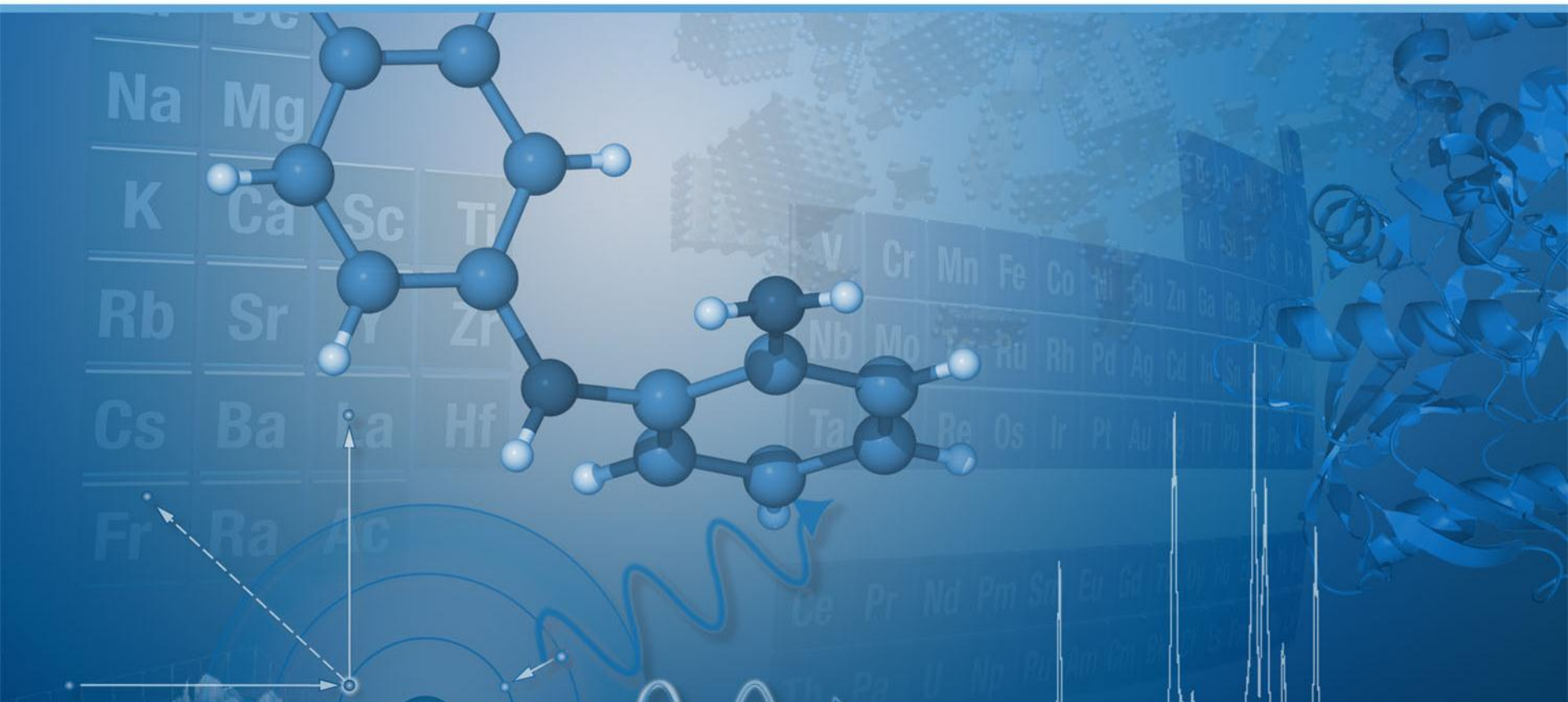
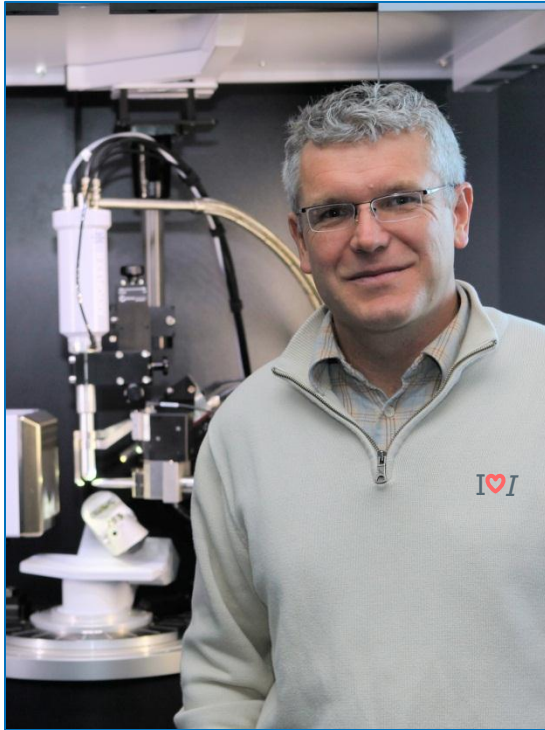


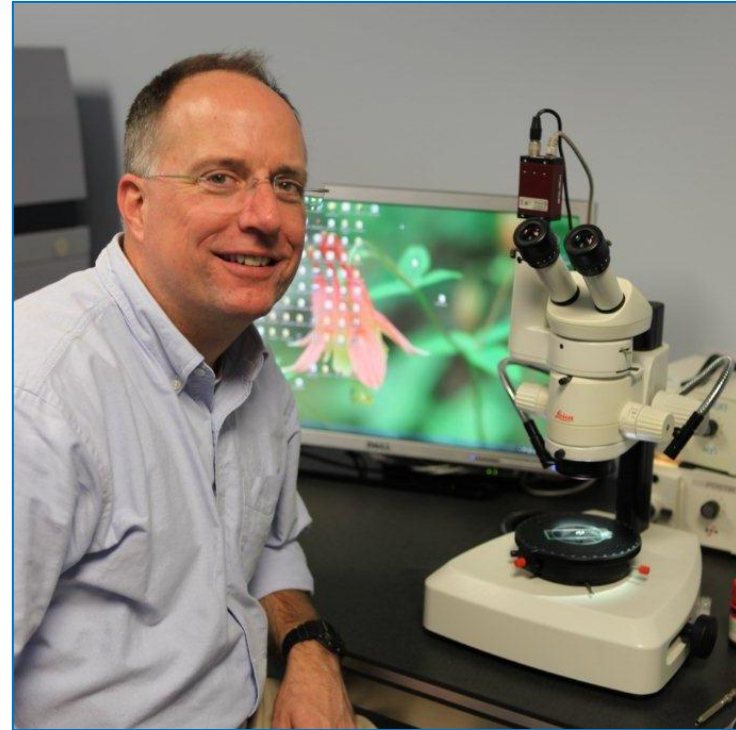
# Fast, Intuitive Structure Determination IV: Space Group Determination and Structure Solution



# Welcome

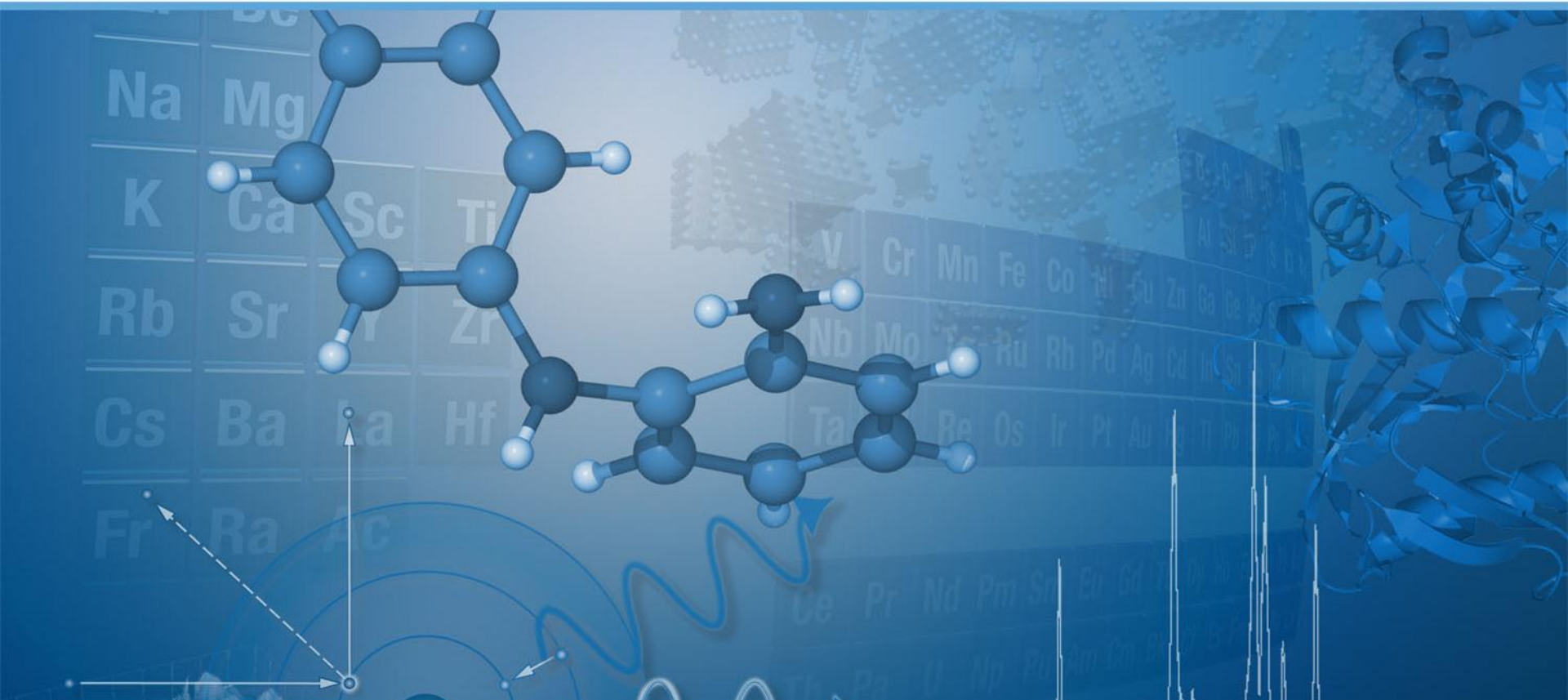


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# Space Group Determination

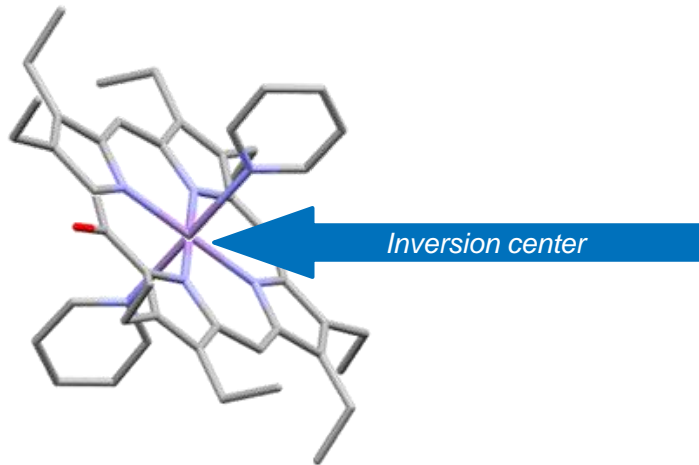


# Overview



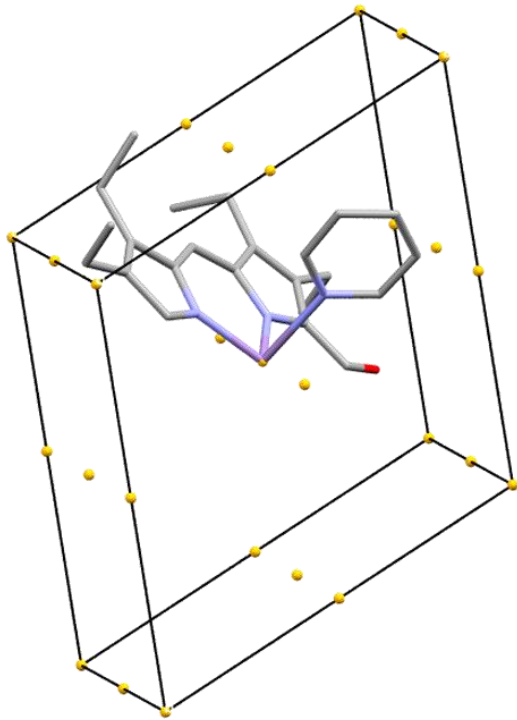
- The space group defines relationships between the asymmetric unit, the contents of the unit cell, and the entire crystal.
- Determining the proper three-dimensional symmetry facilitates the mathematics underlying the structure determination.
- Determination of the space group is made by examination of the Laue symmetry,  $|E|$  statistics, and systematic absences.

# Crystallographic symmetry



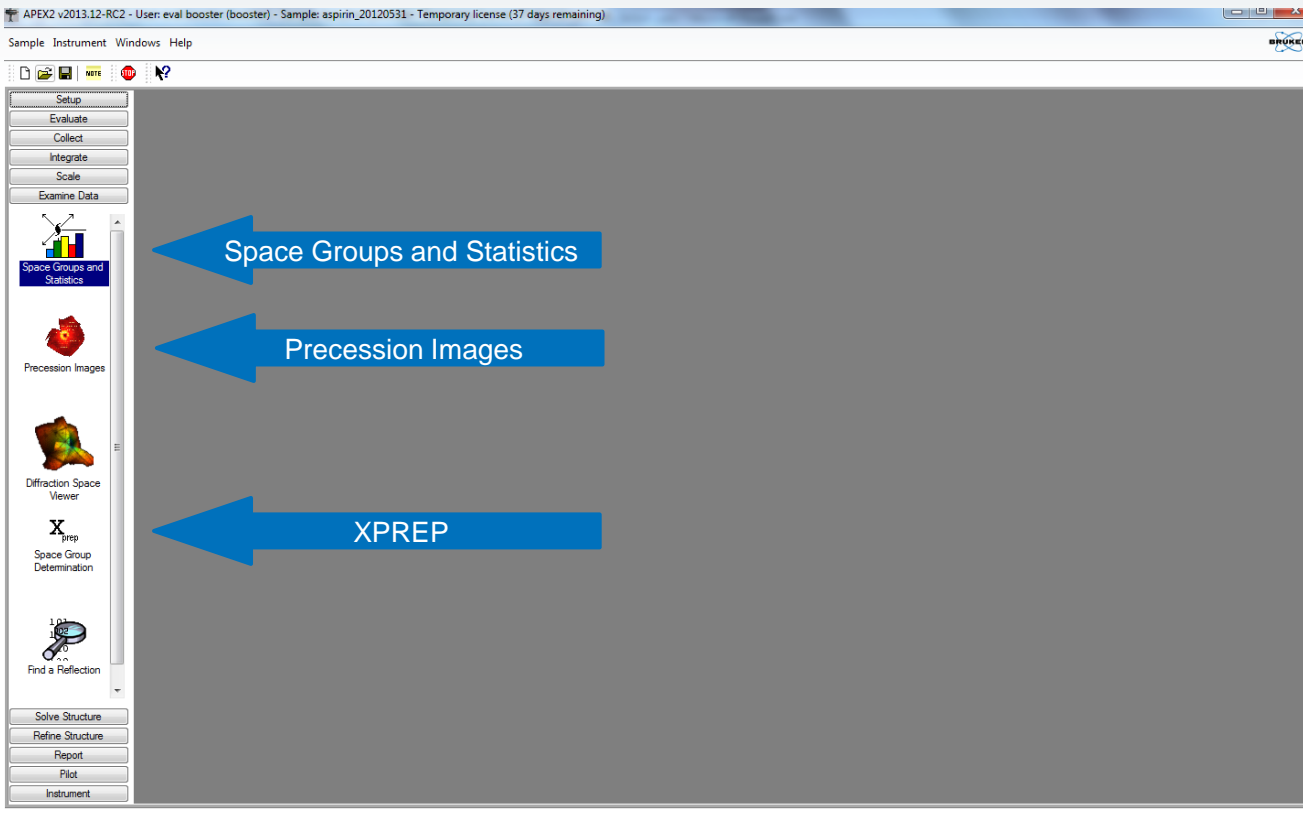
- Symmetry defines structure.
- Asymmetric unit: smallest set of atoms to generate crystal structure from symmetry elements of space group.
- Asymmetric unit possesses no crystallographic symmetry except the identity element.

# Unit Cell



- The unit cell is the smallest repeating set.
- Neighboring sets can be generated by translation.

# Determining the Space Group with APEX2



- The Examine Data set of tools.
- Space Groups and Statistics: GUI for XPREP.
- Precession Images: inspect reciprocal lattice layers.
- XPREP: Engine for data analysis.



# Space Groups and Statistics

The screenshot shows the Bruker software interface with several panels. A top panel contains file selection fields for 'hkl file' (mo\_aspirin\_20120531\_0m.hkl) and 'p4p file' (mo\_aspirin\_20120531\_0m.p4p). Below this, an 'Input Files' section shows 'hkl file: bcn29.hkl' and 'p4p file: bcn299\_0m.p4p'. A central 'Unit Cell' table displays parameters for two different data sets. The bottom panel, 'Experimental Parameters', shows 'Formula: C9H8O4', 'Formula Type' (Chemical Formula selected), and 'Radiation Type: Mo'. A checkbox labeled 'Must be chiral' is circled in red.

	a	b	c	alpha	beta	gamma
cell	11.2508	6.5459	11.2615	90	95.930	90
cell esds	0.0006	0.0004	0.0006	0	0.002	0

	a	b	c	alpha	beta	gamma
cell	15.4666	11.4793	15.6793	90	112.8366	90
cell esds	0.0003	0.0002	0.0003	0	0.0006	0

Experimental Parameters

Formula:

Formula Type:  
 Chemical Formula  
 Protein Sequence

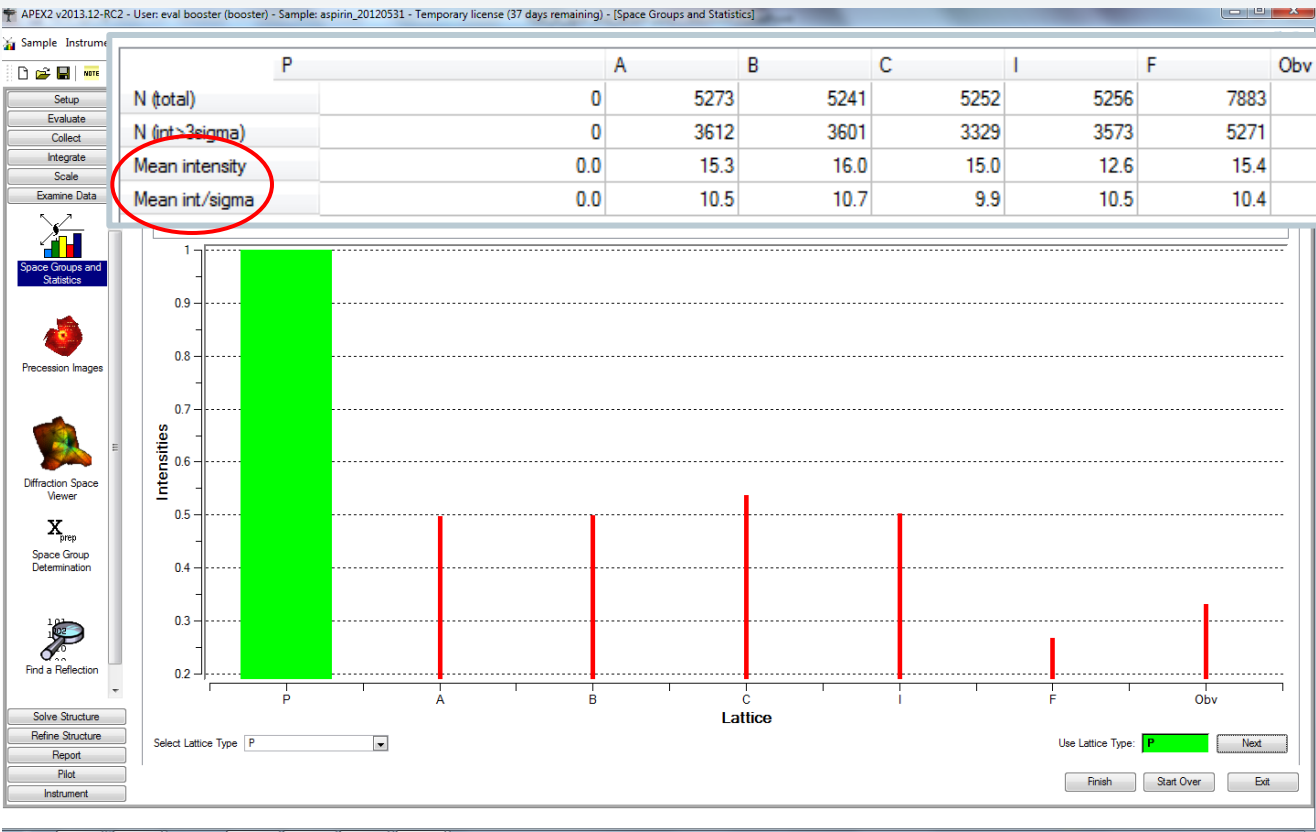
Must be chiral

Radiation Type:

- Cell dimensions.
- Formula and radiation.



# Lattice Exceptions



on for

- For condition to be met,  $\langle I \rangle$  and  $\langle I/\sigma \rangle$  approach zero.

# Space Group Determination

Bravais Lattice

Option	A	B	C	Alpha	Beta	Gamma	Volume	R(sym)
<input type="radio"/> Bravais Lattices								
<input type="radio"/> ORTHORHOMBIC C-lattice	15.074	16.721	6.546	90.00	90.00	89.95	1649.87	0.570
<input checked="" type="radio"/> MONOCLINIC P-lattice	11.251	6.546	11.262	90.00	95.93	90.00	824.93	0.025
<input type="radio"/> MONOCLINIC C-lattice	16.721	15.074	6.546	90.00	90.00	90.05	1649.87	0.601
<input type="radio"/> MONOCLINIC C-lattice						5	1649.87	0.615
<input type="radio"/> Retain Original Cell								

Systematic absence exceptions

E-value statistics

Non-centrosymmetric: 0.736      Mean |E<sup>2</sup>-1|: 1.004      Centrosymmetric: 0.968

Identical indices and Friedel opposites combined before calculating R(sym)

Space Group	No.	Type	Axes	CSD	R(sym)	N(eq)	Syst. Abs.	CFOM
<input checked="" type="radio"/> P2(1)/c	# 14	centro	4	19410	0.025	1505	0.8 / 9.0	1.32

- Bravais lattice determination.
- Systematic

- Calculation of |E<sup>2</sup>-1|.
- Possible space groups.

# Space group selection



The screenshot shows the APEX2 software interface. The main window displays the 'Space Group Determination' results. A table lists Bravais Lattices with their respective parameters. Below this, a dialog box titled 'Identical indices and Friedel opposites combined before calculating R(sym)' is open, showing a table of space groups. A dropdown menu is visible, listing various space groups including P1, P-1, P2, P2(1), C2, Pm, Pc, Cm, Cc, P2/m, and P1.

Option	A	B	C	Alpha	Beta	Gamma	Volume	R(sym)
Bravais Lattices								
ORTHORHOMBIC C-lattice	15.074	16.721	6.546	90.00	90.00	89.95	1649.87	0.570
MONOCLINIC P-lattice	11.251	6.546	11.262	90.00	95.93	90.00	824.93	0.025
MONOCLINIC C-lattice	16.721	15.074	6.546	90.00	90.00	90.05	1649.87	0.601
MONOCLINIC I-lattice	15.074	16.721	6.546	90.00	90.00	89.95	1649.87	0.615
Retain Original Cell								

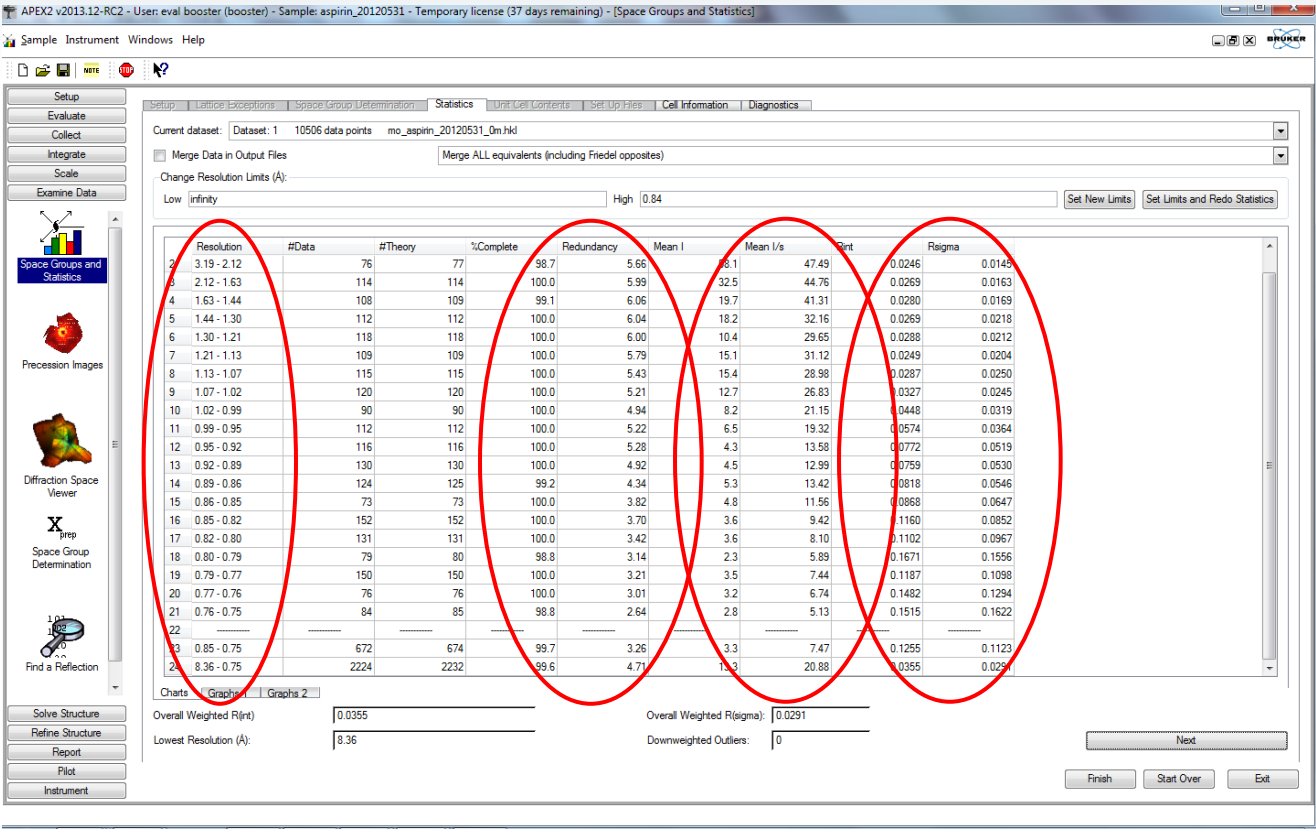
  

Space Group	No.	Type	Axes	CSD	R(sym)	N(eq)	Syst. Abs.	CFOM
Space Groups								
P2(1)/c	# 14	centro	4	19410	0.025	1505	0.8 / 9.0	1.32

- Manual selection of space group.



# Summary Statistics



- Ranked by resolution shells
- Completeness and redundancy
- Intensity and I/σ
- R(int) and R(sigma)

# Unit Cell Contents



The screenshot shows the Bruker APEX2 software interface. The main window displays the following information:

- Tentative Z (units/cell): 4.0
- Formula: C<sub>9</sub>H<sub>8</sub>O<sub>4</sub>
- Rho: 1.451
- Non-H atomic volume: 15.9

Buttons for "Update Z Units" and "Update Formula" are visible next to their respective fields. The interface also includes a sidebar with various tools like "Space Groups and Statistics", "Precession Images", "Diffraction Space Viewer", "Space Group Determination", and "Find a Reflection". At the bottom, there are buttons for "Finish", "Start Over", "Exit", and "Next".

- Chemical formula
- Value of Z
- Density
- Non-hydrogen atomic volume

# Set Up Files



Instruction File: `mo_aspirin_20120531_0ma`

```
TITL mo_aspirin_20120531_0ma in P2(1)/c
CELL 0.71073 11.26150 6.54590 11.25080 90.0000 95.9297 90.0000
ZERR 4.00 0.00060 0.00040 0.00060 0.0000 0.0020 0.0000
LATT 1
SYMM -X, 0.5+Y, 0.5-Z
SFAC C H O
UNIT 36 32 16
TEMP -173.150
TREF
HKLF 4
END
```

Buttons: Write Instruction File, Accept, Start Over, Exit

Left sidebar menu: Setup, Evaluate, Collect, Integrate, Scale, Examine Data, Space Groups and Statistics, Precession Images, Diffraction Space Viewer, X<sub>prep</sub> Space Group Determination, Find a Reflection, Solve Structure, Refine Structure, Report, Plot, Instrument

- Instructions for SHELX solution programs
- HKL file with current orientation and limits.

# XPREP



```
+++++
+ XPREP - Reciprocal space exploration - Version 2013/3 for Windows +
+ COPYRIGHT(c) 2013 Bruker-AXS All Rights Reserved +
+++++

Screen size: 1440 x 900
Window size: 640 x 799
Font size: 8 x 16 ( 125 x 206 )
Number of colors: 256

When xprep is started without a filename on the command line, the filename
is prompted for and then the type of data (SHELX, SCALEPACK, XDS or XENGEN)
requested. To generate ideal data, a SHELX .ins or .res file, if necessary
made from a PDB file using SHELXPRO or XPRO, should be given.

'xprep name' reads a SHELX HKLF 4 format file name.hkl, then tries to find
name.spin or name.p4p to extract the cell dimensions and their esds.
'xprep name1 name2' reads name1.hkl and name2.p4p (or name2.spin).

-Ln on the command line allocates space for 1000000n data (default n=4).

** Data multiplied by 0.1000 to bring onto reasonable scale **

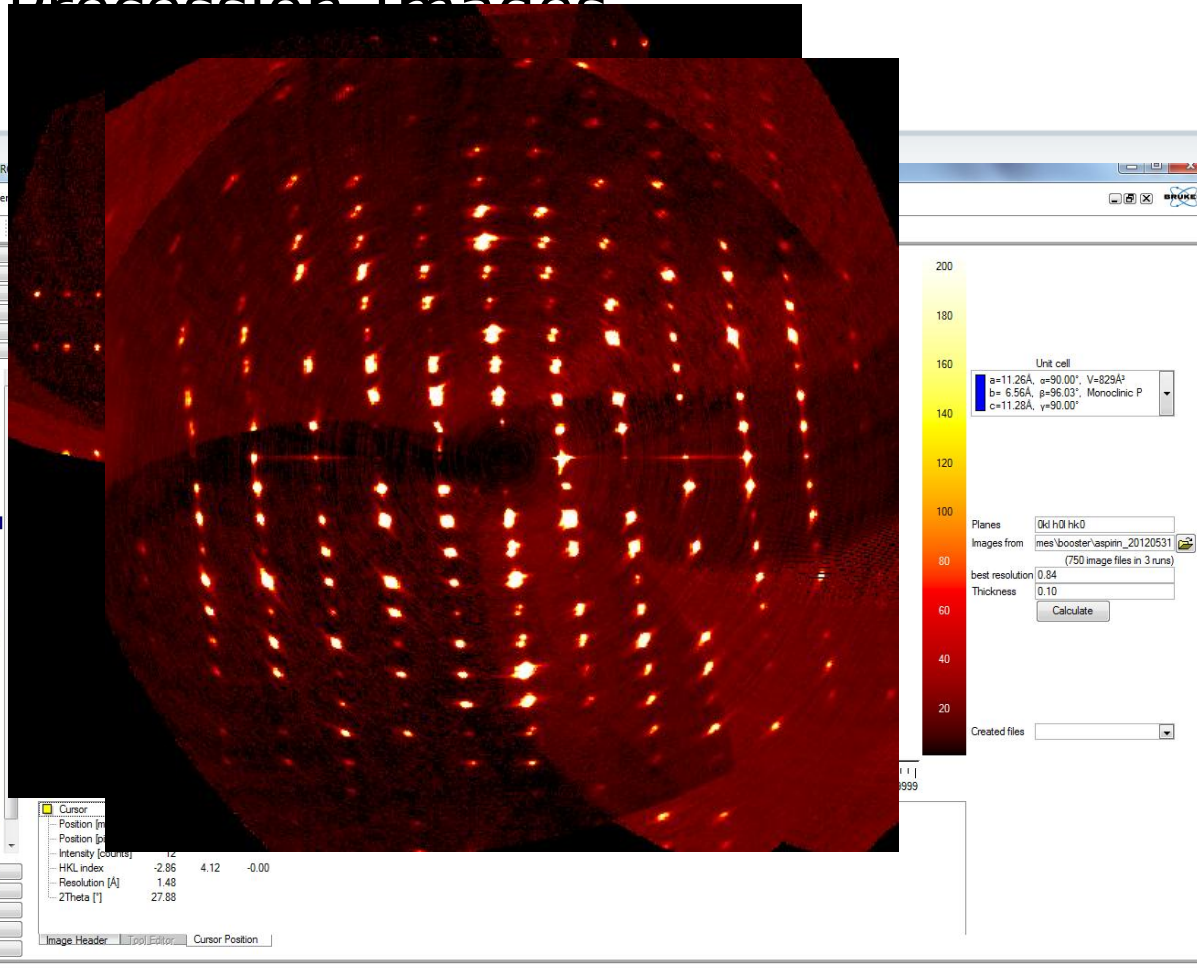
10506 Reflections read from file mo_aspirin_20120531_0m.hkl
Mean (I/sigma) = 10.43

Lattice exceptions: P A B C I F Obv Rev All
N (total) = 0 5273 5241 5252 5256 7883 7002 7021 10506
N (int>3sigma) = 0 3612 3601 3329 3573 5271 4815 4816 7192
Mean intensity = 0.0 15.3 16.0 15.0 12.6 15.4 15.4 15.8 15.3
Mean int/sigma = 0.0 10.5 10.7 9.9 10.5 10.4 10.3 10.5 10.5

Lattice type [P, A, B, C, I, F, O(obv.), R(rev. rhomb. on hex. axes)]
Select option [P]: █
```

- XPREP drives the Space Groups and Statistics plug-in.
- Full functionality of XPREP is retained in separate plug-in.

# Precession Images



- Precession images created from collected frames.
- On hk0 image,  $0k0 = 2n \rightarrow 2_1$  element.
- On h0l image,  $h = 2n \rightarrow a$ -glide element.

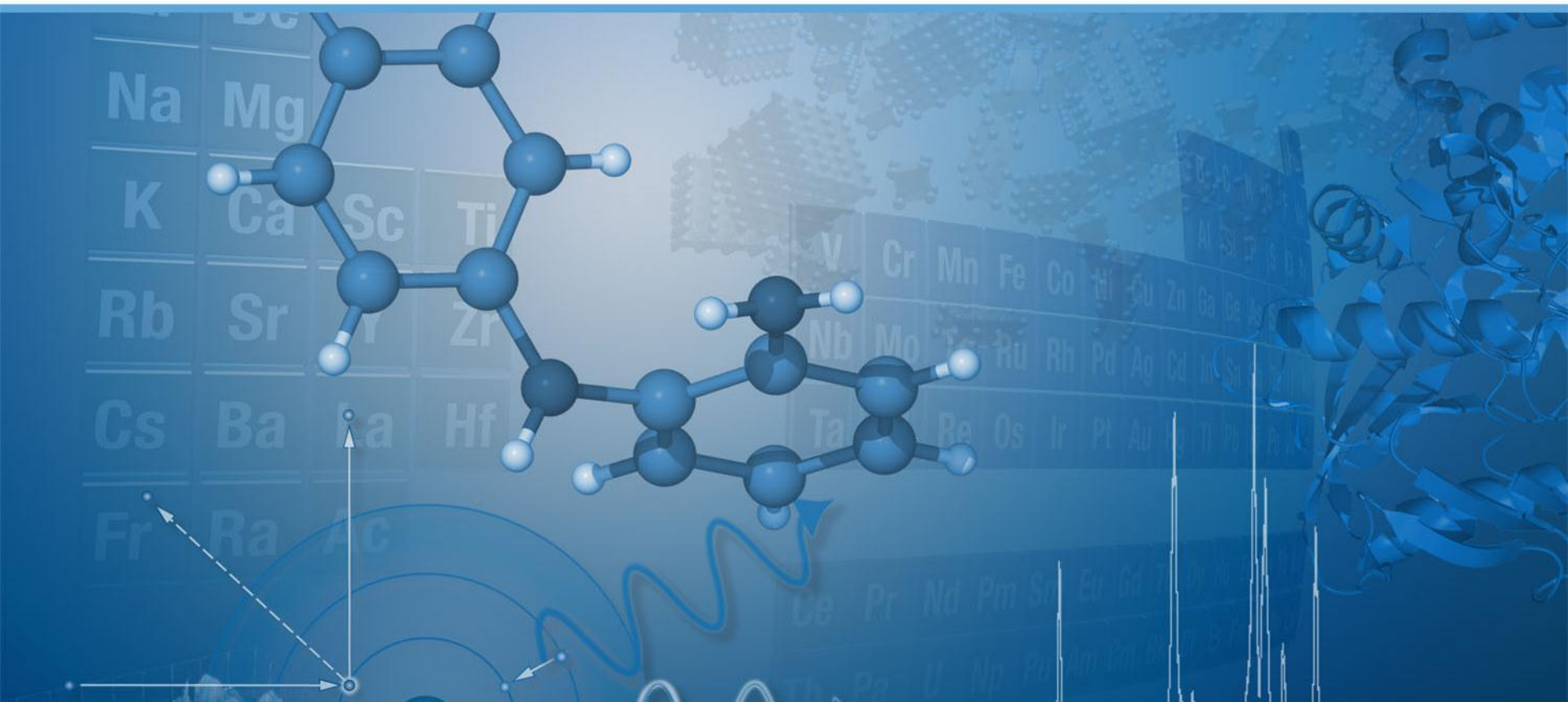


# Space Group Determination



- APEX2 has outstanding capabilities for data analysis and space group determination through George Sheldrick's XPREP.
- Precession images are useful for diagnosing difficult questions of symmetry.
- The tools of APEX2 facilitate space group assignment, leading to success with structure solution and refinement.

# Structure solution with APEX2 software



# Structure solution with APEX2 software

- APEX2 software provides a powerful interface for interactive structure solution
- The "Structure Solution" plugin is a wrapper around George Sheldrick's programs for structure solution and includes
  - XS for Direct Methods
  - XS for Patterson Methods
  - XM for "dual space methods"
  - XT for "Intrinsic phasing"
- Data statistics
- Intelligent default parameters
- Manual input
- Molecule viewer

# The Phase Problem

- A diffraction pattern produced by shooting monochromatic X-rays at a crystal can be understood as the Fourier transform of the complete electron density of the crystal structure. In principle the electron density can be simply reconstructed by Fourier synthesis.
- In reality, the problem is that only the intensities of the waves of the diffraction pattern can be recorded. The information about the phase of the wave, the relative timing when each wave hits, is lost in the experiment
- The problem of elucidating the phases when only the magnitudes are known is referred to as the “Phase Problem”

# Structure solution

- Crystallographers consider a crystal structure to be solved when the phases of enough reflections are well enough determined so that most if not all of the atoms in the unique part of the unit cell are revealed.
- The problem of elucidating the phases when only the magnitudes are known is referred to as the "phase problem".
- There are several ways to solve the crystal structure of a small molecule compound.

# I want that structure...

OK, once I get some phase information from you I can start with the structure design

How about you start designing first and then I'll fit it in with the phases.

But I can't create a structure until I have some phases

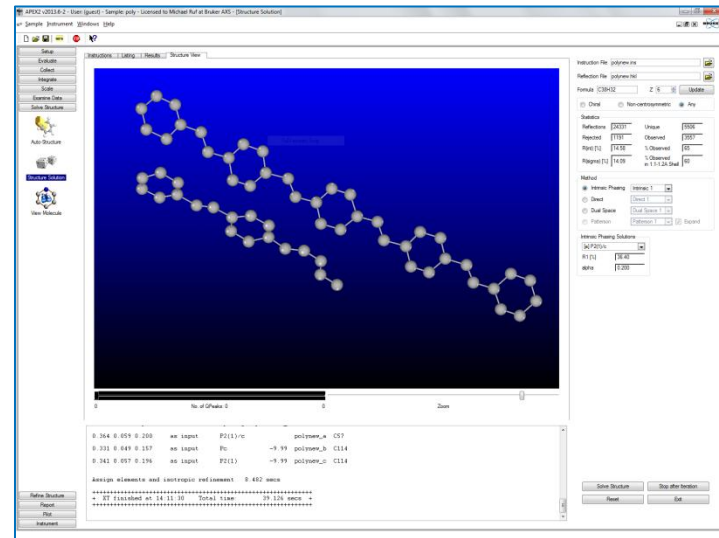
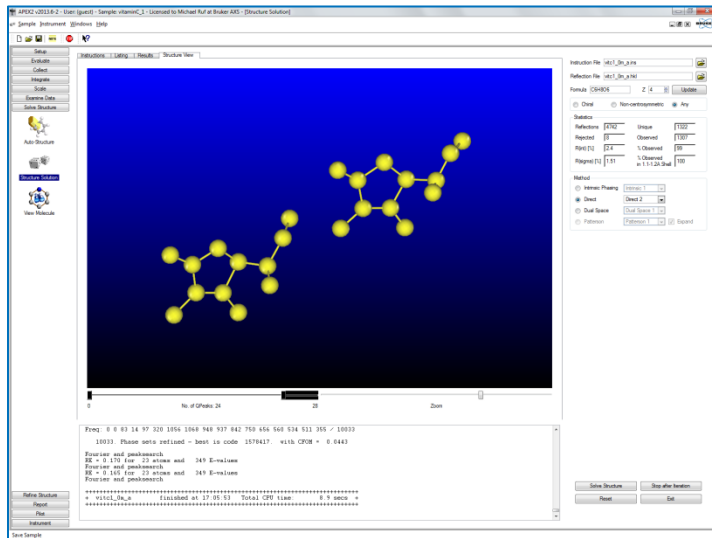
No, where should I get phases from until I see a structure



# Structure solution with APEX2



- Traditional direct methods, Patterson methods and dual space methods have been an integral part of the APEX2 structure solution plugin from day one and have provided fast and effective structure solution for years.
- The latest addition and the current default method of the solution plugin are Intrinsic Phasing implemented with SHELXT.



# The Structure Solution plugin



- Easy and intuitive to use
- Intelligent defaults
- Easy setup



# The Structure Solution plugin



APX2 v2013.6-2 - User: (guest) - Sample: camph - Licensed to Michael Ruf at Bruker AXS - [Structure Solution]

Sample Instrument Windows Help

Setup  
Evaluate  
Collect  
Integrate  
Scale  
Examine Data  
Solve Structure

Auto-Structure  
Structure Solution  
View Molecule

Instructions Listing Results Structure View

Instruction File Camph\_0m.ins  
Reflection File Camph\_0m.hkl  
Formula C10H16O4 Z 4 Update

Chiral Non-centrosymmetric Any

Statistics  
Reflections 1272 Unique 789  
Rejected 1 Observed 629  
R(int) [%] 5.28 % Observed 80  
R(sigma) [%] 9.49 % Observed in 1.1-1.2Å Shell 91

Method  
Intrinsic Phasing Intrinsic 1  
Direct Direct 1  
Dual Space Dual Space 1  
Pattern Patterson 1 Expand

Intrinsic Phasing Solutions  
P2(1)  
R1 [%] 26.50  
alpha 0.024

No. of QPeaks: 0  
Zoom

Space group determination: 0.056 secs  
R1 Rweak Alpha Orientation Space group Flack\_x File Formula  
0.265 0.160 0.024 as input P2(1) 0.21 Camph\_0m\_a C22 O6

Assign elements and isotropic refinement 0.267 secs  
+++++  
+ XT finished at 10:17:53 Total time: 8.770 secs +  
+++++

Refine Structure  
Report  
Plot  
Instrument

Solve Structure Stop after Iteration  
Reset Exit

New Sample

- Scrollable log file display
- Structure display



# The Structure Solution plugin

APX2 v2013.6-2 - User: (guest) - Sample: campb - Licensed to Michael Ruf at Bruker AXS - [Structure Solution]

Sample Instrument Windows Help

Setup Evaluate Collect Integrate Scale Examine Data Solve Structure

Auto-Structure Structure Solution View Molecule

Instructions Listing Results Structure View

```
REM Solution 1 R1 0.265 Rweak 0.160, Alpha = 0.0243 in P2(1)
REM Flack x = 0.209 ( 0.273 ) from Parsons' quotients
REM Formula C22 O6
TITL Campb_0m in P2(1)
CELL 1.34180 7.6908 11.6542 12.5846 90.000 105.468 90.000
ZERR 4.00 0.0010 0.0018 0.0015 0.000 0.009 0.000
LATT -1
SFAC -X, 1/2+Y, -Z
SFAC C H O
UNIT 40 64 16
TEMP -179.350
SHEL 999 0.800
L.S. 10
BOND
LIST 6
FHAP 2
PLAN 20
ANIS
DELI
O001 3 0.32161 0.33399 0.22004 11.00000 0.04943 8.21
O002 3 0.45581 0.45314 0.08325 11.00000 0.05176 7.85
O003 3 0.21312 0.36454 0.70090 11.00000 0.05791 7.81
O004 3 0.57759 0.38556 0.34131 11.00000 0.05327 7.80
O005 3 0.70995 0.50927 0.20198 11.00000 0.05142 7.26
C006 1 0.43644 0.33473 0.32119 11.00000 0.03775 7.16
C007 1 0.04747 0.49708 -0.18492 11.00000 0.02767 6.98
C008 1 0.13548 0.30517 0.62314 11.00000 0.04540 6.77
C009 1 -0.03806 0.28770 0.59768 11.00000 0.03727 6.63
C00A 1 0.21841 0.31789 0.44256 11.00000 0.03740 6.25
C00B 1 0.23287 0.24266 0.54624 11.00000 0.04020 6.17
C00C 1 0.59593 0.50512 0.10112 11.00000 0.03941 6.15
C00D 1 0.81458 0.50463 -0.01963 11.00000 0.04564 6.13
C00E 1 0.77431 0.54933 -0.14298 11.00000 0.04051 6.00
C00F 1 0.37612 0.26091 0.40305 11.00000 0.04253 5.96
C00G 3 0.80106 0.40882 -0.27883 11.00000 0.07992 5.84
C00H 1 0.43677 0.22601 0.60096 11.00000 0.04543 5.84
C00I 1 0.65981 0.57426 0.01574 11.00000 0.04635 5.68
C00J 1 0.26892 0.44220 0.47628 11.00000 0.04803 5.63
C00K 1 0.00214 0.52840 0.04985 11.00000 0.05586 5.43
C00L 1 0.56755 0.54005 -0.19745 11.00000 0.04493 5.35
C00M 1 0.52431 0.23576 0.50772 11.00000 0.04935 5.33
C00N 1 0.72608 0.69327 0.06504 11.00000 0.06254 5.19
C00O 1 0.50118 0.59026 -0.09125 11.00000 0.05378 5.17
C00P 1 0.87484 0.47935 -0.20750 11.00000 0.05177 5.16
C00Q 1 0.78362 0.37478 -0.01491 11.00000 0.06641 5.04
C00R 1 0.14677 0.12323 0.51742 11.00000 0.06066 4.73
C00S 1 0.03874 0.31345 0.35695 11.00000 0.05419 4.55
HKLIF 4
END
```

Statistics

Reflections	1272	Unique	789
Rejected	1	Observed	629
R(int) [%]	5.28	% Observed	80
R(sigma) [%]	9.49	% Observed in 1.1-1.2Å Shell	91

Method

Intrinsic Phasing  Direct  Dual Space  Patterson

Intrinsic Phasing Solutions

[a] P2(1)

R1 [%] 26.50

alpha 0.024

Space group determination: 0.056 secs

R1	Rweak	Alpha	Orientation	Space group	Flack_x	File	Formula
0.265	0.160	0.024	as input	P2(1)	0.21	Campb_0m_a	C22 O6

Assign elements and isotropic refinement 0.267 secs

+++++  
+ XT finished at 10:17:53 Total time secs +  
+++++

Refine Structure Report Plot Instrument

Solve Structure Stop after Iteration Reset Exit

- Listing display tab
- Numerical results display tab

# Patterson methods

- Patterson methods employ Fourier maps with the squared amplitudes of the structure factor as coefficients and phase angles all assumed to be  $0^\circ$  .
- These maps give peaks corresponding to all vectors between any given pair of points. The peak heights are proportional to the atomic numbers of atoms in the structure and the peaks can be used to derive the positions of atoms .
- Traditionally Patterson methods were the first choice for the solution of structures containing a few heavy atoms.
- Patterson, A. L. (1935).

# Patterson methods



Instructions Listing Results Structure View

Statistics

Reflections	4416	Unique	1241
Rejected	210	Observed	1072
R(int) [%]	7.53	% Observed	86
R(sigma) [%]	8.06	% Observed in 1.1-1.2Å Shell	96

Method

Patterson Patterson 1 Expand

```
PATT nv 1 dmin 1.80 res1 0.84 Nsup 138 Zmin 5.80 maxet 8
FMAP code 6
PLAN npeaks 80 del1 0.500 del2 1.500
MORE verbosity 1
TIME t 9999999.

Patterson and peaksearch
Patt sup on vector 1 0.8990 0.1648 0.0901 Height 237. Length 2.62
PATFOM = 67.5 Corr. Coeff. = 77.1 SYMFOM = 99.9 for 4 heavy atoms
+++++
```

- Two default settings
- Option for partial structure expansion

# Direct methods

- The term “direct methods” refers to a mathematical-statistical approach that tries to solve the phase problem by limiting the possible relationships between phase and intensity to a range of probabilities.
- The key point behind the direct method derives from invoking prior structural knowledge, usually that the crystal is composed of discrete atoms, with atoms being small and distinct points relative to the spaces between them.
- MULTAN (Main *et al.*, 1980),  
SHELXS, XS (Sheldrick, 1990),  
SAYTAN (Debaerdemaeker *et al.*, 1985)  
and SIR (Burla *et al.*, 1989)

# Direct Methods



APEX2 v2013.6-2 - User: (guest) - Sample: camph - Licensed to Michael Ruf at Bruker AXS - [Structure Solution]

Sample Instrument Windows Help

Setup Evaluate Collect Integrate Scale Examine Data Solve Structure

Auto-Structure Structure Solution View Molecule

Instructions Listing Results Structure View

Instruction File Camph\_0m.ins  
Reflection File Camph\_0m.hkl  
Formula C10H16O4 Z 4 Update

Chiral  Non-centrosymmetric  Any

Statistics

Reflections	1272	Unique	789
Rejected	1	Observed	629
R(int) [%]	5.28	% Observed	30
R(sigma) [%]	9.49	% Observed in 1.1-1.2Å Shell	31

Method

Intrinsic Phasing Intrinsic 1  
 Direct Direct 1  
 Dual Space Dual Space 1  
 Patterson Patterson 1 Expand

Solve Structure Stop after iteration  
Reset Exit

0 No. of QPeaks: 27 43 Zoom

```
Freq: 0 2 47 1 1 6 0 1 4 11 18 27 28 16 18 13 13 10 4 4 3 3 7 1 4 2 / 256
256. Phase sets refined - best is code 1767049. with CFOM = 0.0386
Fourier and peaksearch
RE = 0.225 for 29 atoms and 507 E-values
Fourier and peaksearch
RE = 0.230 for 27 atoms and 507 E-values
Fourier and peaksearch
+++++
+ Camph_0m finished at 14:41:12 Total CPU time: 0.5 secs +
+++++
```

Refine Structure Report Plot Instrument

- Three default settings
- Increasing exhaustiveness of search

# Dual space methods



- Shake-and-bake differs from conventional direct methods by employing a minimal function which is optimized through alternate cycles of reciprocal space phase and real space filtering.
- Reciprocal space refinement employs density modification and real-space filtering impose the phase constraints that are implicit in real space.
- The shake-and-bake technique has been successfully used to determine the structures of several small proteins.
- *SnB* (Miller *et al.*, 1994; Weeks & Miller, 1999),
- SHELXD, XM (Sheldrick, 1997, 1998)

# Dual Space Methods

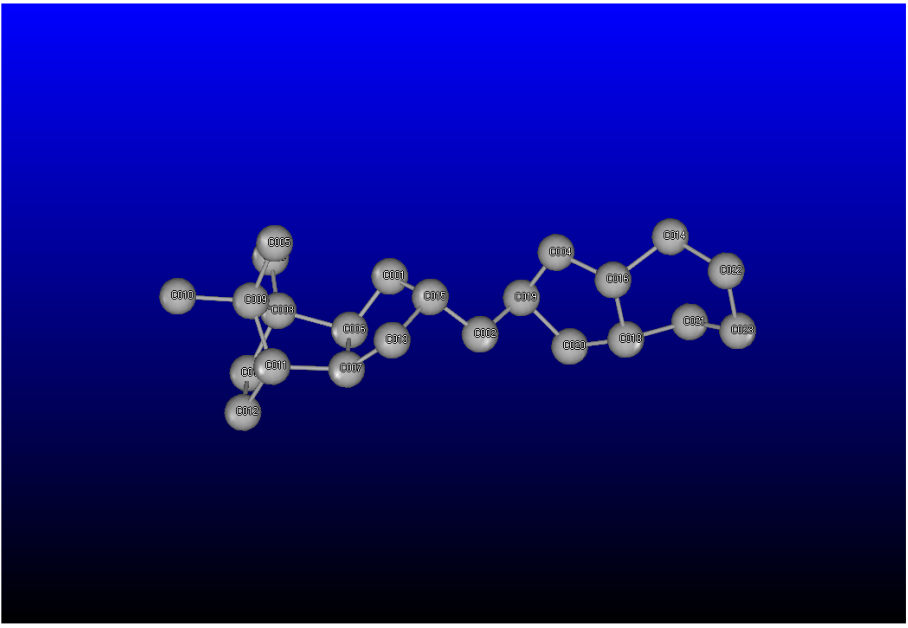


APX2 v2013.6-2 - User: (guest) - Sample: furan - Licensed to Michael Ruf at Bruker AXS - [Structure Solution]

Sample Instrument Windows Help

Setup Evaluate Collect Integrate Scale Examine Data Solve Structure

Auto-Structure Structure Solution View Molecule



No. of QPeaks: 0

Zoom

Instruction File: furan\_0m.ins  
Reflection File: furan\_0m.hkl  
Formula: C10H20N5O4 Z: 4

Chiral Non-centrosymmetric Any

Statistics

Reflected	10658	Unique	2020
Rejected	43	Observed	1976
R(int) [%]	3.76	% Observed	98
R(sigma) [%]	2.45	% Observed in 1.1-1.2Å Shell	99

Method

Intrinsic Phasing Intrinsic 1  
Direct Direct 1  
**Dual Space Dual Space 1**  
Pattern Patterson 1  Expand

Solve Structure Stop after iteration  
Reset Exit

```
Try 2. CPU 4. CC All/Weak 22.9 / 12.2. CFOM 35.1. best 41.8. Best FCC 34.8
Try 3. CPU 1. CC All/Weak 26.3 / 15.5. CFOM 41.8. best 41.8. Best FCC 37.0
Try 4. CPU 2. CC All/Weak 24.0 / 12.8. CFOM 36.8. best 41.8. Best FCC 37.0
Try 5. CPU 2. CC All/Weak 21.2 / 10.1. CFOM 31.3. best 46.6. Best FCC 37.0
Try 6. CPU 1. CC All/Weak 23.9 / 13.8. CFOM 37.7. best 46.6. Best FCC 37.0
Try 7. CPU 4. CC All/Weak 28.2 / 18.5. CFOM 46.6. best 46.6. Best FCC 41.1
Try 8. CPU 3. CC All/Weak 21.0 / 10.5. CFOM 31.6. best103.9. Best FCC 41.1
Try 9. CPU 2. CC All/Weak 21.9 / 11.2. CFOM 33.2. best103.9. Best FCC 41.1
Try 10. CPU 1. CC All/Weak 55.4 / 48.5. CFOM103.9. best103.9. Best FCC 81.2

+++++
+ furan_0m finished at 15:27:01 Elapsed time: 0.47 secs +
+++++
```

- Two default settings
- Increasing exhaustiveness of search
- Default 2 determines the number of atoms to be searched for from the volume and the symmetry



# Charge flipping



- Charge flipping is also an iterative algorithm for reconstructing electron densities from diffraction amplitudes.
- It works on high resolution diffraction data using Fourier recycling. Modification in real space changes the sign of charge density below a threshold, while in reciprocal space the Fourier map is modified without any weighting.
- Compared to traditional direct methods it requires much less prior information.
- Charge flipping needs neither symmetry nor an assumption of atoms. This makes it particularly suitable for structure solution of modulated structures and quasicrystals.
- (Oszlanyi and Suto, 2004; 2005).
- SUPERFLIP Palatinus (2004).


# Fragment Search



- The algorithm locates a fragment of known geometry by integrated Patterson, packing, and direct methods
- A rotation search can find the orientation of a search model of any size and allows one torsional degree of freedom.
- A translation search may locate up to two independent fragments of any size and can take known atoms at fixed positions into account .
- PATSEE (Egert, 1985)

# Fragment Search – model calculation



 **Molecular Networks**  
Inspiring Chemical Discovery

Search

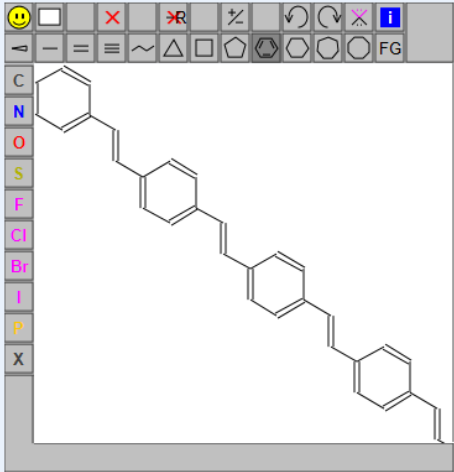
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Home » Online Demo - Interactive 3D Structure Generation with CORINA

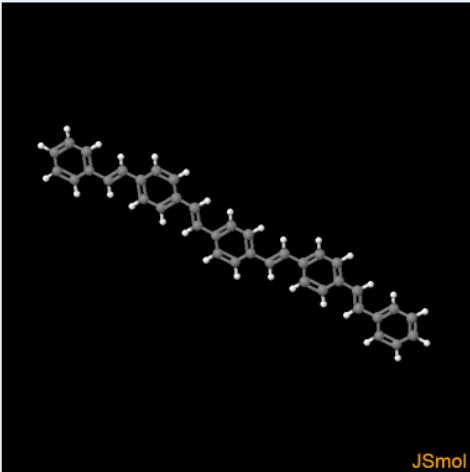
## Online Demo - Interactive 3D Structure Generation with CORINA

Please draw a structure with the integrated molecule editor on the left-hand side. The 3D structure will automatically be calculated by CORINA and displayed on the right-hand side. Below the JSmol/Jmol visualization window two links are provided to download the structure as PDB or MOL file.

The functionality of this online service is also described in a short user guide saved as [slide show](#) or [PDF file](#).



Help how to input structures



JSmol

Background

Scheme

Surface

Interactive

Download 3D structure as [PDB](#) or [MOL](#) file

- [http://www.molecular-networks.com/online\\_demos/corina\\_demo\\_interactive](http://www.molecular-networks.com/online_demos/corina_demo_interactive)

# Intrinsic Phasing



- Intrinsic Phasing plays to the strengths of direct methods solving structures best in space group P1. With the Laue group known, equivalent intensities are averaged and the data is then expanded to P1.
- A departure from classical direct methods is to start the structure solution process not from random phases but from a Patterson superposition minimum function.
- The initial phases provided by the structure solution are then used to determine the appropriate space group which provides the symmetry information for averaging phases for calculating improved electron densities.
- Further dual-space recycling is performed to improve the quality of the electron density. Dual-space recycling employs random omit maps where a certain percentage of the peaks are randomly omitted and only the remaining atoms are used to calculate phases.

# Intrinsic Phasing



- The free lunch algorithm has been implemented to use density modification to calculate phases for reflections that have not been measured completing the data to a given resolution.
- Atoms are then assigned to the density's maxima.
- This method proves to work amazingly well and is less demanding on completeness and data quality compared to other direct methods.
  
- SHELXT, XT (Sheldrick, 2013)

# Intrinsic Phasing



- The most powerful method in Structure solution
- Gives the most complete models
- 15 years ago it took a week to solve this structure with molecular modeling and PATSEE

# Intrinsic Phasing



The screenshot shows the Bruker APEX2 software interface. The main window displays a 3D ball-and-stick model of a polymer chain. On the right, the 'Method' panel is open, showing 'Intrinsic Phasing' selected with 'Intrinsic 1' as the method. Below it, the 'Intrinsic Phasing Solutions' panel shows a dropdown menu with '[a] P2(1)/c' selected, and R1 [%] at 36.40 and alpha at 0.200. The top right of the interface shows the formula C38H32, Z 6, and statistics for reflections (24331 total, 1191 rejected, 5506 unique, 3557 observed).

Solves the structure in P1 and finds the correct space group in the given Laue group. If multiple solutions are plausible they can be accessed through a pull-down box.

- The most powerful method in Structure solution
- Gives the most complete models
- 15 years ago it took a week to solve this structure with molecular modeling and PATSEE

# Intrinsic Phasing



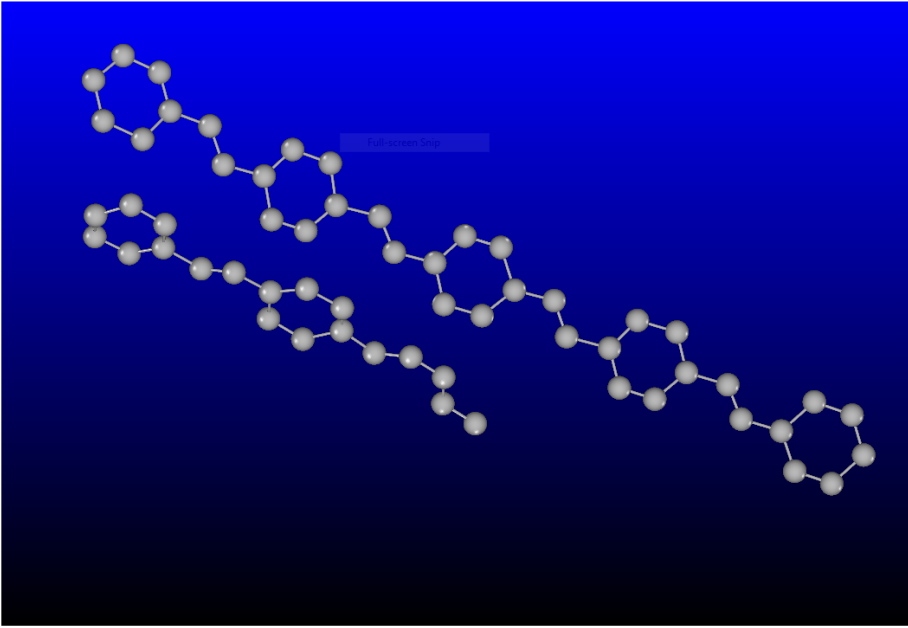
APEX2 v2013.6-2 - User: (guest) - Sample: poly - Licensed to Michael Ruf at Bruker AXS - [Structure Solution]

Sample Instrument Windows Help

Setup Evaluate Collect Integrate Scale Examine Data Solve Structure

Auto-Structure Structure Solution View Molecule

Instructions Listing Results Structure View



Instruction File: polynev.ins  
Reflection File: polynev.hkl  
Formula: C38H32 Z: 6 Update  
 Chiral  Non-centrosymmetric  Any

Statistics

Reflections	24331	Unique	5506
Rejected	1191	Observed	3557
R(int) [%]	14.58	% Observed	85
R(sigma) [%]	14.09	% Observed in 1.1-1.2Å Shell	60

Method

Intrinsic Phasing Intrinsic 1  
 Direct Direct 1  
 Dual Space Dual Space 1  
 Patterson Patterson 1 Expand

Intrinsic Phasing Solutions

[a] P2(1)/c  
R1 [%] 36.40  
alpha 0.200

No. of QPeaks: 0 Zoom

```
0.364 0.059 0.200 as input P2(1)/c polynev_a C57
0.331 0.049 0.157 as input Pc -9.99 polynev_b C114
0.341 0.057 0.196 as input P2(1) -9.99 polynev_c C114
```

Assign elements and isotropic refinement 8.482 secs

```
+++++
+ XT finished at 14:11:30 Total time 39.126 secs +
+++++
```

Refine Structure Report Pilot Instrument

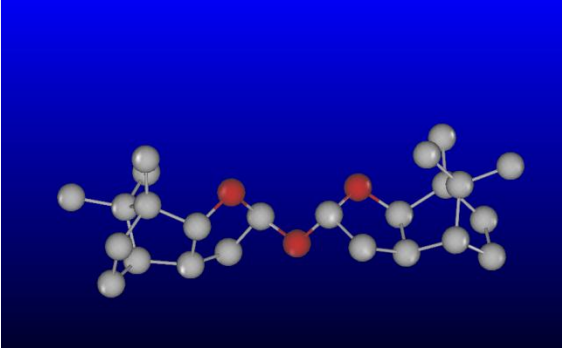
Solve Structure Stop after iteration  
Reset Exit

- The most powerful method in Structure solution
- Gives the most complete models
- 15 years ago it took a week to solve this structure with molecular modeling and PATSEE

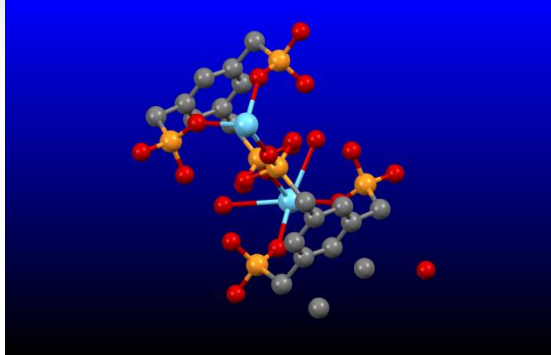


# So how powerful is Intrinsic Phasing

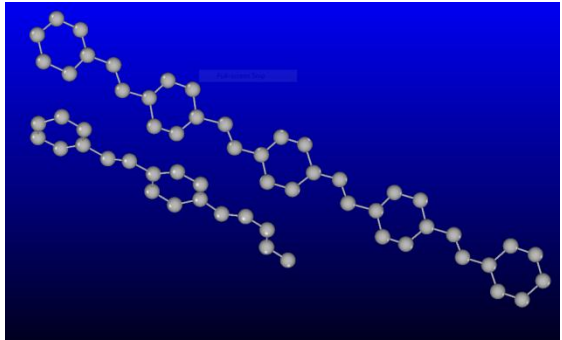
Furan  
in 3s



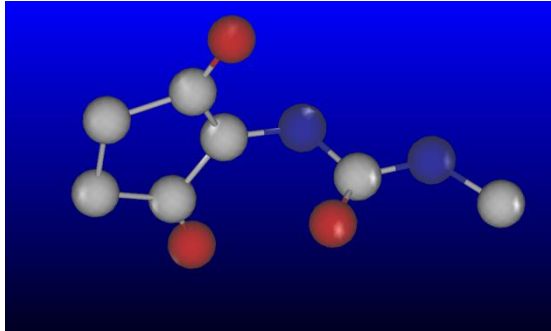
MOF  
in 20s



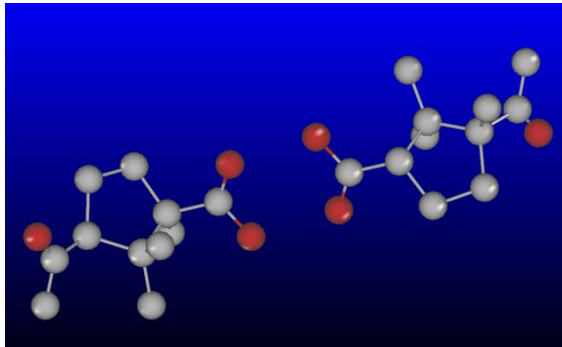
"Poly"  
in 40s



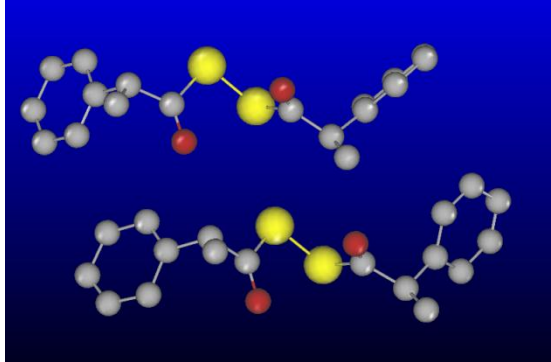
Carbamate  
in 1s

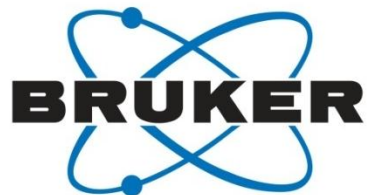


Camphoric  
acid in 11s



Disulfide  
6s





**MIT** Department of Chemistry  
X-Ray Diffraction Facility



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<http://web.mit.edu/x-ray/bmit14.html>



# Questions and Answers

## Any questions?

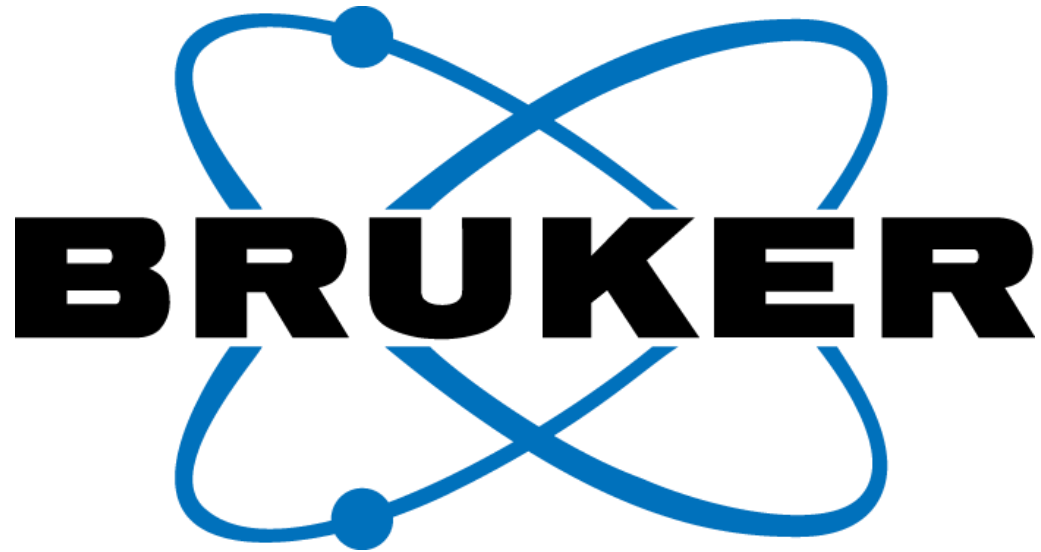
Please type any questions you may have for our speakers in the [Q&A panel](#) and click Send.

## How did we do?

When you exit the webinar, please fill out our [evaluation survey](#) to let us know. We appreciate your feedback.

**Thank you!**





Innovation with Integrity