



Skoltech

LOMONOSOV MOSCOW
STATE UNIVERSITY



Elettra Sincrotrone Trieste



Russian Science
Foundation

Crystallography and Crystal Chemistry
VIII International School-Conference of
Young Scientists 2023

*Software and
approaches in
structural refinement
for battery materials*



Dr. Ivan Trussov

PhD in Chemistry

Center for Energy Science and Technology

Skoltech, Moscow, Russian Federation

November 10th, 2023

A quick look back

J. Appl. Cryst. (1969). 2, 65

A Profile Refinement Method for Nuclear and Magnetic Structures

BY H. M. RIETVELD

Reactor Centrum Nederland, Petten (N.H.), The Netherlands

(Received 29 November 1968)

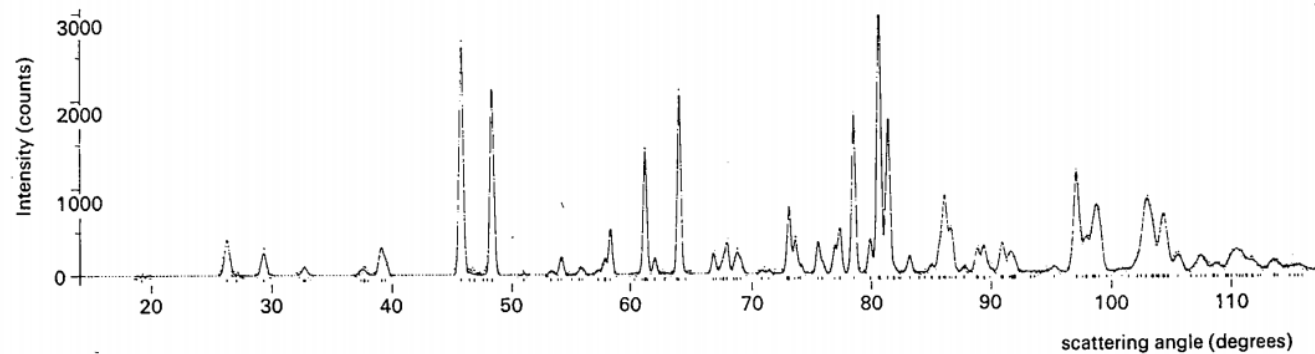


Fig. 5. Neutron powder diffraction diagram of Sr₂UO₅ measured at $\lambda = 2.565 \text{ \AA}$; — calculated profile, measured profile.

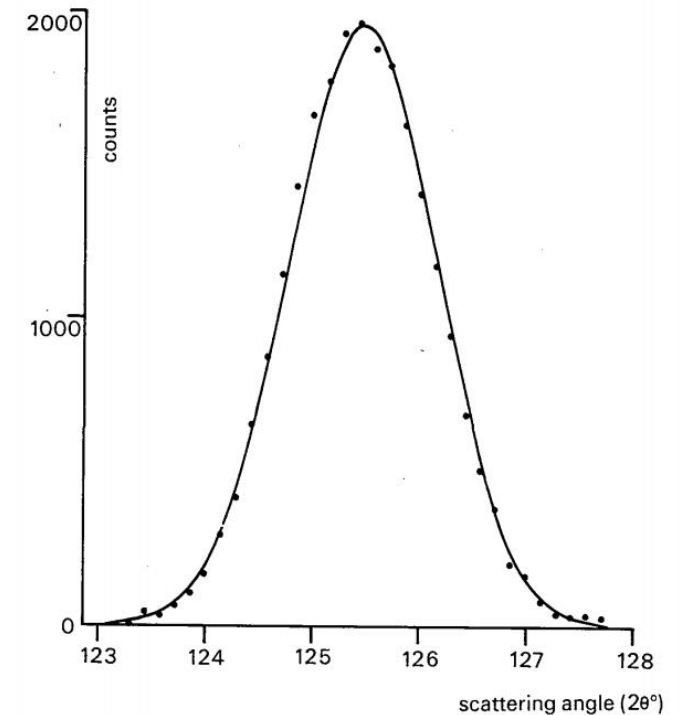


Fig. 1. Comparison of a measured diffraction peak,, with a calculated Gaussian peak profile, —.

A quick look back



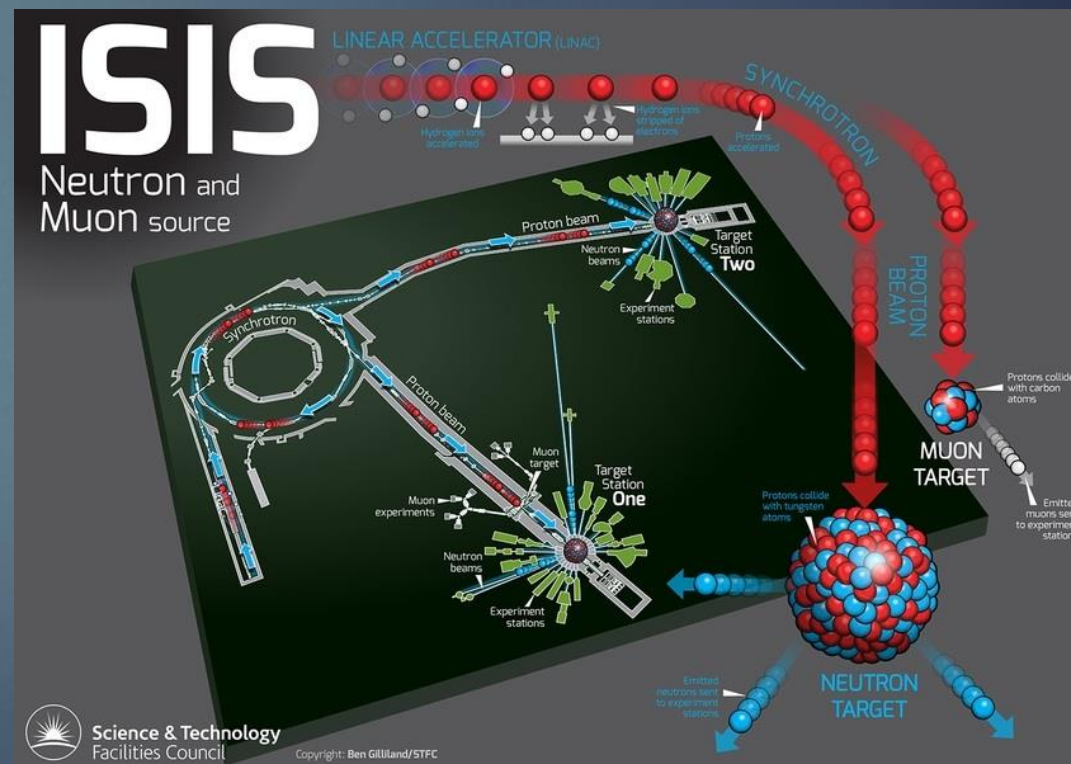
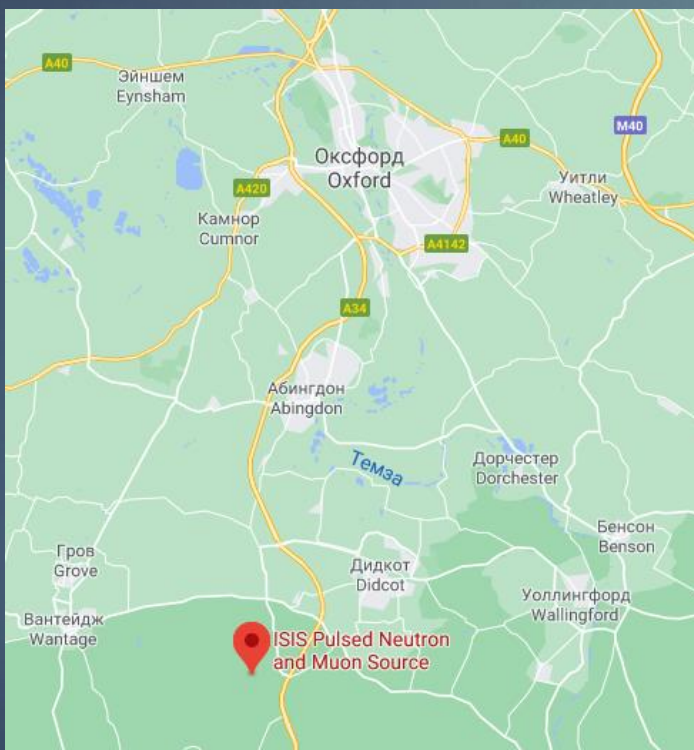
Electrologica X-8

A quick look back

Corpus ID: 60486565

The Cambridge Crystallography Subroutine Library. Extended Mark 2 users manual

[P. Brown, J. C. Matthewman](#) · Published 1981 · Computer Science



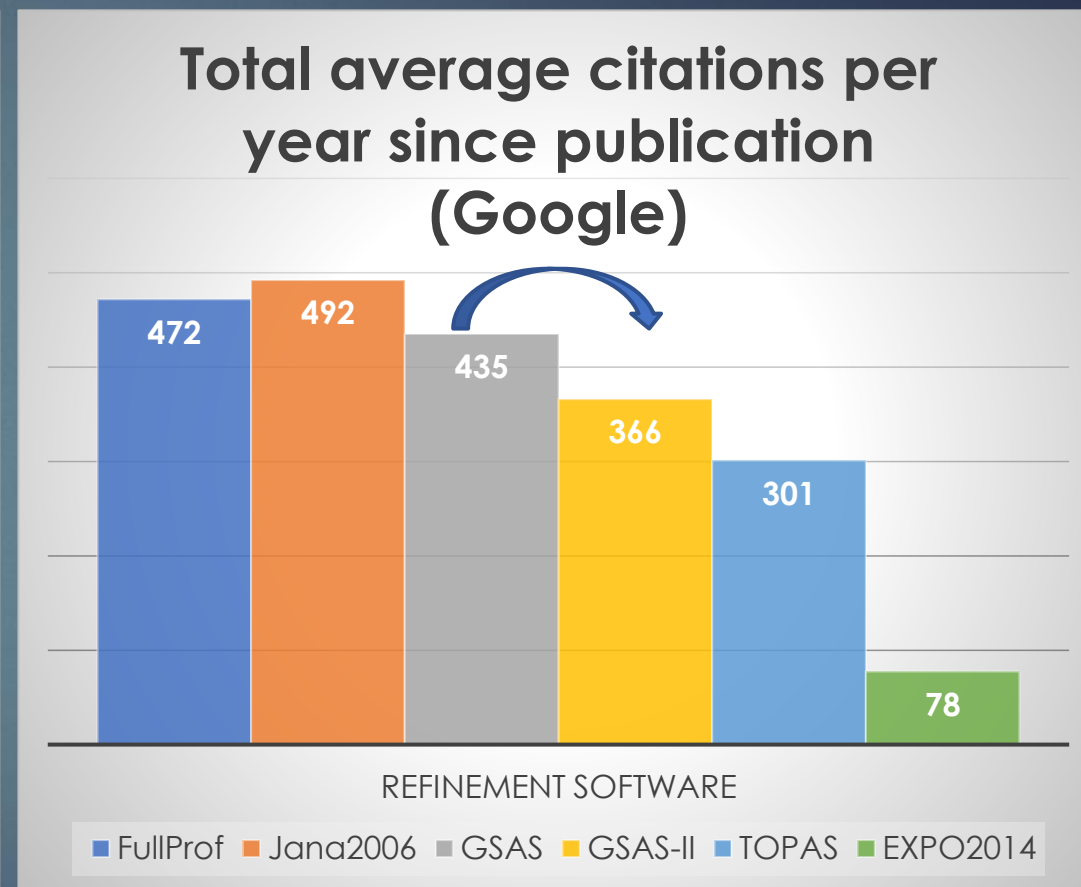
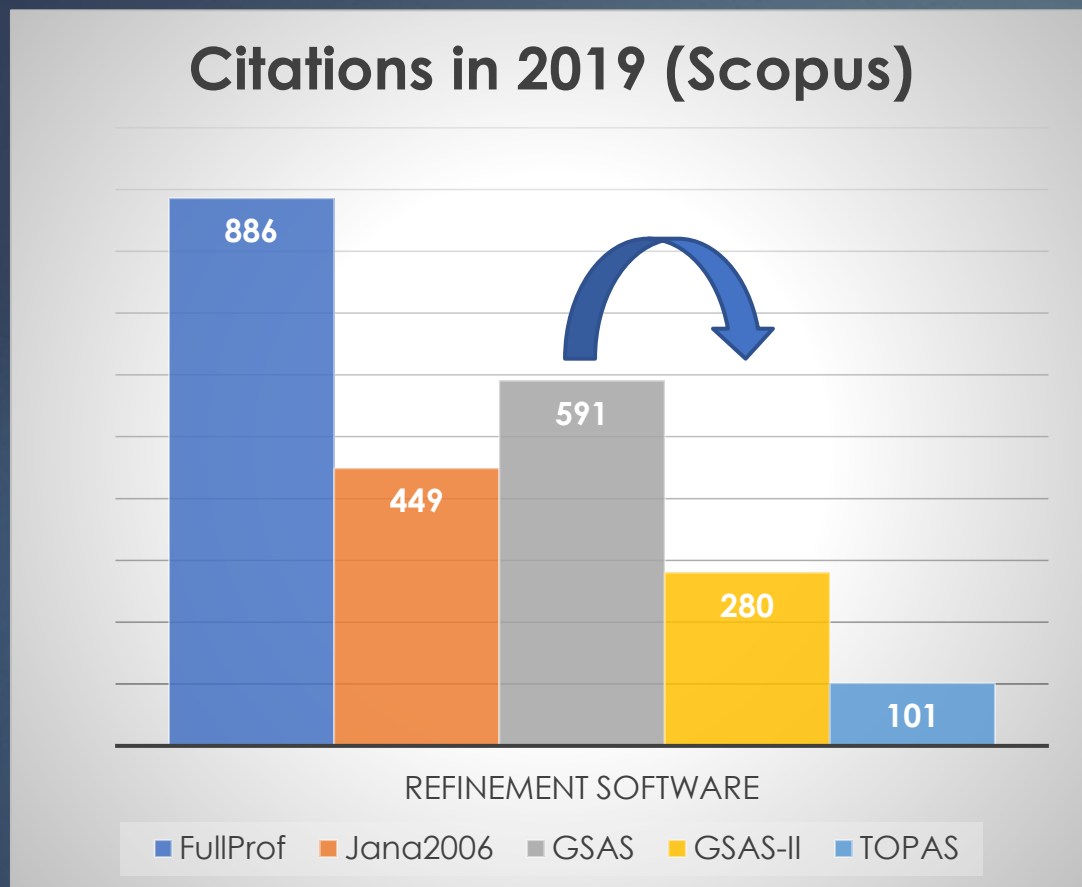
Refinement the way just like elders did

You will need:

- Nicely printed graph,
- Scissors,
- Scales,
- Keen eye,
- Steady hands.



What are the options today?*



*Disclaimer: there are more

Jana2006 (V. Petříček, M. Dušek and L. Palatinus)

Institute of Physics, Academy of Sciences of the Czech Republic

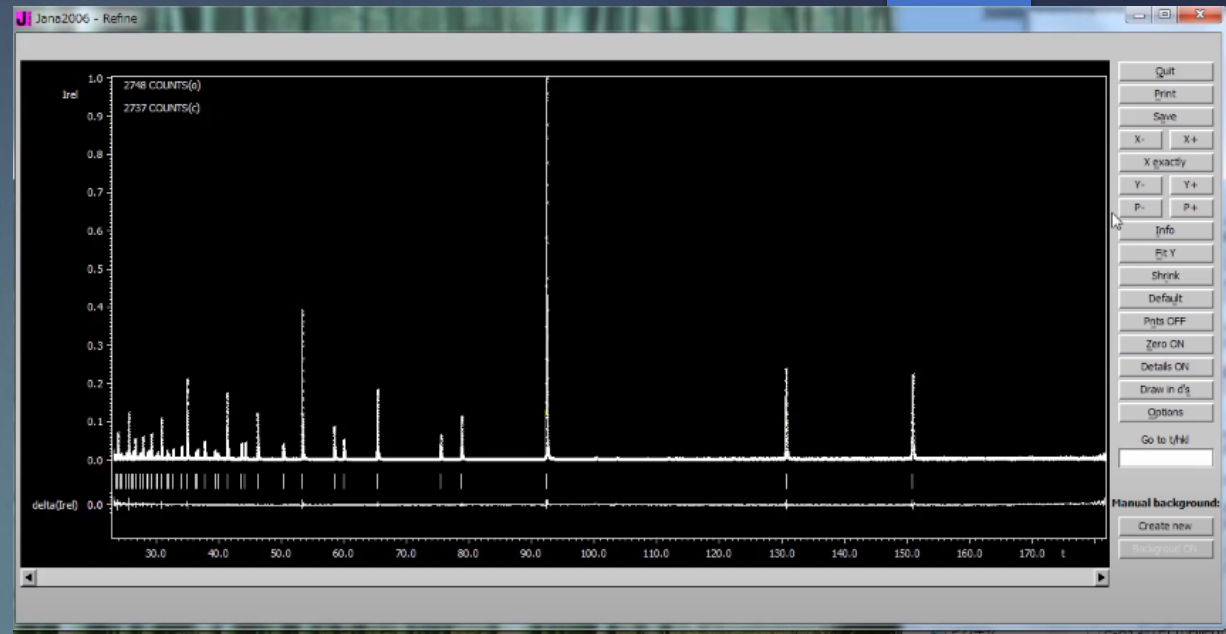
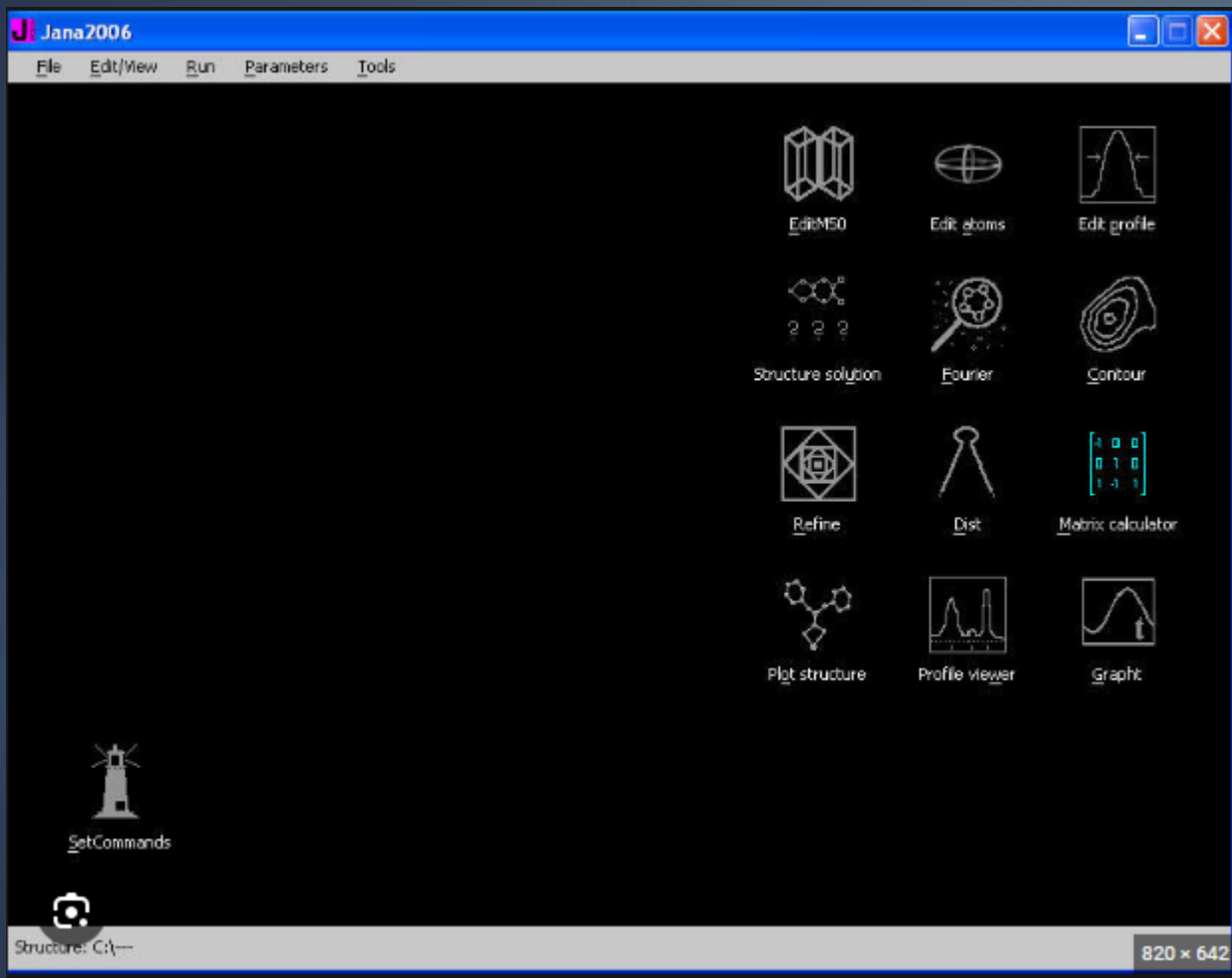
▶ Capabilities

- ▶ Rietveld/Pawley refinement (magnetic structures) (XRD, ND, TOF)
- ▶ **Modulated structures refinement**
- ▶ Fourier mapping
- ▶ Charge flipping
- ▶ Monte Carlo / Simulated annealing
- ▶ Strain/size analysis
- ▶ Indexing
- ▶ Stacking faults
- ▶ Small-Angle scattering
- ▶ Single-Crystal refinement



- Reliable
- Rather Simple
- Easy to link to externals
- Wide tutorial base
- **Free**

Jana2006



FullProf (J. Rodriguez-Carvajal)

ESRF France

▶ Capabilities

- ▶ Rietveld/Pawley refinement (magnetic structures) (XRD, ND, TOF)
- ▶ **Magnetic structure refinement**
- ▶ Fourier mapping
- ▶ Charge flipping
- ▶ Monte Carlo / Simulated annealing
- ▶ Strain/size analysis
- ▶ Indexing
- ▶ Stacking faults
- ▶ Small-Angle scattering
- ▶ Single-Crystal refinement



- Well-established
- OriginPro integration
- **Free**

FullProf

The image displays two software windows. The top window is the 'FullProf Suite ToolBar' with a menu bar (File, Programs, Settings, FP Dimensions, Run a Script, Help) and a toolbar. Below it is the 'Editor of PCR Files' window showing a 'FullProf Program' window with the following text:

```
=> CPU Time: 1.945 seconds  
=> 0.032 minutes  
  
=> END Date:22/02/2019 Time => 14:26:42.893
```

Below this text is a plot of 'Intensity (arb. units)' vs. 'Cycle:100'. The y-axis ranges from -5000 to 40000. The plot shows a series of peaks, with the most prominent one at approximately cycle 30 reaching an intensity of nearly 40,000.

The bottom window is 'OriginPro 8.5' showing a graph of 'Intensity (arb. units)' vs. 'Cycle (!)'. The y-axis ranges from 0 to 40000. The plot shows a series of peaks, with the most prominent one at approximately cycle 30 reaching an intensity of nearly 40,000. A blue arrow points from the 'Easy & Best' text to the OriginPro window.

Easy & Best

FullProf → Origin

The Windows taskbar at the bottom shows the following icons: Start button, File Explorer, Google Chrome, Microsoft Word, EN (Excel), RPS (RStudio), ED 2.0 (ED 2.0), FullProf, and a system tray with the date '22-Feb-19' and time '2:33 PM'.

FullProf

The image displays the FullProf Suite software interface. The main window, titled "FullProf Suite ToolBar", features a menu bar with "File", "Programs", "Settings", "FP Dimensions", "Run a Script", and "Help". Below the menu is a toolbar with various icons for file operations and analysis. The "Working Directory" is set to "c:\FullProf_Suite\Examples\". The "Code File:" field is empty, and the "Date:" is "24/08/2016".

In the foreground, the "Editor of PCR Files" window is open. It has a menu bar with "File", "Editor", "Tools", "Templates", "Help", and "Exit". The toolbar includes icons for file management and analysis. The main area shows a plot of a diffraction pattern with the text "FullProf PCR Editor" overlaid. The x-axis is labeled "2 θ (°)" and ranges from 17 to 49. The y-axis ranges from -200 to 1000. The plot shows several sharp peaks, with the most prominent ones around 20, 30, and 45 degrees. Below the plot, it says "Copyright (c) 2002-2005. JGP - JRC".

To the right of the plot in the Editor window is an "Information" panel with several tabs: "General", "Patterns", "Phases", "Refinement", "Constraints", "Box/Restrains", and "Output". The "General" tab is selected, showing fields for "Title, type of job: Rietveld, Integrated Intensities, Simulated Annealing, ..." and "Type of Patterns, profile, background, diffraction geometry, user-given scattering factors ...". Other tabs like "Phases" and "Refinement" are also visible.

At the bottom of the Editor window, there are status indicators: "Profiles: 0", "Phases: 0", "24/8/2016", and "16:16:41".

In the background, another window shows a diffraction pattern plot with the x-axis labeled "2 θ " and the y-axis ranging from -200 to 200. The plot shows a series of peaks, with the most prominent ones around 30, 40, and 50 degrees.

GSAS-II (R. Von-Dreele and B. Toby)

Argonne National Laboratory, US

▶ Capabilities

- ▶ Rietveld/Pawley refinement (magnetic structures) (XRD, ND, TOF)
 - ▶ Fourier mapping
 - ▶ Charge flipping
 - ▶ Monte Carlo / Simulated annealing
 - ▶ Strain/size analysis
 - ▶ Sequential refinement
 - ▶ Indexing
 - ▶ Combined refinement
 - ▶ Stacking faults
 - ▶ 2D image data processing
 - ▶ Small-Angle scattering
 - ▶ Single-Crystal refinement
- Stable
 - Reliable
 - Quick
 - Simple
 - Easy import/export
 - Free



GSAS-II

- ▶ 50 variables
- ▶ 4189 observations
- ▶ ~2.5 seconds per cycle

GSAS-II project: KNNT0.gpx

File Data Calculate Import Export | Select tab Compute | Help

Project: KNNT0.gpx

General Data Atoms Draw Options Draw Atoms RB Models Map peaks MC/SA RMC Texture Pawley reflect

Phase name: **KNNT0** Phase type: nuclear Space group: P 21 3 Modulated?

Refine unit cell: Unit cell: a = 9.87705 Vol = 963.568

Density: 3.163

Elements	K	O	P	Ti
Isotope				
Nat. Abund.				
No. per cell	8.0	48.0	12.0	8.0
Atom weight	39.098	15.999	30.974	47.900
Bond radii	2.58	1.09	1.48	1.66
Angle radii	2.38	0.89	1.28	1.46
van der Waals radii	2.75	1.70	2.08	1.70

Default color: █ █ █ █

Pawley controls: Do Pawley refinement? Pawley dmin: 1.0 Pawley dmax: 100.0 Pawley neg. wt.: 0.0

Fourier map controls: Map type: Reflection sets: Select reflection sets

Map grid step: 0.25 Peak cutoff %: 50.0

Charge flip controls: Reflection sets: Select reflection sets Normalizing element: None

Map grid step: 0.25 k-Factor (0.1-1.2): 0.1 k-Max (>=10.0): 20.0

Test HKLs: 0 0 2 2 0 0 1 1 1 0 2 0 1 2 3

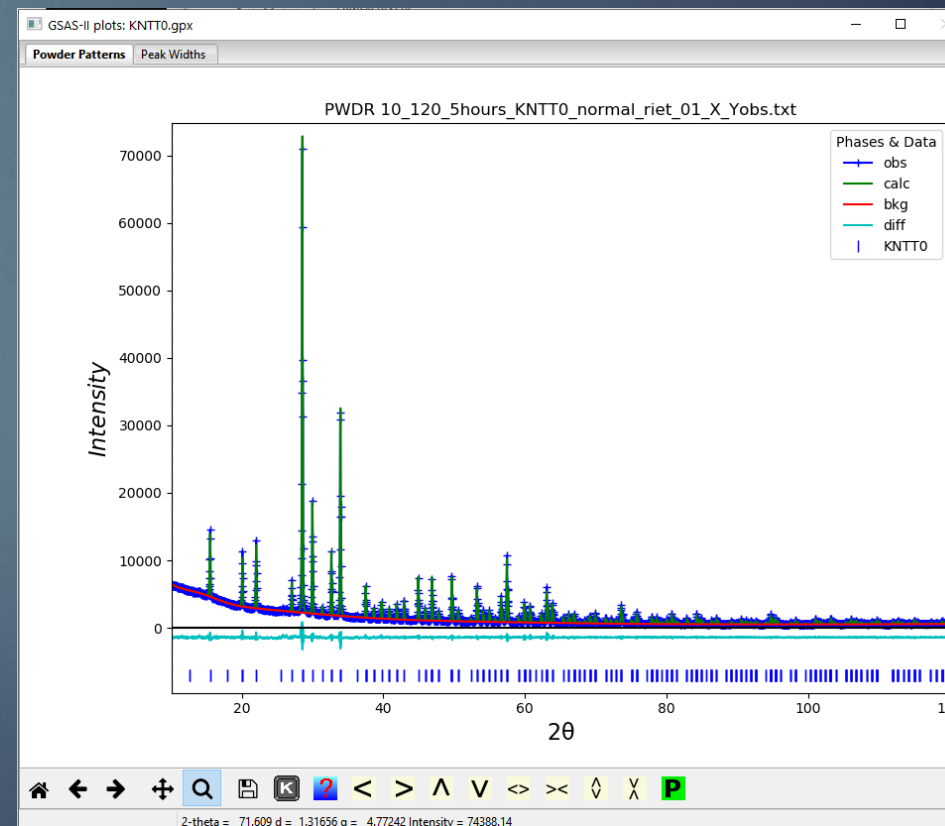
Monte Carlo/Simulated Annealing controls: Reflection set from: d-min: 2.8

MC/SA runs: 1 MC/SA Refine at: 10.0 % of ranges.

MC/SA schedule: log slope: 0.9

Annealing schedule: Start temp: 0.7 Final temp: 0.1 No. trials: 250

Mouse RB drag/drop to reorder



GSAS-II project: KNNT0.gpx

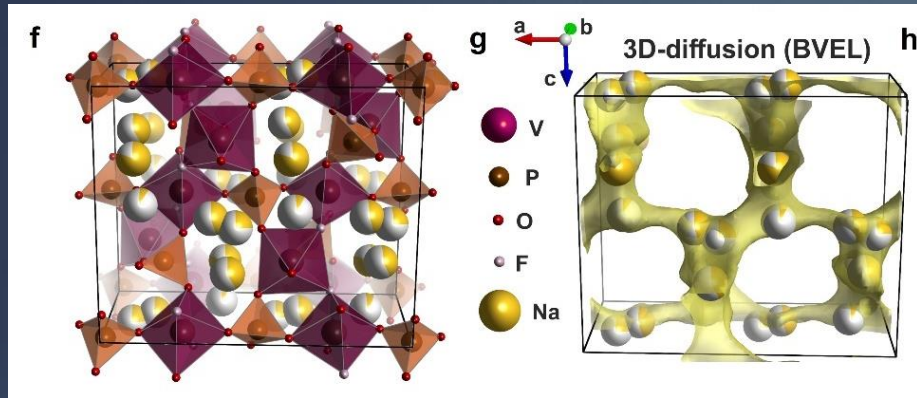
File Data Calculate Import Export | Select tab Edit Atoms Compute | Help

Project: KNNT0.gpx

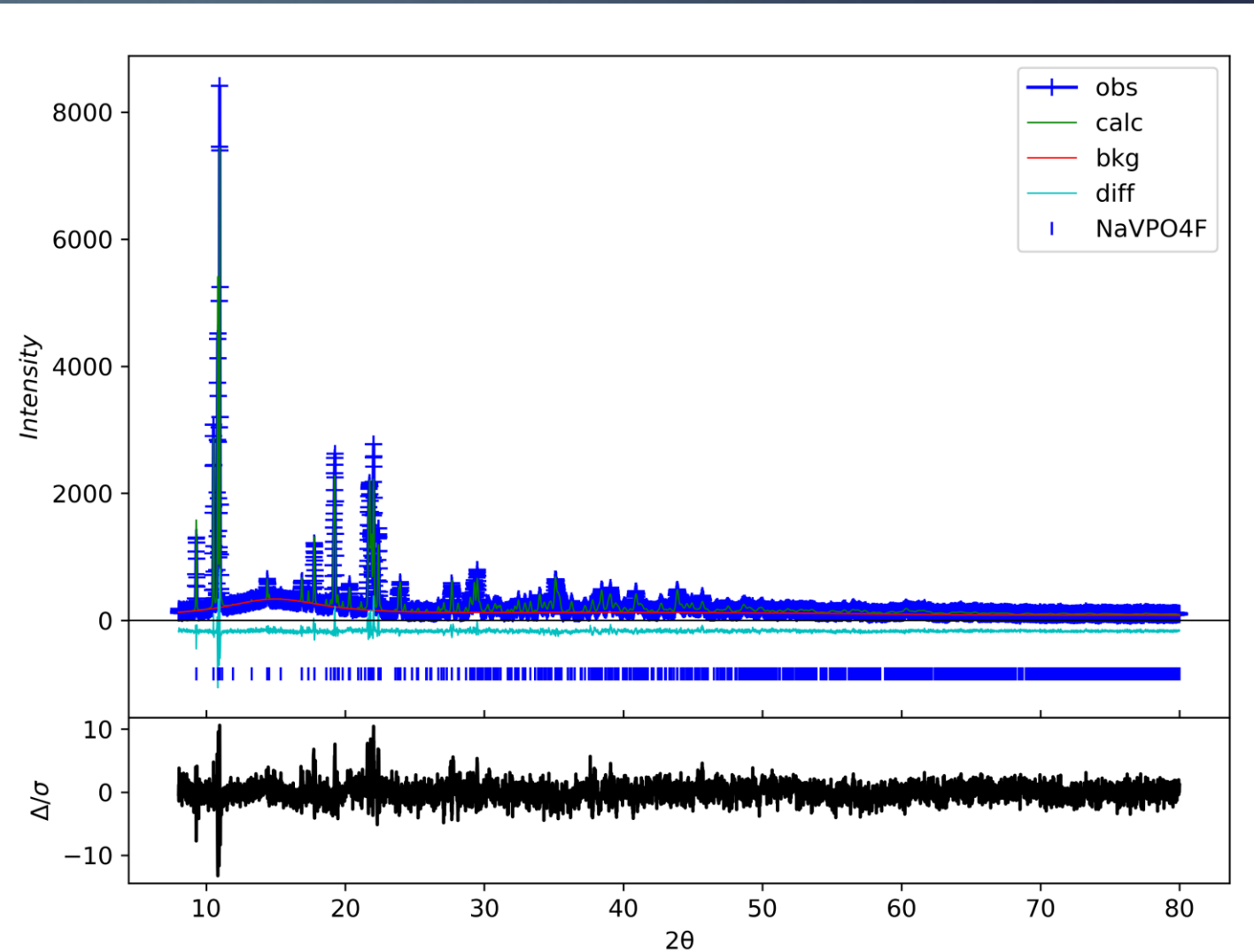
General Data Atoms Draw Options Draw Atoms RB Models Map peaks MC/SA RMC Texture Pawley reflect

	Name	Type	refine	x	y	z	frac	site sym	mult	I/A	Uiso	U11	U22	U33
0	K1	K	XU	0.29412	0.29412	0.29412	1.0000	3(111)	4	I	0.01647			
1	K2	K	XU	0.06469	0.06469	0.06469	1.0000	3(111)	4	I	0.02162			
2	O1	O	XU	0.64756	0.50264	0.42299	1.0000	1	12	I	0.00199			
3	O2	O	XU	0.76789	0.47451	0.20525	1.0000	1	12	I	0.00620			
4	O3	O	XU	0.57924	0.31457	0.26667	1.0000	1	12	I	0.00525			
5	O4	O	XU	0.53174	0.55643	0.20202	1.0000	1	12	I	0.00633			
6	P1	P	XU	0.62820	0.45912	0.27490	1.0000	1	12	I	0.00236			
7	Ti1	Ti	XU	0.58724	0.58724	0.58724	1.0000	3(111)	4	I	0.00179			
8	Ti2	Ti	XU	0.85709	0.85709	0.85709	1.0000	3(111)	4	I	0.00416			

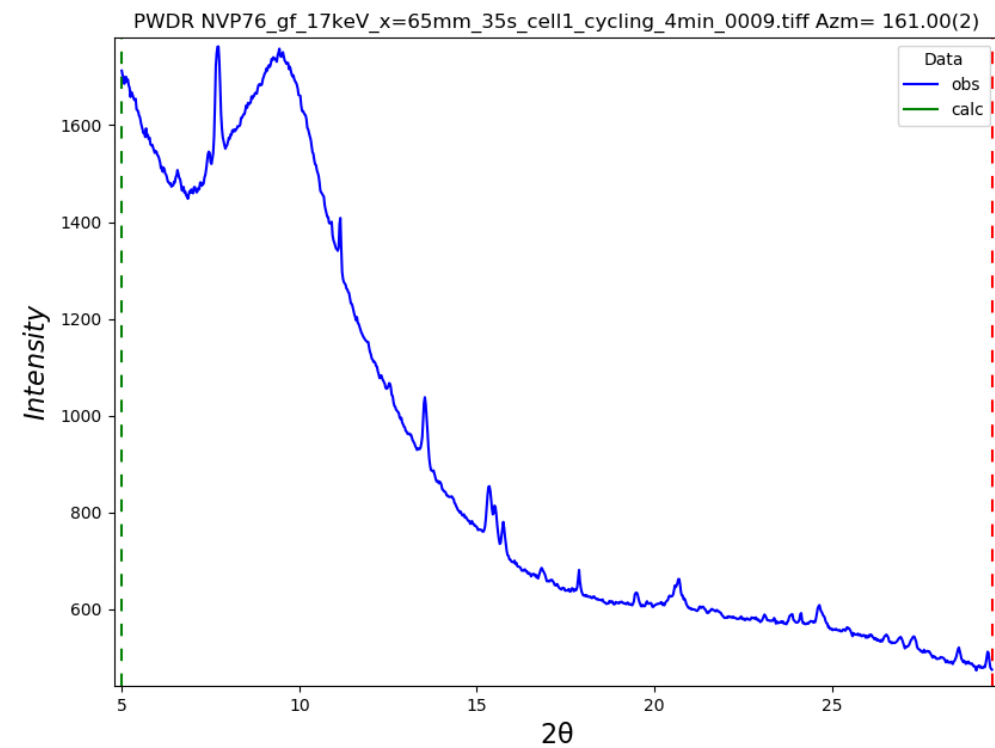
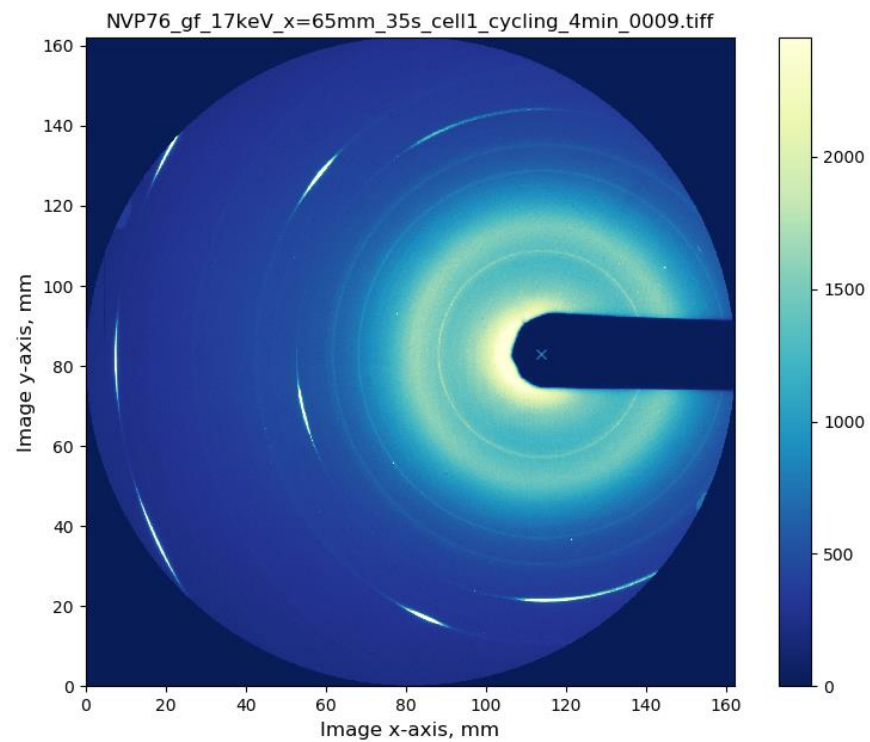
GSAS-II: Rietveld refinement



Real-life case: refinement of
synchrotron data (Elettra)



GSAS-II: 2D integration

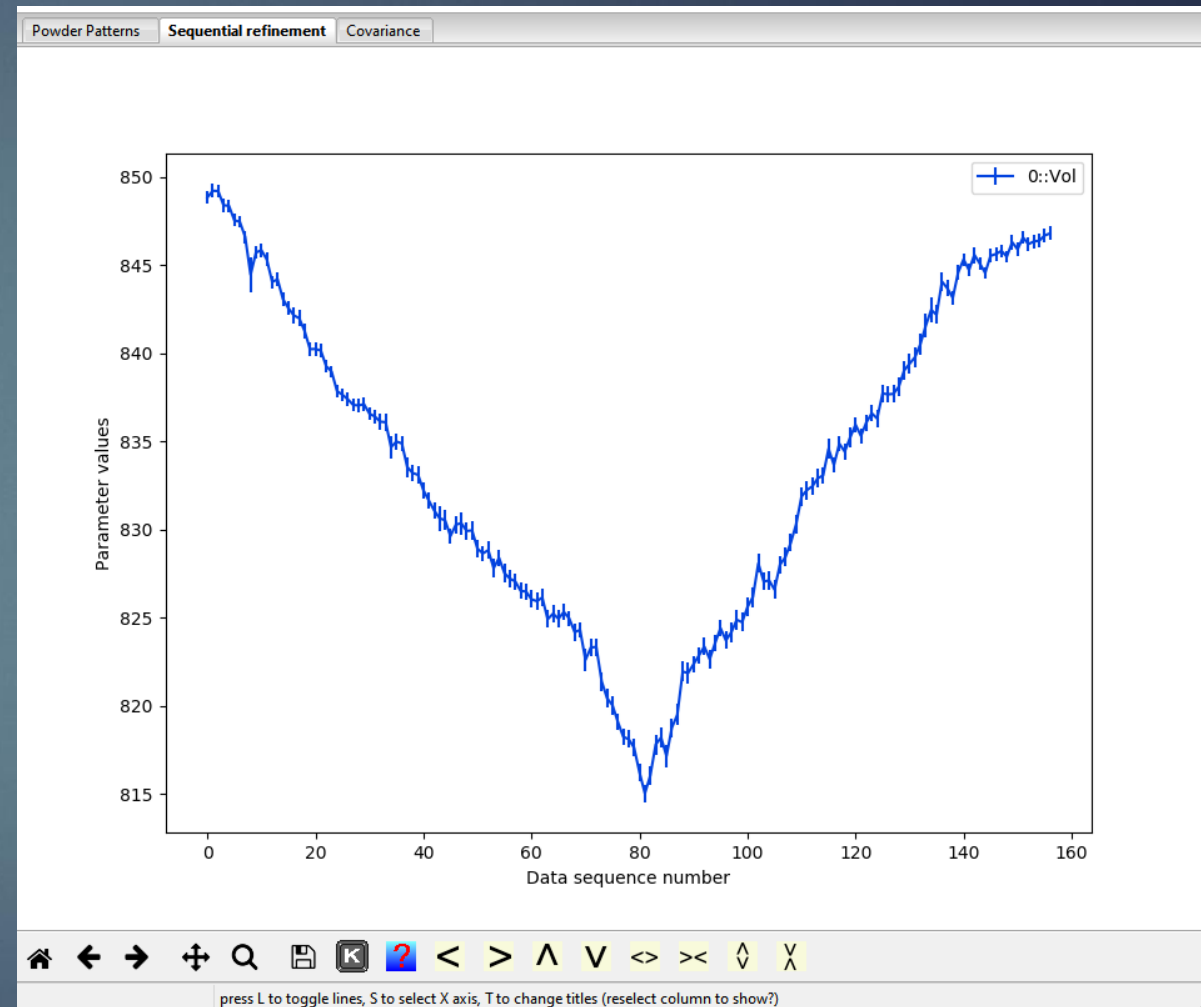


Integration

GSAS-II: sequential refinement

Operando data processing

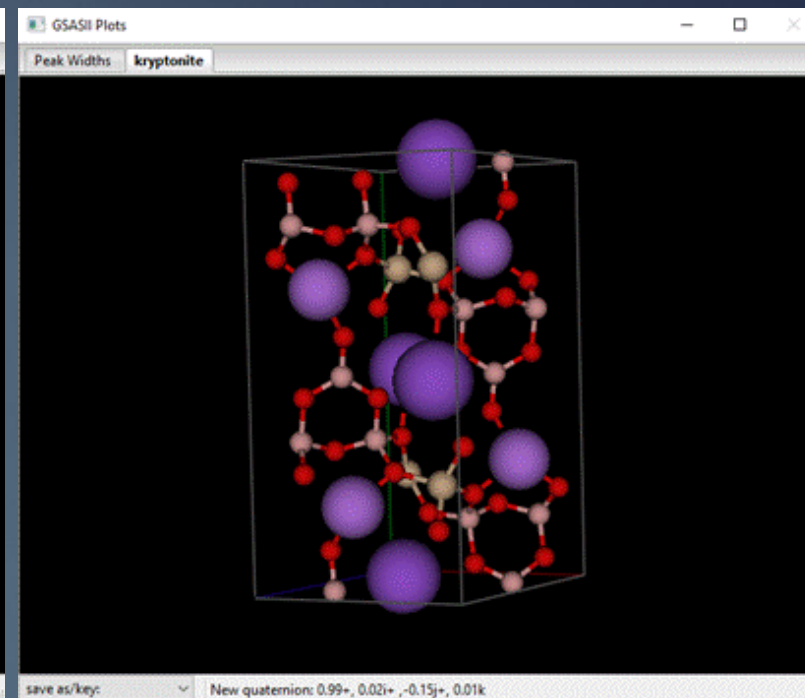
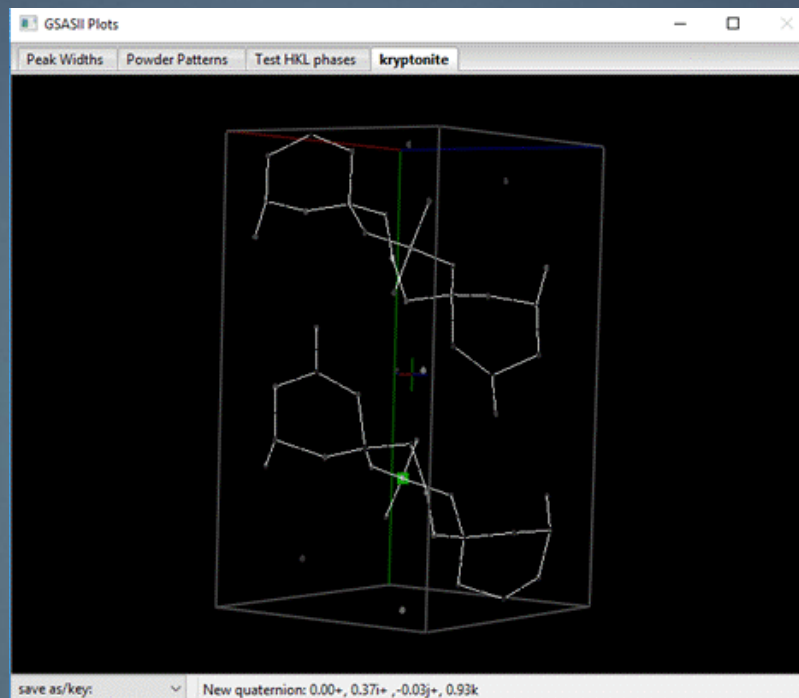
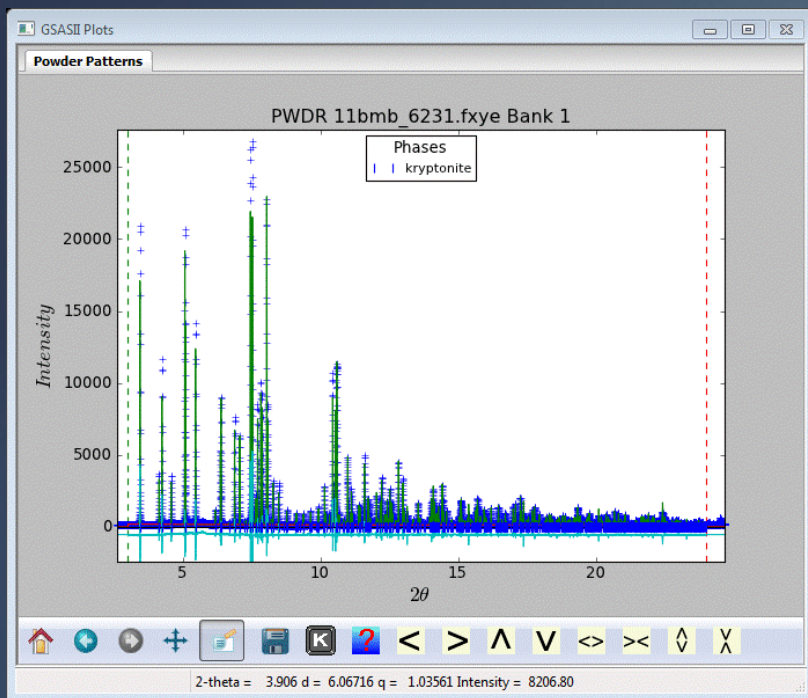
No.	Use	Rwp	$\Delta\chi^2$ (%)	0:a	0:b	0:c	0:Vol	0:Scale
1	<input checked="" type="checkbox"/>	1.646	0.03441	12.71165	6.29707	10.60430	848.833	1.38387
2	<input checked="" type="checkbox"/>	1.631	-0.03114	12.71326	6.29758	10.60679	849.210	1.38889
3	<input checked="" type="checkbox"/>	1.632	0.03624	12.71267	6.29848	10.60556	849.192	1.37282
4	<input checked="" type="checkbox"/>	1.605	0.09778	12.70801	6.29767	10.60079	848.391	1.36416
5	<input checked="" type="checkbox"/>	1.633	0.05971	12.70778	6.29681	10.60198	848.354	1.41886
6	<input checked="" type="checkbox"/>	1.620	-0.07627	12.70155	6.29650	10.59744	847.533	1.40277
7	<input checked="" type="checkbox"/>	1.620	0.00458	12.70059	6.29751	10.59555	847.455	1.41119
8	<input checked="" type="checkbox"/>	1.609	-0.08063	12.69641	6.29314	10.59569	846.600	1.41083
9	<input checked="" type="checkbox"/>	4.469	-0.06099	12.68734	6.29080	10.59025	844.448	1.31111
10	<input checked="" type="checkbox"/>	1.583	0.05825	12.69314	6.28560	10.60000	845.710	1.42267
11	<input checked="" type="checkbox"/>	1.581	0.01577	12.69896	6.28204	10.60278	845.840	1.32732
12	<input checked="" type="checkbox"/>	1.588	-0.11884	12.69667	6.27738	10.60602	845.319	1.36950
13	<input checked="" type="checkbox"/>	1.575	-0.10347	12.69850	6.26764	10.60497	844.045	1.44215
14	<input checked="" type="checkbox"/>	1.588	-0.07454	12.69800	6.26594	10.61002	844.186	1.33812
15	<input checked="" type="checkbox"/>	1.571	0.13419	12.69610	6.25856	10.60999	843.063	1.41862
16	<input checked="" type="checkbox"/>	1.564	0.06156	12.69140	6.25551	10.61272	842.556	1.35540
17	<input checked="" type="checkbox"/>	1.639	0.09152	12.68631	6.25276	10.61649	842.147	1.32481
18	<input checked="" type="checkbox"/>	1.661	0.01574	12.68391	6.25082	10.61979	841.988	1.33254
19	<input checked="" type="checkbox"/>	1.631	0.09673	12.67983	6.24741	10.61985	841.263	1.30670
20	<input checked="" type="checkbox"/>	1.549	0.26961	12.67467	6.24304	10.61859	840.233	1.41128
21	<input checked="" type="checkbox"/>	1.553	-0.15096	12.67360	6.24276	10.62008	840.242	1.34953
22	<input checked="" type="checkbox"/>	1.526	-0.06469	12.67279	6.24047	10.62353	840.153	1.41071
23	<input checked="" type="checkbox"/>	1.505	0.06548	12.66713	6.23671	10.62347	839.267	1.44959
24	<input checked="" type="checkbox"/>	1.517	-0.15059	12.66565	6.23420	10.62509	838.959	1.40847
25	<input checked="" type="checkbox"/>	1.492	0.06009	12.65993	6.22928	10.62434	837.859	1.40929
26	<input checked="" type="checkbox"/>	1.513	0.05393	12.65654	6.22754	10.62746	837.647	1.36172
27	<input checked="" type="checkbox"/>	1.519	0.08939	12.65467	6.22655	10.62744	837.389	1.38533
28	<input checked="" type="checkbox"/>	1.449	-0.08490	12.65092	6.22419	10.63055	837.069	1.35197
29	<input checked="" type="checkbox"/>	1.464	-0.02011	12.64785	6.22428	10.63268	837.044	1.30875
30	<input checked="" type="checkbox"/>	1.469	-0.27831	12.64811	6.22483	10.63234	837.109	1.31613
31	<input checked="" type="checkbox"/>	1.482	0.82426	12.64136	6.22323	10.63400	836.578	1.32899
32	<input checked="" type="checkbox"/>	1.631	-0.15331	12.64219	6.22280	10.63195	836.413	1.34877
33	<input checked="" type="checkbox"/>	1.695	0.06348	12.63780	6.22147	10.63421	836.122	1.32938
34	<input checked="" type="checkbox"/>	1.760	-0.14802	12.63675	6.22149	10.63468	836.092	1.33667
35	<input checked="" type="checkbox"/>	1.897	-0.01079	12.62708	6.21810	10.63064	834.680	1.03925
36	<input checked="" type="checkbox"/>	1.701	-0.03920	12.62957	6.21721	10.63405	834.993	1.14717
37	<input checked="" type="checkbox"/>	1.656	0.04444	12.62953	6.21780	10.63485	834.895	1.24025
38	<input checked="" type="checkbox"/>	1.711	0.08864	12.62267	6.21174	10.63089	833.555	1.10014
39	<input checked="" type="checkbox"/>	1.620	0.03796	12.61940	6.21212	10.62861	833.211	1.23680
40	<input checked="" type="checkbox"/>	1.664	-0.05032	12.61837	6.21044	10.63106	833.110	1.17901
41	<input checked="" type="checkbox"/>	1.671	0.06106	12.61708	6.20558	10.62929	832.234	1.25821



156 powder histograms dataset
~ 15 min for the whole run

NaVOHPO₄ vs. Na

GSAS-II: charge flipping



Generation of electron density map

Identification of the atoms and refinement

Tutorial: subversion.xray.aps.anl.gov/pyGSAS/Tutorials/CFjadarite

Topas Bruker/Academic (A. Coelho and J. Evans), BRUKER

▶ Capabilities

- ▶ Rietveld/Pawley refinement (magnetic structures) (XRD, ND, TOF)
- ▶ Fourier mapping
- ▶ Charge flipping
- ▶ Monte Carlo / Simulated annealing
- ▶ Strain/size analysis
- ▶ Sequential refinement
- ▶ Indexing
- ▶ Combined refinement
- ▶ Stacking faults
- ▶ Parametric refinement
- ▶ Small-Angle scattering
- ▶ Single-Crystal refinement
- ▶ Pair Distribution Function
- ▶ Fundamental approach/ W/K_β contamination/tube tails
- ▶ Cloud computing using Amazon Web Services

- Stable
- Reliable
- Very Fast!
- Large data processing
- Customizable
- Programmable

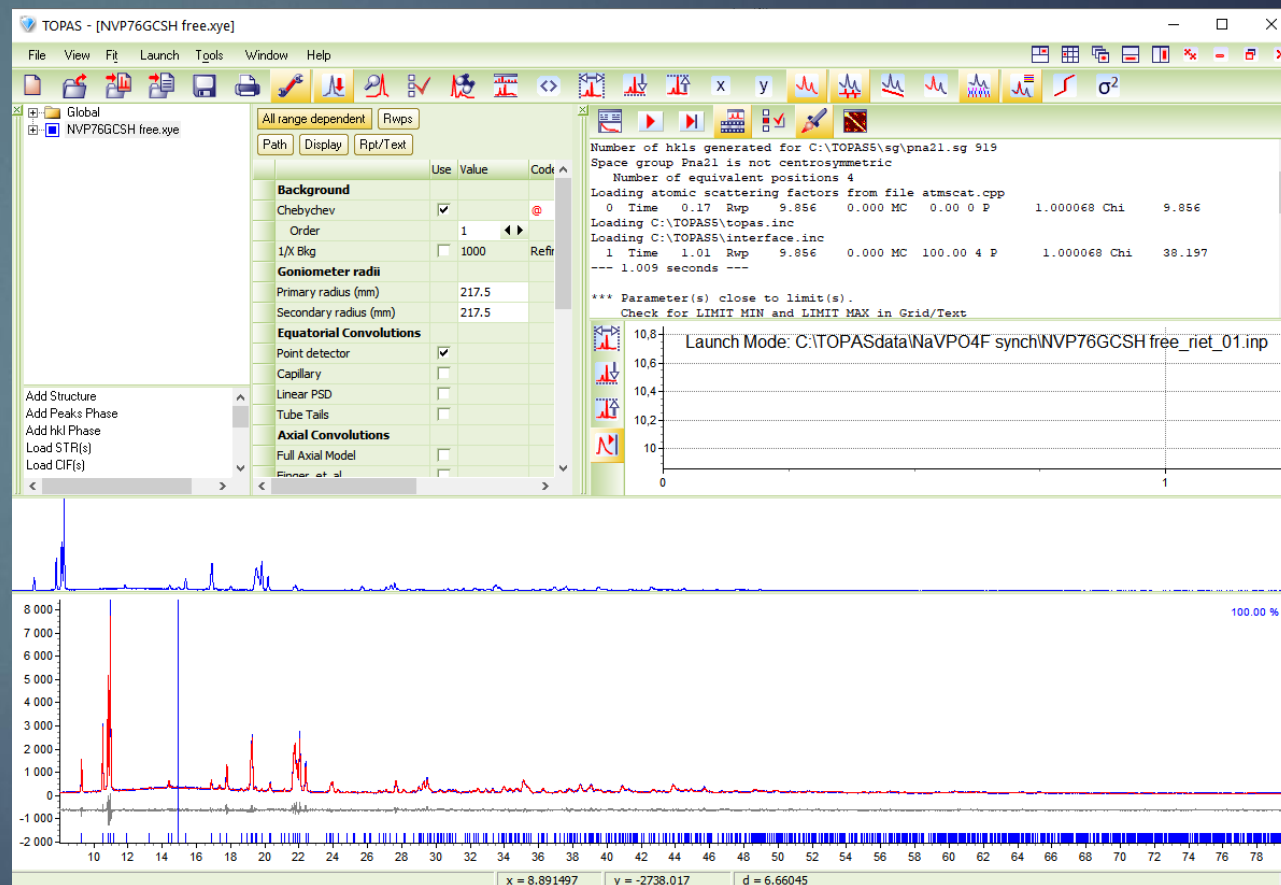


TOPAS (in combination with jEdit)

```
/* Rietveld refinement comprising two phases */
xdd File_Name.xy
  CuKa5(0.001) ` Five emission profile lines
  Radius(217.5)
  LP_Factor(26.4)
  Full_Axial_Model(12, 15, 12, 2.3, 2.3)
  Slit_Width(0.1)
  Divergence(1)
  Zero_Error(@, 0)
  bkg @ 0 0 0 0 0 0
  STR(R-3C, "Corundum Al2O3")
    Trigonal(@ 4.759, @ 12.992)
      site Al          z @ 0.3521 occ Al+3 1 beq @ 0.3
      site O  x @ 0.3062 z 0.25    occ O-2 1 beq @ 0.3
      scale @ 0.001
      CS_L(@, 100)
      r_bragg 0
  STR(Fm-3m, Fluorite)
    Cubic(@ 5.464)
      site Ca          occ Ca 1 beq @ 0.5
      site F  x 0.25  y 0.25 z 0.25 occ F 1 beq @ 0.5
      scale @ 0.001
      CS_L(@, 100)
      r_bragg 0
```

Figure 1

TOPAS example input file written in the INP script comprising readable text. Keywords in green, macros in blue, refined parameters in red, comments in purple.



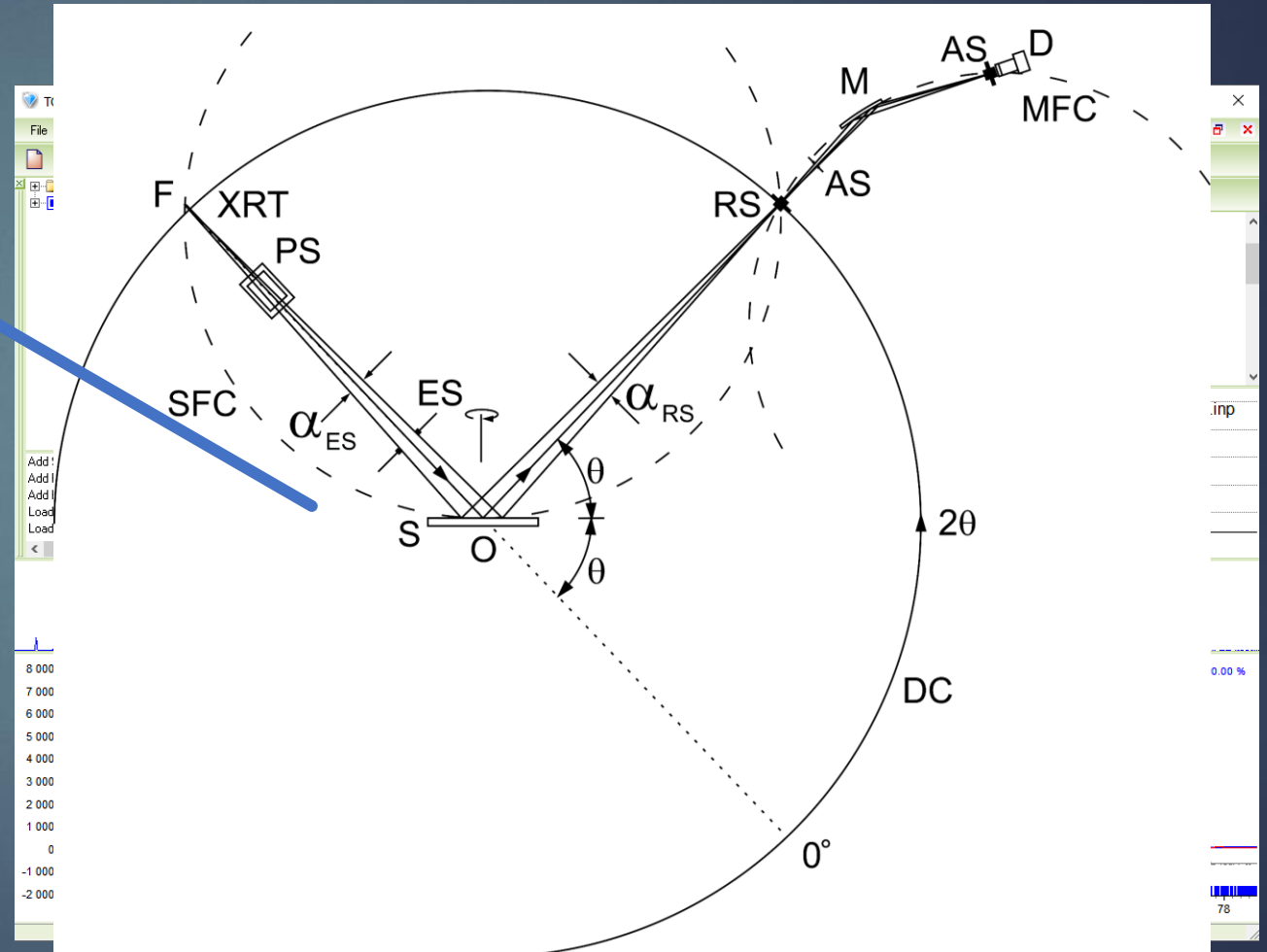
TOPAS (in combination with jEdit)

Fundamental approach to diffraction profile description

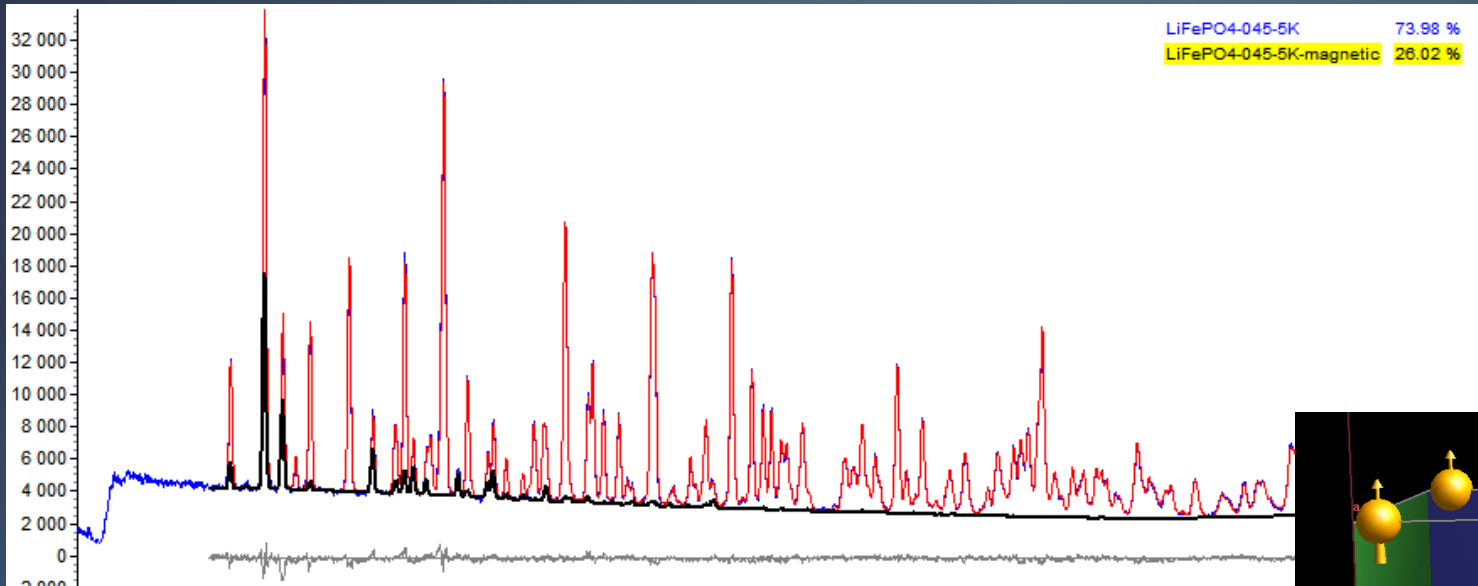
```
/* Rietveld refinement comprising two phases */
xdd File Name.xy
CuKa5(0.001) \ Five emission \ file lines
Radius(217.5)
LP_Factor(26.4)
Full_Axial_Model(12, 15, 12, 2.3, 2.3)
Slit_Width(0.1)
Divergence(1)
Zero_Error(0)
bkg @ 0 0 0 0 0 0
STR(R-3C, "Corundum Al2O3")
  Trigonal(@ 4.759, @ 12.992)
  site Al          z @ 0.3521 occ Al+3 1 beq @ 0.3
  site O  x @ 0.3062 z 0.25   occ O-2  1 beq @ 0.3
  scale @ 0.001
  CS_L(@, 100)
  r_bragg 0
STR(Fm-3m, Fluorite)
  Cubic(@ 5.464)
  site Ca          occ Ca 1 beq @ 0.5
  site F  x 0.25  y 0.25 z 0.25 occ F 1 beq @ 0.5
  scale @ 0.001
  CS_L(@, 100)
  r_bragg 0
```

Figure 1

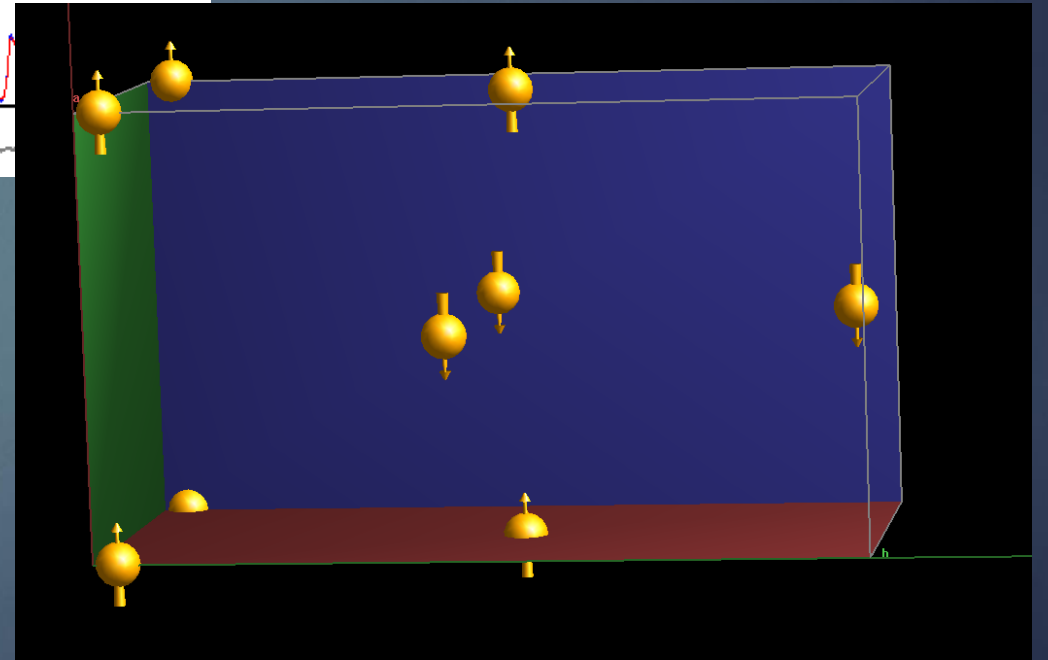
TOPAS example input file written in the INP script comprising readable text. Keywords in green, macros in blue, refined parameters in red, comments in purple.



TOPAS: Magnetic Structure Refinement



LiFePO_4 at 5K



TOPAS: Symmetry mode refinement

ISODISTORT: distortion

Space Group: 221 Pm-3m Oh-1, Lattice parameters: a=3.76000, b=3.76000, c=3.76000, alpha=90.00000, beta=90.00000, gamma=90.00000

Default space-group preferences: monoclinic axes a(b)c, monoclinic cell choice 1, orthorhombic axes abc, origin choice 2, hexagonal axes, SSG standard setting

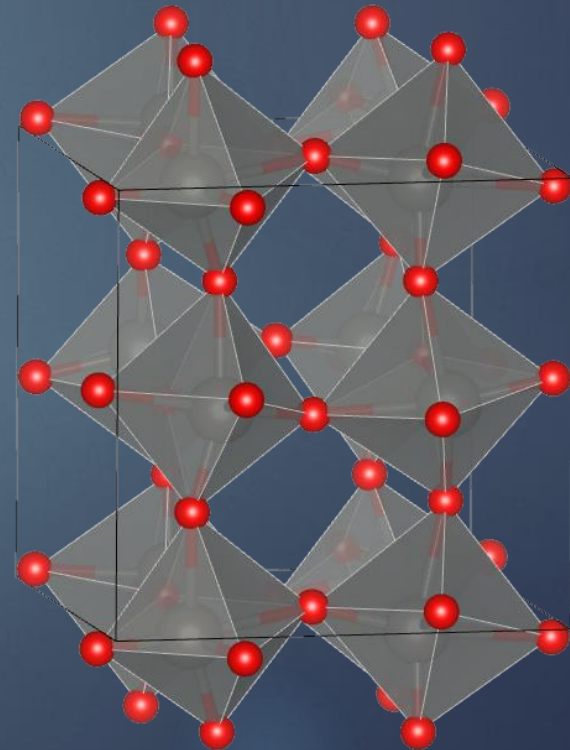
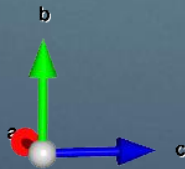
W 1a (0,0,0), O 3d (1/2,0,0)

Include strain, displacive ALL distortions

Reading CIF file...

Done.

Life example
WO₃ refinement
demo



TOPAS: Exhaustive Symmetry Search

J|A|C|S
JOURNAL OF THE AMERICAN CHEMICAL SOCIETY

Article

pubs.acs.org/JACS

An Exhaustive Symmetry Approach to Structure Determination: Phase Transitions in $\text{Bi}_2\text{Sn}_2\text{O}_7$

James W. Lewis,[†] Julia L. Payne,[†] Ivana Radosavljevic Evans,[†] Harold T. Stokes,[‡] Branton J. Campbell,[‡]
and John S. O. Evans^{*,†}

[†]Department of Chemistry, University Science Site, Durham University, South Road, Durham DH1 3LE, United Kingdom

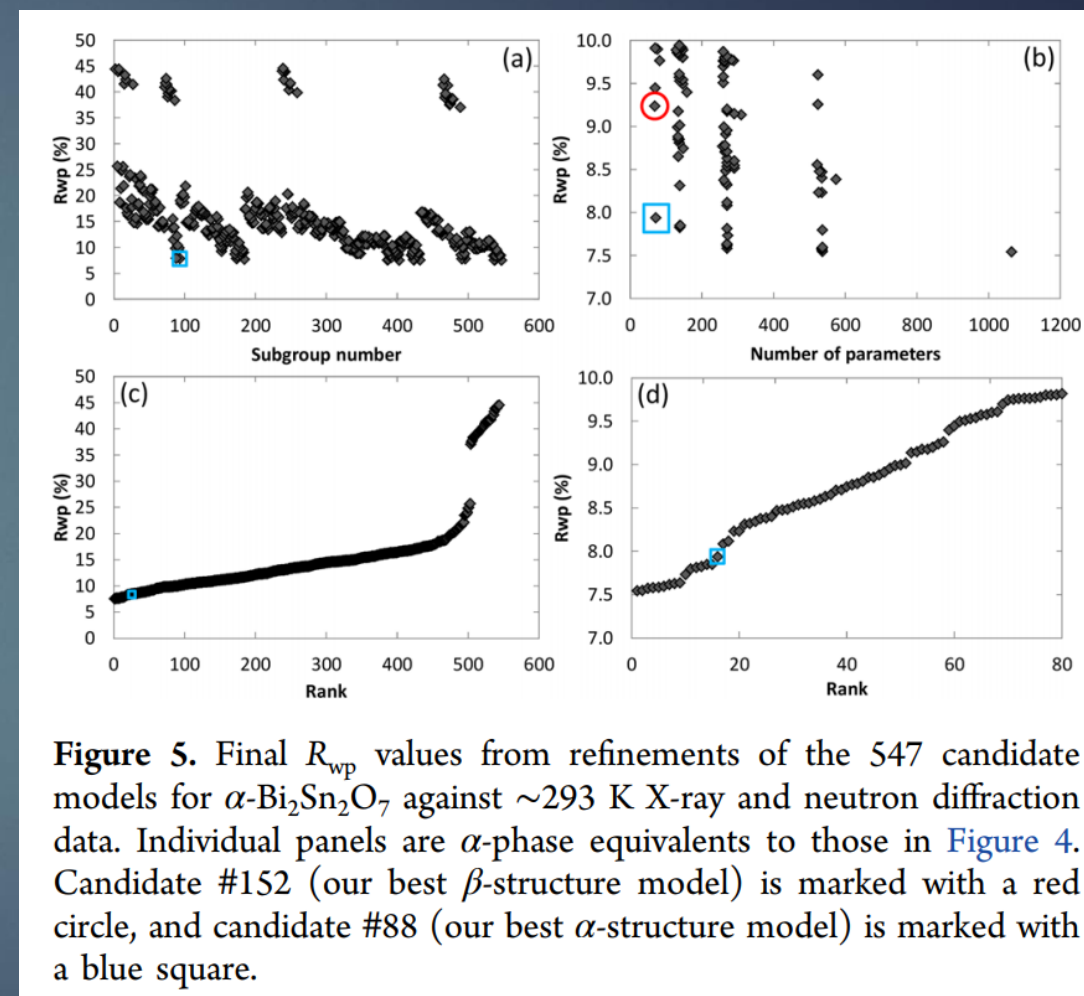
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Automatic search over 547 intermediate subgroups

Assisted with ISODISTORT

https://community.dur.ac.uk/john.evans/topas_workshop/tutorial_exhaustive_symmetry.htm



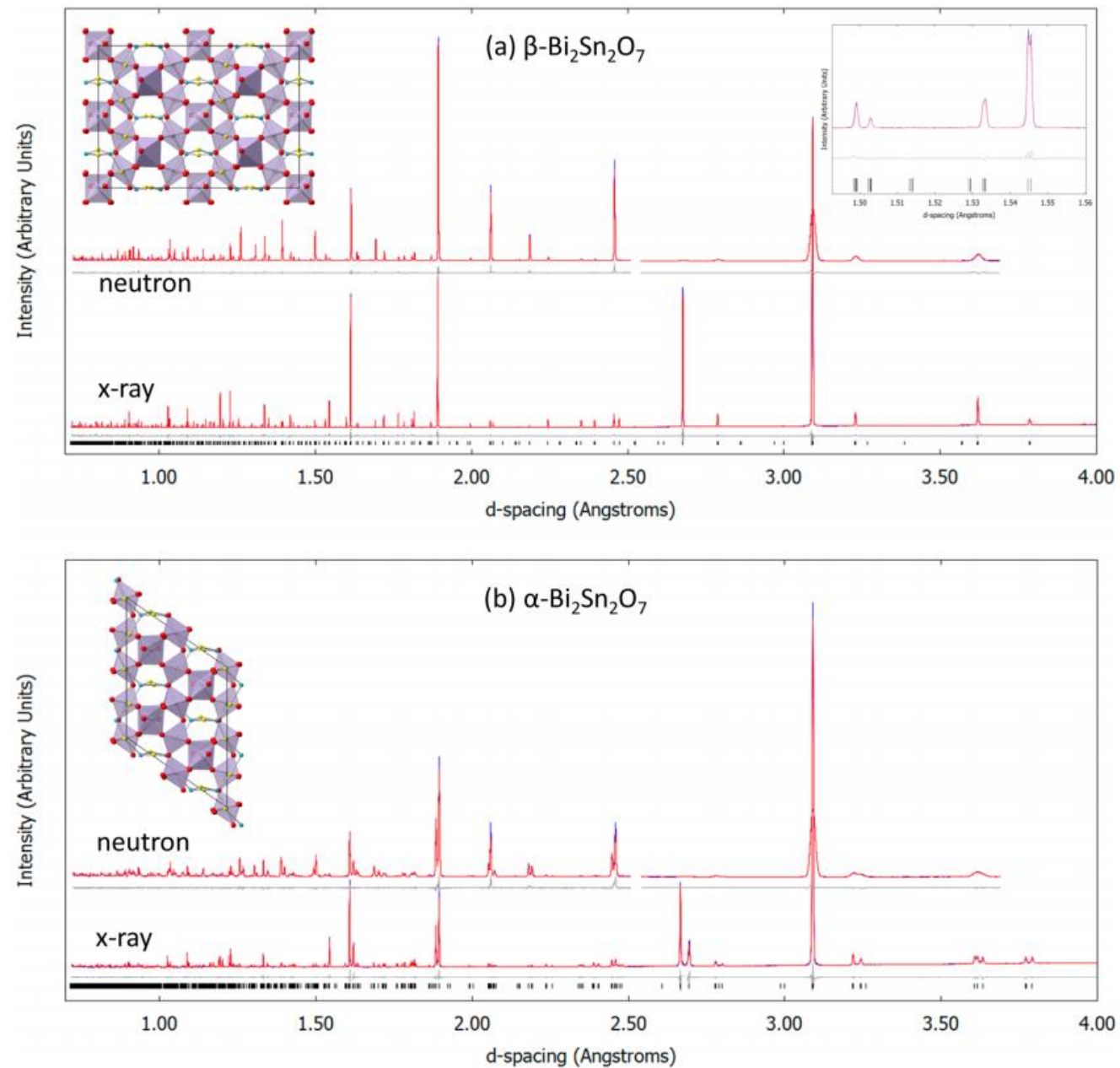
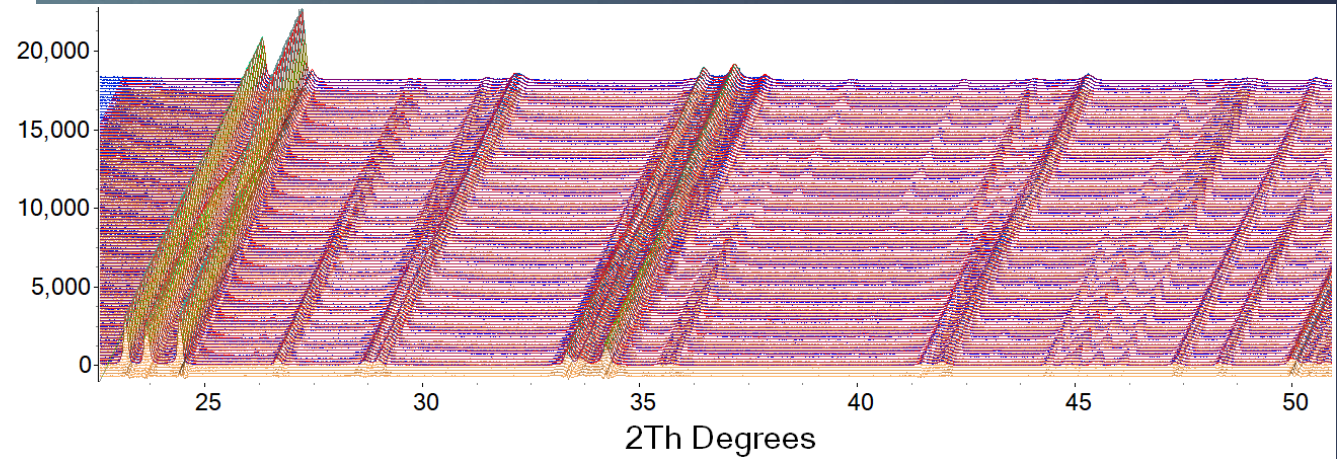
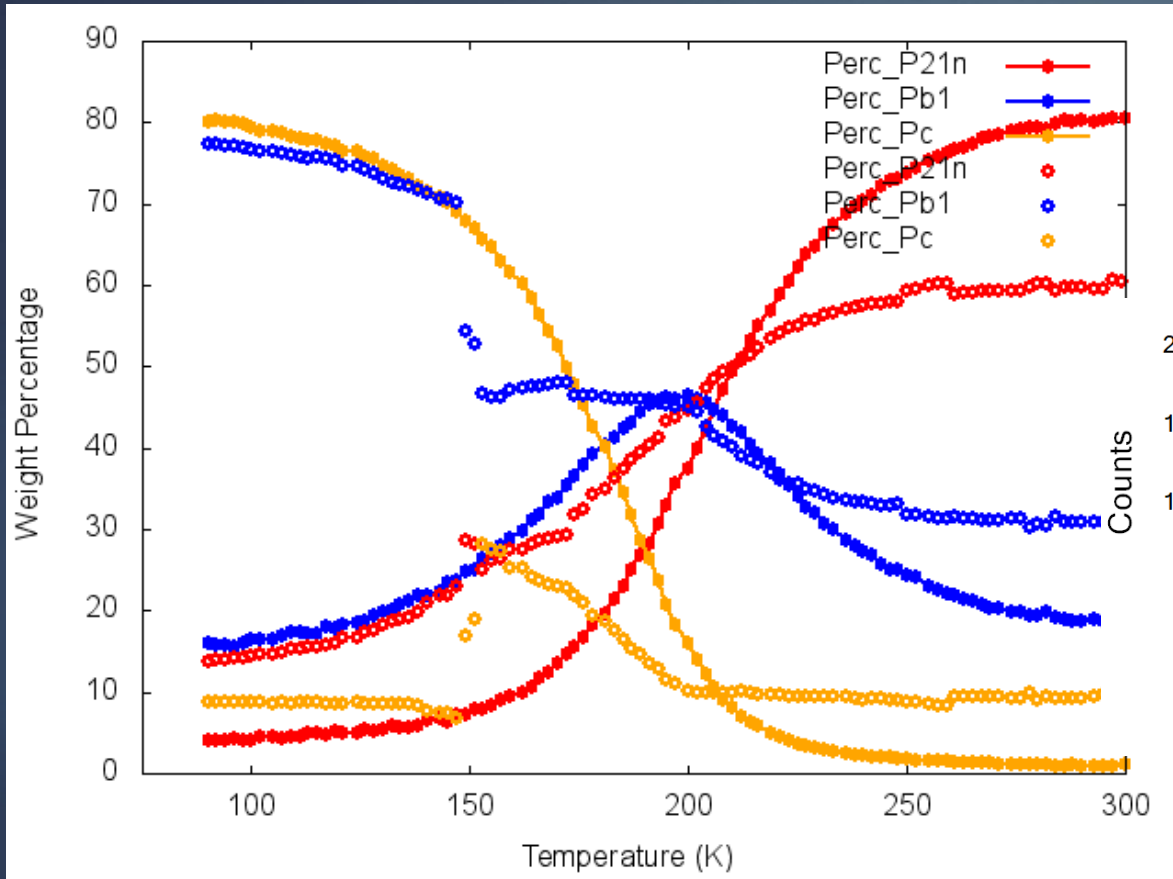


Figure 6. Final Rietveld fits for (a) β - $\text{Bi}_2\text{Sn}_2\text{O}_7$ and (b) α - $\text{Bi}_2\text{Sn}_2\text{O}_7$ models. Neutron data have been scaled and offset vertically for plotting. Neutron data for $d > 2.5$ Å are from the lower resolution 90° data bank. Inset to (a) shows X-ray fit in the region of the (4 8 0) and (0 8 8) reflections at $d \approx 1.55$ Å, which would be unsplit for a metrically cubic cell. Structure insets are views down $[0\ 1\ 0]$, key as in Figure 1.

TOPAS: Parametric refinement



G.W. Graham and J. Evans, Parametric Rietveld refinement, *J. Appl. Cryst.* (2007). 40, 87–95

TOPAS: Parametric refinement

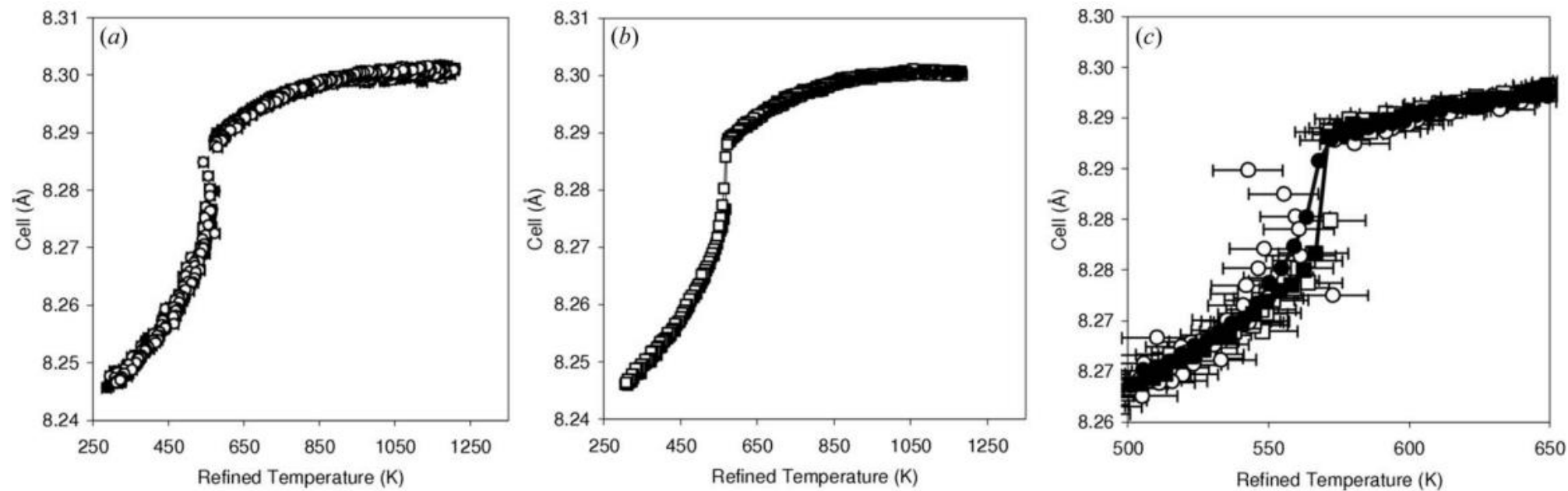
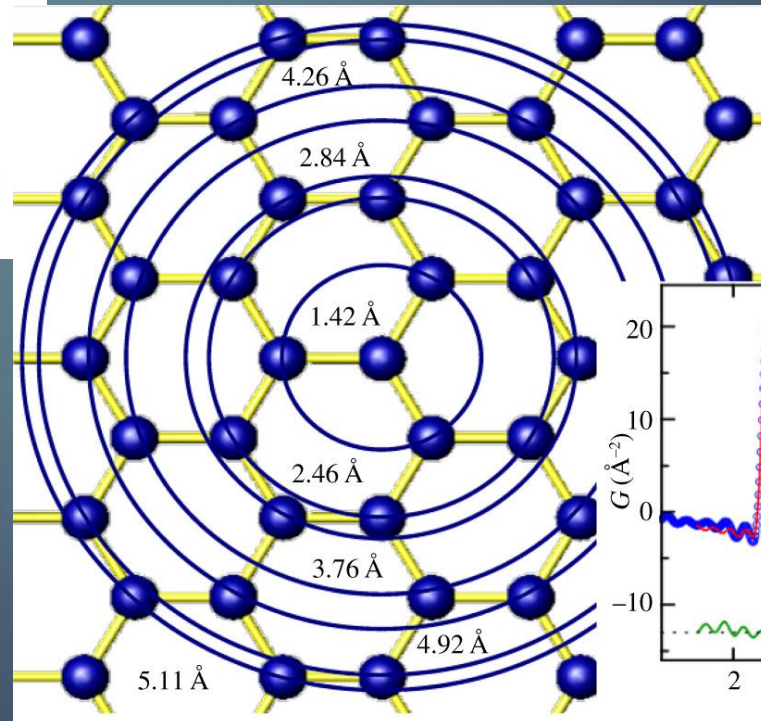
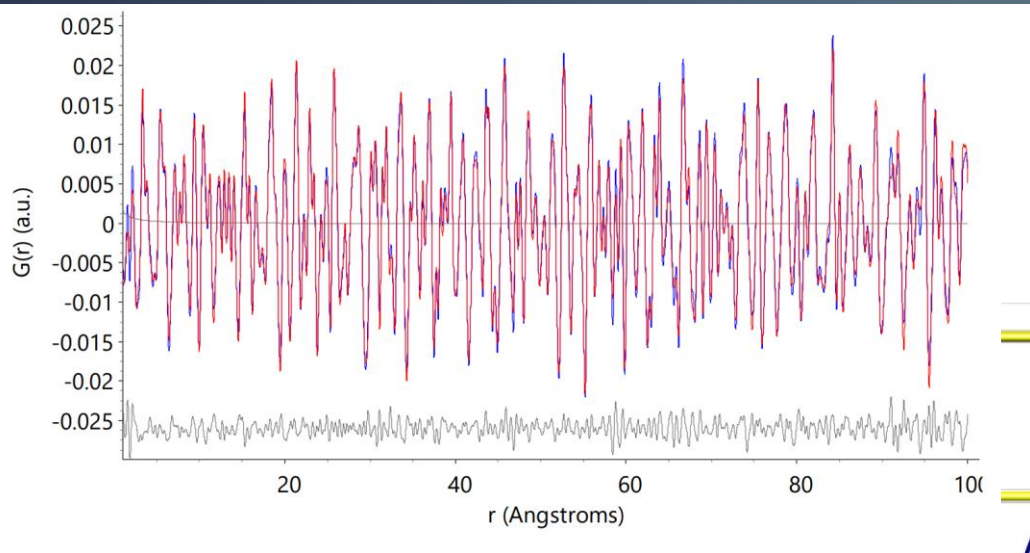


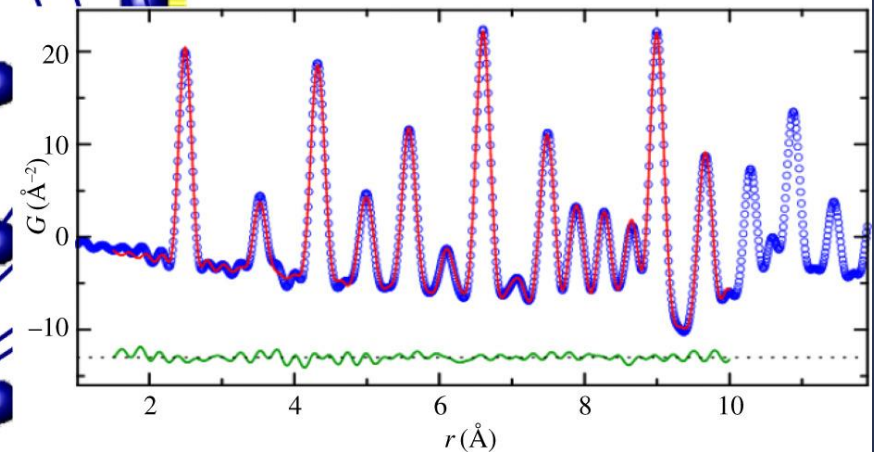
Figure 8

Cell parameters from (a) independent and (b) parametric fitting of 871 and 435 data sets; closed points, warming; open points, cooling. (c) The region close to the phase transition. Data taken on warming are represented by squares; cooling data by circles; open symbols represent independent fitting; closed symbols represent parametric fitting.

TOPAS: Pair Distribution Function



pair distribution function (PDF) gives the probability of finding an atom at a distance 'r' from a given atom.



Conclusions

A ZOO of
software

Refinement
schools

The Power
of Habits

APPROACHES ARE LIMITED BY ONLY YOUR IMAGINATION

And by a bit of a knowledge on how to use tools...

Thx

