

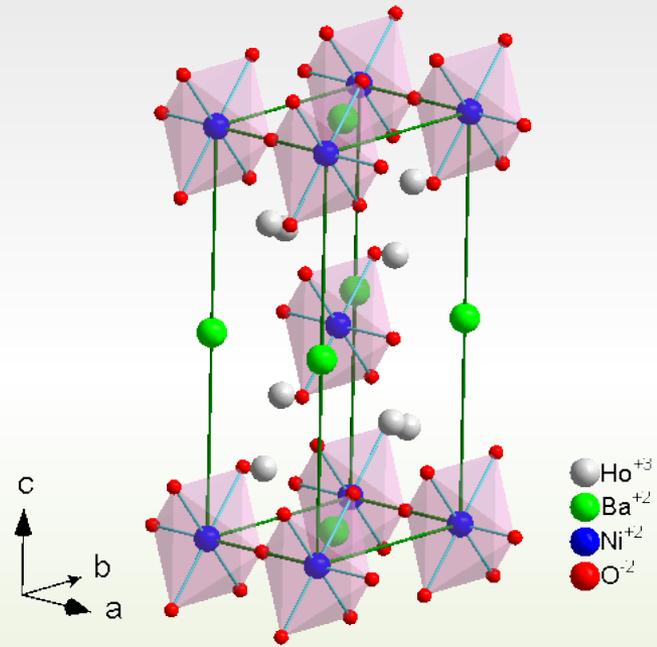
Magnetic structure determination of $\text{Ho}_2\text{BaNiO}_5$ using FullProf Suite and SARAh



Orthorhombic (Space group: $Immm$)
 $a=3.764 \text{ \AA}$, $b=5.761 \text{ \AA}$, $c=11.336 \text{ \AA}$)

NiO_6 octahedra form chains along the a-axis.

3D Antiferromagnetic ordering at $T_N \sim 53 \text{ K}$



Eur. Phys. J. B 24, 59-70 (2001)

THE EUROPEAN
 PHYSICAL JOURNAL B
 EDP Sciences
 © Società Italiana di Fisica
 Springer-Verlag 2001

Neutron diffraction study of the magnetic ordering in the series R_2BaNiO_5 (R = Rare Earth)

E. García-Matres^{1,a}, J.L. Martínez², and J. Rodríguez-Carvajal^{3,b}

¹ Institut Laue-Langevin, BP 156, 38042, Grenoble Cedex, France

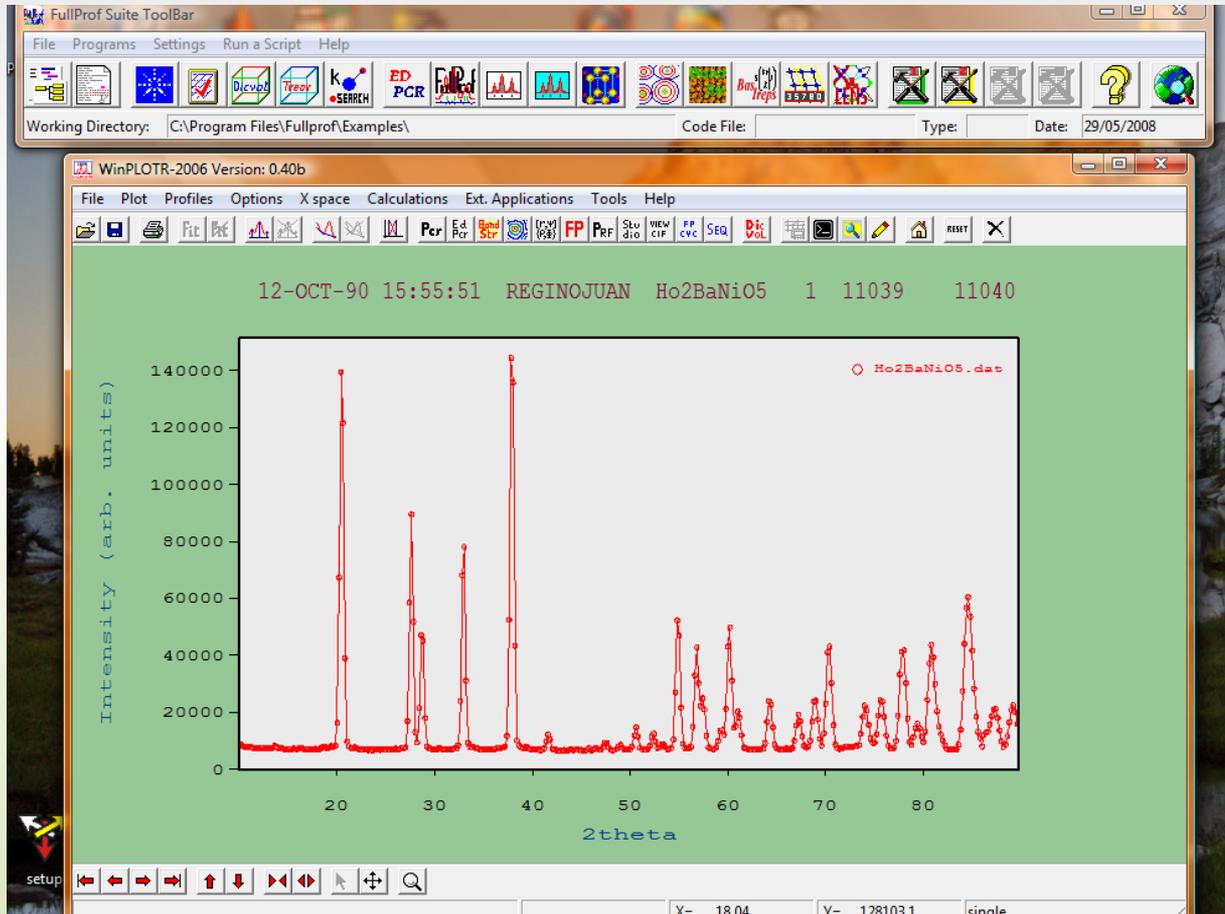
² Instituto de Ciencia de Materiales (CSIC), Fac. Ciencias (C-4), Universidad Autónoma de Madrid, 28049 Madrid, Spain

³ Laboratoire Léon Brillouin (CEA-CNRS), Centre d'Études de Saclay, 91191 Gif-sur-Yvette Cedex, France

Atom	Wyck.	Site	x/a	y/b	z/c
Ho	4j	mm2	1/2	0	0.2025(4)
Ni	2a	mmm	0	0	0

STARTING INFORMATION

- Neutron powder diffraction data collected at D1B –ILL at 1.5 K using $\lambda = 2.524 \text{ \AA}$ (File : Ho2BaNiO5.dat)
- Instrument resolution file: (d1b_ill.irf)
- Crystal structure known (File: Ho2BaNiO5.cif)

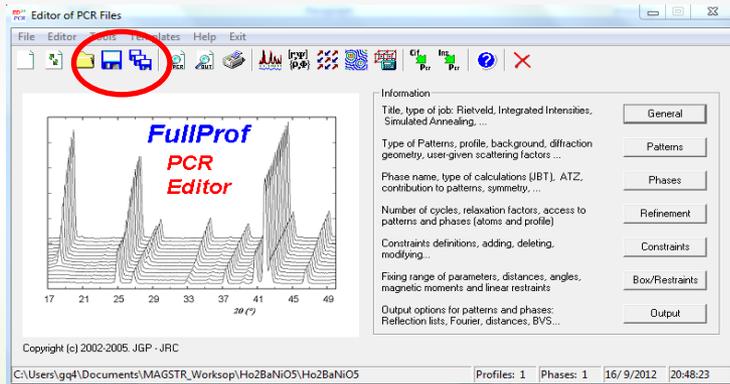
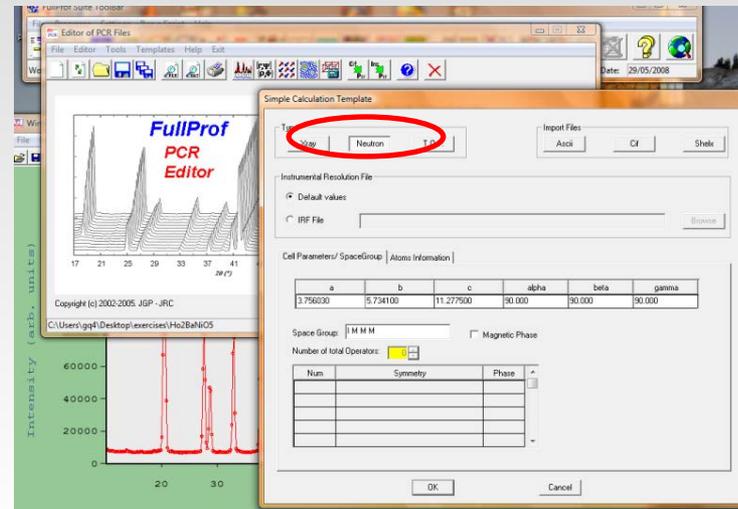


STEPS FOR MAGNETIC STRUCTURE DETERMINATION

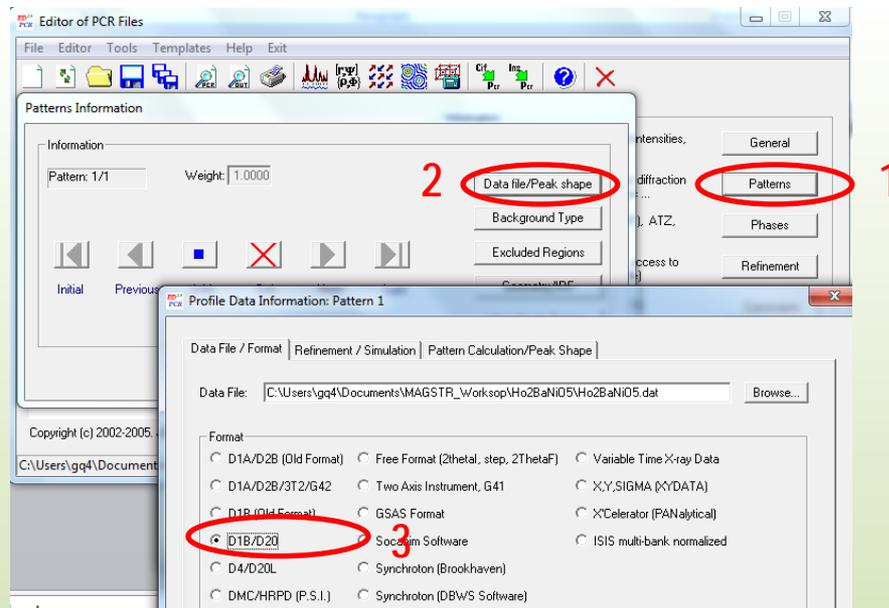
- ✓ refining the crystal structure for the paramagnetic state ($T > T_N$ or T_C)
→ obtain all the relevant structural and profile parameters
- ✓ preparing a PCR file and performing a refinement of the low temperature data ($T < T_N$) with fixed structural parameters (without a magnetic model)
→ identify the magnetic contribution to the diffraction pattern
 - ✓ indexing the magnetic reflections
→ use *k-search* to determine the propagation vector(s) k_m
- ✓ Performing symmetry analysis (propagation vector, space group, atomic position)
→ use *Basireps* or *SARAh* to get IRs and Basis vectors
- ✓ Adding the magnetic phase to the PCR file (using the symmetry information) and solve the magnetic structure using trial and error methods
- ✓ Magnetic structure model visualization using FpStudio program

➤ use **EdPCR** to create the input file for FullProf (*.PCR)

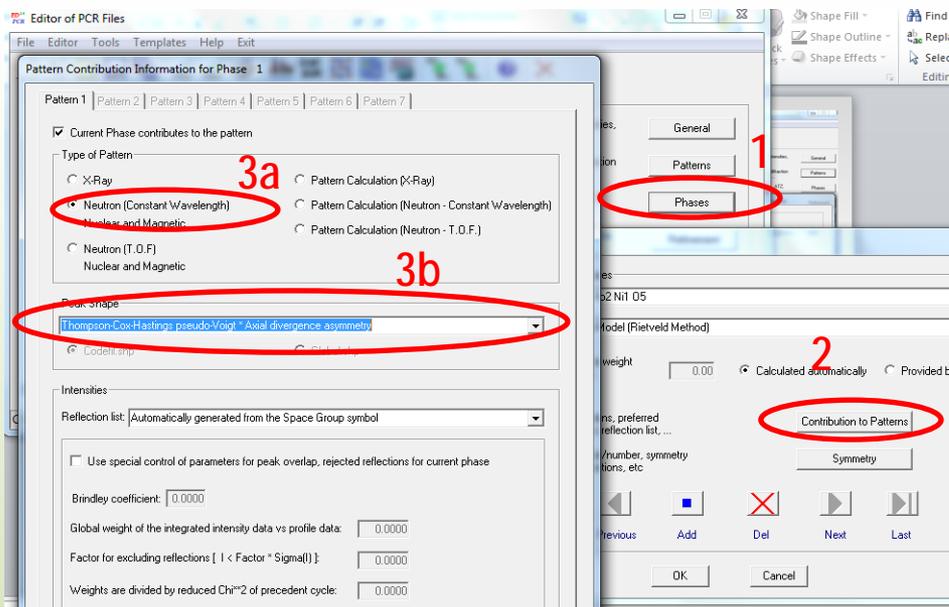
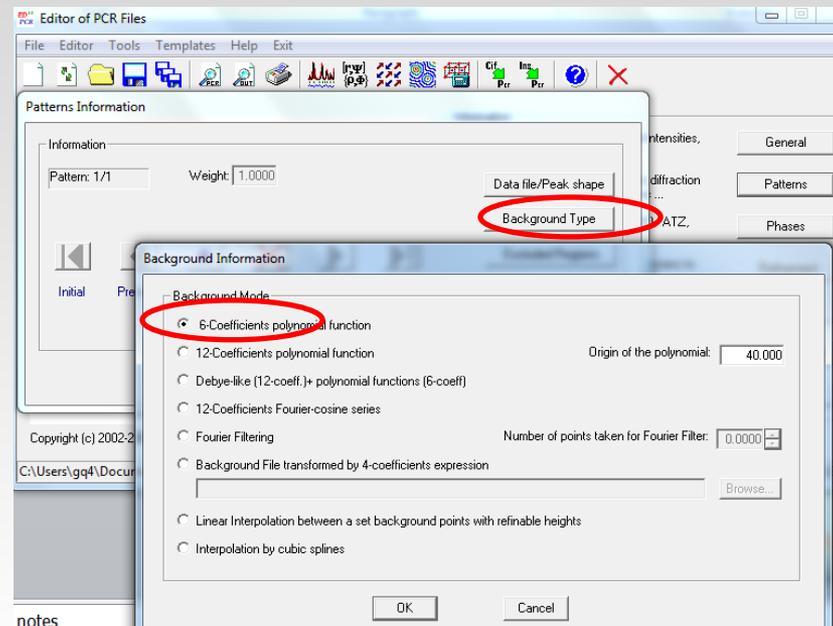
- import the crystallographic information by clicking on “CIF to PCR”
- in the new window, select the “Neutron” tab for the type of calculations
- use the “Browse” button to upload the instrument resolution file “IRF” (**d1b_ill.irf**)



- save the PCR file by clicking the “Save” button
- open the “Patterns” tab (1) and then the “Data file/ peak shape” (2) and select the “D1B/D20” for the data file format (3)

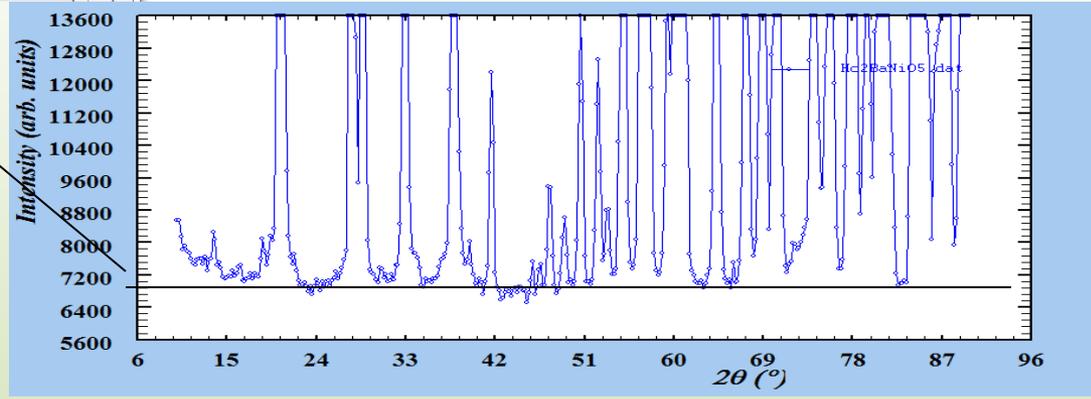
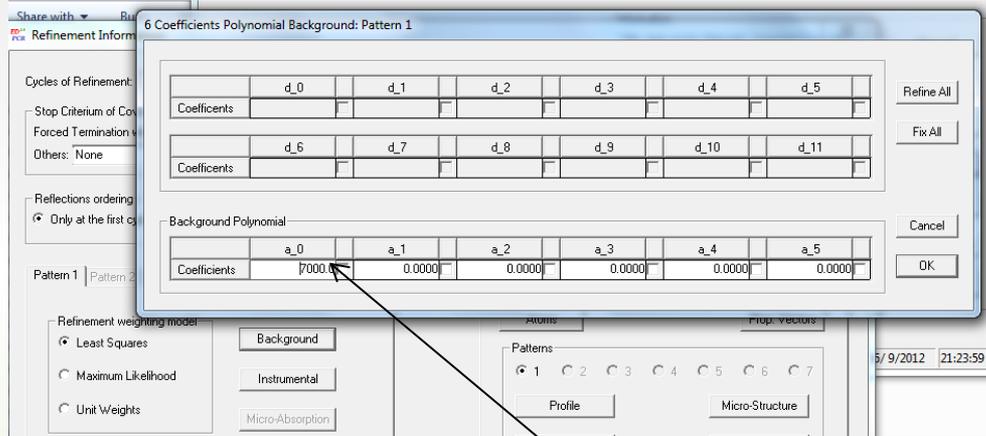
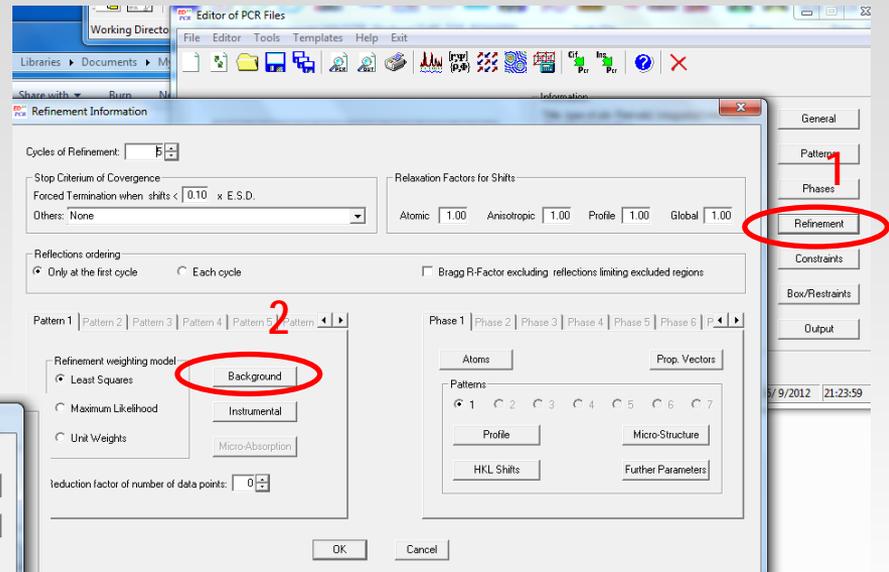


- “Refinement/Simulation” tab, make sure that “Neutron-CW” option is selected, wavelength is “User defined”
 $\lambda_1 = \lambda_2 = 2.524 \text{ \AA}$
- “pattern calculation” the “Thompson-Cox-Hastings pseudo-Voigt” peak shape is chosen
- For the background information, select the “6-coefficients polynomial function”



- From the main window of EdPcr, open the “Phases” tab (1) and then click on the “Contribution to patterns” (2) and then select the “current phase contributes to the pattern” & “neutron (constant wavelength)” (3a) and “Thompson-Cox-Hastings pseudo-Voigt” for the peak shape (3b), Reflection list : “Automatically generated from space group”

- Open the “Refinement” (1) and then the “Background” and add value for the “a₀” coefficient (~7000, read from the data file) that will give a first flat approximation for the background



- From the same “Refinement” window (1) , click on the “Profile” tab and and set a number for the “Scale factor” (~ 50 for this example). The number of “cycles of refinement” can also be increased at this time
- save the PCR file by clicking the “Save” button, every time a change has been made

The screenshot displays the MagSTR software interface. The 'Refinement Information' window is open, showing 'Cycles of Refinement' set to 5. The 'Profile Parameters: Phase 1 Pattern 1' dialog box is also open, with the 'Scale' coefficient set to 50.000. The 'Refinement' tab is selected in the right-hand sidebar.

Refinement Information Window:

- Cycles of Refinement: 5
- Relaxation Factors for Shifts: 1.00 Anisotropic 1.00 Profile 1.00 Global 1.00
- Bragg R-Factor excluding reflections limiting excluded regions
- Phase 1 | Phase 2 | Phase 3 | Phase 4 | Phase 5 | Phase 6 | P
- Atoms | Prop. Vectors
- Patterns: 1 (selected), 2, 3, 4, 5, 6, 7
- Profile | Micro-Structure
- HKL Shifts | Further Parameters

Profile Parameters: Phase 1 Pattern 1 Dialog Box:

Factors:

Coefficients	Scale	Overall B-factor
	50.000	0.0000

Cell Parameters:

Coefficients	a	b	c	alpha	beta	gamma
	3.756031	5.734100	11.277499	90.000	90.000	90.000

FWHM / Shape Parameters | Asymmetry Parameters | Preferred Orientation

FWHM Parameters:

Coefficients	U	V	W	IG
	0.000000	0.000000	0.000000	0.000000

Shape Parameters:

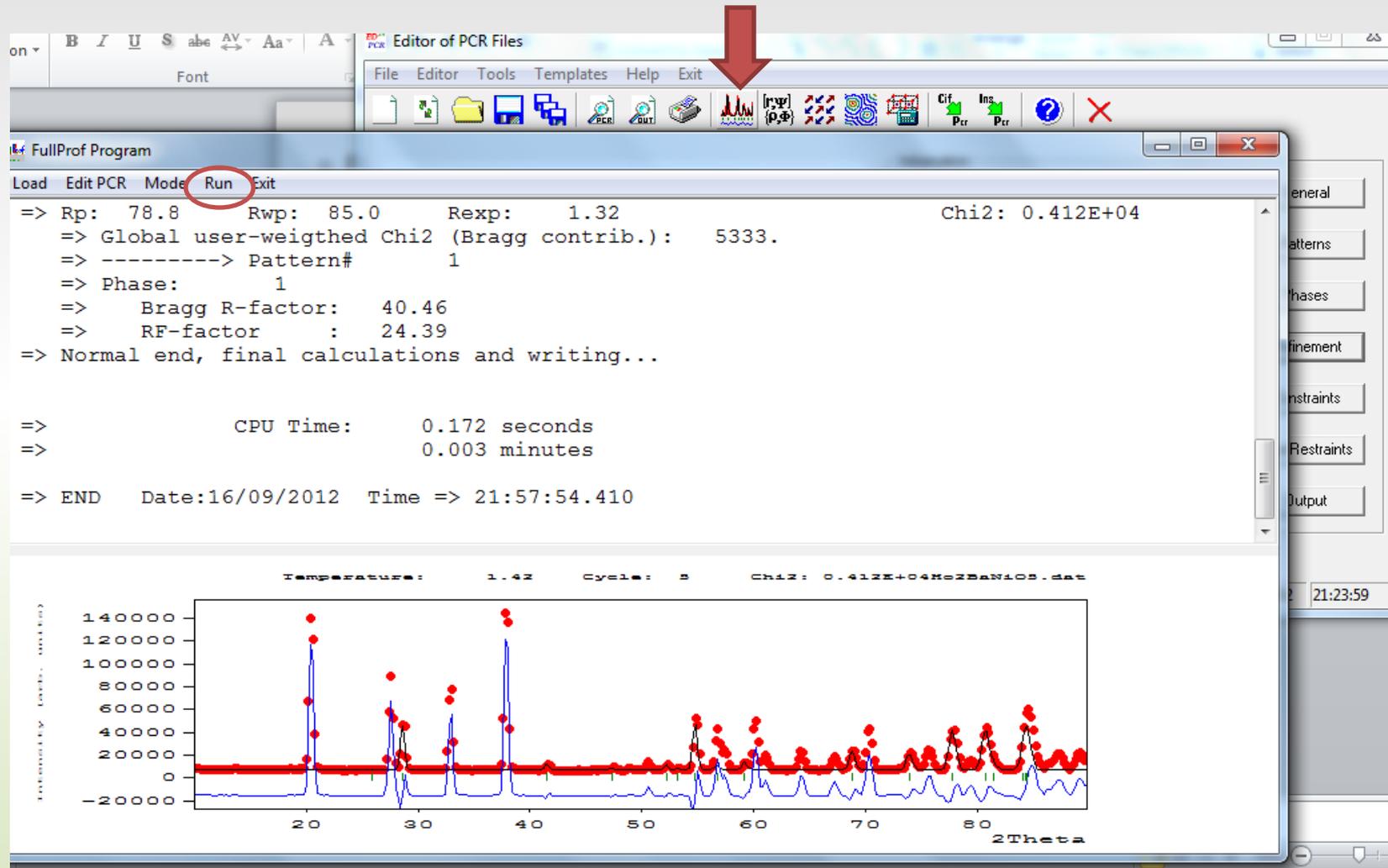
Coefficients	X	Y	SZ
	0.000000	0.000000	0.000000

Buttons: Refine All, Fix All

Right Sidebar: General, Patterns, Phase 1, Refinement (selected), Constrains, Box/Restraints, Output

Status: 9/2012 21:23:59

- Run the Fullprof program by click on button indicated below. All the parameters are fixed at this time.



- ✓ You can run the refinement again by allowing the scale factor, lattice parameters, some of the background coefficients and the 2theta zero to vary
- ✓ **Refined parameters** appear in blue or red (with additional constraints)

Profile Parameters: Phase 1 Pattern 1

Factors

	Scale	Overall B-factor
Coefficients	52.856	0.0000

Cell Parameters

	a	b	c	alpha	beta	gamma
Coefficients	3.751848	5.733387	11.270996	90.000	90.000	90.000

FWHM / Shape Parameters Asymmetry Parameters Preferred Orientation

FWHM Parameters

	U	V	W	IG
Coefficients	0.000000	0.000000	0.000000	0.000000

Buttons: Refine All, Fix All

- ✓ **Atomic parameters** (fractional atomic positions, thermal factors, occupation) can be accessed through Refinement → Phase # tab → Atoms

Atoms Information: Phase 1

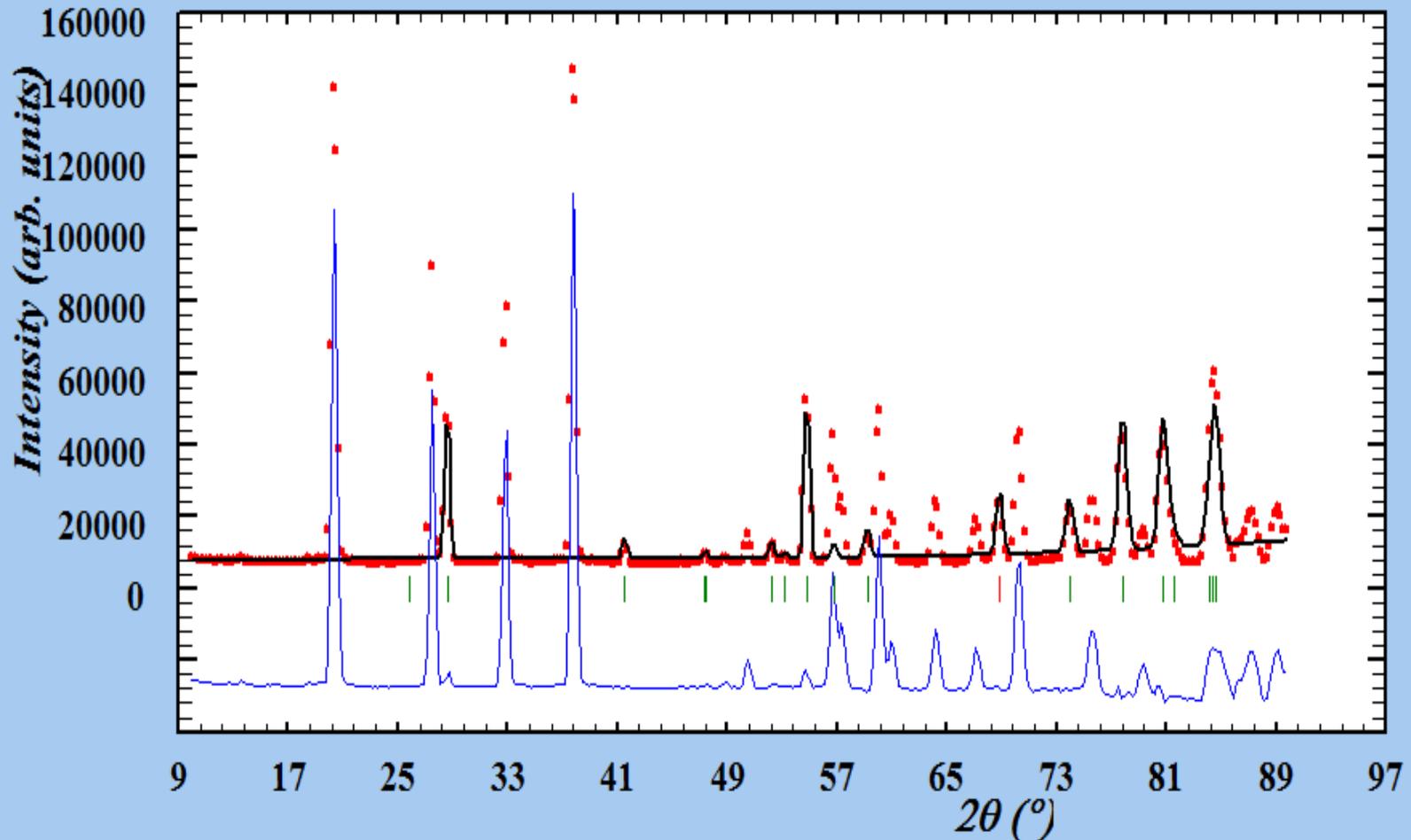
List of Atoms

Number of Atoms: 5

	Label	Ntyp	X	Y	Z	B	Occ	Therm. Fact.
Atom # 1	Ho1	Ho	0.50000	0.00000	0.20178	0.30000	0.25000	Isotropic
Atom # 2	Ba1	Ba	0.50000	0.50000	0.00000	0.30000	0.12500	Isotropic
Atom # 3	Ni1	Ni	0.00000	0.00000	0.00000	0.30000	0.12500	Isotropic
Atom # 4	O1	O	0.00000	0.24224	0.14892	0.30000	0.50000	Isotropic

Anisotropic Thermal Factors / Form Factors

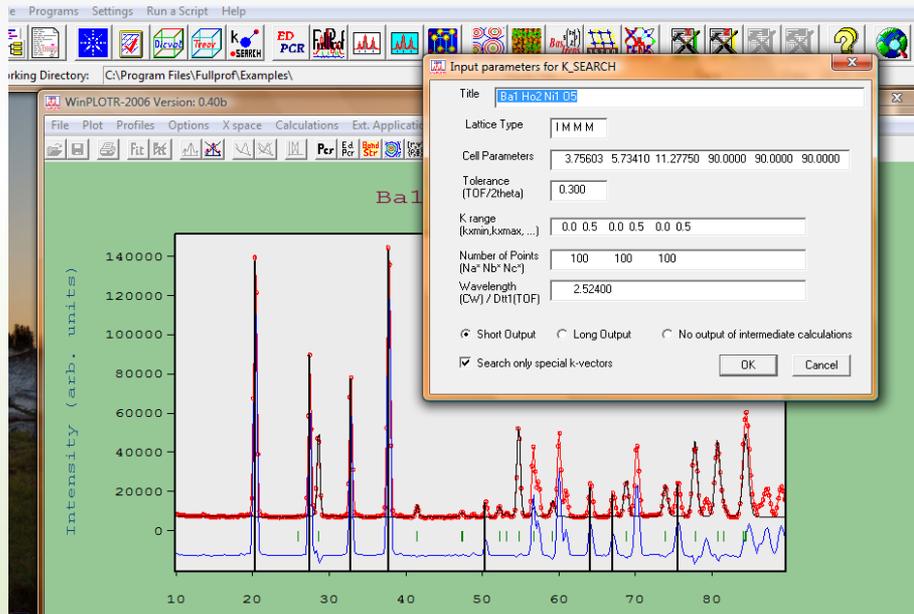
Ba1 Ho2 Ni1 O5



- ✓ Open the PRF file (Rietveld plot) by using the [Winplotr program](#). The result will look something similar to the figure above
- ✓ The reflections that are left unindexed are all magnetic in origin

INDEX THE MAGNETIC REFLECTIONS USING THE k-search program

- open the PRF file using **WinPlotr-2006** program and select the un-indexed reflections to create the input file for "k-search" program. For doing this, in the menu of winplotr click on "Calculations"- "peak detection"- "enable". After enabling, go again to "Calculations"- "peak detection" and "insert peak". After selecting the magnetic peaks, go to "save peaks" to save them as "K-search format"



- run "k-search" program to find the propagation vector and see the results listed in the file "k_search.kup"

=> List of satellites (hkl)+(Kx,Ky,Kz) for the best solution:

				Kx=0.5000	Ky=0.0000	Kz=0.5000			
H	K	L	n	D* (cal)	D* (obs)	2Th (cal)	2Th (obs)	2Th (obs-cal)	
1	0	1	1	0.1403	0.1398	20.3982	20.3261	-0.0721	
1	0	-1	1	0.1882	0.1880	27.4762	27.4512	-0.0250	
1	1	0	1	0.2238	0.2237	32.8159	32.7950	-0.0209	
1	1	2	1	0.2566	0.2564	37.7840	37.7571	-0.0269	
1	0	-3	1	0.3377	0.3371	50.4500	50.3532	-0.0968	
1	0	5	1	0.4206	0.4205	64.1262	64.0944	-0.0318	
-1	1	0	1	0.4380	0.4375	67.1170	67.0208	-0.0962	
1	2	-3	1	0.4855	0.4854	75.5671	75.5454	-0.0217	

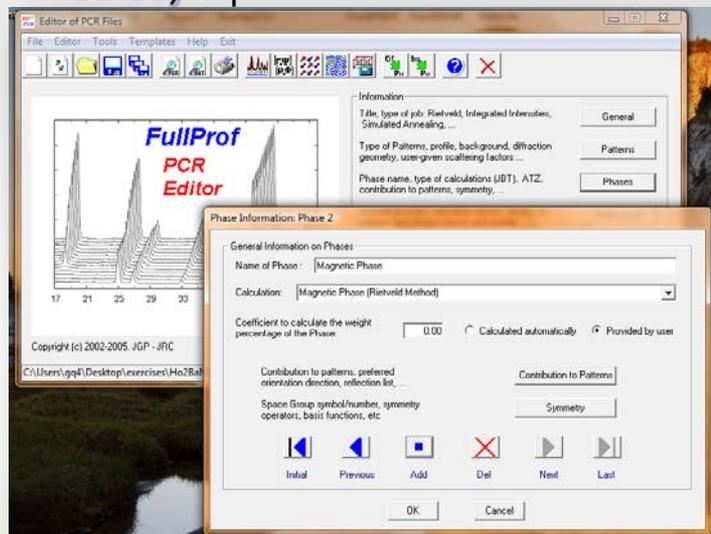
=> Best R-factor: 0.9461 % for propagation vector:

k = (0.5000 0.0000 0.5000)

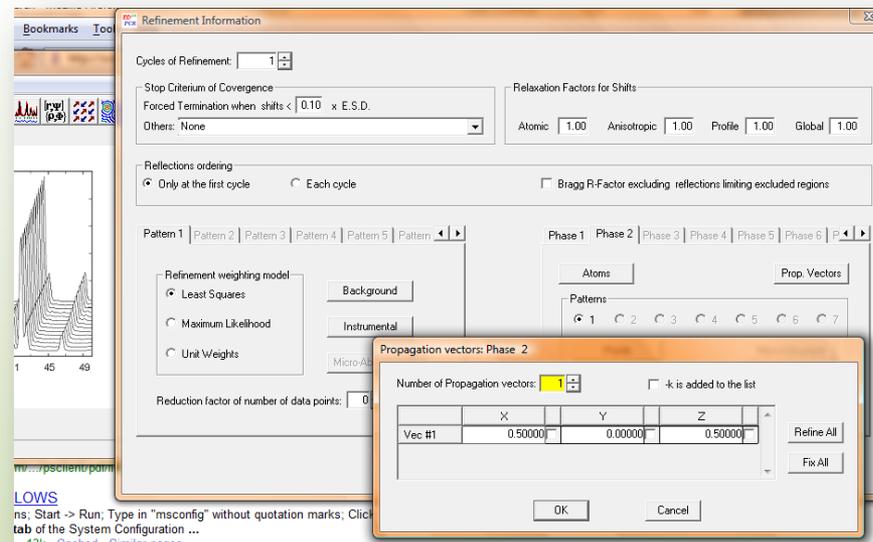
for the $\text{Ho}_2\text{BaNiO}_5 \rightarrow k_m = (0.5, 0, 0.5)$

➤ ADDING THE MAGNETIC PHASE AS A SECOND PHASE TO THE PCR

- ✓ use PCR Editor to introduce the magnetic phase as a second phase. Go to the "Phases" tab and click on the "Add" button. You can name (ex. *magphase*) the new phase as you wish, and in the "calculation" tab select the "Magnetic phase (Rietveld Method)" option.



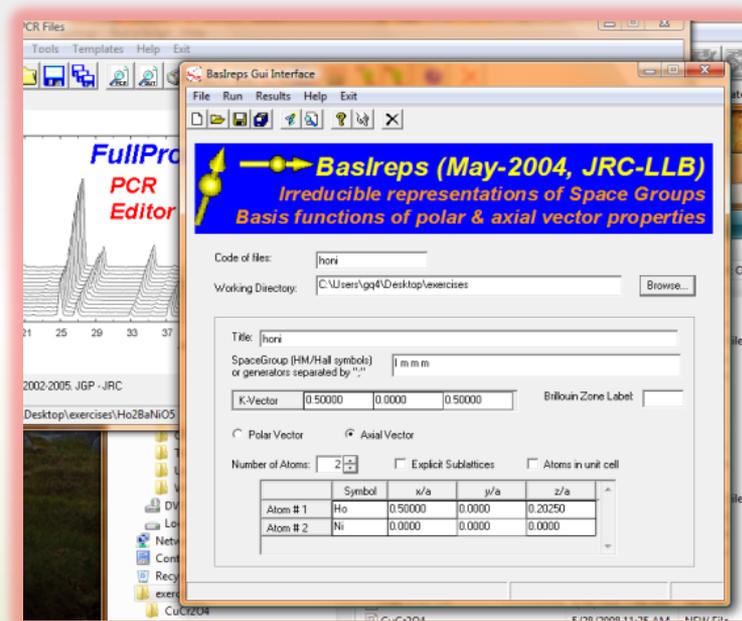
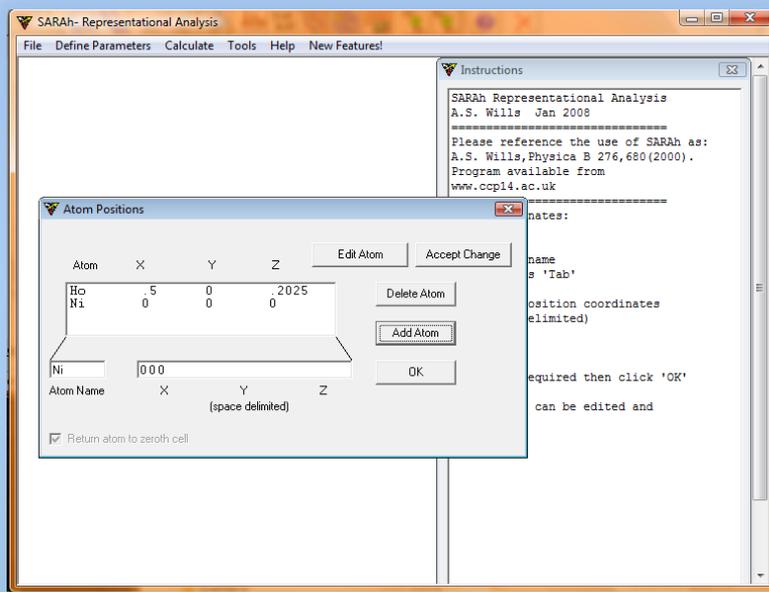
- ✓ the propagation vector for the magnetic phase needs to be added into the PCR file. For doing that, you need to click on "Refinement" button and then select the "Phase 2" and "Prop. Vectors"



- ✓ you can also open the PCR file using your default text editor at this time and verify that the second phase has been successfully added. Don't worry about the symmetry at this time.

➤ PERFORM SYMMETRY ANALYSIS

- ✓ use the **SARAh** program or **Baslreps** to generate the Irreducible representations and basis vectors associated with $k_m = (0.5, 0, 0.5)$. Both programs require as an input the k_m vector, space group and atom positions of the magnetic ion.



- ✓ for this example we will use the program **SARAh**. See the software's website for the tutorial on how to run the program. The program generates a summary file containing the basis vectors components for the two magnetic ions. The file is located in SARAh program's folder.

- ✓ The result of the symmetry analysis is also summarized in a TEX file, in Sarah directory, as shown in this capture:

Ho

IR	BV	Atom	BV components					
			$m_{\parallel a}$	$m_{\parallel b}$	$m_{\parallel c}$	$im_{\parallel a}$	$im_{\parallel b}$	$im_{\parallel c}$
Γ_1	ψ_1	1	0	4	0	0	0	0
		2	0	4	0	0	0	0
Γ_2	ψ_2	1	4	0	0	0	0	0
		2	-4	0	0	0	0	0
	ψ_3	1	0	0	4	0	0	0
		2	0	0	-4	0	0	0
Γ_3	ψ_4	1	4	0	0	0	0	0
		2	4	0	0	0	0	0
	ψ_5	1	0	0	4	0	0	0
		2	0	0	4	0	0	0
Γ_4	ψ_6	1	0	4	0	0	0	0
		2	0	-4	0	0	0	0

Table 1: Basis vectors for the space group $I m m m$ with $k_{-55} = (.5, 0, .5)$. The decomposition of the magnetic representation for the Ho site $(.5, 0, .2025)$ is $\Gamma_{Mag} = 1\Gamma_1^1 + 2\Gamma_2^1 + 2\Gamma_3^1 + 1\Gamma_4^1$. The atoms of the nonprimitive basis are defined according to 1: $(.5, 0, .2025)$, 2: $(.5, 0, .7975)$.

Γ_1 constraints moments to lie along the *b*-axis

Γ_3 constraints moments to lie in the *ac*-plane

Ni

IR	BV	Atom	BV components					
			$m_{\parallel a}$	$m_{\parallel b}$	$m_{\parallel c}$	$im_{\parallel a}$	$im_{\parallel b}$	$im_{\parallel c}$
Γ_1	ψ_1	1	0	4	0	0	0	0
Γ_3	ψ_2	1	4	0	0	0	0	0
		1	0	0	4	0	0	0

Table 2: Basis vectors for the space group $I m m m$ with $k_{-55} = (.5, 0, .5)$. The decomposition of the magnetic representation for the Ni site $(0, 0, 0)$ is $\Gamma_{Mag} = 1\Gamma_1^1 + 0\Gamma_2^1 + 2\Gamma_3^1 + 0\Gamma_4^1$. The atom of the primitive basis is defined according to 1: $(0, 0, 0)$.

- ✓ If the two sites (Ni and Ho) order according to the same representation only the representations 1 and 3 are allowed.

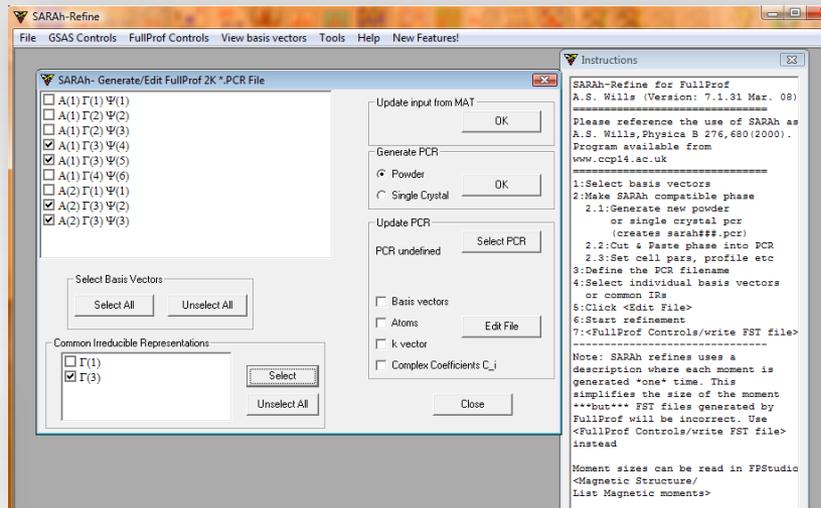
✓ “SARAh Refine” program can be used to generate the magnetic phase for the PCR (FullProf) format (see Sarah manual for more details). In our case , it will generate the file “sarah71.pcr”

✓ You’ll need to select the basis vectors corresponding to one of the two common Irreducible Representations (gamma3 or Γ_3 in our case).

```

sarah71.pcr - Notepad
File Edit Format View Help
  2   1   1  -2   2
! Rea1(0)-Imaginary(1) indicator for C1
0 0
!
SYMM X, Y, Z
BASR 2 0 0 0 0 0 2
BASI 0 0 0 0 0 0 0
BASR 4 0 0 0 0 0 4
BASI 0 0 0 0 0 0 0
SYMM -X+1, Y, -Z+1
BASR 2 0 0 0 0 0 2
BASI 0 0 0 0 0 0 0
BASR 0 0 0 0 0 0 0
BASI 0 0 0 0 0 0 0
!
! Atom Typ Mag Vek X Y Z Biso Occ C1 C2 C3
! C4 C5 C6 C7 C8 C9 MagPh
HO1 MH03 1 0 .50000 .00000 .20250 .30000 1.00000 0.000 0.000 0.000
! 0.000 0.000 0.000 0.000 0.000 0.000 .00000
! 0.00 0.00 0.00 0.00 0.00 0.00
NI2 MN13 2 0 .00000 .00000 .00000 .30000 1.00000 0.000 0.000 0.000
! 0.000 0.000 0.000 0.000 0.000 0.000 .00000
! 0.00 0.00 0.00 0.00 0.00 0.00
! ----- Profile Parameters for Pattern # 1
! Scale Shape1 Bov Str1 Str2 Str3 Strain-Model
! 10.0 0.0000 0.0000 0.0000 0.0000 0.0000 0
! 0.00000 0.00 0.00 0.00 0.00 0.00
! u v w X Y GauS1z LorS1z Size-Model
! 1.08239 -0.23233 0.25618 0.00000 0.00000 0.00000 0.00000 0
! 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00
! a b c alpha beta gamma
!
! 273
! 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000
! Pref1 Pref2 Asy1 Asy2 Asy3 Asy4
! 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000
! 0.00 0.00 0.00 0.00 0.00 0.00
! Propagation vectors:
! .5000000 .0000000 .5000000 Propagation Vector 1
! 0.0000000 0.0000000 0.0000000

```

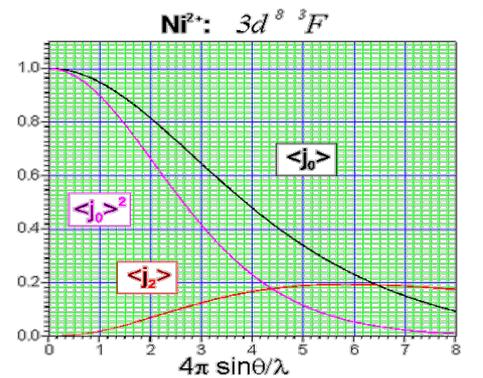
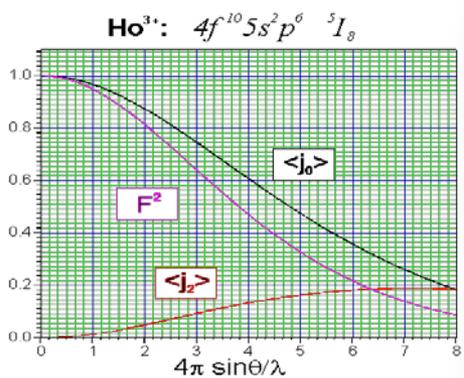
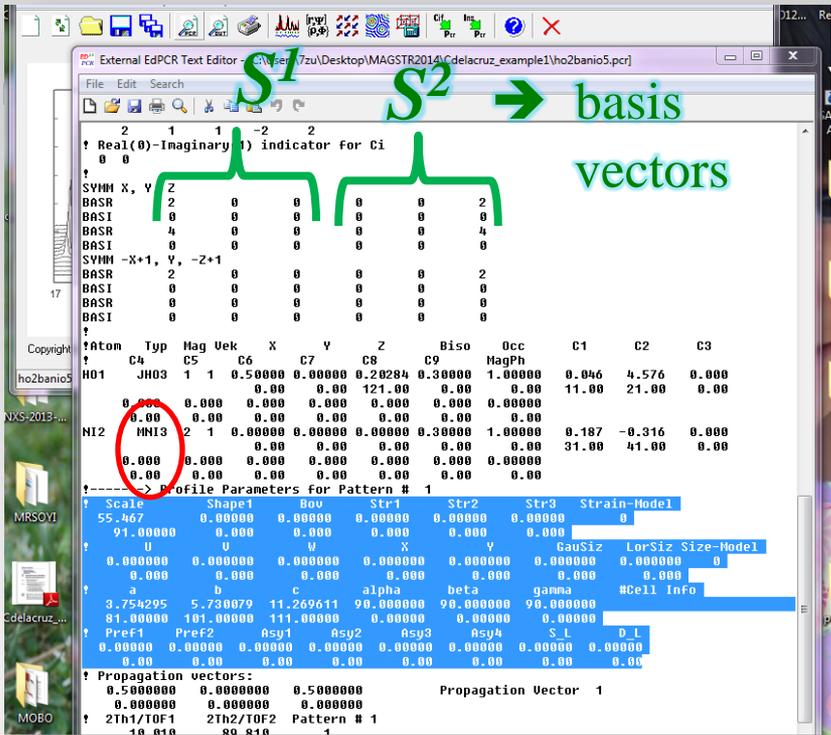


✓ Note that the selected model Γ_3 constrains the magnetic moments of Ho and Ni to lie in the ac-plane

✓ Open the PCR file generated by Sarah (“sarah71.pcr”), copy the entire content of the file and PASTE it over the section of the second phase of your Ho2BaNiO5 PCR file.

✓ once the magnetic phase is defined into your PCR file, examine the profile parameter section; you'll need to set the profile parameters for the magnetic phase (phase 2) the same as you have in the structural phase (phase 1). Copy/paste that section from the phase1 to the phase 2. Make sure that you are not removing the line defining the propagation vector, at the end of the phase 2 section.

✓ note that the scale factor and the lattice parameters of the structural and magnetic phase need to be constrained to have the same values in both the nuclear and magnetic phases.



$$S_{kjs} = \sum_{n\lambda} C_{n\lambda}^v S_{n\lambda}^{k v} (js)$$

Fourier coefficient for calculation of m_{ijs} at each site

$$S_k = C_1 S^1 + C_2 S^2$$

✓ make sure that the correct parameters for the magnetic scattering form factors are used **JHO3** for the magnetic rare earth Ho^{3+} and **MNI3** for the transition metal ion Ni^{3+}

$$\chi(\vec{\delta}) = \langle \chi^0(\vec{\delta}) \rangle + \left(1 - \frac{\gamma}{J}\right) \langle \chi^J(\vec{\delta}) \rangle$$

International Tables of Crystallography, Volume C, ed. by AJC Wilson, Kluwer Ac. Pub., 1998, p. 513

MAGNETIC STRUCTURE REFINEMENT

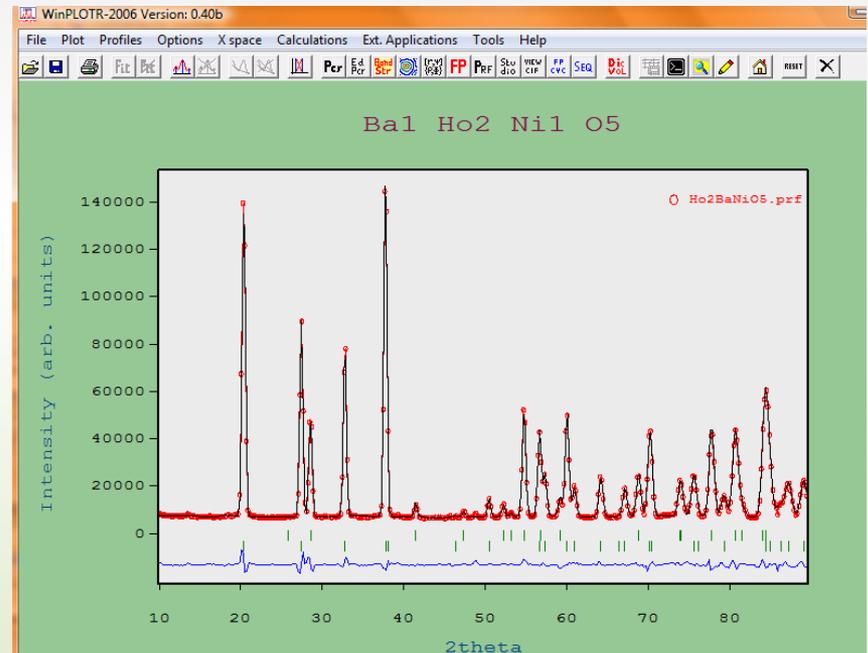
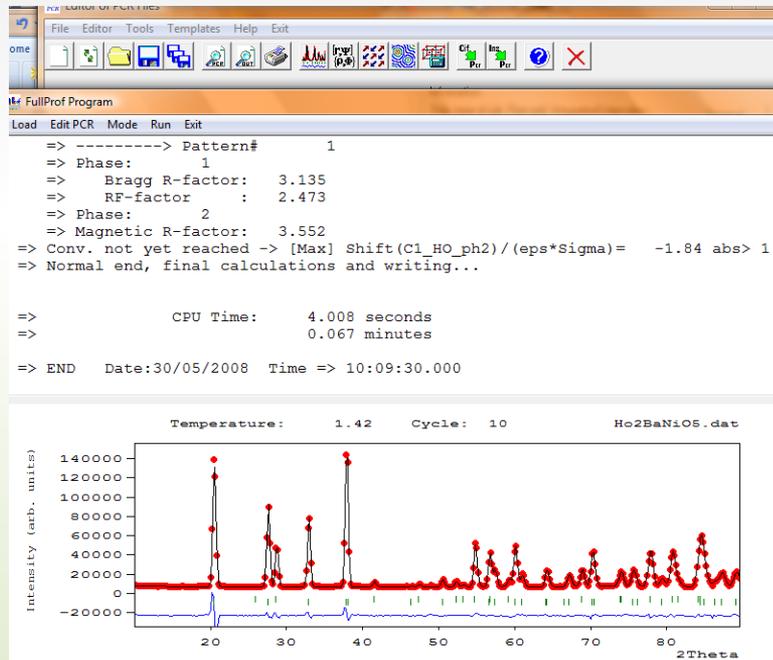
✓ select the basis vector coefficients C1 and C2 for the two independent magnetic ions (Ho and Ni) to be refined

Basis Functions Coefficients

	C1		C2		C3		C4	
Atom # 1	2.00000	<input checked="" type="checkbox"/>	2.00000	<input checked="" type="checkbox"/>	0.00000	<input type="checkbox"/>	0.00000	<input type="checkbox"/>
Atom # 2	0.12300	<input checked="" type="checkbox"/>	0.18300	<input checked="" type="checkbox"/>	0.00000	<input type="checkbox"/>	0.00000	<input type="checkbox"/>

✓ run the refinement using the FullProf program

✓ start to refine additional parameters (profile, lattice ...) to obtain a good quality fit.



MAGNETIC MOMENT DETERMINATION

- ✓ Check the output file (*.out) from FullProf. Verify that the magnetic structure model and the magnitude of the Ho and Ni moments are meaningful

```

External EdPCR Text Editor - [C:\Users\7zu\Desktop\MAGSTR2014\Cdelacruz_example1\Ho2BaNiO5.out]
File Edit Search
-----
=> Phase 2 Name: Magnetic Phase
-----
=> New parameters, shifts, and standard deviations
-----
Atom      x      dx      sx      y      dy      sy      z      dz      sz      B      dB      sB      occ.
HO1       0.50000 0.00000 0.00000 0.00000 0.00000 0.00000 0.20250 0.00000 0.00000 0.30000 0.00000 0.00000 1.00000
NI2       0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0.30000 0.00000 0.00000 1.00000

=> Coefficients of basis vectors, shifts, and standard deviations:
-----
Atom      C1      dC1      sC1      C2      dC2      sC2      C3      dC3      sC3
HO1       0.889718 0.000000 0.065527 9.029646 0.000000 0.054908 0.000000 0.000000 0.000000
          0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000
          0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000
          0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000
NI2       0.765226 0.000000 0.125650 -1.242781 0.000000 0.050806 0.000000 0.000000 0.000000
          0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000
          0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000
          0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000
-----
Line:1708 Col:30
NUM INS
  
```

The moment m_{ljs} is calculated from the refined values of the Fourier components S_{kjs}

$$m_{ljs} = \sum_{\{k\}} S_{kjs} \exp\{-2\pi i k R_l\}$$

$$S_{kjs} = \sum_{n\lambda} C_{n\lambda}^v S_{n\lambda}^{k v}(js)$$

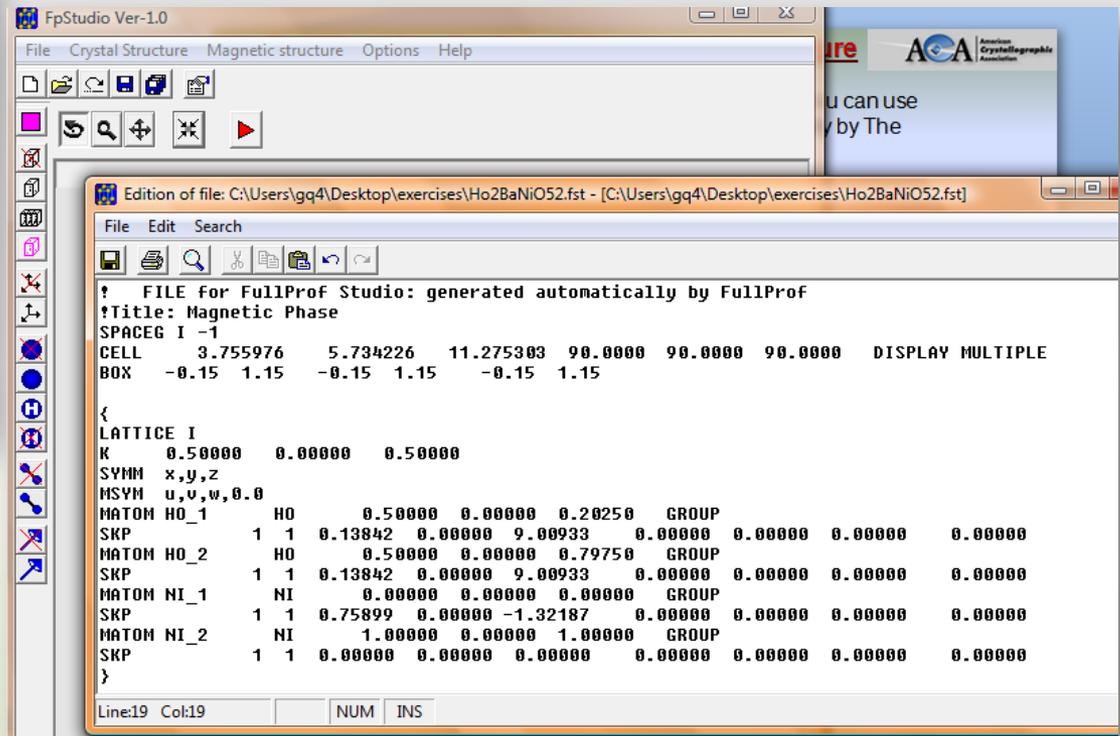
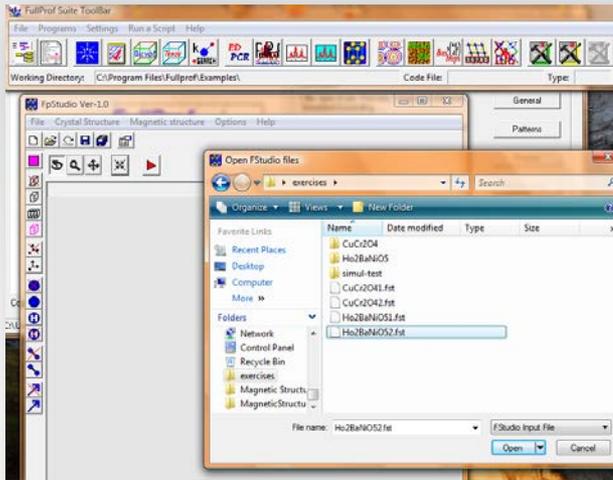
Ho: $M_x = 0.09(6) \mu_B$; $M_z = 9.03(5) \mu_B$

Ni: $M_x = 0.77(12) \mu_B$; $M_z = -1.24(5) \mu_B$

the moment of Ho is nearly parallel to the c-axis and the Ni-moment is canted by ~ 29 deg with respect to the c-axis

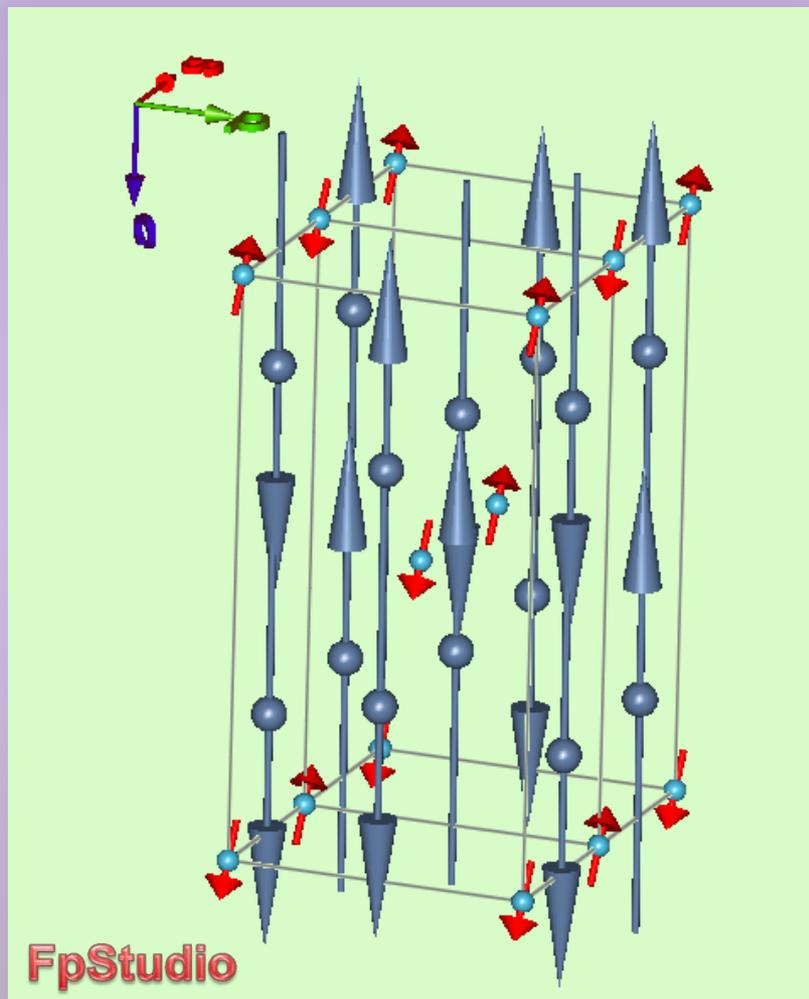
➤ VISUALIZATION OF THE MAGNETIC STRUCTURE

- ✓ to visualize the determined magnetic structure you can use **FpStudio** program. It reads ***.fst** files, generated automatically by The Fullprof or SARAh



- ✓ **FpStudio** uses Fourier coefficients notation (u,v,w). You can edit the input file if necessary..

CONGRATULATIONS ! Here is your magnetic structure



- ✓ To see list of magnetic moments at each site:
Magnetic structure → List magnetic moments

Atom : H01_1 H0

x	y	z	Translation	k	MSYM	m(a)	m(b)	m(c)	Mtot
0.500	0.000	0.203	(0, 0, 0)	1	1	0.090	0.000	9.030	
			(0, 1, 0)	1	1	0.090	0.000	9.030	9.030
			(0, 0, 0)	1	1	0.090	0.000	9.030	9.030
			(1, 0, 0)	1	1	-0.090	0.000	-9.030	

Ho

Atom : NI2_1 NI

x	y	z	Translation	k	MSYM	m(a)	m(b)	m(c)	Mtot
0.000	0.000	0.000	(0, 0, 0)	1	1	0.765	0.000	-1.243	
			(0, 0, 1)	1	1	-0.765	0.000	1.243	1.459
			(0, 1, 0)	1	1	0.765	0.000	-1.243	1.459
			(0, 1, 1)	1	1	-0.765	0.000	1.243	1.459
			(1, 0, 0)	1	1	-0.765	0.000	1.243	1.459
			(1, 0, 1)	1	1	0.765	0.000	-1.243	

Ni