#### Uses of X-ray Crystallography

#### September, 2004

#### This lecture will cover:

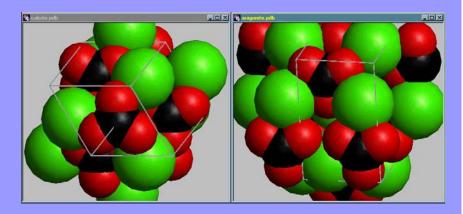
Health and Safety

What we can use the method for

Outline of theory

Outline of practice

#### Historical View of Crystallography

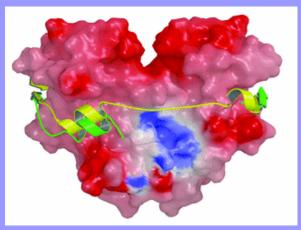


The origins are in mineralogy. The spatial arrangements of atoms explain the properties

#### Health and Safety

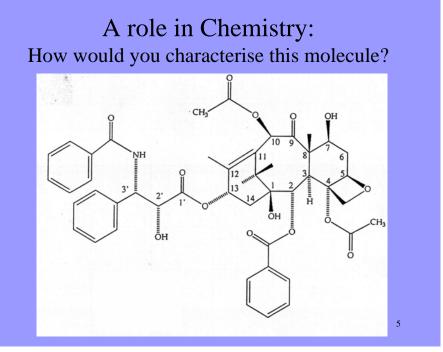
- X-rays have the potential to cause serious radiation burns.
- The equipment is safety-interlocked to current standards.
- The interlocks are checked weekly.
- People wishing to use the equipment must be trained and registered.
- Members of chemistry may observe the equipment in use without registering.

#### And the other end of the scale -

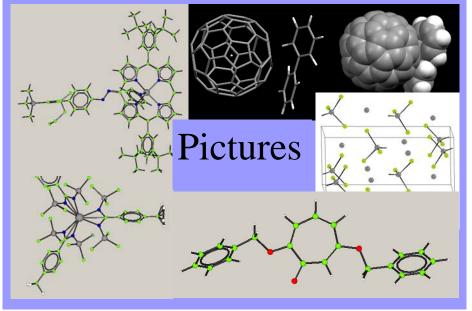


Interaction of a Plague pathogen with a protein molecule.

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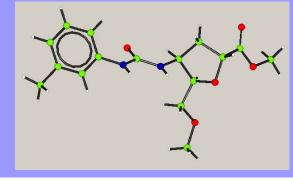


#### What do we want?

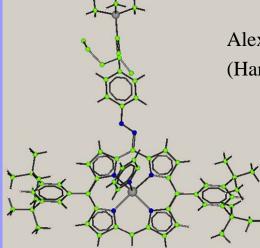


## Why do we want crystal structures?

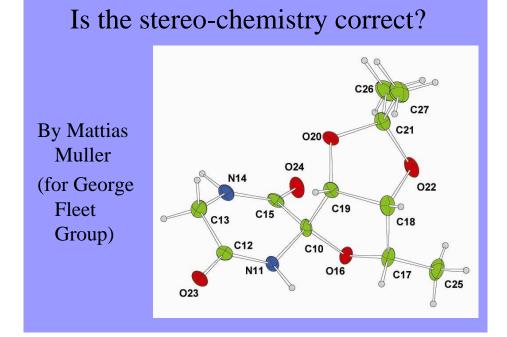
- Gross structure atom types and connectivity
- Stereo chemistry
- Fine detail bond lengths, angles and torsion angles
- Electron density distributions
- Crystal Structure



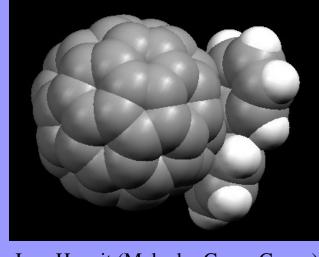
#### Have we made what we thought we had made?



Alexander Kripovacik (Harry Anderson Group)



#### What does it look like?



Jane Haggit (Malcolm Green Group)

## Single Crystal X-ray Structure Analysis

Pros:

Usually gives definitive 3-dimensional information Usually gives all of the structure

Usually very fast – 1hr-24 hrs.

Inexpensive on consumables –  $\pounds 10-\pounds 50$  per structure Cons:

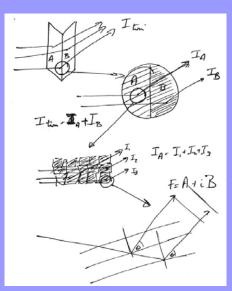
Material is in solid state

Needs single crystals

May fail altogether

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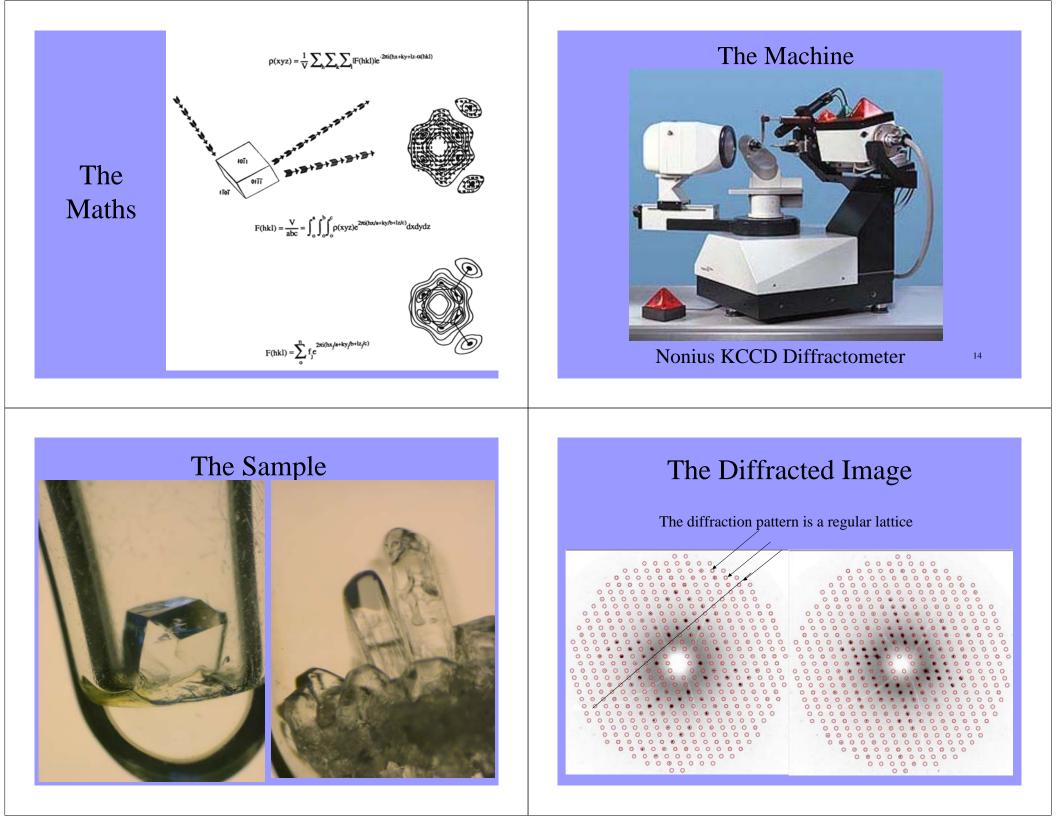
#### The Physics



#### The crystal acts as a 3D diffraction grating. Monochromatic Xrays falling on the crystal interfere constructively when the Bragg angle is satisfied.

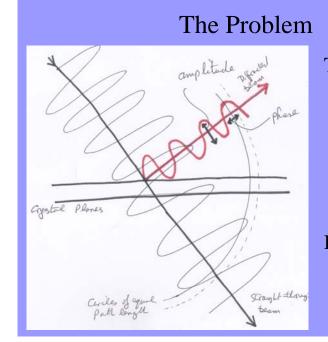
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The emergent beams have an intensity and a phase



11.471	8.223	14.272	90.000	93.177	90.000	p2
0 0	1 8167.4	225.5	0	1 5	1570.9	39.8
0 0	2 1832.6	95.3	0	1 6	826.1	18.2
0 <u>0</u> 0 <u>0</u>	3 1282.5	62.6	0	1 7	751.8	15.3
0 0	4 466.4	21.3	0	1 8	538.8	11.7
	5 472.4	19.8	0	1 9	741.9	26.2
	6 1676.1	67.2	0	1 10	78.7	8.0
0 0	7 198.8	8.3	0	1 11	483.1	15.7
0 0	8 564.3	15.9	0	1 12	105.1	10.4
	9 69.7	27.7	0	1 13	485.8	24.2
0 0 1	9.3	8.4	0	1 14	308.0	16.6
0 0 1	146.8	14.7	0	115	26.2	9.1
0 0 1	23.2	11.5	0	1 16	39.4	10.2
0 0 1	8.4	10.9	0	1 17	48.2	10.9
0 0 1	4 213.1	19.8	0	2 1	2997.1	83.6
0 0 1	195.4	23.8	0	2 2 2 3		102.9
0 0 1	42.5	15.2	0	2 3	803.0	20.5
0 0 1		14.5	0	2 4	696.9	17.3
0 1	1 9068.2	212.0	0	2 5	142.5	4.7
0 1	2 1097.4	28.8	0	2 6	533.1	9.7
0 1	3 2421.4	60.5	0	2 7	2357.4	44.7

The experiment yields the intensity of many thousands of unique 'reflections'<sup>17</sup>



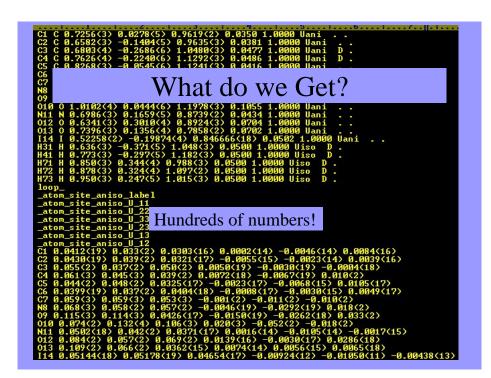
The phase of a diffracted beam is actually the phase lag with respect to the incident beam. It is not easy to measure.

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#### The Solution

We cannot easily measure the phases, but in the 1950's it was realised that there must be relationships between the phases, so that if a few are known, the rest can be estimated.

Modern DIRECT METHODS programs 'guess' some starting phases, and then try to select the best guess. This is measured by 'figures of merit'



#### Exchange of Results

This is usually done via text (ASCII) files. A program is needed to convert the data into pictures and tables.

- Cif files: Crystallographic Information File format. This has become an international standard.
- SHELX files: After the name of a widely used crystallographic program.
- PDB files: Protein Data Bank format. Often used by modelling and graphics programs.

## **Graphics Programs**

- There are dozens available from free viewers to expensive modelling packages
- Mercury: Free from CCDC. Has some knowledge of symmetry operations. Reads cif files. Will output bitmap files.
- Encifer: Free from CCDC. As above, but also enables you to read, edit and validate the syntax of cif files. Only outputs cif files.
- ViewerLite: Free from Accelrys. Reads PDB files, will output JPG, TIF etc.
- ORTEP: Free with WINGX. A fully functional crystallographic plotting program. Reads cif and SHELX files.

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## DEMO

## Structure solution from data input to final picture and tables

## Converting cif files to Tables

Microsoft Excel. You will need to use a text editor to isolate the bit of the cif you want to process.

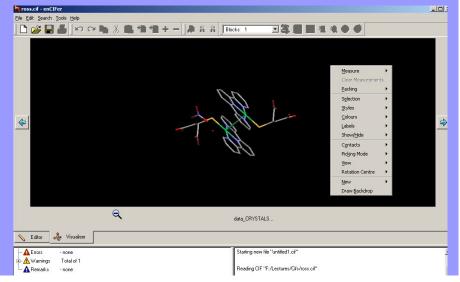
Microsoft Word. You will have to fiddle with left, right and decimal tabs to make a nice table

Use the IUCr web service *printcif*. http://journals.iucr.org/services/cif/printcif.html

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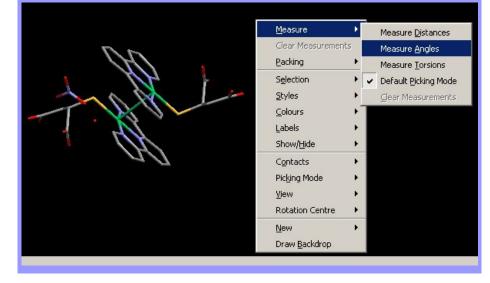
## Encifer

#### Visualisation module



## Encifer

#### Measuring geometric parameters



# Validating the Contents of a cif file

The IUCr has both defined the syntax of a cif file, and set criteria for the quality of the data contained in the file. This can be validated with:

Checkcif as a web service.

http://journals.iucr.org/services/cif/checkcif.html

PLATON in WINGX. The program can be downloaded from:

http://www.chem.gla.ac.uk/~louis/software/wingx/

**PLATON Validation** PLATON/CHECK-(181101) versus check.def version of 16/11/01 for entry: CRYSTALS Data From: publish.cif - Data Type: CIF Bond Precision C-C = 0.0047 A CELL 0.71073 9.724 5.631 16.284 SpaceGroup from Symmetry P21 Reported P\_1 21 1 90.00 92. наll: P 2yb 92.01 90.00 891.08 MoietyFormula C15 H24 N4 07 Reported C15 H24 N4 07 prmula C15 H24 N4 07 SumFormula C15 H24 N4 07 Reported 372.38[Calc] 372.38[Rep Dx,gcm-3 = 1.388[Rep 2[Rep 0.111[Rep 1.388[Cal 7 2[Ca]c 0.111[Ca]c Mu (mm-1) = F000 396.0[Calc] 396.0[Rep] F000 = 396.0[Calc], 396.0[Rep]
\* Reported T limits: Tmin=0.990 Tmax=1.000 'MULTI-SCAN'
Calculated T limits: Tmin=0.997 Tmin'=0.255 Tmax=0.999
\* Reported Hmax= 12, Kmax= 7, Lmax= 21, Nref= 2204 , Th(max)= 27.47
\* Calculated Hmax= 12, Kmax= 7, Lmax= 21, Nref= 2262( 4105), Ratio= 0.97( 0.54)
\* R= 0.0542( 2204), wR2= 0.1059( 2204), S = 0.947, Npar= 244 >>> The Following ALERTS were generated <<< 063\_ALERT A Crystal Probably too Large for Beam Size .... 12.30 mm 220\_ALERT A Large Non-Solvent C Ueq(max)/Ueq(min) . 4.83 Ratio #\_\_\_\_\_ \_\_\_\_\_ 028\_ALERT B -diffrn-measured-fraction-theta-max low ..... 0.97 222\_ALERT B Large Non-SOlvent H ueq(max)/ueq(min). 242\_ALERT B Large Non-SOlvent H ueq(max)/ueq(min). 242\_ALERT B Check Low U(eq) as Compared to Neighbors .... 411\_ALERT B Short Inter H...H Contact: H(101)... H(211) = 432\_ALERT B Short Inter X...Y Contact: 0(19) ... C(25) = 4.36 Ratio C(16) 2.06 Ang. 2.89 Ang. \_\_\_\_\_ 089\_ALERT C Poor Data / Parameter ratio ..... 125\_ALERT C No \_symmetry\_space\_group\_name\_Hall given .... 142\_ALERT C su on b - Axis small or Missing (x 100000) ... 143\_ALERT C su on c - Axis small or Missing (x 100000) ... 9.03 20 Ang. 50 Ang.

## **PLATON Validation**

Alerts are ranked in severity.

- A level: Must either be corrected or explained in the text of a publication.
- B level: Must be corrected or explained in a note to the editor.
- C level: May indicate a problem.

>>> The Following ALERTS were generated <<<

063_ALERT A Crystal Probably too Large for Beam Size 220_ALERT A Large Non-Solvent C Ueq(max)/Ueq(min) . #	12.30 mm 4.83 Ratio
7 228_ALERT B -diffrn-measured-fraction-theta-max low 222_ALERT B Large Non-Solvent H Ueq(max)/Ueq(min) . 242_ALERT B Check Low U(eq) as Compared to Neighbors	0.97 4.36 Ratio C(16)
411_ALERT B Short Inter HH Contact: H(101) H(211) = 432_ALERT B Short Inter XY Contact: 0(19) C(25) =	2.06 Ang. 2.89 Ang.

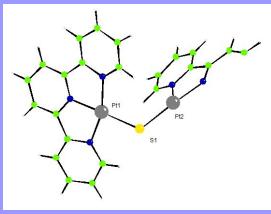
## CCDC – The Cambridge Crystallographic Data Centre

CCDC maintains and distributes the CSD (Cambridge Structural Database), plus software for searching, viewing and analysing crystal structures.

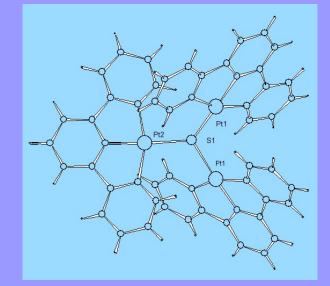
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#### Example: <sup>1</sup>/<sub>2</sub> molecule in asymmetric unit

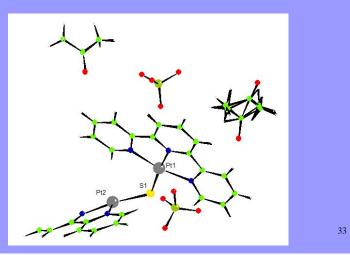
The crystallographic entity is ½ of the molecule. The second half (which shares the S) is generated by crystallographic symmetry.



#### Example: The full molecule The completed molecule has a propeller shape

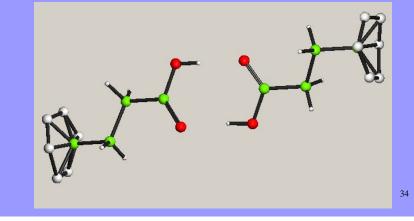


Example: Solvent of crystallisation As well as the ClO4 counter ions, there is acetone of solvation.



Example: Disorder

There are 2 molecules in the asymmetric unit, forming a hydrogen bonded dimer.Both terminal CF3 groups are disordered.



#### Advanced X-ray Course

Anyone intending to do their own X-ray analyses, or anyone simply wishing to learn more about crystallography, should come to the 2-day (6hr) intensive course.

Possible dates: Monday & Tuesday 18 & 19 October