

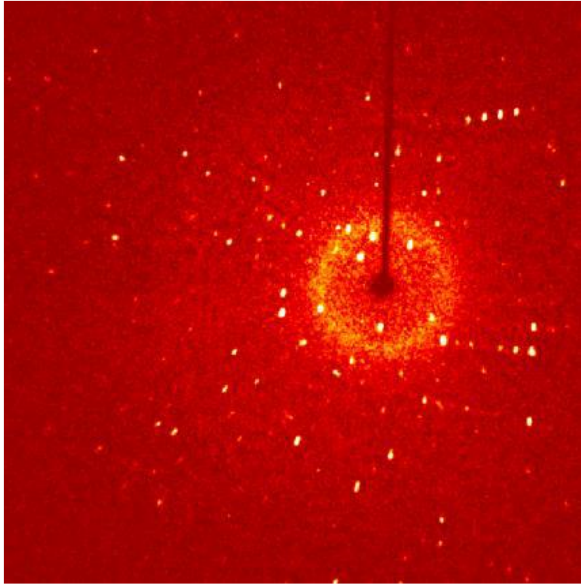
## T6. Modeling disorder: Solvent masks

Slides and sample data from Dr. Brian Patrick, UBC

Edits and presentation by Dr. Louise Dawe, WLU

Based on: Spek, A.L. *Acta Cryst.* (2015). C**71**, 9–18.

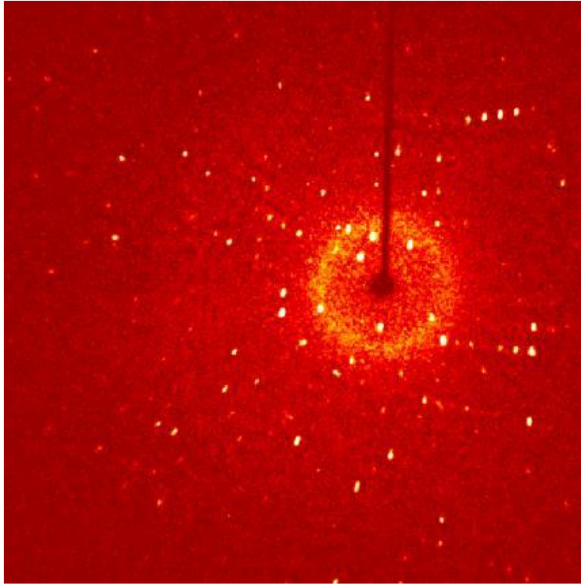
<https://journals.iucr.org/c/issues/2015/01/00/ln3172/ln3172.pdf>



Integrate reflections



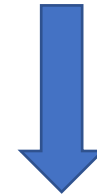
$$F_o = \sqrt{I / Lp}$$



Integrate reflections



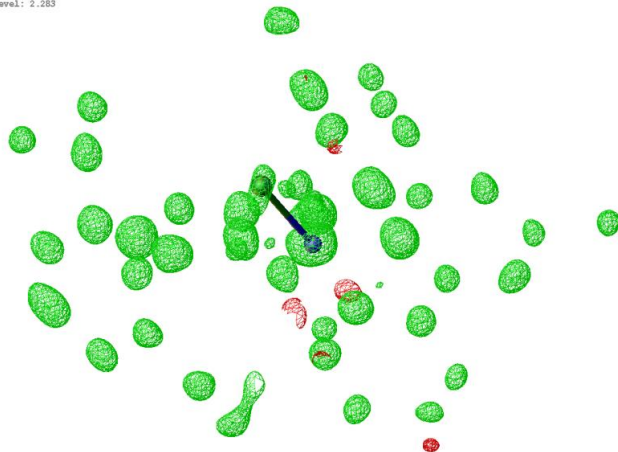
$$F_o = \sqrt{I / Lp}$$



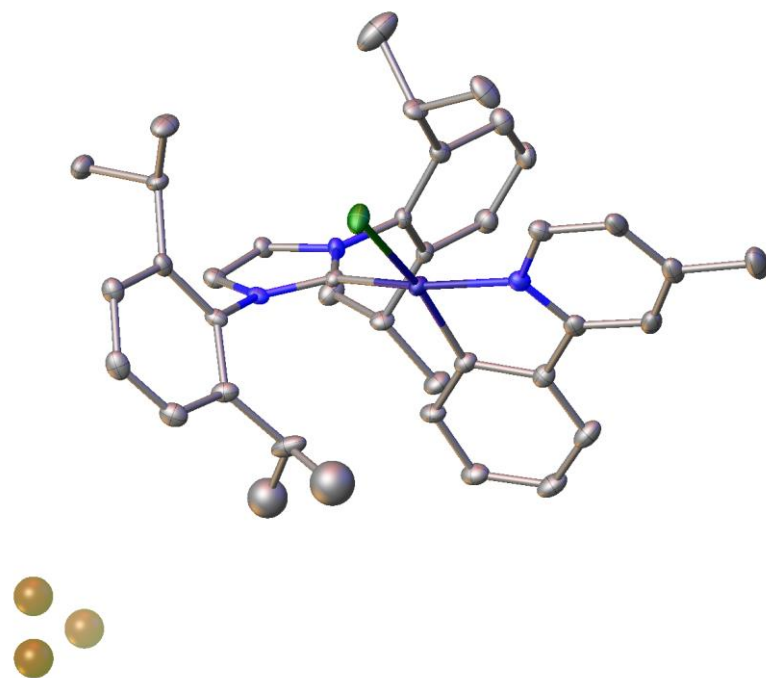
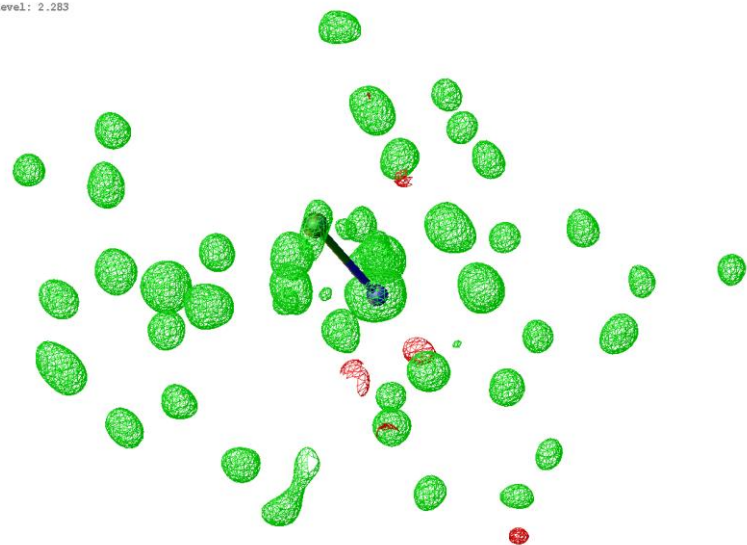
$$\rho(xyz) = \frac{1}{V} \sum_{hkl} \bar{F}_{hkl} \cos 2\pi(hx + ky + lz)$$



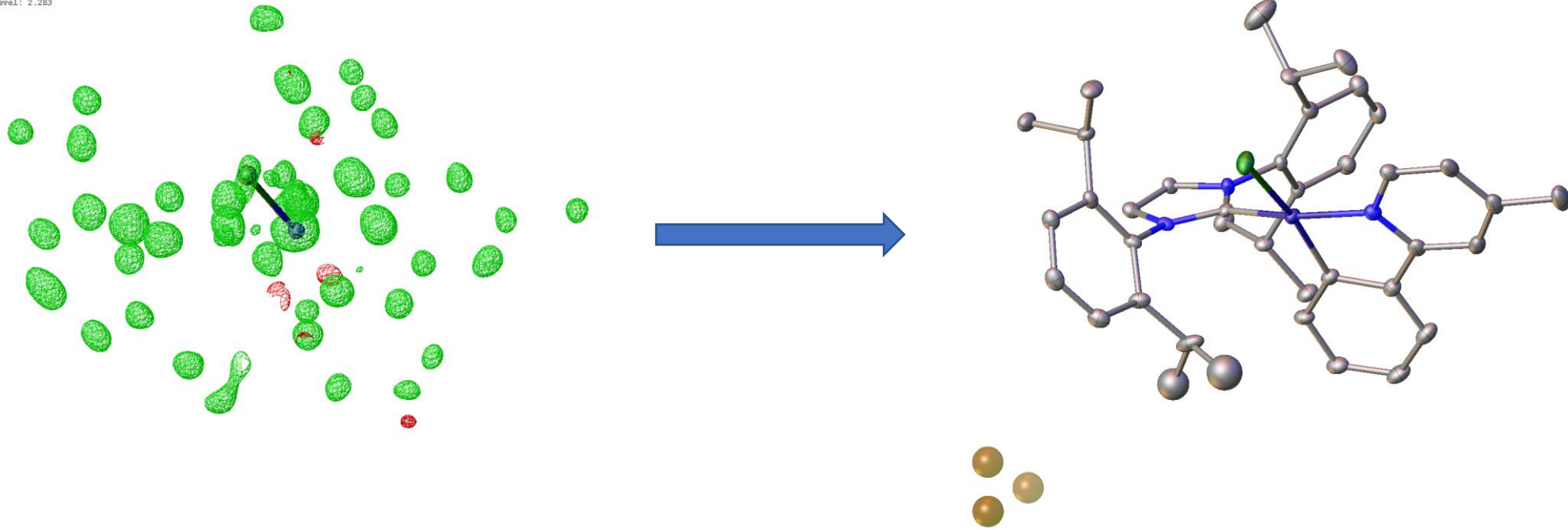
Current level: 2.283



Current level: 2.283



Current level: 2.283



Use scattering factors and coordinates (x, y, z) for each atom (j) in the unit cell to calculate structure factors (F) for each reflection.

$$\vec{F}(hkl) = \sum f_j \exp[2\pi i(hx_j + ky_j + lz_j)]$$

Least-squares refinement tries to minimize

$$\sum_{hkl} w' (F_o^2 - F_c^2)^2$$




Your measured intensities

The diagram consists of a central mathematical equation at the top. Two blue arrows originate from the equation. One arrow points from the summation index  $hkl$  down to the text 'Your measured intensities'. The other arrow points from the calculated structure factor term  $F_c^2$  down to the text 'Calculated from your model'.

Calculated from your model

Each atom in your model contributes to the calculated structure factor.

Least-squares refinement tries to minimize

$$\sum_{hkl} w' (F_o^2 - F_c^2)^2$$
The diagram shows the equation  $\sum_{hkl} w' (F_o^2 - F_c^2)^2$  with two blue arrows. One arrow originates from the  $\sum_{hkl}$  term and points down and to the left towards the text 'Your measured intensities'. The other arrow originates from the  $F_c^2$  term and points down and to the right towards the text 'Calculated from your model'.

Your measured intensities

Calculated from your model

The closer your model approximates the electron density in your unit cell, the smaller the difference.

# Solvent Masking via PLATON's SQUEEZE

Identifies solvent accessible regions in the unit cell.

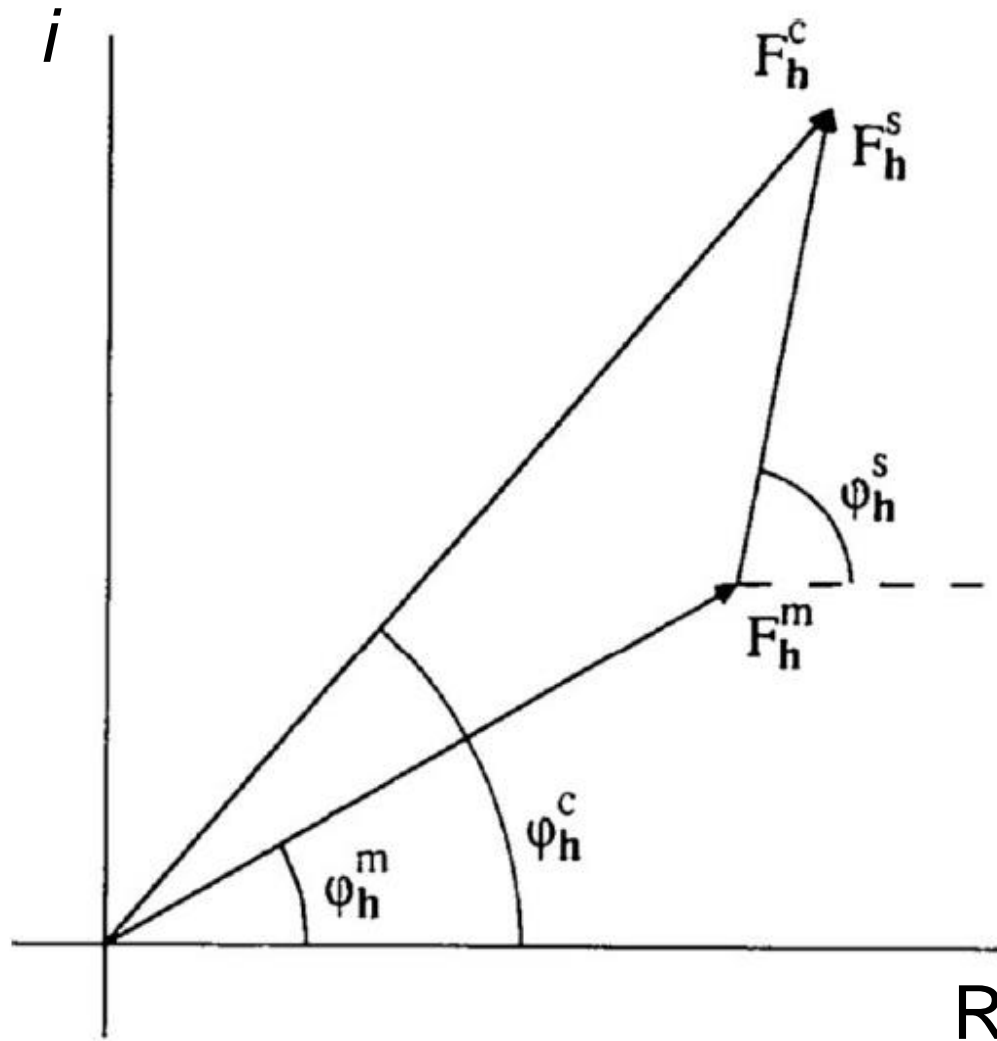
Calculates unresolved (unmodeled) electron density in that region.

SQUEEZE calculates the solvent contribution to the structure factors by back-Fourier transformation of the electron density found in the solvent-accessible region

$$F_{calc} = F_{Main} + F_{Solvent}$$



# Solvent Masking via PLATON's SQUEEZE

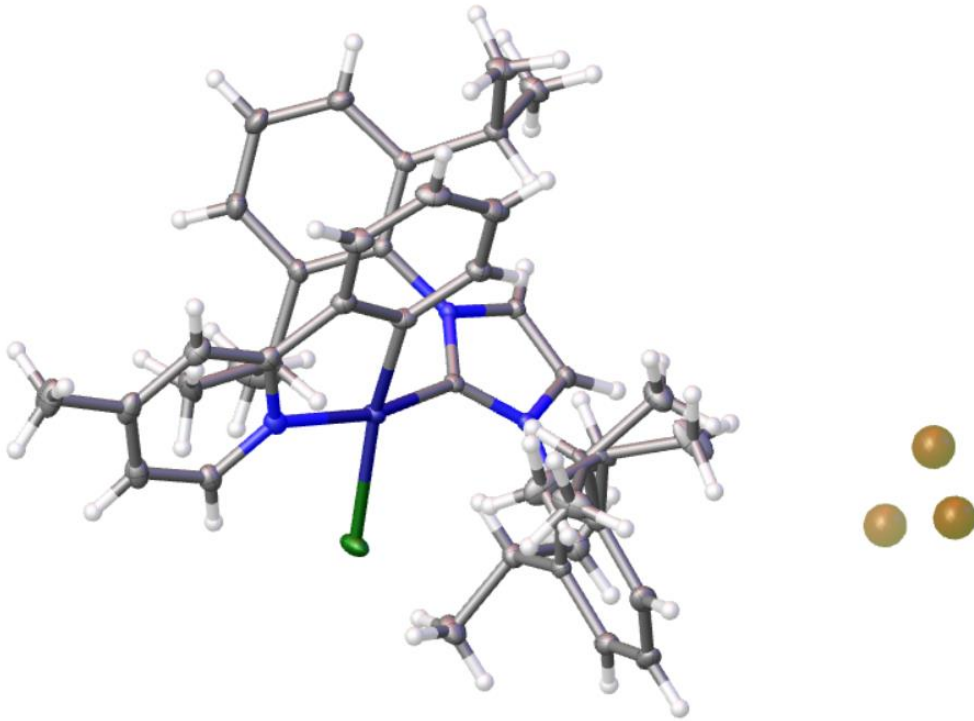


$$F_{calc} = F_{Main} + F_{Solvent}$$

- Refine everything in the main structure, including non-solvent disorder and hydrogen atoms.
- Refinement must include the ACTA and LIST 4 command in the .ins file. This will create the .cif and .fcf in a format that can be used by PLATON SQUEEZE.
- Twinned data with HKLF5 or TWIN/BASF data requires LIST 8 (not 4).

- Initiate PLATON/SQUEEZE. It will:
  - Search for solvent accessible voids
  - Calculate the electron density in each void
  - Calculate the correction ( .fab file) required to each reflection to remove that electron density from the void.

- Initiate PLATON/SQUEEZE. It will:
  - Creates new .ins file (name\_sq.ins) containing the ABIN instruction
  - Creates new .hkl file (name\_sq.hkl), identical to original .hkl file
  - Creates new .fab file (name\_sq.fab), includes the solvent contribution to the calculated structure factors



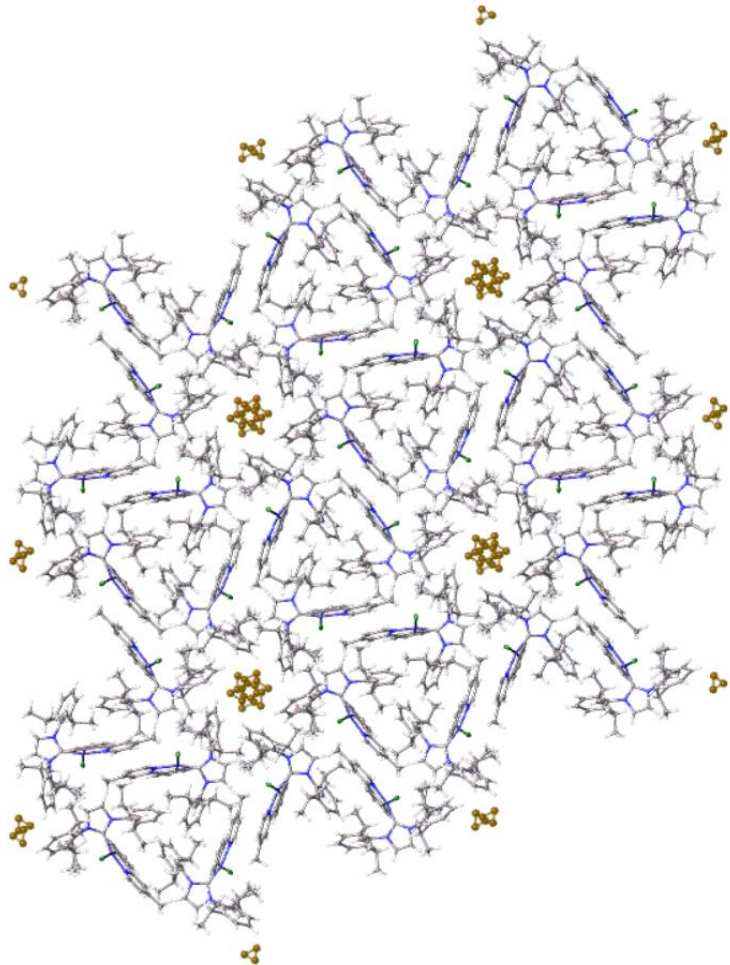
As a first step, you can explore the disordered solvent. Some suggestions:

- CTRL + Q to connect the three largest peaks
- GROW
- PACK
- MATR 3

Olex2

File Edit View Structure Mode Tools Model Select Help

C  
H  
Cl  
N  
Ni  
Q



**solvent** *P6<sub>5</sub>*  
C:\Users\ldawe\OneDrive - Wilfrid Laurier  
C39H46ClN3Ni

$a = 23.7330(14)$   $\alpha = 90^\circ$   $Z = 6$   
 $b = 23.7330(14)$   $\beta = 90^\circ$   $Z' = 1$   
 $c = 10.7187(9)$   $\gamma = 120^\circ$   $V = 5228.5(6)$

$R_1 = 3.41\%$   
 $wR_2 = 10.85\%$

$d \text{ min (Mo)} = 0.71$   $|I/\sigma(I)| = 53.1$   $R_{\text{int}} = 4.12\%$   $\text{Full } 50.5^\circ = 100$   
 $2\theta = 60.1^\circ$   $\text{Shift} = -0.009$   $\text{Max Peak} = 1.9$   $\text{Min Peak} = -0.3$   $\text{GooF} = 1.165$   $\text{Hooft} = .002(2)$

Refinement Finished

Home Work View Tools Info

Recent Files

Electron Density Peaks

Peaks Select Delete

Transparency

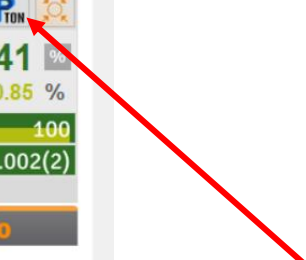
Label	Height
Q1	1.890
Q2	1.530
Q3	1.010
Q4	0.830
Q5	0.390
Q6	0.390
Q7	0.360
Q8	0.350
Q9	0.340
Q25	0.280

Refinement Indicators

Bad Reflections

Reflection Statistics

Reflection Statistics Summary



As a first step, you can explore the disordered solvent. Some suggestions:  
Navigate to INFO → Electron Density Peaks

FUSE

Launch PLATON (if you do not have the PTON button, you can launch from the folder that hosts pwt.exe).

# PLATON

A Multipurpose Crystallographic Tool

(C) 1980-2022 A.L. Spek - Version: 51222 [WEB: May 23, 2023]

GRAPHICS	GEOM-CALC	VOIDS FLIP	SYMMETRY	ABSORPTION	REPORT	MISC-TOOLS
PlutonAuto	Calc All	Calc Solv	Addsym	MULscanABS	Validation	System-S
Ortep-Plot	Calc Intra	Calc K.P.I	Addsym-EQL	ABSPstScan	Asym-Vlew	fcf2hkl
NewmanPlot	Calc Inter	Squeeze	Addsym-EXT	ABSTompa	FCF-Valid	Expand2P1
Ring-Plots	Calc Coord	Hybrid	Addsym-PLT	ABSGauss	DiffFourier	FCF-Gener
Plane-Plot	Calc Metal	CalcFCFsqr	Addsym-SHX	ABSxtal	ANALofVAR	HKLF-Gener
PolyPlot	Calc Geom	ContourSol	Newsym	ABSSphere	ByvoetPair	HKL-Transf
ContourDif	Calc Hbond	Solv F3D	Nonsym	ShxAbs	AsymExpect	Exar-Res
Contour-Fo	Calc TMA	Solv Plot	LePage	AnomDisVal	Asym-Valid	Ans-Res
AutoMolFit	L.S.-Plane	CavityPlot	Delhed	AnomDisPlt	SupplMater	Rename-Res
hkl2Powder	DihedAngle	Calc SASA	Molsym	MuPLot	Expect-hkl	Auto-Renum
SimPowderP	AngleLines	Flip Menu	SPGRfromEX		CSD-Cell	Create-spf
RadDistFun	AngLsplLin	Flip Show	Asym		CSD-Quest	Create-res
Patterson	CremerPopl	Flip Patt	ASYMaverFR		StructTidy	Create-clf
ShelxtPlot	BondValenc	Flipper 25	LePageTwin	XtLPLanAgl	StralnAnal	Create-pdb
	Volcal	Structure?		Xtal Habit		HFIX-Res
WLLsonPlot	R/S-CIP					clf2fcf
PLutoNatl v	Mol Volume		TwLnRotMat			clf2shel xl

Xtal Data (CIF ) solvent.clf- Set 2( ): solvent  
 Refl Data (LIST4 ) solvent.fcf [ FCF ] ( ): solvent

Browser - HELP

<http://www.platonsoft.nl/PLATON-MANUAL.pdf>

[http://www.platonsoft.nl/PLATON\\_HOW\\_TO.pdf](http://www.platonsoft.nl/PLATON_HOW_TO.pdf)

INPUT INSTRUCTIONS via KEYBOARD or LEFT-MOUSE-CLICKS (HELP with RIGHT CLICKS)

PLATON 10
OptionMenus
NoMove
Join-Expand
Organic
Round
Parentheses
Label-Alias
R/S-Determ
Norm-H-bond
NoSymm
NoDisorder
LstARU RCel
LstCellSymm
ListAtoms
ListBonds
List Uij
Exclude H
MinQPeakHgt
MinQPeakDis
Q-Peak-Incl
KeyInstruct
Prev Next
SAVE-InstrS
ENTRY-LIST
Reset End
Exit
MenuActive

2. Apply a solvent mask.

1. Visualize the solvent accessible region.

Values below for gridpoints and volumes in []  
refer to areas where atom centers may reside.

Area	#GridPoint	VolPerc.	Vol(A <sup>3</sup> )	X(av)	Y(av)	Z(av)	Eigenvector(frac)	Sig(Ang)
1	34650[ 9462]	5	262[ 71.6]	0.000	0.000	-0.023	1 -0.058 0.055 1.000	3.16
							2 0.979 1.000 0.000	1.53
							3 -1.000 0.937 -0.803	1.40

x	y	z	Shortest Contacts within 4.5 Ang. (Excl. H)
1	0.000	0.000-0.023	C20 3.47; C21 3.94; C19 4.16;

:: Note: use CALC VOID (not CALC SOLU) for Packing Index.

Report the Distance from VOID-CG to Boundary in EU-Directions

Nr	MinEU1	MaxEU1	MinEU2	MaxEU2	MinEU3	MaxEU3	MaxDist (Ang)
1	-6.78	6.38	-3.87	1.87	-2.85	2.86	6.78

:: ADP <C24A 0.005 0.020 0.072 - RATIO(MAX/MIN) = 15.1 prolate

:: TRMX = ( 1.00 0.00 0.00/ 0.00 1.00 0.00/ 0.00 0.00 1.00)  
:: CELL = 23.733 23.733 10.719 90.000 90.000 120.000

:: Reflection Data are READ from File : solvent.fcf - ( OBS-Data)  
W: No Reflections Supplied !

:: END Statement Executed for this Entry  
:: \*\*\* FILES for Final Refinement with SHELXL201n \*\*\*

:: SQUEEZE ins on :solvent\_sq.ins  
:: SQUEEZE hkl on :solvent\_sq.hkl  
:: SQUEEZE fab on :solvent\_sq.fab  
:: SQUEEZE cif on :solvent\_sq.sqf  
:: SQUEEZE xyz on :solvent\_sq.sqz

1. Return to OLEX2.
2. Open solvent\_sq.ins.
3. Change your hkl file to solvent\_sq.hkl.
4. Refine.
5. Examine the result (including the CIF).