

DIRDIF - Fragment Searching to easily  
solve structures which direct methods  
won't



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(But really Paul Beurskens et al, University of  
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# DIRDIF - The Real Thing



*Mariken van  
Nieuwmege*

- P.T. Beurskens, G. Beurskens, R de Gelder, S. Garcia-Granda, R. Gould & J.M.M Smits, Crystallography Laboratory, the University of Nijmegen.
- Windows realisation by Louis Ferrugia, The University of Glasgow
- Examples from Simon Parsons, The University of Edinburgh

# DIRDIF - the general idea

**Strengthen Direct Methods by making use of known structural features**

<b>Heavy atoms</b>	<b>-</b>	<b>PATTY</b>
<b>Known molecular structure</b>	<b>-</b>	<b>ORIENT</b>
<b>Known molecular orientation</b>	<b>-</b>	<b>TRACOR</b>
<b>Known position</b>	<b>-</b>	<b>DIFTAN</b>

# PATTY Example: $\text{Rh}(\text{C}_5\text{H}_5)\{\text{B}(\text{C}_4\text{H}_5\text{N}_2\text{S})_3\}\text{Cl}$

$P-1$  ;  $V = 2618 \text{ \AA}^3$  ;  $Z = 4$  ; data poor

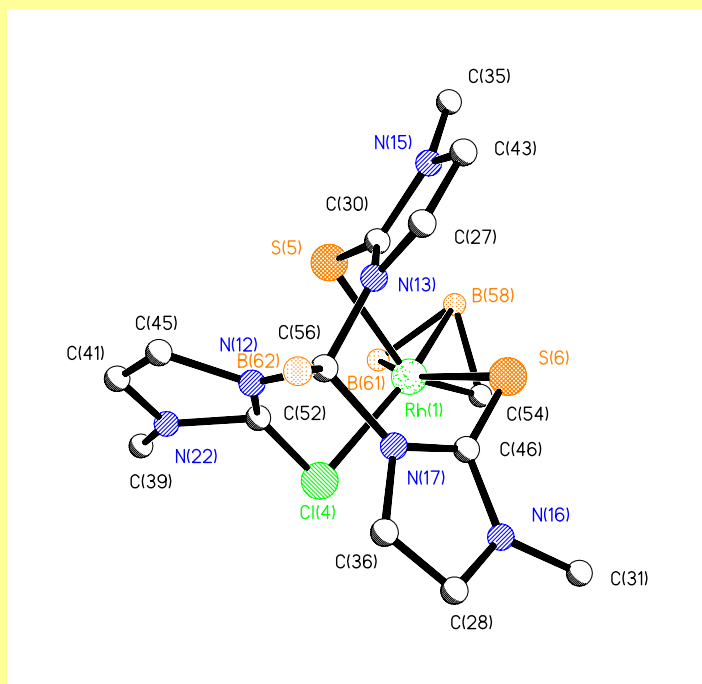
Related compound:  $\text{Cd}(\text{Br})\{\text{C}_4\text{H}_5\text{N}_2\text{S}\}_3$

$P-1$  ;  $V = 1337 \text{ \AA}^3$  ;  $Z = 2$  ; data very good

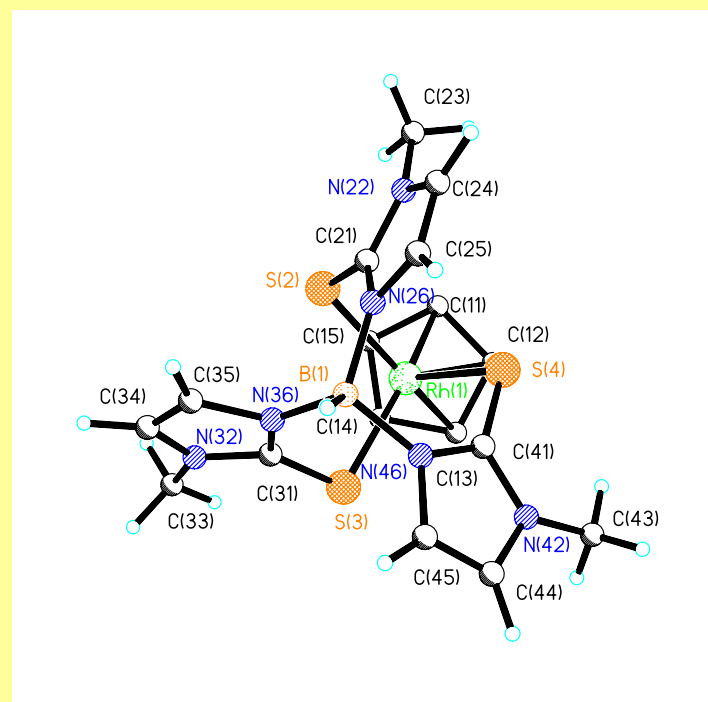
(but not, of course, known about until later!)

# Patterson for $\text{Rh}(\text{C}_5\text{H}_5)\{\text{B}(\text{C}_4\text{H}_5\text{N}_2\text{S})_3\}$

1	6000.	0.0000	0.0000	0.0000	0.00
2	2762.	0.0402	-0.1273	-0.4576	8.73
3	1774.	0.2821	0.3041	-0.1894	6.61
4	1134.	-0.3419	-0.4948	0.1759	8.46
5	1084.	0.2122	0.3148	-0.0738	4.98
6	1074.	0.0587	0.1962	0.0148	2.47
7	1036.	-0.2006	0.0525	-0.0485	2.46
8	1035.	0.4790	0.2530	-0.1397	7.18
9	1015.	-0.0707	0.0107	0.1178	2.48
10	920.	0.2423	0.4265	0.2664	6.98



**DIRDIF solution**



**Refined structure**

# S18DEN : Patterson

$C_{126}H_{108}S_{18}$  ;  $P2_1/c$ :  $V = 3800\text{\AA}^3$  :  $Z = 2$

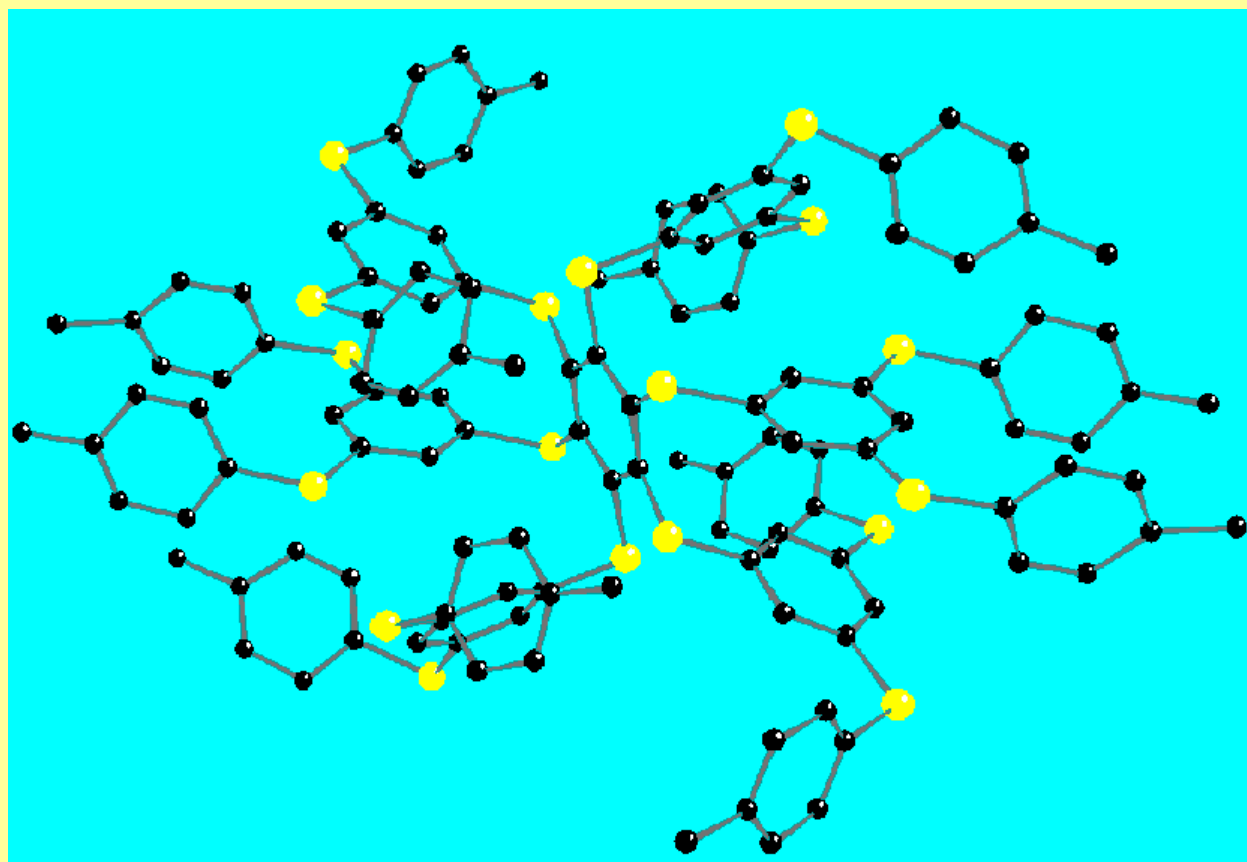
Peak	height	x	y	z	length
1	6000.	0.0000	0.0000	0.0000	0.00
2	461.	0.0000	0.2053	0.5000	8.92
3	416.	0.0000	0.1524	0.5000	8.57
4	390.	0.0000	0.3350	0.5000	10.13
5	367.	0.1657	0.1813	0.2520	5.44
6	367.	0.0000	0.0373	0.5000	8.14
7	363.	-0.1338	0.0346	0.2463	5.52
8	348.	0.0584	0.0000	0.0681	1.32
9	343.	0.2914	0.0000	0.0219	5.71
10	338.	0.0320	0.5000	0.1696	9.44

# S18DEN: Patterson solution and final refinement

- S1      0.000    0.000    0.002
- S2      0.002    -0.003    0.003
- S3      0.000    0.000    0.010
- S4      -0.001    -0.001    0.000
- S5      -0.002    0.001    0.004
- S6      0.000    0.000    0.000
- S7      -0.001    0.005    0.000
- S8      0.002    -0.005    0.008
- S9 (not found in Patterson)



# S18DEN - DIRDIF SOLUTION



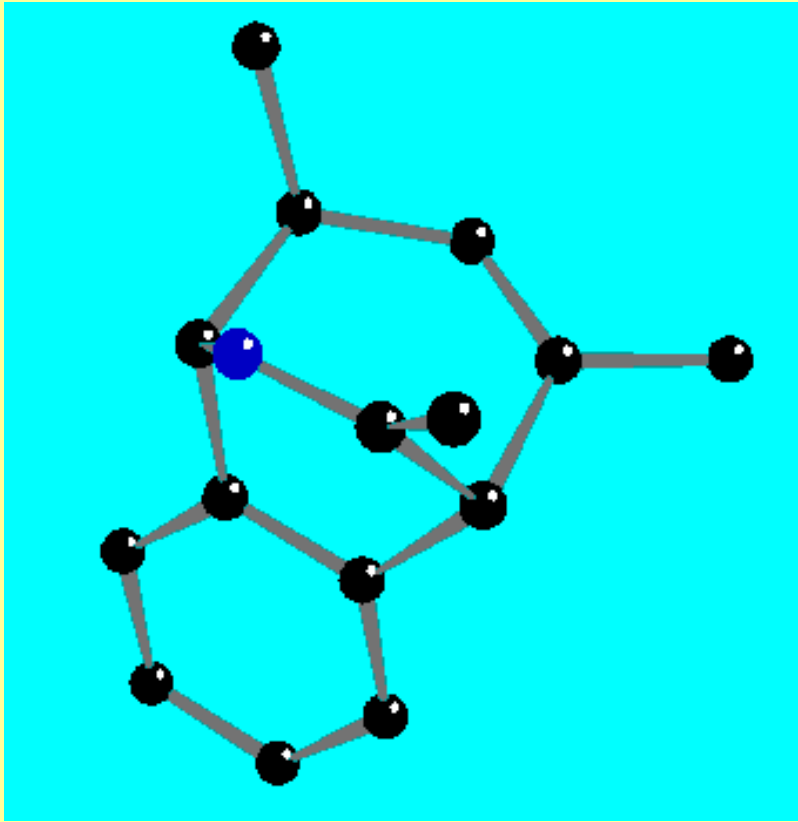
# Orient Test: CHNM13

a	b	c	$\alpha$	$\beta$	$\gamma$
8.280	12.915	41.666	90	90.00	90

$C_{30}H_{23}N$  :  $Z = 8$

**124 atoms in asymmetric unit -  
strong hint of twinning!**

# ORIENT - the general principle



- Calculate sharpened Patterson from data
- Calculate vector map from fragment
- Rotate calculated map to achieve best overlap with Patterson.
- Here C<sub>15</sub>N

# CHNM13 Patterson

Peak	height	x	y	z	length
1	1397.	0.0000	0.0532	0.5000	20.84
2	1241.	0.2103	0.0000	-0.4999	20.90
3	1006.	0.0332	0.0000	0.0269	1.15
4	865.	0.0009	0.0869	0.0140	1.26
5	636.	0.0000	0.1872	0.0000	2.42
6	464.	0.0030	0.4896	0.2497	12.18
7	457.	0.4502	0.2590	-0.0001	5.01
8	389.	-0.2460	0.4897	0.2496	12.34
9	374.	0.2252	0.4884	0.2506	12.34
10	350.	0.1415	0.0894	0.0390	2.31

# ORIENT - Matching the Vectors

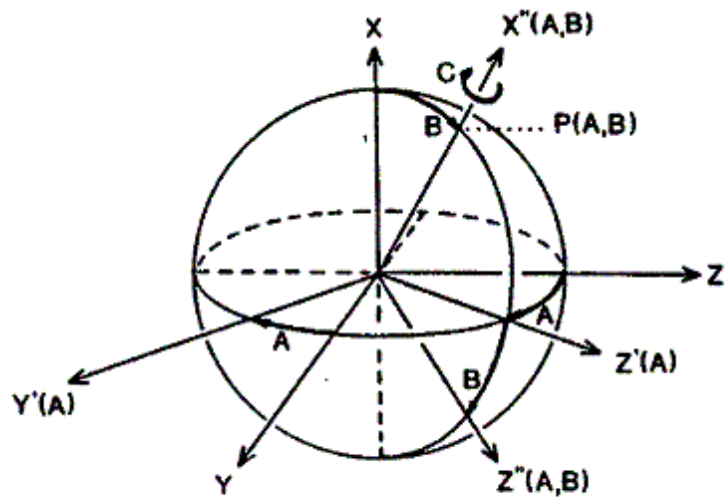


Figure 1. Definition of Eulerian angles

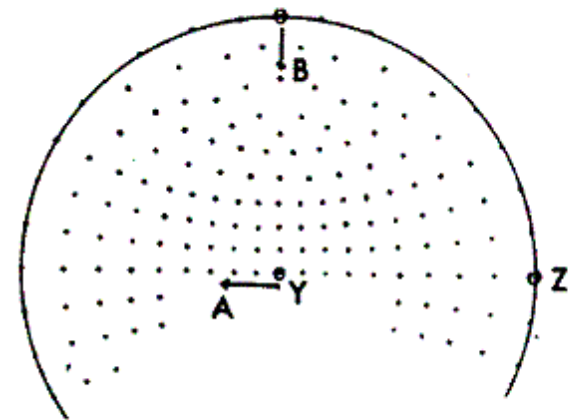


Figure 2. The coarse (A,B) grid plotted on a Wulff net, i.e., a stereographic projection of points  $P(A,B)$

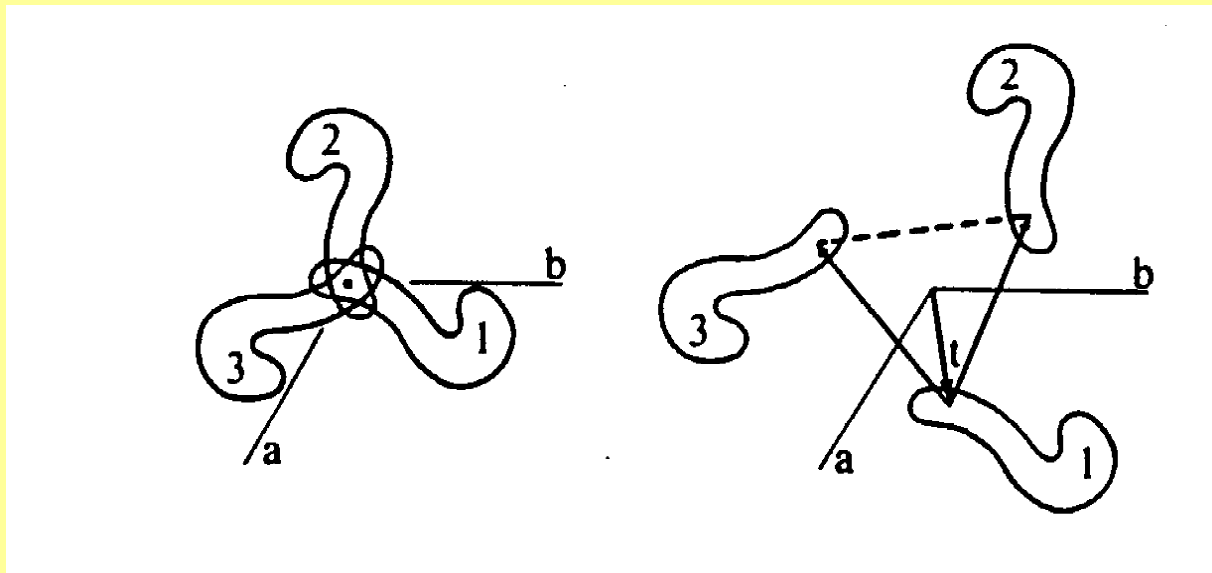
# ORIENT RESULTS

Set	A	B	C	ISIG
1	216.40	69.40	199.80	392
2	184.40	32.40	176.40	346
3	170.80	33.60	174.20	328
4	90.70	40.20	16.80	309
5	346.40	71.40	87.60	288
6	145.20	61.40	27.60	282

(with  $Z' = 2$ , at least two correct orientations are present)

# TRACOR - general principle

- Calculate shift of oriented fragment relative to symmetry elements



# TRACOR Results

**Class 2: origin not fixed in  $b$ -direction**

**Fourier is calculated in  $ac$ -plane:**

$$a = 8.280, c = 41.666 \text{ \AA}, \beta = 90.00^\circ$$

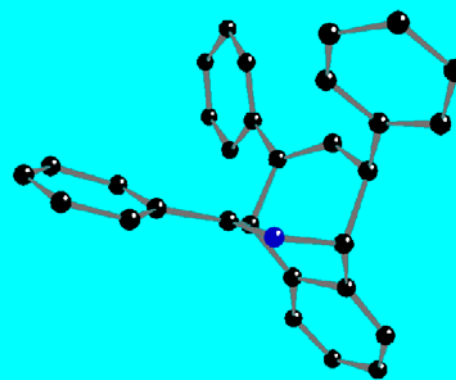
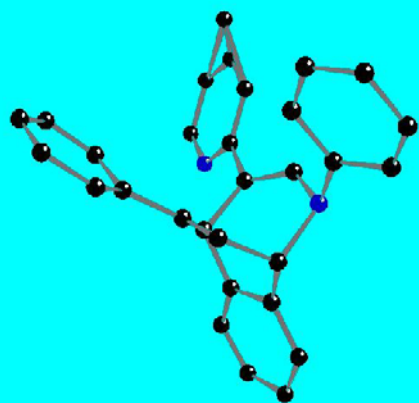
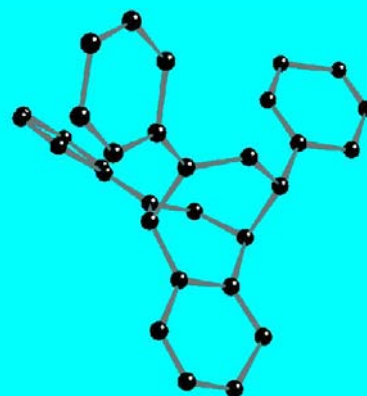
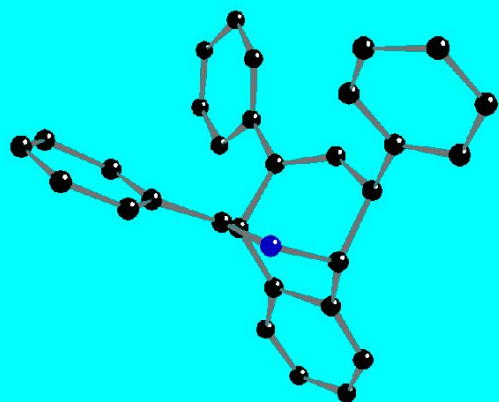
**No close contacts**

**Possible shift vectors:**

<b>FOM</b>	<b><math>t_x</math></b>	<b><math>t_y</math></b>	<b><math>t_z</math></b>
<b>1 912.</b>	<b>0.14858</b>	<b>0.00000</b>	<b>0.00627</b>



# CHNM13 – Results for 4 molecules



# CHNM13 – The end of the story

- Refinement converged unconvincingly
- Twinned refinement with  $[100]$  as twin axis gave 60:40 composition for twins.
- Solution is probably due to the ability to the Fourier expansion to delete the weaker component on geometrical grounds.