

# Electron Crystallography Workshop

## Basel, August 2008

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Image processing in 2D: MRC software for real space images

MRC programs

Unbending

## **5 main steps**

**after acquisition of images**

**before interpretation of map**

1. Processing of individual images in 2D (CCUNBENDK, MAKETRAN, etc)
2. Merging (ORIGTILTK) image amplitudes and phases
3. Electron diffraction integration (BACKAUTOK, AUTOINDEXK, PICKPROFK)
4. Merging electron diffraction data (MERGEDIFF)
5. Combining image and electron diffraction data (LATLINEK)

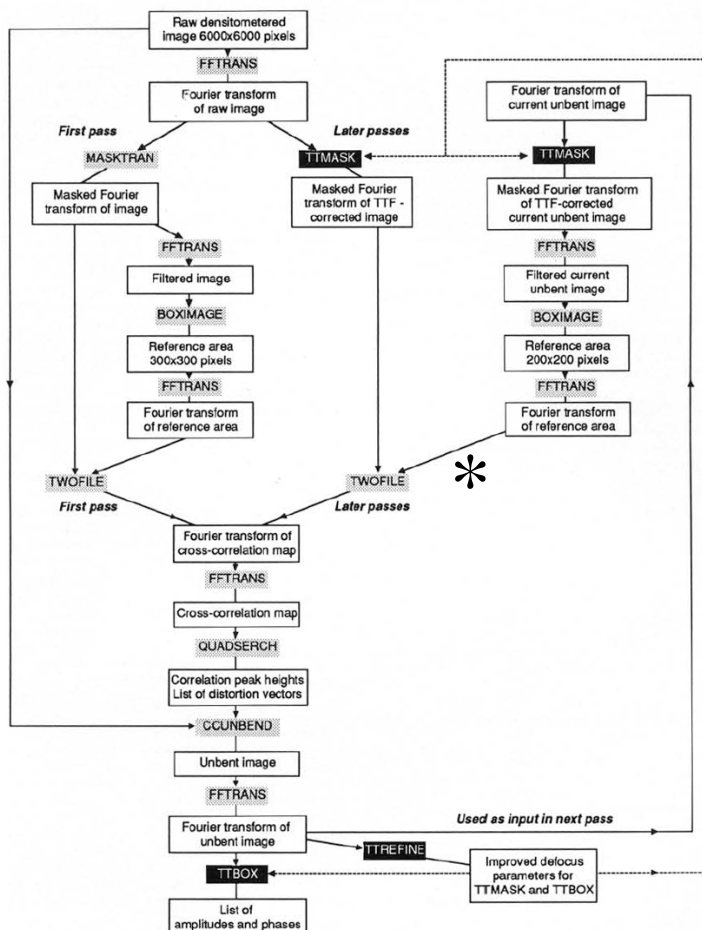
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Aim to combine graphical plots with concise summaries



Henderson et al (1990) JMB

Dashed lines - information  
Full lines - data

\* Could use MAKETRAN  
for reference area  
without any defocus

Kunji et al (2000) PNAS

**TABLE I**  
Brief Description of Current MRC Programs

Two-dimensional crystals		
1. EMTILT		Calculate tilt angles from lattice parameters.
2. MASKTRANA		Mask transform for filtering, like TRMASK.
3. AUTOCORRL		Autocorrelation calc + expansion – use with QUADSERCH.
4. QUADSERCHB		Correlation peak search on lattice, with profile fit.
5. CCUNBENDD	K	Unbend image using list of peaks from QUADSERCH.
6. MMBOX	A	Read amplitudes and phases from transform and display surrounding box.
7. MMLATREF		Lattice parameter refinement based on MMBOX.
8. TTBOX	K	Correct for tilted transfer function, gives amplitudes and phases.
9. TTMASK		Combined MASKTRAN and TTBOX, masking + TTF corr on tilted images.
10. TTREFINE	A	Refine defocus, astigmatism, tilt params on tilted images.
11. TTBOXREF	Defunct	Lattice parameter refinement on images with TTF correction.
12. CTFSEARCH	A	Refine or search for correct defocus, astigmatism, on data from untilted images.
13. CTFAPPLY	K	Apply CTF to data from MMBOX, with graphical output.
14. ORIGTILTC	K	Combine data from different images using crystal symmetry.
15. LLFIT		Lattice line fitting for smooth curves and structure factors.
16. LATLINED	K	Agard's least squares latline fit of amplitudes and phases.
17. ALLSPACE	A	Determine space group, origin, beamtilt on single image.
18. AVRGPAGES		Overall averaging of projection data from ORIGTILT.
19. AVRGAMPHS		Overall averaging of amplitude and phase projection data.
20. MAKETRAN		Create reference transform from MTZ file with given defocus.
21. SCALIMAMP3D		Scales image amplitudes to selected reference data.
(1, Shaw and Hills (1981); 4,5,12,13,14,16, Henderson <i>et al.</i> (1986); 8,9,10, Henderson <i>et al.</i> (1990); 14, Amos <i>et al.</i> (1982); 16, Agard (1983); 17, Valpuesta <i>et al.</i> (1994); 21, Havelka <i>et al.</i> (1995))		
Electron diffraction patterns		
1. BACKAUTO	K	Calculate radial background and find centre of pattern.
2. AUTOINDEX	K	Find two simplest lattice vectors automatically.
3. PICKAUTO	K, PICKPROFK	Integrate and background correct electron diffraction spots.
4. MERGEDIFF		Merge e.d. data and do a host of corrections.
5. AVRGFDEL		Average multiple measurements of delta-F from MERGEDIFF.
6. SYNCFIT	P3	Fit lattice line curves to output from MERGEDIFF.
7. F2MTZ		Convert formatted data (A,P) to MTZ format (CCP4 Suite).
8. AVRGINTENS		Overall averaging of electron diffraction intensities in projection.
(1,2,3,6, Baldwin and Henderson (1984); 4, Ceska and Henderson (1990))		

**TABLE I (ctd)**

### General processing

HEADER	Print out information in header records
LABEL	Image handling of various kinds
FFTRANS	Fast Fourier transform
BOXIMAGE	Box off an area leaving in original position
TAPEREDGE	Taper edge of an image to remove spikes in transform
TWOFIELD	Linear combination, or multiply/divide data in two files

### General display

LASERPLOT	Made redundant by PLOT2K library, directly into postscript
HISTO K	Make histogram of densities in an image
CURVY 2K	Produces graph, now direct to postscript
Ximdisp	LMB raster graphics display for X-terminals
SURF, LIGHT	Produces shaded surface representation of 3D maps

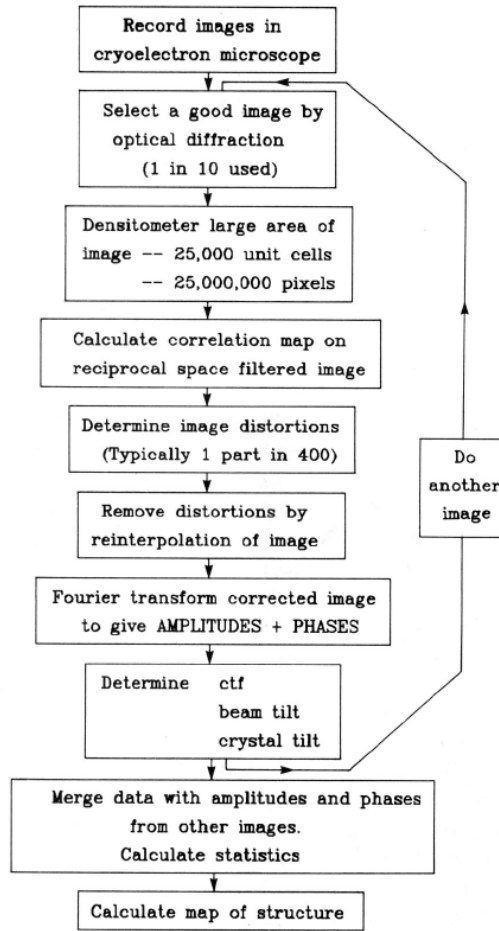
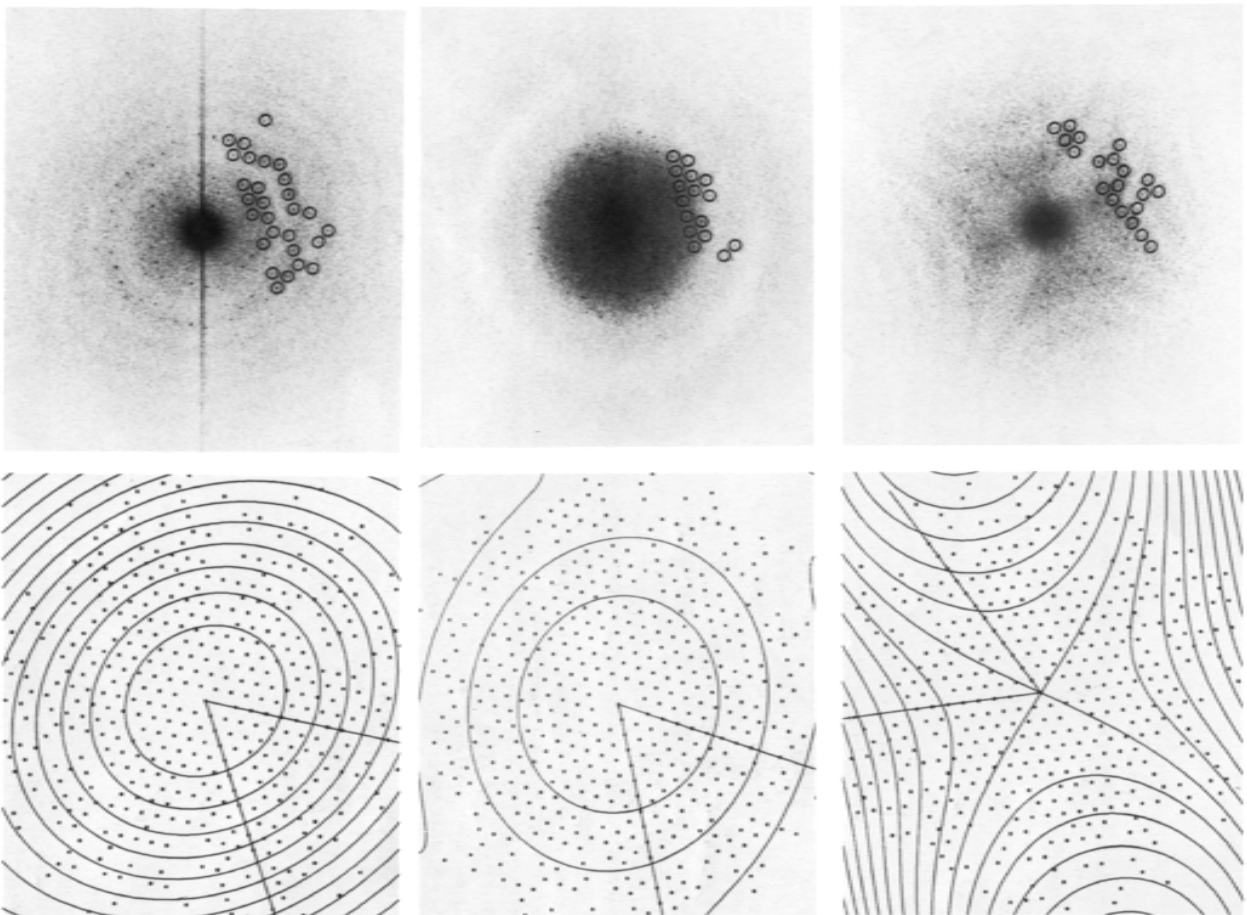


Fig. 2. Optical diffraction patterns and computer generated plots from three typical images. Some of the higher resolution spots in the optical diffraction patterns have been circled for clarity. In the computer plots, the zeroes in the contrast transfer functions are indicated by lines and all spots detected above the noise level are plotted. The top image is almost exactly in focus but contains about 4500 Å of astigmatism. The middle image is underfocused by 2000 Å with very little astigmatism. The bottom image is more highly defocused (1300 Å) with slightly more astigmatism. In terms of information content, the three images are equally good.



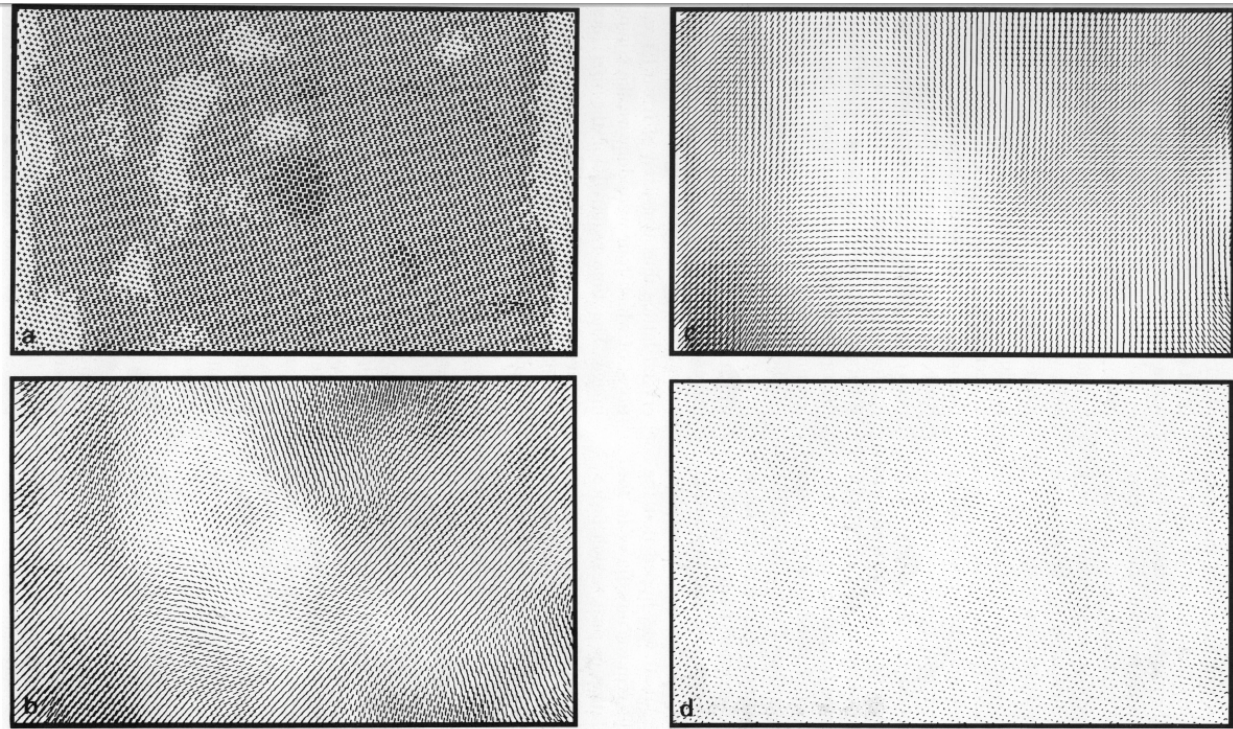
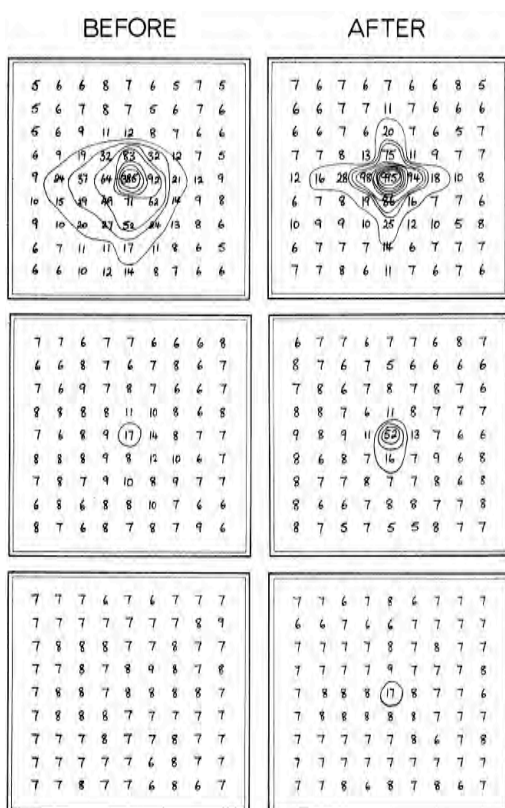


Fig. 3. The map of the peaks in the cross-correlation function: (a) Heights of cross-correlation peaks. Darker symbols indicate higher correlation. In the centre the correlation is 1.0 since it is from this area that the reference area was chosen. Other symbols ( $\times$  and  $+$ ) indicate correlations of above 0.5 and above 0.3 respectively. (b) Vector displacements of centres of gravity of correlation peaks from the positions predicted based on a perfect lattice. Vectors are plotted as  $20\times$  bigger than the size of the actual displacement. In the centre, the displacement is zero since this is the reference area. (c) Plot of the actual distortion correction that is used to reinterpolate the raw image. (d) Plot of the vector displacement, carried out in precisely the same way as in (b), except that the starting image was the image produced by application of the corrections shown in (c). The resulting plot shows no residual deviations above 1 Å. The average remaining error is substantially less than 0.5 Å.

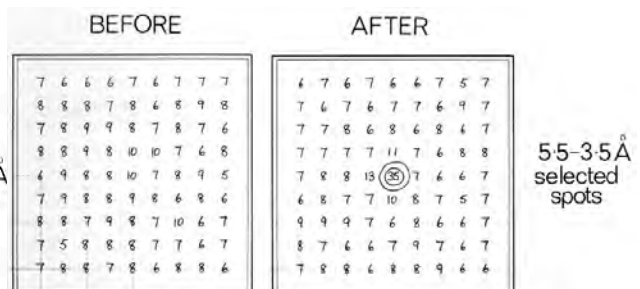


$\infty-7.0\text{Å}$

7.0-5.5Å

5.5-3.5Å

### Improvement by unbending



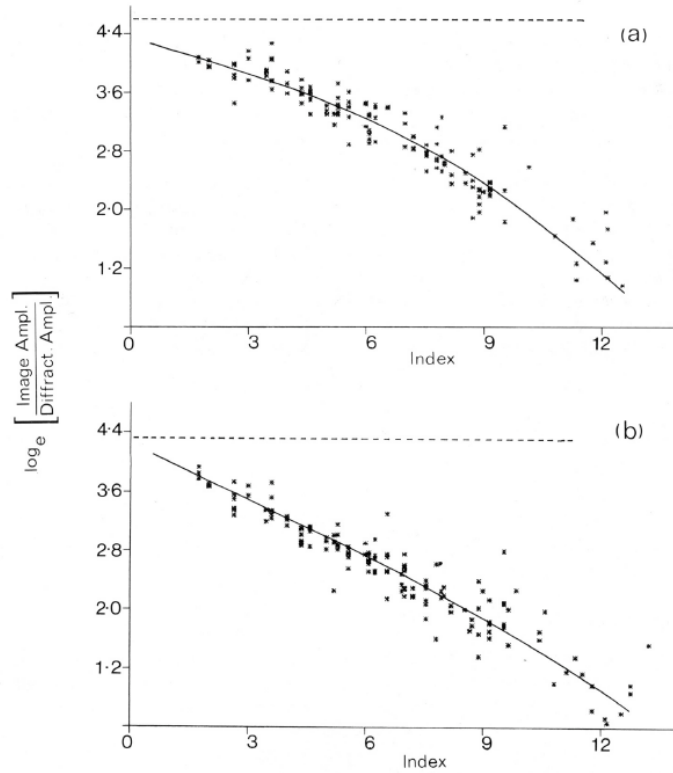


Fig. 5. Plots from two typical images comparing the ratio of image amplitude to electron diffraction pattern amplitude as a function of resolution. In both cases, the loss of contrast is approximately a factor of 30 between low resolution and 4 Å resolution. Along the abscissa, an index of 12 corresponds to 4.5 Å resolution. In (a), the relationship is clearly non-linear, whereas in (b) the points are more nearly on a straight line. The dashed line at the top of each plot indicates the theoretical level of contrast which would have occurred if the image were perfect.

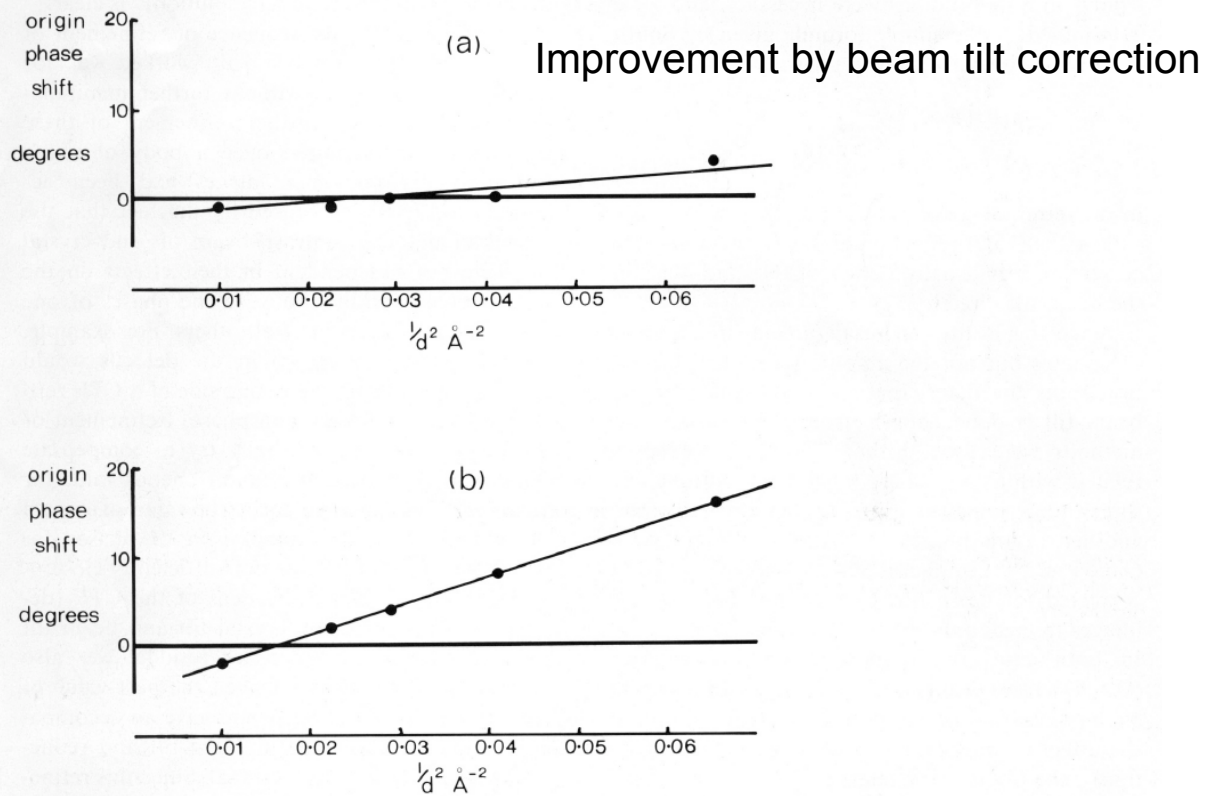


Fig. 6. Dependence of the position of the phase origin determined as a function of resolution in directions (a) perpendicular to  $b^*$  and (b) perpendicular to  $a^*$ . The determination of phase origin was made by comparing the phases of spots which are related by the crystallographic three-fold axis with one another. As demonstrated by the line drawn through the points, the position of the phase origin varies linearly with  $1/d^2$ , where  $d$  is the spacing of the Fourier component. The origin phase shift is plotted in terms of the effect on the phase of the (1,0) or (0,1) reflection. Thus a  $10^\circ$  phase shift corresponds to an origin shift of 1.5 Å for purple membrane.

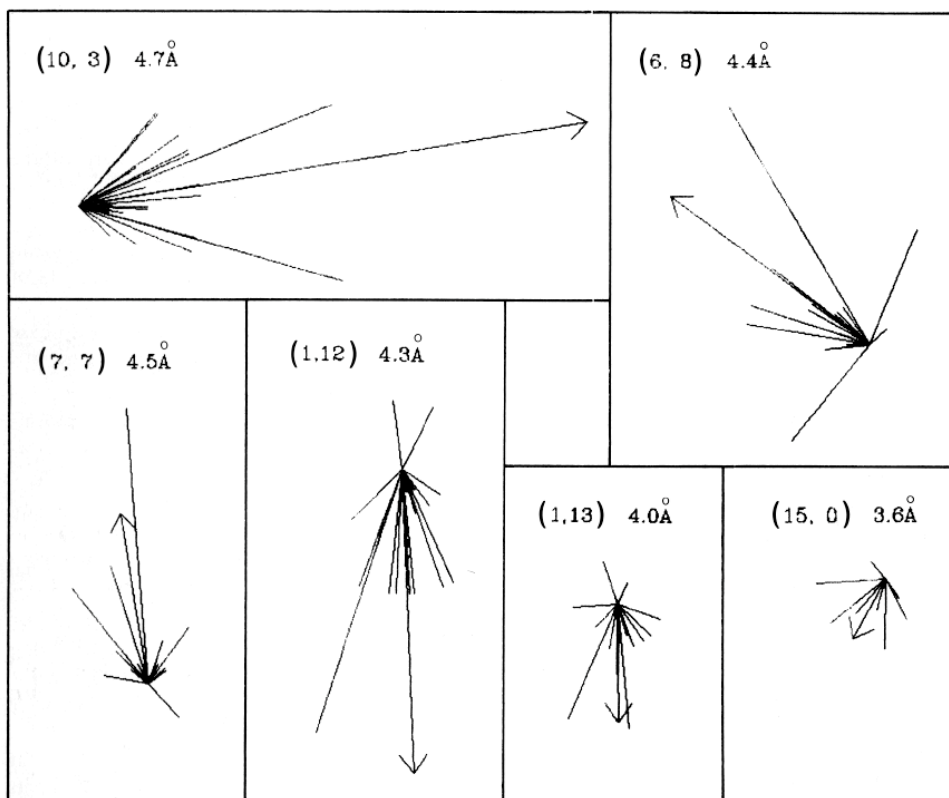
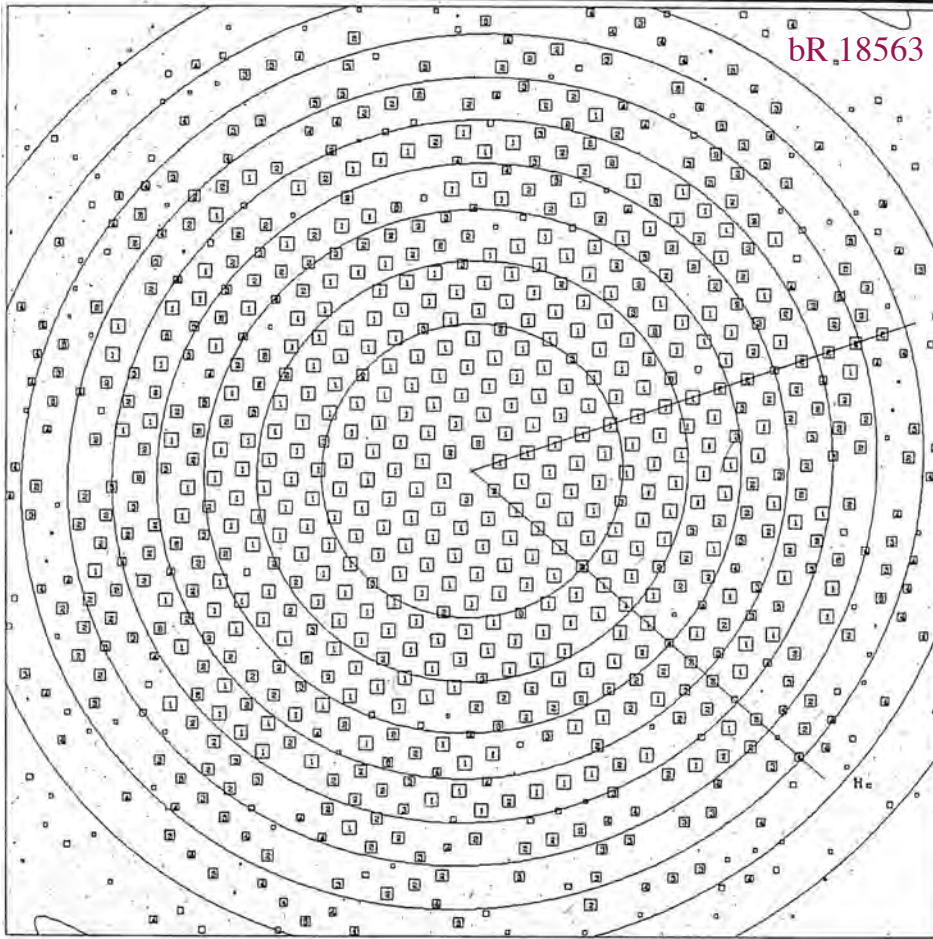


Fig. 7. Graphical comparison of all phases determined for six spots with resolution beyond 4.7 Å. Phases are plotted as vectors on a polar diagram with the length of each vector being proportional to  $1/IQ^2$ . Thus the strongest spots show up as longer vectors. The result of the summation of all the vectors is also shown as a vector, but this is plotted at 1/4 of its true length. The direction of this vector is our best estimate of the phase of the Fourier component in the structure, and its length can be used to provide an estimate of the error.

Table 2  
Summary of data for each image

Image	No. of phases <sup>a)</sup>	Overall phase residual	Defocus (Å)	Astig. (Å)	Beam tilt (mrad)
7415	217	26.2	242	4485	1.63
35978	256	27.8	1922	205	1.59
14980	200	25.3	2038	625	3.32
14981	178	28.1	3753	475	2.26
14983	205	28.6	3770	420	2.41
14984	240	21.7	3323	894	2.61
14988	249	22.0	5028	855	2.44
15004	239	34.7	-595	963	1.41
15006	255	23.4	1357	975	1.73
15025	231	25.1	1088	1025	2.62
15026	218	24.9	1125	850	2.28
14450	119 (5.5Å)	29.3	1730	260	2.88
14456	132 (5.5Å)	30.8	-1275	250	2.40

<sup>a)</sup> Resolution is 3.5 Å in all cases except where otherwise stated.



FILM NUMBER 18563 Date of last edit: 15.4.88

MICROSCOPE SULEIKA  
DATE MEASURED 12.5.87 (TO 3.5A)

AX	AY	BX	BY	ISIZE	ISIZE	DSTEP	XMAG	CS	KV
106.667	-92.150	132.933	46.013	4320	4320	12.5	71043	1.35	100
ASTAR		BSTAR	GAMMASTAR	TILTAXIS	TILTANGLE	(EMTILT)			
140.960		140.671	59.916	(4.37)					

REVHK 0 ROT180 1 (SGNXCH) 0 CELL 62.45

DISTORTION CORRECTION: Date DFMID1 DFMID2 ANGAST TILTAXIS TILTANGL

1) 13.05.87 - - - - -

STATISTICS: AFTER RUN (sometimes after further refinement of parameters)

ORIGTILT: TAXA TANGL ORIGH ORIGK TILTH TILTK RES PHSRESID #PHASES DATASET

1+R) 49.001 0.243 -108.41 -118.70 0.38 -0.24 3.5 29.57 345 MERGOUT.APH

TREFINE: TEMP FACTORS RFAC #AMPS #IQ<8 RES PHSRESID #PHASES DATASET

	a	b	c	RFAC	#AMPS	#IQ<8	RES	PHSRESID	#PHASES	DATASET
1+R)	0.02037	0.01902	0.02058	15.69	126	125	6.5	18.28	126	CMBND
1+R)	0.01686	0.01551	0.01659	19.78	428	344	3.5	43.45	428	CMBND

WMBOX: 100/7 7/5.5 5.5/3.5 All

1+R) DFMID1	DFMID2	ANG	H				
2981	3152	29.03	#1-4	2888	273	93	293
TILTAXIS	TILTANGL	#1-7	104	61	180	345	
-89.825	-0.243	#poss	105	69	254	428	

1+W) DFMID1	DFMID2	ANG	H				
2981	3152	29.03	#1-4	4085	307	102	2586
TILTAXIS	TILTANGL	#1-7	104	59	142	305	
-89.825	-0.243	#poss	104	65	189	358	
			105	69	253	427	

%refamp 100.0 40.8 15.5

CORRELATION COEFFS (IMAGE vs DIFFRACTION)

1+R)	Rfactor between scaled reference amps and image amps 0.1389		
INP-7.0A	par1	45deg	perp
	0.992	0.992	0.995
	35	35	35
7.0A-5.5A	0.989	0.996	0.991
	23	23	23
5.5A-3.5A	0.955	0.933	0.969
	84	85	84

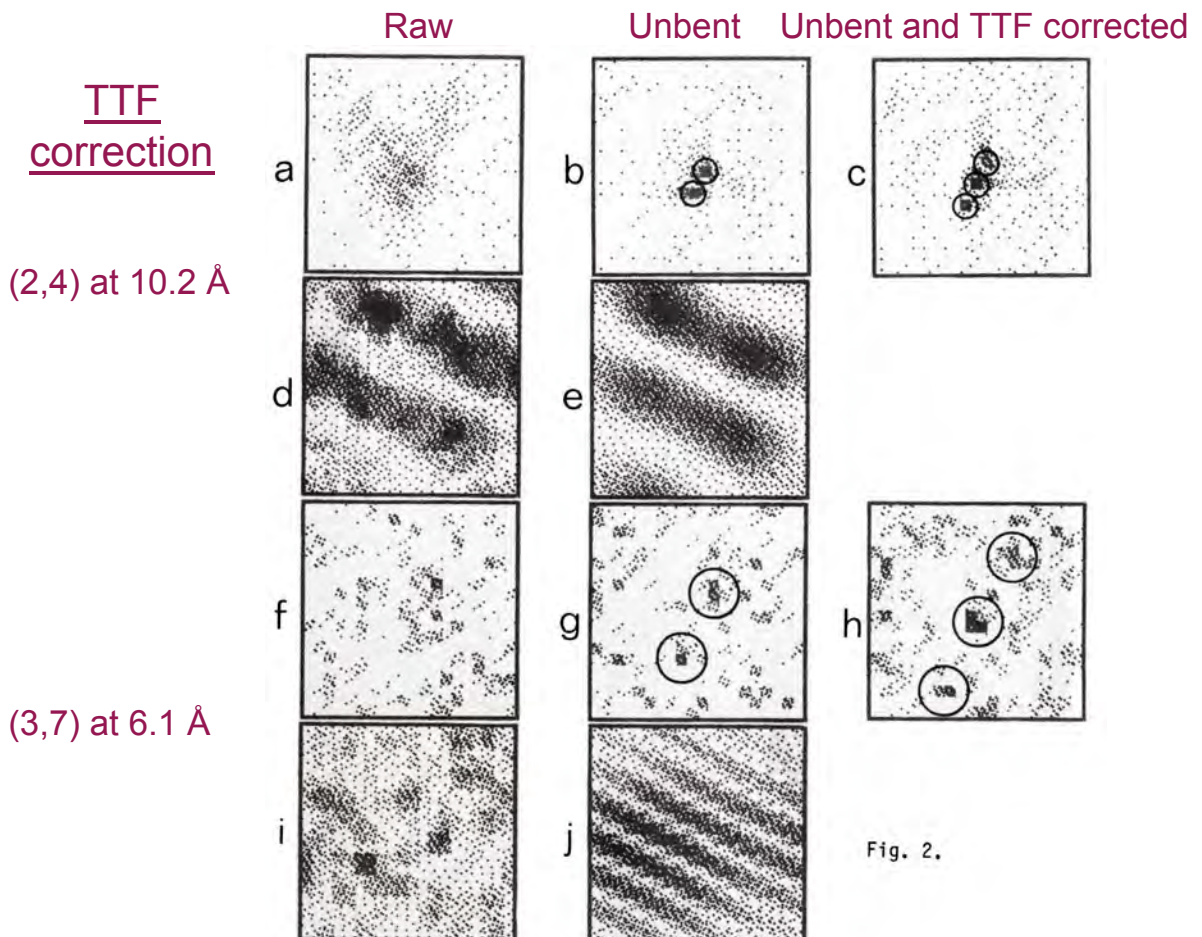
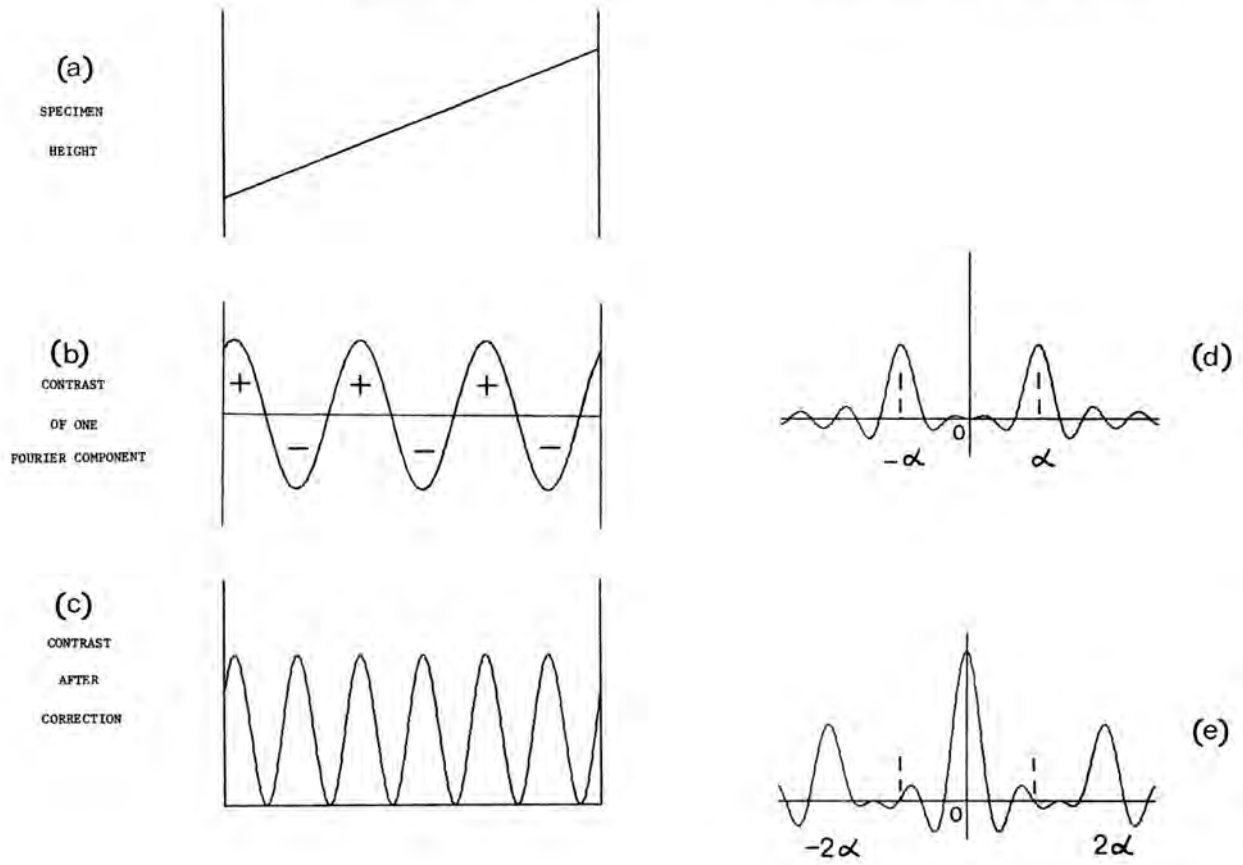
COMMENTS, CURRENT STATUS ETC.

Processing complete. Best image so far. Continued to 2.8A.

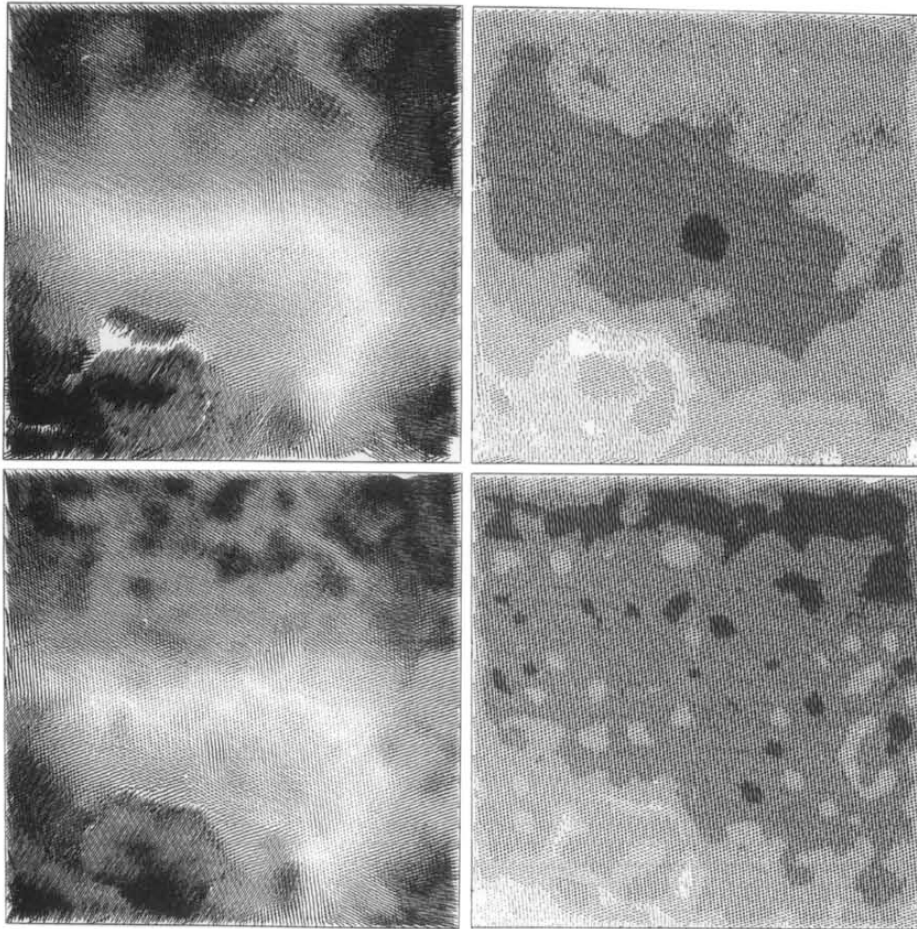


IMAGES

FOURIER TRANSFORMS



51056



Paralel

Perpendicular

6 5 5 7 6 10 8 11 8 7 7 6 6 7 8	6 6 5 10 5 7 7 6 8 6 7 9 7 11 8	7 Å
7 8 7 7 8 11 12 35 10 9 6 5 8 7 6	7 9 8 7 7 8 13 17 9 7 8 6 7 7 5	
5 7 10 8 8 10 7 19 11 10 7 7 6 6 7	7 6 8 6 7 8 7 12 6 7 6 8 6 7 6	
8 5 7 8 6 8 8 17 11 6 6 9 7 7 6	6 6 7 9 8 7 7 12 8 6 9 7 6 6 7	5.5 Å
7 6 11 32 9 12 10 25 6 7 9 6 8 6 7	7 6 9 10 8 9 11 16 7 6 7 8 7 8 7	
10 11 15 34 76 40 13 88 12 9 11 7 7 6	7 6 7 14 13 15 22 28 12 8 8 8 7 7 6	
7 10 12 21 46 224 125 231 53 7 14 11 7 10 7	8 8 9 10 11 31 119 140 21 13 13 12 6 9 9	
9 11 20 23 43 62 332 302 51 41 27 19 14 11	16 12 11 25 46 64 282 308 268 59 44 20 10 9 9	
7 9 8 7 14 18 23 219 168 255 47 12 10 7 5	8 7 9 7 11 9 21 60 30 22 13 7 10 7 6	3.5 Å
8 8 8 8 9 9 11 45 17 21 47 51 16 8 7	7 6 6 7 9 9 13 22 10 10 15 11 8 8 8	
6 8 8 7 7 9 9 24 6 15 11 10 11 8 5	5 7 5 7 7 7 10 12 9 6 9 7 7 7 6	
8 6 6 6 9 8 10 27 7 13 10 8 6 8 9	7 8 8 7 6 7 14 14 7 8 6 5 6 7 7	
5 6 7 6 7 13 11 29 11 11 8 7 7 5 6	7 7 6 5 6 8 9 13 9 7 6 6 7 6 7	
8 6 7 7 8 6 11 45 14 10 8 7 6 11 7	6 6 5 4 10 6 11 20 12 8 8 6 6 7 8	
6 6 7 5 6 7 8 14 7 10 12 5 5 7 7	7 7 8 6 7 7 8 13 6 7 7 7 6 6 5	
7 8 8 5 6 8 6 8 8 5 7 7 11 7 8	6 8 7 6 8 7 7 8 6 7 6 7 9 7 6	7 Å
8 8 6 8 6 4 6 8 6 6 5 6 7 8 6	6 5 7 7 6 4 8 8 7 8 5 6 7 8 5	
8 6 5 8 7 8 8 7 7 6 6 9 6 9	7 6 5 9 8 6 9 7 5 7 6 6 6 8 6	
15 13 9 9 6 10 7 9 11 8 8 5 11 6 7	11 8 5 5 7 7 6 8 7 6 6 6 11 6 7	
17 41 37 11 8 6 5 8 6 3 5 5 6 9 6	8 11 6 6 7 8 11 8 6 8 7 6 6 8 8	
8 6 19 9 7 8 7 10 8 10 7 8 7 6 6	8 6 8 7 8 6 8 7 5 7 5 8 5 8 7	5.5 Å
5 7 7 8 9 10 8 41 18 8 10 8 5 8 5	7 6 6 8 8 7 8 7 6 9 8 7 5 7 6	
7 9 9 10 10 12 67 227 59 10 9 7 10 6 8	8 7 7 7 6 7 15 35 5 6 5 5 8 6 7	
7 8 6 9 7 11 12 46 15 9 9 7 10 8 6	7 6 9 5 8 6 6 6 6 8 8 9 8 7 10	
8 7 5 10 10 5 7 11 3 7 7 9 17 11 8	8 5 7 9 5 7 6 9 9 6 8 6 9 8 6	
7 5 6 6 5 6 6 13 10 9 6 6 19 31 16	7 6 7 6 6 8 9 7 6 7 6 7 10 9 6	7 Å
5 8 9 6 7 10 8 9 7 10 5 11 9 23 17	8 8 8 7 8 9 7 9 7 9 8 7 7 8 7	
6 6 9 7 7 6 7 9 5 6 6 8 7 9 9	5 10 7 7 7 7 8 7 7 7 7 10 9 7 9	
9 7 8 7 7 11 7 10 6 6 8 5 8 7 5	10 6 7 7 8 8 6 7 5 9 7 6 7 5 9	
7 7 8 5 9 6 8 10 3 9 8 6 7 8 5	7 8 9 11 11 8 7 8 7 5 8 8 6 6 6	
7 8 6 7 6 9 7 7 6 6 7 7 5 8 6	7 6 6 6 7 8 7 7 8 8 6 7 7 7 8	7 Å
6 8 7 7 8 9 6 8 7 7 7 7 6 7 6	9 8 8 7 6 7 7 7 7 8 7 6 6 7 7	
8 7 7 8 6 6 8 7 5 7 7 6 8 8 7	7 6 6 7 7 7 6 6 7 7 6 7 8 7 6	
8 7 8 7 8 8 7 6 8 8 6 6 5 8 7	7 8 9 6 7 7 7 7 6 7 8 7 7 7 6	
7 8 8 8 7 6 8 8 7 7 7 6 6 7 7	8 8 8 8 7 7 7 7 6 7 7 7 8 7 7	
7 7 6 8 7 7 6 8 7 7 7 6 7 7 7	6 7 8 7 7 6 7 6 6 7 7 6 6 7 7	3.5 Å
8 8 7 6 6 7 11 14 8 7 7 7 7 8 7	7 8 7 6 7 7 8 11 9 6 7 6 6 7 6	
7 7 9 7 8 7 10 47 17 8 7 7 7 8 6	7 9 7 7 7 7 8 16 10 8 8 7 7 9 7	
6 6 7 7 7 8 7 9 7 7 8 6 7 6 6	8 7 8 7 6 5 7 8 10 7 7 9 7 8 7	
8 6 6 7 8 7 7 8 8 6 6 9 7 7 7	7 7 7 6 6 7 7 7 8 8 8 8 7 6 7	
7 7 7 7 6 7 8 7 7 7 6 7 9 7	8 8 7 7 6 7 8 6 6 7 7 7 7 7 6	7 Å
7 6 8 7 6 9 6 7 7 6 7 7 7 7 7	7 7 7 7 8 7 6 7 7 7 8 8 7 8 7 7	
8 8 7 7 6 7 7 8 8 7 6 7 7 6 6	8 7 7 6 7 7 7 7 7 6 8 6 7 8 7	
6 5 6 6 8 8 8 8 7 7 8 8 6 7 7	7 6 7 7 6 7 7 8 6 7 7 6 6 7 7	
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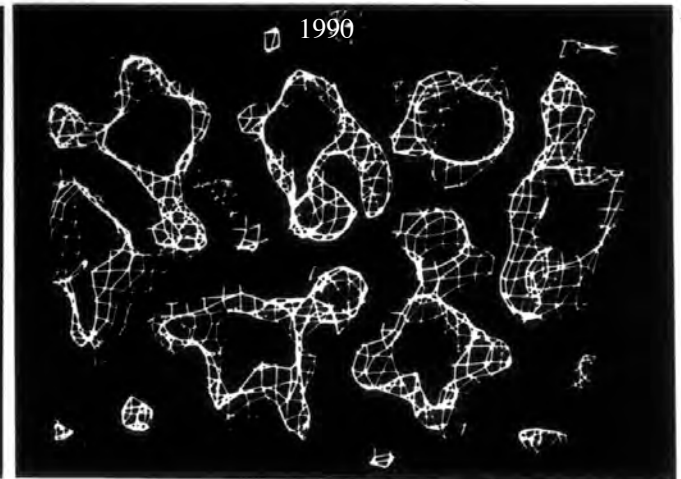
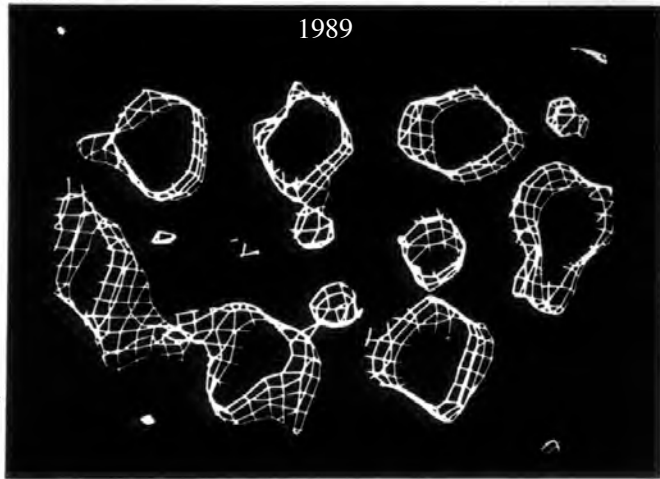
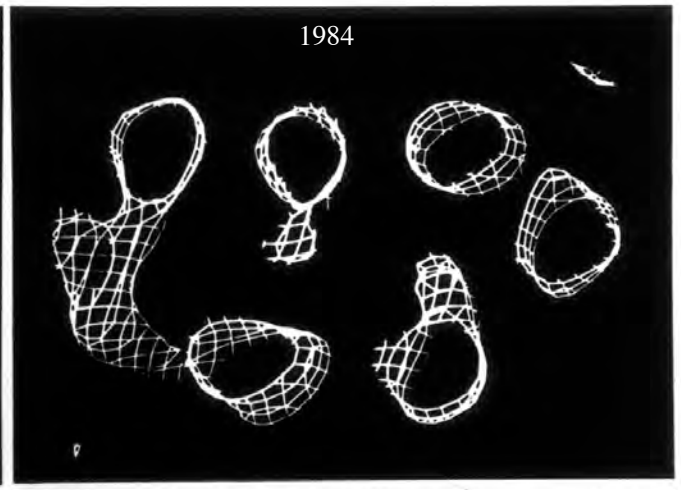
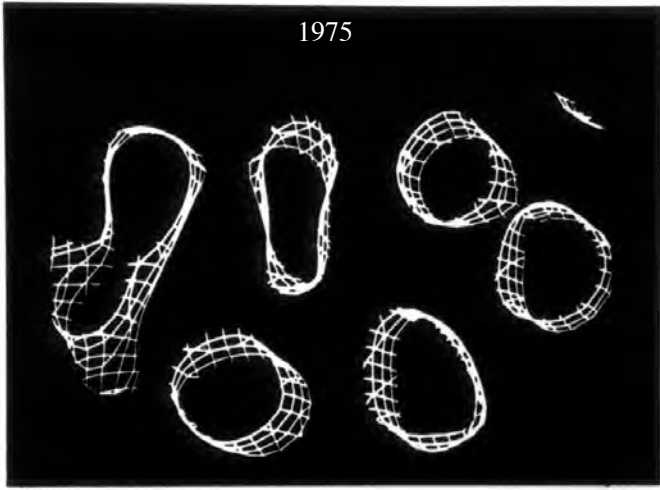
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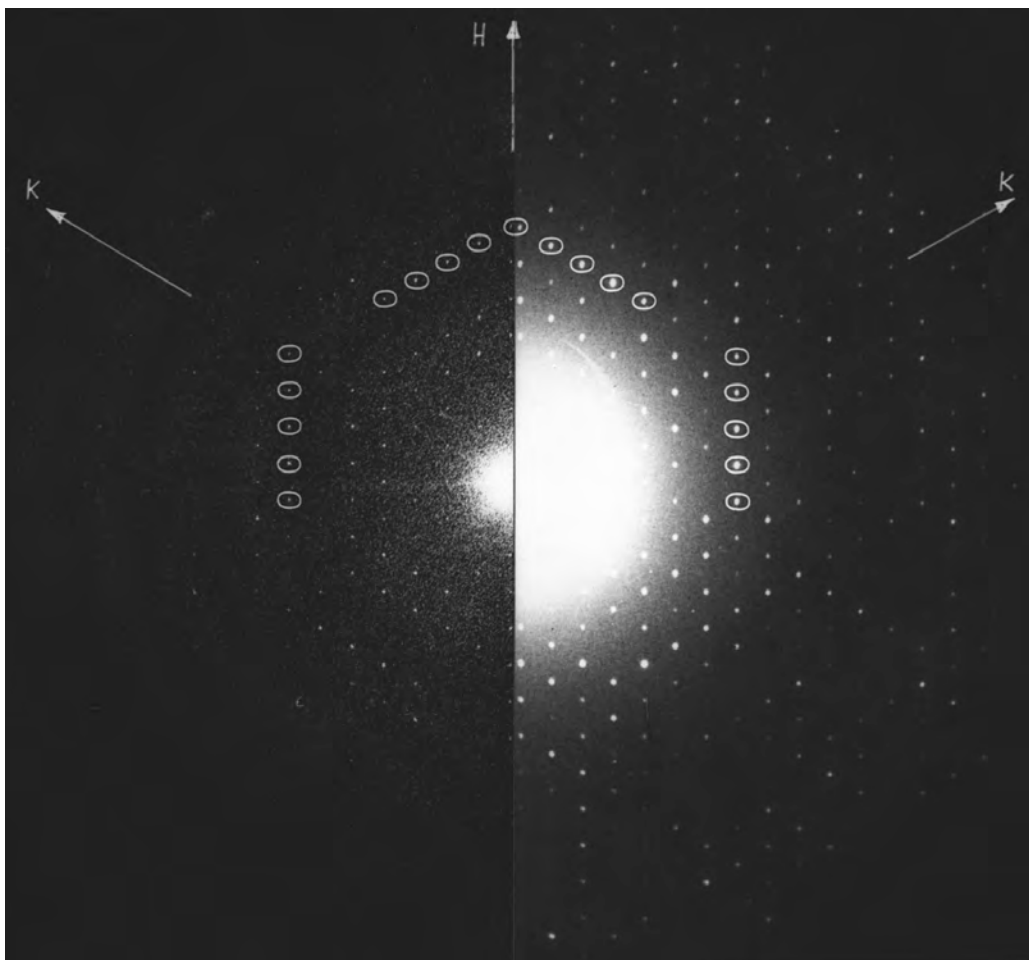
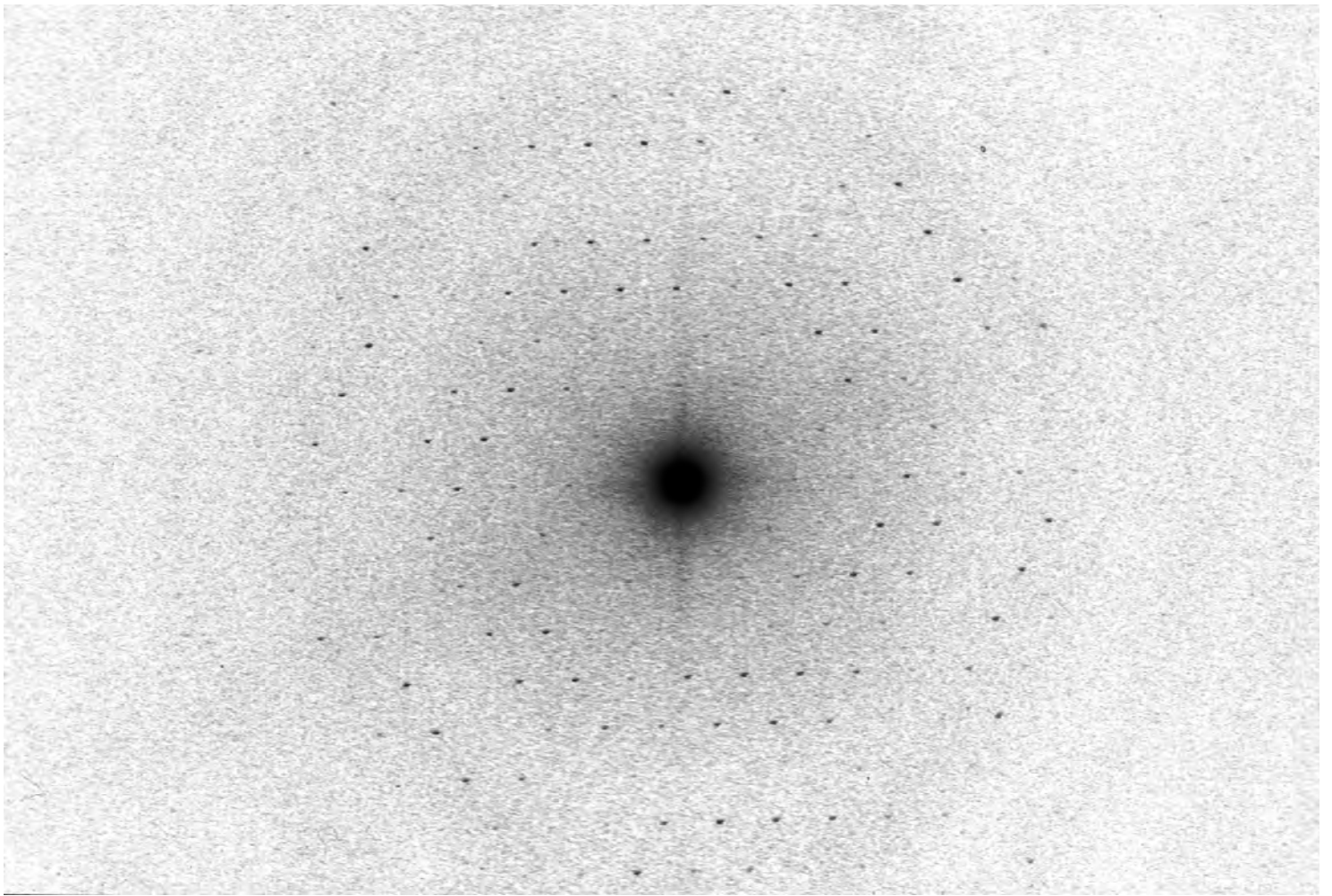
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  ASTAR  BSTAR  GAMMASTAR  TILTAXIS  TILTANGLE  (EMTILT)
174.621 154.412 73.184 61.323 -41.246 ; TAXA = -43.239
REVHR 0 ROT180 0 (SGNKCH) 0 CELL 62.45
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2C) 11.5.89 3028 2873 32.64 61.323 -41.246
3C) 15.5.89 3028 2951 28.08 61.323 -41.246
3K) 17.5.89 3028 2951 28.08 61.323 -41.246
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STATISTICS: AFTER RUN (sometimes after further refinement of parameters)
ORIGTILT: TAXA TANGL ORIGH ORIGR TILTH TILTK RES PHSRESID #PHASES DATASE#
1+R) -43.18 -42.45 -104.8 -172.0 - - 6.5 50.64 85 CMBND
2+R) -43.22 -41.21 -106.3 -172.1 - - 6.5 52.93 91 CMBND
3+R) -42.93 -40.54 -108.9 -169.9 - - 6.5 51.05 90 CMBND
3K+R) -42.75 -40.75 -107.5 -170.7 - - 6.5 50.82 90 CMBND
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TTREFINE: TEMP FACTORS RFAC #AMPS #IQ<8 RES PHSRESID #PHASES DATASE#
          a b c
2+R) 0.02909 0.01749 0.00454 0.17 95 90 6.5 54.00 95 CMBND
3+R) 0.02877 0.01687 0.00371 0.17 95 89 6.5 54.47 95 CMBND
3K+R) 0.02687 0.01672 0.00516 0.17 95 91 6.5 54.90 95 CMBND
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3+R) 0.02405 0.01659 0.00520 0.27 321 208 3.5 62.94 133 CMBND
3K+R) 0.02281 0.01632 0.00511 0.27 321 214 3.5 62.29 133 CMBND
-----
TTBOX:
          100/7 7/5.5 5.5/3.5 100/7 7/5.5 5.5/3.5 All
          parallel to tilt perp
1+R) DFMID1 DFMID2 ANG H 855 69 25 702 23 8 43%
      3028 2873 32.6 #1-4 38 16 25 32 4 6 12%
      TILTAXIS TILTANGL #1-7 40 23 45 37 12 24 18%
      61.3 -41.2 #poss 40 26 97 38 26 97 32%
-----
2+R) DFMID1 DFMID2 ANG H 1919 193 41 860 27 13 76%
      3028 2951 28.08 #1-4 40 23 33 37 9 14 15%
      TILTAXIS TILTANGL #1-7 40 23 52 38 17 42 21%
-----
3+R) DFMID1 DFMID2 ANG H 2091 222 43 905 26 13 81%
      3027 2970 18.72 #1-4 40 23 32 36 11 18 16%
      TILTAXIS TILTANGL #1-7 40 23 52 38 15 41 20%
      % refamp 100.0 44.9 16.4 118.9 25.3 6.2
3K+R) DFMID1 DFMID2 ANG H 2065 227 47 908 35 16 80%
      3032 2987 19.73 #1-4 40 23 38 36 12 17 16%
      TILTAXIS TILTANGL #1-7 40 23 55 38 17 42 21%
      % refamp 100.0 45.8 17.4 120.1 31.4 7.8
-----
CORRELATION COEFFS (IMAGE vs DIFFRACTION)
3+R) par1 45deg perp 3K+R) par1 45deg perp Rfactor between
INF-7.0A 0.981 0.962 0.909 0.978 0.961 0.906 scaled reference
          26 26 25 26 26 25 amps and image
7.0A-5.5A 0.951 0.954 0.166 0.959 0.948 0.159 amps : 0.22
          18 17 17 18 17 17
5.5A-3.5A 0.919 0.660 0.474 0.934 0.718 0.473
          64 65 63 64 64 63
-----
COMMENTS, CURRENT STATUS ETC.
----- This is the best tilted image so far. Best results from 3rd pass
with 25,52 knots.

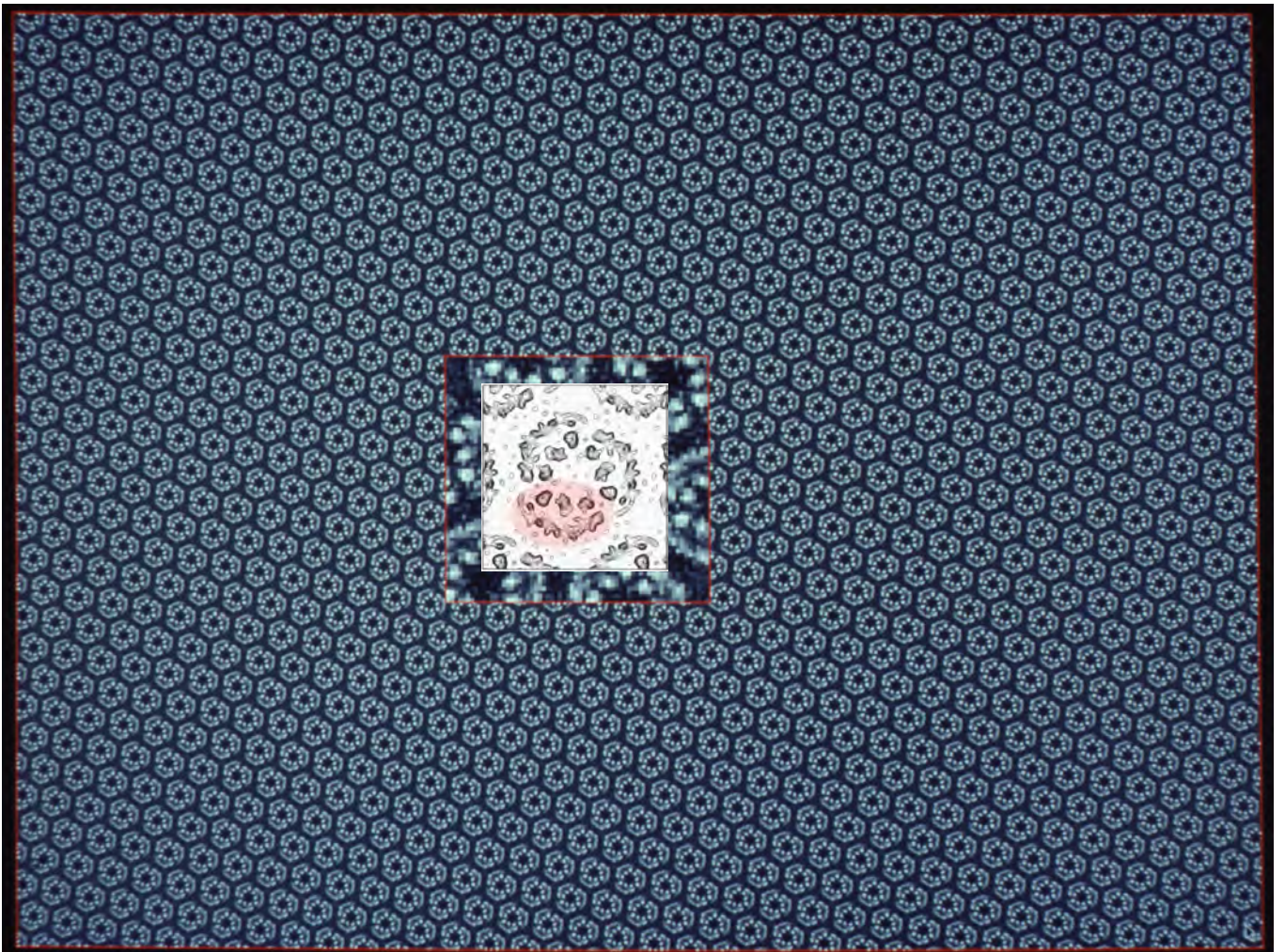
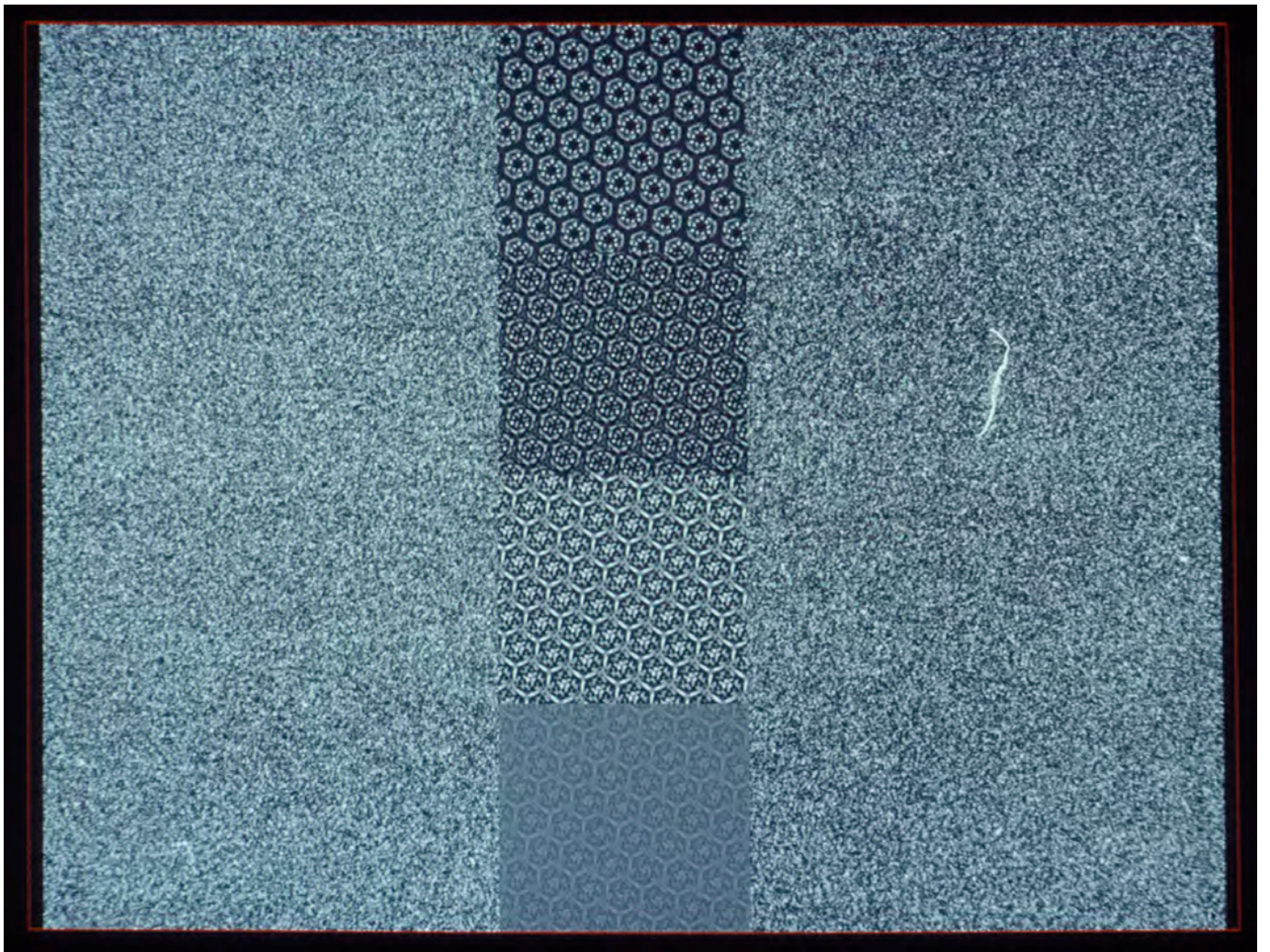
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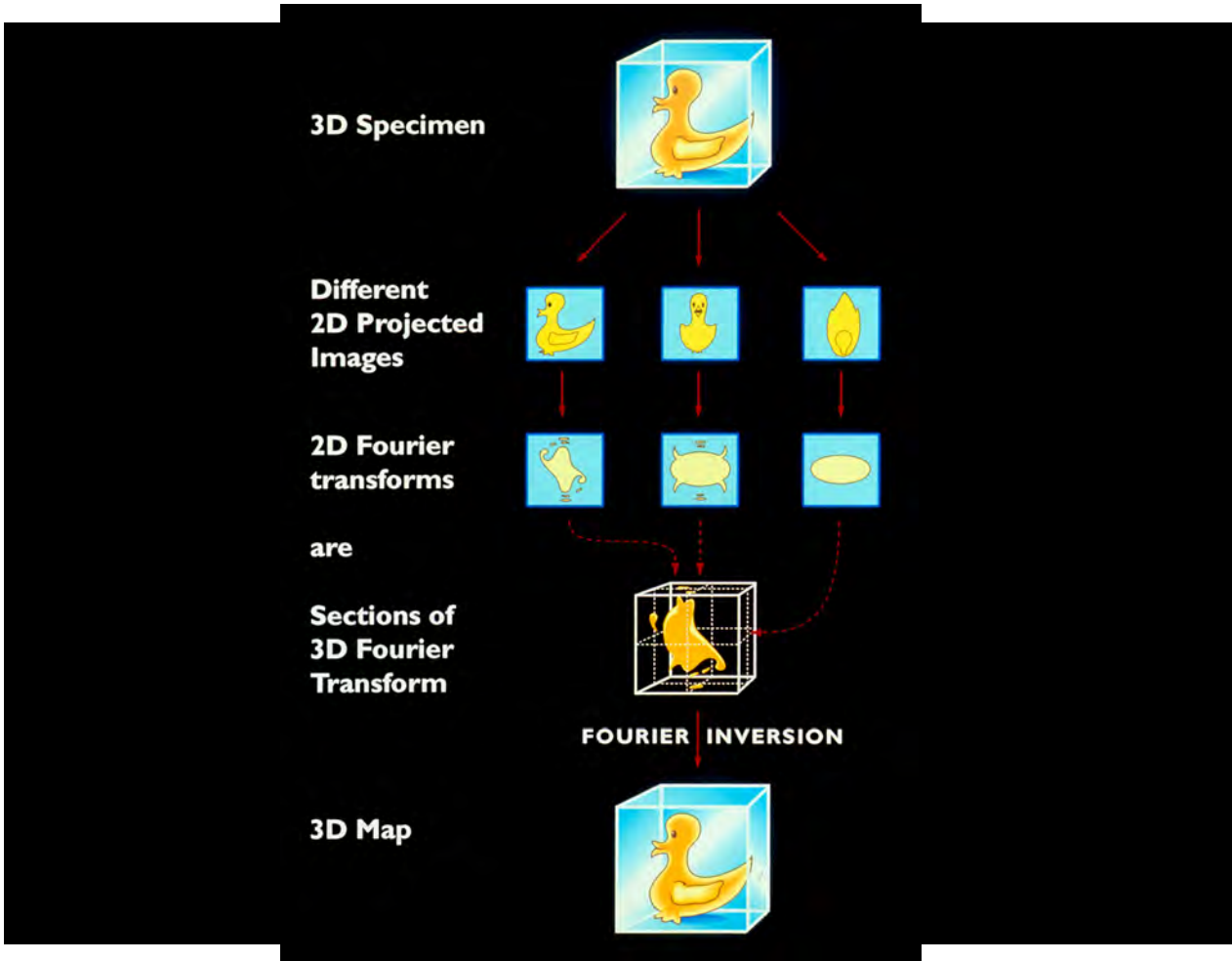
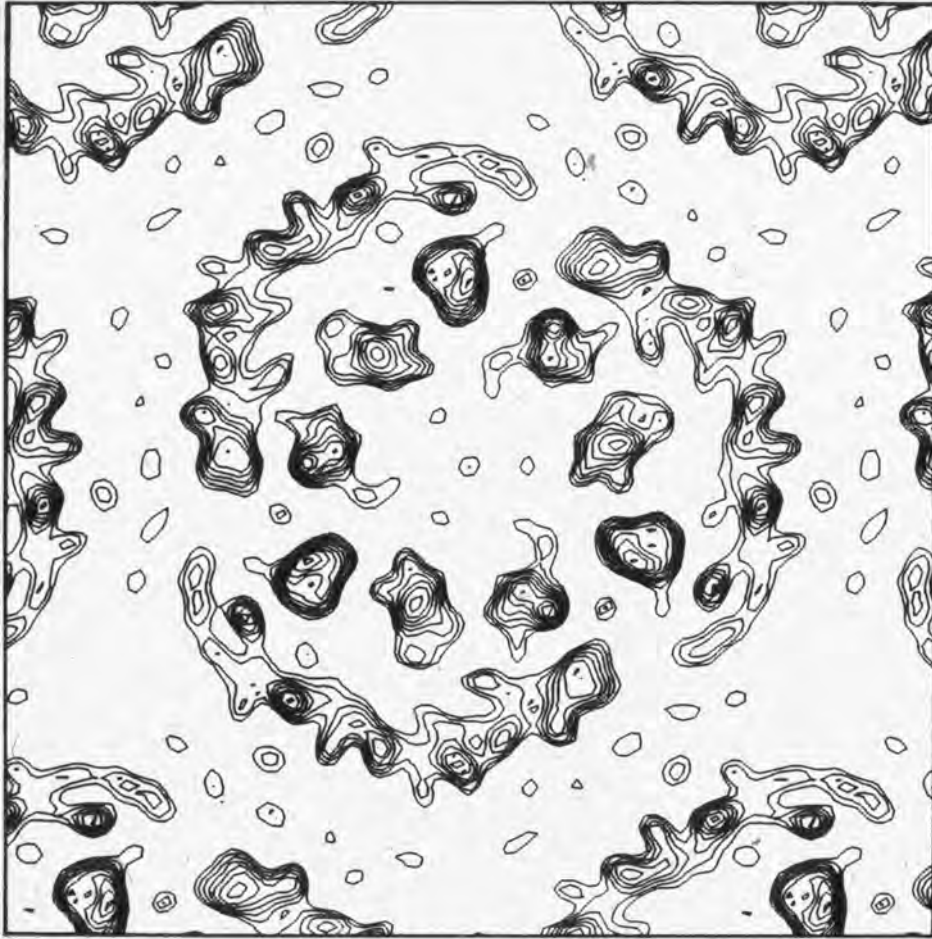
## Bacteriorhodopsin - from 7 Å to 3.5 Å

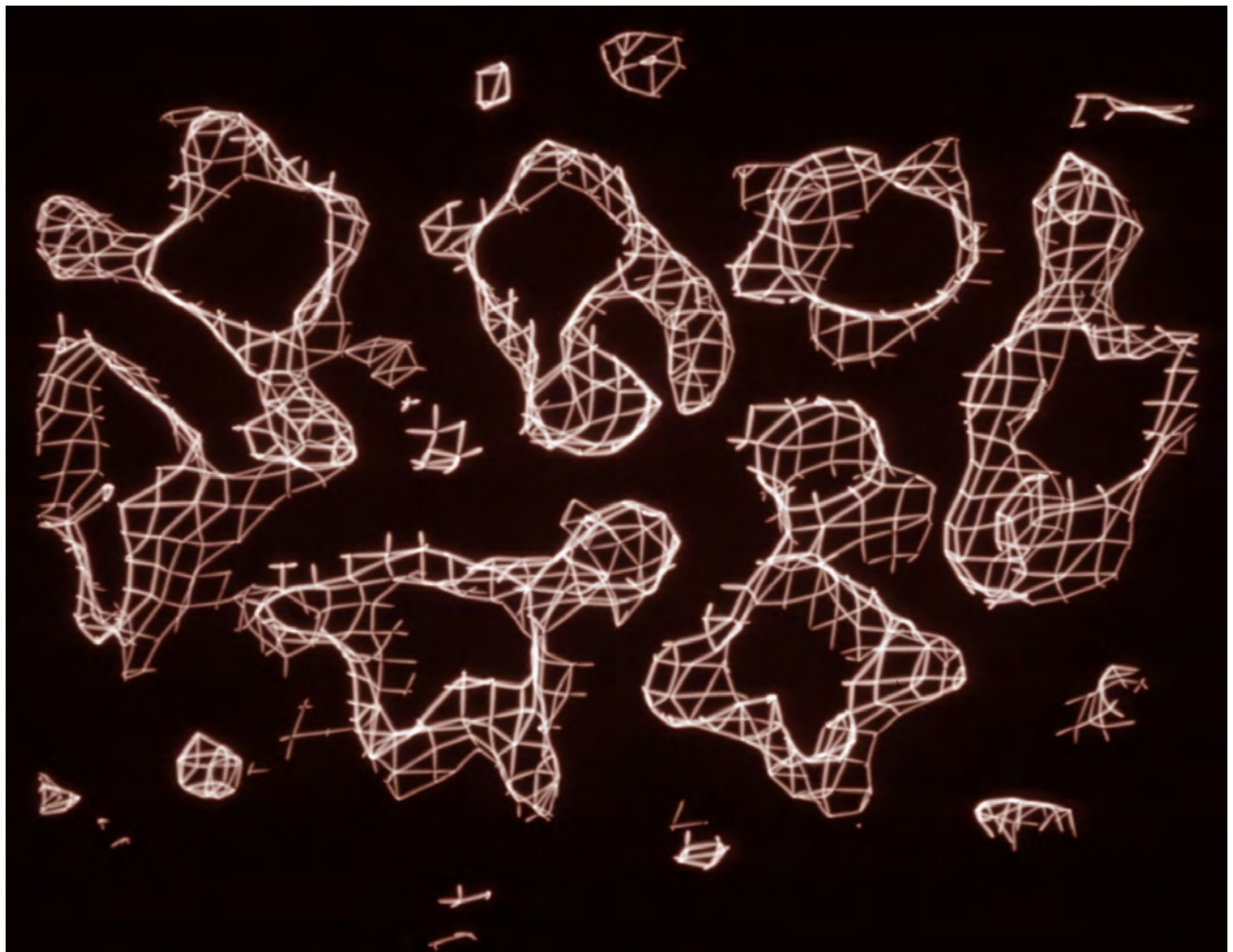
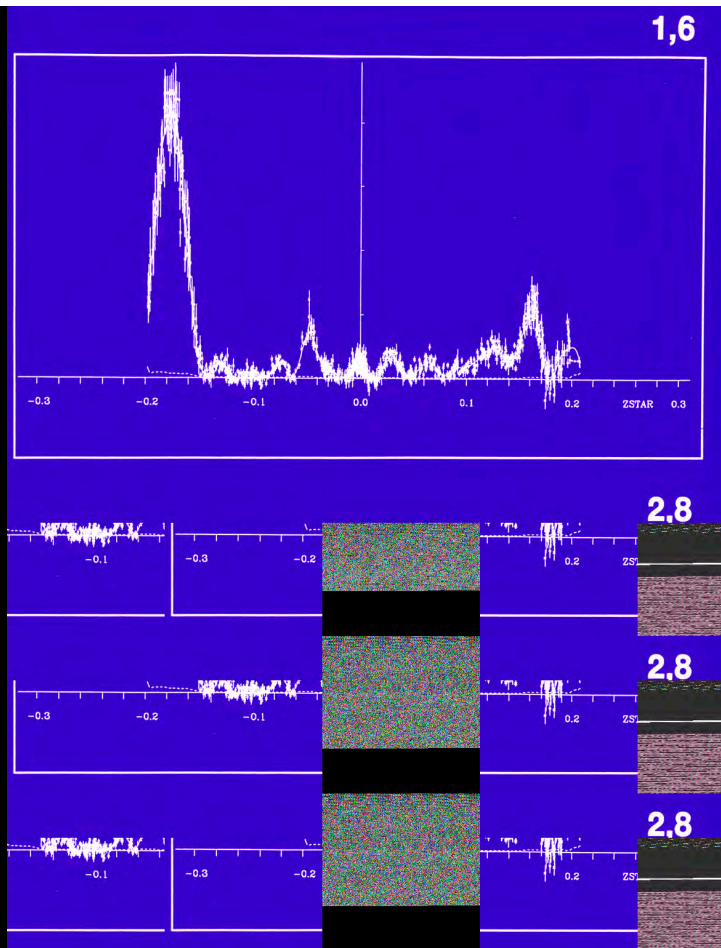
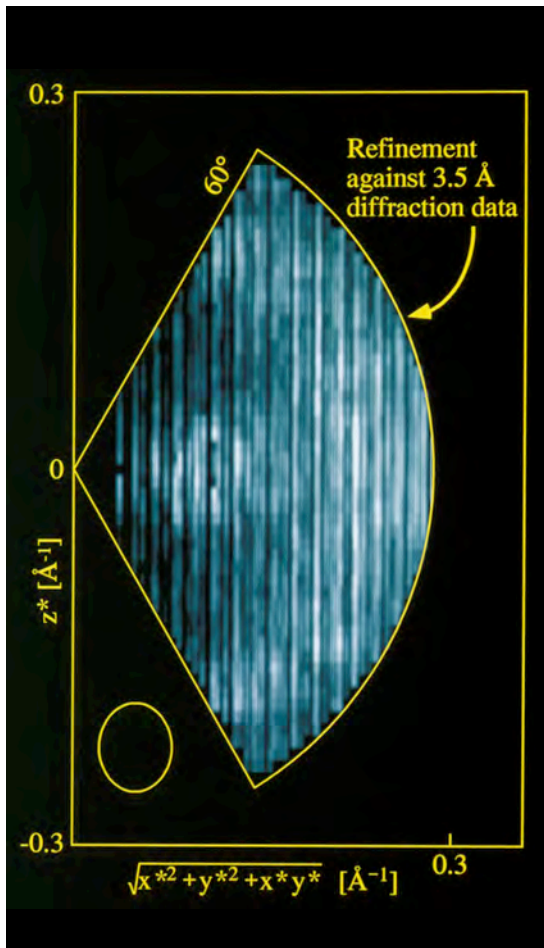
**Bigger crystals by fusion**  
**Cold stages – liquid nitrogen and helium**  
**Unbending**  
**Beam tilt**  
**Tilt transfer function**  
**(Field emission guns)**





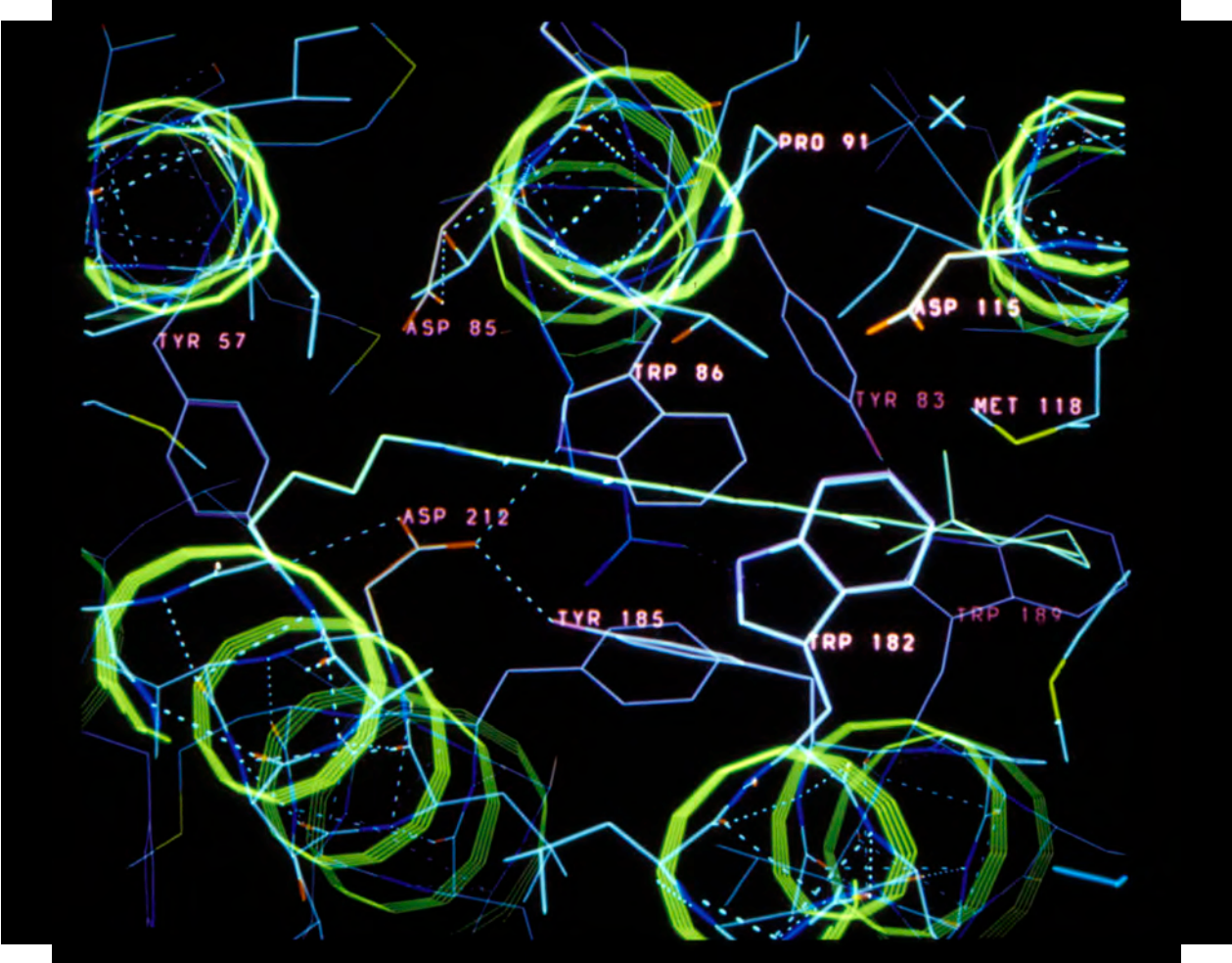
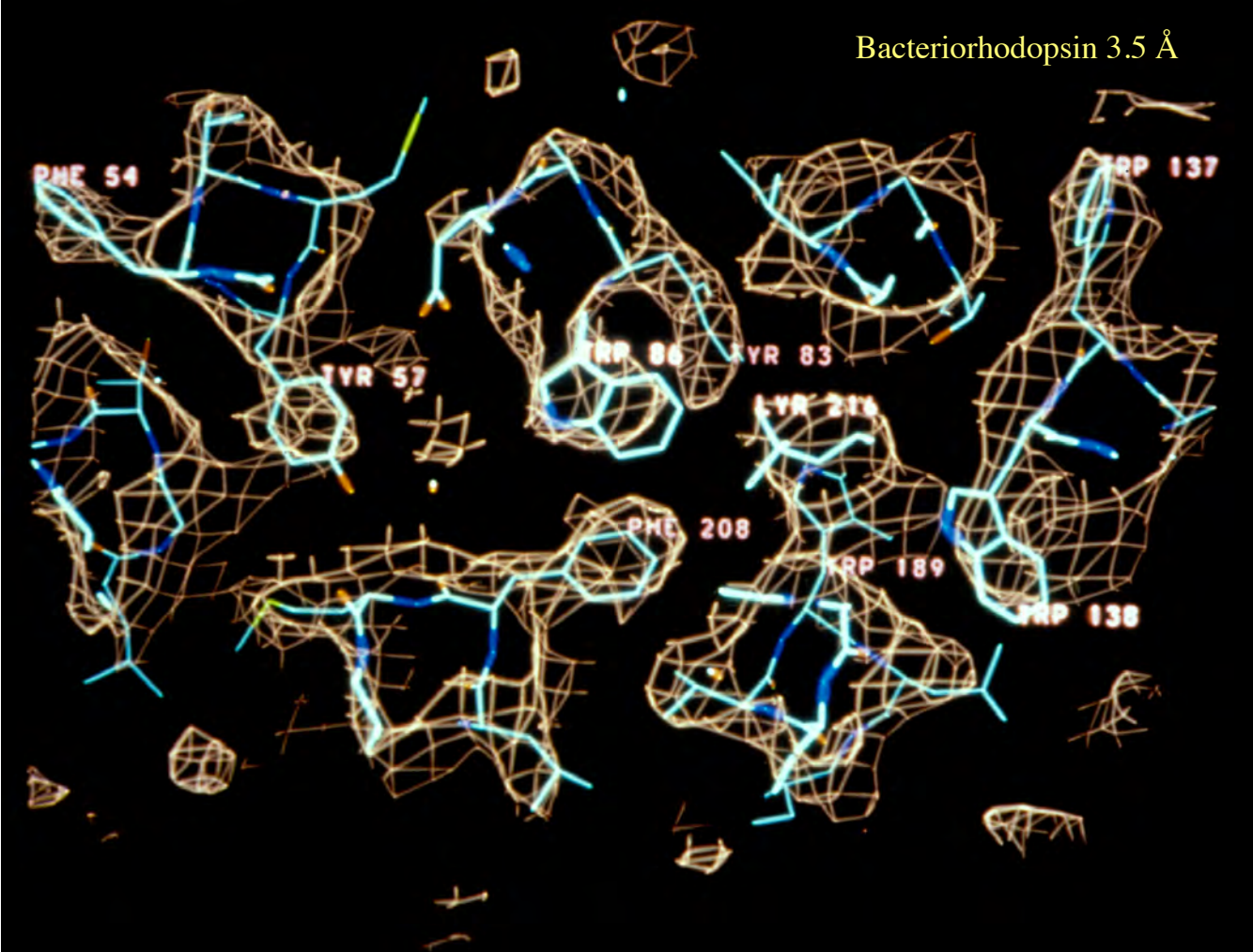


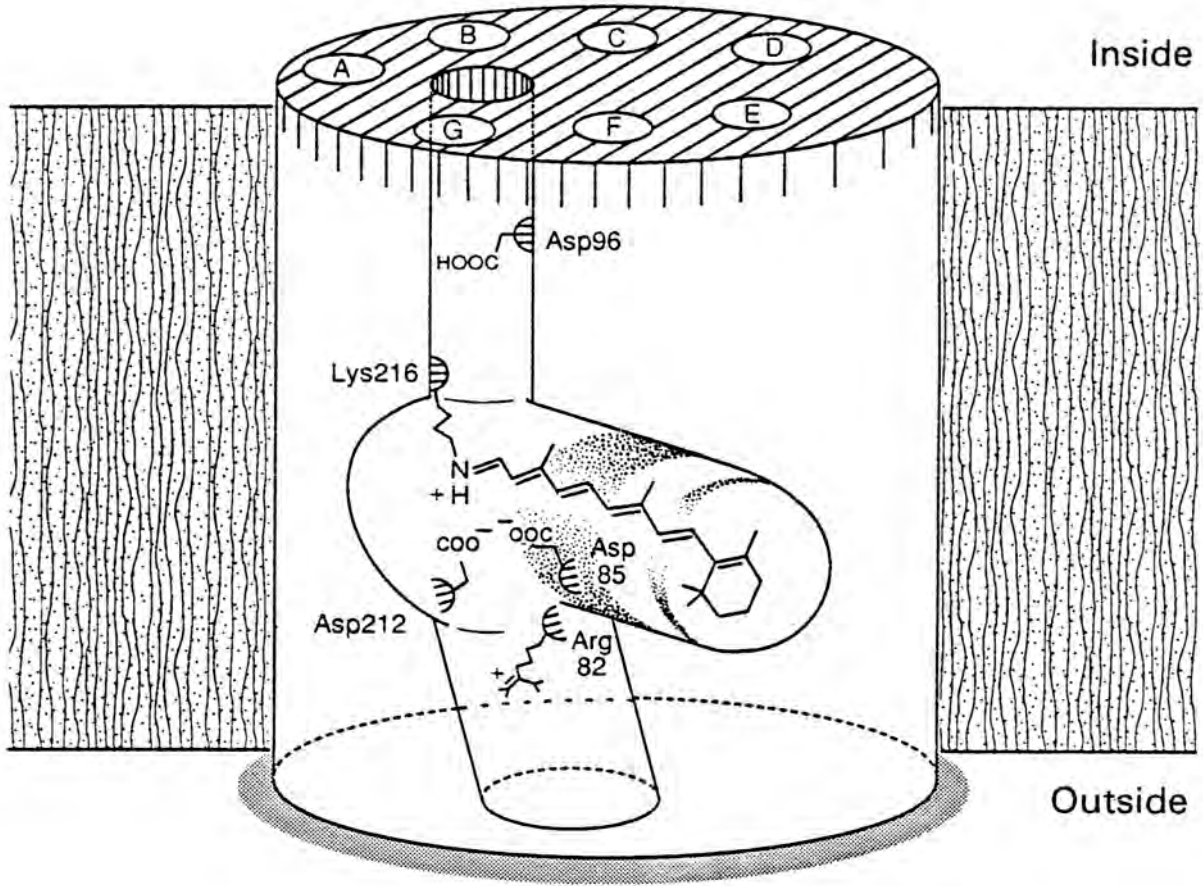
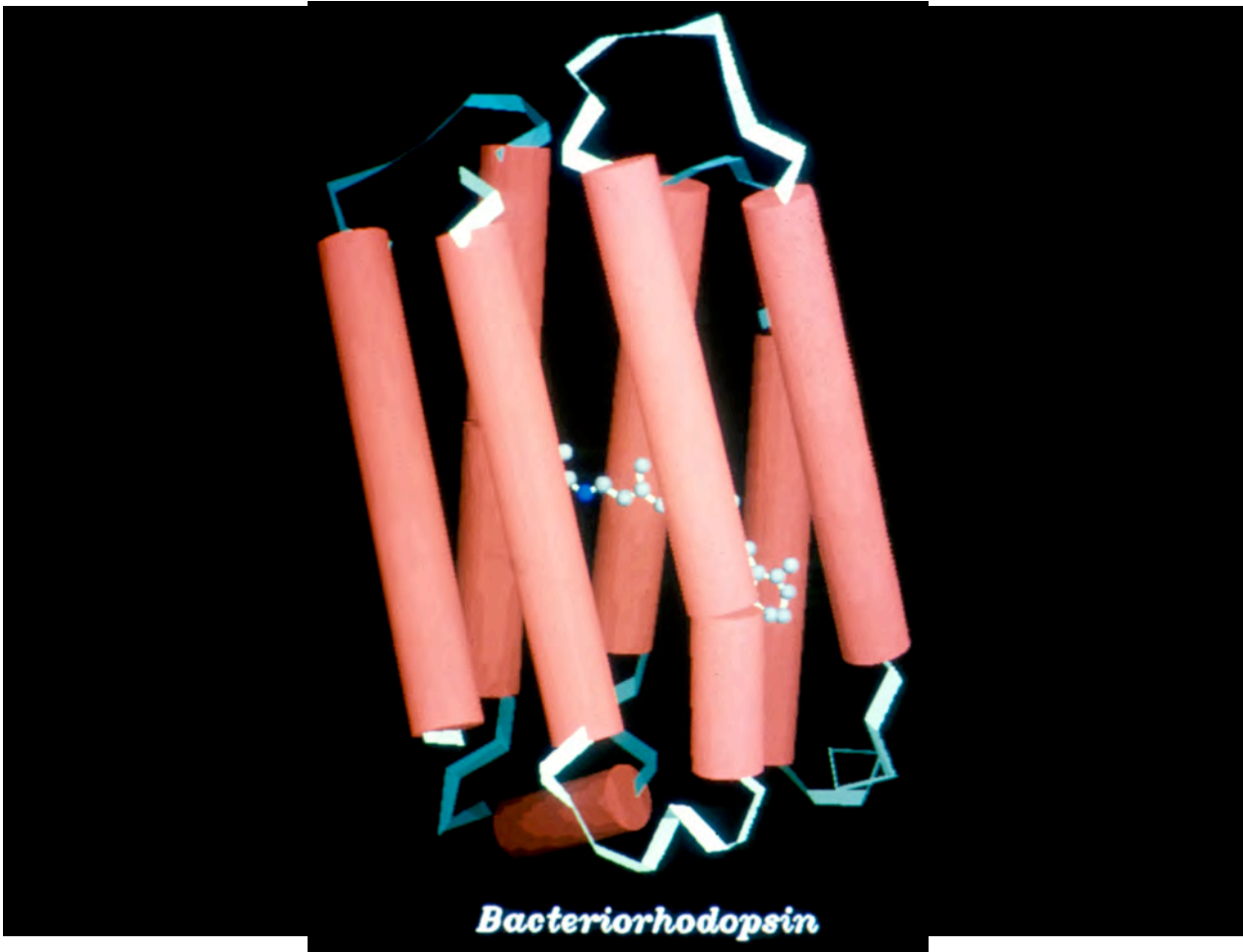


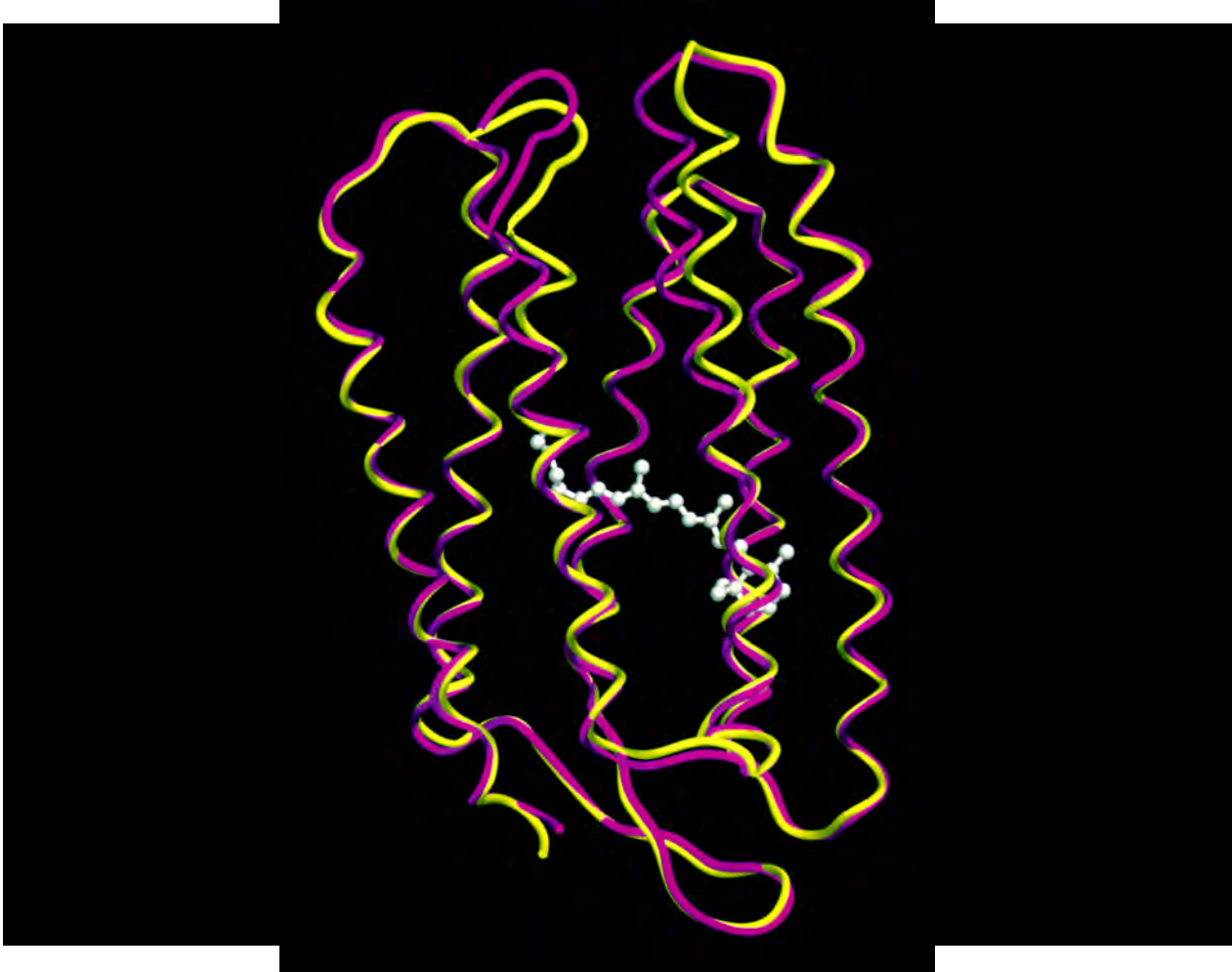




Bacteriorhodopsin 3.5 Å







### 3D structures from 2D crystals

Bacteriorhodopsin	3.5 Å	*
Bacteriorhodopsin	3.0 Å	*
DOC bacteriorhodopsin	6.0 Å	
Bacteriorhodopsin p22121	6.5 Å	
Porin PhoE	6.0 Å	
Plant LHC-II	3.4 Å	*
Rhodopsin frog p2	6.5 Å	
Tubulin dimer	3.7 Å	*
Aquaporin-1	3.7 Å	*
Aquaporin-4	3.2 Å	*
Aquaporin-0	1.9 Å	*
Halorhodopsin	5.0 Å	
Glutathione transferase	3.2 Å	*
SecYEG complex	8.0 Å	
Plant photosystem II RC	8.0 Å	
Neurospora H <sup>+</sup> -ATPase	8.0 Å	
Gap junction channel	7.5 Å	
NhaA Na/H antiporter	7.0 Å	
Glycerol channel GlpF	6.9 Å	
Oxalic acid transporter OxlT	6.0 Å	
EmrE multidrug transporter	7.0 Å	

## Problems & pitfalls

- Space group determination
- Twinning
- Comparison to X-ray structures

### The 17\* Two-Sided Plane Groups Allowed For Biological Molecules

Unit cell	Two-sided plane groups	Corresponding 3-dimensional space group	Projection symmetry
oblique	p1	P1	p1
	p21	P2( <i>c</i> -axis unique)	p2
rectangular	p12	P2( <i>b</i> -axis unique)	pm
	p12 <sub>1</sub>	P2 <sub>1</sub>	pg
	c12	C2	cm
	p222	P222	pmm
	p222 <sub>1</sub>	P222 <sub>1</sub>	pmg
	p22 <sub>1</sub> 2 <sub>1</sub>	P22 <sub>1</sub> 2 <sub>1</sub>	pgg
	c222	C222	cmm
square	p4	P4	p4
	p422	P422	p4m
	p42 <sub>1</sub> 2	P42 <sub>1</sub> 2	p4g
hexagonal	p3	P3	p3
	p312	P312	p3m1
	p321	P321	p31m
	p6	P6	p6
	p622	P622	p6m

The two-sided plane group nomenclature was first proposed by W.T. Holser (*Z.krystallogr.* **110**, 266-28, (1958)). His nomenclature has the following main rules.

- (a) Cell type is indicated first by small letter, *p* or *c* (primitive or centred)
- (b) The axis perpendicular to the plane is always chosen as the *z*-axis.
- (c) The symmetry along this axis is always described by the first symbol following the cell type.

e.g. p3 p4<sub>2</sub>2

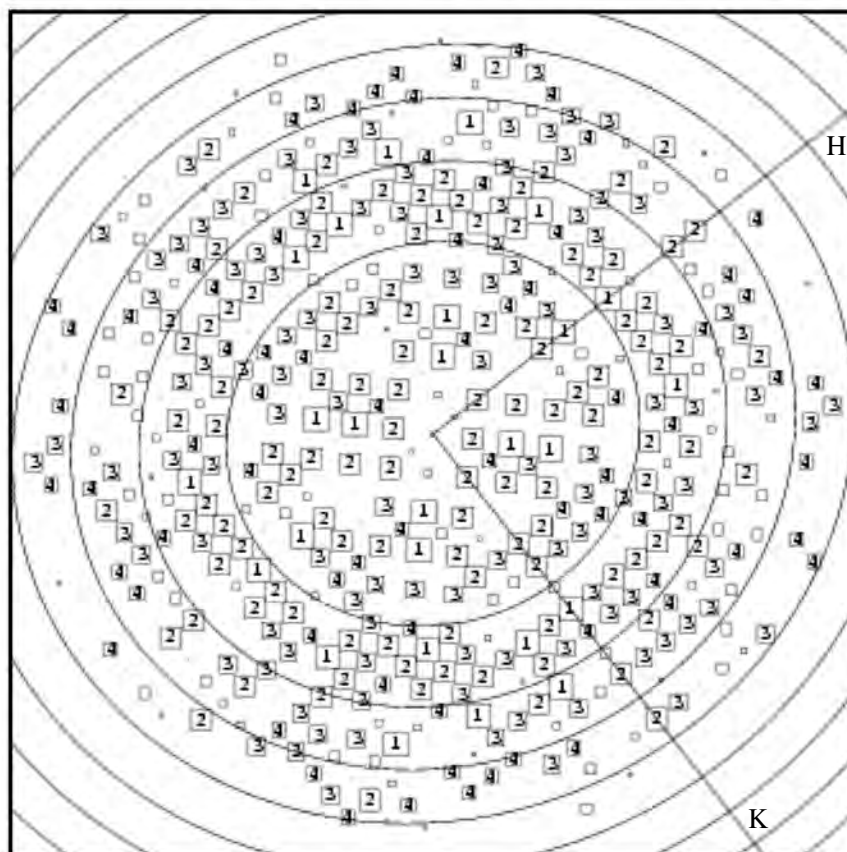
\* Note that there 80 two-sided plane groups in total, of which there are only 17 which do not contain inversion centres or mirror or glide planes.

```

C##### ALLSPACE #####
C Table of phase comparisons to be made
C - not comparable
C 1 directly identical
C H differ by 180 * H JSIMPLE = number to compare directly
C K differ by 180 * K JSCREW = number to compare + 180 * M
C HK differ by 180 * (H+K) where M = H*JH180 + K*JK180
C
C
C SPACEGROUP H=-h +h -h +k +k -k -k +h -h +k -k -h +h -h +h JSIMPLE
C H= -k +k -k +k JSCREW
C ref in
C prog # symb K=+k -k -k +h -h +h -h -h +h -h +h +h -h +k -k JH180
C K= -k +k -k +k JK180
C 1 1 p1 - - - - - - - - - - - - - - - 0 0 - -
C 2 2 p2 - - 1 - - - - - - - - - - - - - - 1 0 - -
C 3 3b p12 1 - - - - - - - - - - - - - - - 1 0 - -
C 4 "a" " - 1 - - - - - - - - - - - - - - - 1 0 - -
C 5 4b p121 K - - - - - - - - - - - - - - - 0 1 - 180
C 6 "a" " - H - - - - - - - - - - - - - - - 0 1 180 -
C 7 5b c12 1 - - - - - - - - - - - - - - - 1 0 - -
C 8 "a" " - 1 - - - - - - - - - - - - - - - 1 0 - -
C 9 6 p222 1 1 1 - - - - - - - - - - - - - - 3 0 - -
C 10 7b p2221 H H 1 - - - - - - - - - - - - - - 1 2 180 -
C 11 "a" " K K 1 - - - - - - - - - - - - - - 1 2 - 180
C 12 8 p22121 HK HK 1 - - - - - - - - - - - - - - 1 2 180 180
C 13 9 c222 1 1 1 - - - - - - - - - - - - - - 3 0 - -
C 14 10 p4 - - 1 - 1 1 - - - - - - - - - - 3 0 - -
C 15 11 p422 1 1 1 1 1 1 - - - - - - - - - - 7 0 - -
C 16 12 p4212 HK HK 1 1 HK HK 1 - - - - - - - - 3 4 180 180
C 17 13 p3 - - - - - - - - - - 1 - 1 - - - - 2 0 - -
C 18 14 p312 - - - - - 1 - 1 1 - 1 - - - 5 0 - -
C 19 15 p321 - - - 1 - - - 1 - 1 - 1 - - 5 0 - -
C 20 16 p6 - - 1 - - - - - 1 1 1 1 - - 5 0 - -
C 21 17 p622 - - 1 1 - - 1 1 1 1 1 1 1 1 11 0 - -
C
C Notes:-
C 1. Compare all possible pairs of phases each with error E.
C 2. Error comparing 2 different reflections is 1.414 * E.
C 3. Error comparing reflections to its Friedel is 2.0 * E.
C 4. So Friedel comparisons should have less weight ???
C 5. Note that the convention in the two dimensional spacegroups is that
C the first in-plane symmetry axis is the a-axis. Therefore,
C when ALLSPACE indicates that the spacegroup has the in-plane
C axis along b, it is better to switch the indexing to ensure
C compatibility with the normal convention as programmed in
C ORIGIN, rather than using the REVHK option in ORIGIN,
C which will switch the indexing on input.

```

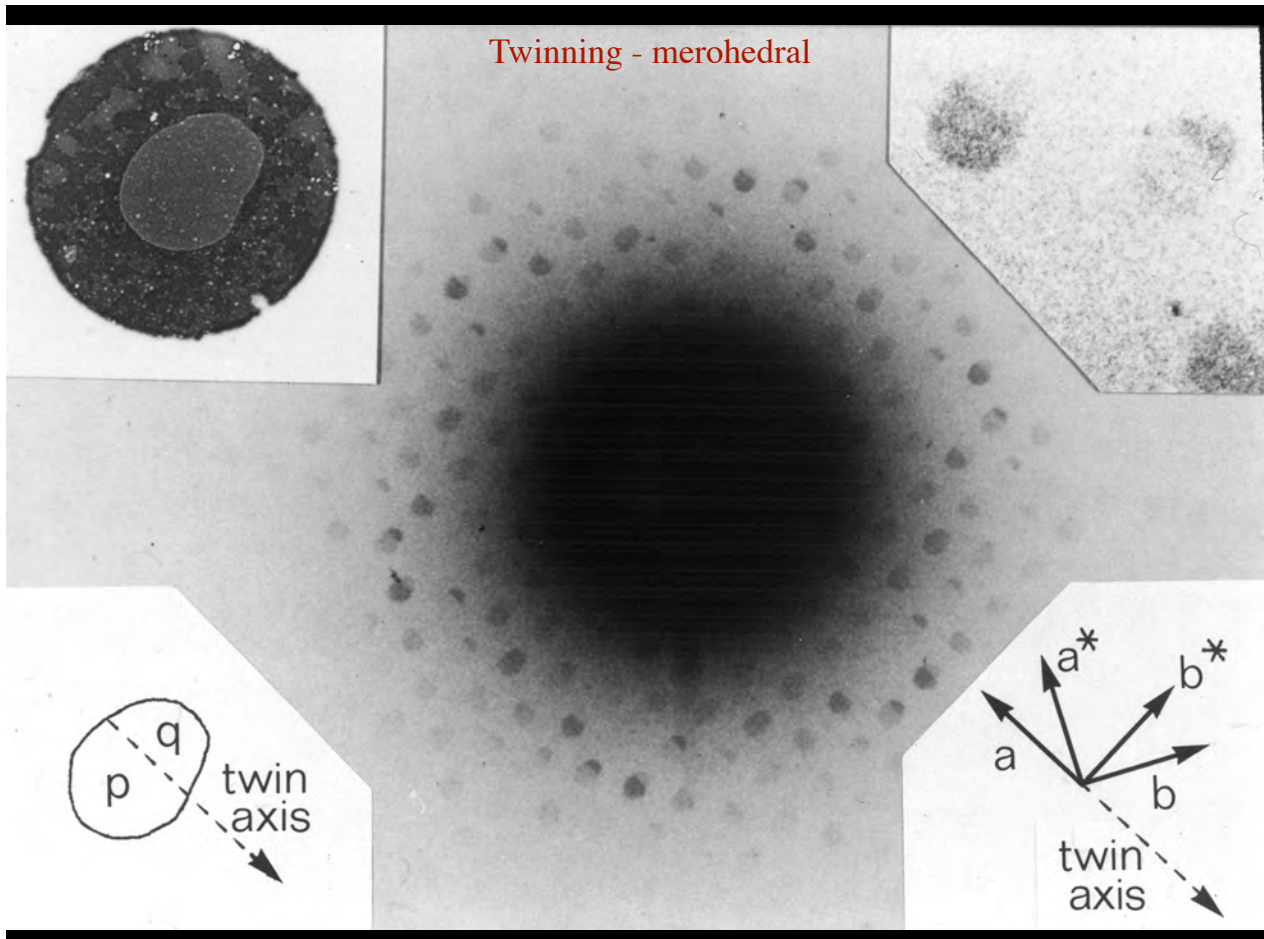
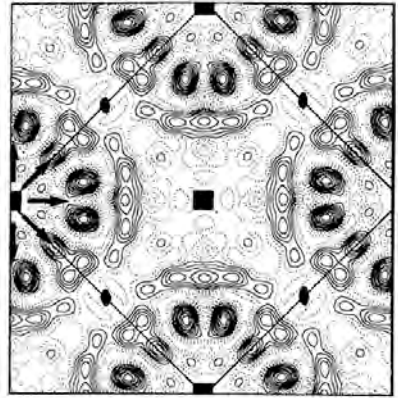
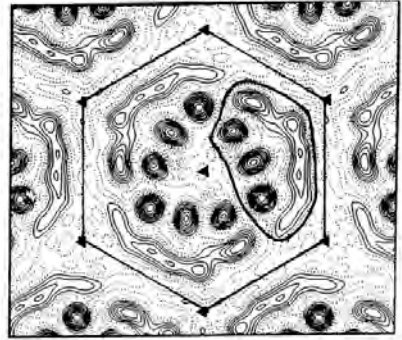
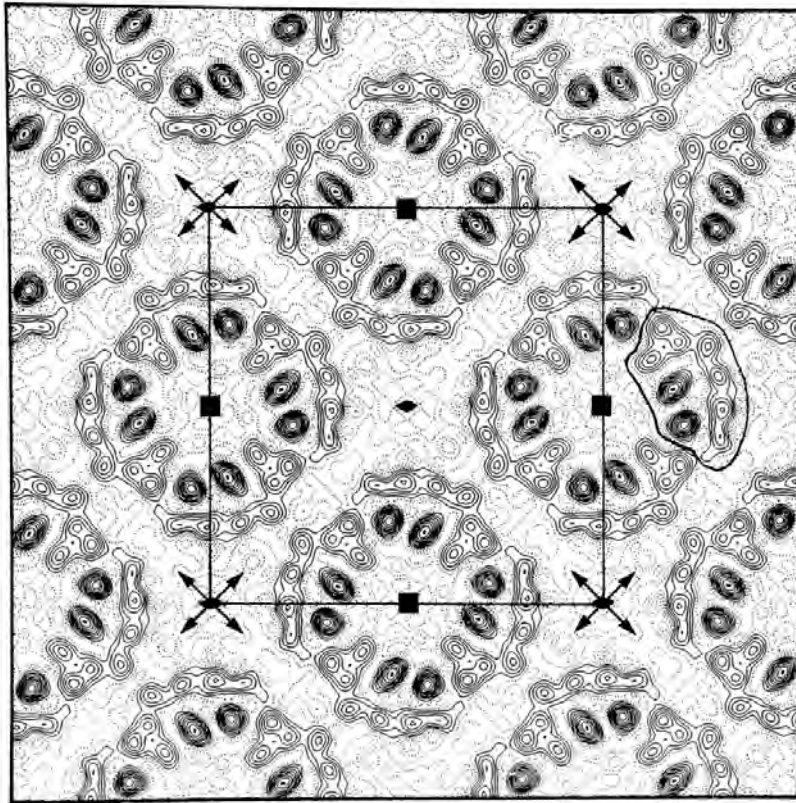
Halorhodopsin CTFg000 defocus=5650,7050,15, 19.2.94, CTF refinement



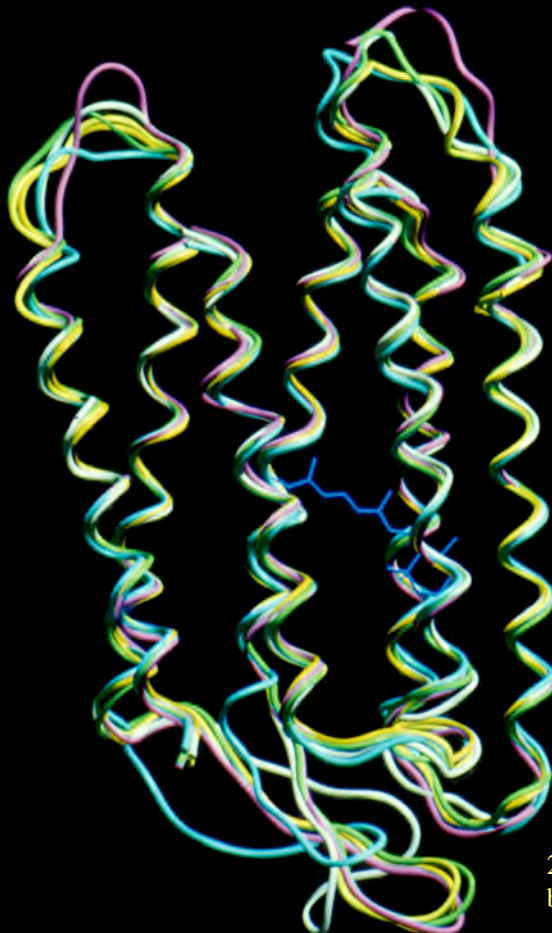
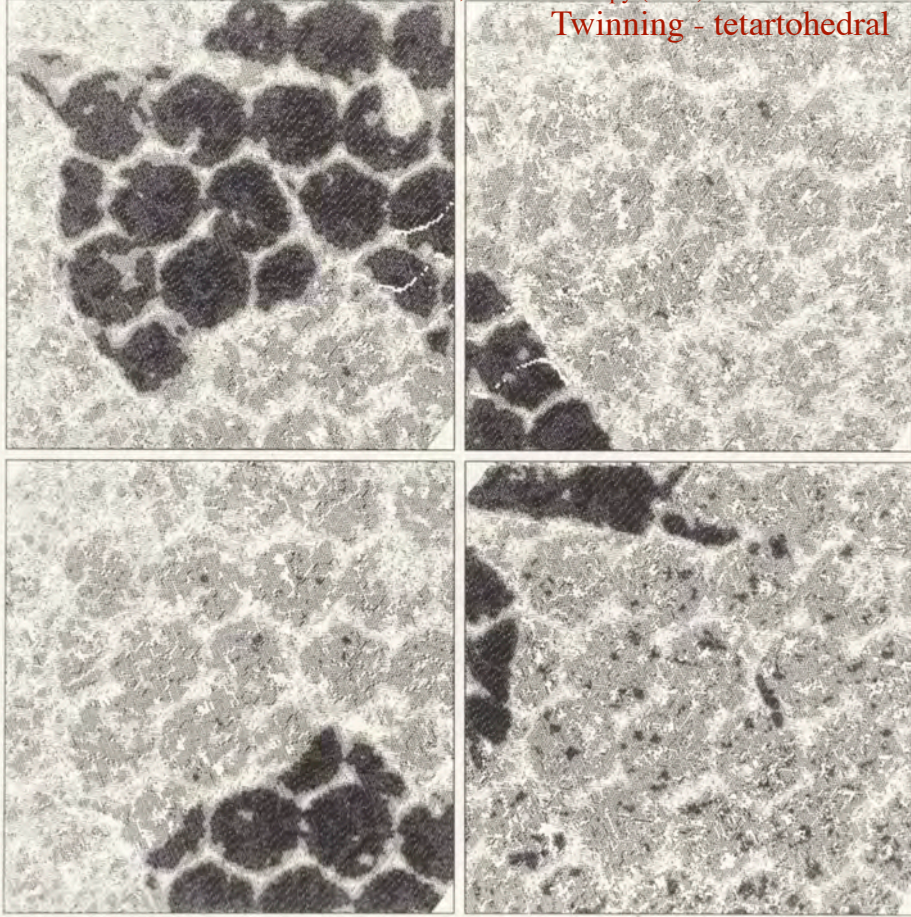
Halorhodopsin film 2464s

SPACEGROUP	Phase resid(No) v.other spots (90 random)	Phase resid(No) v.theoretical (45 random)	OX	OY	Target residual based on statistics taking Friedel weight into account
1 p1	34.4 432	25.9 432			
2 p2	42.8* 216	21.4 432	130.1	-21.6	51.7
3b p12_b	77.7 167	11.3 14	-49.5	12.0	35.2
3a p12_a	80.1 169	30.1 18	-180.0	-21.8	35.4
4b p121_b	29.3* 167	10.1 14	-139.7	120.0	35.2
4a p121_a	21.4* 169	9.3 18	138.0	68.1	35.4
5b c12_b	77.7 167	11.3 14	-49.5	12.0	35.2
5a c12_a	80.1 169	30.1 18	-180.0	-21.8	35.4
6 p222	64.9 552	21.5 432	-49.7	158.3	41.2
7b p2221b	59.6 552	37.7 432	-139.5	-111.9	41.2
7a p2221a	63.0 552	37.8 432	-139.7	68.2	41.2
8 p22121	32.3* 552	21.5 432	130.2	158.2	41.2
9 c222	64.9 552	21.5 432	-49.7	158.3	41.2
10 p4	30.8* 528	21.5 432	130.1	-21.7	41.5
11 p422	57.2 1173	21.5 432	130.1	158.1	37.6
12 p4212	28.2* 1173	21.6 432	130.1	158.1	37.6

\* = acceptable  
! = should be considered  
\ = possibility



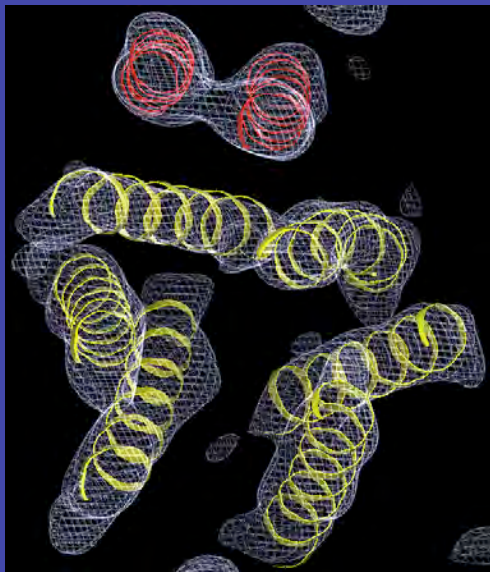
Twinning - tetartohedral



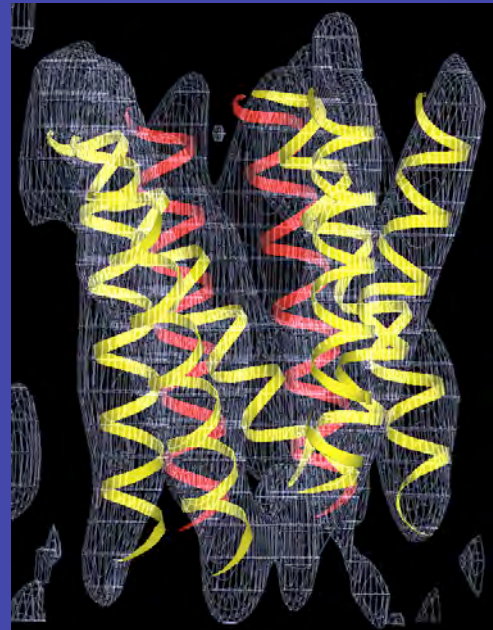
2 EM and 4 X-ray  
bacteriorhodopsin structures



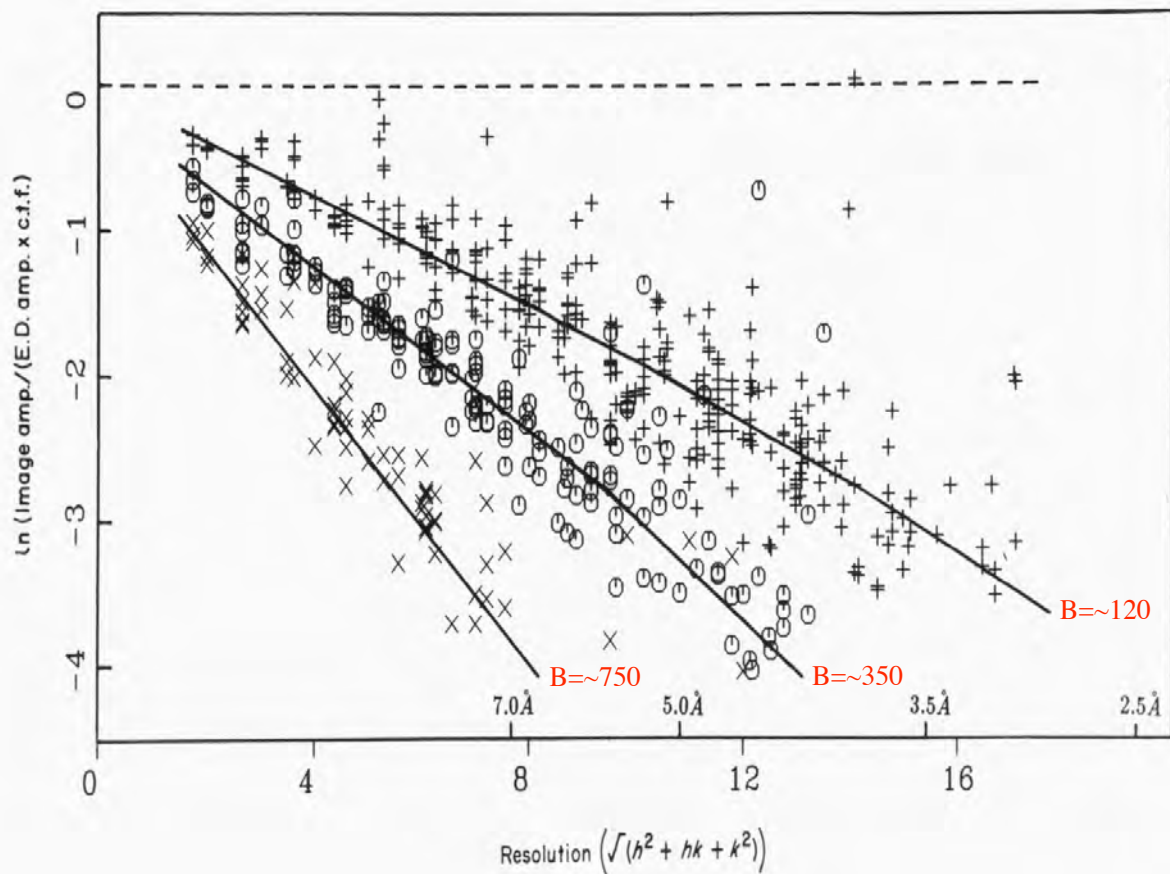
The multidrug transporter EmrE is an asymmetric homodimer  
Tate & Ubarretxena-Belandia, EMBO J. (2003) 22, 6175

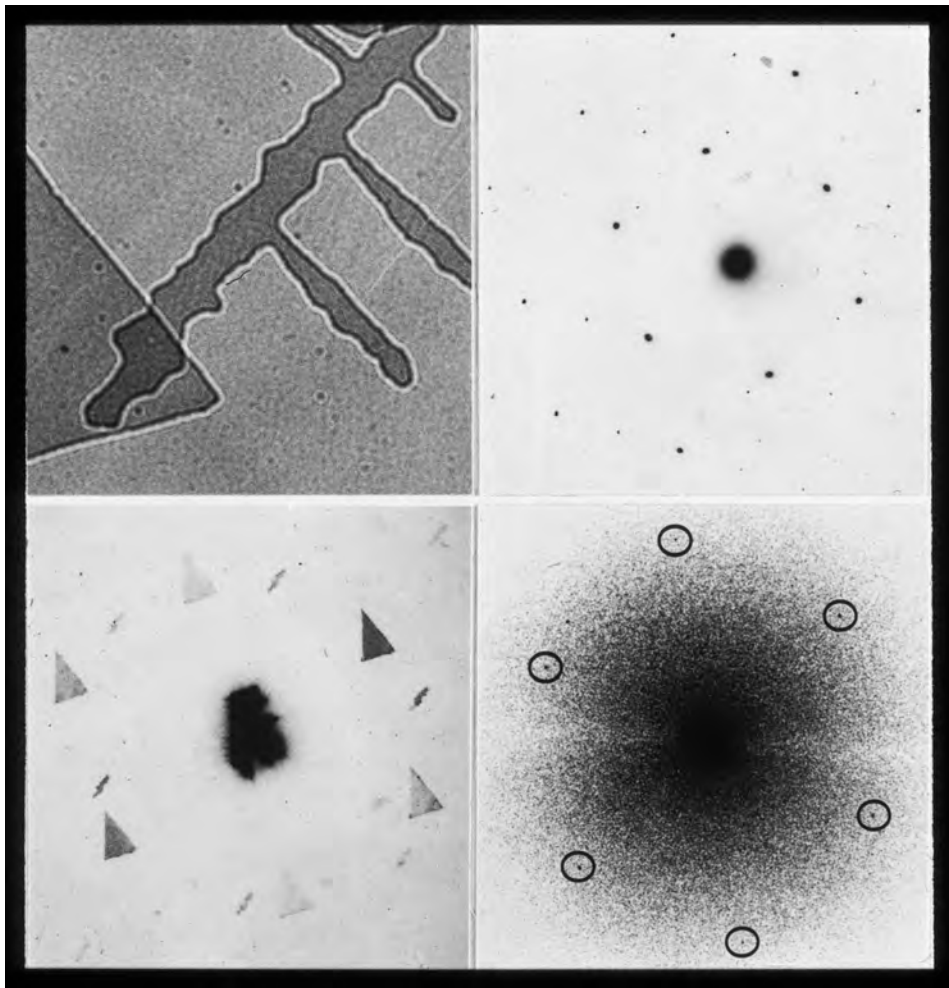


Top view

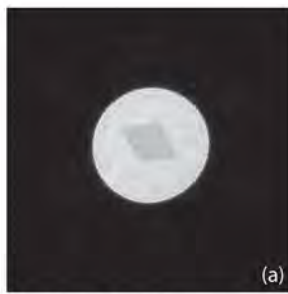


Side view

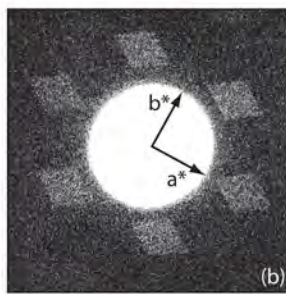




A17044/thinC\_122p



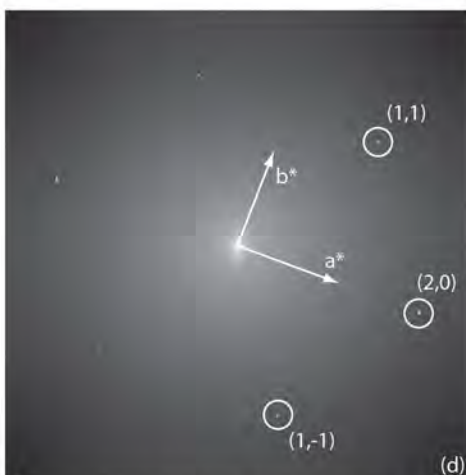
bright field defocused eldiff



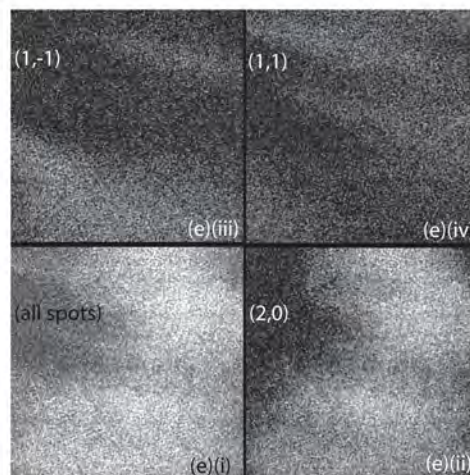
dark field defocused eldiff



dark field stretched contrast



power spectrum from micrograph



pseudo-dark-field images

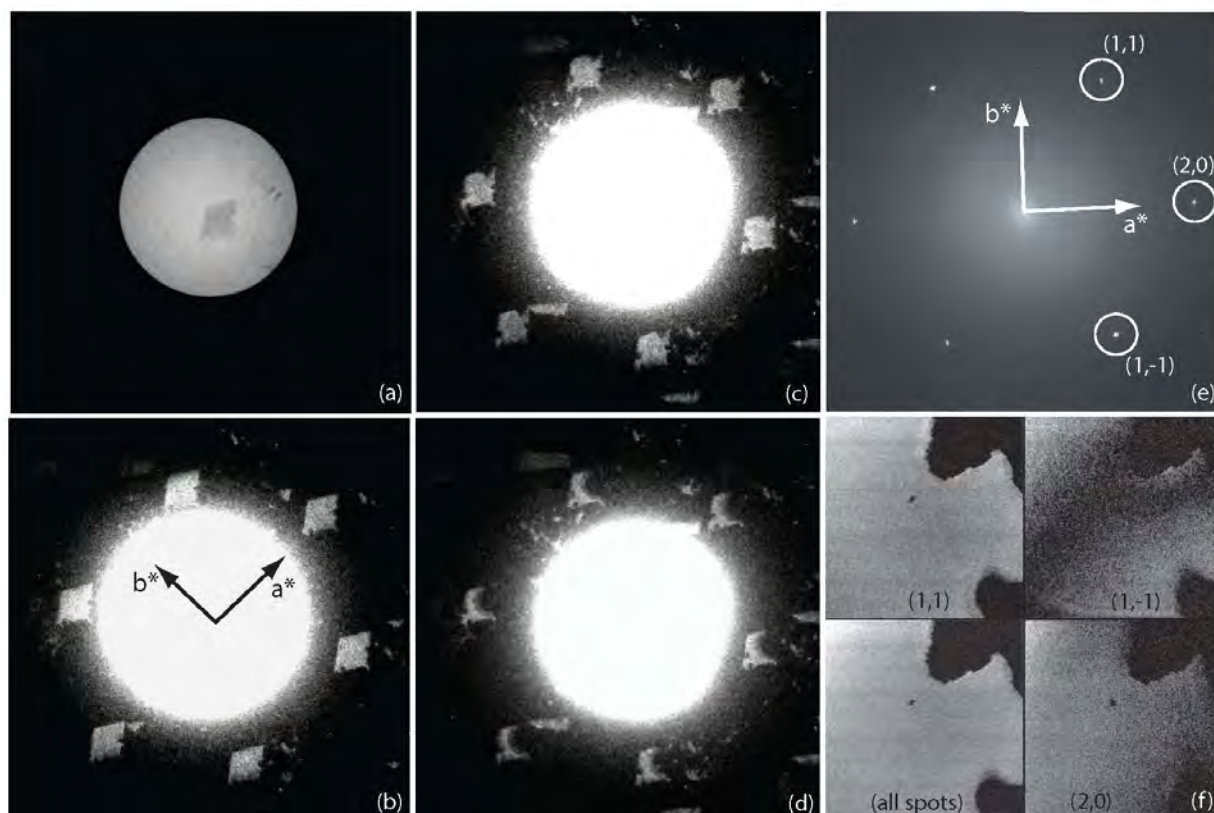


Figure 6

Table 1 - image contrast

Image	Description	Overall image area 1.5 $\mu\text{m}$ square		Selected image area 0.15 $\mu\text{m}$ square		% theoretical - range of values for either overall or selected area		
		$I_g/I_0$	$F_g/F_0$	$I_g/I_0$	$F_g/F_0$	Compared to electron diffraction	Corrected for detector MTF	Corrected for inelastic scattering
A17044	300kV thinC floodbeam	$0.4\text{-}2.0 \times 10^{-4}$	0.006-0.014	$0.4\text{-}4.6 \times 10^{-4}$	0.006-0.021	2.7-9.7 %	10-44 %	11-47 %
011643	300kV thinC microspotscan	$4.3\text{-}7.5 \times 10^{-4}$	0.021-0.027	$3.9\text{-}15.7 \times 10^{-4}$ *	0.020-0.039 *	9.1-17.7 %	41-63 %	43-67 %
A16973	120kV thickC nanospotscan	$1.7\text{-}3.5 \times 10^{-4}$	0.013-0.019	$4.9\text{-}8.4 \times 10^{-4}$	0.022-0.029	4.8-10.7 %	27-47 %	37-64 %
A16984	120kV thickC nanospotscan	$(0.3\text{-}2.4 \times 10^{-4})$	(0.005-0.015)	$0.4\text{-}3.3 \times 10^{-4}$	0.007-0.018	2.6-6.6 %	14-29 %	19-40 %
para 22may image07	thinC Medipix 120kV	$1.7\text{-}5.1 \times 10^{-4}$ **	0.013-0.023 **	-	-	4.8-8.5 %	10-18 %	18-20 %
A02026	300kV thickC floodbeam	$(0.8\text{-}2.8 \times 10^{-4})$	(0.009-0.017)	$3.2\text{-}12.3 \times 10^{-4}$	0.018-0.035	8.2-15.9 %	30-59 %	35-70 %
A02027	300kV thickC floodbeam	$(2.4\text{-}5.8 \times 10^{-4})$	(0.015-0.024)	$4.5\text{-}16.6 \times 10^{-4}$	0.021-0.041	6.8-18.8 %	31-79 %	36-93 %
A02030	300kV thickC floodbeam	-	-	$3.7\text{-}8.6 \times 10^{-4}$	0.019-0.029	8.6-13.2 %	39-49 %	46-58 %
A03133	300kV thickC floodbeam	$2.5\text{-}5.7 \times 10^{-4}$	0.016-0.024	$7.9\text{-}15.7 \times 10^{-4}$	0.028-0.040	7.3-18.2 %	33-67 %	39-79 %
A03134	300kV thickC floodbeam	$1.3\text{-}7.0 \times 10^{-4}$	0.012-0.026	$1.3\text{-}12.1 \times 10^{-4}$	0.011-0.035	5.0-15.9 %	23-59 %	27-70 %
A03141	300kV thickC floodbeam	$0.9\text{-}6.8 \times 10^{-4}$	0.010-0.026	$5.9\text{-}31.8 \times 10^{-4}$	0.024-0.056	4.4-25.6 %	16-95 %	19-112 %

## Notes to Table 1:

\* The selected area in this case was only 0.11  $\mu\text{m}$  square, which was the size of each spot in the spotscan raster.

\*\* The area in this case was only 0.1  $\mu\text{m}$  square, which was the full size of the Medipix II-Quad detector.

The smallest and largest values given in columns 3 to 9 correspond to the weakest and strongest of the three reflections at  $\sim 4$  Å resolution.

To calculate the % theoretical, the raw  $F_g/F_0$  image values must first be divided by the values expected from electron diffraction, which are 0.22 for 300keV images, or 0.27 for 120keV images, as shown in column 7. All three reflections at  $\sim 4$  Å have very similar electron diffraction intensities.

The MTF envelope correction used to calculate column 8 has been taken from Fig. 5 in reference [5] for film (1/0.18 and 1/0.23 for (2,0) and (1,1) respectively) and Medipix (1/0.40 and 1/0.47) at 120keV and from Fig. 6 for film at 300keV (1/0.22 and 1/0.27 for (2,0) and (1,1) respectively). The MTF correction is larger for the (2,0) reflection because it is at higher resolution, 3.7 Å compared with 4.1 Å for the (1,1) and (1,-1) reflections. A further correction for the contrast reduction due to inelastic scattering is shown in column 9. The correction factors are 1.06 for thin carbon at 300keV, 1.12 for thin carbon at 120keV, 1.18 for thick carbon at 300keV and 1.37 for thick carbon at 120keV.

The numbers in brackets for some of the images in columns 3 and 4 are lower than they should be because the crystal was smaller than the overall image area. The area of A02030 included several twinned and untwinned crystals, so no numbers are given for the overall image area for that image.

## Key considerations

- Tilt-transfer-function (TTF, TTBOX, etc)
- Creating reference area using MAKETRAN
- Size of reference box (optimize)

## Other problems

- Better images on thick carbon
- Flatness of 2D crystals
- Treatment as single molecules/unit cells

## Lessons from 2D for single particle EM

- Beam tilt
- Differential magnification

Grigorieff, Beckmann & Zemlin, JMB, 1995

**Table 2.** Average signal-to-background ratio of all spot intensities in the resolution range 3.0 Å to 4.0 Å, obtained for one image using different reference areas to find the position of unit cells

Area in pixel	Unit cells	% Fourier averaging	Reflections found with $IQ \leq 7$	Signal/Background
300 × 300	73	99	79	10/7
200 × 200	33	98	88	25/7
130 × 130	14	91	107	41/7
70 × 70	4	80	100	37/7
34 × 34	1	0	70	4/7
Unprocessed image			40	0/7

In each case, Fourier averaging was applied to the image before unbending except in the last two rows. The value (in %) in the third column refers to the area masked out by the Fourier mask applied to the image transform. The signal-to-background ratio was calculated after subtraction of the background from each integrated spot intensity. The total number of reflections in the chosen range was 222. The signal refers to the average intensity above background at the position expected for the diffraction peaks from the crystal. The background is the average intensity in the immediately surrounding area; it is normalized to 7. The standard deviation of the background is the background fluctuation after the intensity of all reflections has been averaged. It was determined to be 1.0 for the single molecule cross-correlation in the second last row. Thus, a peak of 4 is above a background of 7 by  $4 \times$  the standard deviation. The signal-to-background ratio for the unprocessed image was included for comparison in the last row.

## Acknowledgements

**bR**  
7 Å Unwin  
3.5 Å Baldwin, Downing, Lepault, Zemlin  
3D map Baldwin, Ceska, Zemlin, Beckman, Downing  
Refinement Grigorieff

**hR**  
7 Å Havelka, Oesterhelt  
5 Å Kunji

paraffin  
Bob Glaeser, Greg McMullan, Wasi Faruqi