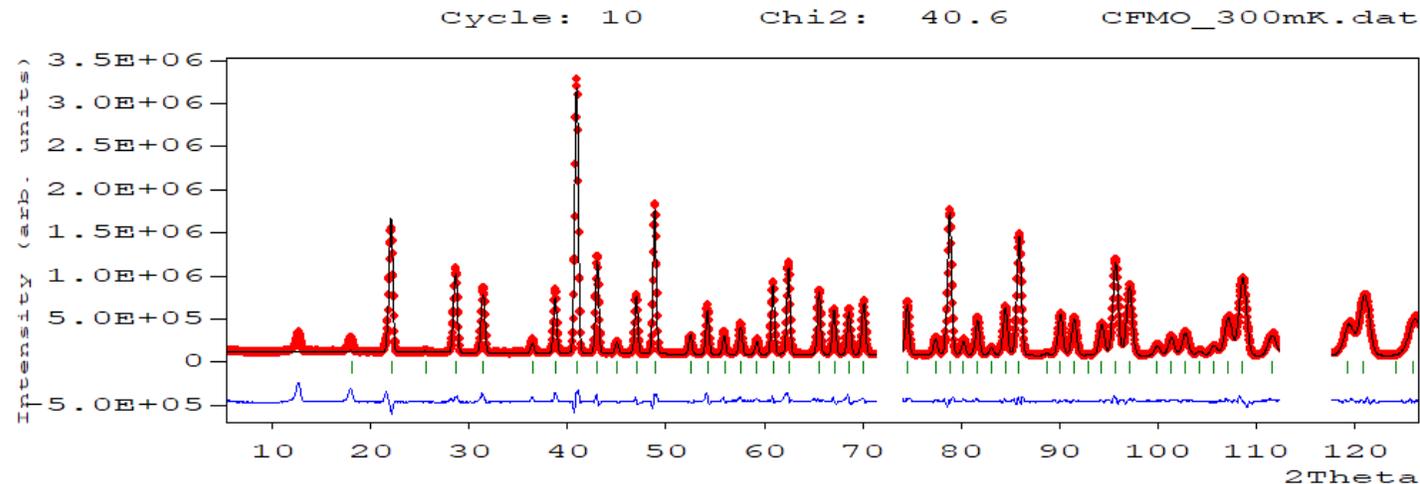
- Run refinement against the 0.3 K data
- “CFMO_300mK.dat”
- This looks good, with the extra magnetic peaks.
- Could refine lattice constants since the the temperature changed, but fits looks close that this isn't needed yet.

```
FullProf Program
=> Expected :          1.46          1.8695
=> Conventional Rietveld R-factors for Pattern:          1
=> Rp: 10.00   Rwp: 13.1   Rexp: 2.05          Chi2: 40.6
=> Global user-weighted Chi2 (Bragg contrib.): 29.39
=> -----> Pattern#          1
=> Phase:          1
=> Bragg R-factor: 3.077
=> RF-factor      : 1.998

=> Convergence reached at this CYCLE !!!!: CYCLE No.          1
=> R-Factors: 6.10   9.31   Chi2: 40.6   DW-Stat.: 0.1079   Patt#: 1
=> Expected :          1.46          1.8695
=> Conventional Rietveld R-factors for Pattern:          1
=> Rp: 10.00   Rwp: 13.1   Rexp: 2.05          Chi2: 40.6
=> Global user-weighted Chi2 (Bragg contrib.): 43.97
=> -----> Pattern#          1
=> Phase:          1
=> Bragg R-factor: 3.077
=> RF-factor      : 1.998
=> Normal end, final calculations and writing...

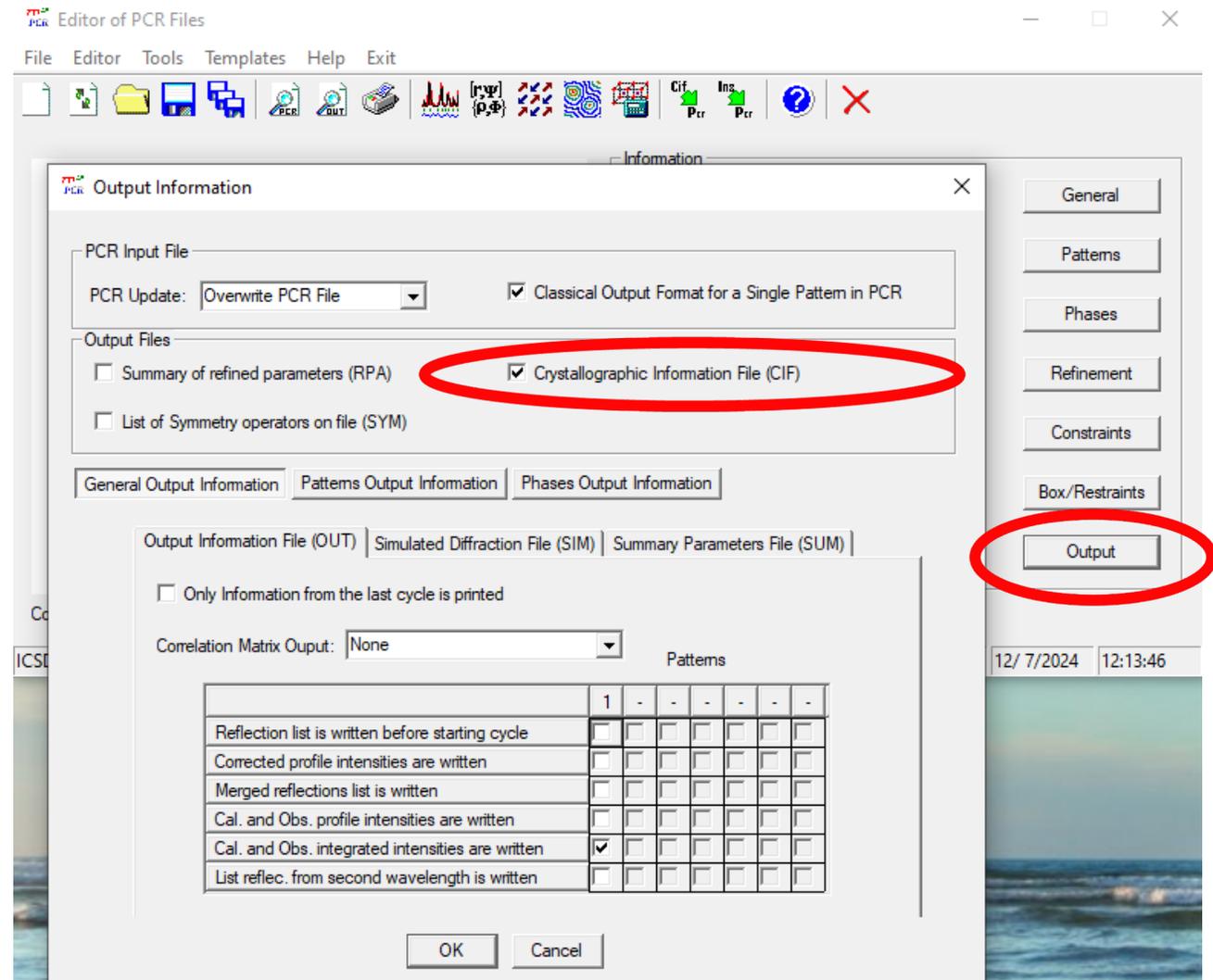
=> CPU Time: 0.752 seconds
=> 0.013 minutes

=> END   Date:12/07/2024   Time => 12:09:52.995
```



Step 1: Refine the crystal structure using FullProf

- Go into the “Output” tab to create a cif file after each refinement.
- This is a good way to check the structure makes sense.
- We will also use this as the starting point for our magnetic model.
- CHECK your folder to see all the files that are output when you run Fullprof.
- Link this cif file to open with VESTA



$\text{Cs}_2\text{Fe}_2(\text{MoO}_4)_3$: Refinement Strategy

- This example will use the Bilbao Crystallographic Server (<http://www.cryst.ehu.es/>) and follow these steps:
 - Step 1: Refine the crystal structure using FullProf
 - **Step 2: Determine the k-vector by indexing the magnetic reflections using k-search**
 - Step 3: Create test magnetic space groups using MAXMAGN on the Bilbao Crystallographic Server. Save these as mcif files.
 - Step 4: Convert the mcif file into a .pcr file using mCIF2PCR.
 - Step 5: Use the created .pcr file to fit the nuclear and magnetic neutron data using Fullprof to determined the magnetic structure.

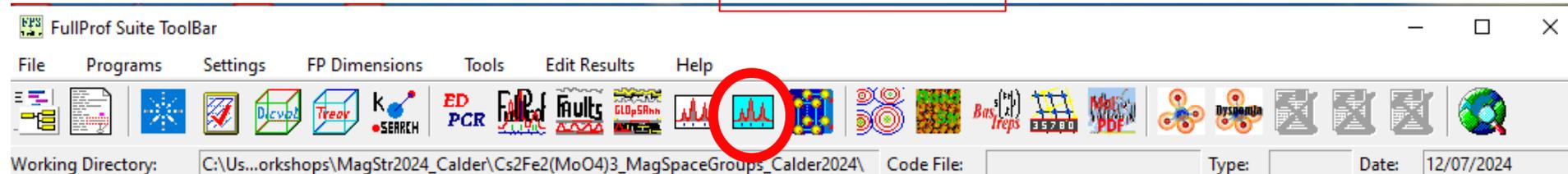
To determine the k-vector from powder data need to know the crystal structure and then index the magnetic peaks.

We have just refined the crystal structure.

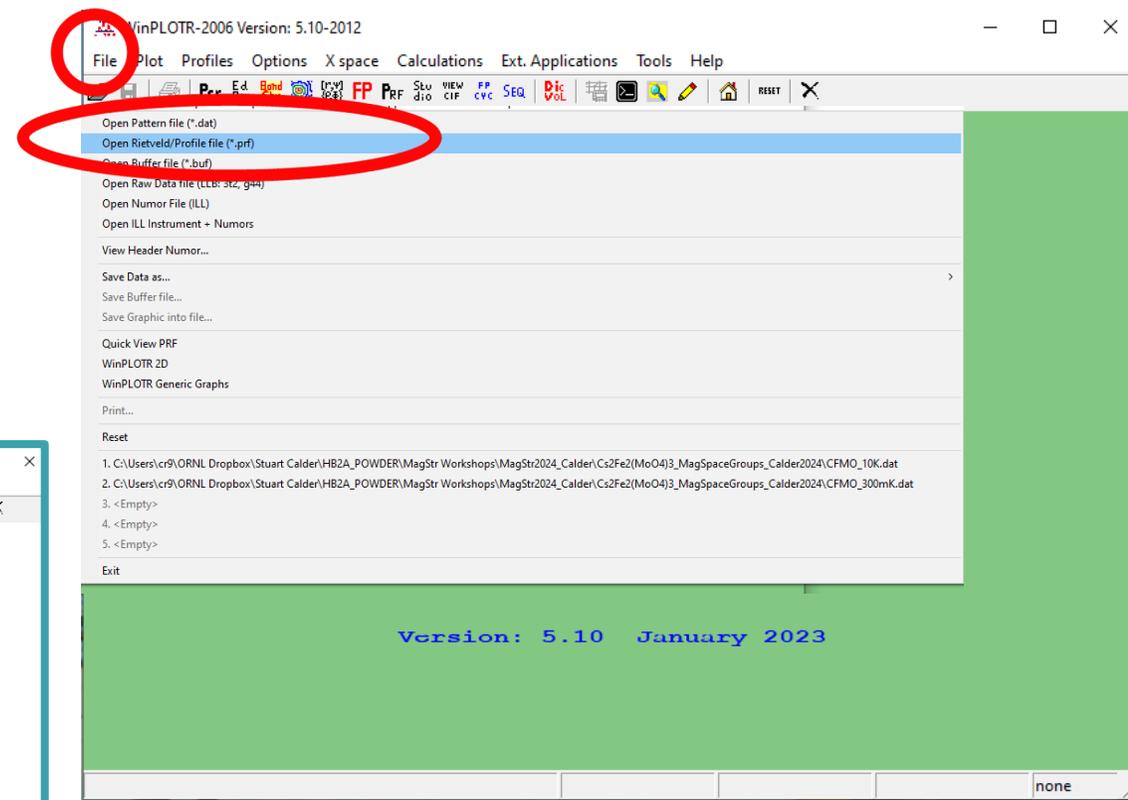
So we will load in this model and use the “k-search” feature in Fullprof

Determine the k-vector

WinPlotr-2006

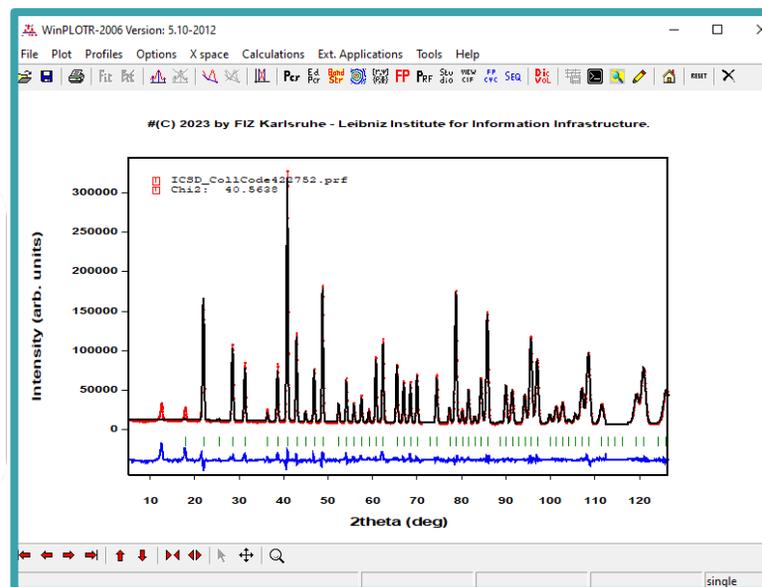


- k-search is run in WinPlotr-2006.
- Open the .prf file:
 - “File”>”Open Rietveld/Profile file (*.prf)”
 - Select the prf file



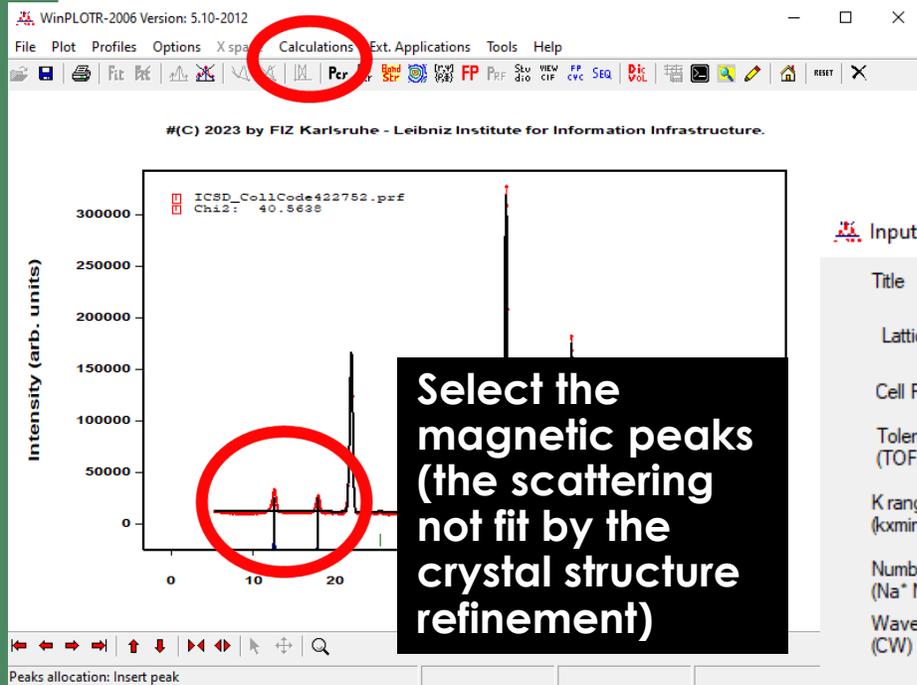
backup
ICSD_CollCode422752

NOTE: If the background changes to white this is a good sign. If it stays green, you might have issues with running k-search. Try running it, if issues then reopen a different way.



Determine the k-vector

- Now the magnetic peaks need to be indexed to find the propagation vector that defines the magnetic unit cell.
- Select “Calculations”> “peak detection”>”enable” . After enabling, go again to “Calculations”> “peak detection” > “insert peak”. After clicking on magnetic peaks, go to “save peaks” to save them as “K-search format”. Run k-search.



Input structural model, this is pulled from prf file

k=(0,0,0)

Determine the k-vector

A commensurate k-vector was found. If multiple k-vectors seem reasonable, then test them all!

In some cases no solutions are found.

This could indicate an incommensurate structure.

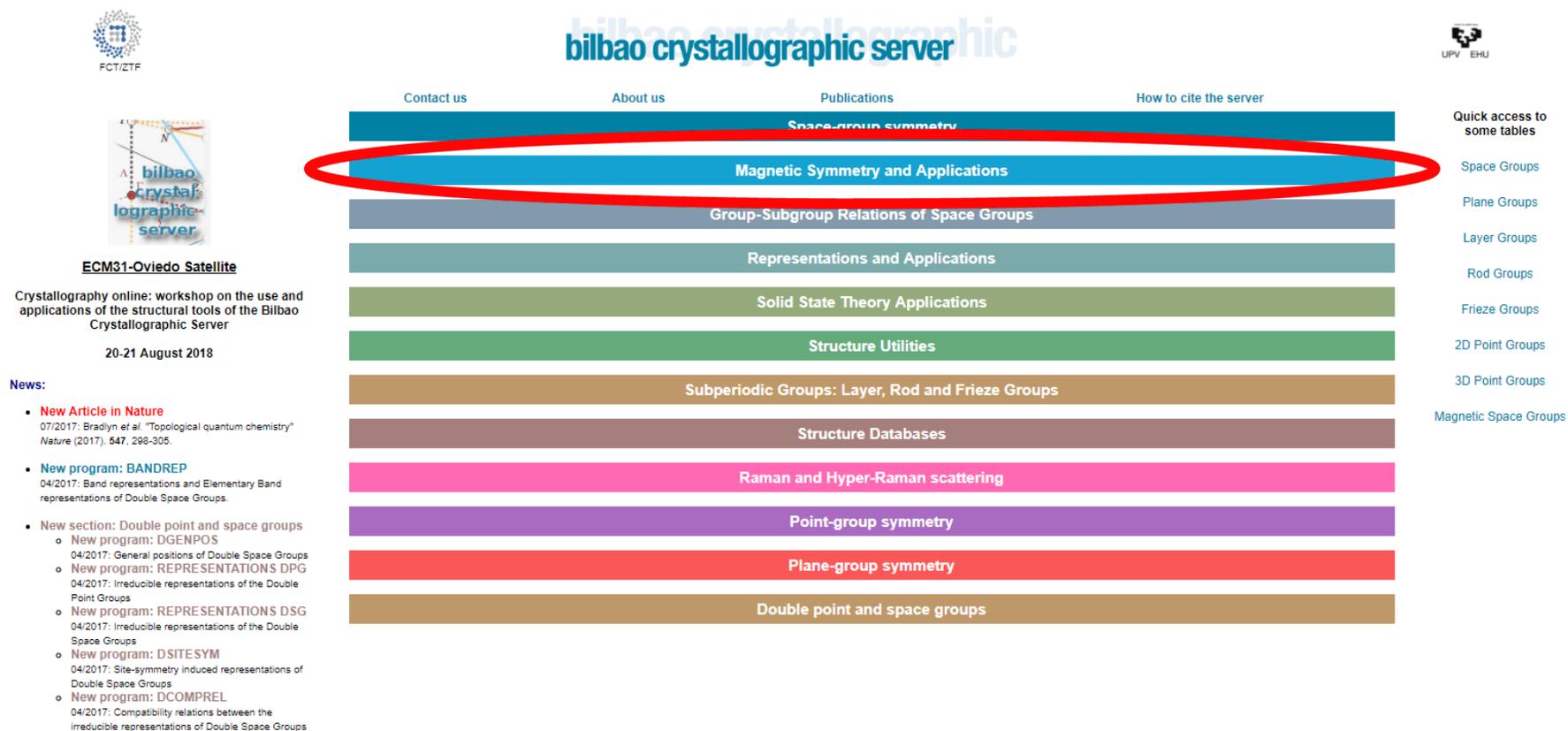
Determine an incommensurate structure uniquely from powders is very challenging. There is an example later in this workshop that looks at this case.

$\text{Cs}_2\text{Fe}_2(\text{MoO}_4)_3$: Refinement Strategy

- This example will use the Bilbao Crystallographic Server (<http://www.cryst.ehu.es/>) and follow these steps:
 - Step 1: Refine the crystal structure using FullProf
 - Step 2: Determine the k-vector by indexing the magnetic reflections using k-search
 - **Step 3: Create test magnetic space groups using MAXMAGN on the Bilbao Crystallographic Server. Save these as mcif files.**
 - Step 4: Convert the mcif file into a .pcr file using mCIF2PCR.
 - Step 5: Use the created .pcr file to fit the nuclear and magnetic neutron data using Fullprof to determined the magnetic structure.

Step 3: Creating mCIF file

- Go to Bilbao Crystallographic Server: <http://www.cryst.ehu.es/>
- Select “Magnetic Symmetry and Applications” to open the drop-down menu



The screenshot shows the Bilbao Crystallographic Server website. The main navigation bar includes links for "Contact us", "About us", "Publications", and "How to cite the server". Below this is a horizontal menu with various categories, where "Magnetic Symmetry and Applications" is highlighted with a red oval. To the right of the main menu is a "Quick access to some tables" section with links to "Space Groups", "Plane Groups", "Layer Groups", "Rod Groups", "Frieze Groups", "2D Point Groups", "3D Point Groups", and "Magnetic Space Groups".

ECM31-Oviedo Satellite
Crystallography online: workshop on the use and applications of the structural tools of the Bilbao Crystallographic Server
20-21 August 2018

News:

- **New Article in Nature**
07/2017: Bradlyn et al. "Topological quantum chemistry" *Nature* (2017), 547, 298-305.
- **New program: BANDREP**
04/2017: Band representations and Elementary Band representations of Double Space Groups.
- **New section: Double point and space groups**
 - New program: DGENPOS
04/2017: General positions of Double Space Groups
 - New program: REPRESENTATIONS DPG
04/2017: Irreducible representations of the Double Point Groups
 - New program: REPRESENTATIONS DSG
04/2017: Irreducible representations of the Double Space Groups
 - New program: DSITESYM
04/2017: Site-symmetry induced representations of Double Space Groups
 - New program: DCOMPREL
04/2017: Compatibility relations between the irreducible representations of Double Space Groups

Step 3: Creating mCIF file

- Then select “MAXMAGN”

bilbao crystallographic server

Contact us

About us

Publications

How to cite the server

Space-group symmetry

Magnetic Symmetry and Applications

MGENPOS	General Positions of Magnetic Space Groups
MWYCKPOS	Wyckoff Positions of Magnetic Space Groups
MNORMALIZER	Normalizers of Magnetic Space Groups
IDENTIFY MAGNETIC GROUP	Identification of a Magnetic Space Group from a set of generators in an arbitrary setting
BNS2OG	Transformation of symmetry operations between BNS and OG settings
mCIF2PCR	Transformation from mCIF to PCR format (FullProf).
MPOINT	Magnetic Point Group Tables
MAGNEXT	Extinction Rules of Magnetic Space Groups
MAXMAGN	Maximal magnetic space groups for a given space group and a propagation vector
MAGMODELIZE	Magnetic structure models for any given magnetic symmetry
STRCONVERT	Convert & Edit Structure Data (supports the CIF, mCIF, VESTA, VASP formats -- with magnetic information where available)
k-SUBGROUPSMAG ⚠	Magnetic subgroups consistent with some given propagation vector(s) or a supercell
MAGNDATA ⚠	A collection of magnetic structures with portable cif-type files
MVISUALIZE	3D Visualization of magnetic structures with Jmol
MTENSOR ⚠	Symmetry-adapted form of crystal tensors in magnetic phases
MAGNETIC REP.	Decomposition of the magnetic representation into irreps
Get_mirreps	Irreps and order parameters in a paramagnetic space group- magnetic subgroup phase transition

Step 3: Creating mCIF file

- Now the crystal structure and k-vector have been determined the magnetic structure can be found by testing model magnetic space groups.
- This can be done in FullProf by creating a .mcif file from the Bilbao Crystallographic Server.

Step 3: Creating mCIF file

- **[1]** Need to have a propagation vector. This was determined using k-search in fullprof (to be (0,0,0)).
- **[2]** Input the space group number of the crystal structure (or choose from a list of all space groups)- Note: if you have a cif file this step is not necessary.
- **[2]** Check the box “Structure data of the paramagnetic phase will be included”. This allows you to input a .cif file.

Bilbao Crystallographic Server → MAXMAGN

Help

MAXMAGN: Maximal magnetic space groups for a given a propagation vector and resulting magnetic structural models

MAXMAGN: Maximal magnetic space groups for a given a propagation vector and resulting magnetic structural models

MAXMAGN provides the possible magnetic space groups that can be assigned to a 1-k commensurate magnetic phase assuming that the magnetic symmetry is a maximal one. The space group of the paramagnetic phase (parent group) and the observed propagation vector are required as input. Optionally, the parent paramagnetic structure can be introduced (by hand or by a cif file). In this latter case the program provides the constrains for the different possible symmetries and cif-like files can be produced. These files permit the different alternative models to be analyzed, refined,

2

Structure data of the paramagnetic phase will be included Non-conventional setting

Please, enter the label of the space group of the paramagnetic phase (parent group)

1

Please, enter the propagation vector k:

Step 3: Creating mCIF file

- Choose .cif file (crystal structure only).
The one for this example is the one outputted from Fullprof, so will contain the correct crystal parameters at low temperature.
- Upload the cif file.

Bilbao Crystallographic Server → MAXMAGN - Maximal magnetic space groups

Parent paramagnetic structure cif file

Option 1: Please submit a structure file (CIF format):

ICSD_CollCode422752.cif

No space group provided. The space group indicated in the cif file will be taken.

Bilbao Crystallographic Server
<http://www.cryst.ehu.es>



Step 3: Creating mCIF file

- The paramagnetic phase information is displayed.
 - Select the magnetic atom(s). This case is there are two Fe ions.
 - Push Submit. This may take a few seconds to run the calculations.....

Bilbao Crystallographic Server → MAXMAGN - Maximal magnetic space groups

Parent phase structure data: Magnetic Atoms

Parent space group: $P2_13$ (No. 198)

Lattice parameters (Angstroms and degrees): a=10.89220, b=10.89220, c=10.89220, alpha=90.0000, beta=90.0000, gamma=90.0000

Atoms: Please select the magnetic ones

N	Atom name	Atom type	Wyckoff Position	Coordinates	Magnetic?
1	Cs1	Cs	4a	0.17935 0.32065 0.67935	<input type="checkbox"/>
2	Mo1	Mo	12b	0.29978 0.62310 0.52710	<input type="checkbox"/>
3	Fe1	Fe	4a	0.33726 0.33726 0.33726	<input checked="" type="checkbox"/>
4	O1	O	12b	0.27437 0.46199 0.45051	<input type="checkbox"/>
5	Cs2	Cs	4a	0.45806 0.05806 0.54194	<input type="checkbox"/>
6	Fe2	Fe	4a	0.61176 0.61176 0.61176	<input checked="" type="checkbox"/>
7	O2	O	12b	0.45457 0.67094 0.51574	<input type="checkbox"/>
8	O3	O	12b	0.25546 0.60404 0.68066	<input type="checkbox"/>
9	O4	O	12b	0.20847 0.73550 0.45177	<input type="checkbox"/>

Submit

Step 3: Creating mCIF file

Maximal magnetic space groups for the parent space group $P2_13$ (No. 198) and the propagation vector $k = (0, 0, 0)$

Maximal subgroups which allow non-zero magnetic moments for at least one atom are coloured

N	Group (BNS)	Transformation matrix	General positions	Properties	Magnetic structure
1	$P2_13$ (#198.9) Go to a subgroup	$\begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \end{pmatrix}$ Alternatives (domain-related)	Show	Systematic absences MAGNEXT Tensor properties MTENSOR	Show
2	$P2_1'2_1'2_1$ (#19.27) Go to a subgroup	$\begin{pmatrix} 0 & 0 & 1 & 1/4 \\ 0 & 1 & 0 & 1/4 \\ -1 & 0 & 0 & 1/4 \end{pmatrix}$ Alternatives (domain-related)	Show	Systematic absences MAGNEXT Tensor properties MTENSOR	Show

- The possible maximal magnetic space groups are displayed in grey
- To view magnetic structure and export mcif file click on “Show” in last column.

Step 3: Creating mCIF file: Check #1

Magnetic Structure

Selected magnetic space group: 1- $P2_13$ (#198.9)

Setting of the parent group

Parent space group $P2_13$ (No. 198)

Lattice parameters: a=10.89220, b=10.89220, c=10.89220, alpha=90.0000, beta=90.0000, gamma=90.0000

[Go to setting standard (a, b, c ; 0, 0, 0)]

[Go to an alternative setting]

Export data to MCIF file/Visualize Go to a subgroup

Bilbao Crystallographic Server → MAXMAGN - Maximal magnetic space groups Help

Maximal magnetic space groups for the parent space group $P2_13$ (No. 198) and the propagation vector $k = (0, 0, 0)$

Maximal subgroups which allow non-zero magnetic moments for at least one atom are coloured

N	Group (BNS)	Transformation matrix	General positions	Properties	Magnetic structure
1	$P2_13$ (#198.9) Go to a subgroup	$\begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \end{pmatrix}$ Alternatives (domain-related)	Show	Systematic absences MAGNEXT Tensor properties MTENSOR	Show
2	$P2_1'2_1'2_1'$ (#19.27) Go to a subgroup	$\begin{pmatrix} 0 & 0 & 1 & 1/4 \\ 0 & 1 & 0 & 1/4 \\ -1 & 0 & 0 & 1/4 \end{pmatrix}$ Alternatives (domain-related)	Show	Systematic absences MAGNEXT Tensor properties MTENSOR	Show

Atomic positions, Wyckoff positions and Magnetic Moments

N	Atom	New WP	Multiplicity	Magnetic moment	Values of M_x, M_y, M_z
1	Cs1 Cs 0.82065 0.82065 0.82065	$(x,x,x m_x, m_x, m_x) (-x+1/2, -x, x+1/2 -m_x, -m_x, m_x)$ $(-x, x+1/2, -x+1/2 -m_x, m_x, -m_x) (x+1/2, -x+1/2, -x m_x, -m_x, -m_x)$	4	-	-
2	Mo1 Mo 0.29978 0.62310 0.52710	$(x,y,z m_x, m_y, m_z) (-x+1/2, -y, z+1/2 -m_x, -m_y, m_z)$ $(-x, y+1/2, -z+1/2 -m_x, m_y, -m_z) (x+1/2, -y+1/2, -z m_x, -m_y, -m_z)$ $(z,x,y m_z, m_x, m_y) (z+1/2, -x+1/2, -y m_z, -m_x, -m_y)$ $(-z+1/2, -x, y+1/2 -m_z, -m_x, m_y) (-z, x+1/2, -y+1/2 -m_z, m_x, -m_y)$ $(y,z,x m_y, m_z, m_x) (-y, z+1/2, -x+1/2 -m_y, m_z, -m_x)$ $(y+1/2, -z+1/2, -x m_y, -m_z, -m_x) (-y+1/2, -z, x+1/2 -m_y, -m_z, m_x)$	12	-	-
3	Fe1 Fe 0.33726 0.33726 0.33726	$(x,x,x m_x, m_x, m_x) (-x+1/2, -x, x+1/2 -m_x, -m_x, m_x)$ $(-x, x+1/2, -x+1/2 -m_x, m_x, -m_x) (x+1/2, -x+1/2, -x m_x, -m_x, -m_x)$	4	(M_x, M_x, M_x)	$M_x = 0.00000$
4	O1 O 0.27437 0.48199 0.45051	$(x,y,z m_x, m_y, m_z) (-x+1/2, -y, z+1/2 -m_x, -m_y, m_z)$ $(-x, y+1/2, -z+1/2 -m_x, m_y, -m_z) (x+1/2, -y+1/2, -z m_x, -m_y, -m_z)$ $(z,x,y m_z, m_x, m_y) (z+1/2, -x+1/2, -y m_z, -m_x, -m_y)$ $(-z+1/2, -x, y+1/2 -m_z, -m_x, m_y) (-z, x+1/2, -y+1/2 -m_z, m_x, -m_y)$ $(y,z,x m_y, m_z, m_x) (-y, z+1/2, -x+1/2 -m_y, m_z, -m_x)$ $(y+1/2, -z+1/2, -x m_y, -m_z, -m_x) (-y+1/2, -z, x+1/2 -m_y, -m_z, m_x)$	12	-	-
5	Cs2 Cs 0.04194 0.04194 0.04194	$(x,x,x m_x, m_x, m_x) (-x+1/2, -x, x+1/2 -m_x, -m_x, m_x)$ $(-x, x+1/2, -x+1/2 -m_x, m_x, -m_x) (x+1/2, -x+1/2, -x m_x, -m_x, -m_x)$	4	-	-
6	Fe2 Fe 0.61176 0.61176 0.61176	$(x,x,x m_x, m_x, m_x) (-x+1/2, -x, x+1/2 -m_x, -m_x, m_x)$ $(-x, x+1/2, -x+1/2 -m_x, m_x, -m_x) (x+1/2, -x+1/2, -x m_x, -m_x, -m_x)$	4	(M_x, M_x, M_x)	$M_x = 0.00000$

Bilbao Crystallographic Server  For comments, please mail to administrador.bcs@ehu.es

- The Fe ions have a magnetic moment (M_x, M_x, M_x)
- Shows the moment is constrained to be along 111 direction.
- Makes refinement easier!

Step 3: Creating mCIF file:

Check #2

Selected magnetic space group: 2- $P2_1'2_1'2_1$ (#19.27)

Setting of the parent group

Parent space group $P2_13$ (No. 198)

Lattice parameters: a=10.89220, b=10.89220, c=10.89220, alpha=90.0000, beta=90.0000, gamma=90.0000

[Go to setting standard (-c, b, a ; 1/4, 1/4, 1/4)]
 [Go to an alternative setting]

Export data to MCIF file/Visualize Go to a subgroup

Bilbao Crystallographic Server → MAXMAGN - Maximal magnetic space groups Help

Maximal magnetic space groups for the parent space group $P2_13$ (No. 198) and the propagation vector $k = (0, 0, 0)$

Maximal subgroups which allow non-zero magnetic moments for at least one atom are coloured

N	Group (BNS)	Transformation matrix	General positions	Properties	Magnetic structure
1	$P2_13$ (#198.9) Go to a subgroup	$\begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \end{pmatrix}$ Alternatives (domain-related)	Show	Systematic absences MAGNEXT Tensor properties MTENSOR	Show
2	$P2_1'2_1'2_1$ (#19.27) Go to a subgroup	$\begin{pmatrix} 0 & 0 & 1 & 1/4 \\ 0 & 1 & 0 & 1/4 \\ -1 & 0 & 0 & 1/4 \end{pmatrix}$ Alternatives (domain-related)	Show	Systematic absences MAGNEXT Tensor properties MTENSOR	Show

Bilbao Crystallographic Server For comments, please mail to administrator.bcs@ehu.es

Atomic positions, Wyckoff positions and Magnetic Moments

N	Atom	New WP	Multiplicity	Magnetic moment	Values of M_x, M_y, M_z
1	Cs1 Cs 0.82065 0.82065 0.82065	$(x,x,x m_x, m_y, m_z) (-x+1/2, -x, x+1/2 m_x, m_y, -m_z)$ $(-x, x+1/2, -x+1/2 m_x, -m_y, m_z) (x+1/2, -x+1/2, -x m_x, -m_y, -m_z)$	4	-	-
2	Mo1_1 Mo 0.29978 0.62310 0.52710	$(x,y,z m_x, m_y, m_z) (-x+1/2, -y, z+1/2 m_x, m_y, -m_z)$ $(-x, y+1/2, -z+1/2 m_x, -m_y, m_z) (x+1/2, -y+1/2, -z m_x, -m_y, -m_z)$	4	-	-
	Mo1_2 Mo 0.52710 0.29978 0.62310	$(z,x,y m_x, m_y, m_z) (z+1/2, -x+1/2, -y m_x, -m_y, -m_z)$ $(-z+1/2, -x, y+1/2 m_x, m_y, -m_z) (-z, x+1/2, -y+1/2 m_x, -m_y, m_z)$	4	-	-
	Mo1_3 Mo 0.62310 0.52710 0.29978	$(y,z,x m_x, m_y, m_z) (-y, z+1/2, -x+1/2 m_x, -m_y, m_z)$ $(y+1/2, -z+1/2, -x m_x, -m_y, -m_z) (-y+1/2, -z, x+1/2 m_x, m_y, -m_z)$	4	-	-
3	Fe1 Fe 0.33726 0.33726 0.33726	$(x,x,x m_x, m_y, m_z) (-x+1/2, -x, x+1/2 m_x, m_y, -m_z)$ $(-x, x+1/2, -x+1/2 m_x, -m_y, m_z) (x+1/2, -x+1/2, -x m_x, -m_y, -m_z)$	4	(M_x, M_y, M_z)	$M_x = 0.00000$ $M_y = 0.00000$ $M_z = 0.00000$
4	O1_1 O 0.27437 0.48199 0.45051	$(x,y,z m_x, m_y, m_z) (-x+1/2, -y, z+1/2 m_x, m_y, -m_z)$ $(-x, y+1/2, -z+1/2 m_x, -m_y, m_z) (x+1/2, -y+1/2, -z m_x, -m_y, -m_z)$	4	-	-
	O1_2 O 0.45051 0.27437 0.48199	$(z,x,y m_x, m_y, m_z) (z+1/2, -x+1/2, -y m_x, -m_y, -m_z)$ $(-z+1/2, -x, y+1/2 m_x, m_y, -m_z) (-z, x+1/2, -y+1/2 m_x, -m_y, m_z)$	4	-	-
	O1_3 O 0.48199 0.45051 0.27437	$(y,z,x m_x, m_y, m_z) (-y, z+1/2, -x+1/2 m_x, -m_y, m_z)$ $(y+1/2, -z+1/2, -x m_x, -m_y, -m_z) (-y+1/2, -z, x+1/2 m_x, m_y, -m_z)$	4	-	-
5	Cs2 Cs 0.04194 0.04194 0.04194	$(x,x,x m_x, m_y, m_z) (-x+1/2, -x, x+1/2 m_x, m_y, -m_z)$ $(-x, x+1/2, -x+1/2 m_x, -m_y, m_z) (x+1/2, -x+1/2, -x m_x, -m_y, -m_z)$	4	-	-
6	Fe2 Fe 0.61176 0.61176 0.61176	$(x,x,x m_x, m_y, m_z) (-x+1/2, -x, x+1/2 m_x, m_y, -m_z)$ $(-x, x+1/2, -x+1/2 m_x, -m_y, m_z) (x+1/2, -x+1/2, -x m_x, -m_y, -m_z)$	4	(M_x, M_y, M_z)	$M_x = 0.00000$ $M_y = 0.00000$ $M_z = 0.00000$
	O2_1 O 0.45457 0.67094 0.51574	$(x,y,z m_x, m_y, m_z) (-x+1/2, -y, z+1/2 m_x, m_y, -m_z)$ $(-x, y+1/2, -z+1/2 m_x, -m_y, m_z) (x+1/2, -y+1/2, -z m_x, -m_y, -m_z)$	4	-	-

- The Fe ions have a magnetic moment (M_x, M_y, M_z)
- This time the moments are unconstrained.

Step 3: Creating mCIF file

- MVISUALIZE lets you quickly check magnetic structure.

Magnetic Structure

Selected magnetic space group: 1- $P2_13$ (#198.9)

Setting of the parent group

Parent space group $P2_13$ (No. 198)

Lattice parameters: a=10.89220, b=10.89220, c=10.89220, alpha=90.0000, beta=90.0000, gamma=90.0000

Go to an alternative setting

Export data to mCIF file/Visualize

Atomic positions, Wyckoff positions and Magnetic Moments

N	Atom	New WP	Multiplicity	Magnetic moment	Values of M_x, M_y, M_z
1	Cs1 Cs	0.82065 0.82065 0.82065 (x,x,x m_x, m_x, m_x) (-x+1/2, -x, x+1/2 $-m_x, -m_x, m_x$) (-x, x+1/2, -x+1/2 $-m_x, m_x, -m_x$) (x+1/2, -x+1/2, -x $m_x, -m_x, -m_x$)	4	-	-
2	Mo1 Mo	0.29978 0.62310 0.52710 (x,y,z m_x, m_y, m_z) (-x+1/2, -y, z+1/2 $-m_x, -m_y, m_z$) (-x, y+1/2, -z+1/2 $-m_x, m_y, -m_z$) (x+1/2, -y+1/2, -z $m_x, -m_y, -m_z$) (z,x,y m_z, m_x, m_y) (z+1/2, -x+1/2, -y $m_z, -m_x, -m_y$) (-z+1/2, -x, y+1/2 $-m_z, -m_x, m_y$) (-z, x+1/2, -y+1/2 $-m_z, m_x, -m_y$) (y,z,x m_y, m_z, m_x) (-y, z+1/2, -x+1/2 $-m_y, -m_z, -m_x$) (y+1/2, -z+1/2, -x $m_y, -m_z, -m_x$) (-y+1/2, -z, x+1/2 $-m_y, -m_z, m_x$)	12	-	-
3	Fe1 Fe	0.33726 0.33726 0.33726 (x,x,x m_x, m_x, m_x) (-x+1/2, -x, x+1/2 $-m_x, -m_x, m_x$) (-x, x+1/2, -x+1/2 $-m_x, m_x, -m_x$) (x+1/2, -x+1/2, -x $m_x, -m_x, -m_x$)	4	(M_x, M_x, M_x)	$M_x = 1.1$
4	O1 O	0.27437 0.48199 0.45051 (x,y,z m_x, m_y, m_z) (-x+1/2, -y, z+1/2 $-m_x, -m_y, m_z$) (-x, y+1/2, -z+1/2 $-m_x, m_y, -m_z$) (x+1/2, -y+1/2, -z $m_x, -m_y, -m_z$) (z,x,y m_z, m_x, m_y) (z+1/2, -x+1/2, -y $m_z, -m_x, -m_y$) (-z+1/2, -x, y+1/2 $-m_z, -m_x, m_y$) (-z, x+1/2, -y+1/2 $-m_z, m_x, -m_y$) (y,z,x m_y, m_z, m_x) (-y, z+1/2, -x+1/2 $-m_y, -m_z, -m_x$) (y+1/2, -z+1/2, -x $m_y, -m_z, -m_x$) (-y+1/2, -z, x+1/2 $-m_y, -m_z, m_x$)	12	-	-
5	Cs2 Cs	0.04194 0.04194 0.04194 (x,x,x m_x, m_x, m_x) (-x+1/2, -x, x+1/2 $-m_x, -m_x, m_x$) (-x, x+1/2, -x+1/2 $-m_x, m_x, -m_x$) (x+1/2, -x+1/2, -x $m_x, -m_x, -m_x$)	4	-	-
6	Fe2 Fe	0.61176 0.61176 0.61176 (x,x,x m_x, m_x, m_x) (-x+1/2, -x, x+1/2 $-m_x, -m_x, m_x$) (-x, x+1/2, -x+1/2 $-m_x, m_x, -m_x$) (x+1/2, -x+1/2, -x $m_x, -m_x, -m_x$)	4	(M_x, M_x, M_x)	$M_x = 1.2$
7	O2 O	0.45457 0.67094 0.51574 (x,y,z m_x, m_y, m_z) (-x+1/2, -y, z+1/2 $-m_x, -m_y, m_z$) (-x, y+1/2, -z+1/2 $-m_x, m_y, -m_z$) (x+1/2, -y+1/2, -z $m_x, -m_y, -m_z$) (z,x,y m_z, m_x, m_y) (z+1/2, -x+1/2, -y $m_z, -m_x, -m_y$) (-z+1/2, -x, y+1/2 $-m_z, -m_x, m_y$) (-z, x+1/2, -y+1/2 $-m_z, m_x, -m_y$) (y,z,x m_y, m_z, m_x) (-y, z+1/2, -x+1/2 $-m_y, -m_z, -m_x$) (y+1/2, -z+1/2, -x $m_y, -m_z, -m_x$) (-y+1/2, -z, x+1/2 $-m_y, -m_z, m_x$)	12	-	-

mCIF file of the structure

Submit this mcif file to MVISUALIZE for 3D visualization of the estructure using Jmol:

Download mCIF file: [bcs_file.mcif](#)
[The preview text below is non-editable, only copy-allowed]

```

# #CIF_2.0
# Created by the Bilbao Crystallographic Server
    
```

MVISUALIZE: 3D Visualization of magnetic structures with Jmol

MVISUALIZE Main Page

Show/Hide File

BMS: P 2_13

JSmol

help console Execute

Note: If the application stops working right or any malfunction is observed, it is probably a temporal problem due to the cache memory of your browser. Clear your web browser cache to solve it. If you still observe any malfunction, write an e-mail to cryst@wm.lcu.edu explaining the problem in detail.

We want to know input the model into Fullprof to see if it fits the data.
To do this we first download an mcif file.
Then convert this mcif into a Fullprof pcr
This is the same way a crystal structure refinement is done.

Step 3: Creating mCIF file:

- We will choose the allowed magnetic structure 2 ($P2_13$ (#198.9)) for this example.
- But all should be checked to ensure the solution is uniquely correct or to determine equivalent solutions.
- If none of the shown maximal magnetic space groups work → go to a subgroup

Step 3: Creating mCIF file

Maximal magnetic space groups for the parent space group $P2_13$ (No. 198) and the propagation vector $k = (0, 0, 0)$

Maximal subgroups which allow non-zero magnetic moments for at least one atom are coloured

N	Group (BNS)	Transformation matrix	General positions	Properties	Magnetic structure
1	$P2_13$ (#198.9) Go to a subgroup	$\begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \end{pmatrix}$ Alternatives (domain-related)	Show	Systematic absences MAGNEXT Tensor properties MTENSOR	Show
2	$P2_1'2_1'2_1'$ (#19.27) Go to a subgroup	$\begin{pmatrix} 0 & 0 & 1 & 1/4 \\ 0 & 1 & 0 & 1/4 \\ -1 & 0 & 0 & 1/4 \end{pmatrix}$ Alternatives (domain-related)	Show	Systematic absences MAGNEXT Tensor properties MTENSOR	Show

mCIF file of the structure

Submit this mcif file to MVISUALIZE for 3D visualization of the structure using Jmol: [Submit to MVISUALIZE](#)

[Download mCIF file: bcs_file.mcif](#)

```

#CIF_2.0
# Created by the Bilbao Crystallographic Server
# http://www.cryst.ehu.es
# Date: 15/07/2024 23:48:50
# ICSD_CollCode422752.cif

data_5yOhtAoR
_audit_creation_date 2024-07-15
_audit_creation_method "Bilbao Crystallographic Server"

_citation_journal_abbrev ?
_citation_journal_volume ?
_citation_page_first ?
_citation_page_last ?
_citation_article_id ?
_citation_year ?
_citation_DOI ?

loop_
_citation_author_name
  
```

Selected magnetic space group: 1- $P2_13$ (#198.9)
 Setting of the parent group
 Parent space group $P2_13$ (No. 198)
 Lattice parameters: a=10.89220, b=10.89220, c=10.89220, alpha=90.0000, beta=90.0000, gamma=90.0000

[Export data to mCIF file/Visualize](#) [Go to a subgroup](#)

Atomic positions, Wyckoff positions and Magnetic Moments

N	Atom	New WP	Multiplicity	Magnetic moment
1	Cs1 Cs 0.82065 0.82065 0.82065	(x,x,x m_x, m_x, m_x) (-x+1/2, -x, x+1/2 $-m_x, -m_x, m_x$) (-x, x+1/2, -x+1/2 $-m_x, m_x, -m_x$) (x+1/2, -x+1/2, -x $m_x, -m_x, m_x$)	4	-
2	Mo1 Mo 0.29978 0.62310 0.52710	(x,y,z m_x, m_x, m_x) (-x+1/2, -y, z+1/2 $-m_x, -m_y, m_z$) (-x, y+1/2, -z+1/2 $-m_x, m_y, -m_z$) (x+1/2, -y+1/2, -z $m_x, -m_y, -m_z$) (z, x, y m_z, m_x, m_y) (z+1/2, -x+1/2, -y $m_z, -m_x, -m_y$) (-z+1/2, -x, y+1/2 $-m_z, -m_x, m_y$) (-z, x+1/2, -y+1/2 $-m_z, m_x, -m_y$) (y, z, x m_y, m_z, m_x) (-y, z+1/2, -x+1/2 $-m_y, m_z, -m_x$) (y+1/2, -z+1/2, -x $m_y, -m_z, -m_x$) (-y+1/2, -z, x+1/2 $-m_y, -m_z, m_x$)	12	-
3	Fe1 Fe 0.33726 0.33726 0.33726	(x,x,x m_x, m_x, m_x) (-x+1/2, -x, x+1/2 $-m_x, -m_x, m_x$) (-x, x+1/2, -x+1/2 $-m_x, m_x, -m_x$) (x+1/2, -x+1/2, -x $m_x, -m_x, -m_x$)	4	(M_x, M_x, M_x) $M_x = [1.1]$
4	O1 O 0.27437 0.48199 0.45051	(x,y,z m_x, m_x, m_x) (-x+1/2, -y, z+1/2 $-m_x, -m_y, m_z$) (-x, y+1/2, -z+1/2 $-m_x, m_y, -m_z$) (x+1/2, -y+1/2, -z $m_x, -m_y, -m_z$) (z, x, y m_z, m_x, m_y) (z+1/2, -x+1/2, -y $m_z, -m_x, -m_y$) (-z+1/2, -x, y+1/2 $-m_z, -m_x, m_y$) (-z, x+1/2, -y+1/2 $-m_z, m_x, -m_y$) (y, z, x m_y, m_z, m_x) (-y, z+1/2, -x+1/2 $-m_y, m_z, -m_x$) (y+1/2, -z+1/2, -x $m_y, -m_z, -m_x$) (-y+1/2, -z, x+1/2 $-m_y, -m_z, m_x$)	12	-
5	Cs2 Cs 0.04194 0.04194 0.04194	(x,x,x m_x, m_x, m_x) (-x+1/2, -x, x+1/2 $-m_x, -m_x, m_x$) (-x, x+1/2, -x+1/2 $-m_x, m_x, -m_x$) (x+1/2, -x+1/2, -x $m_x, -m_x, -m_x$)	4	(M_x, M_x, M_x) $M_x = [1.2]$
6	Fe2 Fe 0.61176 0.61176 0.61176	(x,x,x m_x, m_x, m_x) (-x+1/2, -x, x+1/2 $-m_x, -m_x, m_x$) (-x, x+1/2, -x+1/2 $-m_x, m_x, -m_x$) (x+1/2, -x+1/2, -x $m_x, -m_x, -m_x$)	4	(M_x, M_x, M_x) $M_x = [1.2]$
7	O2 O 0.45457 0.67094 0.51574	(x,y,z m_x, m_x, m_x) (-x+1/2, -y, z+1/2 $-m_x, -m_y, m_z$) (-x, y+1/2, -z+1/2 $-m_x, m_y, -m_z$) (x+1/2, -y+1/2, -z $m_x, -m_y, -m_z$) (z, x, y m_z, m_x, m_y) (z+1/2, -x+1/2, -y $m_z, -m_x, -m_y$) (-z+1/2, -x, y+1/2 $-m_z, -m_x, m_y$) (-z, x+1/2, -y+1/2 $-m_z, m_x, -m_y$) (y, z, x m_y, m_z, m_x) (-y, z+1/2, -x+1/2 $-m_y, m_z, -m_x$) (y+1/2, -z+1/2, -x $m_y, -m_z, -m_x$) (-y+1/2, -z, x+1/2 $-m_y, -m_z, m_x$)	12	-

1. Input values for magnetic moment

NOTE: In this case $M_x (=M_y=M_z)$, when we run Fullprof it will constrain them to remain the same. But if M_x, M_y, M_z are allowed to be different, as for the second magnetic space group (#19.27) then be careful when adding the moments. If you make them all the same Fullprof will potentially constrain them to always be the same, which is incorrect. ALWAYS PUT DIFFERENT MOMENT SIZES HERE!

Step 4: Creating a pcr from an mcif file

- Go back to the main page on server and open mCIF2PCR

bilbao crystallographic server

Contact us

About us

Publications

How to cite the server

Space-group symmetry

Magnetic Symmetry and Applications

MGENPOS	General Positions of Magnetic Space Groups
MWHYCKPOS	Wyckoff Positions of Magnetic Space Groups
MKVEC	The k-vector types and Brillouin zones of Magnetic Space Groups
IDENTIFY MAGNETIC GROUP	Identification of a Magnetic Space Group from a set of generators in an arbitrary setting
BNS2OG	Transformation of symmetry operations between BNS and OG settings
mCIF2PCR	Transformation from mCIF to PCR format (FullProf).
MPOINT	Magnetic Point Group Tables
MAGNEXT	Extinction Rules of Magnetic Space Groups
MAXMAGN	Maximal magnetic space groups for a given space group and a propagation vector
MAGMODELIZE	Magnetic structure models for any given magnetic symmetry
STRCONVERT	Convert & Edit Structure Data (supports the CIF, mCIF, VESTA, VASP formats -- with magnetic information where available)
k-SUBGROUPSMAG	Magnetic subgroups consistent with some given propagation vector(s) or a supercell
MAGNDATA	A collection of magnetic structures with portable cif-type files
MVISUALIZE	3D Visualization of magnetic structures with Jmol
MTENSOR 	Symmetry-adapted form of crystal tensors in magnetic phases
MAGNETIC REP.	Decomposition of the magnetic representation into irreps
Get_mirreps	Irreps and order parameters in a paramagnetic space group- magnetic subgroup phase transition

$\text{Cs}_2\text{Fe}_2(\text{MoO}_4)_3$: Refinement Strategy

- This example will use the Bilbao Crystallographic Server (<http://www.cryst.ehu.es/>) and follow these steps:
 - Step 1: Refine the crystal structure using FullProf
 - Step 2: Determine the k-vector by indexing the magnetic reflections using k-search
 - Step 3: Create test magnetic space groups using MAXMAGN on the Bilbao Crystallographic Server. Save these as mcif files.
 - **Step 4: Convert the mcif file into a .pcr file using mCIF2PCR.**
 - Step 5: Use the created .pcr file to fit the nuclear and magnetic neutron data using Fullprof to determined the magnetic structure.

Step 4: Creating a pcr from an mcif file

mCIF2PCR: Transformation from mCIF to PCR format (FullProf).

mCIF_to_PCR

Given a magCIF file, it produces a PCR template that can be used as input for FullProf (the program mCIF_to_PCR (FullProf) is used). By default the provided PCR file is intended for a simulation. The file can be then modified by hand for a refinement of the model.

Choose a structure file (mCIF format):

Choose File bcs_file_MSG198p9.mcif Convert

1

2

Bilbao Crystallographic Server
http://www.cryst.ehu.es



- **[1]** Choose the mcif we just created through MAXMAGN
- **[2]** Click convert

The file has been successfully converted.

[Click to download it](#)

- This will convert the file and “Click to download it” will download the .pcr file
- We will use this .pcr file in the next step.

$\text{Cs}_2\text{Fe}_2(\text{MoO}_4)_3$: Refinement Strategy

- This example will use the Bilbao Crystallographic Server (<http://www.cryst.ehu.es/>) and follow these steps:
 - Step 1: Refine the crystal structure using FullProf
 - Step 2: Determine the k-vector by indexing the magnetic reflections using k-search
 - Step 3: Create test magnetic space groups using MAXMAGN on the Bilbao Crystallographic Server. Save these as mcif files.
 - Step 4: Convert the mcif file into a .pcr file using mCIF2PCR.
 - **Step 5: Use the created .pcr file to fit the nuclear and magnetic neutron data using Fullprof to determined the magnetic structure.**

Step 5: Refining the magnetic structure with Fullprof

- Pcr file created contains a single phase with crystal structure and magnetic ions described by a magnetic space group.
- The downloaded pcr file calculates the pattern based on default values.
- We could change the defaults in the .pcr file in the same way as done for the examples created from a .cif file.
- To do this we work down the Tabs in the GUI (General/Patterns/Phases/Refinement) and/or edit the text file.

BUT, since we already have a working pcr file for the nuclear phase, we can just paste in the magnetic portion of interest

Step 5: Refining the magnetic structure with Fullprof

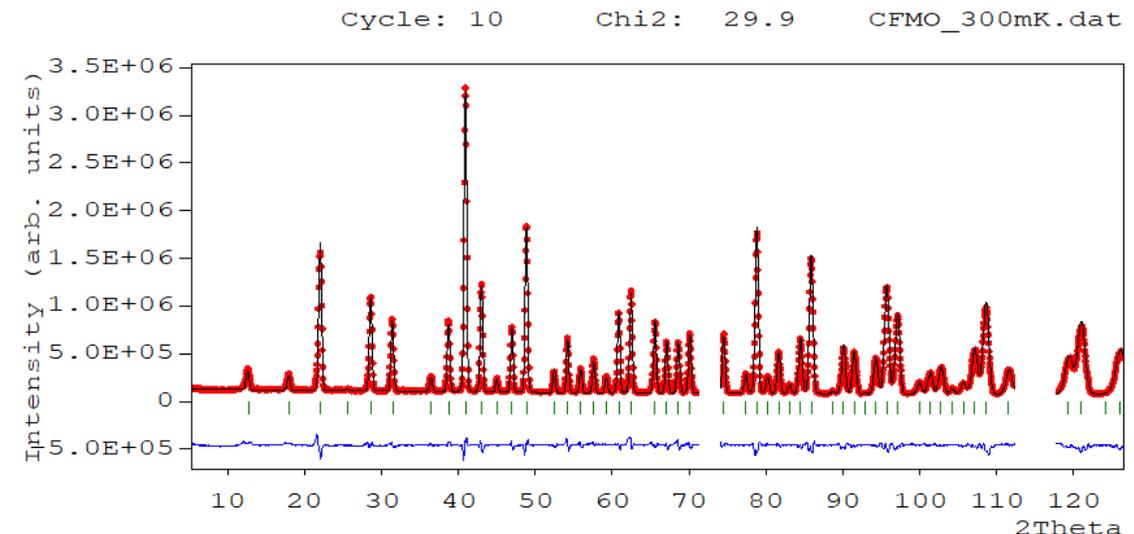
- Run the refinement.
- The moments vary automatically.
- The fit looks close, with all the new magnetic scattering being captured.
- Refining the background, lattice constants, etc will improve the fit slightly.
- But note the chi2 is fairly high (16 is about the lowest.) This is because of the background. This is likely due to short range magnetic order.
- NOTE: do not just rely on chi2 or Rw values, these are often less important than looking at the fit and understanding why the numbers are what they are.

```
FullProf Program
=> Bragg R-factor: 6.104
=> RF-factor : 3.888
=> Nuclear R-factor: 6.006
=> Magnetic R-factor: 10.41
=> Pure Magnetic R-factor: 22.31

=> Convergence reached at this CYCLE !!!!: CYCLE No. 6
=> R-Factors: 6.31 7.99 Chi2: 29.9 DW-Stat.: 0.1371 Patt#: 1
=> Expected : 1.46 1.8712
=> Conventional Rietveld R-factors for Pattern: 1
=> Rp: 10.3 Rwp: 11.2 Rexp: 2.05 Chi2: 29.9
=> Global user-weighted Chi2 (Bragg contrib.): 30.81
=> -----> Pattern# 1
=> Phase: 1
=> Bragg R-factor: 6.104
=> RF-factor : 3.888
=> Nuclear R-factor: 6.006
=> Magnetic R-factor: 10.41
=> Pure Magnetic R-factor: 22.31
=> Normal end, final calculations and writing...

=> CPU Time: 0.984 seconds
=> 0.016 minutes

=> END Date:16/07/2024 Time => 09:36:48.937
```



Step 5: Refining the magnetic structure with Fullprof

- This fit captures the magnetic scattering.
- There was another maximal magnetic space group. The same procedure should be done to check how that model works.
- You should find that it is unstable and so we can define $P2_13$ (#198.9) as the determined magnetic space group

Bilbao Crystallographic Server → MAXMAGN - Maximal magnetic space groups Help

**Maximal magnetic space groups for the parent space group $P2_13$ (No. 198)
and the propagation vector $k = (0, 0, 0)$**

Maximal subgroups which allow non-zero magnetic moments for at least one atom are coloured

N	Group (BNS)	Transformation matrix	General positions	Properties	Magnetic structure
1	$P2_13$ (#198.9) Go to a subgroup	$\begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \end{pmatrix}$ Alternatives (domain-related)	Show	Systematic absences MAGNEXT Tensor properties MTENSOR	Show
2	$P2_1'2_1'2_1'$ (#19.27) Go to a subgroup	$\begin{pmatrix} 0 & 0 & 1 & 1/4 \\ 0 & 1 & 0 & 1/4 \\ -1 & 0 & 0 & 1/4 \end{pmatrix}$ Alternatives (domain-related)	Show	Systematic absences MAGNEXT Tensor properties MTENSOR	Show

Bilbao Crystallographic Server
<http://www.cryst.ehu.es>



For comments, please mail to
administrador.bcs@ehu.es

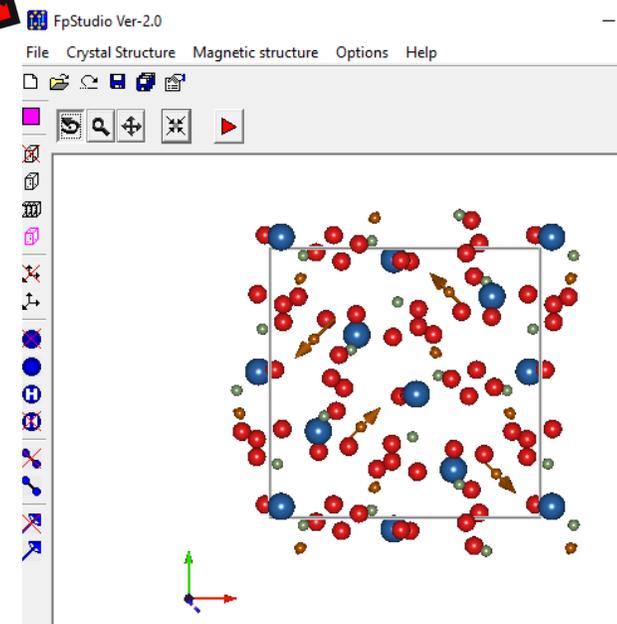
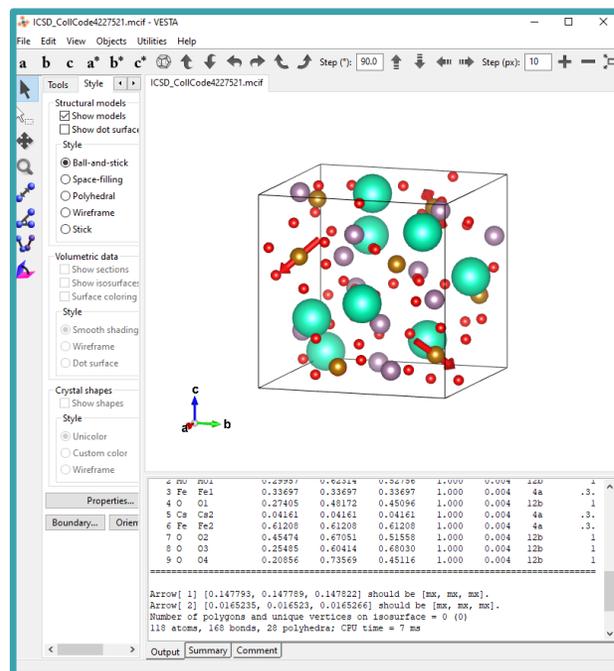
Step 5: Refining the magnetic structure with Fullprof

- From the refinement the moments are predominately only on one site.
- The magnetic structure can be viewed in Fpstudio. The moment sizes can be seen in the drop down menu: "Magnetic structure">"list magnetic moments"
- The mcif file can also be viewed with VESTA.

Atoms Information: Phase 1

Atom #	Label	Ntyp	Mag. Rot.	Prog. V...	X	Y	Z	B	Occ
Atom # 1	Cs1	Cs	1	0	0.82093	0.82093	0.82093	0.30000	0.33333
Atom # 2	Mo1	Mo	1	0	0.29957	0.62314	0.52756	0.30000	1.00000
Atom # 3	Fe1	MFE2	1	0	0.33697	0.33697	0.33697	0.30000	0.33333
Atom # 4	O1	O	1	0	0.27405	0.48172	0.45096	0.30000	1.00000

Atom #	Re[x]	Re[y]	Re[z]	Im[x]	Im[y]	Im[z]	MPhase
Atom #3	1.60983	1.60983	1.60982	0.00000	0.00000	0.00000	0.00000
Atom #6	0.18266	0.18266	0.18263	0.00000	0.00000	0.00000	0.00000



Moment sizes with errors are in the .sum file

Step 5: Refining the magnetic structure with Fullprof

- Always ask “does this magnetic model make sense?”
- The moment sizes are very different, but within plausible ranges for Fe.
- Look at supporting data and calculations in the manuscript.
- The different Fe moment sizes are expected.
- Therefore we can present this magnetic model as the magnetic structure.

==> MAGNETIC MOMENT PARAMETERS:

Name	Mx	sMx	My	sMy	Mz	sMz	M	sM	MPhas	sMPhas
Fe1	1.610(18)		1.610(18)		1.610(18)		2.7883(321)		0.0000(0)	
Fe2	0.183(53)		0.183(53)		0.183(53)		0.3164(922)		0.0000(0)	

Moment sizes with errors are in the .sum file

Cs₂Fe₂(MoO₄)₃—A Strongly Frustrated Magnet with Orbital Degrees of Freedom and Magnetocaloric Properties

Published as part of *Chemistry of Materials virtual special issue “In Memory of Prof. Francis DiSalvo”*.

Lenka Kubíčková, Anna Katharina Weber, Martin Panthöfer, Stuart Calder, and Angela Möller*

Cite This: <https://doi.org/10.1021/acs.chemmater.4c01262>

Read Online

ACCESS |

Metrics & More

Article Recommendations

Supporting Information

ABSTRACT: We report an in-depth study of the thermodynamic and magnetocaloric properties of a strongly frustrated magnet, Cs₂Fe₂(MoO₄)₃. The underlying structure belongs to the double trillium lattice, which consists of two Fe^{II} ($S = 2$) sites with easy-axis and easy-plane single-ion anisotropy. Detailed ⁵⁷Fe Mössbauer spectroscopic investigations along with ligand-field calculations support the existence of disparate ground states. The antiferromagnetic ordered structure is presented by the propagation vector $k = (0,0,0)$ with noncollinear magnetic moments of 2.97 μ_B (Fe1) and 0.17 μ_B (Fe2), respectively. Strong and disordered magnetic correlations exist in the temperature regime between $T_N \approx 1.0$ K and $|\theta_{CW}| \approx 22$ K. The large degeneracy of the ground state is investigated in terms of its magnetocaloric response. Magnetization and specific heat measurements indicate a significant magnetocaloric cooling efficiency, making this rare-earth-free compound a promising candidate for cryogenic magnetic refrigeration applications, with refrigeration capacity of 79 J kg⁻¹ for $\Delta(\mu_0H) = 8$ T.

