

## Supplementary Material

**Table 1. Data-collection statistics**

<b>Resolution range (Å)</b>	<b><math>R_{\text{merge}}</math> (%)</b>	<b>Completeness (%)</b>
30.00–5.06	7.9	93.9
5.06–4.02	5.3	97.6
4.02–3.51	6.4	97.1
3.51–3.19	5	96.5
3.19–2.96	8	96
2.96–2.79	8.3	96.3
2.79–2.65	13.6	96.3
2.65–2.53	14.5	95.6
2.53–2.43	22.2	96
2.43–2.35	23	97.3
All reflections	5.6	96.3

**Table 2. Tabulated  $R$  indices**

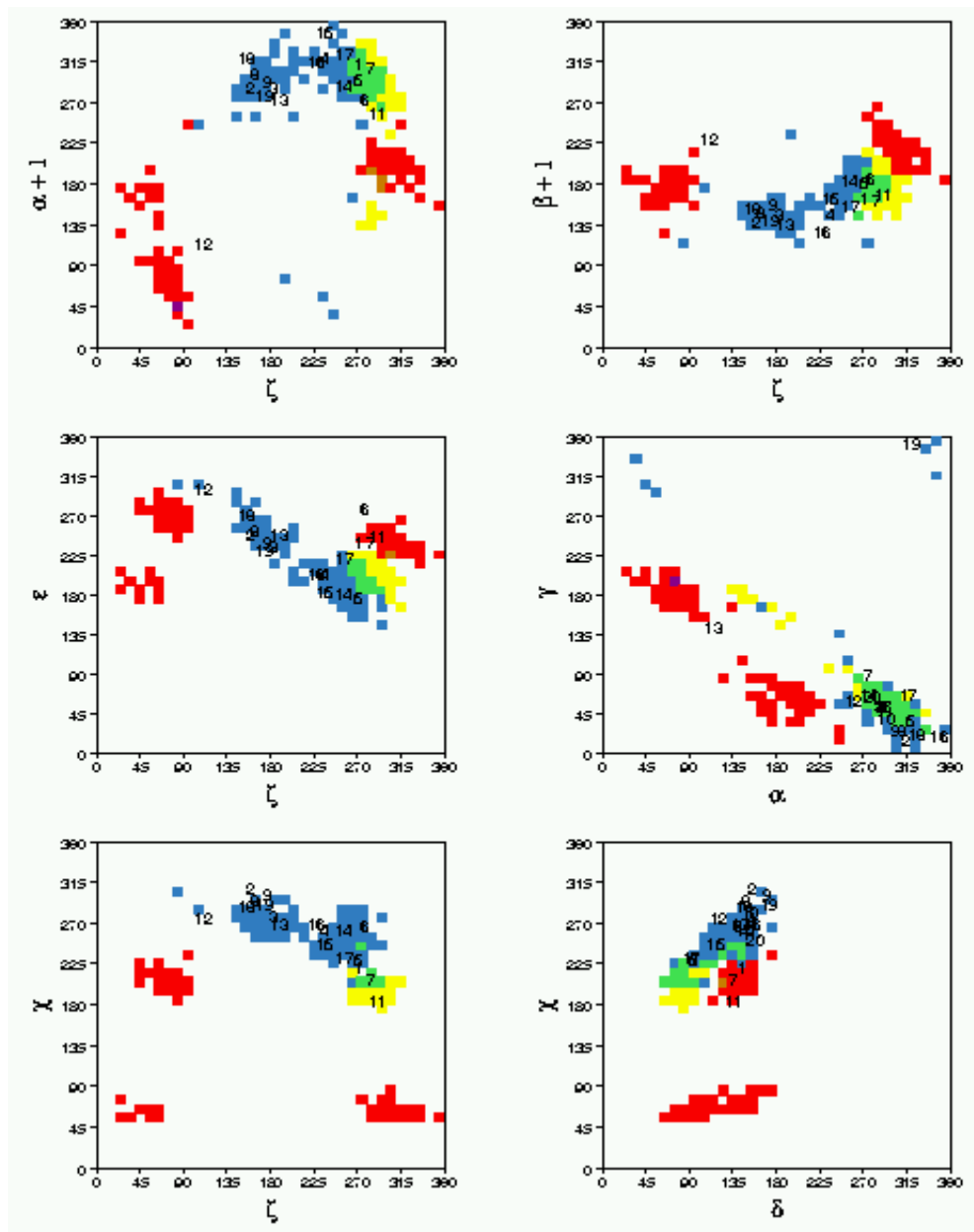
<b>Resolution range (Å)</b>	<b>No. ref used</b>	<b>% obs</b>	<b><math>R</math></b>	<b><math>R_{\text{free}}</math> ref.</b>	<b><math>R_{\text{free}}</math></b>
30.00–10.00	80	85.42	0.15	2	0.05
10.00–5.97	132	95.97	0.18	11	0.16
5.97–4.66	182	98.94	0.2	4	0.17
4.66–3.95	207	96	0.2	9	0.16
3.95–3.49	230	96.48	0.23	17	0.29
3.49–3.16	254	97.08	0.22	12	0.36
3.16–2.91	267	96.89	0.27	13	0.35
2.91–2.71	294	96.83	0.28	11	0.44
2.71–2.55	317	96.14	0.31	7	0.54
2.55–2.35	323	97.43	0.31	18	0.44
Overall	2286	96.41	22.64	104	26.78

**Table 3. *B*-value analysis**

Values generated from *BAVERAGE* from the *CCP4* program suite.

<b>Residue/chain</b>	<b><i>B</i><sub>av</sub></b>	<b>RMS <i>B</i></b>	<b>Residue/chain</b>	<b><i>B</i><sub>av</sub></b>	<b>RMS <i>B</i></b>
C/A	43.8	4.81	C/B	50.4	8.64
C/A	47.1	11.05	C/B	48.2	10.76
G/A	50.6	9.48	G/B	46.2	8.84
G/A	50.3	10.47	G/B	46.5	11.29
T/A	50.6	7.88	T/B	51.7	11.24
A/A	42.6	7.7	A/B	46.2	11.87
C/A	42.2	6.68	C/B	47.8	10.55
C/A	47.2	9.35	C/B	43.3	8.59
G/A	54.3	7.48	G/B	50.3	11.28
G/A	48.4	6.18	G/B	53.4	10.12

## DNA Scattergrams



Produced during deposition to the NDB with ADIT.

Based on analysis of selected structures of resolution at least 1.9 Å, A-DNA (yellow), B-DNA (blue), Z-DNA (red), A and B (green), A and Z (orange), B and Z (purple), A, B and Z (brown). [B. Schneider et al. (1997). *Biopolymers*, **42**, 113–124]