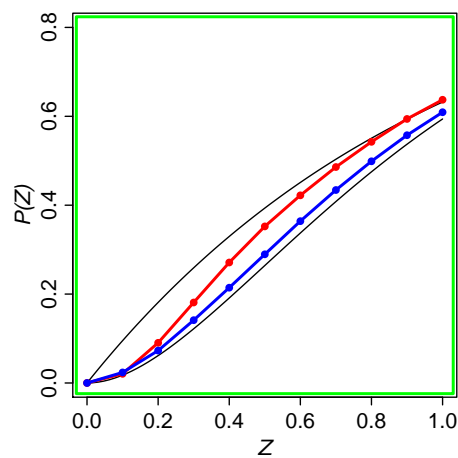
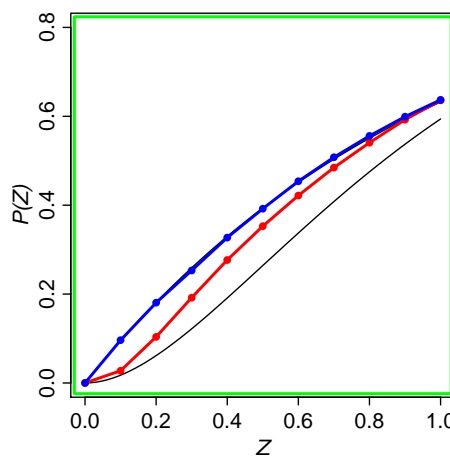
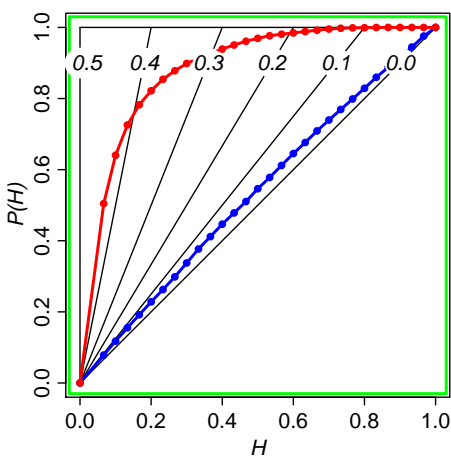
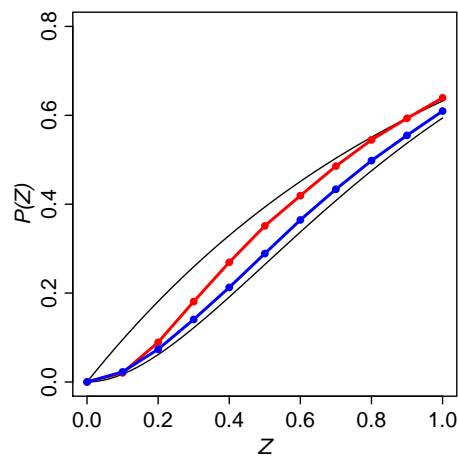
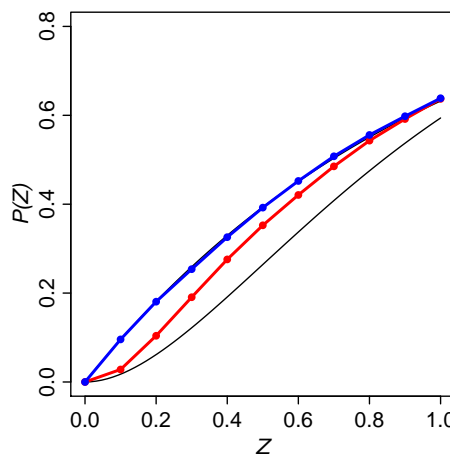
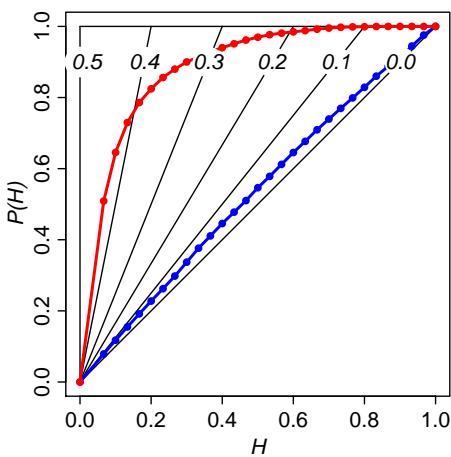
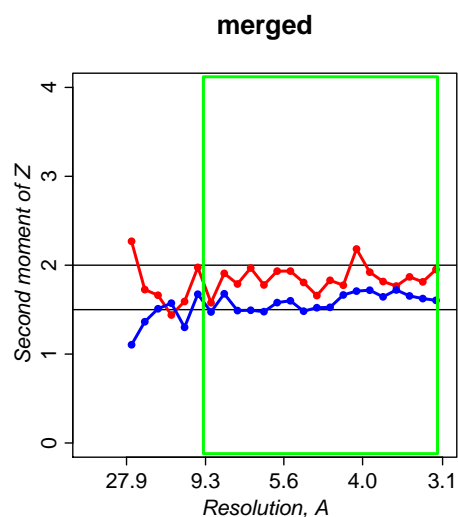
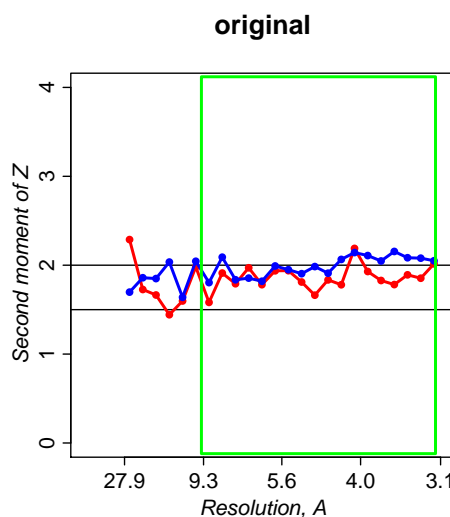
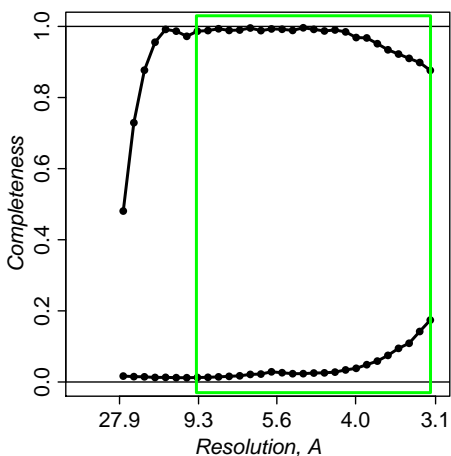
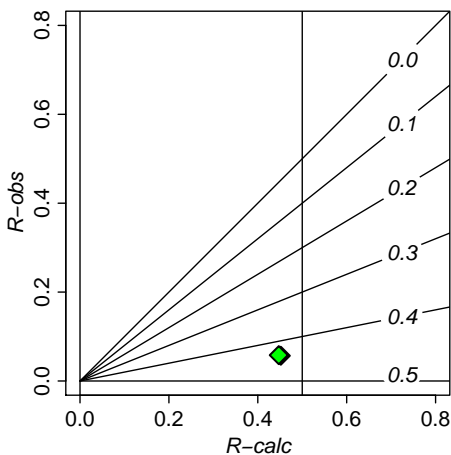


1a38

	original	merged
s.g.	P 65	-
p.g.	12021	12027
a.u.	2	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	39.3	-
R'	-	-
R-free	47.8	-
R'-free	-	-
residues per monomer	DNA 0	protein 221

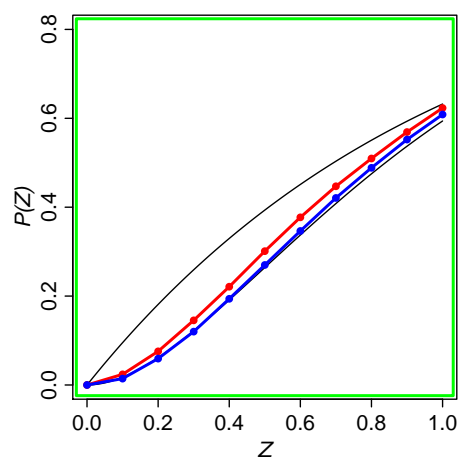
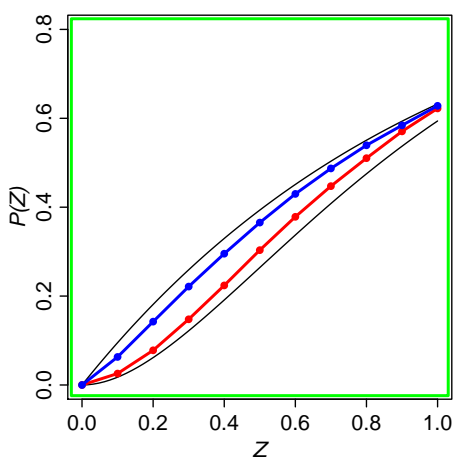
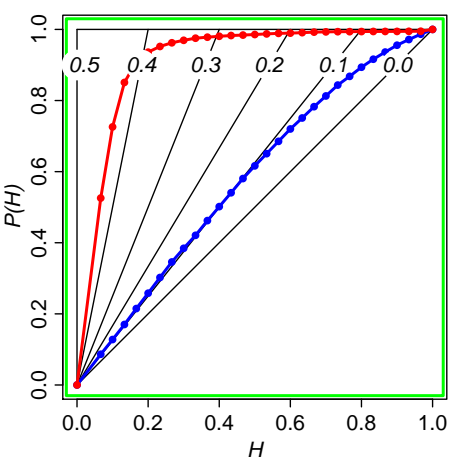
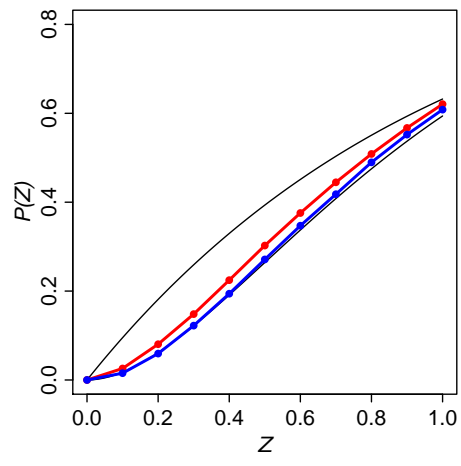
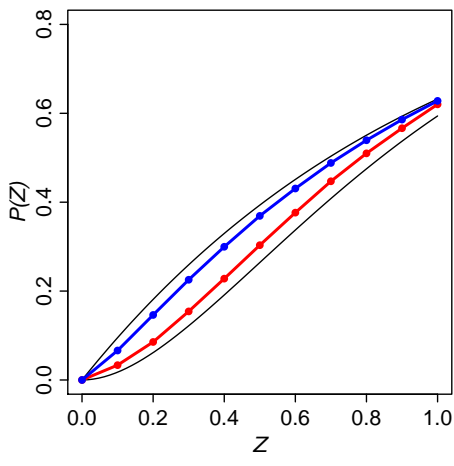
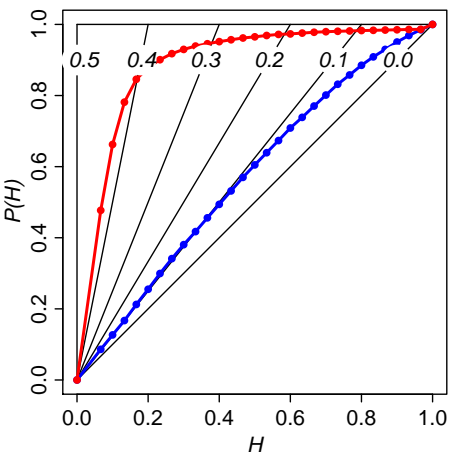
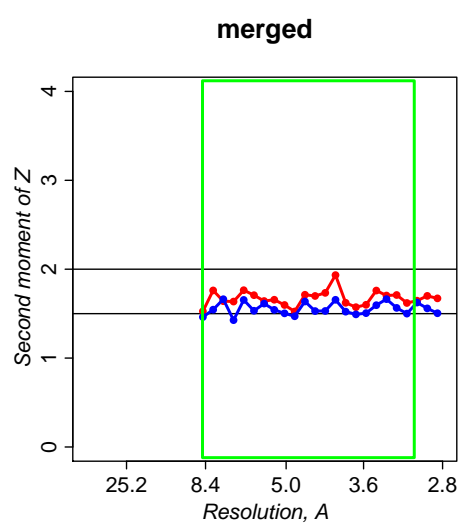
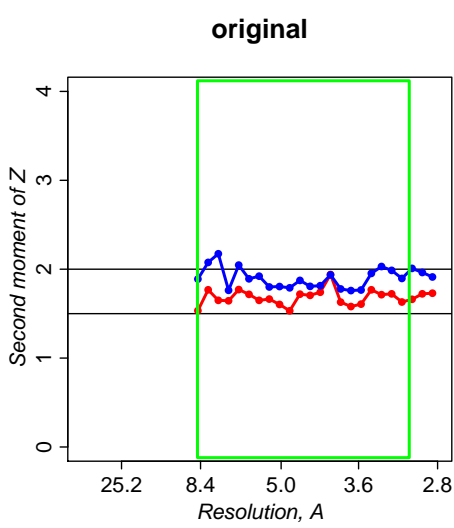
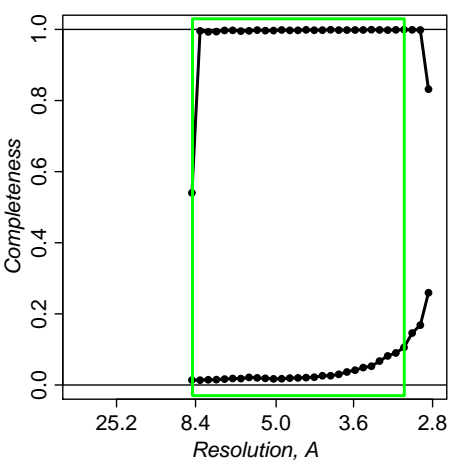
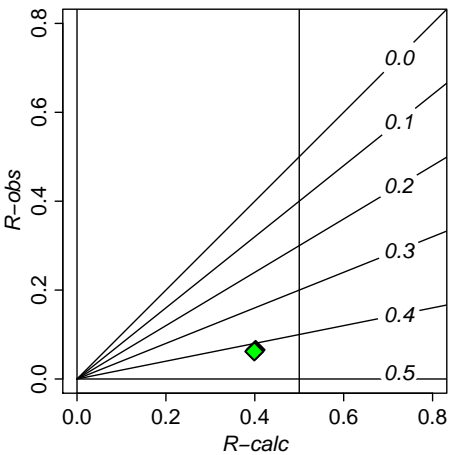
s < f/100	408	1.95 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	29.0-3.1	9.9-3.1
unique	22,039	21,365
measured	20,975	20,341
used	17,852	17,450
NCS	translation	rotation
r.m.s.d. (A)	31.84	0.17
angle (o)	179.41	0.60



1a4o

	original	merged
s.g.	P 65	-
p.g.	12021	12027
a.u.	4	-
p.t.	2	-
p.o.	2	-
r.m.s.d. (A)	-	-
R	29.3	-
R'	-	-
R-free	37.5	-
R'-free	-	-
residues per monomer	DNA 0	protein 197

s < f/100	34	0.12 %
s <= 0	0	0.00 %
f <= 0	283	1.00 %
s,f <= 0	0	0.00 %
range (A)	9.0-2.8	9.0-3.0
unique	28,744	23,205
measured	28,360	23,160
used	25,160	20,442
NCS	translation	rotation
r.m.s.d. (A)	1.04	0.37
angle (o)	3.63	0.78



1a6p

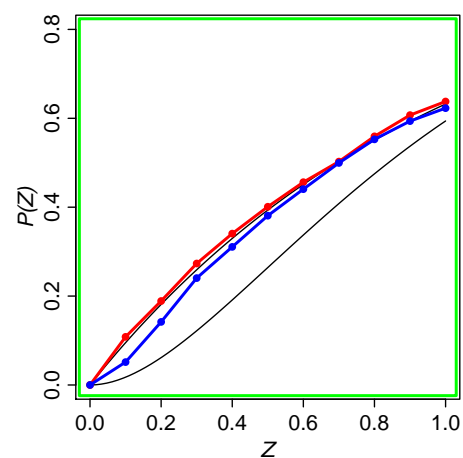
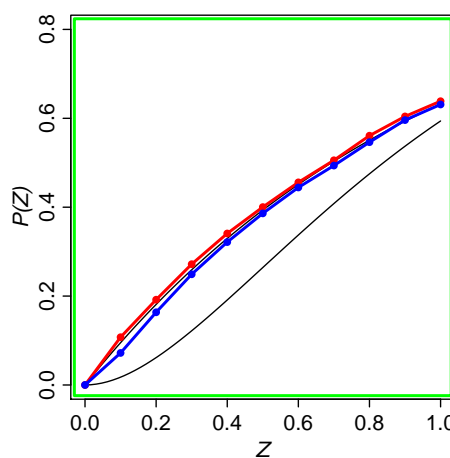
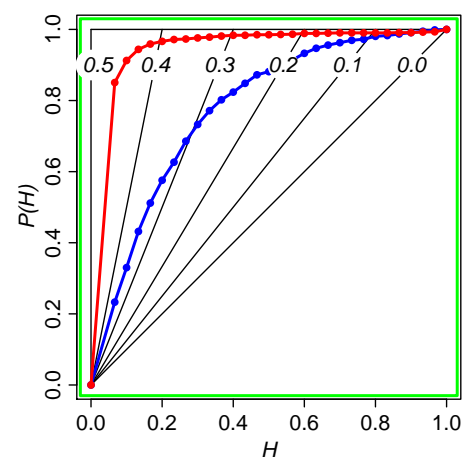
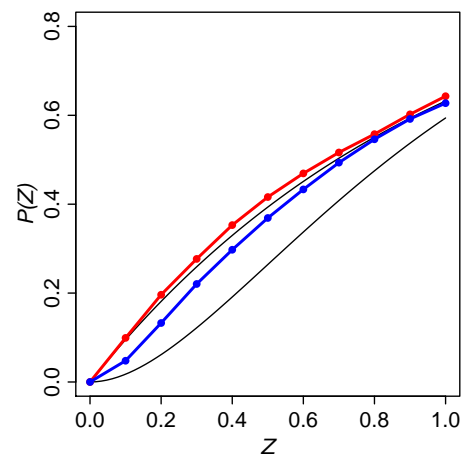
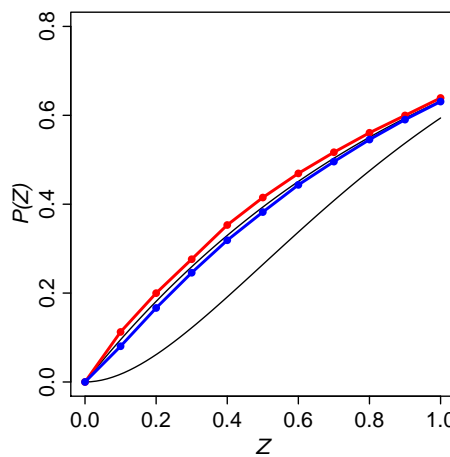
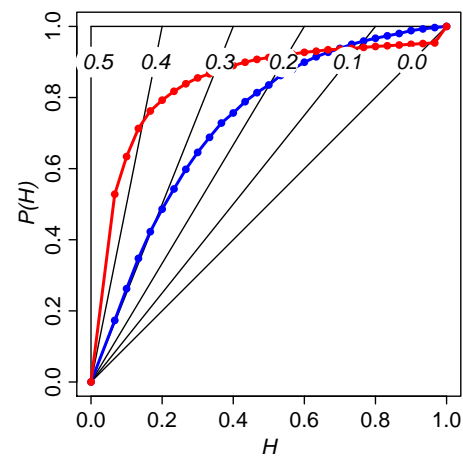
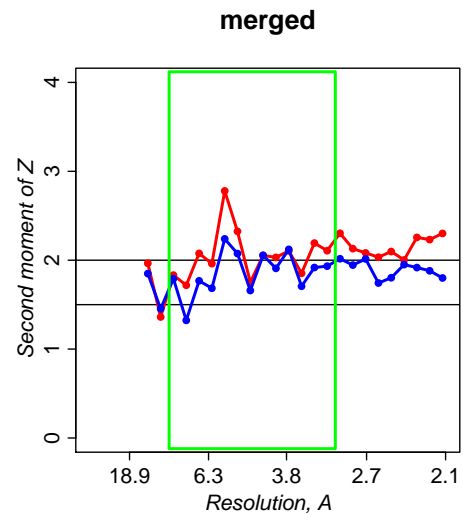
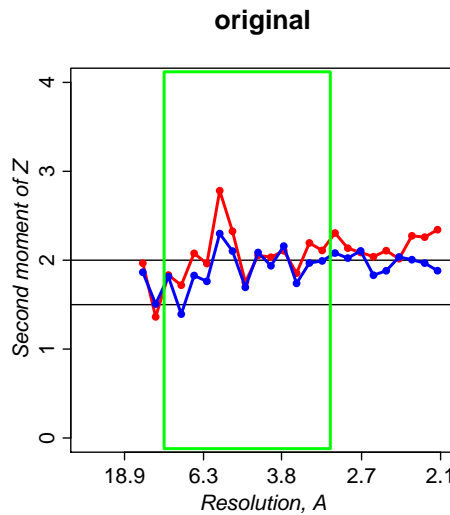
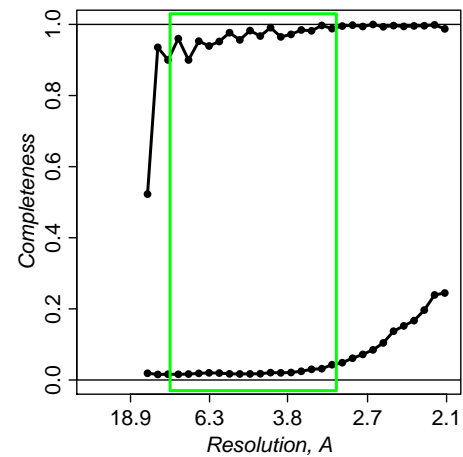
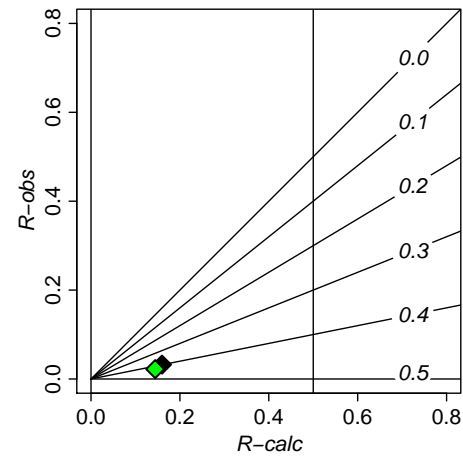
	original	merged
s.g.	P 43	P 43 21 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.22
R	25.7	
R'	26.2	27.2
R-free	28.1	
R'-free	30.8	32.4

s < f/100	62	0.59 %
s <= 0	0	0.00 %
f <= 0	398	3.82 %
s,f <= 0	0	0.00 %

range (A)	14.5–2.1	9.9–3.0
unique	10,548	3,467
measured	10,424	3,383
used	8,834	2,666

NCS	translation	rotation
r.m.s.d. (A)	34.03	0.22
angle (o)	179.87	0.13

residues per monomer	DNA	protein
	0	94



1a75

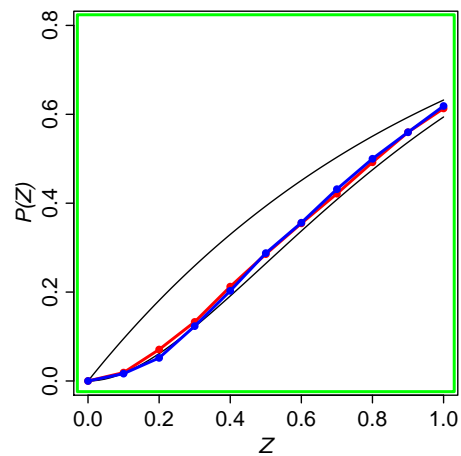
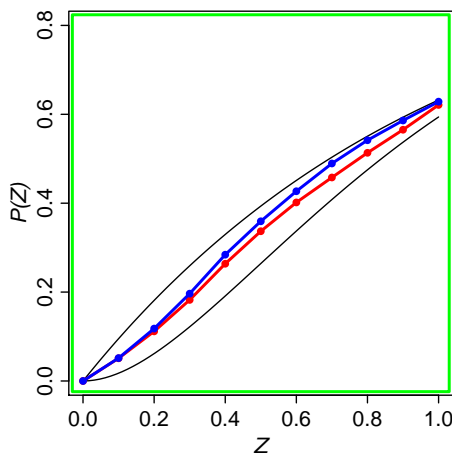
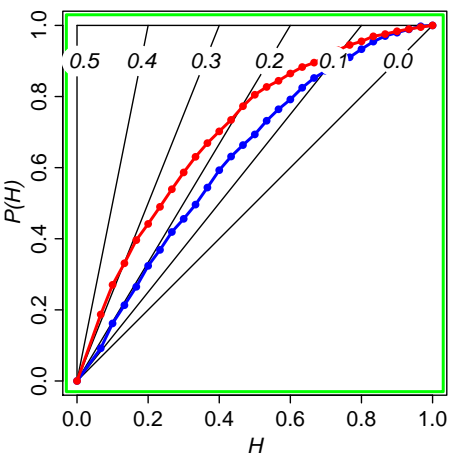
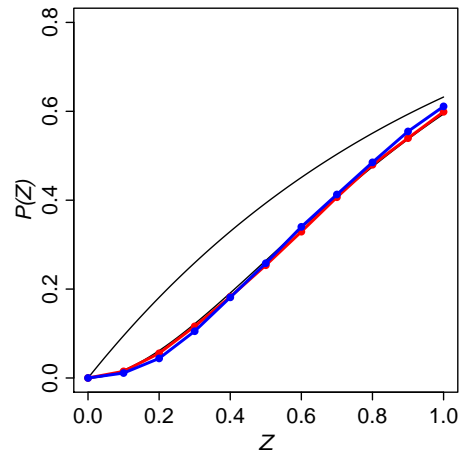
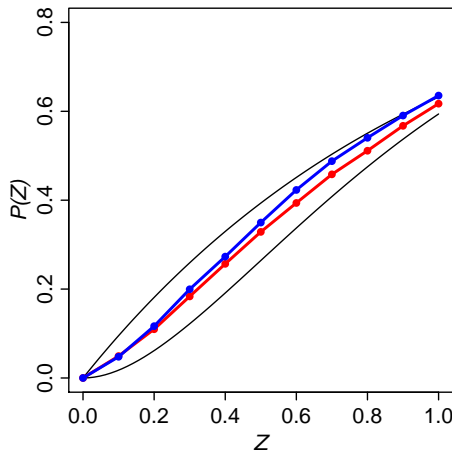
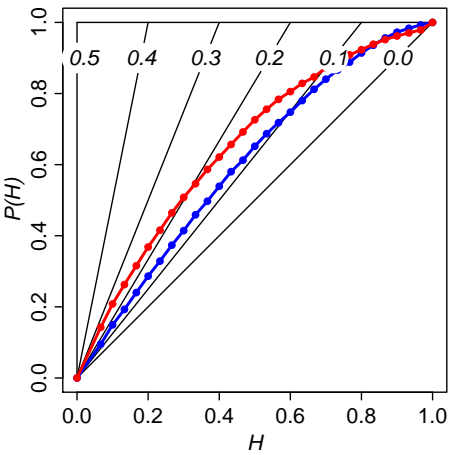
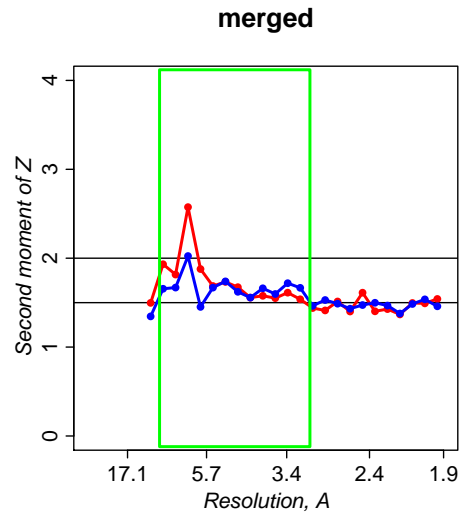
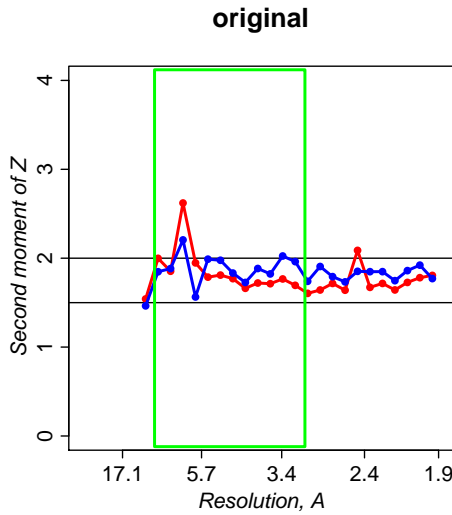
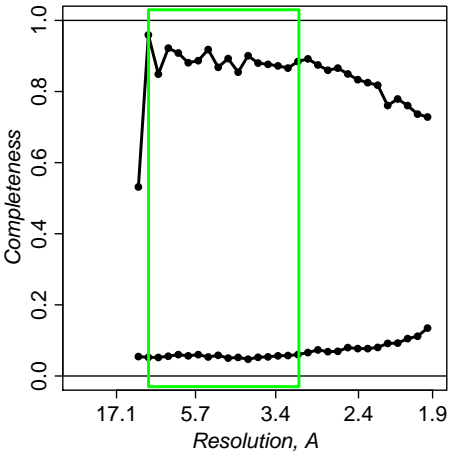
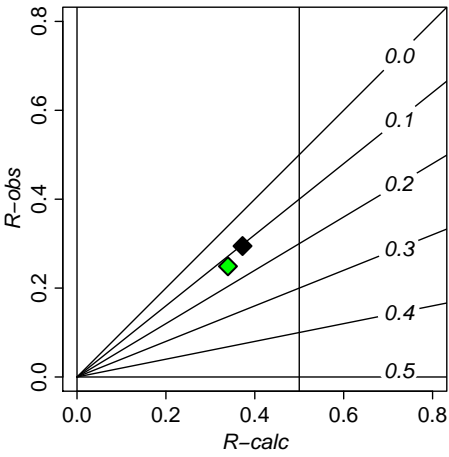
	original	merged
s.g.	P 1 21 1	P 21 21 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		1.31
R	29.5	
R'	33.7	35.4
R-free	32.6	
R'-free	37.2	38.2

residues per monomer	DNA	protein
	0	106

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	166	1.34 %
s,f <= 0	0	0.00 %

range (A)	12.0–1.9	9.9–3.0
unique	15,097	3,836
measured	12,412	3,380
used	9,010	2,524

NCS	translation	rotation
r.m.s.d. (A)	18.77	1.05
angle (o)	175.58	4.78



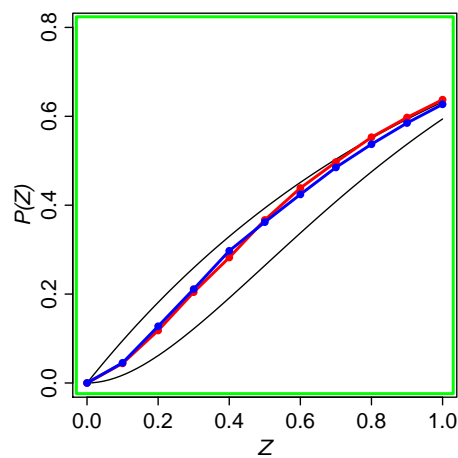
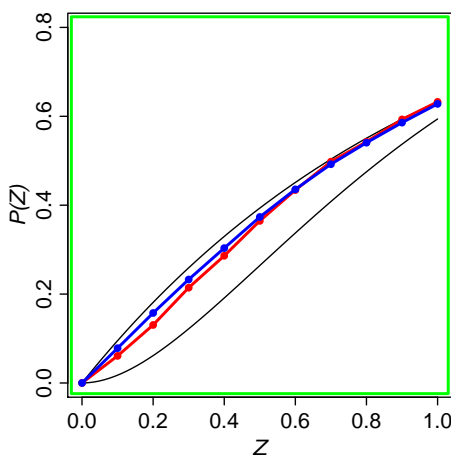
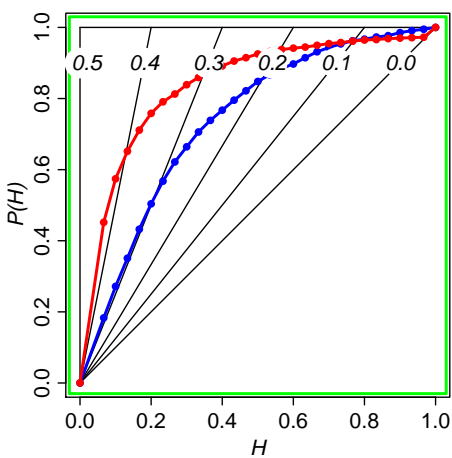
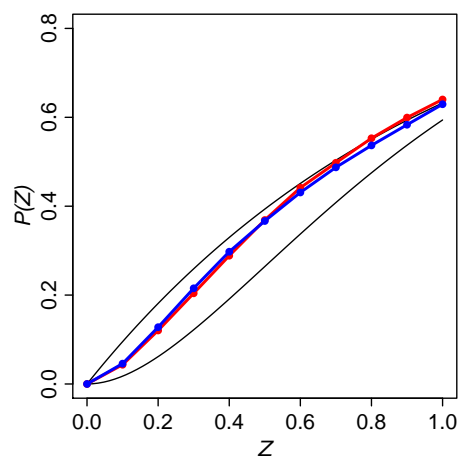
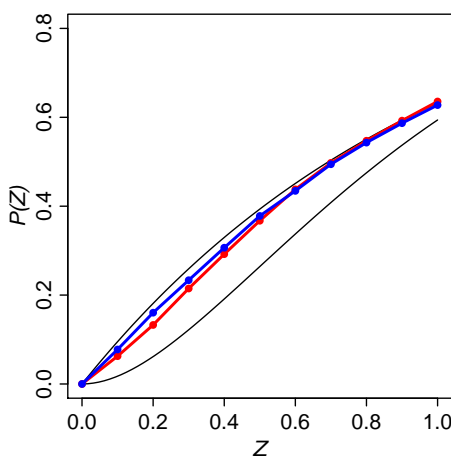
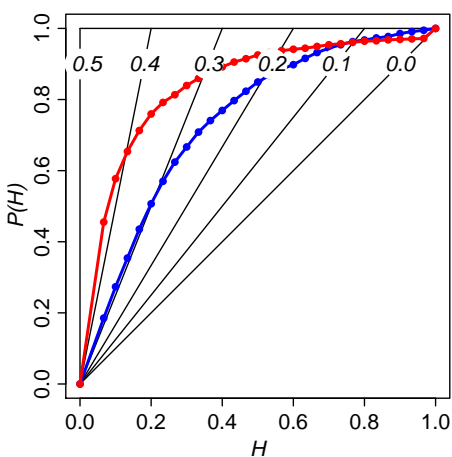
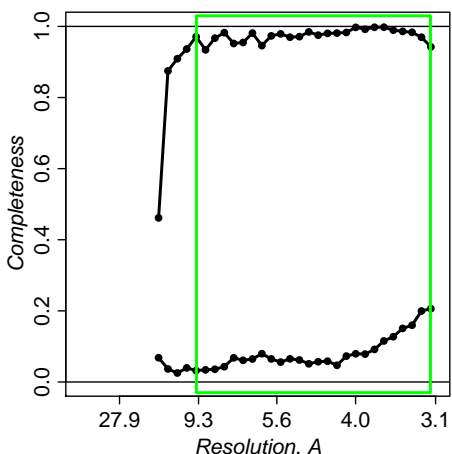
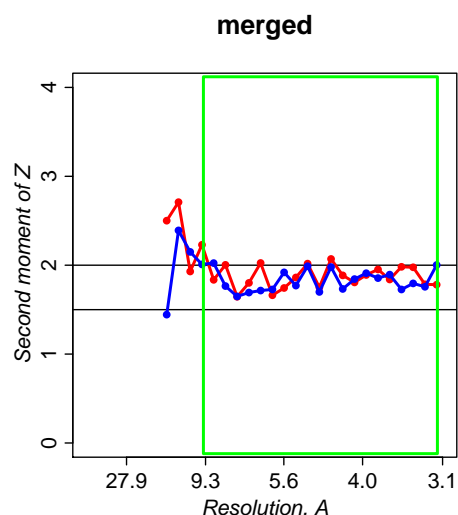
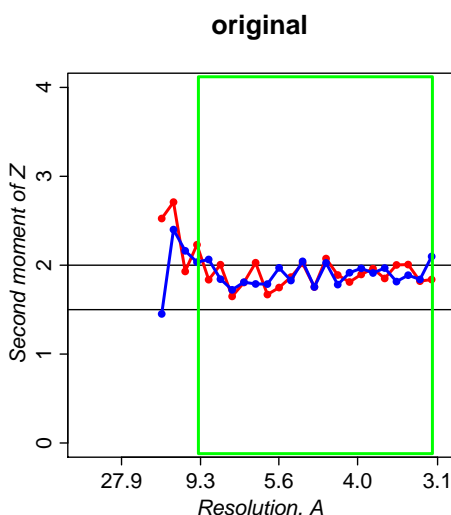
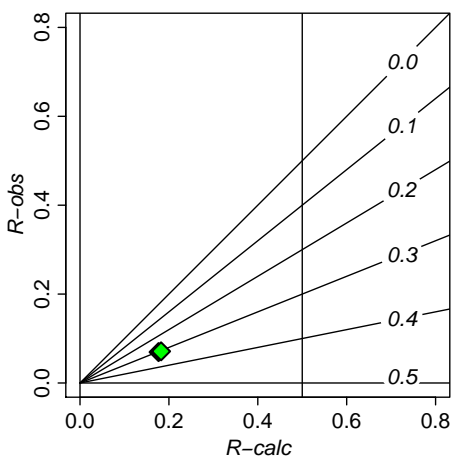
1a7b

	original	merged
s.g.	P 21 21 21	P 41 21 2
p.g.	10003	10205
a.u.	4	2
p.t.	2	2
p.o.	4	4
r.m.s.d. (A)		0.34
R	21.8	
R'	22.4	23.0
R-free	30.9	
R'-free	31.2	31.4
residues per monomer	DNA 0	protein 93

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	178	2.32 %
s,f <= 0	0	0.00 %

range (A)	14.9–3.1	9.9–3.1
unique	7,870	7,670
measured	7,684	7,503
used	6,196	6,092

NCS	translation	rotation
r.m.s.d. (A)	13.41	0.33
angle (o)	41.30	0.23



1a8g

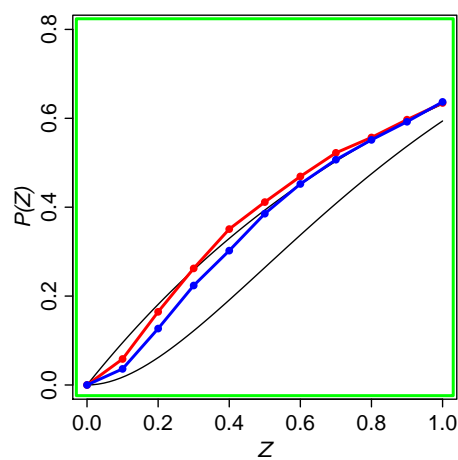
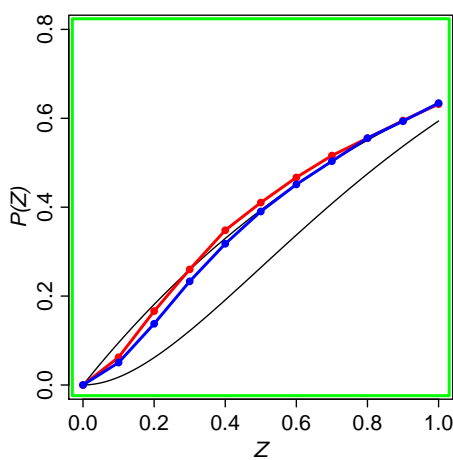
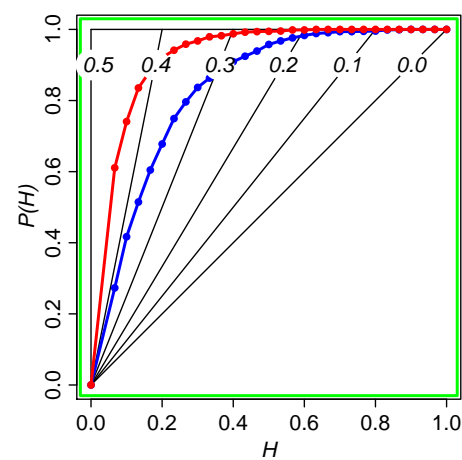
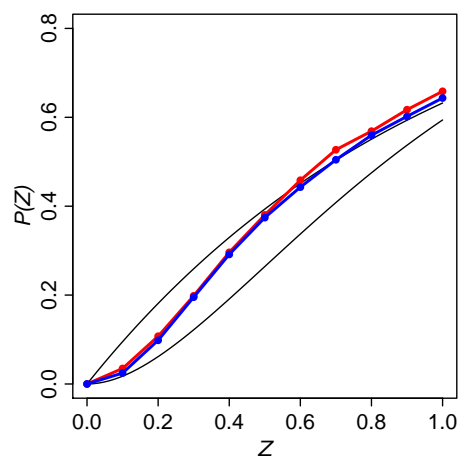
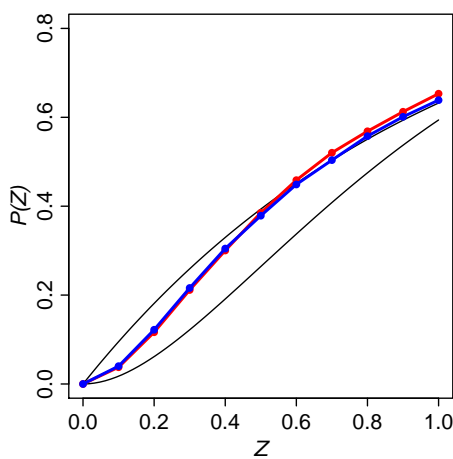
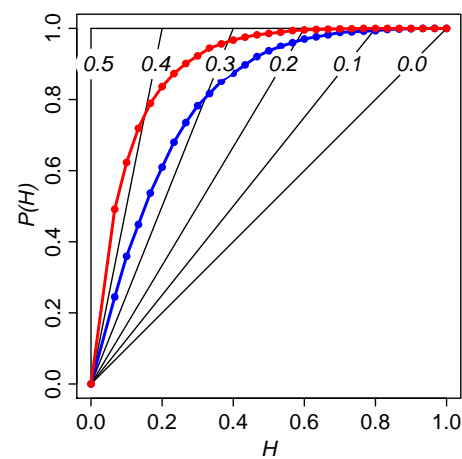
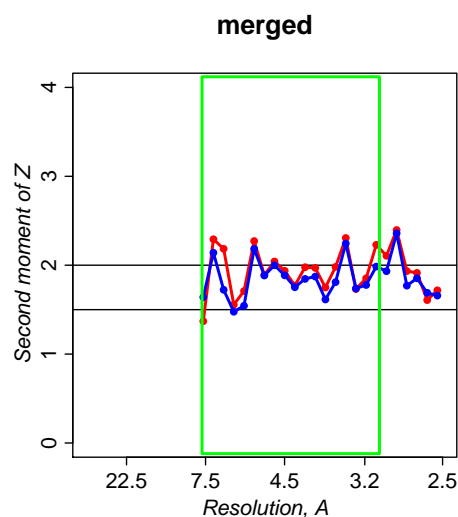
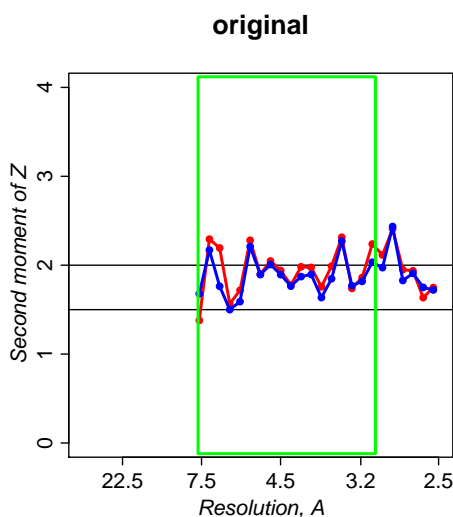
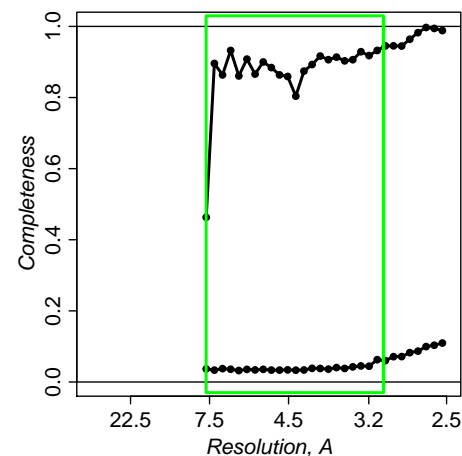
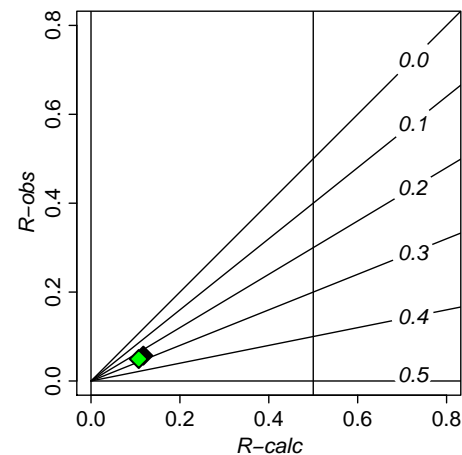
	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.25
R	22.9	
R'	23.9	25.0
R-free	29.2	
R'-free	34.4	32.5

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	8.0–2.5	8.0–3.0
unique	5,992	3,617
measured	5,566	3,252
used	4,638	2,600

NCS	translation	rotation
r.m.s.d. (A)	19.51	0.25
angle (o)	179.84	0.27

residues per monomer	DNA	protein
	0	99



1aar

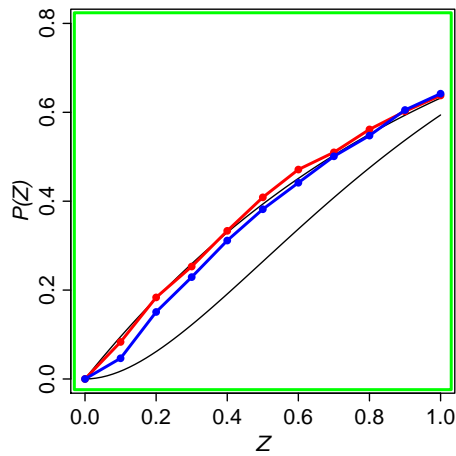
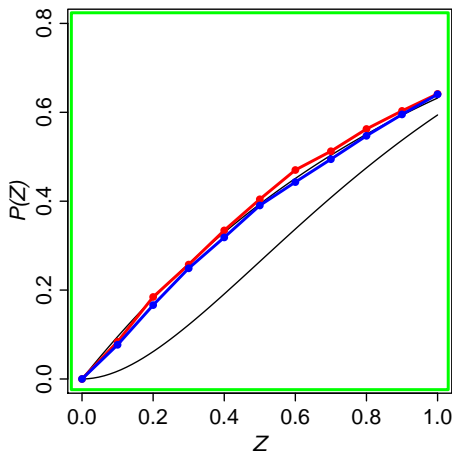
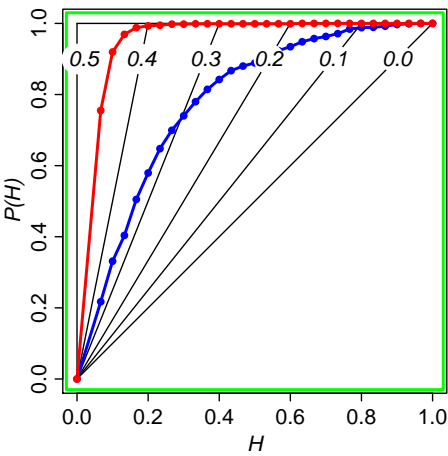
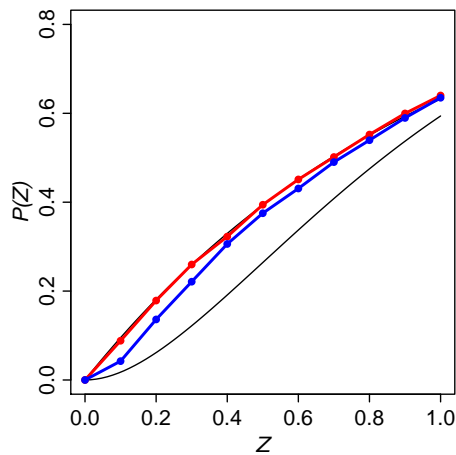
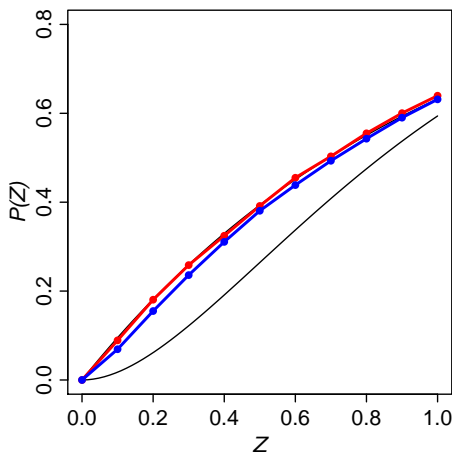
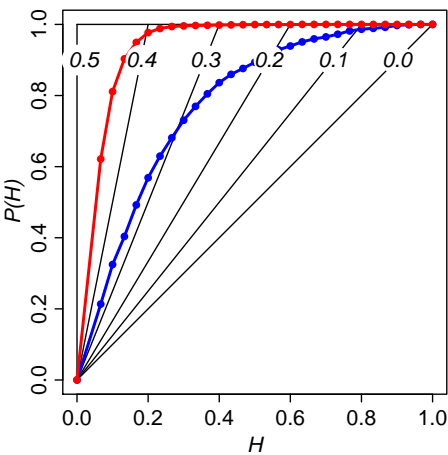
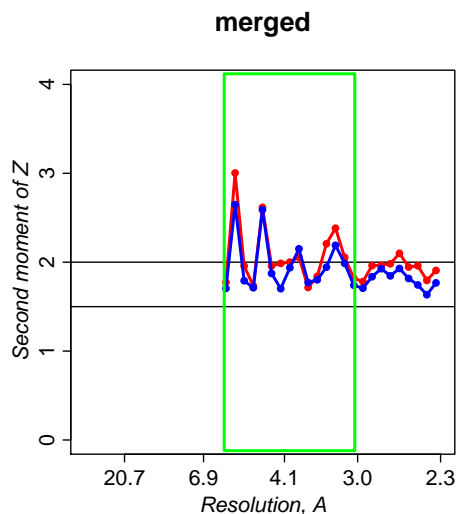
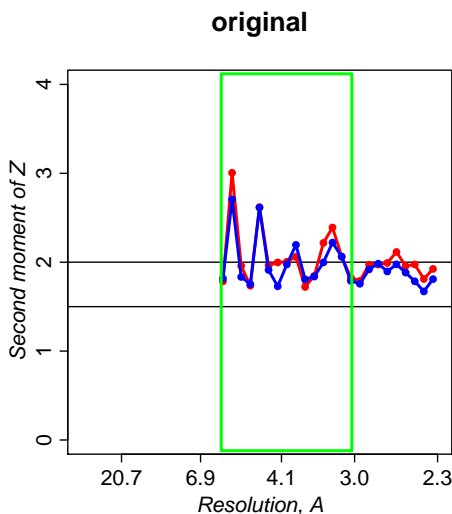
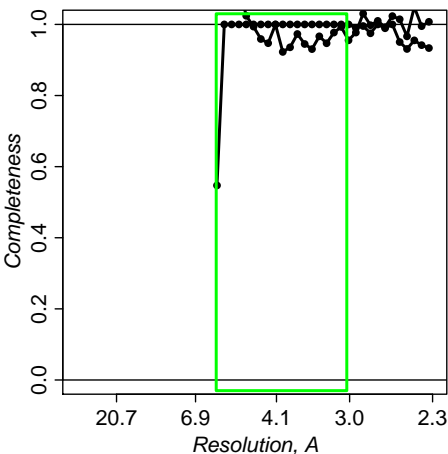
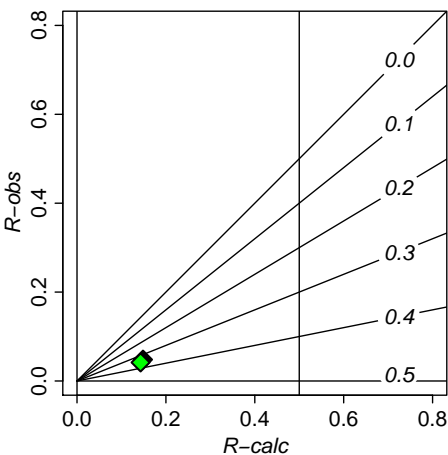
	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		1.46
R	20.2	
R'	21.2	21.9
R-free	26.2	
R'-free	28.3	28.2

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	6.0–2.3	6.0–3.0
unique	5,171	2,187
measured	5,074	2,187
used	4,712	2,016

NCS	translation	rotation
r.m.s.d. (A)	19.40	1.46
angle (o)	177.48	2.92

residues per monomer	DNA	protein
	0	76



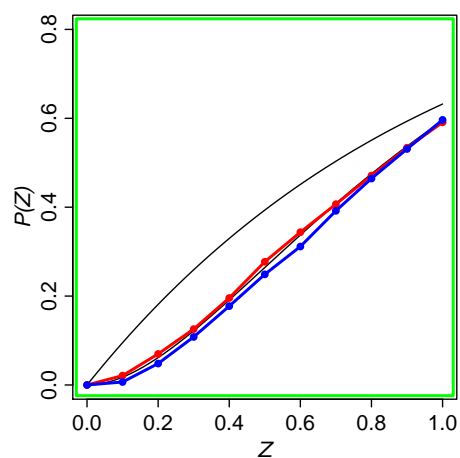
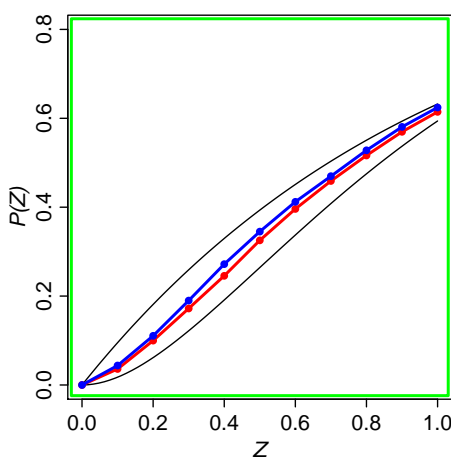
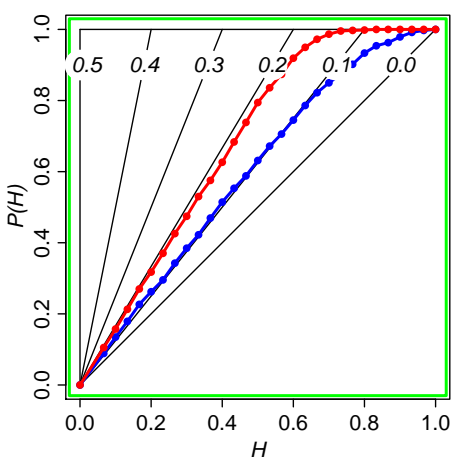
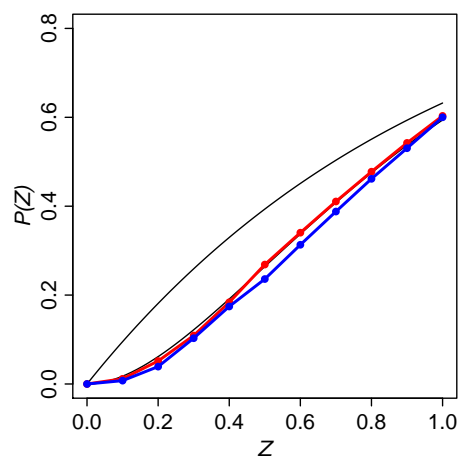
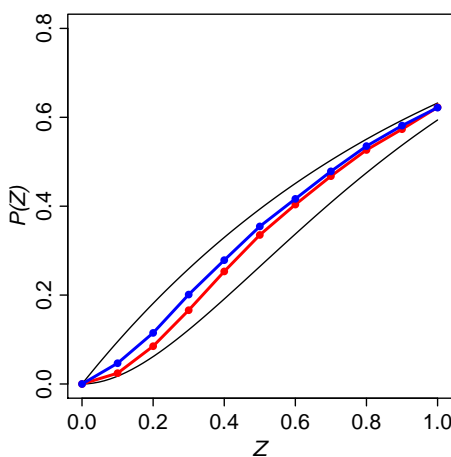
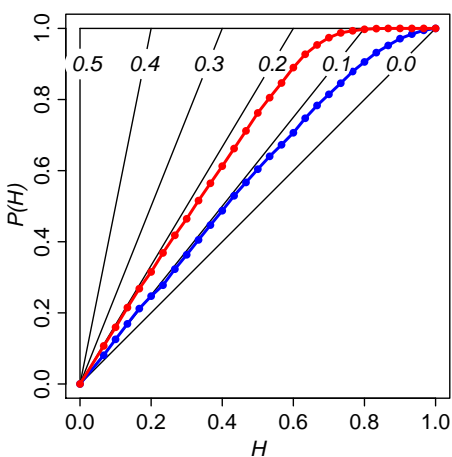
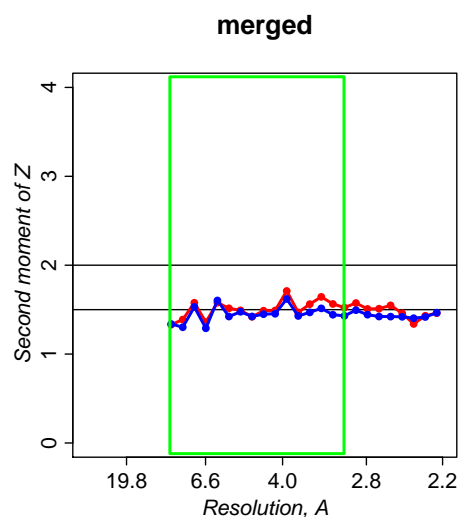
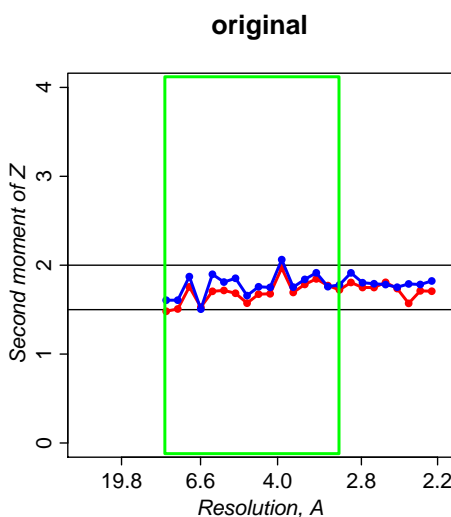
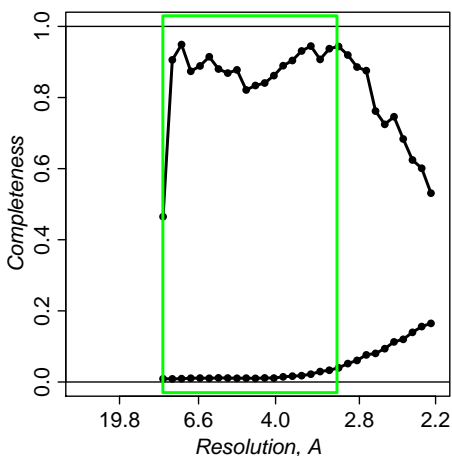
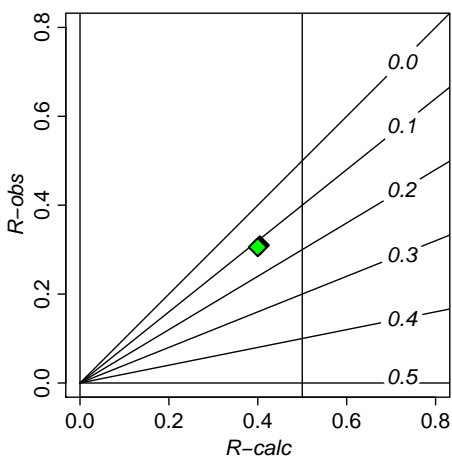
1ab6

	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		4.67
R	21.1	
R'	-	-
R-free	26.1	
R'-free	-	-
residues per monomer	DNA 0	protein 125

s < f/100	1466	17.81 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	10.0–2.2	9.9–3.0
unique	10,158	4,967
measured	8,233	4,444
used	6,386	3,608

NCS	translation	rotation
r.m.s.d. (A)	20.52	3.04
angle (o)	166.94	15.51



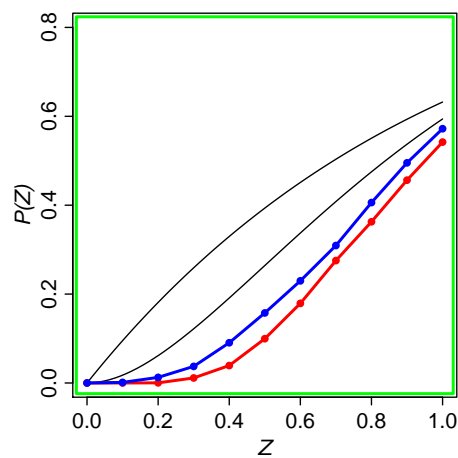
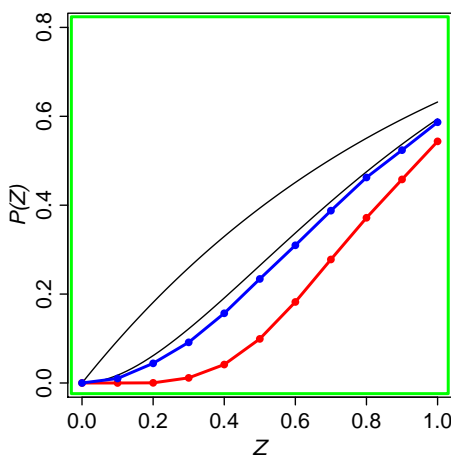
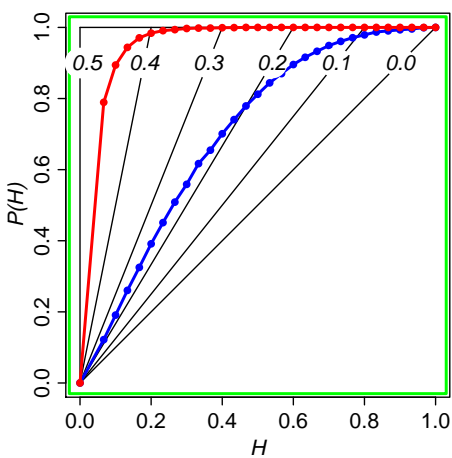
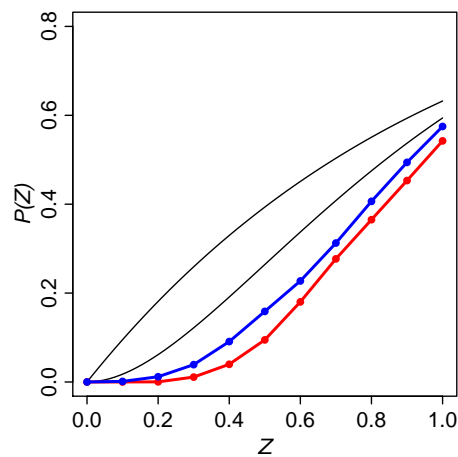
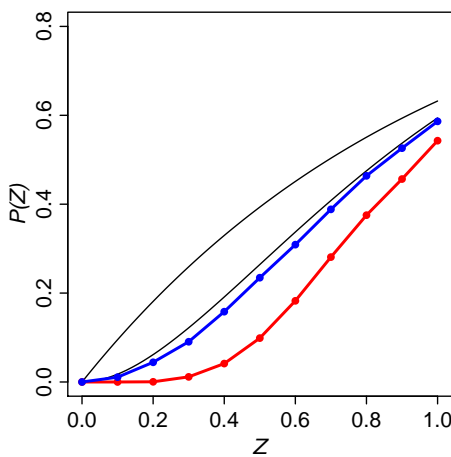
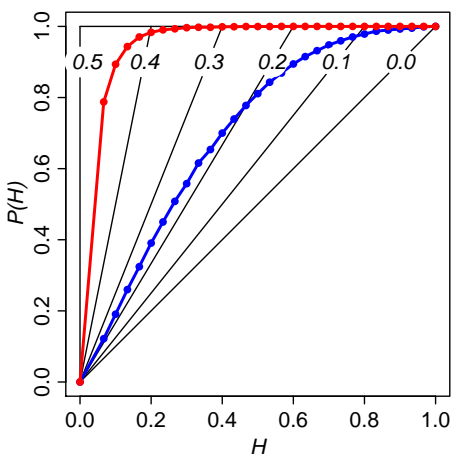
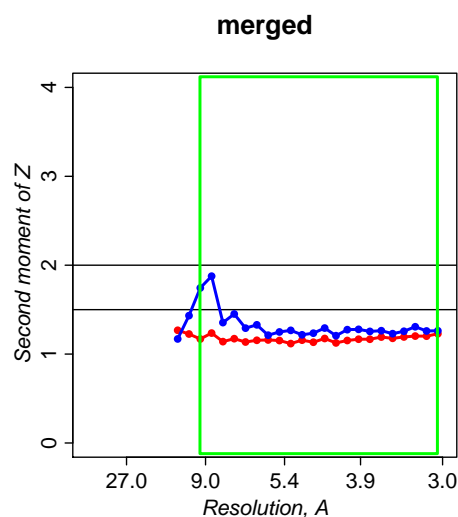
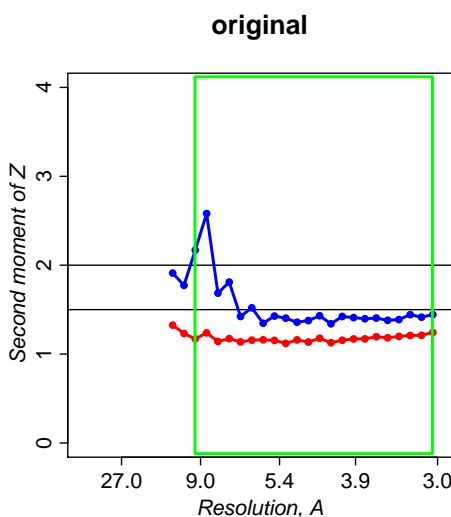
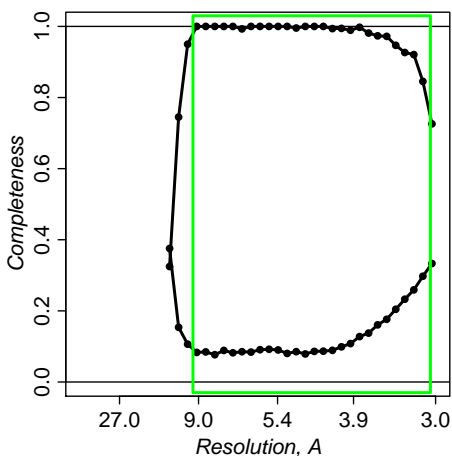
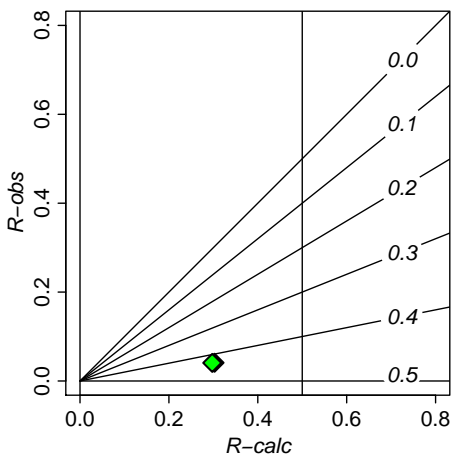
1aow

	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	23.9	-
R'	-	-
R-free	31.1	-
R'-free	-	-
residues per monomer	DNA 0	protein 309

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	12.5-3.0	9.9-3.0
unique	8,584	8,371
measured	8,114	7,992
used	7,480	7,404

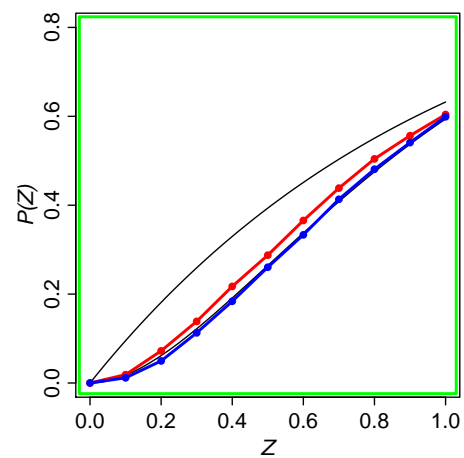
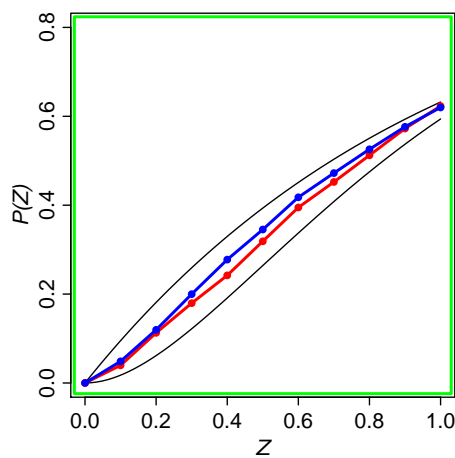
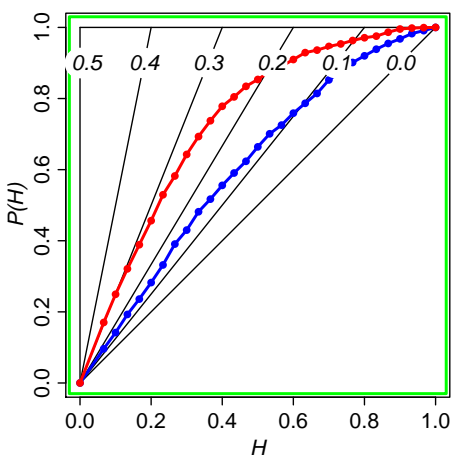
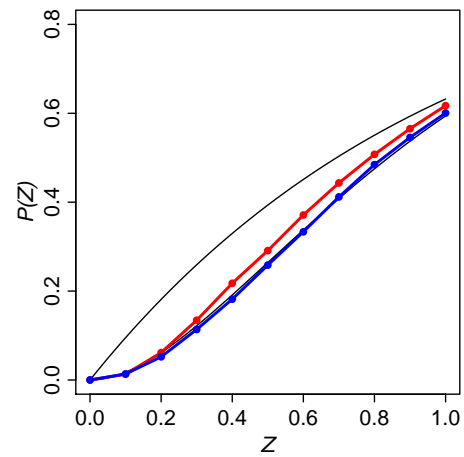
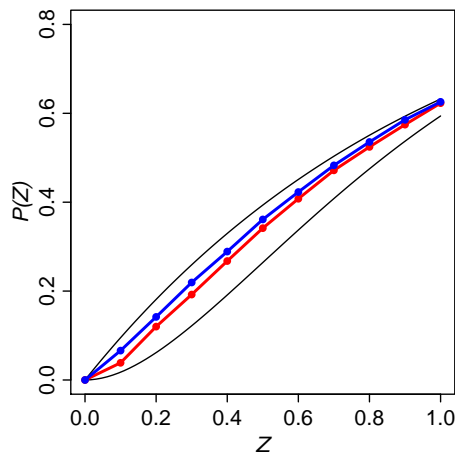
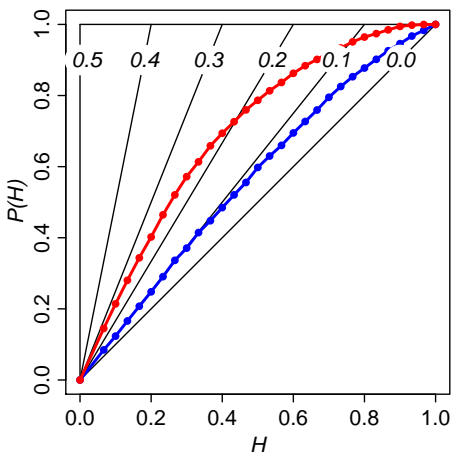
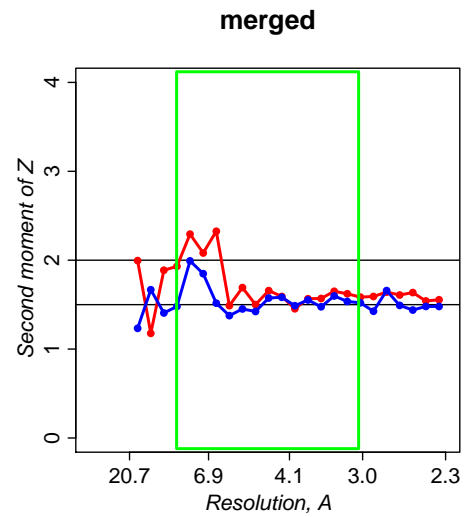
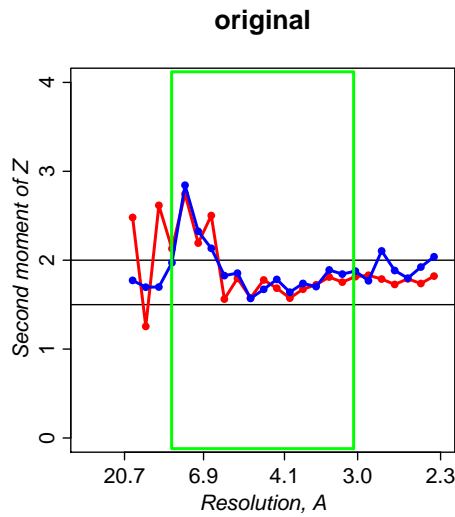
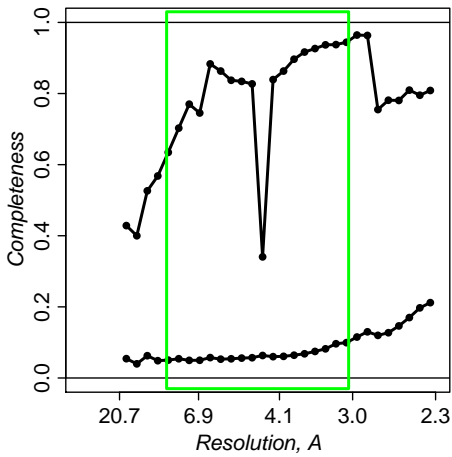
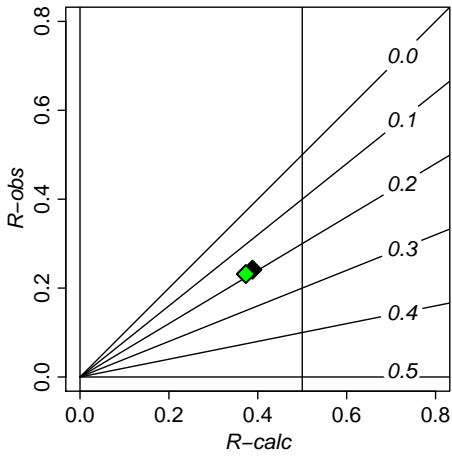
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1ap9

	original	merged
s.g.	P 63	-
p.g.	12021	12027
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	33.6	-
R'	-	-
R-free	41.6	-
R'-free	-	-
residues per monomer	DNA 0	protein 219

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	19.9–2.3	9.9–3.0
unique	10,047	4,439
measured	8,398	3,807
used	7,096	3,090
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1as1

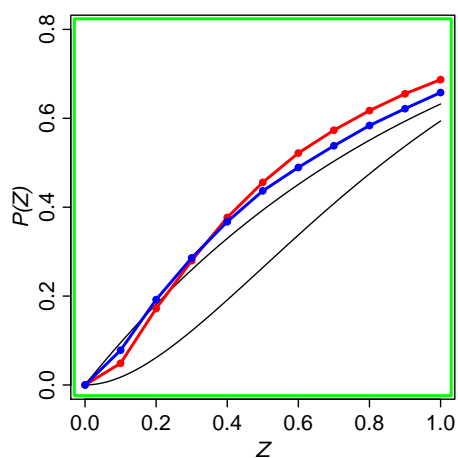
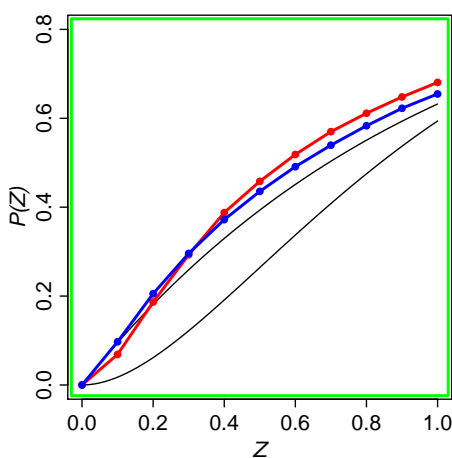
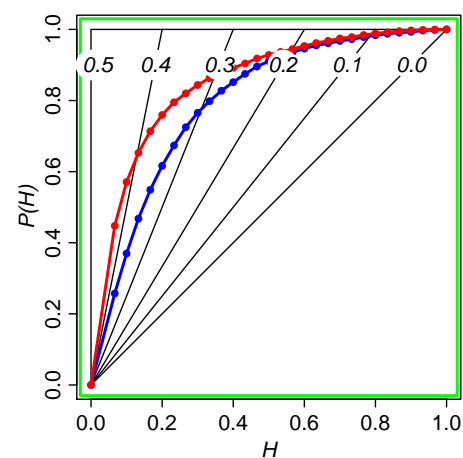
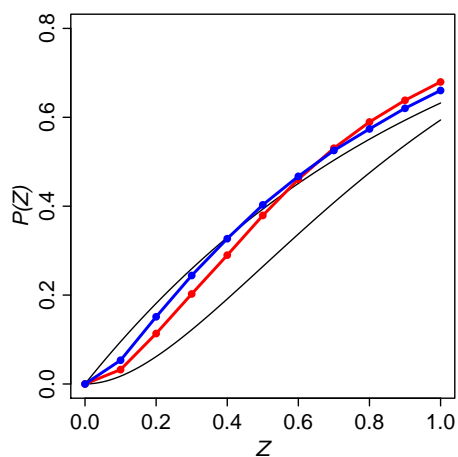
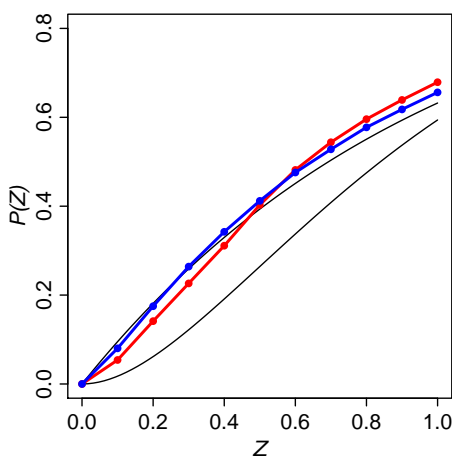
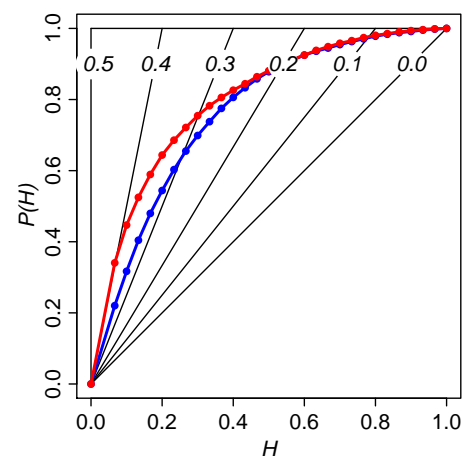
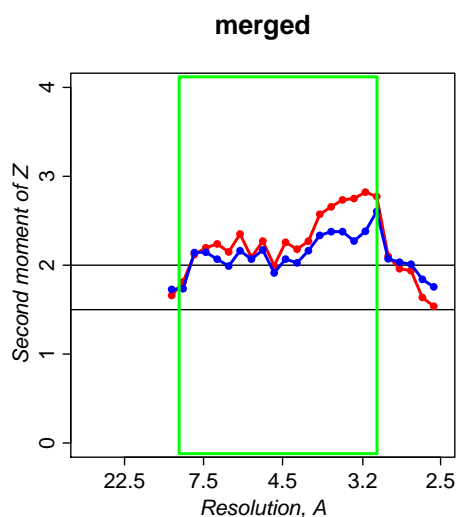
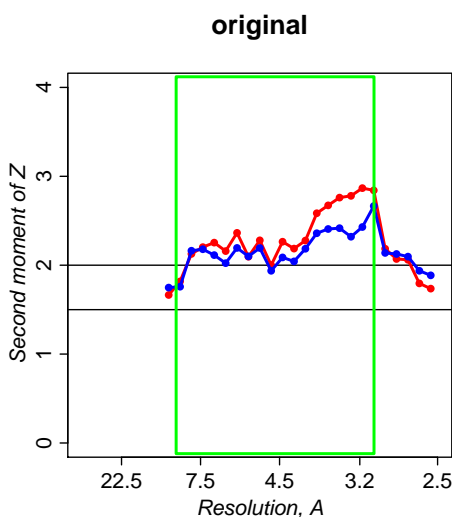
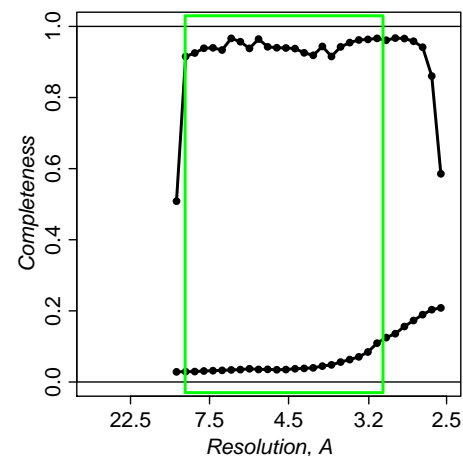
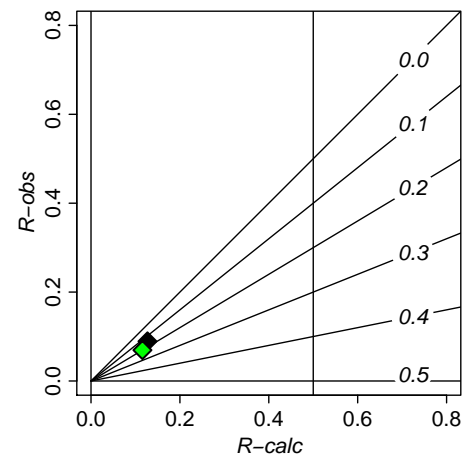
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.30
R	24.0	
R'	24.6	24.1
R-free	28.8	
R'-free	29.6	28.8

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	11.0–2.5	9.9–3.0
unique	35,411	20,592
measured	32,478	19,483
used	28,684	16,934

NCS	translation	rotation
r.m.s.d. (A)	36.37	0.30
angle (o)	179.93	0.07

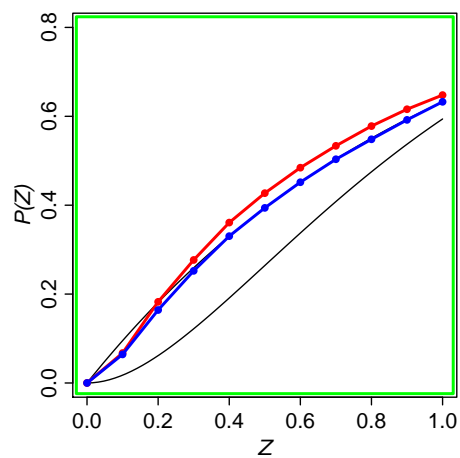
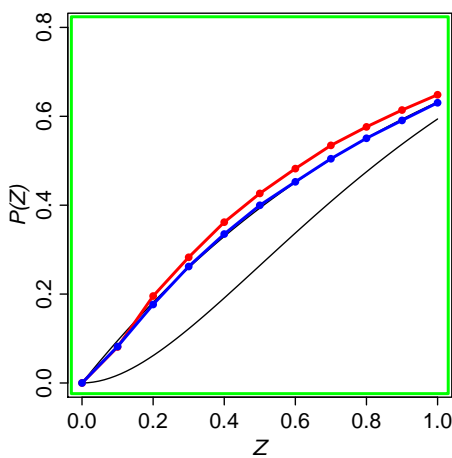
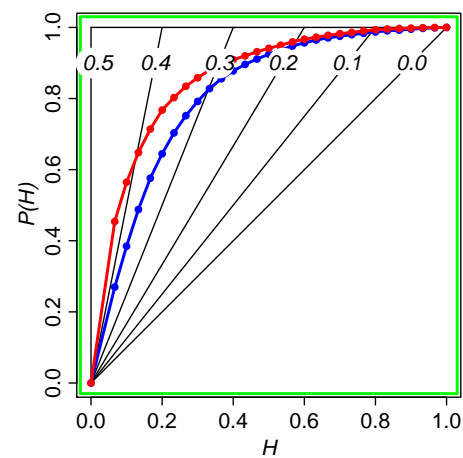
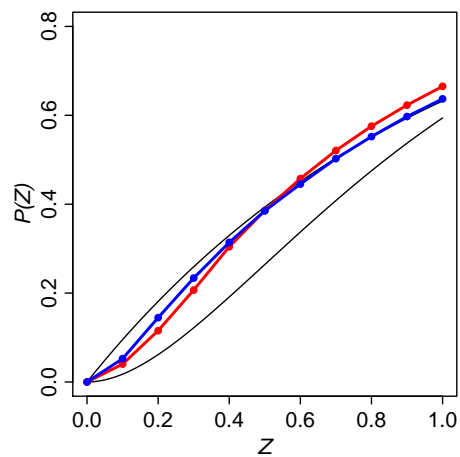
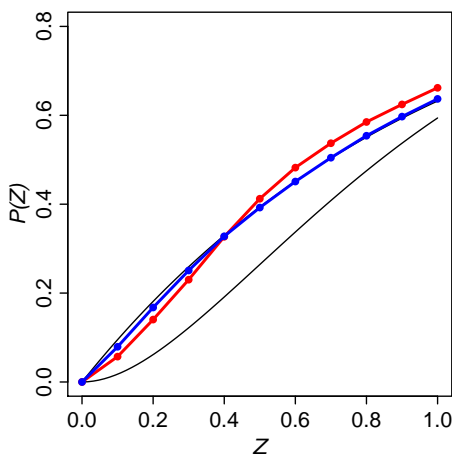
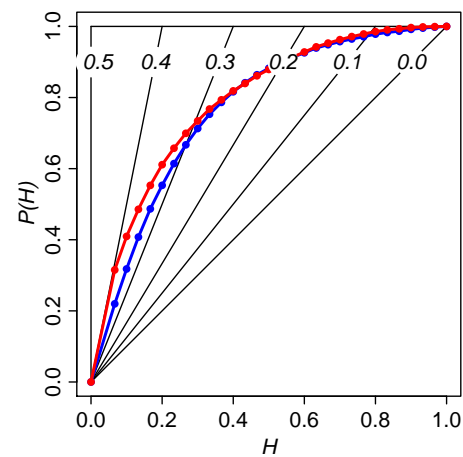
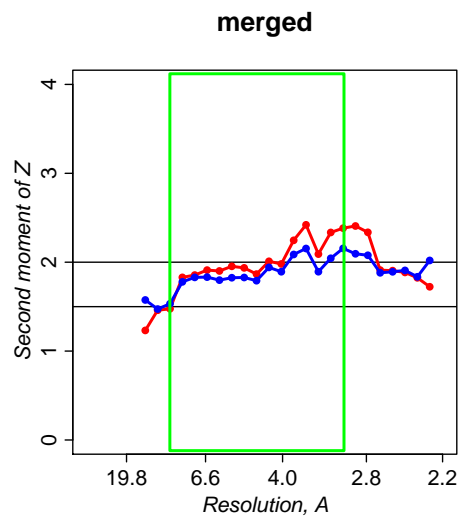
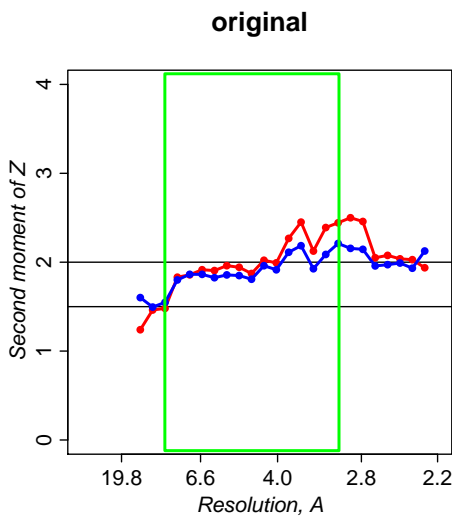
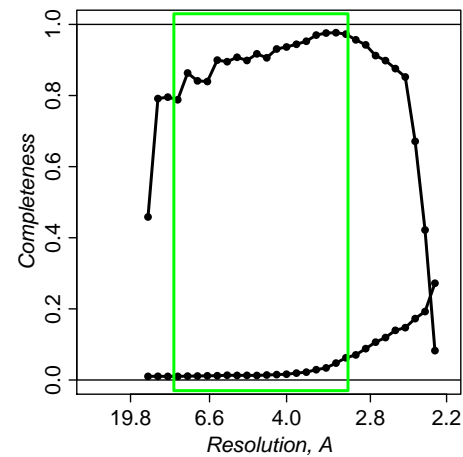
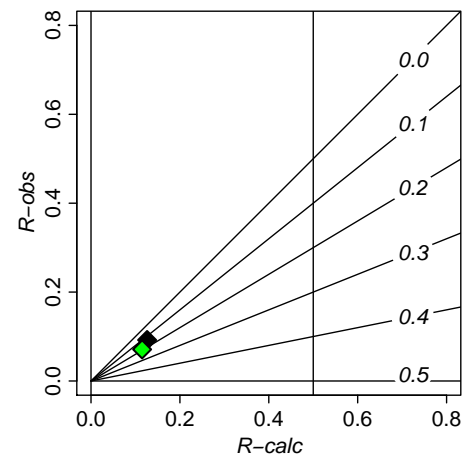
residues per monomer	DNA	protein
	0	396



1asm

	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.24
R	23.6	
R'	24.2	24.1
R-free	27.8	
R'-free	28.3	27.4
residues per monomer	DNA 0	protein 396

s < f/100	3435	8.68 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	15.0–2.2	9.9–3.0
unique	49,354	20,540
measured	39,577	19,251
used	34,434	16,754
NCS	translation	rotation
r.m.s.d. (A)	36.44	0.23
angle (o)	179.97	0.04



1asn

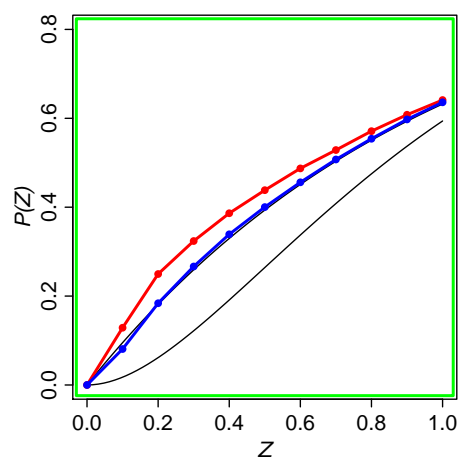
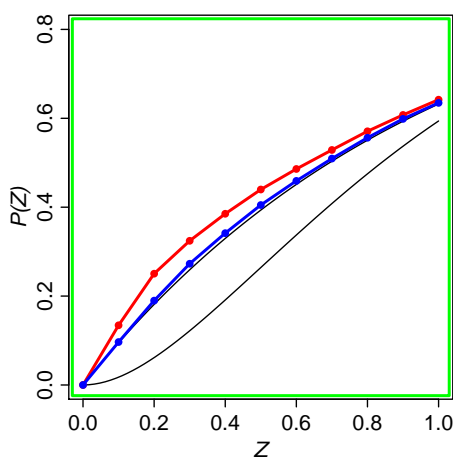
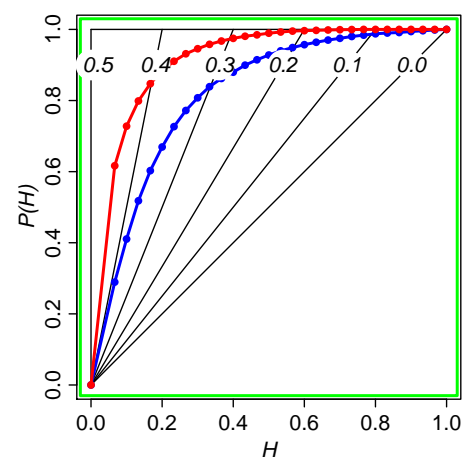
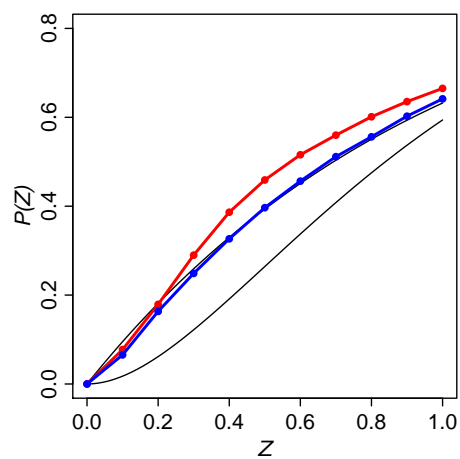
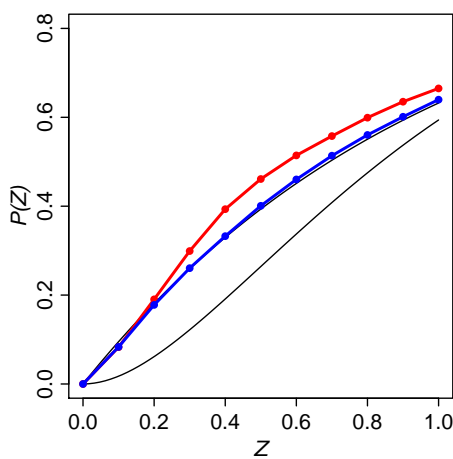
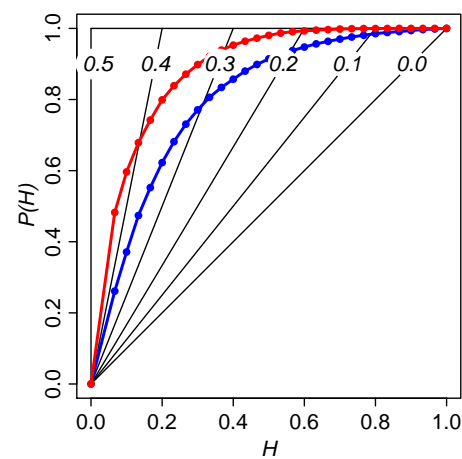
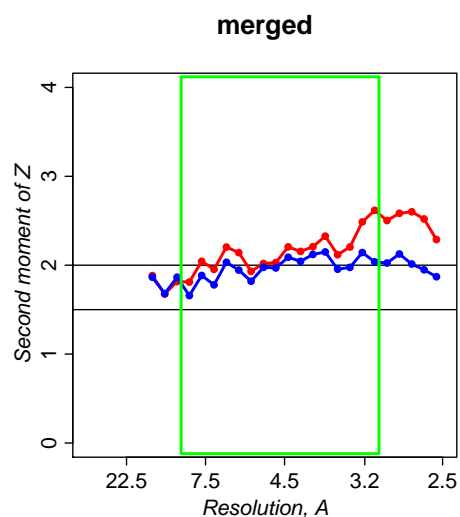
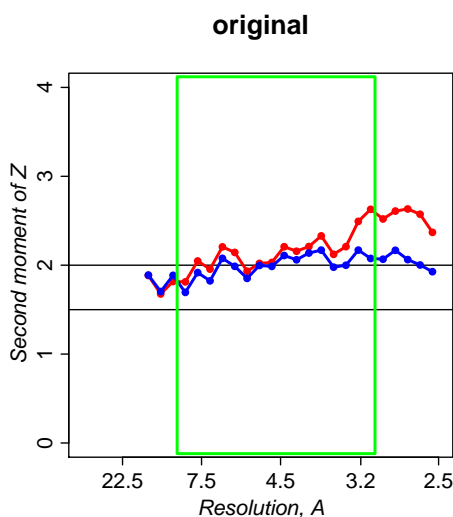
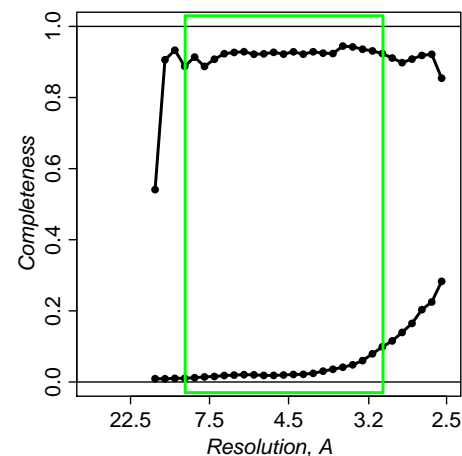
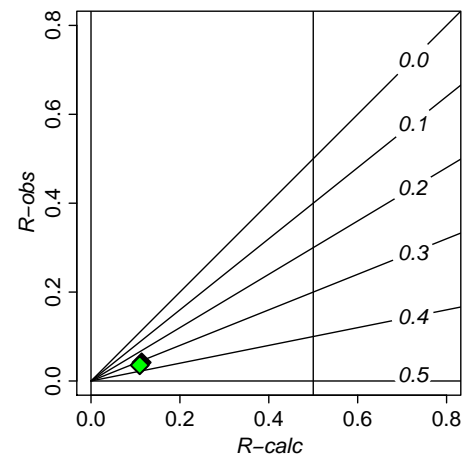
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.25
R	22.6	
R'	23.4	23.7
R-free	26.3	
R'-free	27.4	27.5

s < f/100	1277	3.83 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	15.0–2.5	9.9–3.0
unique	36,341	21,192
measured	33,324	19,664
used	28,716	16,850

NCS	translation	rotation
r.m.s.d. (A)	36.63	0.25
angle (o)	179.97	0.04

residues per monomer	DNA	protein
	0	396



1aw1

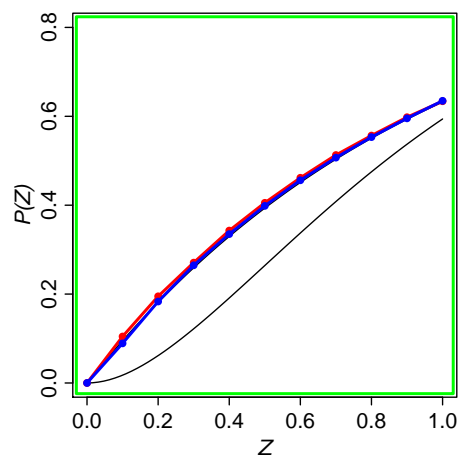
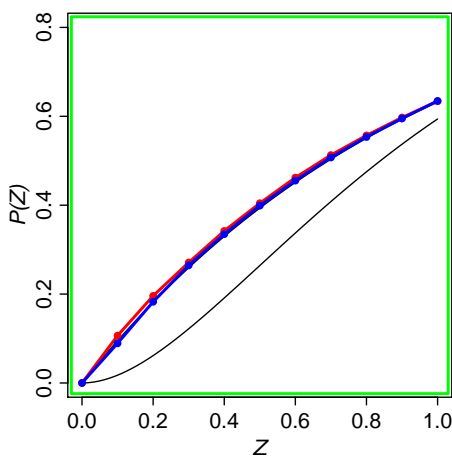
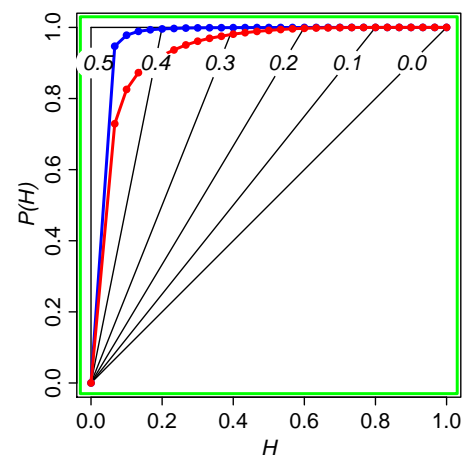
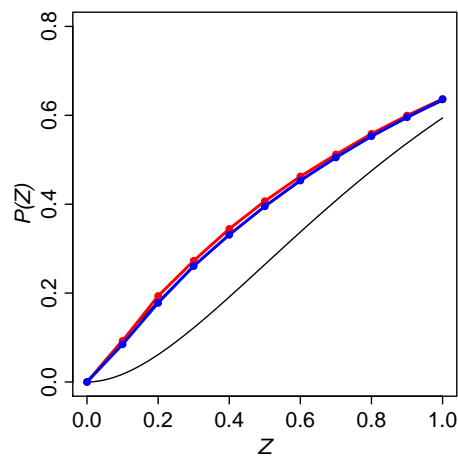
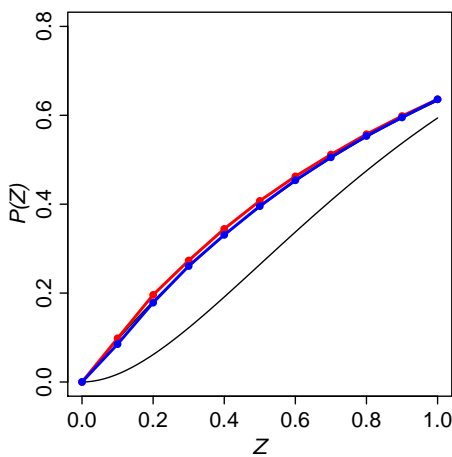
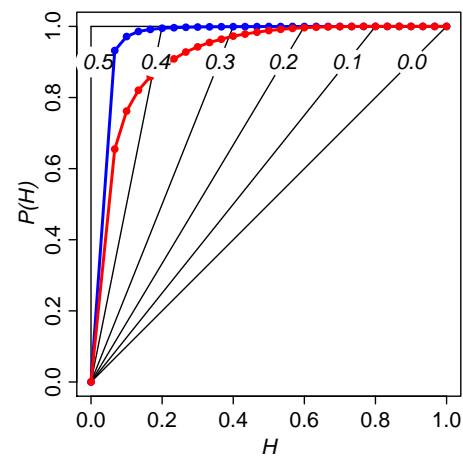
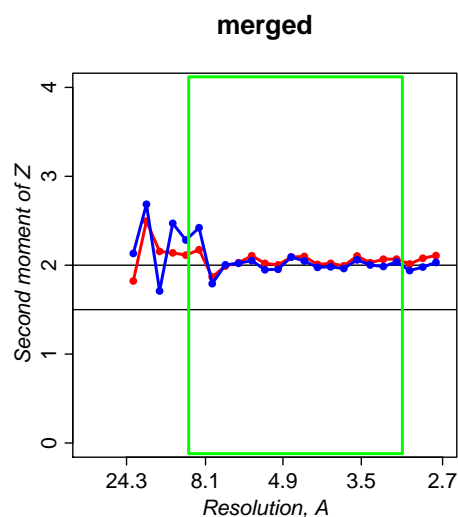
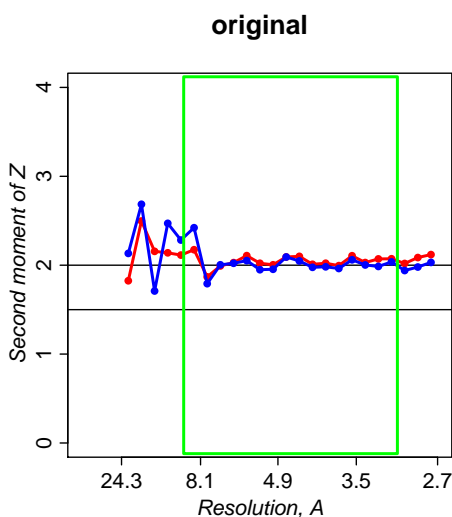
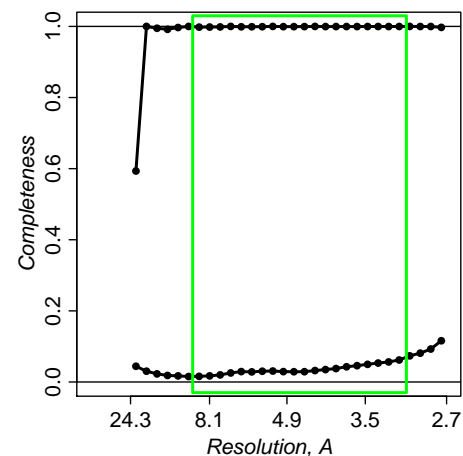
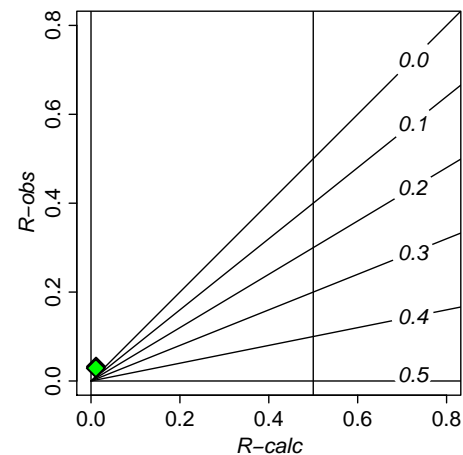
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	8	4
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.02
R	18.7	
R'	18.7	18.8
R-free	24.1	
R'-free	24.1	24.0

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	24.2–2.7	9.9–3.0
unique	59,649	42,380
measured	59,609	42,363
used	56,076	39,744

NCS	translation	rotation
r.m.s.d. (A)	15.48	0.01
angle (o)	65.57	0.02

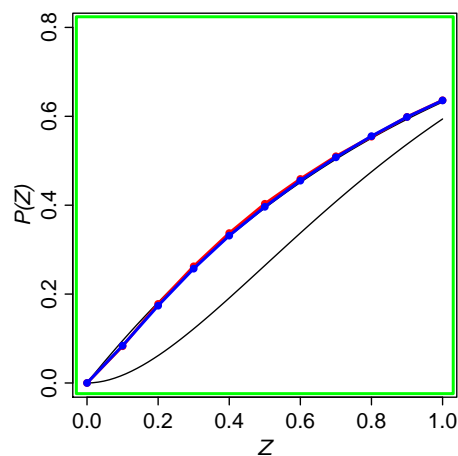
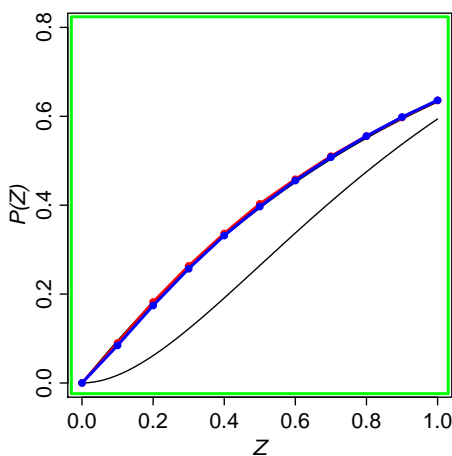
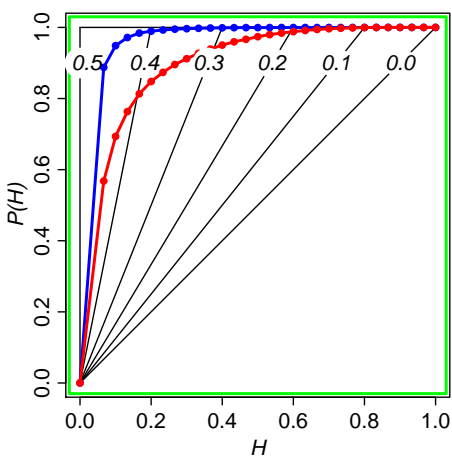
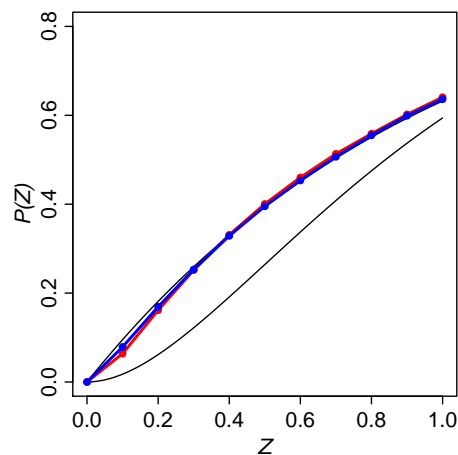
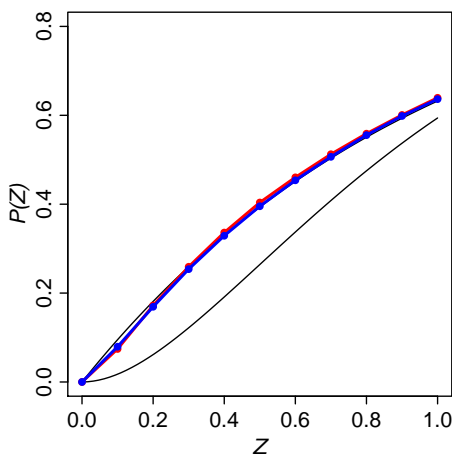
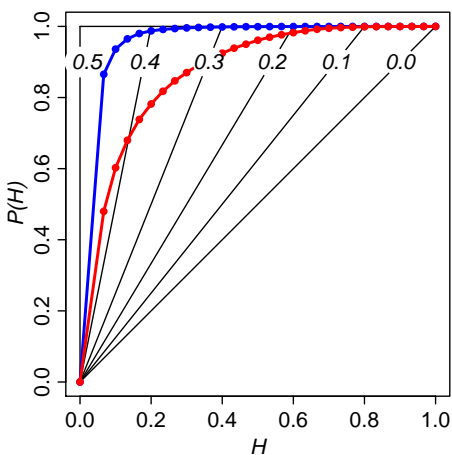
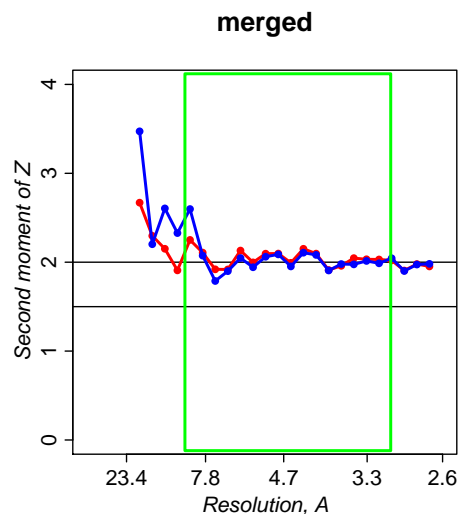
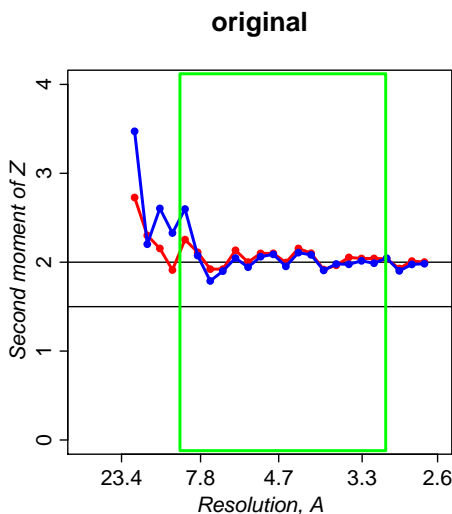
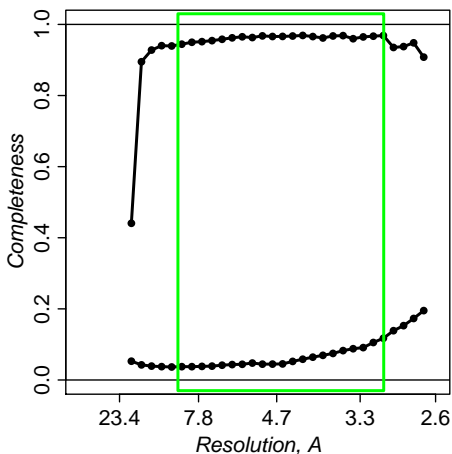
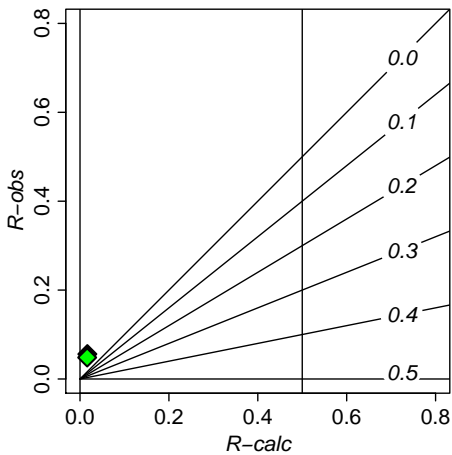
residues per monomer	DNA	protein
	0	254



1aw2

	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	8	4
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.04
R	19.2	
R'	19.2	19.2
R-free	23.6	
R'-free	23.6	23.3
residues per monomer	DNA 0	protein 254

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	20.0–2.7	9.9–3.0
unique	62,949	42,366
measured	60,025	40,867
used	54,480	37,266
NCS	translation	rotation
r.m.s.d. (A)	15.65	0.02
angle (o)	65.44	0.03



1ayp

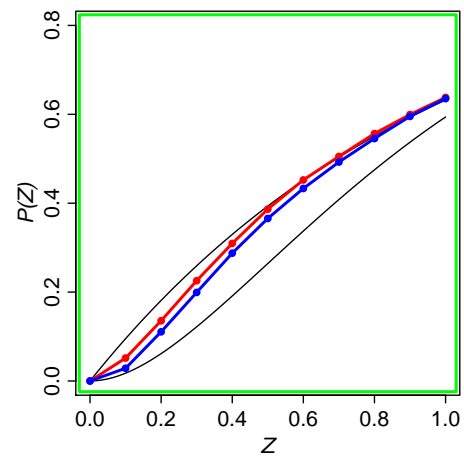
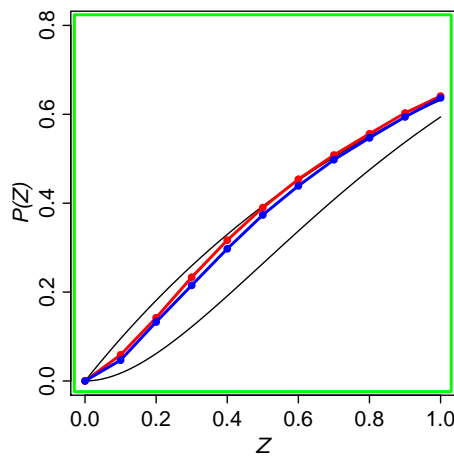
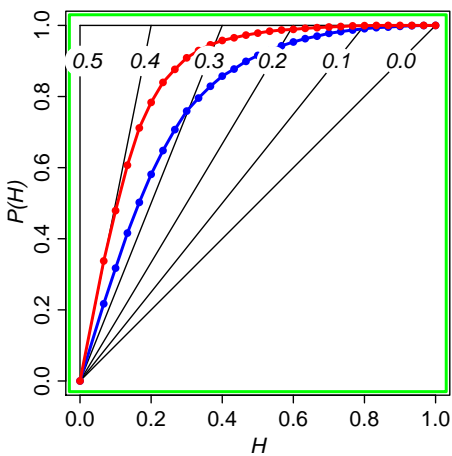
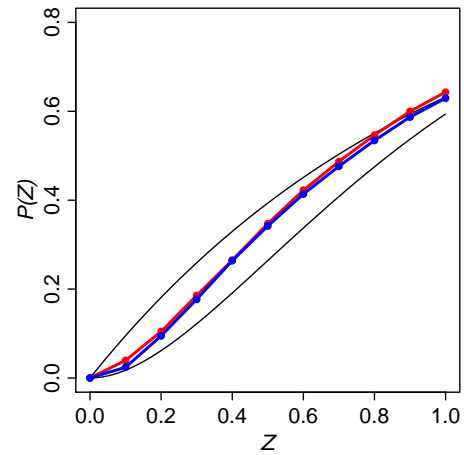
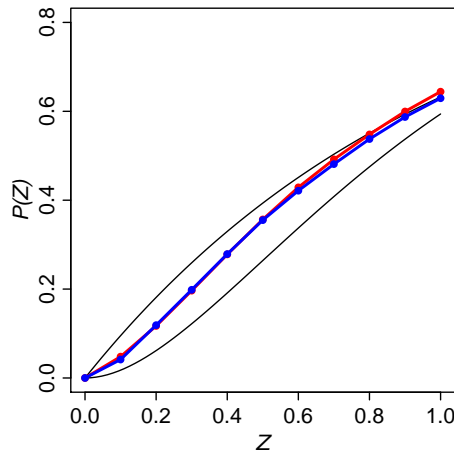
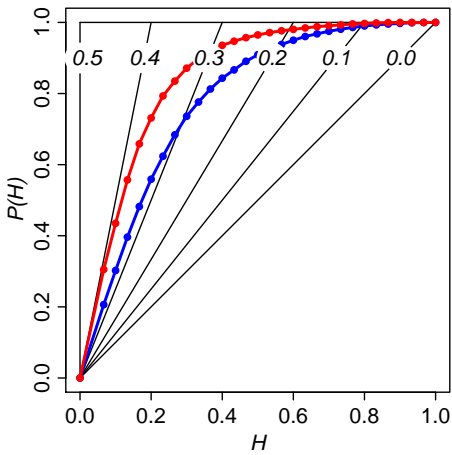
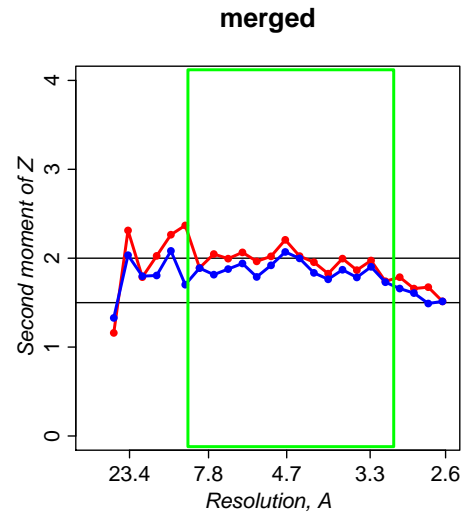
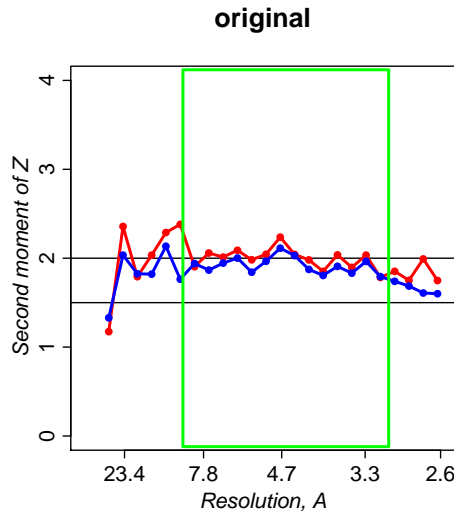
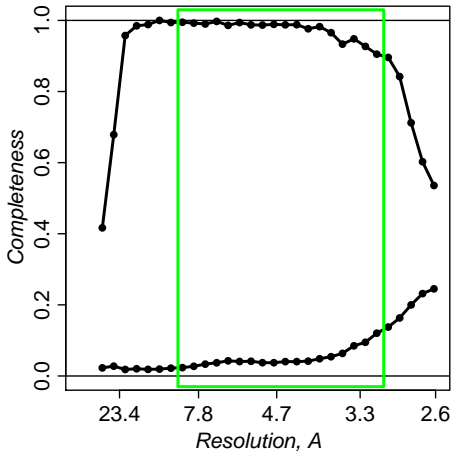
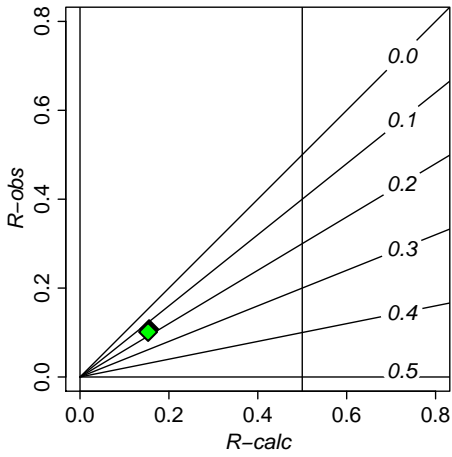
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.40
R	25.4	
R'	26.0	26.7
R-free	31.3	
R'-free	32.7	32.9

residues per monomer	DNA	protein
	0	124

s < f/100	319	1.44 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	55.7–2.6	9.9–3.0
unique	25,870	15,864
measured	22,200	15,191
used	18,732	13,622

NCS	translation	rotation
r.m.s.d. (A)	11.77	0.35
angle (o)	59.18	0.22



1b0w

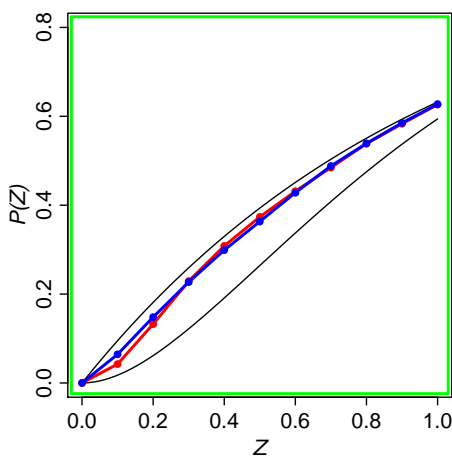
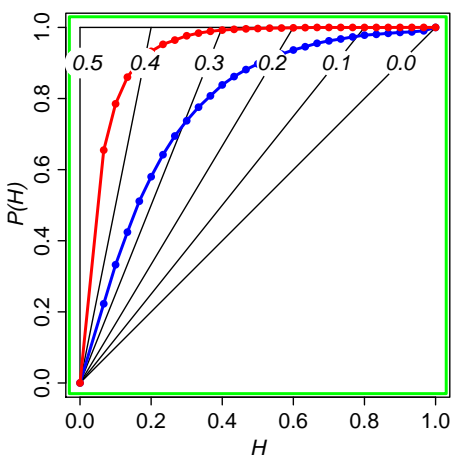
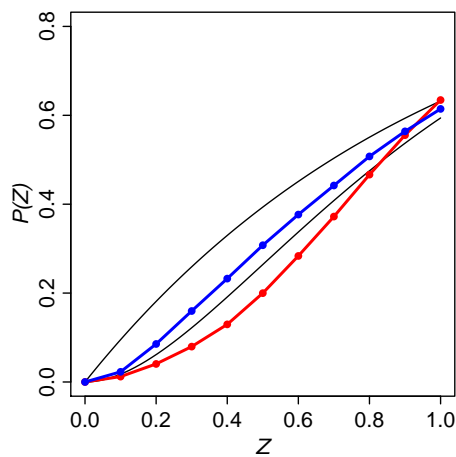
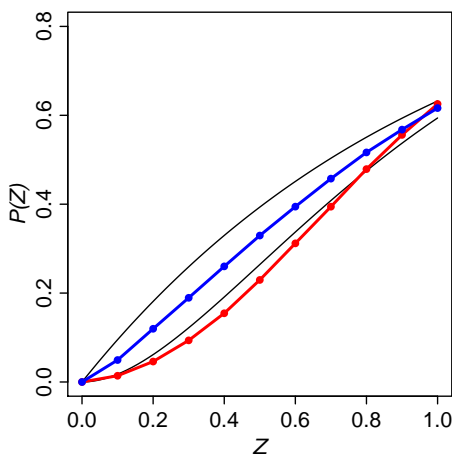
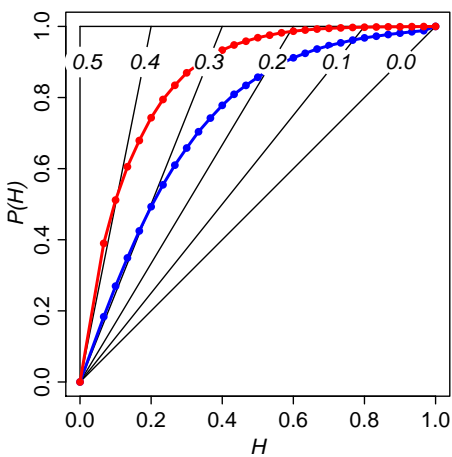
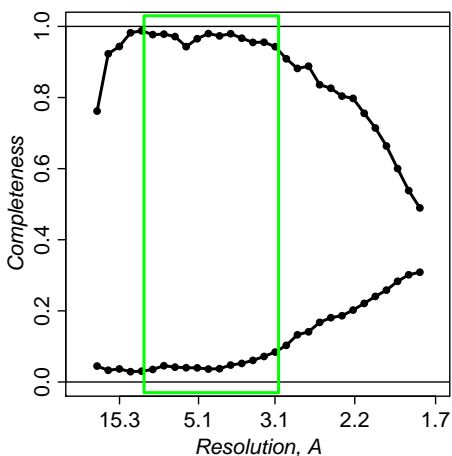
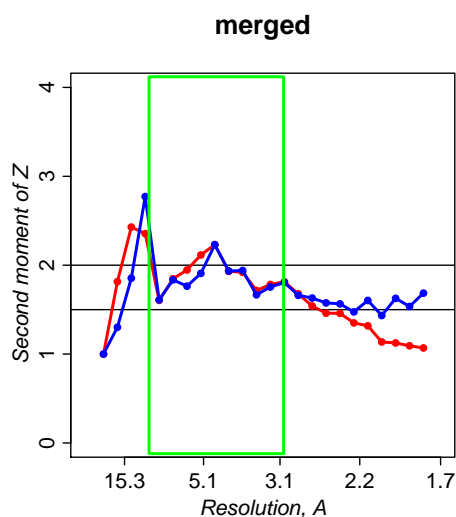
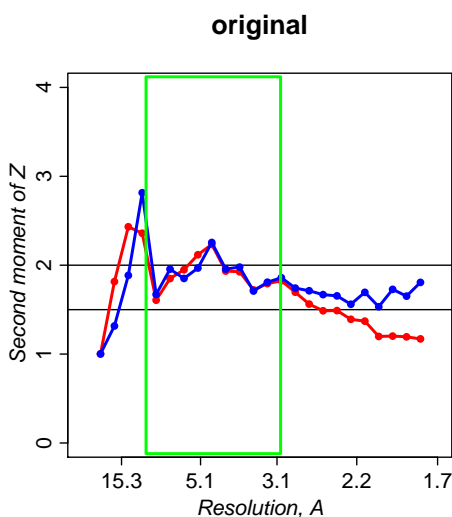
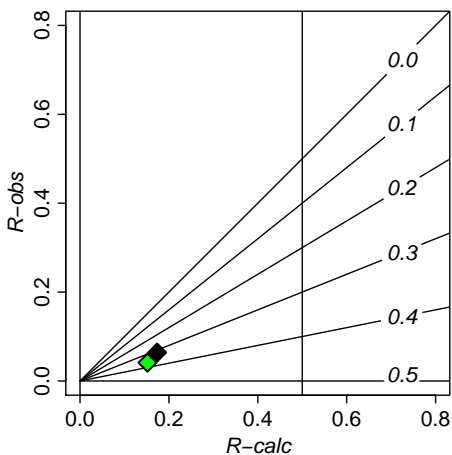
	original	merged
s.g.	C 2 2 2 1	P 61 2 2
p.g.	10003	12027
a.u.	3	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.18
R	26.6	
R'	26.5	28.1
R-free	29.5	
R'-free	29.5	31.6

residues per monomer	DNA	protein
	0	108

s < f/100	1	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	52.5-1.8	9.9-3.0
unique	46,234	9,152
measured	35,139	8,806
used	23,031	7,014

NCS	translation	rotation
r.m.s.d. (A)	10.83	0.19
angle (o)	59.88	0.08



1b49

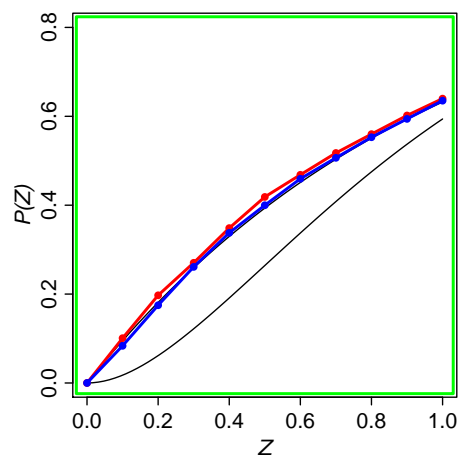
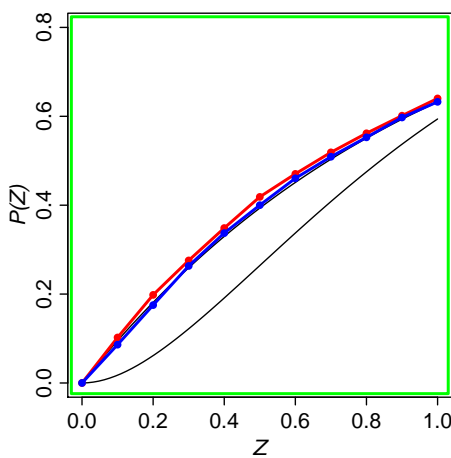
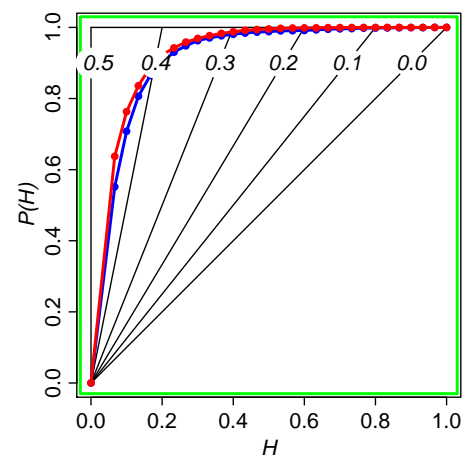
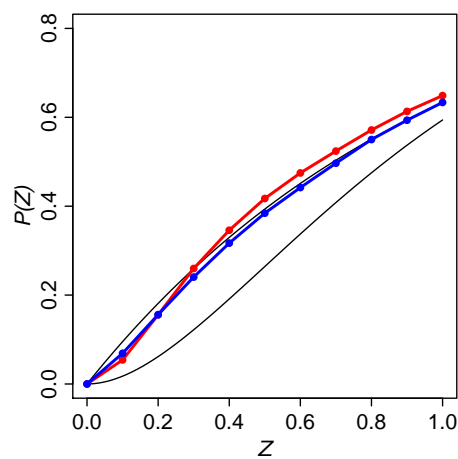
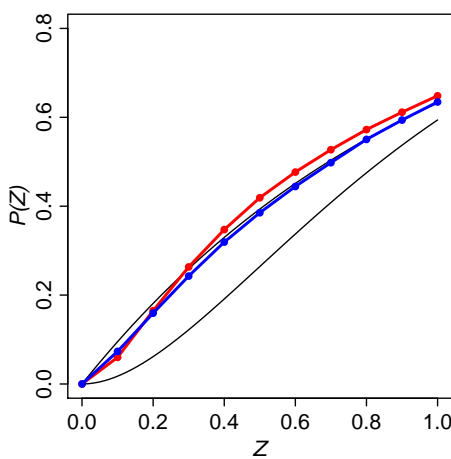
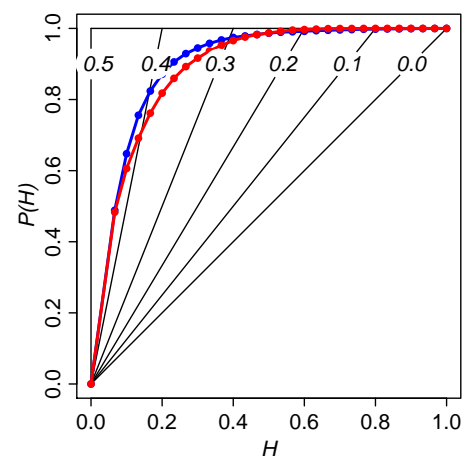
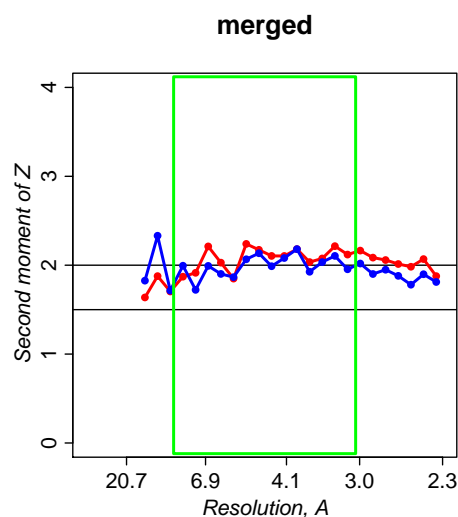
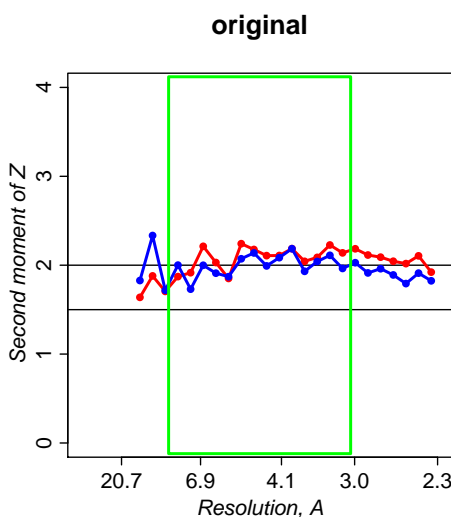
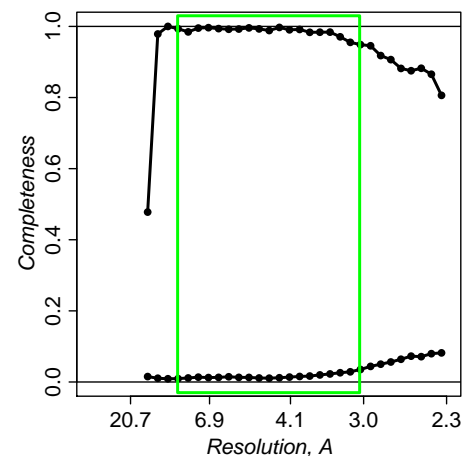
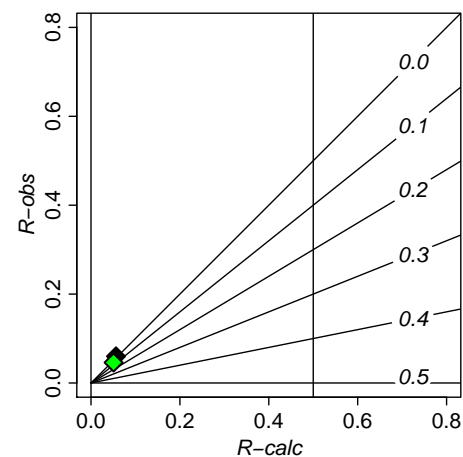
	original	merged
s.g.	C 1 2 1	I 2 2 2
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.05
R	20.9	
R'	20.9	21.5
R-free	24.6	
R'-free	24.7	24.6

s < f/100	3398	12.97 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	15.9–2.3	9.9–3.0
unique	28,283	12,532
measured	26,192	12,295
used	22,332	10,820

NCS	translation	rotation
r.m.s.d. (A)	29.59	0.05
angle (o)	179.99	0.01

residues per monomer	DNA	protein
	0	241



1b5d

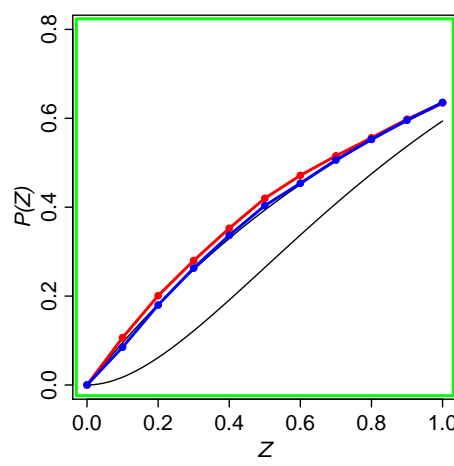
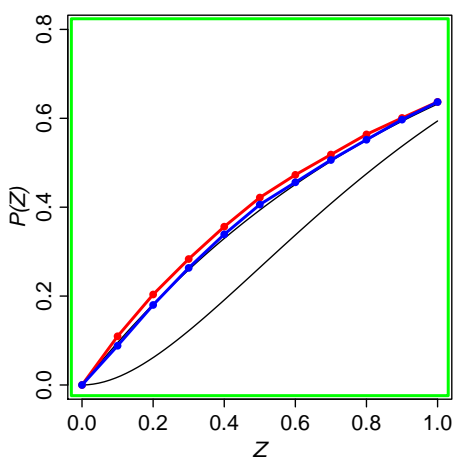
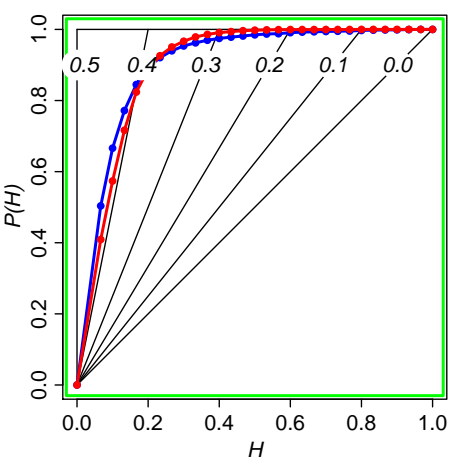
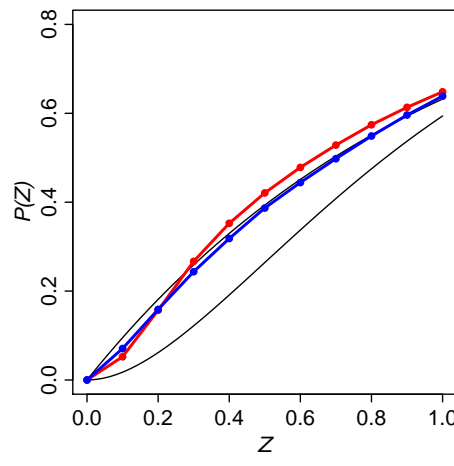
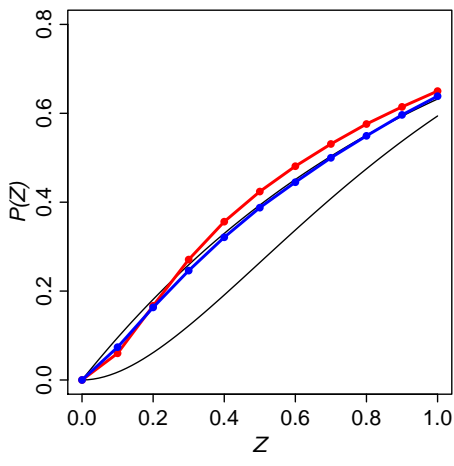
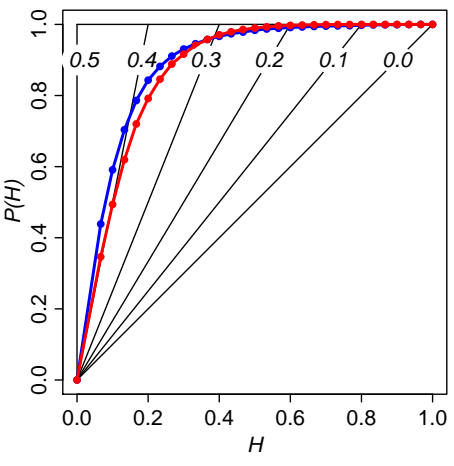
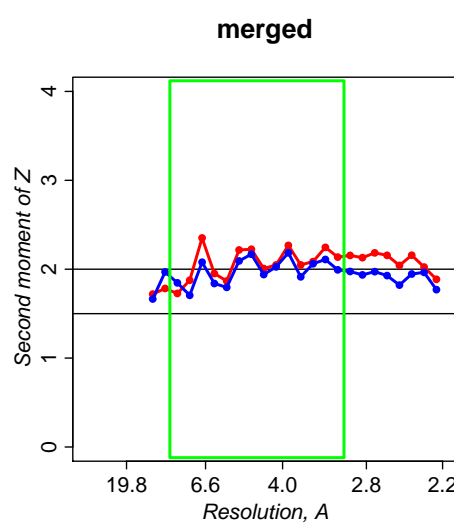
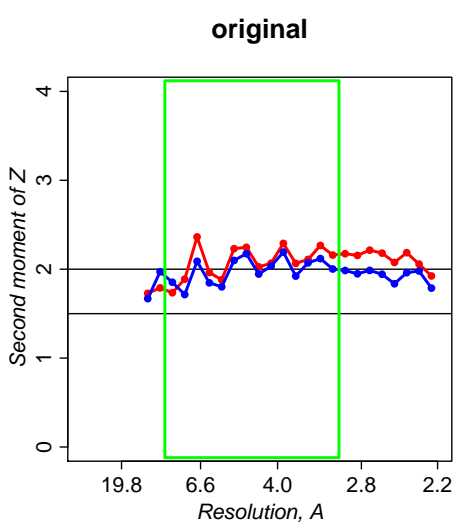
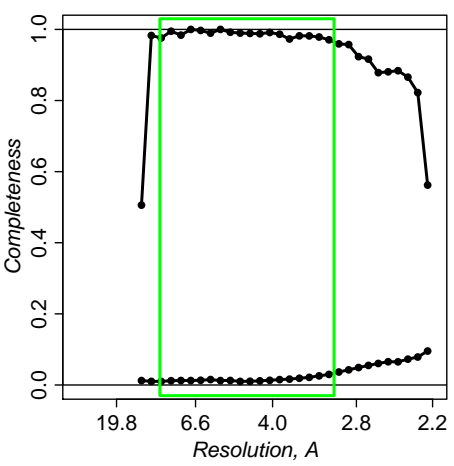
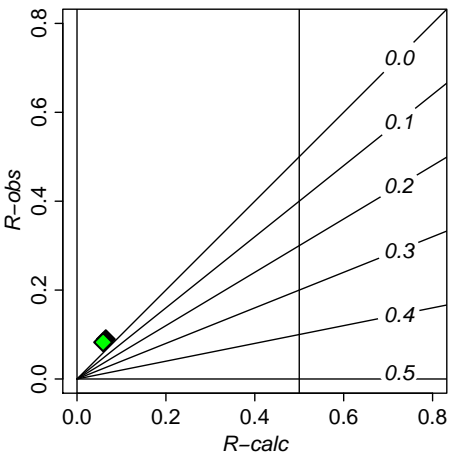
	original	merged
s.g.	C 1 2 1	I 2 2 2
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.05
R	21.6	
R'	21.8	22.0
R-free	24.8	
R'-free	24.8	24.4

residues per monomer	DNA	protein
	0	246

s < f/100	3380	11.59 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	13.1–2.2	9.9–3.0
unique	32,429	12,614
measured	29,170	12,394
used	24,986	10,974

NCS	translation	rotation
r.m.s.d. (A)	30.17	0.05
angle (o)	179.99	0.02



1b5e

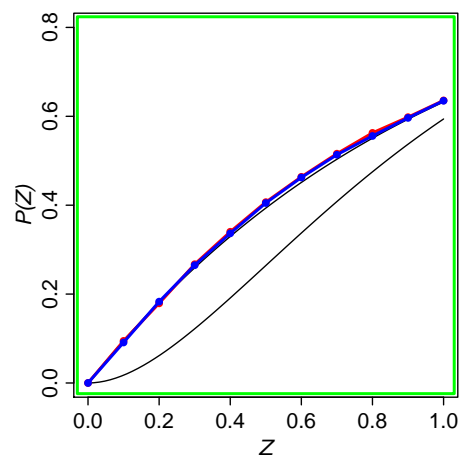
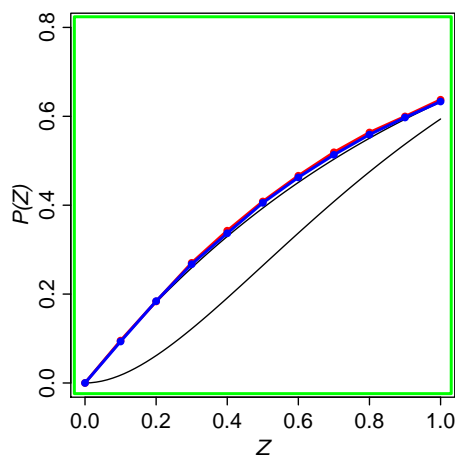
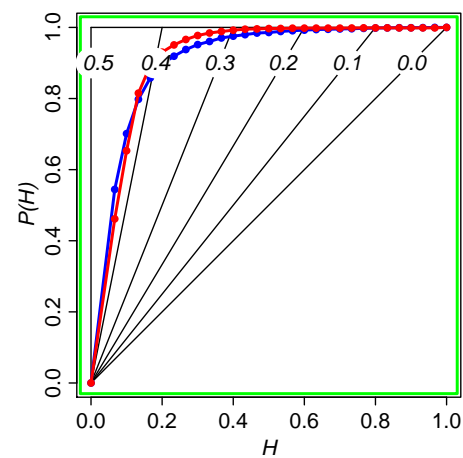
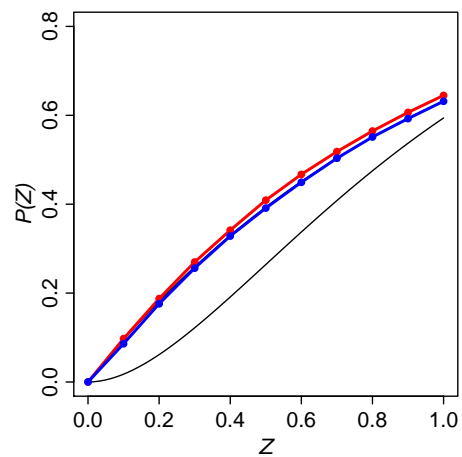
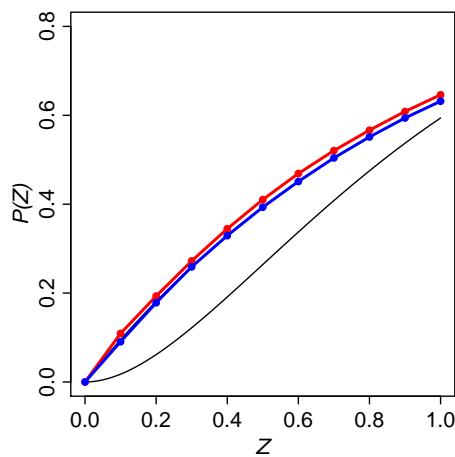
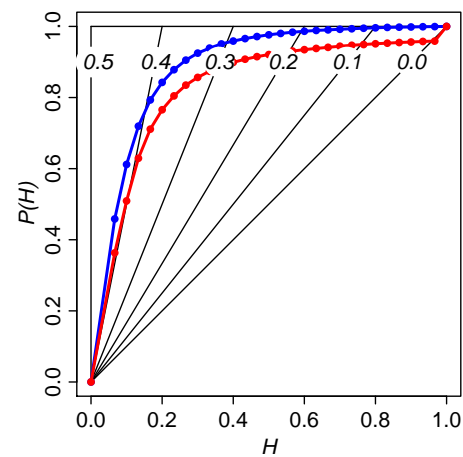
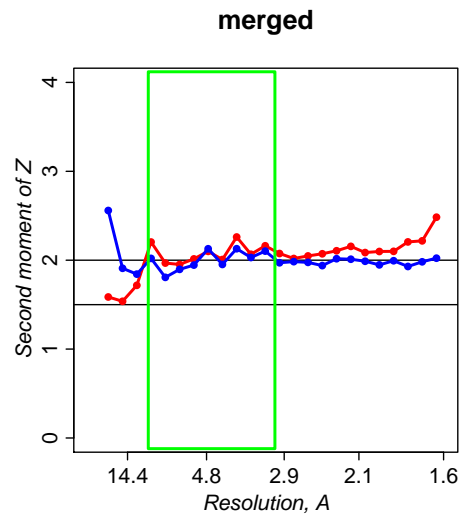
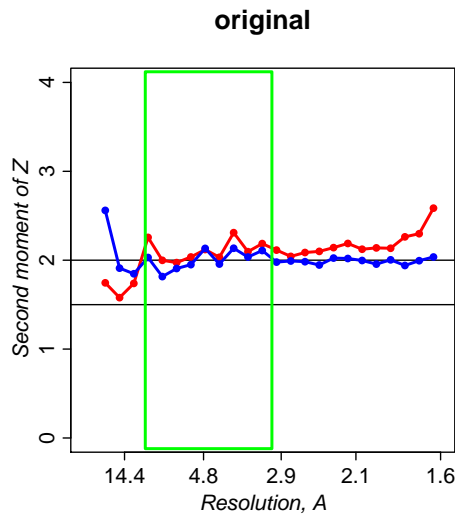
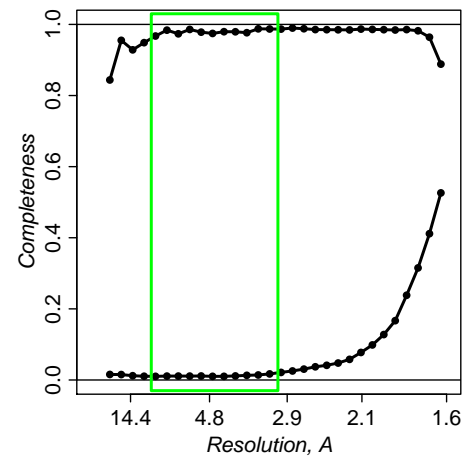
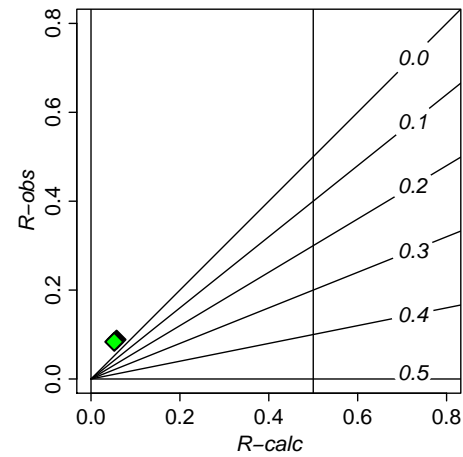
	original	merged
s.g.	C 1 2 1	I 2 2 2
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.05
R	24.7	
R'	24.7	24.9
R-free	26.0	
R'-free	25.9	26.0

s < f/100	6294	7.86 %
s <= 0	0	0.00 %
f <= 0	2403	3.00 %
s,f <= 0	0	0.00 %

range (A)	43.4–1.6	9.9–3.0
unique	82,184	12,338
measured	80,033	12,114
used	73,708	10,670

NCS	translation	rotation
r.m.s.d. (A)	29.57	0.05
angle (o)	179.99	0.03

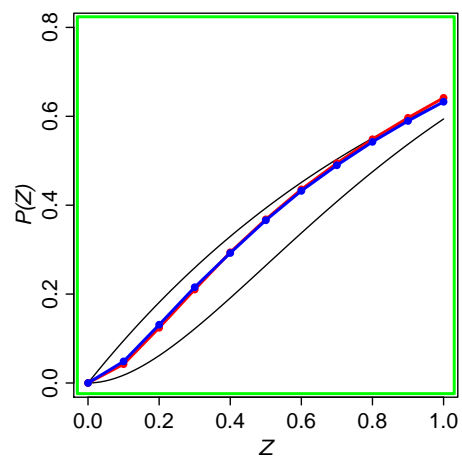
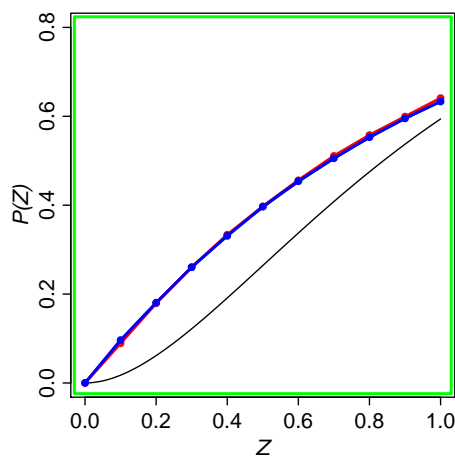
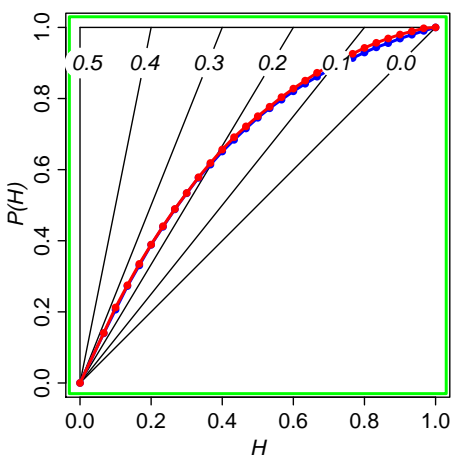
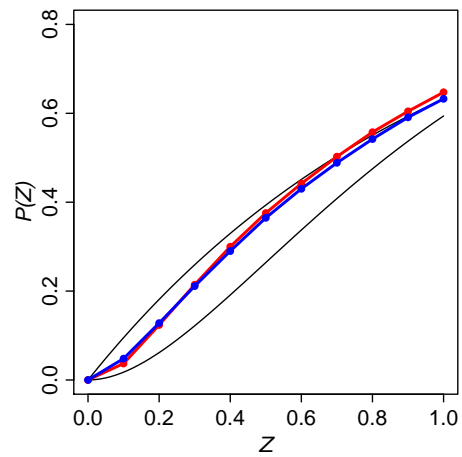
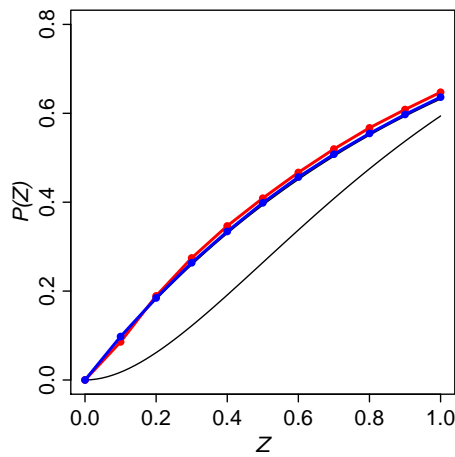
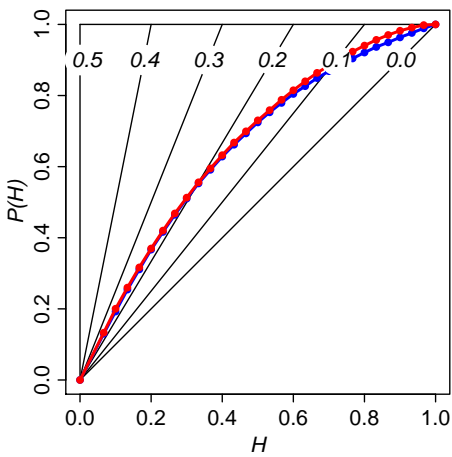
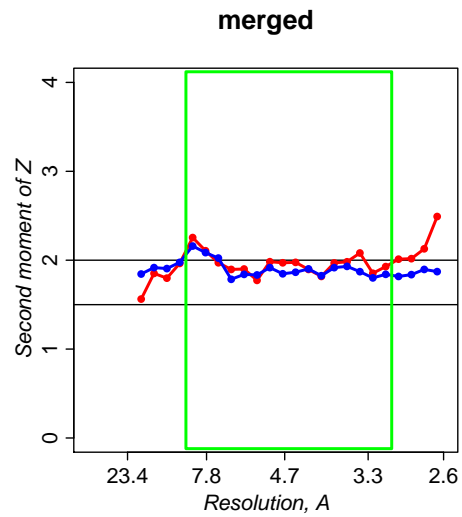
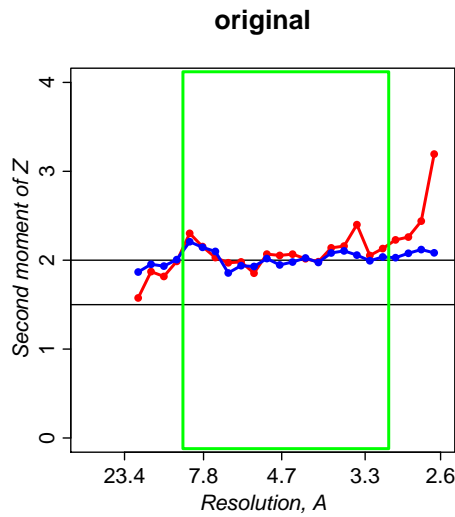
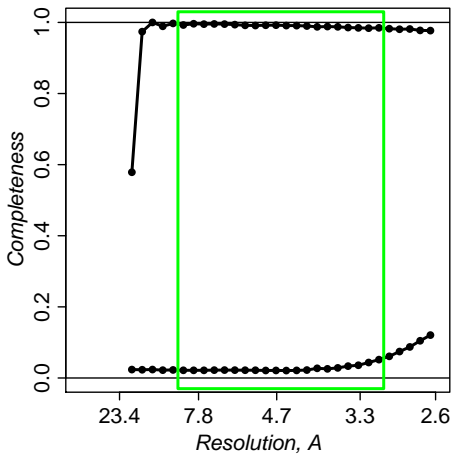
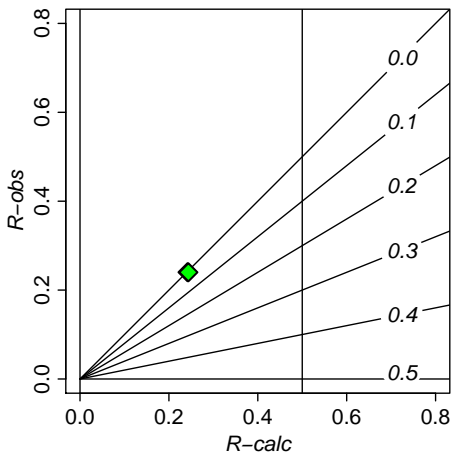
residues per monomer	DNA	protein
	0	241



1b6c

	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.74
R	22.5	
R'	22.5	22.5
R-free	27.3	
R'-free	27.3	26.9
residues per monomer	DNA 0	protein 433

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	19.8–2.6	9.9–3.0
unique	58,605	37,185
measured	57,741	36,755
used	54,974	35,700
NCS	translation	rotation
r.m.s.d. (A)	34.93	0.64
angle (o)	179.78	0.73



1b8z

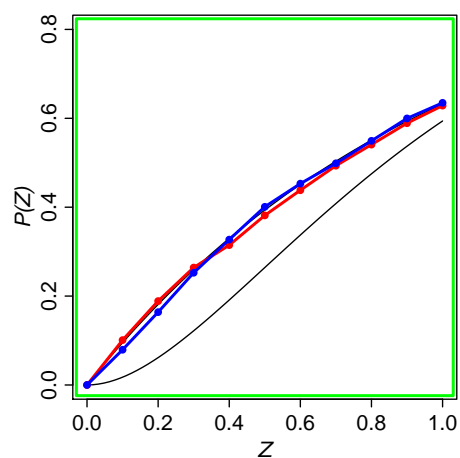
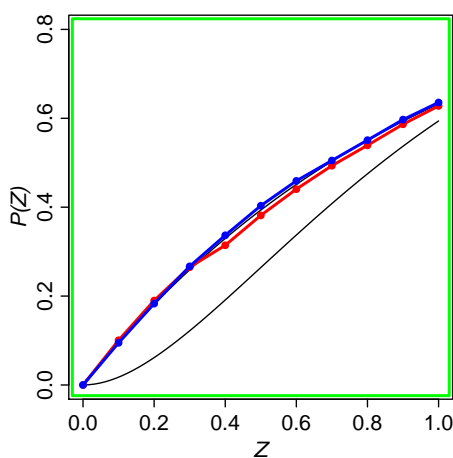
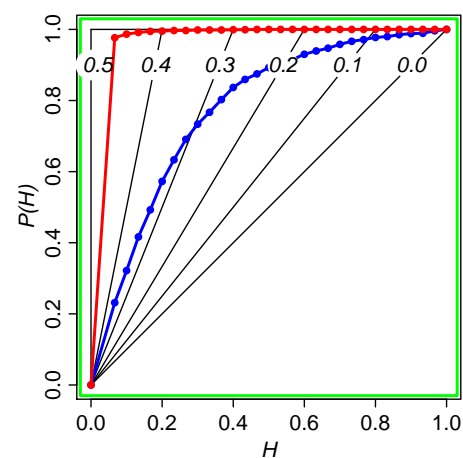
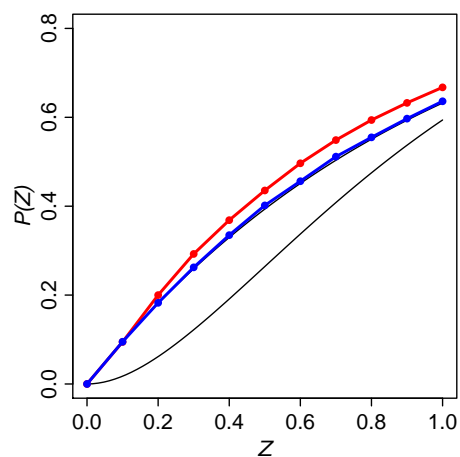
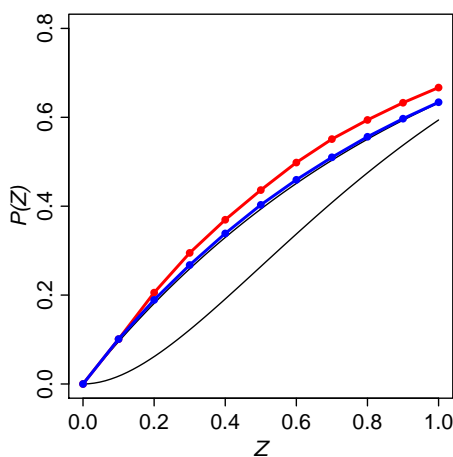
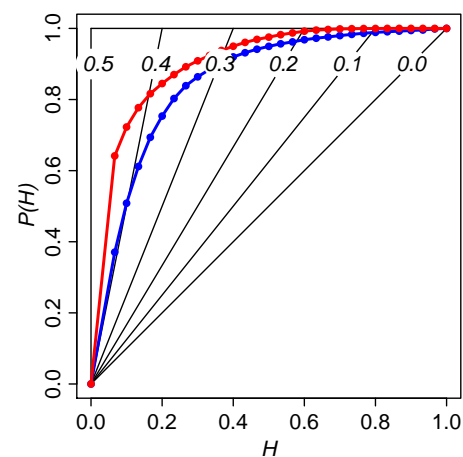
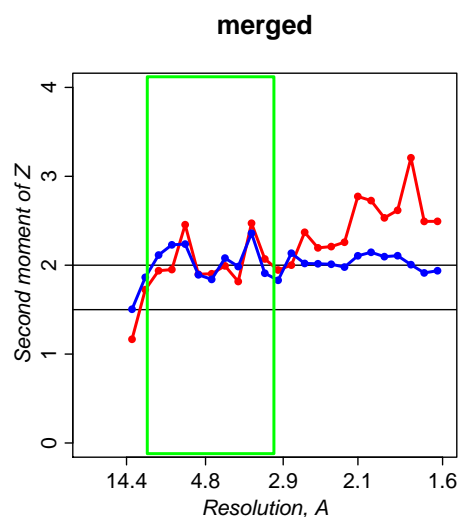
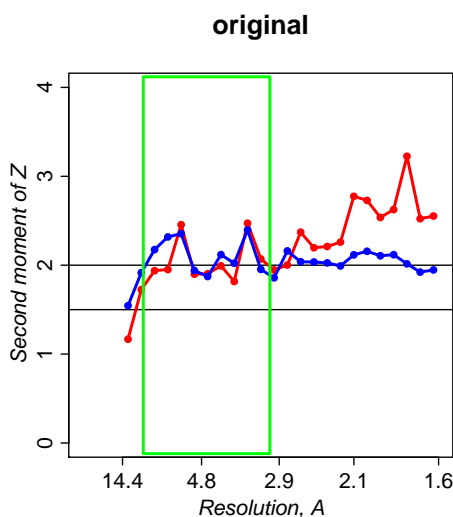
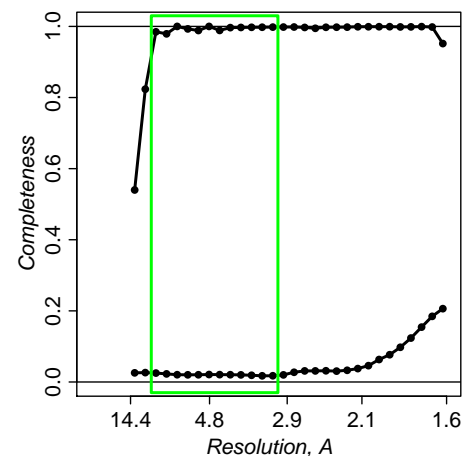
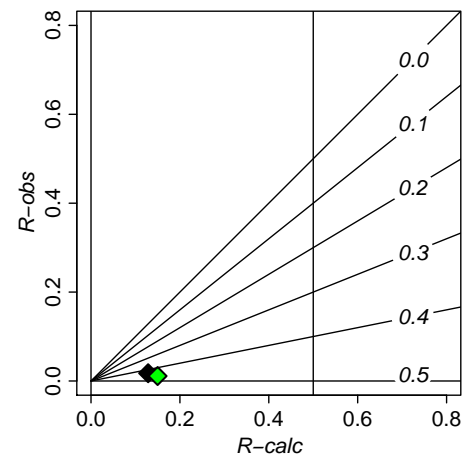
	original	merged
s.g.	P 43	P 43 21 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.10
R	26.5	
R'	26.7	27.5
R-free	25.2	
R'-free	25.6	25.5

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	14.8–1.6	9.9–3.0
unique	21,694	3,208
measured	21,552	3,193
used	19,106	2,566

NCS	translation	rotation
r.m.s.d. (A)	20.99	0.10
angle (o)	179.83	0.19

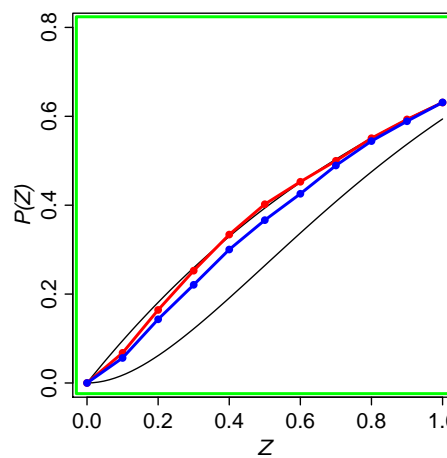
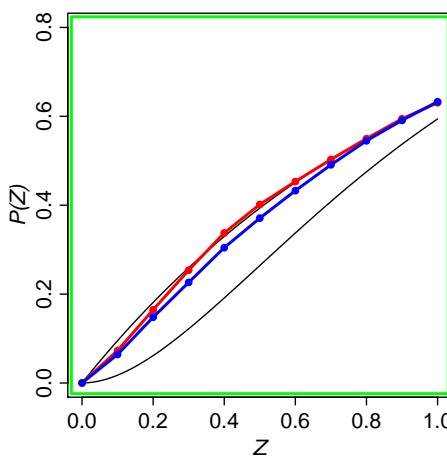
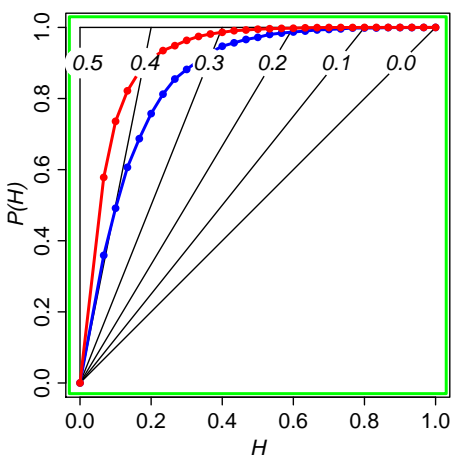
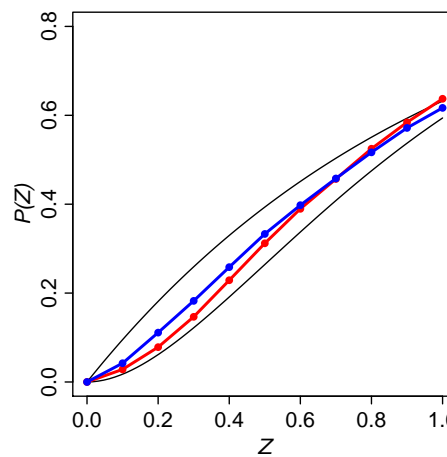
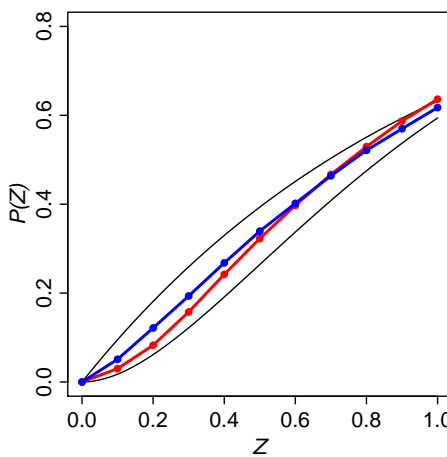
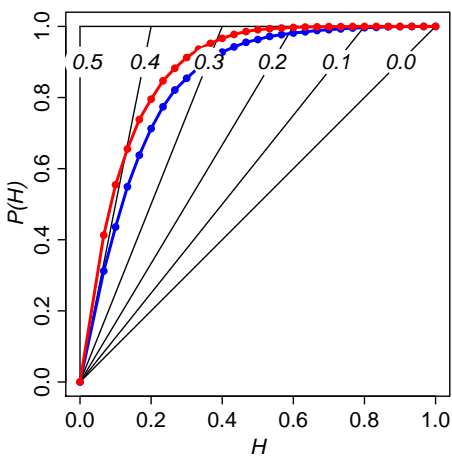
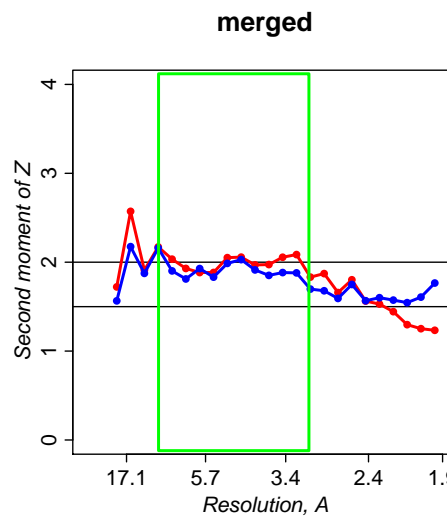
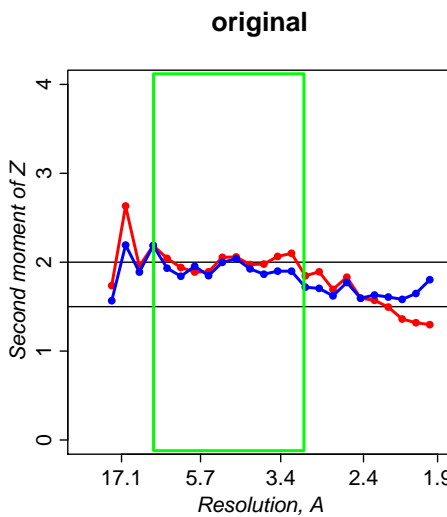
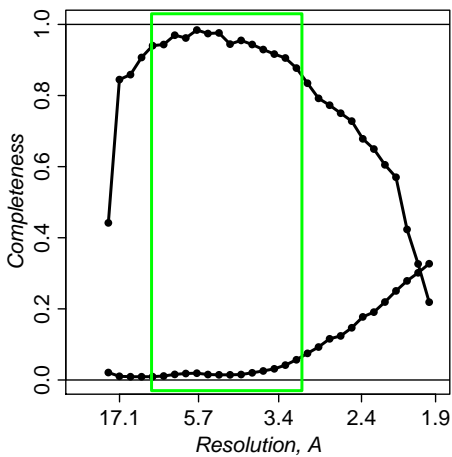
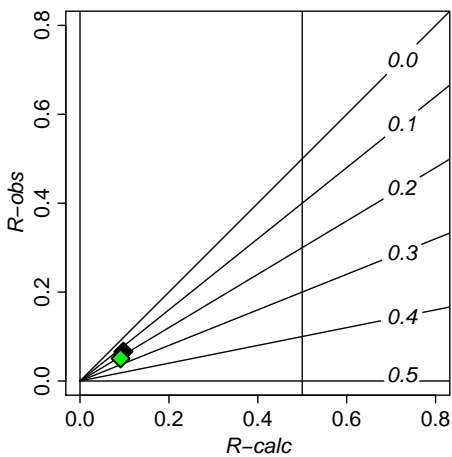
residues per monomer	DNA	protein
	0	67



1bay

	original	merged
s.g.	14	14 2 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.11
R	23.0	
R'	23.5	24.6
R-free	25.4	
R'-free	26.6	27.5
residues per monomer	DNA 0	protein 193

s < f/100	3016	10.70 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	29.6–1.9	9.9–3.0
unique	42,932	10,793
measured	28,194	10,022
used	21,732	8,682
NCS	translation	rotation
r.m.s.d. (A)	26.29	0.11
angle (o)	179.93	0.08



1bdl

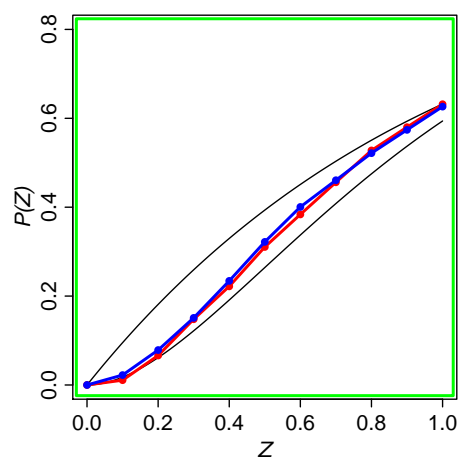
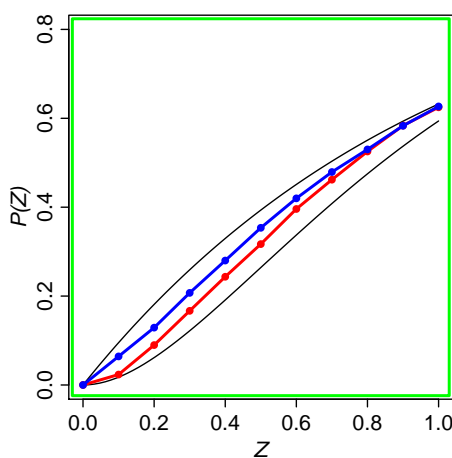
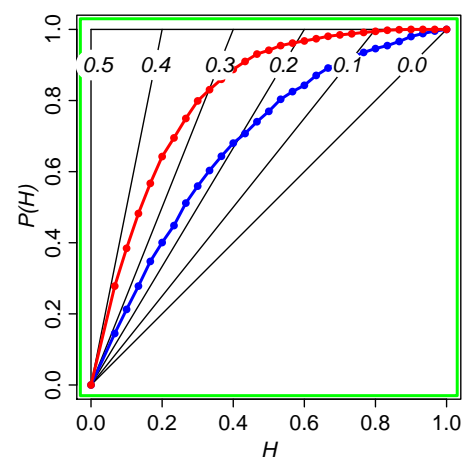
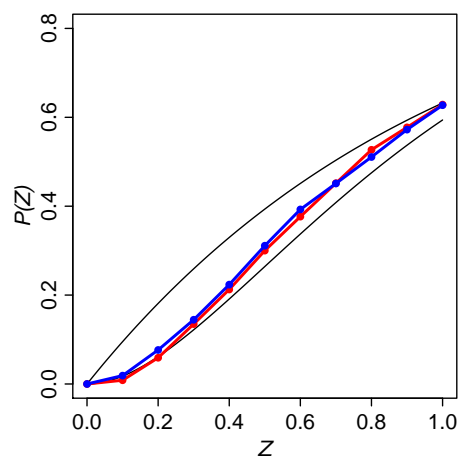
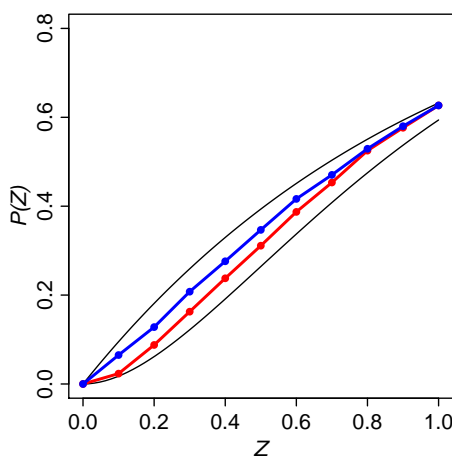
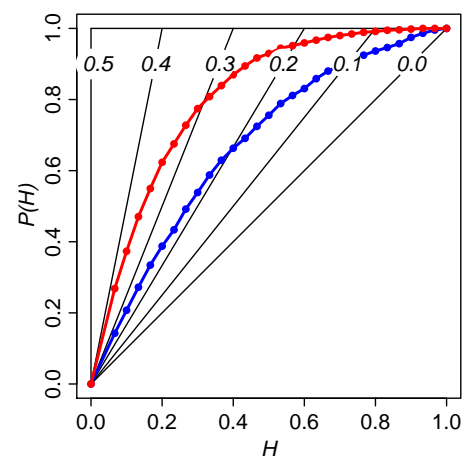
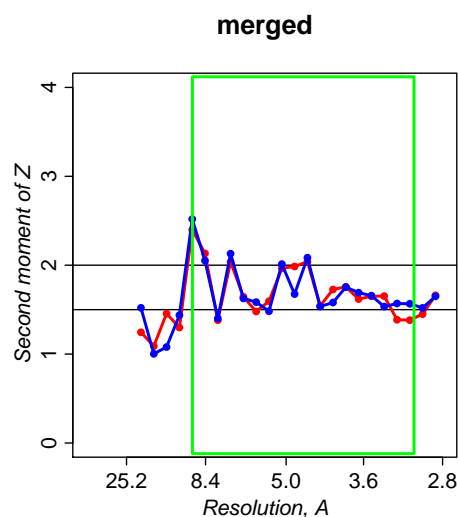
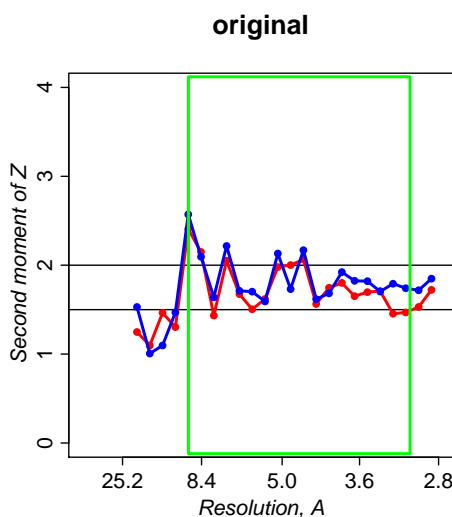
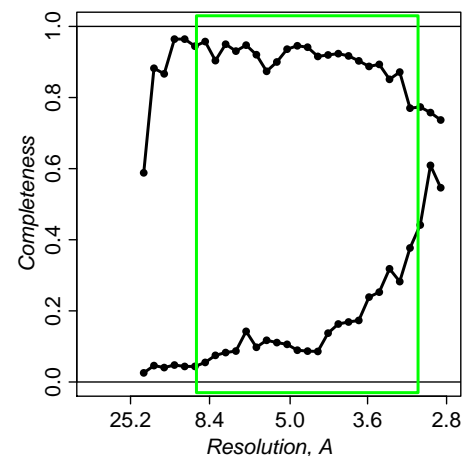
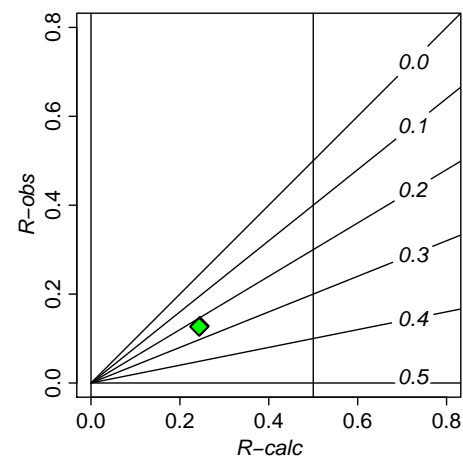
	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.63
R	19.0	
R'	19.7	21.1
R-free	25.9	
R'-free	27.0	30.7

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	20.9–2.8	9.9–3.0
unique	4,712	3,758
measured	4,059	3,331
used	3,086	2,582

NCS	translation	rotation
r.m.s.d. (A)	21.02	0.63
angle (o)	179.43	0.62

residues per monomer	DNA	protein
	0	99



1bdq

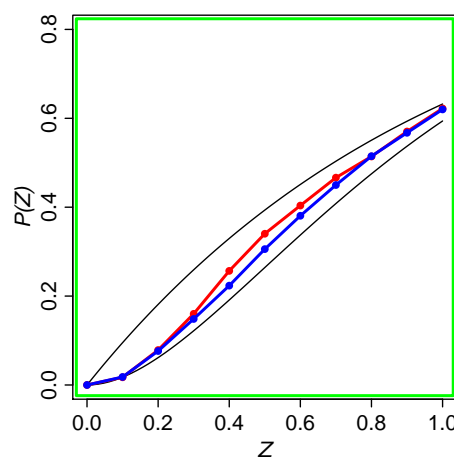
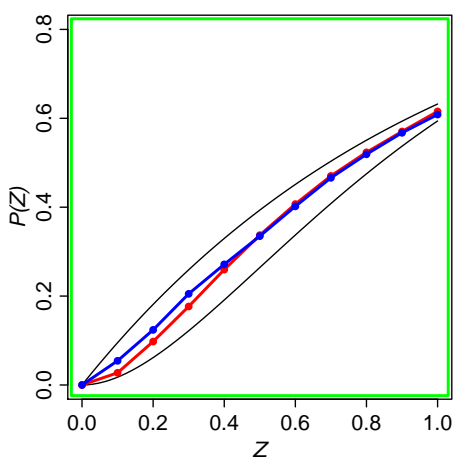
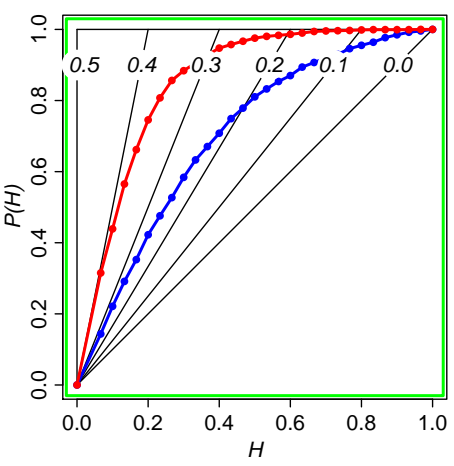
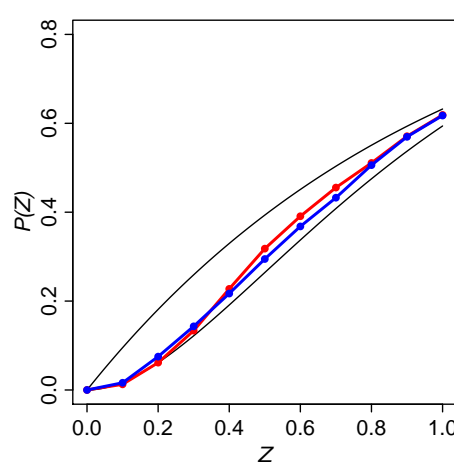
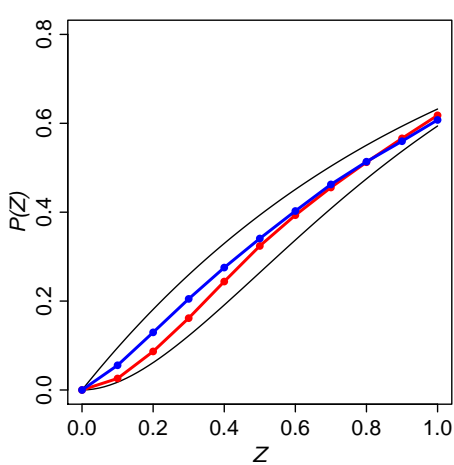
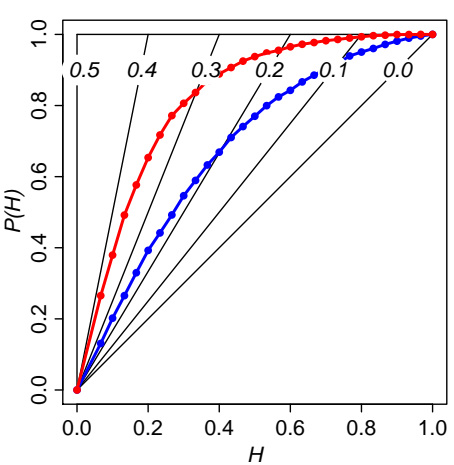
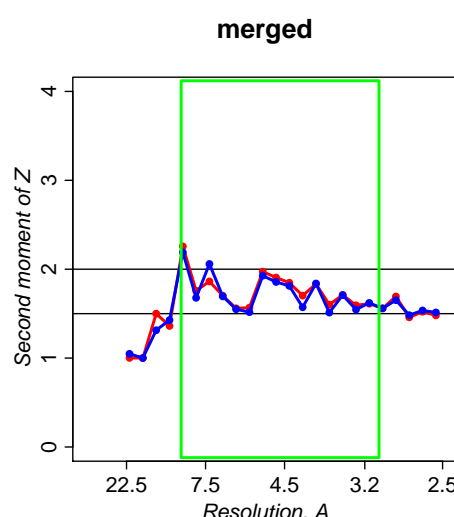
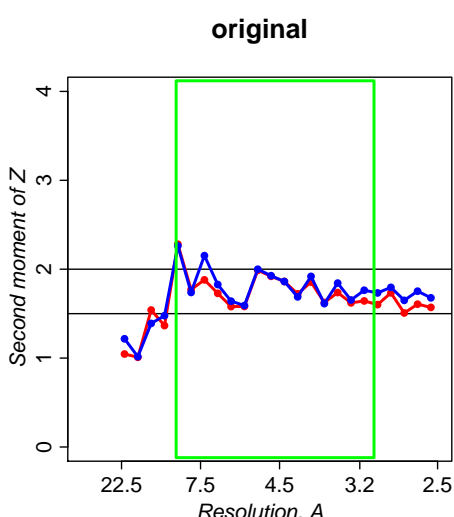
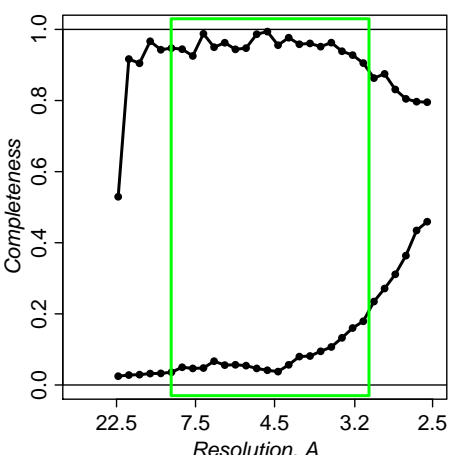
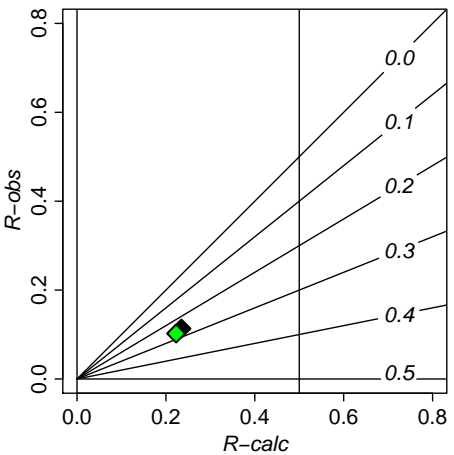
	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.61
R	19.8	
R'	21.0	22.6
R-free	23.9	
R'-free	25.7	28.7

residues per monomer	DNA	protein
	0	99

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	24.8–2.5	9.9–3.0
unique	6,559	3,699
measured	5,863	3,499
used	4,554	2,758

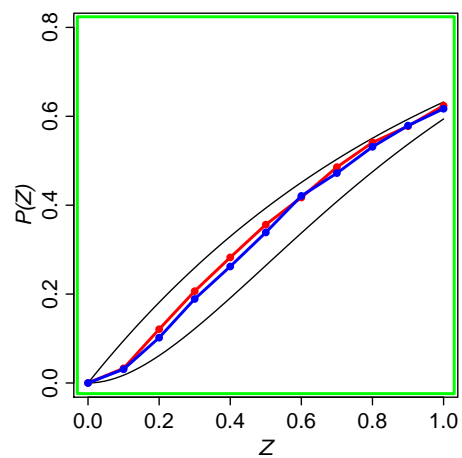
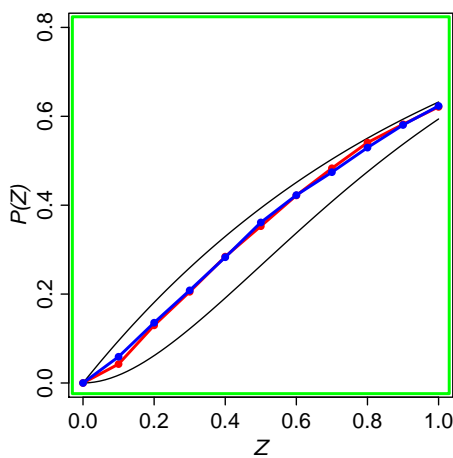
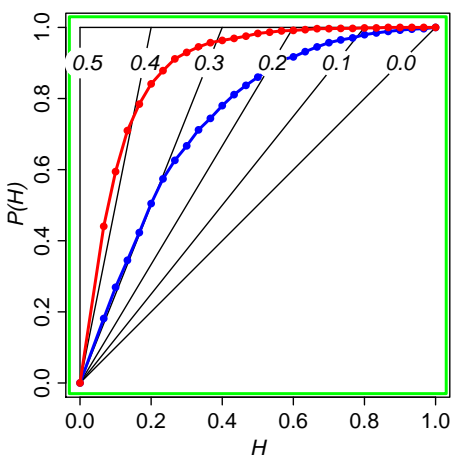
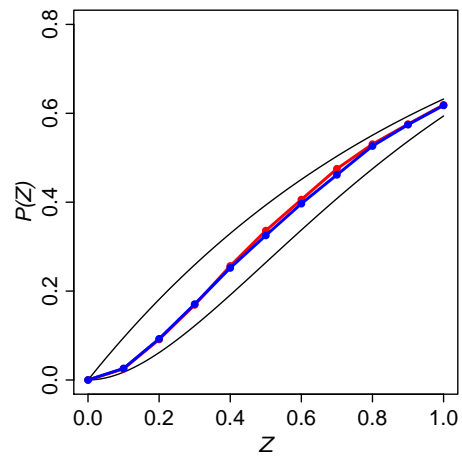
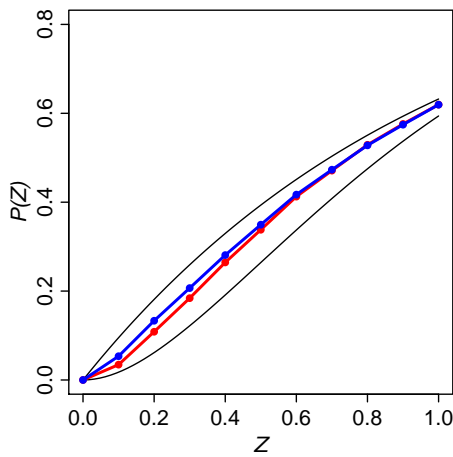
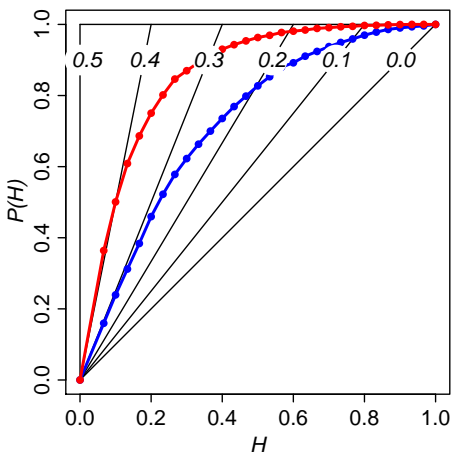
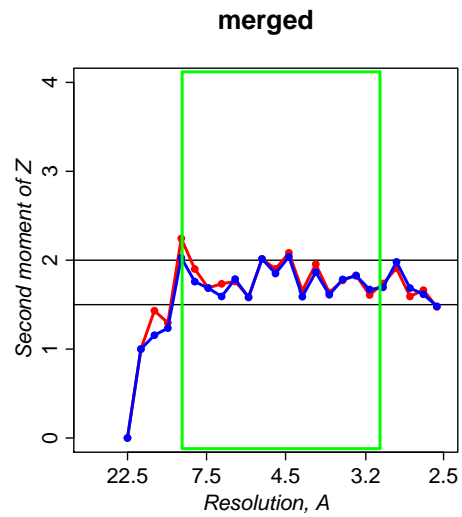
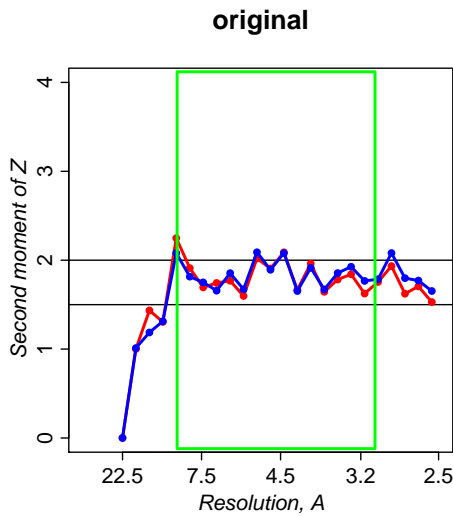
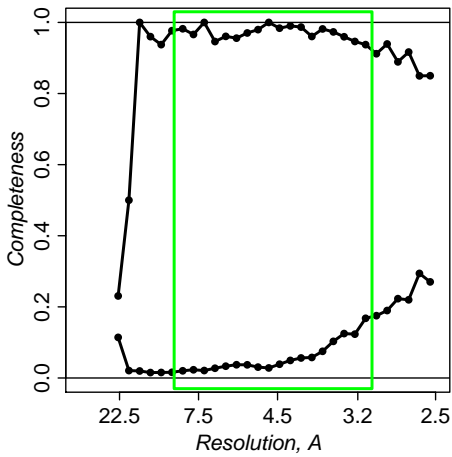
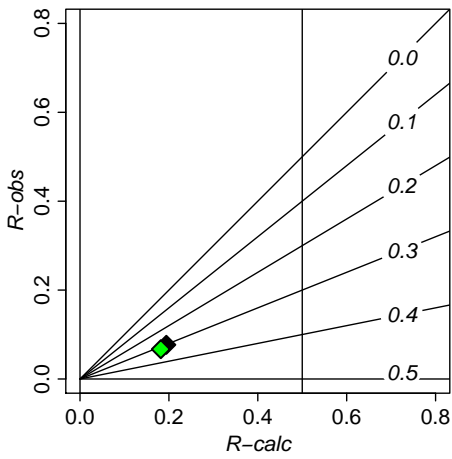
NCS	translation	rotation
r.m.s.d. (A)	22.94	0.60
angle (o)	179.79	0.78



1bdr

	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.36
R	19.9	
R'	20.9	21.8
R-free	23.5	
R'-free	25.2	26.9
residues per monomer	DNA 0	protein 99

s < f/100	6	0.10 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	27.1–2.5	9.9–3.0
unique	6,510	3,671
measured	6,061	3,543
used	4,840	2,830
NCS	translation	rotation
r.m.s.d. (A)	19.59	0.35
angle (o)	179.79	0.66



1bir

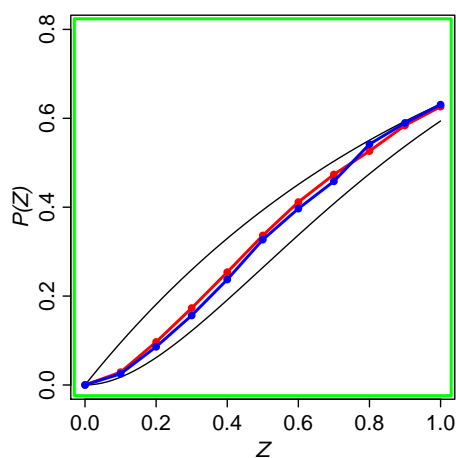
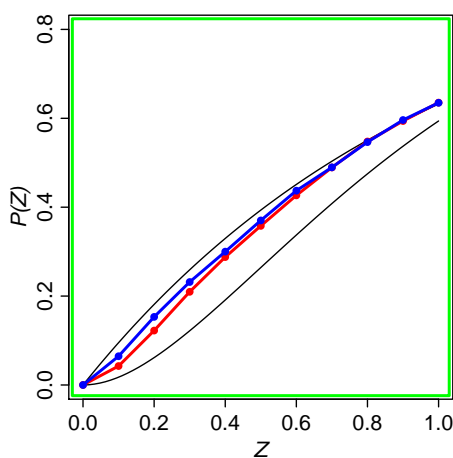
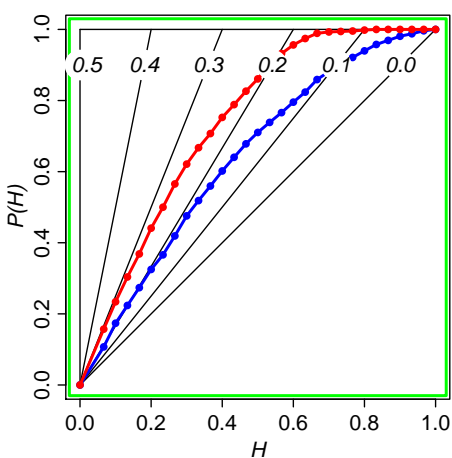
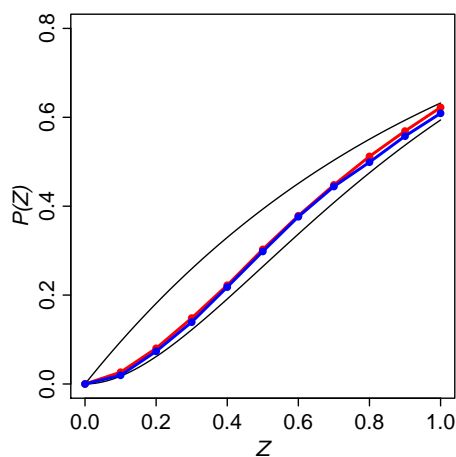
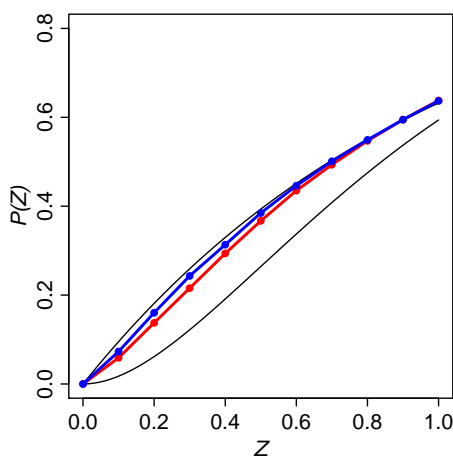
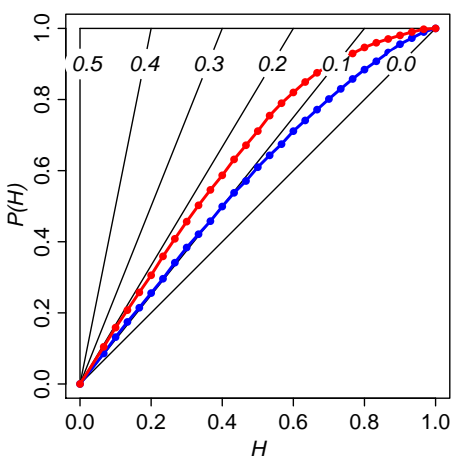
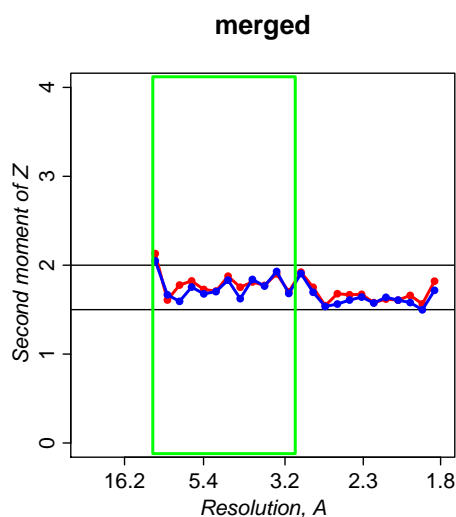
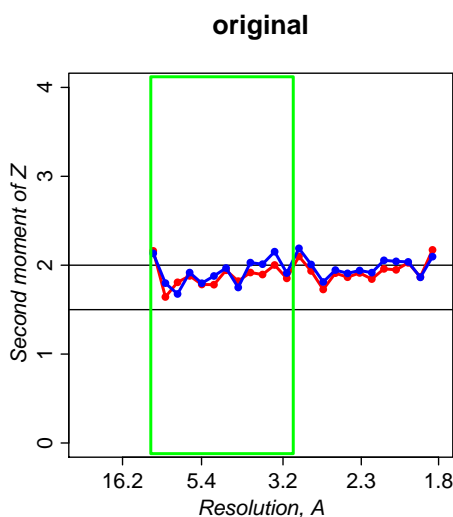
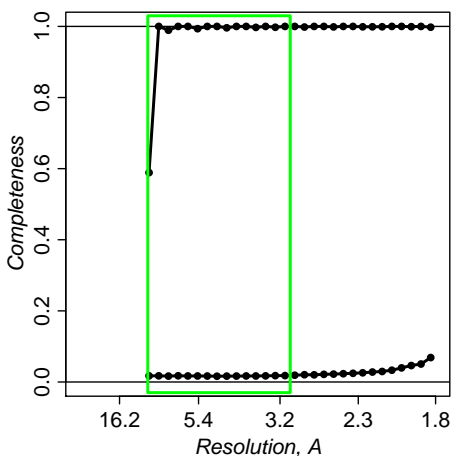
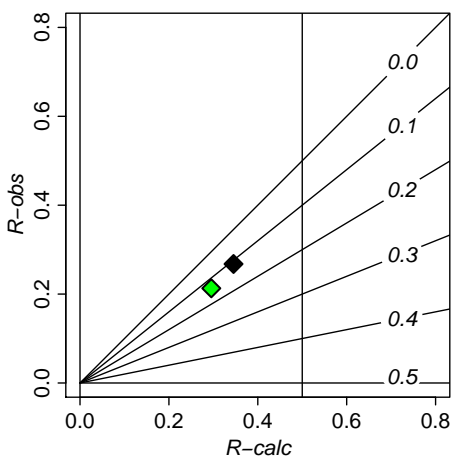
	original	merged
s.g.	P 1 21 1	P 21 21 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.96
R	25.0	
R'	25.2	29.1
R-free	26.3	
R'-free	26.8	32.5

residues per monomer	DNA	protein
	0	104

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	10.0–1.8	9.9–3.0
unique	17,471	3,752
measured	17,457	3,746
used	15,484	3,118

NCS	translation	rotation
r.m.s.d. (A)	20.74	0.93
angle (o)	175.09	4.93



1bre

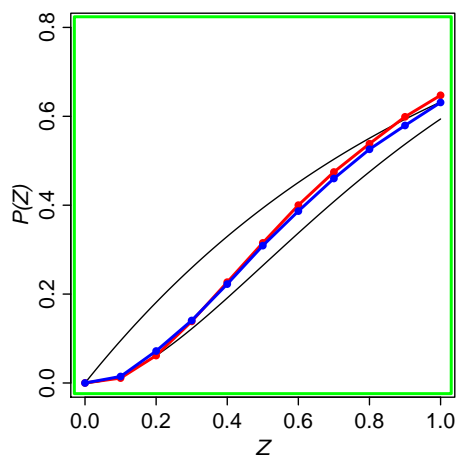
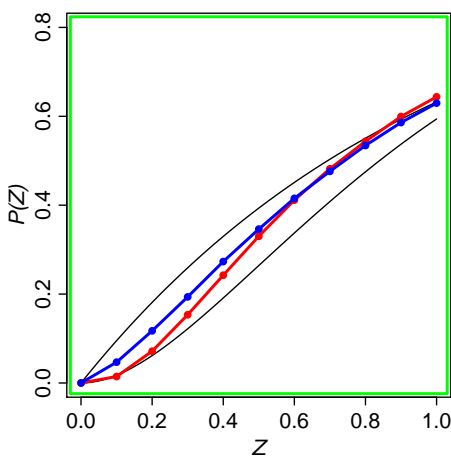
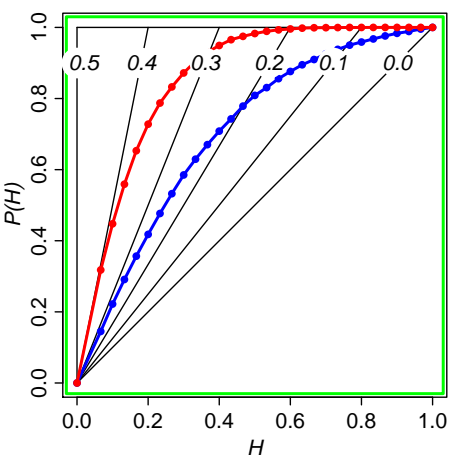
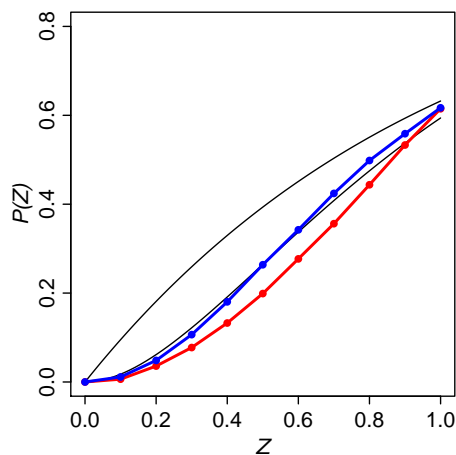
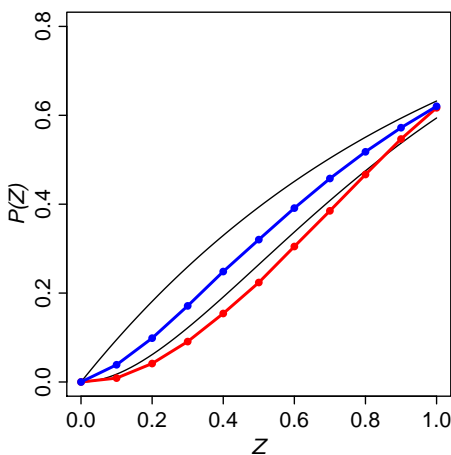
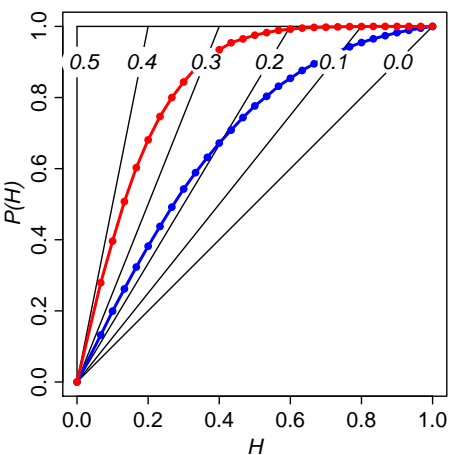
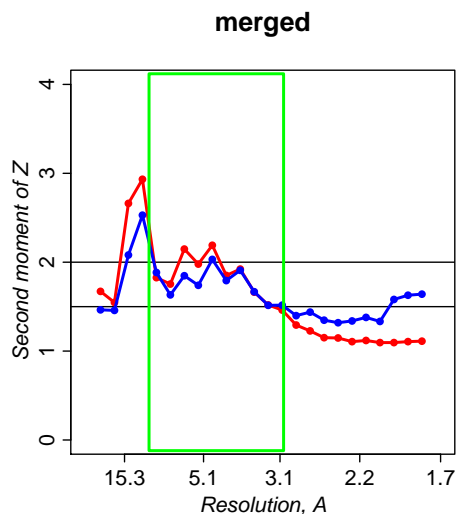
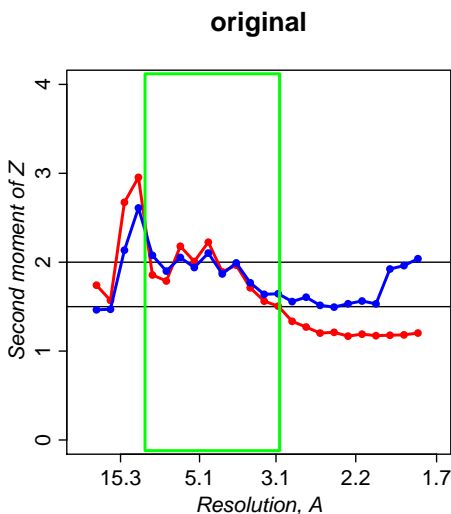
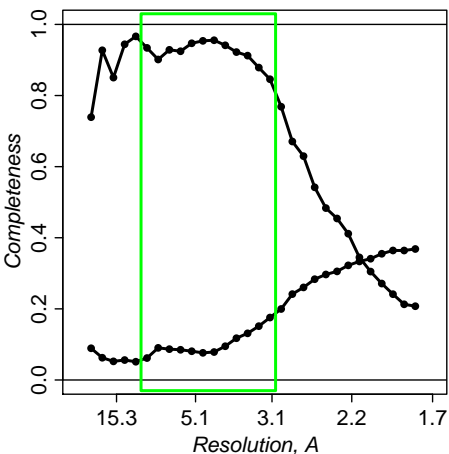
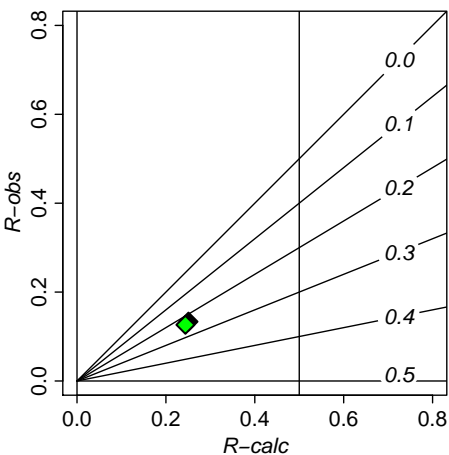
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.73
R	29.6	
R'	30.6	32.1
R-free	33.0	
R'-free	33.1	34.4

s < f/100	2	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	71.2–1.8	9.9–3.0
unique	89,379	17,671
measured	42,839	15,993
used	27,162	13,866

NCS	translation	rotation
r.m.s.d. (A)	10.37	0.66
angle (o)	58.00	0.93

residues per monomer	DNA	protein
	0	107



1bvs

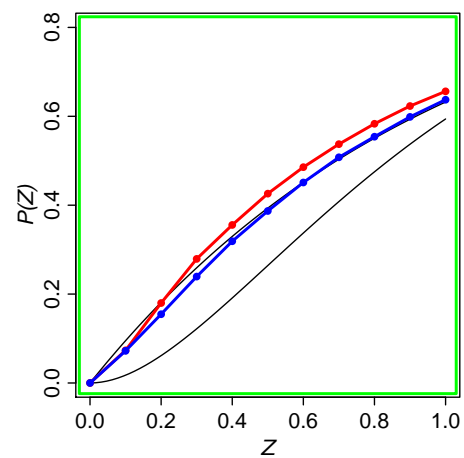
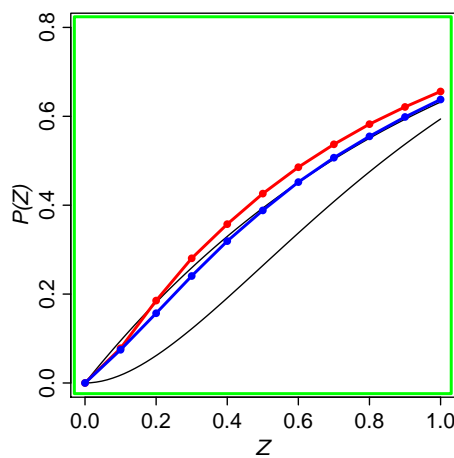
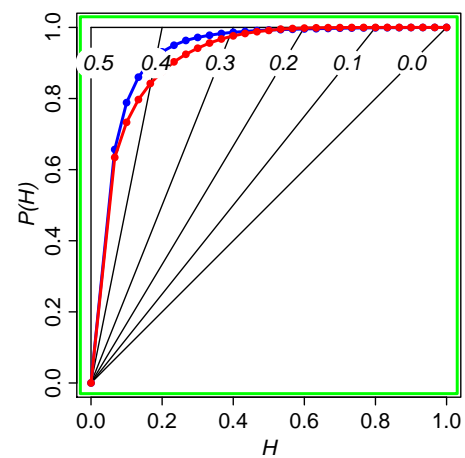
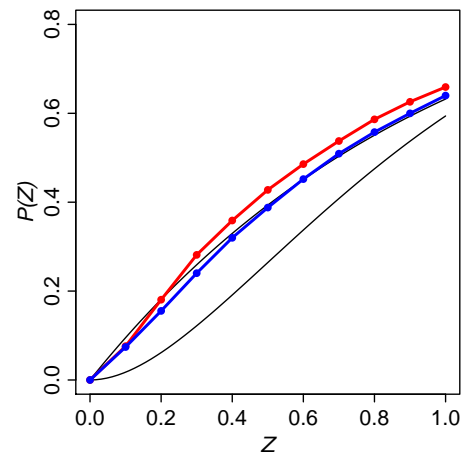
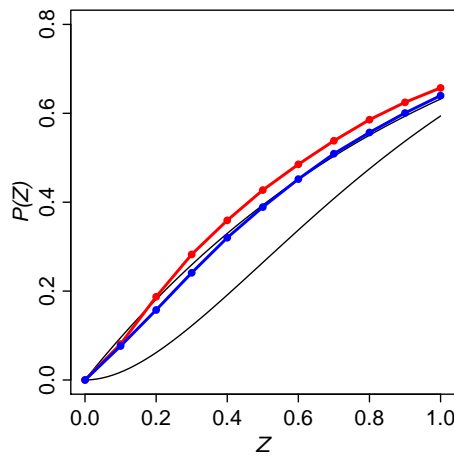
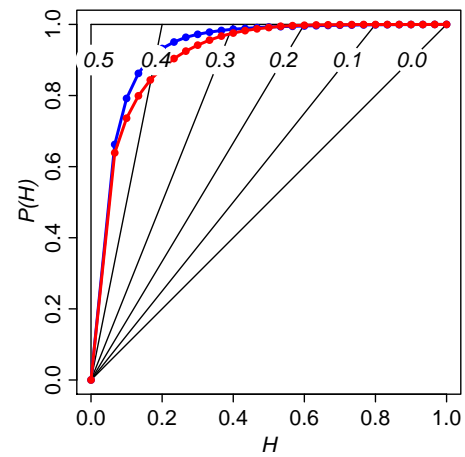
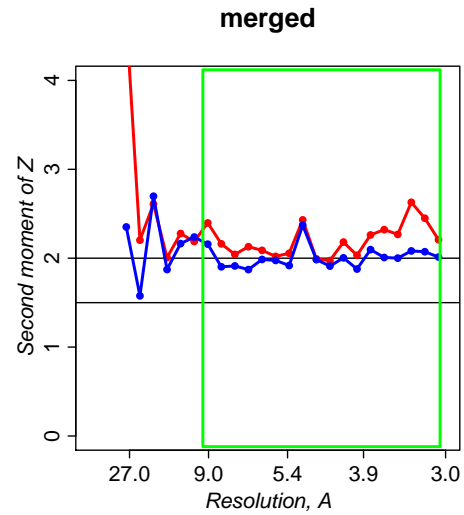
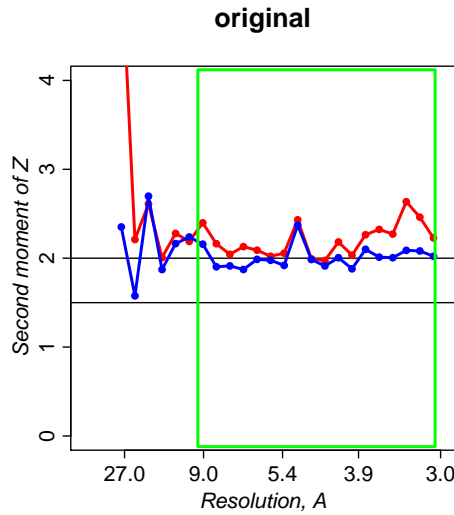
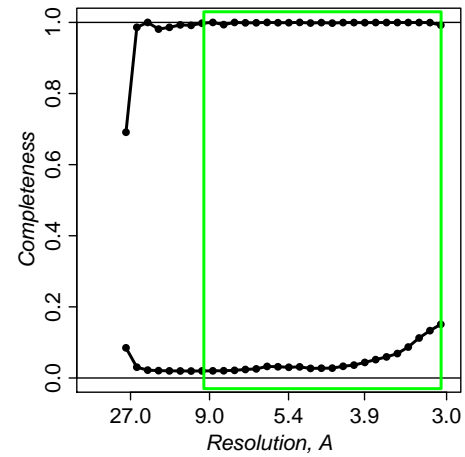
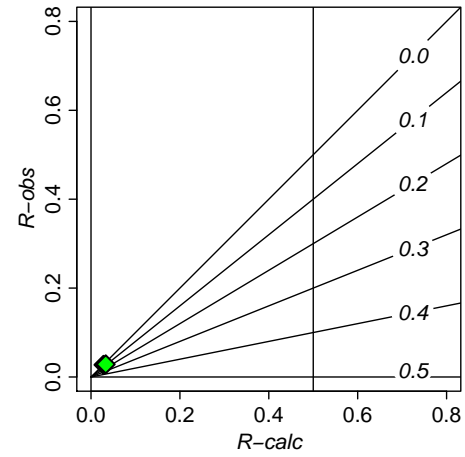
	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	8	4
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.02
R	25.9	
R'	25.9	26.4
R-free	32.1	
R'-free	32.1	32.6

residues per monomer	DNA	protein
	0	182

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	36.1–3.0	9.9–3.0
unique	49,221	47,879
measured	49,147	47,819
used	46,832	45,698

NCS	translation	rotation
r.m.s.d. (A)	14.52	0.01
angle (o)	59.96	0.02



1c03

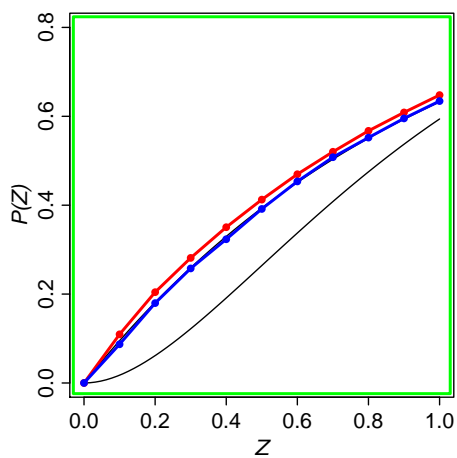
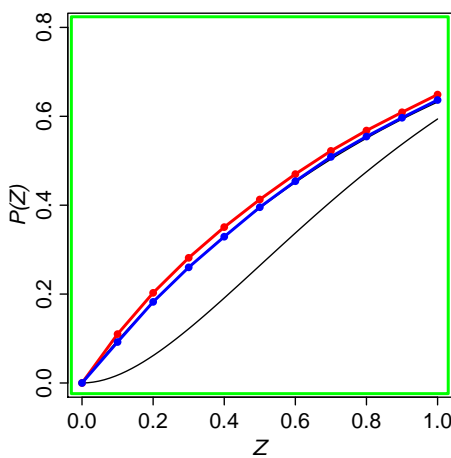
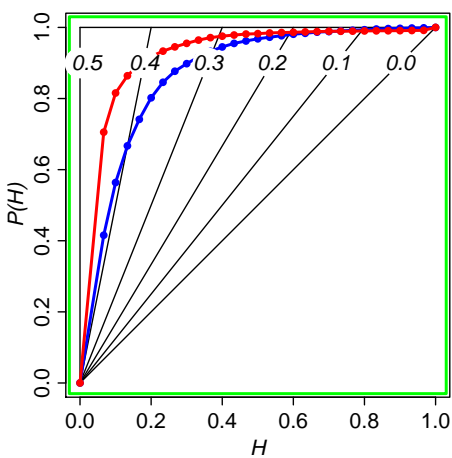
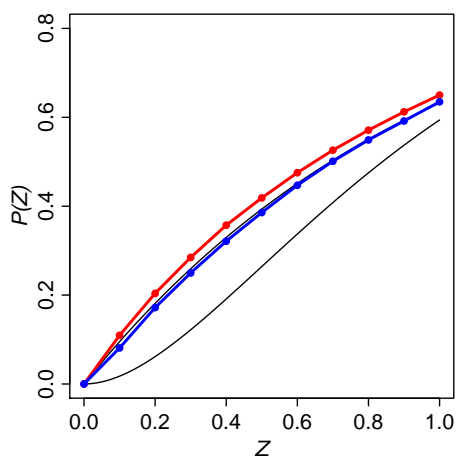
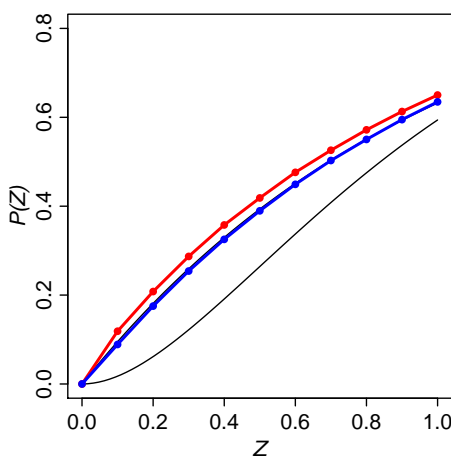
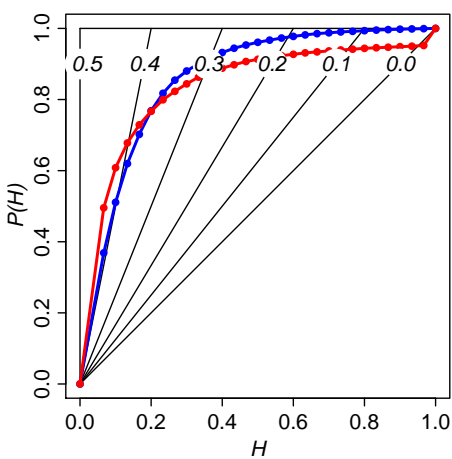
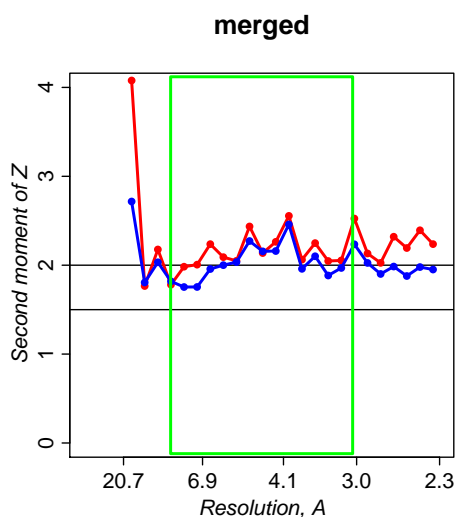
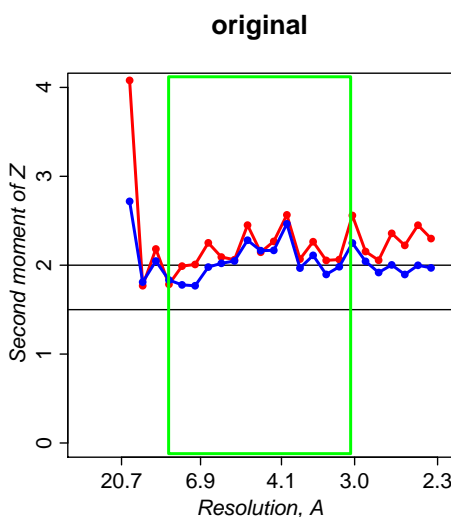
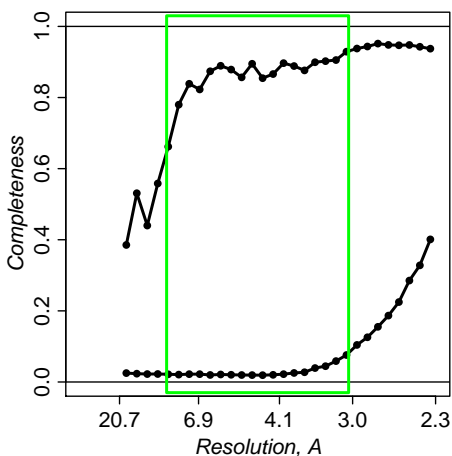
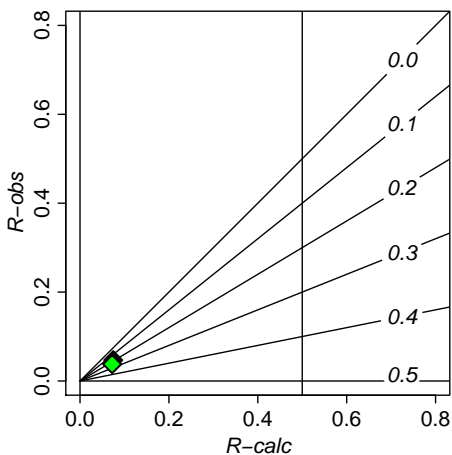
	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.06
R	22.9	
R'	22.9	23.0
R-free	26.2	
R'-free	26.1	26.1

residues per monomer	DNA	protein
	0	163

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	1148	3.26 %
s,f <= 0	0	0.00 %

range (A)	19.9–2.3	9.9–3.0
unique	38,574	16,946
measured	35,254	15,005
used	32,142	13,140

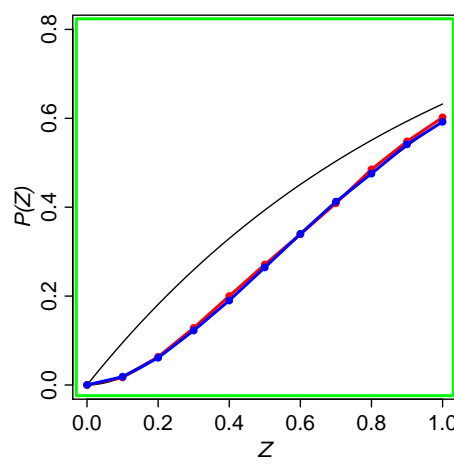
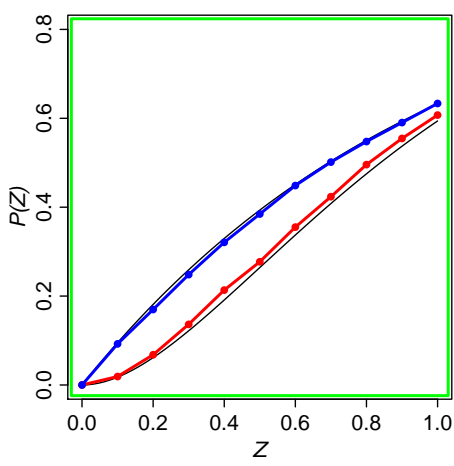
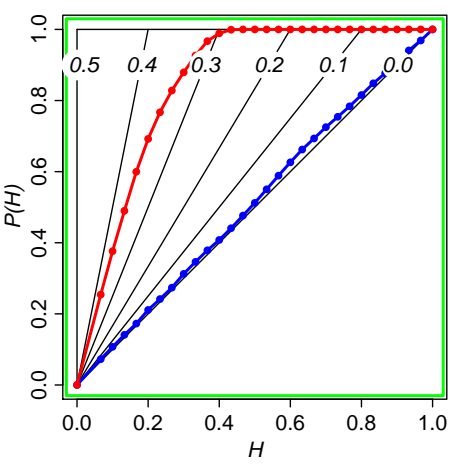
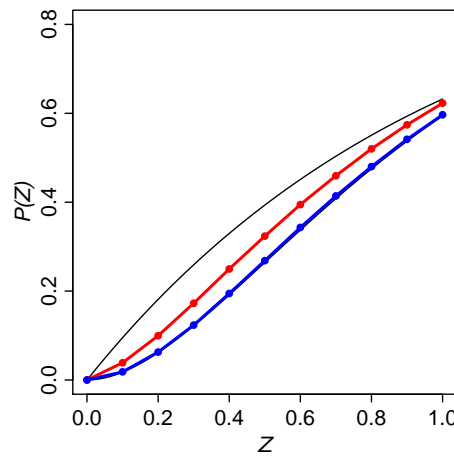
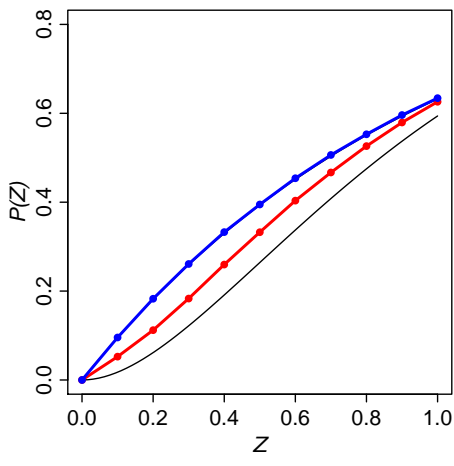
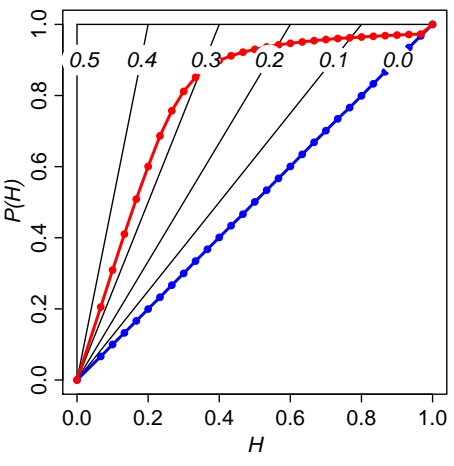
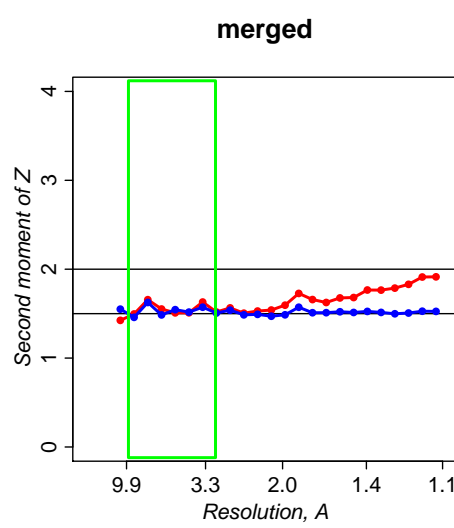
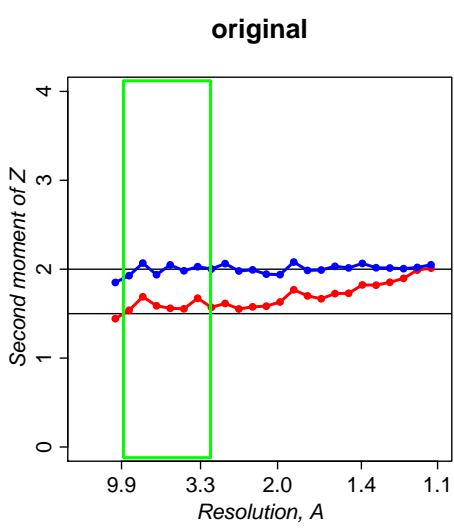
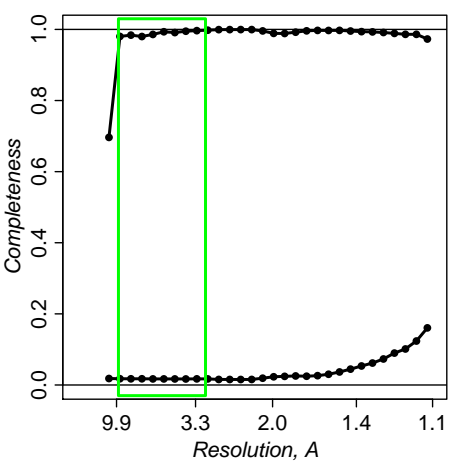
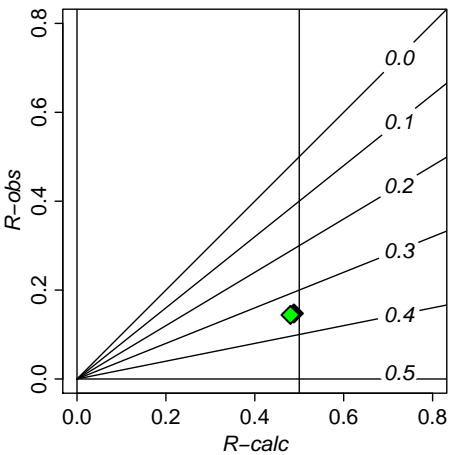
NCS	translation	rotation
r.m.s.d. (A)	23.34	0.06
angle (o)	179.97	0.02



1c5e

	original	merged
s.g.	P 1 21 1	-
p.g.	10001	10003
a.u.	3	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	29.8	-
R'	-	-
R-free	30.4	-
R'-free	-	-
residues per monomer	DNA 0	protein 95

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	1883	1.71 %
s,f <= 0	0	0.00 %
range (A)	14.8-1.1	9.9-3.0
unique	110,989	5,409
measured	109,971	5,365
used	103,954	4,698
NCS	translation	rotation
r.m.s.d. (A)	13.91	15.31
angle (o)	100.78	109.75



1c9t

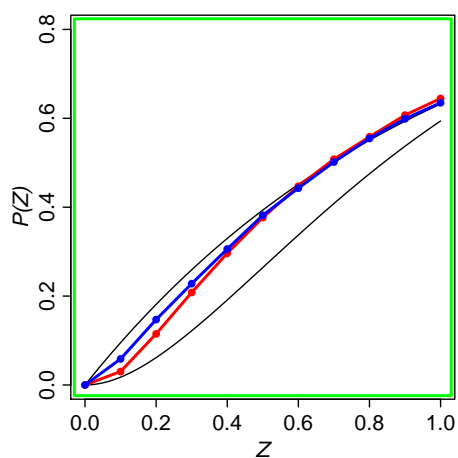
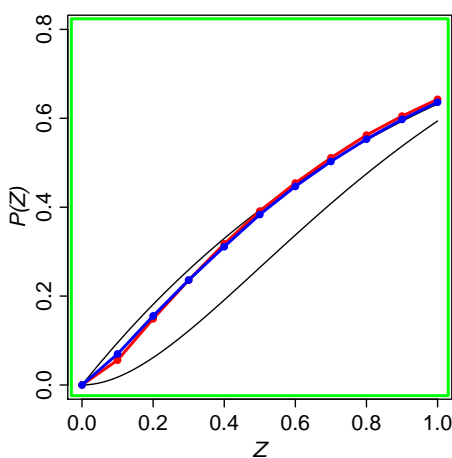
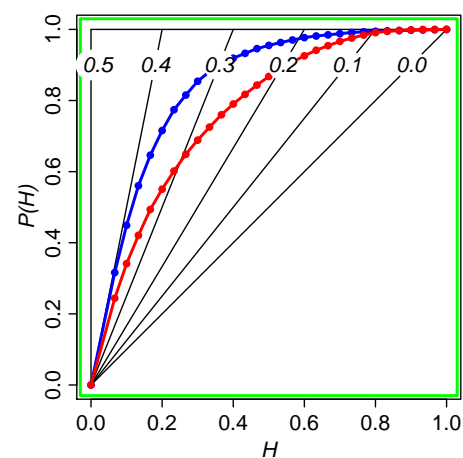
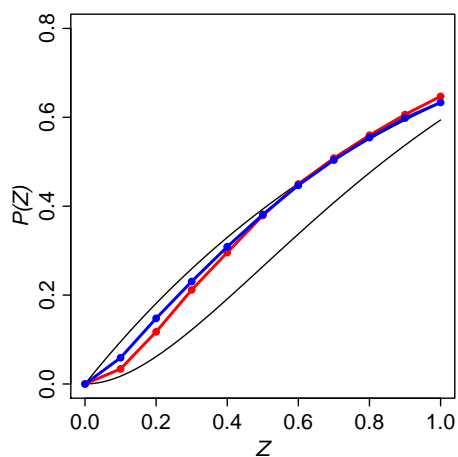
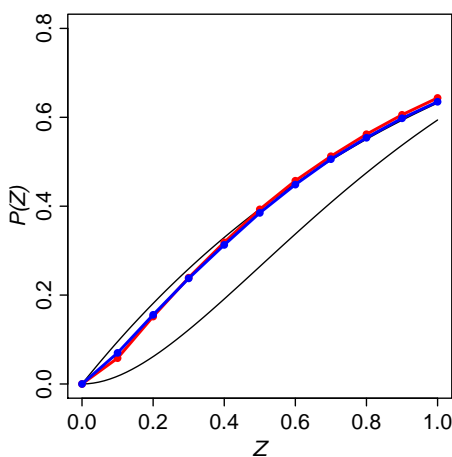
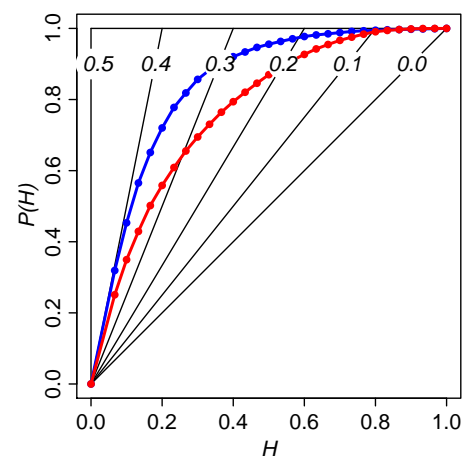
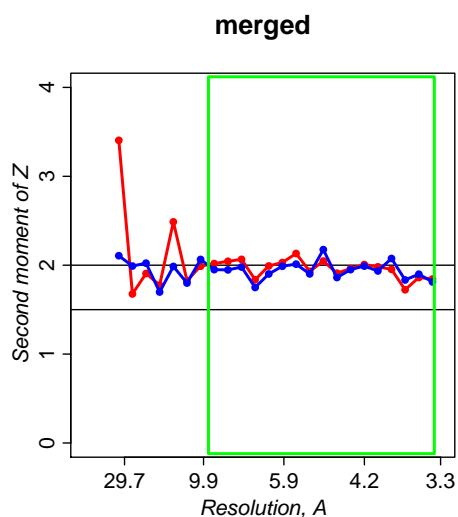
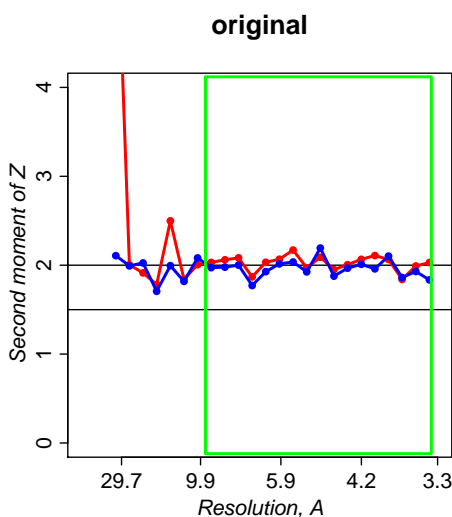
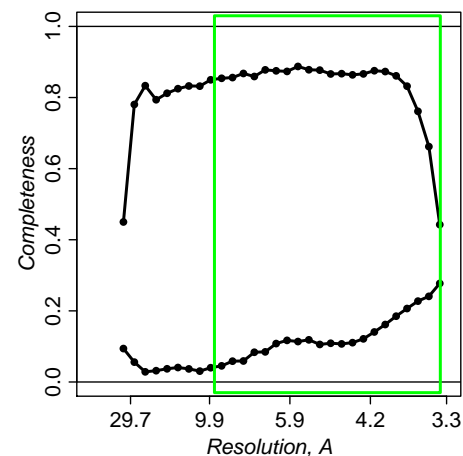
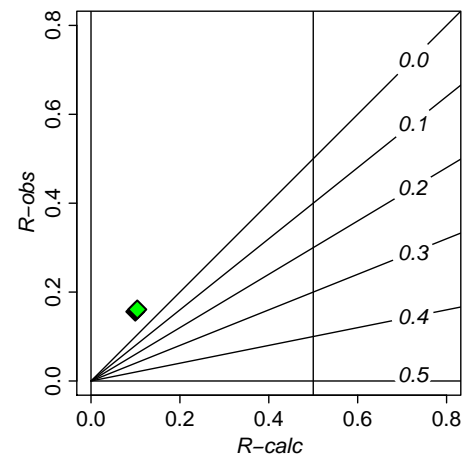
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.13
R	21.2	
R'	21.2	20.9
R-free	29.6	
R'-free	29.4	27.9

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	43.5-3.3	9.9-3.3
unique	29,145	28,023
measured	23,355	22,430
used	19,368	18,632

NCS	translation	rotation
r.m.s.d. (A)	22.15	0.09
angle (o)	104.99	0.06

residues per monomer	DNA	protein
	0	276



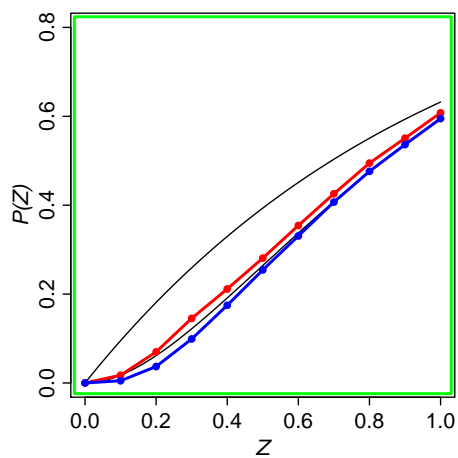
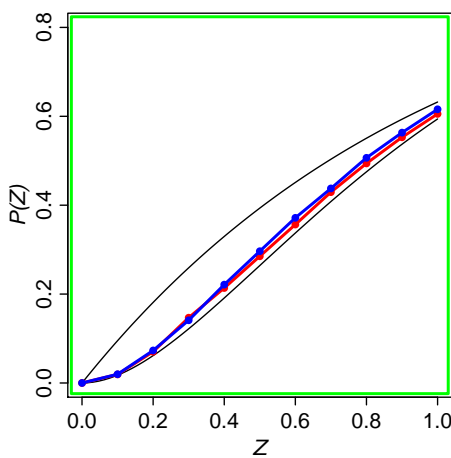
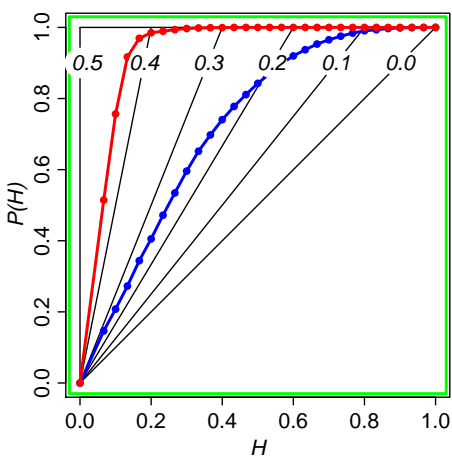
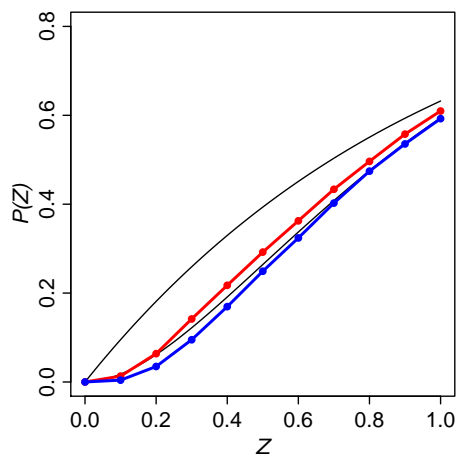
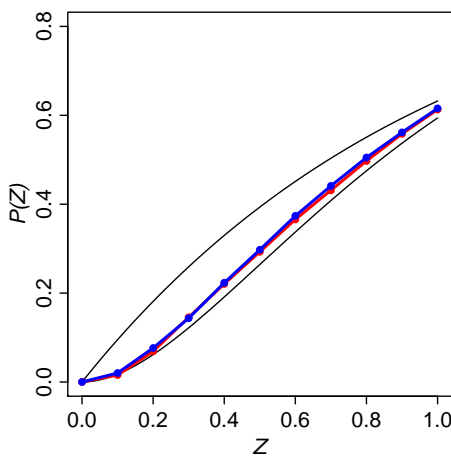
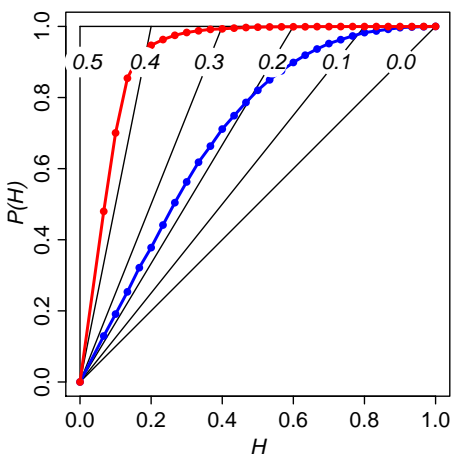
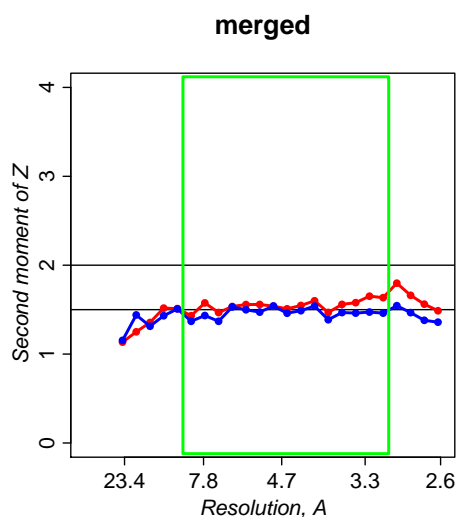
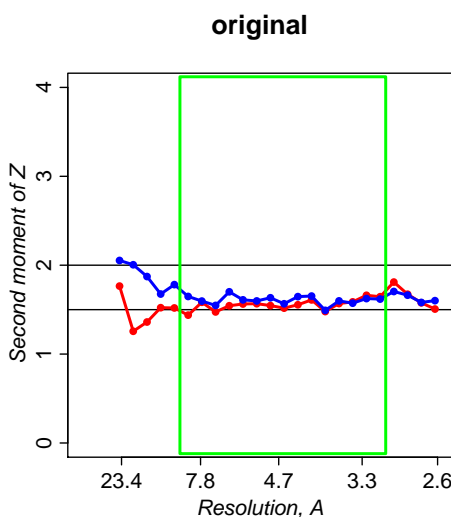
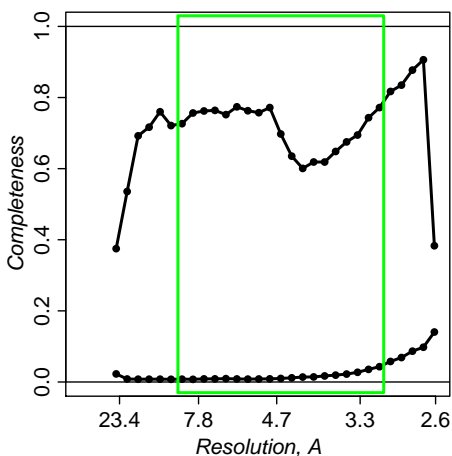
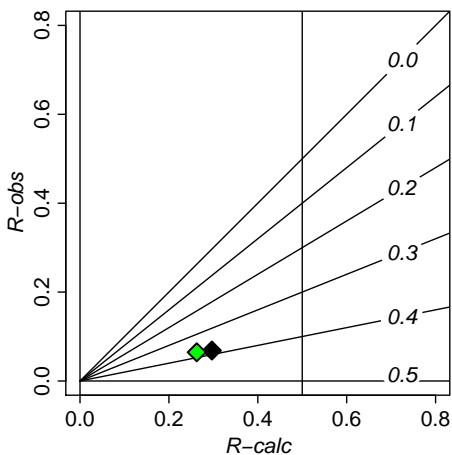
1caw

	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	24.6	-
R'	-	-
R-free	30.2	-
R'-free	-	-
residues per monomer	DNA 0	protein 365

s < f/100	2374	22.44 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	30.1-2.6	9.9-3.0
unique	14,742	9,763
measured	10,578	6,846
used	9,664	6,334

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1chr

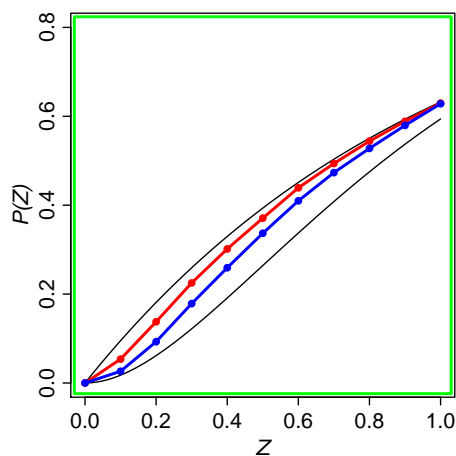
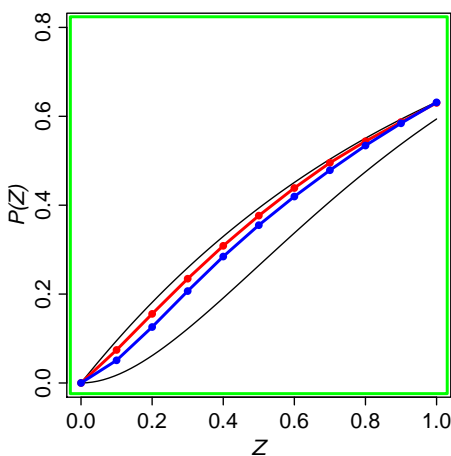
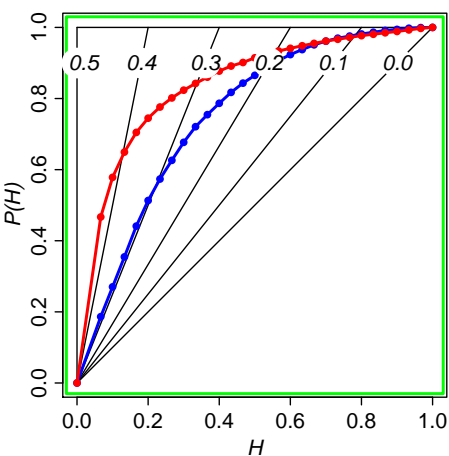
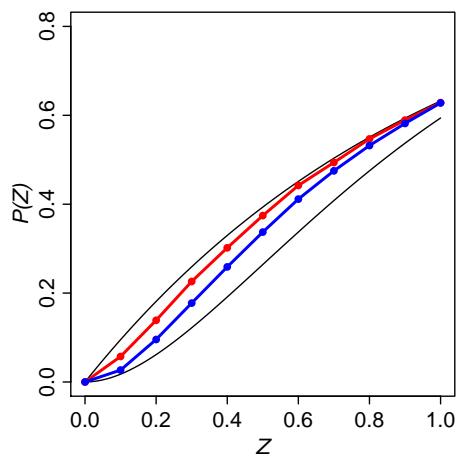
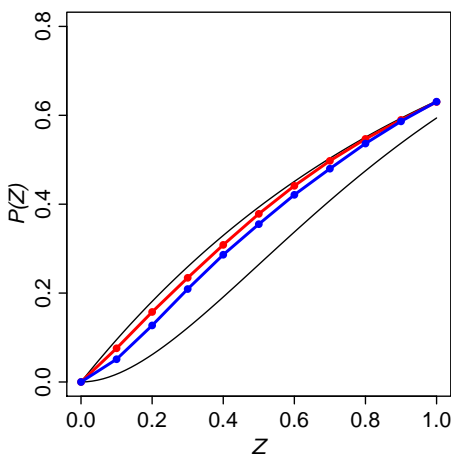
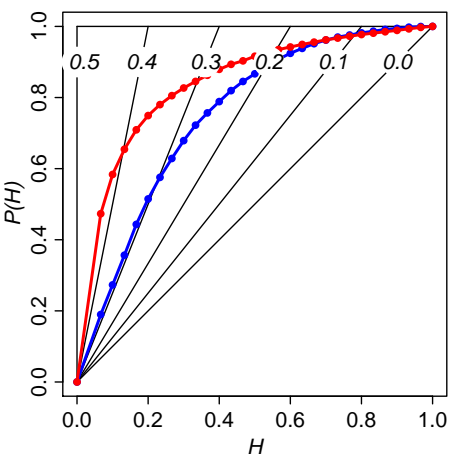
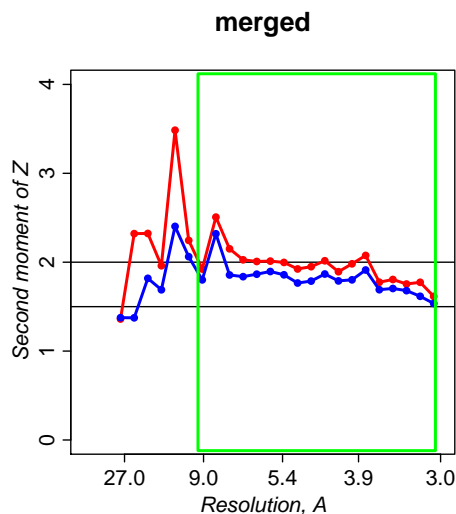
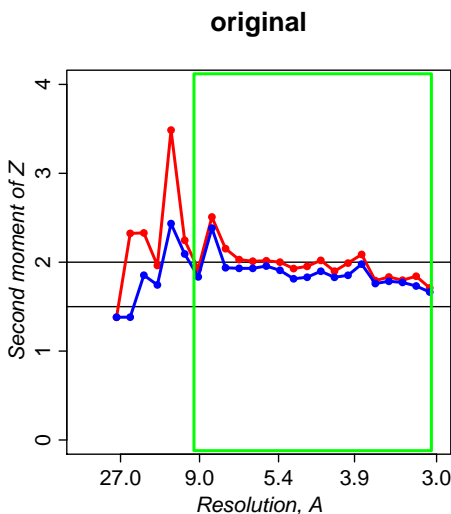
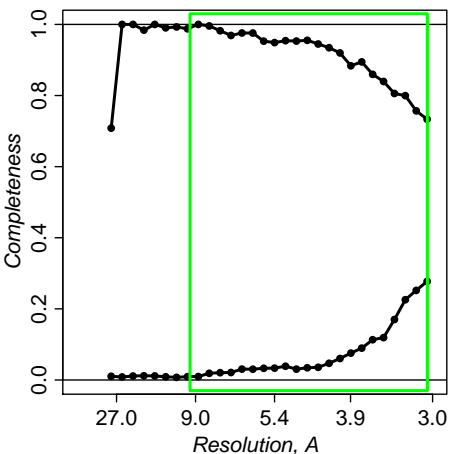
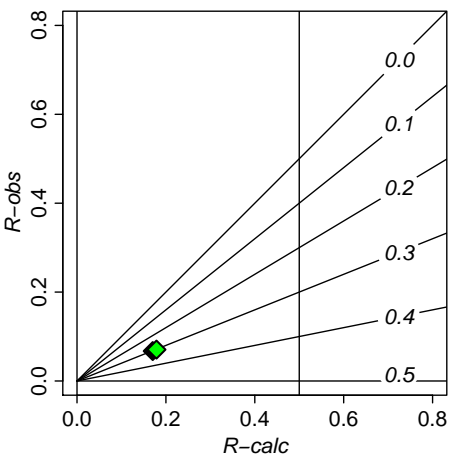
	original	merged
s.g.	14	14 2 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.77
R	22.8	
R'	23.2	24.1
R-free	27.6	
R'-free	27.1	27.2

s < f/100	1776	11.09 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	37.1-3.0	9.9-3.0
unique	18,297	17,778
measured	16,011	15,495
used	13,488	13,120

NCS	translation	rotation
r.m.s.d. (A)	32.52	0.77
angle (o)	179.79	0.23

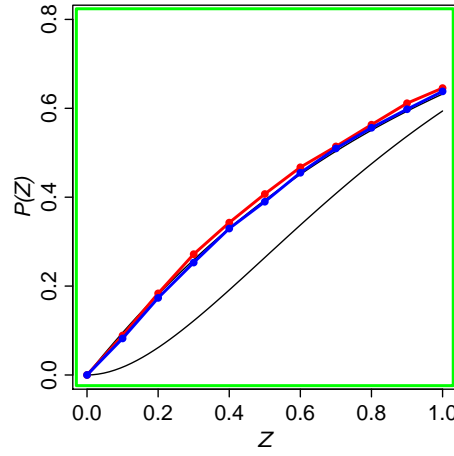
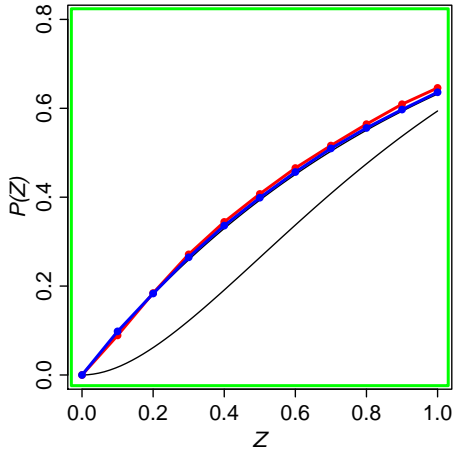
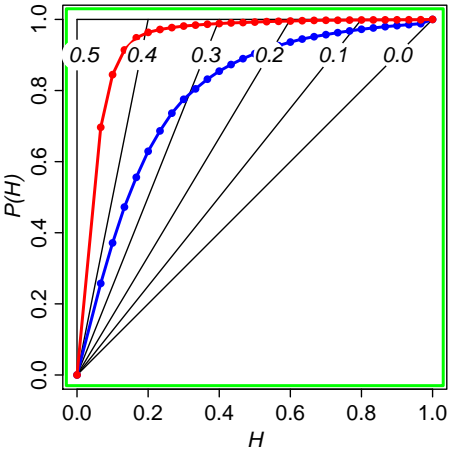
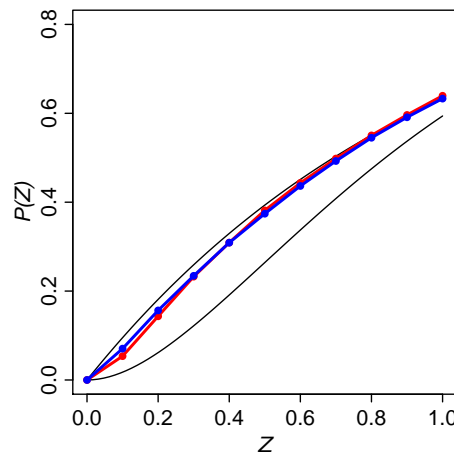
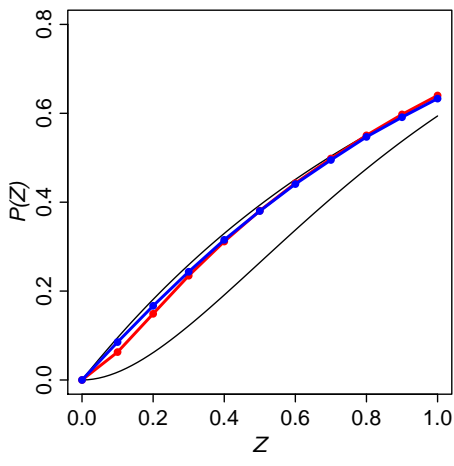
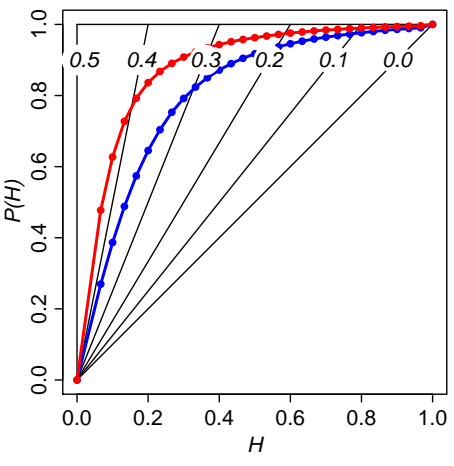
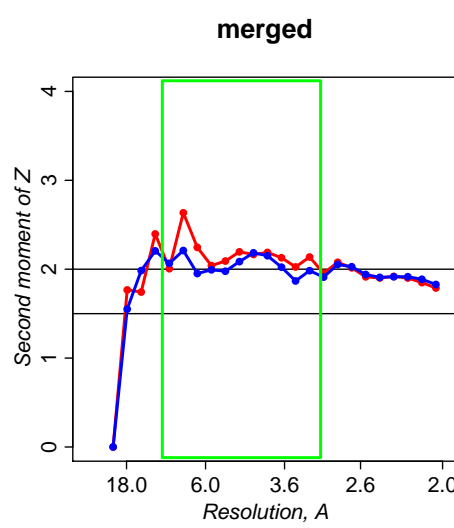
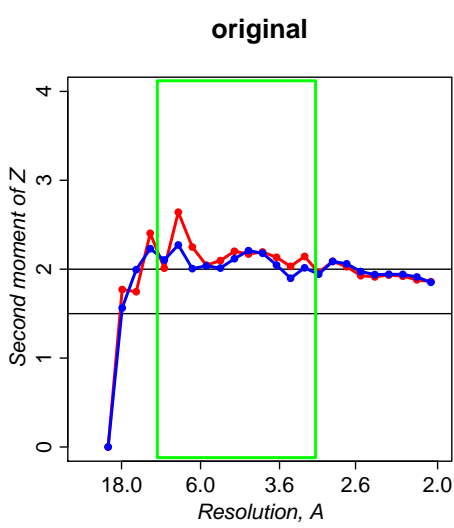
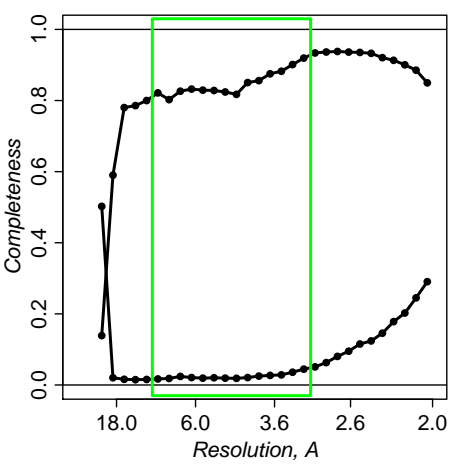
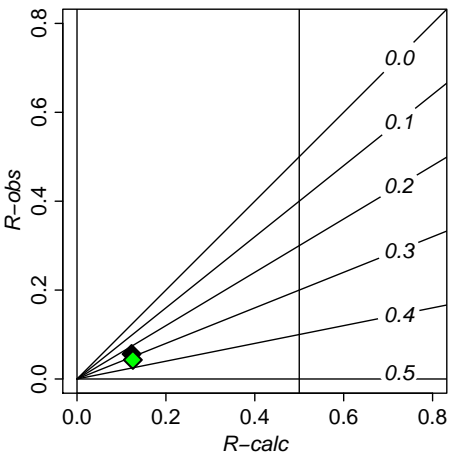
residues per monomer	DNA	protein
	0	370



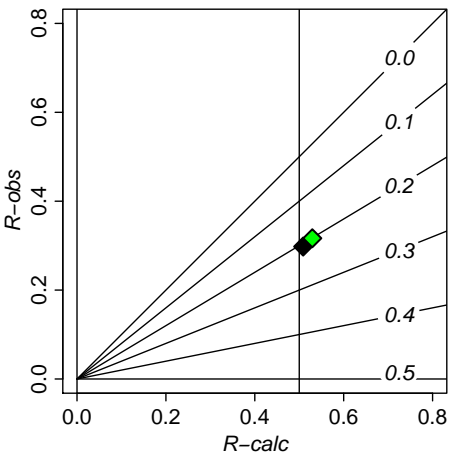
1d01

	original	merged
s.g.	P 1 21 1	P 63
p.g.	10001	12021
a.u.	6	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.10
R	28.7	
R'	28.7	28.3
R-free	30.5	
R'-free	30.2	29.6
residues per monomer	DNA 0	protein 168

s < f/100	388	0.41 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	37.2–2.0	9.9–3.0
unique	106,068	30,694
measured	95,109	26,657
used	80,154	21,966
NCS	translation	rotation
r.m.s.d. (A)	13.77	0.06
angle (o)	59.95	0.05



1d8g

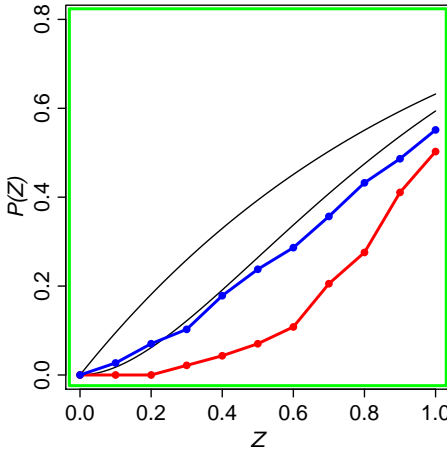
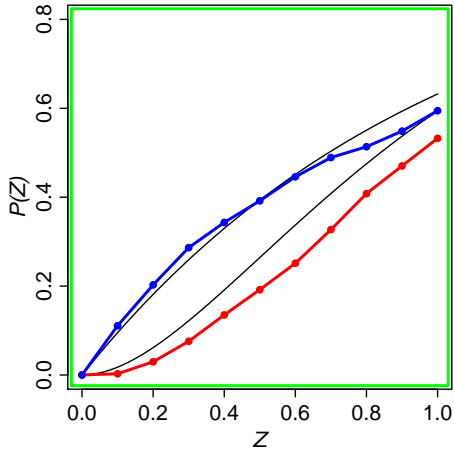
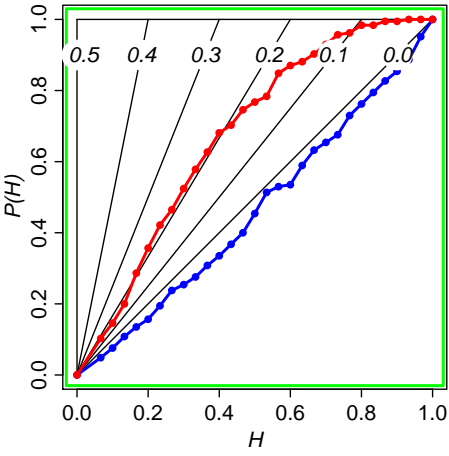
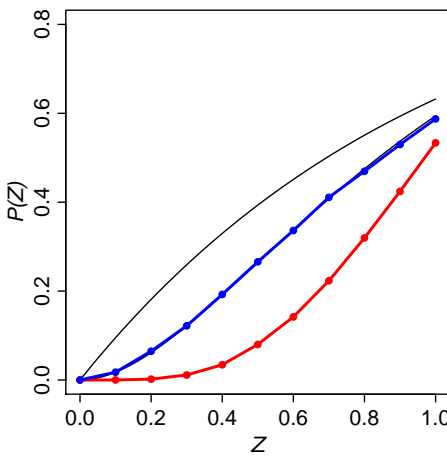
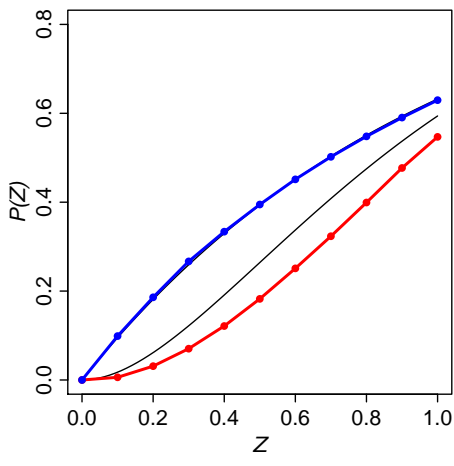
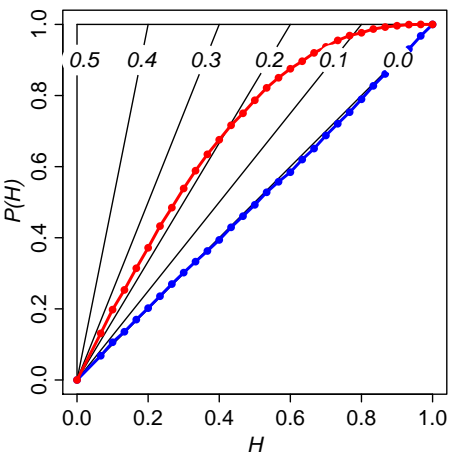
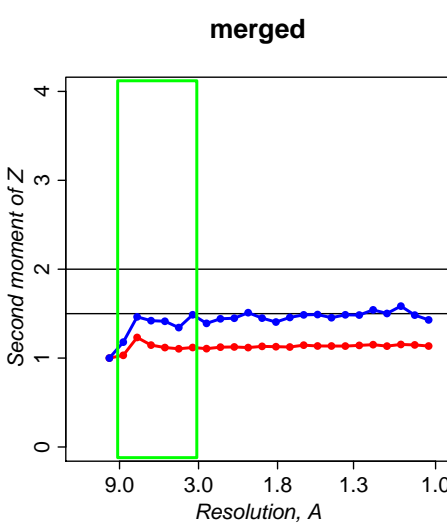
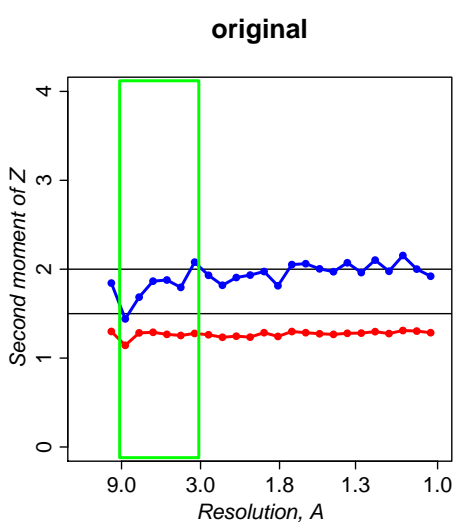
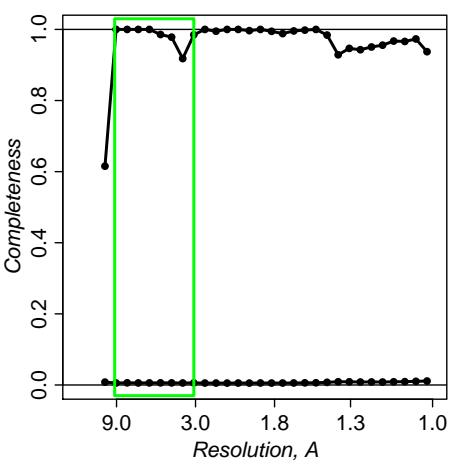


	original	merged
s.g.	C 1 2 1	-
p.g.	10001	10003
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	30.9	-
R'	-	-
R-free	32.2	-
R'-free	-	-

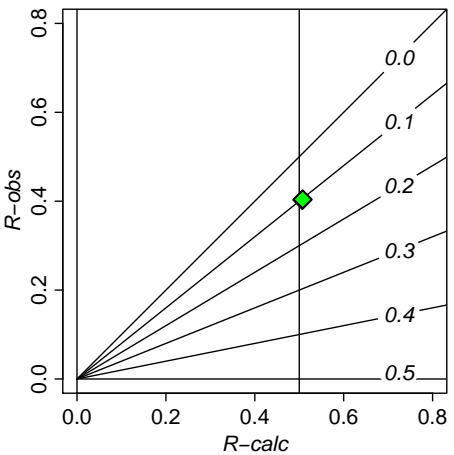
	11050	85.03 %
s < f/100	11050	85.03 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

residues per monomer	DNA	protein
	9	0

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1db2



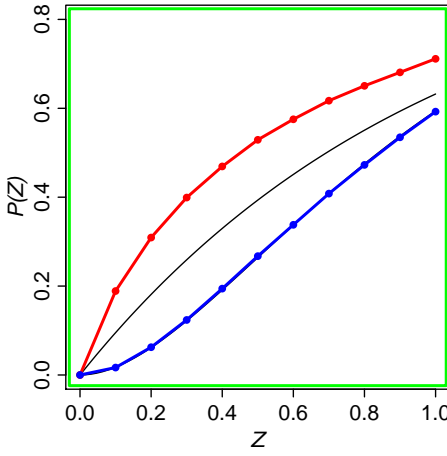
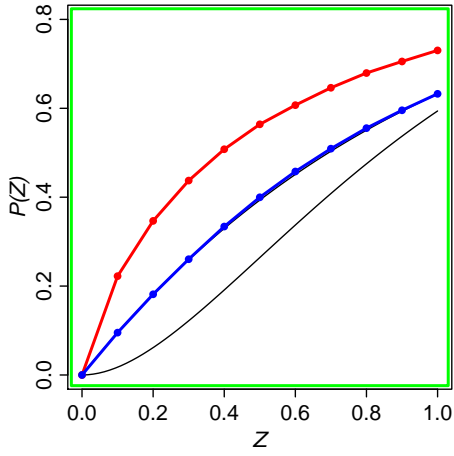
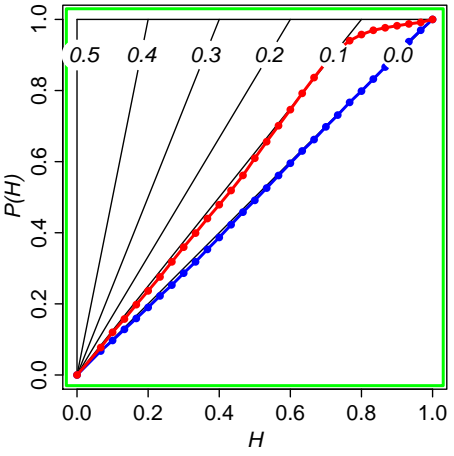
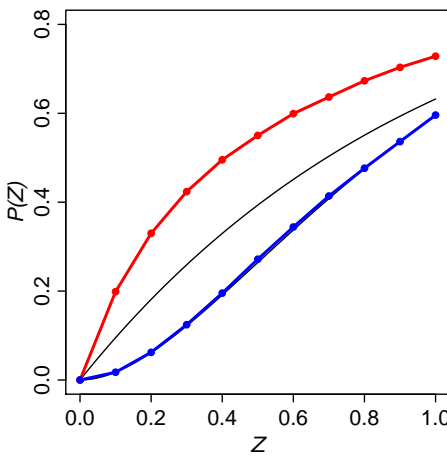
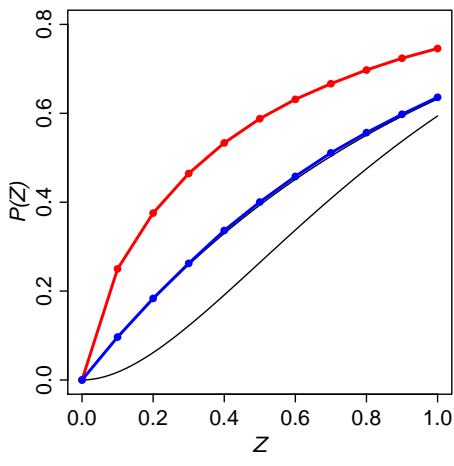
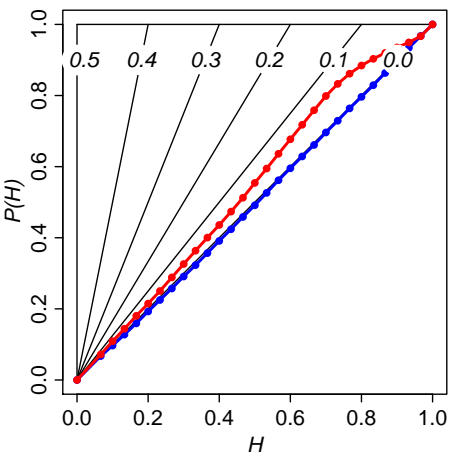
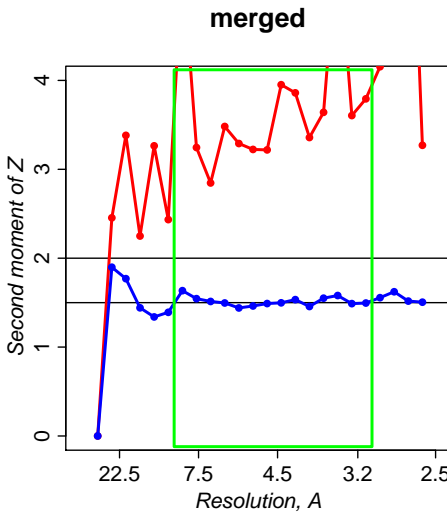
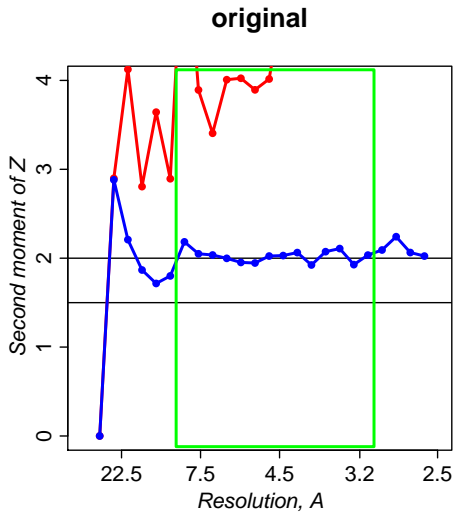
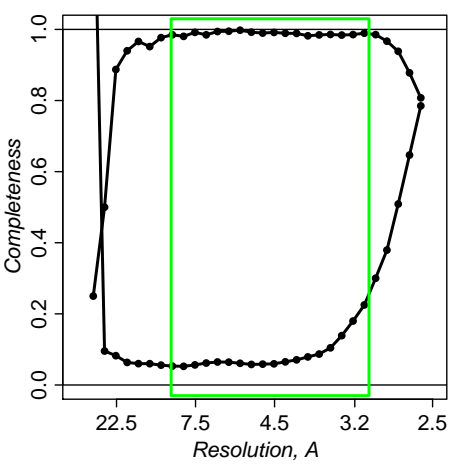
	original	merged
s.g.	P 31 2 1	-
p.g.	10023	12027
a.u.	2	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	59.5	-
R'	-	-
R-free	67.3	-
R'-free	-	-

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	1385	3.45 %
s,f <= 0	0	0.00 %

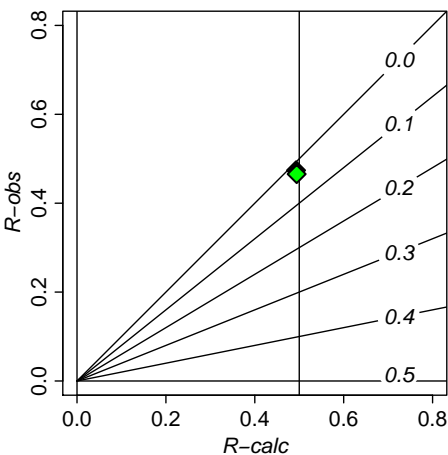
range (A)	83.8-2.5	9.9-3.0
unique	42,110	25,091
measured	40,198	24,786
used	33,018	20,558

NCS	translation	rotation
r.m.s.d. (A)	24.45	16.55
angle (o)	80.35	60.56

residues per monomer	DNA	protein
	0	362



1dbf



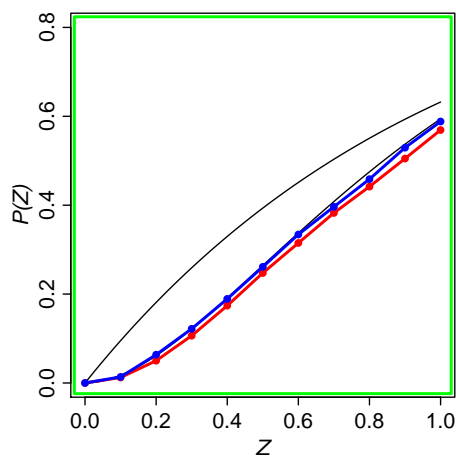
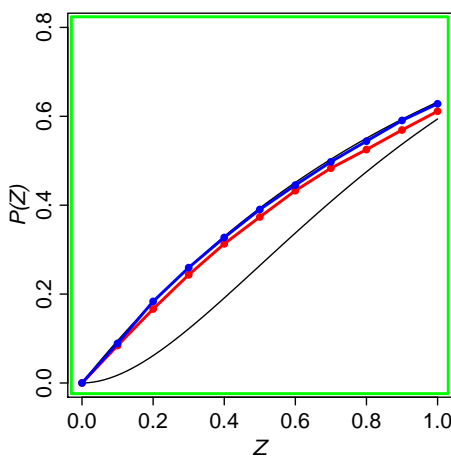
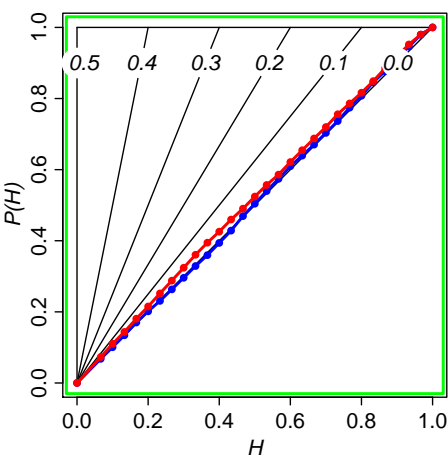
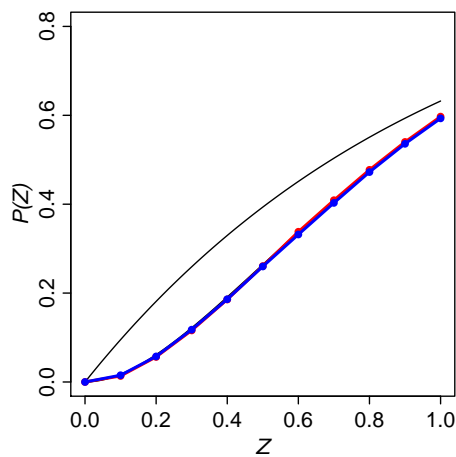
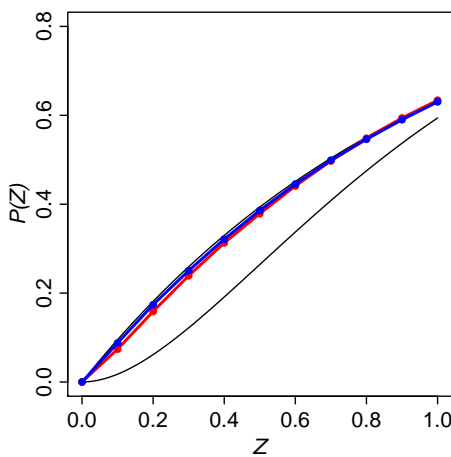
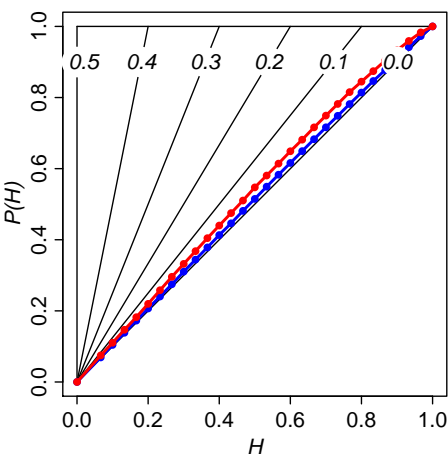
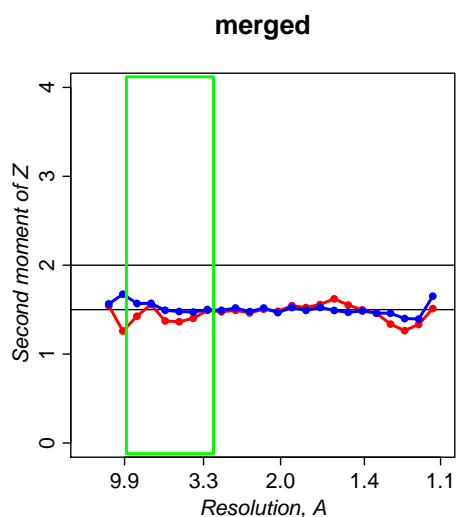
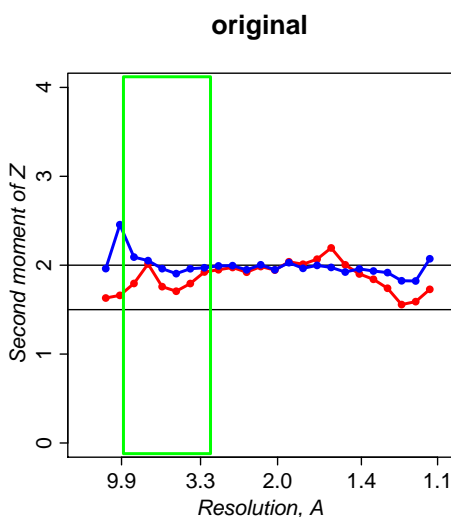
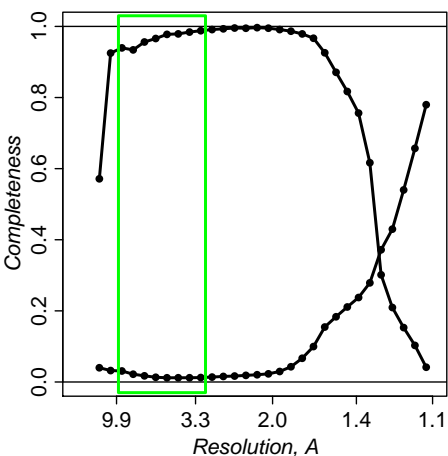
	original	merged
s.g.	P 21 21 21	-
p.g.	10003	10205
a.u.	3	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	30.6	-
R'	-	-
R-free	31.5	-
R'-free	-	-

residues per monomer	DNA	protein
	0	127

s < f/100	5873	6.54 %
s <= 0	2	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	23.4-1.1	9.9-3.0
unique	143,509	7,736
measured	89,868	7,546
used	72,398	6,154

NCS	translation	rotation
r.m.s.d. (A)	18.86	14.35
angle (o)	101.85	70.87



1dc3

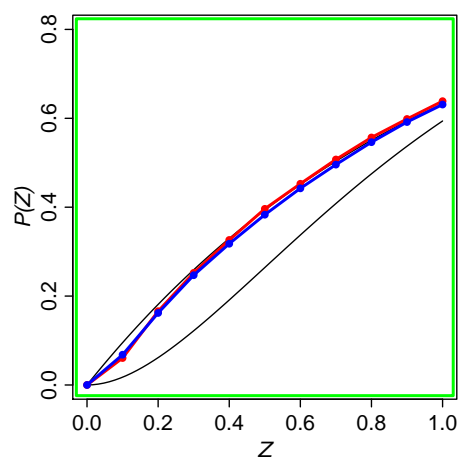
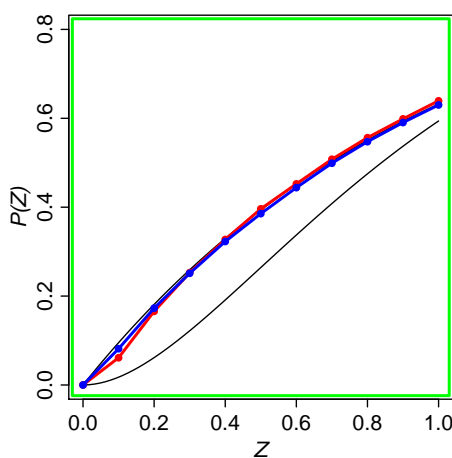
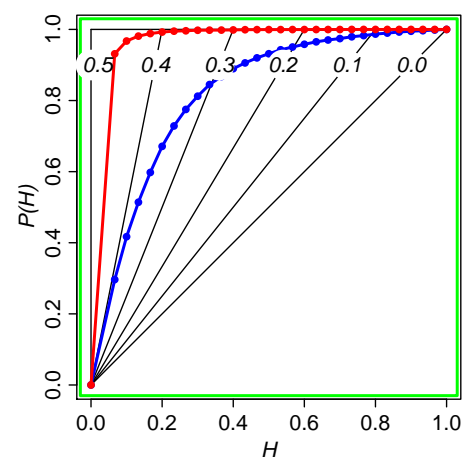
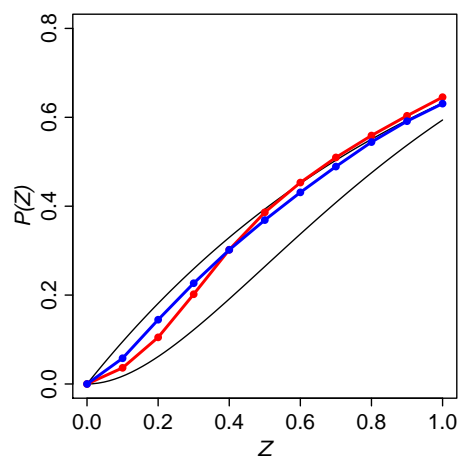
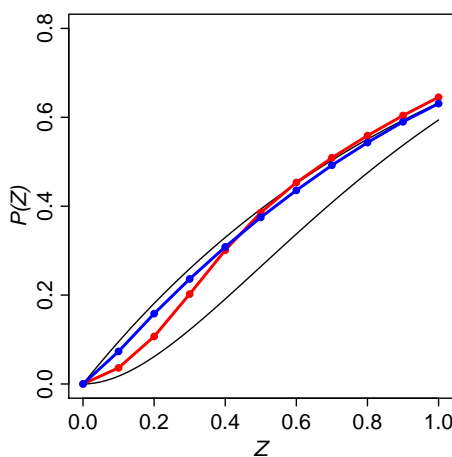
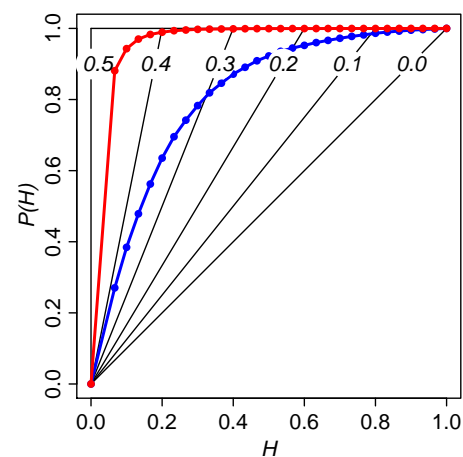
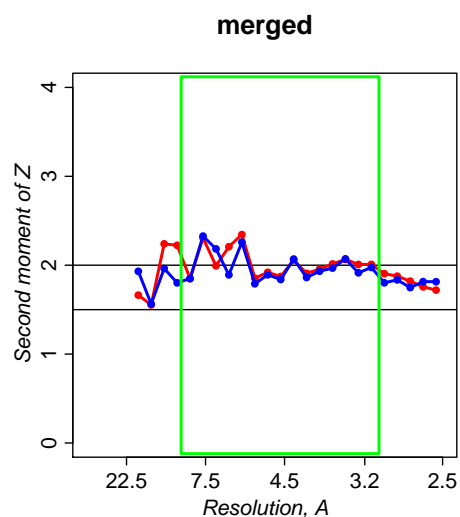
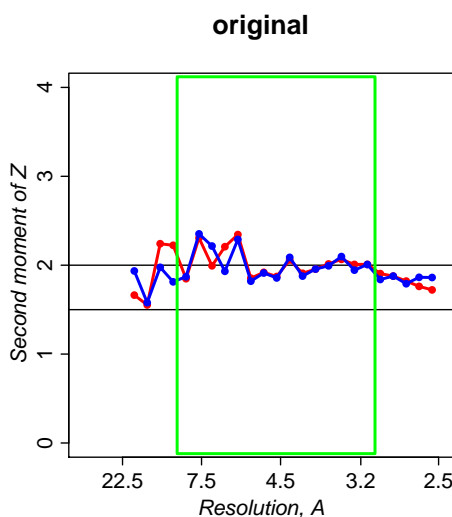
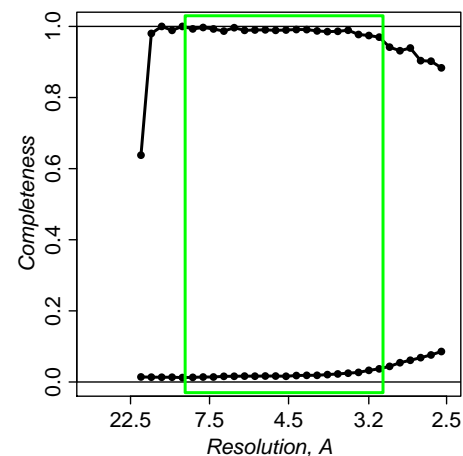
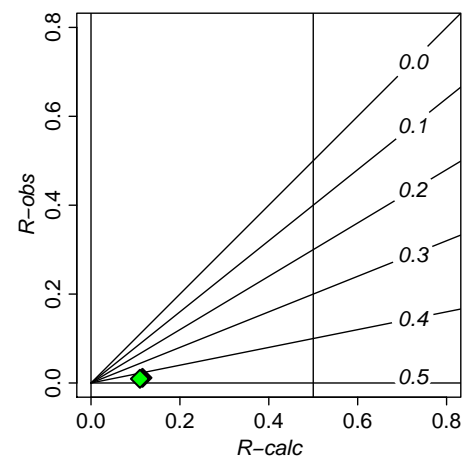
	original	merged
s.g.	1 41	1 41 2 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.17
R	21.8	
R'	22.1	22.6
R-free	23.5	
R'-free	24.4	24.9

s < f/100	398	1.09 %
s <= 0	0	0.00 %
f <= 0	5	0.01 %
s,f <= 0	0	0.00 %

range (A)	19.9–2.5	9.9–3.0
unique	38,355	21,678
measured	36,605	21,330
used	33,554	19,516

NCS	translation	rotation
r.m.s.d. (A)	31.14	0.17
angle (o)	179.98	0.02

residues per monomer	DNA	protein
	0	330



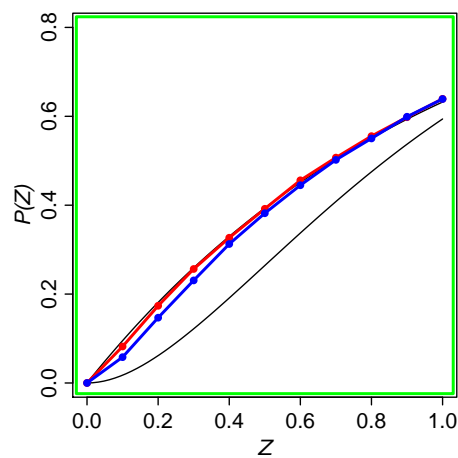
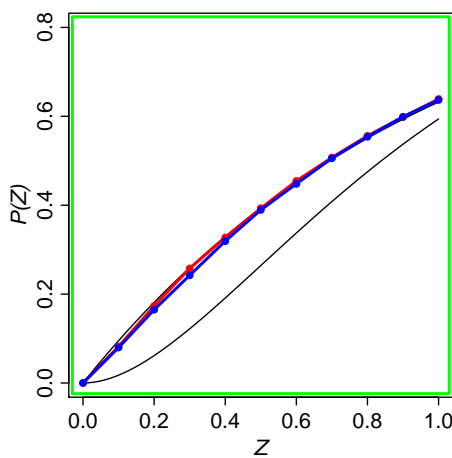
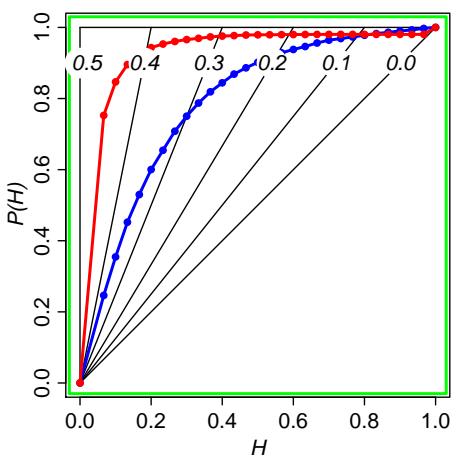
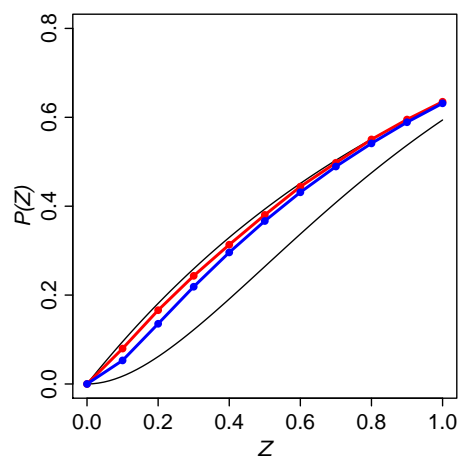
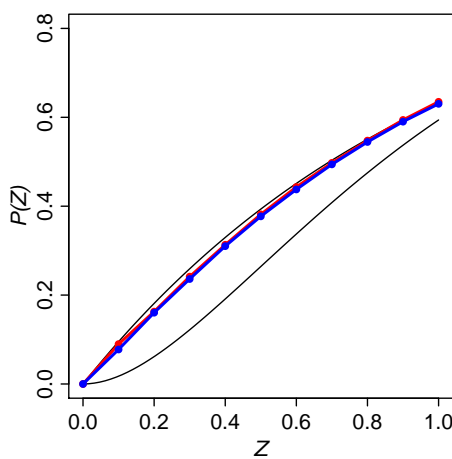
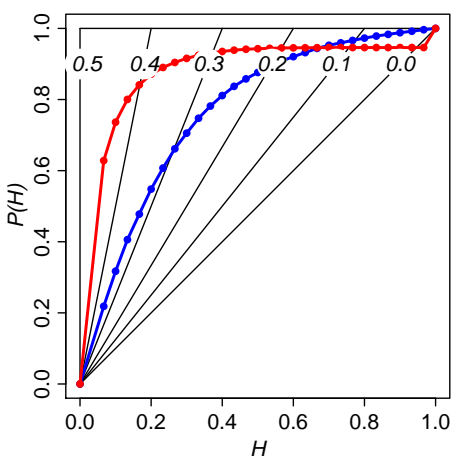
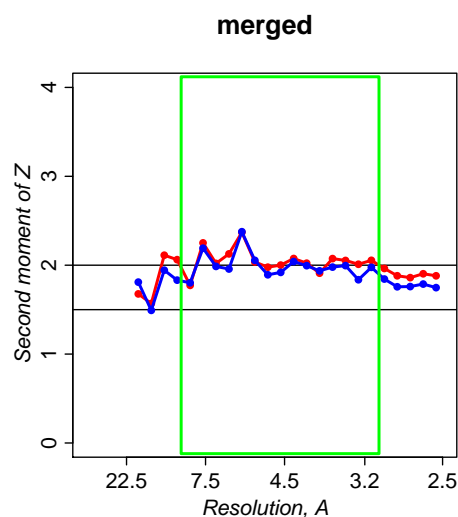
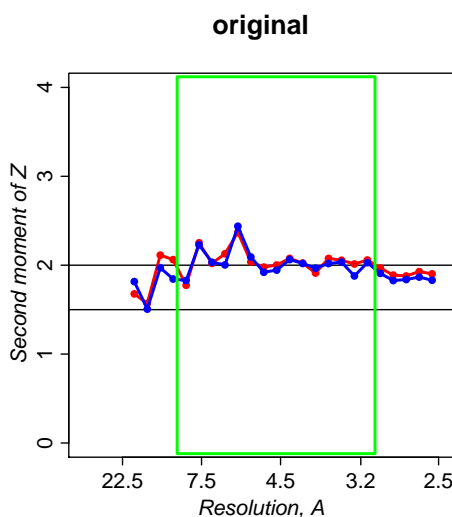
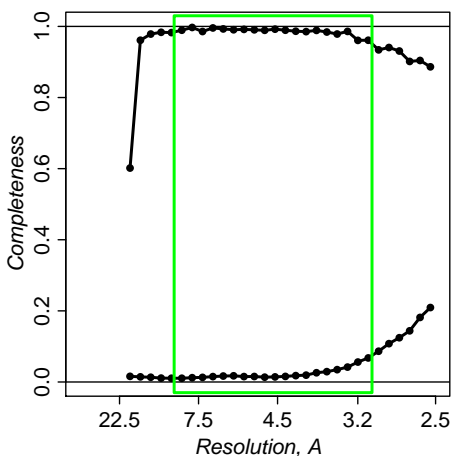
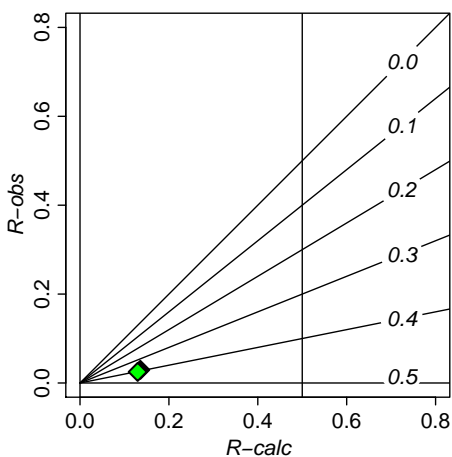
1dc4

	original	merged
s.g.	1 41	1 41 2 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.23
R	21.7	
R'	22.3	23.0
R-free	25.3	
R'-free	25.8	26.5
residues per monomer	DNA 0	protein 330

s < f/100	4319	11.63 %
s <= 0	0	0.00 %
f <= 0	2407	6.48 %
s,f <= 0	0	0.00 %

range (A)	19.8–2.5	9.9–3.0
unique	38,988	22,009
measured	37,130	21,597
used	33,562	19,664

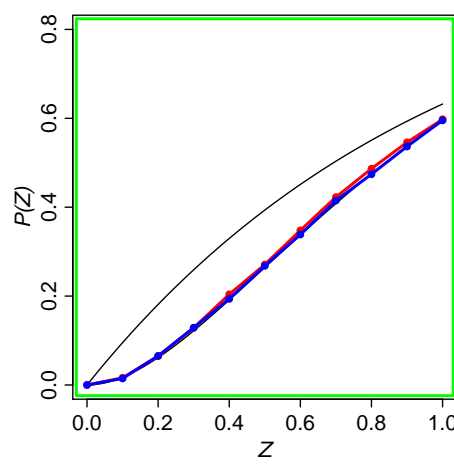
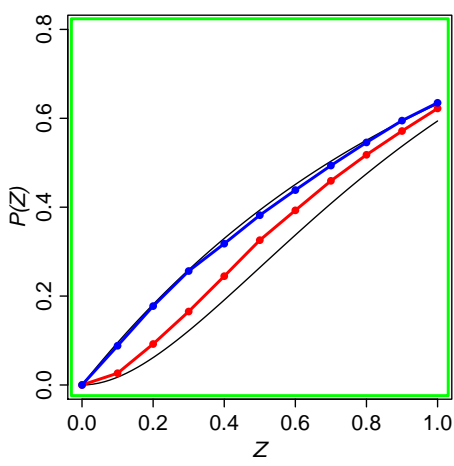
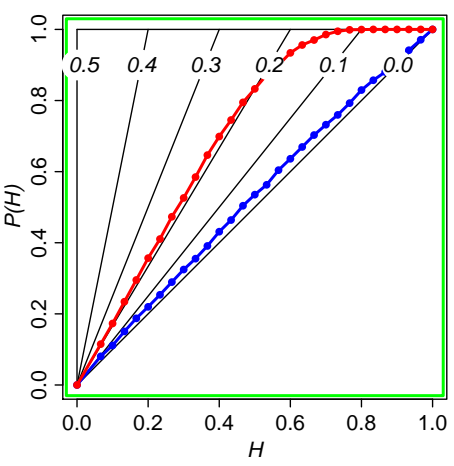
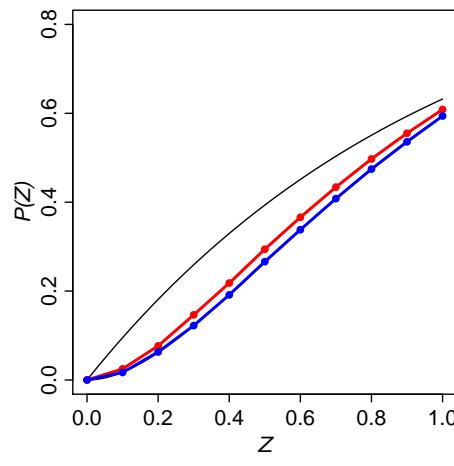
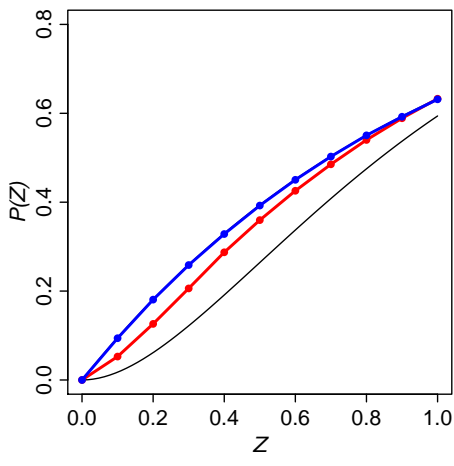
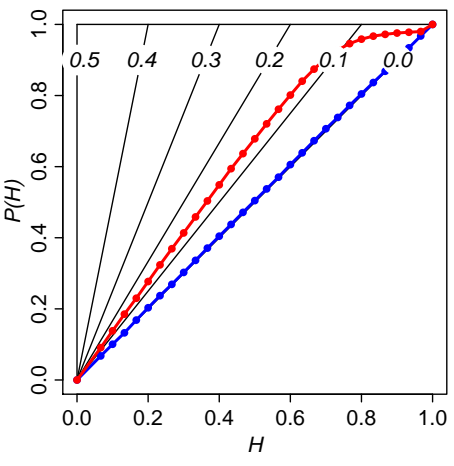
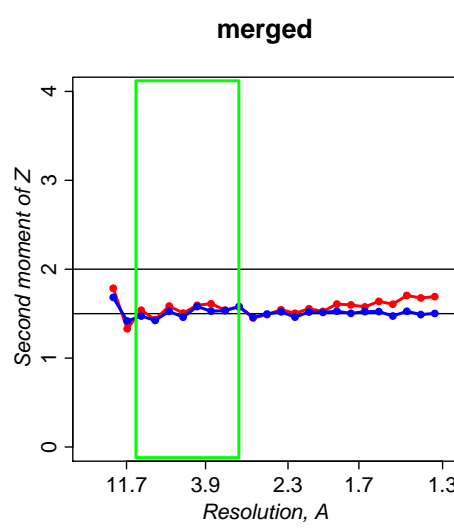
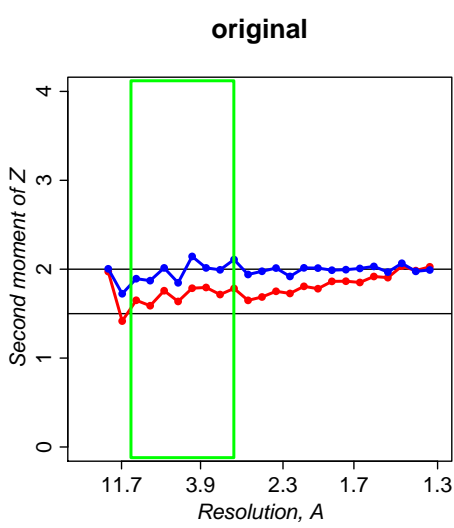
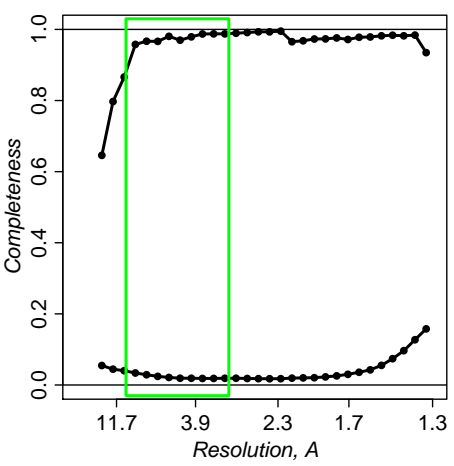
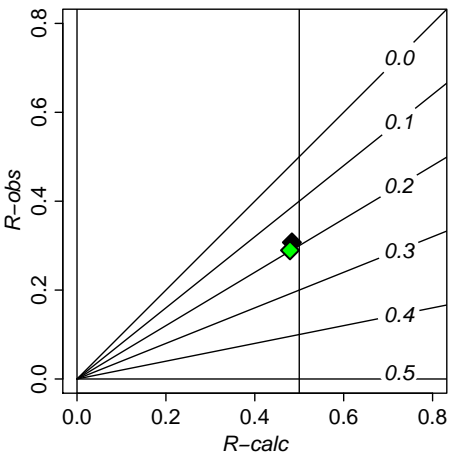
NCS	translation	rotation
r.m.s.d. (A)	26.83	0.23
angle (o)	179.95	0.07



1dcs

	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	26.6	-
R'	-	-
R-free	27.5	-
R'-free	-	-
residues per monomer	DNA 0	protein 279

s < f/100	148	0.21 %
s <= 0	0	0.00 %
f <= 0	851	1.19 %
s,f <= 0	0	0.00 %
<hr/>		
range (A)	24.1-1.3	9.9-3.0
unique	73,446	5,856
measured	71,648	5,737
used	69,066	5,402
<hr/>		
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1ddy

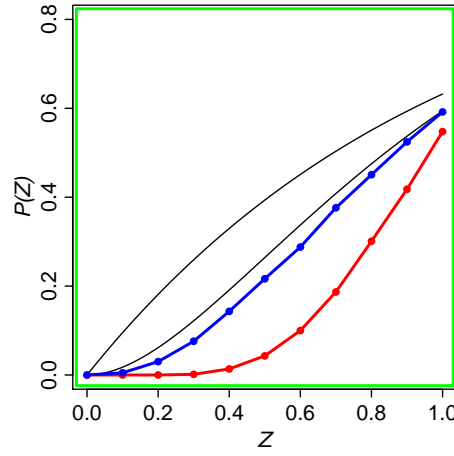
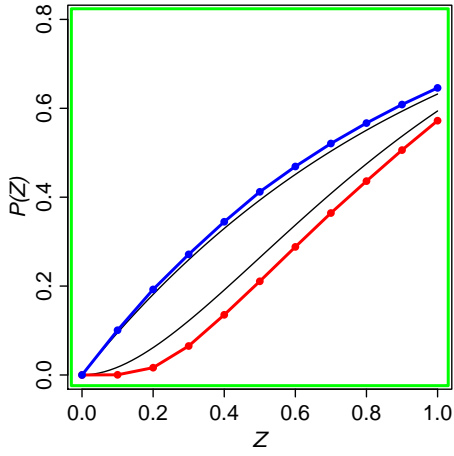
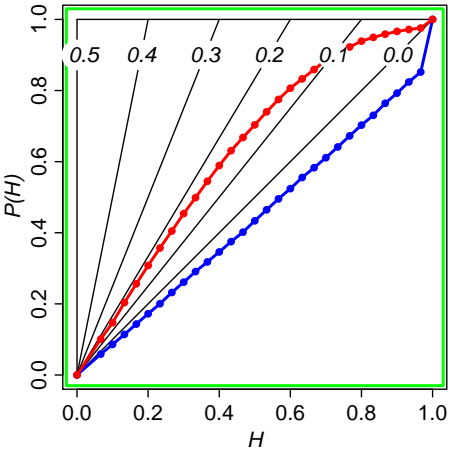
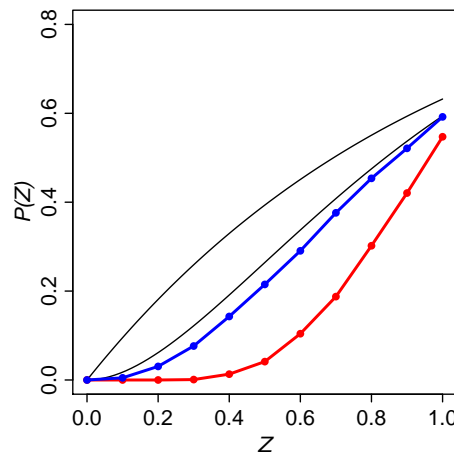
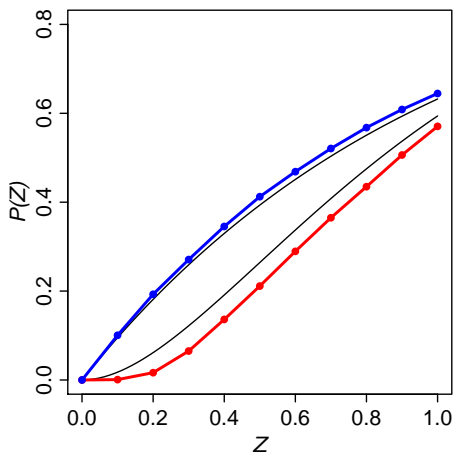
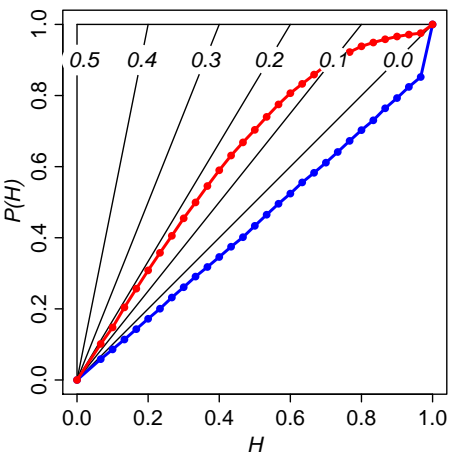
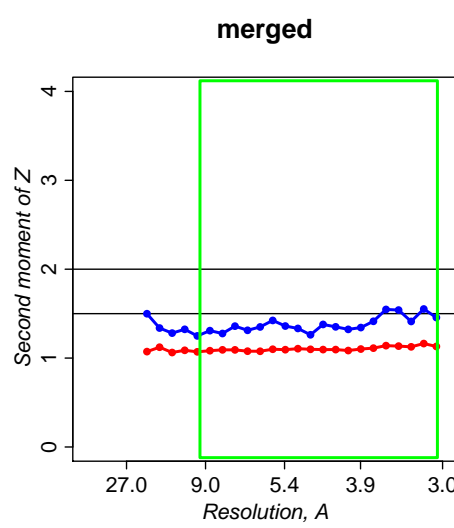
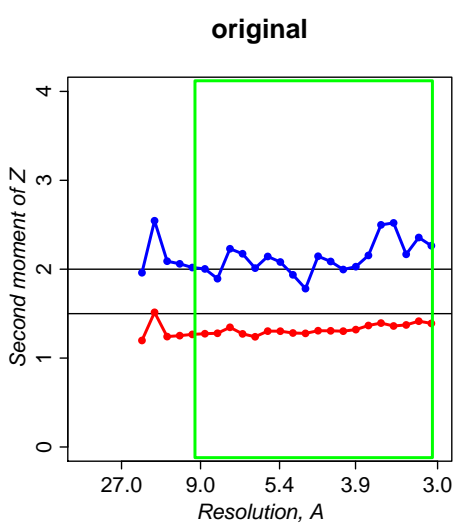
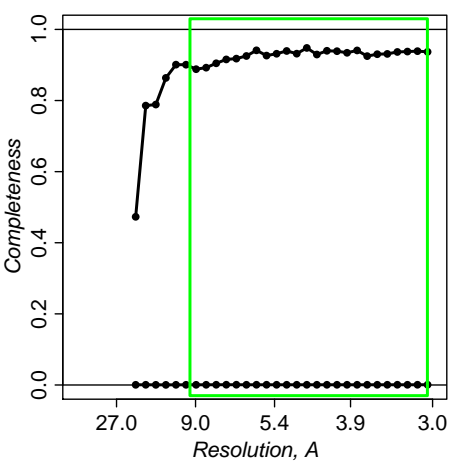
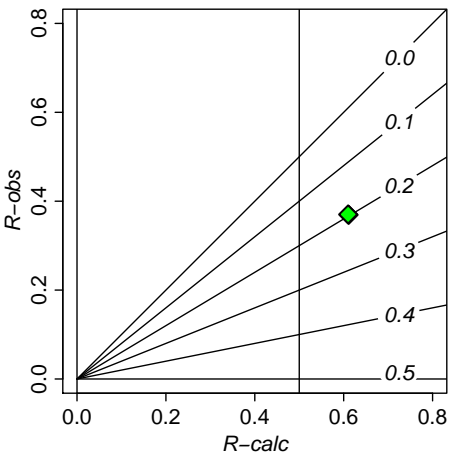
	original	merged
s.g.	C 2 2 2 1	-
p.g.	10003	12027
a.u.	4	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	26.3	-
R'	-	-
R-free	31.3	-
R'-free	-	-

residues per monomer	DNA	protein
	35	0

s < f/100	14244	100.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.9-3.0	9.9-3.0
unique	15,305	14,882
measured	14,244	13,892
used	10,521	10,329

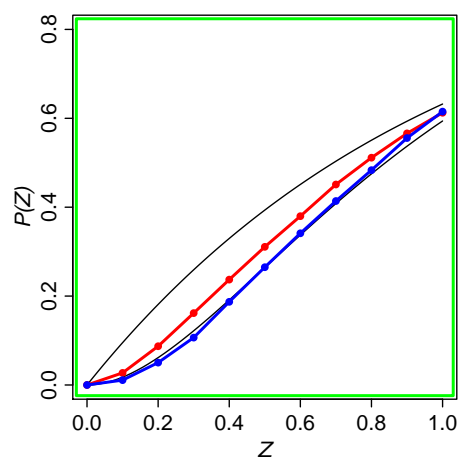
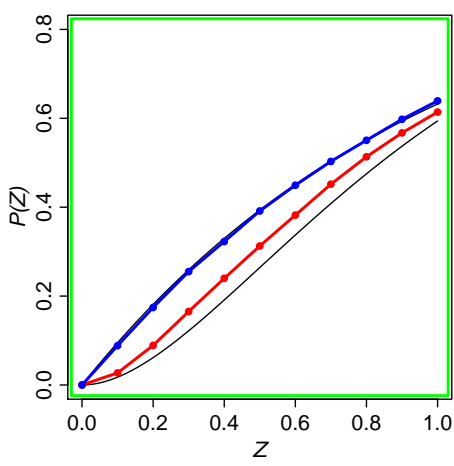
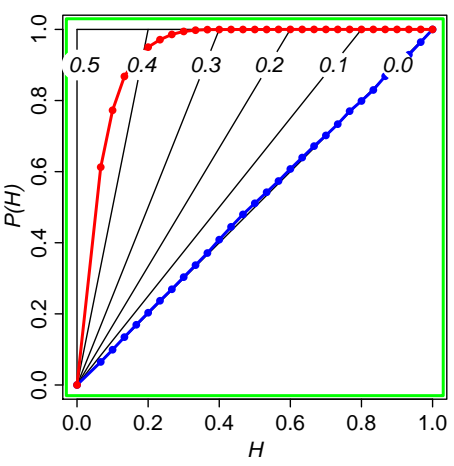
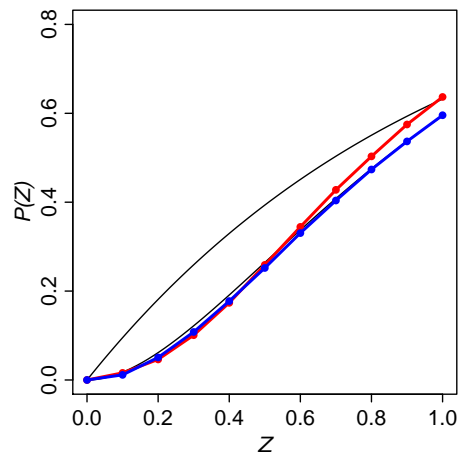
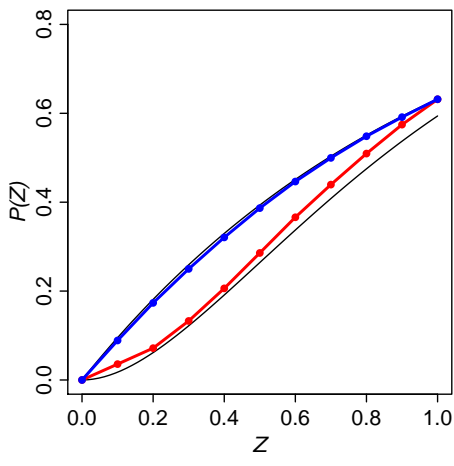
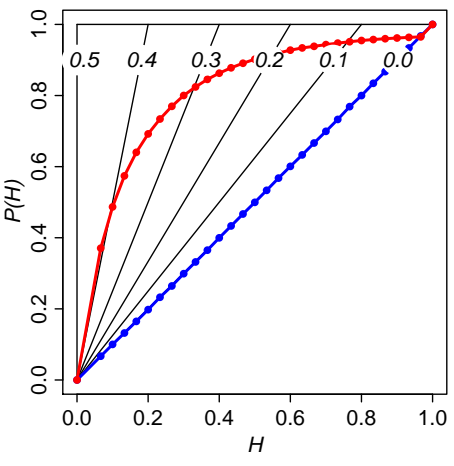
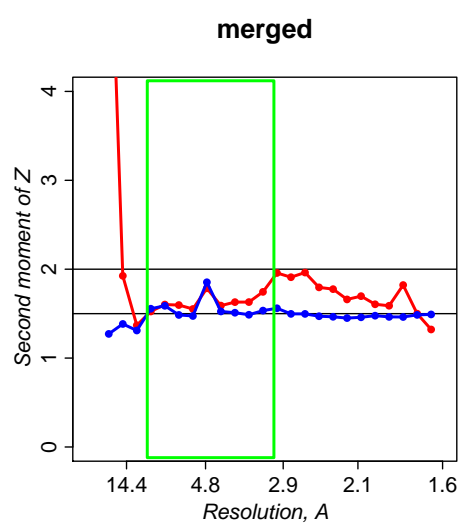
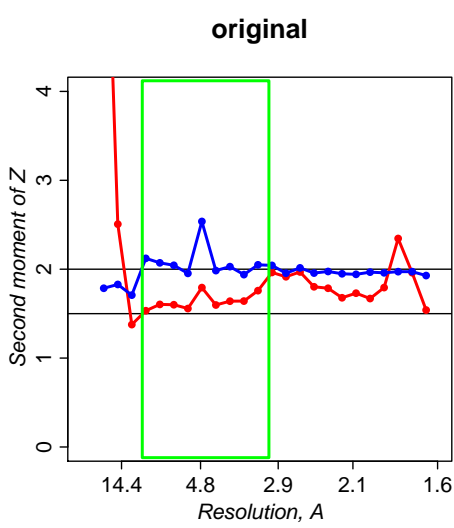
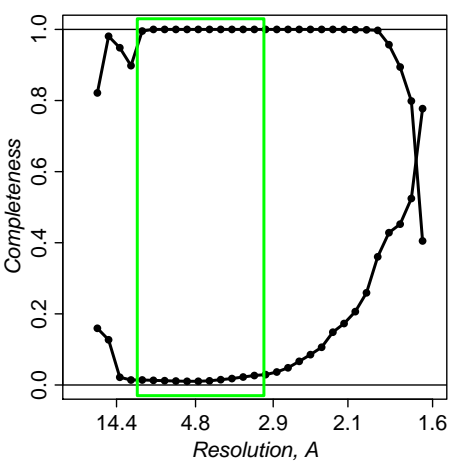
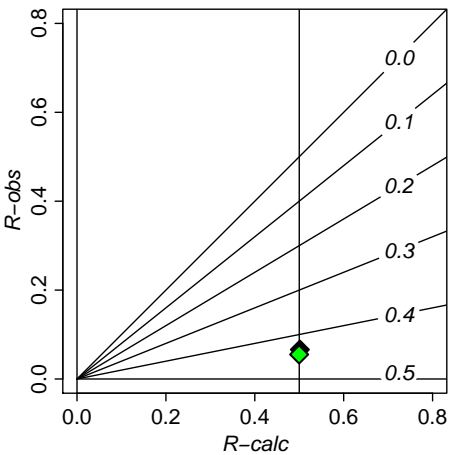
NCS	translation	rotation
r.m.s.d. (A)	5.79	13.13
angle (o)	22.38	55.04



1dgw

	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	32.0	-
R'	-	-
R-free	35.1	-
R'-free	-	-
residues per monomer	DNA 0	protein 346

s < f/100	1995	3.25 %
s <= 0	0	0.00 %
f <= 0	1812	2.95 %
s,f <= 0	0	0.00 %
range (A)	38.6-1.6	9.9-3.0
unique	66,968	10,344
measured	61,474	10,343
used	58,152	9,848
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1dlu

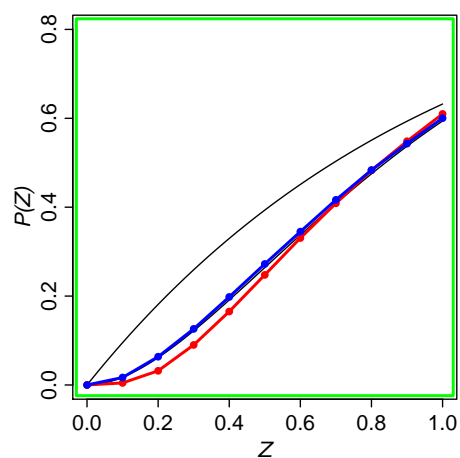
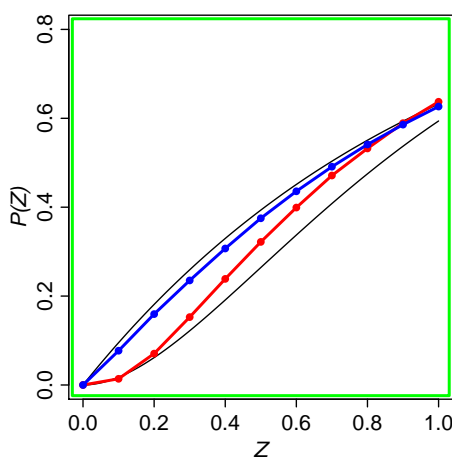
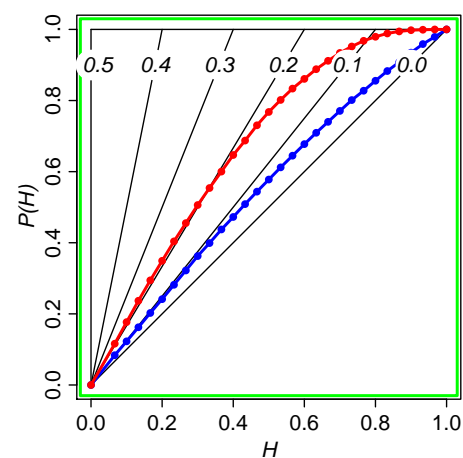
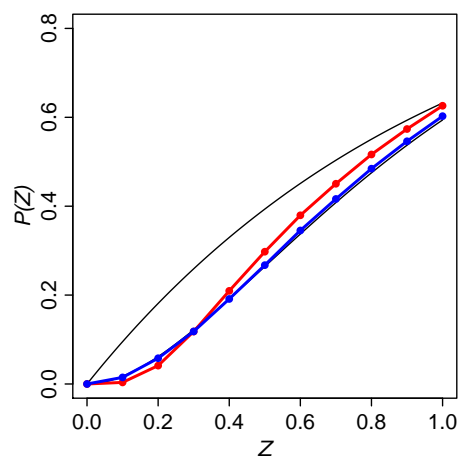
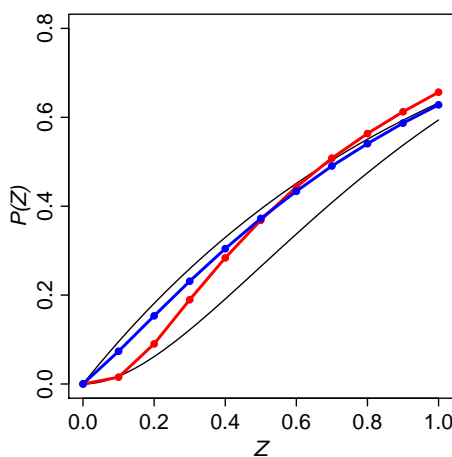
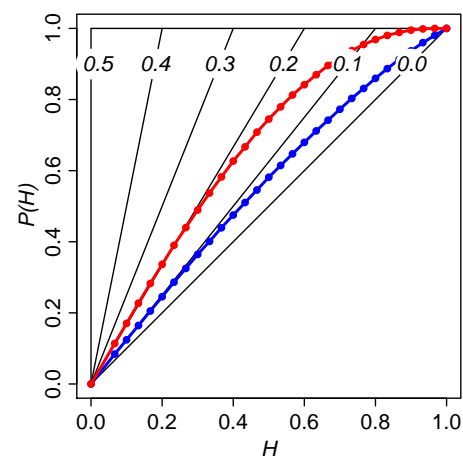
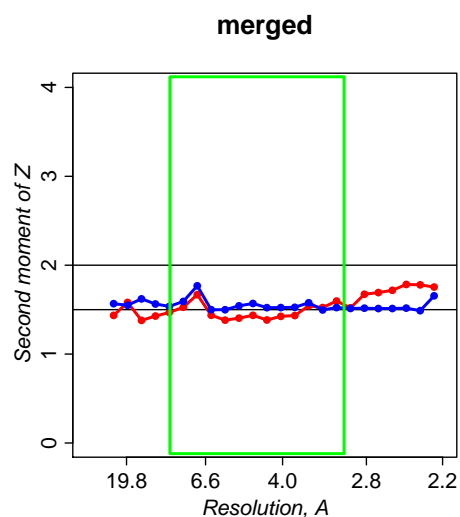
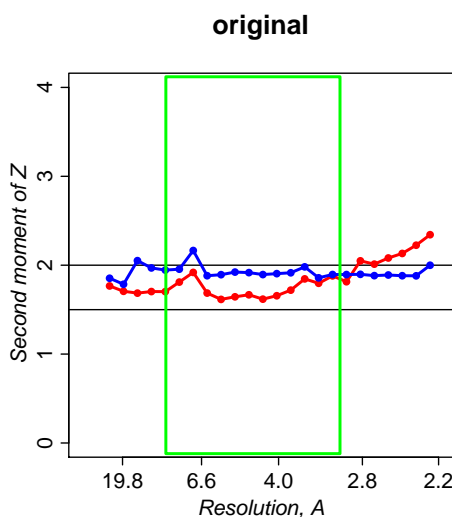
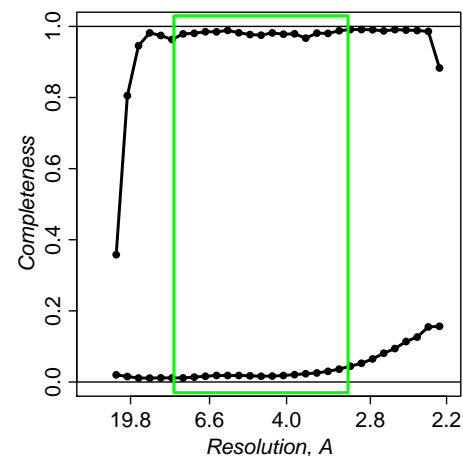
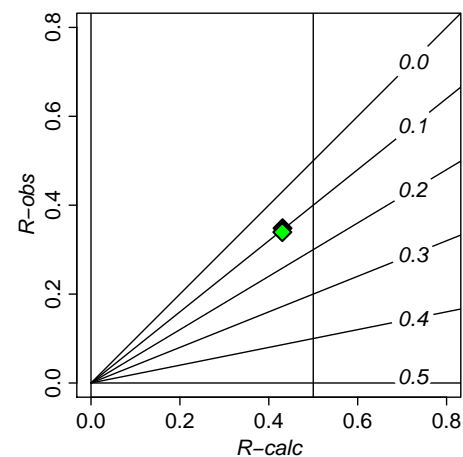
	original	merged
s.g.	P 1 21 1	P 21 21 2
p.g.	10001	10003
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		7.51
R	26.1	
R'	-	-
R-free	27.9	
R'-free	-	-

s < f/100	2109	2.15 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	39.9–2.2	9.9–3.0
unique	100,564	39,288
measured	98,103	38,531
used	86,918	35,746

NCS	translation	rotation
r.m.s.d. (A)	16.49	1.34
angle (o)	63.20	3.94

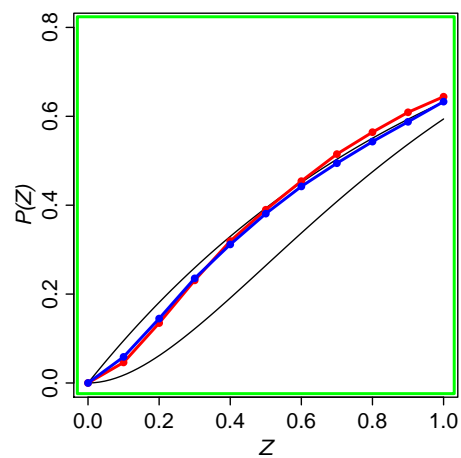
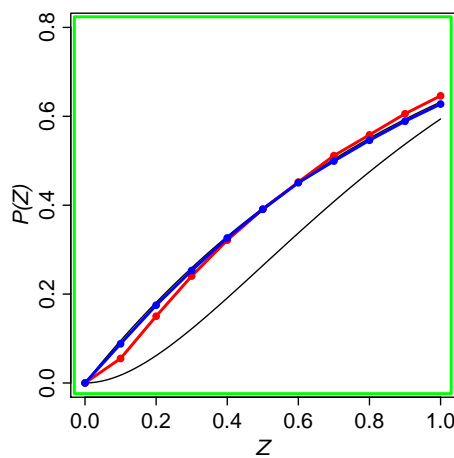
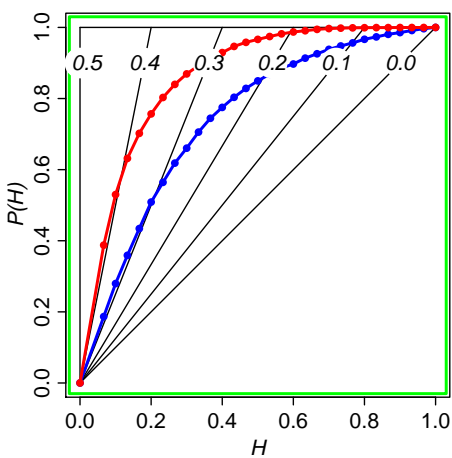
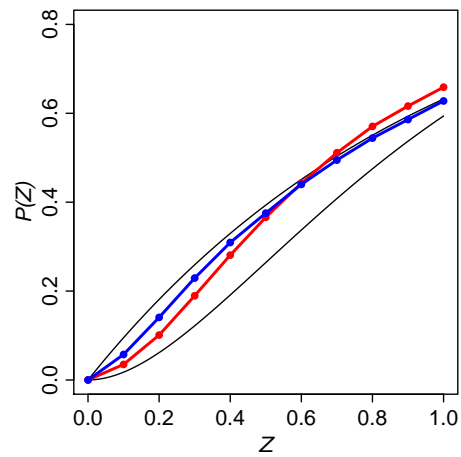
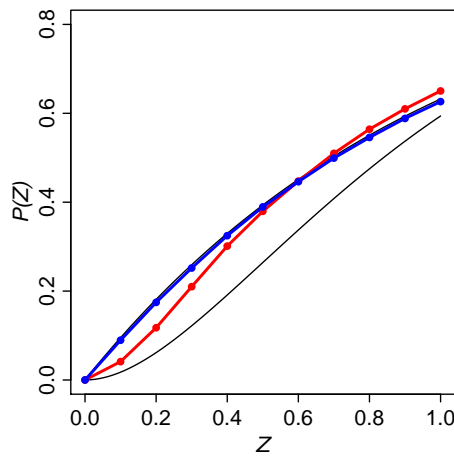
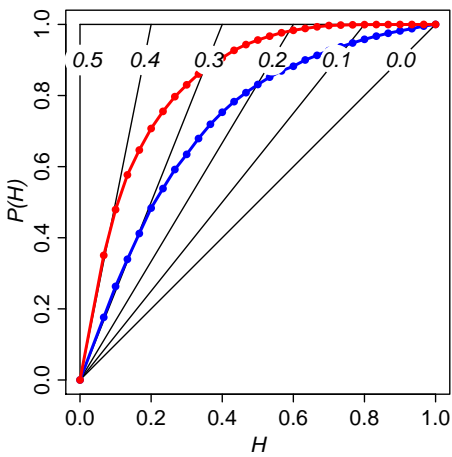
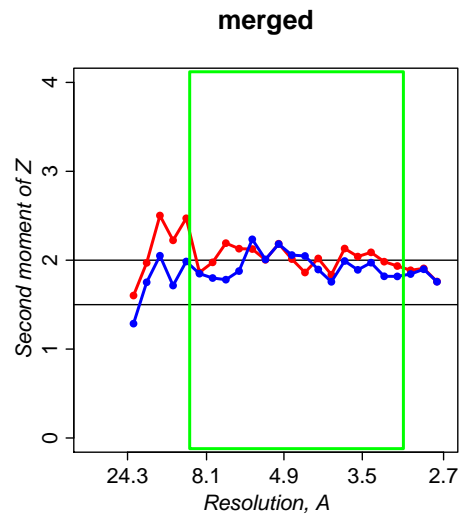
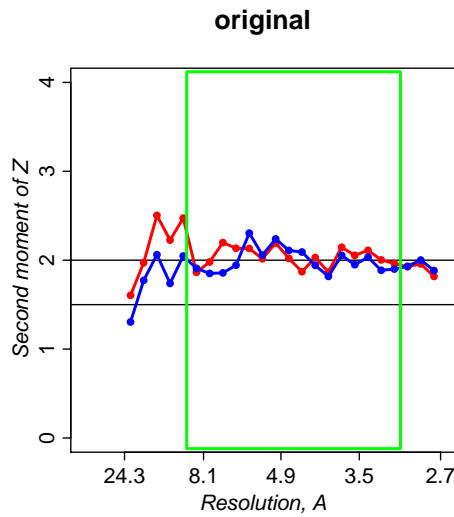
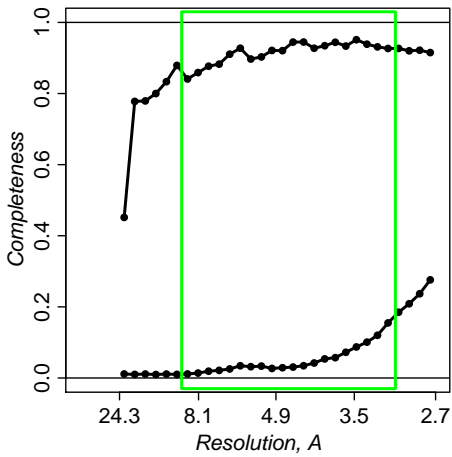
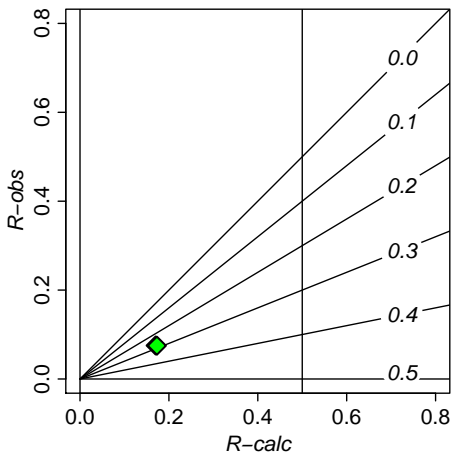
residues per monomer	DNA	protein
	0	389



1ea6

	original	merged
s.g.	P 21 21 21	P 41 21 2
p.g.	10003	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.37
R	23.8	
R'	24.1	24.3
R-free	26.9	
R'-free	26.8	27.1
residues per monomer	DNA 0	protein 304

s < f/100	704	3.53 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	24.7–2.7	9.9–3.0
unique	21,610	15,380
measured	19,939	14,274
used	16,624	11,958
NCS	translation	rotation
r.m.s.d. (A)	26.58	0.32
angle (o)	89.82	0.31



1efq

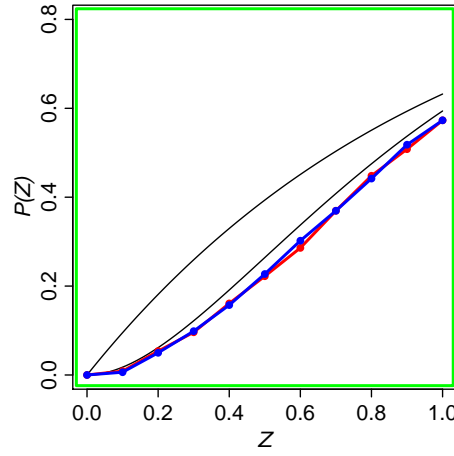
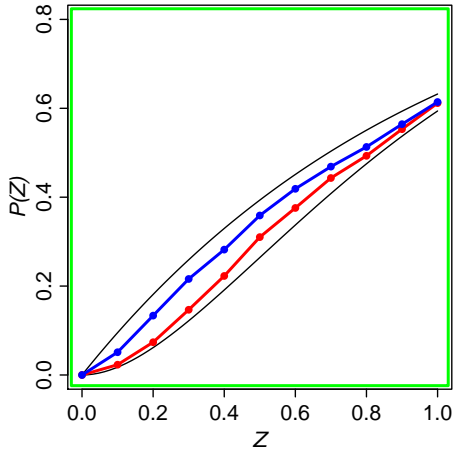
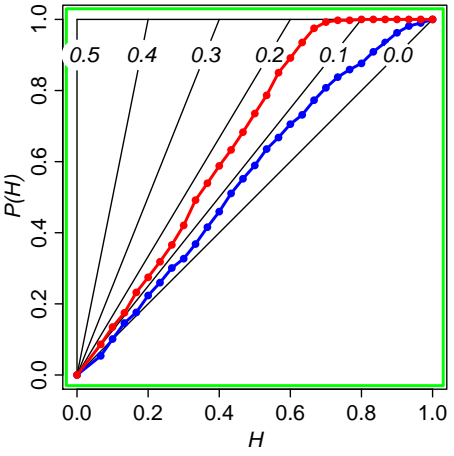
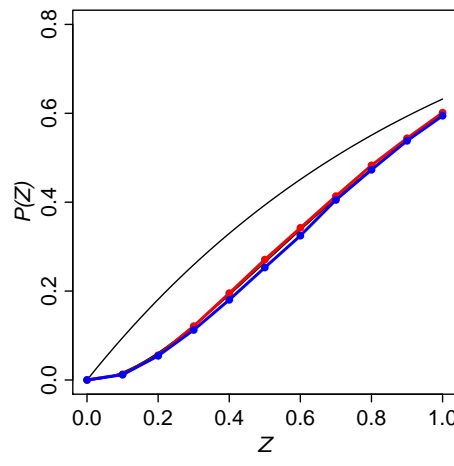
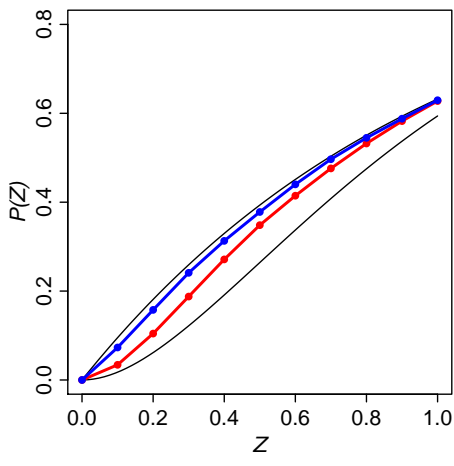
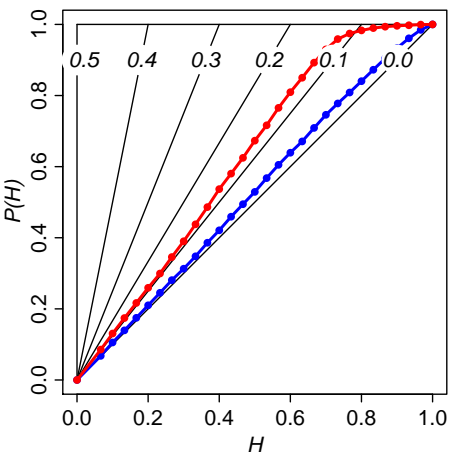
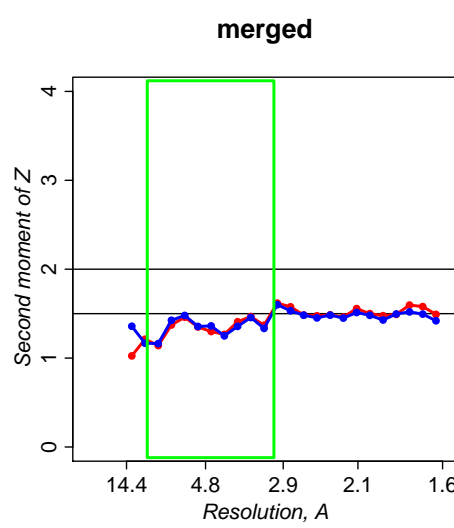
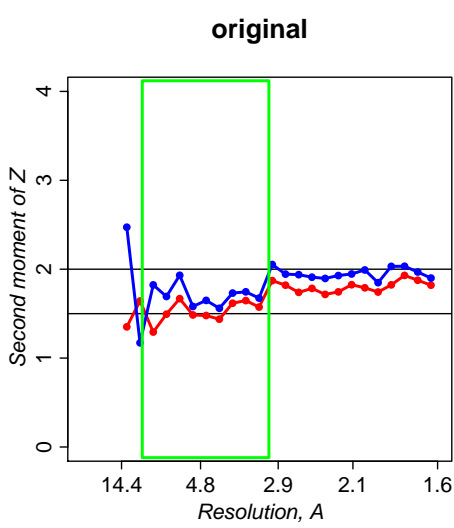
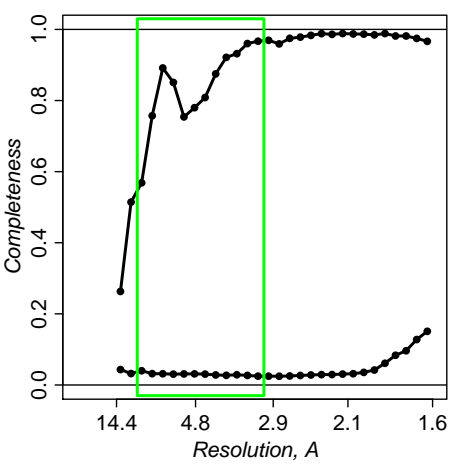
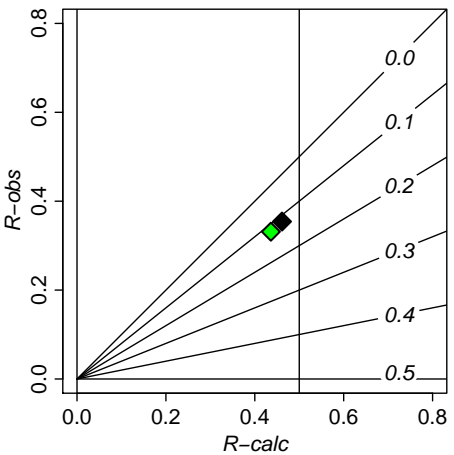
	original	merged
s.g.	P 63	-
p.g.	12021	12027
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	32.7	-
R'	-	-
R-free	34.1	-
R'-free	-	-

residues per monomer	DNA	protein
	0	113

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	14.9-1.6	9.9-3.0
unique	15,736	2,370
measured	15,187	2,105
used	13,192	1,598

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1egw

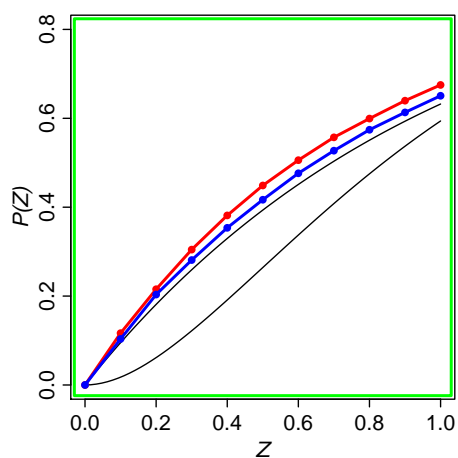
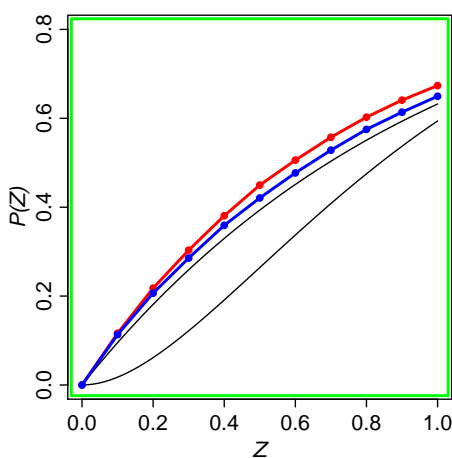
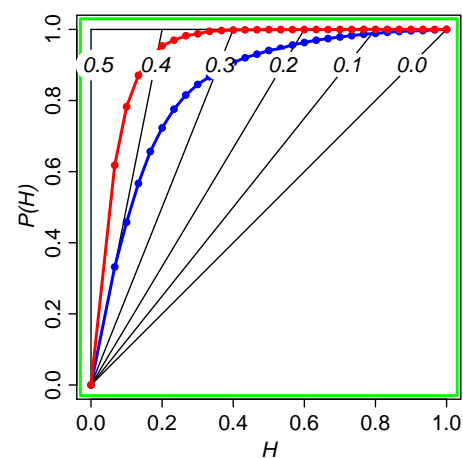
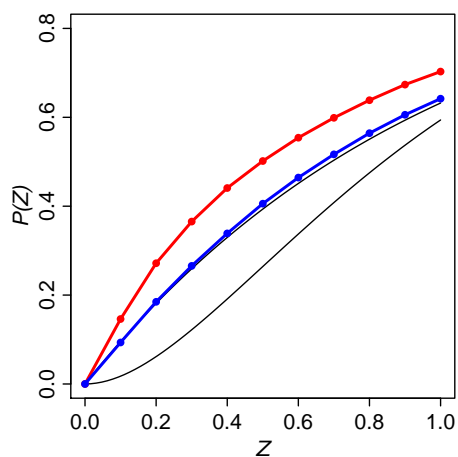
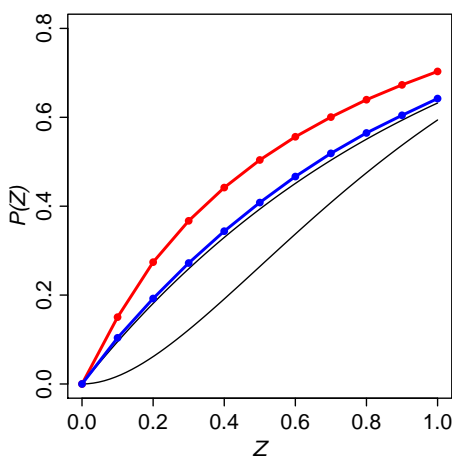
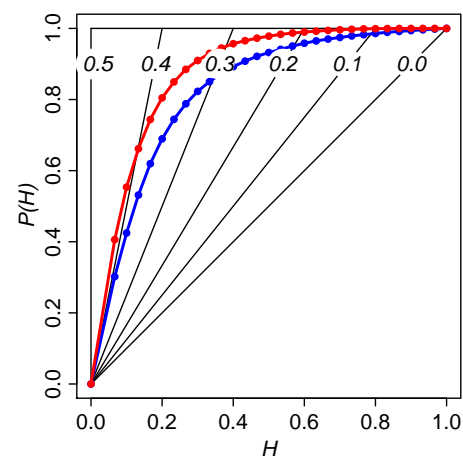
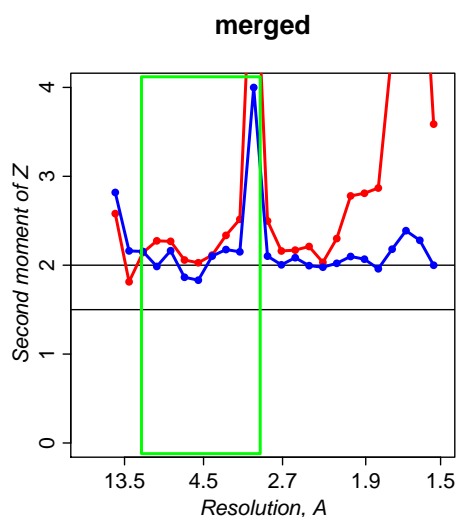
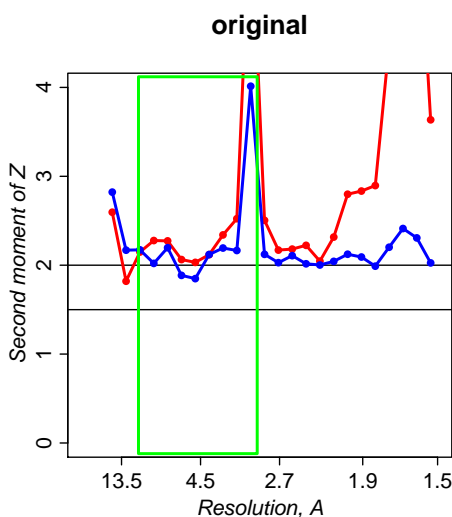
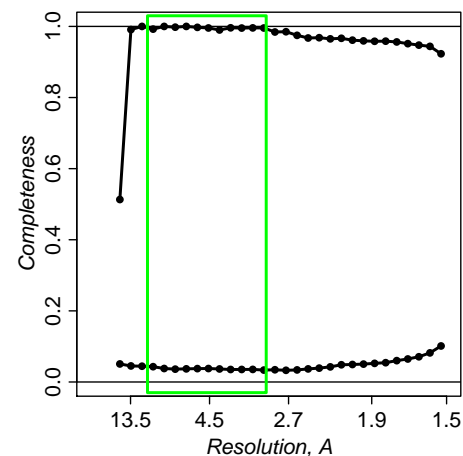
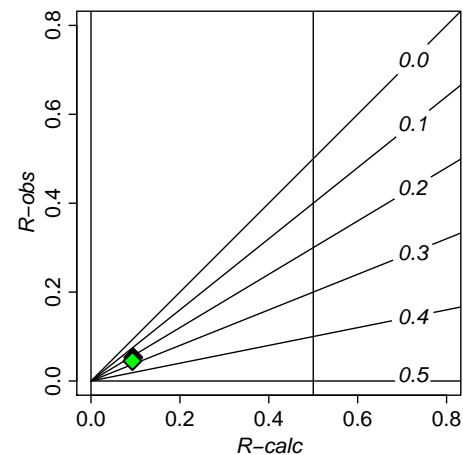
	original	merged
s.g.	P 1	P 1 21 1
p.g.	10000	10001
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.20
R	34.5	
R'	34.5	34.8
R-free	36.1	
R'-free	36.3	36.6

s < f/100	3588	4.14 %
s <= 0	3588	4.14 %
f <= 0	3588	4.14 %
s,f <= 0	3588	4.14 %

range (A)	22.9–1.5	9.9–3.0
unique	90,222	10,975
measured	86,655	10,927
used	80,718	10,312

NCS	translation	rotation
r.m.s.d. (A)	25.54	0.20
angle (o)	179.53	0.48

residues per monomer	DNA	protein
	14	71



1ekv

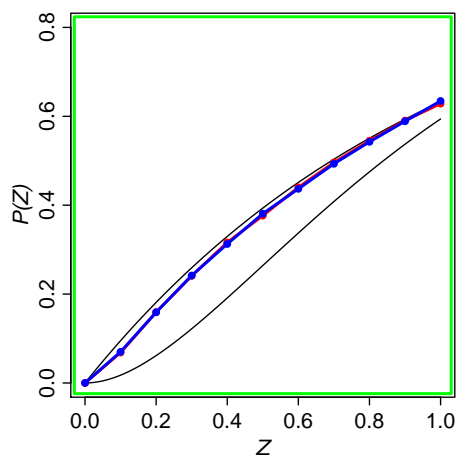
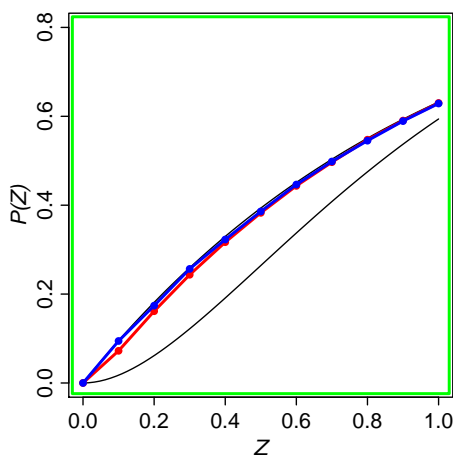
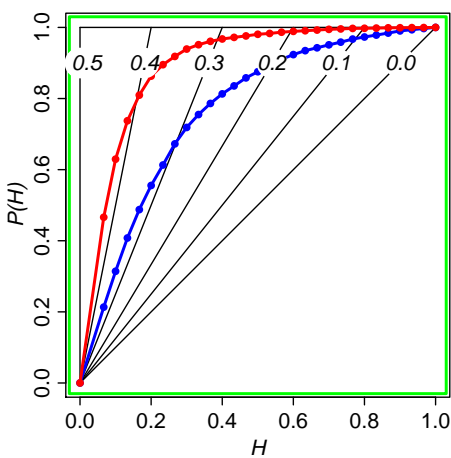
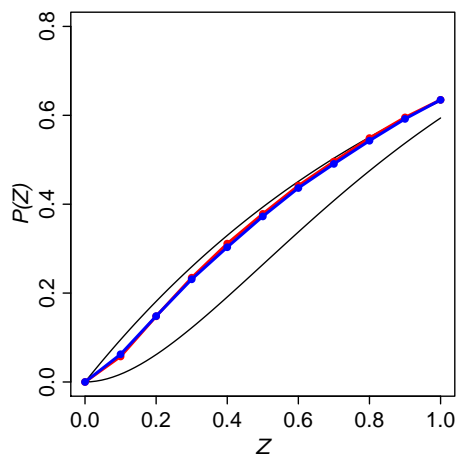
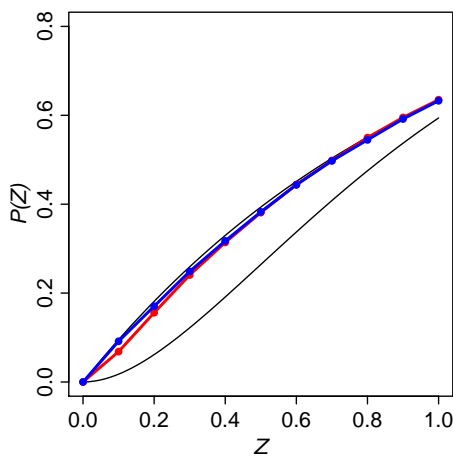
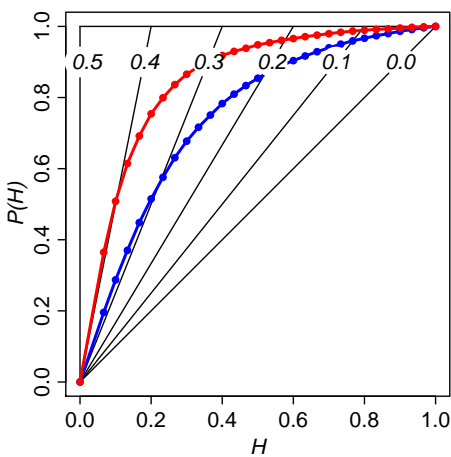
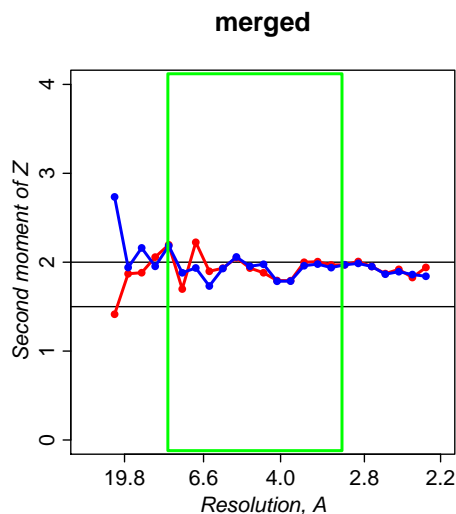
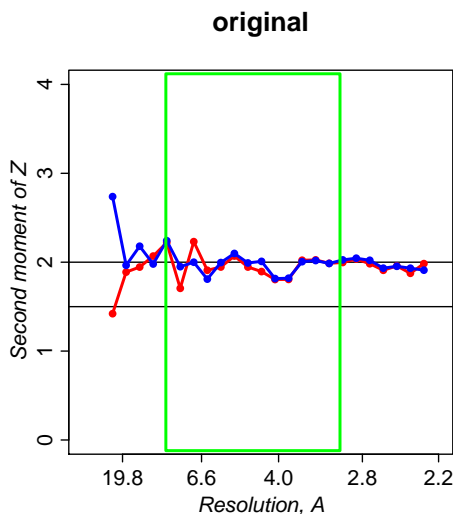
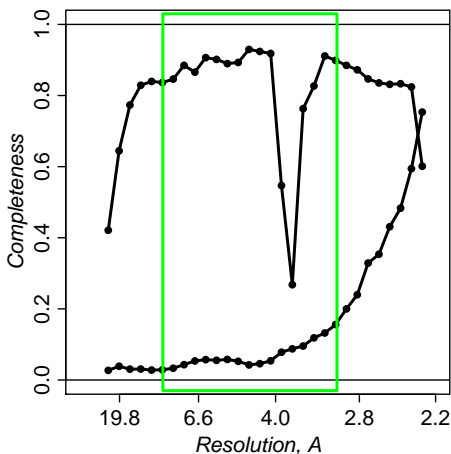
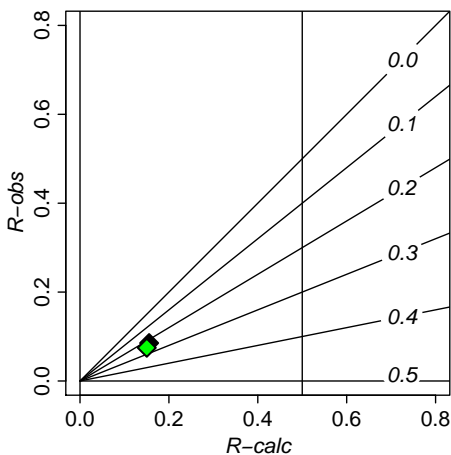
	original	merged
s.g.	P 32	P 32 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.64
R	24.2	
R'	24.7	25.0
R-free	29.4	
R'-free	29.7	29.3

s < f/100	1	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	34.3–2.3	9.9–3.0
unique	39,033	16,022
measured	31,372	12,832
used	25,908	10,698

NCS	translation	rotation
r.m.s.d. (A)	32.91	0.64
angle (o)	179.94	0.12

residues per monomer	DNA	protein
	0	365



1em0

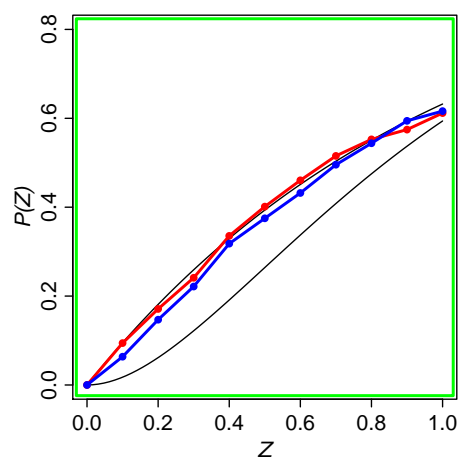
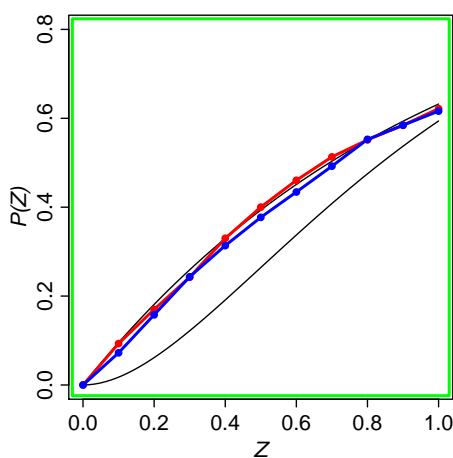
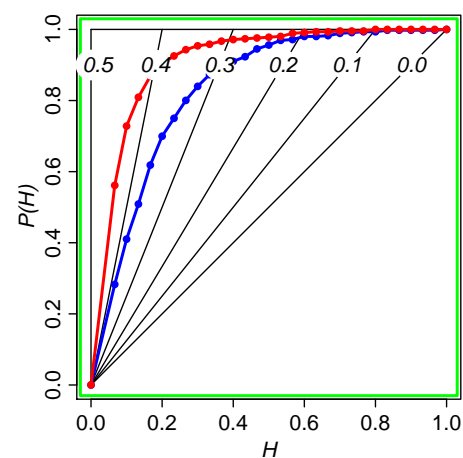
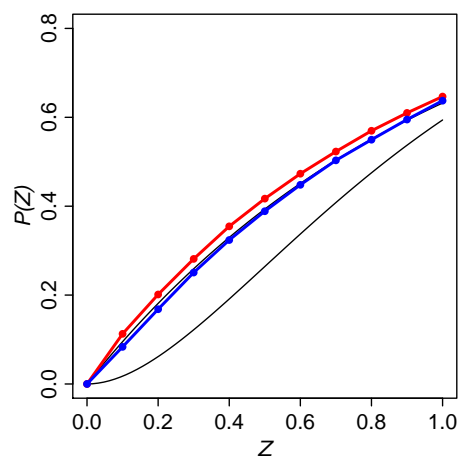
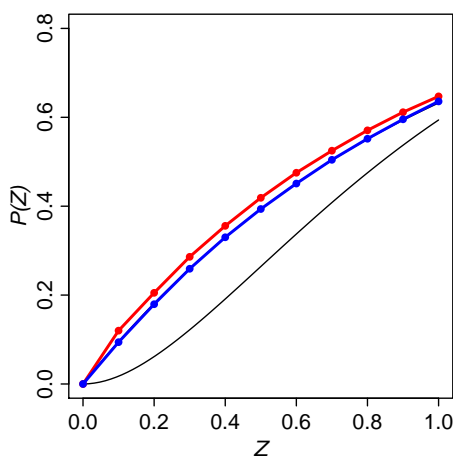
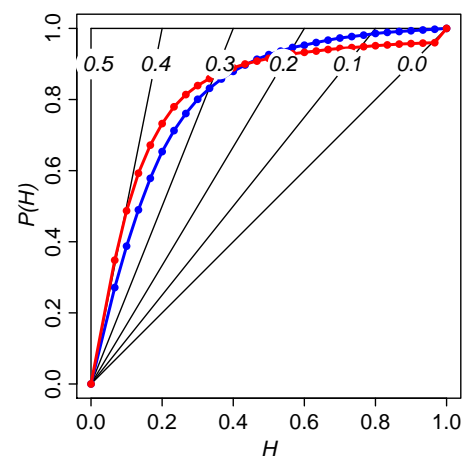
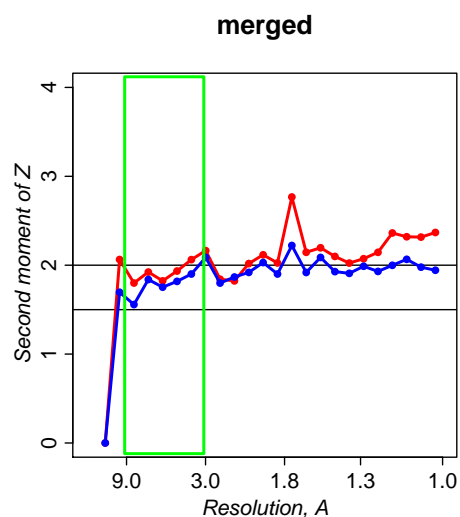
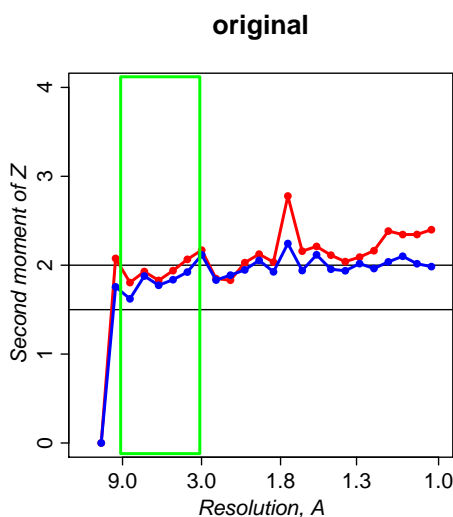
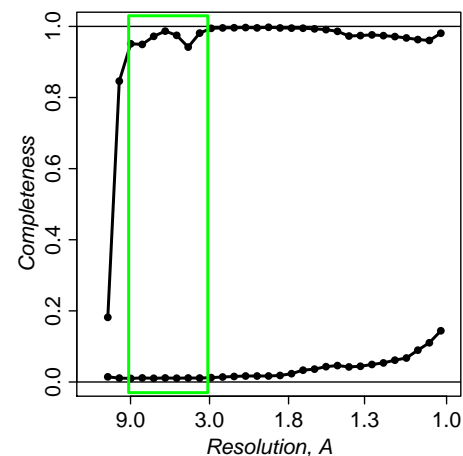
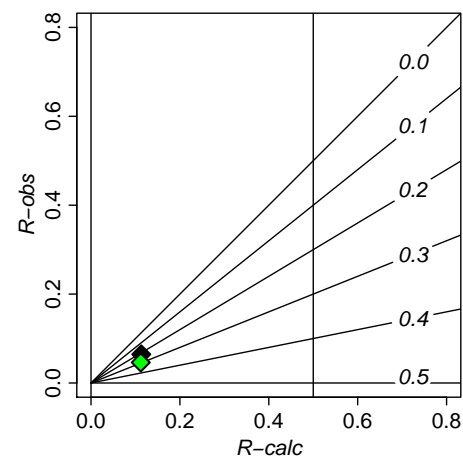
	original	merged
s.g.	P 41	P 41 21 2
p.g.	10201	10205
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.12
R	44.0	
R'	44.0	45.2
R-free	45.9	
R'-free	45.9	46.2

s < f/100	969	2.90 %
s <= 0	0	0.00 %
f <= 0	1080	3.23 %
s,f <= 0	0	0.00 %

range (A)	32.2–1.0	9.9–3.0
unique	34,162	1,265
measured	33,404	1,229
used	30,102	908

NCS	translation	rotation
r.m.s.d. (A)	6.94	0.08
angle (o)	61.34	0.02

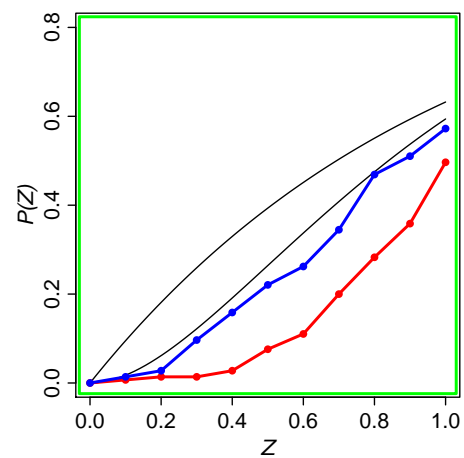
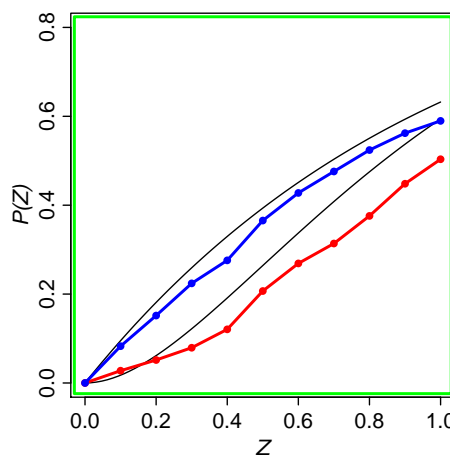
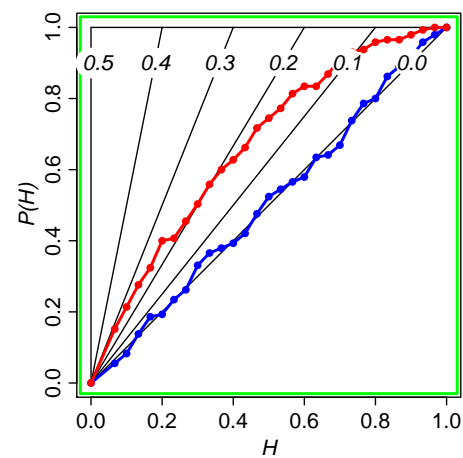
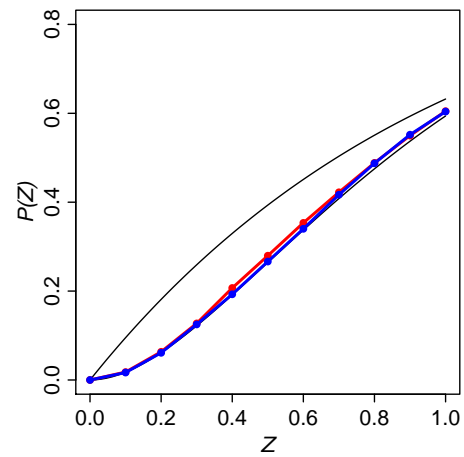
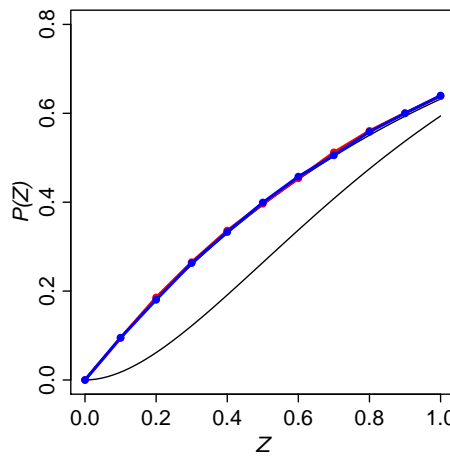
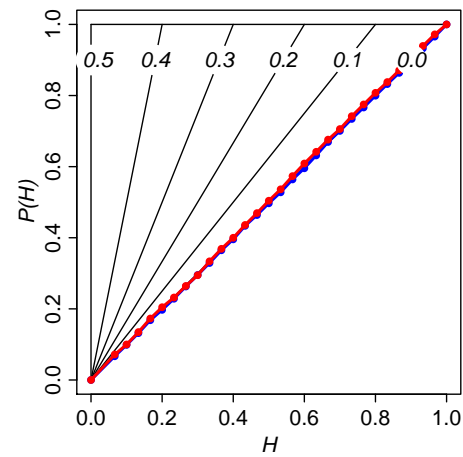
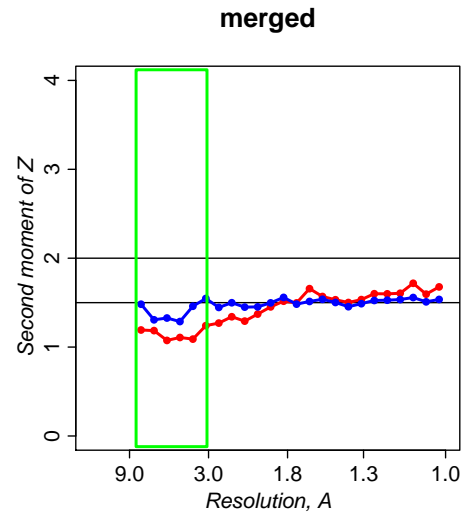
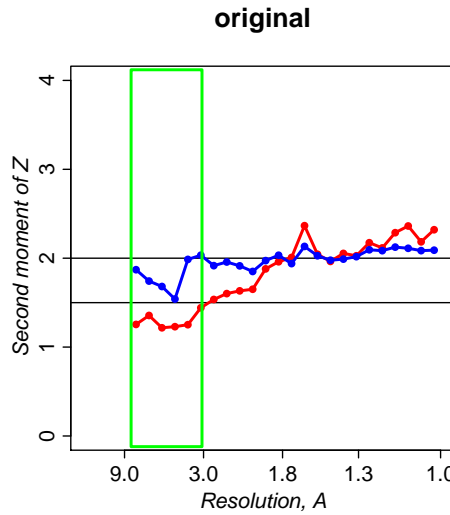
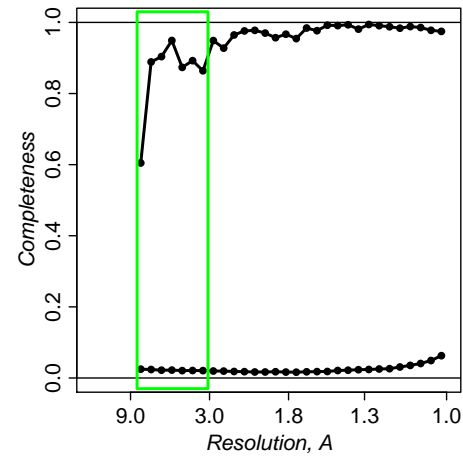
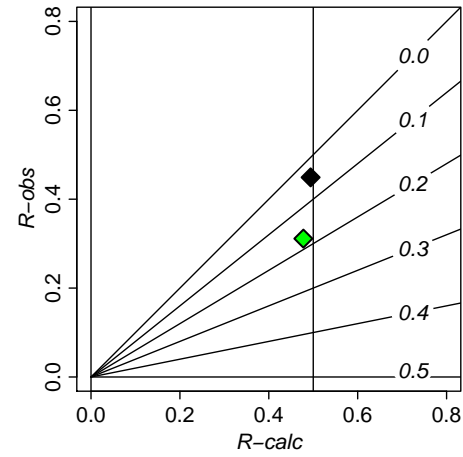
residues per monomer	DNA	protein
	5	0



1en8

	original	merged
s.g.	C 1 2 1	-
p.g.	10001	10003
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	35.9	-
R'	-	-
R-free	34.3	-
R'-free	-	-
residues per monomer	DNA 9	protein 0

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	23	0.18 %
s,f <= 0	0	0.00 %
<hr/>		
range (A)	8.0-1.0	8.0-3.0
unique	13,328	496
measured	13,035	446
used	11,266	290
<hr/>		
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1eoh

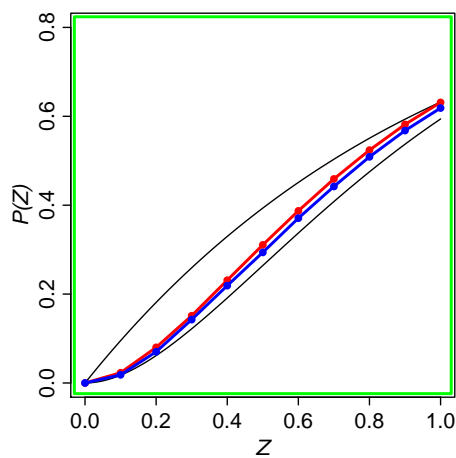
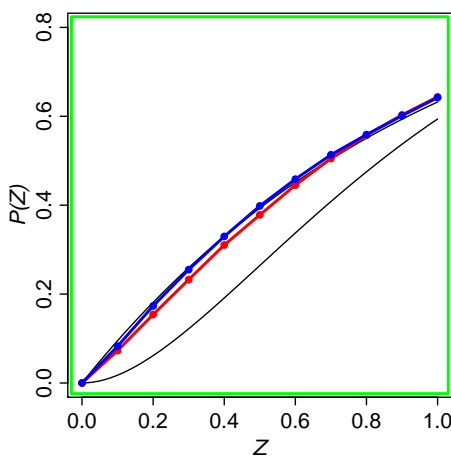
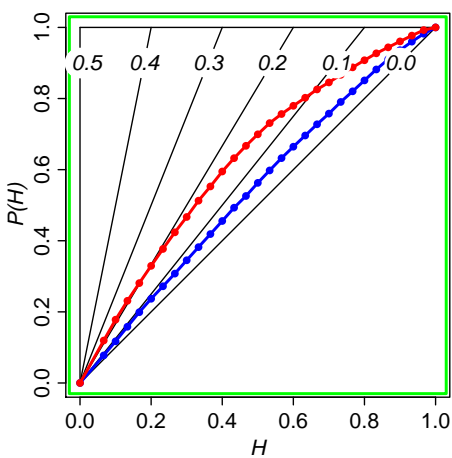
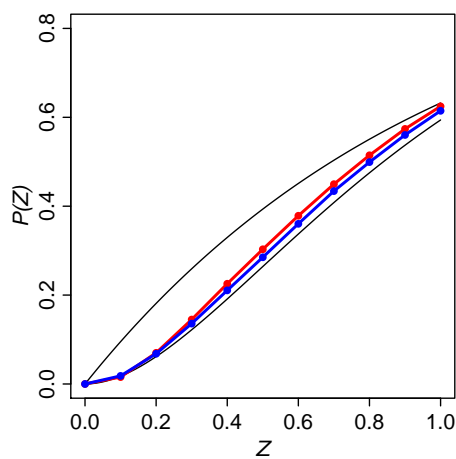
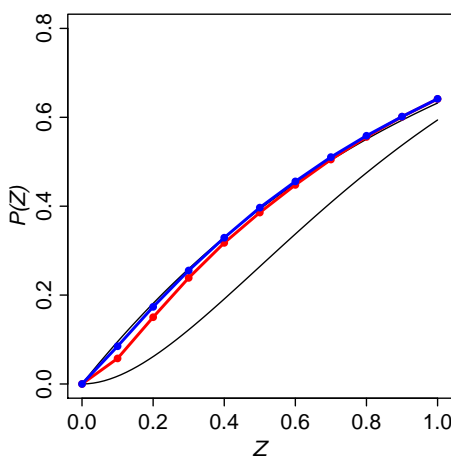
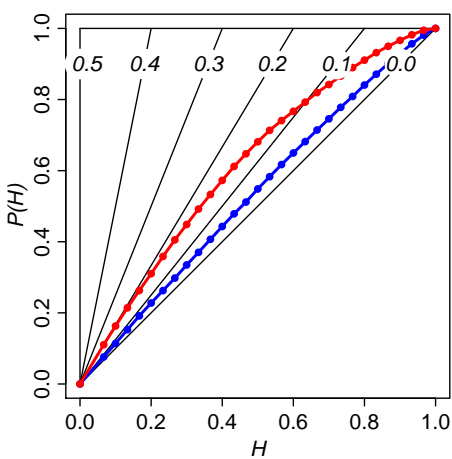
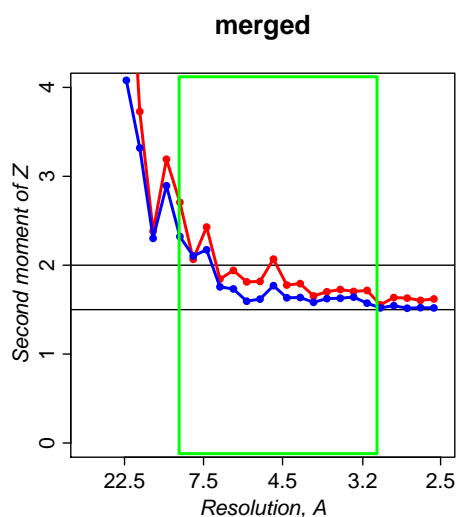
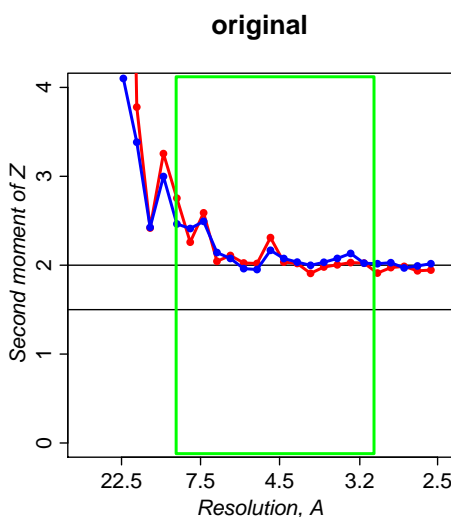
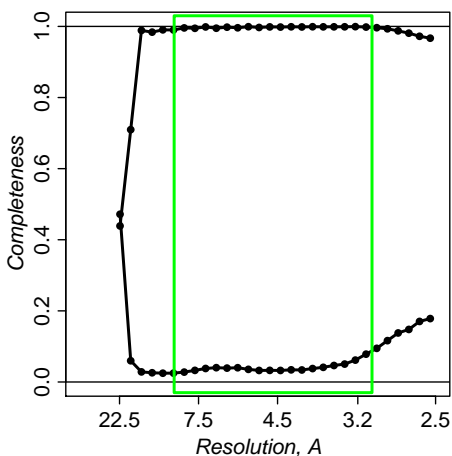
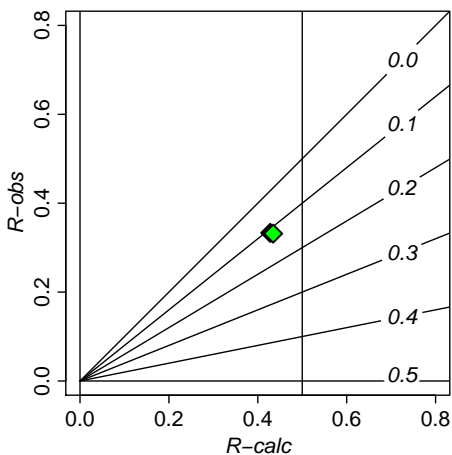
	original	merged
s.g.	P 21 21 21	-
p.g.	10003	10205
a.u.	8	-
p.t.	2	-
p.o.	4	-
r.m.s.d. (A)	-	-
R	24.7	-
R'	-	-
R-free	29.6	-
R'-free	-	-

residues per monomer	DNA	protein
	0	209

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	25.6-2.5	9.9-3.0
unique	58,245	32,996
measured	57,649	32,938
used	49,638	28,472

NCS	translation	rotation
r.m.s.d. (A)	1.01	0.63
angle (o)	4.54	2.36



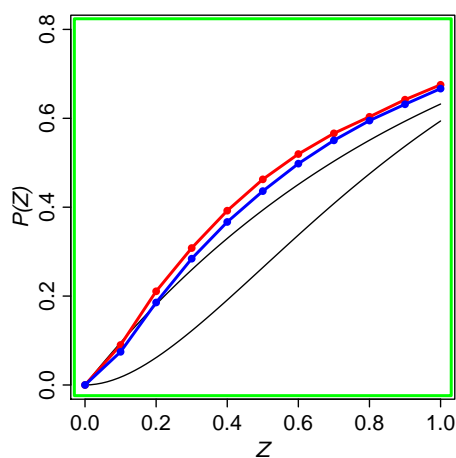
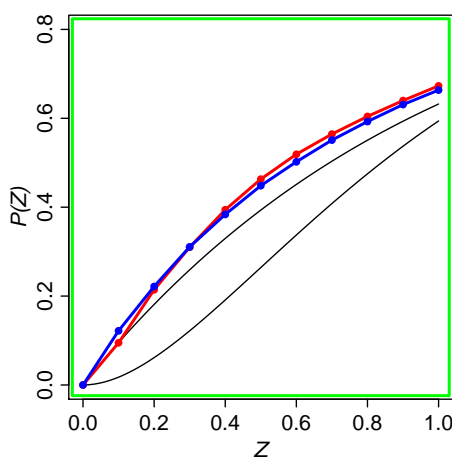
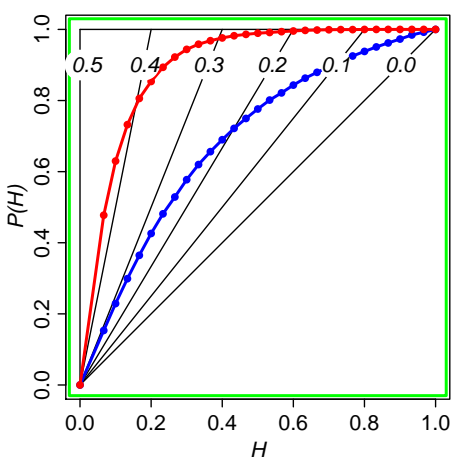
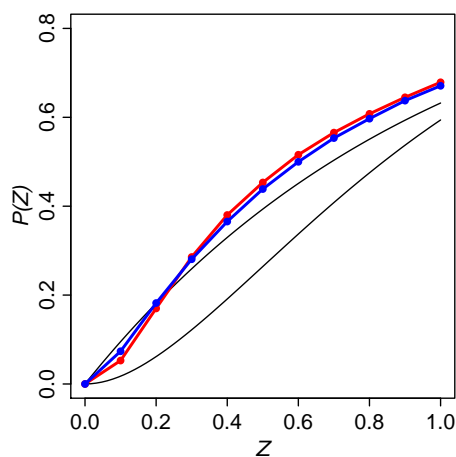
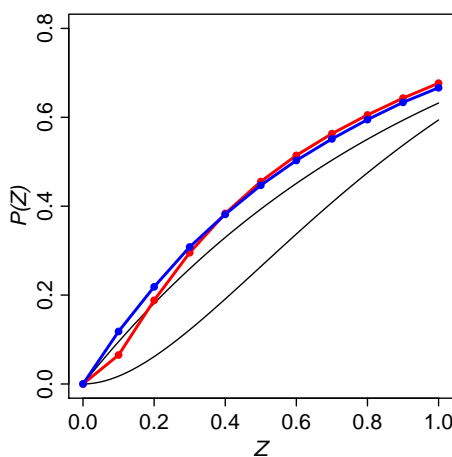
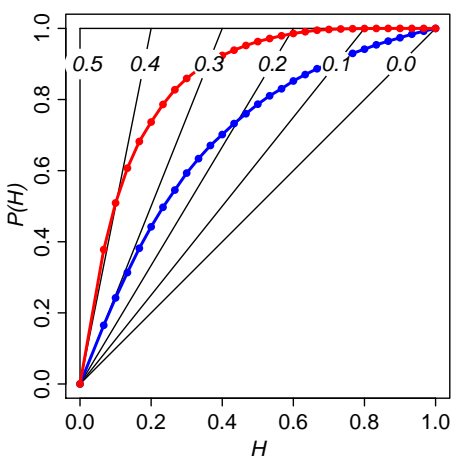
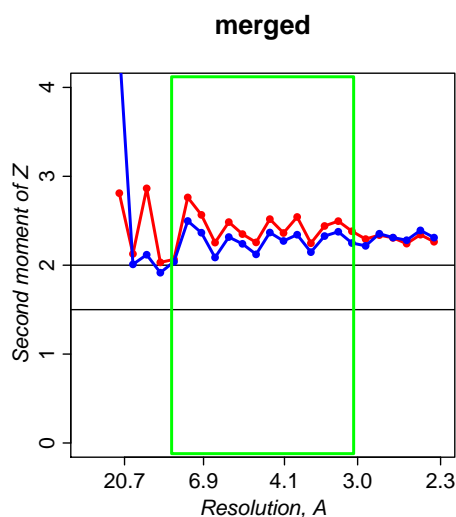
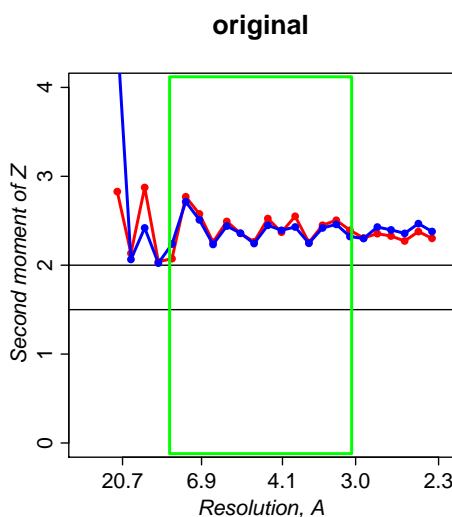
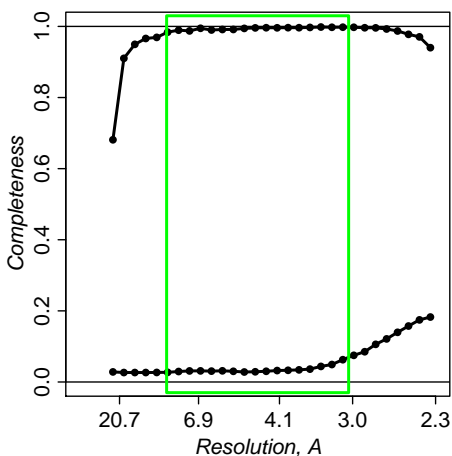
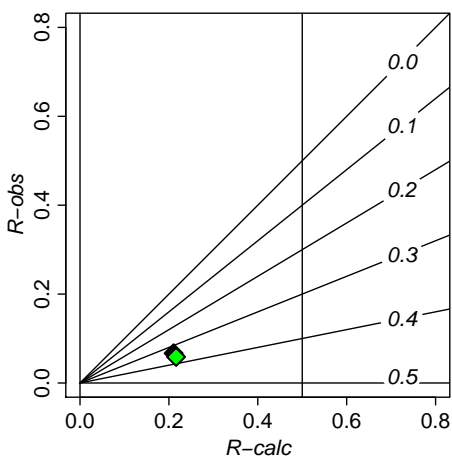
1erj

	original	merged
s.g.	P 31	-
p.g.	10020	10023
a.u.	3	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	25.4	-
R'	-	-
R-free	28.1	-
R'-free	-	-
residues per monomer	DNA 0	protein 348

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.8-2.3	9.9-3.0
unique	54,611	23,881
measured	53,856	23,784
used	50,954	22,480

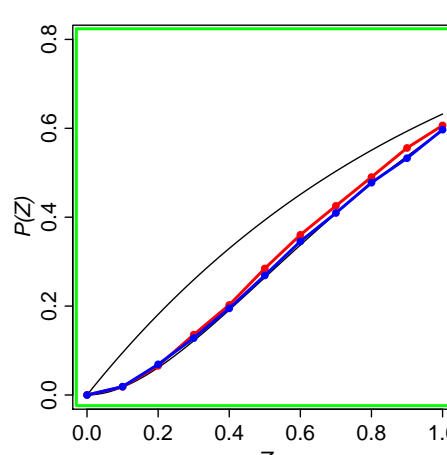
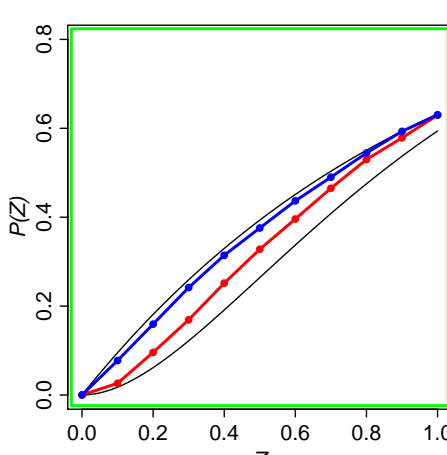
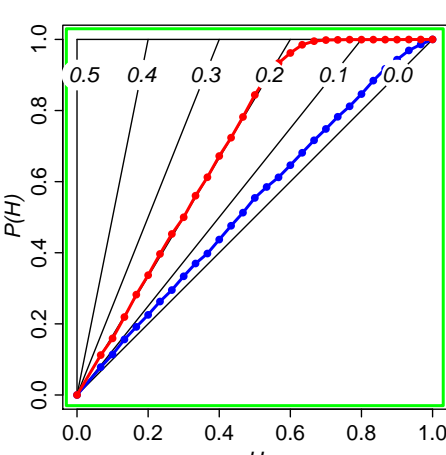
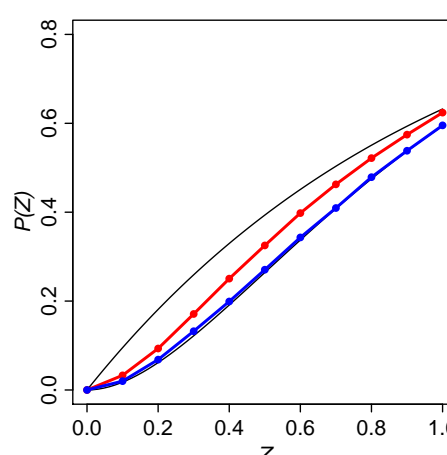
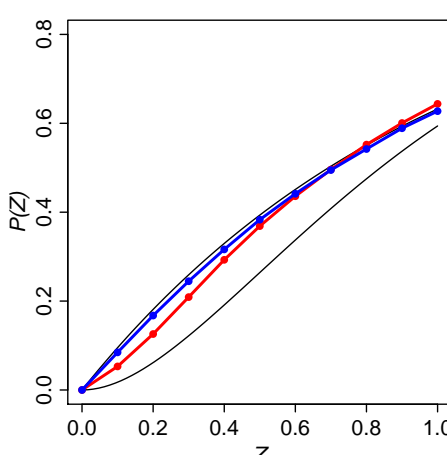
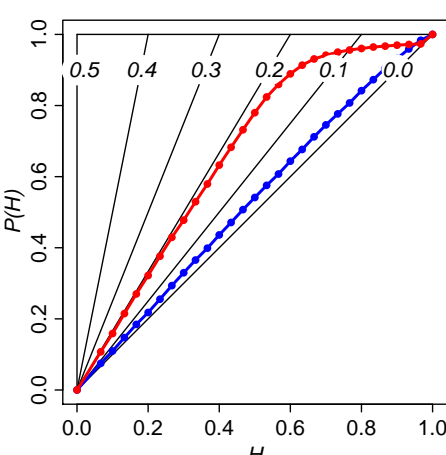
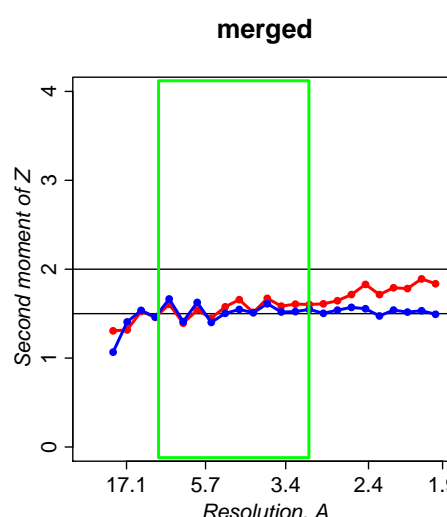
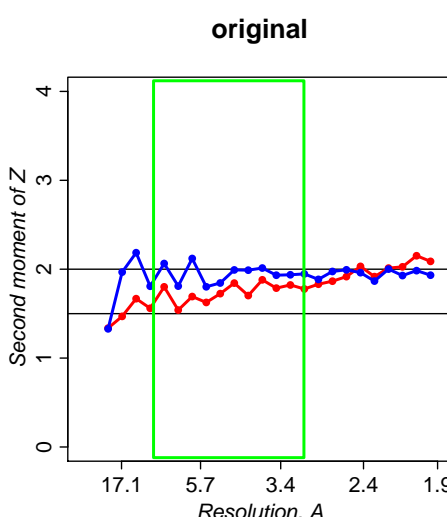
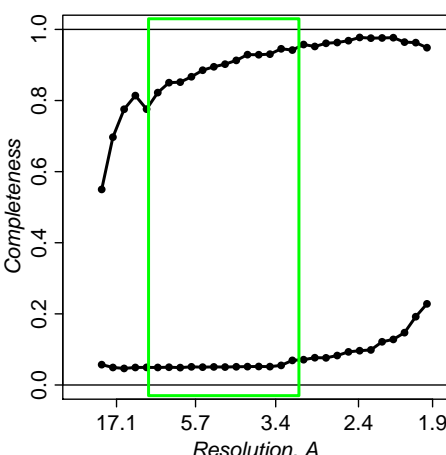
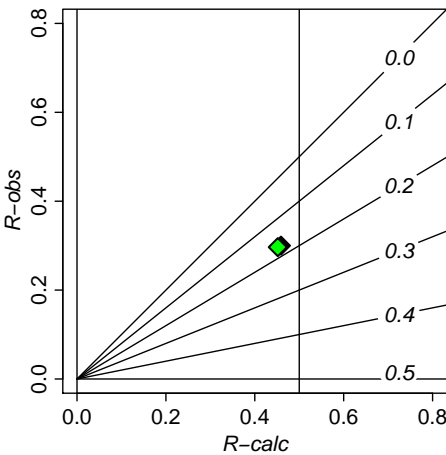
NCS	translation	rotation
r.m.s.d. (A)	0.16	0.11
angle (o)	0.51	0.19



1et5

	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	24.0	-
R'	-	-
R-free	25.9	-
R'-free	-	-
residues per monomer	DNA 0	protein 336

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	490	1.61 %
s,f <= 0	0	0.00 %
<hr/>		
range (A)	35.4-1.9	9.9-3.0
unique	31,960	7,899
measured	30,437	7,242
used	28,214	6,472
<hr/>		
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1eyx

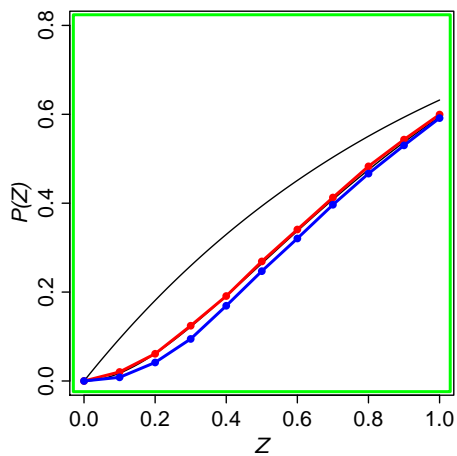
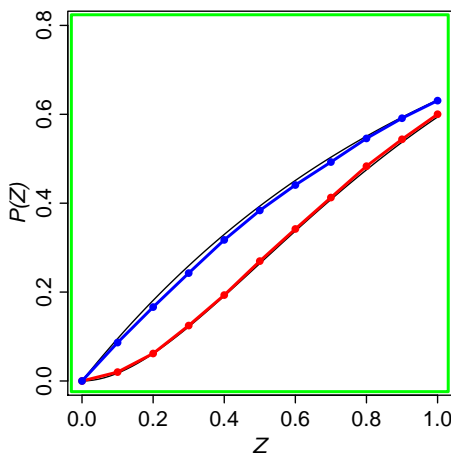
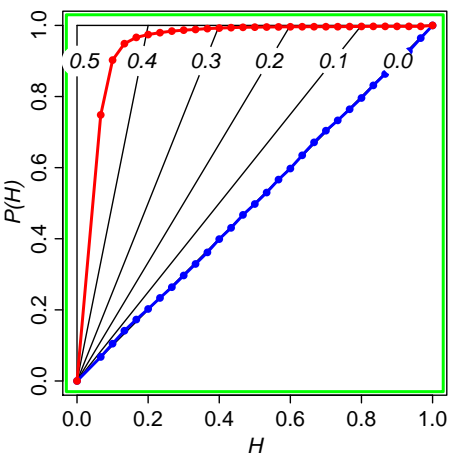
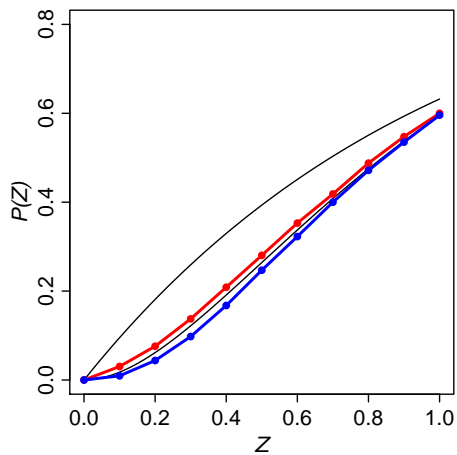
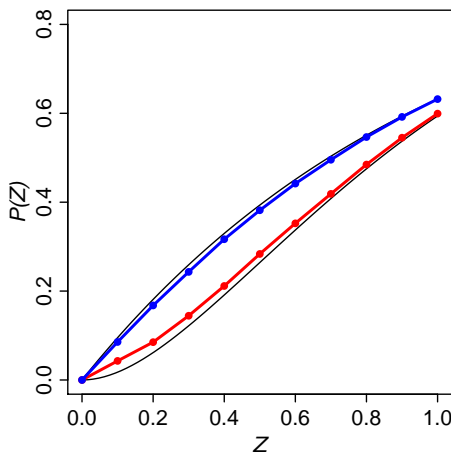
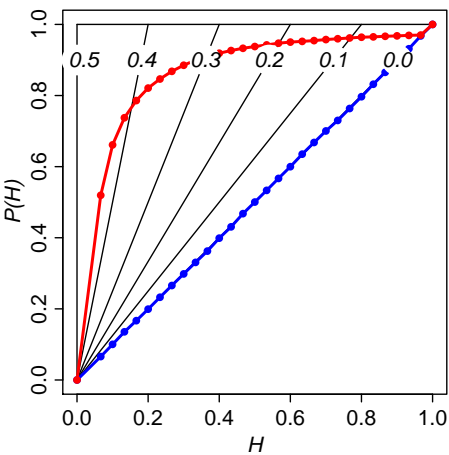
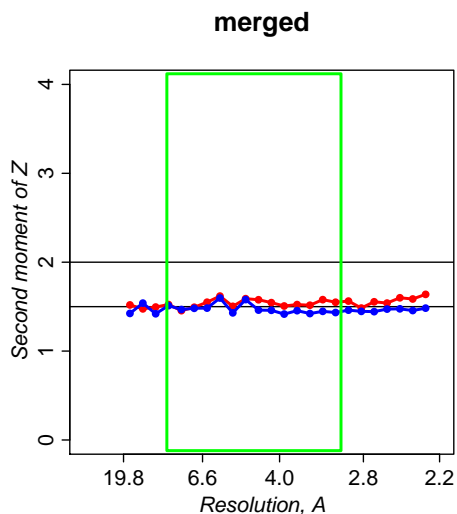
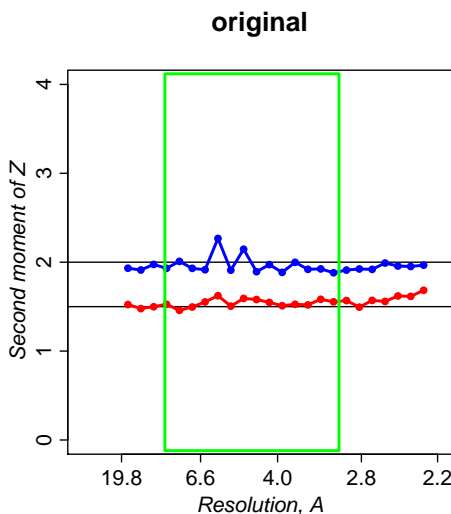
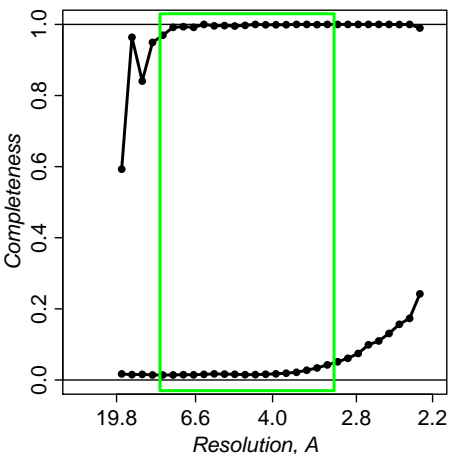
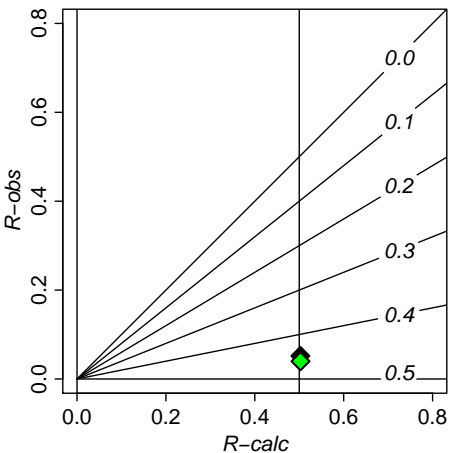
	original	merged
s.g.	H 3	H 3 2
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		5.59
R	30.6	
R'	-	-
R-free	34.9	
R'-free	-	-

residues per monomer	DNA	protein
	0	345

s < f/100	804	2.19 %
s <= 0	0	0.00 %
f <= 0	708	1.93 %
s,f <= 0	0	0.00 %

range (A)	translation	rotation
19.8–2.2	9.9–3.0	
unique	36,744	15,063
measured	36,651	15,035
used	35,634	14,514

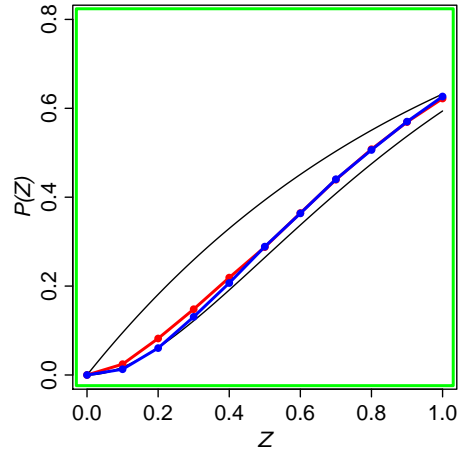
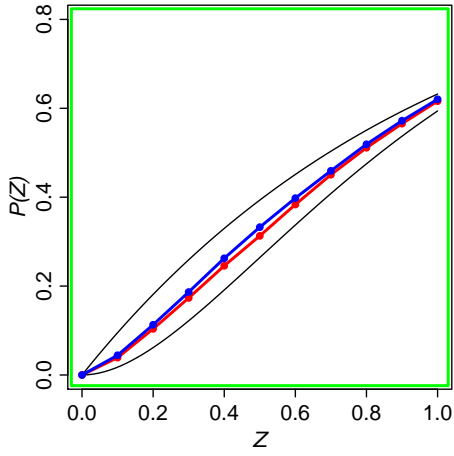
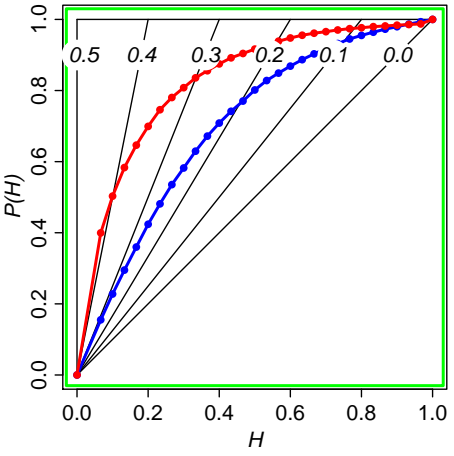
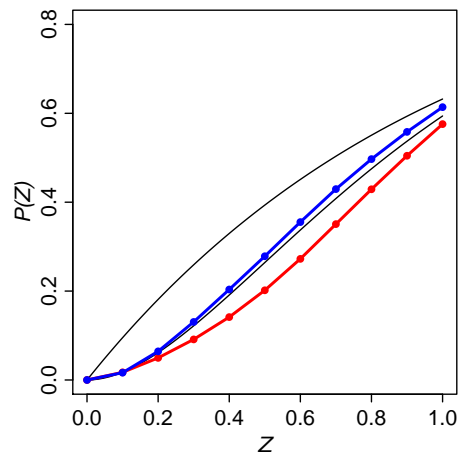
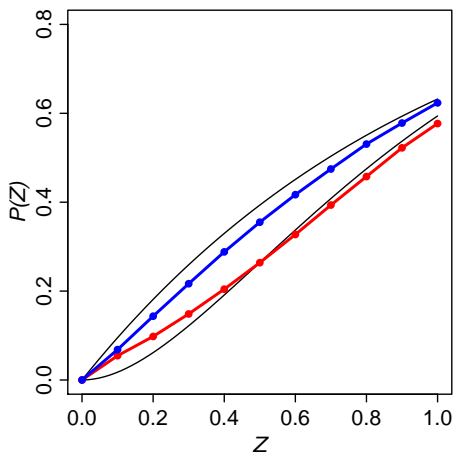
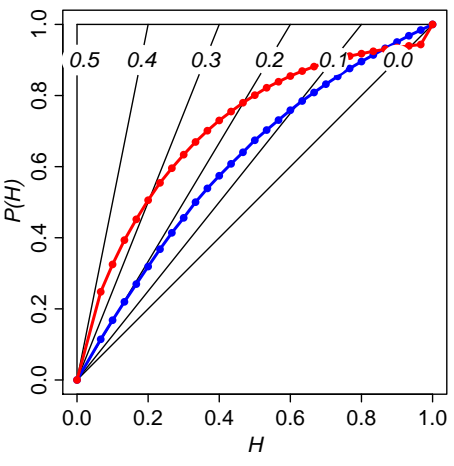
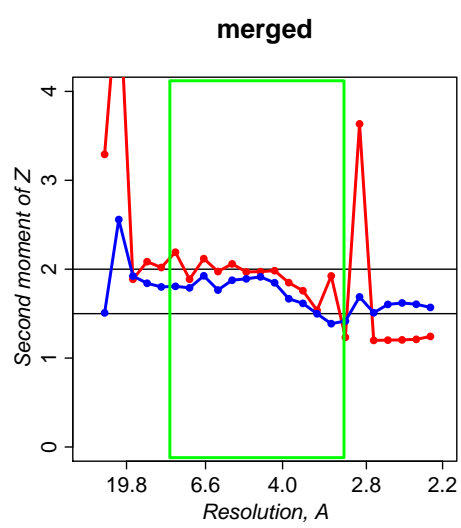
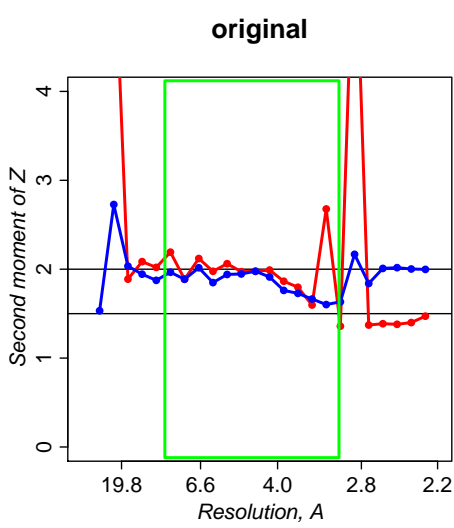
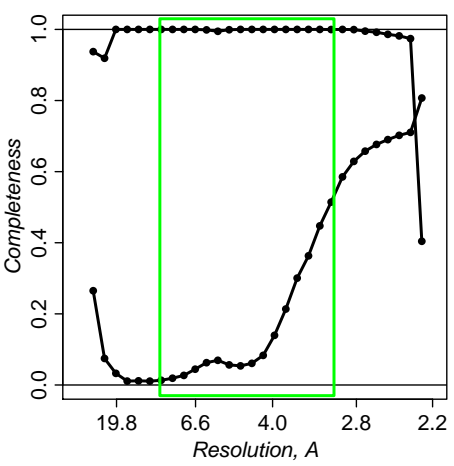
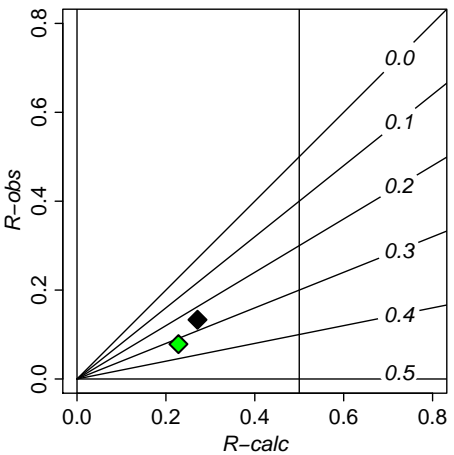
NCS	translation	rotation
r.m.s.d. (A)	28.51	3.49
angle (o)	179.91	8.41



1ezz

	original	merged
s.g.	H 3	H 3 2
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		1.72
R	33.2	
R'	33.7	33.5
R-free	38.6	
R'-free	40.0	38.8
residues per monomer	DNA 0	protein 463

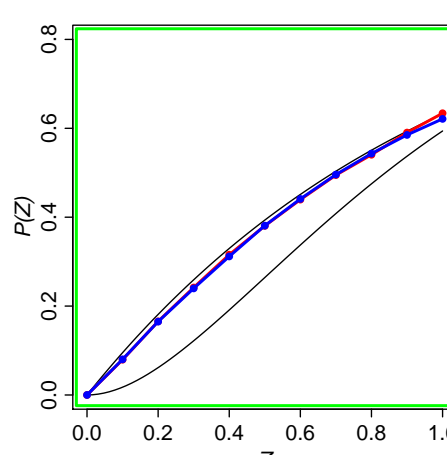
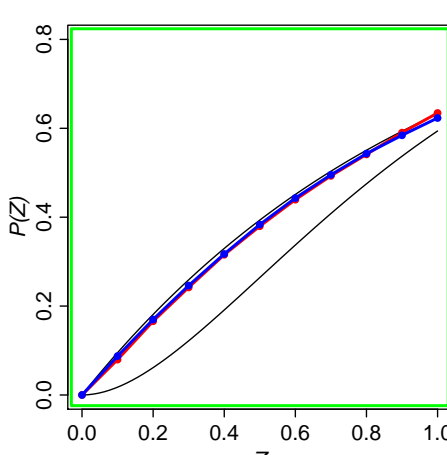
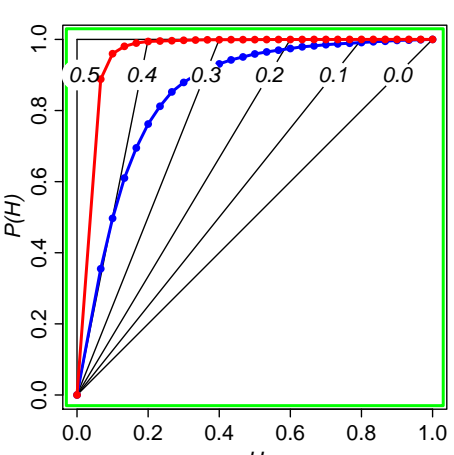
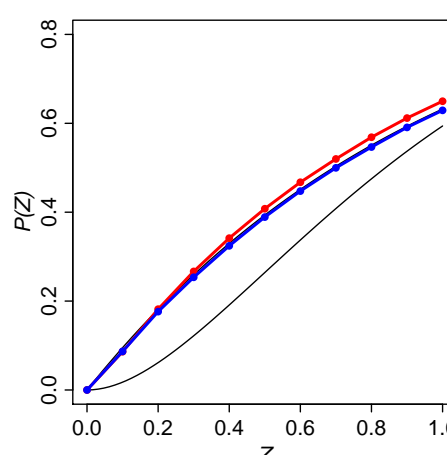
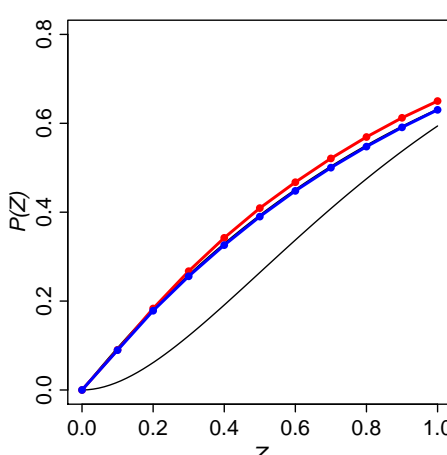
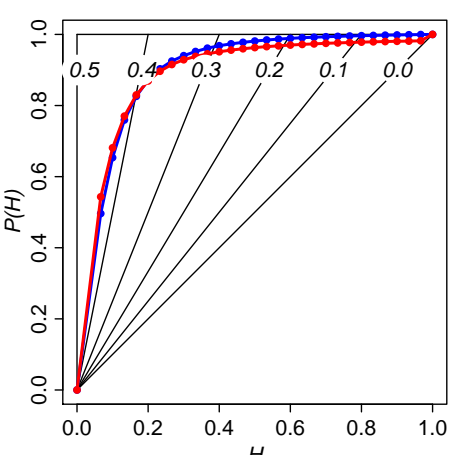
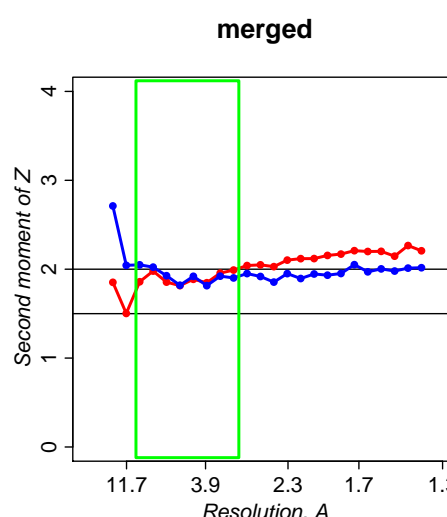
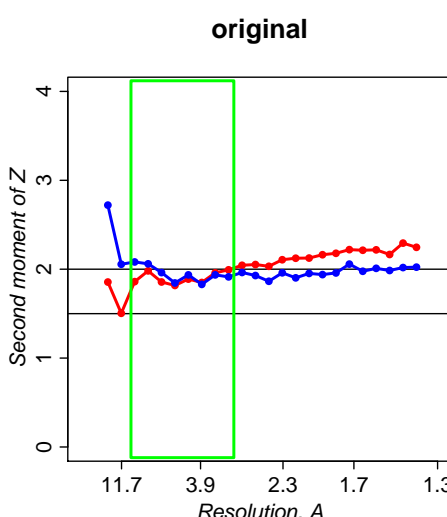
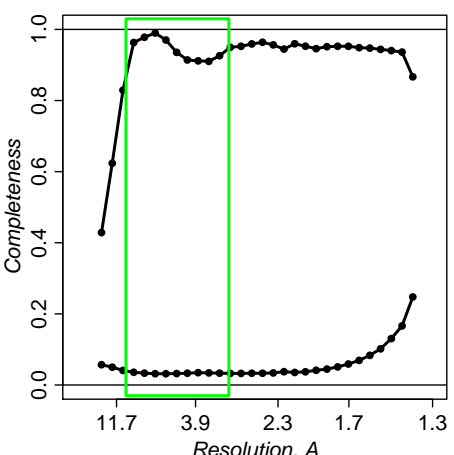
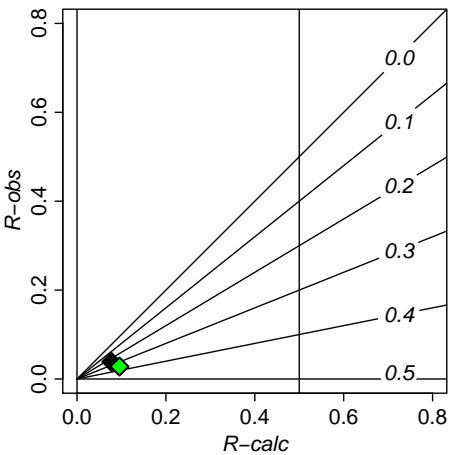
s < f/100	723	1.27 %
s <= 0	0	0.00 %
f <= 0	1758	3.09 %
s,f <= 0	0	0.00 %
range (A)	74.4–2.2	9.9–3.0
unique	60,634	24,311
measured	56,891	24,303
used	53,312	23,100
NCS	translation	rotation
r.m.s.d. (A)	49.60	1.72
angle (o)	179.84	0.43



1f1g

	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.06
R	31.4	
R'	31.4	31.4
R-free	31.4	
R'-free	31.6	31.4
residues per monomer	DNA 0	protein 153

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	2850	1.22 %
s,f <= 0	0	0.00 %
range (A)	24.2–1.4	9.9–3.0
unique	248,192	22,252
measured	233,021	20,750
used	227,982	19,970
NCS	translation	rotation
r.m.s.d. (A)	19.73	0.04
angle (o)	119.82	0.04



1f5t

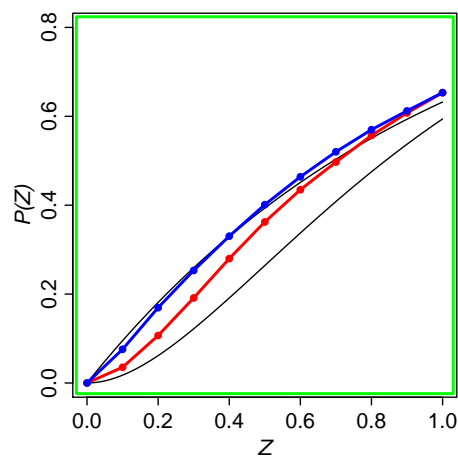
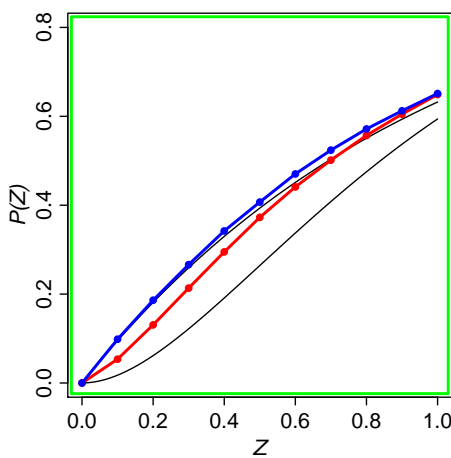
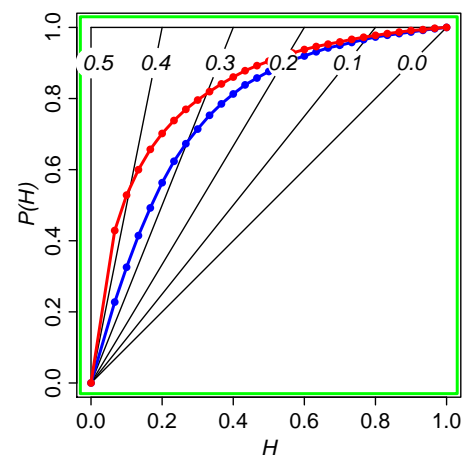
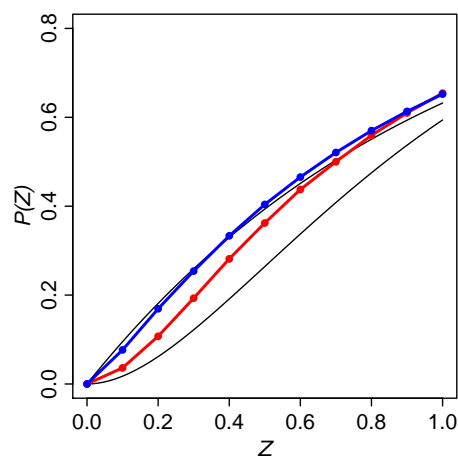
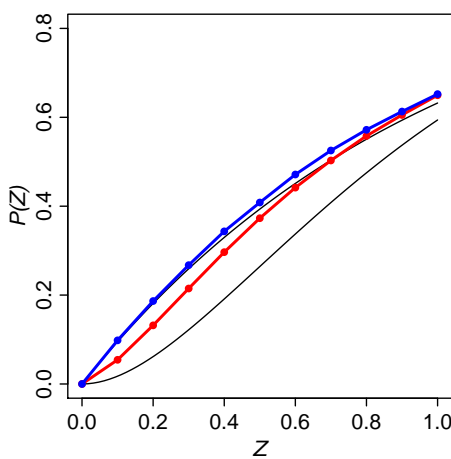
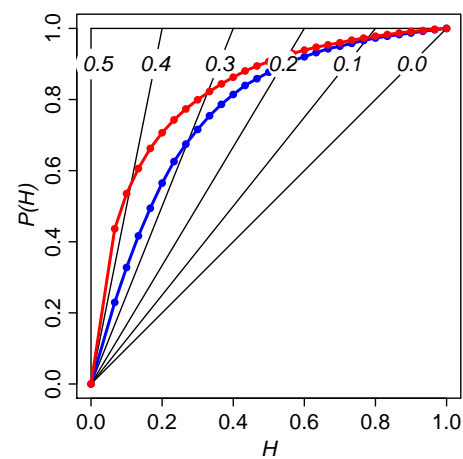
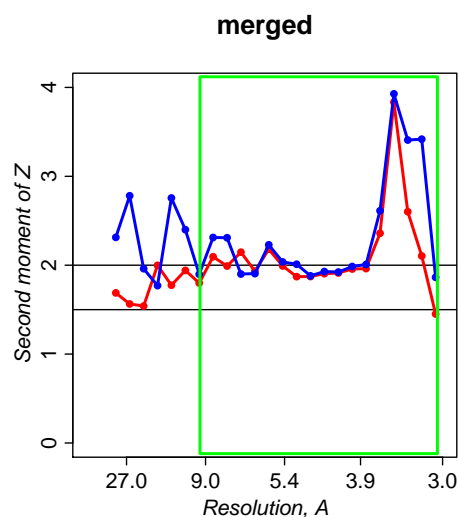
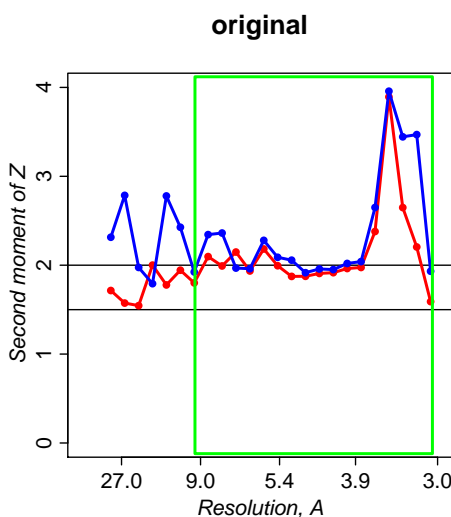
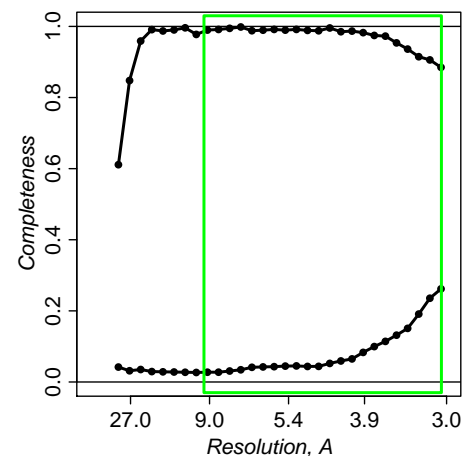
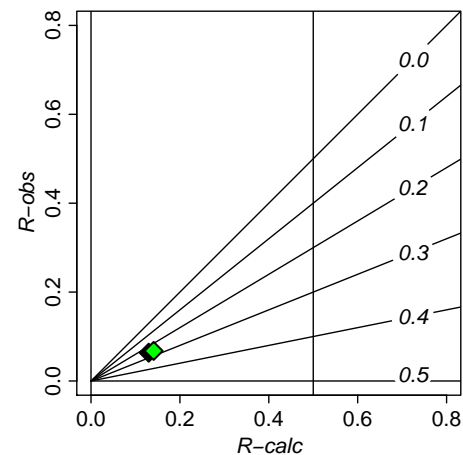
	original	merged
s.g.	P 41	P 41 21 2
p.g.	10201	10205
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		0.27
R	34.3	
R'	34.5	34.7
R-free	37.7	
R'-free	38.2	38.2

s < f/100	1231	3.38 %
s <= 0	1231	3.38 %
f <= 0	1231	3.38 %
s,f <= 0	1231	3.38 %

range (A)	48.8-3.0	9.9-3.0
unique	38,042	36,947
measured	36,445	35,376
used	32,076	31,298

NCS	translation	rotation
r.m.s.d. (A)	5.38	0.26
angle (o)	23.32	0.29

residues per monomer	DNA	protein
	0	120



1f5v

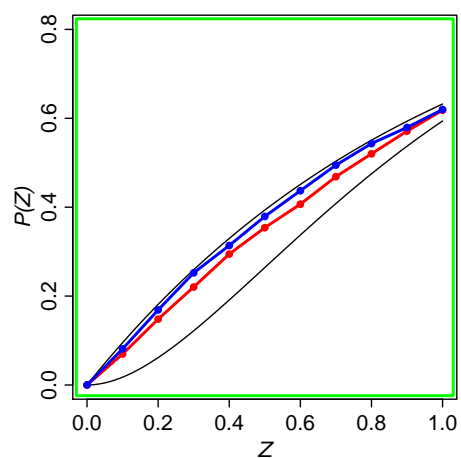
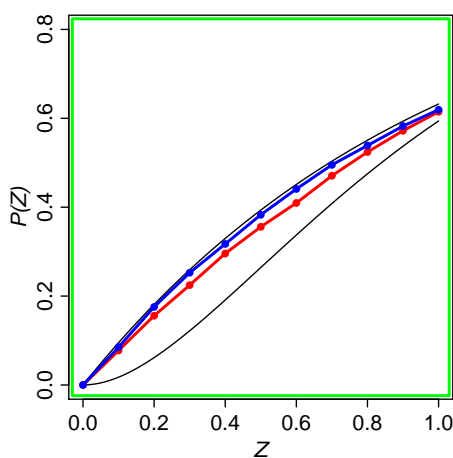
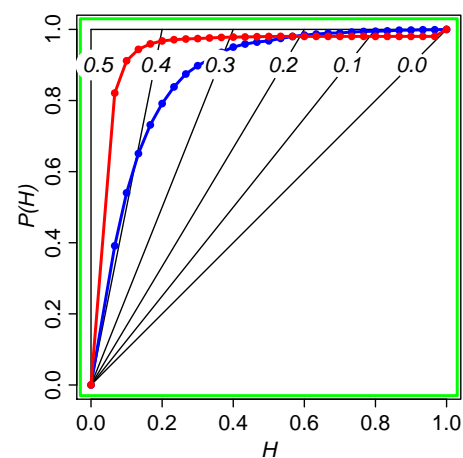
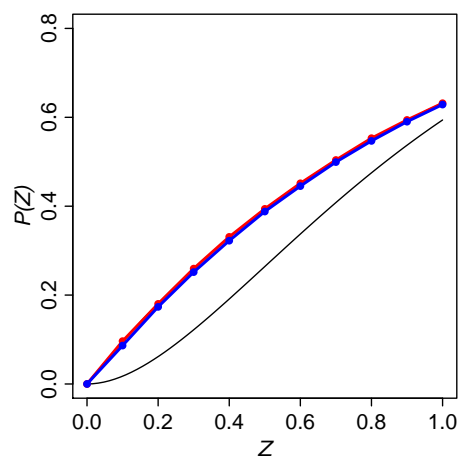
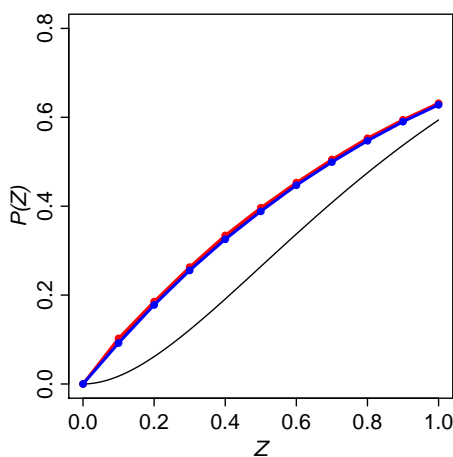
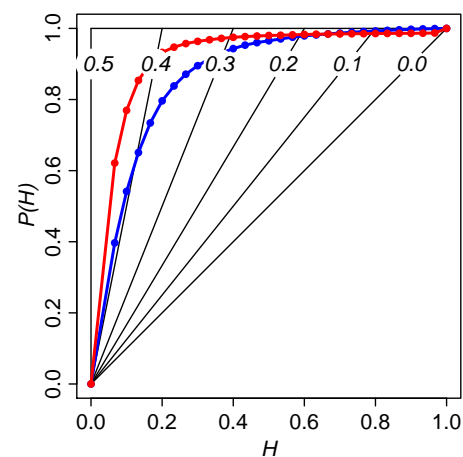
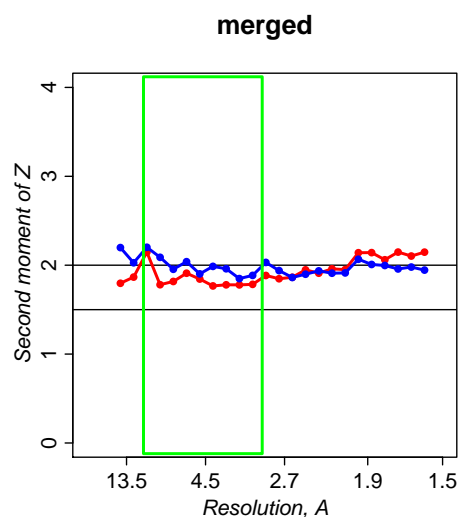
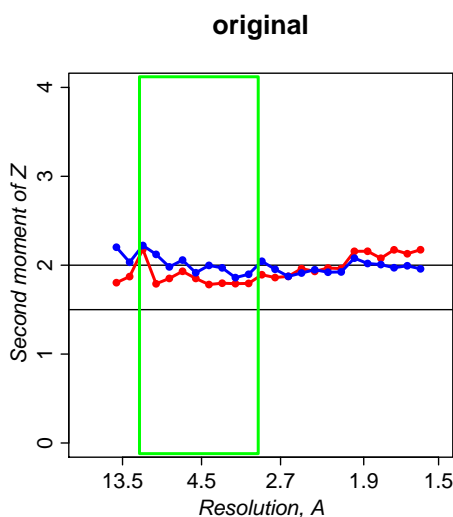
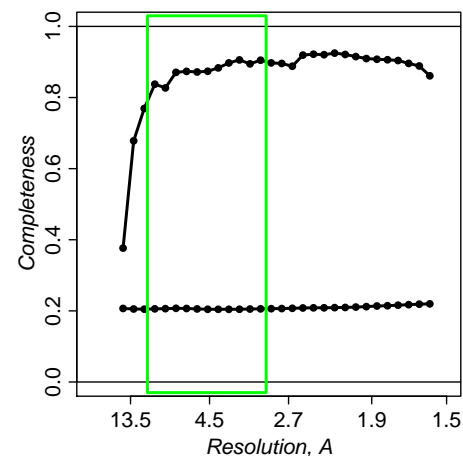
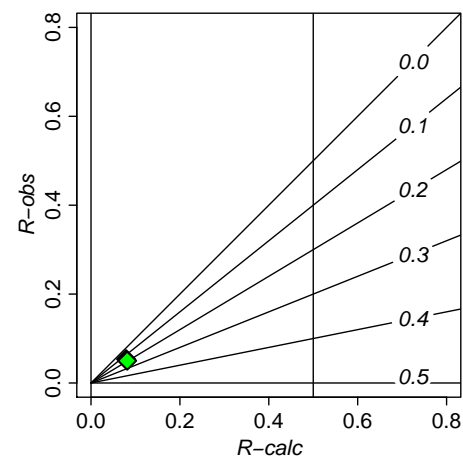
	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.06
R	26.9	
R'	26.9	26.6
R-free	28.2	
R'-free	28.2	27.8

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.9–1.5	9.9–3.0
unique	61,816	8,288
measured	55,608	7,358
used	48,188	6,208

NCS	translation	rotation
r.m.s.d. (A)	33.28	0.06
angle (o)	180.00	0.06

residues per monomer	DNA	protein
	0	240



1f9w

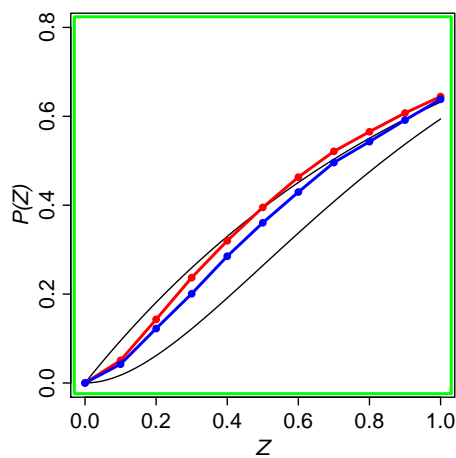
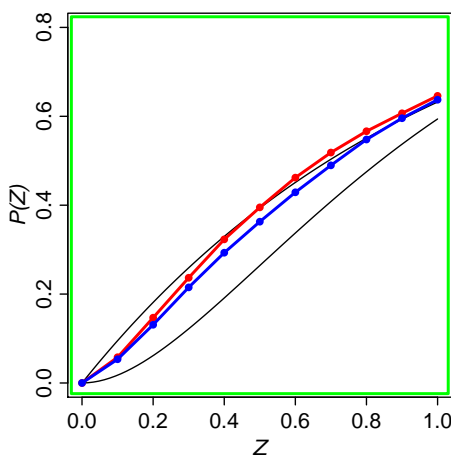
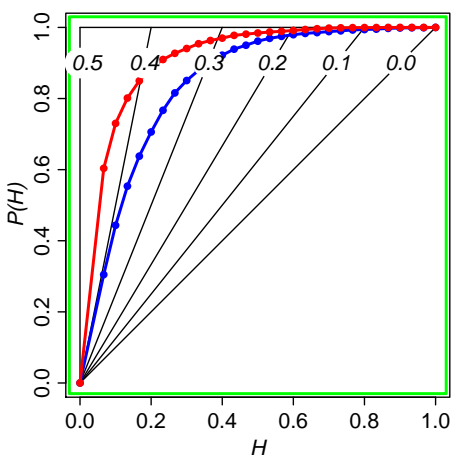
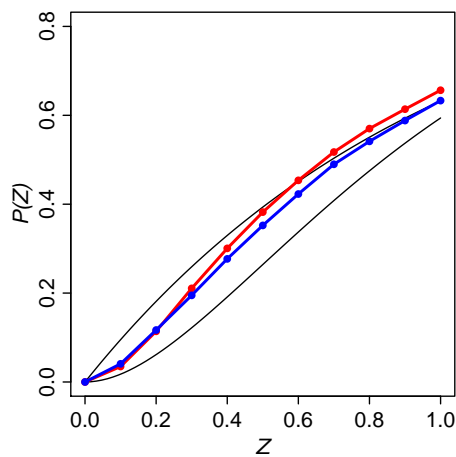
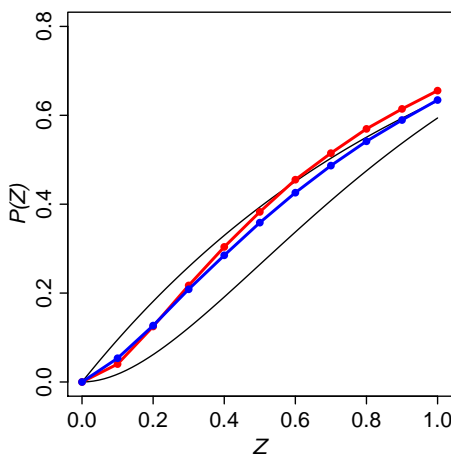
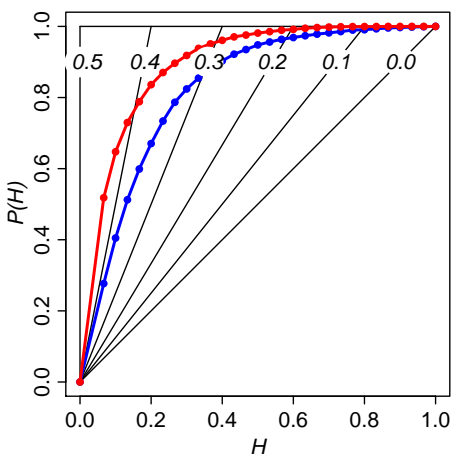
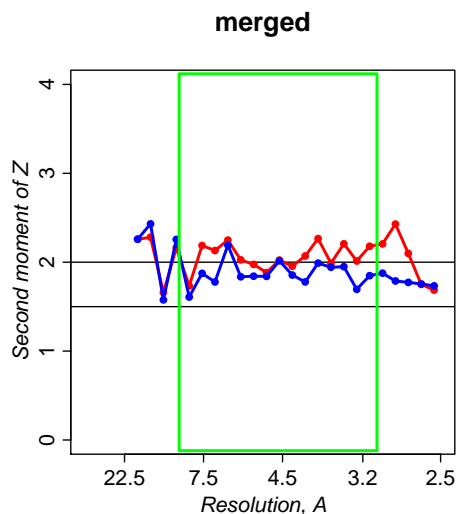
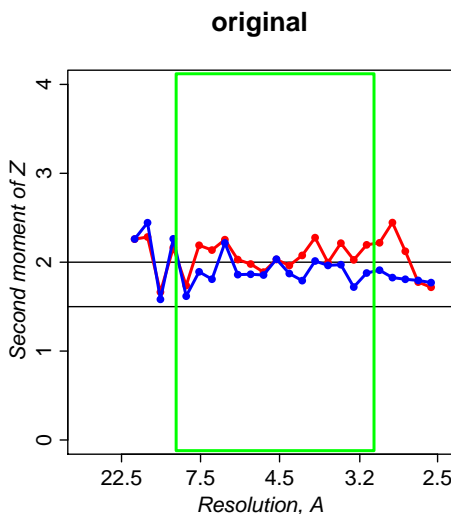
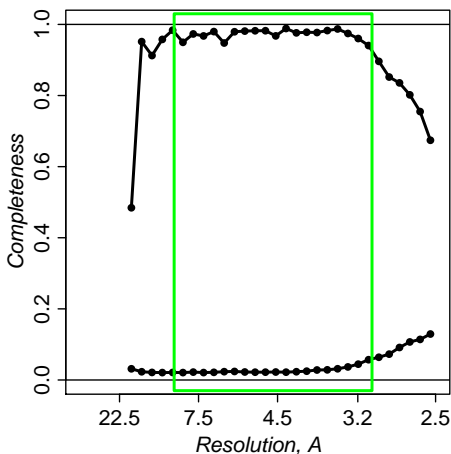
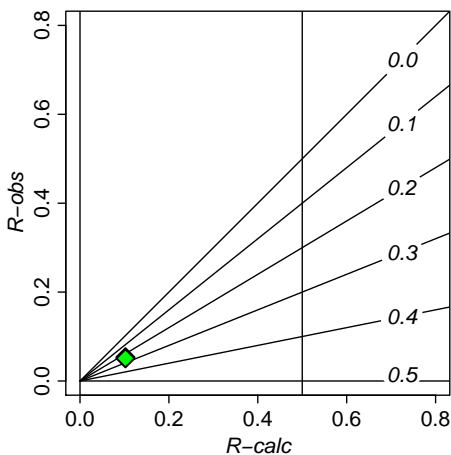
	original	merged
s.g.	P 43	P 43 21 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.03
R	27.6	
R'	27.6	28.8
R-free	34.7	
R'-free	34.6	36.4

residues per monomer	DNA	protein
	0	300

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.2–2.5	9.9–3.0
unique	20,592	11,630
measured	18,420	11,291
used	15,496	9,718

NCS	translation	rotation
r.m.s.d. (A)	28.07	0.02
angle (o)	179.97	0.05



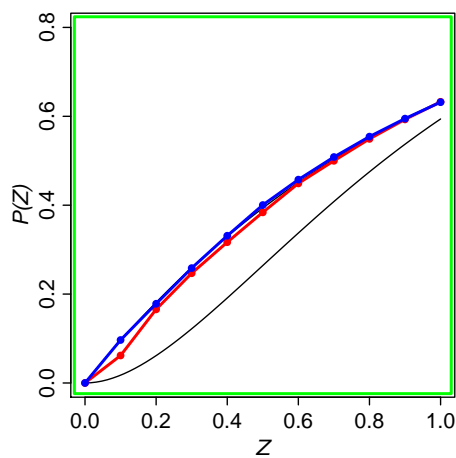
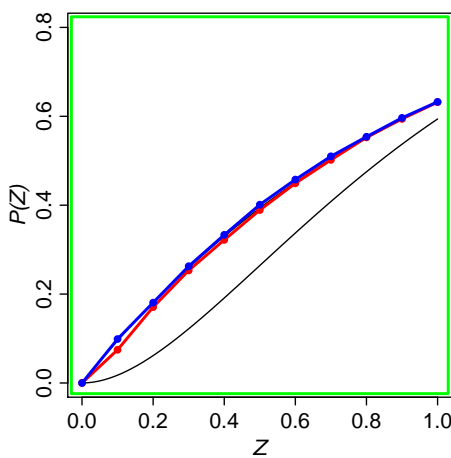
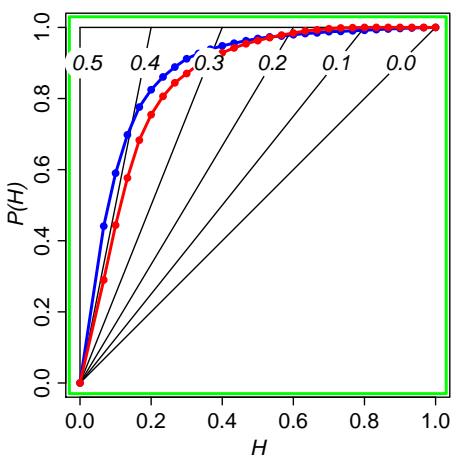
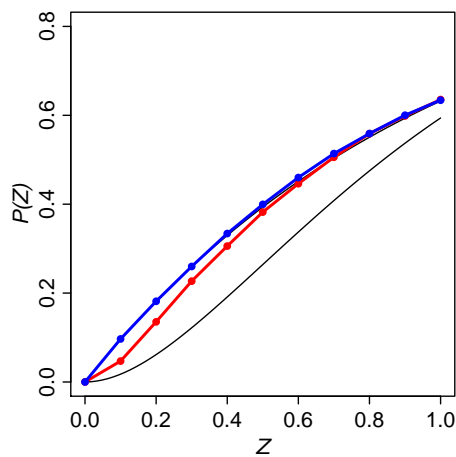
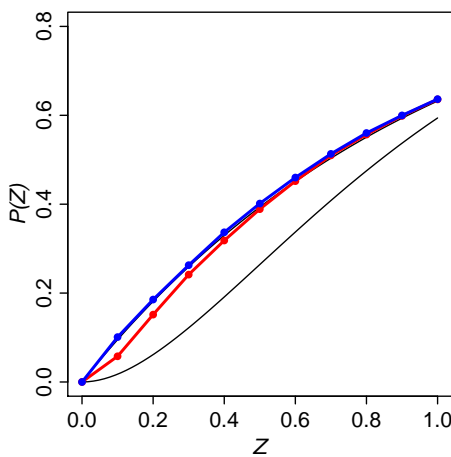
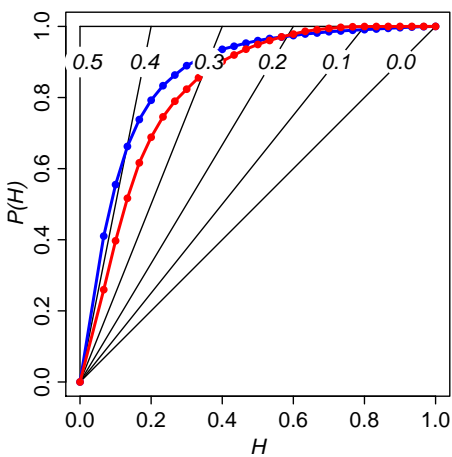
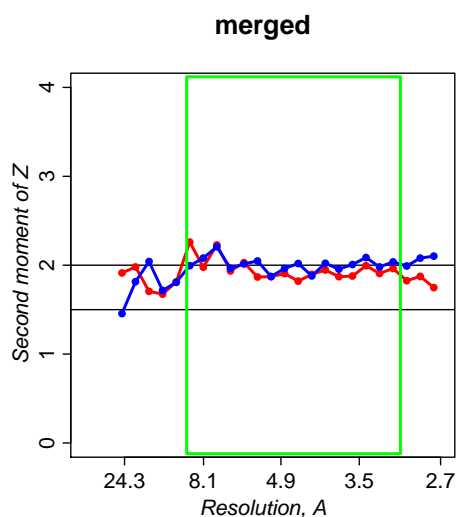
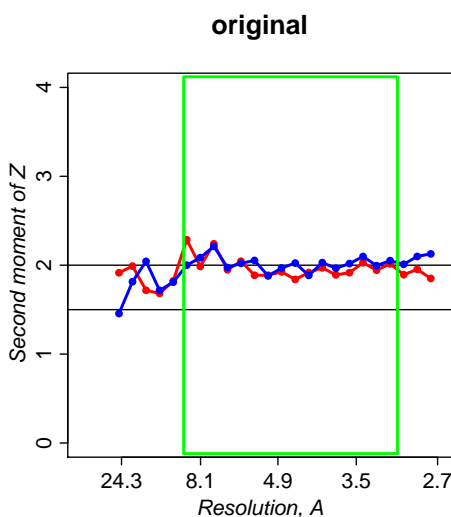
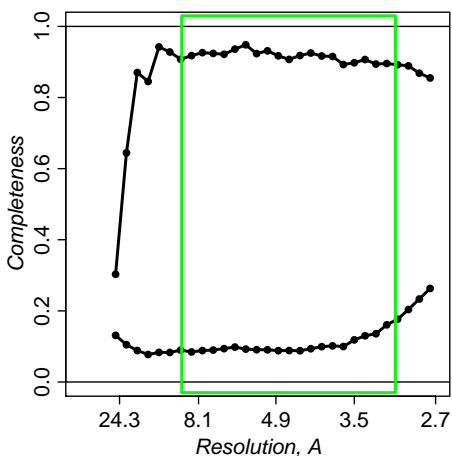
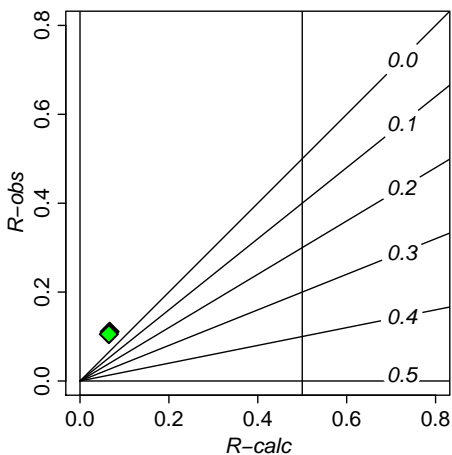
1ffn

	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.10
R	23.2	
R'	23.1	23.5
R-free	28.6	
R'-free	28.5	28.1
residues per monomer	DNA 0	protein 382

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	31.8–2.7	9.9–3.0
unique	24,883	17,601
measured	22,352	16,005
used	20,048	14,454

NCS	translation	rotation
r.m.s.d. (A)	42.32	0.10
angle (o)	180.00	0.01



1ffo

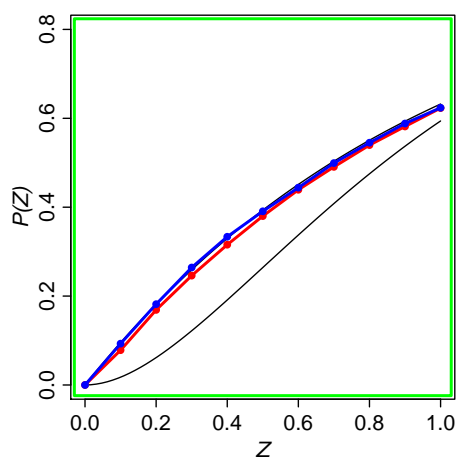
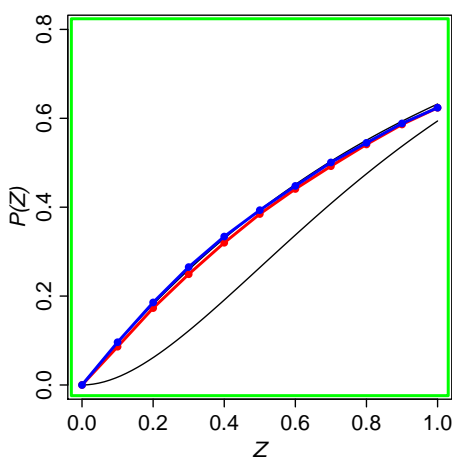
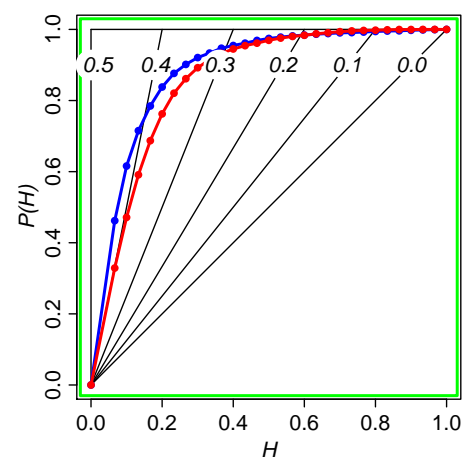
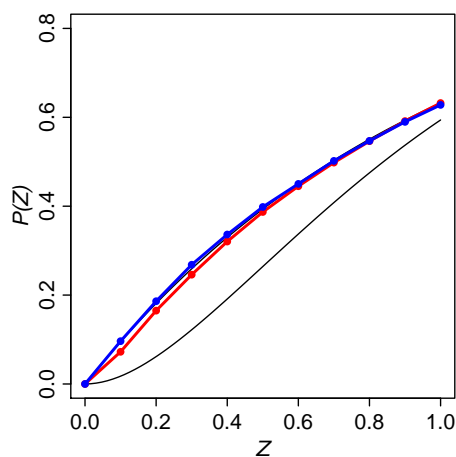
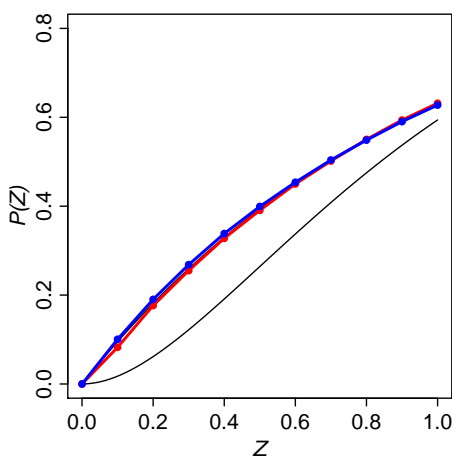
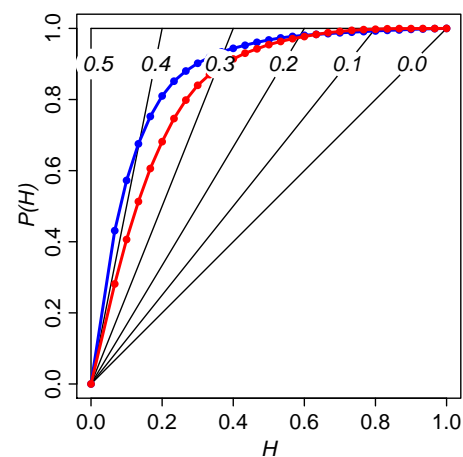
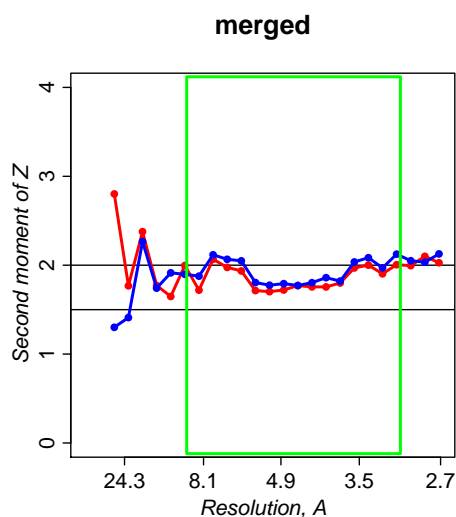
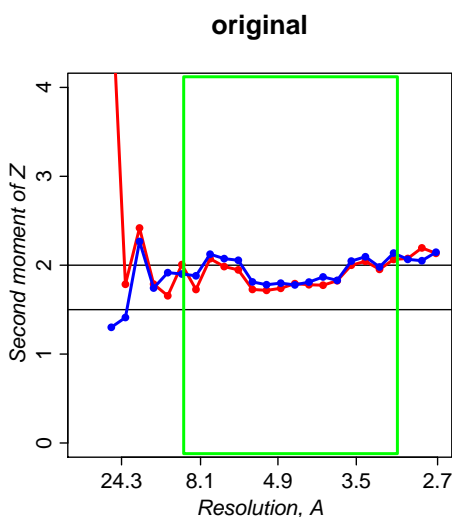
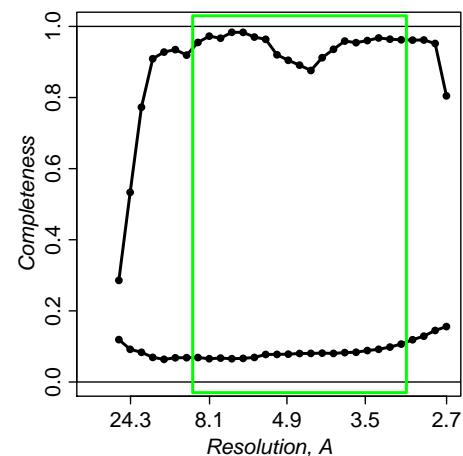
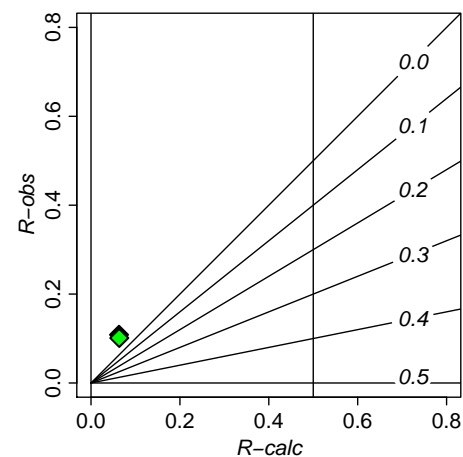
	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.10
R	23.5	
R'	23.5	23.5
R-free	27.7	
R'-free	27.8	27.0

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	43.3–2.7	9.9–3.0
unique	25,996	17,573
measured	24,299	16,636
used	22,006	15,124

NCS	translation	rotation
r.m.s.d. (A)	42.35	0.10
angle (o)	179.97	0.07

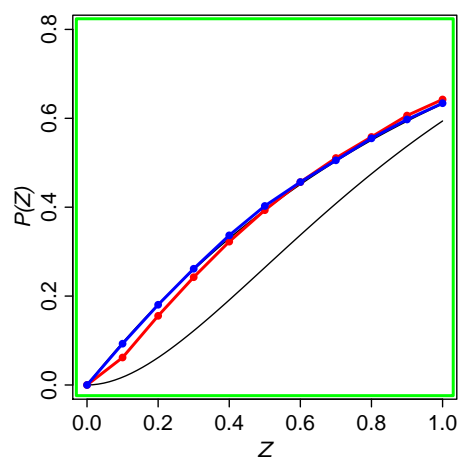
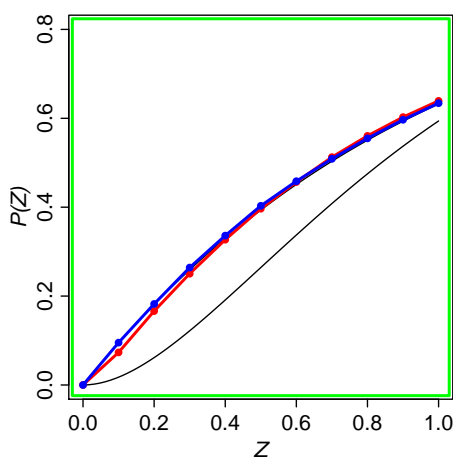
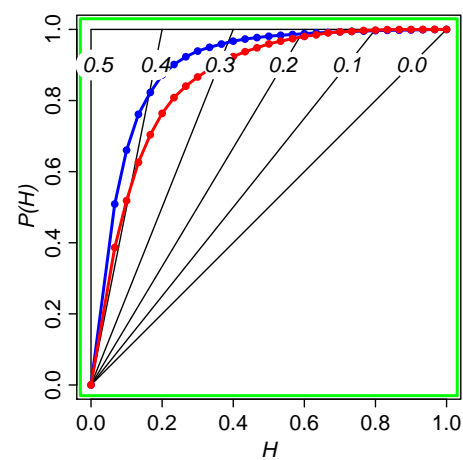
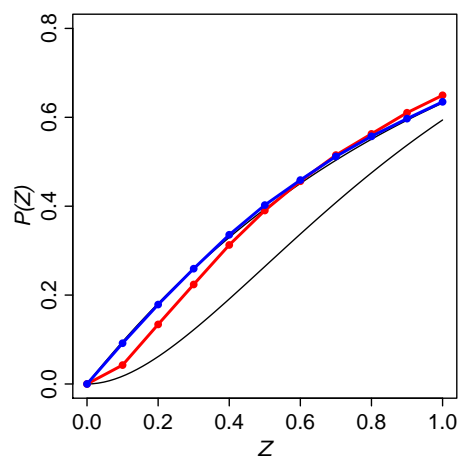
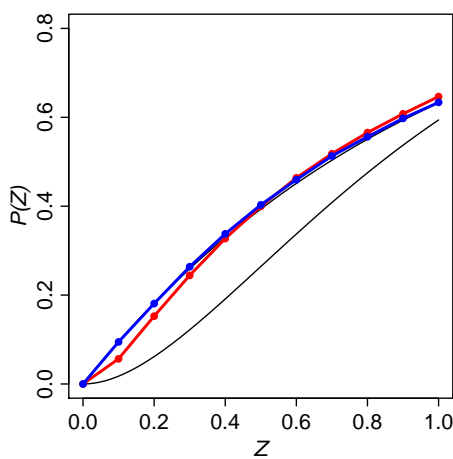
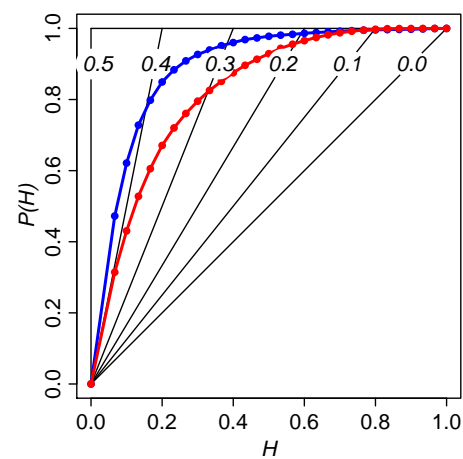
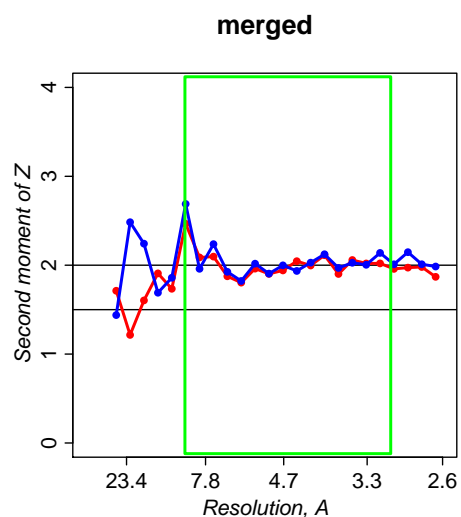
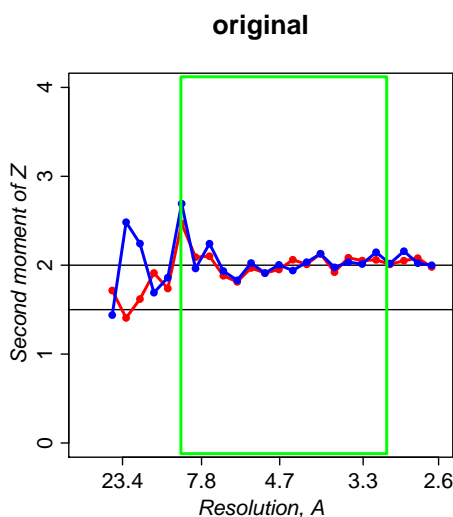
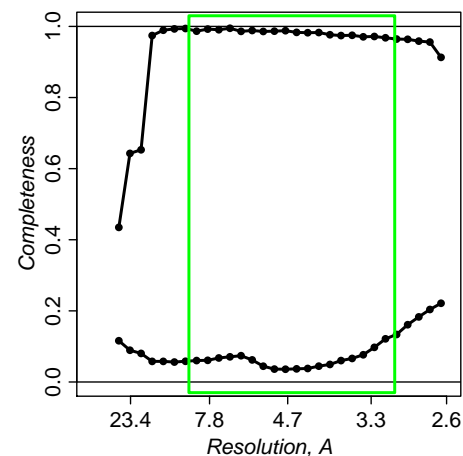
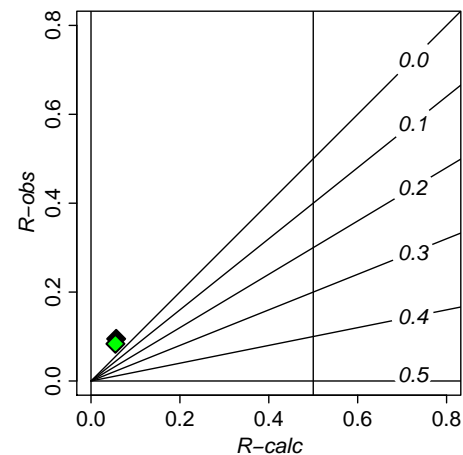
residues per monomer	DNA	protein
	0	382



1ffp

	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.09
R	23.5	
R'	23.4	23.5
R-free	29.2	
R'-free	29.1	28.5
residues per monomer	DNA 0	protein 382

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	41.5–2.6	9.9–3.0
unique	26,496	16,811
measured	25,600	16,439
used	23,698	15,286
NCS	translation	rotation
r.m.s.d. (A)	41.77	0.09
angle (o)	179.98	0.03



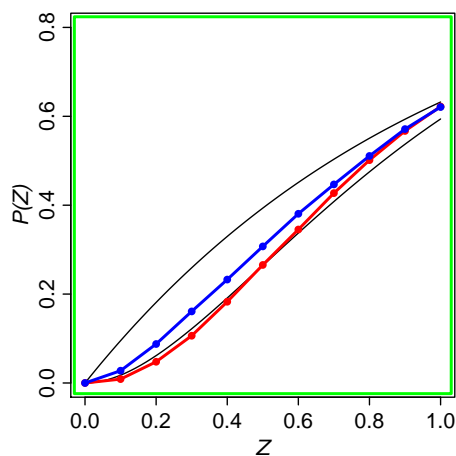
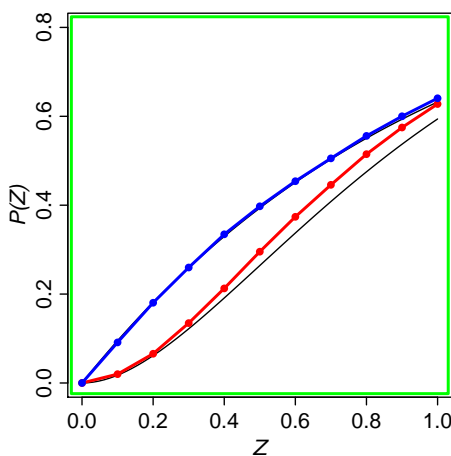
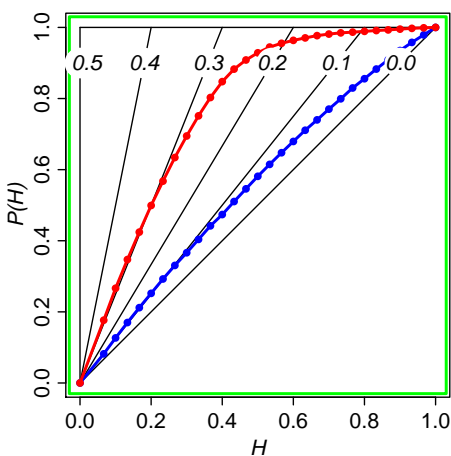
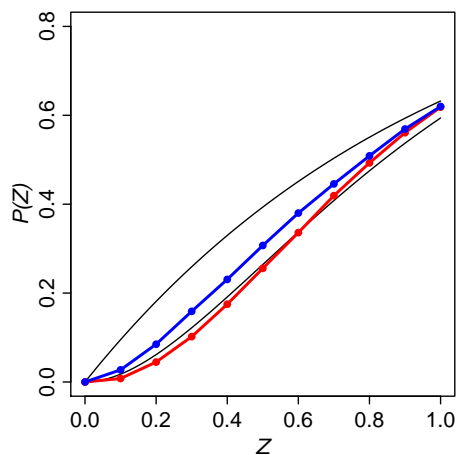
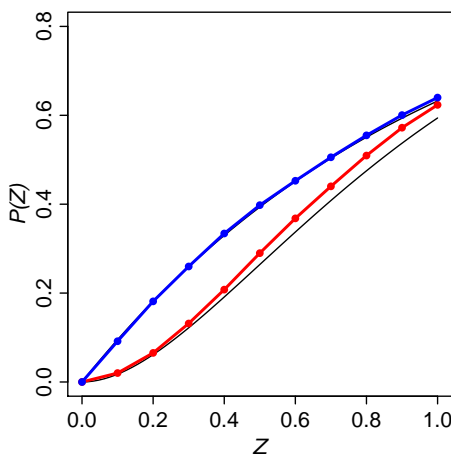
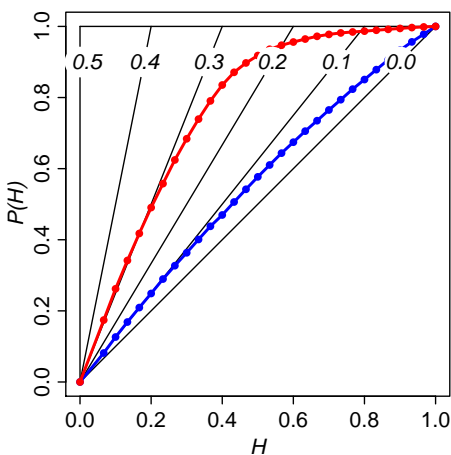
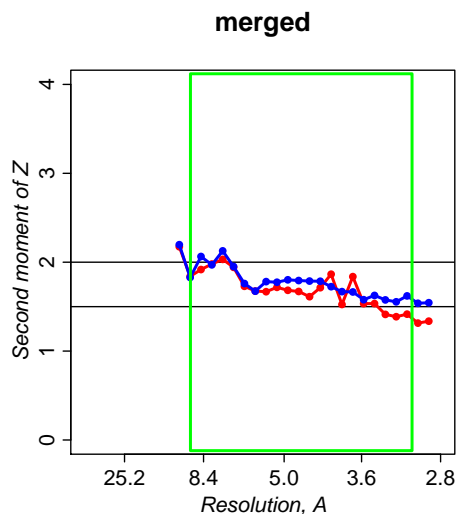
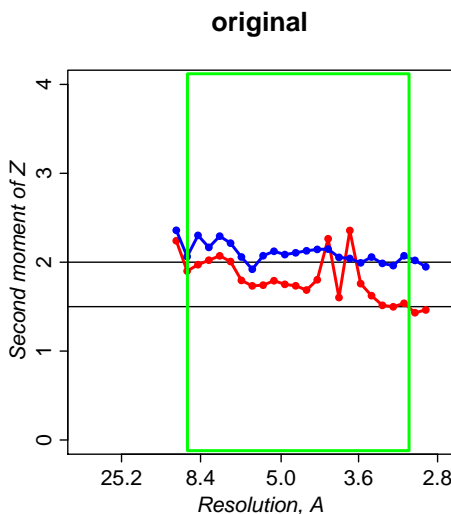
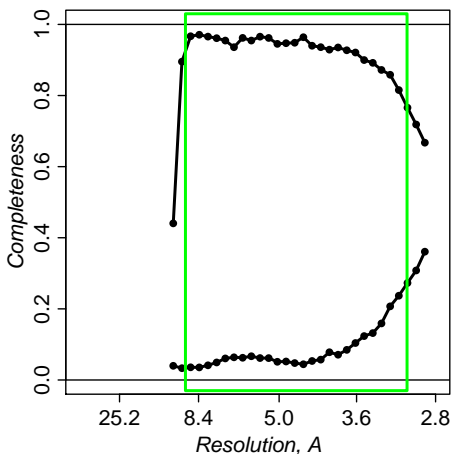
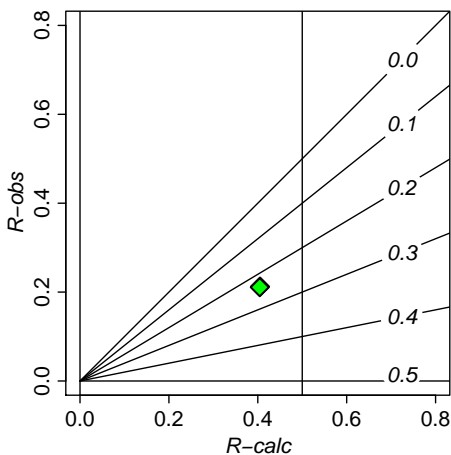
1fhf

	original	merged
s.g.	P 31	-
p.g.	10020	10023
a.u.	3	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	24.7	-
R'	-	-
R-free	29.6	-
R'-free	-	-
residues per monomer	DNA 0	protein 304

s < f/100	268	1.01 %
s <= 0	268	1.01 %
f <= 0	268	1.01 %
s,f <= 0	268	1.01 %

range (A)	11.2-2.9	9.9-3.0
unique	30,561	25,929
measured	26,655	23,425
used	23,060	20,798

NCS	translation	rotation
r.m.s.d. (A)	2.28	0.89
angle (o)	7.68	2.99



1flk

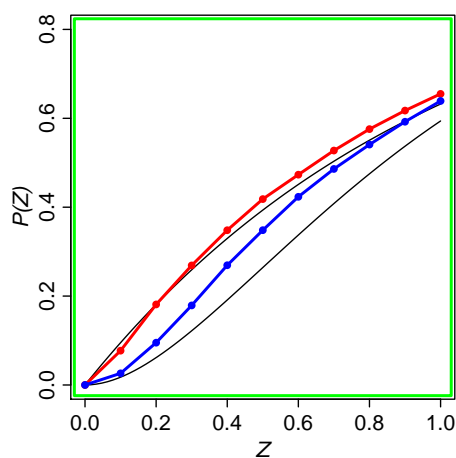
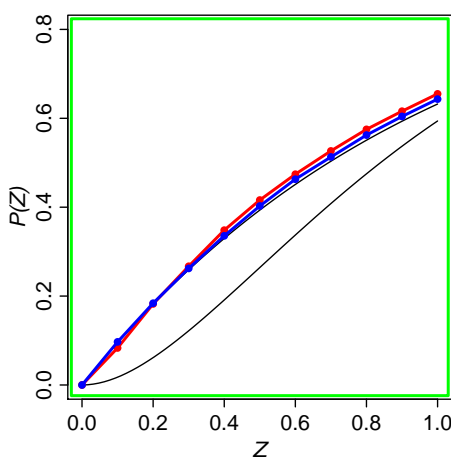
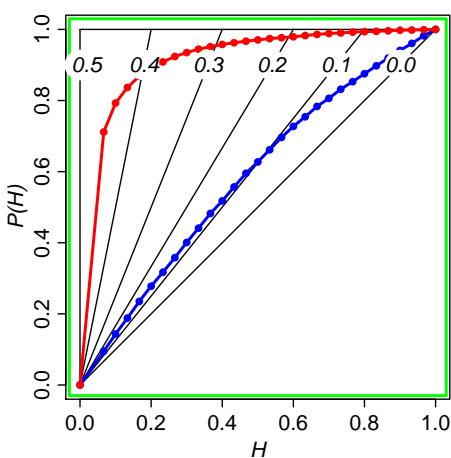
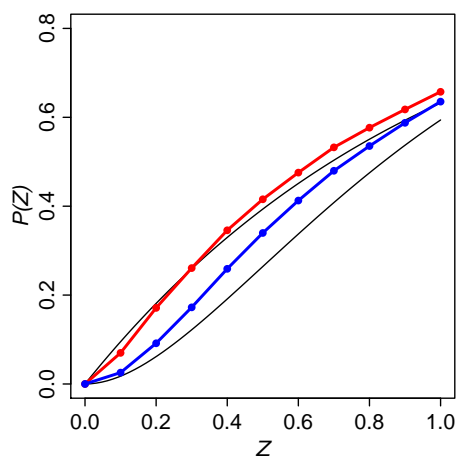
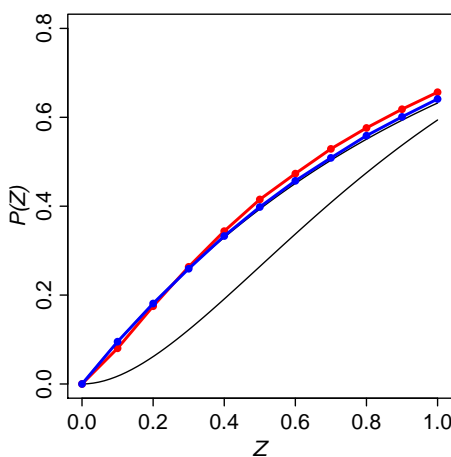
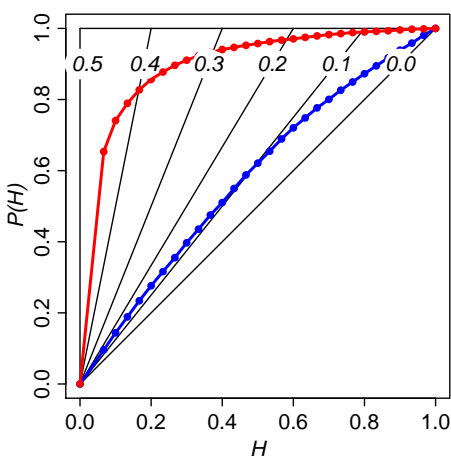
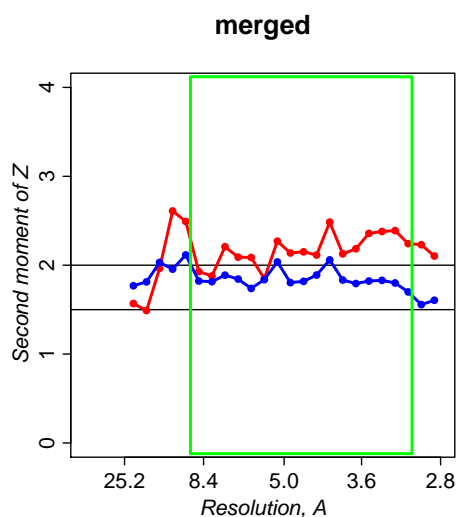
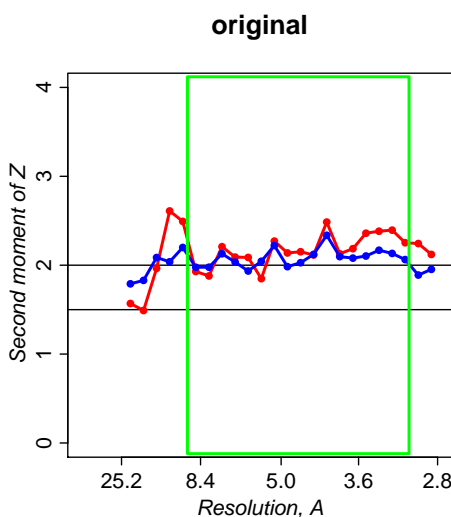
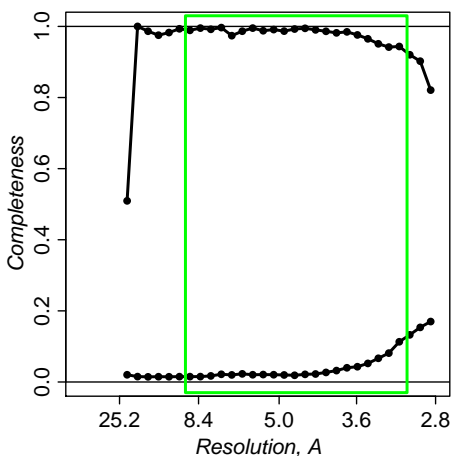
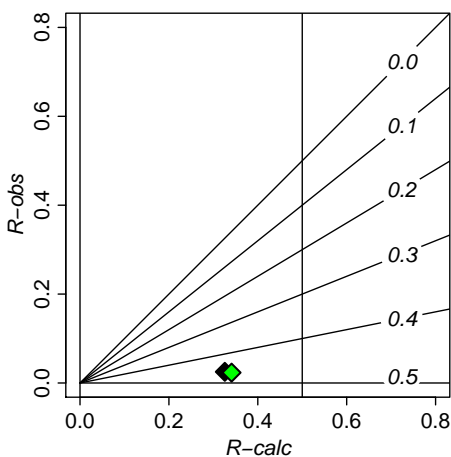
	original	merged
s.g.	H 3	H 3 2
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.97
R	25.9	
R'	25.7	26.5
R-free	28.0	
R'-free	28.1	28.3

residues per monomer	DNA	protein
	0	205

s < f/100	1077	5.39 %
s <= 0	811	4.06 %
f <= 0	811	4.06 %
s,f <= 0	811	4.06 %

range (A)	23.8–2.8	9.9–3.0
unique	21,009	16,571
measured	19,981	16,076
used	18,036	14,650

NCS	translation	rotation
r.m.s.d. (A)	47.80	0.92
angle (o)	179.34	0.91



1fil

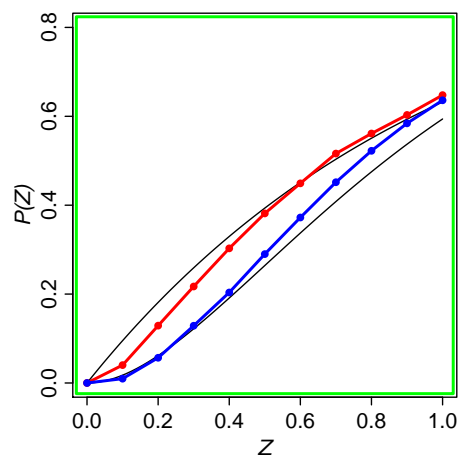
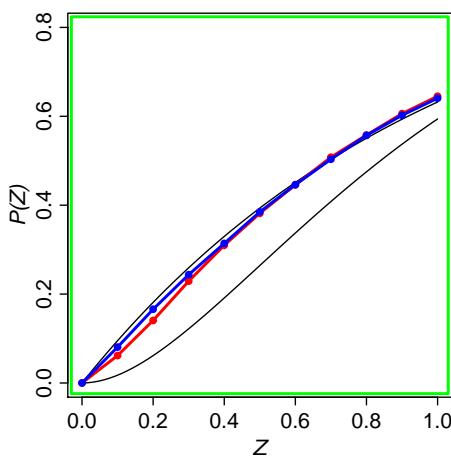
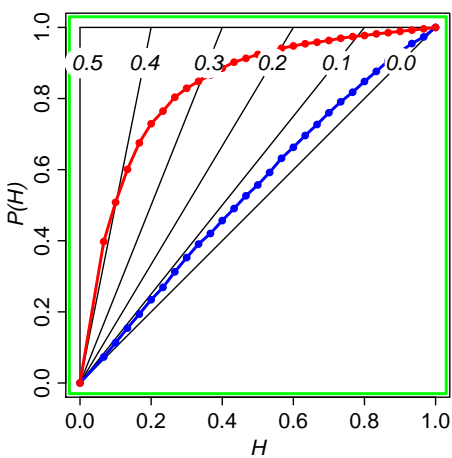
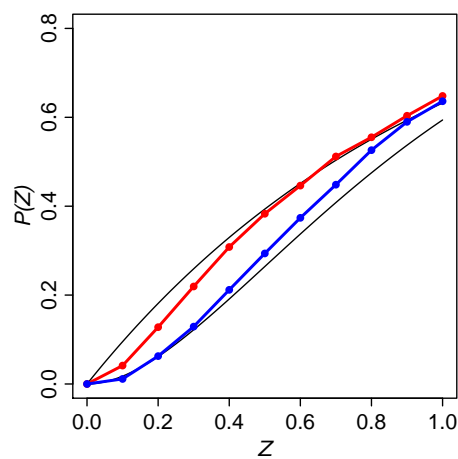
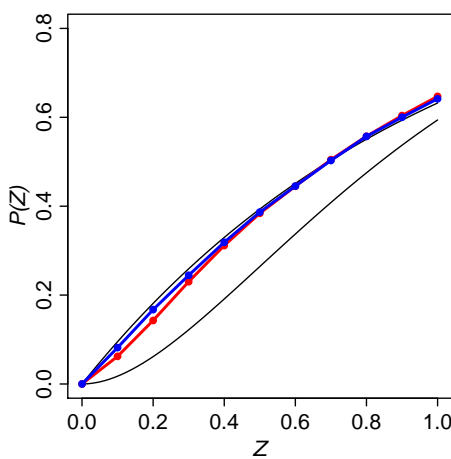
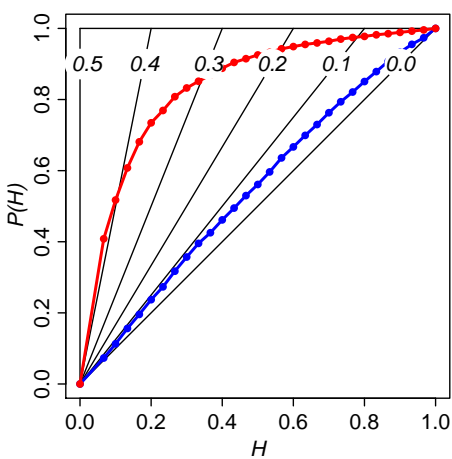
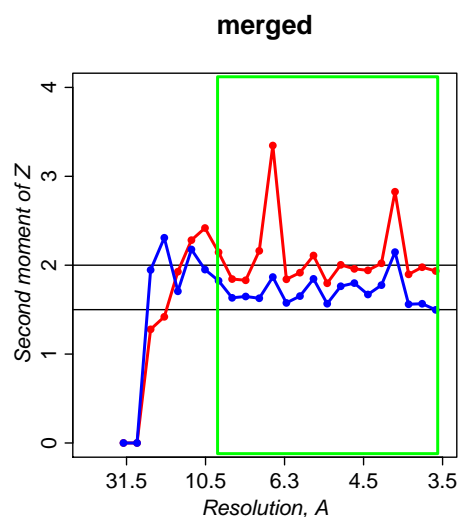
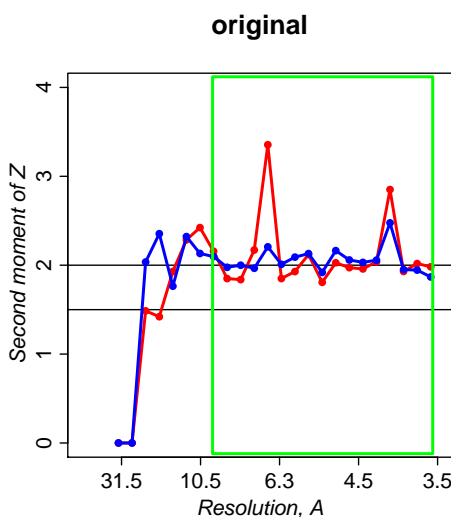
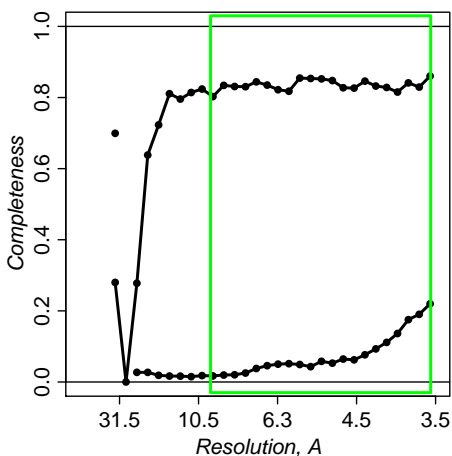
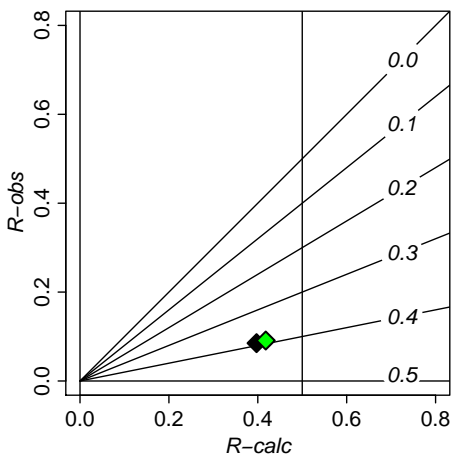
	original	merged
s.g.	P 3 2 1	P 63 2 2
p.g.	10023	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		1.37
R	24.1	
R'	23.4	23.6
R-free	31.8	
R'-free	30.9	30.6

residues per monomer	DNA	protein
	0	205

s < f/100	74	0.78 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	41.9–3.5	9.9–3.5
unique	11,370	10,787
measured	9,436	9,021
used	7,592	7,348

NCS	translation	rotation
r.m.s.d. (A)	14.22	1.29
angle (o)	59.66	0.42



1fnk

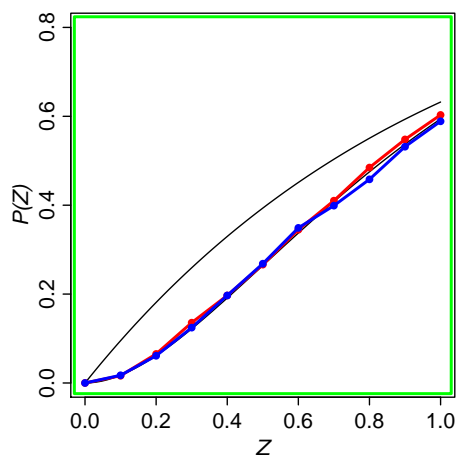
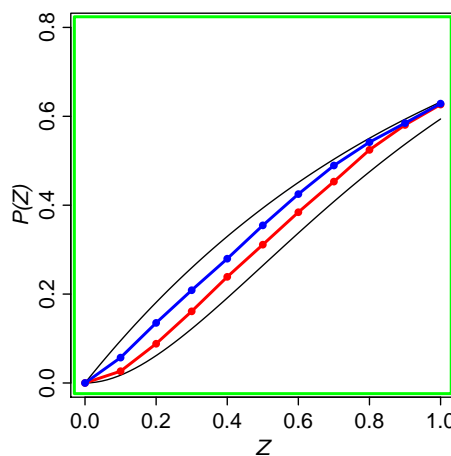
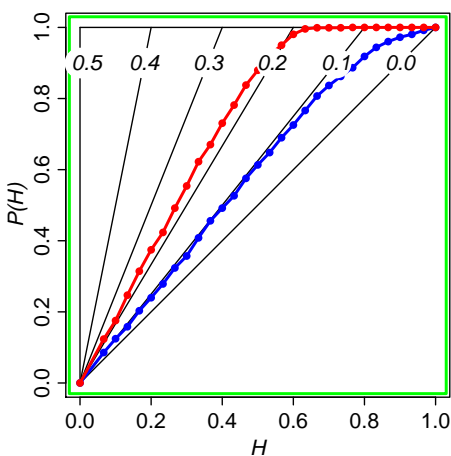
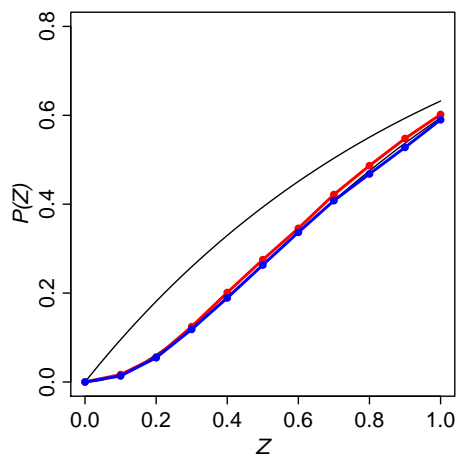
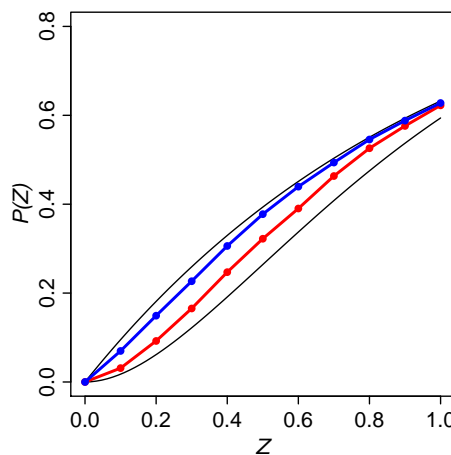
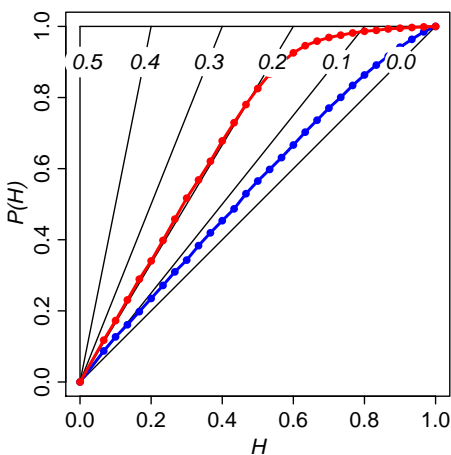
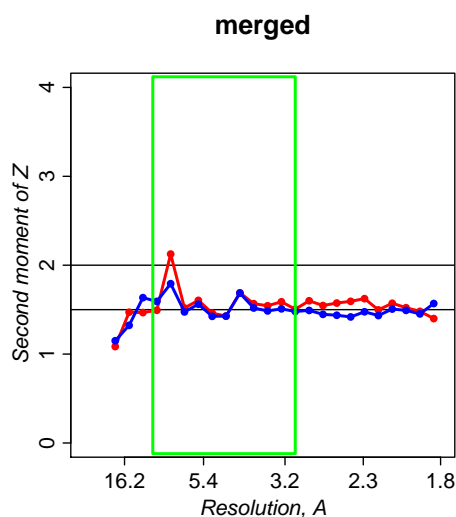
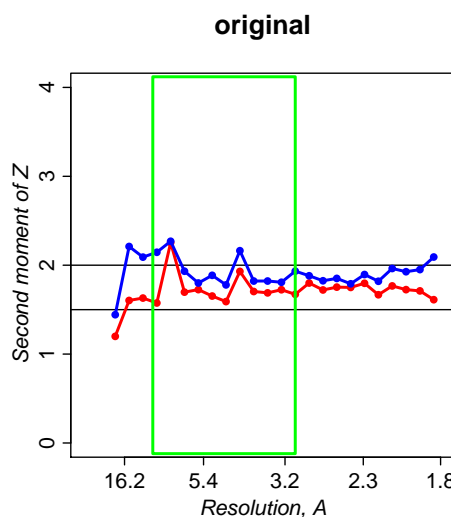
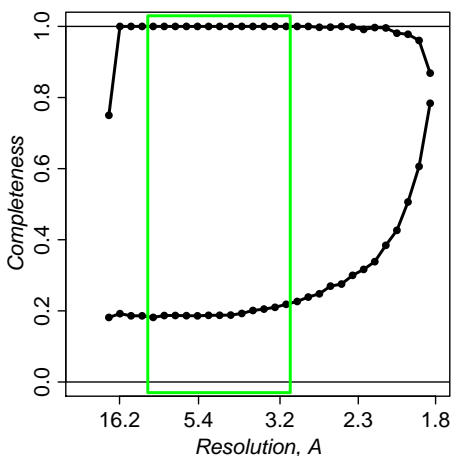
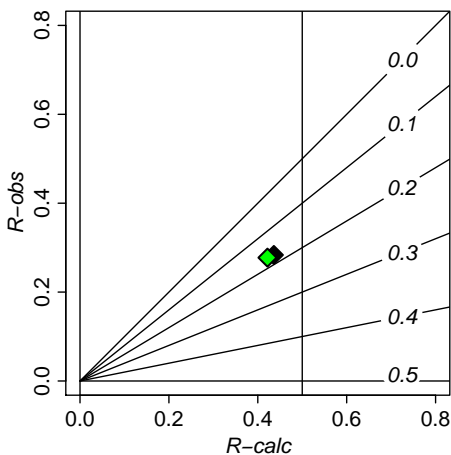
	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	24.7	-
R'	-	-
R-free	26.6	-
R'-free	-	-

residues per monomer	DNA	protein
	0	115

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	27.5-1.8	9.9-3.0
unique	10,107	2,118
measured	9,908	2,118
used	9,254	1,946

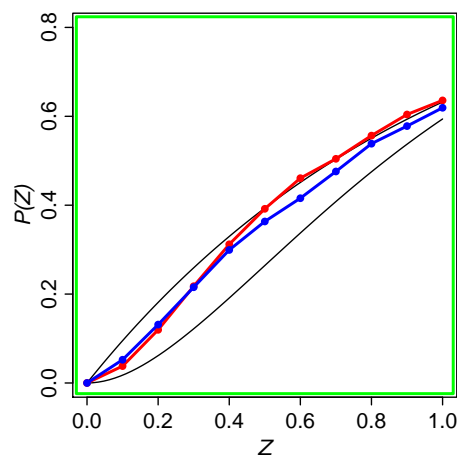
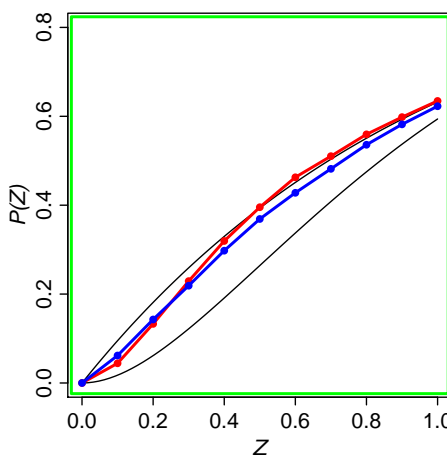
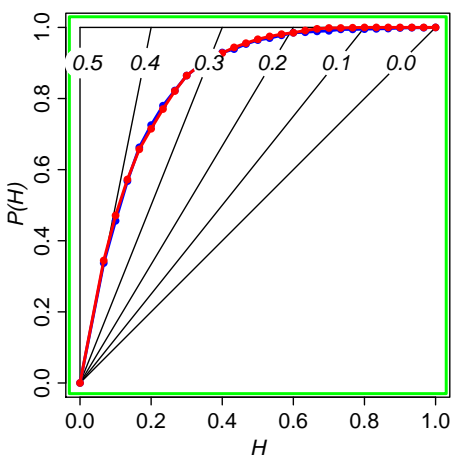
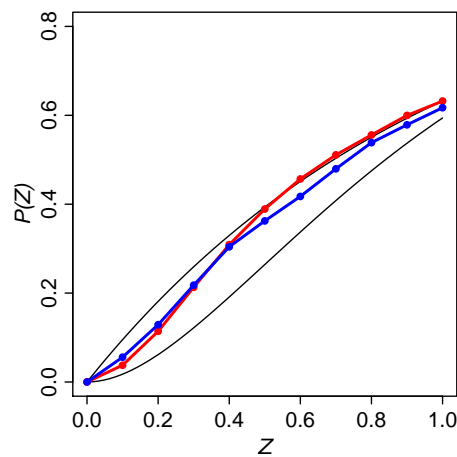
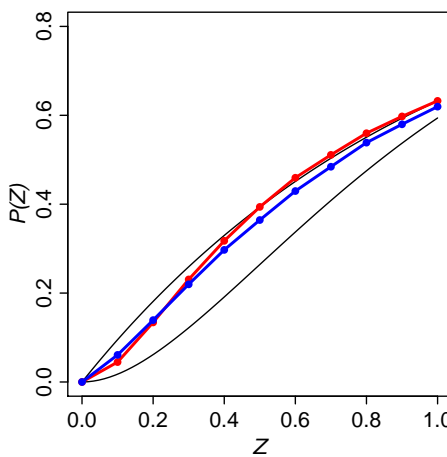
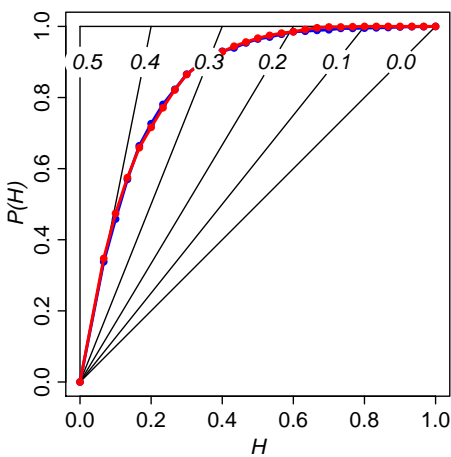
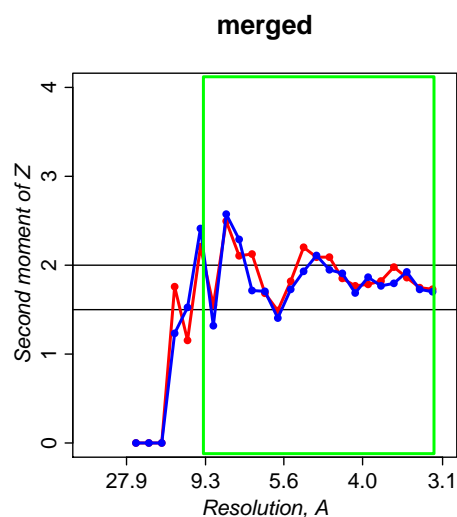
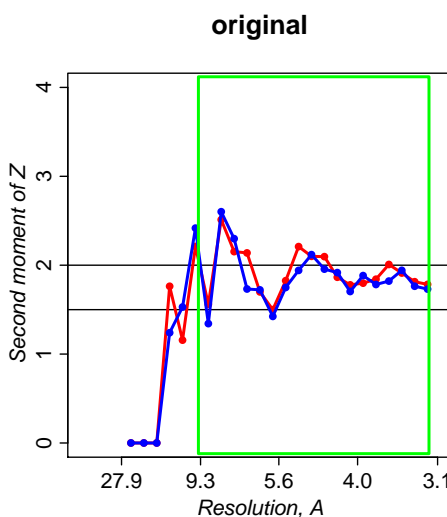
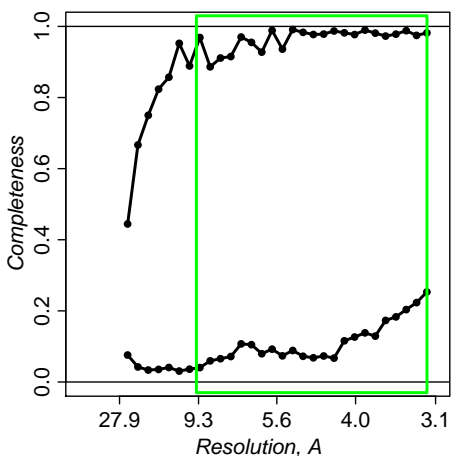
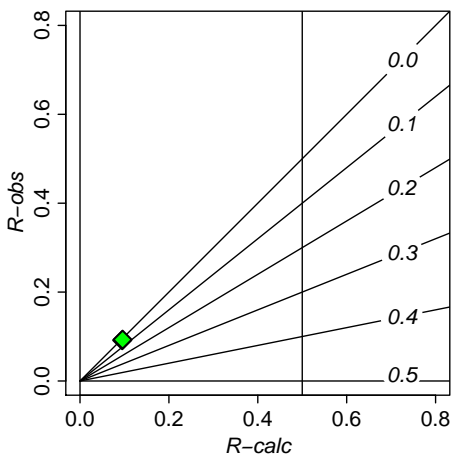
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1fqx

	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.05
R	18.6	
R'	18.8	20.2
R-free	31.7	
R'-free	32.3	32.0
residues per monomer	DNA 0	protein 99

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	26.0–3.1	9.9–3.1
unique	3,362	3,253
measured	3,263	3,171
used	2,544	2,516
NCS	translation	rotation
r.m.s.d. (A)	21.82	0.04
angle (o)	179.87	0.19



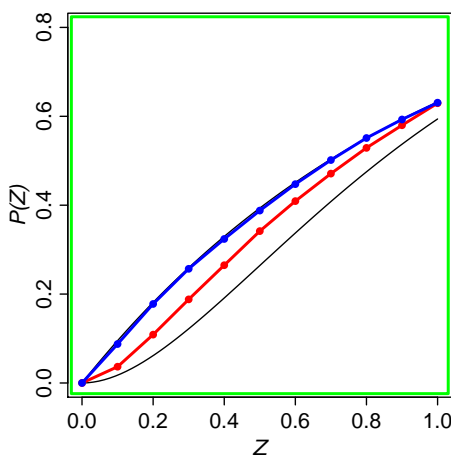
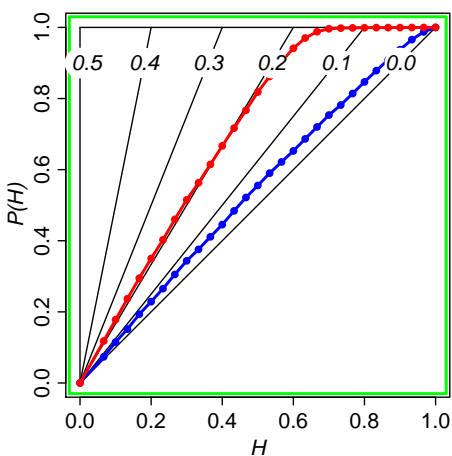
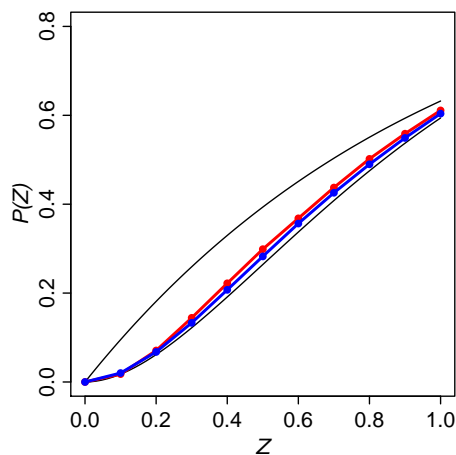
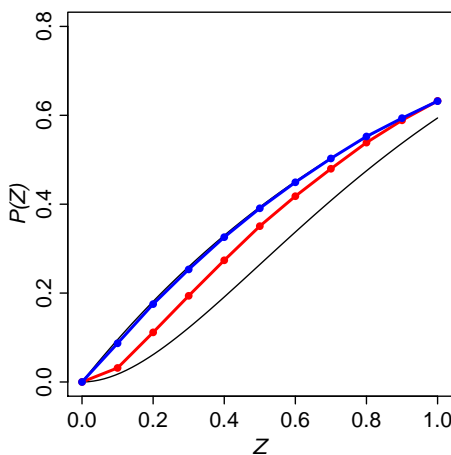
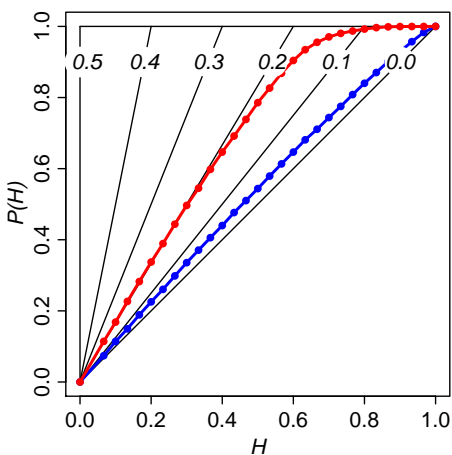
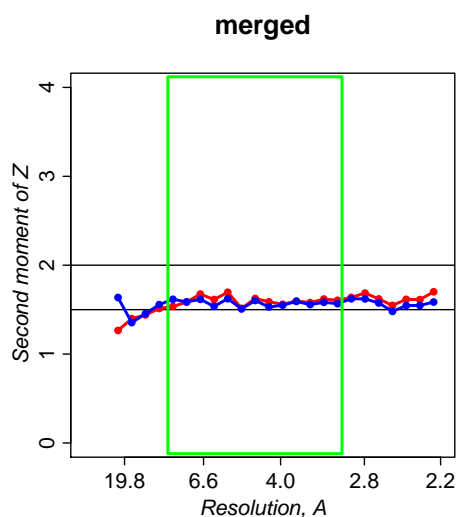
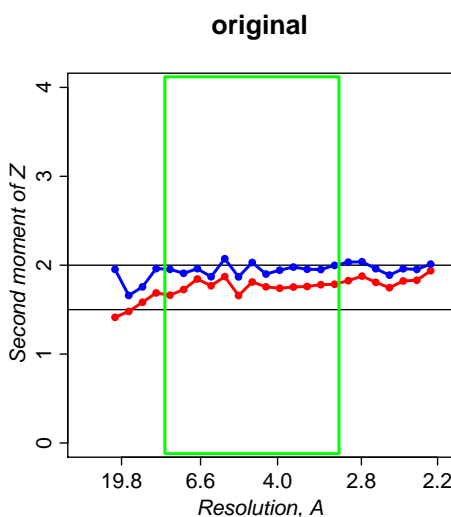
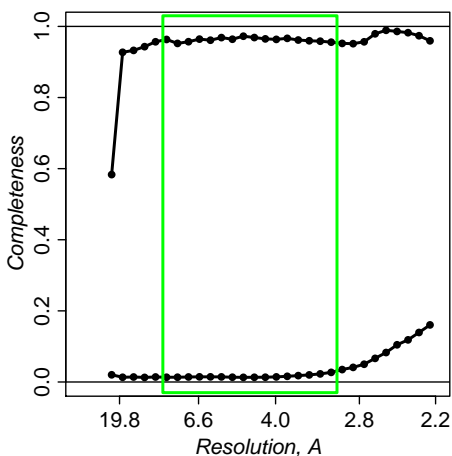
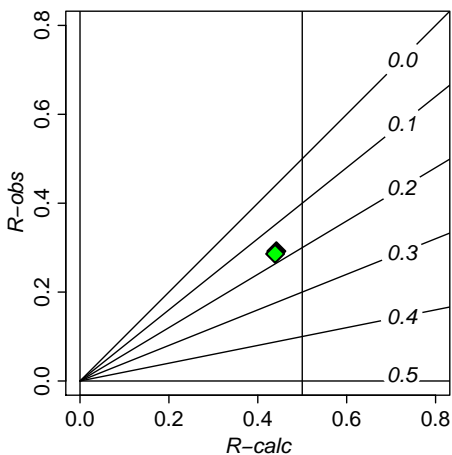
1fro

	original	merged
s.g.	P 43	-
p.g.	10201	10205
a.u.	4	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	23.4	-
R'	-	-
R-free	26.1	-
R'-free	-	-
residues per monomer	DNA 0	protein 176

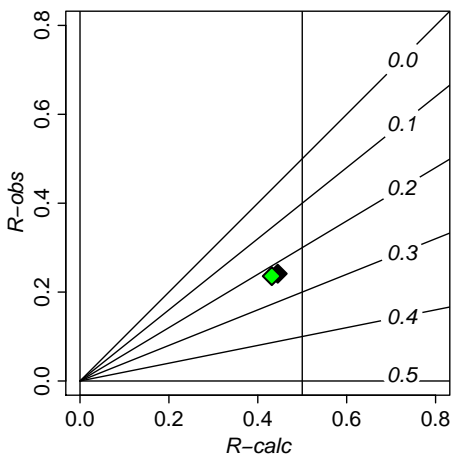
s < f/100	977	2.75 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.9-2.2	9.9-3.0
unique	36,709	14,982
measured	35,502	14,411
used	32,166	12,688

NCS	translation	rotation
r.m.s.d. (A)	18.15	0.66
angle (o)	79.92	2.50



1ft2



	original	merged
s.g.	P 65	-
p.g.	12021	12027
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (Å)	-	-
R	21.2	-
R'	-	-
R-free	25.8	-
R'-free	-	-

s < f/100	3822	22.32 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

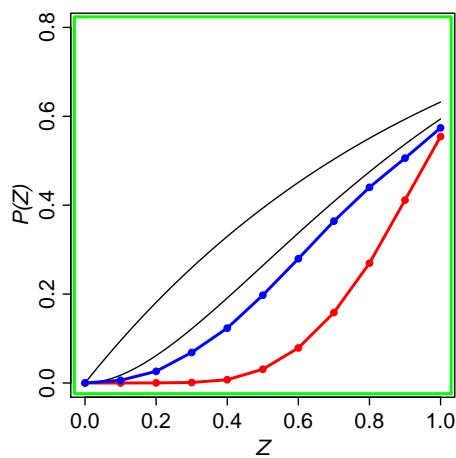
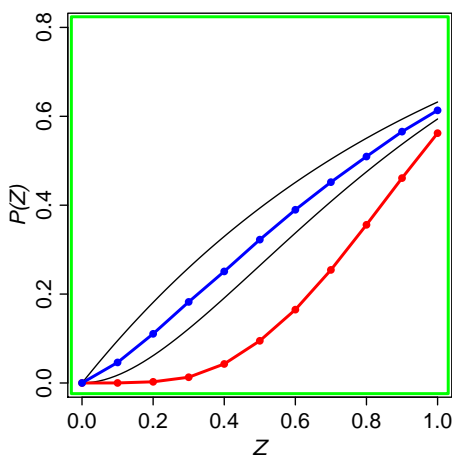
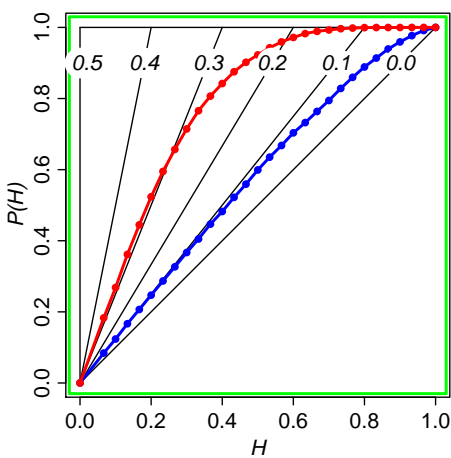
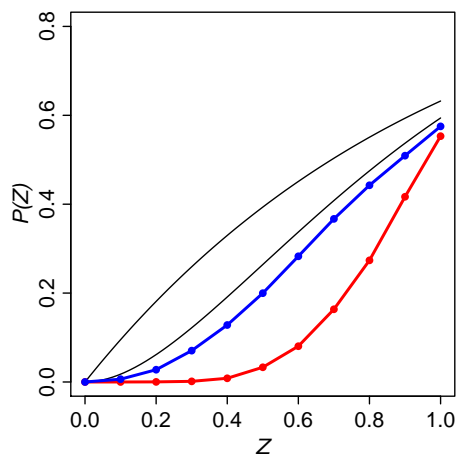
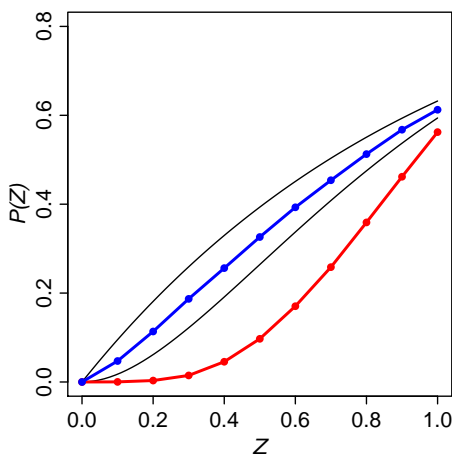
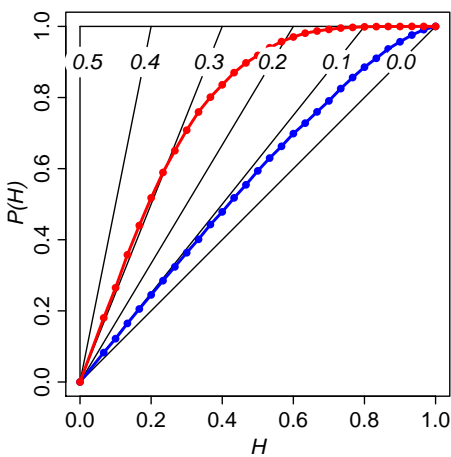
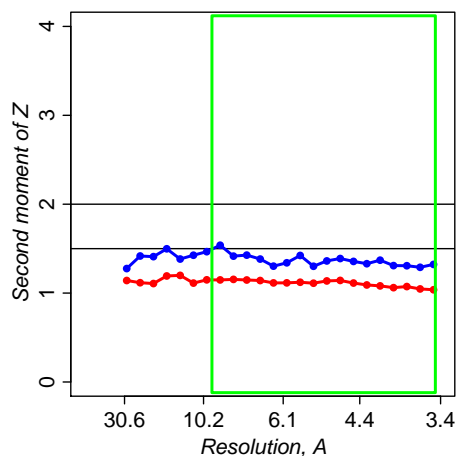
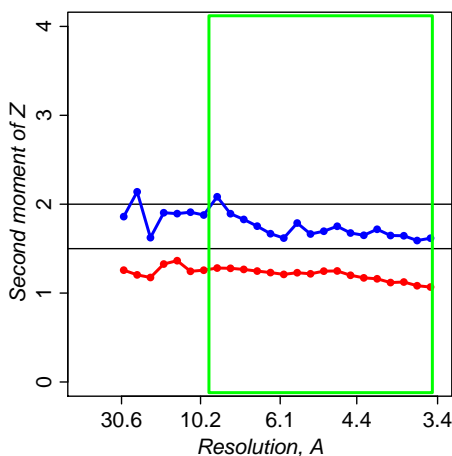
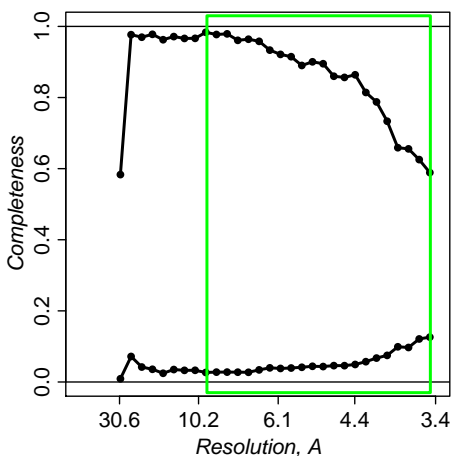
range (Å)	34.5-3.4	9.9-3.4
unique	21,473	20,571
measured	17,125	16,252
used	12,742	12,134

NCS	translation	rotation
r.m.s.d. (Å)	-	-
angle (°)	-	-

residues per monomer	DNA	protein
	0	716

original

merged



1fv1

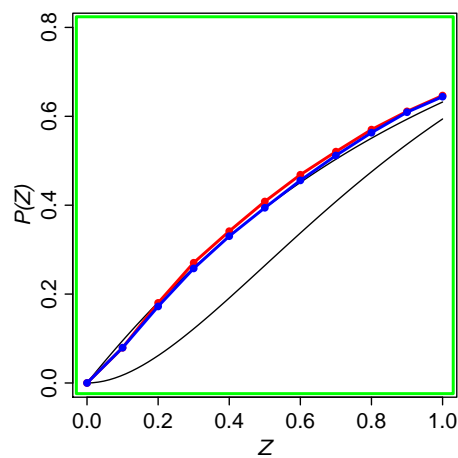
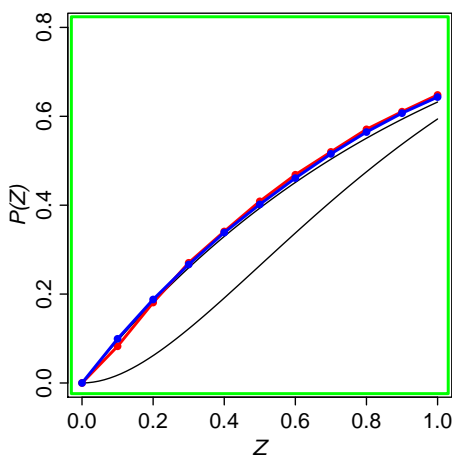
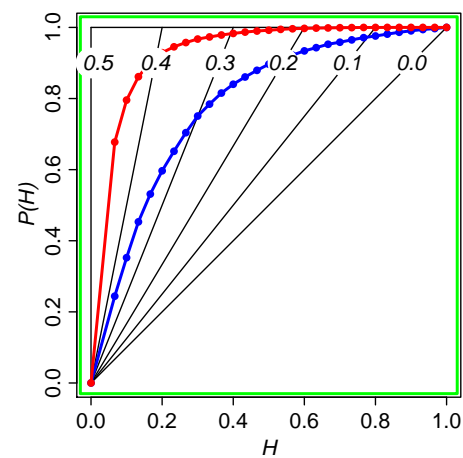
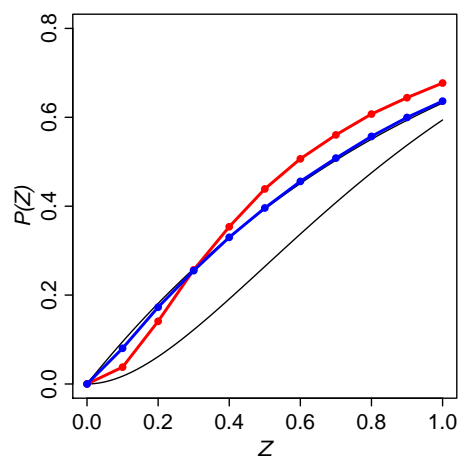
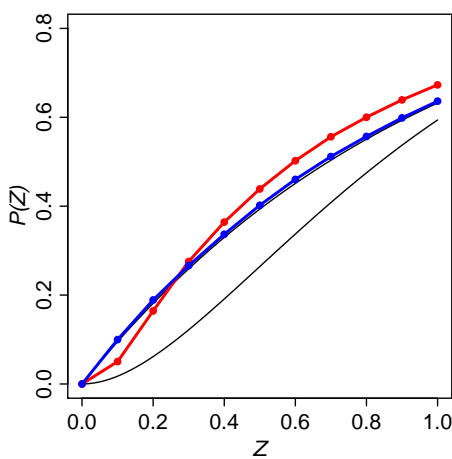
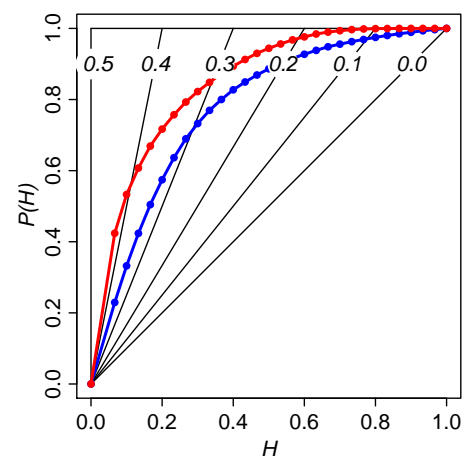
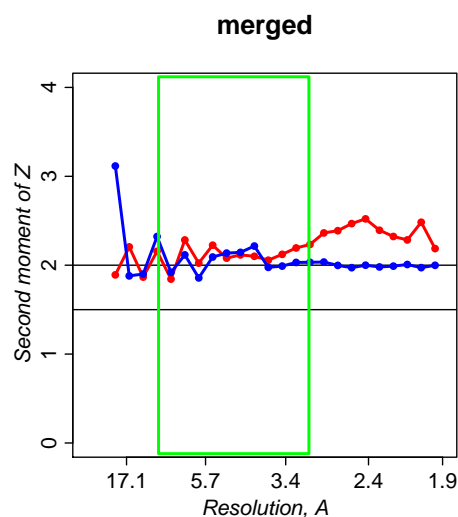
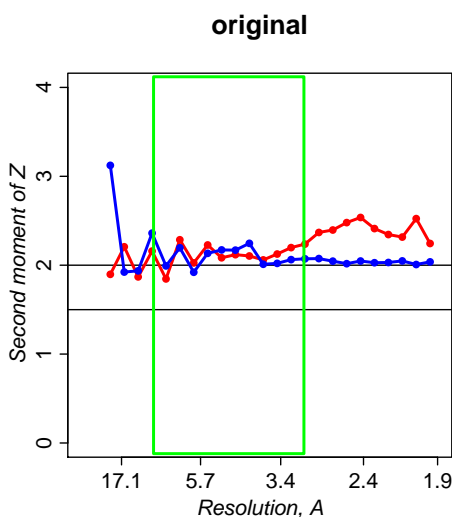
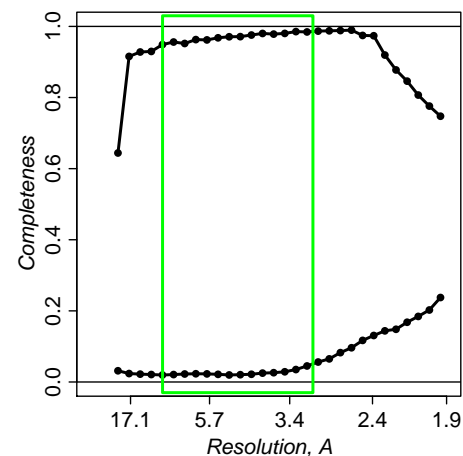
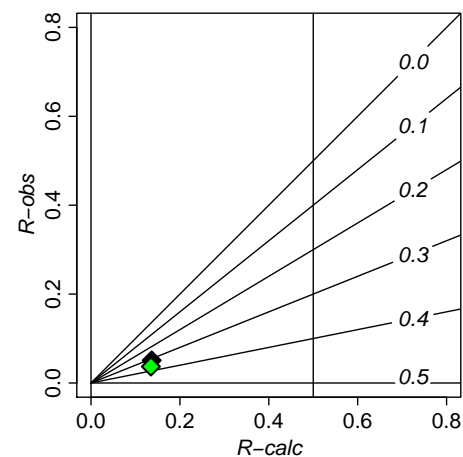
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.38
R	27.2	
R'	27.6	27.6
R-free	28.8	
R'-free	29.1	29.7

s < f/100	2	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	31.6–1.9	9.9–3.0
unique	70,594	17,599
measured	63,975	17,187
used	58,084	15,502

NCS	translation	rotation
r.m.s.d. (A)	38.57	0.37
angle (o)	179.88	0.13

residues per monomer	DNA	protein
	0	386



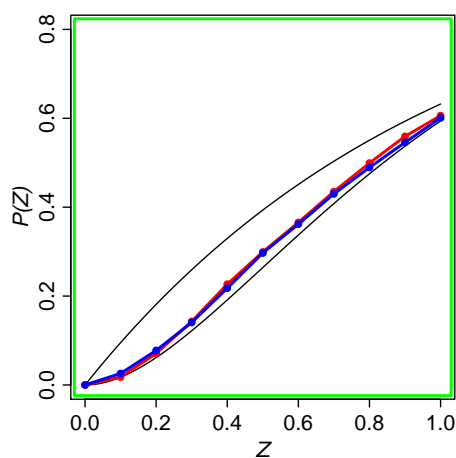
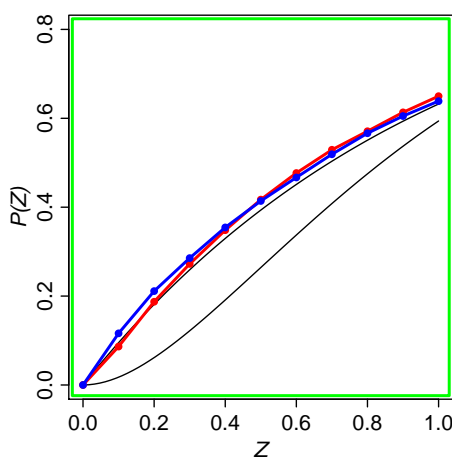
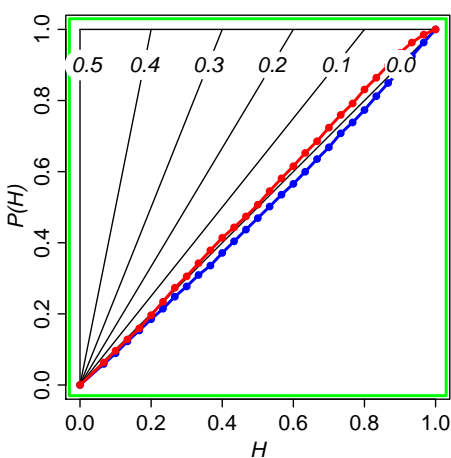
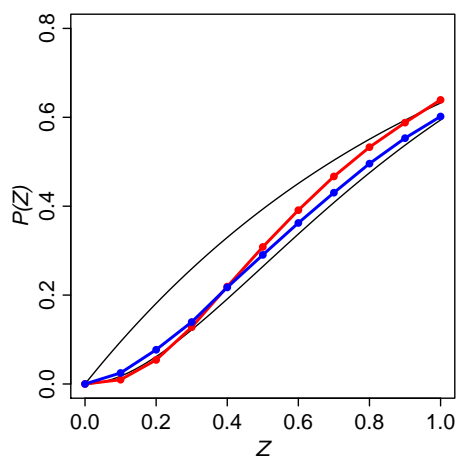
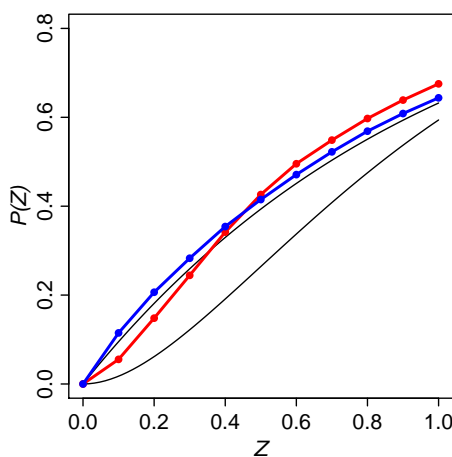
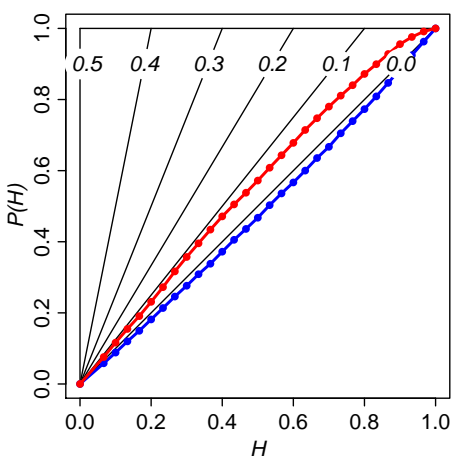
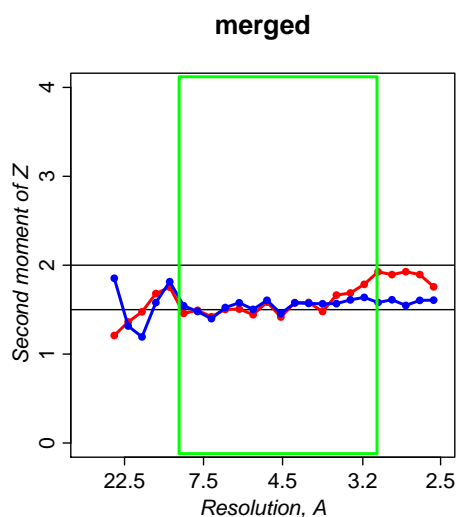
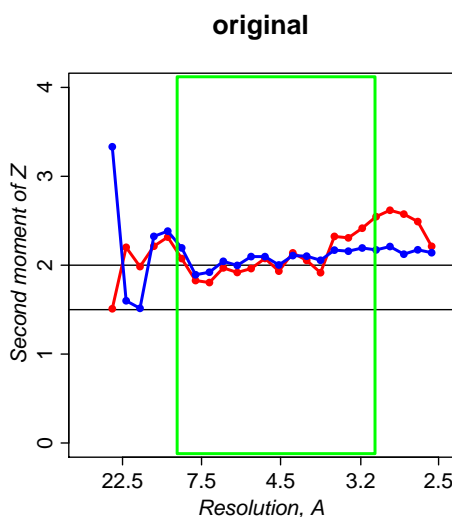
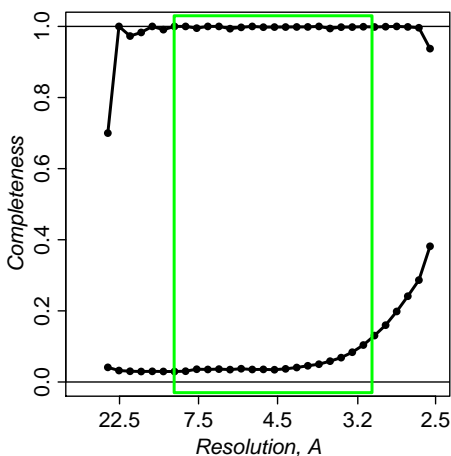
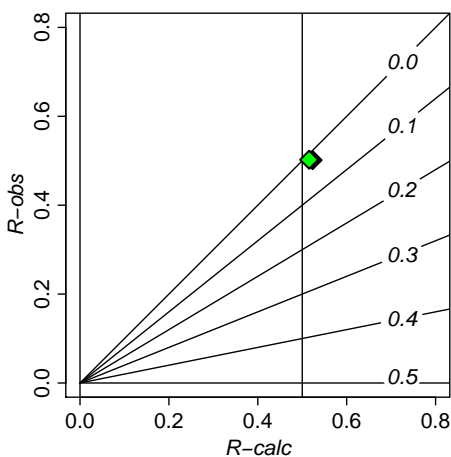
1fv2

	original	merged
s.g.	P 1 21 1	-
p.g.	10001	10003
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	25.9	-
R'	-	-
R-free	33.2	-
R'-free	-	-
residues per monomer	DNA 0	protein 451

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	39.9-2.5	9.9-3.0
unique	19,229	10,877
measured	19,086	10,856
used	16,528	9,284

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



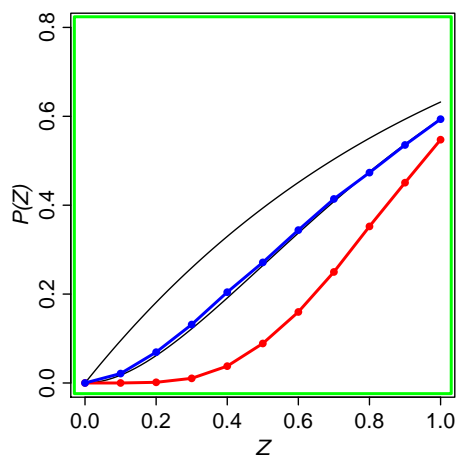
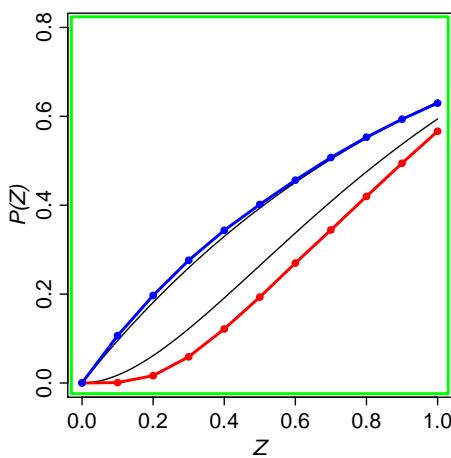
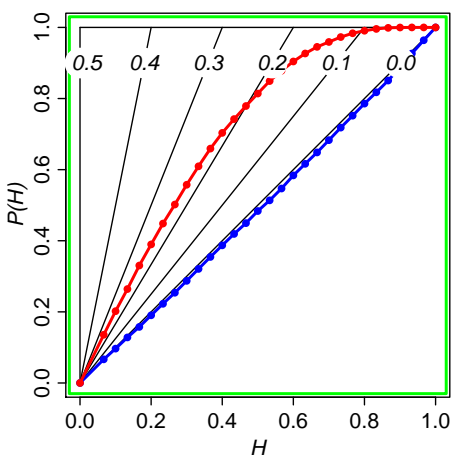
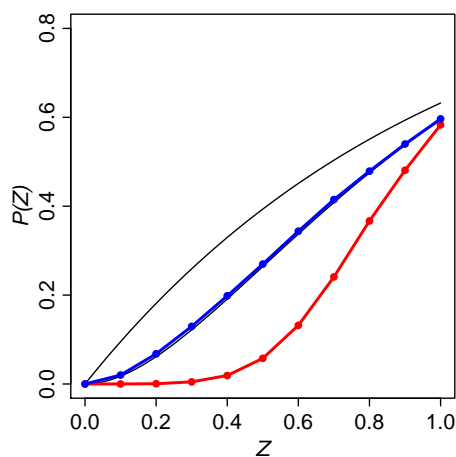
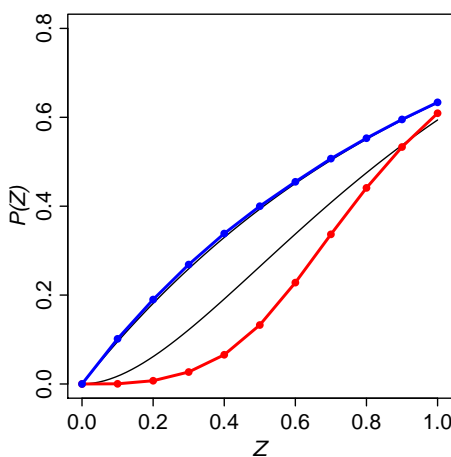
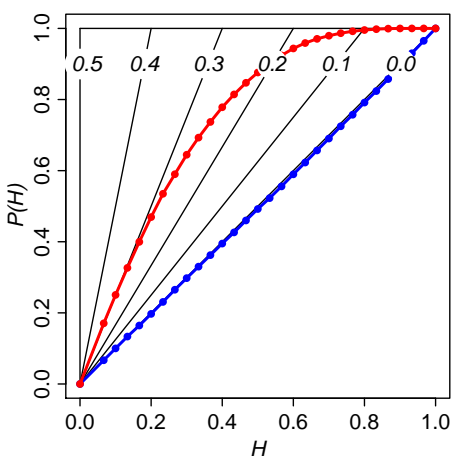
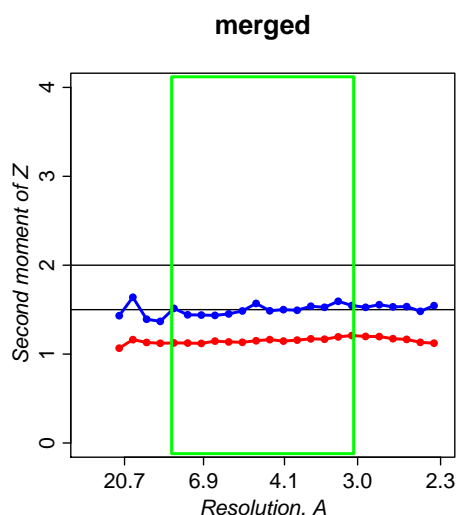
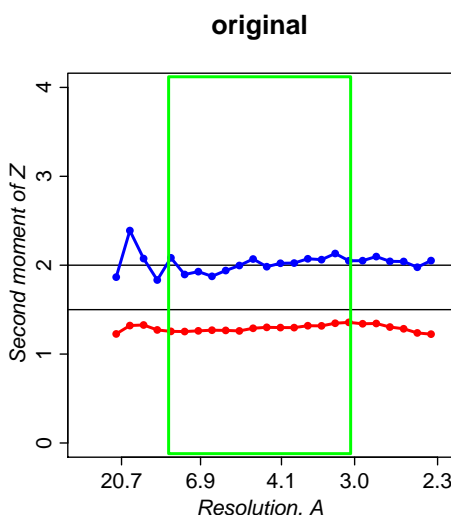
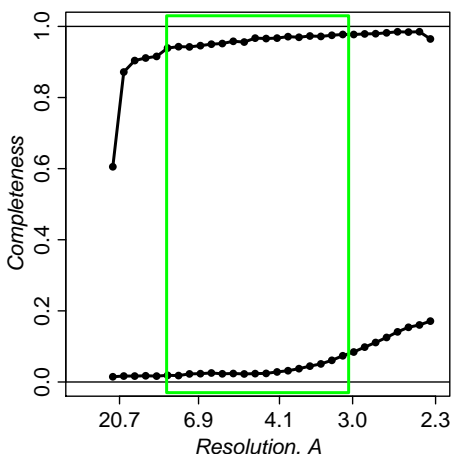
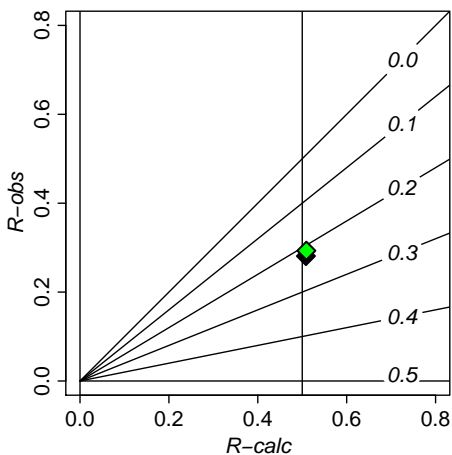
1fv3

	original	merged
s.g.	P 1 2 1 1	P 2 1 2 1 2
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		26.33
R	28.0	
R'	-	-
R-free	31.8	
R'-free	-	-
residues per monomer	DNA 0	protein 451

s < f/100	440	0.89 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.9–2.3	9.9–3.0
unique	51,011	22,475
measured	49,640	21,743
used	45,308	19,456

NCS	translation	rotation
r.m.s.d. (A)	44.23	13.73
angle (o)	168.24	43.47



1fx9

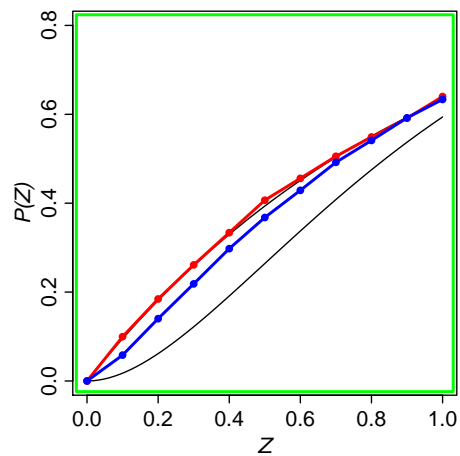
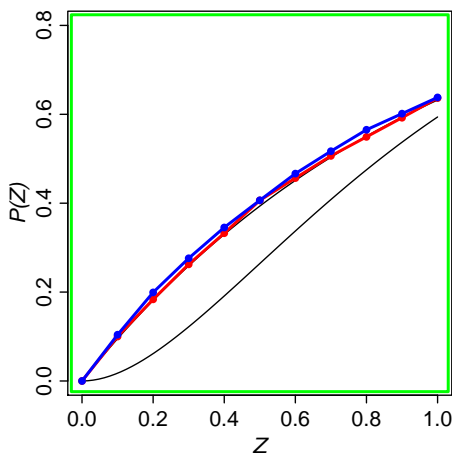
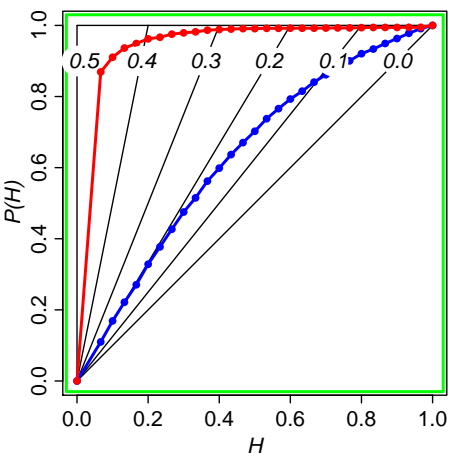
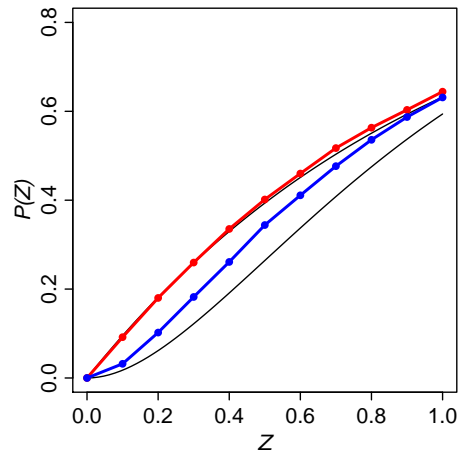
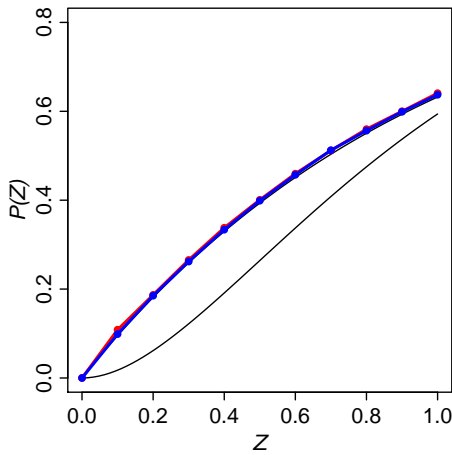
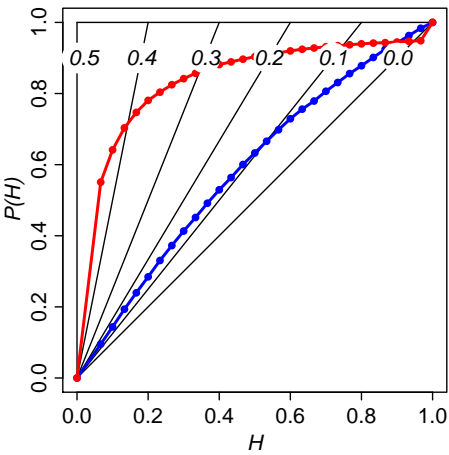
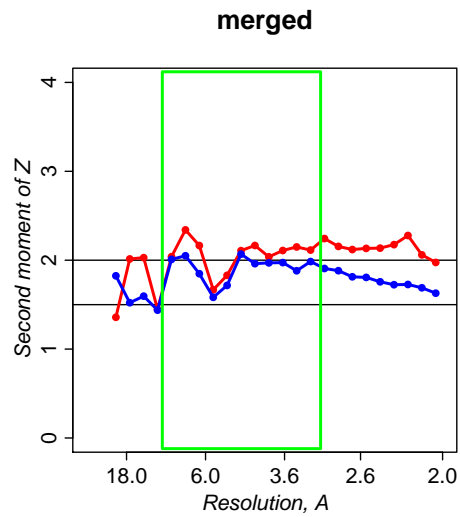
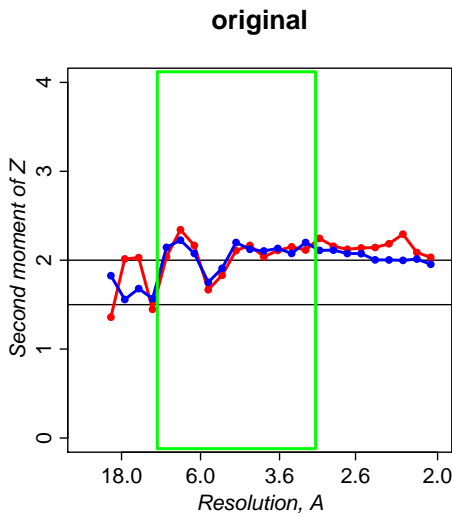
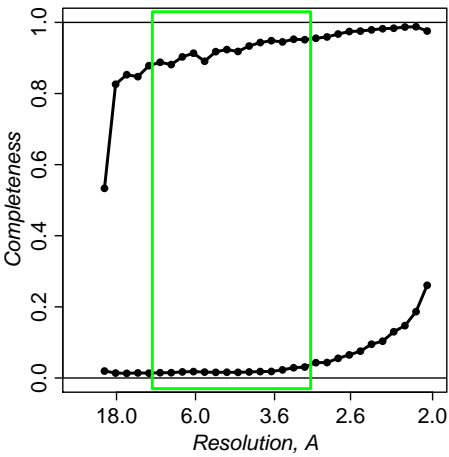
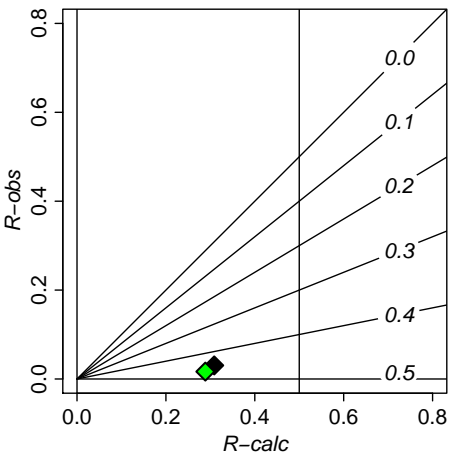
	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.39
R	27.4	
R'	27.7	28.4
R-free	29.3	
R'-free	27.8	29.6

residues per monomer	DNA	protein
	0	124

s < f/100	400	2.06 %
s <= 0	0	0.00 %
f <= 0	752	3.88 %
s,f <= 0	0	0.00 %

range (A)	translation	rotation
32.5–2.0	9.9–3.0	
unique	20,104	5,760
measured	19,386	5,388
used	18,010	4,846

NCS	translation	rotation
r.m.s.d. (A)	23.51	0.39
angle (o)	179.83	0.23



1fxf

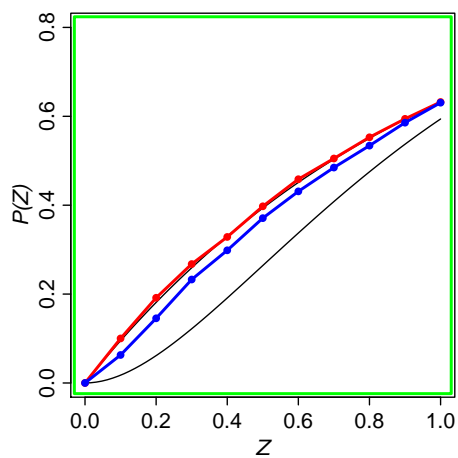
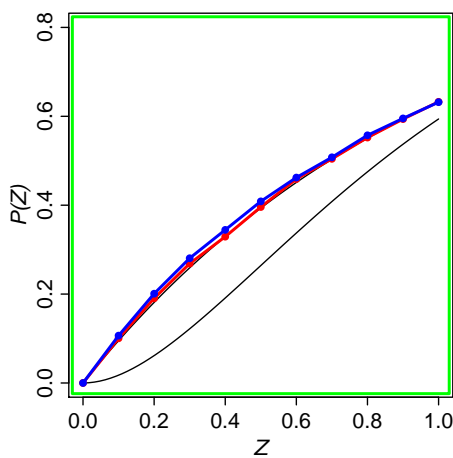
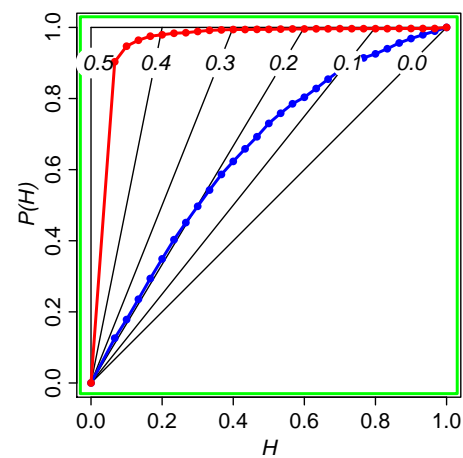
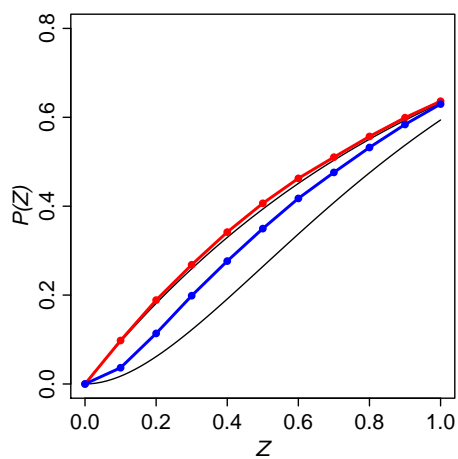
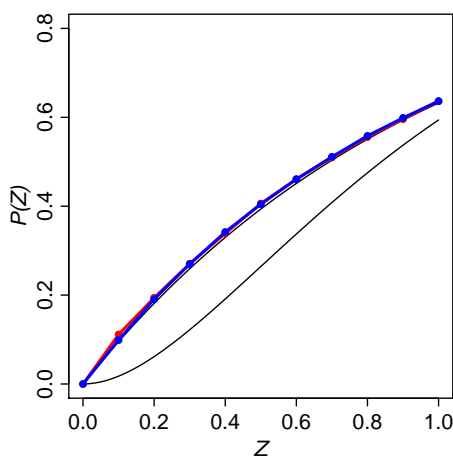
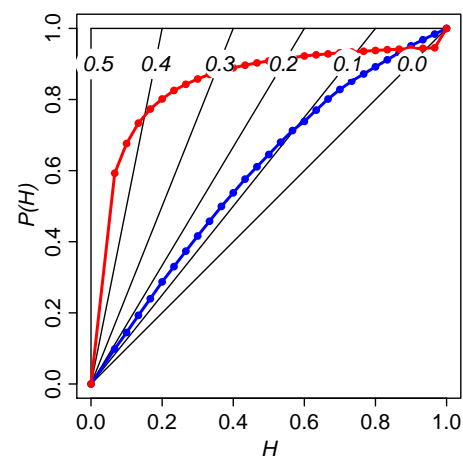
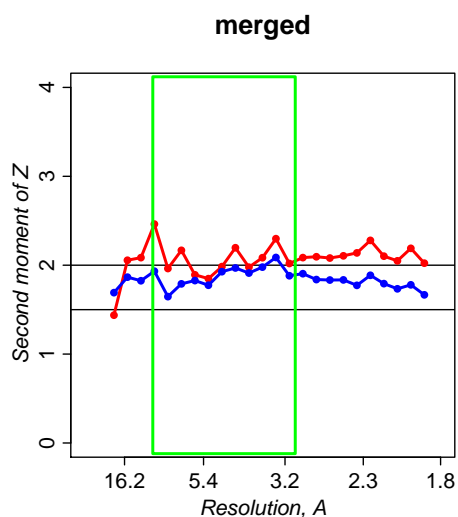
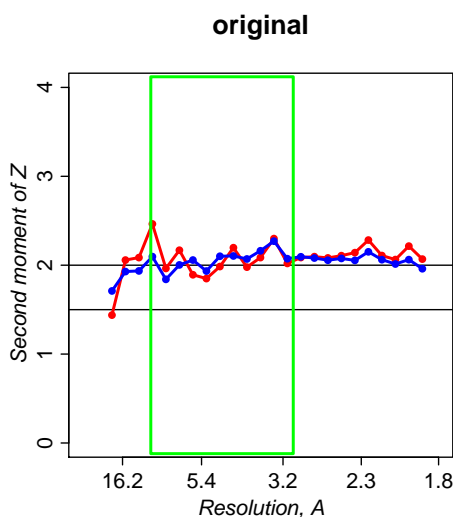
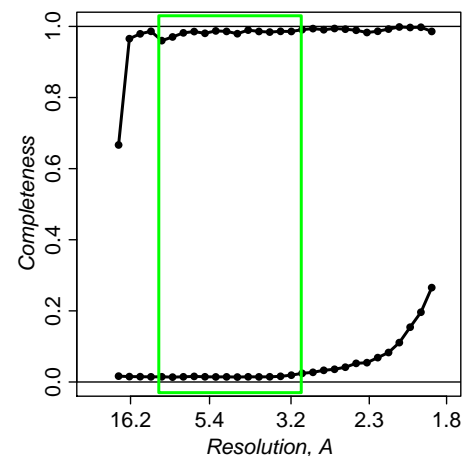
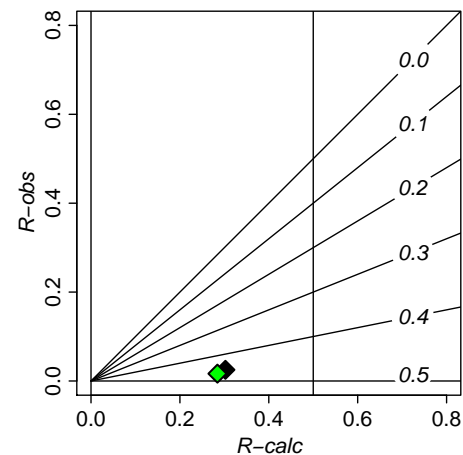
	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.33
R	28.0	
R'	28.5	29.4
R-free	31.5	
R'-free	32.7	33.8

s < f/100	613	2.44 %
s <= 0	0	0.00 %
f <= 0	975	3.88 %
s,f <= 0	0	0.00 %

range (A)	28.9–1.8	9.9–3.0
unique	25,367	5,768
measured	25,119	5,681
used	23,338	5,078

NCS	translation	rotation
r.m.s.d. (A)	21.93	0.33
angle (o)	179.84	0.31

residues per monomer	DNA	protein
	0	124



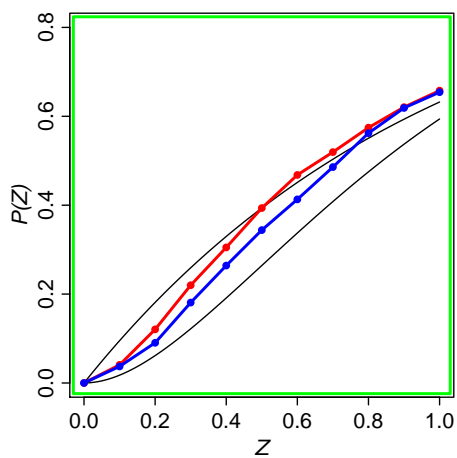
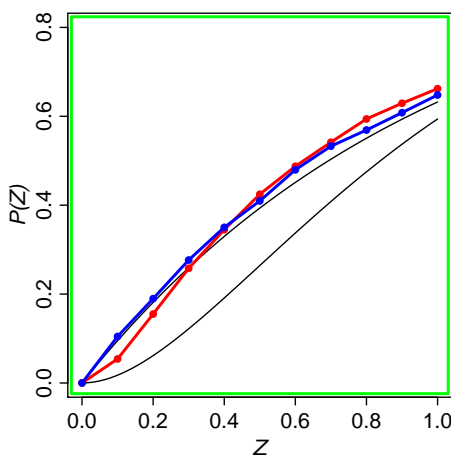
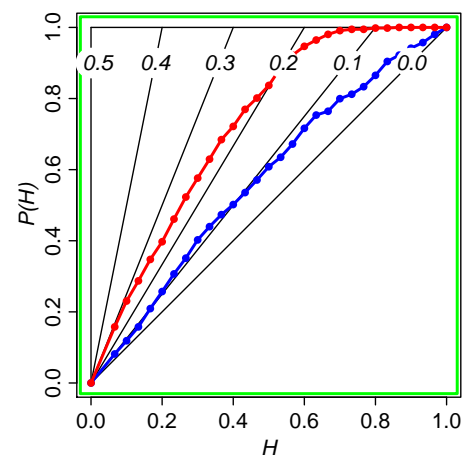
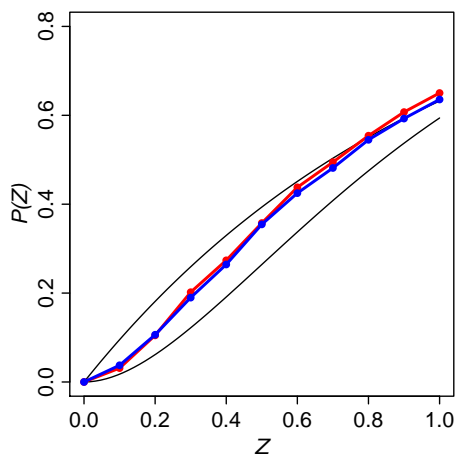
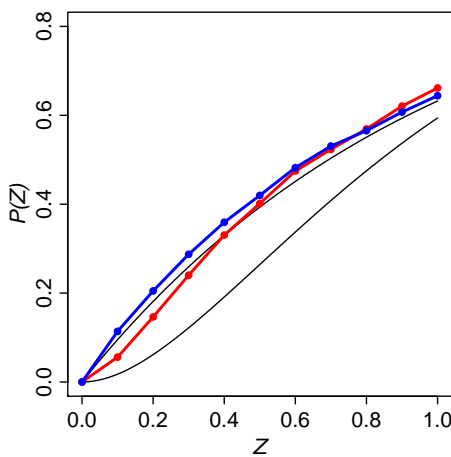
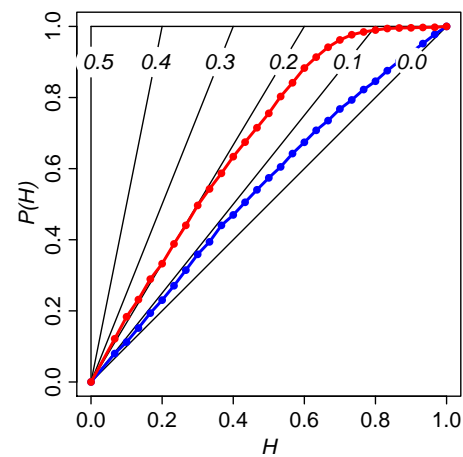
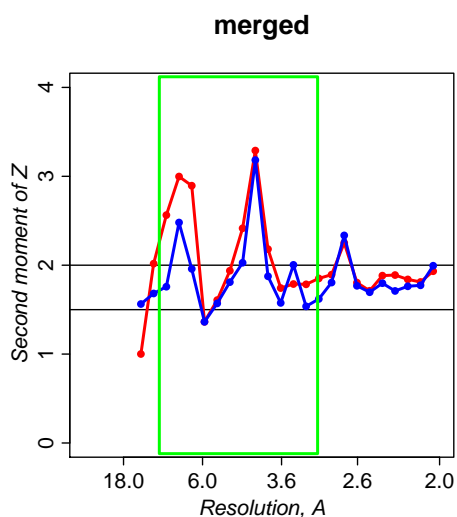
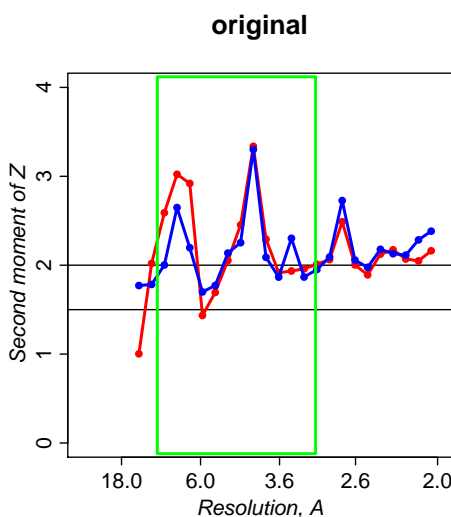
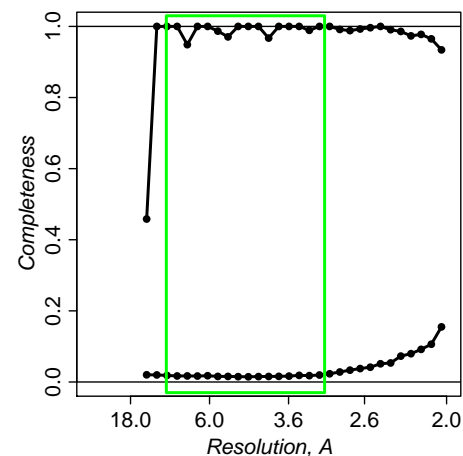
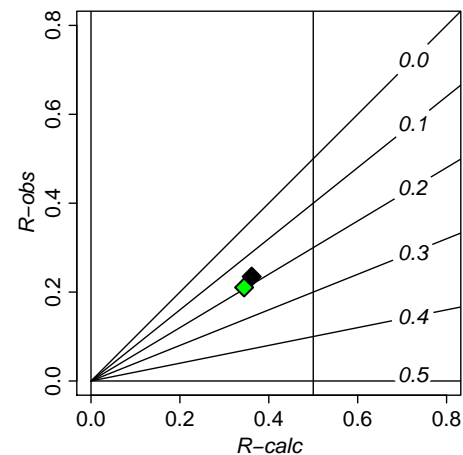
1g1i

	original	merged
s.g.	P 21 21 2	P 4 21 2
p.g.	10003	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.82
R	28.0	
R'	31.0	32.9
R-free	33.2	
R'-free	36.1	39.8
residues per monomer	DNA 0	protein 43

s < f/100	76	1.39 %
s <= 0	76	1.39 %
f <= 0	76	1.39 %
s,f <= 0	76	1.39 %

range (A)	14.1–2.0	9.9–3.0
unique	5,543	1,681
measured	5,450	1,670
used	4,100	1,126

NCS	translation	rotation
r.m.s.d. (A)	7.52	0.74
angle (o)	81.15	9.08



1g39

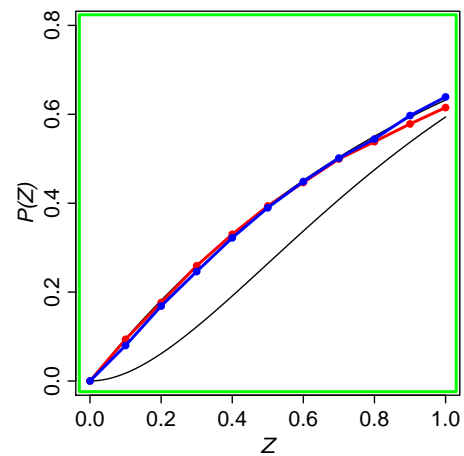
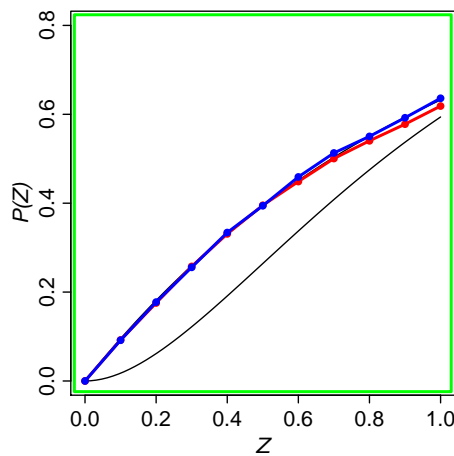
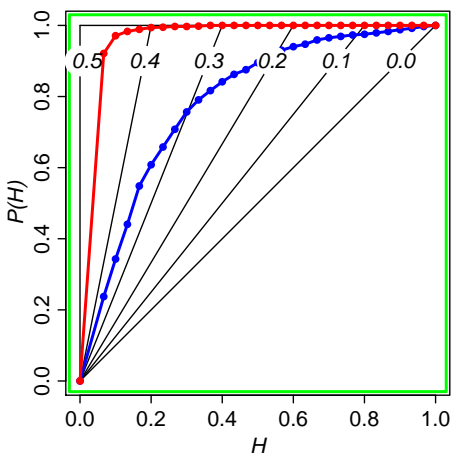
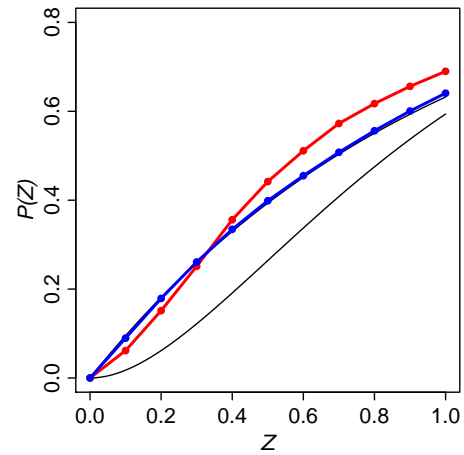
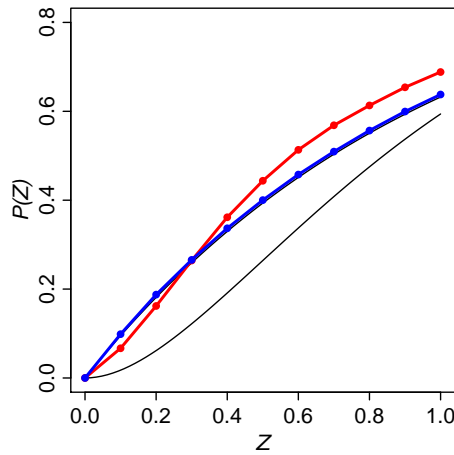
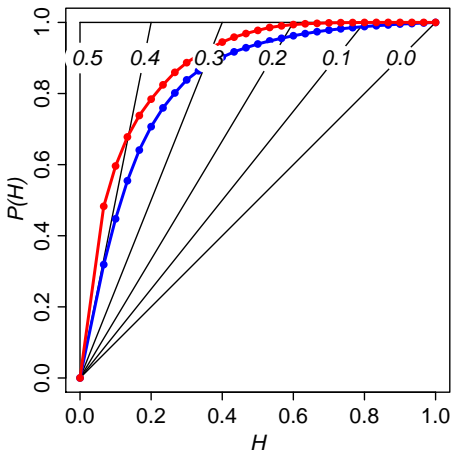
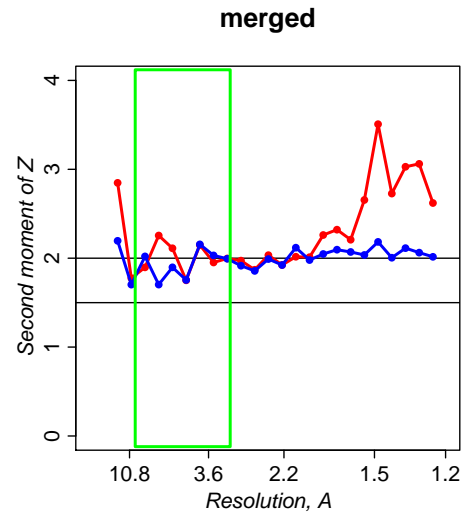
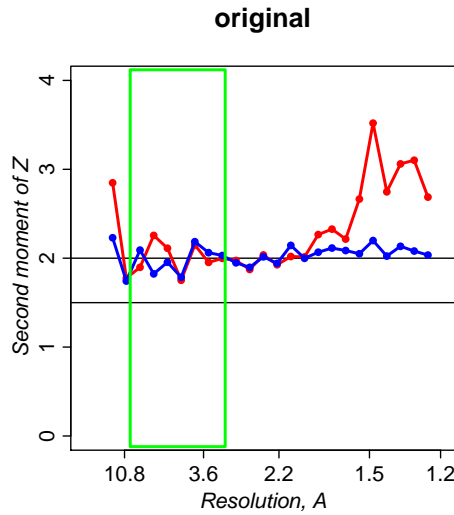
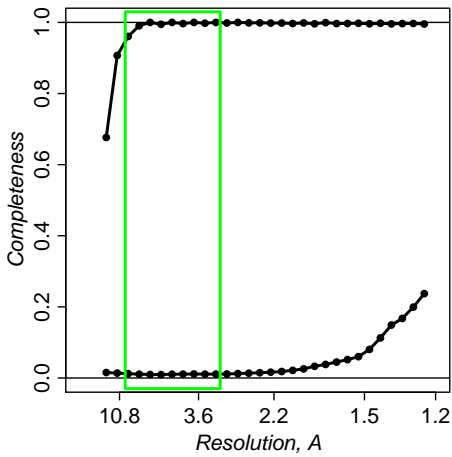
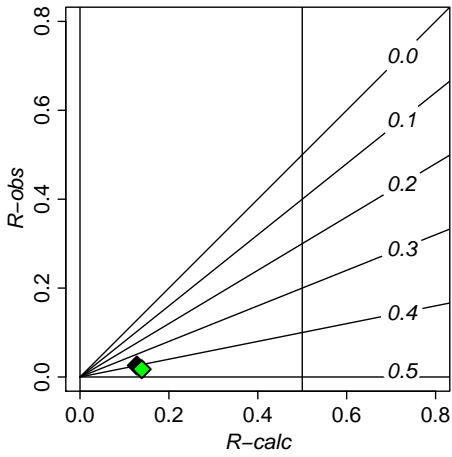
	original	merged
s.g.	P 1 21 1	P 21 21 2
p.g.	10001	10003
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.27
R	37.0	
R'	37.3	37.8
R-free	34.5	
R'-free	34.1	34.7

residues per monomer	DNA	protein
	0	27

s < f/100	1804	4.90 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	20.6–1.2	9.9–3.0
unique	36,912	2,496
measured	36,802	2,489
used	33,386	1,994

NCS	translation	rotation
r.m.s.d. (A)	11.31	0.12
angle (o)	83.23	0.06



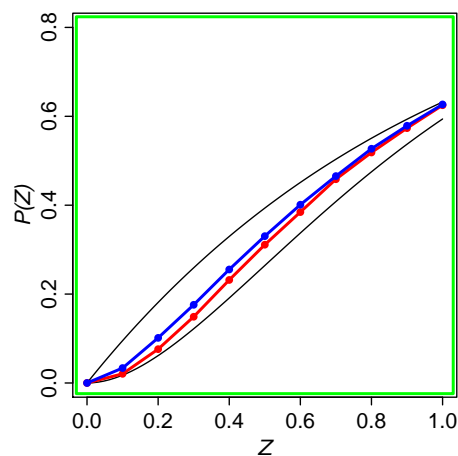
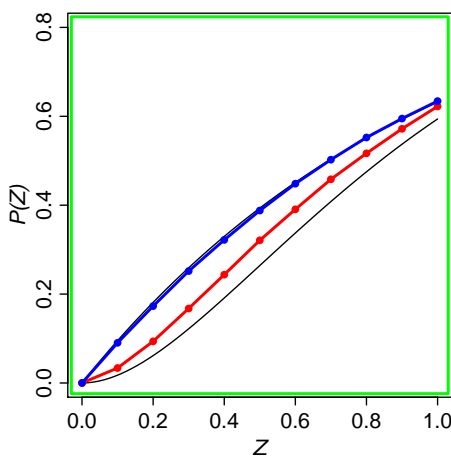
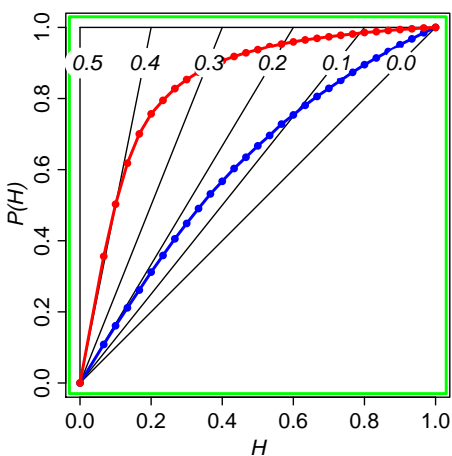
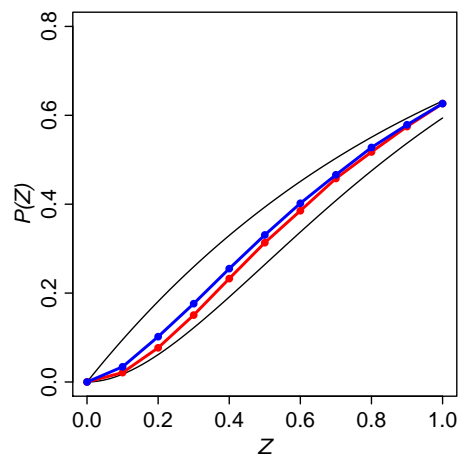
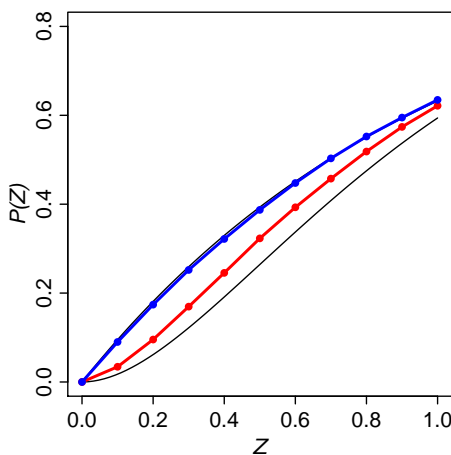
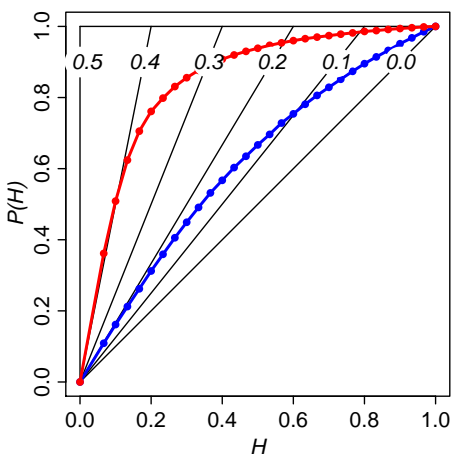
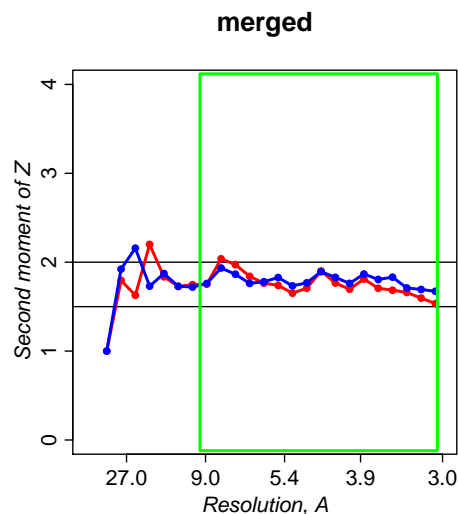
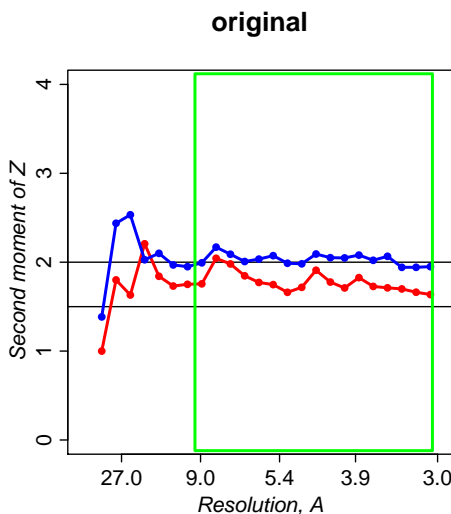
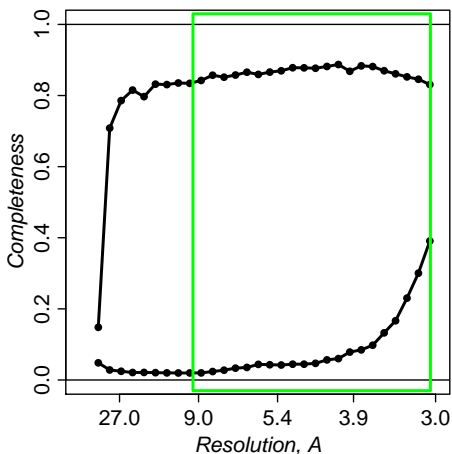
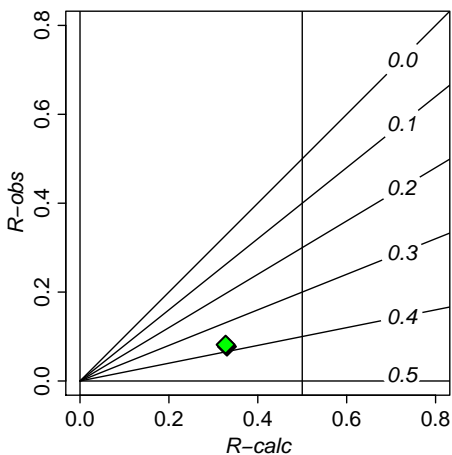
1g4a

	original	merged
s.g.	P 3 2 1	-
p.g.	10023	12027
a.u.	2	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	39.2	-
R'	-	-
R-free	44.2	-
R'-free	-	-
residues per monomer	DNA 0	protein 356

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	85.0-3.0	9.9-3.0
unique	53,962	52,320
measured	46,550	45,218
used	40,610	39,652

NCS	translation	rotation
r.m.s.d. (A)	18.58	0.80
angle (o)	59.94	0.39



1g4b

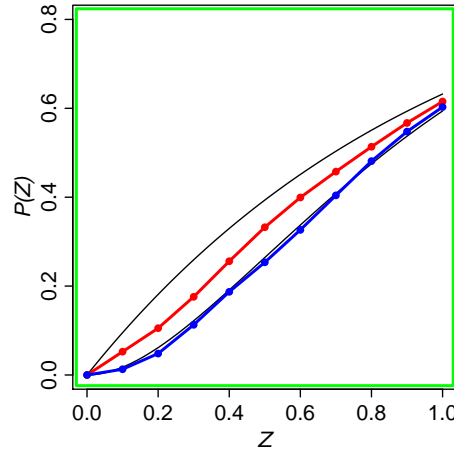
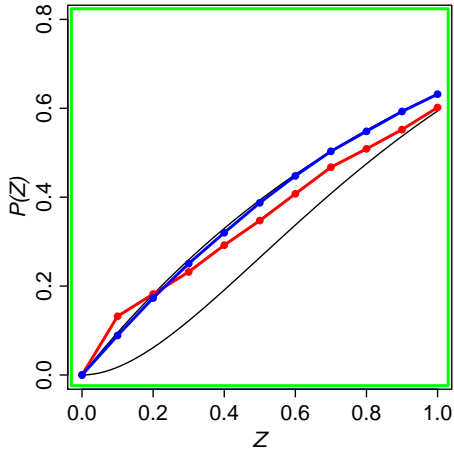
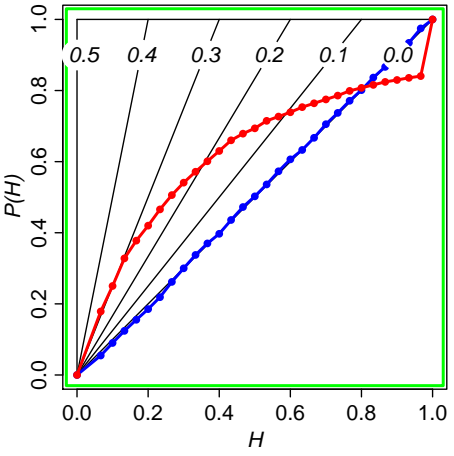
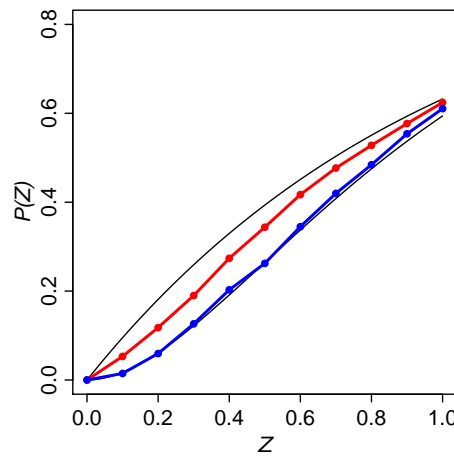
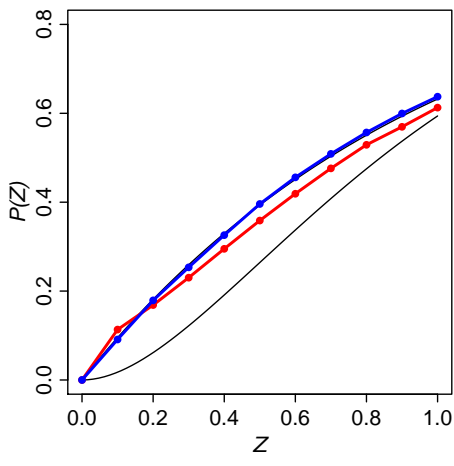
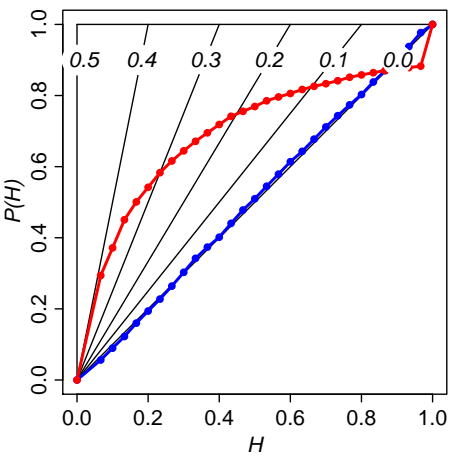
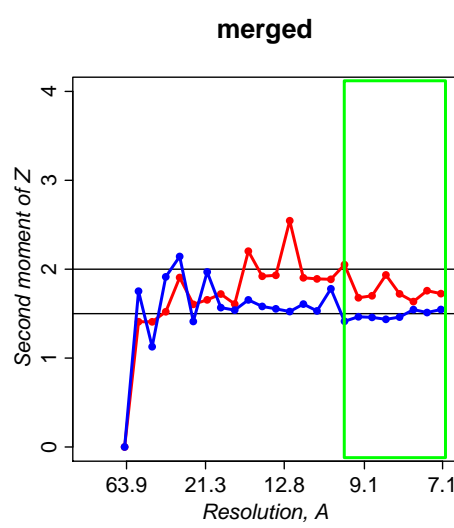
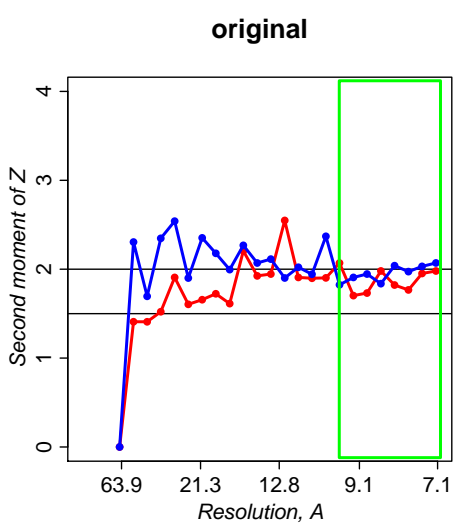
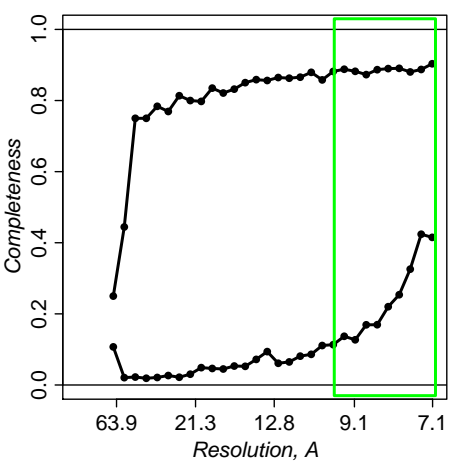
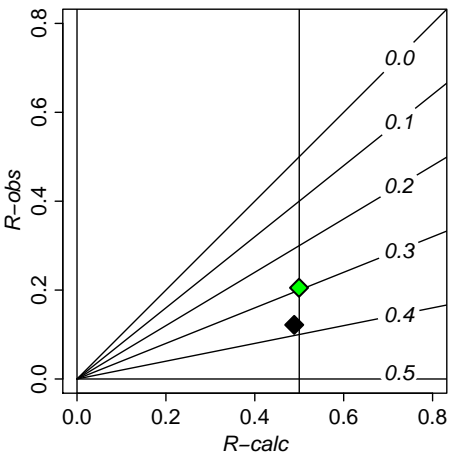
	original	merged
s.g.	P 3 2 1	-
p.g.	10023	12027
a.u.	4	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	34.9	-
R'	-	-
R-free	52.2	-
R'-free	-	-

residues per monomer	DNA	protein
	0	393

s < f/100	4	0.06 %
s <= 0	0	0.00 %
f <= 0	439	6.85 %
s,f <= 0	0	0.00 %

range (A)	82.1-7.0	9.9-7.0
unique	7,347	4,651
measured	6,405	4,125
used	4,940	3,306

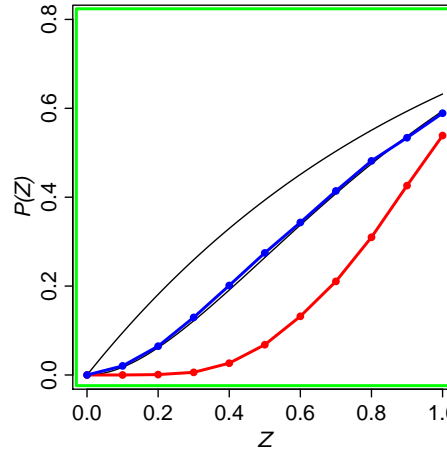
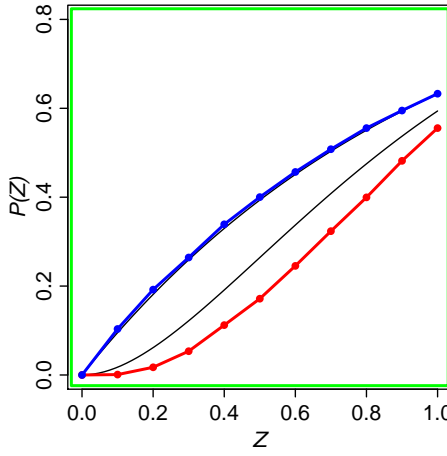
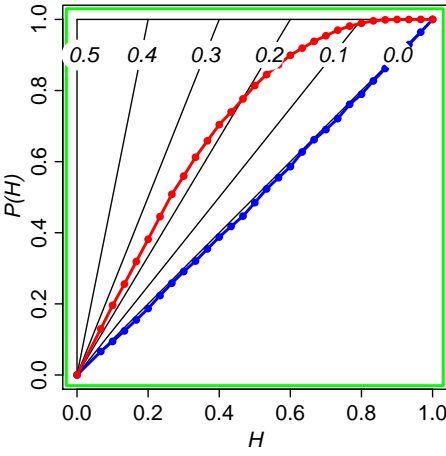
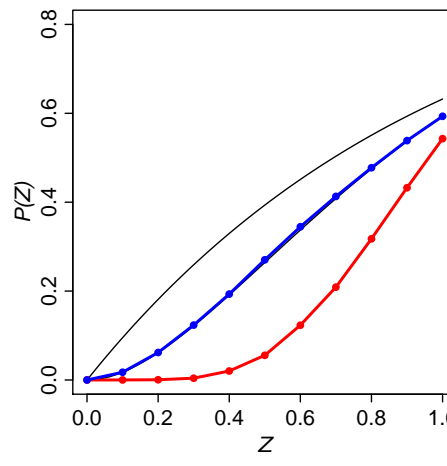
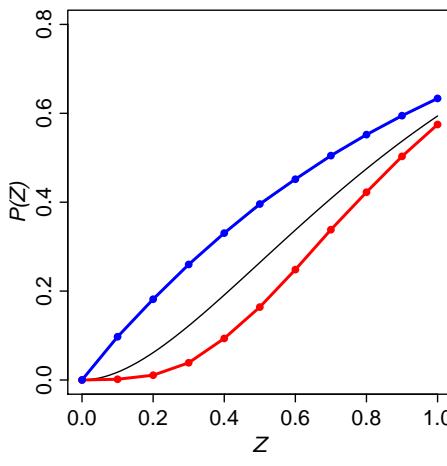
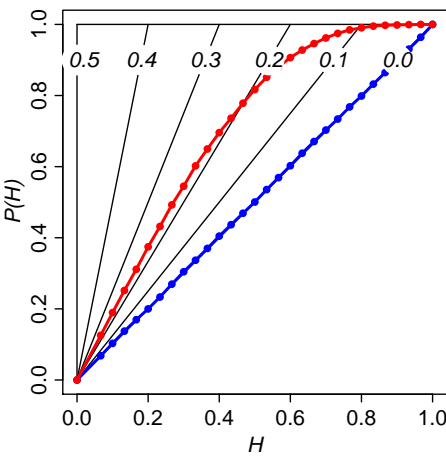
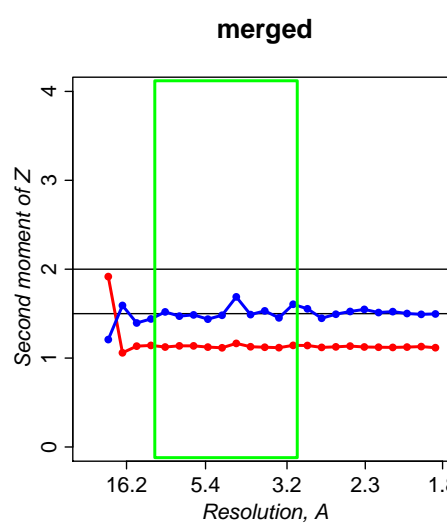
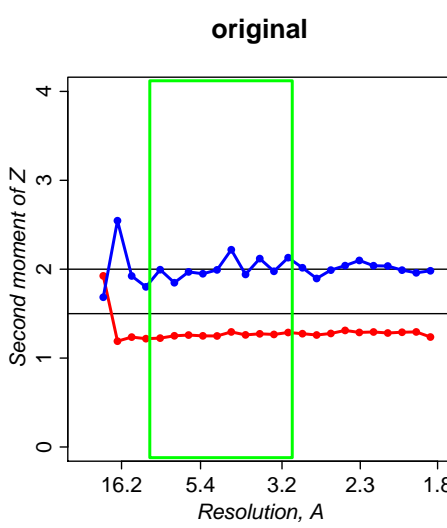
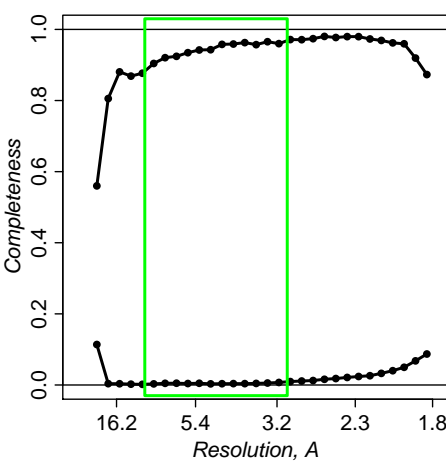
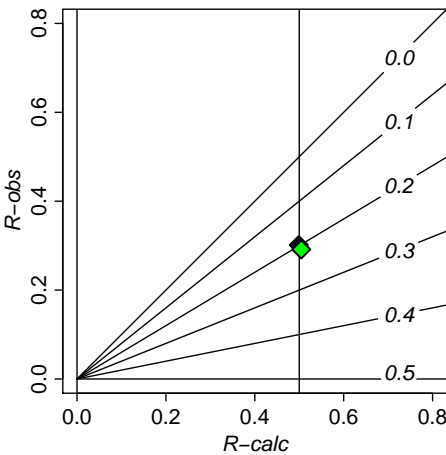
NCS	translation	rotation
r.m.s.d. (A)	3.33	1.02
angle (o)	10.18	1.88



1g7f

	original	merged
s.g.	P 21 21 21	-
p.g.	10003	10205
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	30.1	-
R'	-	-
R-free	31.2	-
R'-free	-	-
residues per monomer	DNA 0	protein 297

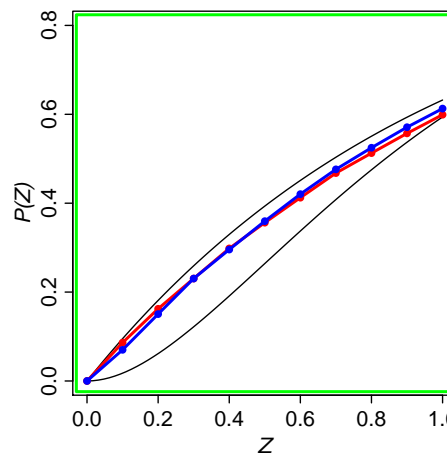
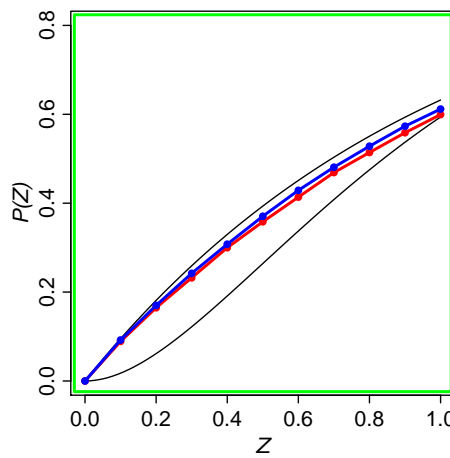
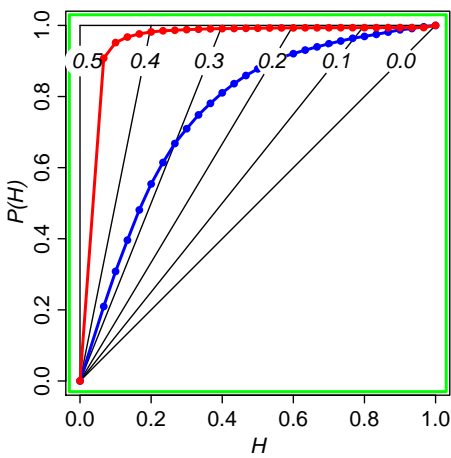
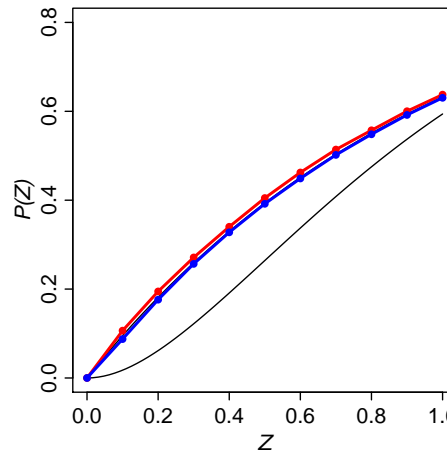
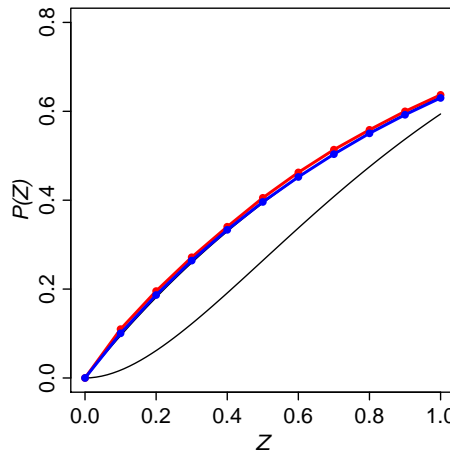
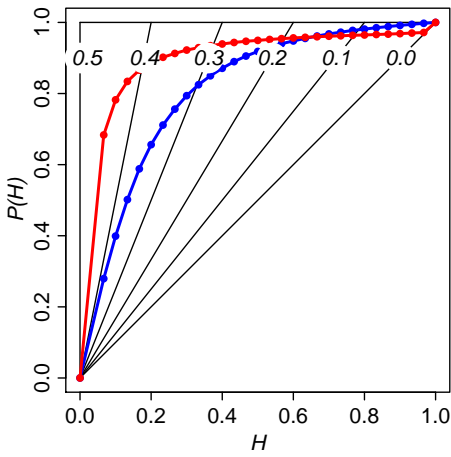
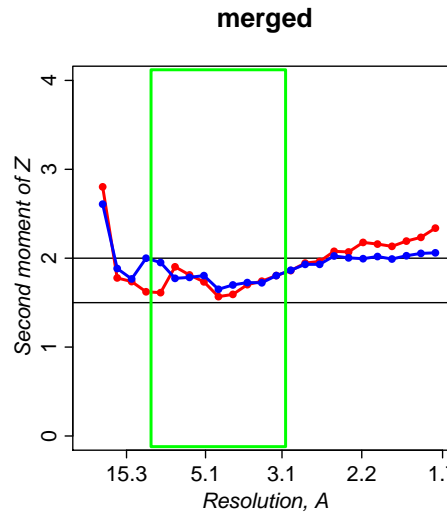
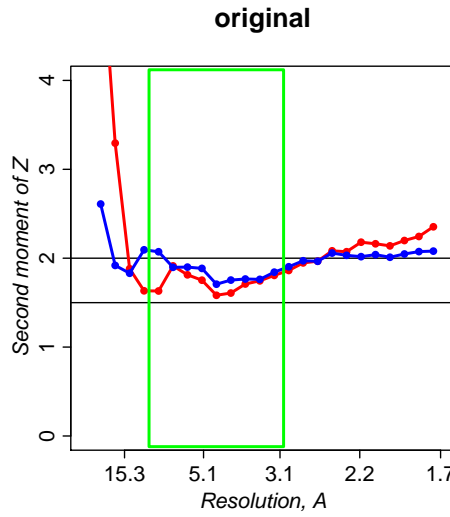
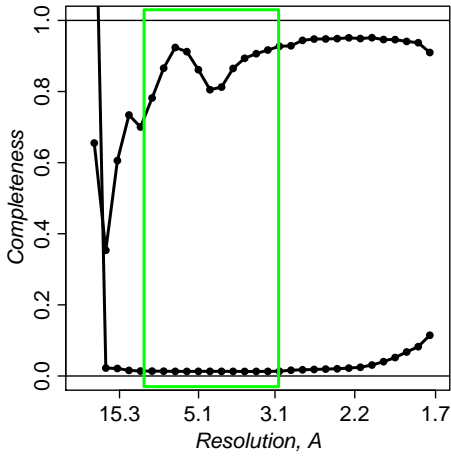
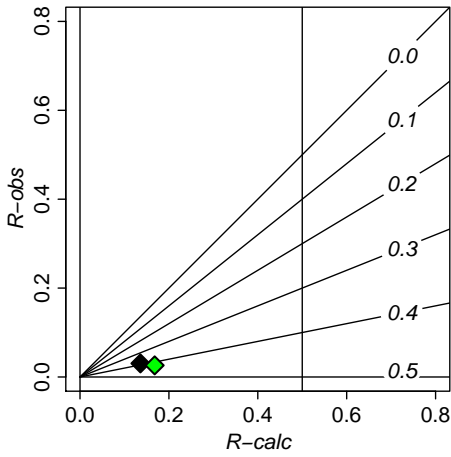
s < f/100	14855	41.89 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	45.3-1.8	9.9-3.0
unique	37,202	8,061
measured	35,465	7,682
used	29,740	6,446
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1gc0

	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.13
R	26.3	
R'	26.6	26.8
R-free	28.6	
R'-free	28.8	29.1
residues per monomer	DNA 0	protein 353

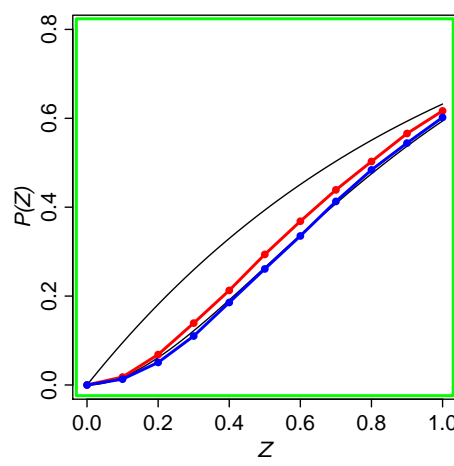
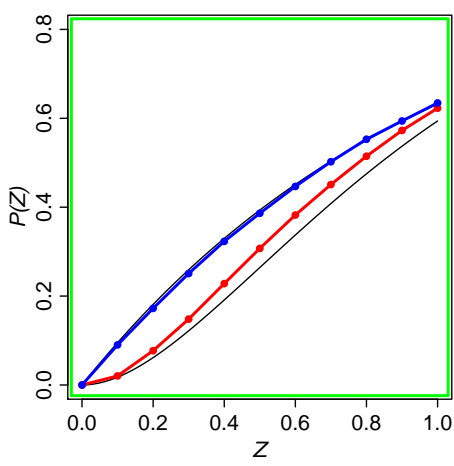
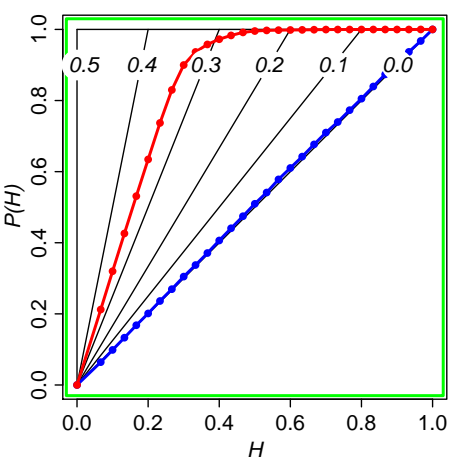
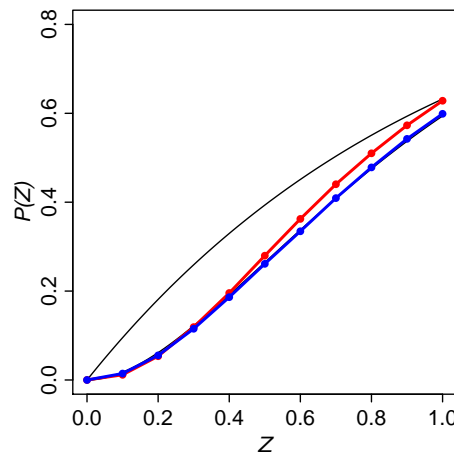
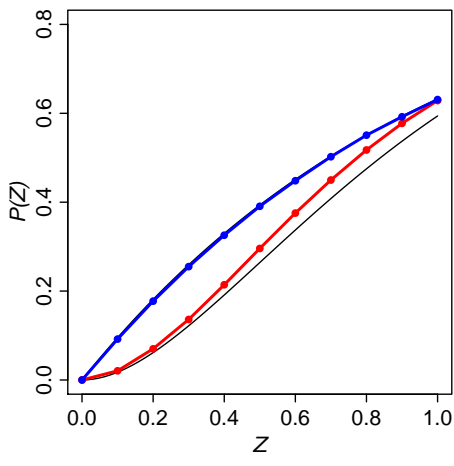
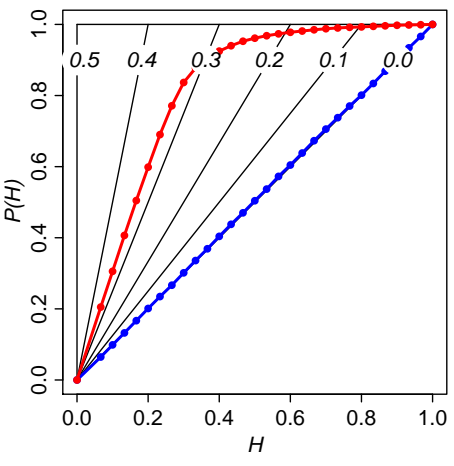
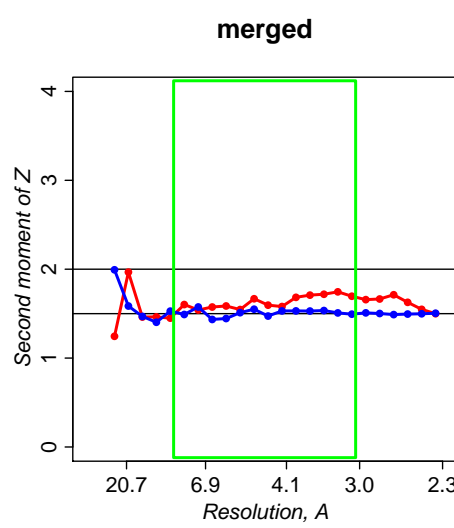
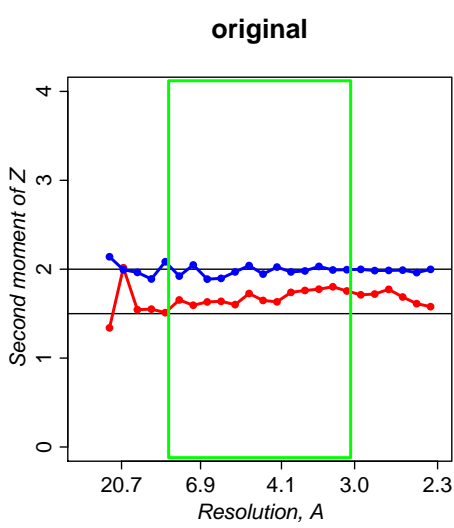
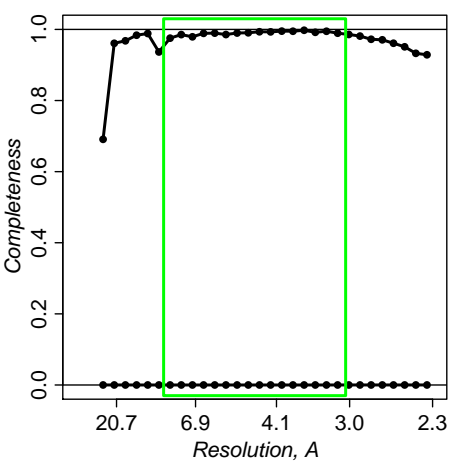
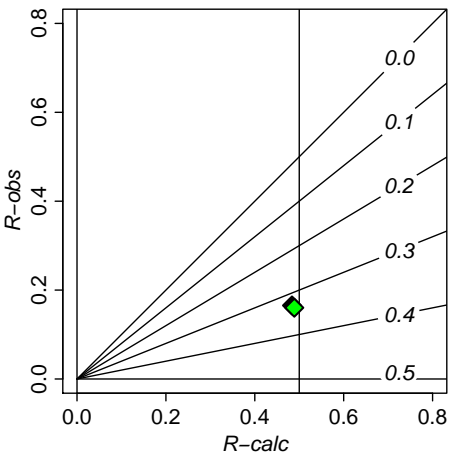
s < f/100	2370	1.58 %
s <= 0	0	0.00 %
f <= 0	2829	1.89 %
s,f <= 0	0	0.00 %
range (A)	71.6–1.7	9.9–3.0
unique	161,009	28,464
measured	149,546	25,093
used	138,374	22,724
NCS	translation	rotation
r.m.s.d. (A)	31.32	0.12
angle (o)	179.99	0.02



1gd8

	original	merged
s.g.	P 41	-
p.g.	10201	10205
a.u.	9	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	29.1	-
R'	-	-
R-free	31.7	-
R'-free	-	-
residues per monomer	DNA 0	protein 105

s < f/100	65159	100.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	40.0-2.3	9.9-3.0
unique	67,076	29,491
measured	65,159	29,238
used	59,304	26,528
NCS	translation	rotation
r.m.s.d. (A)	1.08	0.58
angle (o)	5.44	2.12



1gwy

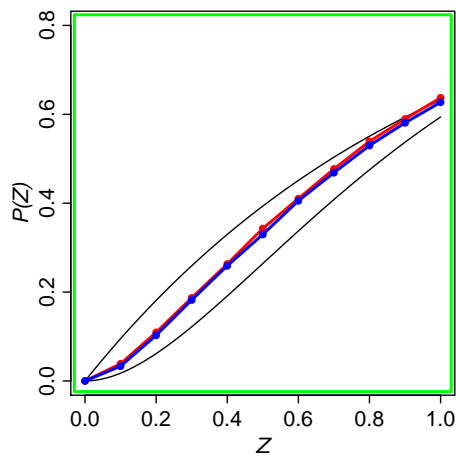
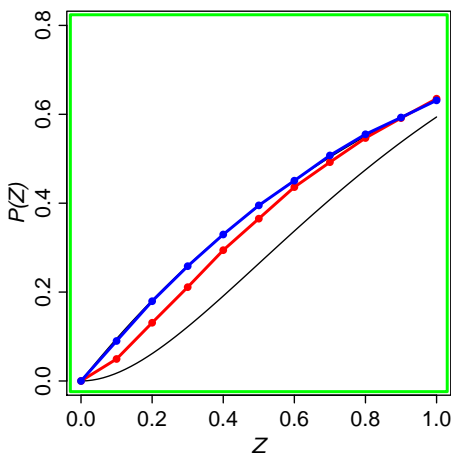
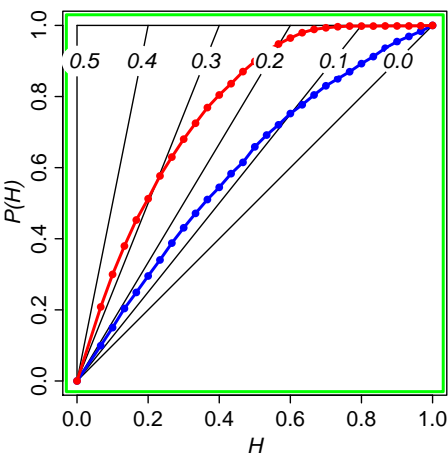
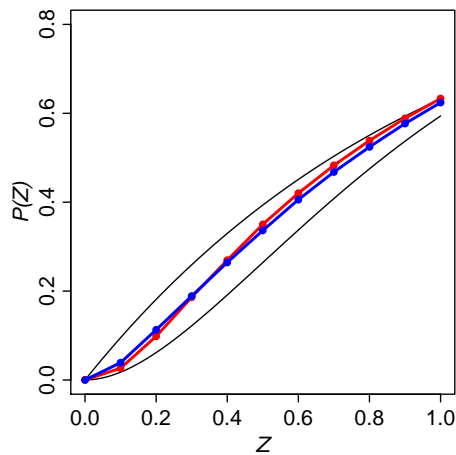
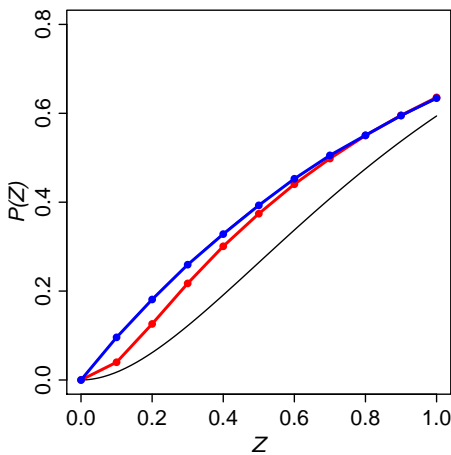
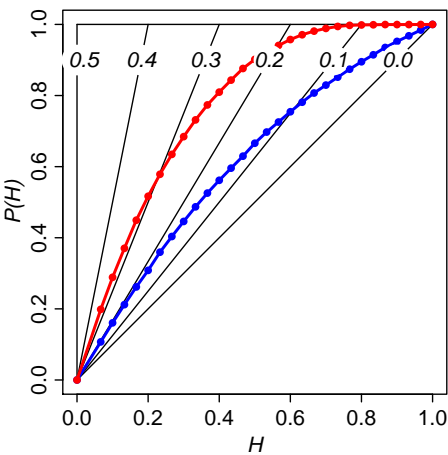
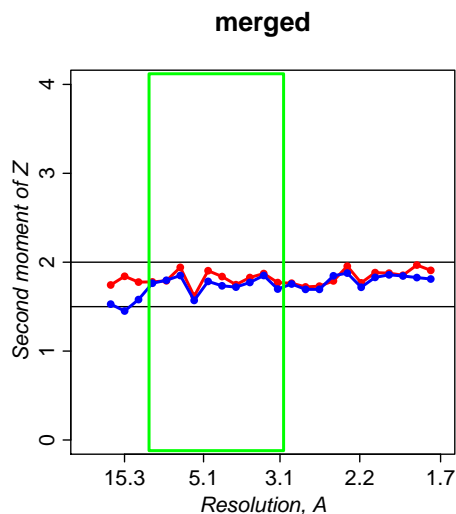
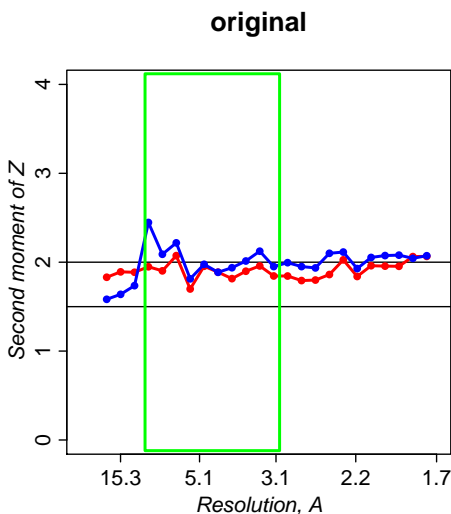
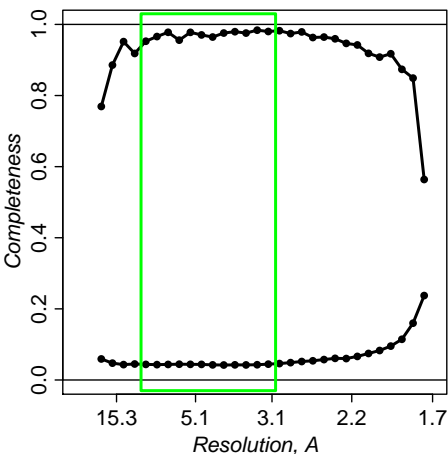
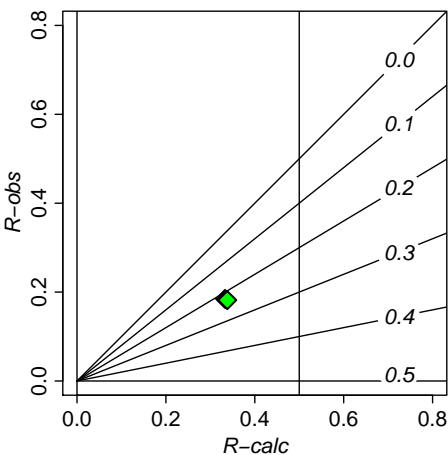
	original	merged
s.g.	P 1 21 1	P 21 21 2
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		2.84
R	27.0	
R'	39.4	38.7
R-free	29.6	
R'-free	41.7	41.4

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	32.3–1.7	9.9–3.0
unique	35,364	6,453
measured	31,855	6,295
used	26,722	5,324

NCS	translation	rotation
r.m.s.d. (A)	23.93	0.25
angle (o)	179.78	0.23

residues per monomer	DNA	protein
	0	175



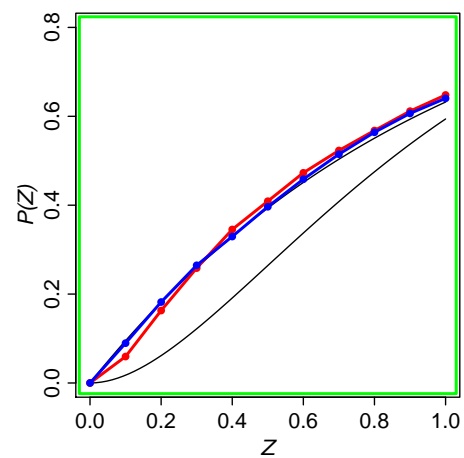
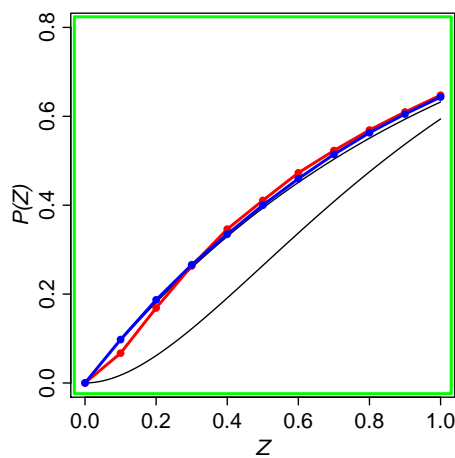
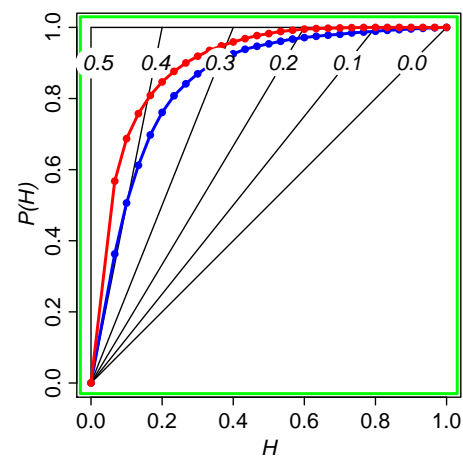
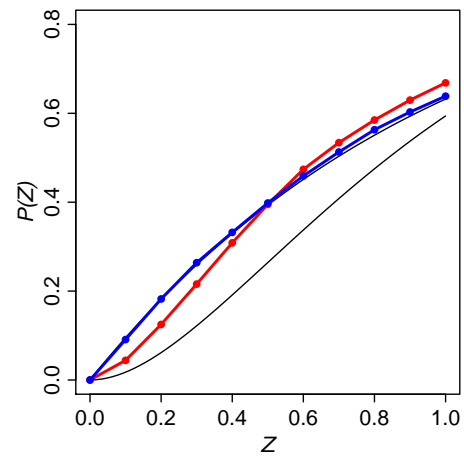
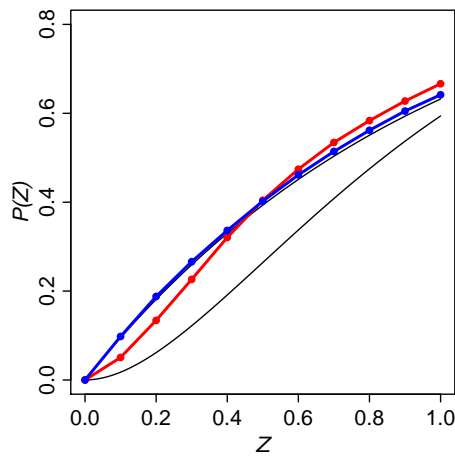
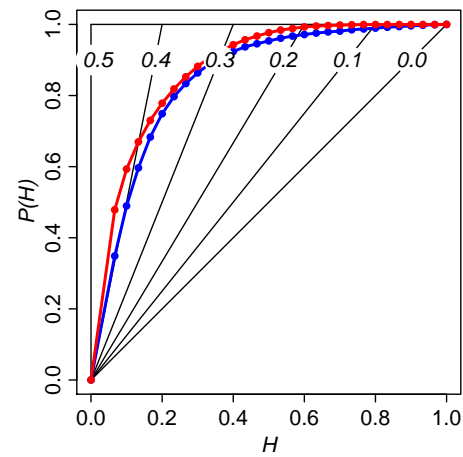
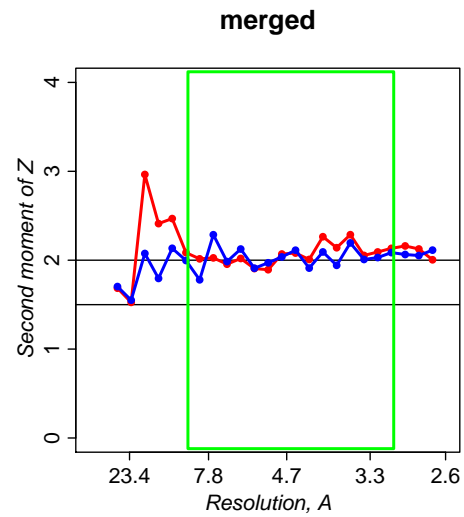
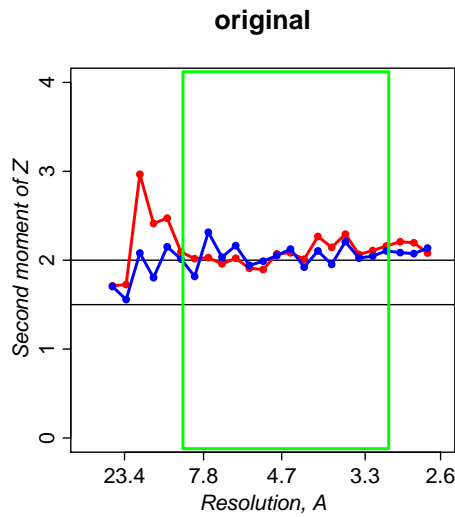
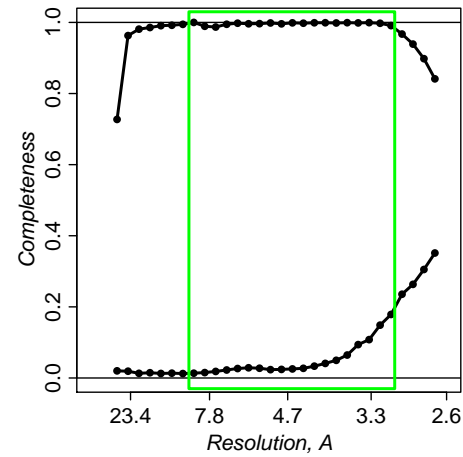
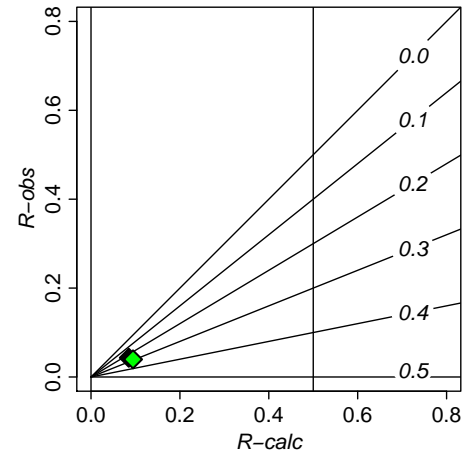
1gzm

	original	merged
s.g.	P 31	P 64
p.g.	10020	12021
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.14
R	23.0	
R'	23.0	23.2
R-free	25.5	
R'-free	25.1	24.7
residues per monomer	DNA 0	protein 328

s < f/100	299	1.15 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	45.0–2.6	9.9–3.0
unique	26,936	17,968
measured	26,063	17,908
used	24,556	17,370

NCS	translation	rotation
r.m.s.d. (A)	19.22	0.14
angle (o)	59.95	0.08



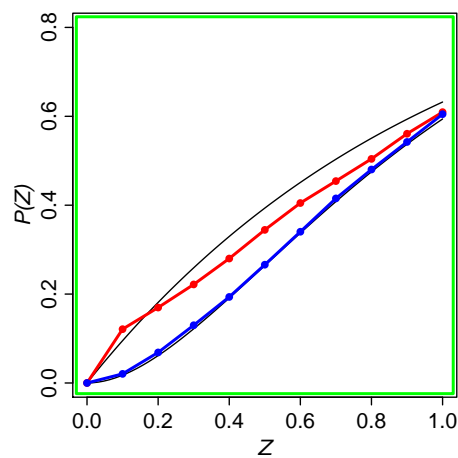
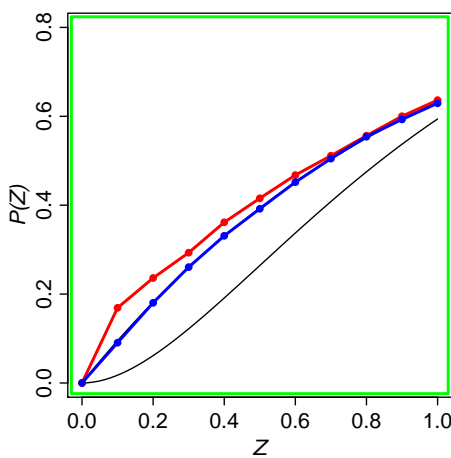
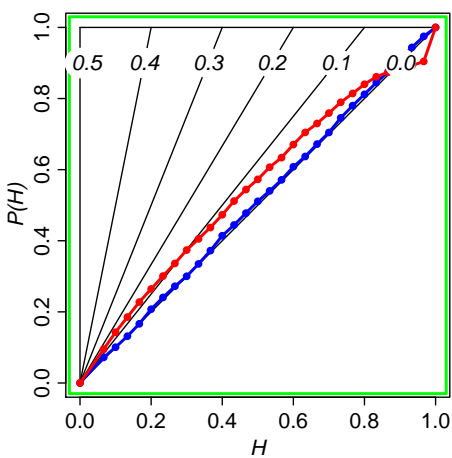
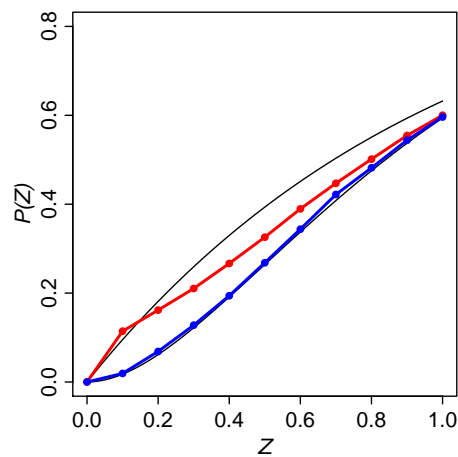
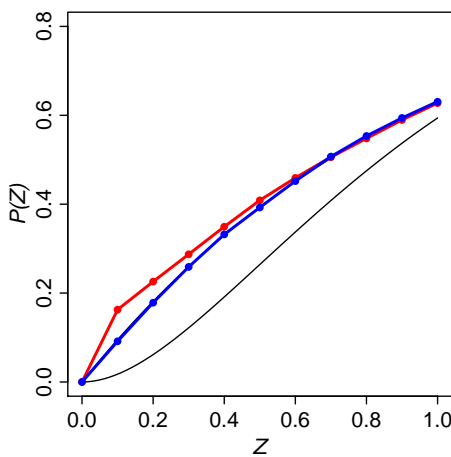
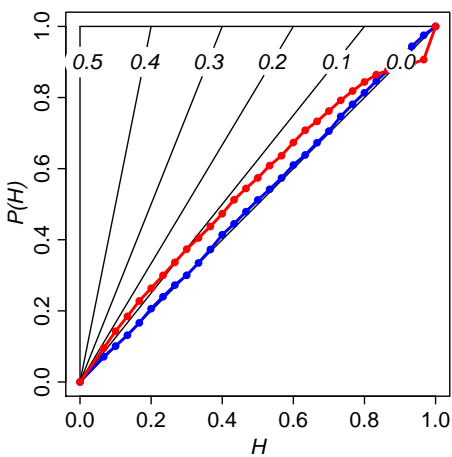
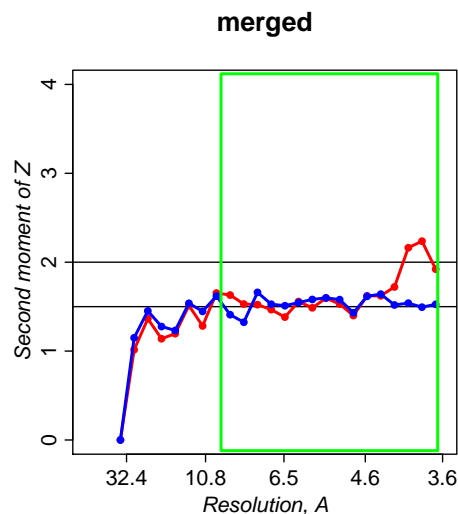
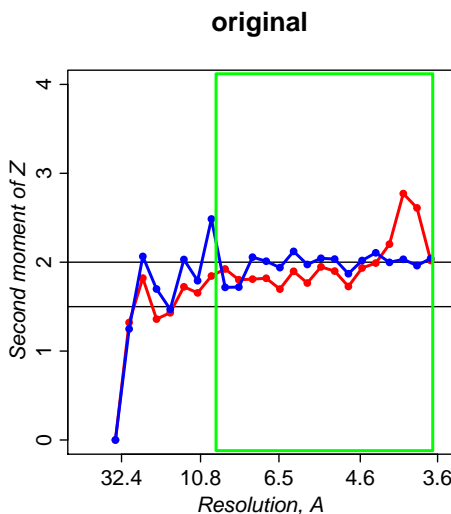
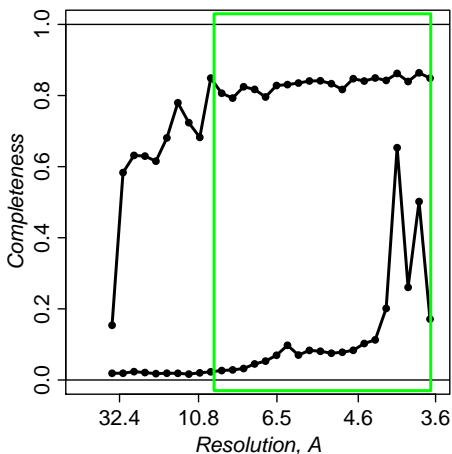
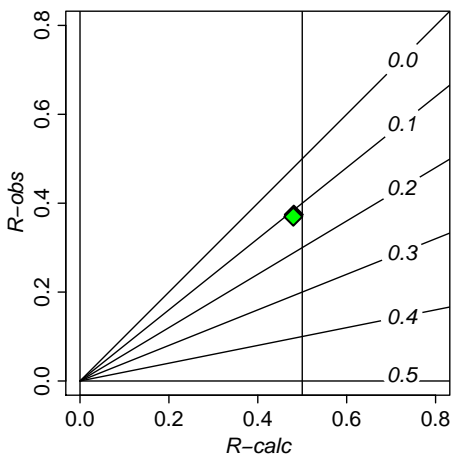
1h6e

	original	merged
s.g.	P 64	-
p.g.	12021	12027
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	26.5	-
R'	-	-
R-free	30.3	-
R'-free	-	-
residues per monomer	DNA 0	protein 229

s < f/100	19	0.28 %
s <= 0	0	0.00 %
f <= 0	714	10.69 %
s,f <= 0	0	0.00 %

range (A)	48.2-3.6	9.9-3.6
unique	8,022	7,612
measured	6,680	6,396
used	4,898	4,730

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1h9m

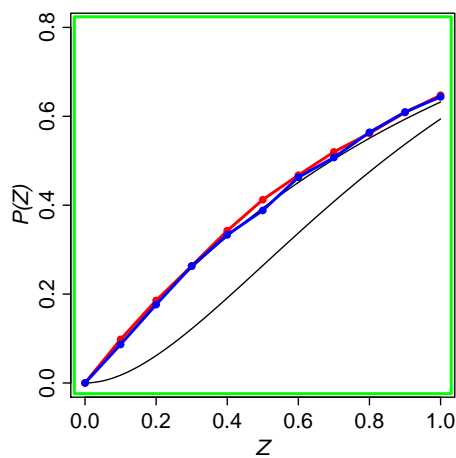
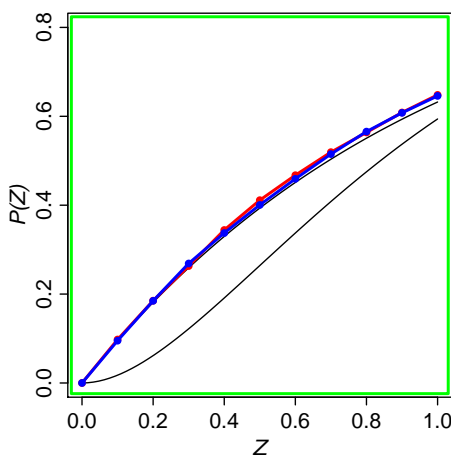
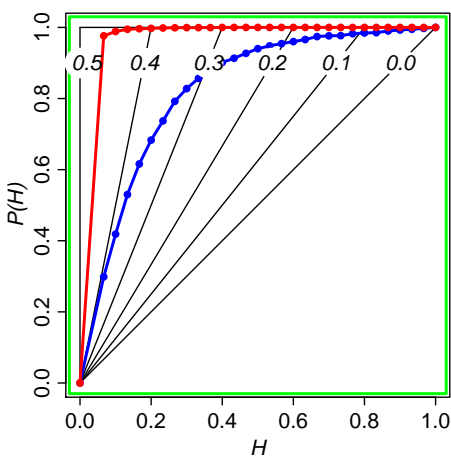
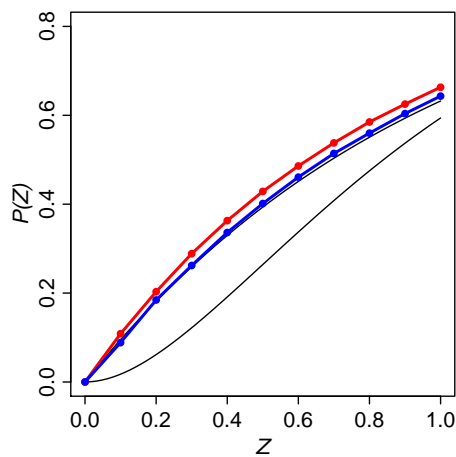
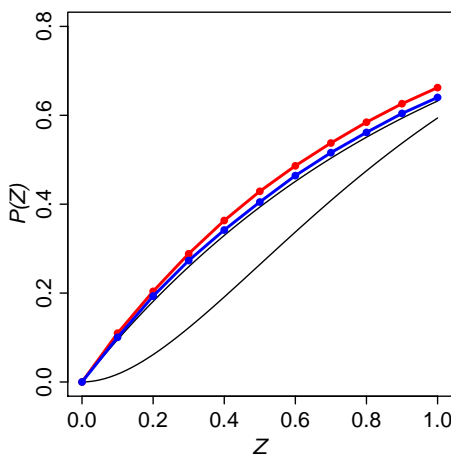
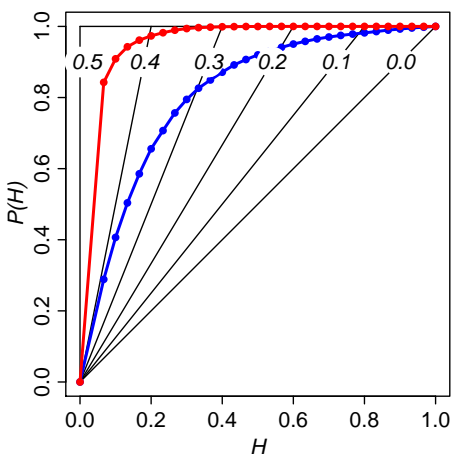
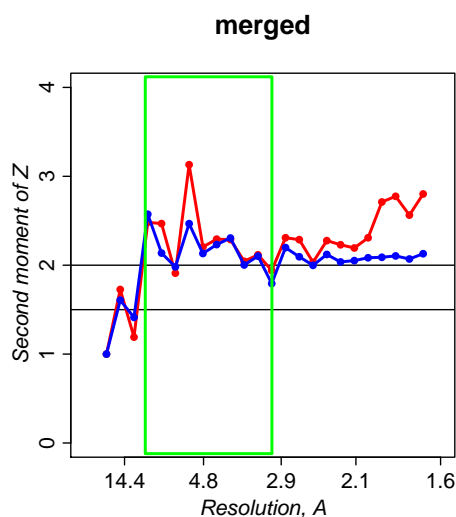
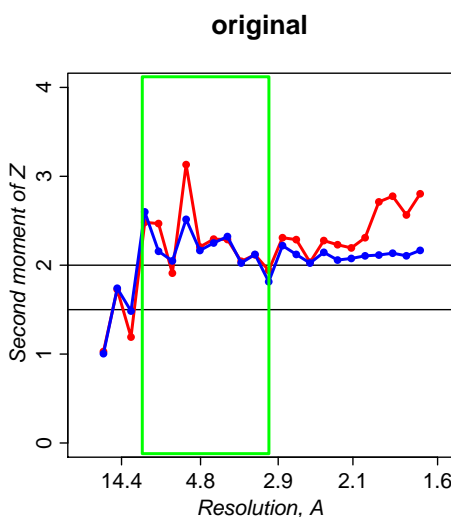
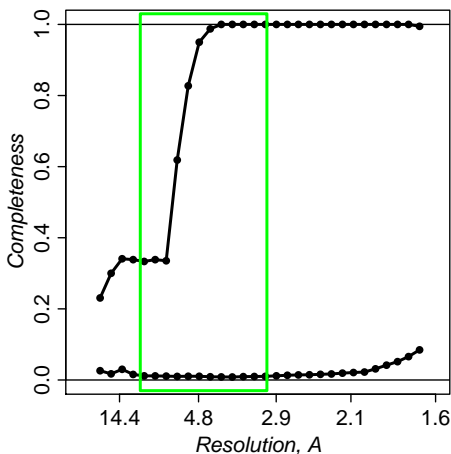
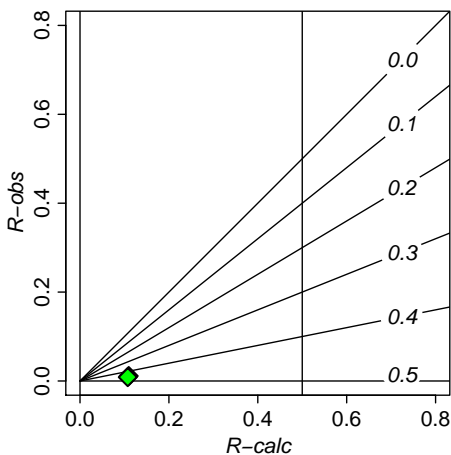
	original	merged
s.g.	H 3	H 3 2
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.22
R	33.2	
R'	33.5	34.1
R-free	37.2	
R'-free	36.3	36.4

residues per monomer	DNA	protein
	0	141

s < f/100	3351	12.09 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	39.0–1.6	9.9–3.0
unique	28,241	4,553
measured	27,725	4,137
used	26,474	3,804

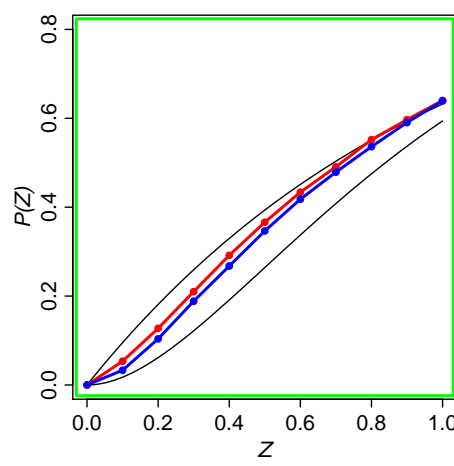
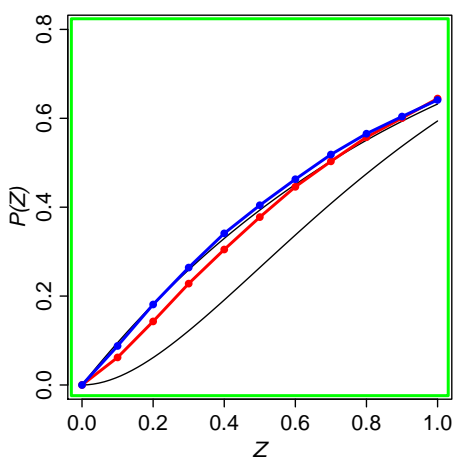
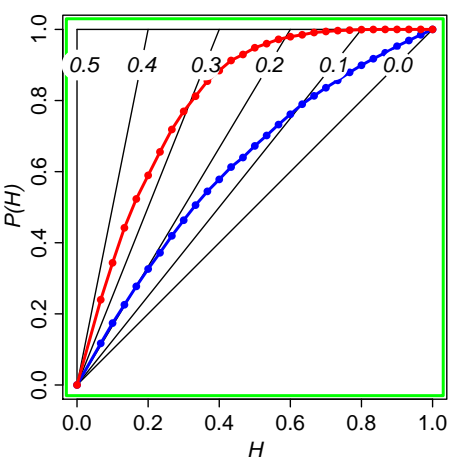
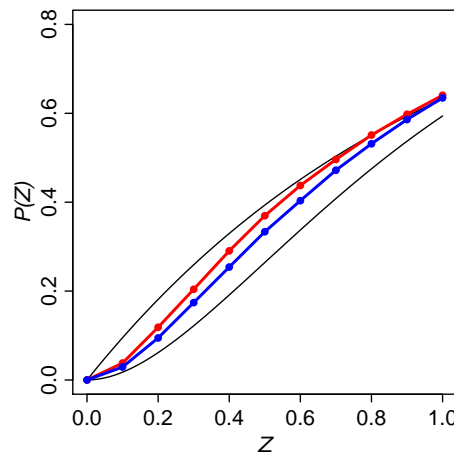
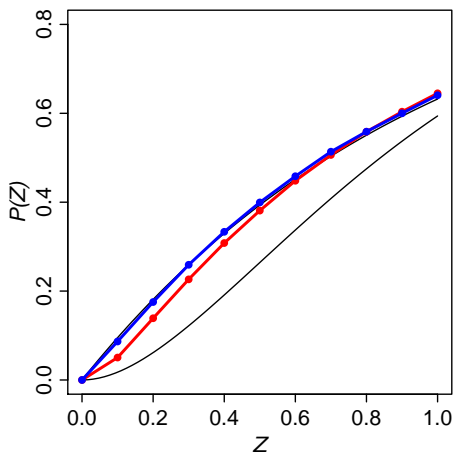
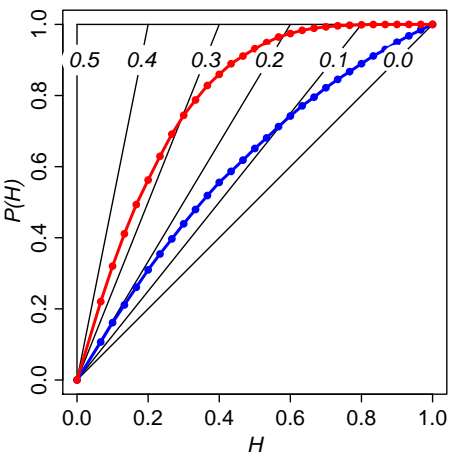
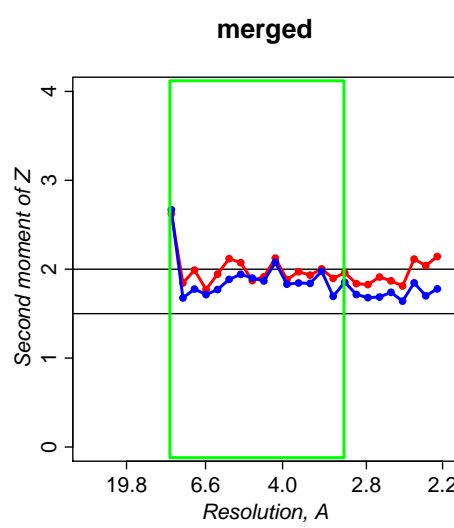
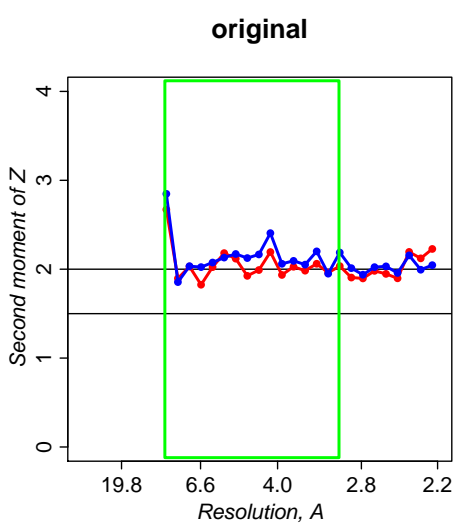
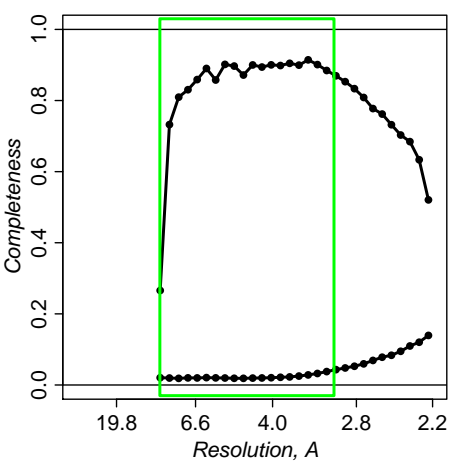
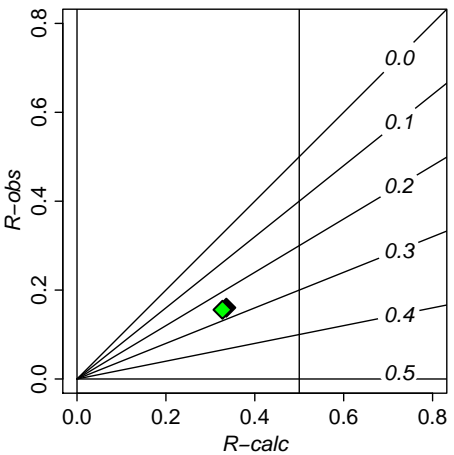
NCS	translation	rotation
r.m.s.d. (A)	27.21	0.22
angle (o)	179.91	0.11



1hbh

	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		8.11
R	24.1	
R'	-	-
R-free	26.9	
R'-free	-	-
residues per monomer	DNA 0	protein 288

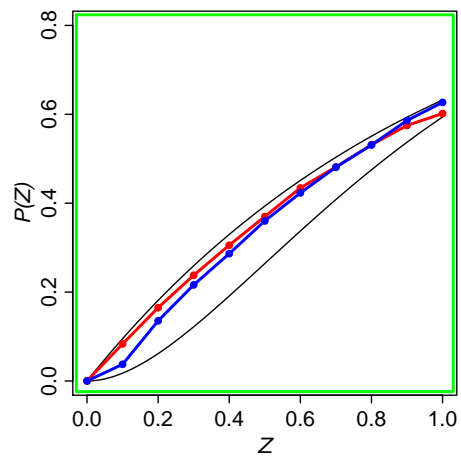
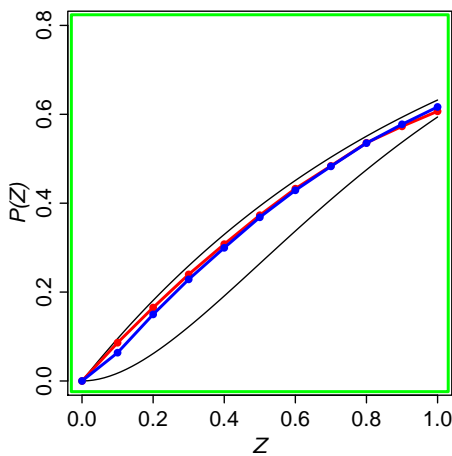
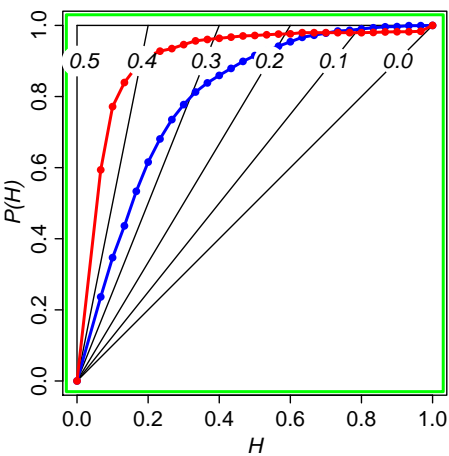
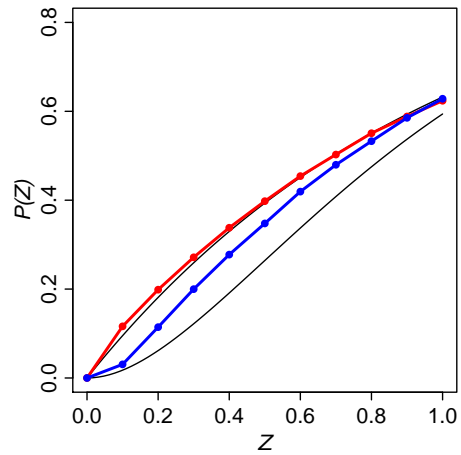
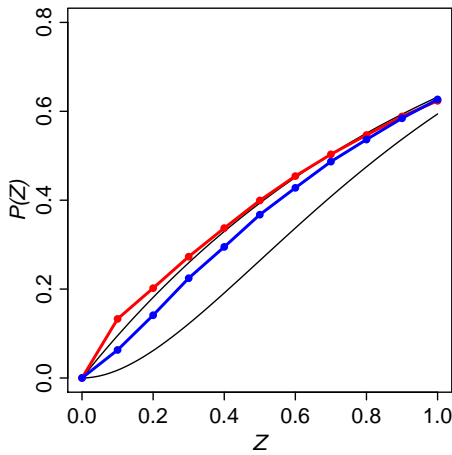
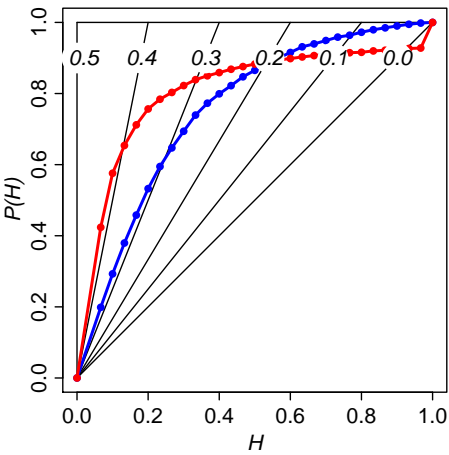
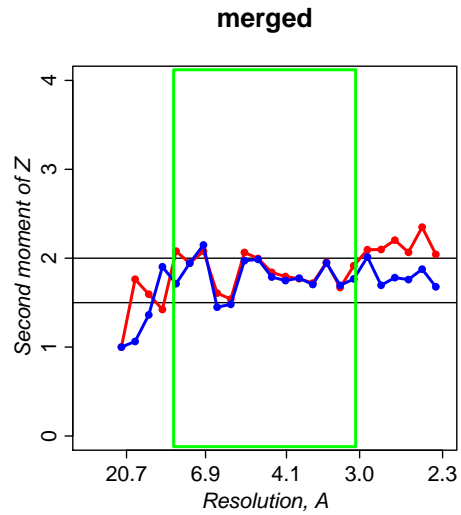
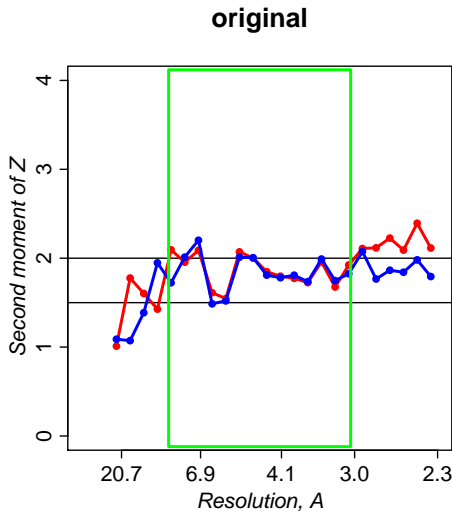
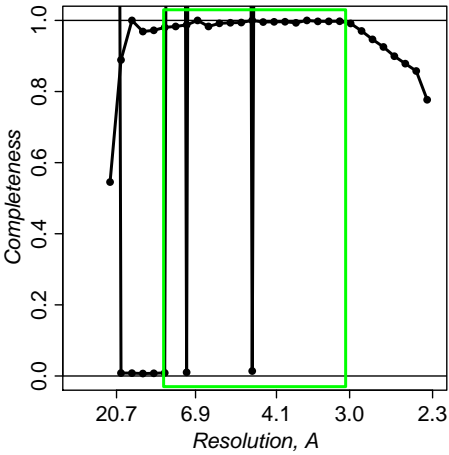
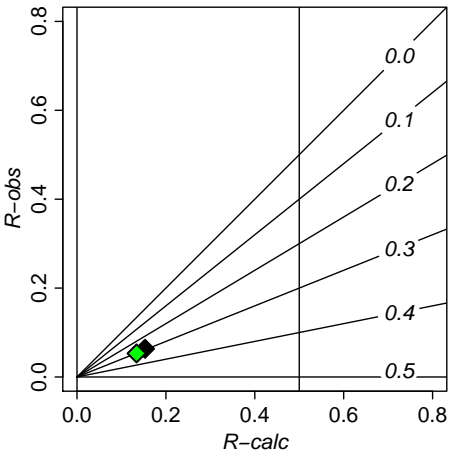
s < f/100	8896	30.27 %
s <= 0	8896	30.27 %
f <= 0	8896	30.27 %
s,f <= 0	8896	30.27 %
range (A)	10.0–2.2	9.9–3.0
unique	37,574	14,587
measured	29,393	12,885
used	22,800	10,612
NCS	translation	rotation
r.m.s.d. (A)	35.44	0.24
angle (o)	179.51	0.58



1hbv

	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.27
R	22.4	
R'	22.7	24.8
R-free	26.7	
R'-free	28.1	31.1
residues per monomer	DNA 0	protein 99

s < f/100	1062	13.19 %
s <= 0	0	0.00 %
f <= 0	624	7.75 %
s,f <= 0	0	0.00 %
range (A)	29.7–2.3	9.9–3.0
unique	8,584	3,781
measured	8,054	3,765
used	6,592	3,030
NCS	translation	rotation
r.m.s.d. (A)	22.56	0.27
angle (o)	179.86	0.24



1hci

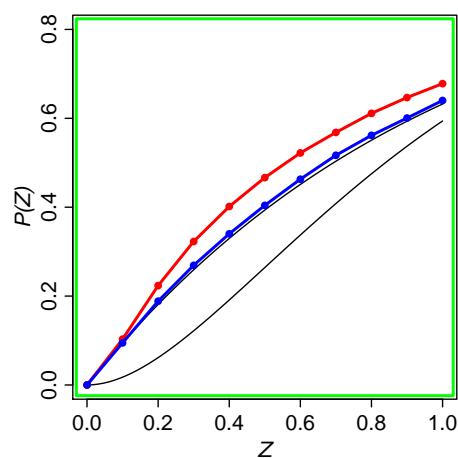
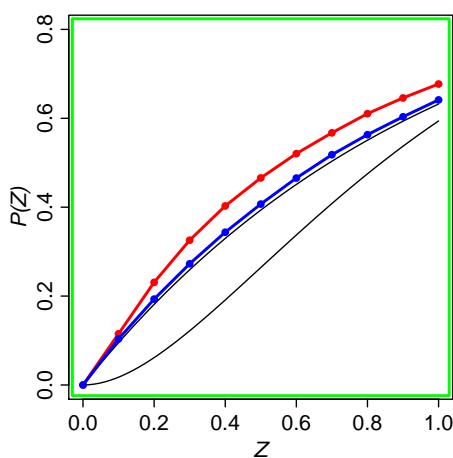
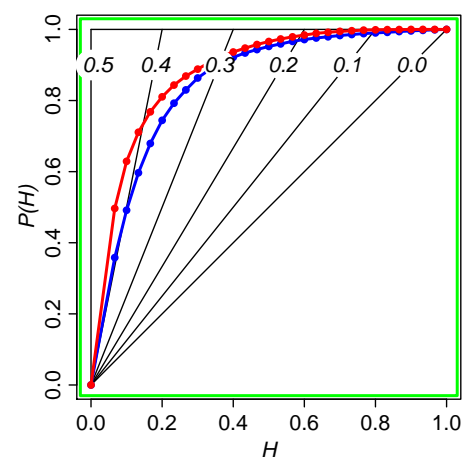
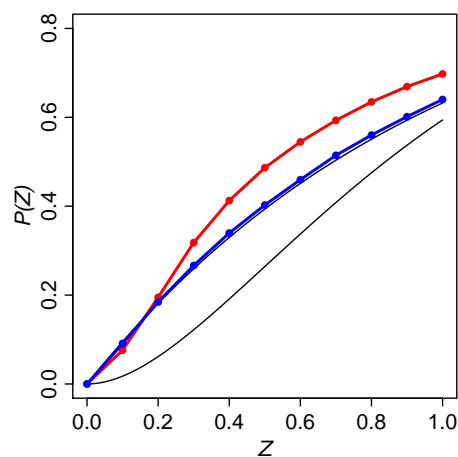
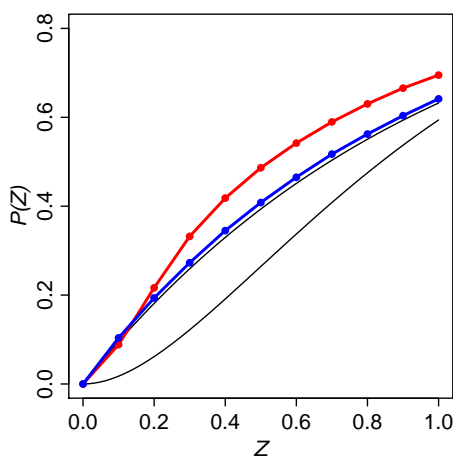
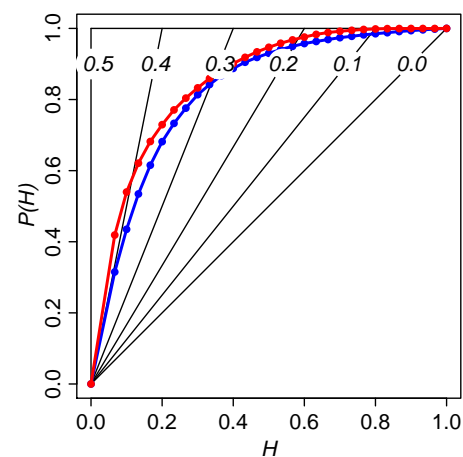
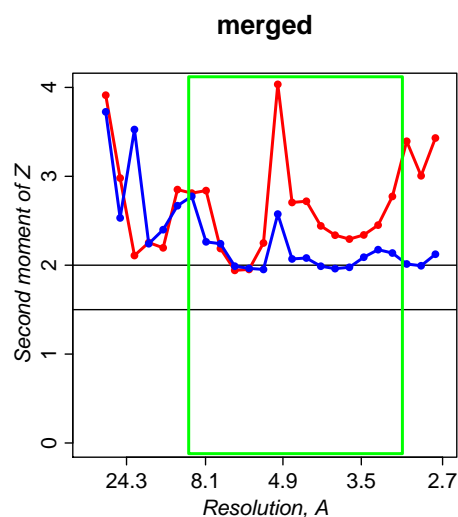
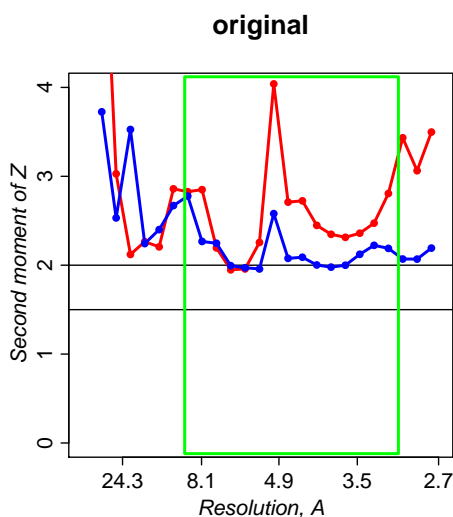
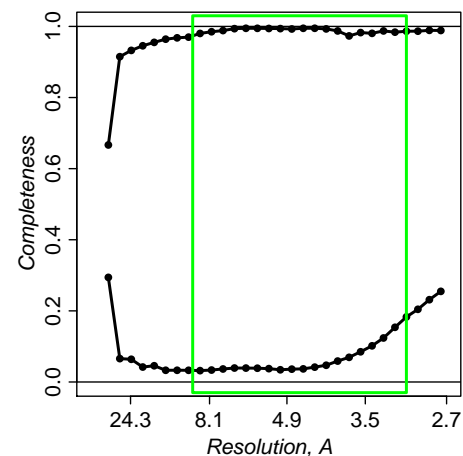
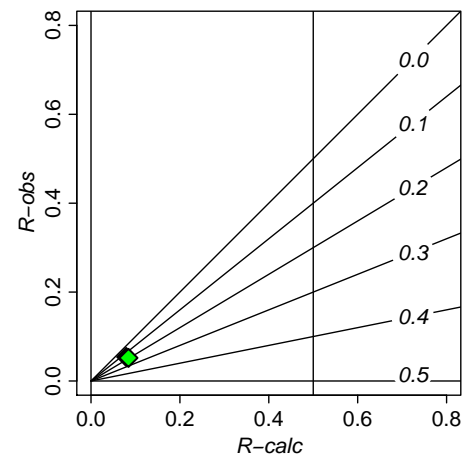
	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.02
R	28.5	
R'	28.5	28.9
R-free	32.4	
R'-free	32.4	32.7

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	82.8–2.7	9.9–3.0
unique	71,718	50,806
measured	70,769	50,148
used	66,128	46,736

NCS	translation	rotation
r.m.s.d. (A)	137.36	0.02
angle (o)	179.97	0.06

residues per monomer	DNA	protein
	0	475



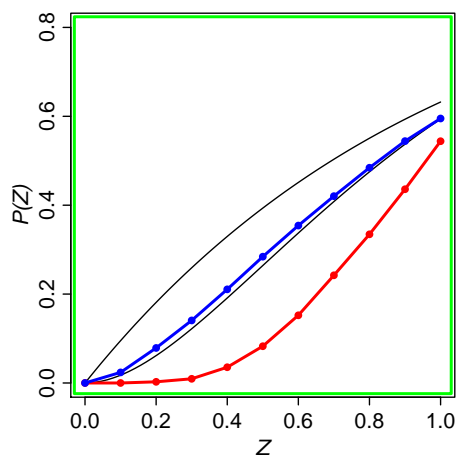
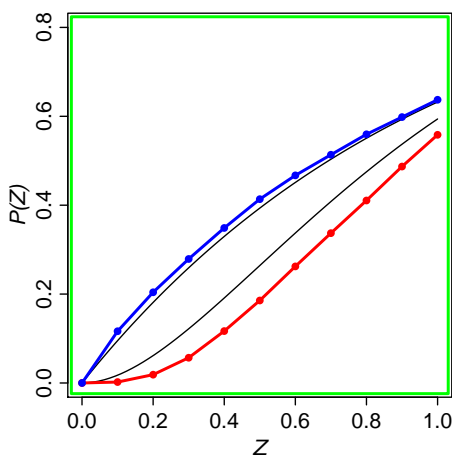
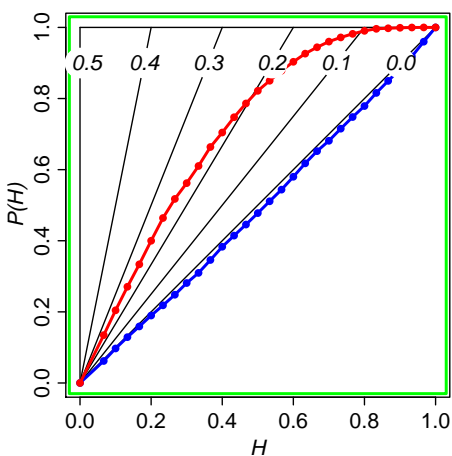
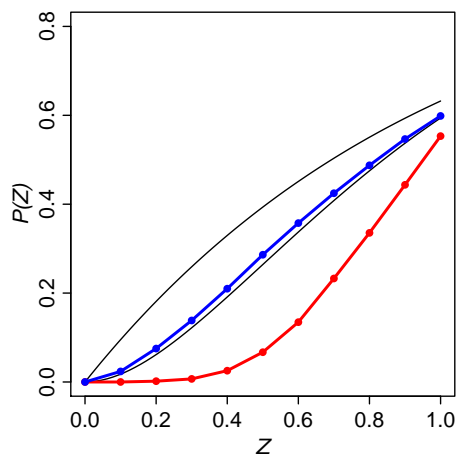
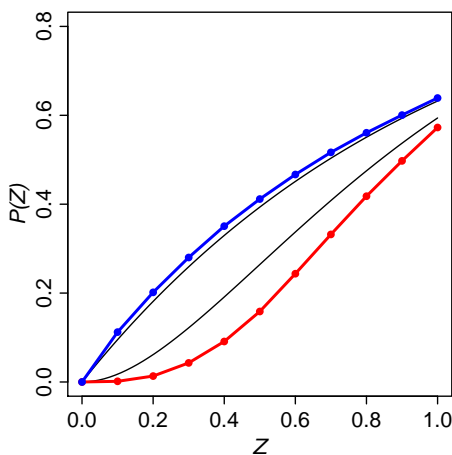
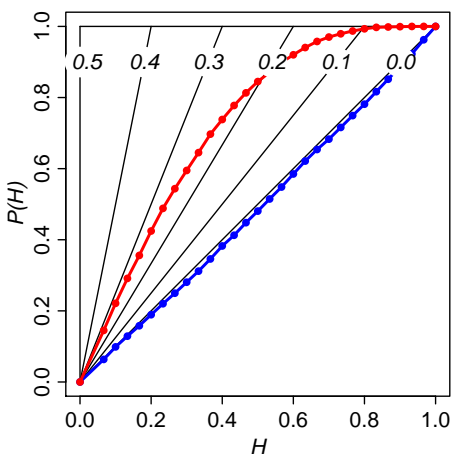
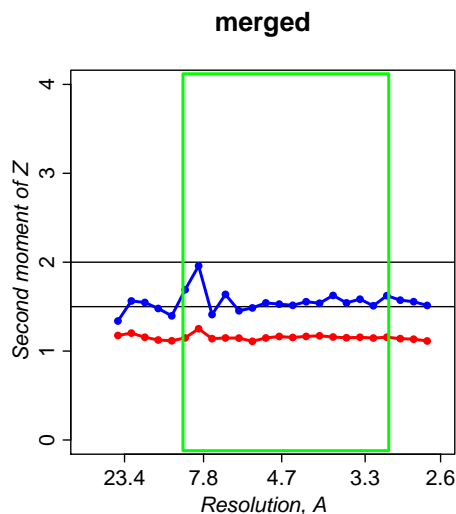
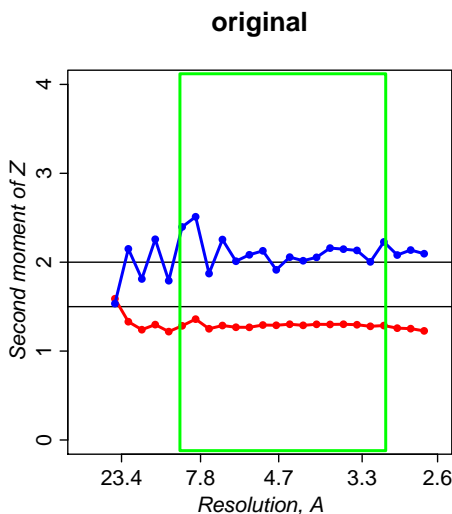
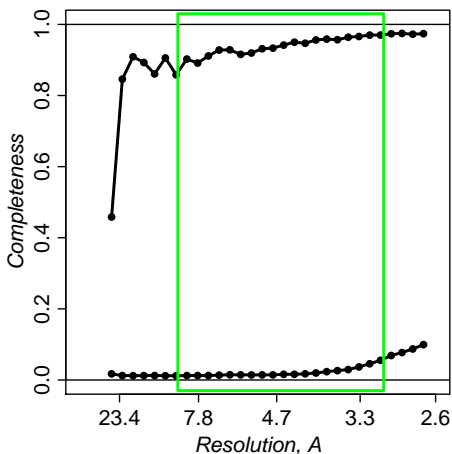
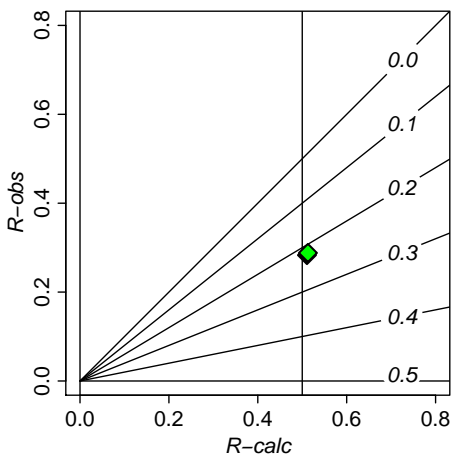
1hk1

	original	merged
s.g.	P 1 21 1	-
p.g.	10001	10003
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	25.7	-
R'	-	-
R-free	30.9	-
R'-free	-	-
residues per monomer	DNA 0	protein 553

s < f/100	838	4.97 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	35.3-2.6	9.9-3.0
unique	17,621	11,823
measured	16,849	11,239
used	14,712	9,768

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



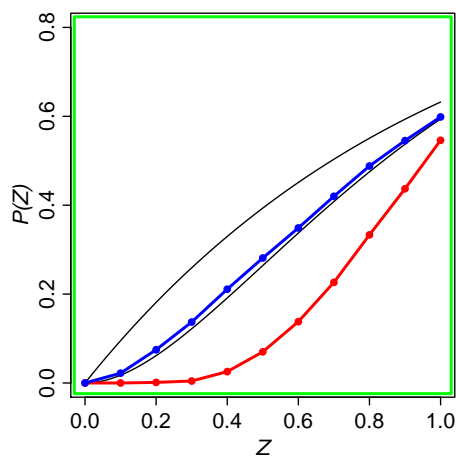
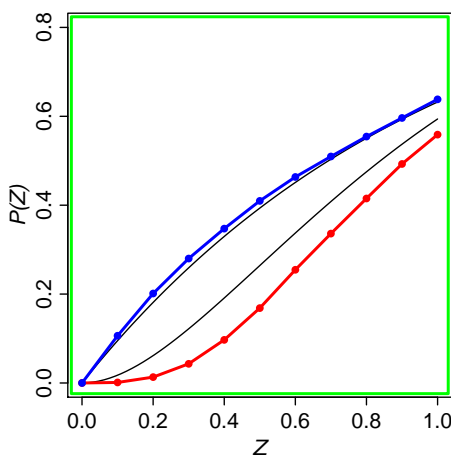
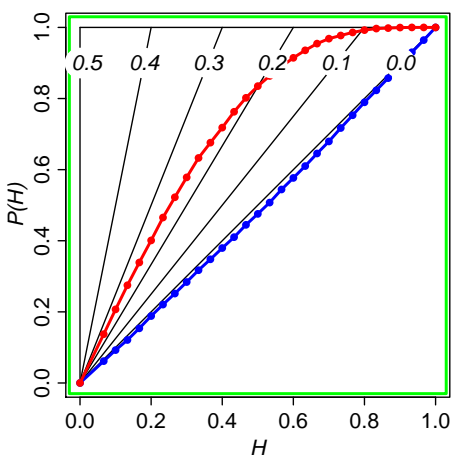
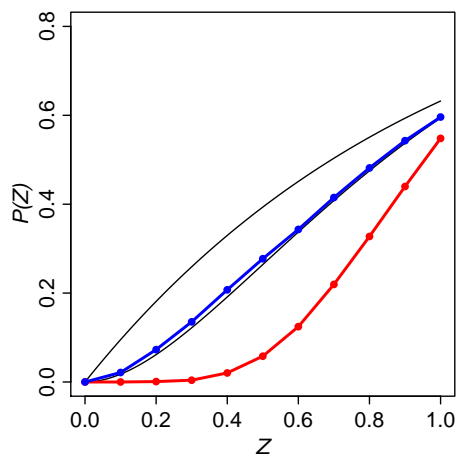
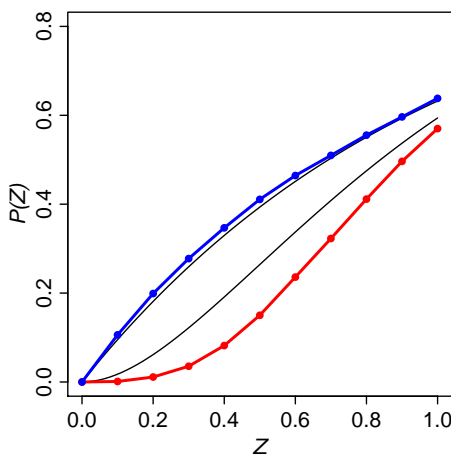
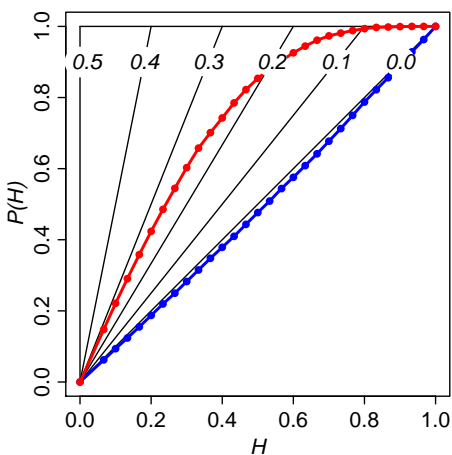
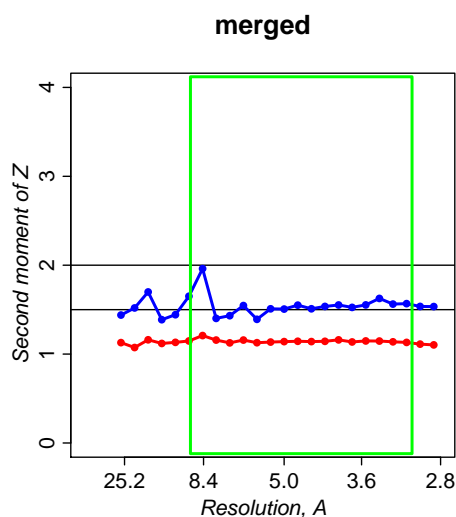
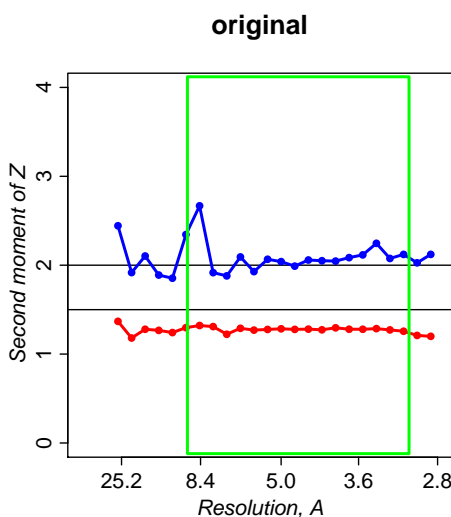
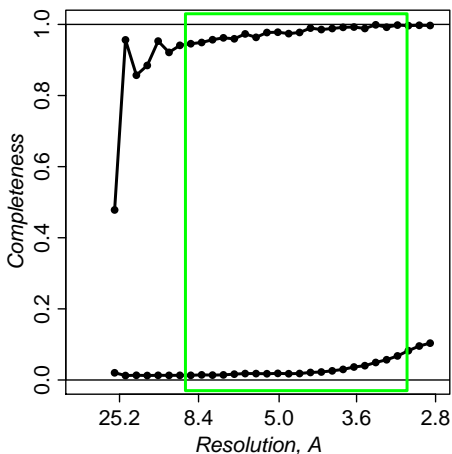
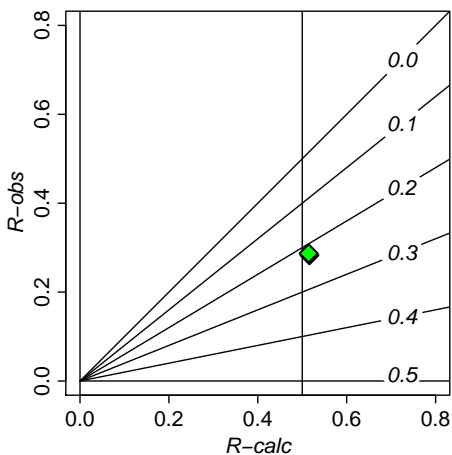
1hk2

	original	merged
s.g.	P 1 21 1	-
p.g.	10001	10003
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	25.4	-
R'	-	-
R-free	32.9	-
R'-free	-	-
residues per monomer	DNA 0	protein 560

s < f/100	439	2.99 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	34.1-2.8	9.9-3.0
unique	14,890	11,770
measured	14,684	11,600
used	13,078	10,442

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



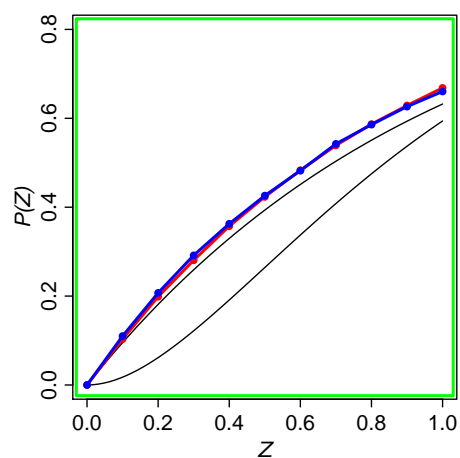
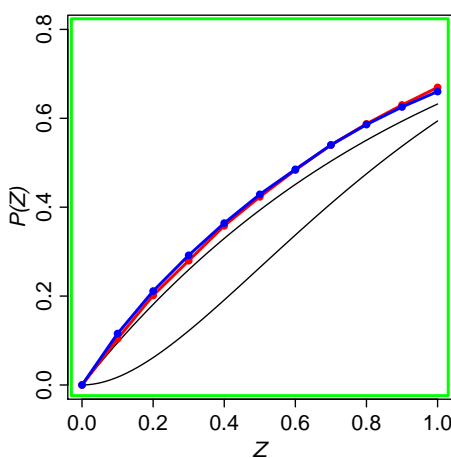
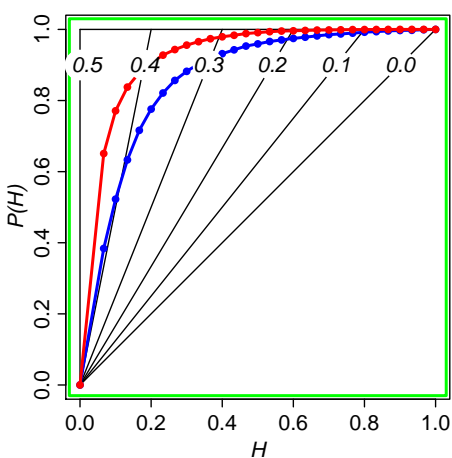
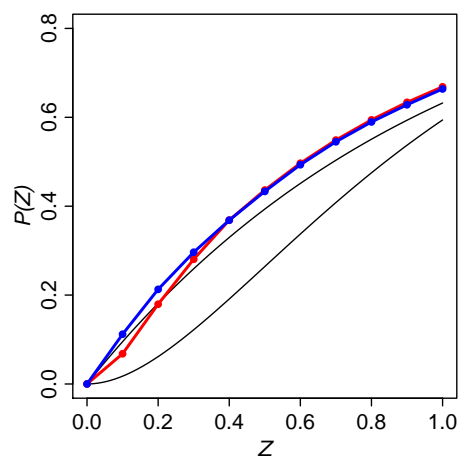
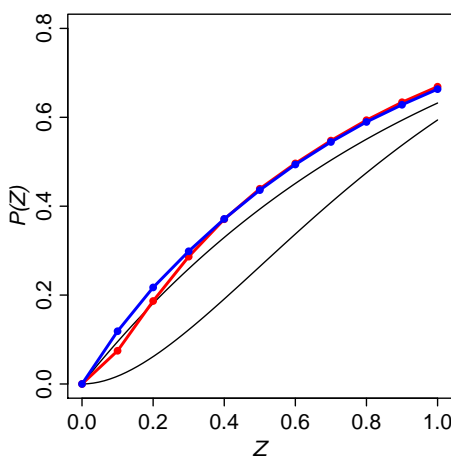
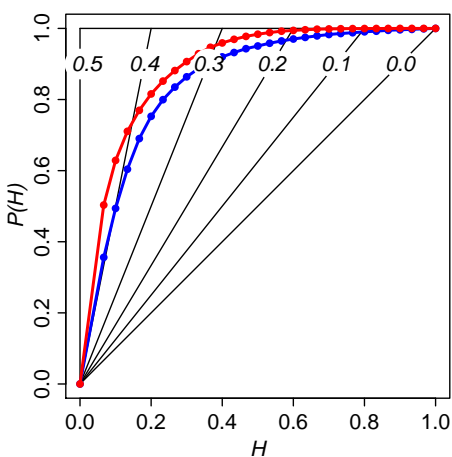
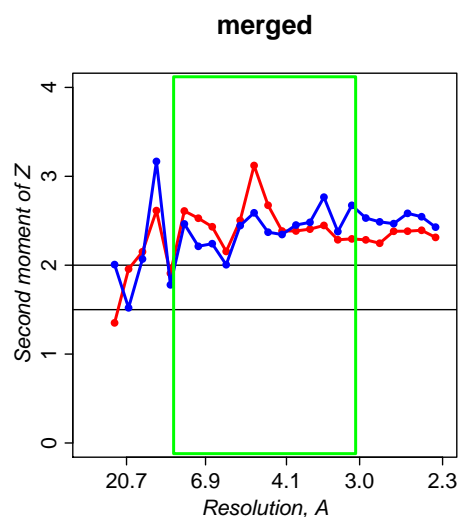
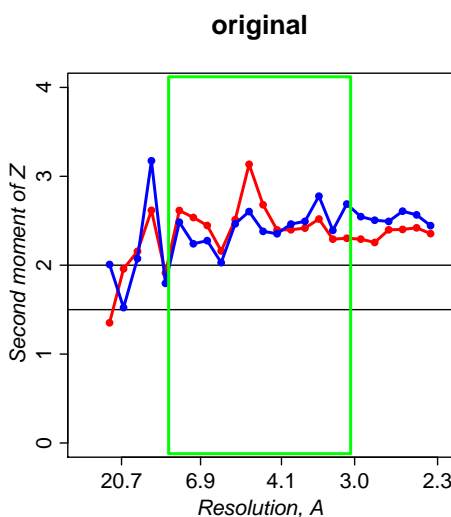
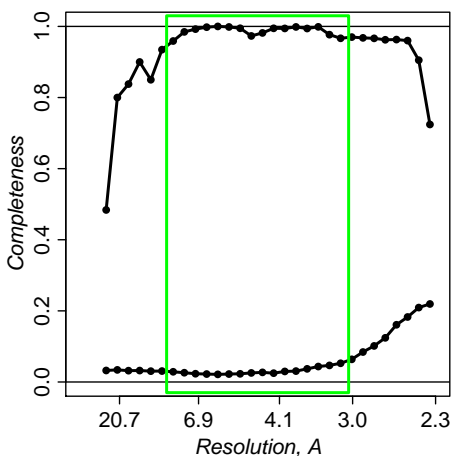
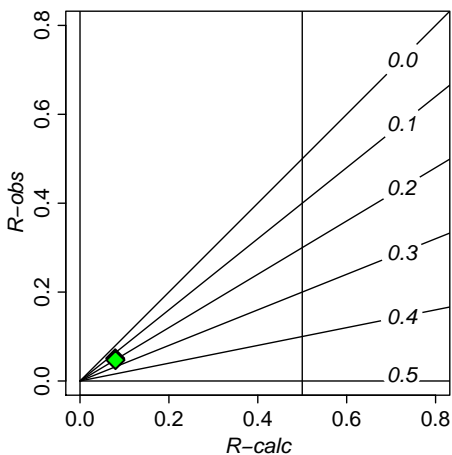
1hm0

	original	merged
s.g.	H 3	H 3 2
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.15
R	25.0	
R'	25.1	25.5
R-free	28.2	
R'-free	28.5	29.2
residues per monomer	DNA 0	protein 440

s < f/100	10	0.03 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	39.7–2.3	9.9–3.0
unique	39,938	17,510
measured	37,758	17,260
used	34,058	15,964

NCS	translation	rotation
r.m.s.d. (A)	52.33	0.15
angle (o)	179.99	0.04



1hm8

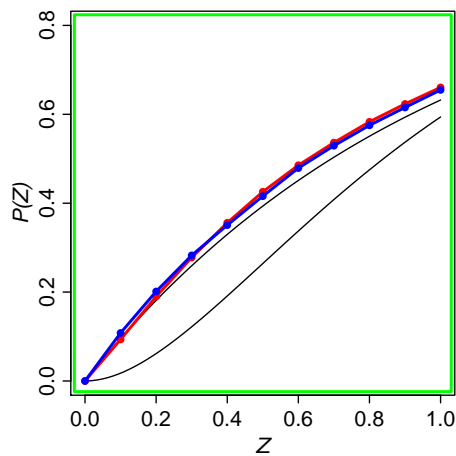
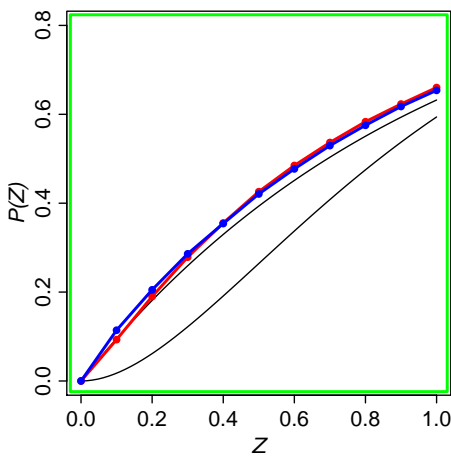
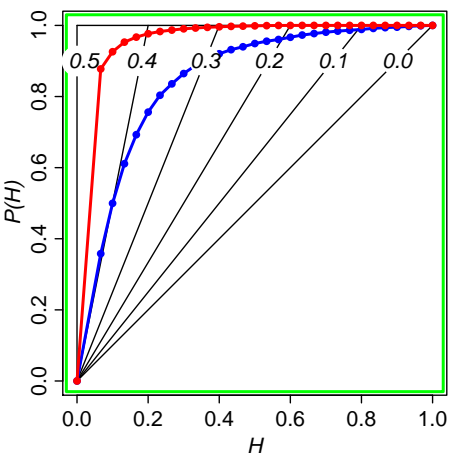
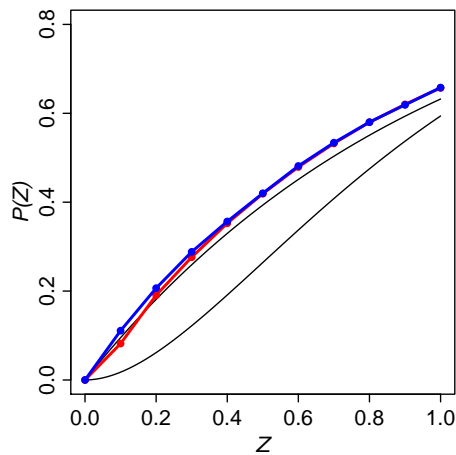
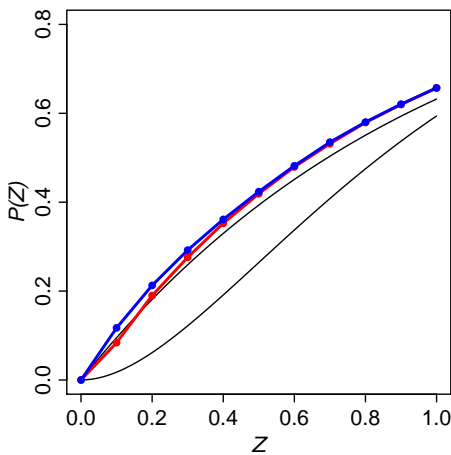
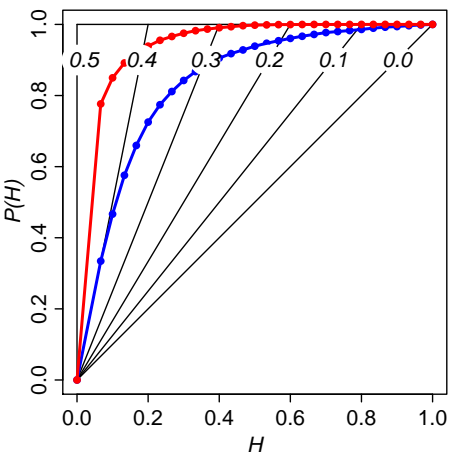
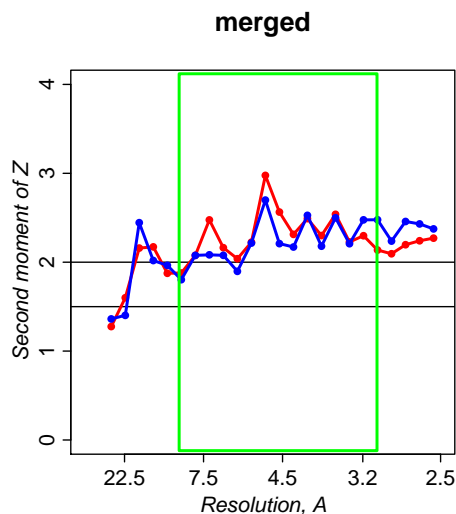
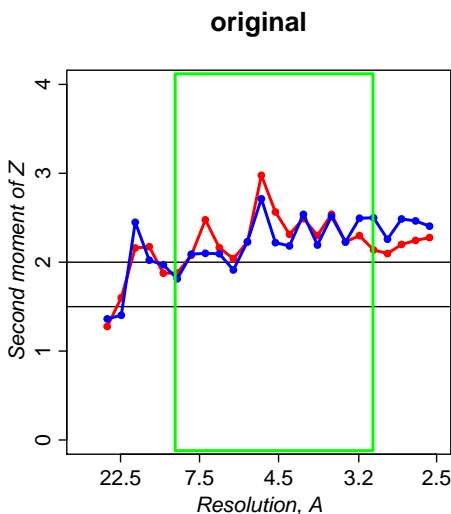
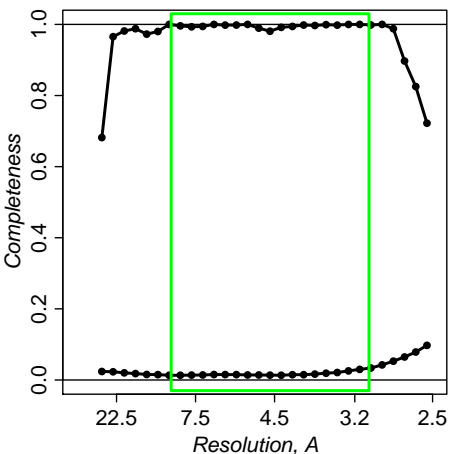
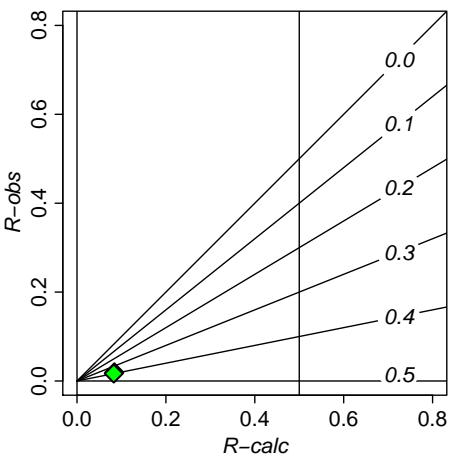
	original	merged
s.g.	H 3	H 3 2
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.03
R	23.1	
R'	23.1	23.8
R-free	26.5	
R'-free	26.6	27.2

s < f/100	3851	13.18 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	46.2–2.5	9.9–3.0
unique	30,804	17,363
measured	29,218	17,305
used	26,644	16,112

NCS	translation	rotation
r.m.s.d. (A)	59.67	0.03
angle (o)	180.00	0.01

residues per monomer	DNA	protein
	0	458



1hm9

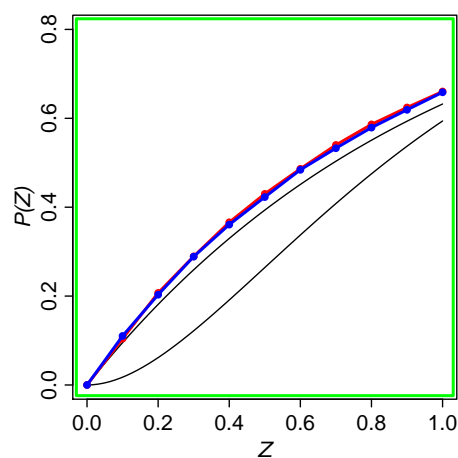
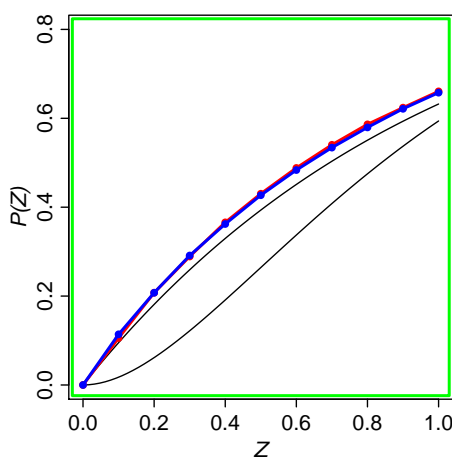
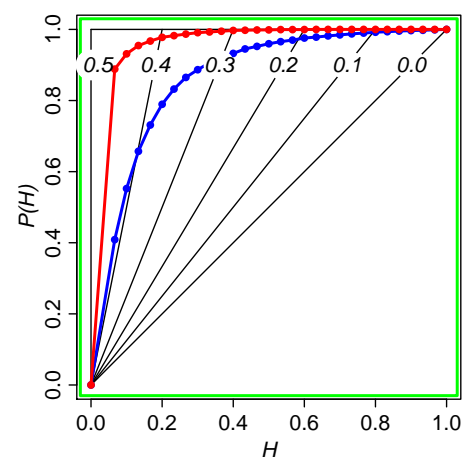
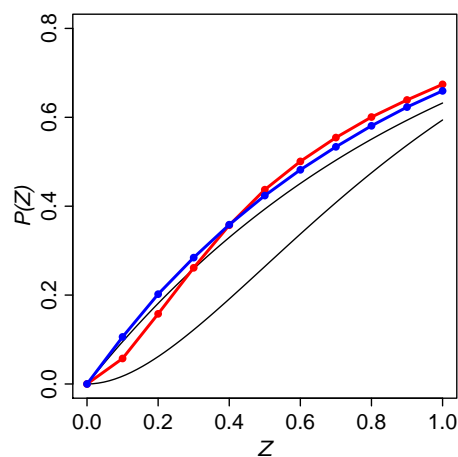
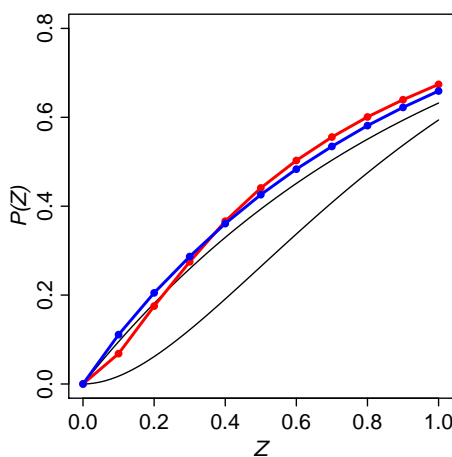
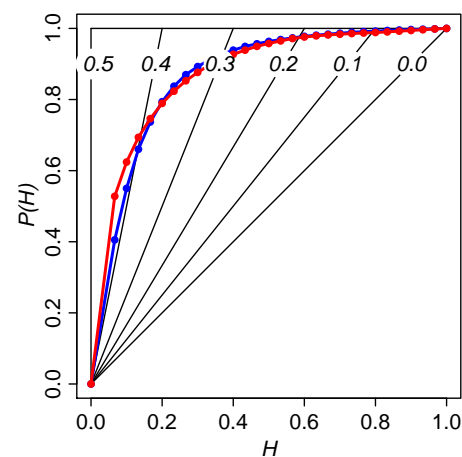
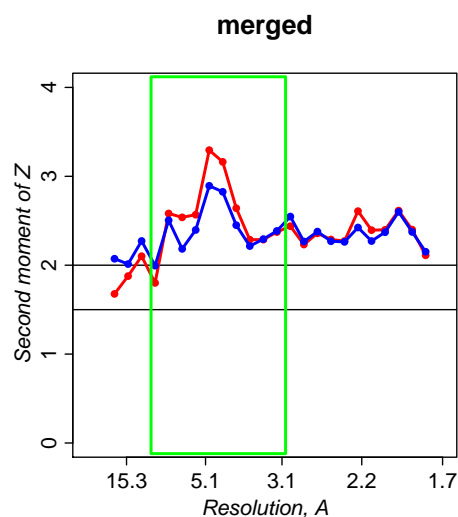
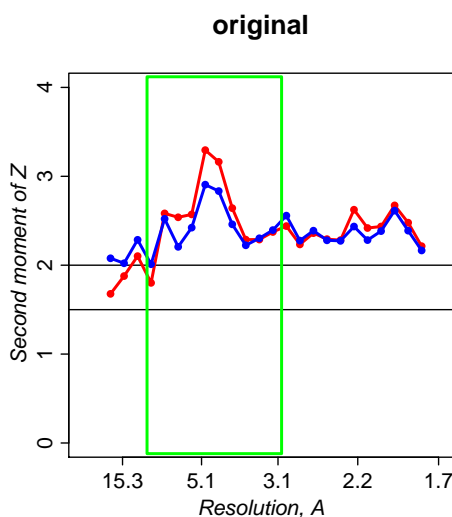
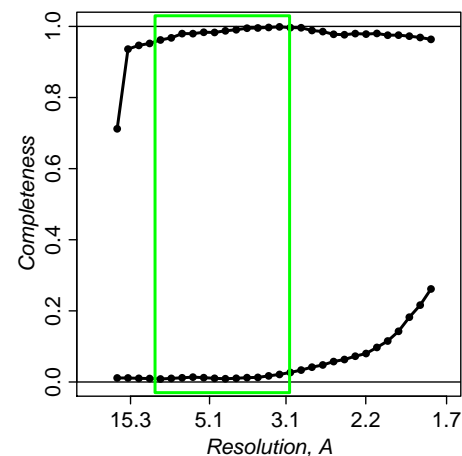
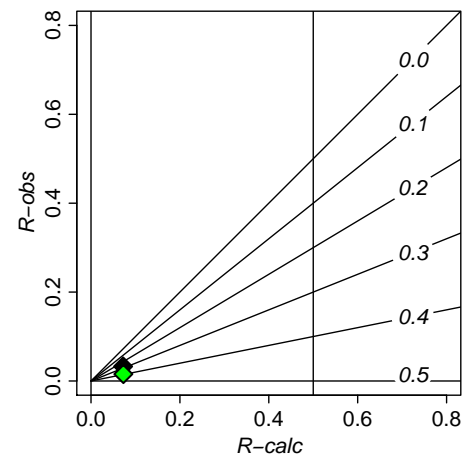
	original	merged
s.g.	H 3	H 3 2
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.05
R	26.5	
R'	26.5	26.5
R-free	29.4	
R'-free	29.5	29.5

s < f/100	8610	10.47 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.1–1.8	9.9–3.0
unique	83,997	16,224
measured	82,248	16,083
used	76,972	14,842

NCS	translation	rotation
r.m.s.d. (A)	54.24	0.05
angle (o)	180.00	0.02

residues per monomer	DNA	protein
	0	458



1hqq

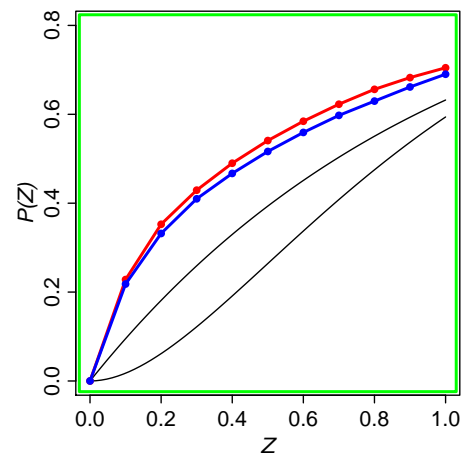
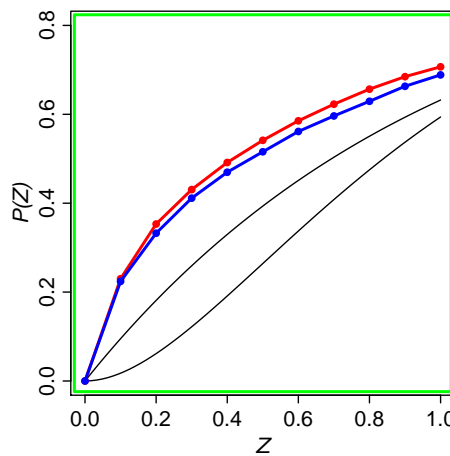
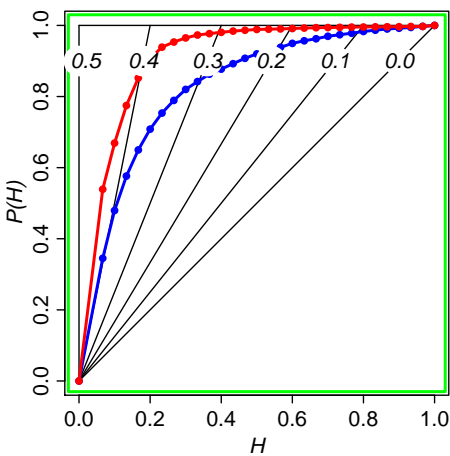
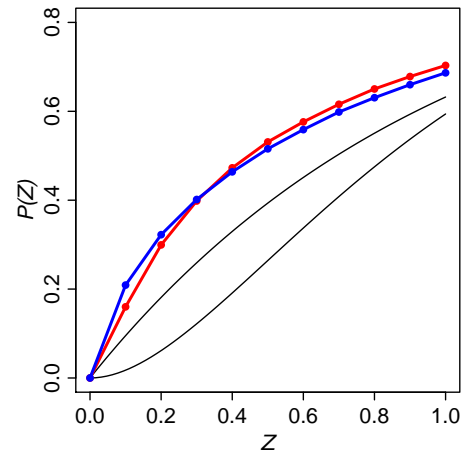
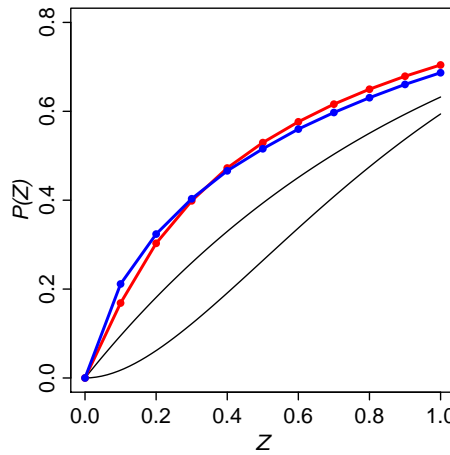
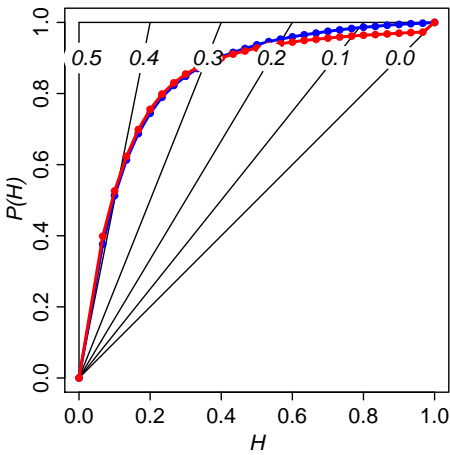
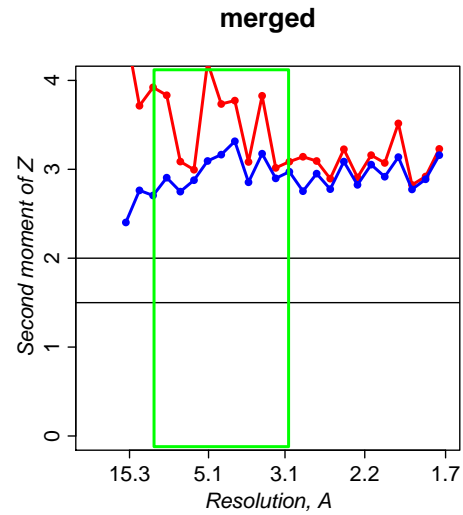
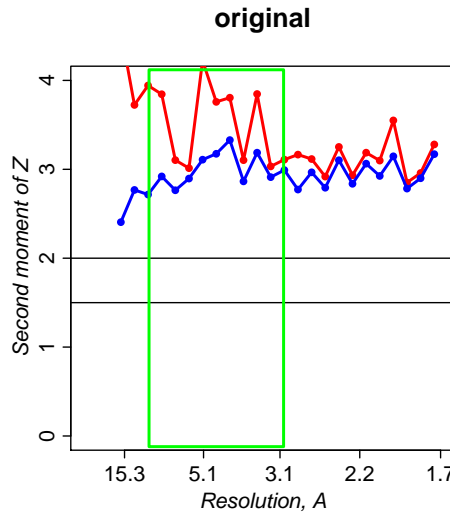
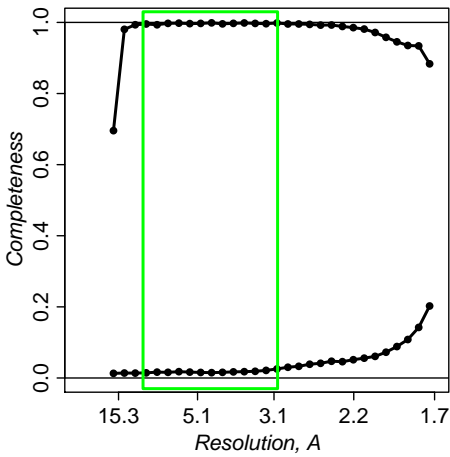
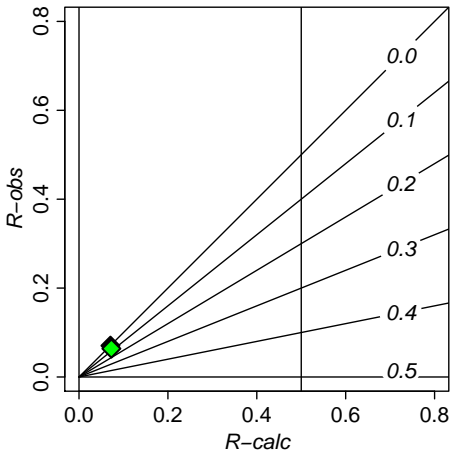
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		0.08
R	26.3	
R'	26.4	26.3
R-free	28.9	
R'-free	29.3	29.5

s < f/100	3361	5.31 %
s <= 0	0	0.00 %
f <= 0	1083	1.71 %
s,f <= 0	0	0.00 %

range (A)	20.8–1.7	9.9–3.0
unique	65,529	11,688
measured	63,318	11,656
used	58,192	10,550

NCS	translation	rotation
r.m.s.d. (A)	0.21	0.06
angle (o)	0.57	0.03

residues per monomer	DNA	protein
	0	132



1hv4

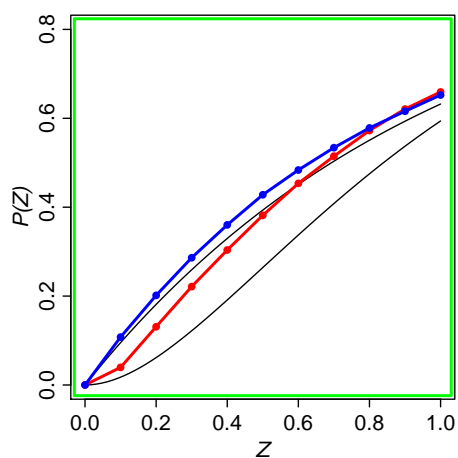
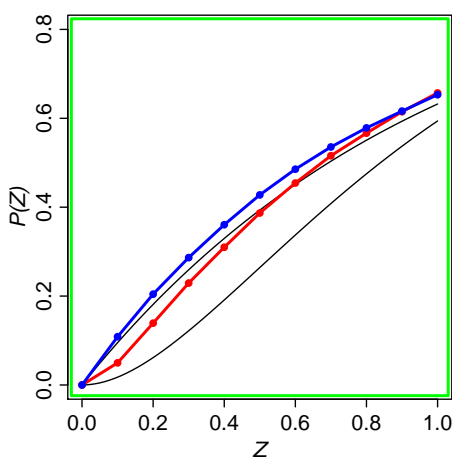
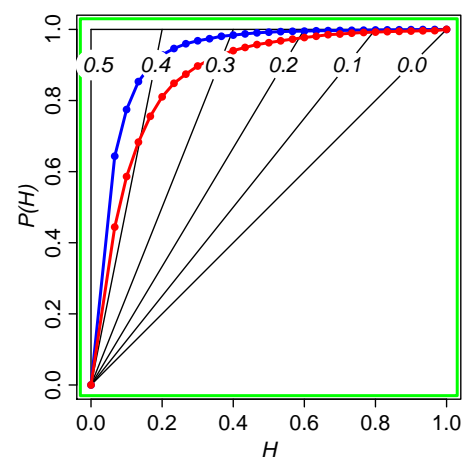
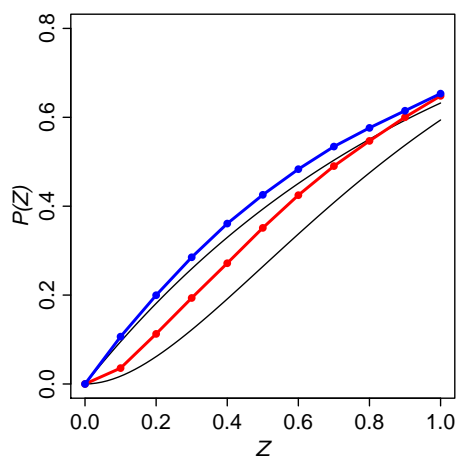
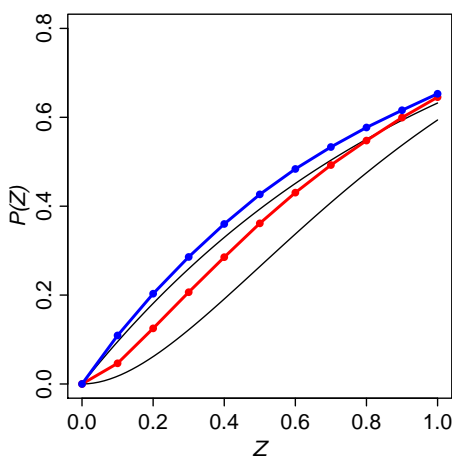
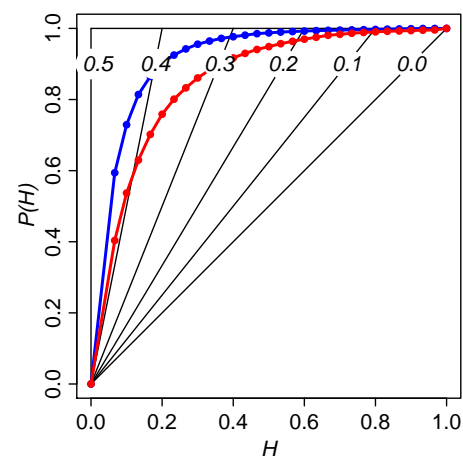
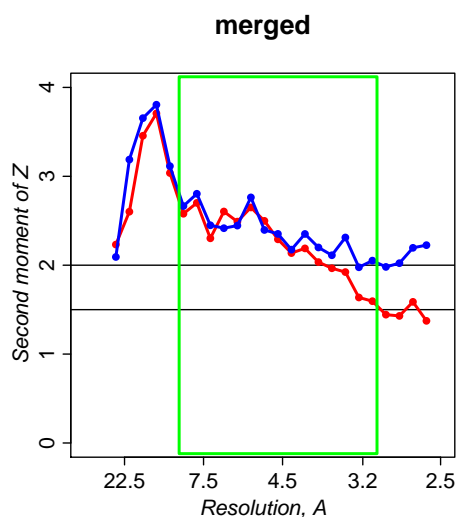
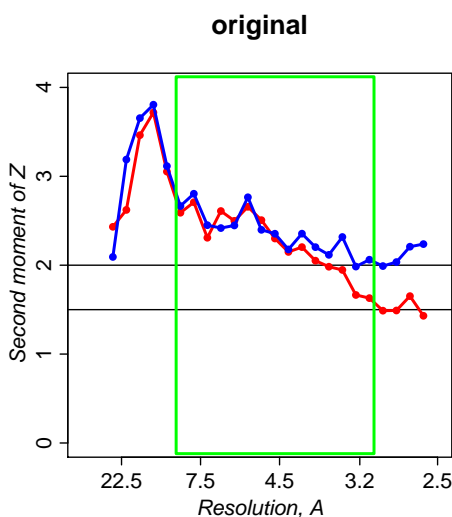
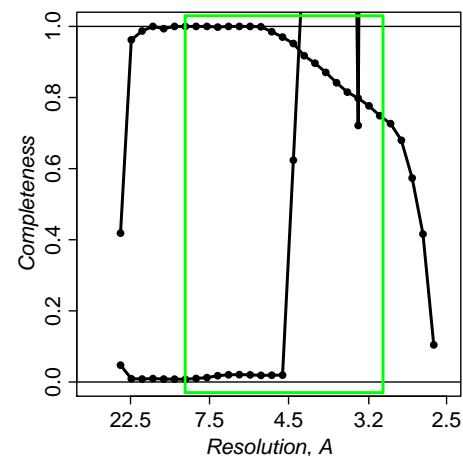
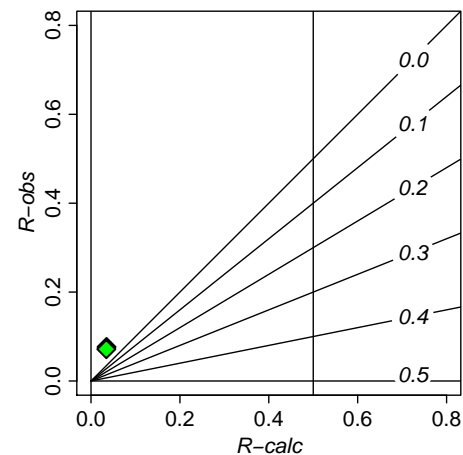
	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	4	2
p.t.	2	2
p.o.	1	2
r.m.s.d. (A)		0.05
R	23.2	
R'	23.2	23.8
R-free	30.1	
R'-free	30.1	30.7

s < f/100	2818	9.19 %
s <= 0	0	0.00 %
f <= 0	72	0.23 %
s,f <= 0	0	0.00 %

range (A)	36.9–2.6	9.9–3.0
unique	42,311	25,566
measured	30,654	22,350
used	25,532	19,288

NCS	translation	rotation
r.m.s.d. (A)	1.57	0.05
angle (o)	6.05	0.04

residues per monomer	DNA	protein
	0	287



1hw1

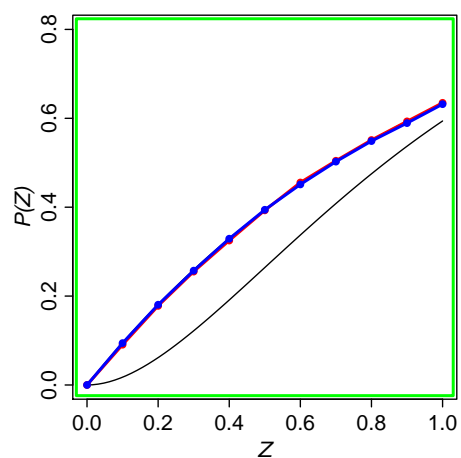
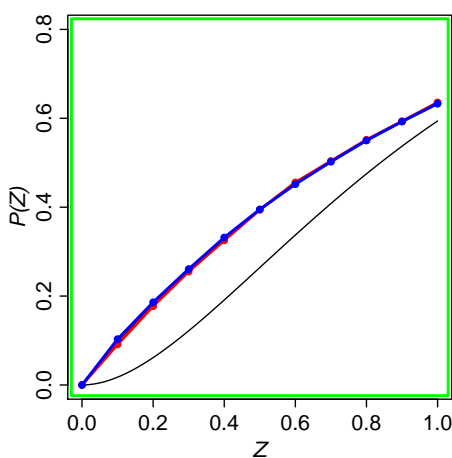
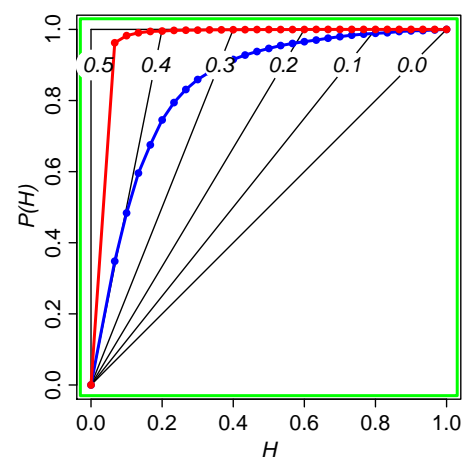
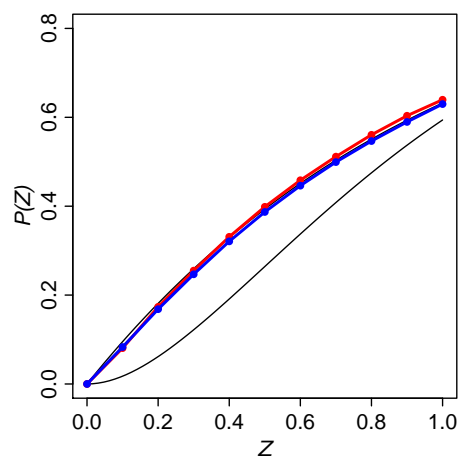
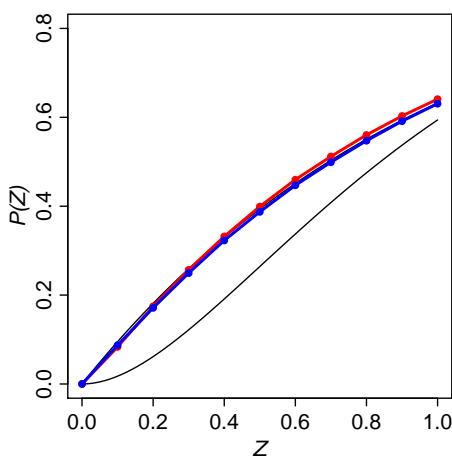
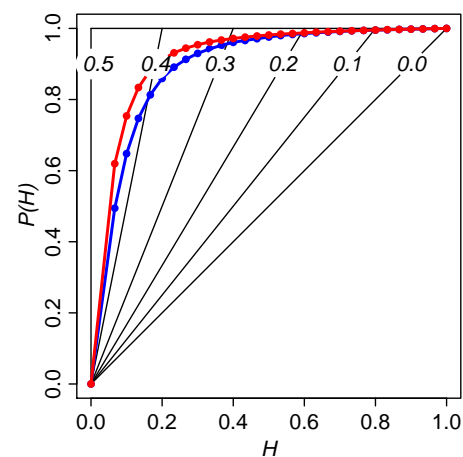
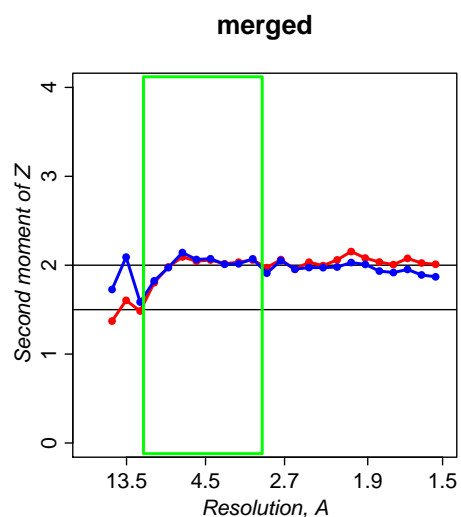
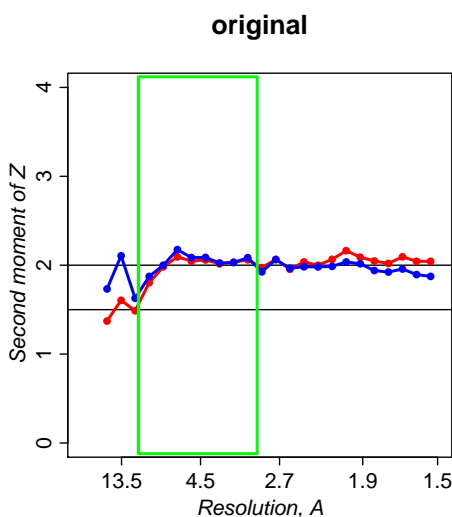
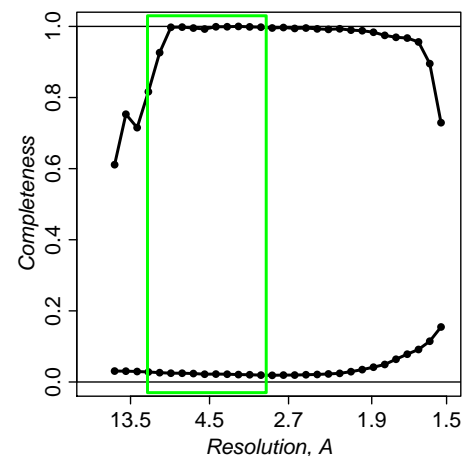
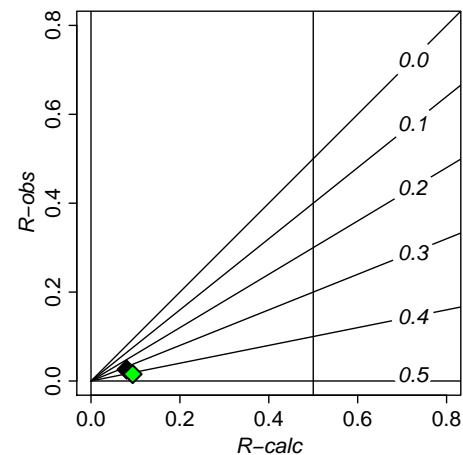
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.04
R	25.7	
R'	25.8	26.1
R-free	26.5	
R'-free	26.7	27.0

s < f/100	1679	2.13 %
s <= 0	1674	2.12 %
f <= 0	1674	2.12 %
s,f <= 0	1674	2.12 %

range (A)	29.7–1.5	9.9–3.0
unique	83,029	10,188
measured	78,956	10,109
used	72,284	9,114

NCS	translation	rotation
r.m.s.d. (A)	28.71	0.04
angle (o)	179.96	0.05

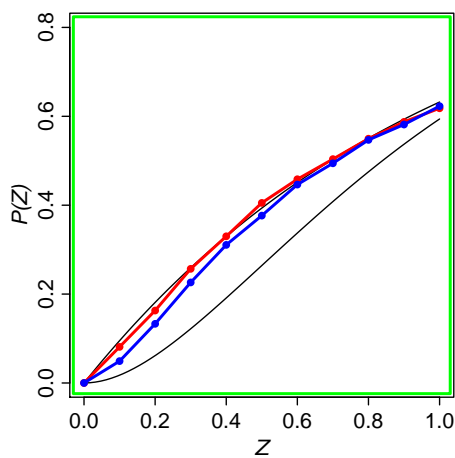
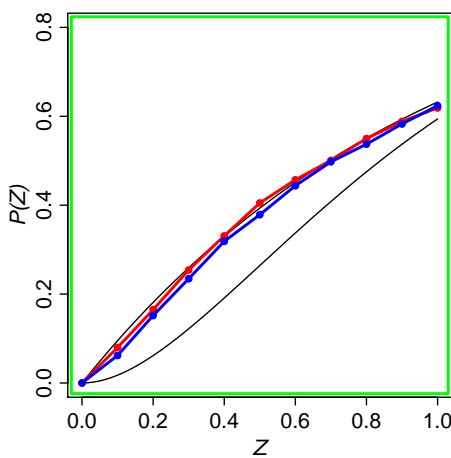
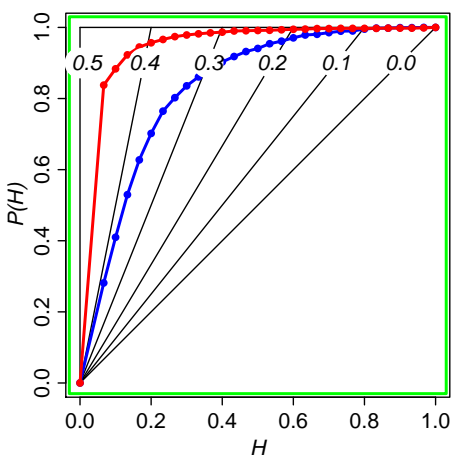
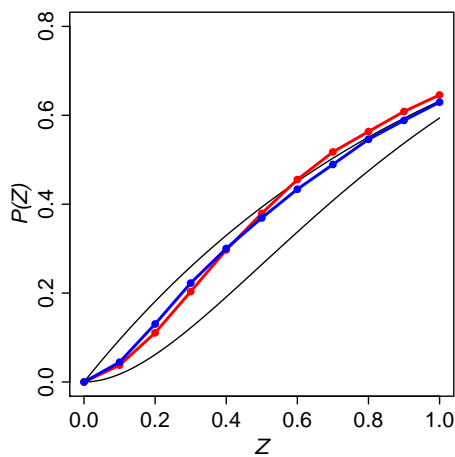
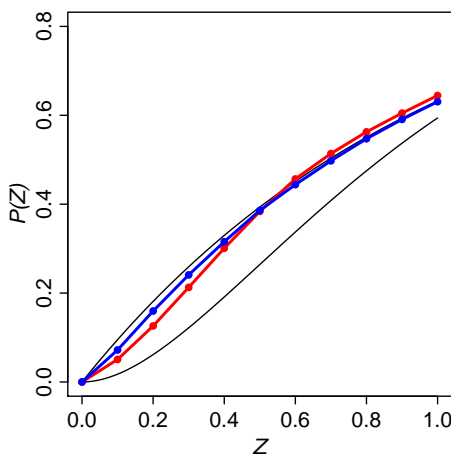
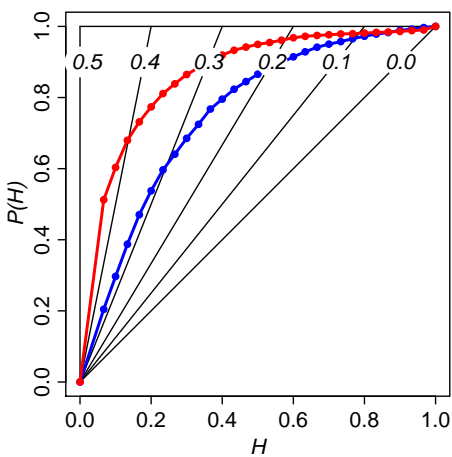
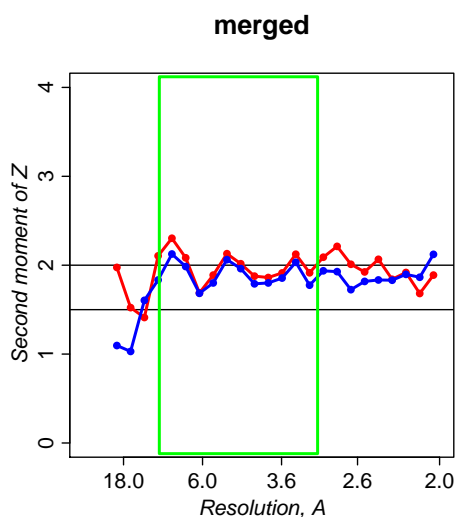
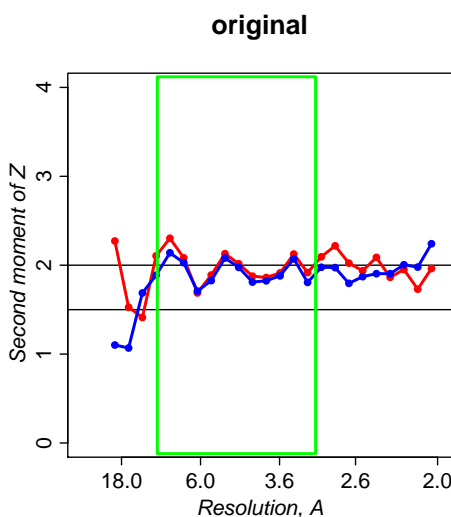
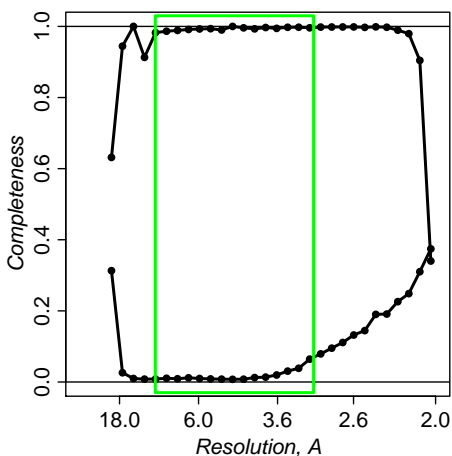
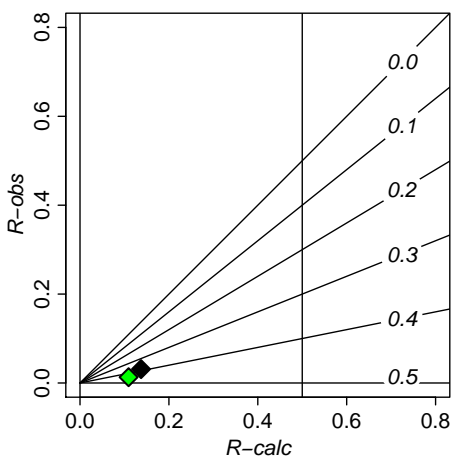
residues per monomer	DNA	protein
	0	226



1hxb

	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.19
R	24.3	
R'	24.9	26.8
R-free	28.6	
R'-free	28.3	30.2
residues per monomer	DNA 0	protein 99

s < f/100	1521	12.63 %
s <= 0	0	0.00 %
f <= 0	74	0.61 %
s,f <= 0	0	0.00 %
range (A)	27.4–2.0	9.9–3.0
unique	12,973	3,741
measured	12,040	3,723
used	10,220	2,992
NCS	translation	rotation
r.m.s.d. (A)	19.54	0.19
angle (o)	179.92	0.09



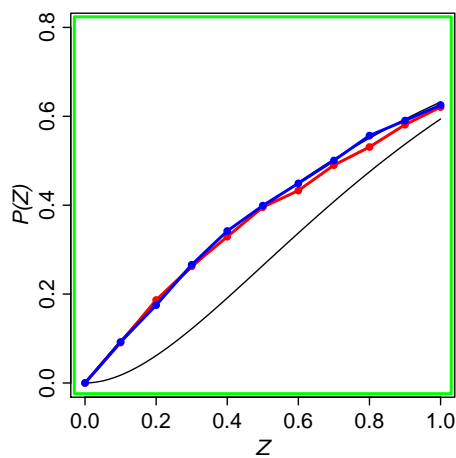
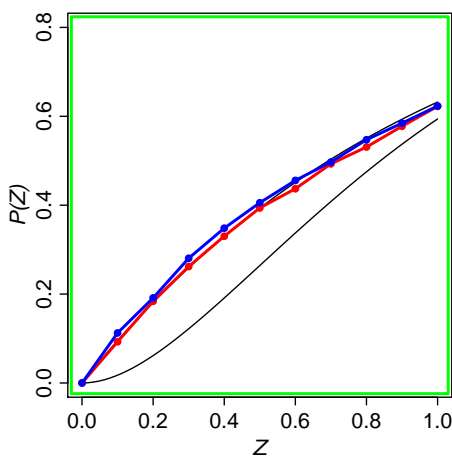
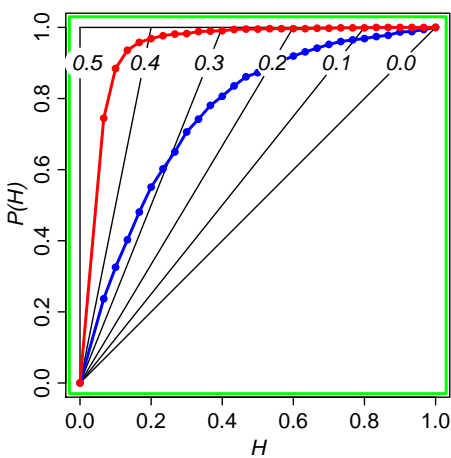
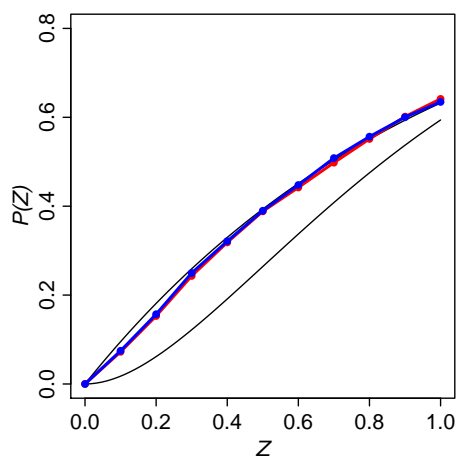
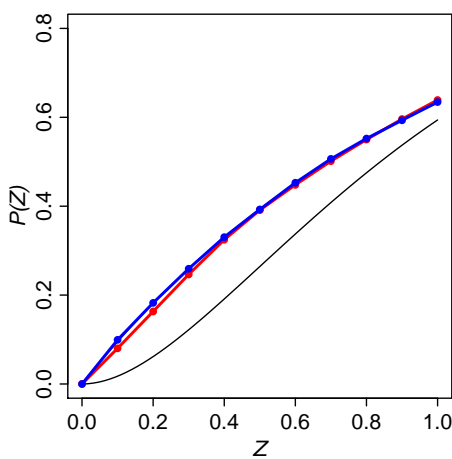
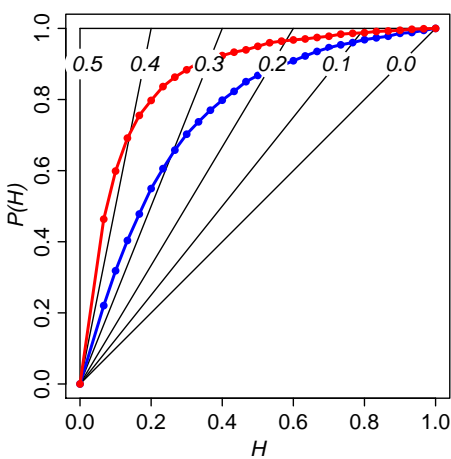
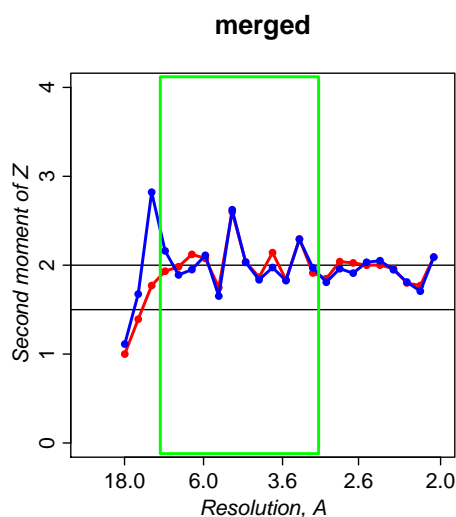
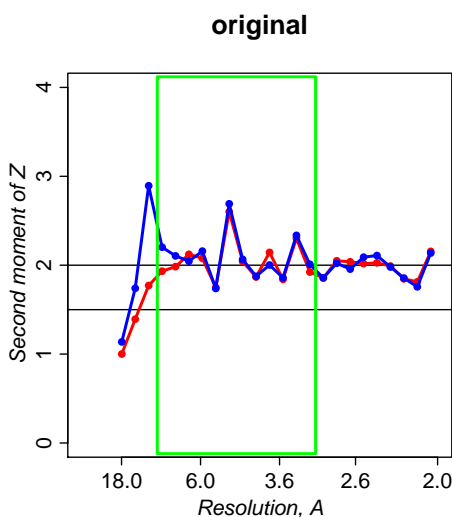
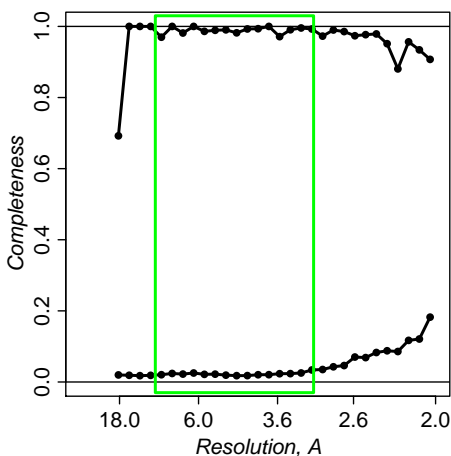
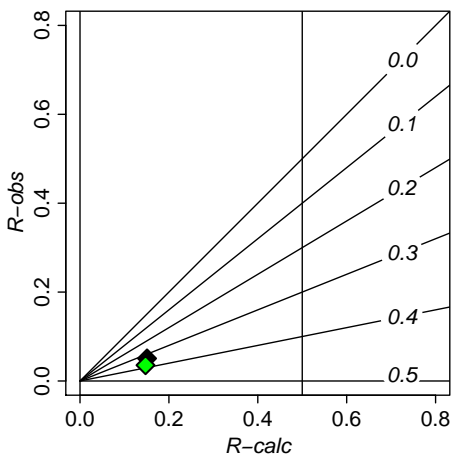
1i0c

	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.16
R	23.7	
R'	23.5	23.9
R-free	24.2	
R'-free	24.1	25.6
residues per monomer	DNA 0	protein 58

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	21.5–2.0	9.9–3.0
unique	6,808	1,977
measured	6,548	1,957
used	5,808	1,706

NCS	translation	rotation
r.m.s.d. (A)	16.85	0.16
angle (o)	179.79	0.24



1i1j

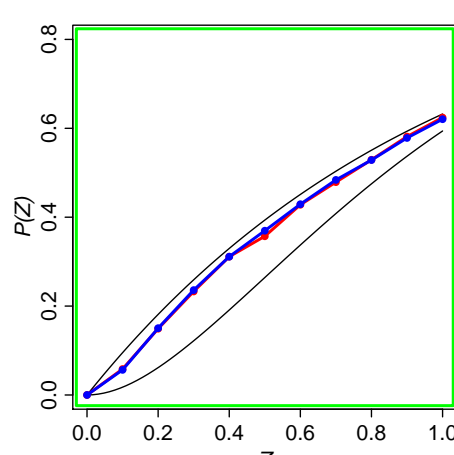
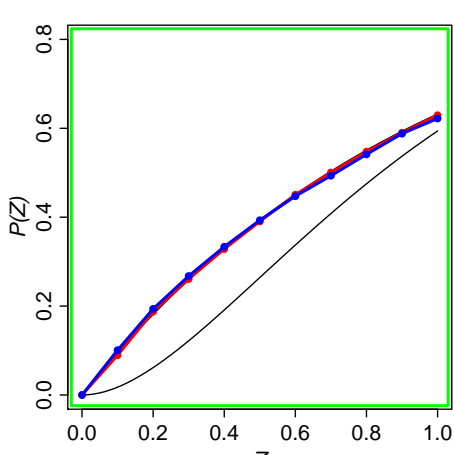
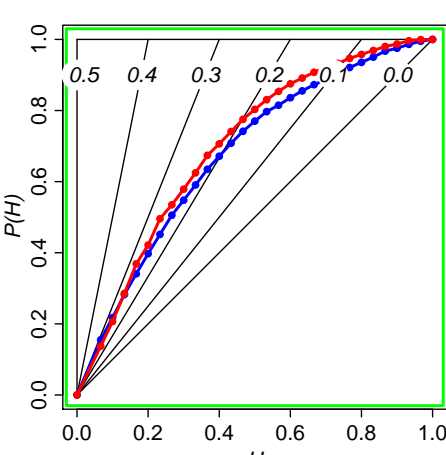
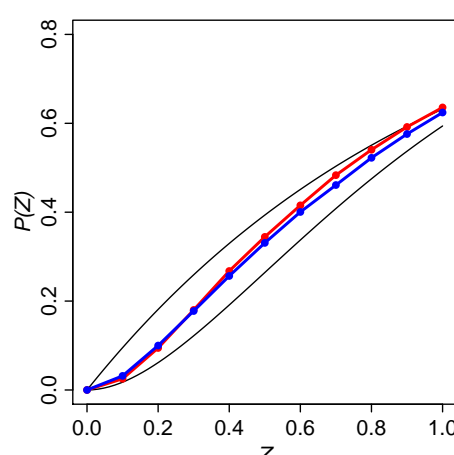
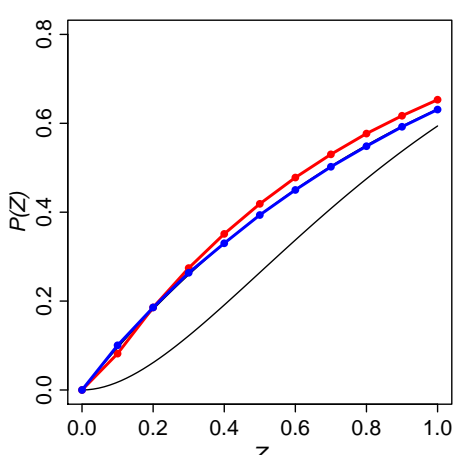
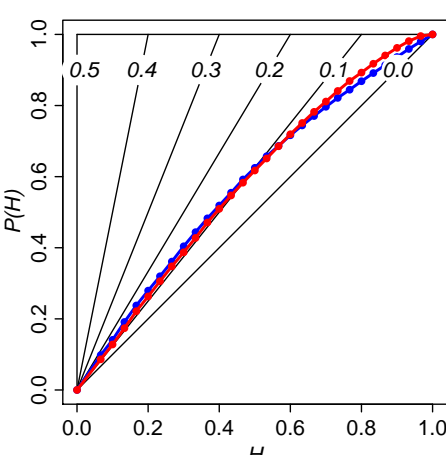
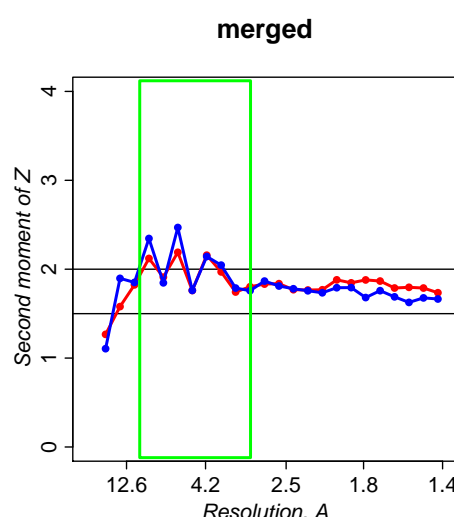
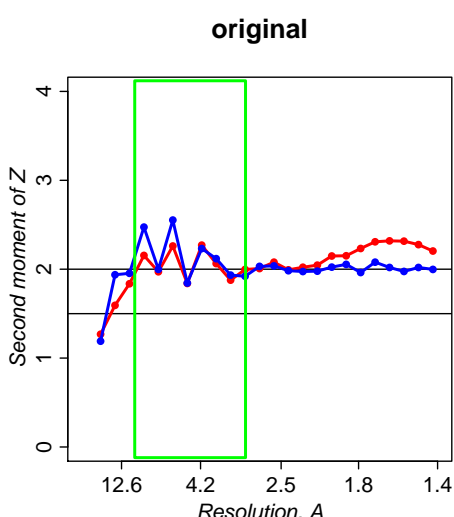
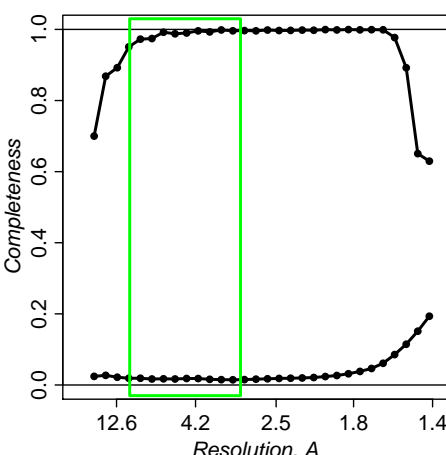
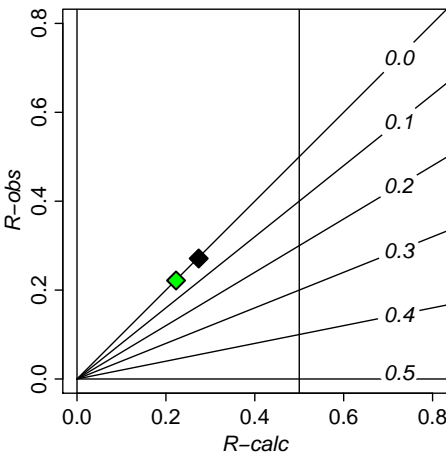
	original	merged
s.g.	P 21 21 21	P 43 21 2
p.g.	10003	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.50
R	28.8	
R'	28.9	28.6
R-free	29.8	
R'-free	30.0	30.8

s < f/100	236	0.62 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	43.9–1.4	9.9–3.0
unique	41,231	4,248
measured	38,165	4,213
used	31,934	3,206

NCS	translation	rotation
r.m.s.d. (A)	15.57	0.35
angle (o)	89.56	1.31

residues per monomer	DNA	protein
	0	104



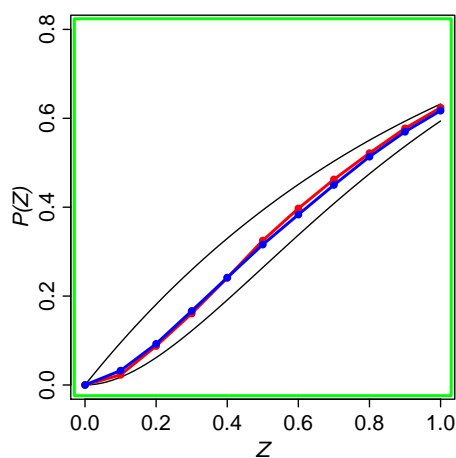
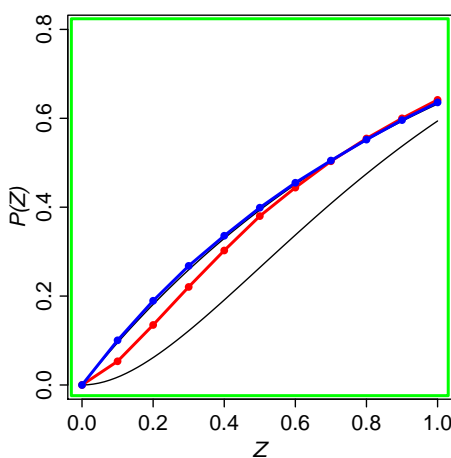
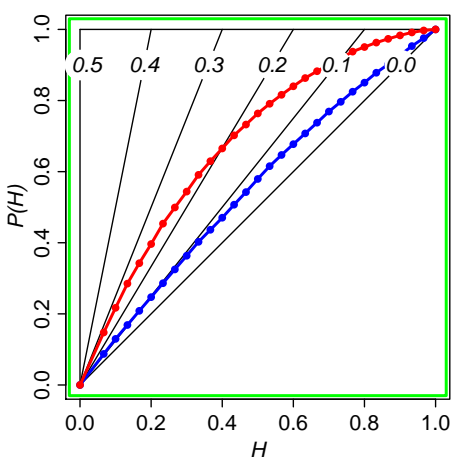
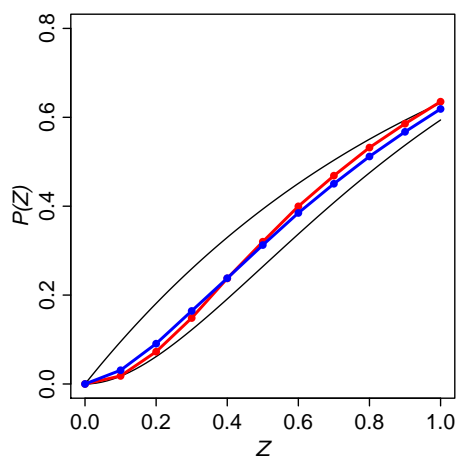
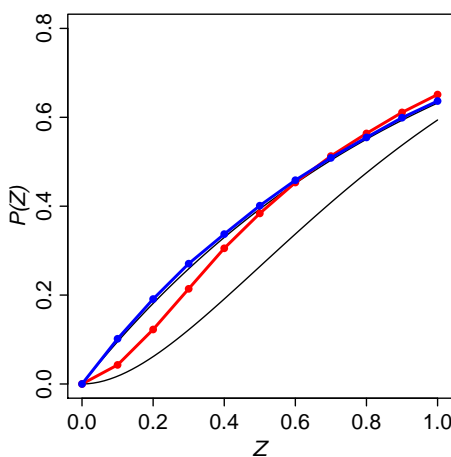
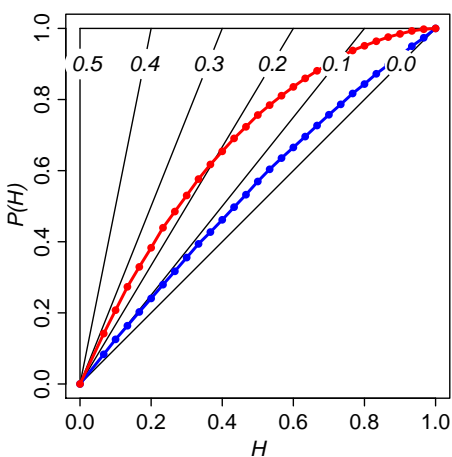
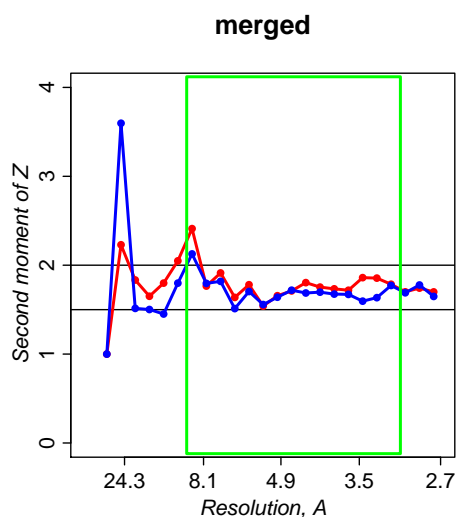
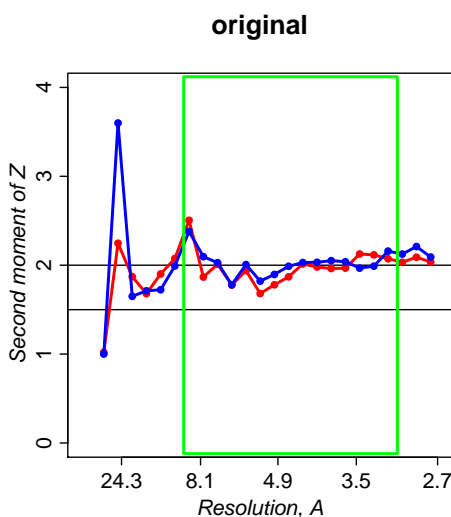
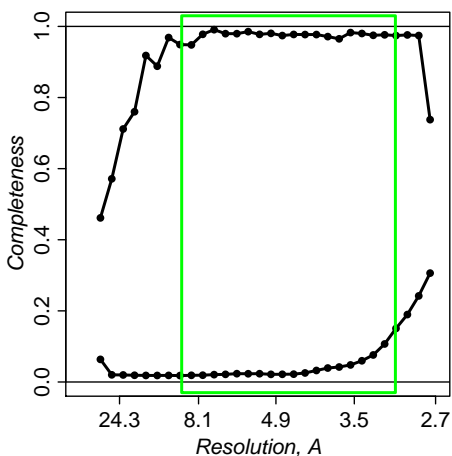
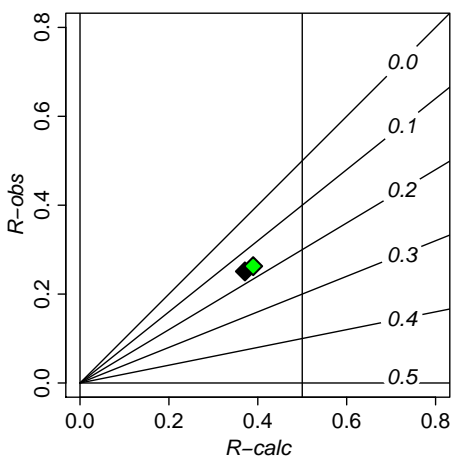
1i5l

	original	merged
s.g.	P 1 21 1	-
p.g.	10001	10003
a.u.	14	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	24.0	-
R'	-	-
R-free	29.6	-
R'-free	-	-
residues per monomer	DNA 0	protein 71

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	65.2-2.7	9.9-3.0
unique	31,219	22,138
measured	29,712	21,608
used	26,894	19,678

NCS	translation	rotation
r.m.s.d. (A)	1.77	18.82
angle (o)	12.05	174.81



1i7m

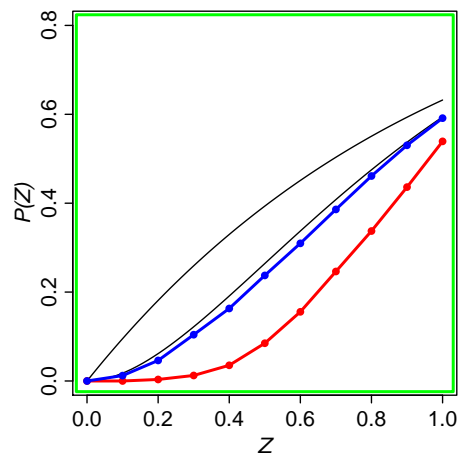
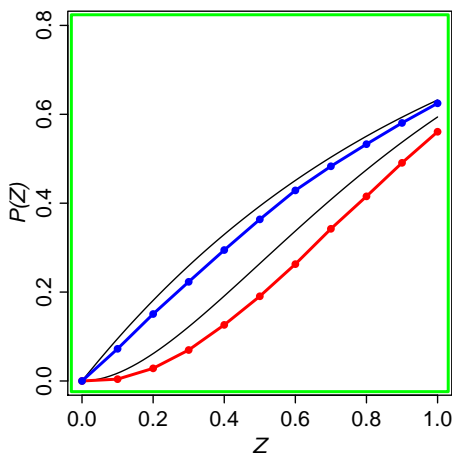
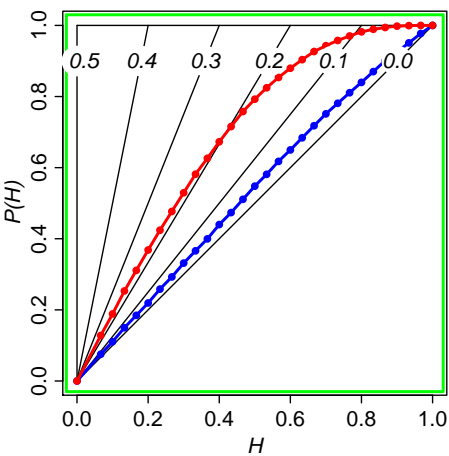
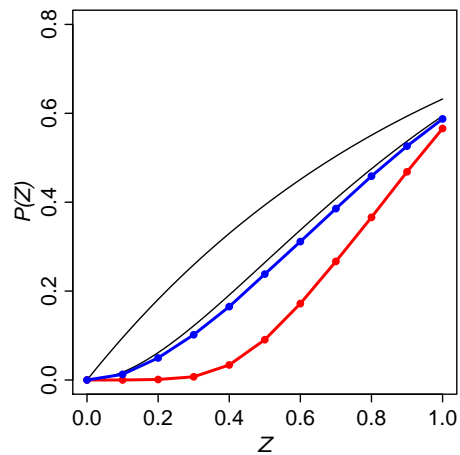
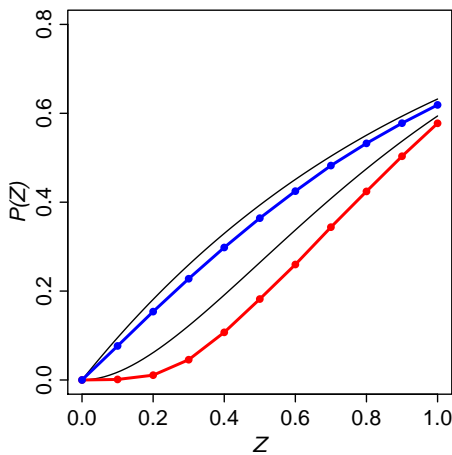
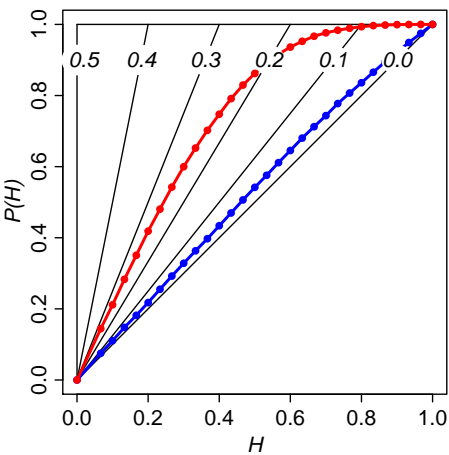
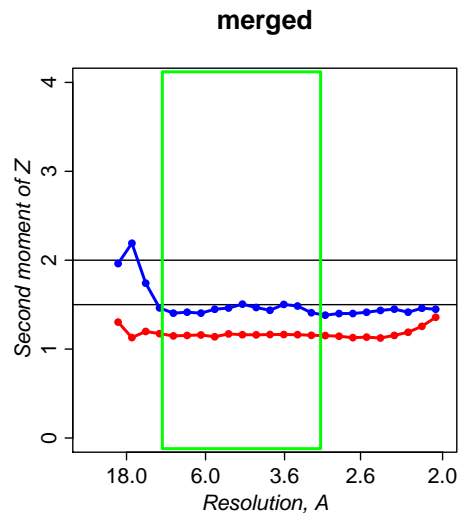
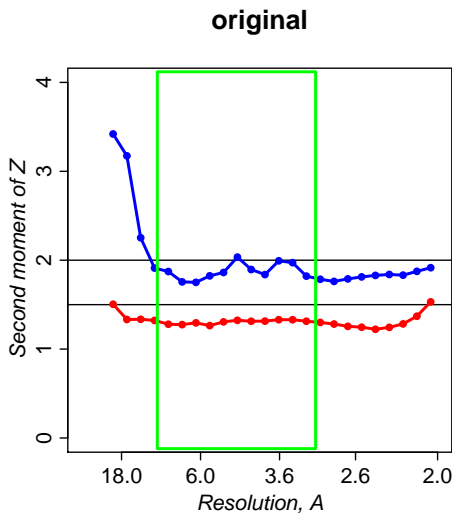
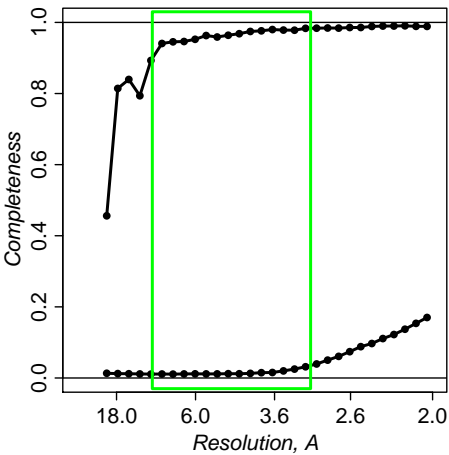
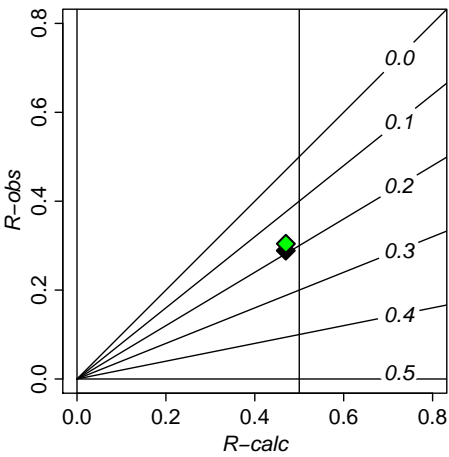
	original	merged
s.g.	P 1 21 1	-
p.g.	10001	10003
a.u.	2	-
p.t.	2	-
p.o.	2	-
r.m.s.d. (A)	-	-
R	28.2	-
R'	-	-
R-free	30.7	-
R'-free	-	-

residues per monomer	DNA	protein
	0	303

s < f/100	5131	10.50 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.4-2.0	9.9-3.0
unique	49,800	14,503
measured	48,878	14,092
used	43,854	12,330

NCS	translation	rotation
r.m.s.d. (A)	2.93	28.06
angle (o)	11.50	168.64



1ic8

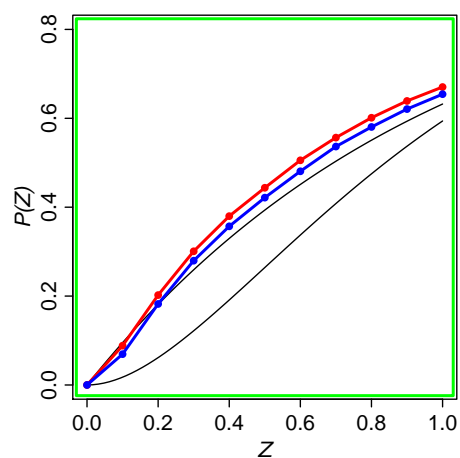
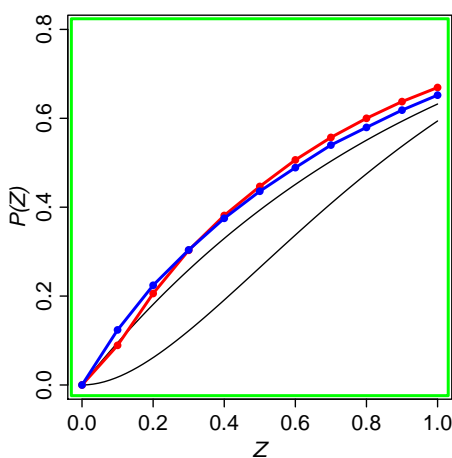
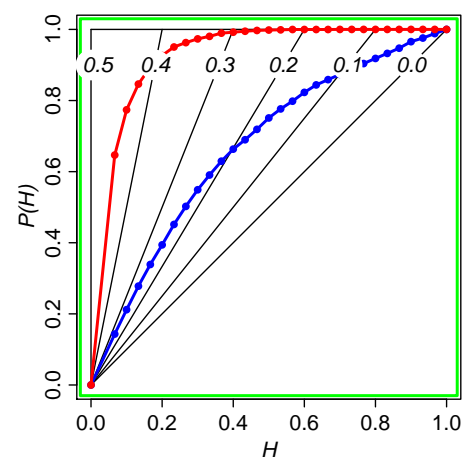
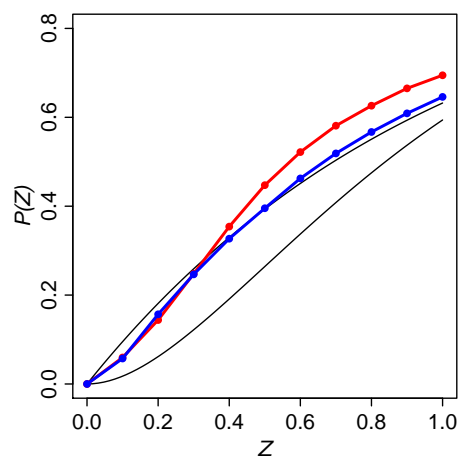
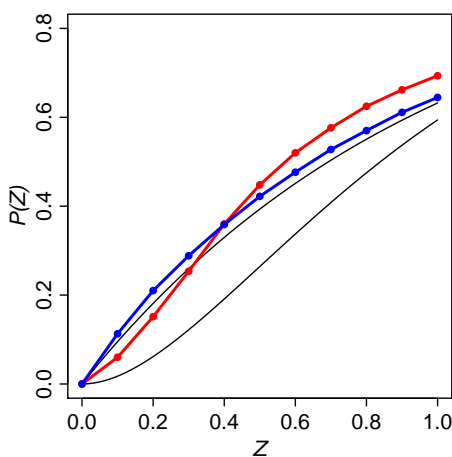
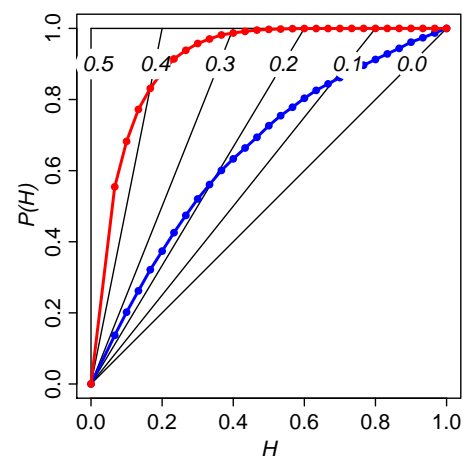
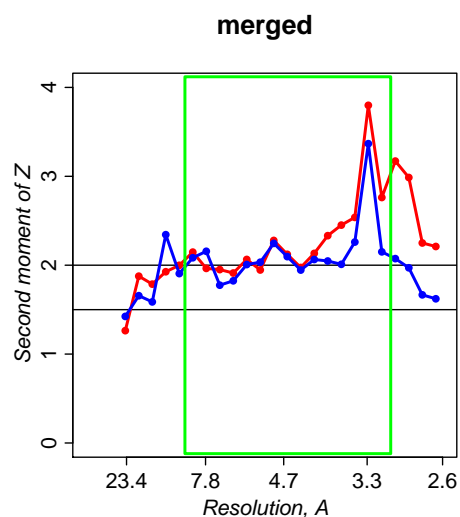
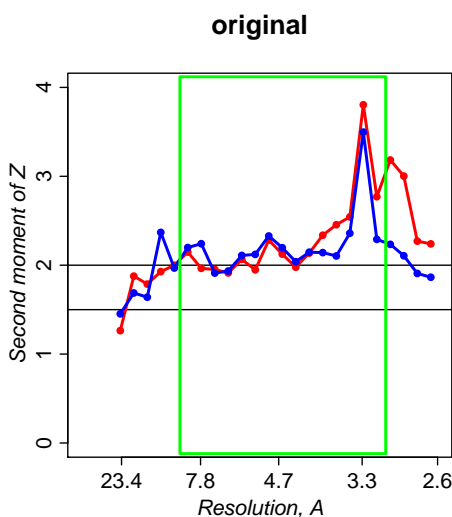
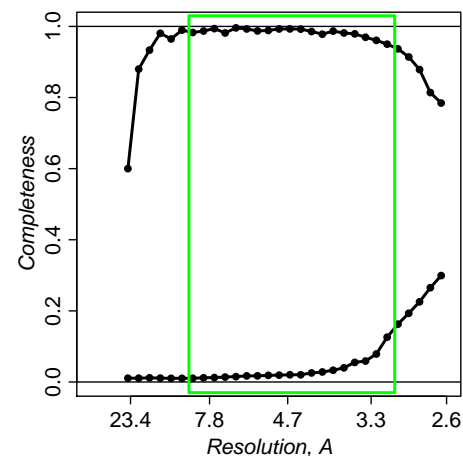
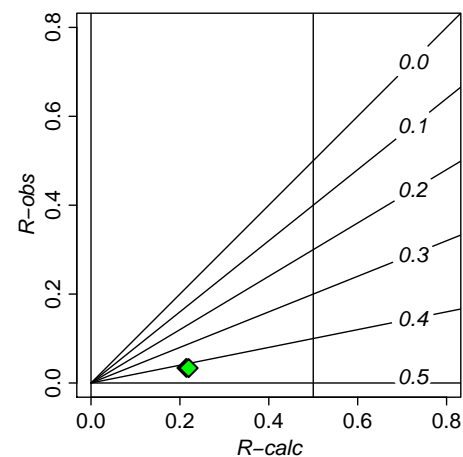
	original	merged
s.g.	P 41	P 41 21 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.88
R	39.2	
R'	40.7	42.1
R-free	47.1	
R'-free	49.8	50.5

s < f/100	686	4.63 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.4–2.6	9.9–3.0
unique	15,891	10,071
measured	14,810	9,829
used	11,978	8,146

NCS	translation	rotation
r.m.s.d. (A)	31.46	0.88
angle (o)	179.57	0.45

residues per monomer	DNA	protein
	0	169



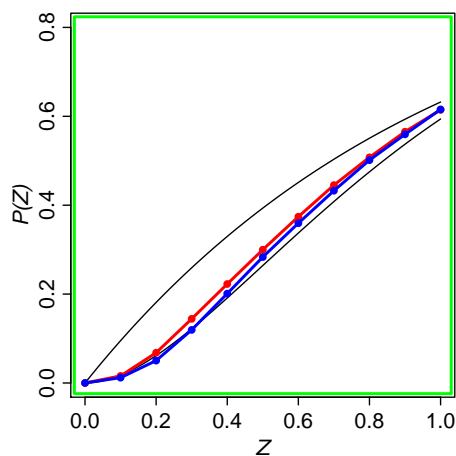
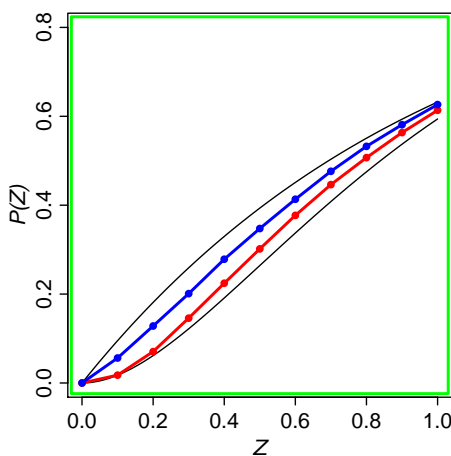
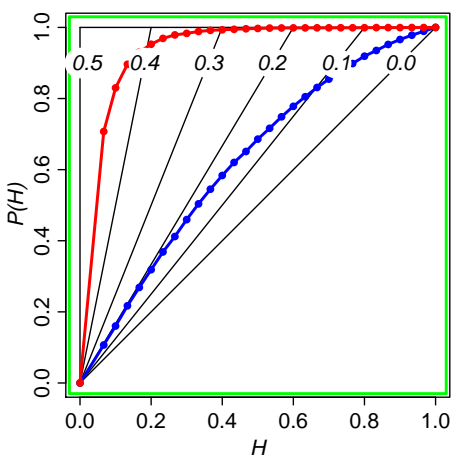
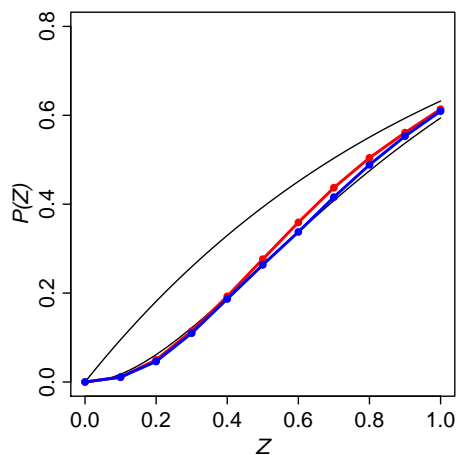
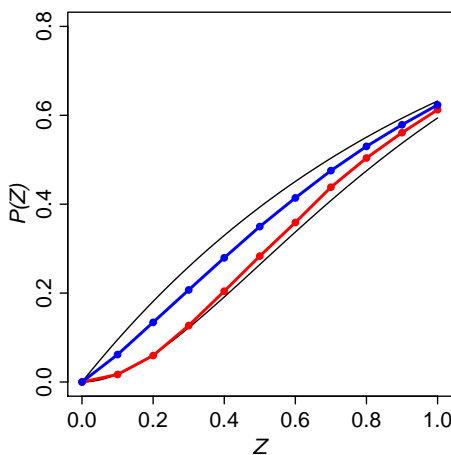
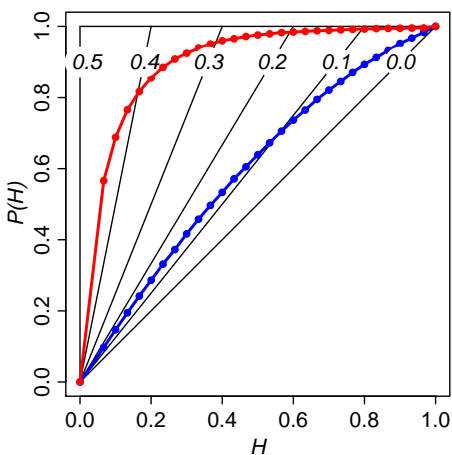
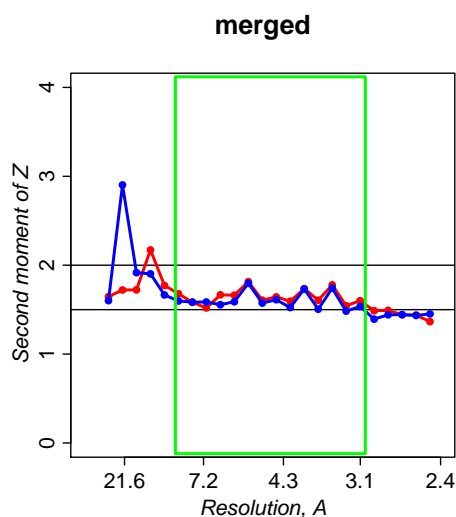
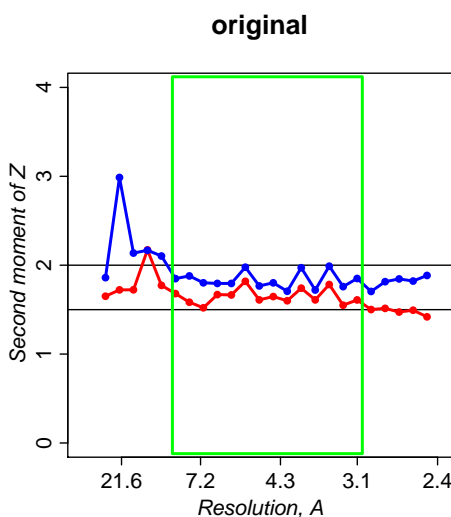
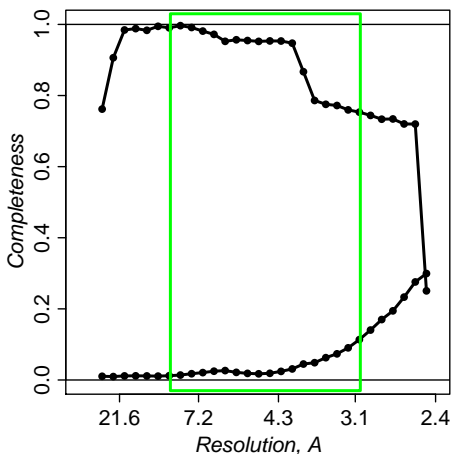
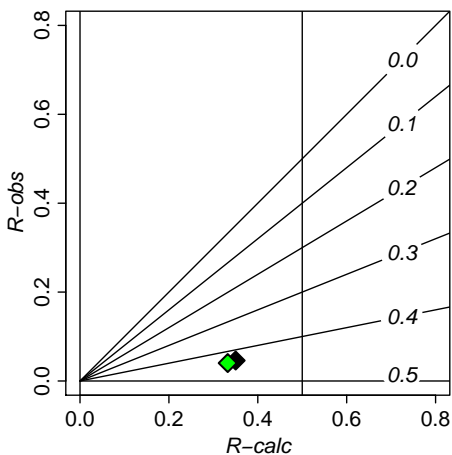
1igj

	original	merged
s.g.	P 1 21 1	-
p.g.	10001	10003
a.u.	2	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	25.1	-
R'	-	-
R-free	31.8	-
R'-free	-	-
residues per monomer	DNA 0	protein 433

s < f/100	1535	5.67 %
s <= 0	0	0.00 %
f <= 0	64	0.24 %
s,f <= 0	0	0.00 %

range (A)	51.7-2.4	9.9-3.0
unique	35,765	18,447
measured	27,090	15,833
used	19,596	12,382

NCS	translation	rotation
r.m.s.d. (A)	34.40	0.75
angle (o)	179.72	0.40



1ihc

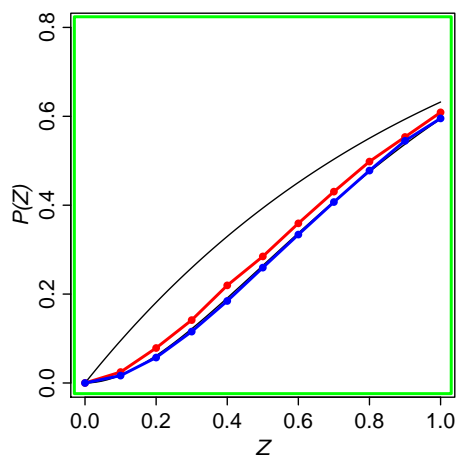
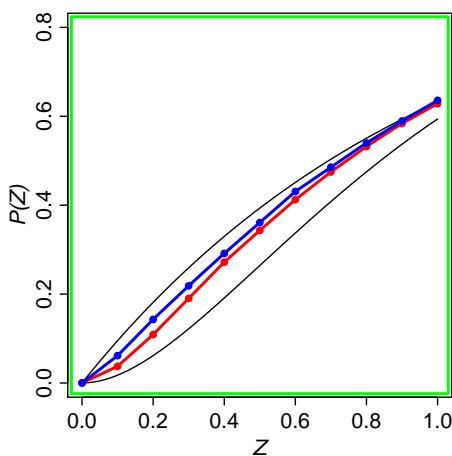
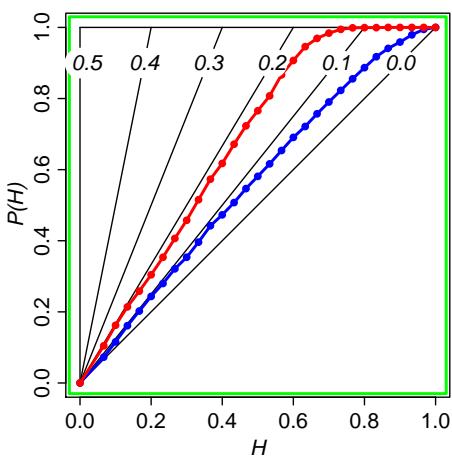
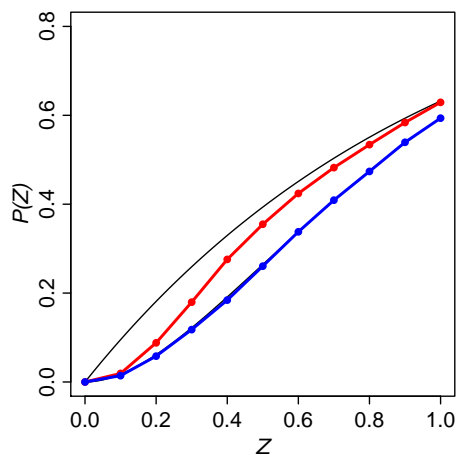
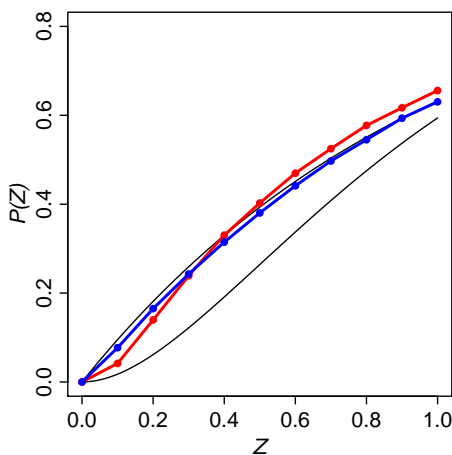
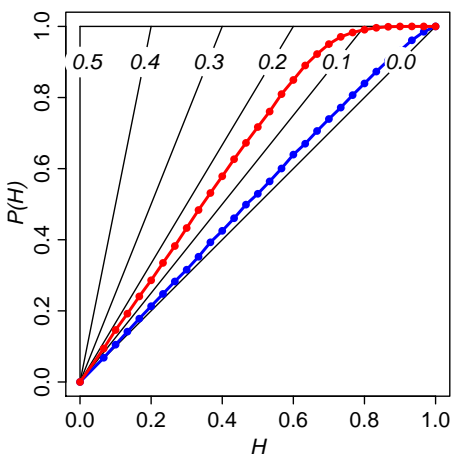
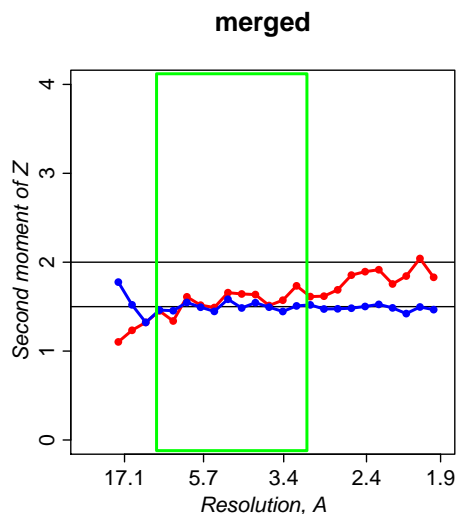
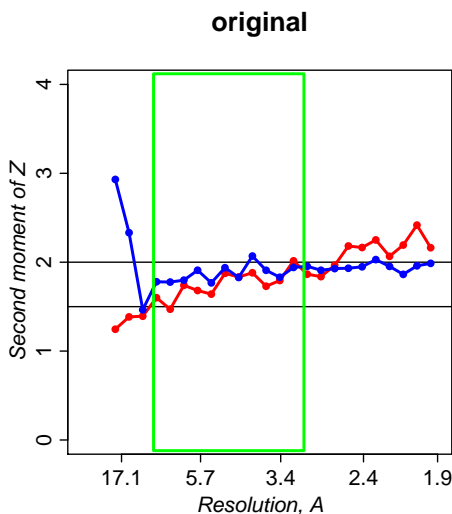
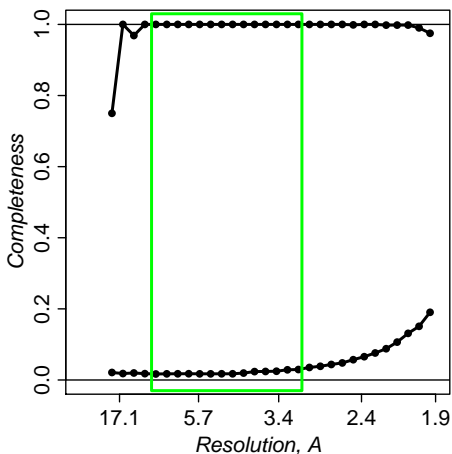
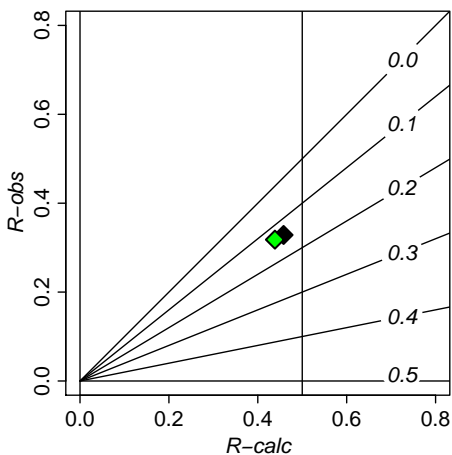
	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	22.4	-
R'	-	-
R-free	25.0	-
R'-free	-	-

residues per monomer	DNA	protein
	0	169

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	25.6-1.9	9.9-3.0
unique	14,563	3,578
measured	14,511	3,578
used	13,532	3,228

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



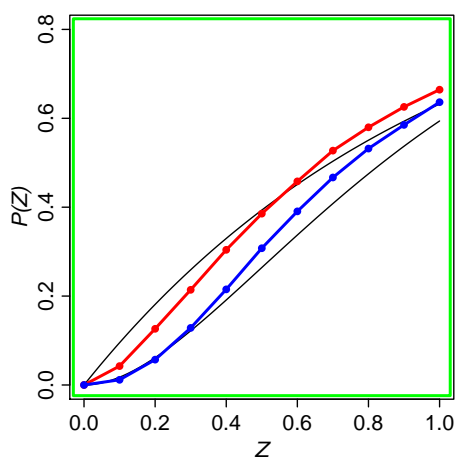
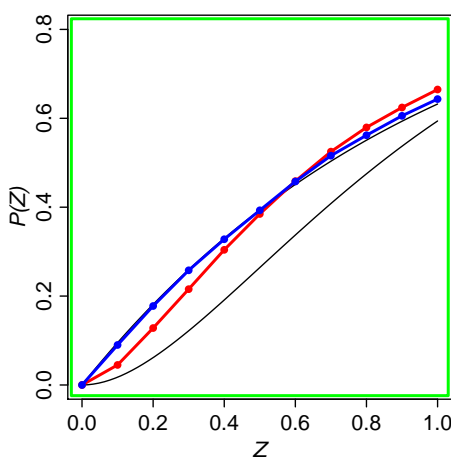
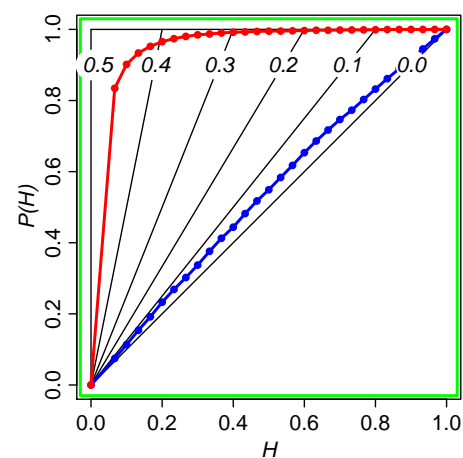
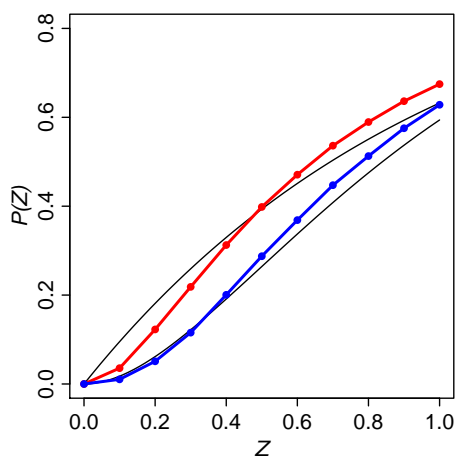
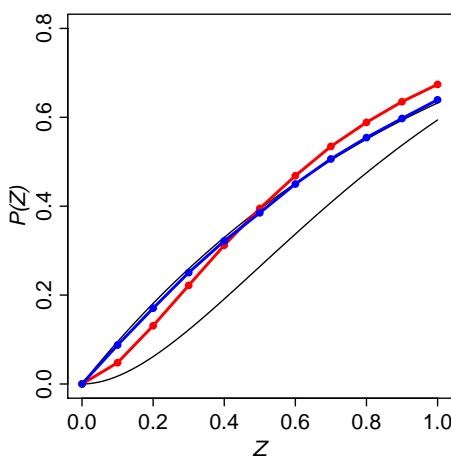
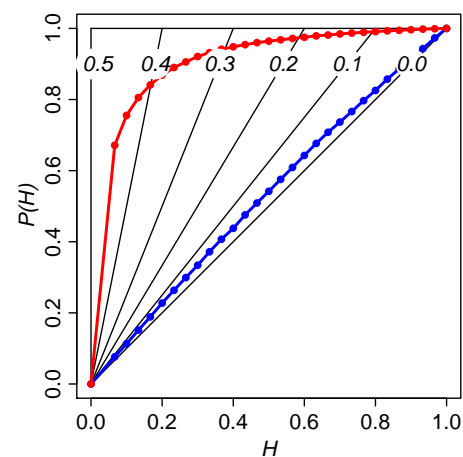
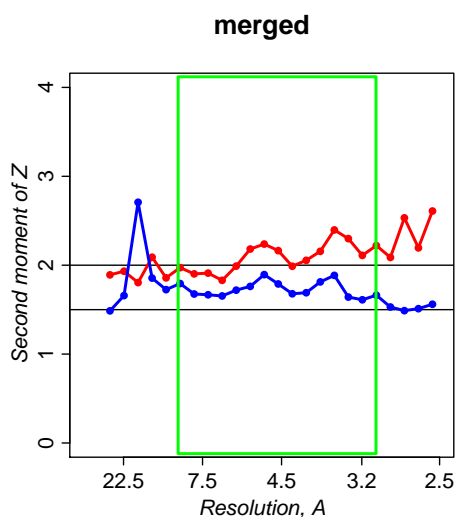
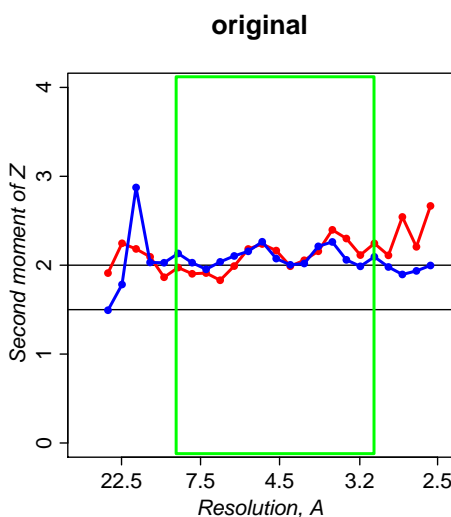
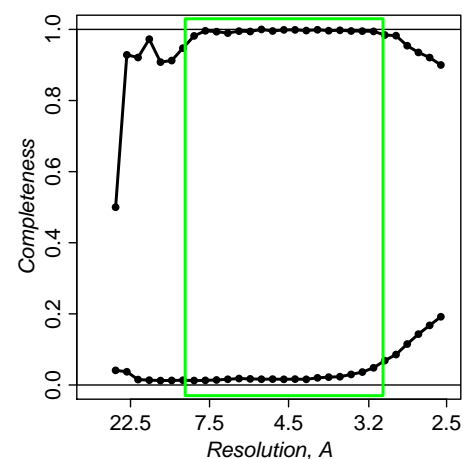
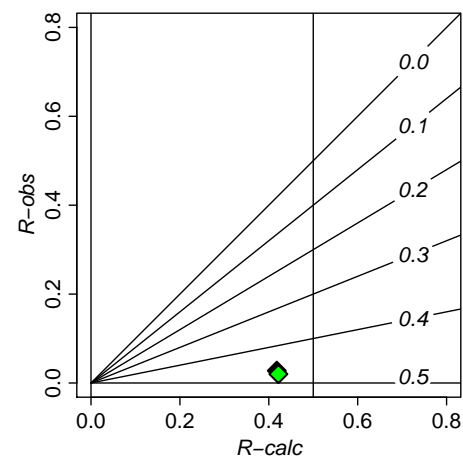
1irm

	original	merged
s.g.	P 32	-
p.g.	10020	10023
a.u.	3	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (Å)	-	-
R	29.8	-
R'	-	-
R-free	36.0	-
R'-free	-	-
residues per monomer	DNA 0	protein 190

s < f/100	1198	4.61 %
s <= 0	750	2.88 %
f <= 0	750	2.88 %
s,f <= 0	750	2.88 %

range (Å)	46.8–2.5	9.9–3.0
unique	26,825	15,122
measured	26,008	15,045
used	23,472	13,700

NCS	translation	rotation
r.m.s.d. (Å)	1.18	0.98
angle (°)	3.68	1.20



1is7

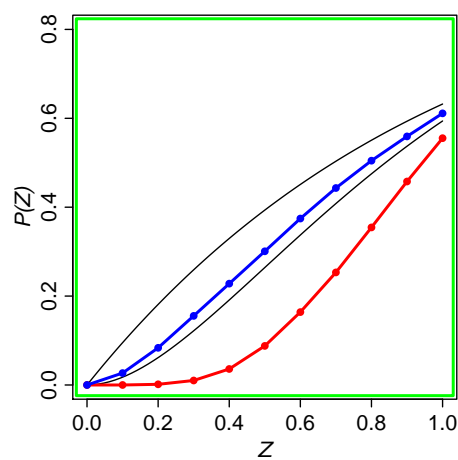
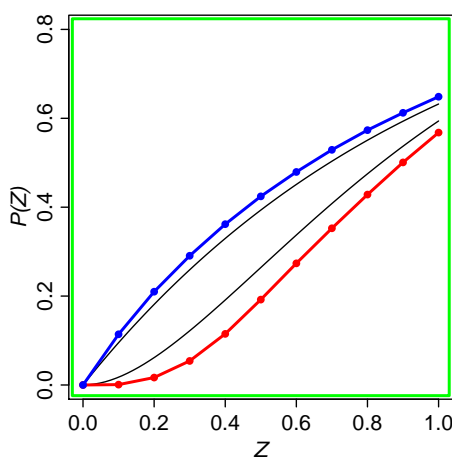
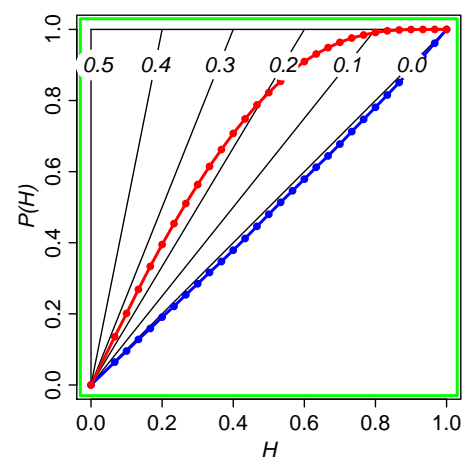
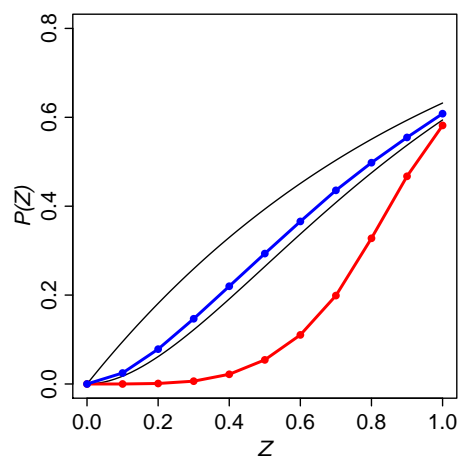
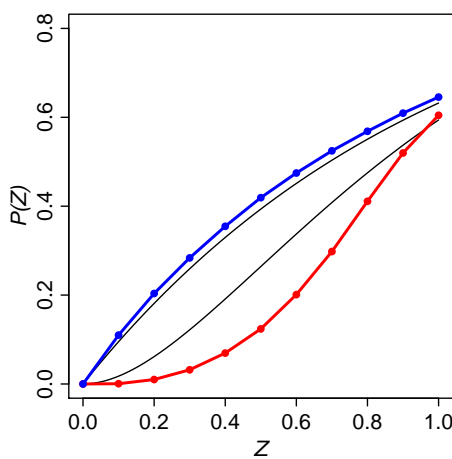
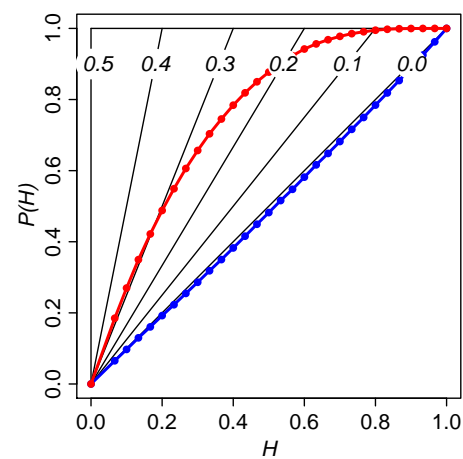
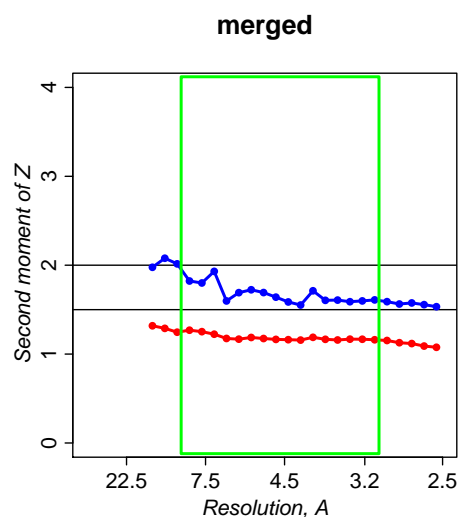
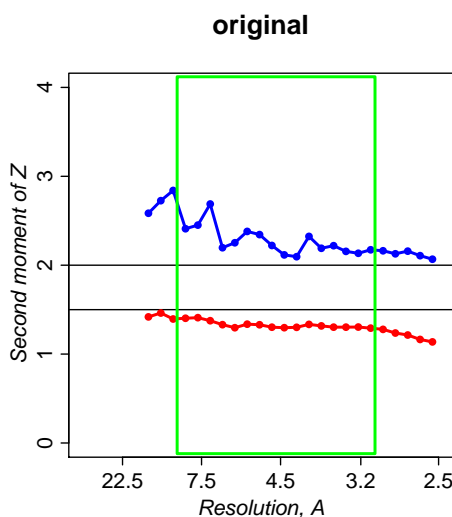
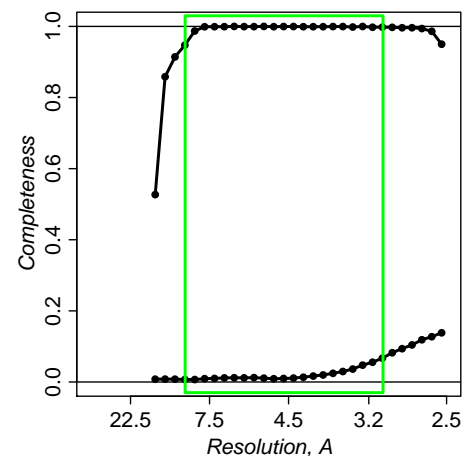
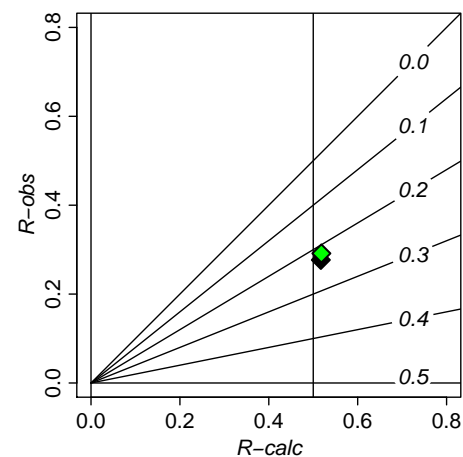
	original	merged
s.g.	P 1 21 1	-
p.g.	10001	10003
a.u.	10	-
p.t.	2	-
p.o.	2	-
r.m.s.d. (A)	-	-
R	26.8	-
R'	-	-
R-free	31.4	-
R'-free	-	-

s < f/100	27144	23.26 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	15.0-2.5	9.9-3.0
unique	117,666	66,681
measured	116,689	66,575
used	108,788	62,486

NCS	translation	rotation
r.m.s.d. (A)	1.12	7.73
angle (o)	4.34	33.57

residues per monomer	DNA	protein
	0	278



1is8

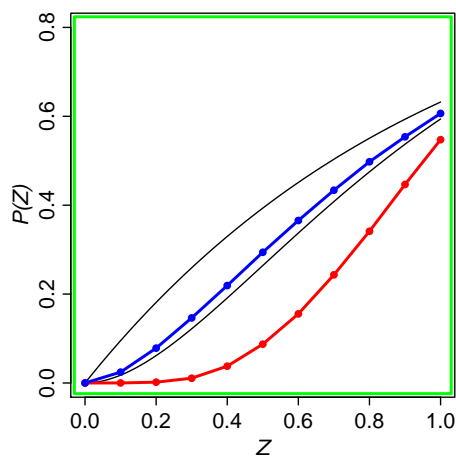
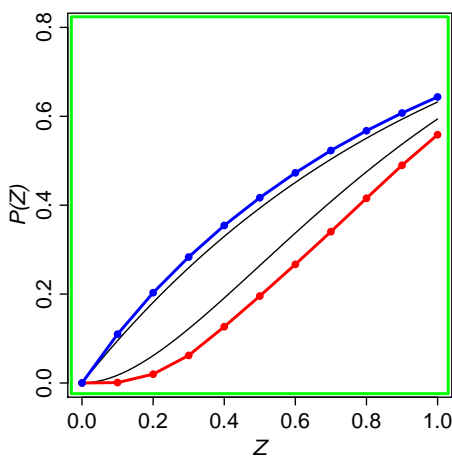
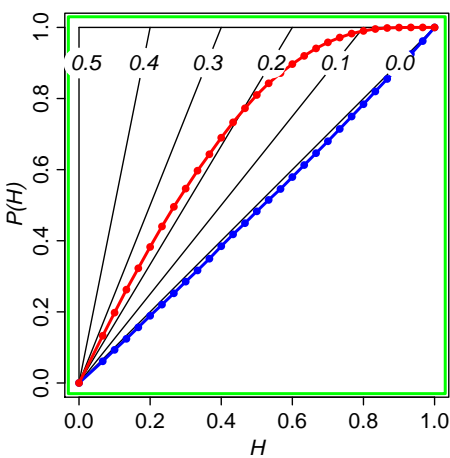
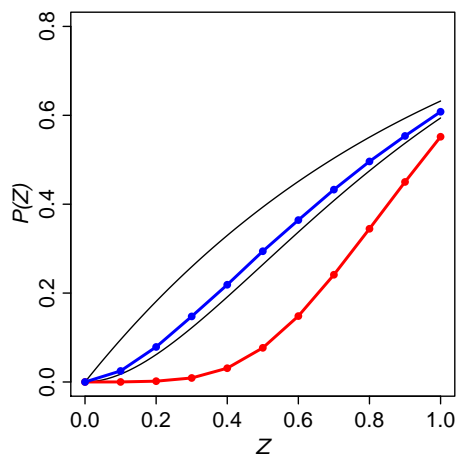
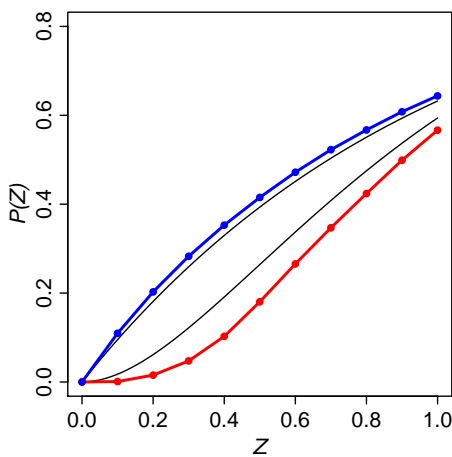
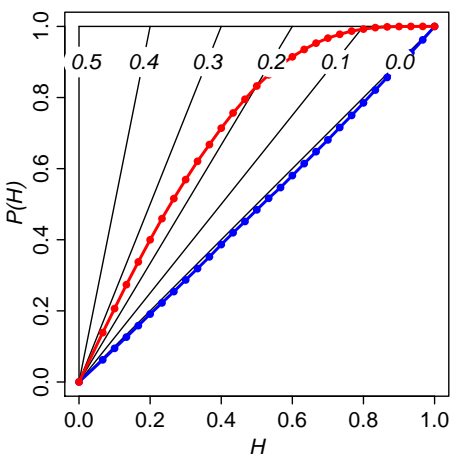
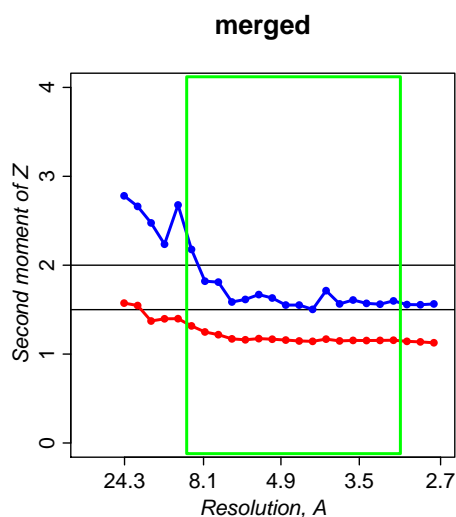
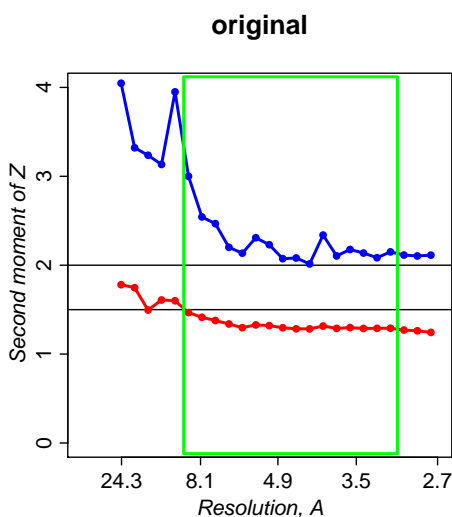
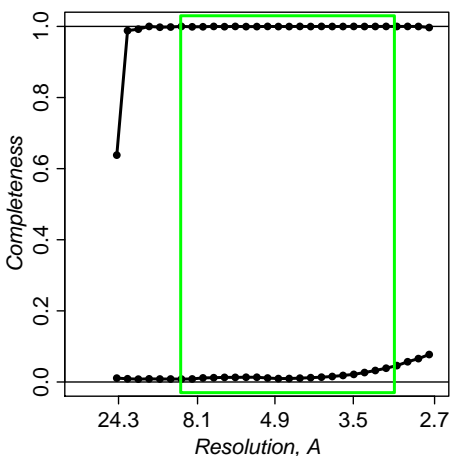
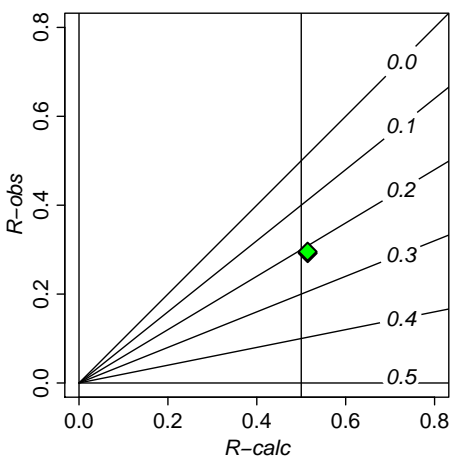
	original	merged
s.g.	P 1 21 1	-
p.g.	10001	10003
a.u.	10	-
p.t.	2	-
p.o.	2	-
r.m.s.d. (A)	-	-
R	24.9	-
R'	-	-
R-free	29.8	-
R'-free	-	-

s < f/100	31947	34.25 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.6-2.7	9.9-3.0
unique	93,329	66,246
measured	93,283	66,233
used	87,002	62,230

NCS	translation	rotation
r.m.s.d. (A)	1.13	7.67
angle (o)	4.67	33.35

residues per monomer	DNA	protein
	0	276



1ixy

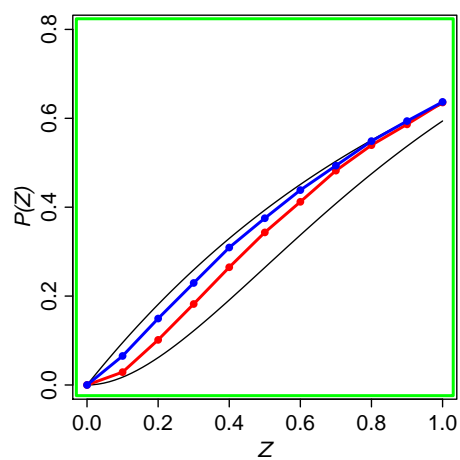
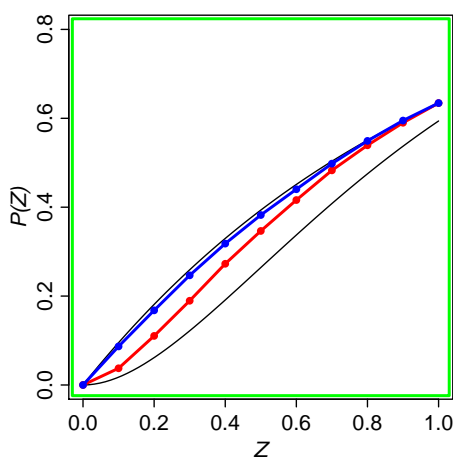
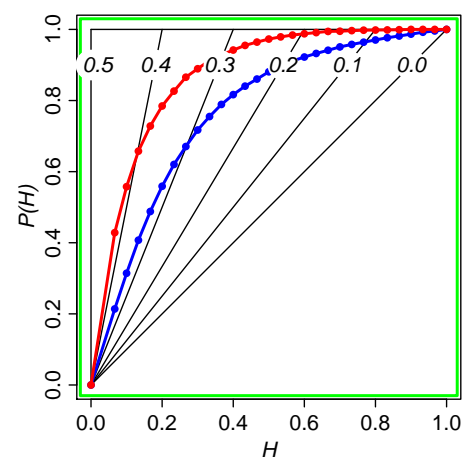
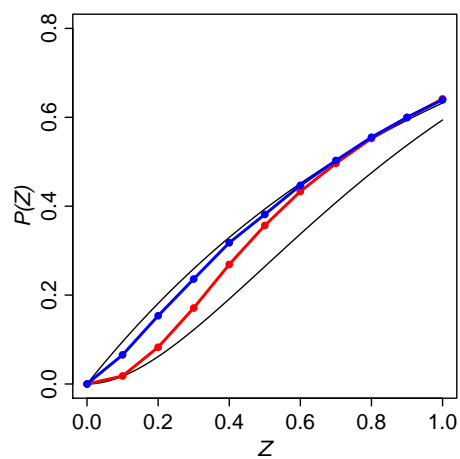
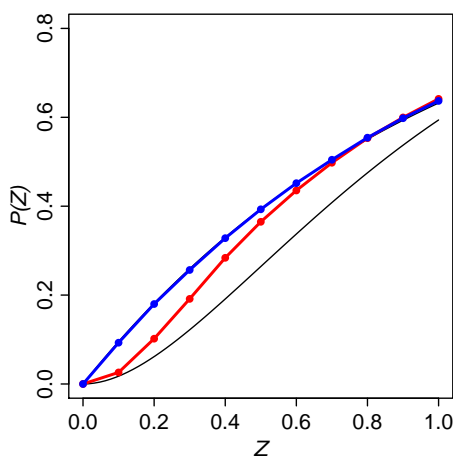
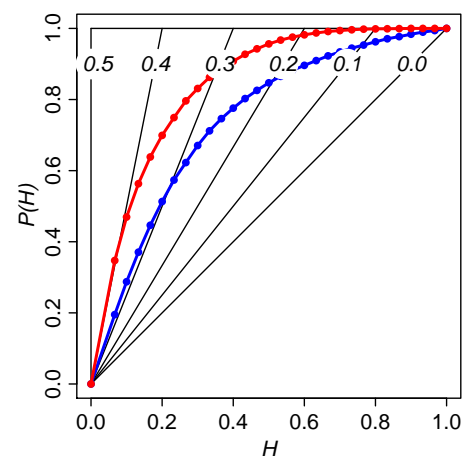
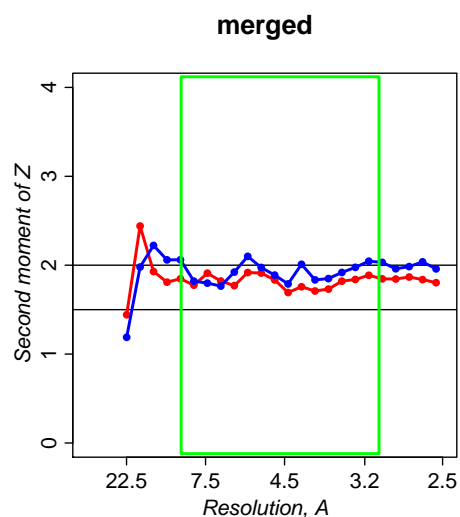
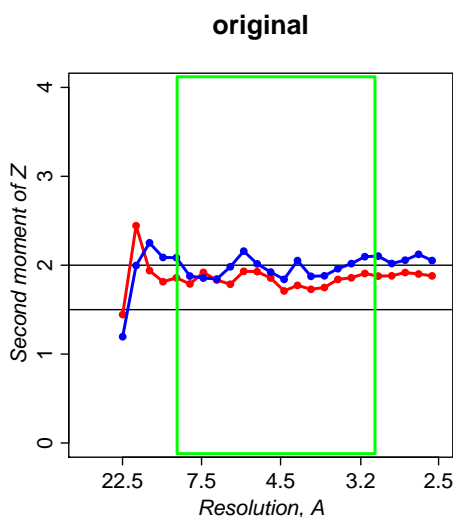
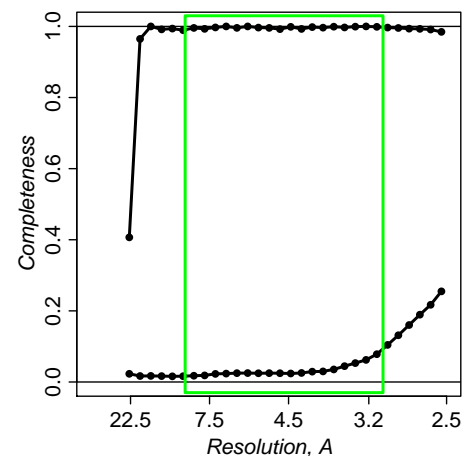
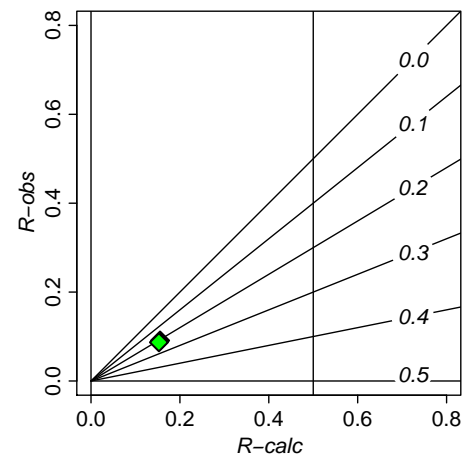
	original	merged
s.g.	P 1 21 1	P 21 21 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.22
R	23.6	
R'	23.9	24.0
R-free	29.2	
R'-free	29.2	28.6

s < f/100	47	0.15 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	27.0–2.5	9.9–3.0
unique	30,590	17,254
measured	30,421	17,211
used	27,158	15,254

NCS	translation	rotation
r.m.s.d. (A)	28.92	0.22
angle (o)	179.86	0.18

residues per monomer	DNA	protein
	23	351



1izn

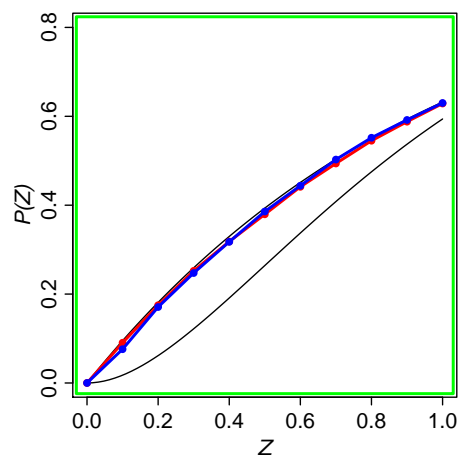
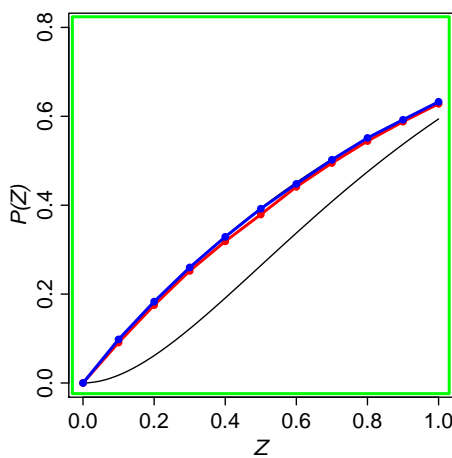
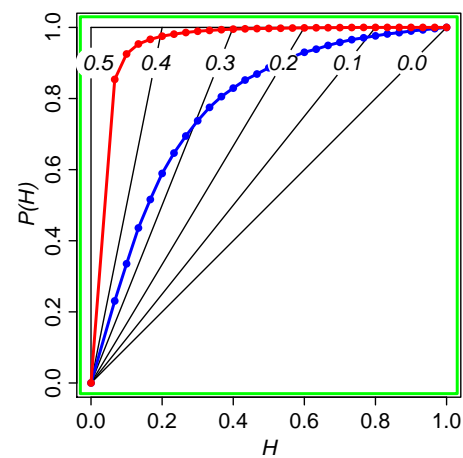
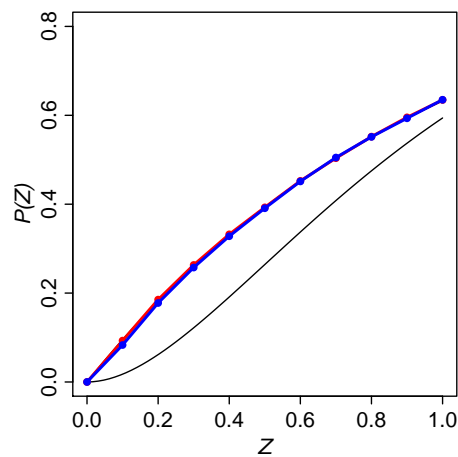
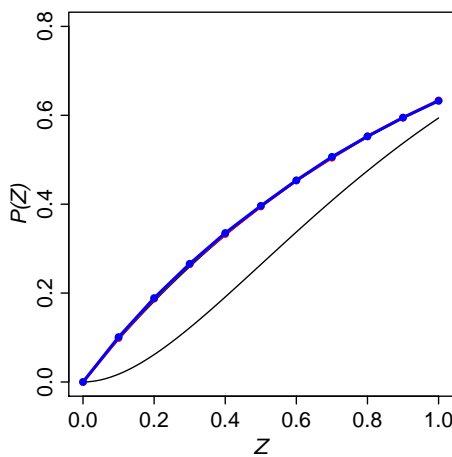
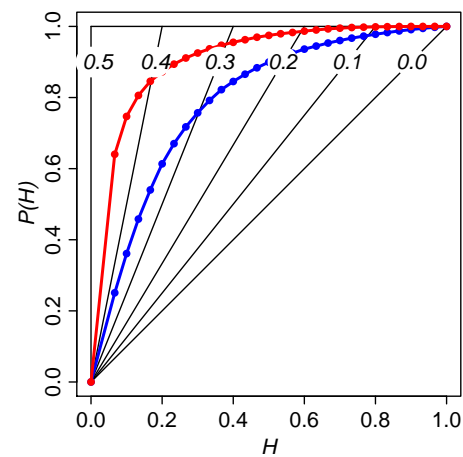
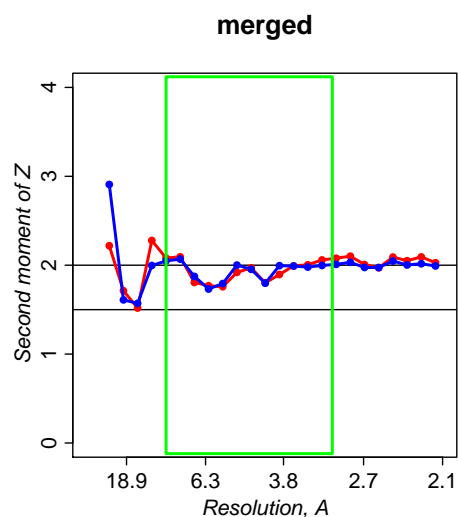
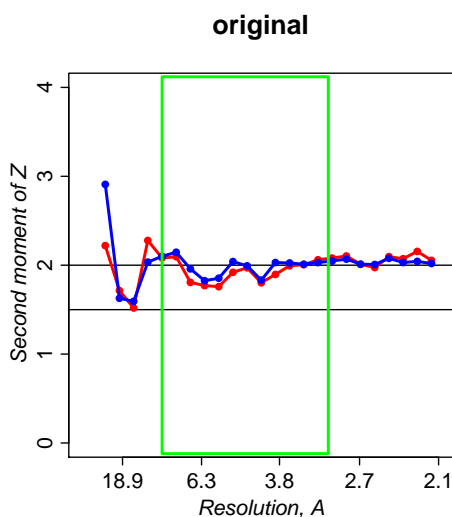
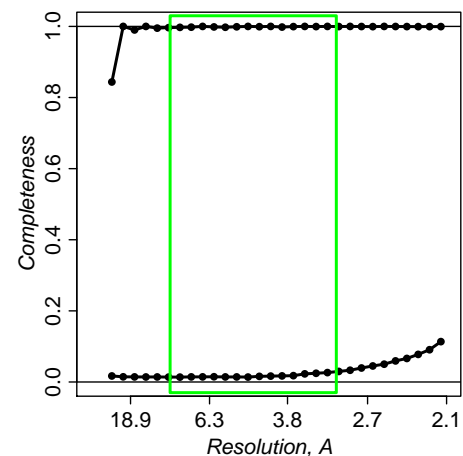
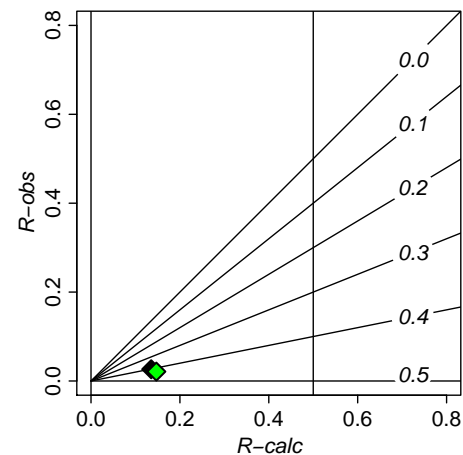
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.44
R	26.4	
R'	27.2	27.2
R-free	29.5	
R'-free	29.6	29.9

s < f/100	16	0.03 %
s <= 0	16	0.03 %
f <= 0	16	0.03 %
s,f <= 0	16	0.03 %

range (A)	49.3–2.1	9.9–3.0
unique	60,220	20,238
measured	60,190	20,224
used	55,624	18,184

NCS	translation	rotation
r.m.s.d. (A)	50.02	0.44
angle (o)	179.92	0.12

residues per monomer	DNA	protein
	0	541



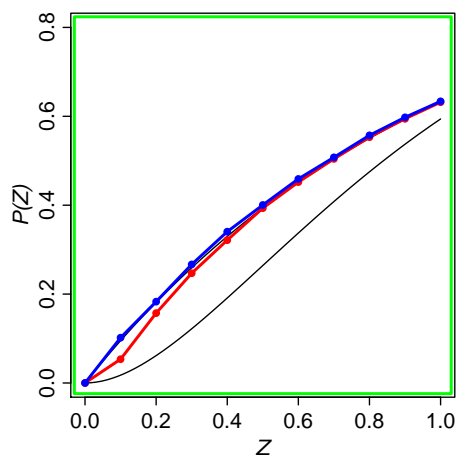
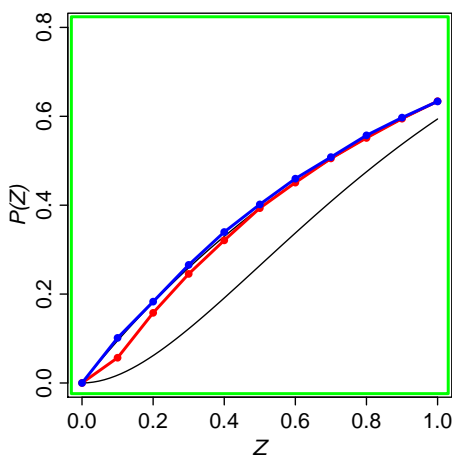
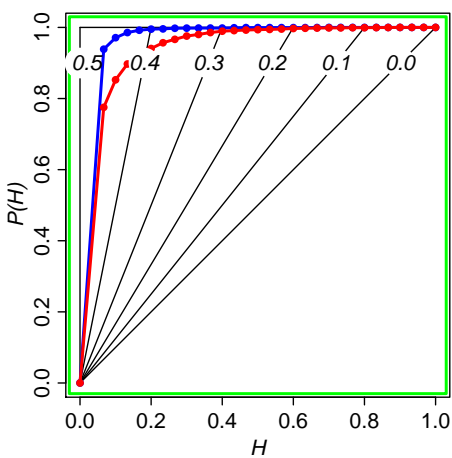
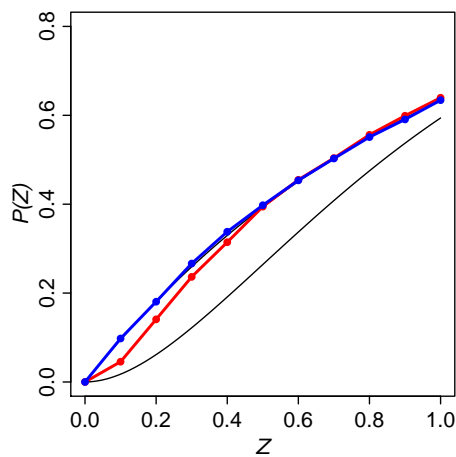
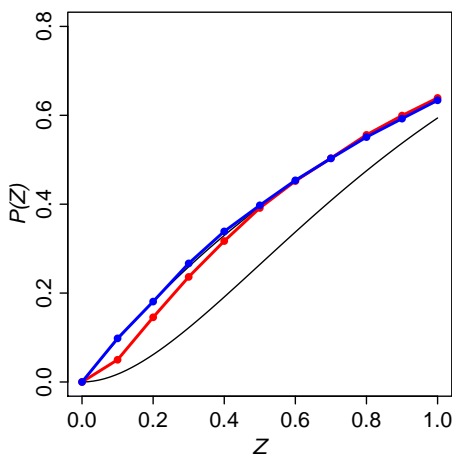
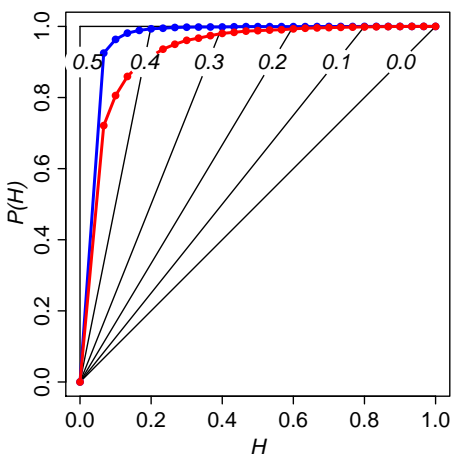
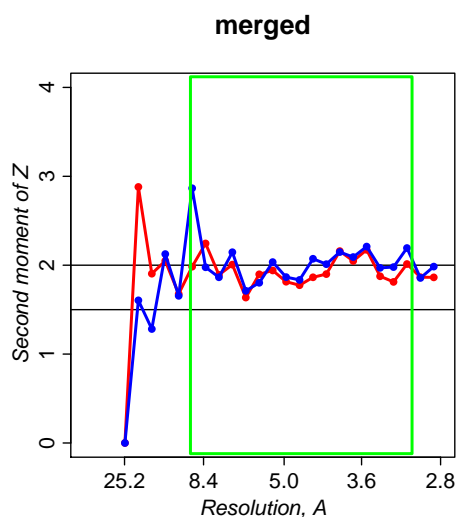
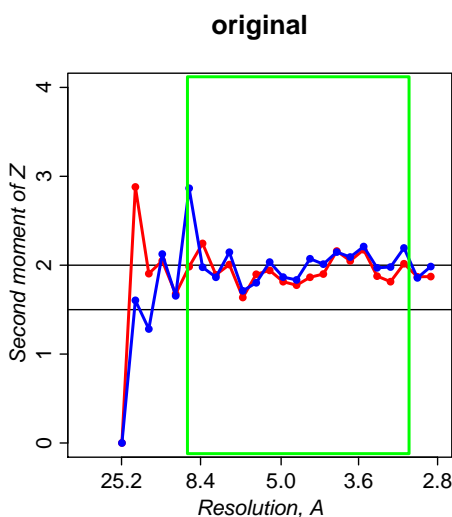
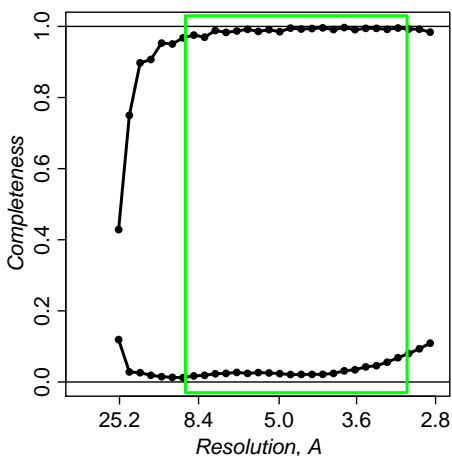
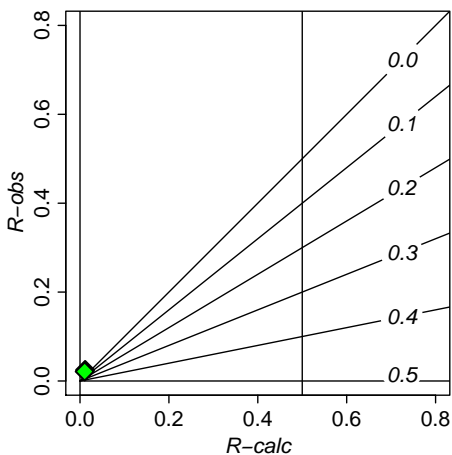
1izy

	original	merged
s.g.	P 65	P 65 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.01
R	21.4	
R'	21.4	22.6
R-free	27.5	
R'-free	27.5	29.2
residues per monomer	DNA 0	protein 276

s < f/100	573	4.70 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	30.0–2.8	9.9–3.0
unique	12,335	9,781
measured	12,202	9,703
used	9,876	7,842

NCS	translation	rotation
r.m.s.d. (A)	26.95	0.01
angle (o)	179.97	0.05



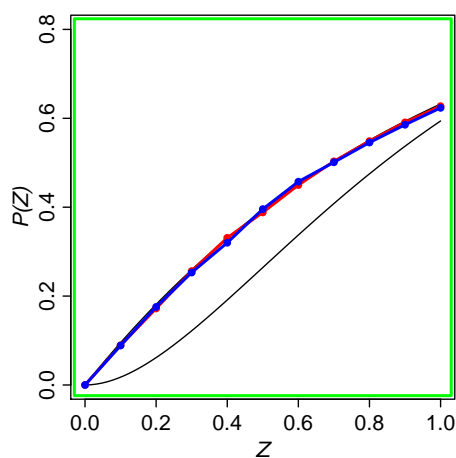
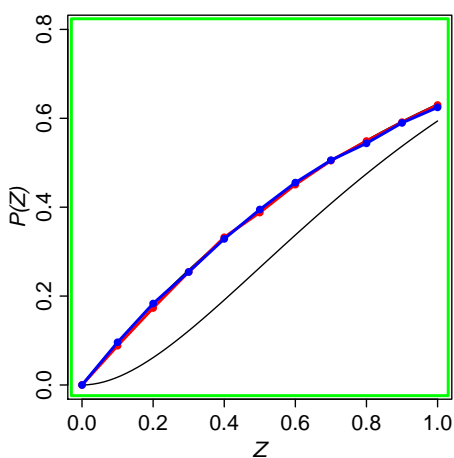
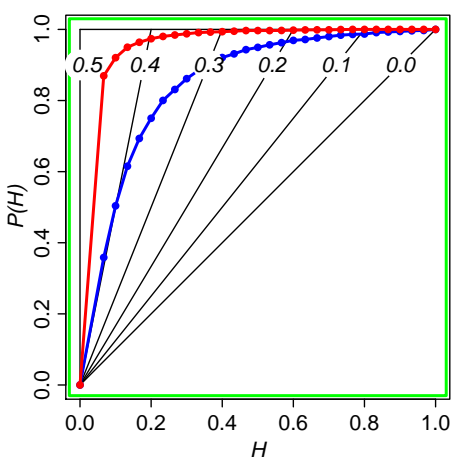
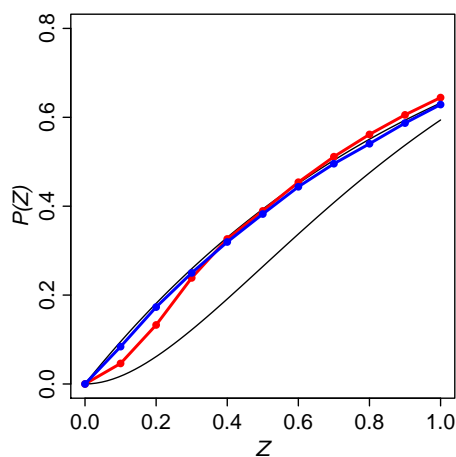
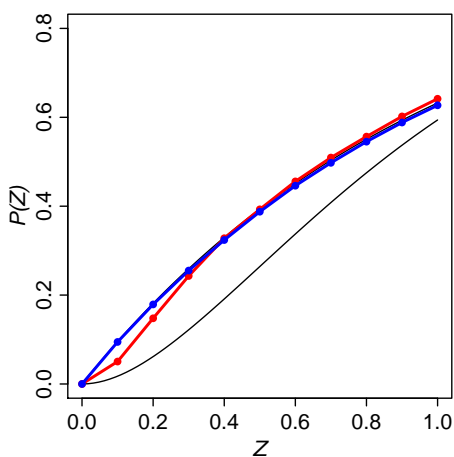
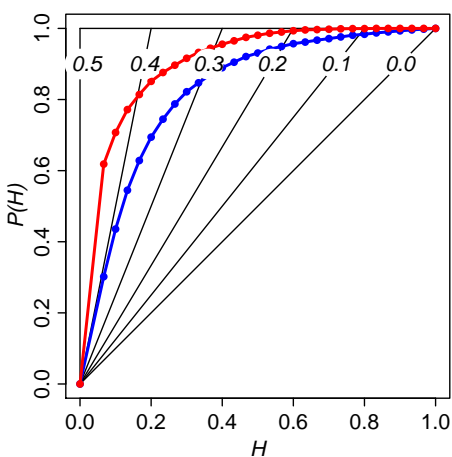
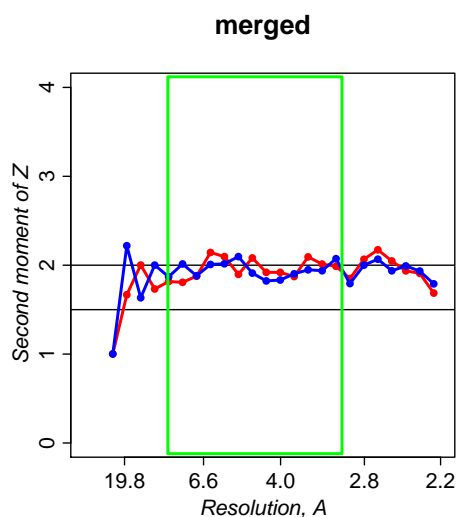
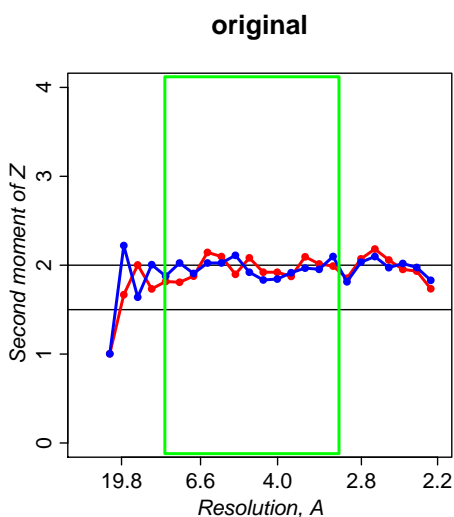
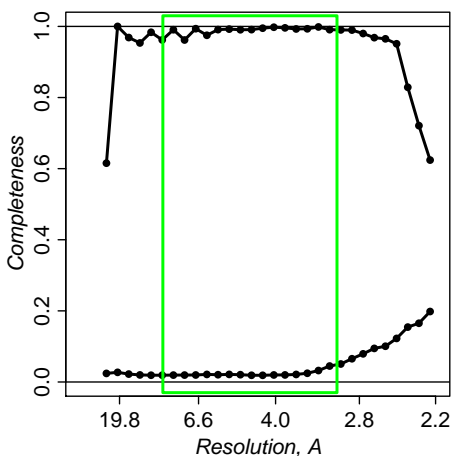
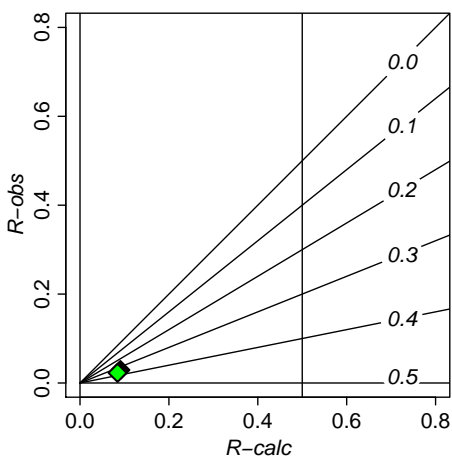
1j1a

	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.09
R	28.7	
R'	28.7	29.3
R-free	32.0	
R'-free	32.1	32.5
residues per monomer	DNA 0	protein 124

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	37.6–2.2	9.9–3.0
unique	15,964	6,153
measured	14,631	6,104
used	12,902	5,560

NCS	translation	rotation
r.m.s.d. (A)	22.61	0.09
angle (o)	179.98	0.03



1j5v

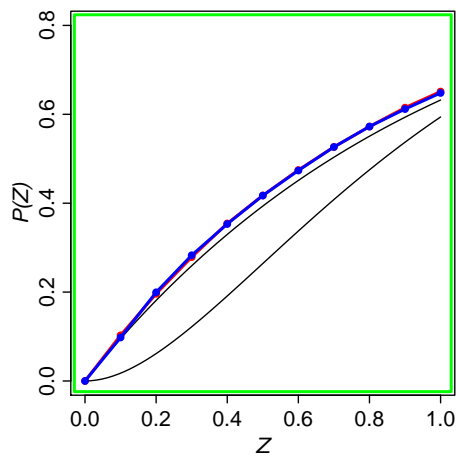
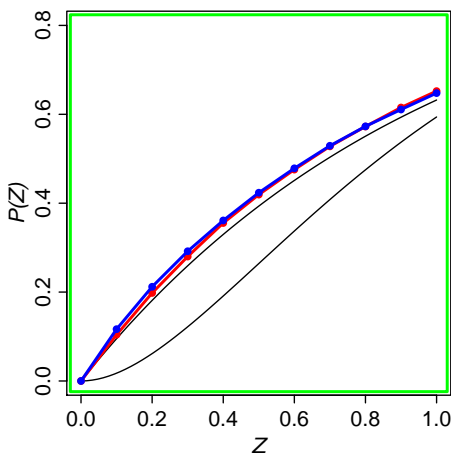
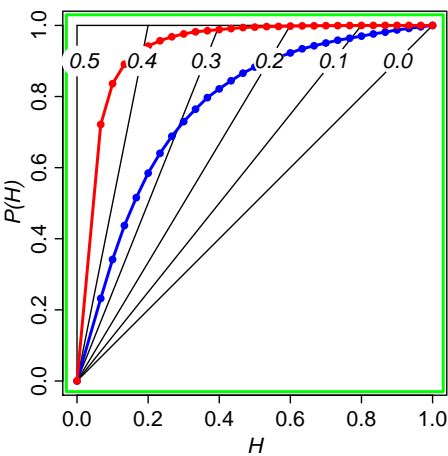
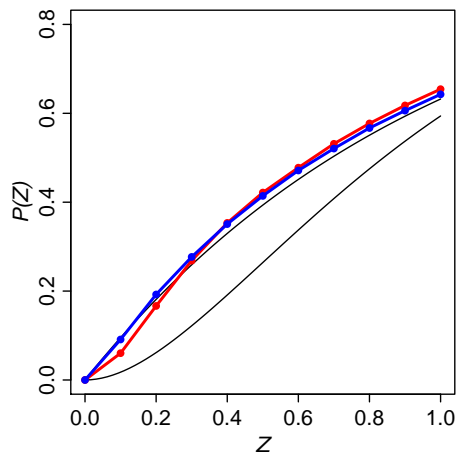
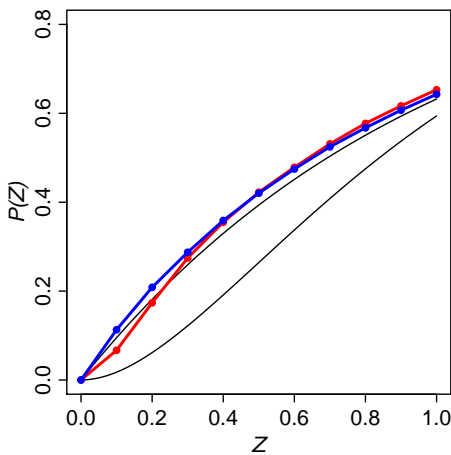
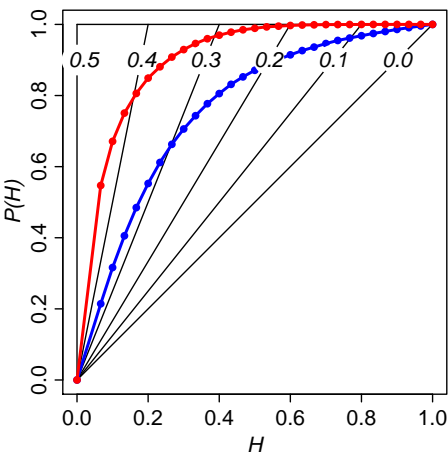
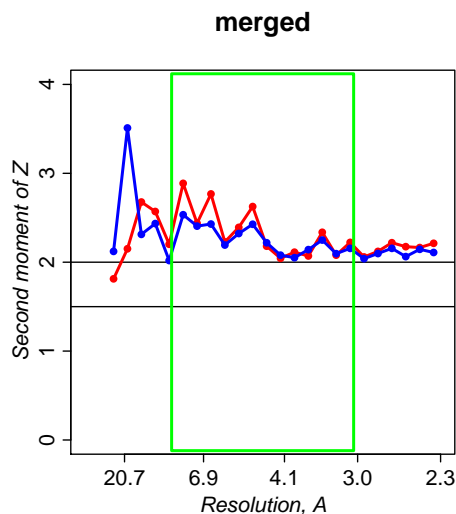
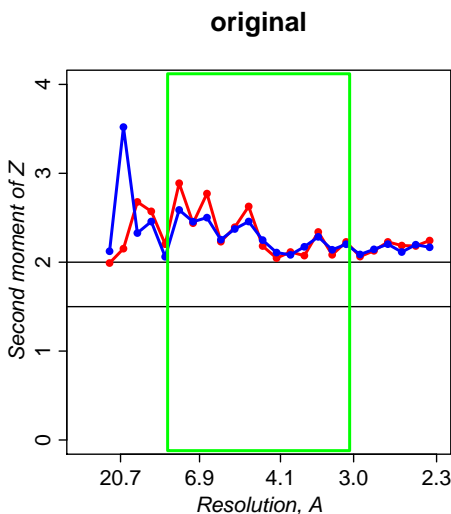
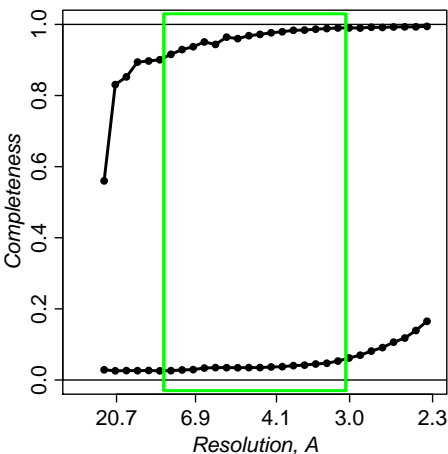
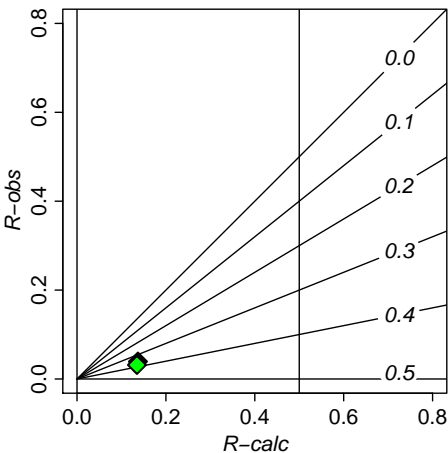
	original	merged
s.g.	H 3	H 3 2
p.g.	10020	10023
a.u.	4	2
p.t.	2	2
p.o.	1	2
r.m.s.d. (A)		0.15
R	24.2	
R'	24.5	24.7
R-free	28.5	
R'-free	28.9	29.4

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	37.9–2.3	9.9–3.0
unique	63,378	27,768
measured	62,352	27,096
used	58,690	25,018

NCS	translation	rotation
r.m.s.d. (A)	1.00	0.12
angle (o)	3.74	0.04

residues per monomer	DNA	protein
	0	320



1ja3

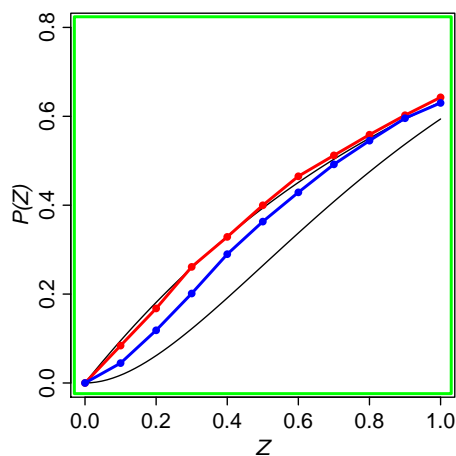
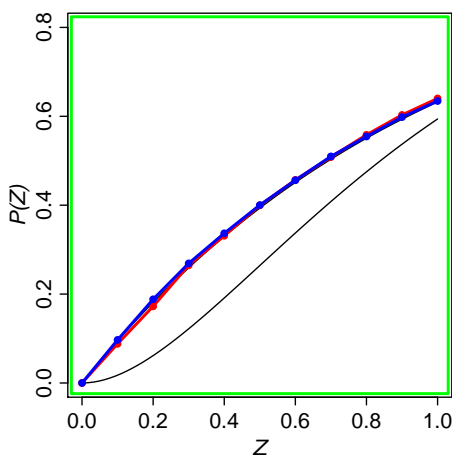
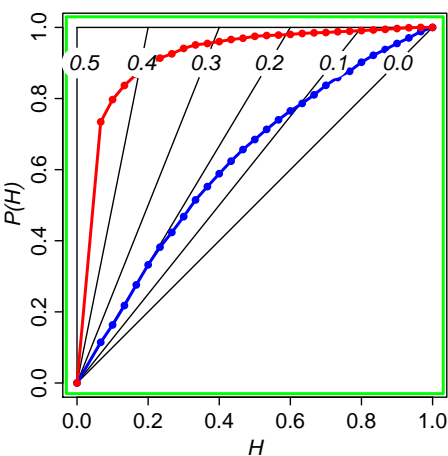
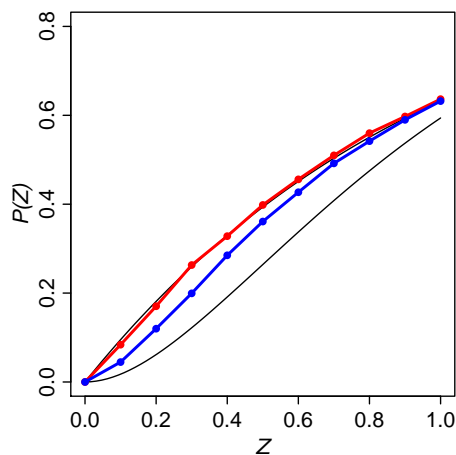
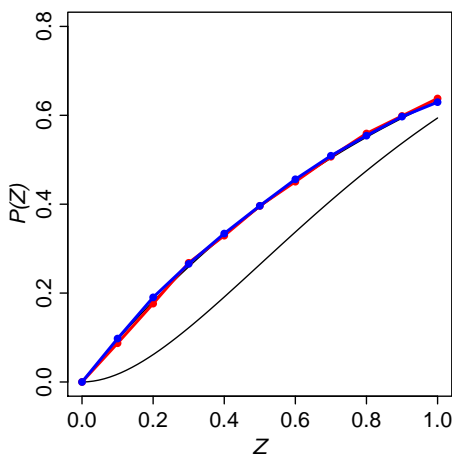
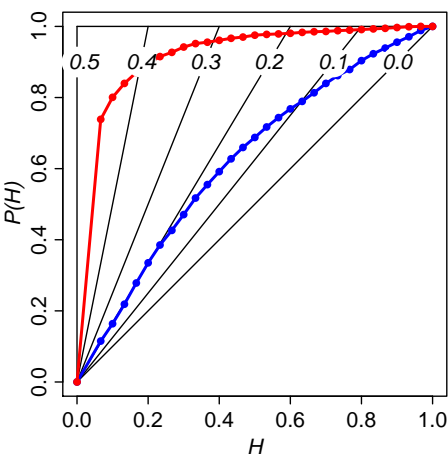
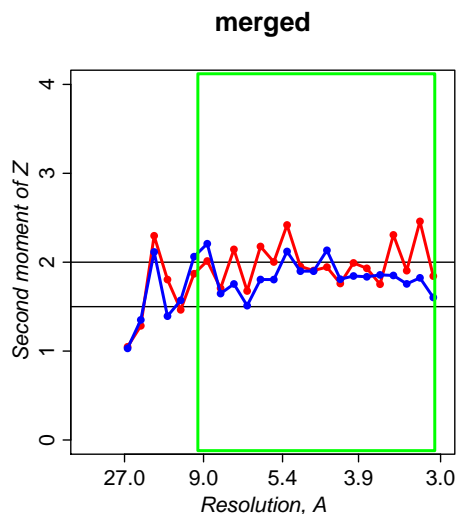
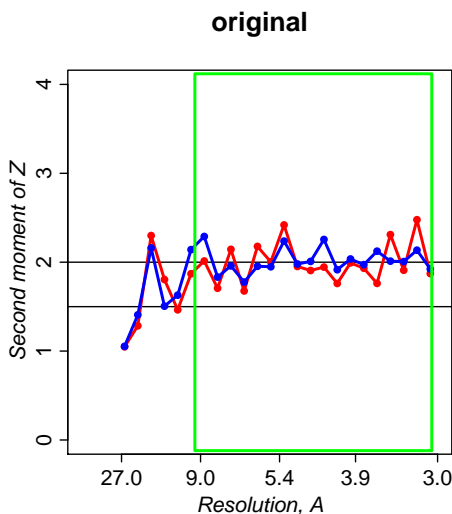
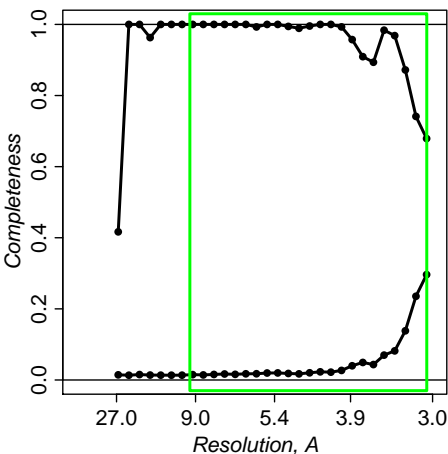
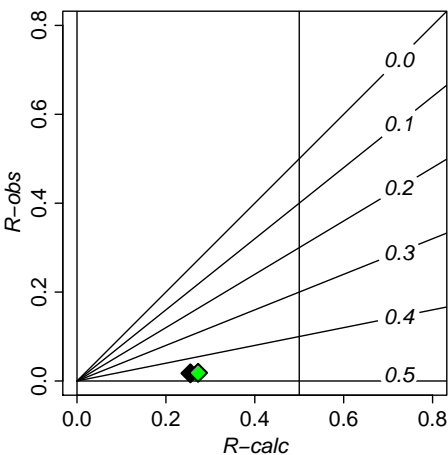
	original	merged
s.g.	H 3	H 3 2
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		1.79
R	25.9	
R'	27.0	27.4
R-free	34.1	
R'-free	33.5	36.5

s < f/100	167	3.24 %
s <= 0	164	3.18 %
f <= 0	164	3.18 %
s,f <= 0	164	3.18 %

range (A)	29.7-3.0	9.9-3.0
unique	5,605	5,450
measured	5,162	5,012
used	4,554	4,438

NCS	translation	rotation
r.m.s.d. (A)	20.56	1.75
angle (o)	177.42	2.66

residues per monomer	DNA	protein
	0	111



1jch

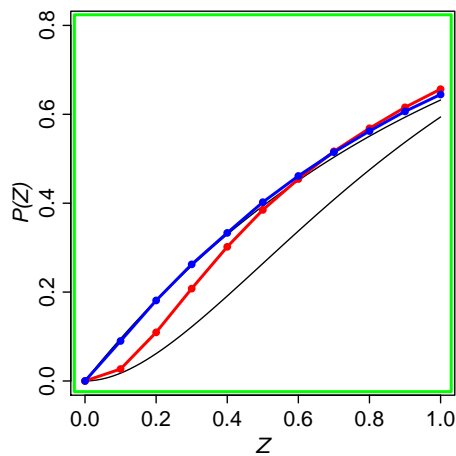
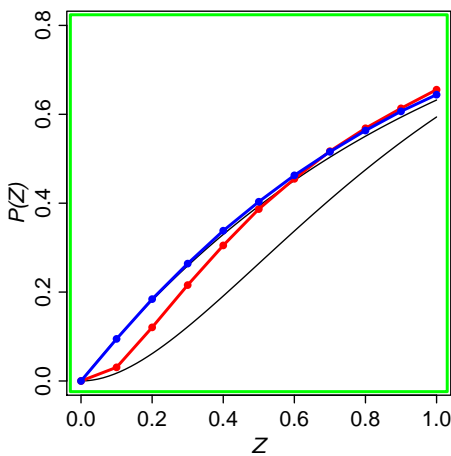
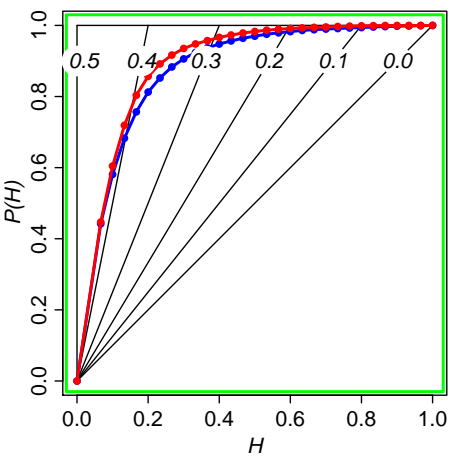
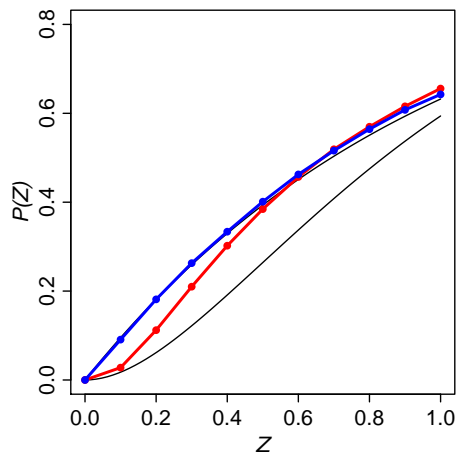
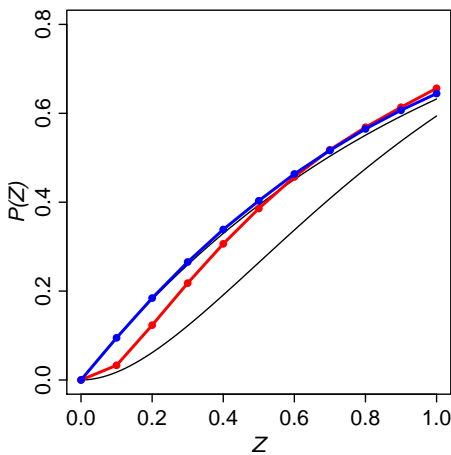
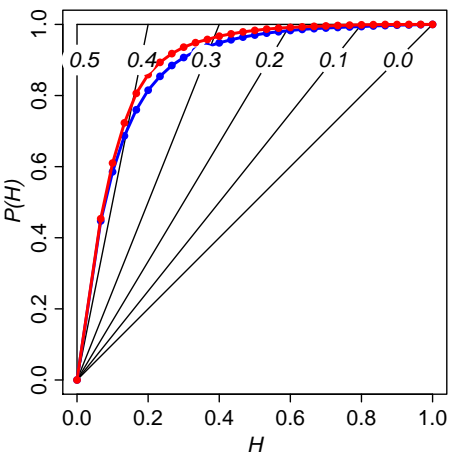
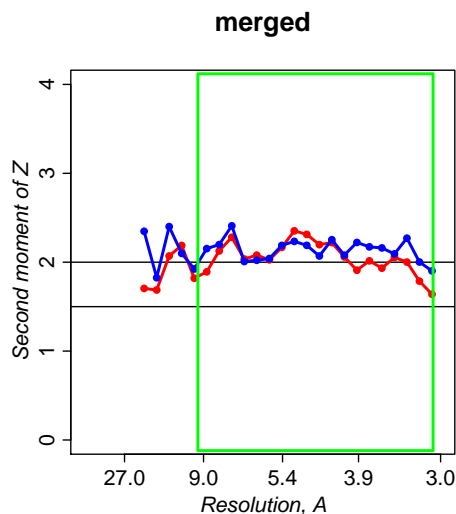
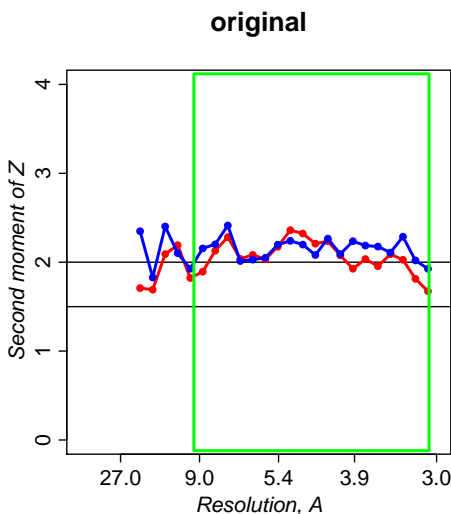
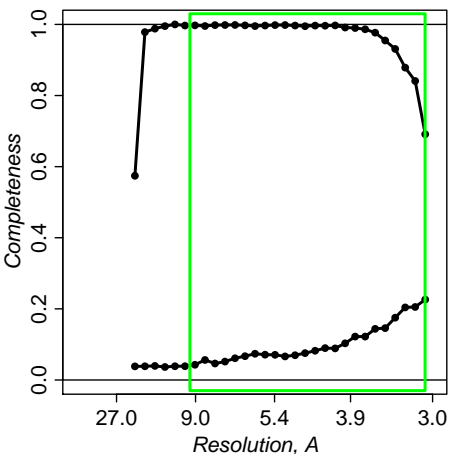
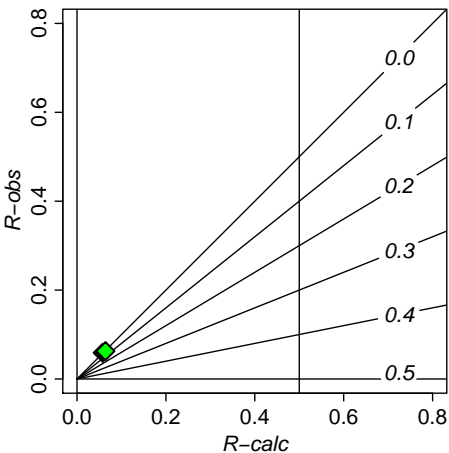
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.19
R	26.3	
R'	26.3	26.8
R-free	31.9	
R'-free	32.0	32.3

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	20.2–3.0	9.9–3.0
unique	39,330	38,311
measured	37,014	36,003
used	33,600	32,772

NCS	translation	rotation
r.m.s.d. (A)	67.31	0.16
angle (o)	179.97	0.48

residues per monomer	DNA	protein
	0	552



1jcn

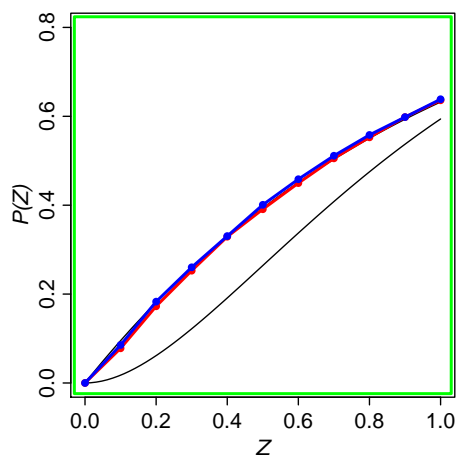
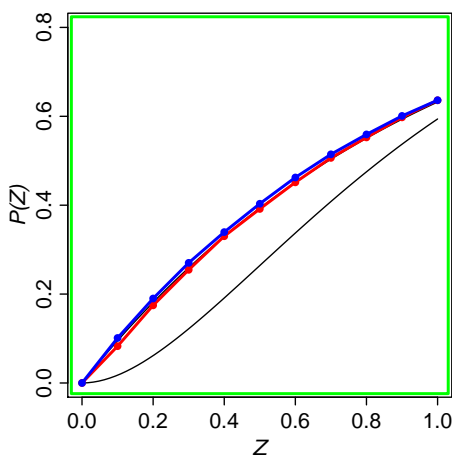
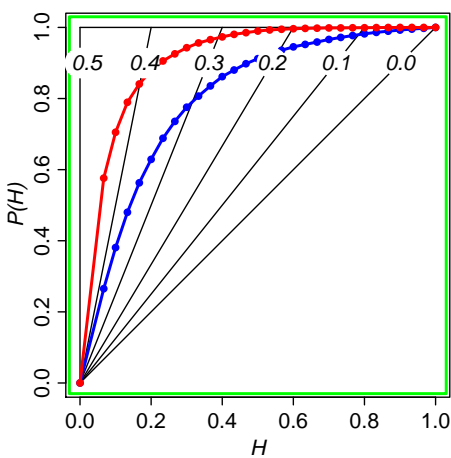
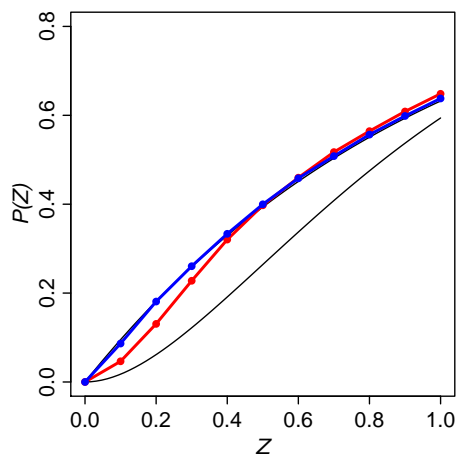
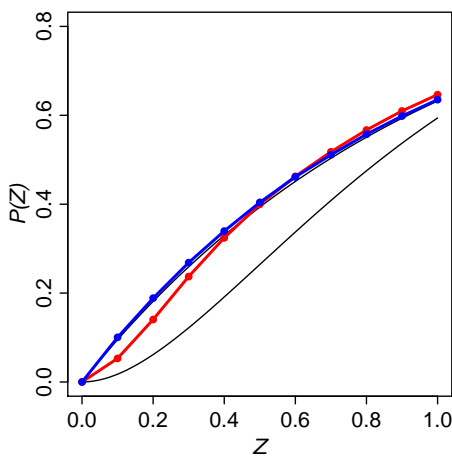
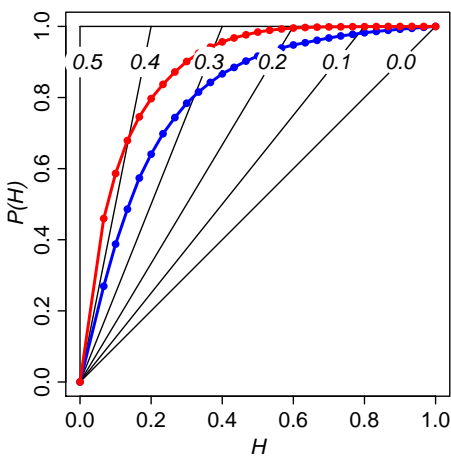
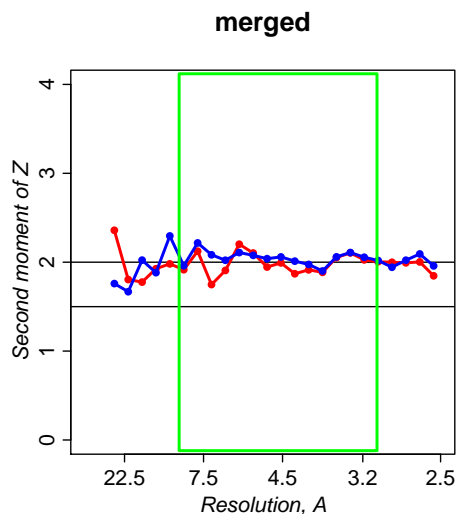
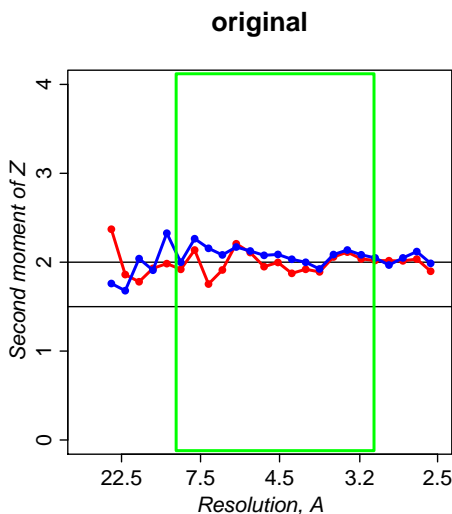
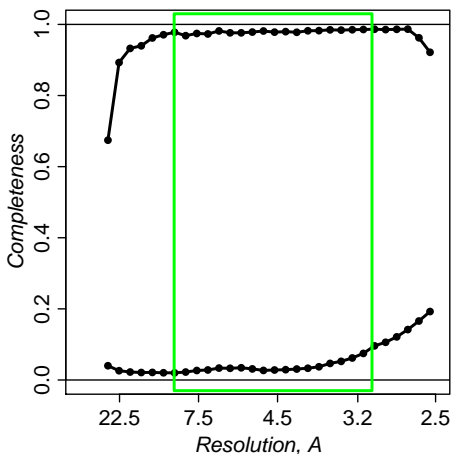
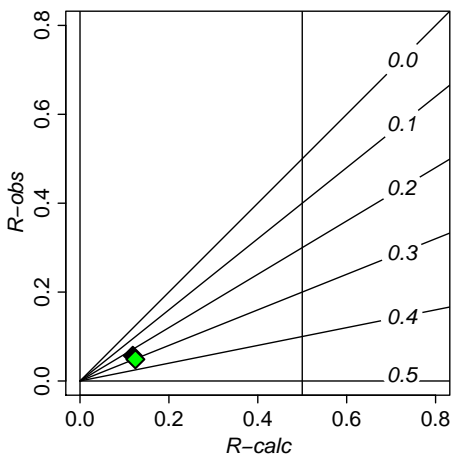
	original	merged
s.g.	14	14 2 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.43
R	27.4	
R'	27.3	27.5
R-free	30.4	
R'-free	30.6	30.9

residues per monomer	DNA	protein
	0	395

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	39.7–2.5	9.9–3.0
unique	45,536	25,671
measured	44,410	25,202
used	41,006	23,118

NCS	translation	rotation
r.m.s.d. (A)	41.40	0.43
angle (o)	179.78	0.23



1je8

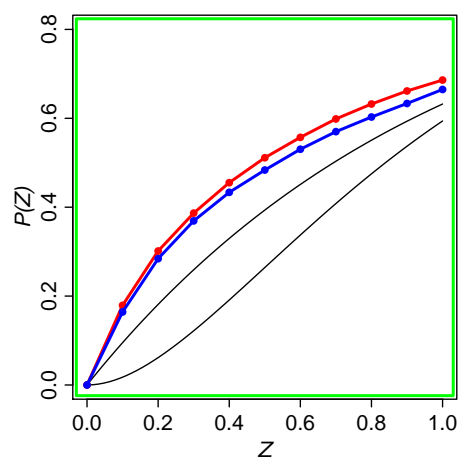
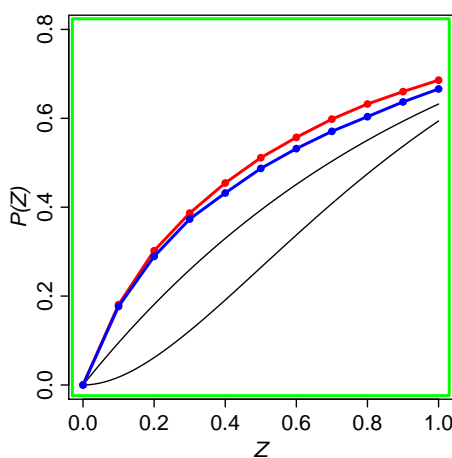
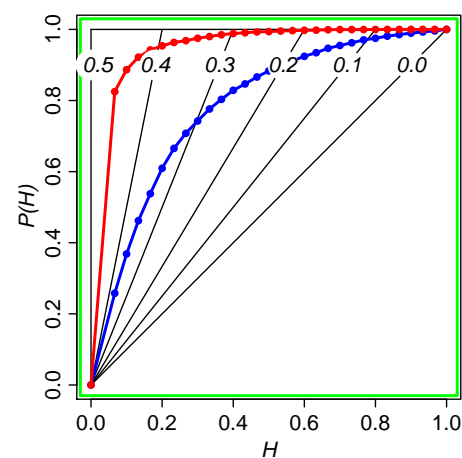
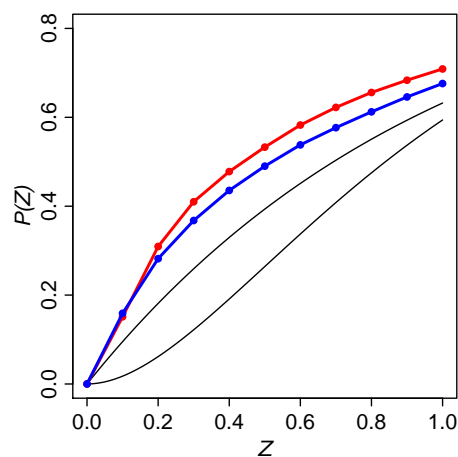
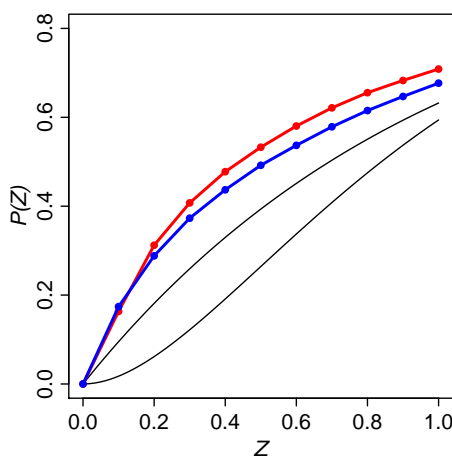
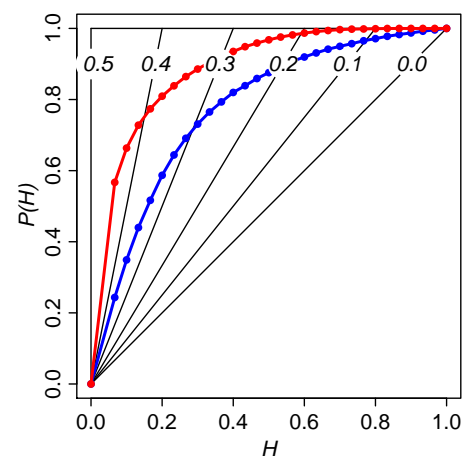
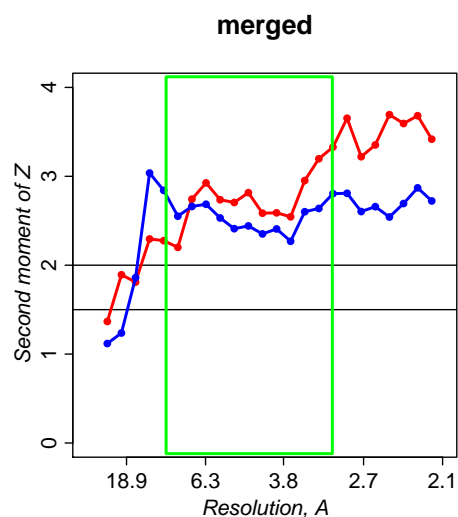
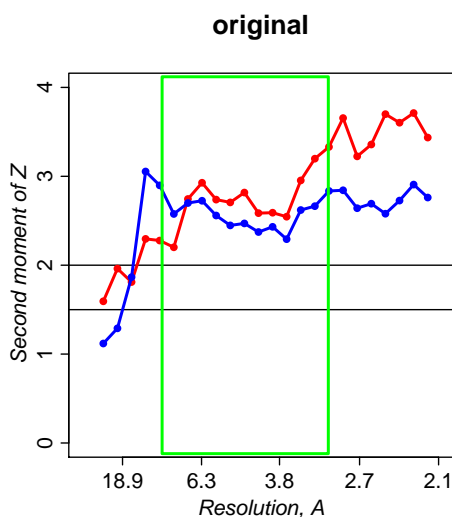
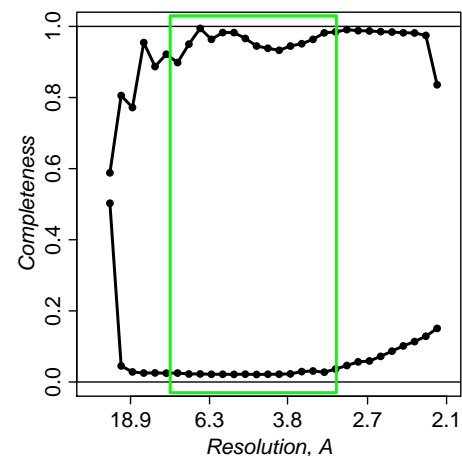
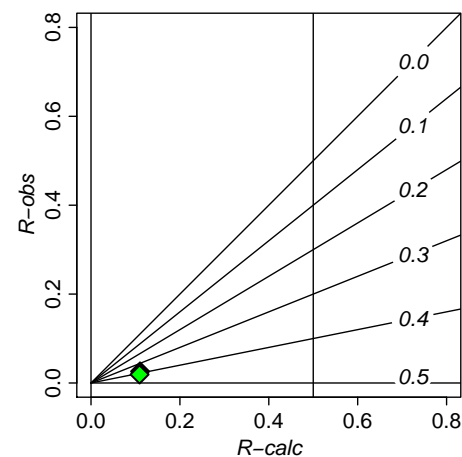
	original	merged
s.g.	P 1 21 1	P 21 21 2
p.g.	10001	10003
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		0.19
R	28.8	
R'	29.1	29.4
R-free	32.8	
R'-free	32.9	33.0

s < f/100	33	0.09 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	56.4–2.1	9.9–3.0
unique	38,050	13,227
measured	36,563	12,709
used	32,522	11,126

NCS	translation	rotation
r.m.s.d. (A)	0.36	0.16
angle (o)	1.48	0.15

residues per monomer	DNA	protein
	19	66



1jig

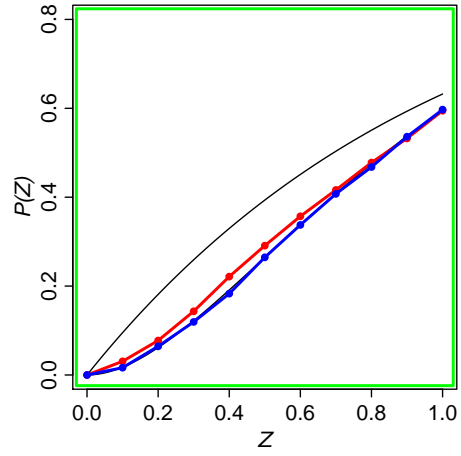
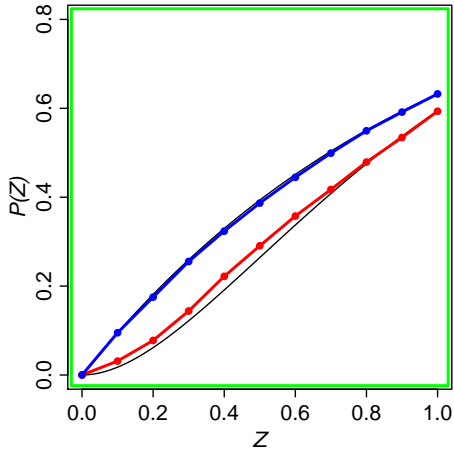
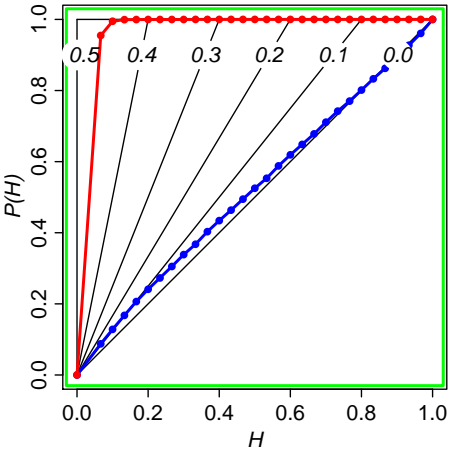
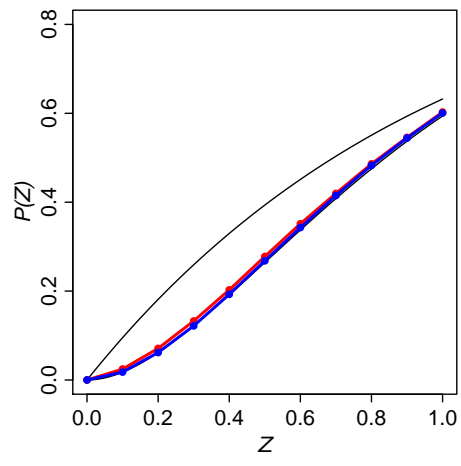
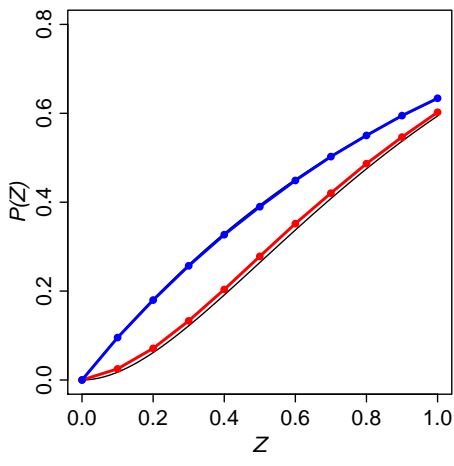
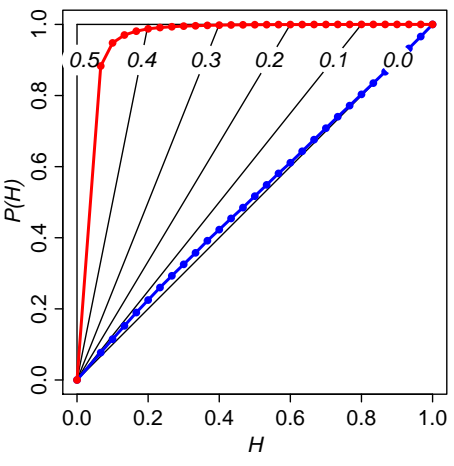
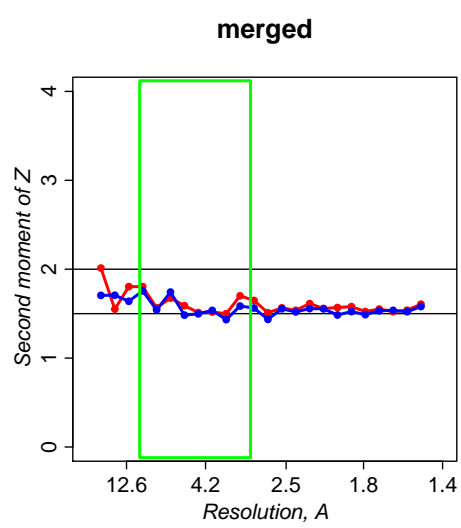
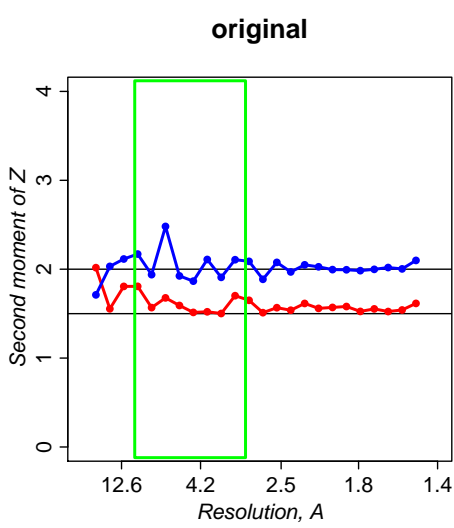
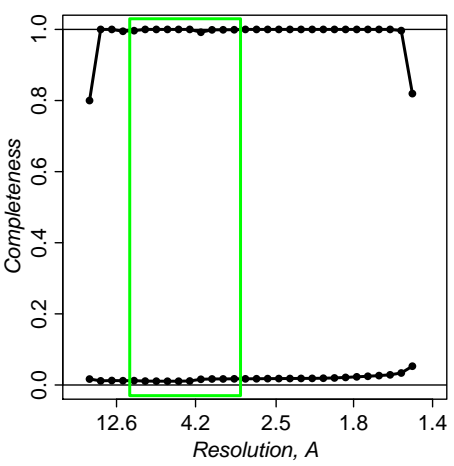
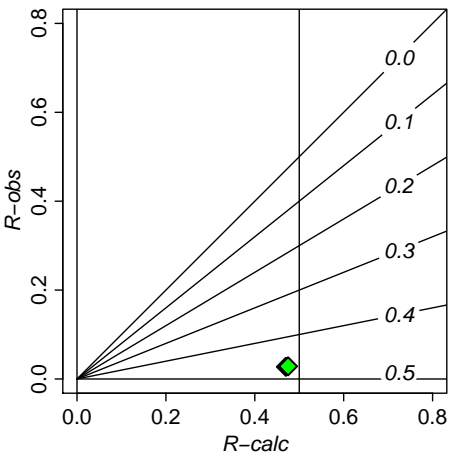
	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	4	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	34.6	-
R'	-	-
R-free	35.6	-
R'-free	-	-

residues per monomer	DNA	protein
	0	146

s < f/100	1974	1.88 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	71.6-1.5	9.9-3.0
unique	107,058	12,026
measured	105,192	12,008
used	100,656	11,118

NCS	translation	rotation
r.m.s.d. (A)	19.84	12.67
angle (o)	119.98	89.99



1jjk

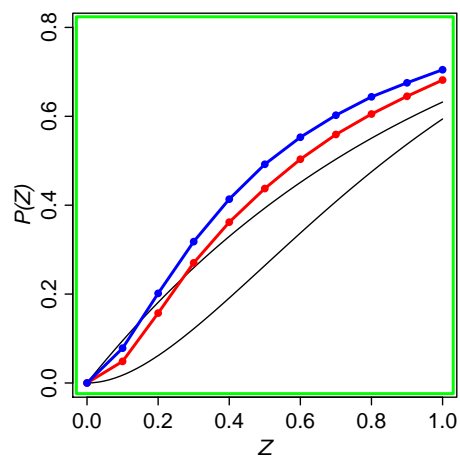
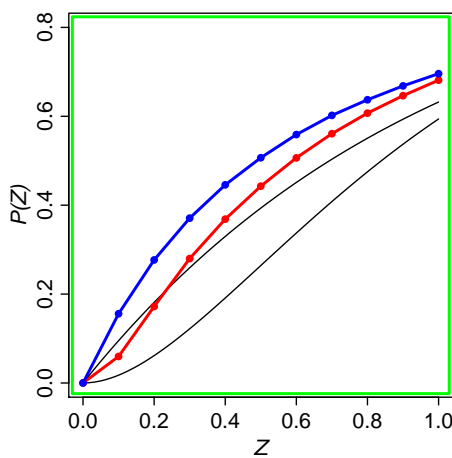
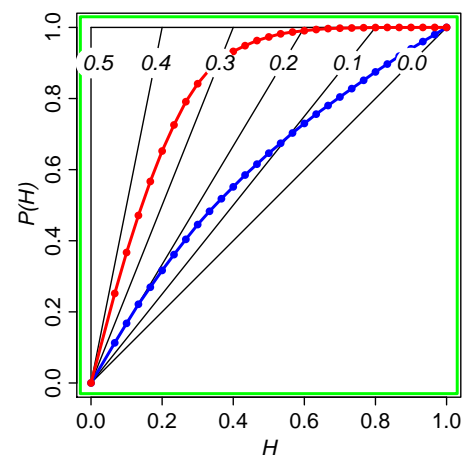
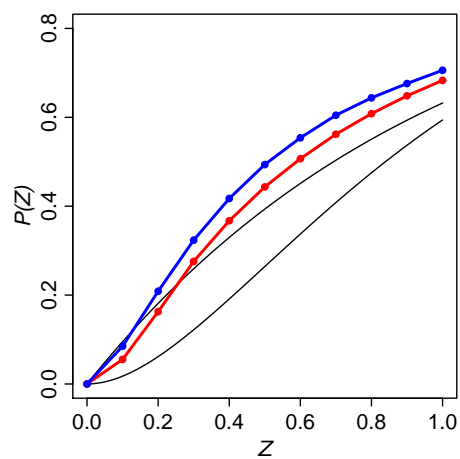
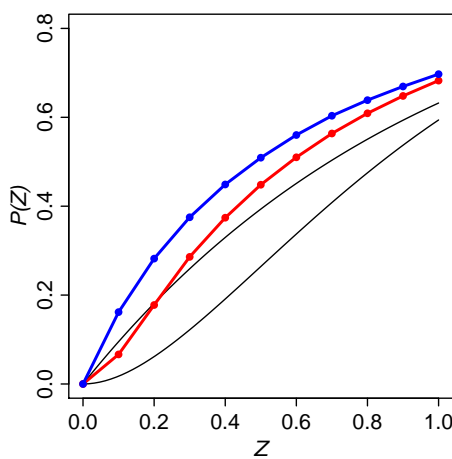
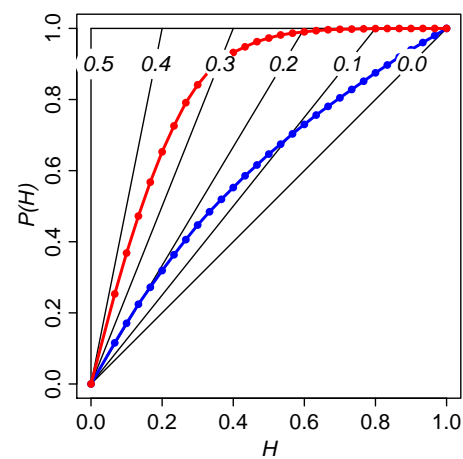
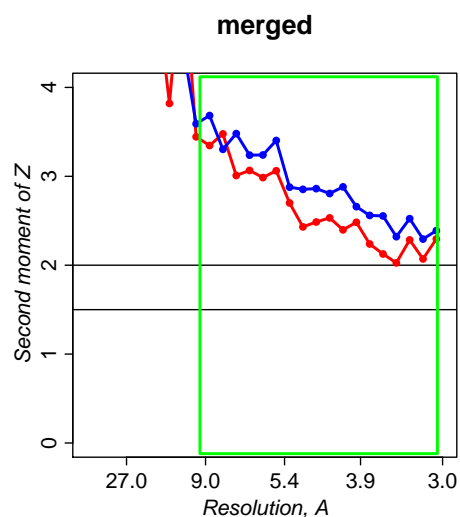
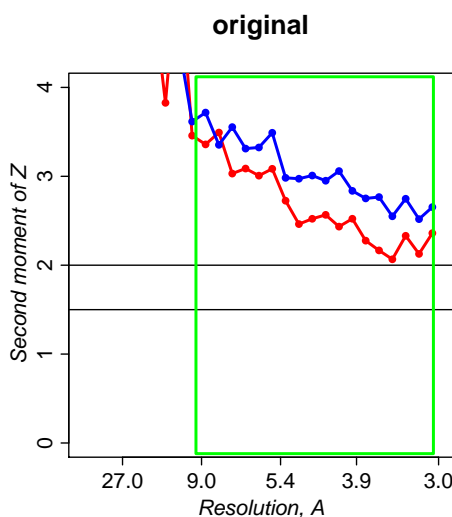
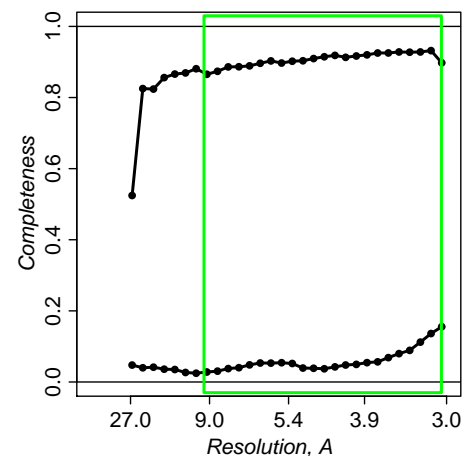
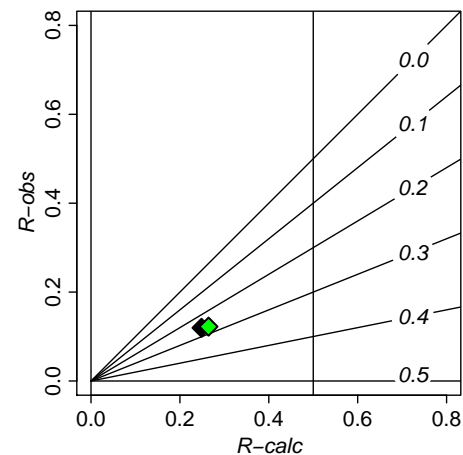
	original	merged
s.g.	P 1 21 1	-
p.g.	10001	10003
a.u.	16	-
p.t.	2	-
p.o.	2	-
r.m.s.d. (A)	-	-
R	28.2	-
R'	-	-
R-free	36.6	-
R'-free	-	-

s < f/100	95	0.15 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.8-3.0	9.9-3.0
unique	71,050	68,806
measured	64,895	63,139
used	57,272	55,944

NCS	translation	rotation
r.m.s.d. (A)	0.43	0.13
angle (o)	1.74	0.51

residues per monomer	DNA	protein
	0	231



1jkt

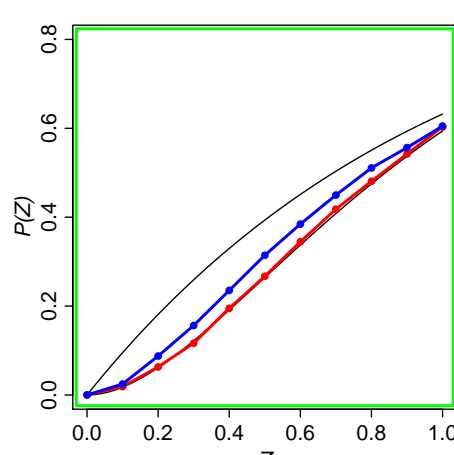
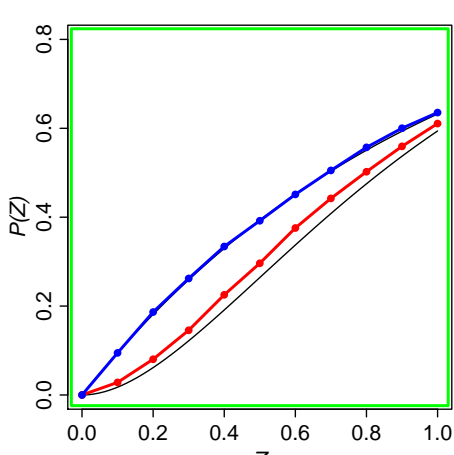
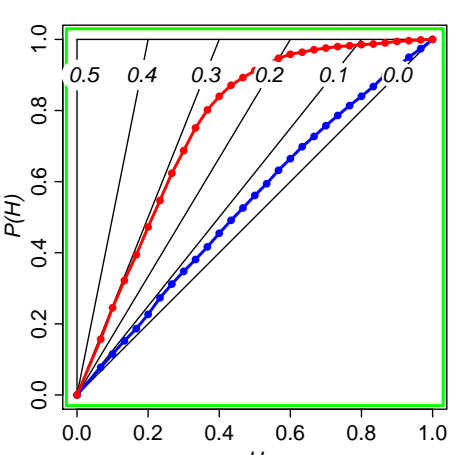
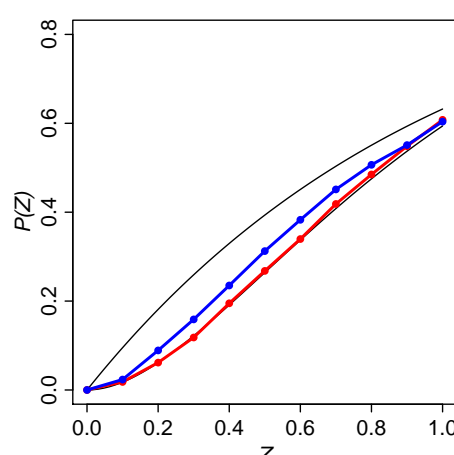
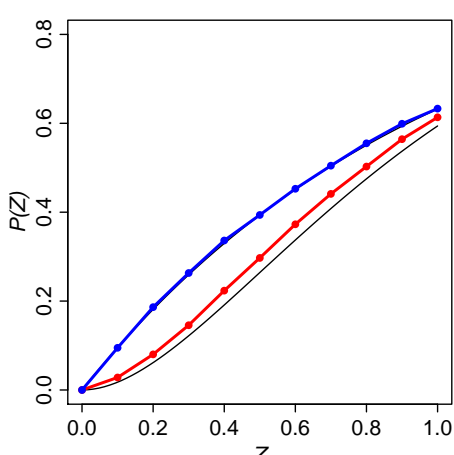
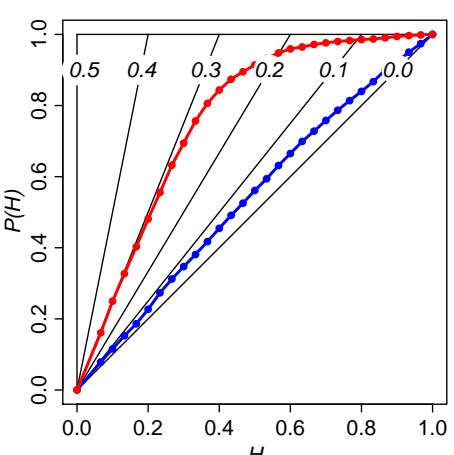
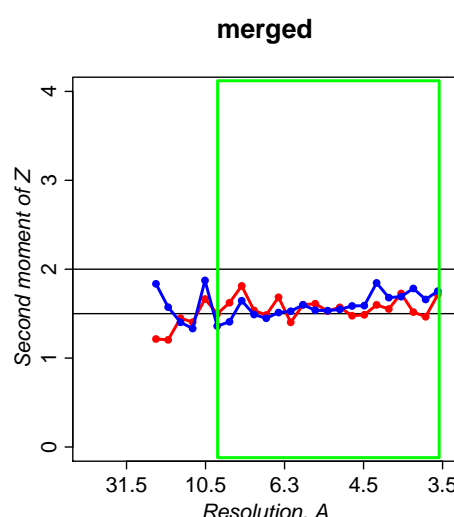
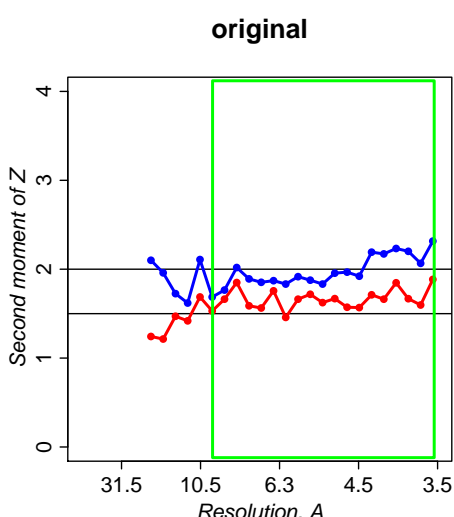
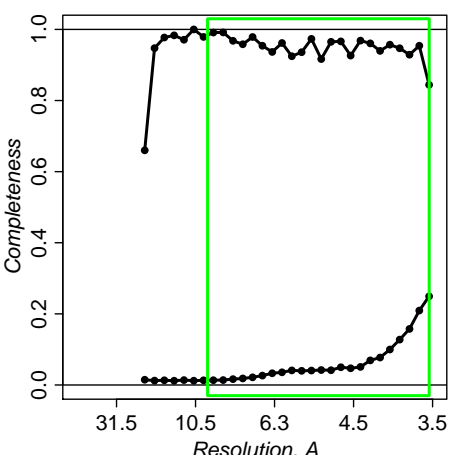
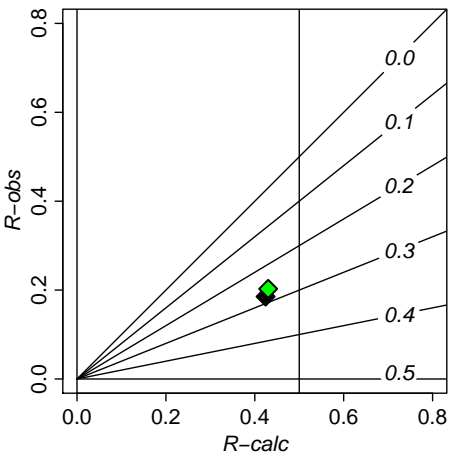
	original	merged
s.g.	P 41	-
p.g.	10201	10205
a.u.	2	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	23.5	-
R'	-	-
R-free	33.8	-
R'-free	-	-

residues per monomer	DNA	protein
	0	276

s < f/100	252	2.95 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.8-3.5	9.9-3.5
unique	9,060	8,699
measured	8,549	8,196
used	7,078	6,864

NCS	translation	rotation
r.m.s.d. (A)	13.25	30.14
angle (o)	45.53	138.09



1jm6

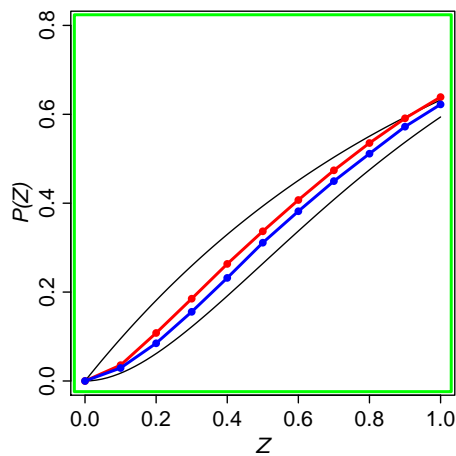
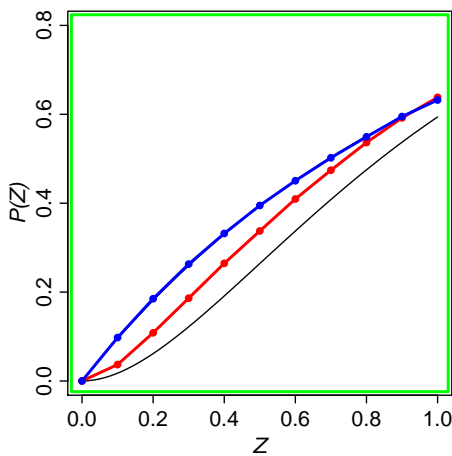
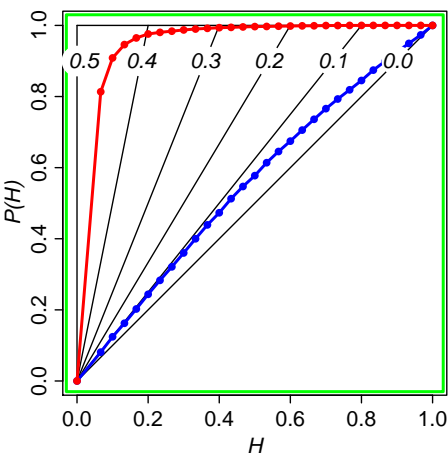
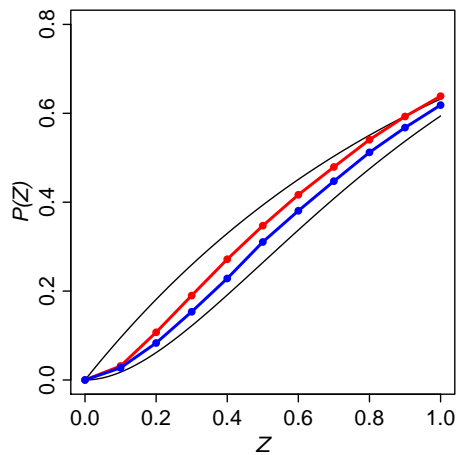
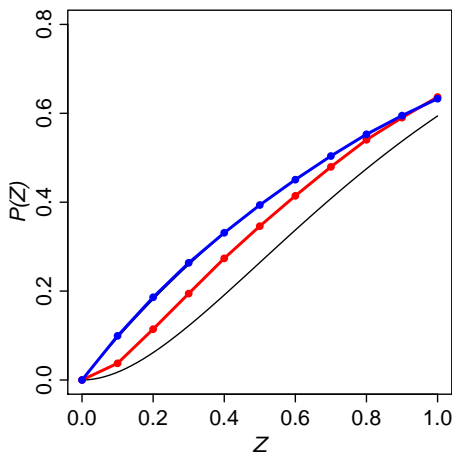
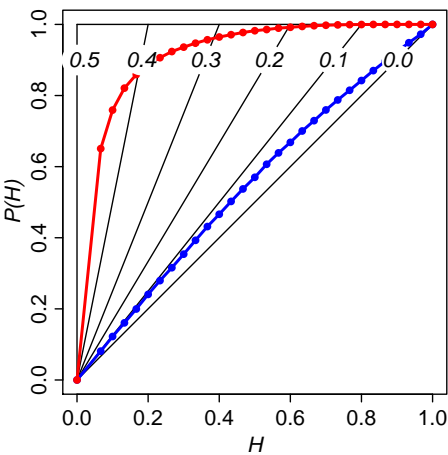
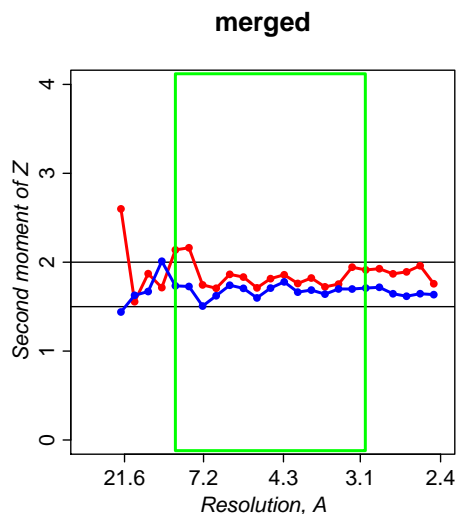
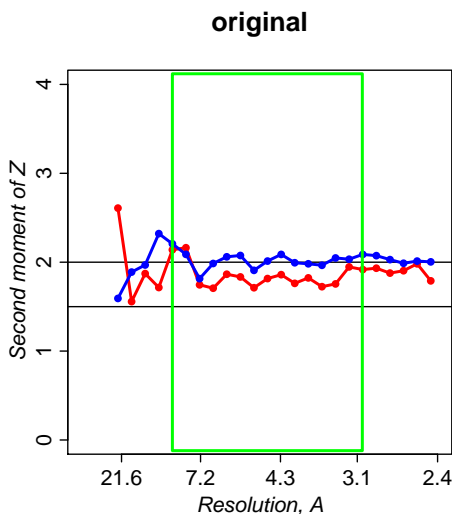
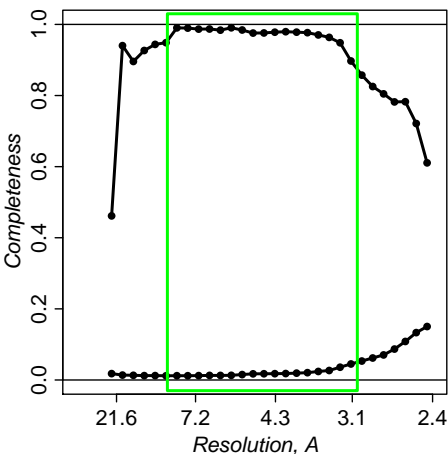
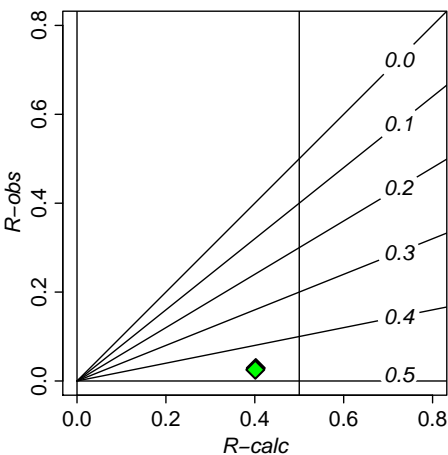
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		9.74
R	28.9	
R'	-	-
R-free	32.0	
R'-free	-	-

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.3–2.4	9.9–3.0
unique	41,403	20,849
measured	35,644	20,005
used	30,798	17,934

NCS	translation	rotation
r.m.s.d. (A)	37.53	0.57
angle (o)	179.91	0.22

residues per monomer	DNA	protein
	0	333



1joe

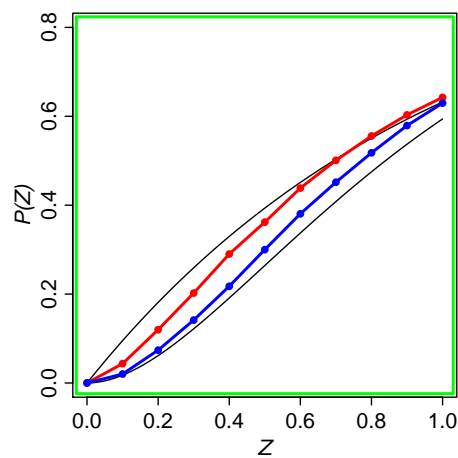
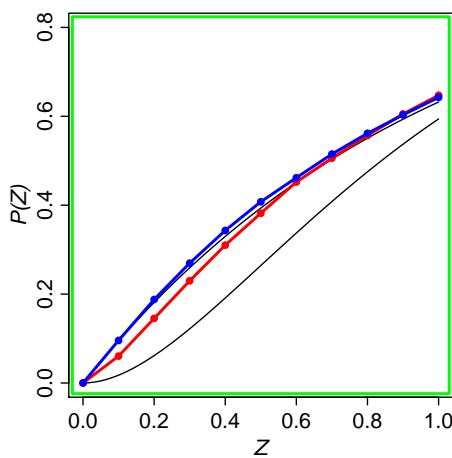
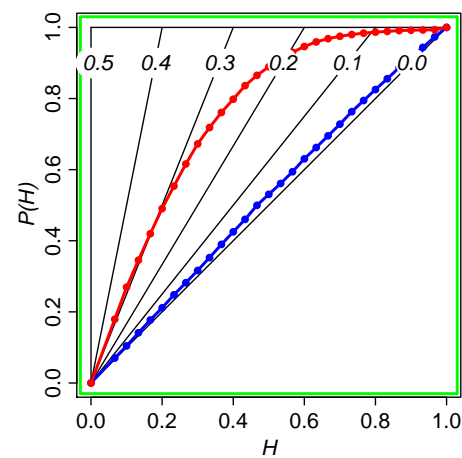
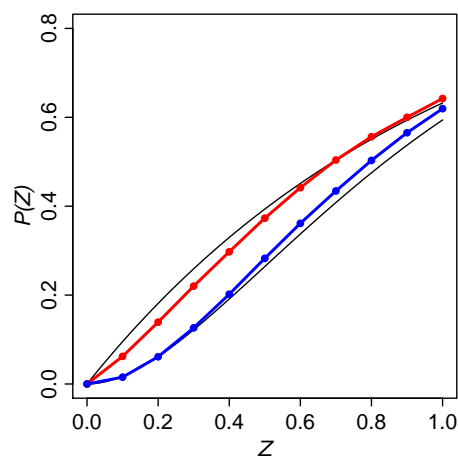
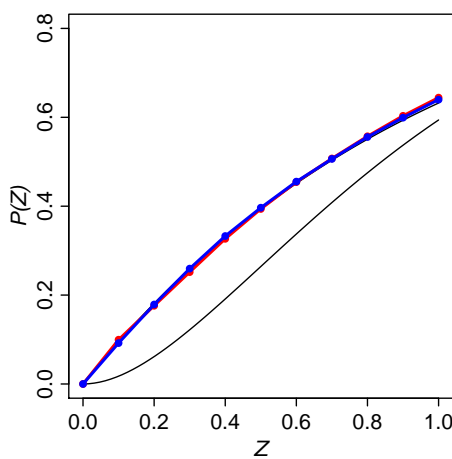
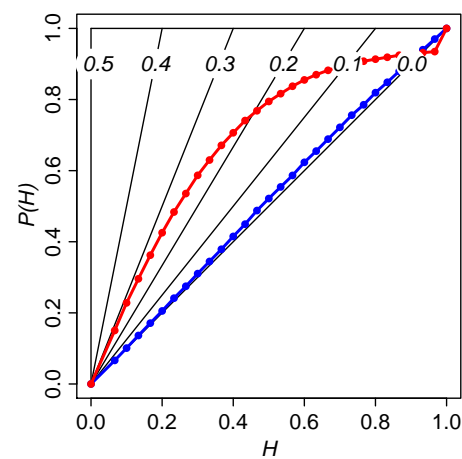
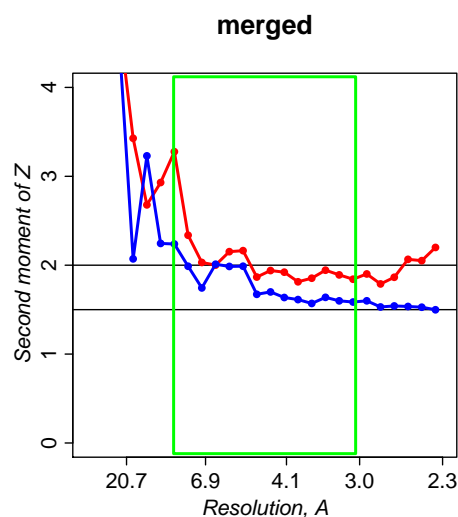
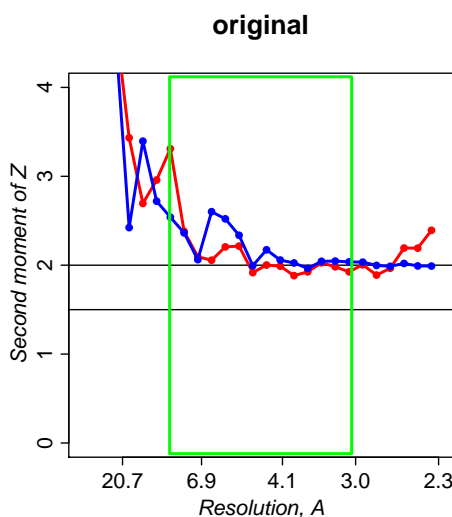
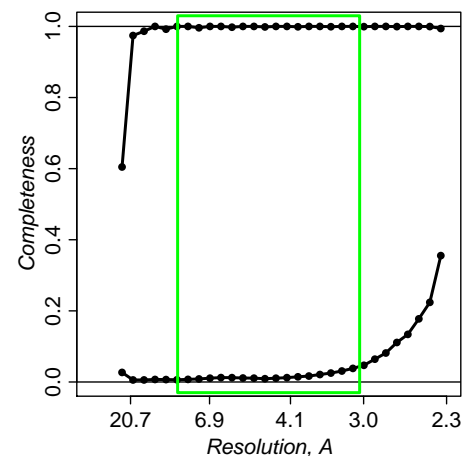
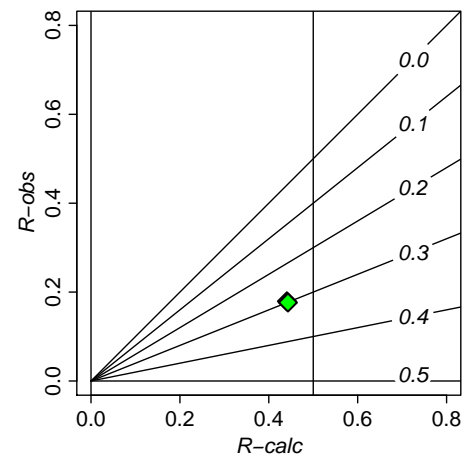
	original	merged
s.g.	P 42	P 42 2 2
p.g.	10201	10205
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		2.47
R	31.5	
R'	35.8	38.2
R-free	35.7	
R'-free	41.1	43.8

s < f/100	4336	14.30 %
s <= 0	0	0.00 %
f <= 0	1433	4.73 %
s,f <= 0	0	0.00 %

range (A)	32.0–2.3	9.9–3.0
unique	30,345	13,415
measured	30,313	13,409
used	26,908	11,576

NCS	translation	rotation
r.m.s.d. (A)	2.47	0.73
angle (o)	11.77	0.75

residues per monomer	DNA	protein
	0	148



1jqh

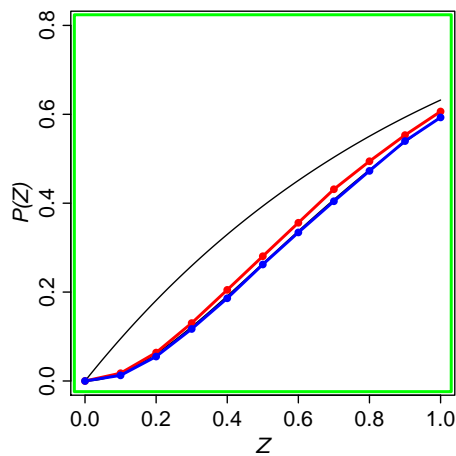
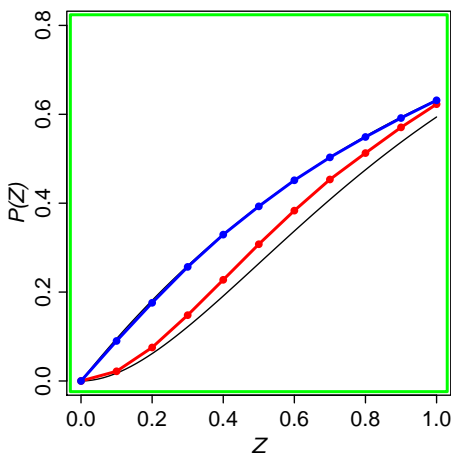
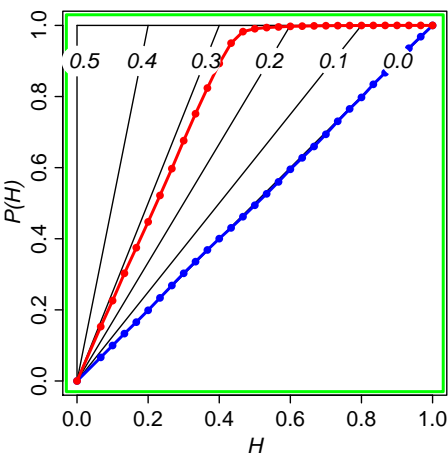
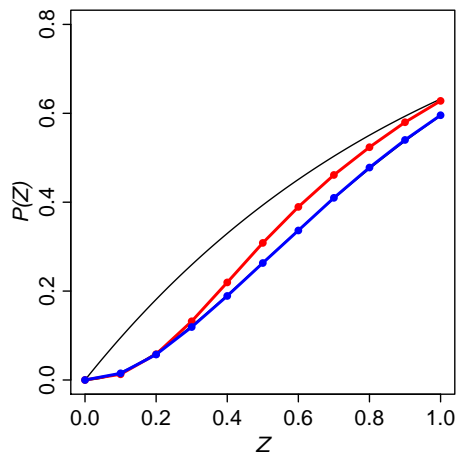
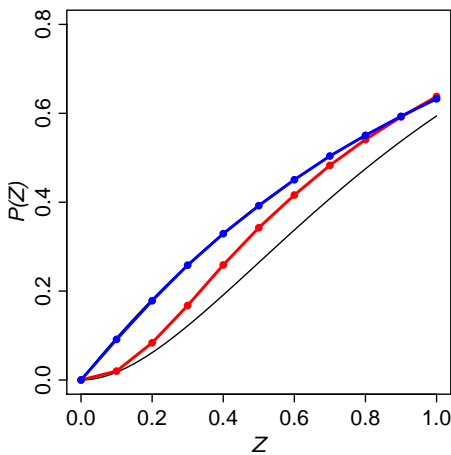
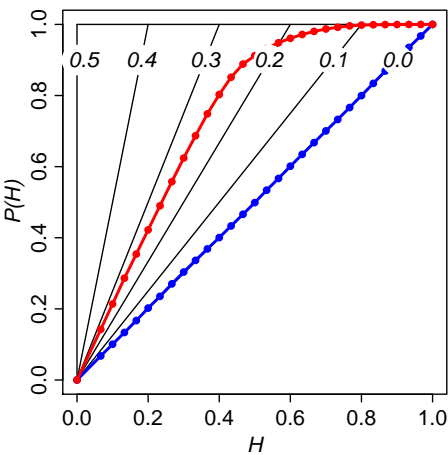
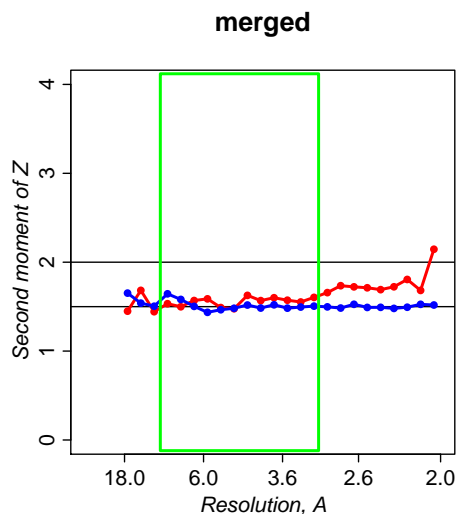
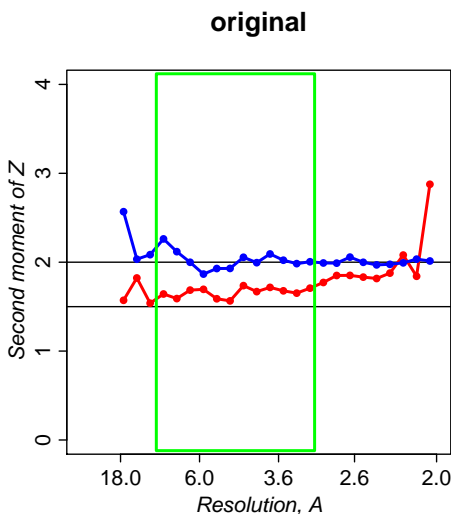
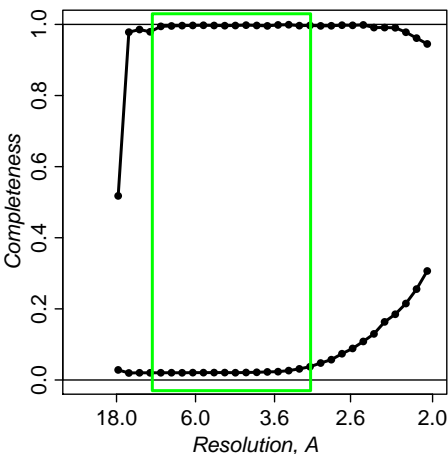
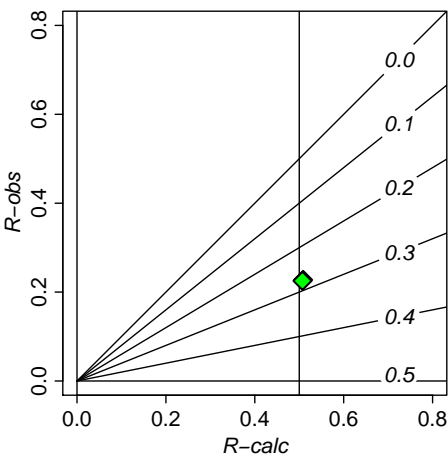
	original	merged
s.g.	P 32	-
p.g.	10020	10023
a.u.	3	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	27.8	-
R'	-	-
R-free	30.9	-
R'-free	-	-

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.8-2.0	9.9-3.0
unique	73,781	21,334
measured	72,800	21,274
used	68,672	19,698

NCS	translation	rotation
r.m.s.d. (A)	4.95	25.63
angle (o)	17.31	162.72

residues per monomer	DNA	protein
	0	287



1jrg

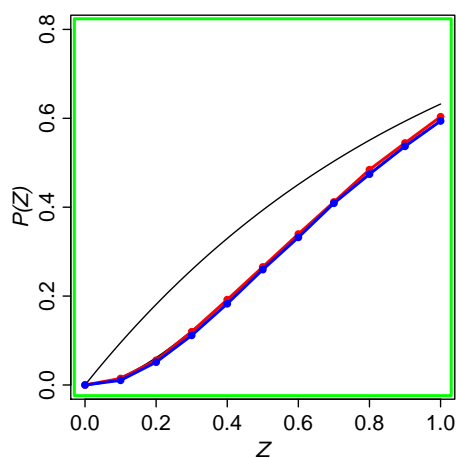
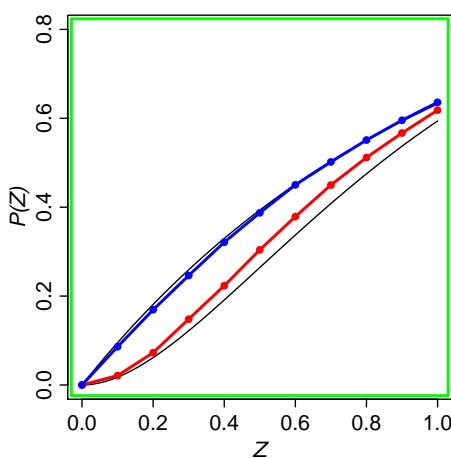
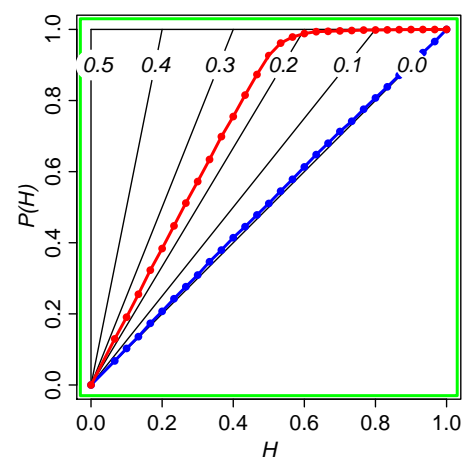
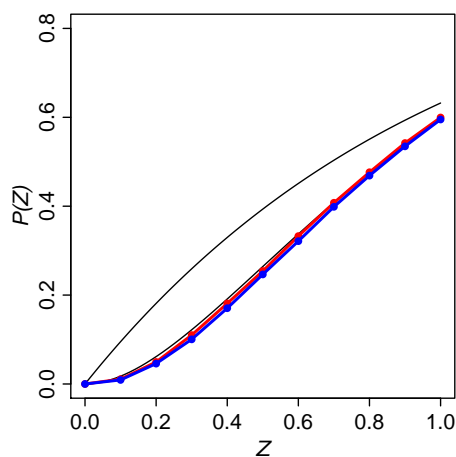
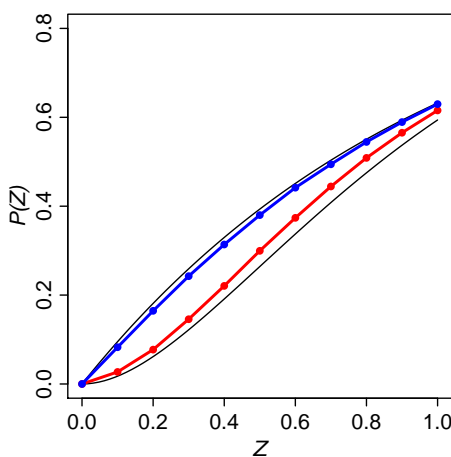
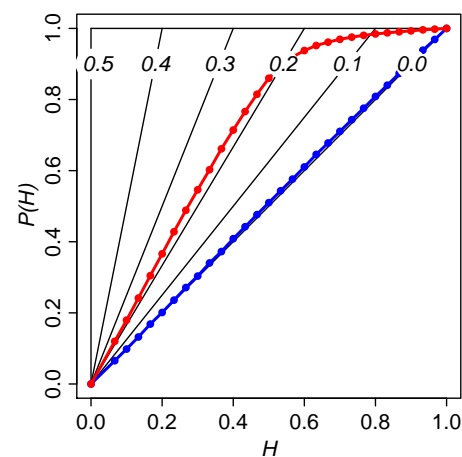
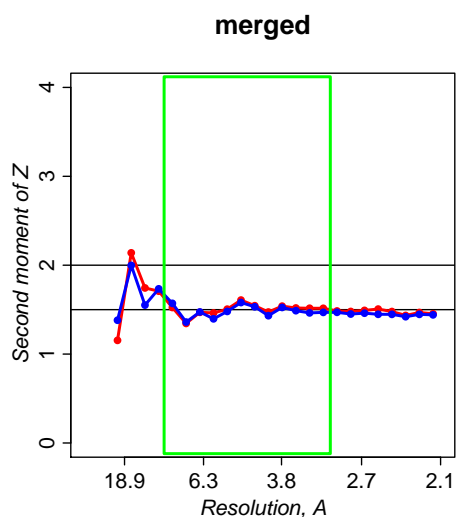
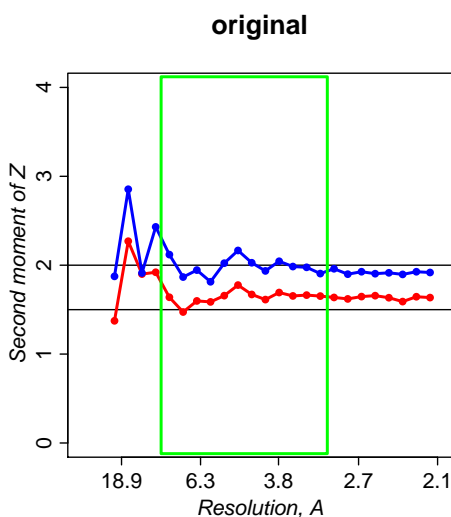
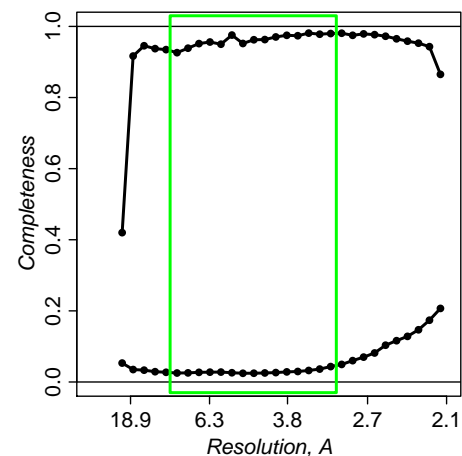
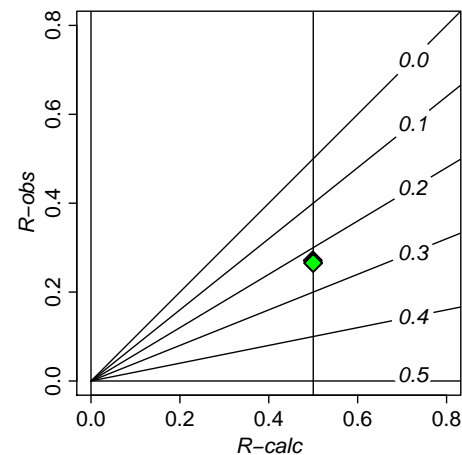
	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	2	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	25.6	-
R'	-	-
R-free	27.9	-
R'-free	-	-

residues per monomer	DNA	protein
	0	350

s < f/100	908	2.10 %
s <= 0	908	2.10 %
f <= 0	908	2.10 %
s,f <= 0	908	2.10 %

range (A)	29.1-2.1	9.9-3.0
unique	45,178	15,189
measured	43,228	14,735
used	39,994	13,592

NCS	translation	rotation
r.m.s.d. (A)	25.77	16.10
angle (o)	128.67	68.20



1jss

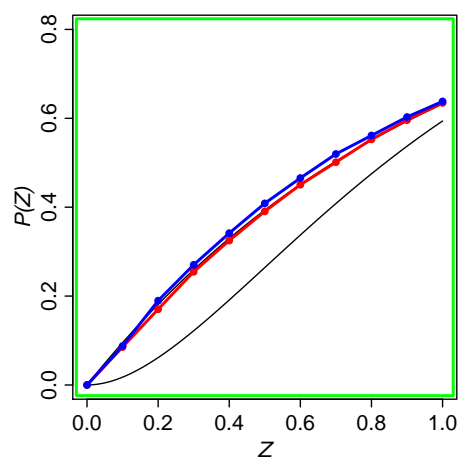
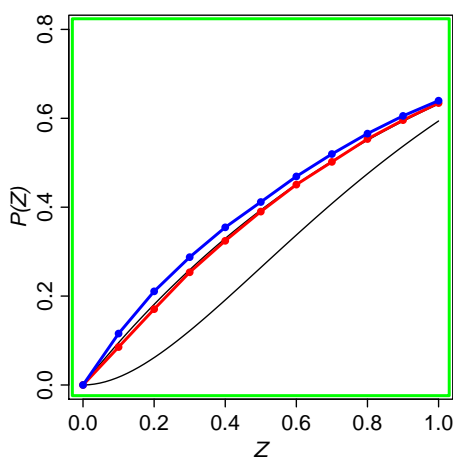
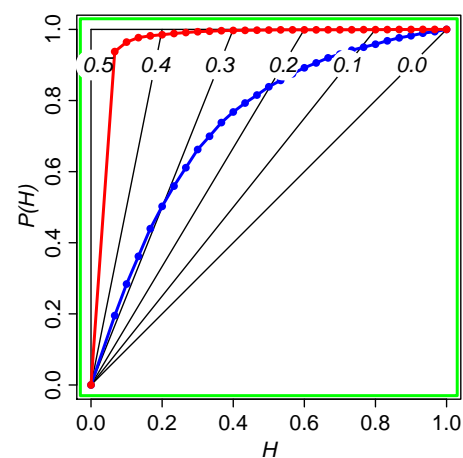
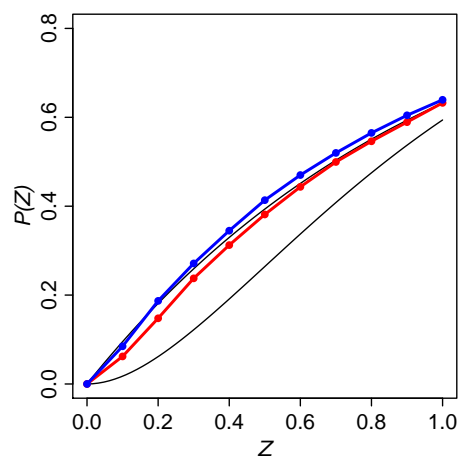
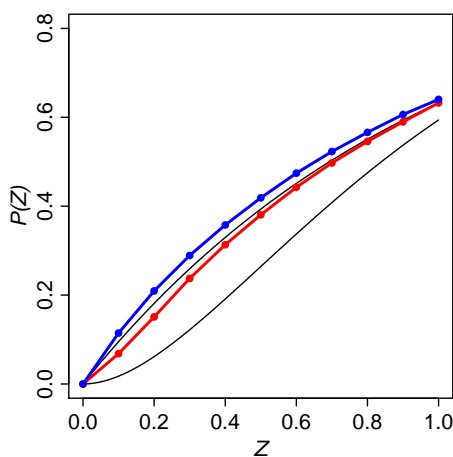
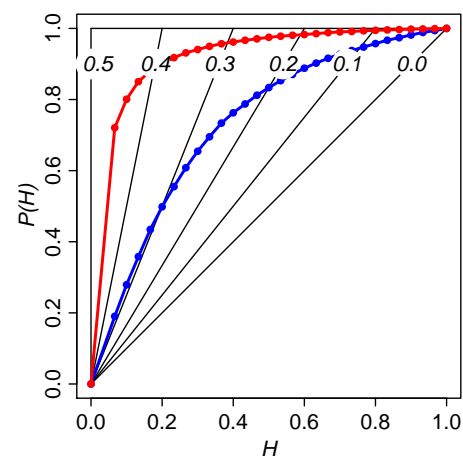
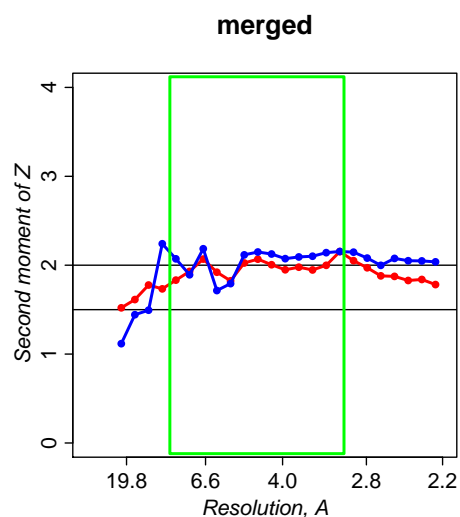
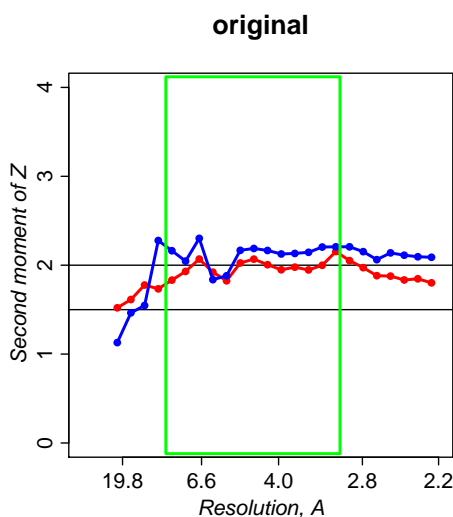
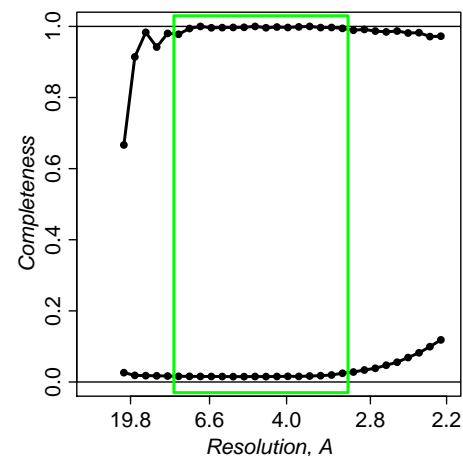
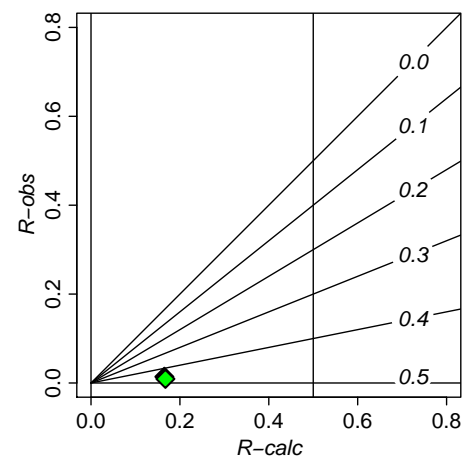
	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.31
R	26.0	
R'	26.6	27.2
R-free	29.1	
R'-free	29.1	30.0

s < f/100	268	1.15 %
s <= 0	268	1.15 %
f <= 0	268	1.15 %
s,f <= 0	268	1.15 %

range (A)	28.5–2.2	9.9–3.0
unique	23,644	9,116
measured	23,341	9,082
used	21,560	8,268

NCS	translation	rotation
r.m.s.d. (A)	27.20	0.31
angle (o)	179.95	0.07

residues per monomer	DNA	protein
	0	199



1jt7

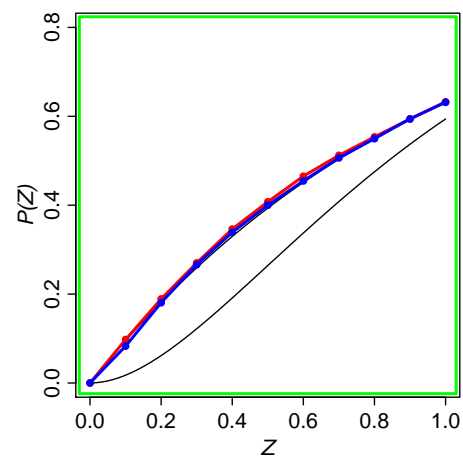
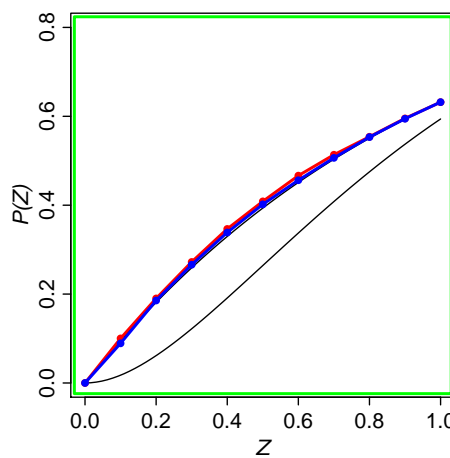
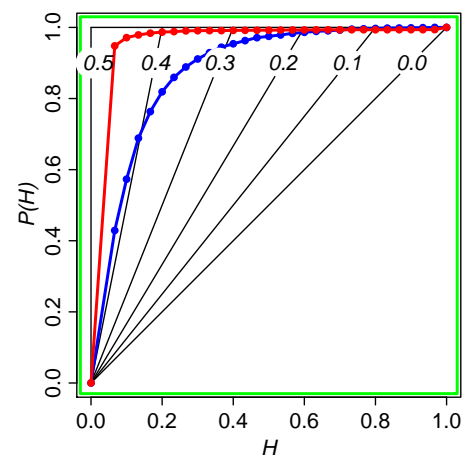
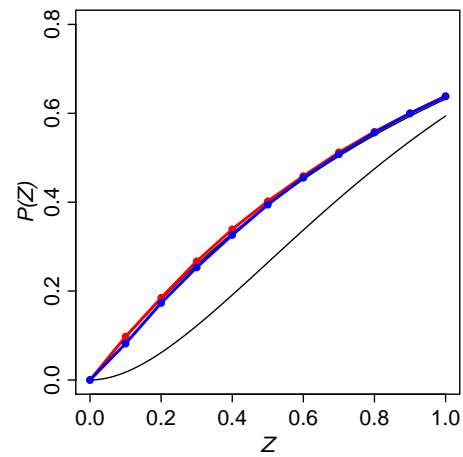
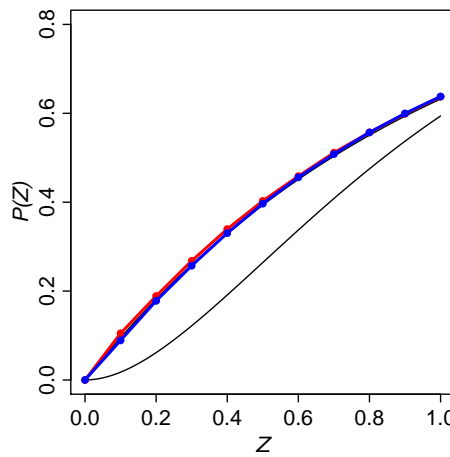
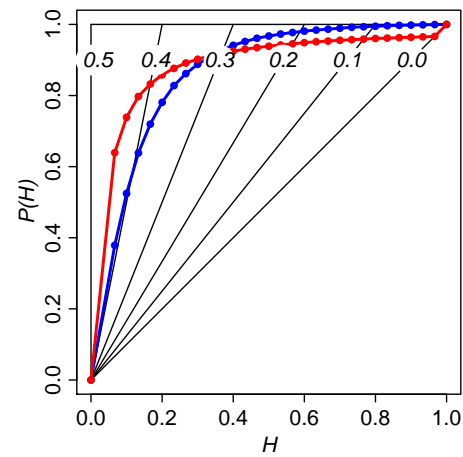
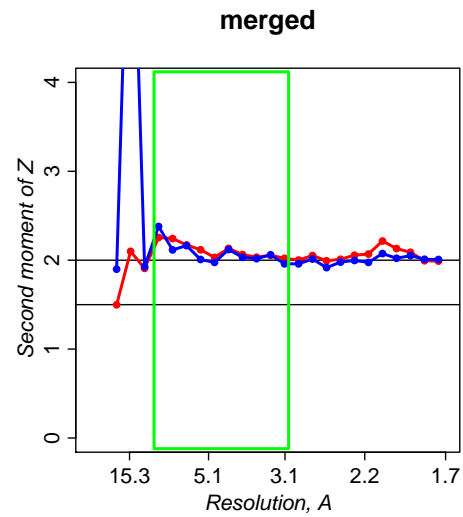
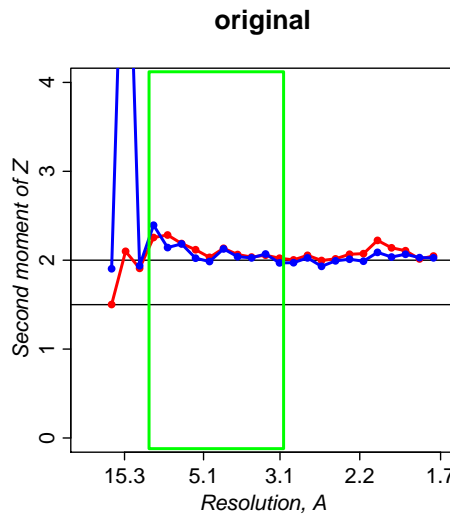
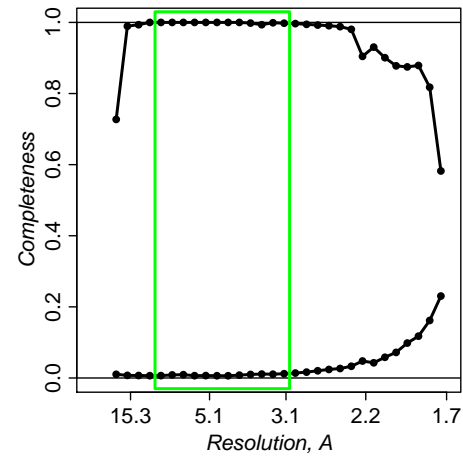
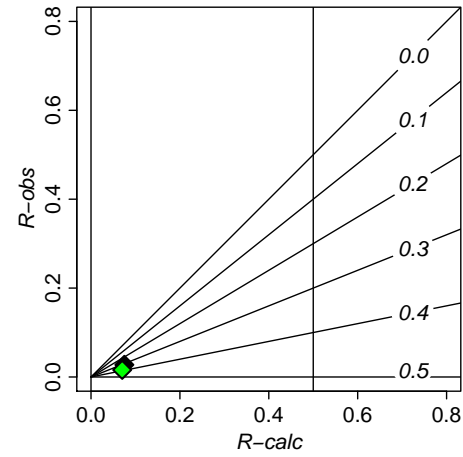
	original	merged
s.g.	C 1 2 1	C 2 2 21
p.g.	10001	10003
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		0.08
R	26.1	
R'	26.1	26.4
R-free	27.1	
R'-free	27.0	27.5

s < f/100	12089	16.38 %
s <= 0	0	0.00 %
f <= 0	1992	2.70 %
s,f <= 0	0	0.00 %

range (A)	30.9–1.7	9.9–3.0
unique	81,512	15,091
measured	73,802	15,067
used	64,744	13,654

NCS	translation	rotation
r.m.s.d. (A)	3.70	0.07
angle (o)	19.36	0.05

residues per monomer	DNA	protein
	0	141



1jtc

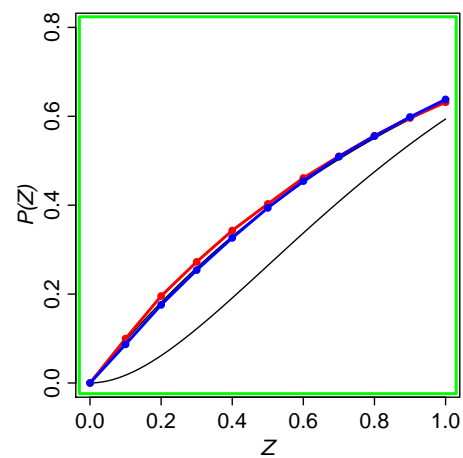
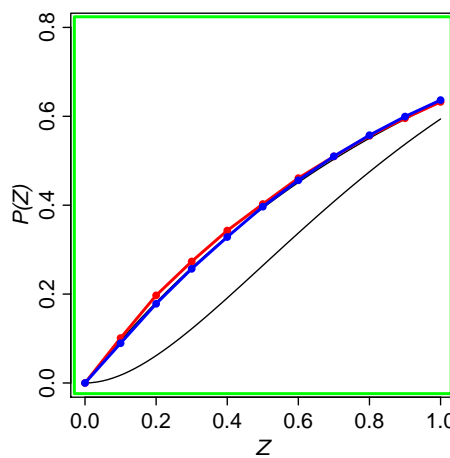
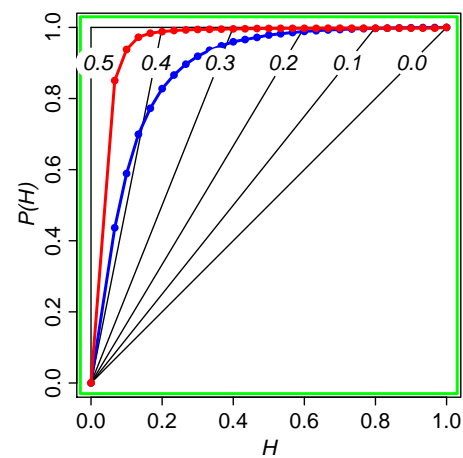
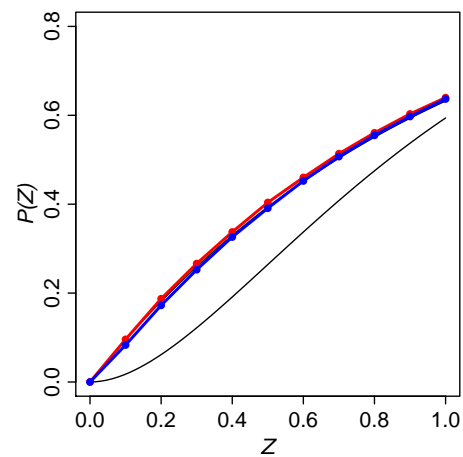
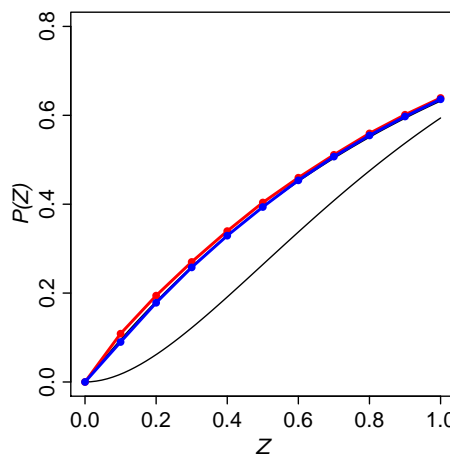
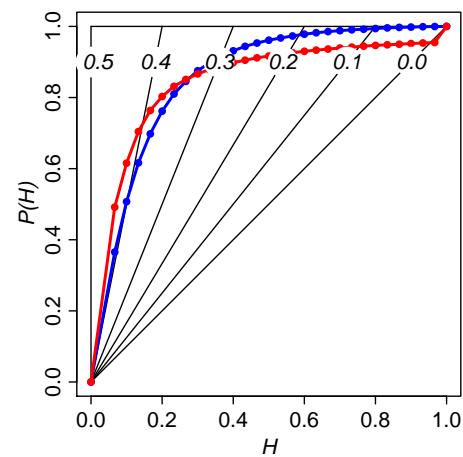
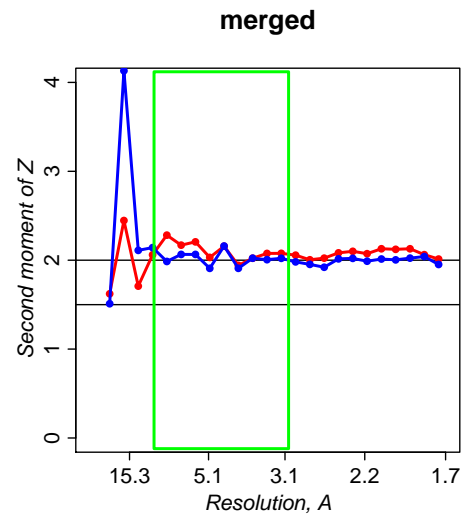
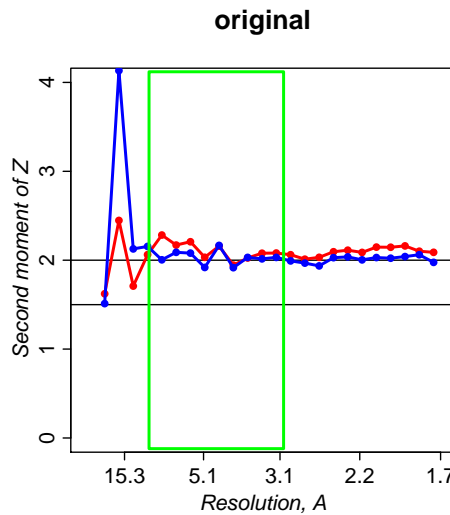
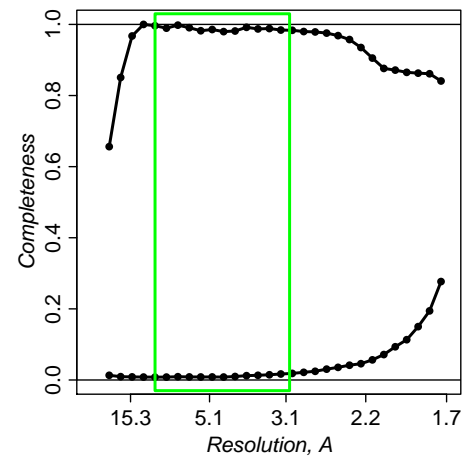
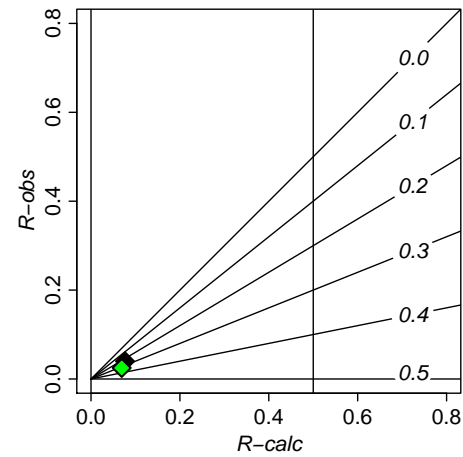
	original	merged
s.g.	C 1 2 1	C 2 2 21
p.g.	10001	10003
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		0.07
R	25.7	
R'	25.8	26.1
R-free	27.1	
R'-free	27.0	27.6

s < f/100	5755	7.70 %
s <= 0	0	0.00 %
f <= 0	2378	3.18 %
s,f <= 0	0	0.00 %

range (A)	48.5–1.7	9.9–3.0
unique	81,315	15,149
measured	74,722	14,945
used	66,362	13,616

NCS	translation	rotation
r.m.s.d. (A)	3.63	0.06
angle (o)	19.12	0.05

residues per monomer	DNA	protein
	0	141



1ju9

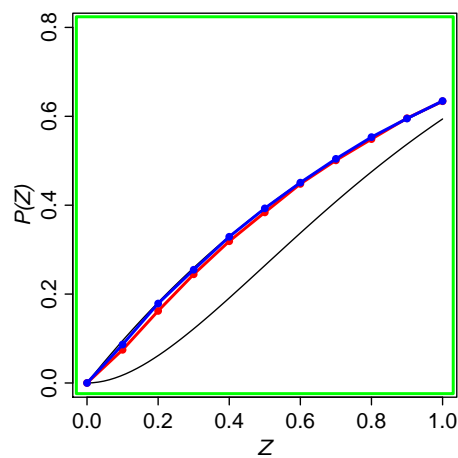
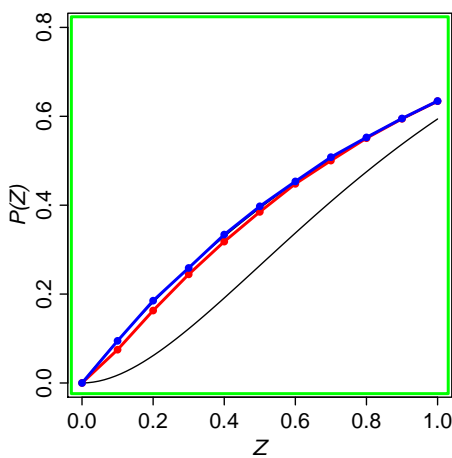
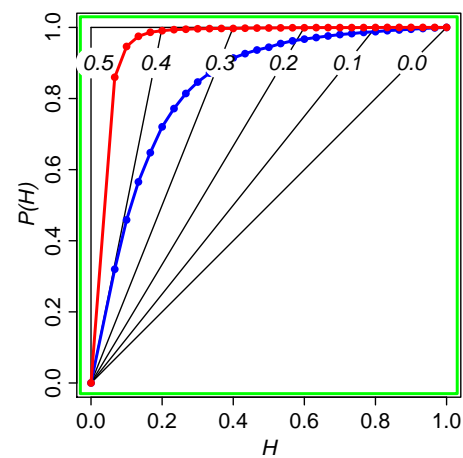
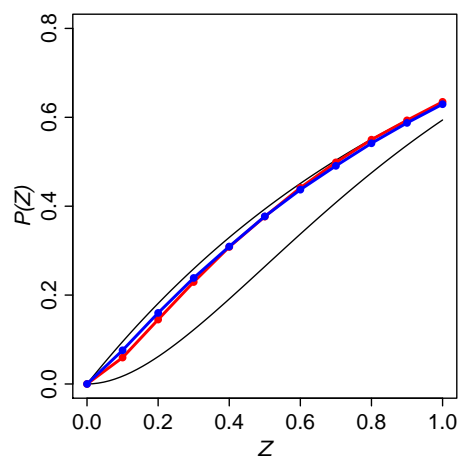
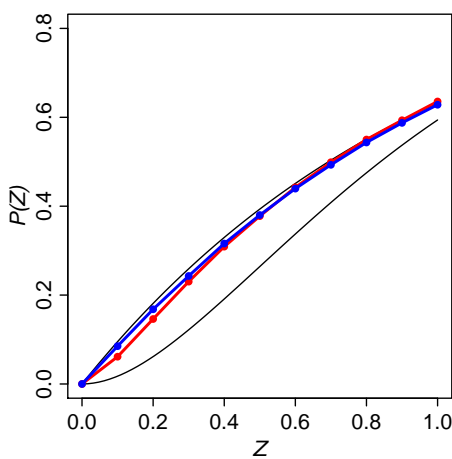
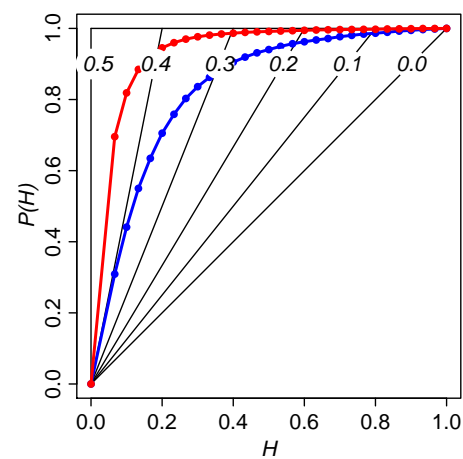
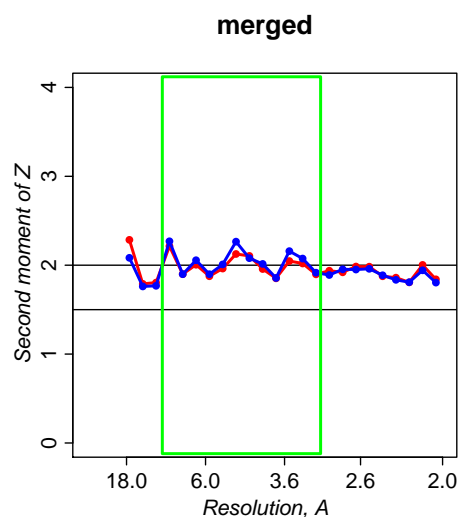
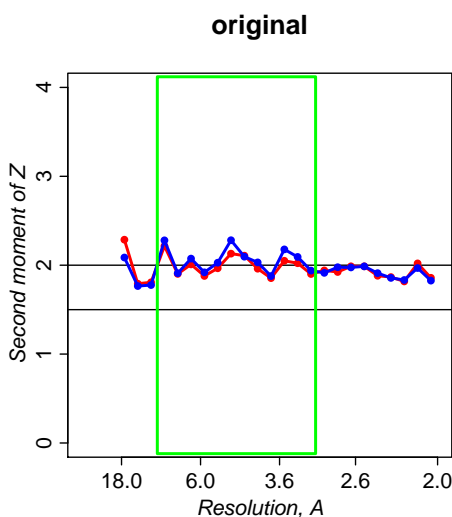
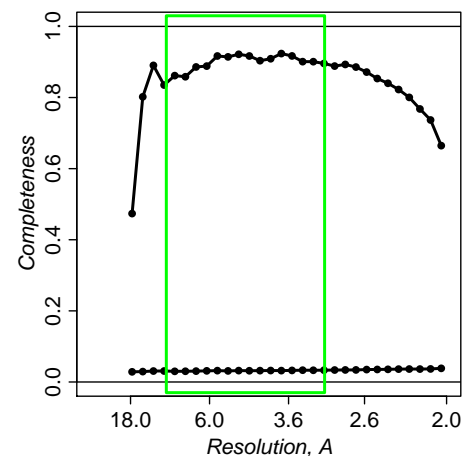
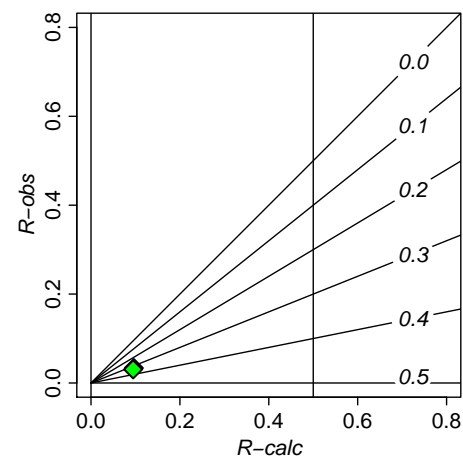
	original	merged
s.g.	P 1 2 1 1	C 2 2 2 1
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.11
R	24.0	
R'	24.1	24.6
R-free	26.5	
R'-free	26.4	27.0

s < f/100	1	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.9–2.0	9.9–3.0
unique	48,711	14,119
measured	40,685	12,779
used	33,986	10,988

NCS	translation	rotation
r.m.s.d. (A)	34.65	0.11
angle (o)	179.97	0.04

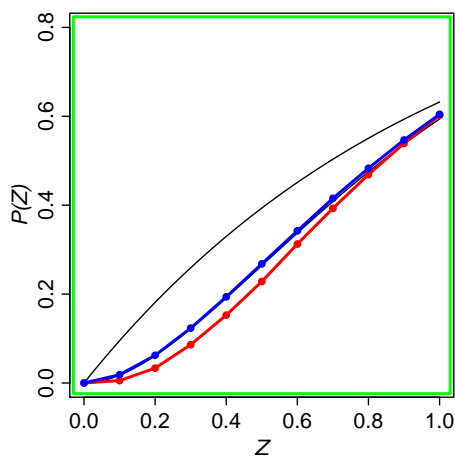
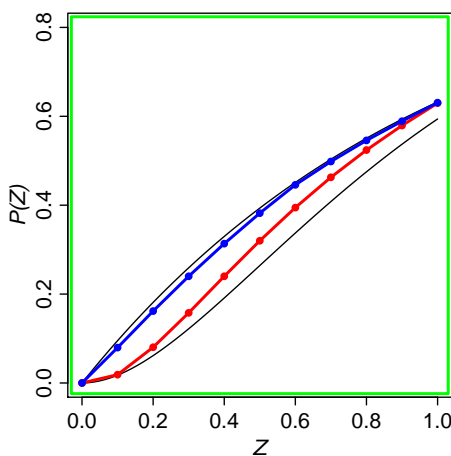
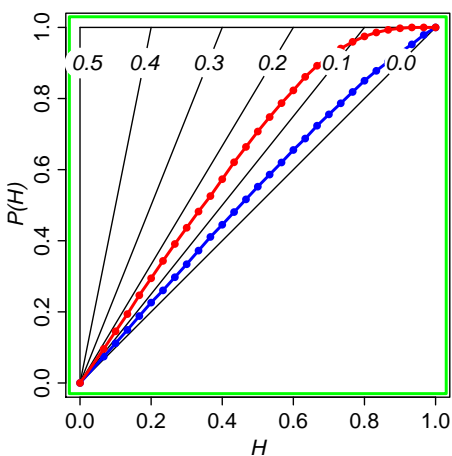
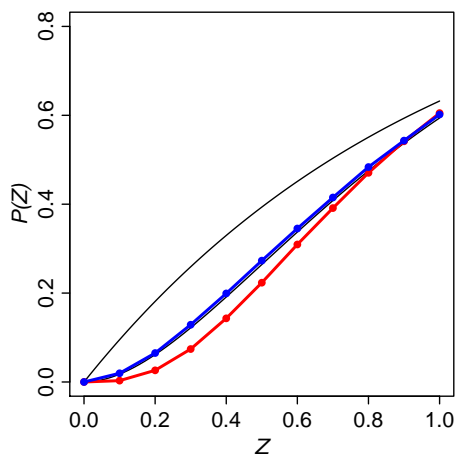
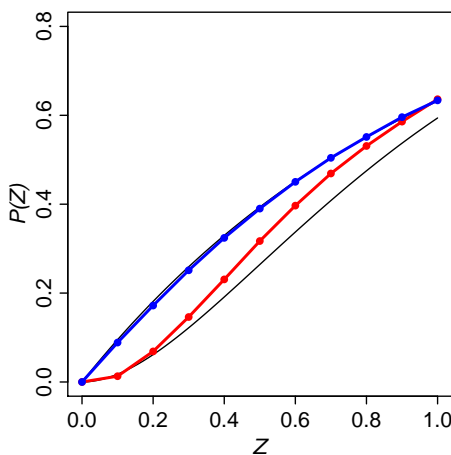
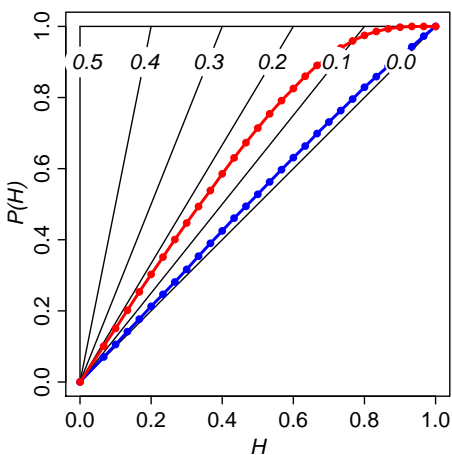
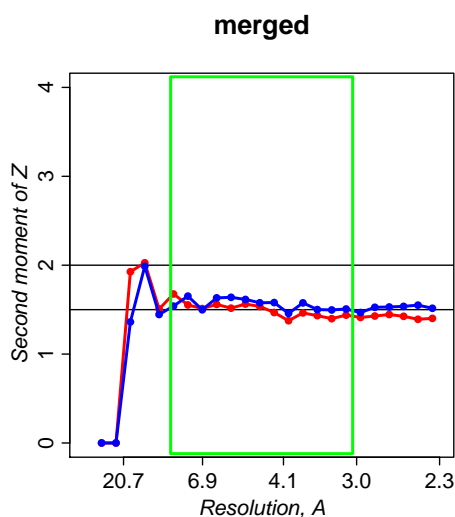
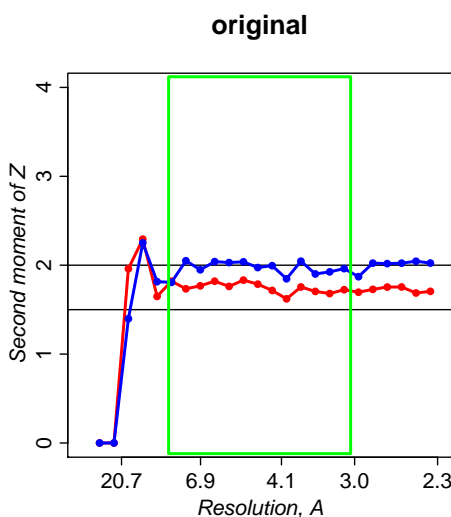
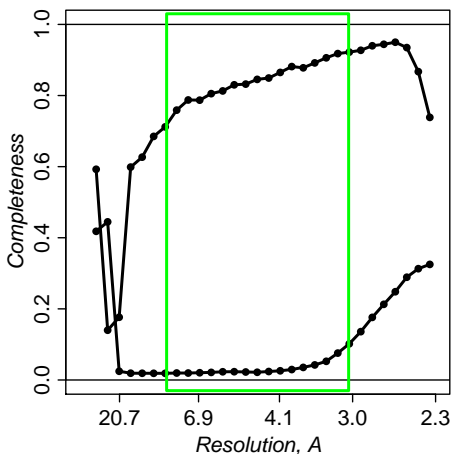
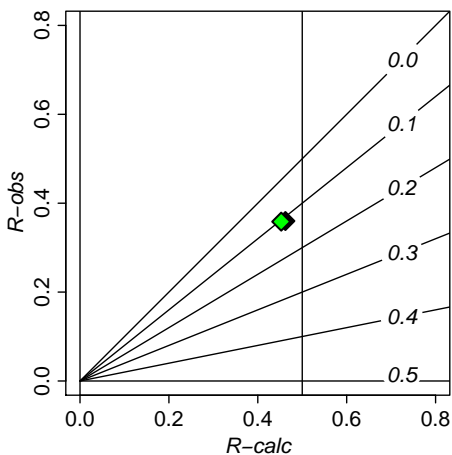
residues per monomer	DNA	protein
	0	374



1jx1

	original	merged
s.g.	P 65	P 65 2 2
p.g.	12021	12027
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		5.77
R	26.1	
R'	-	-
R-free	29.1	
R'-free	-	-
residues per monomer	DNA 0	protein 204

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	78.8-2.3	9.9-3.0
unique	72,415	31,784
measured	63,669	27,681
used	50,016	20,286
NCS	translation	rotation
r.m.s.d. (A)	3.95	3.03
angle (o)	19.58	13.42



1jxo

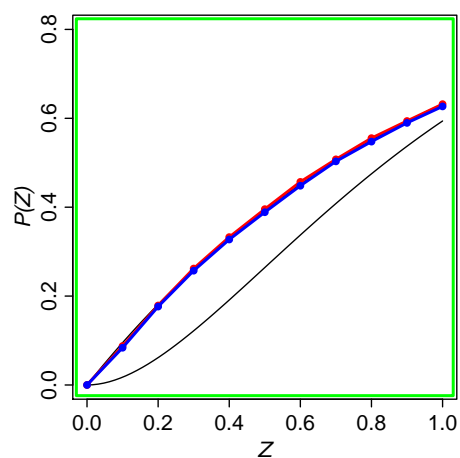
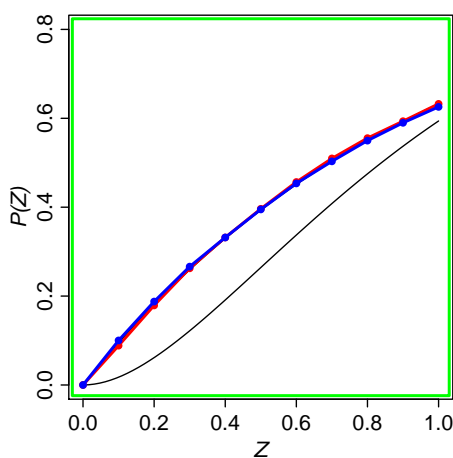
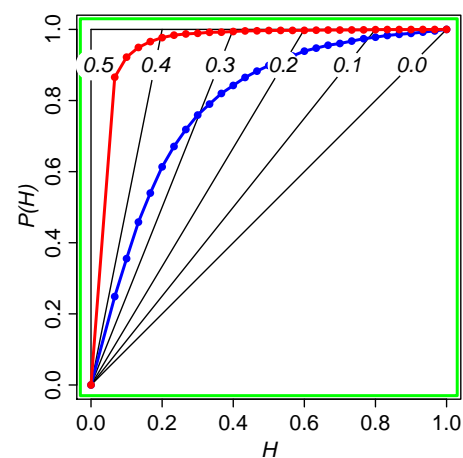
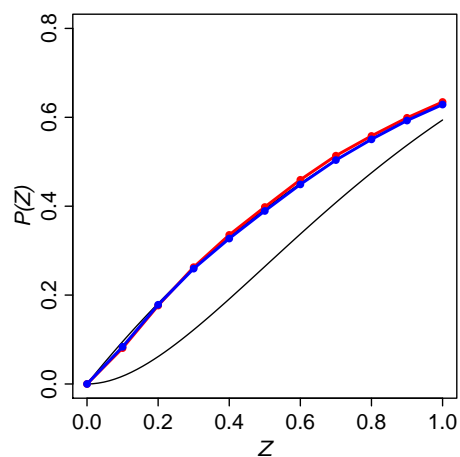
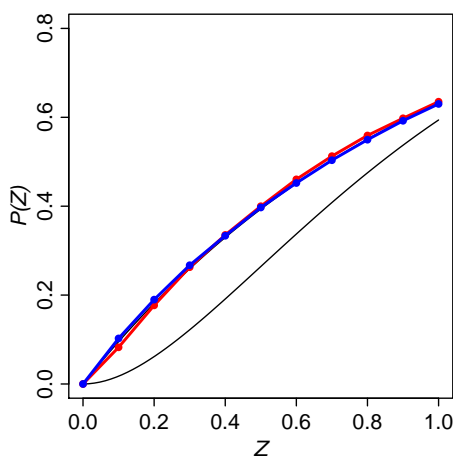
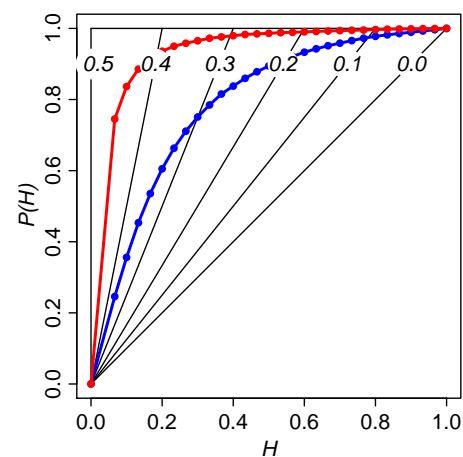
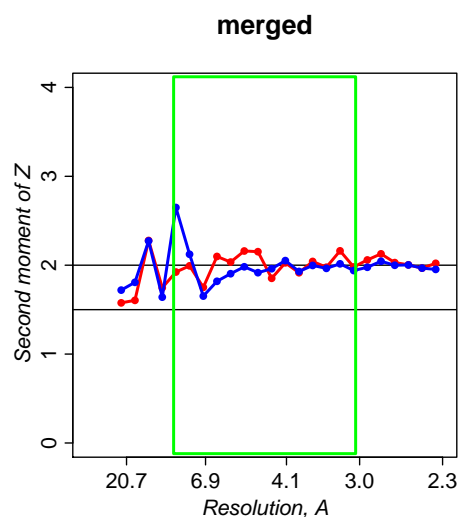
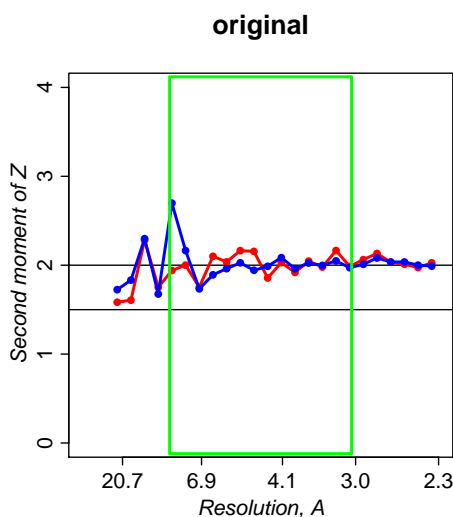
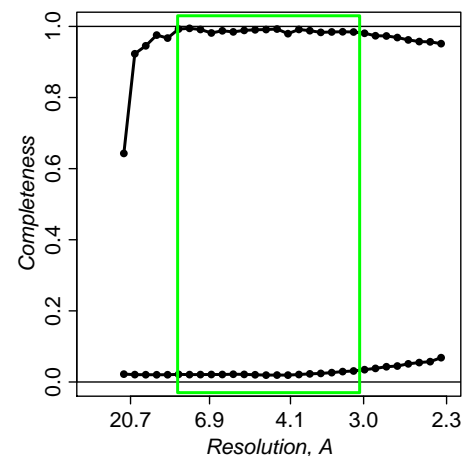
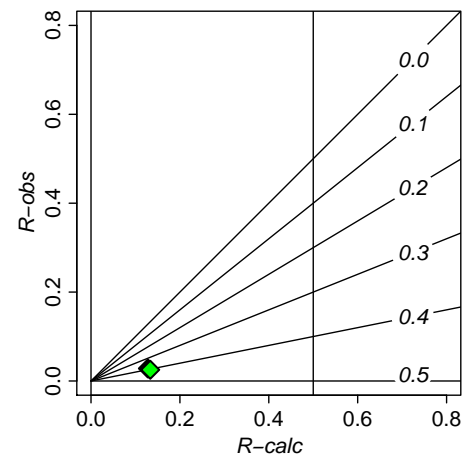
	original	merged
s.g.	P 1	P 1 21 1
p.g.	10000	10001
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.16
R	25.0	
R'	25.2	25.5
R-free	28.6	
R'-free	29.1	28.9

s < f/100	268	1.05 %
s <= 0	268	1.05 %
f <= 0	268	1.05 %
s,f <= 0	268	1.05 %

range (A)	29.9–2.3	9.9–3.0
unique	26,150	11,436
measured	25,456	11,280
used	24,166	10,760

NCS	translation	rotation
r.m.s.d. (A)	35.61	0.16
angle (o)	179.99	0.03

residues per monomer	DNA	protein
	0	261



1k1e

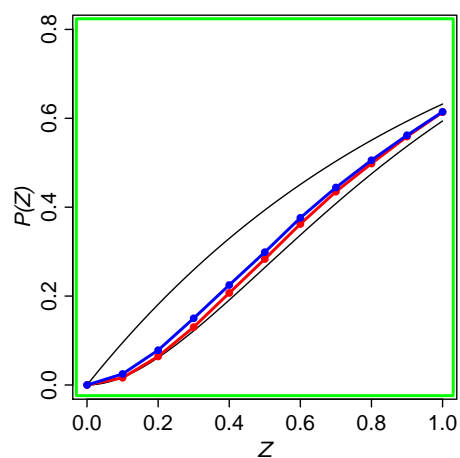
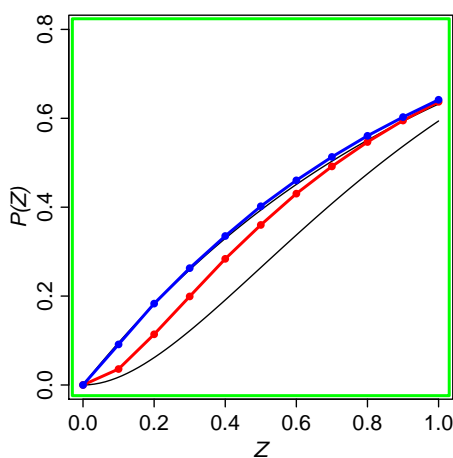
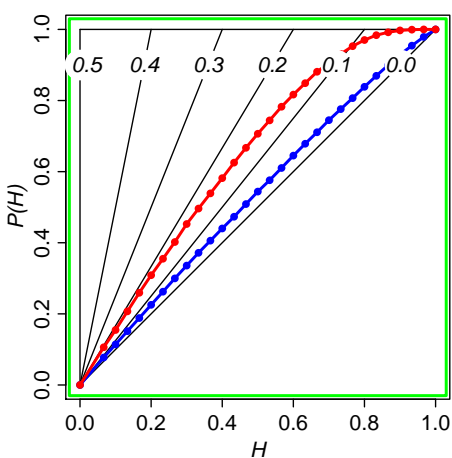
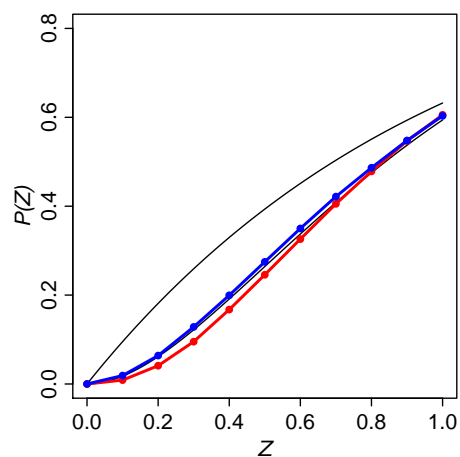
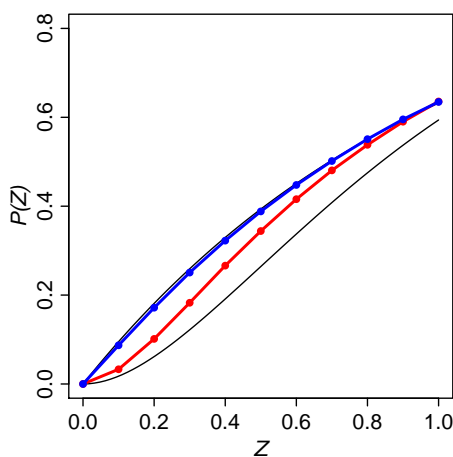
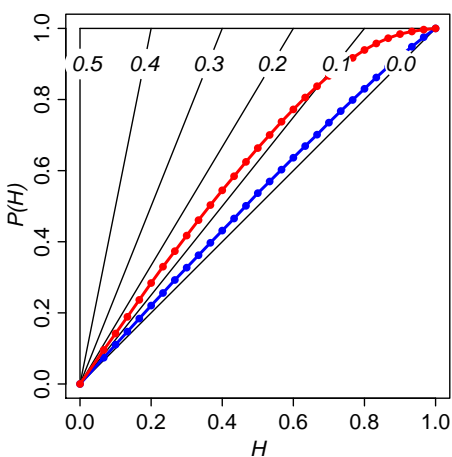
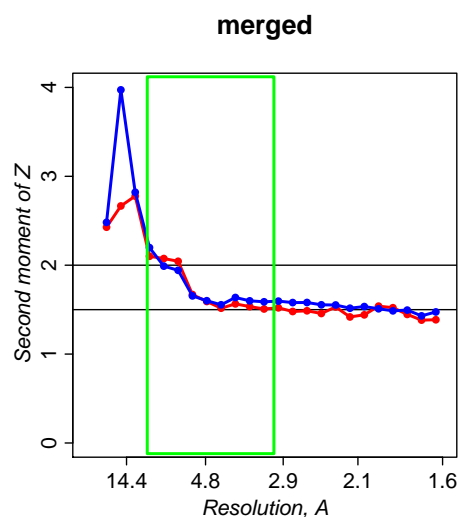
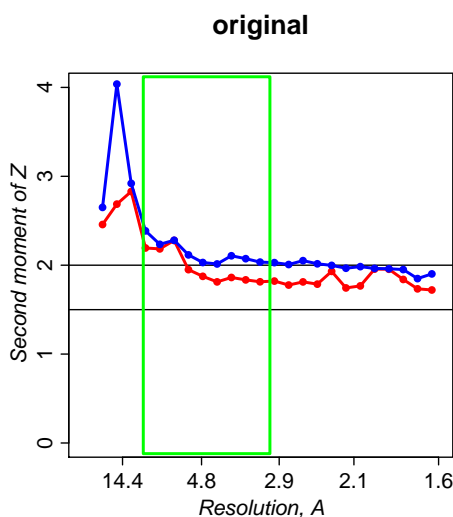
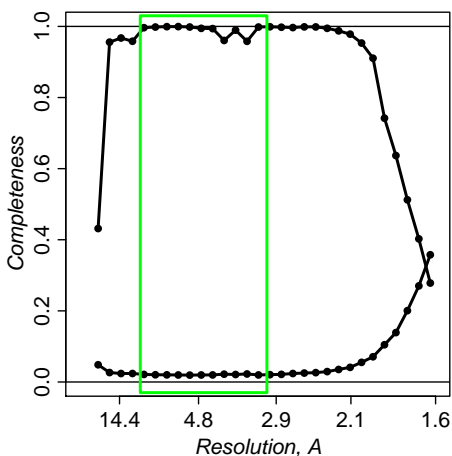
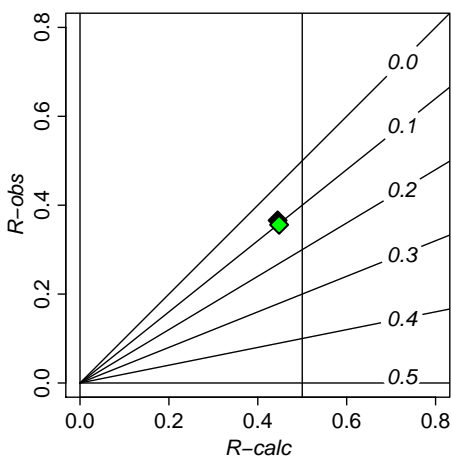
	original	merged
s.g.	C 1 2 1	F 2 2 2
p.g.	10001	10003
a.u.	12	6
p.t.	3	3
p.o.	3	3
r.m.s.d. (A)		4.35
R	30.6	
R'	-	-
R-free	31.7	
R'-free	-	-

residues per monomer	DNA	protein
	0	169

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	46.0-1.6	9.9-3.0
unique	259,283	39,150
measured	204,959	38,629
used	181,148	35,880

NCS	translation	rotation
r.m.s.d. (A)	1.30	0.73
angle (o)	6.27	3.52



1k25

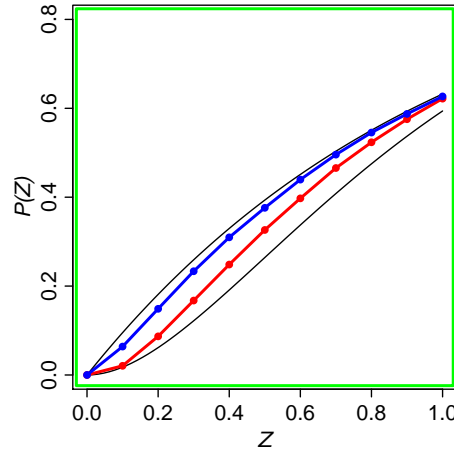
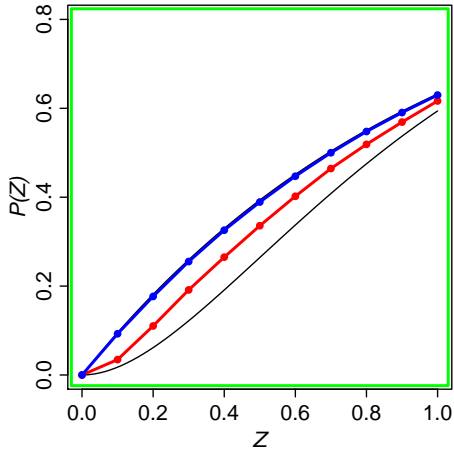
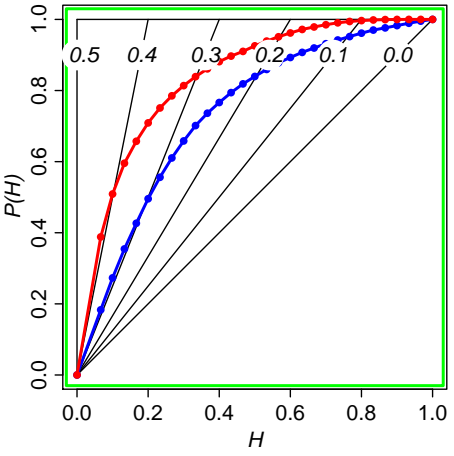
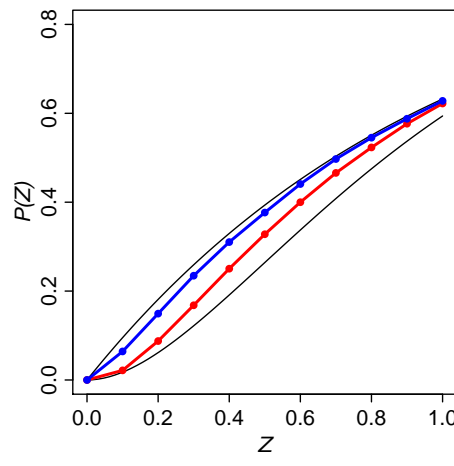
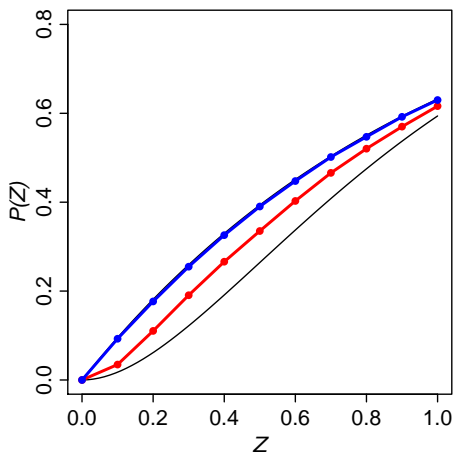
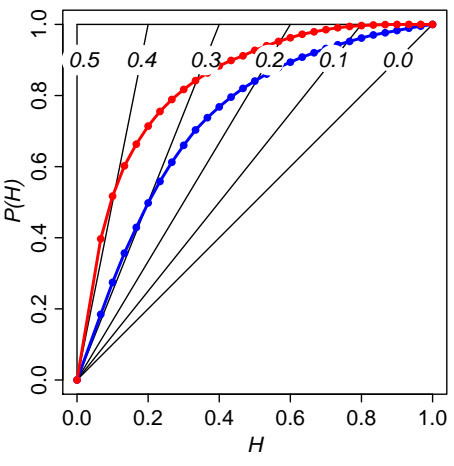
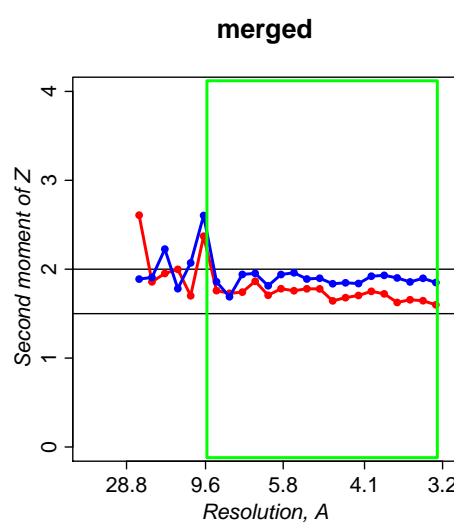
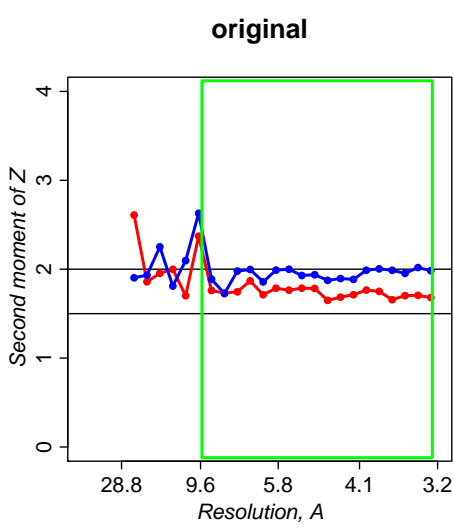
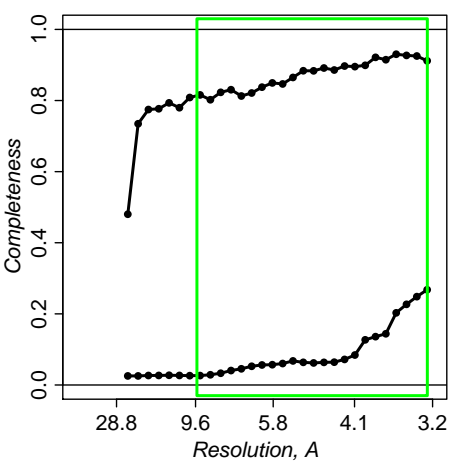
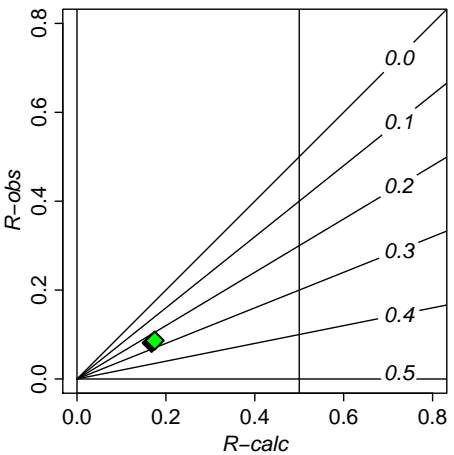
	original	merged
s.g.	P 32	P 62
p.g.	10020	12021
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.35
R	23.8	
R'	23.8	24.0
R-free	31.1	
R'-free	30.9	30.6

residues per monomer	DNA	protein
	0	522

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	24.9–3.2	9.9–3.2
unique	52,394	50,724
measured	46,615	45,314
used	41,082	40,080

NCS	translation	rotation
r.m.s.d. (A)	20.83	0.34
angle (o)	60.00	0.03



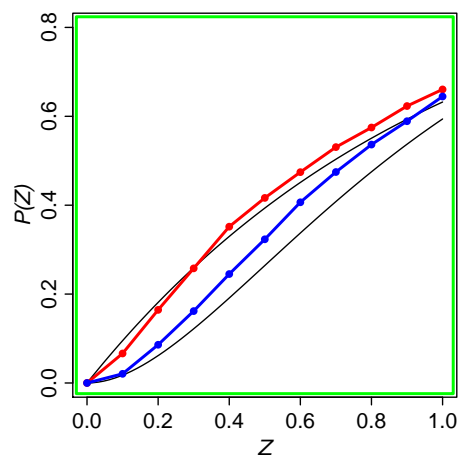
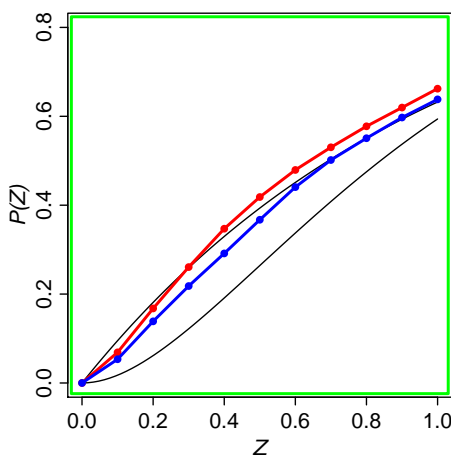
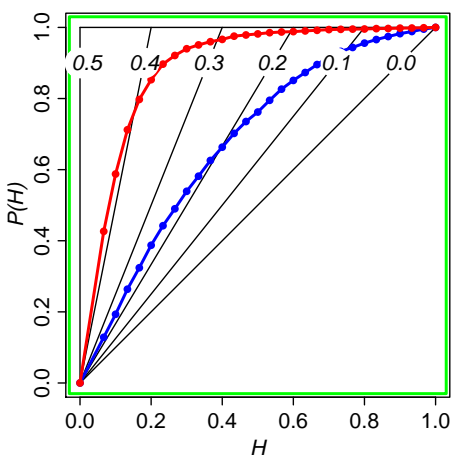
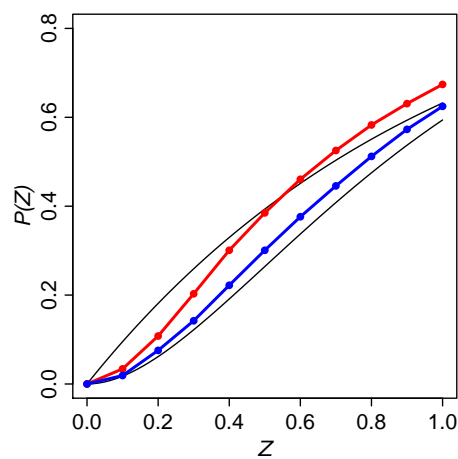
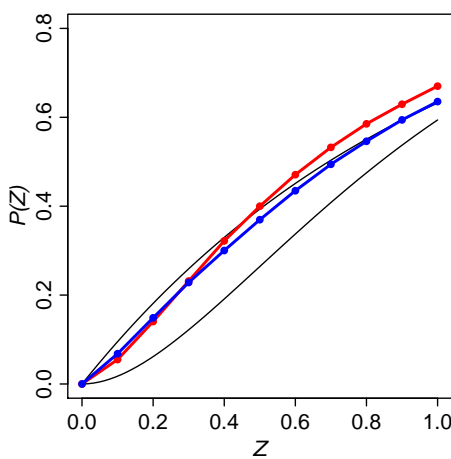
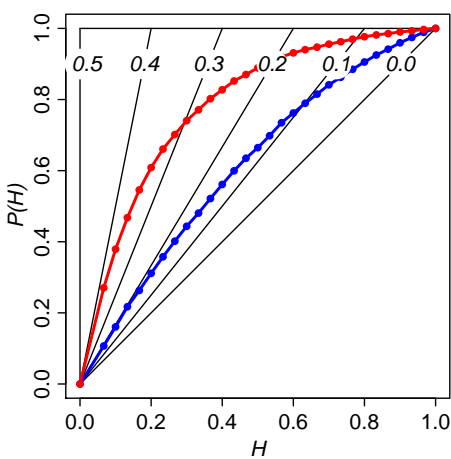
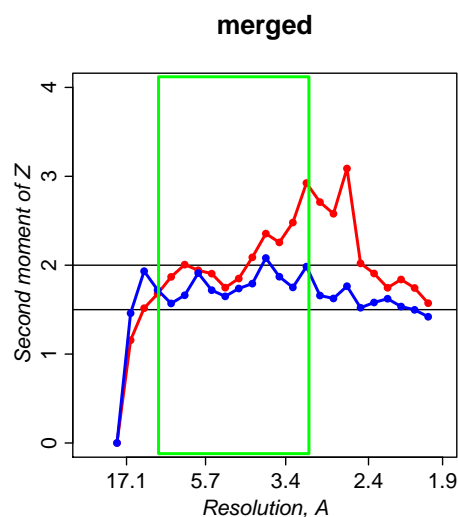
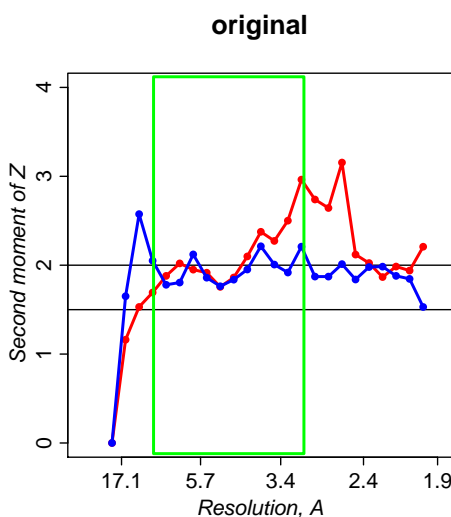
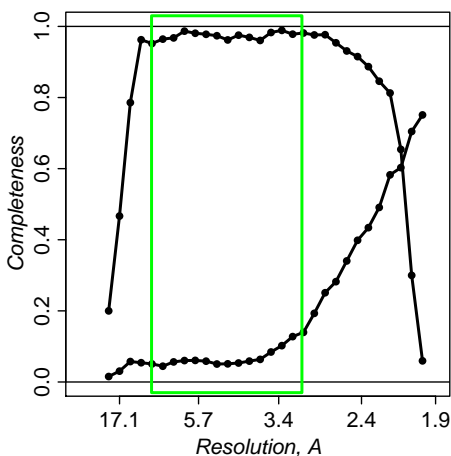
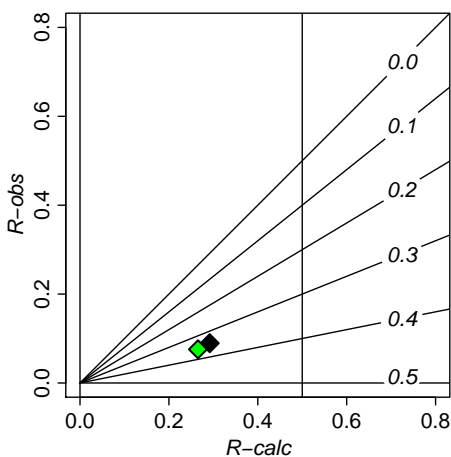
1k7t

	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		5.97
R	29.3	
R'	-	-
R-free	34.2	
R'-free	-	-
residues per monomer	DNA 0	protein 170

s < f/100	349	1.75 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.0-1.9	9.9-3.0
unique	25,453	6,837
measured	19,921	6,669
used	16,428	5,886

NCS	translation	rotation
r.m.s.d. (A)	30.49	0.49
angle (o)	179.87	0.14



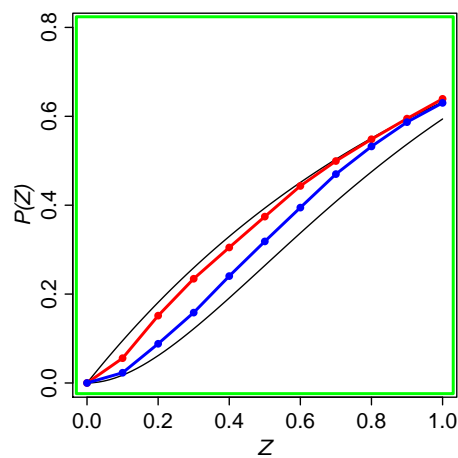
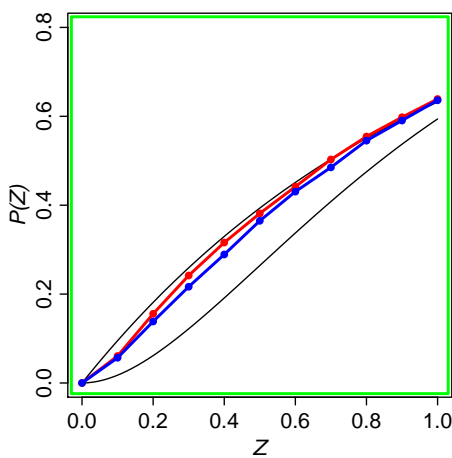
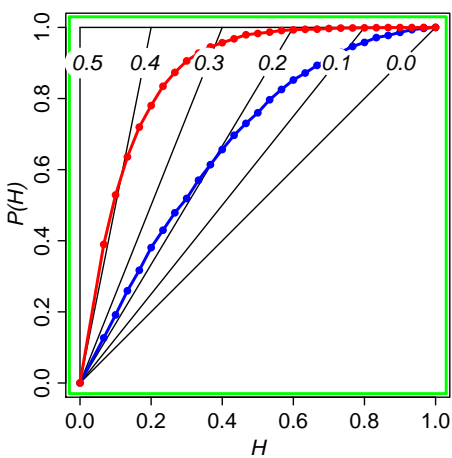
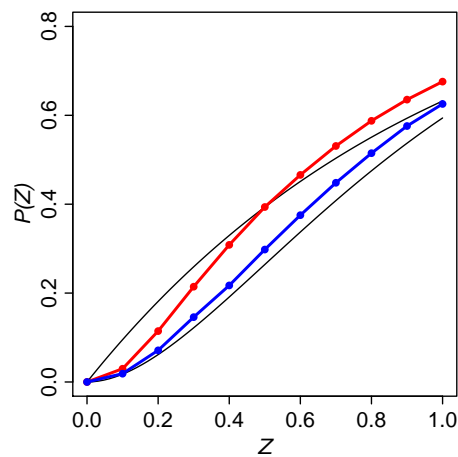
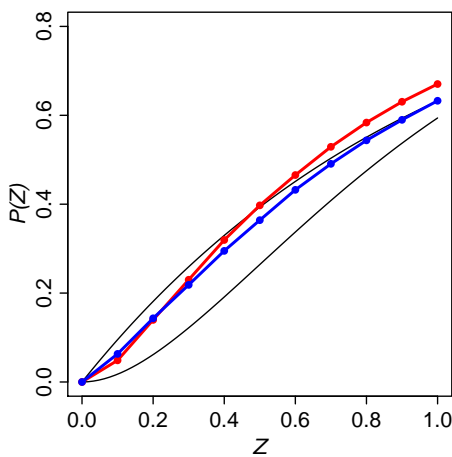
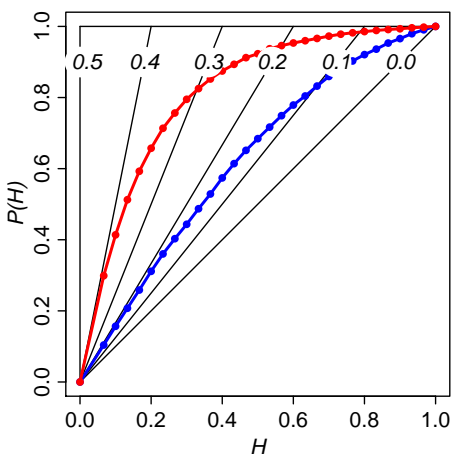
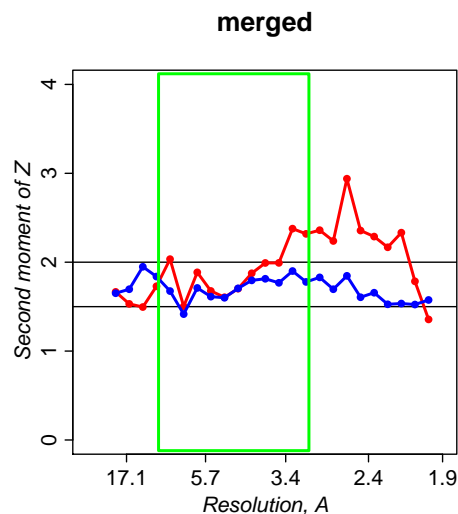
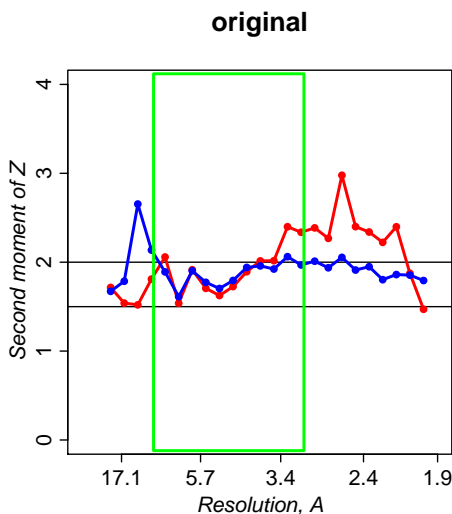
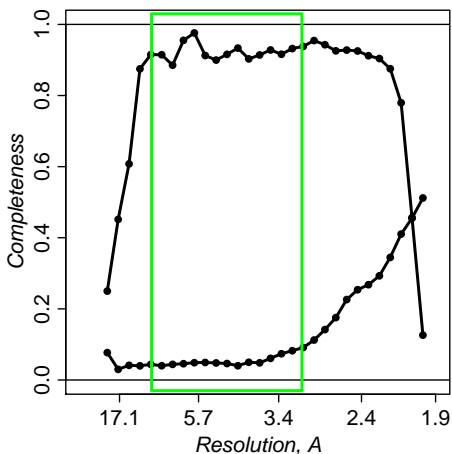
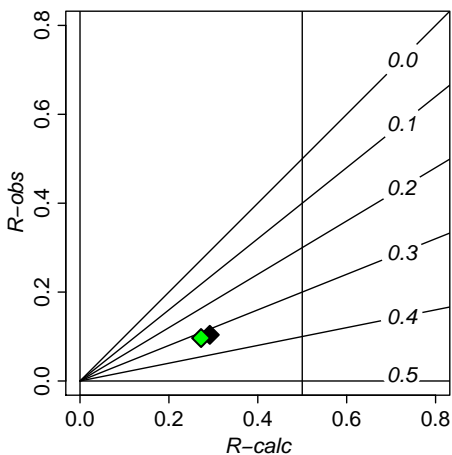
1k7u

	original	merged
s.g.	P 1 2 1 1	C 2 2 2 1
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		6.01
R	27.3	
R'	-	-
R-free	31.4	
R'-free	-	-
residues per monomer	DNA 0	protein 170

s < f/100	665	3.34 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	31.0–1.9	9.9–3.0
unique	24,647	6,623
measured	19,893	6,117
used	16,780	5,268

NCS	translation	rotation
r.m.s.d. (A)	30.16	0.45
angle (o)	179.81	0.20



1k7v

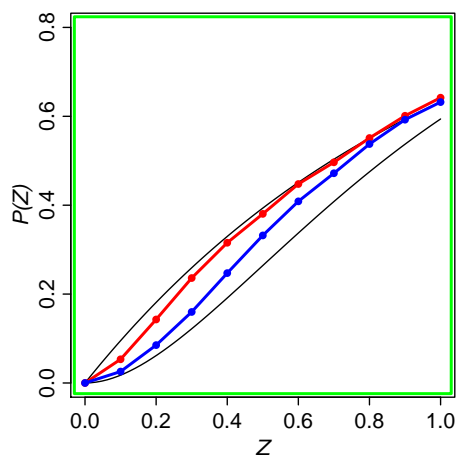
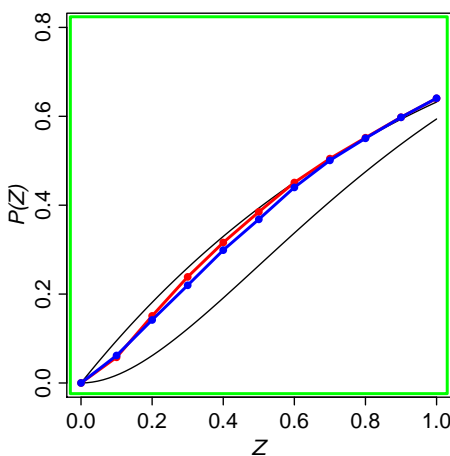
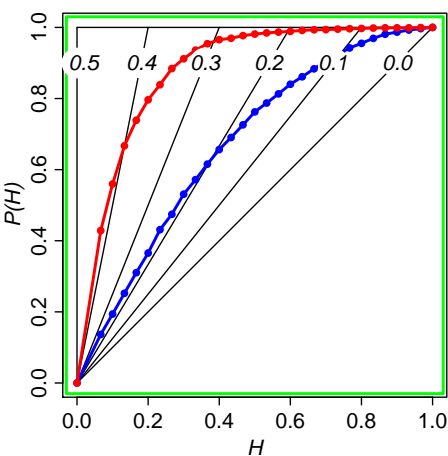
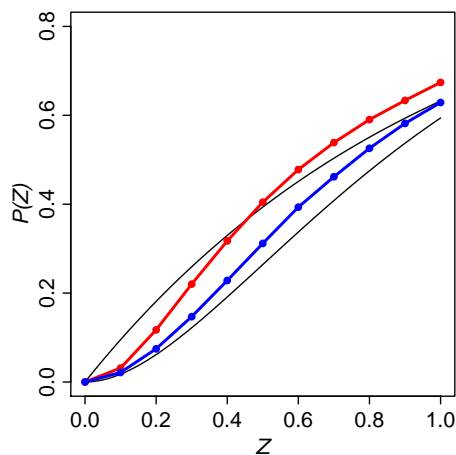
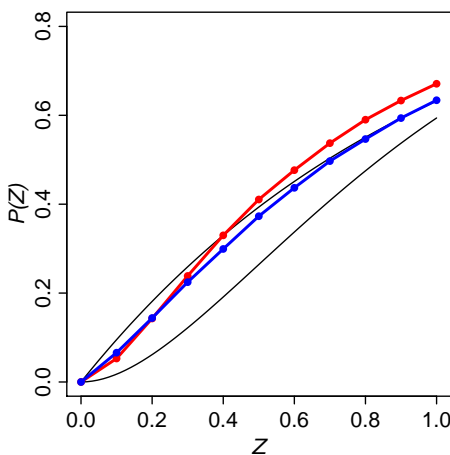
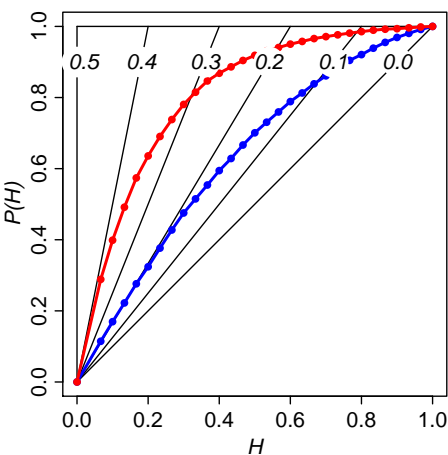
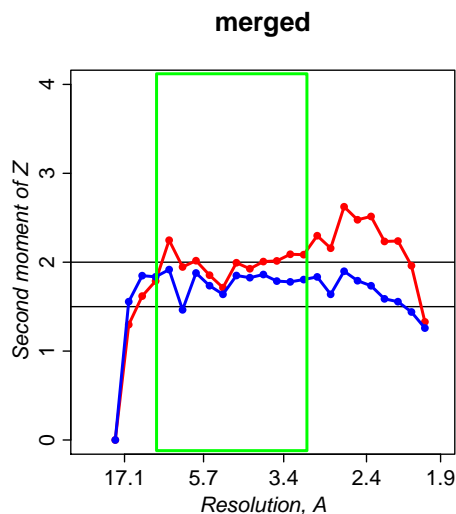
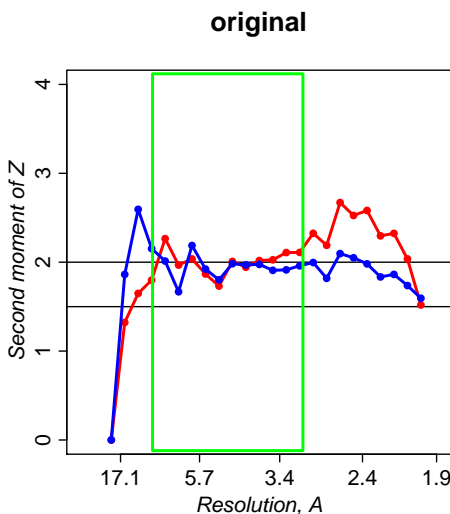
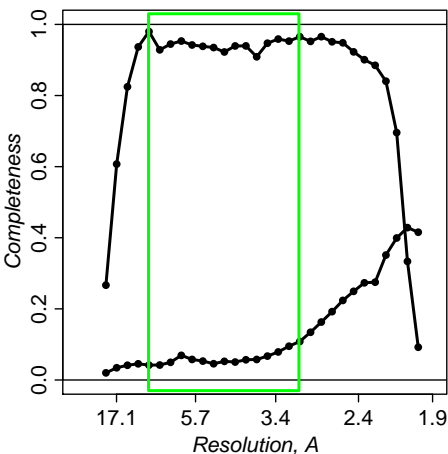
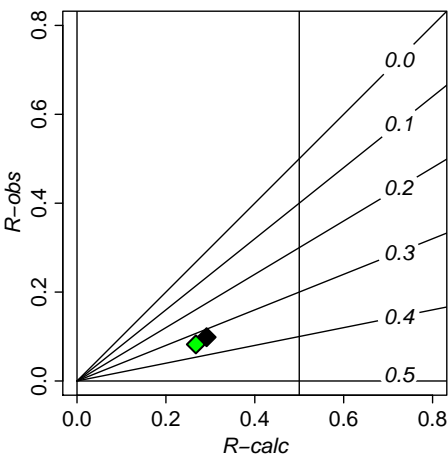
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		6.06
R	29.1	
R'	-	-
R-free	34.2	
R'-free	-	-

s < f/100	310	1.59 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	28.7-1.9	9.9-3.0
unique	24,681	6,670
measured	19,451	6,293
used	15,916	5,404

NCS	translation	rotation
r.m.s.d. (A)	24.55	0.33
angle (o)	179.85	0.22

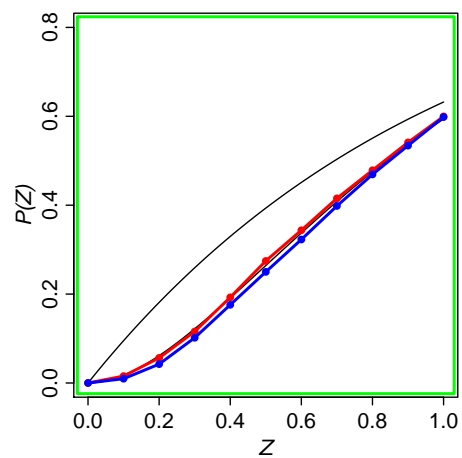
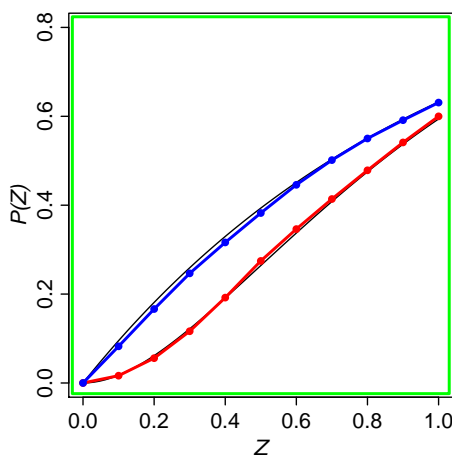
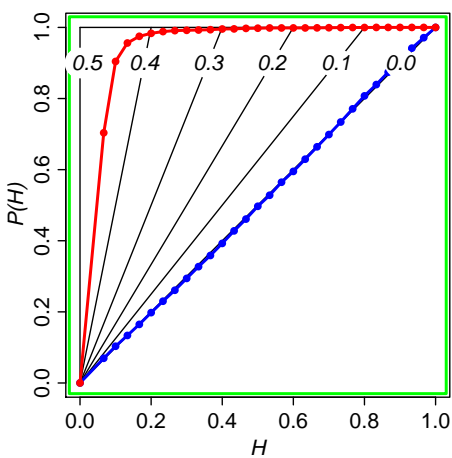
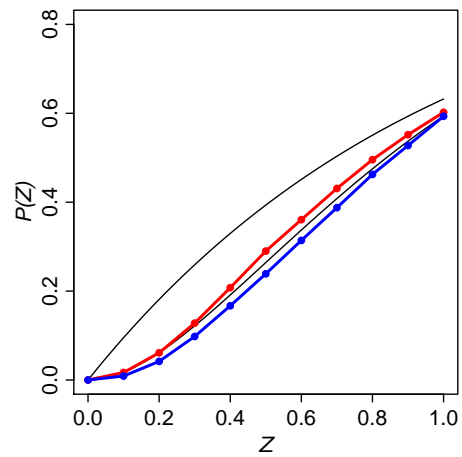
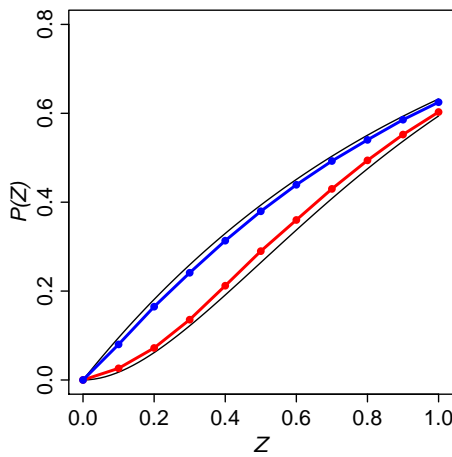
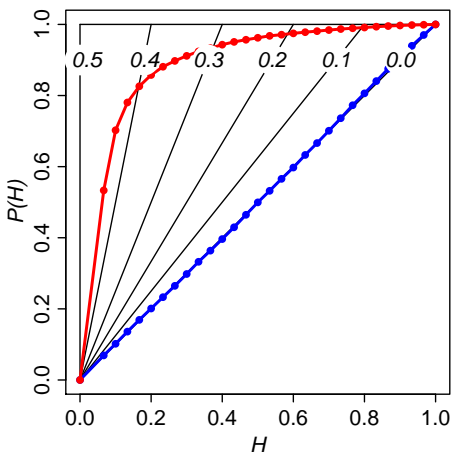
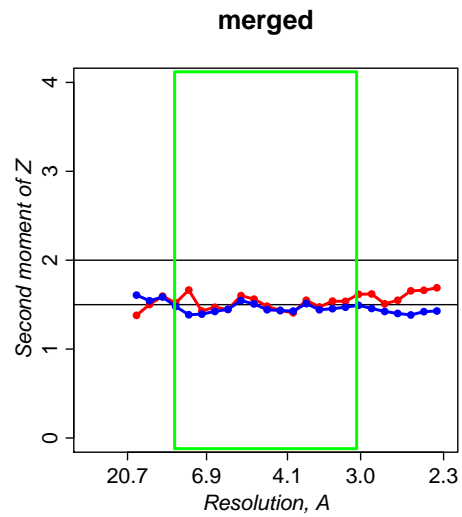
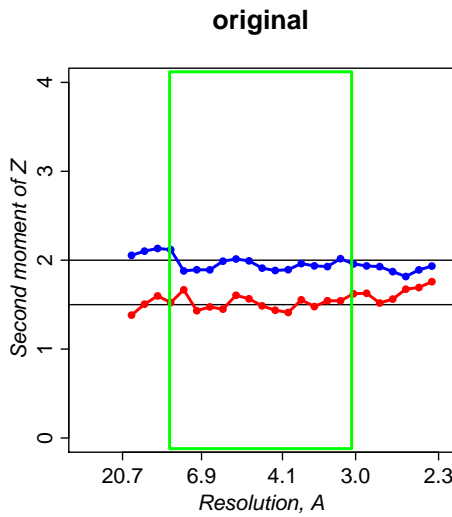
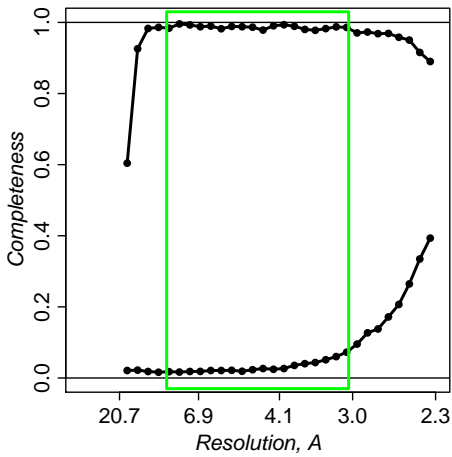
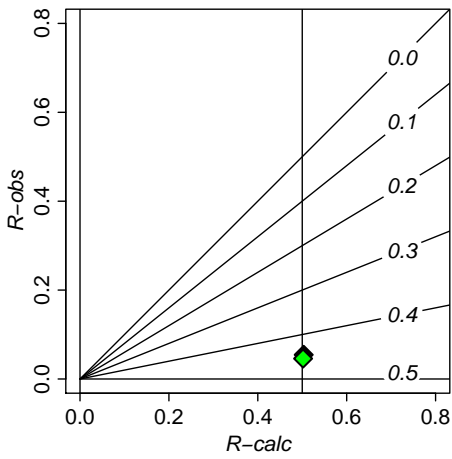
residues per monomer	DNA	protein
	0	170



1k9o

	original	merged
s.g.	P 31 2 1	-
p.g.	10023	12027
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	31.0	-
R'	-	-
R-free	35.1	-
R'-free	-	-
residues per monomer	DNA 0	protein 599

s < f/100	667	2.20 %
s <= 0	665	2.19 %
f <= 0	665	2.19 %
s,f <= 0	665	2.19 %
range (A)	19.5-2.3	9.9-3.0
unique	31,479	13,996
measured	30,331	13,799
used	26,258	11,762
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1kd3

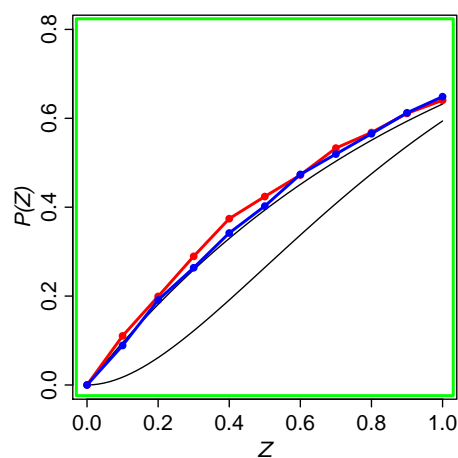
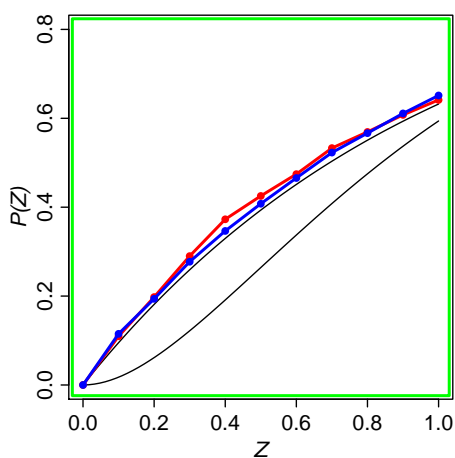
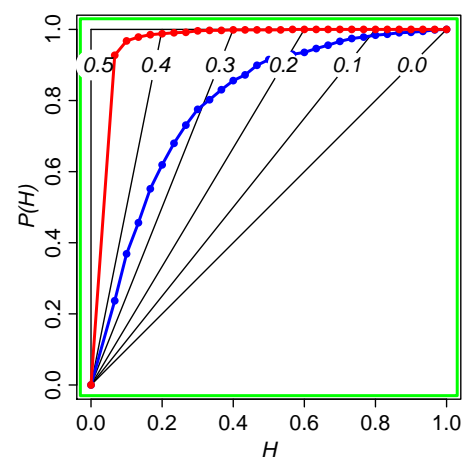
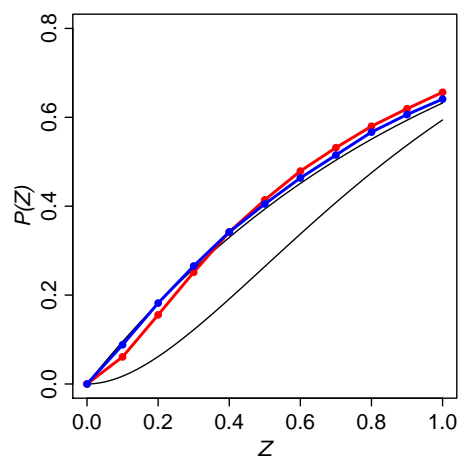
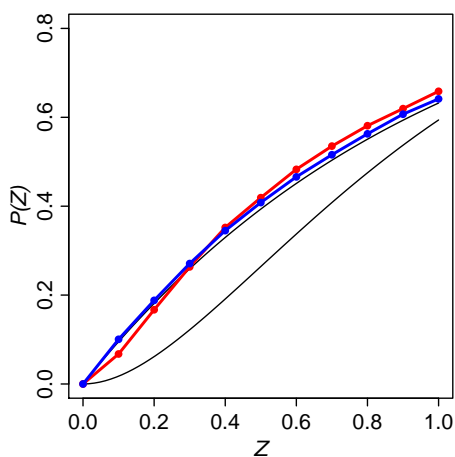
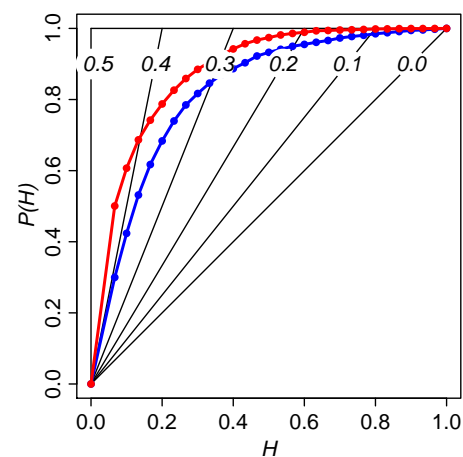
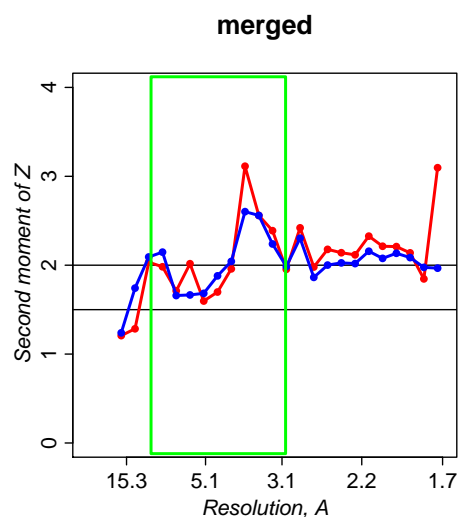
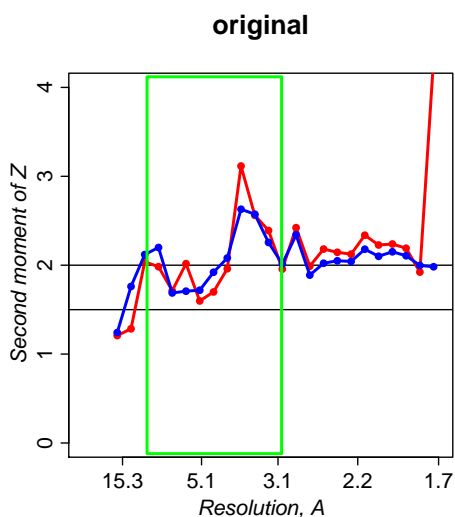
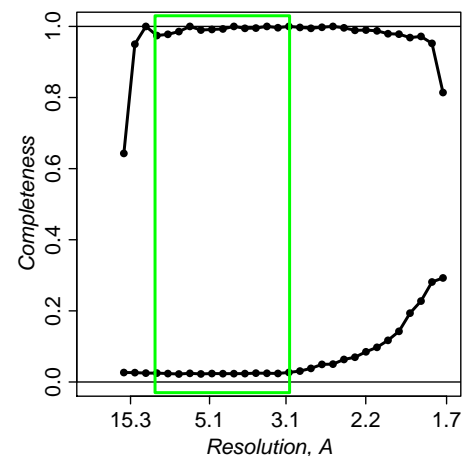
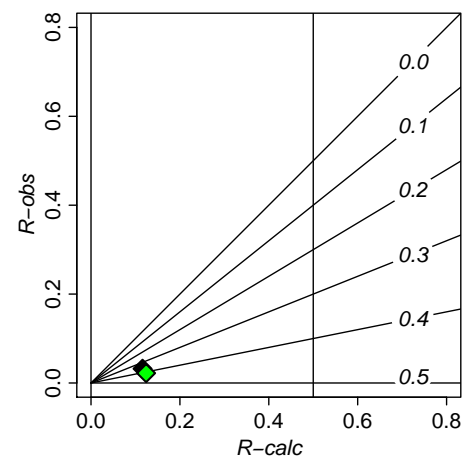
	original	merged
s.g.	P 43	P 43 21 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.05
R	29.6	
R'	29.6	30.4
R-free	27.2	
R'-free	27.2	28.6

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	22.1–1.7	9.9–3.0
unique	10,829	1,923
measured	10,496	1,915
used	8,914	1,480

NCS	translation	rotation
r.m.s.d. (A)	13.95	0.05
angle (o)	179.94	0.09

residues per monomer	DNA	protein
	10	0



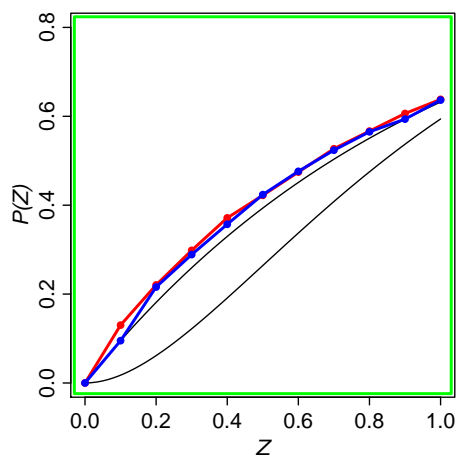
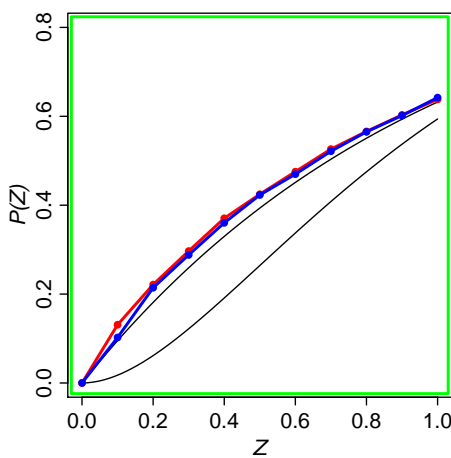
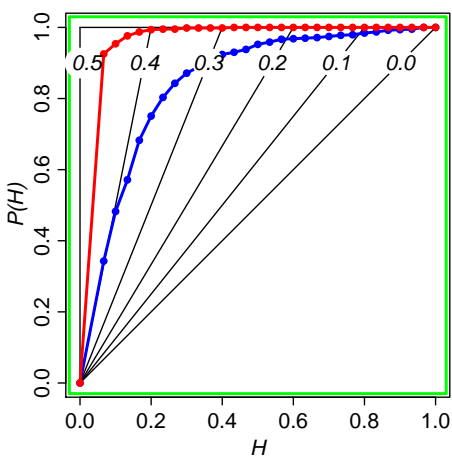
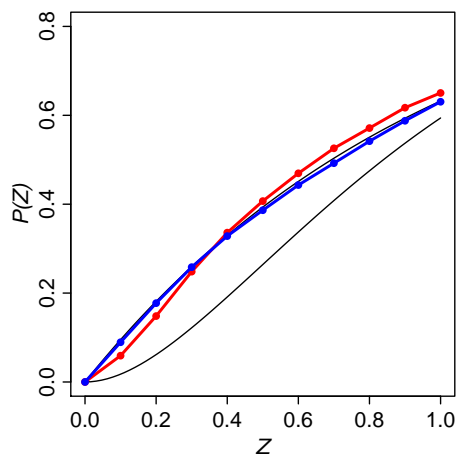
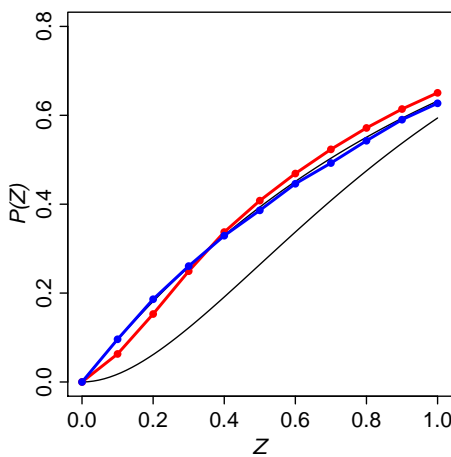
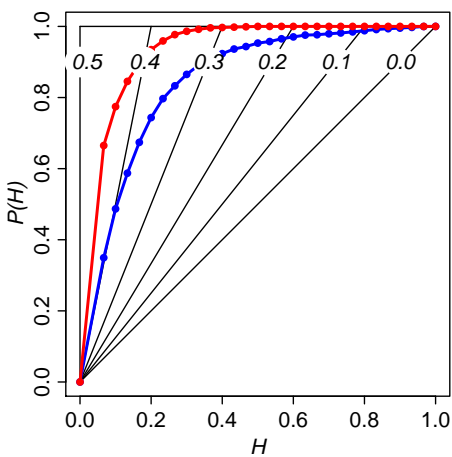
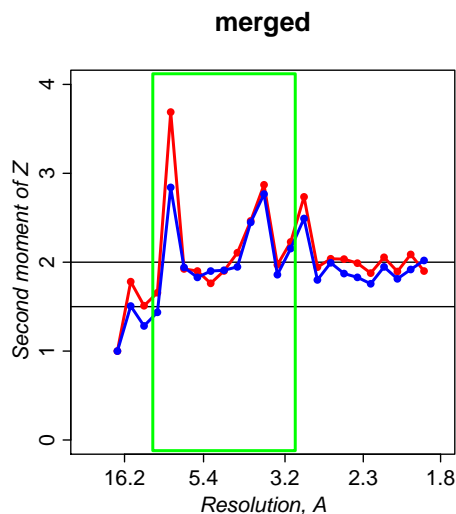
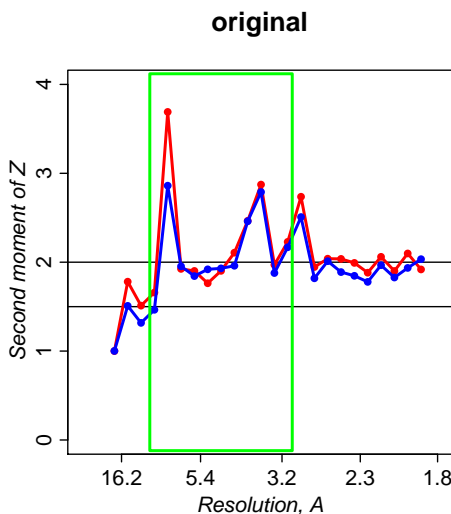
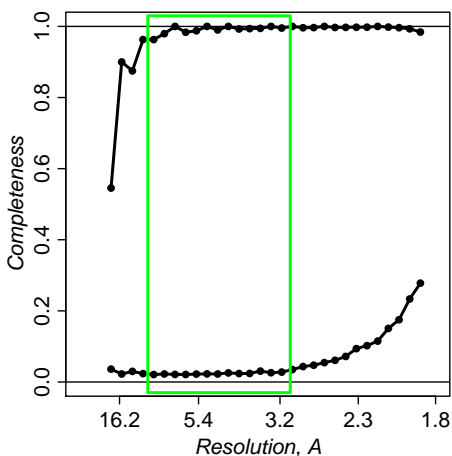
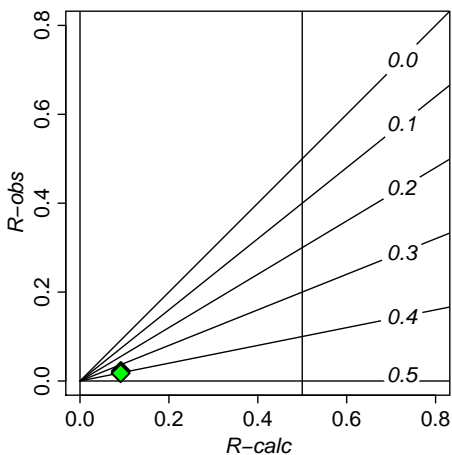
1kd4

	original	merged
s.g.	P 43	P 43 21 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.13
R	37.9	
R'	38.0	39.6
R-free	37.4	
R'-free	37.4	39.1
residues per monomer	DNA 10	protein 0

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	24.9–1.9	9.9–3.0
unique	7,149	1,656
measured	7,113	1,647
used	5,976	1,252

NCS	translation	rotation
r.m.s.d. (A)	13.67	0.12
angle (o)	179.90	0.11



1kd5

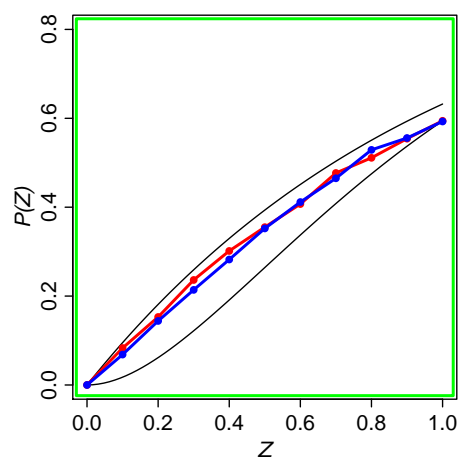
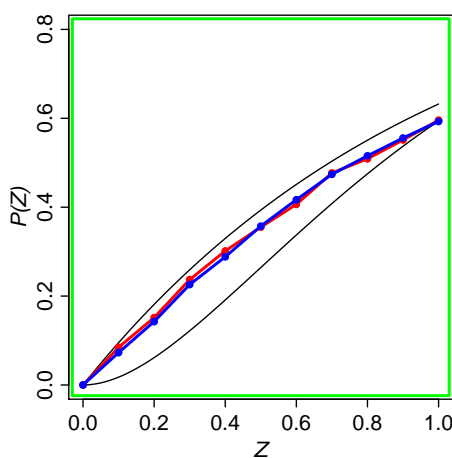
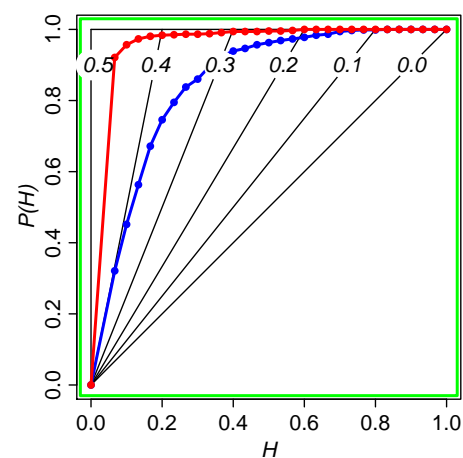
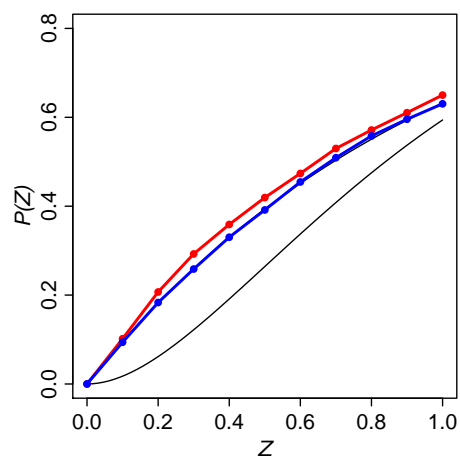
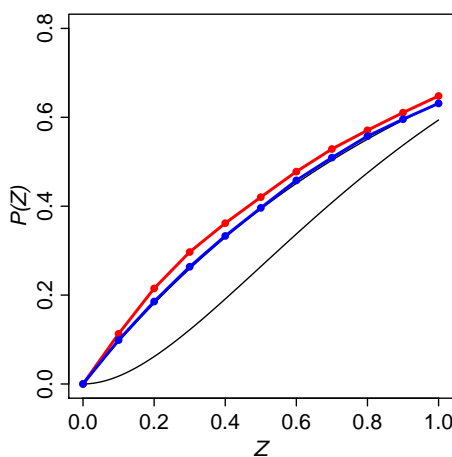
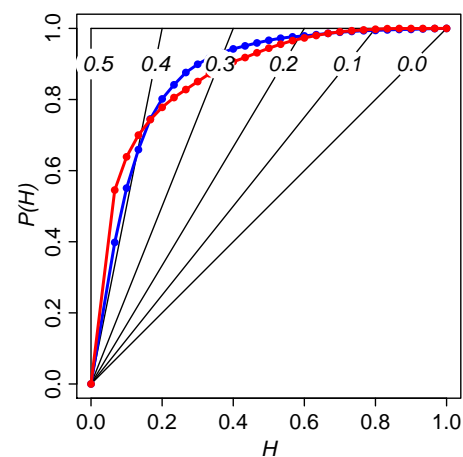
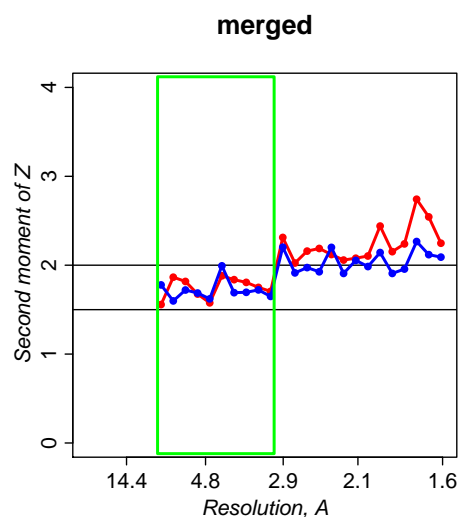
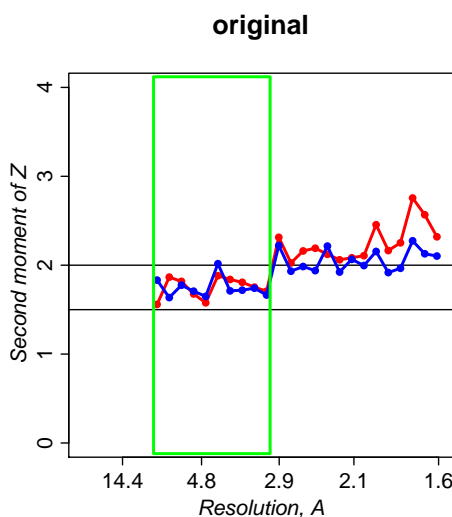
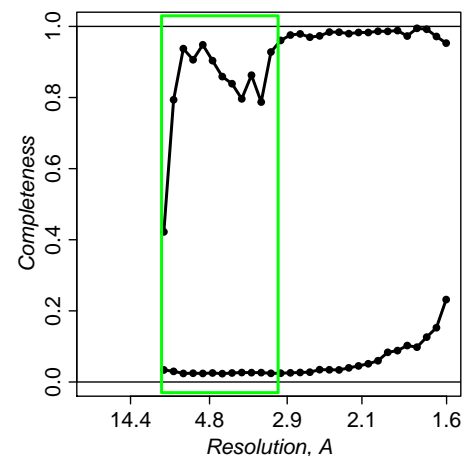
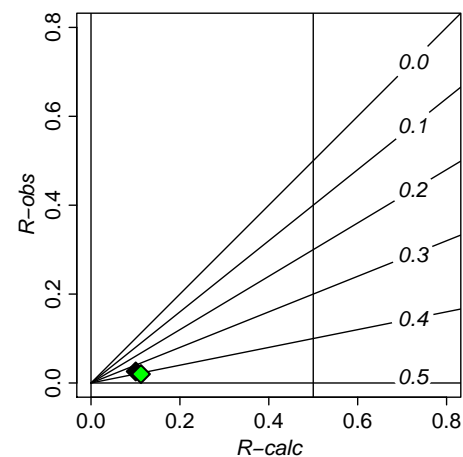
	original	merged
s.g.	P 43	P 43 21 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.04
R	28.6	
R'	28.6	28.9
R-free	27.7	
R'-free	27.7	28.3

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	8.4–1.6	8.4–3.0
unique	14,330	2,048
measured	13,804	1,775
used	11,970	1,346

NCS	translation	rotation
r.m.s.d. (A)	16.20	0.04
angle (o)	179.91	0.10

residues per monomer	DNA	protein
	10	0



1keo

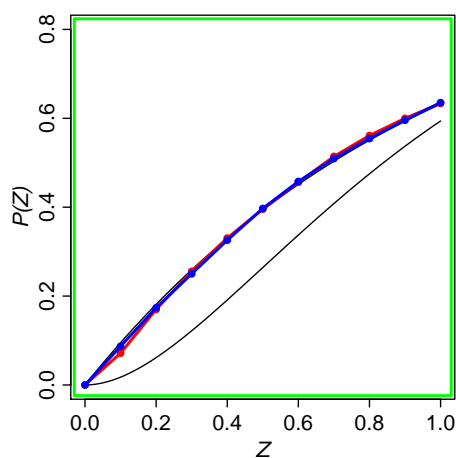
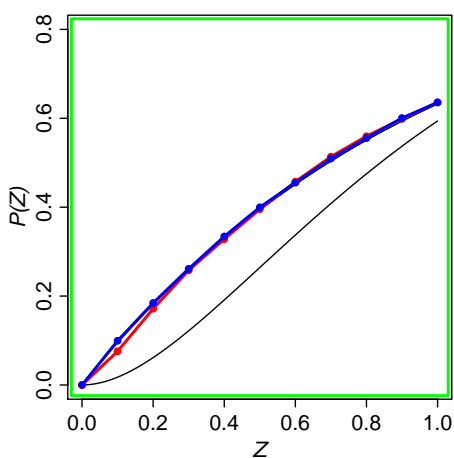
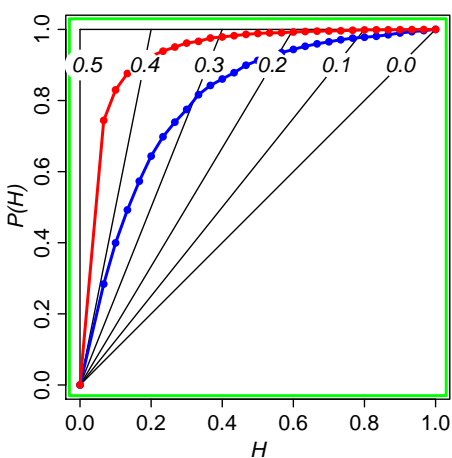
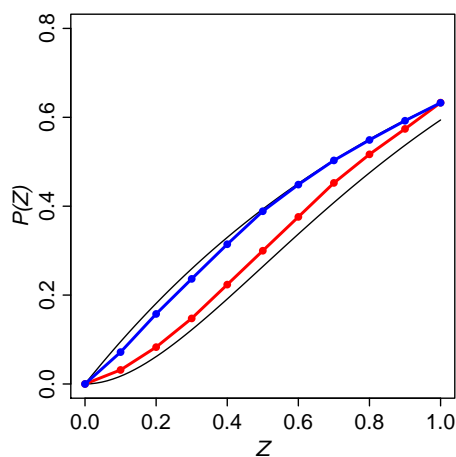
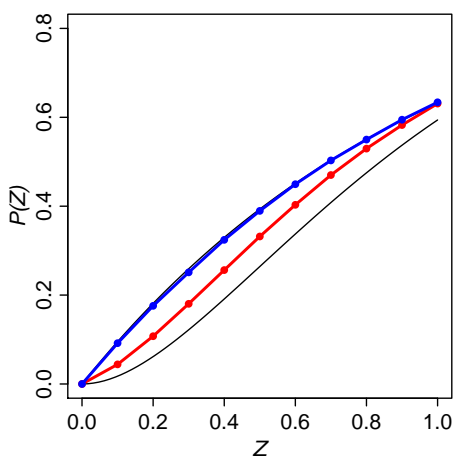
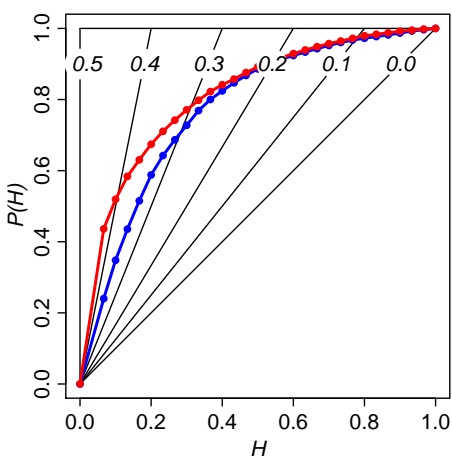
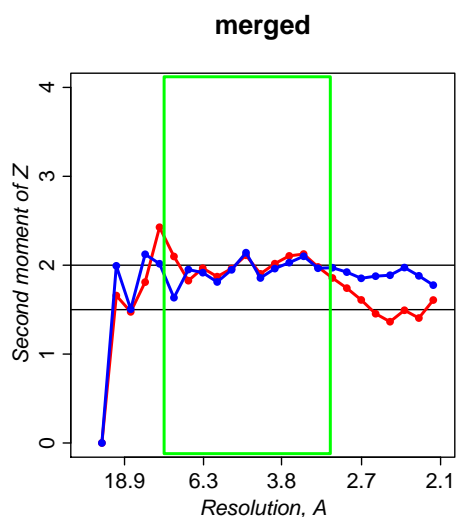
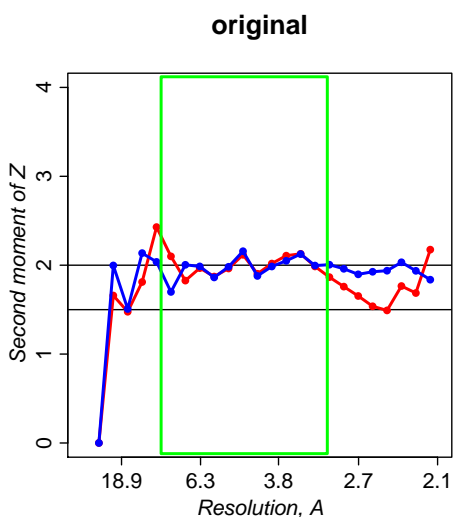
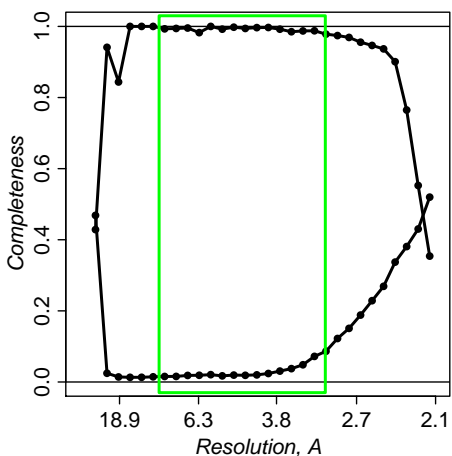
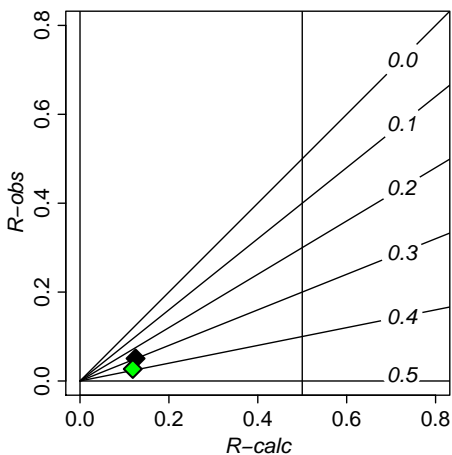
	original	merged
s.g.	14	14 2 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.20
R	25.4	
R'	25.7	26.3
R-free	30.3	
R'-free	31.1	31.2

residues per monomer	DNA	protein
	0	152

s < f/100	26	0.12 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	76.9–2.1	9.9–3.0
unique	24,540	8,365
measured	21,125	8,282
used	18,218	7,298

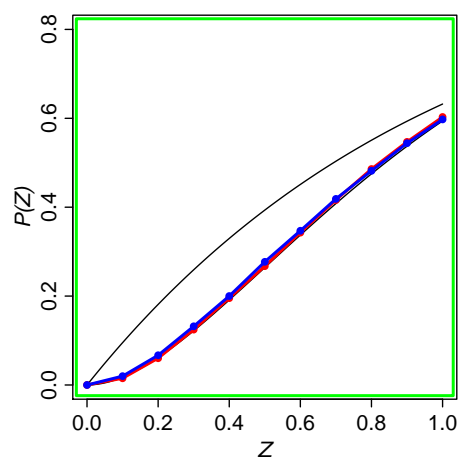
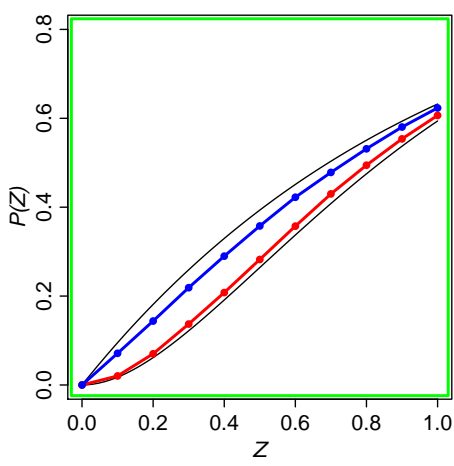
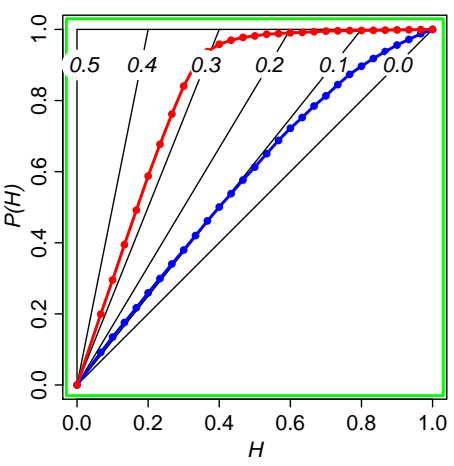
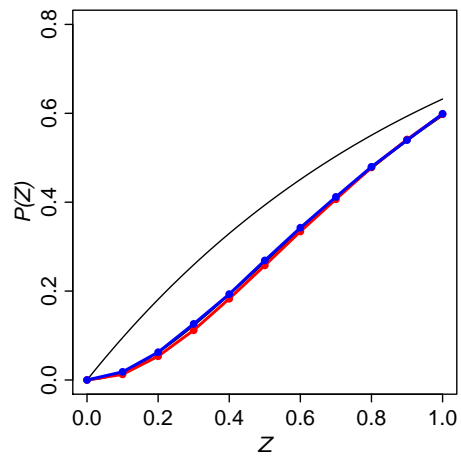
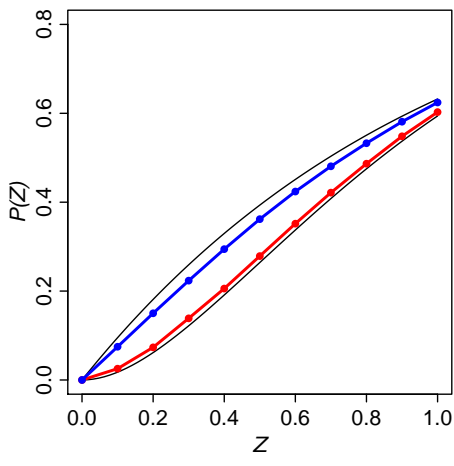
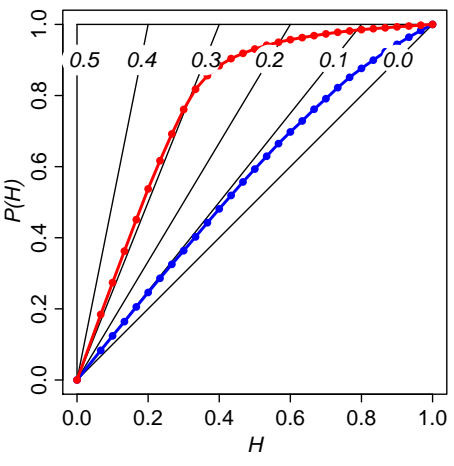
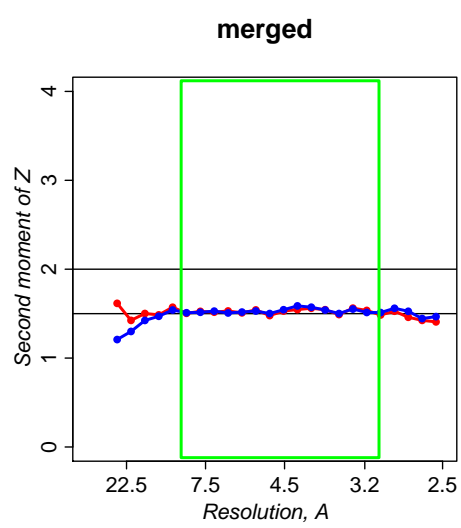
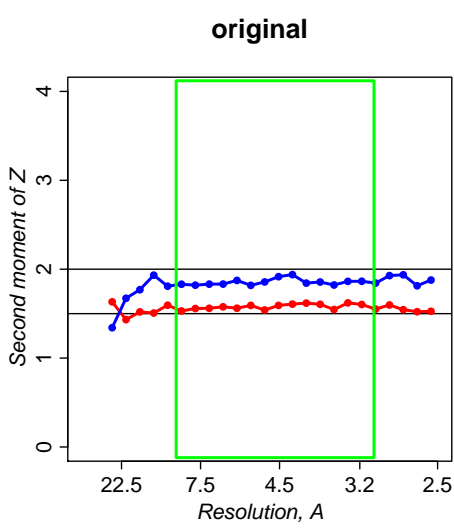
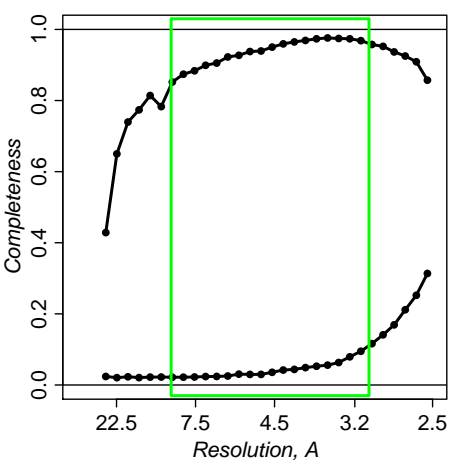
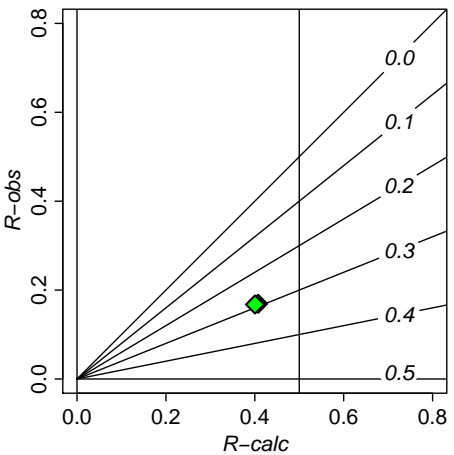
NCS	translation	rotation
r.m.s.d. (A)	26.18	0.19
angle (o)	179.90	0.12



1khu

	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	4	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	26.7	-
R'	-	-
R-free	29.5	-
R'-free	-	-
residues per monomer	DNA 0	protein 184

s < f/100	1562	3.39 %
s <= 0	1562	3.39 %
f <= 0	1562	3.39 %
s,f <= 0	1562	3.39 %
range (A)	38.3-2.5	9.9-3.0
unique	49,223	27,628
measured	46,057	26,405
used	42,630	24,836
NCS	translation	rotation
r.m.s.d. (A)	20.09	14.96
angle (o)	112.45	83.08



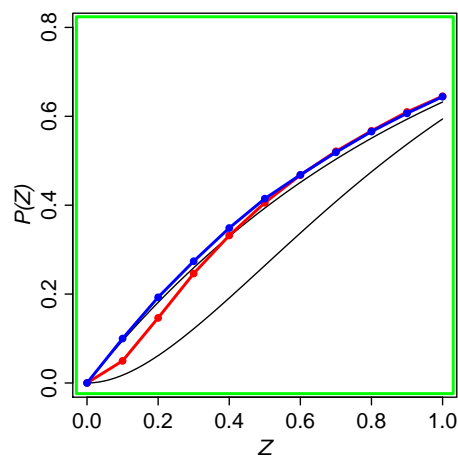
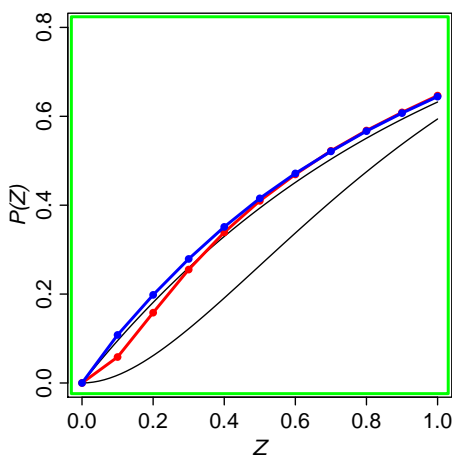
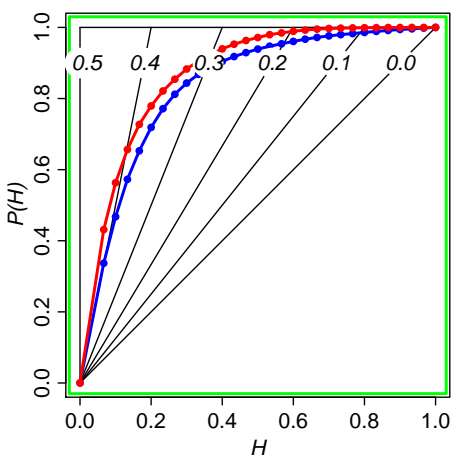
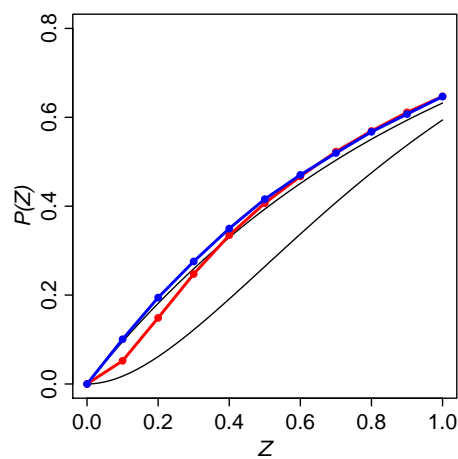
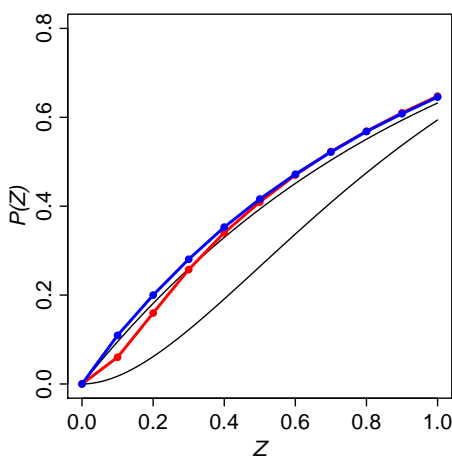
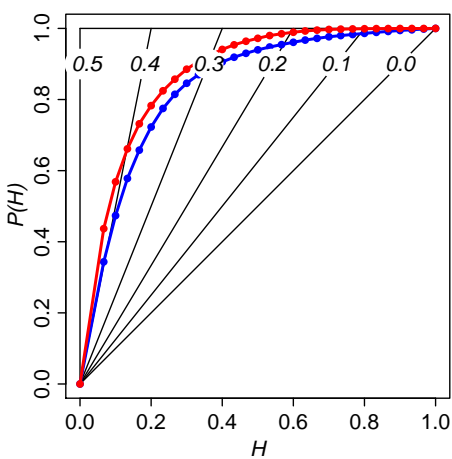
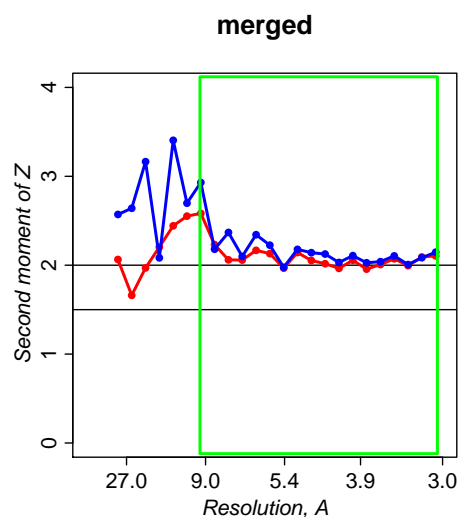
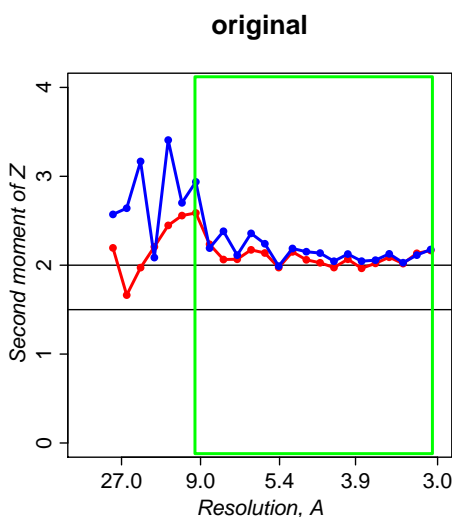
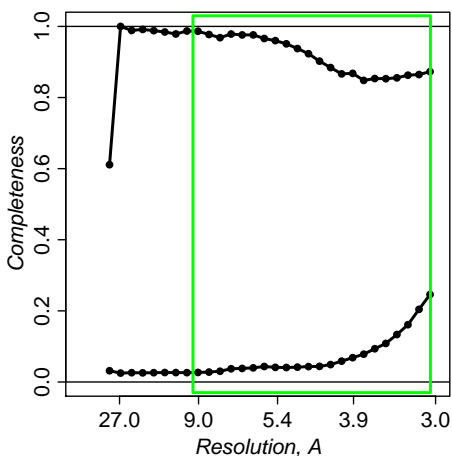
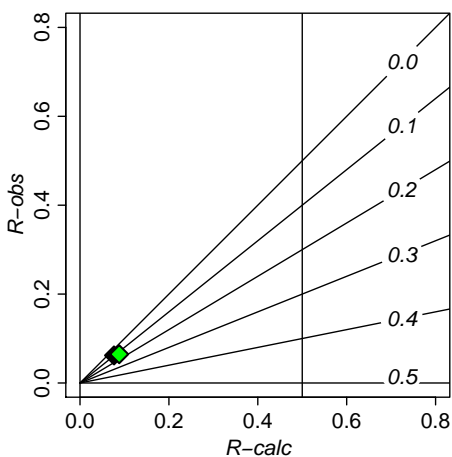
1kiu

	original	merged
s.g.	C 1 2 1	C 2 2 21
p.g.	10001	10003
a.u.	8	4
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		0.04
R	24.9	
R'	24.8	25.2
R-free	33.3	
R'-free	33.3	33.8
residues per monomer	DNA 0	protein 484

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	44.5-3.0	9.9-3.0
unique	80,438	78,148
measured	71,767	69,524
used	61,030	59,188

NCS	translation	rotation
r.m.s.d. (A)	1.52	0.01
angle (o)	2.65	0.02



1klf

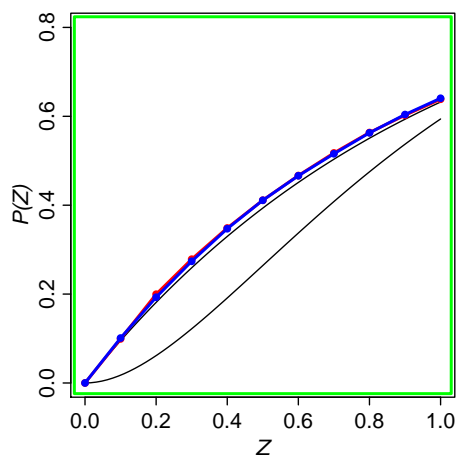
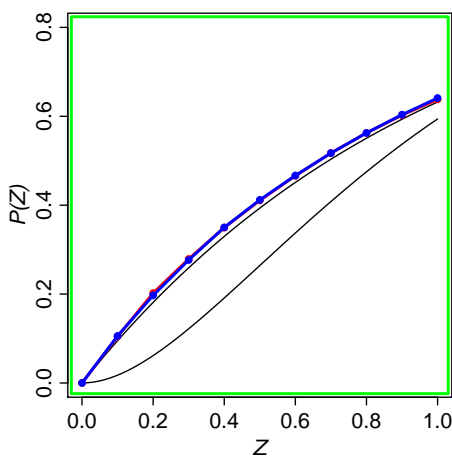
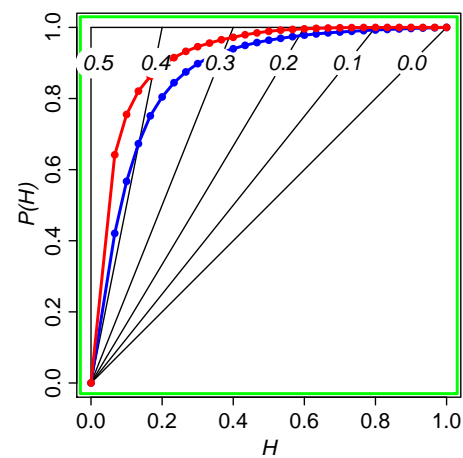
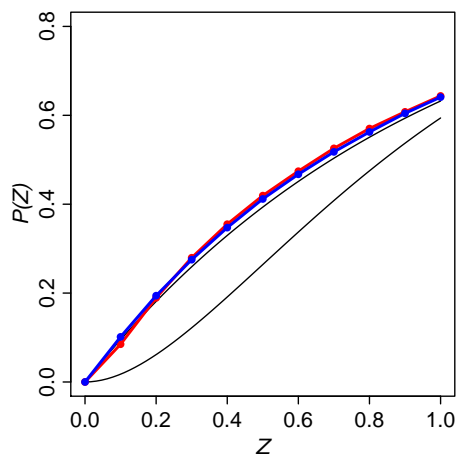
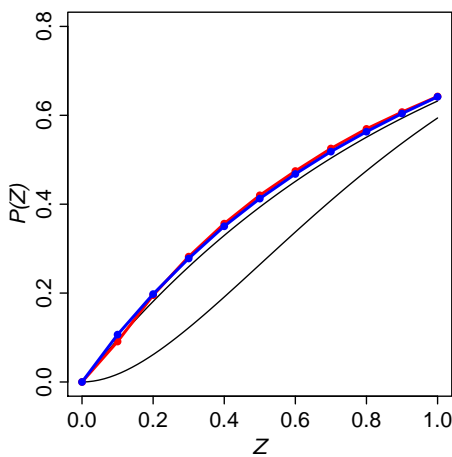
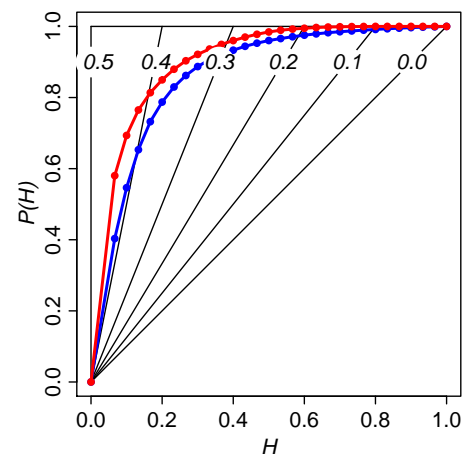
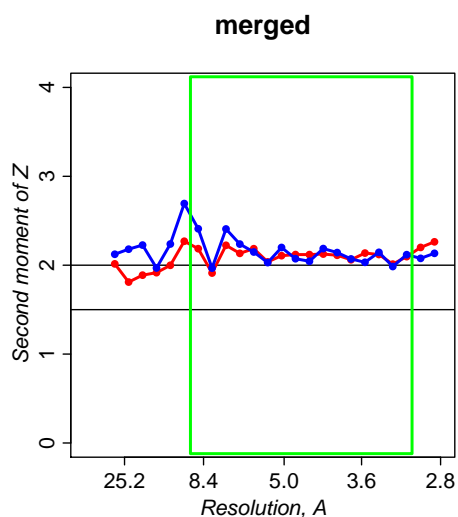
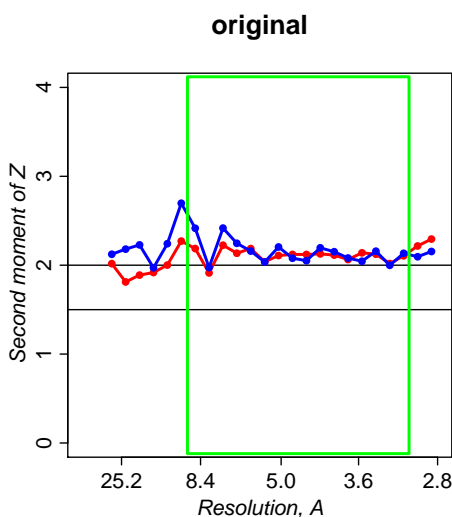
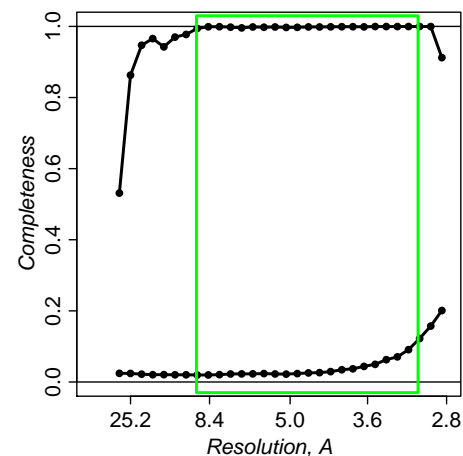
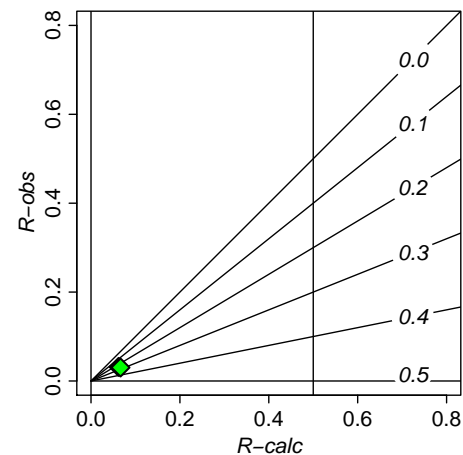
	original	merged
s.g.	C 1 2 1	C 2 2 2 1
p.g.	10001	10003
a.u.	8	4
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		0.06
R	26.9	
R'	26.9	27.3
R-free	34.1	
R'-free	34.1	34.4

s < f/100	16	0.02 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	43.7–2.8	9.9–3.0
unique	100,132	78,633
measured	99,135	78,545
used	93,410	74,290

NCS	translation	rotation
r.m.s.d. (A)	1.96	0.02
angle (o)	4.44	0.03

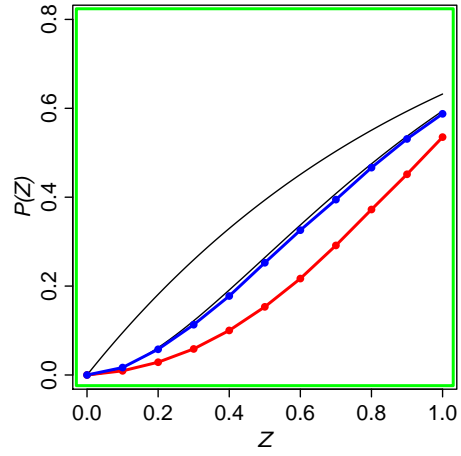
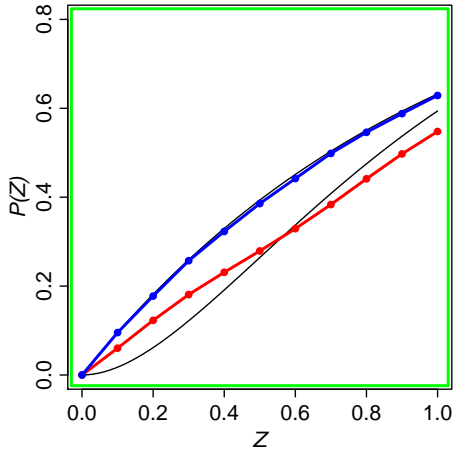
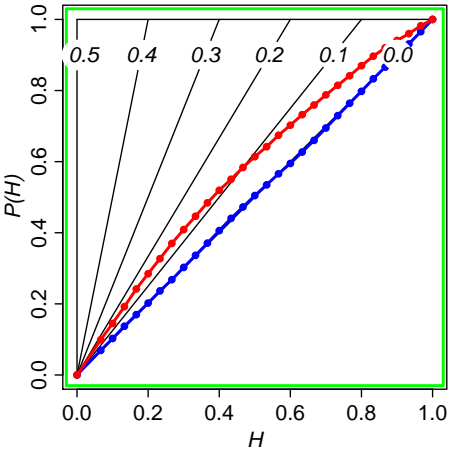
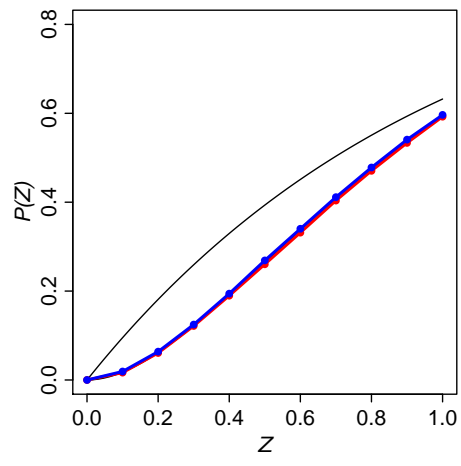
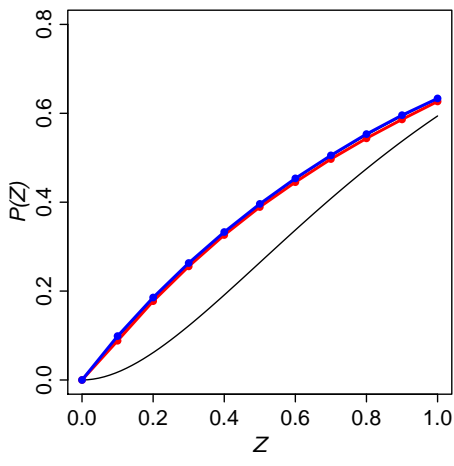
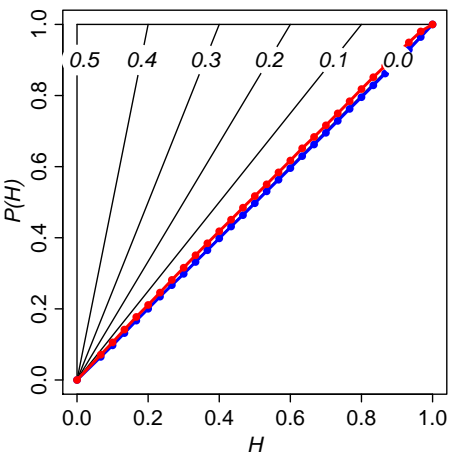
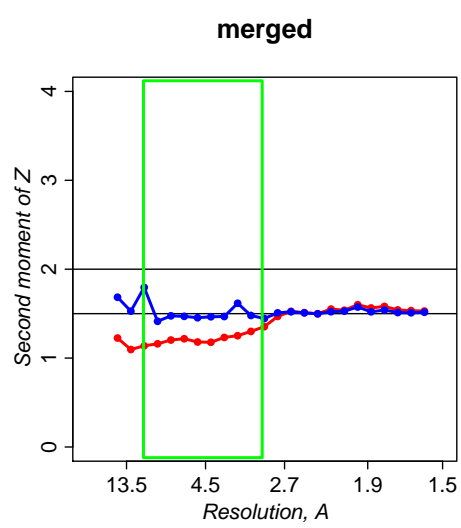
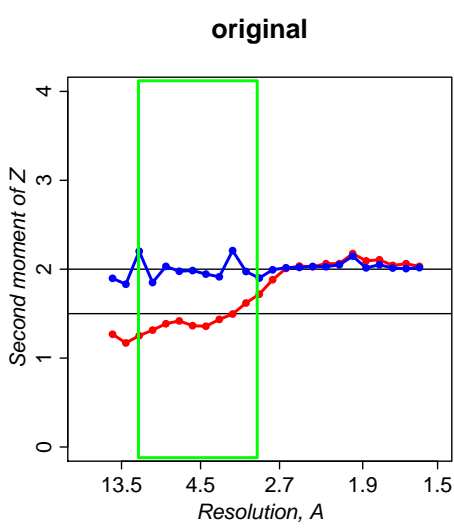
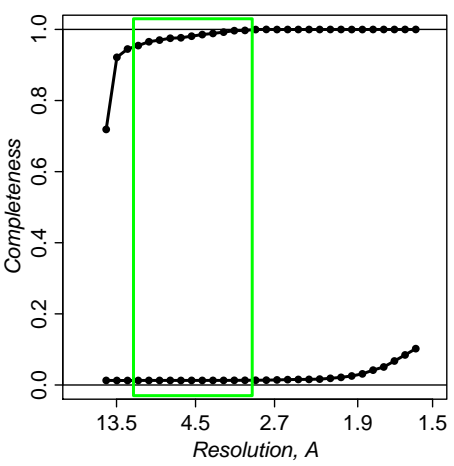
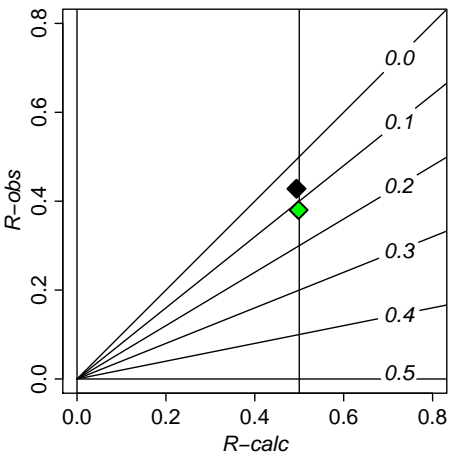
residues per monomer	DNA	protein
	0	484



1kq1

	original	merged
s.g.	P 1 21 1	-
p.g.	10001	10003
a.u.	12	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	30.3	-
R'	-	-
R-free	31.6	-
R'-free	-	-
residues per monomer	DNA 0	protein 60

s < f/100	774	0.67 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	22.4-1.6	9.9-3.0
unique	115,252	15,629
measured	115,018	15,439
used	108,398	13,902
NCS	translation	rotation
r.m.s.d. (A)	8.07	3.63
angle (o)	58.45	25.24



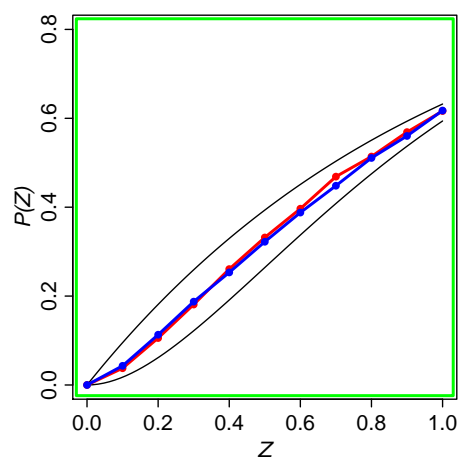
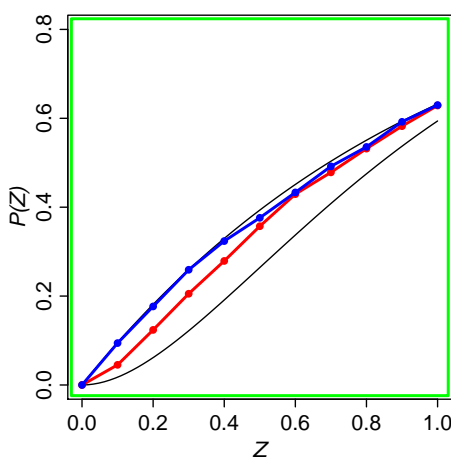
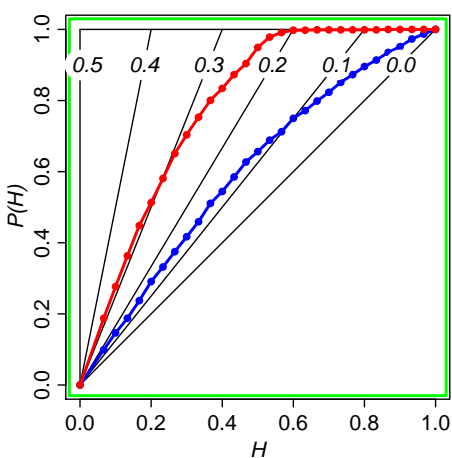
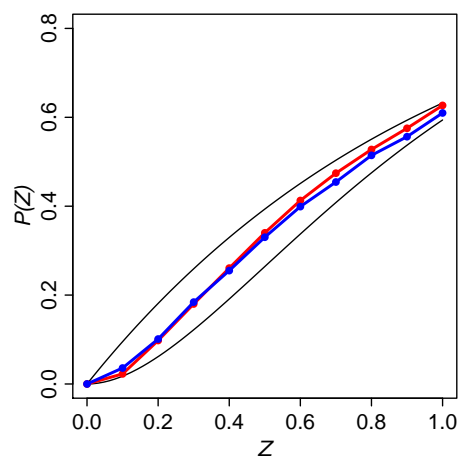
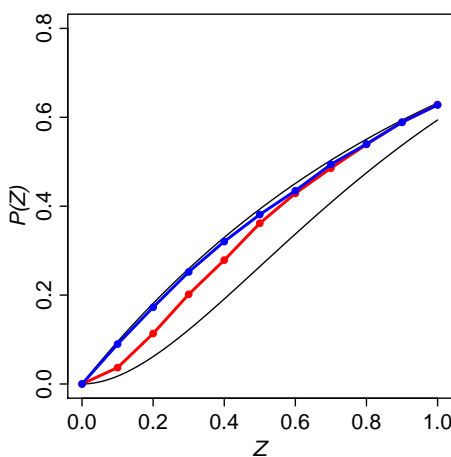
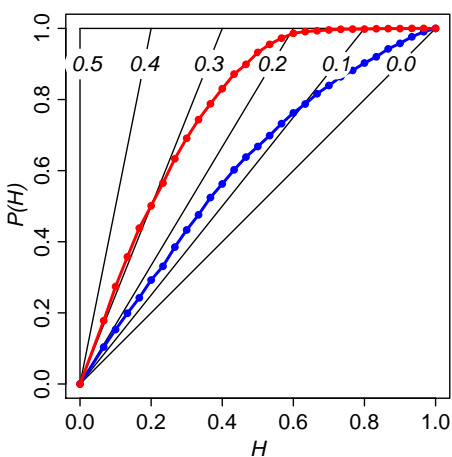
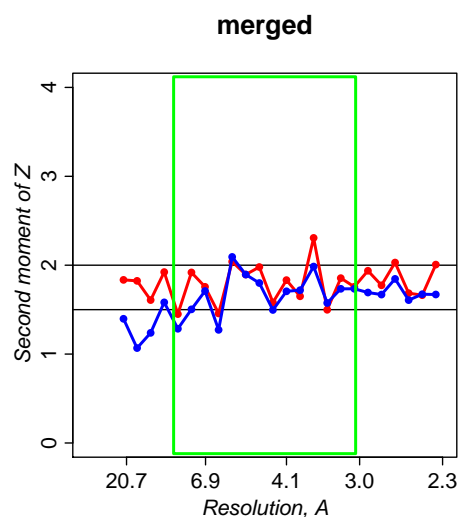
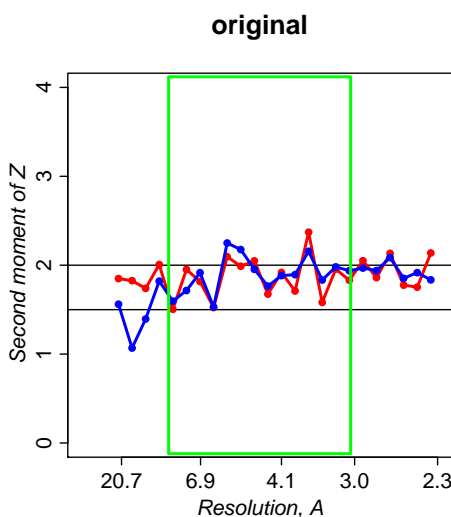
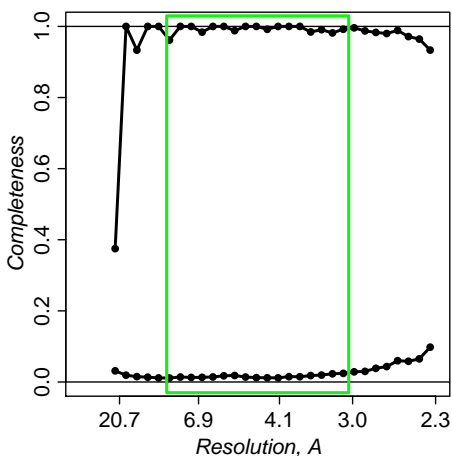
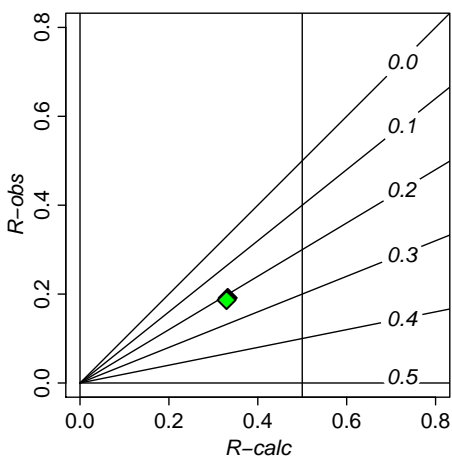
1ku5

	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		7.89
R	24.3	
R'	-	-
R-free	27.8	
R'-free	-	-
residues per monomer	DNA 0	protein 66

s < f/100	399	8.15 %
s <= 0	26	0.53 %
f <= 0	26	0.53 %
s,f <= 0	26	0.53 %

range (A)	27.5-2.3	9.9-3.0
unique	4,991	2,218
measured	4,897	2,202
used	4,234	1,848

NCS	translation	rotation
r.m.s.d. (A)	15.15	0.22
angle (o)	179.78	0.27



1kvo

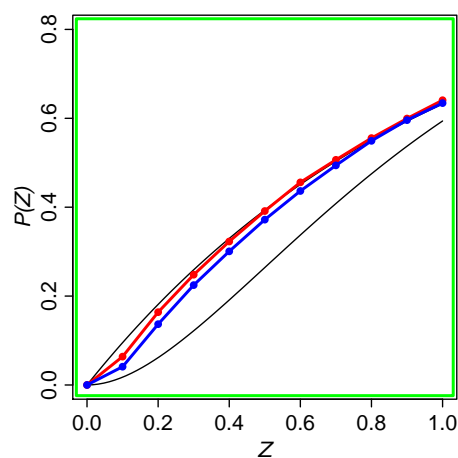
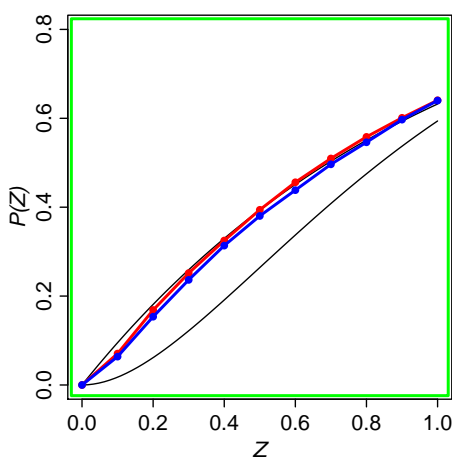
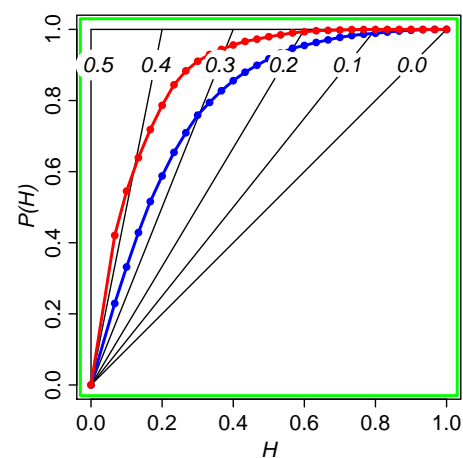
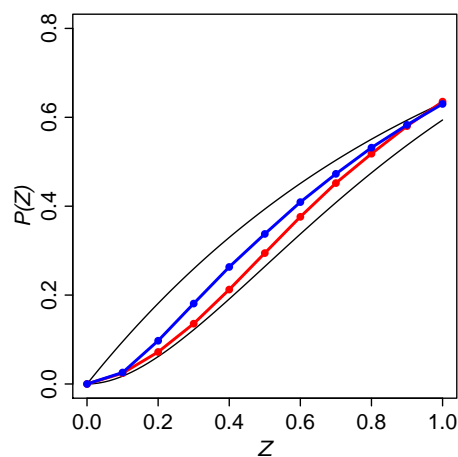
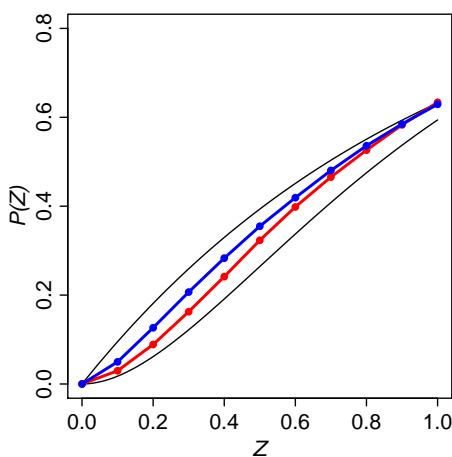
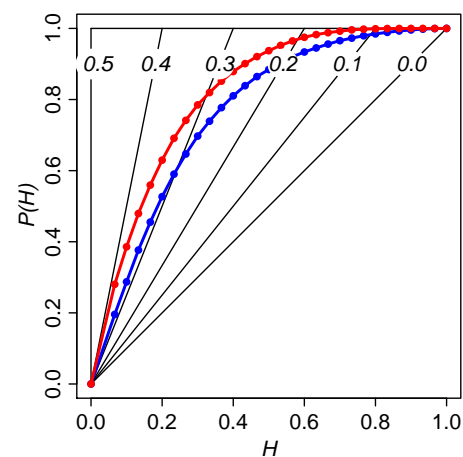
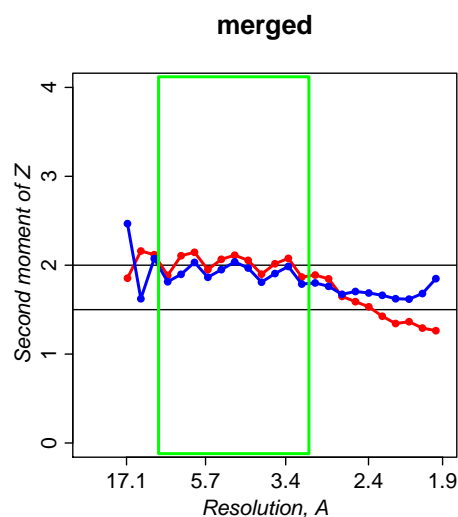
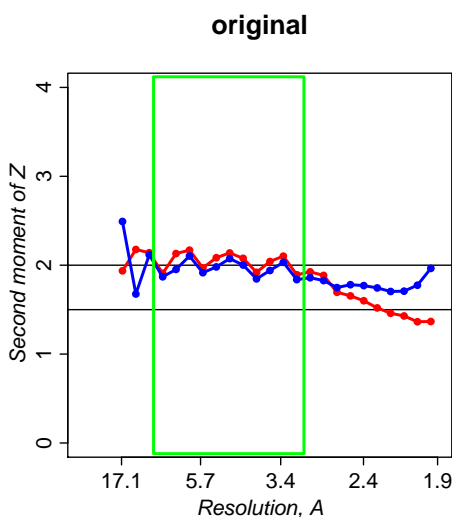
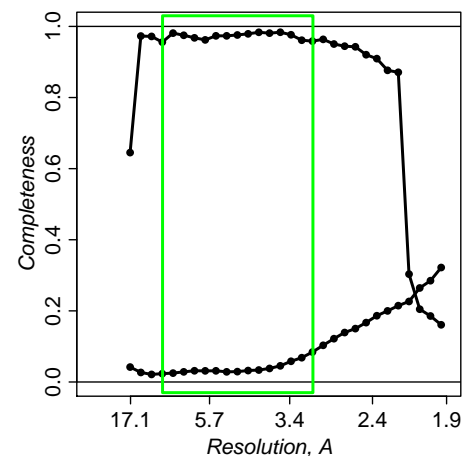
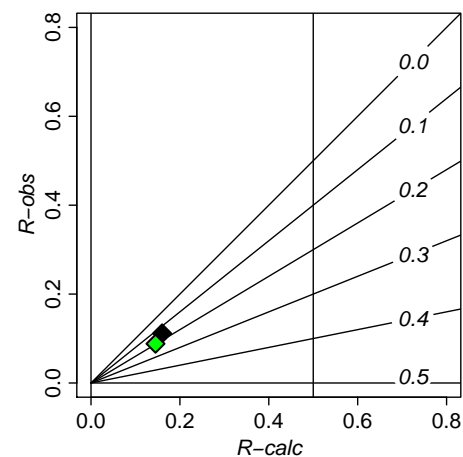
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.25
R	27.6	
R'	28.2	28.2
R-free	30.8	
R'-free	30.9	31.0

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	20.0–1.9	9.9–3.0
unique	63,991	15,944
measured	45,174	15,512
used	39,256	13,962

NCS	translation	rotation
r.m.s.d. (A)	11.87	0.20
angle (o)	59.35	0.16

residues per monomer	DNA	protein
	0	124



1kx1

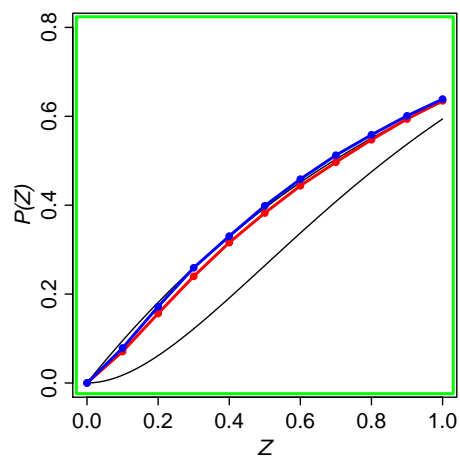
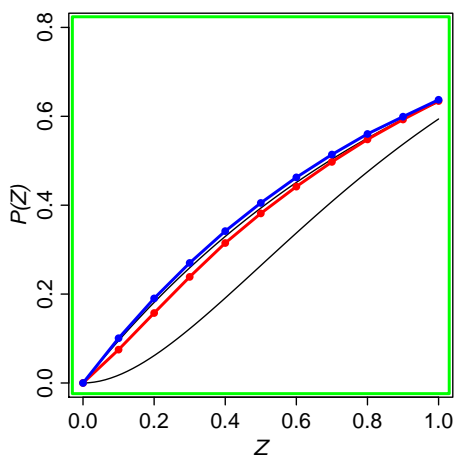
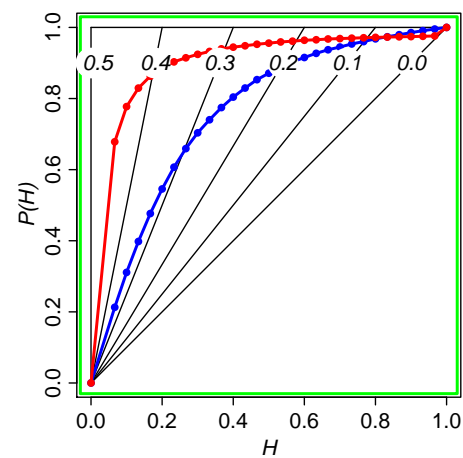
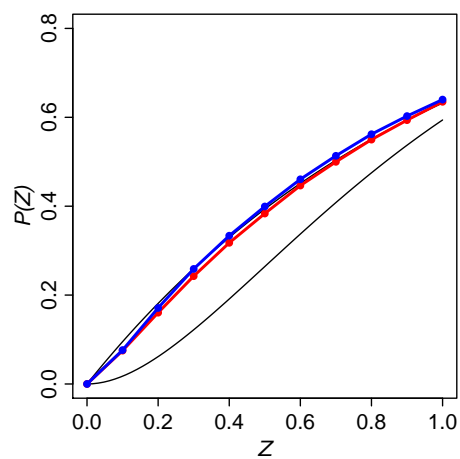
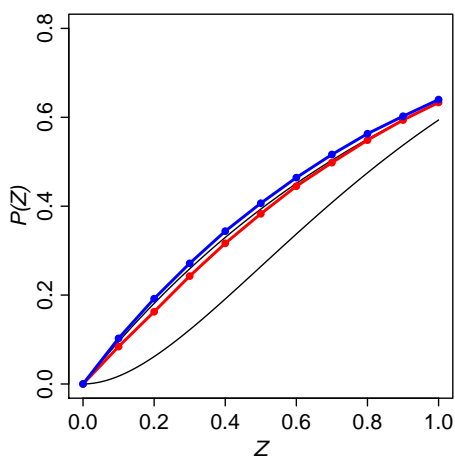
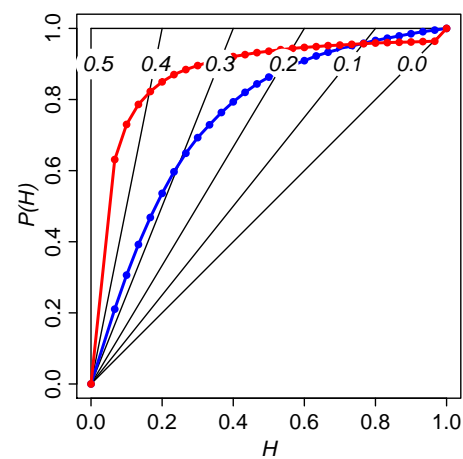
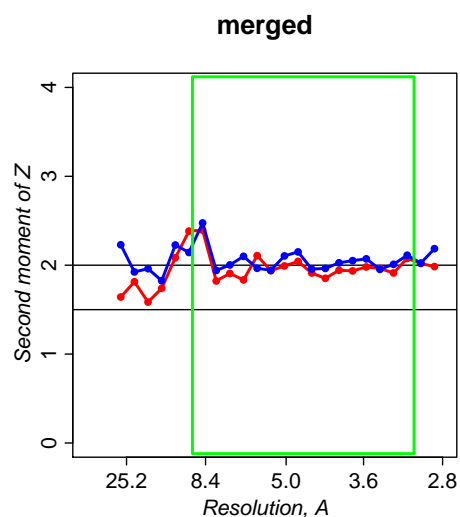
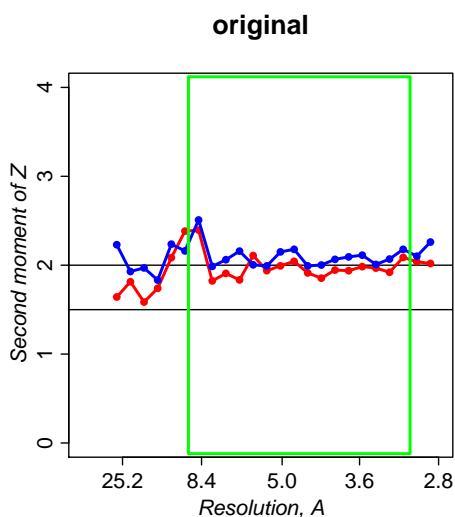
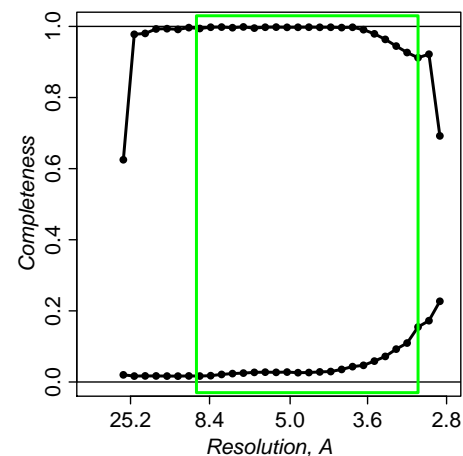
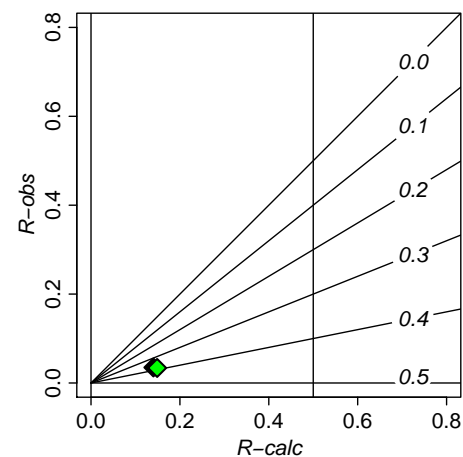
	original	merged
s.g.	P 1 2 1 1	C 2 2 2 1
p.g.	10001	10003
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.25
R	23.1	
R'	23.1	23.8
R-free	27.4	
R'-free	27.1	27.9

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	1066	2.82 %
s,f <= 0	0	0.00 %

range (A)	37.0–2.8	9.9–3.0
unique	39,952	32,280
measured	37,815	31,438
used	34,648	29,106

NCS	translation	rotation
r.m.s.d. (A)	13.93	0.23
angle (o)	66.59	0.28

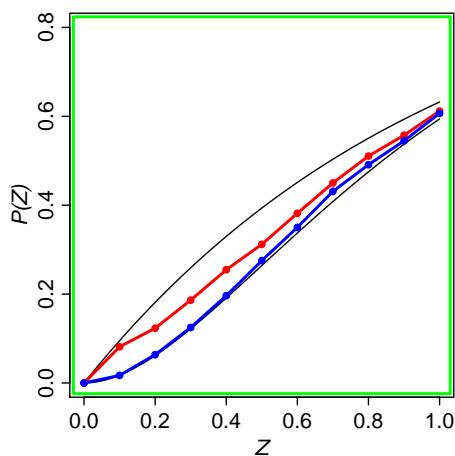
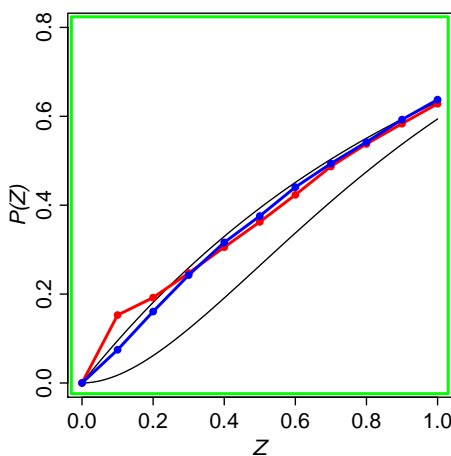
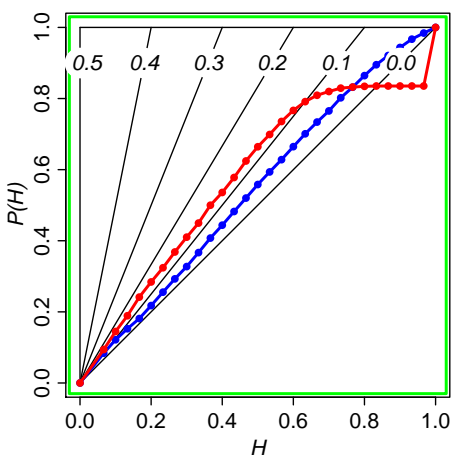
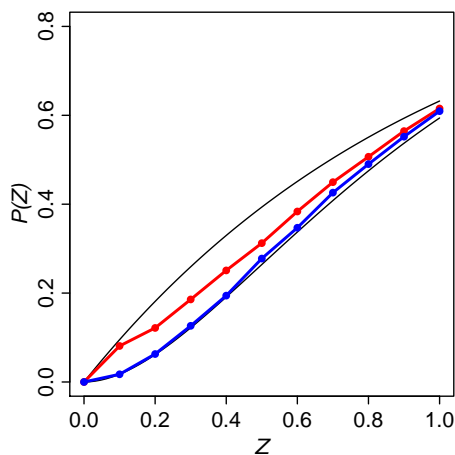
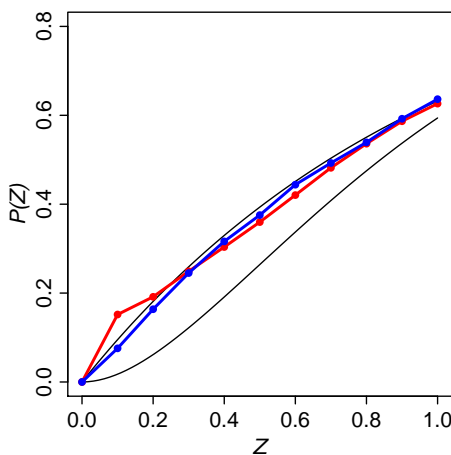
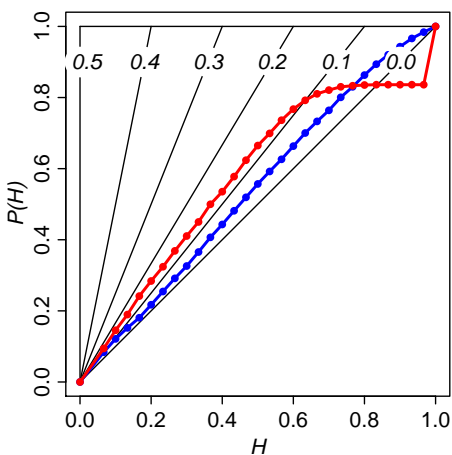
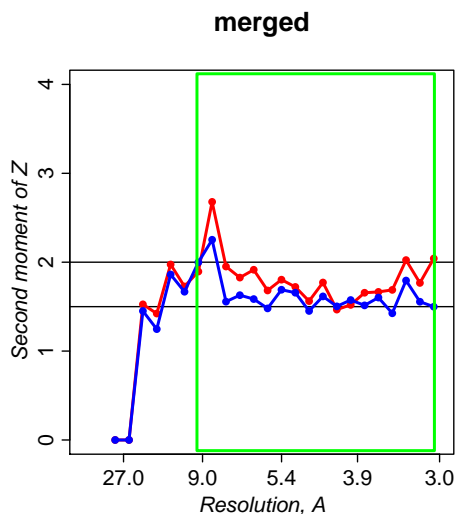
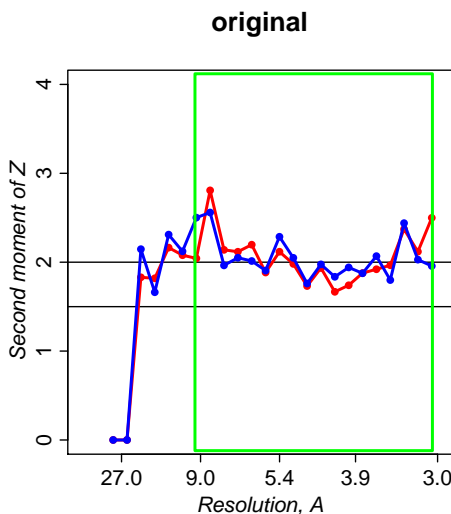
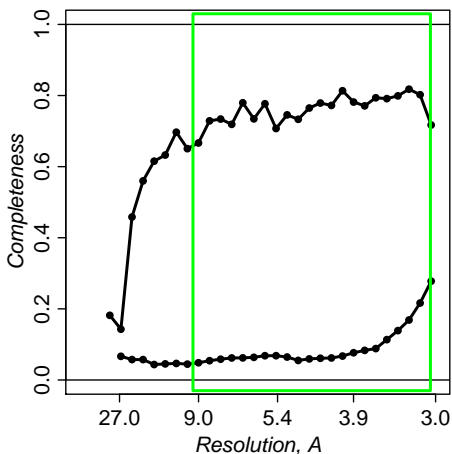
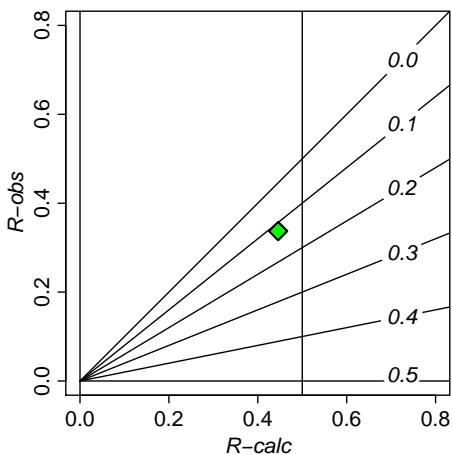
residues per monomer	DNA	protein
	0	149



1kyn

	original	merged
s.g.	P 41	-
p.g.	10201	10205
a.u.	2	-
p.t.	2	-
p.o.	2	-
r.m.s.d. (A)	-	-
R	19.4	-
R'	-	-
R-free	30.2	-
R'-free	-	-
residues per monomer	DNA 0	protein 223

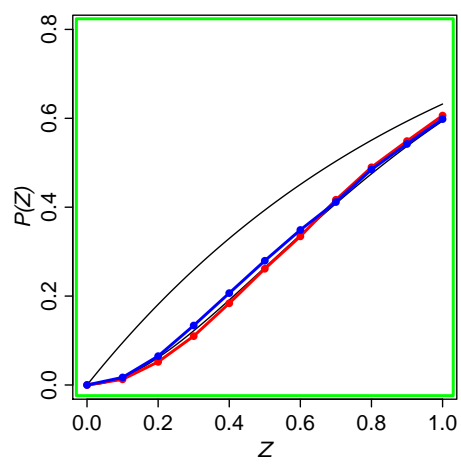
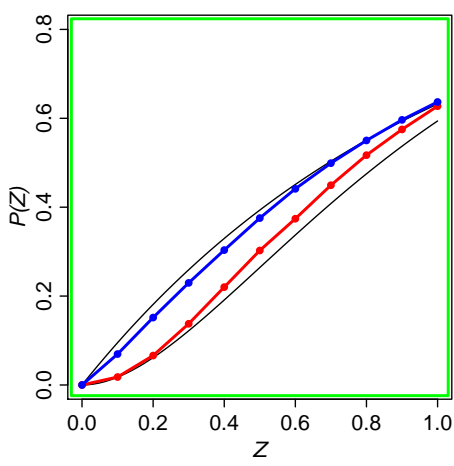
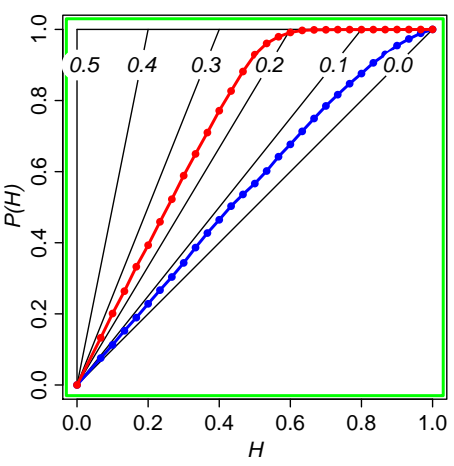
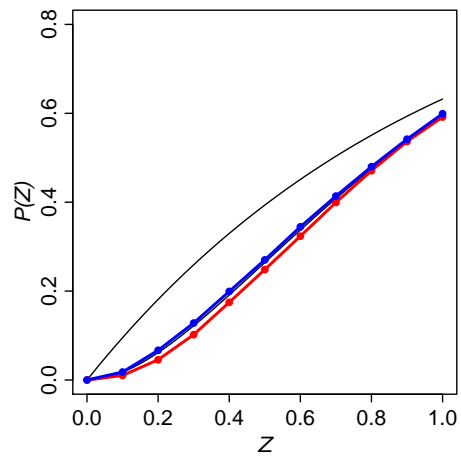
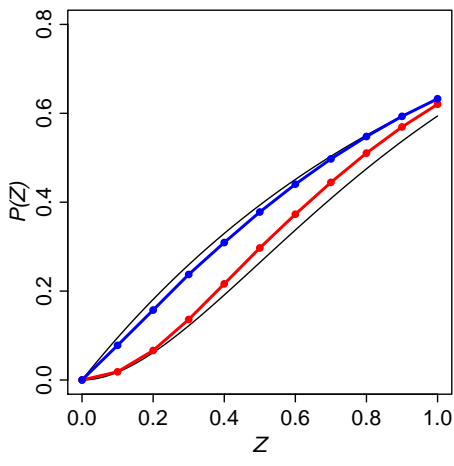
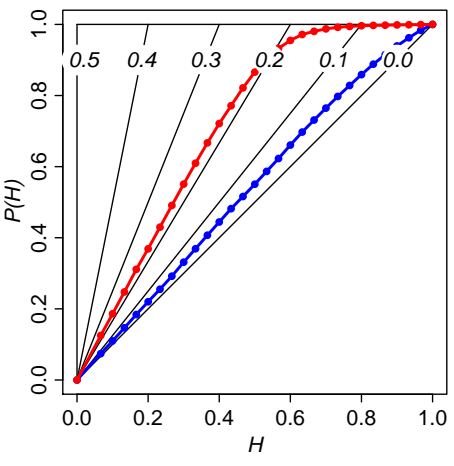
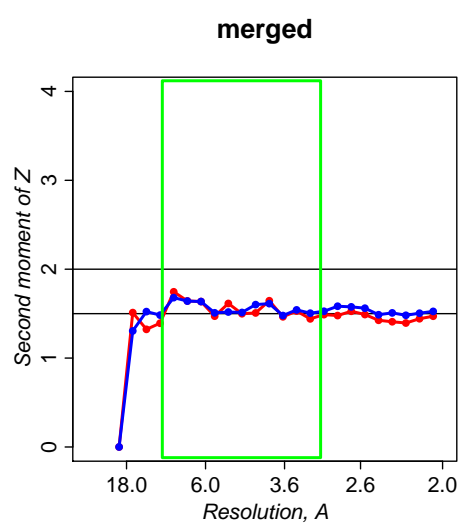
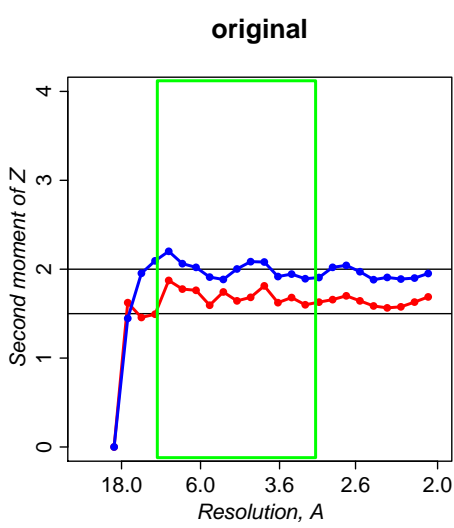
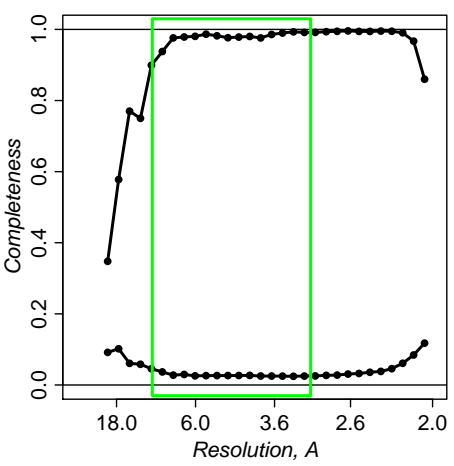
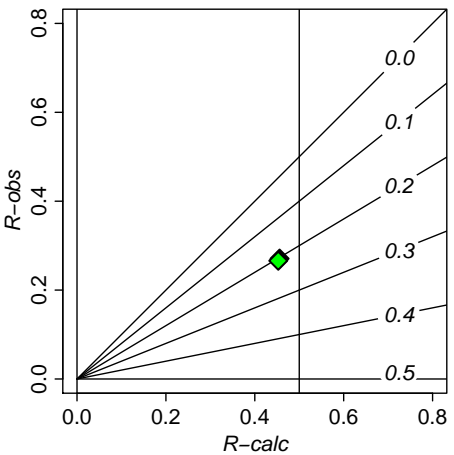
s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	1021	14.45 %
s,f <= 0	0	0.00 %
<hr/>		
range (A)	44.0-3.0	9.9-3.0
unique	9,209	8,862
measured	7,065	6,895
used	5,084	5,014
<hr/>		
NCS	translation	rotation
r.m.s.d. (A)	2.02	25.88
angle (o)	7.78	178.38



111e

	original	merged
s.g.	P 65	P 65 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		9.88
R	25.8	
R'	-	-
R-free	29.6	
R'-free	-	-
residues per monomer	DNA 0	protein 260

s < f/100	112	0.34 %
s <= 0	112	0.34 %
f <= 0	112	0.34 %
s,f <= 0	112	0.34 %
range (A)	28.2-2.0	9.9-3.0
unique	34,186	10,092
measured	33,305	9,926
used	27,760	7,730
NCS	translation	rotation
r.m.s.d. (A)	28.31	5.58
angle (o)	179.18	22.65



1l2g

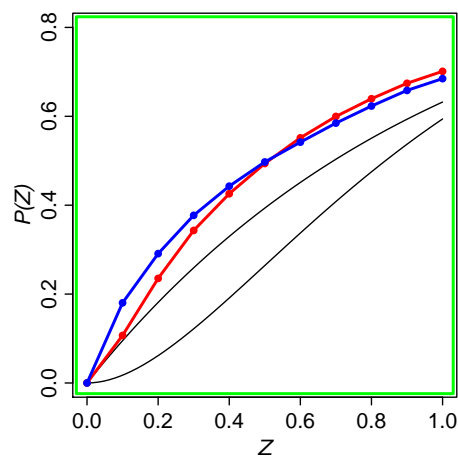
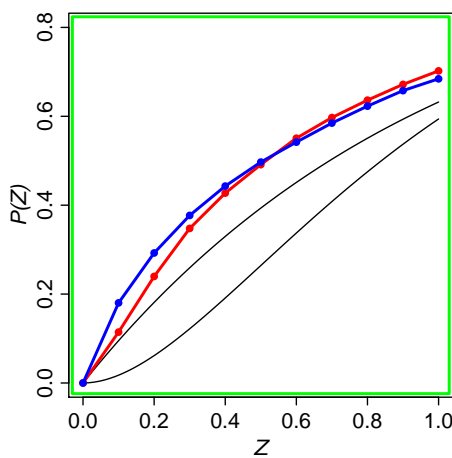
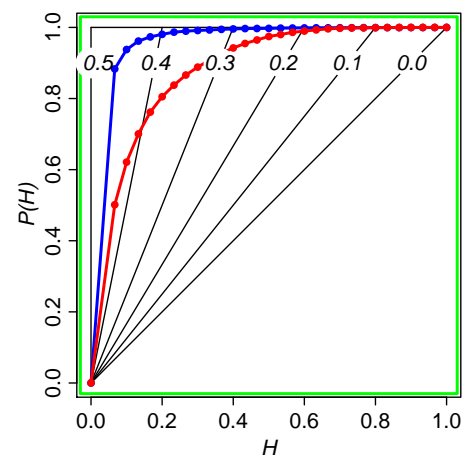
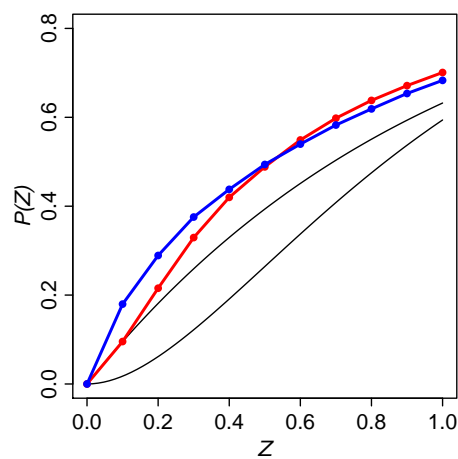
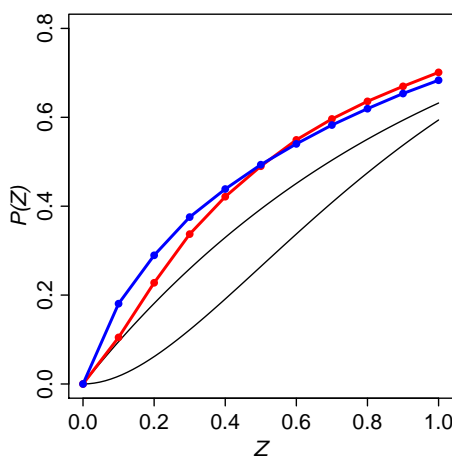
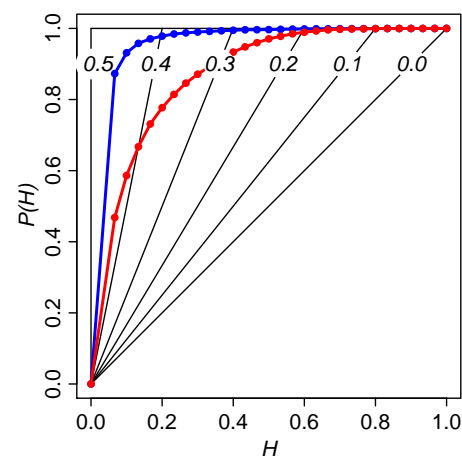
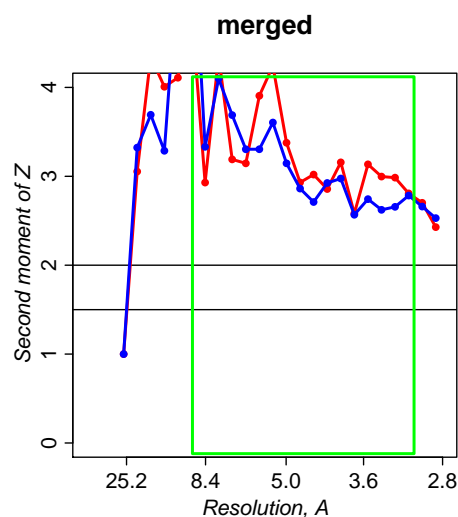
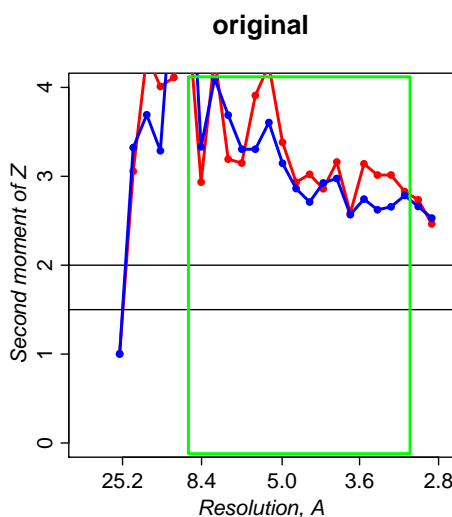
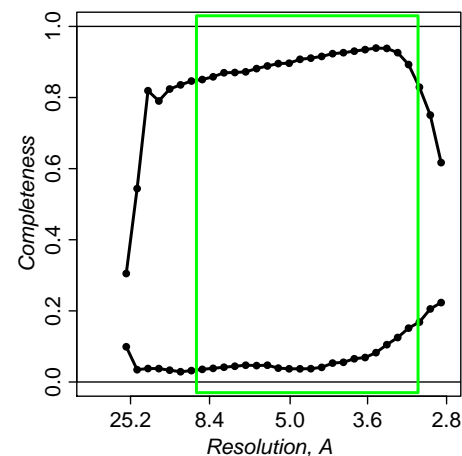
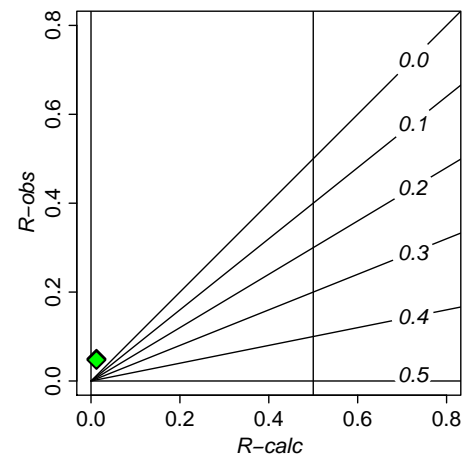
	original	merged
s.g.	P 4	P 4 21 2
p.g.	10201	10205
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		1.41
R	28.4	
R'	28.0	29.0
R-free	34.9	
R'-free	35.1	35.4

s < f/100	186	0.61 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	33.4–2.8	9.9–3.0
unique	35,155	27,796
measured	30,374	25,210
used	24,396	20,698

NCS	translation	rotation
r.m.s.d. (A)	0.49	0.01
angle (o)	1.92	0.04

residues per monomer	DNA	protein
	0	242



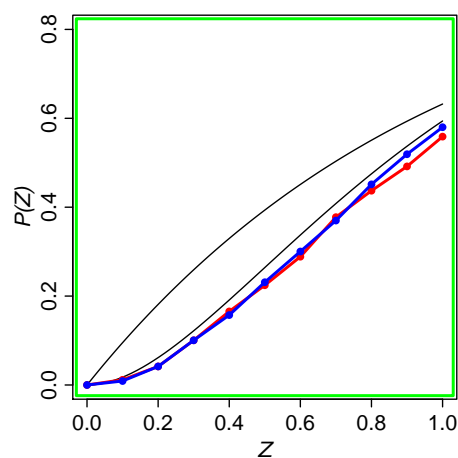
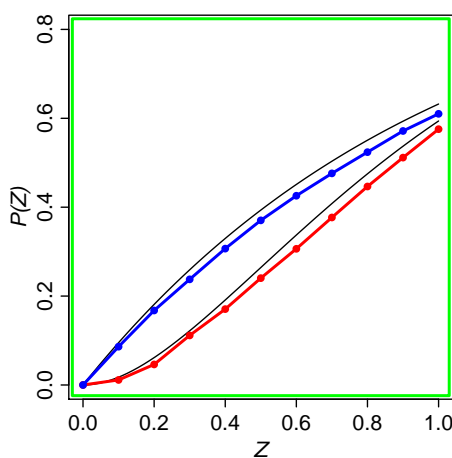
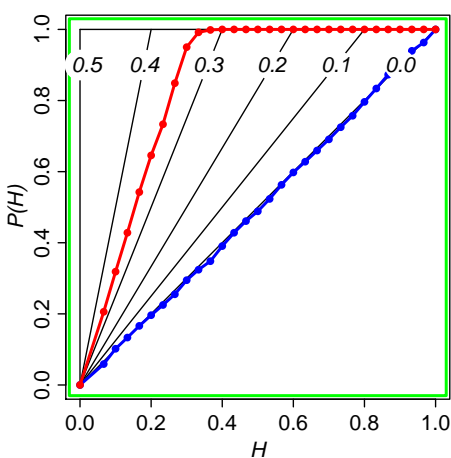
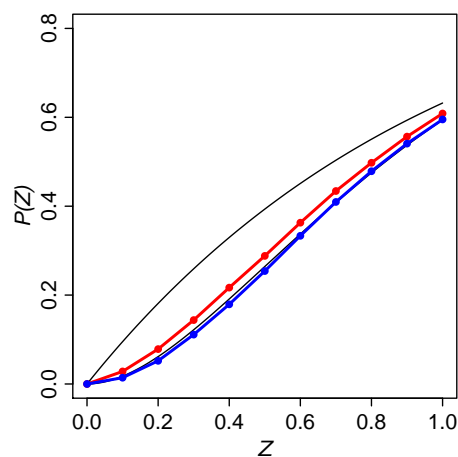
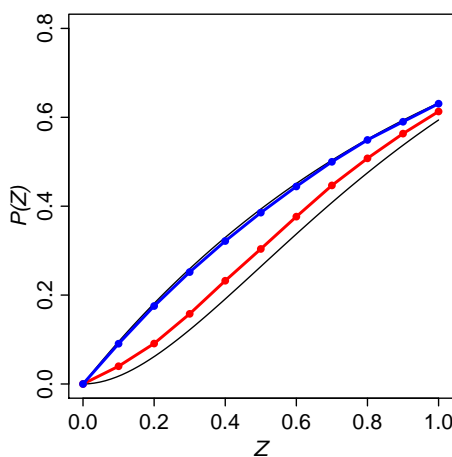
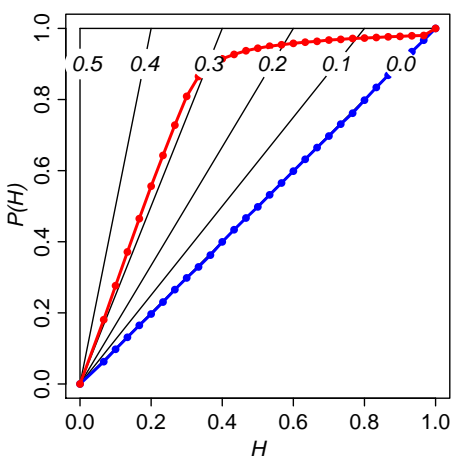
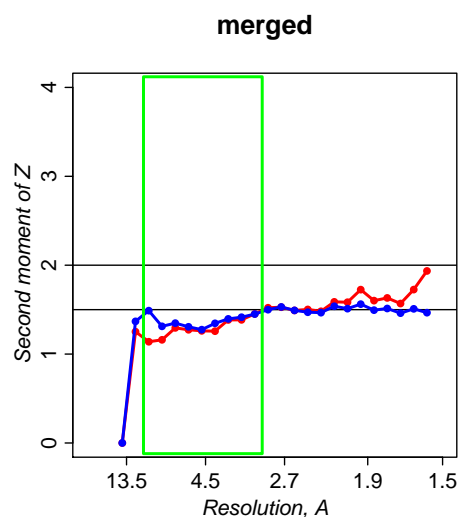
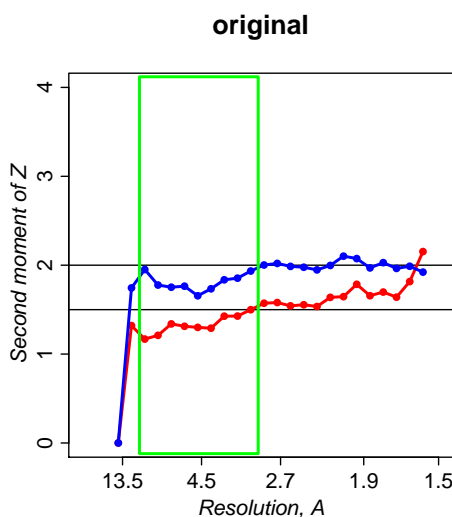
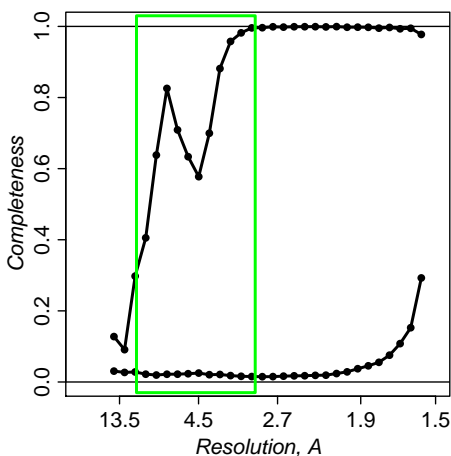
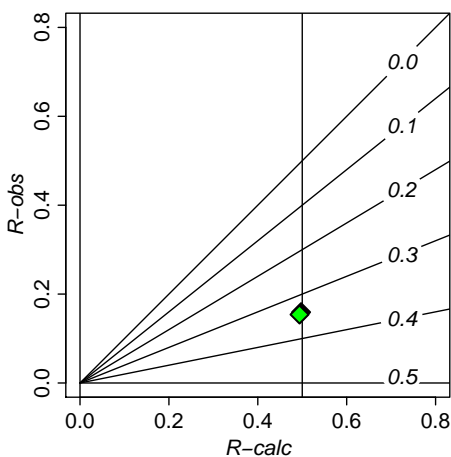
1I2h

	original	merged
s.g.	P 43	-
p.g.	10201	10205
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	30.7	-
R'	-	-
R-free	32.2	-
R'-free	-	-
residues per monomer	DNA 0	protein 144

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	448	1.41 %
s,f <= 0	0	0.00 %

range (A)	18.6-1.5	9.9-3.0
unique	32,765	4,360
measured	31,780	3,615
used	28,678	2,922

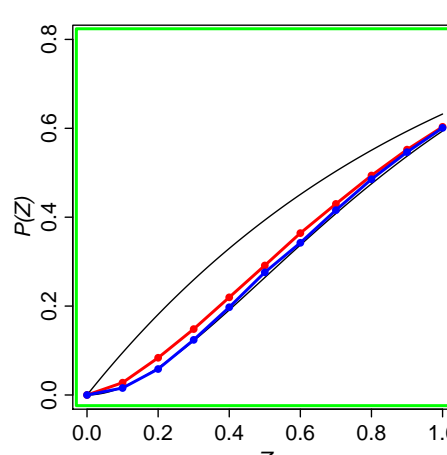
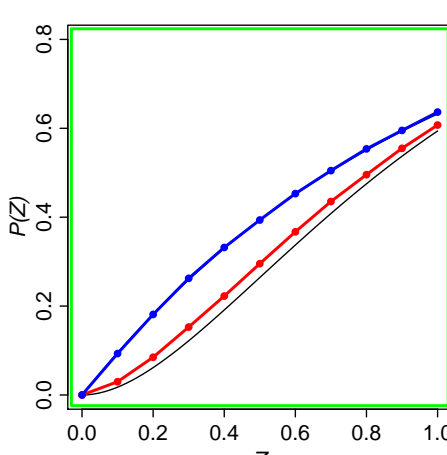
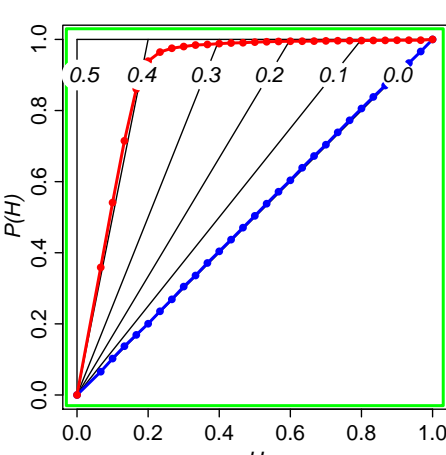
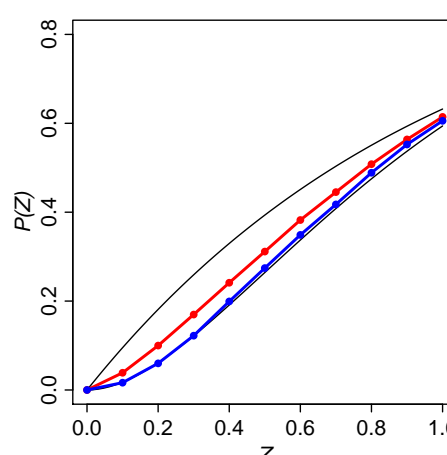
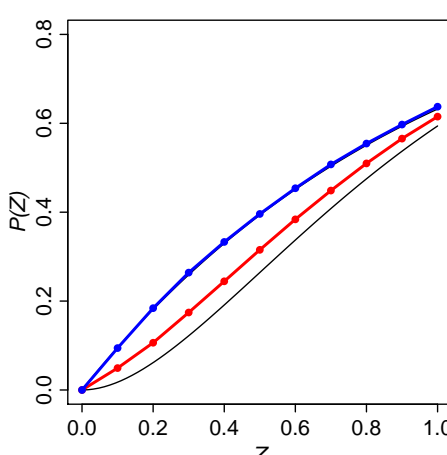
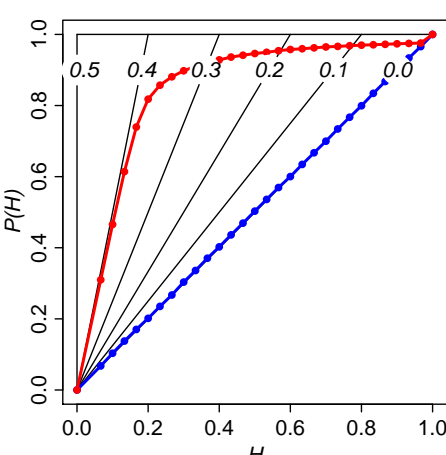
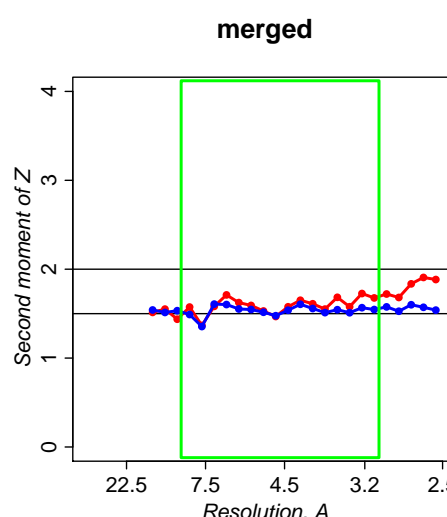
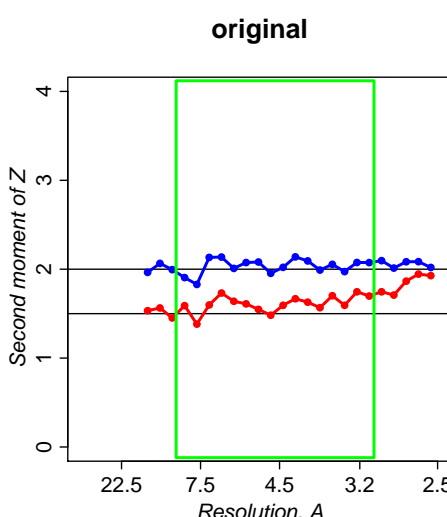
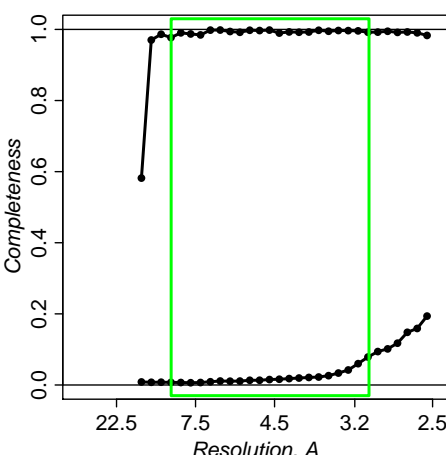
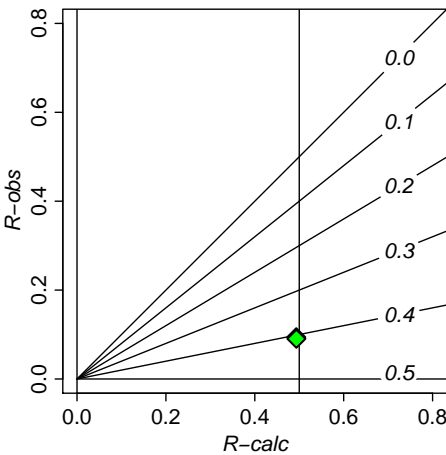
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1l2u

	original	merged
s.g.	P 32 2 1	P 62 2 2
p.g.	10023	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		7.65
R	28.6	
R'	-	-
R-free	30.5	
R'-free	-	-
residues per monomer	DNA 0	protein 223

s < f/100	3157	7.45 %
s <= 0	0	0.00 %
f <= 0	787	1.86 %
s,f <= 0	0	0.00 %
range (A)	14.9–2.5	9.9–3.0
unique	42,696	24,395
measured	42,382	24,255
used	37,808	21,258
NCS	translation	rotation
r.m.s.d. (A)	11.78	3.36
angle (o)	47.06	13.07



1I3d

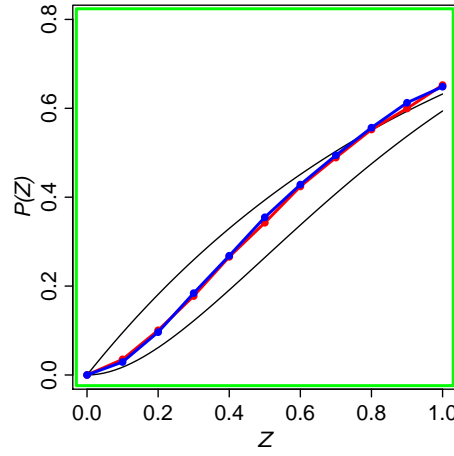
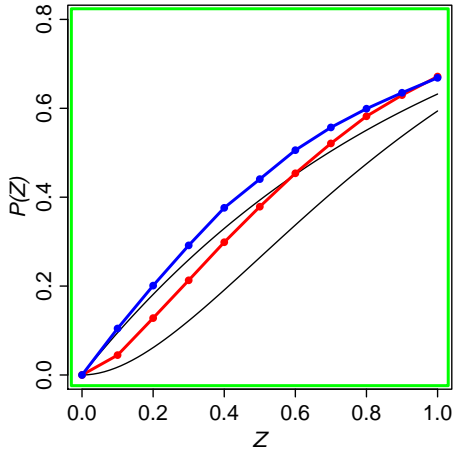
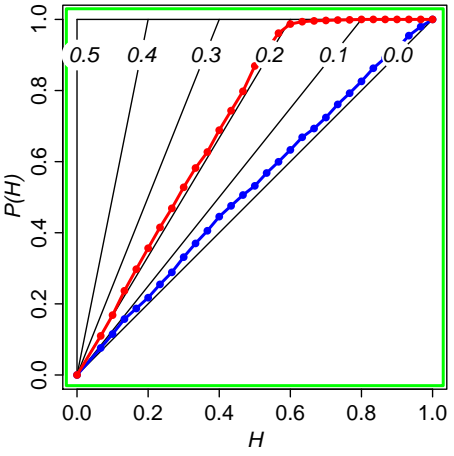
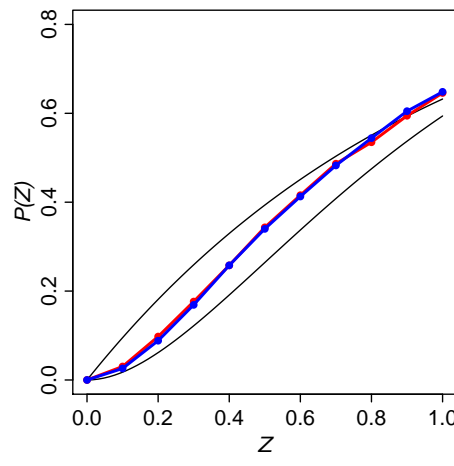
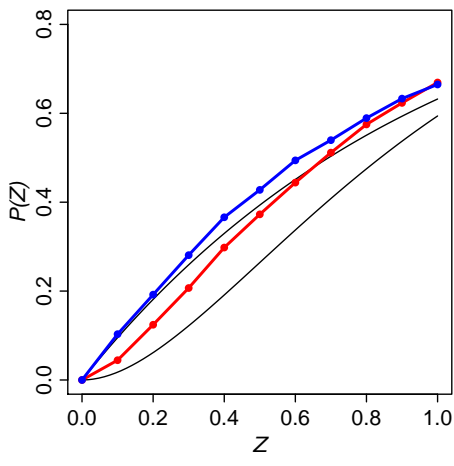
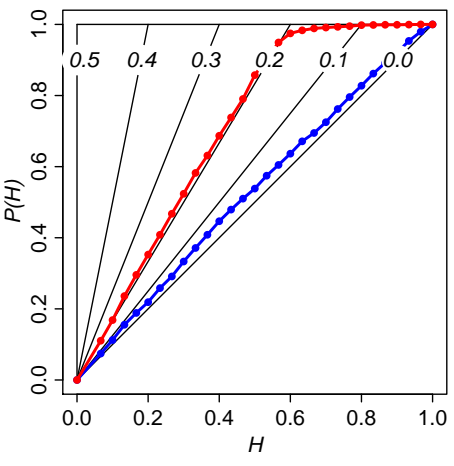
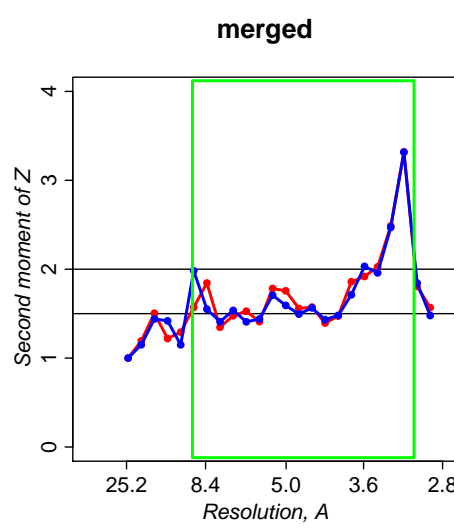
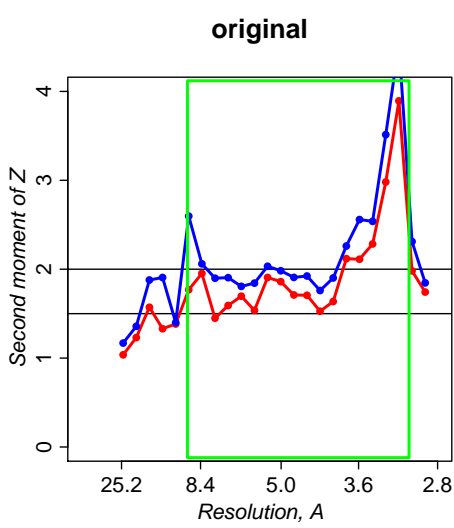
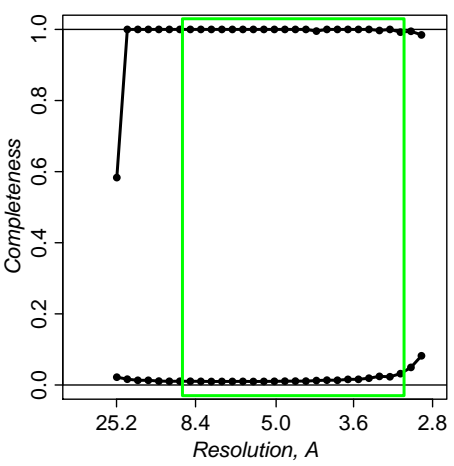
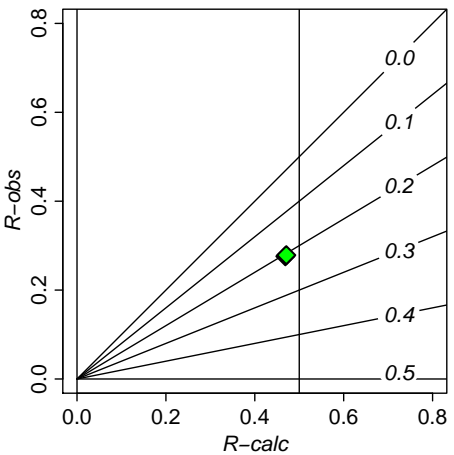
	original	merged
s.g.	1 21 3	-
p.g.	10083	10689
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	25.3	-
R'	-	-
R-free	27.1	-
R'-free	-	-

residues per monomer	DNA	protein
	27	0

s < f/100	896	17.85 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	28.8-2.8	9.9-3.0
unique	5,033	4,173
measured	5,020	4,168
used	4,094	3,402

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



115t

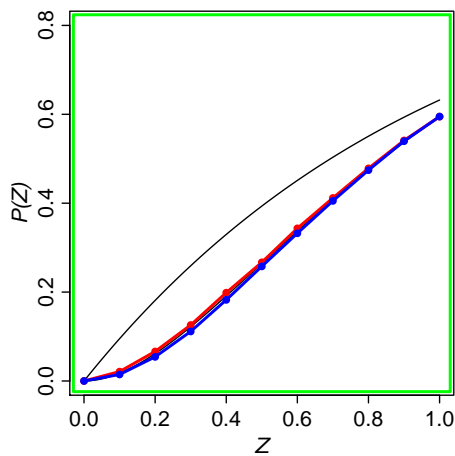
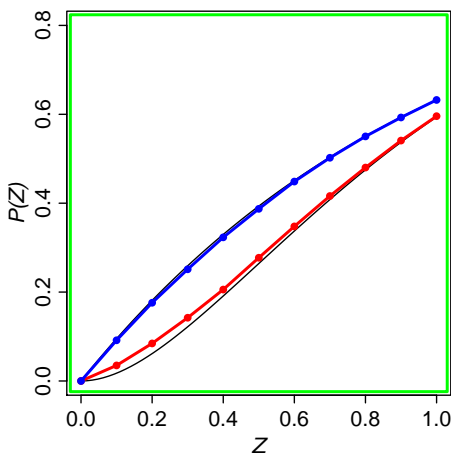
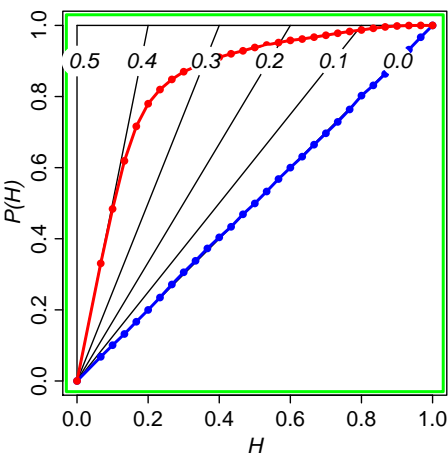
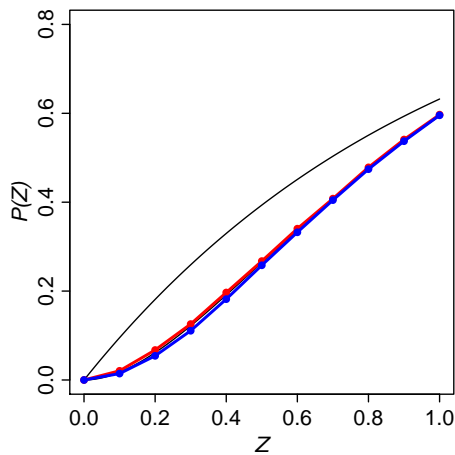
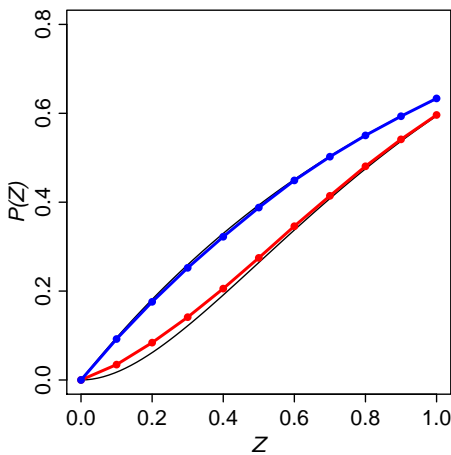
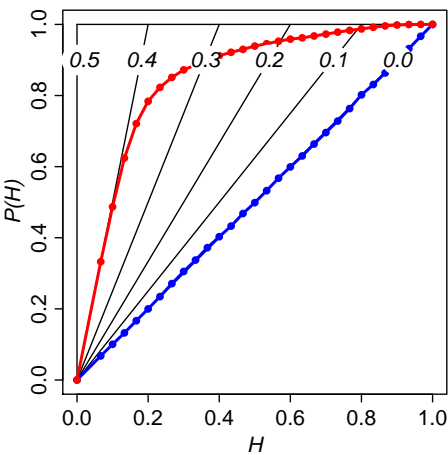
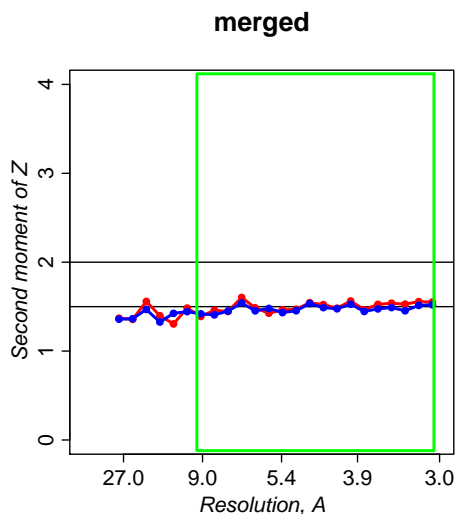
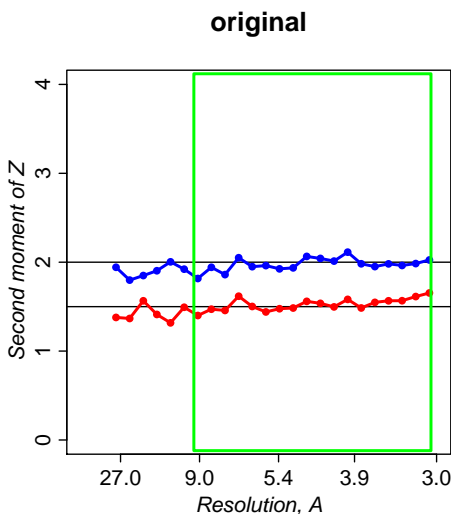
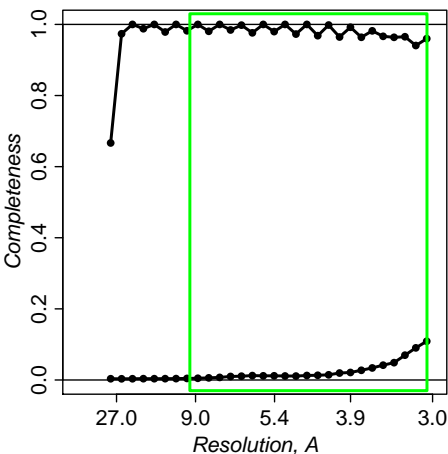
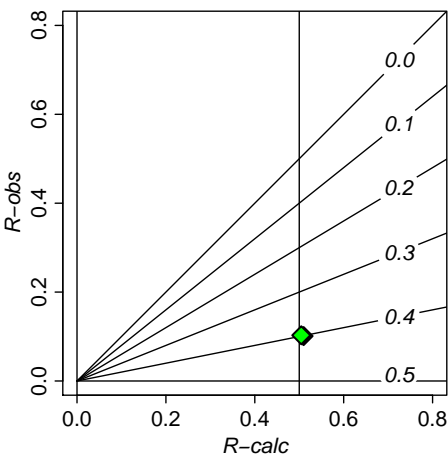
	original	merged
s.g.	P 31	P 61
p.g.	10020	12021
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		12.34
R	25.3	
R'	-	-
R-free	30.3	
R'-free	-	-

s < f/100	5519	22.92 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	37.8-3.0	9.9-3.0
unique	24,724	24,053
measured	24,081	23,415
used	22,852	22,288

NCS	translation	rotation
r.m.s.d. (A)	12.08	7.68
angle (o)	36.73	23.45

residues per monomer	DNA	protein
	0	329



118s

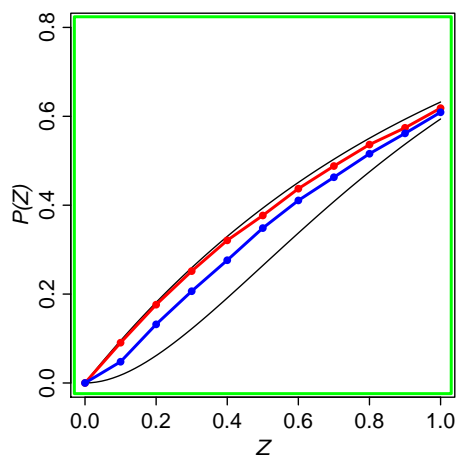
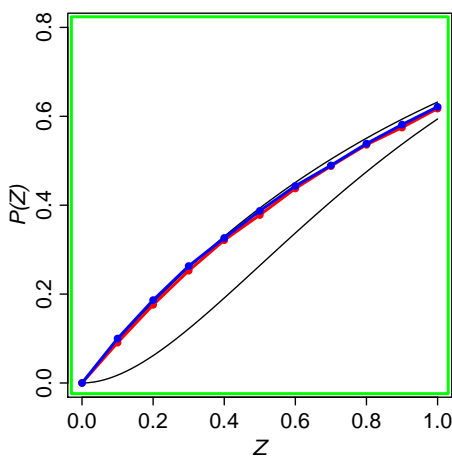
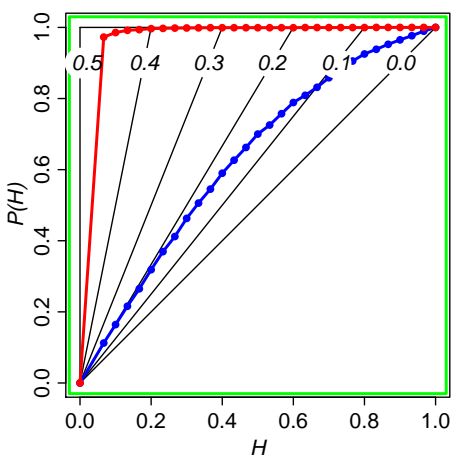
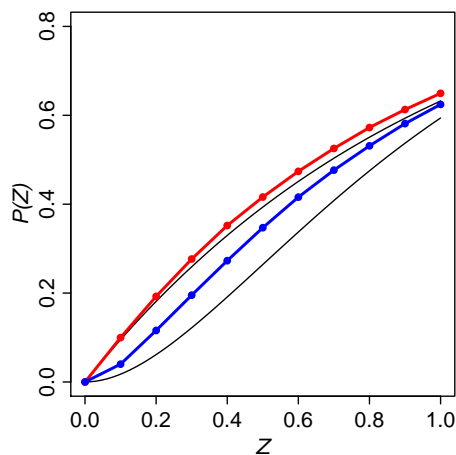
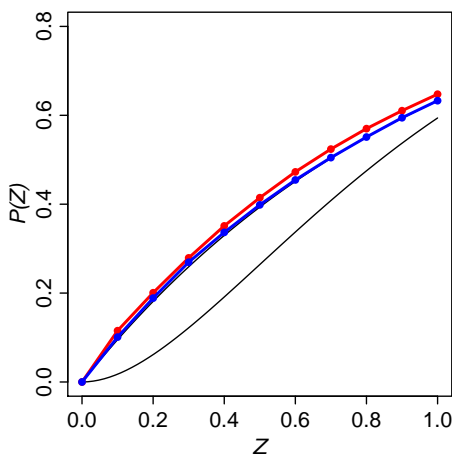
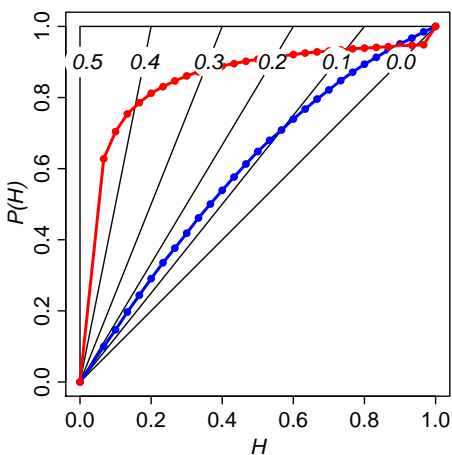
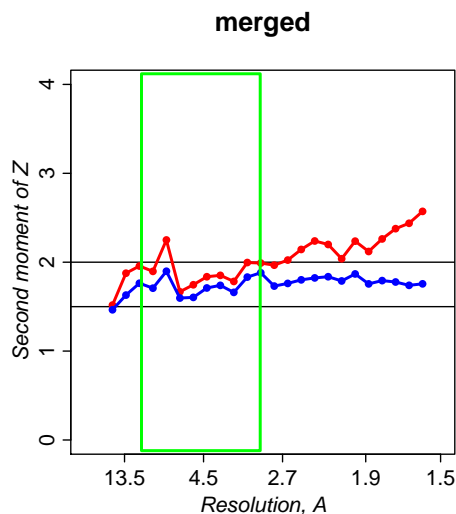
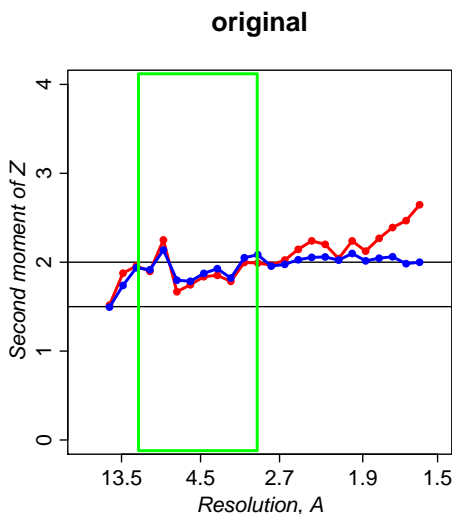
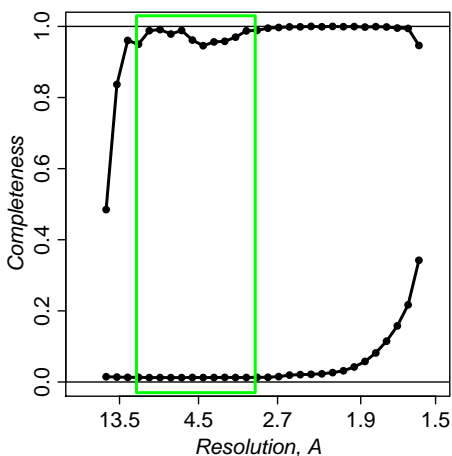
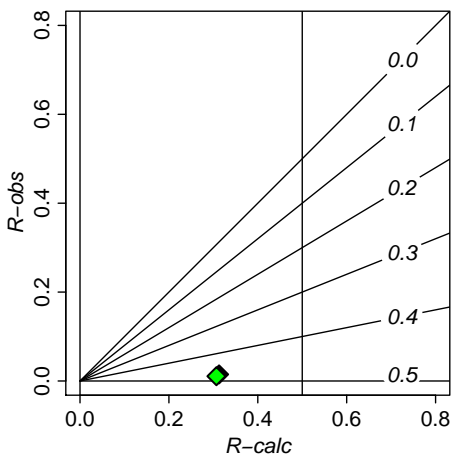
	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.40
R	30.6	
R'	31.4	32.1
R-free	31.6	
R'-free	32.4	33.1

residues per monomer	DNA	protein
	0	124

s < f/100	573	1.33 %
s <= 0	0	0.00 %
f <= 0	1576	3.66 %
s,f <= 0	0	0.00 %

range (A)	25.8–1.5	9.9–3.0
unique	43,494	5,838
measured	43,027	5,675
used	40,502	5,108

NCS	translation	rotation
r.m.s.d. (A)	23.50	0.39
angle (o)	179.89	0.14



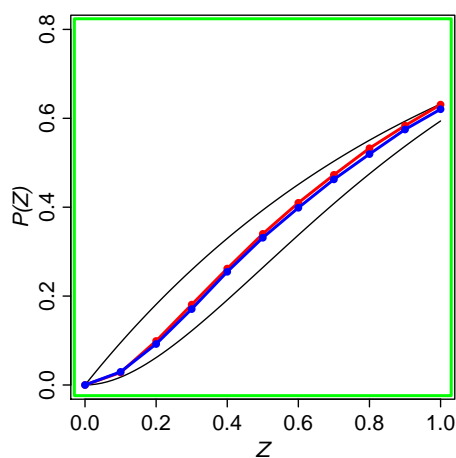
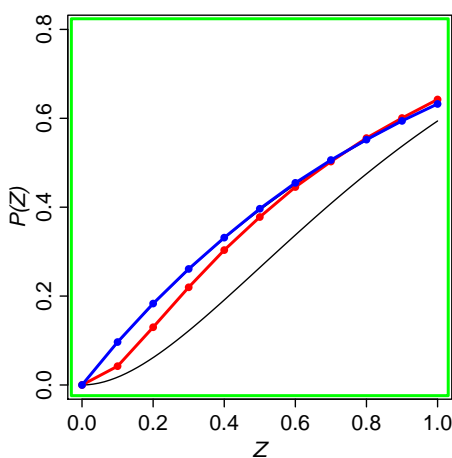
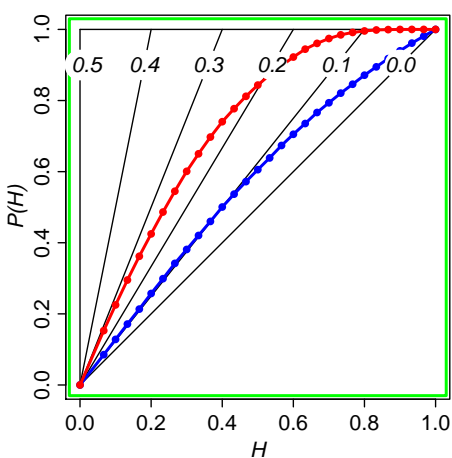
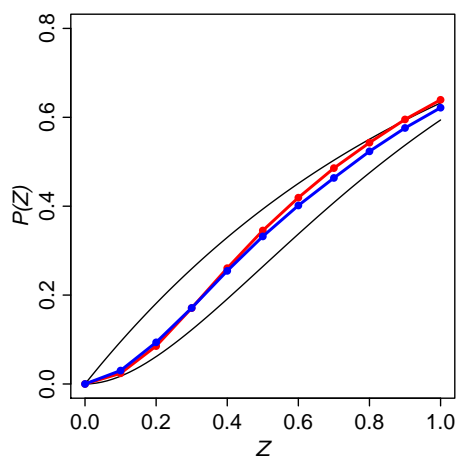
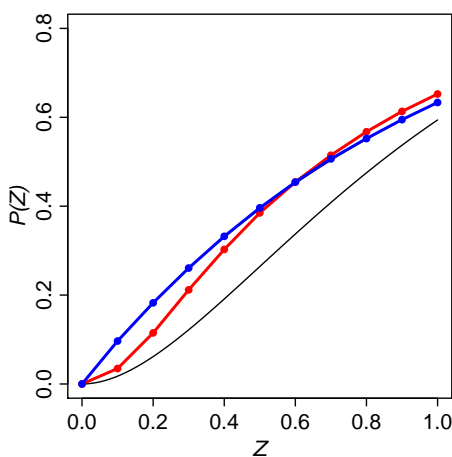
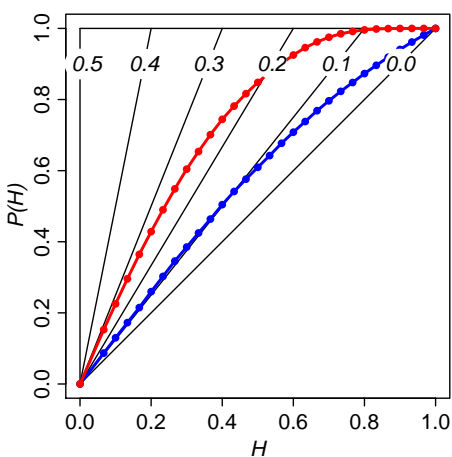
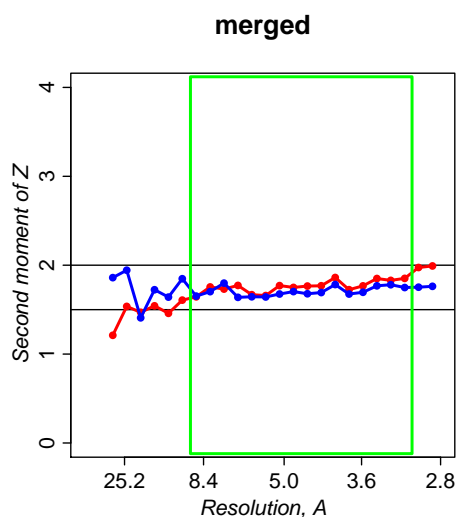
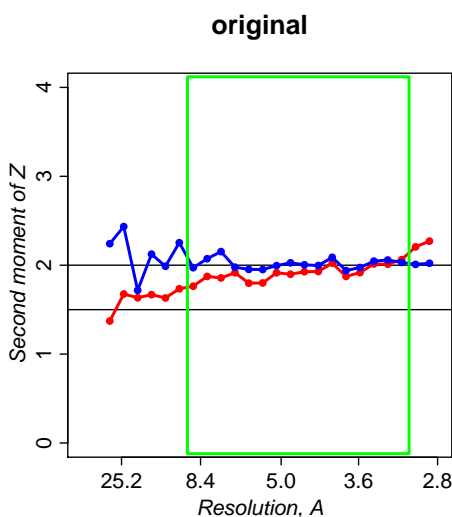
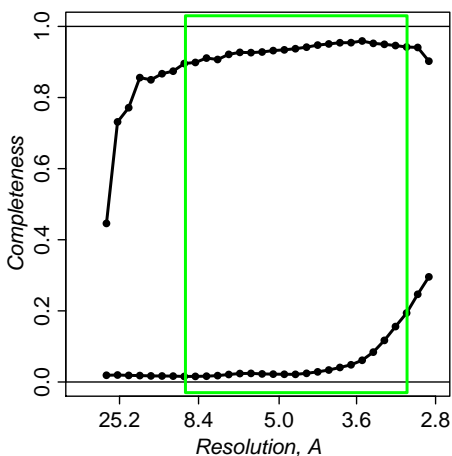
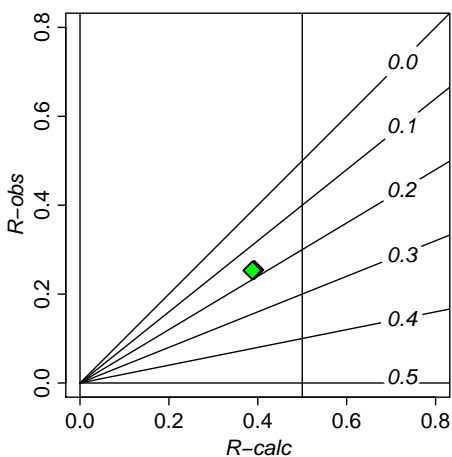
1lb1

	original	merged
s.g.	P 43	-
p.g.	10201	10205
a.u.	4	-
p.t.	2	-
p.o.	2	-
r.m.s.d. (A)	-	-
R	23.7	-
R'	-	-
R-free	27.4	-
R'-free	-	-
residues per monomer	DNA 0	protein 502

s < f/100	707	0.82 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	47.7-2.8	9.9-3.0
unique	91,791	73,277
measured	85,993	69,099
used	76,736	61,664

NCS	translation	rotation
r.m.s.d. (A)	11.47	0.18
angle (o)	37.91	0.37



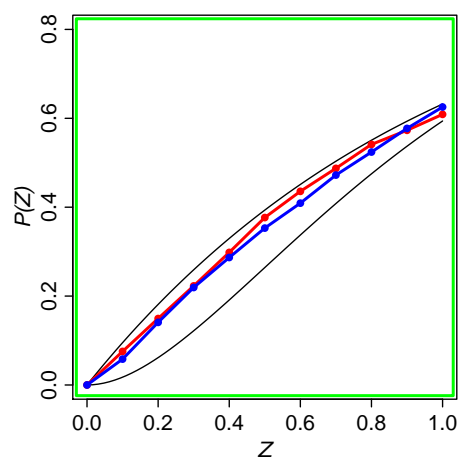
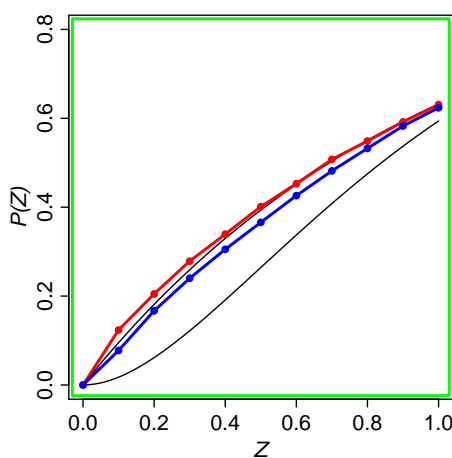
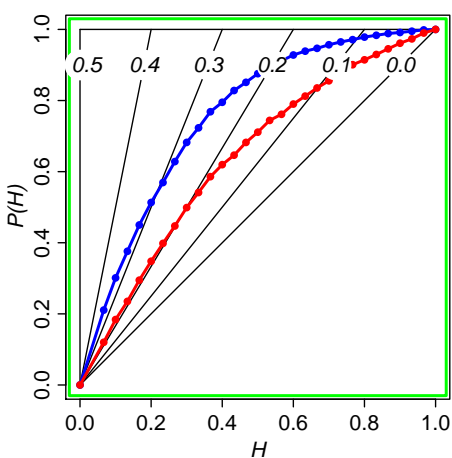
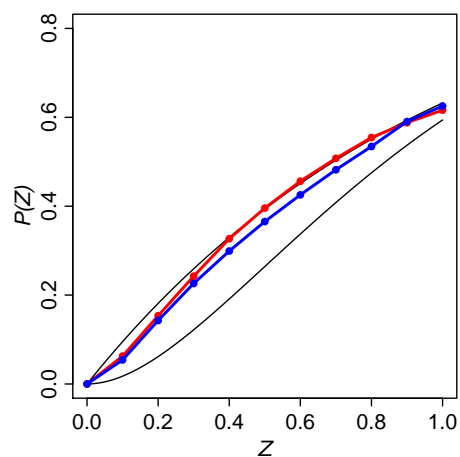
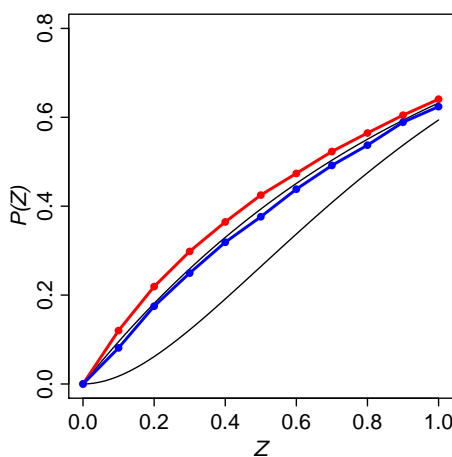
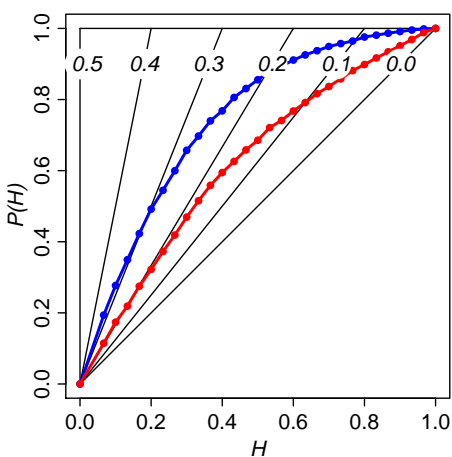
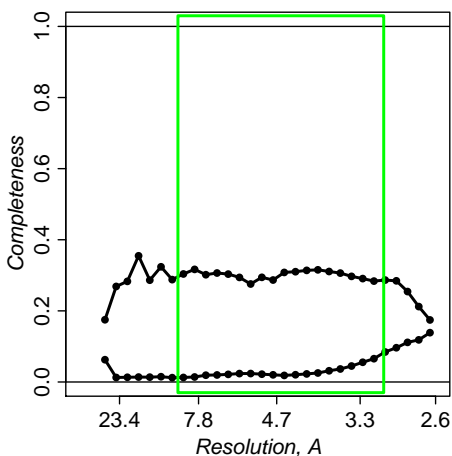
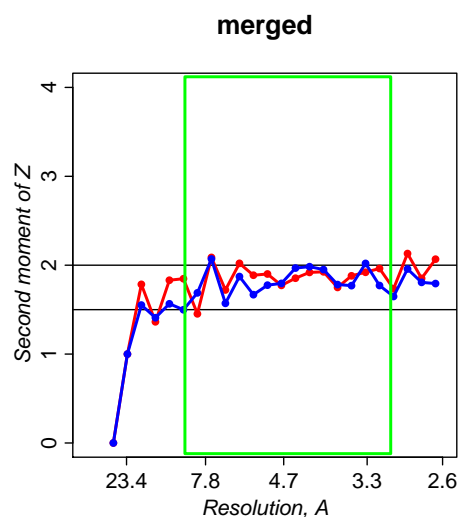
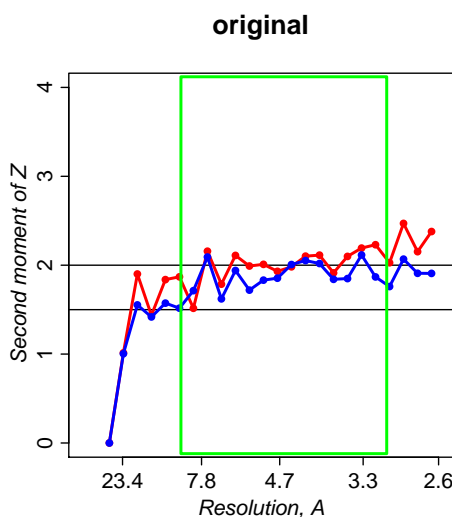
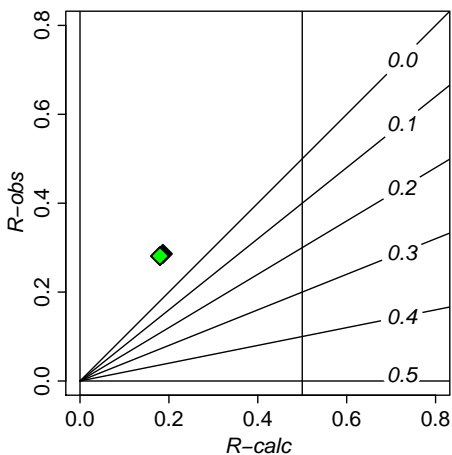
1lbs

	original	merged
s.g.	C 1 2 1	-
p.g.	10001	10003
a.u.	6	-
p.t.	3	-
p.o.	3	-
r.m.s.d. (A)	-	-
R	20.1	-
R'	-	-
R-free	24.4	-
R'-free	-	-
residues per monomer	DNA 0	protein 317

s < f/100	679	4.26 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	47.8-2.6	9.9-3.0
unique	57,887	36,694
measured	15,945	10,976
used	3,892	2,770

NCS	translation	rotation
r.m.s.d. (A)	0.00	0.52
angle (o)	0.00	2.10



1lbw

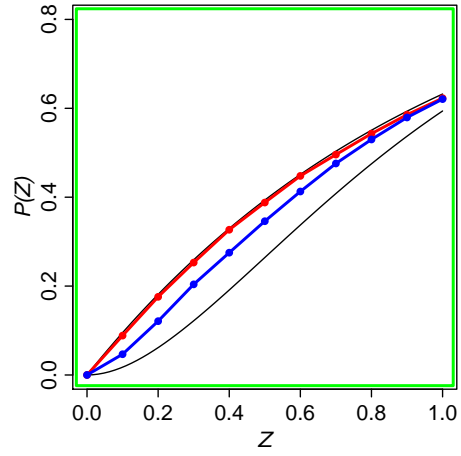
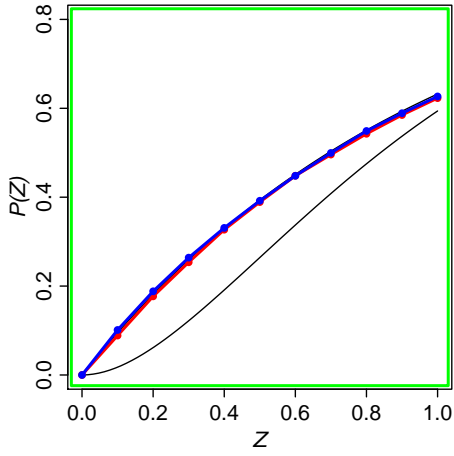
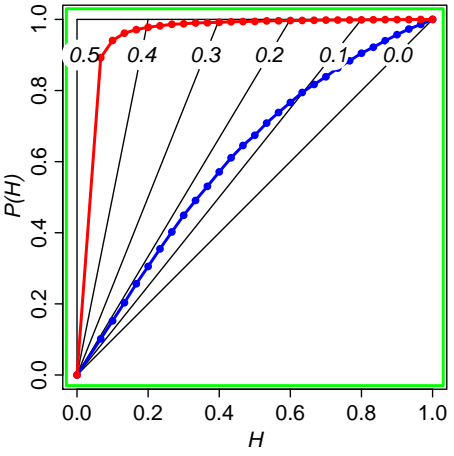
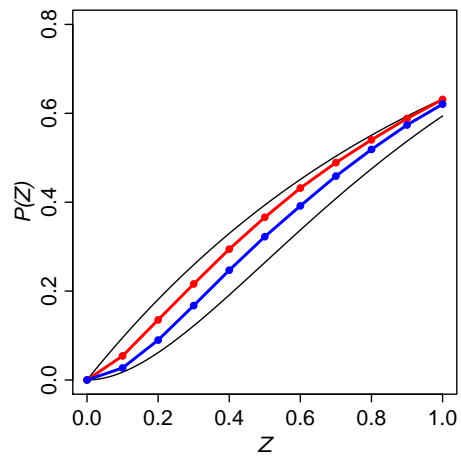
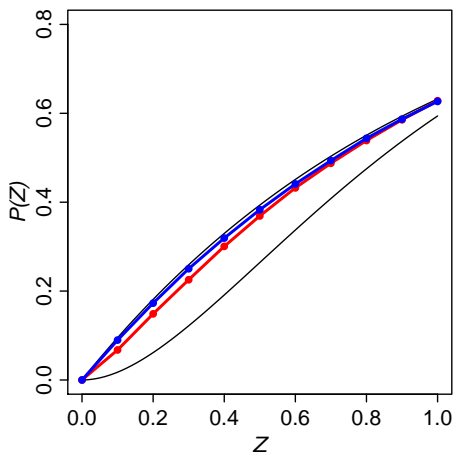
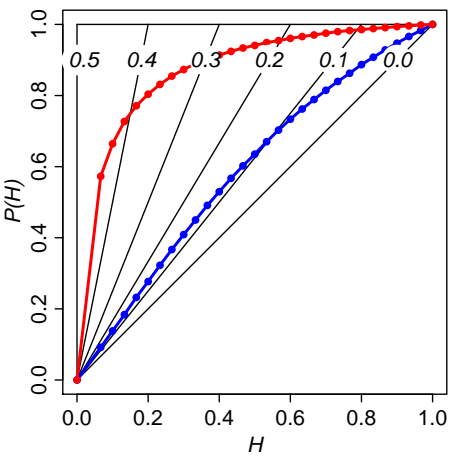
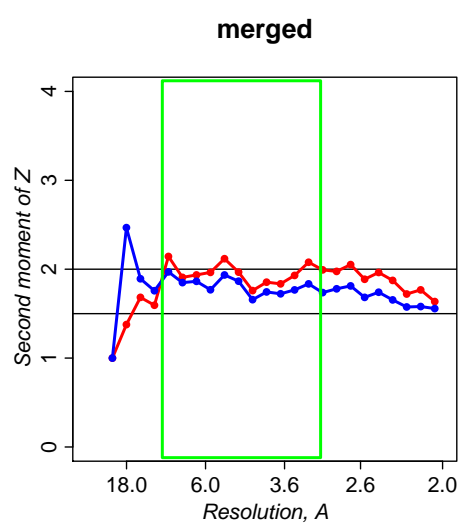
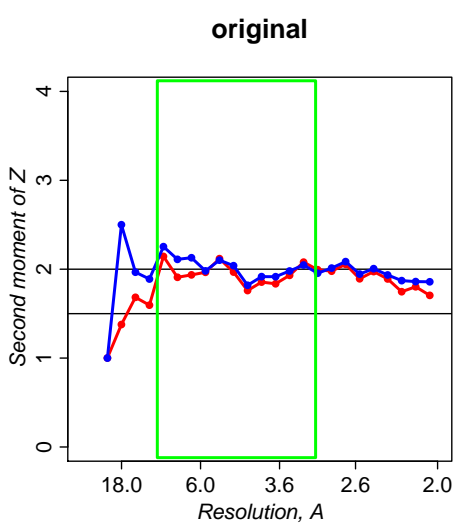
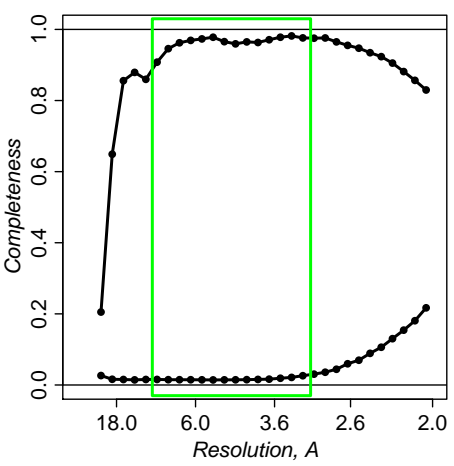
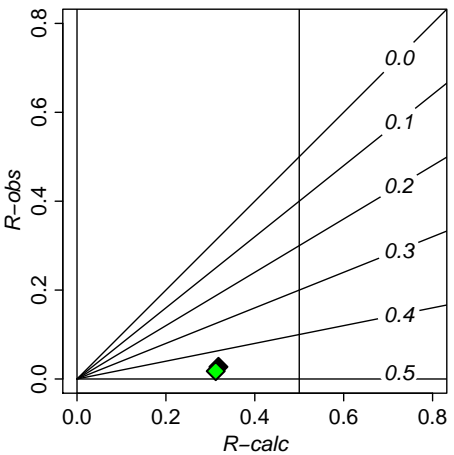
	original	merged
s.g.	P 32	P 32 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.55
R	25.5	
R'	26.1	26.6
R-free	27.5	
R'-free	28.0	28.5

residues per monomer	DNA	protein
	0	252

s < f/100	1379	2.40 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)		
	38.7–2.0	9.9–3.0
unique	62,063	18,024
measured	57,501	17,488
used	51,700	16,014

NCS	translation	rotation
r.m.s.d. (A)	25.31	0.53
angle (o)	179.42	0.62



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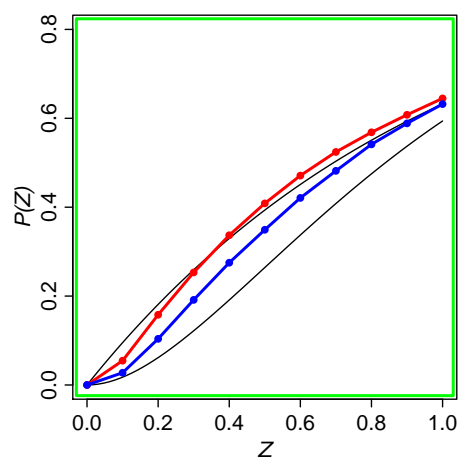
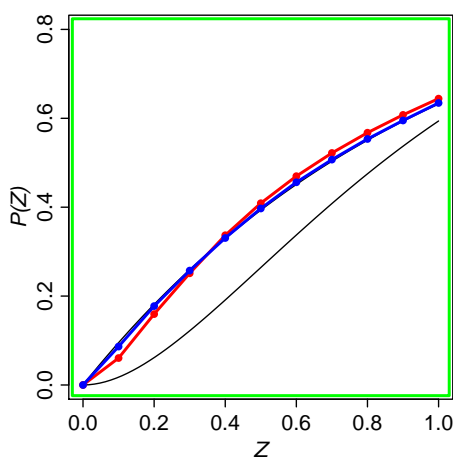
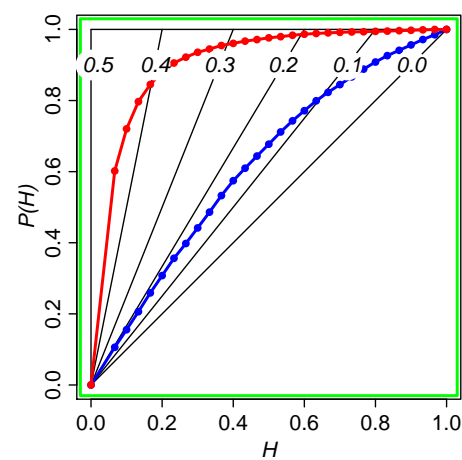
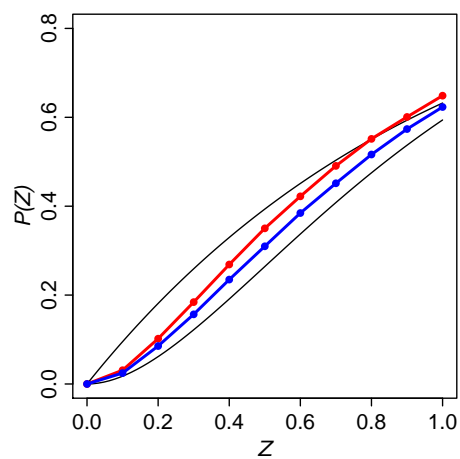
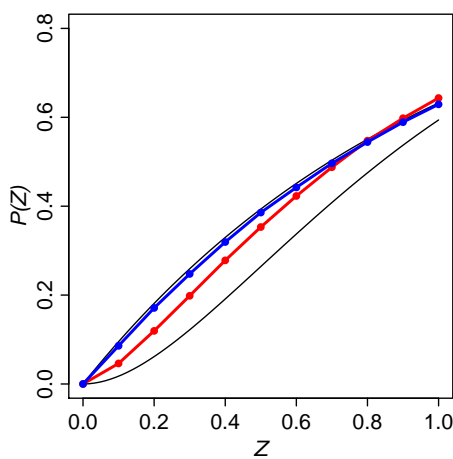
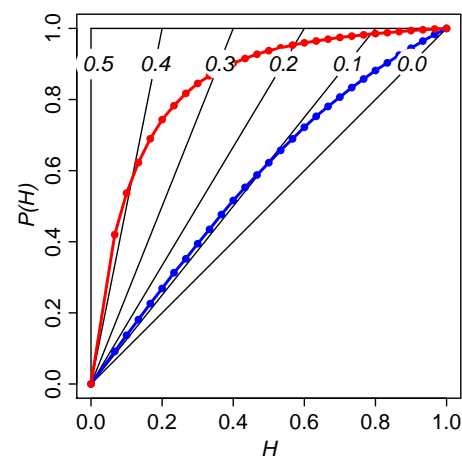
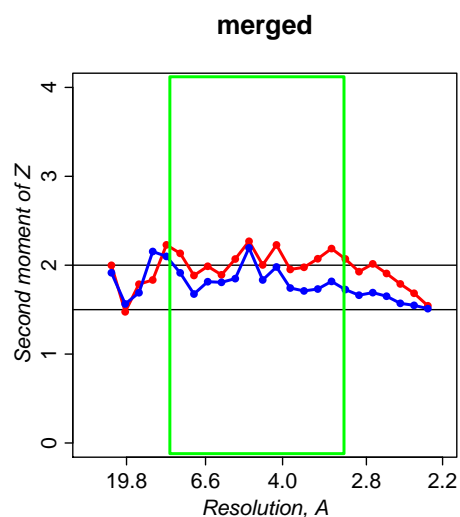
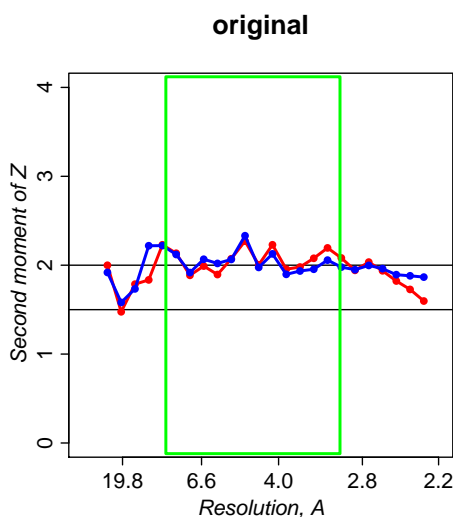
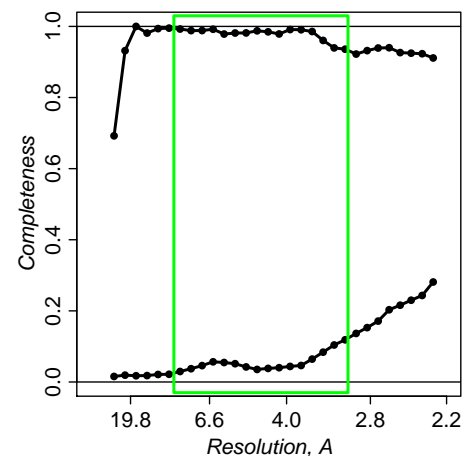
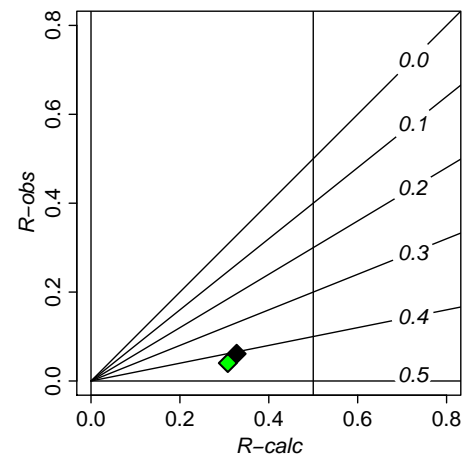
	original	merged
s.g.	P 32	P 32 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.52
R	25.7	
R'	26.4	26.6
R-free	27.5	
R'-free	28.3	27.9

s < f/100	210	0.51 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	44.6–2.2	9.9–3.0
unique	43,598	17,892
measured	41,224	17,376
used	37,478	15,912

NCS	translation	rotation
r.m.s.d. (A)	25.21	0.52
angle (o)	179.84	0.16

residues per monomer	DNA	protein
	0	252



1lbz

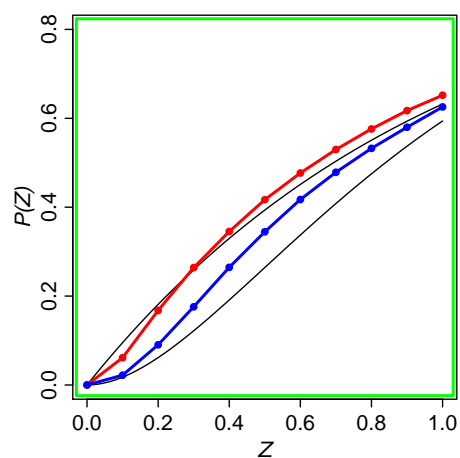
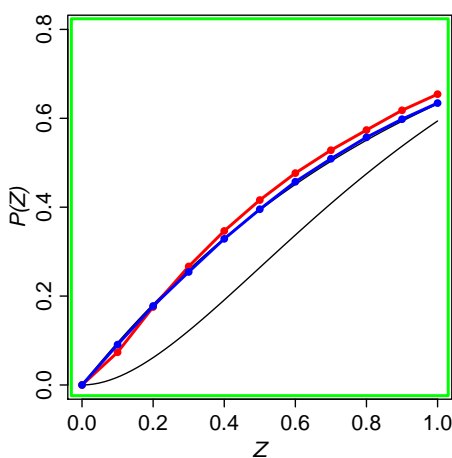
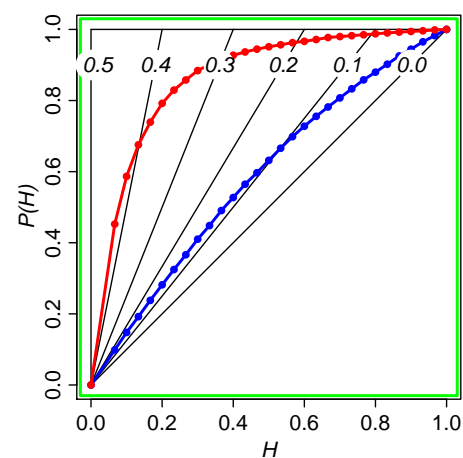
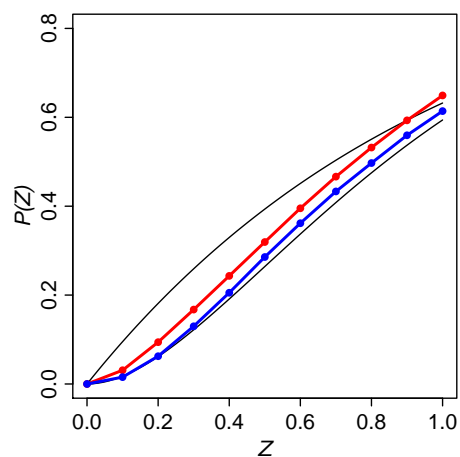
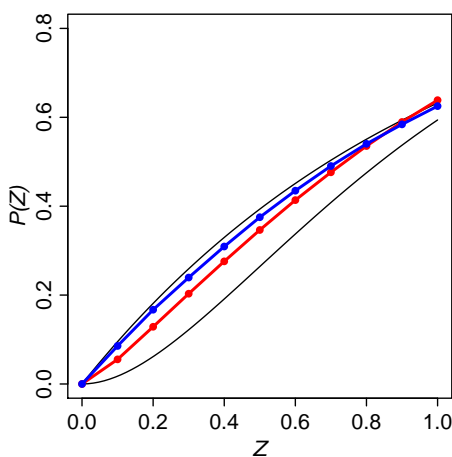
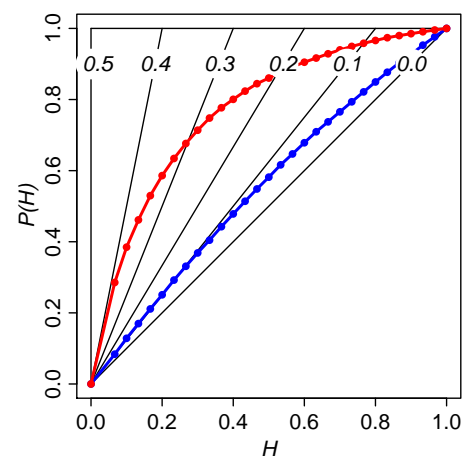
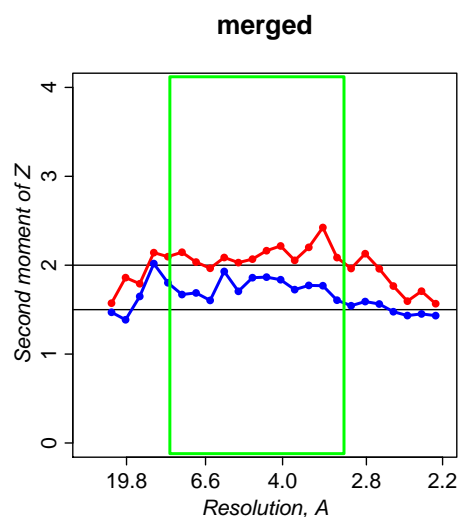
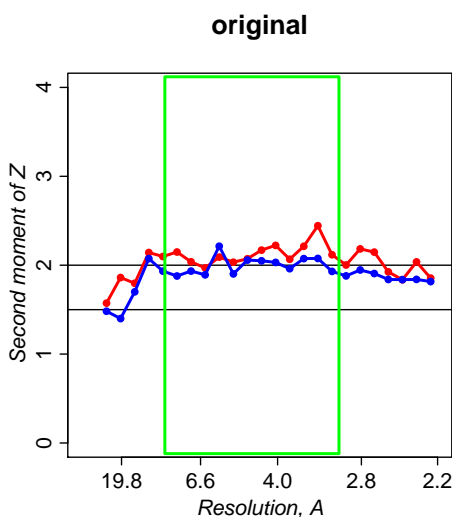
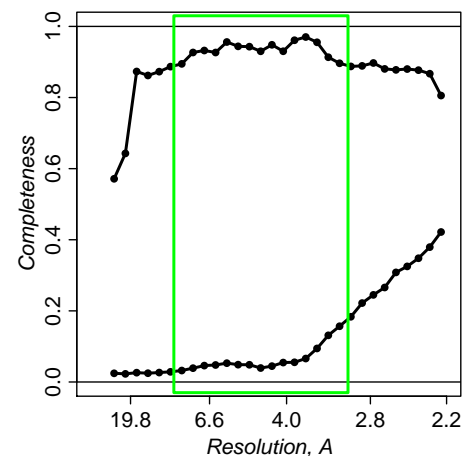
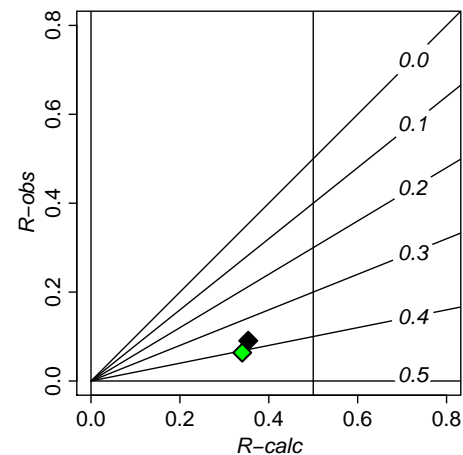
	original	merged
s.g.	P 32	P 32 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.60
R	28.6	
R'	28.3	28.3
R-free	30.9	
R'-free	31.5	31.4

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	44.8–2.2	9.9–3.0
unique	46,921	17,990
measured	41,909	16,777
used	36,084	14,832

NCS	translation	rotation
r.m.s.d. (A)	29.78	0.59
angle (o)	179.65	0.41

residues per monomer	DNA	protein
	0	252



1les

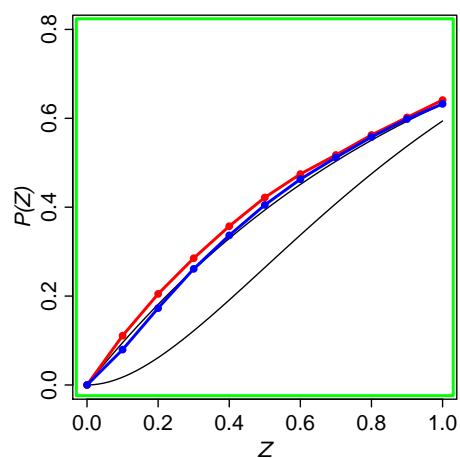
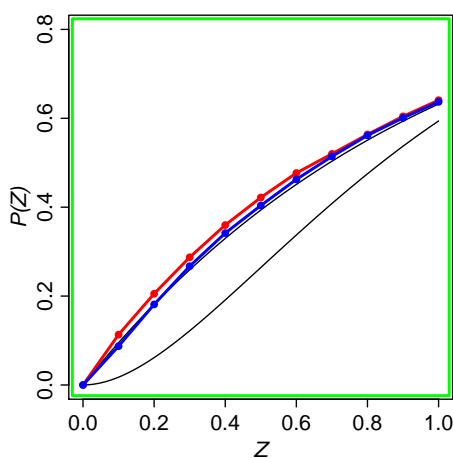
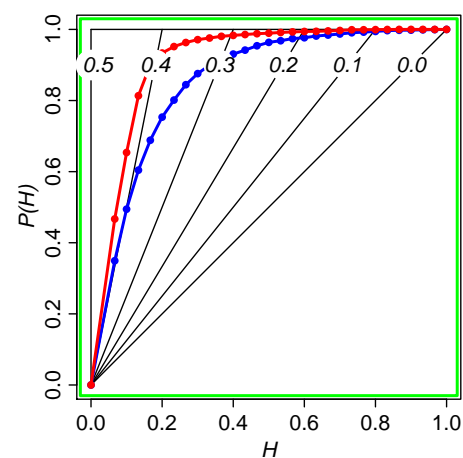
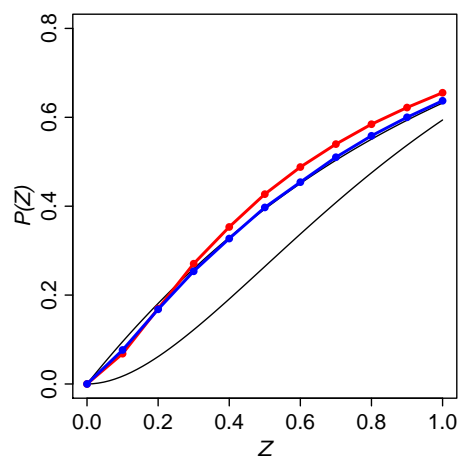
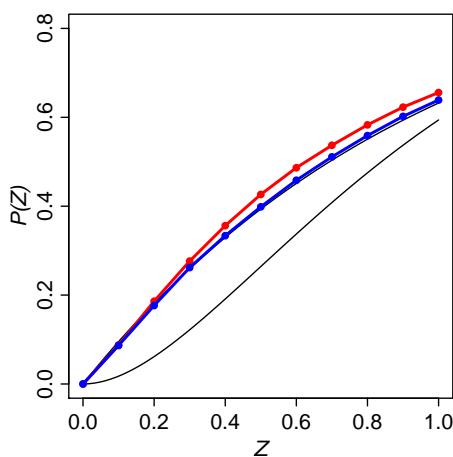
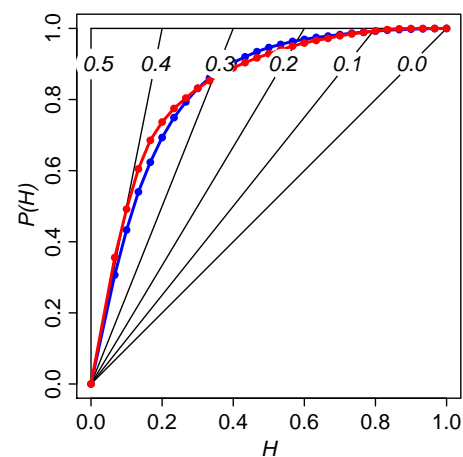
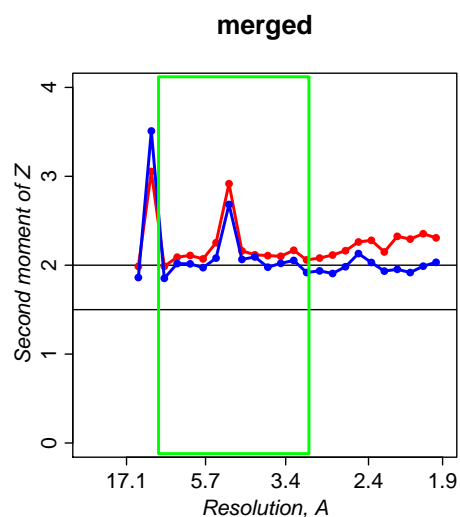
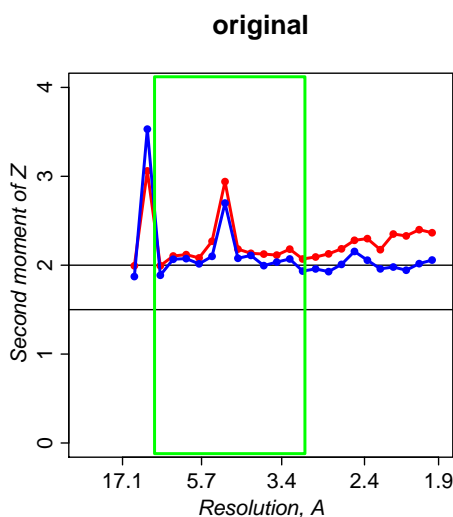
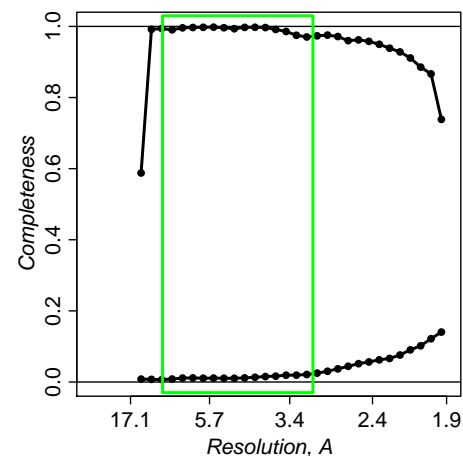
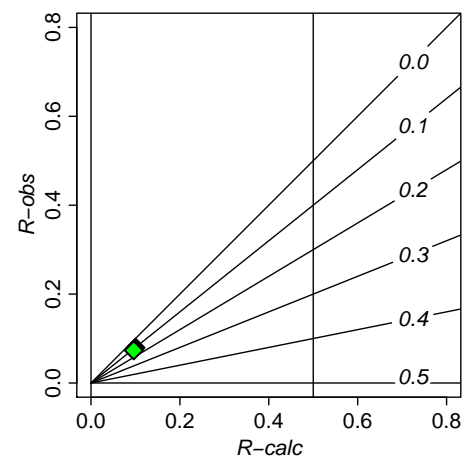
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.10
R	25.2	
R'	26.1	26.1
R-free	28.2	
R'-free	29.2	29.3

s < f/100	3795	9.13 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	15.0–1.9	9.9–3.0
unique	44,723	11,149
measured	41,555	11,012
used	36,618	9,938

NCS	translation	rotation
r.m.s.d. (A)	28.70	0.10
angle (o)	179.97	0.06

residues per monomer	DNA	protein
	0	228



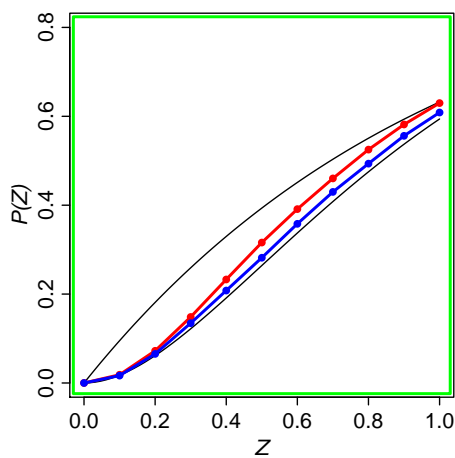
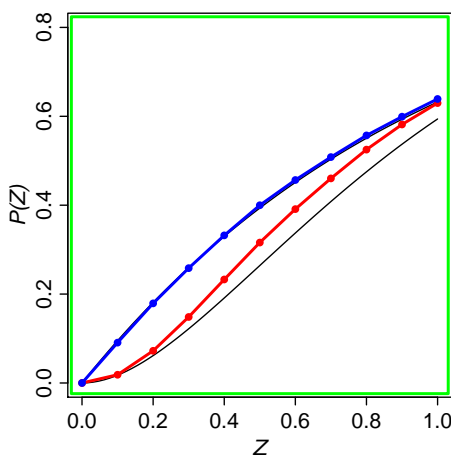
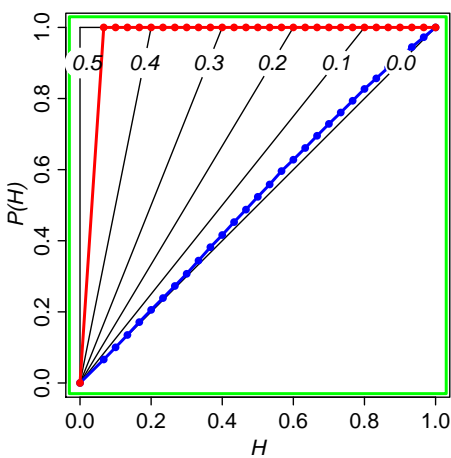
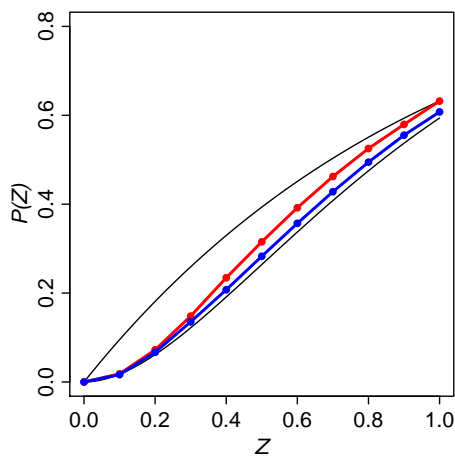
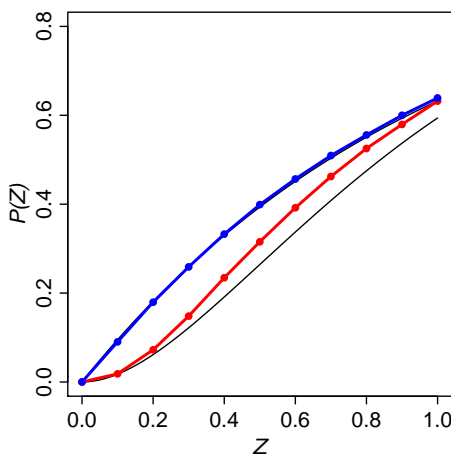
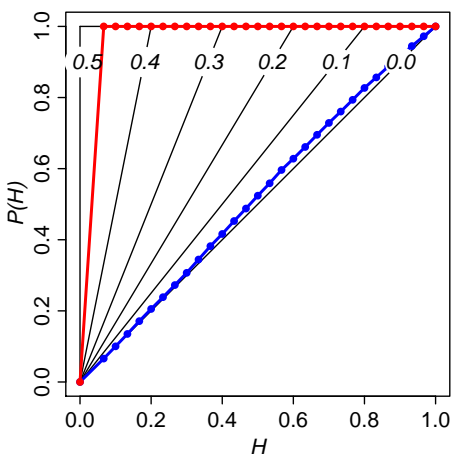
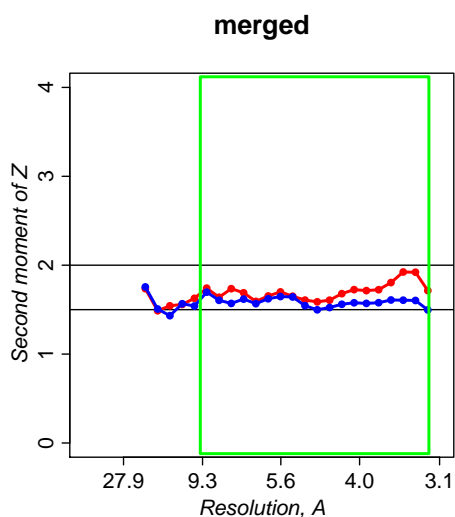
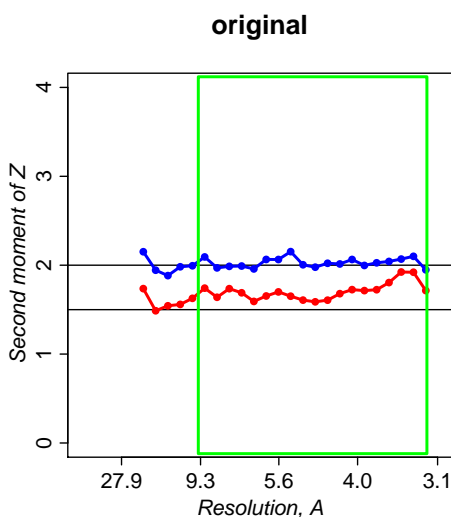
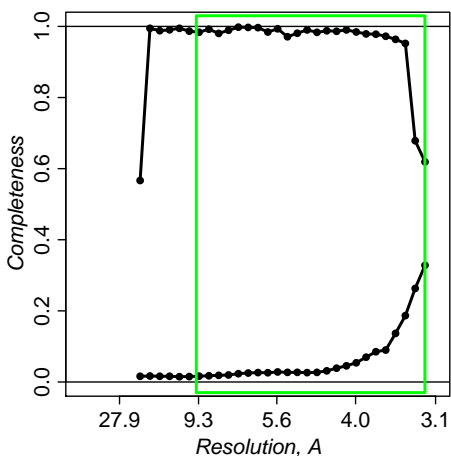
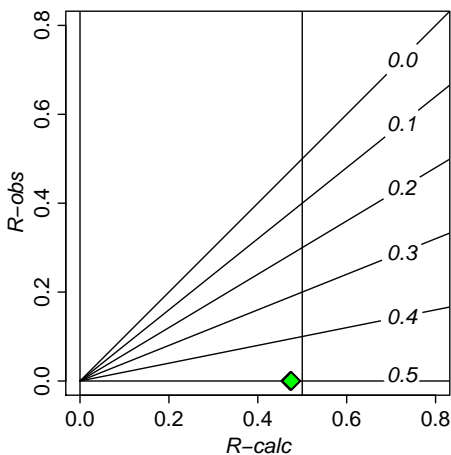
1lj7

	original	merged
s.g.	P 43	P 43 21 2
p.g.	10201	10205
a.u.	10	5
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		6.00
R	24.3	
R'	-	-
R-free	32.8	
R'-free	-	-
residues per monomer	DNA 0	protein 197

s < f/100	276	0.55 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	20.0-3.2	9.9-3.2
unique	53,864	52,280
measured	50,118	48,551
used	46,138	44,940

NCS	translation	rotation
r.m.s.d. (A)	15.07	0.19
angle (o)	71.42	0.52



1lnq

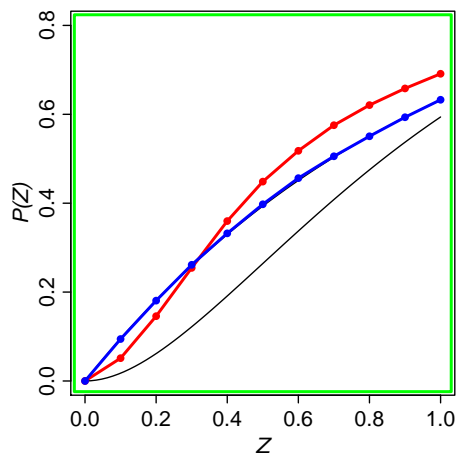
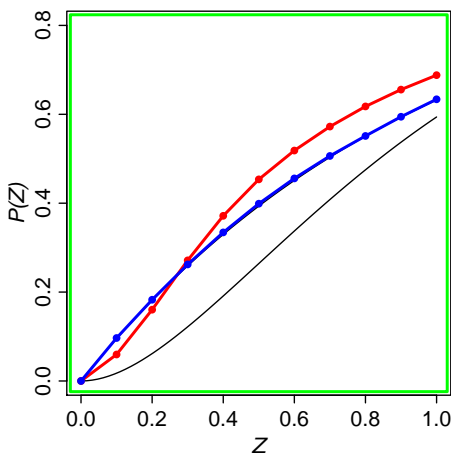
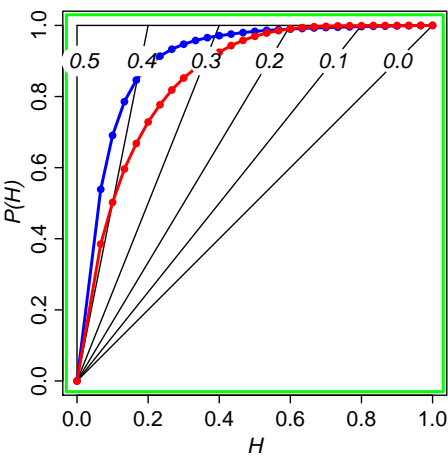
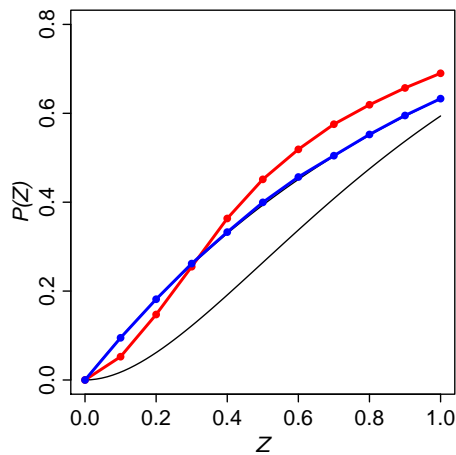
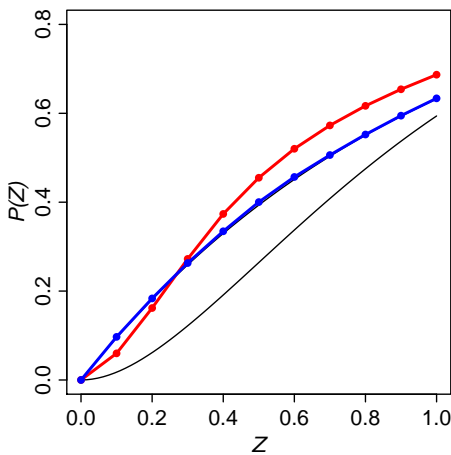
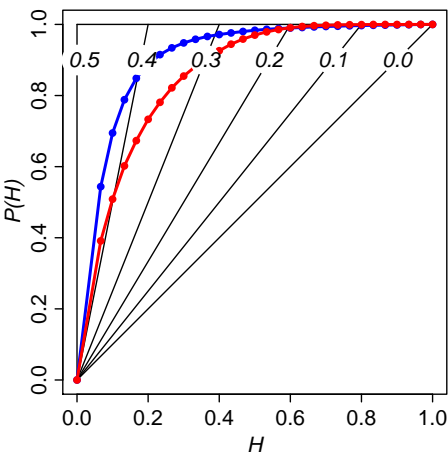
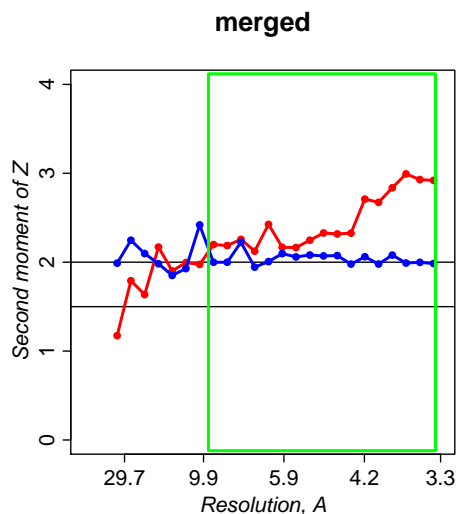
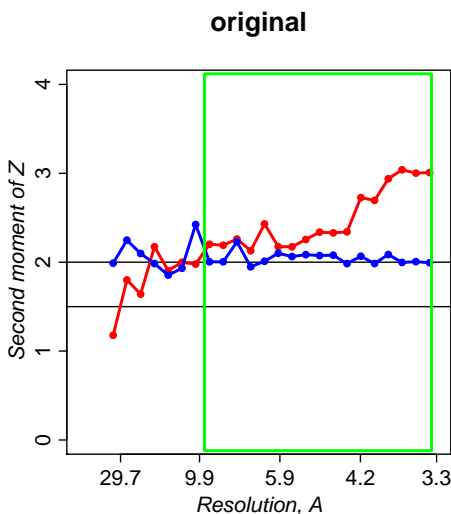
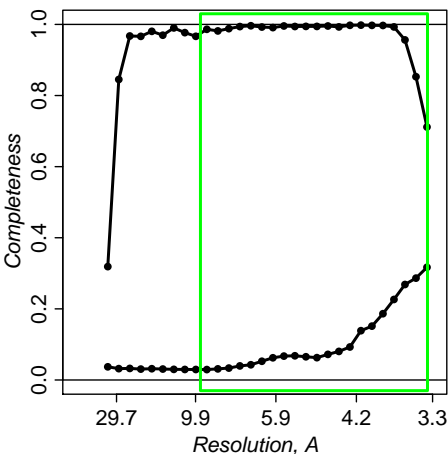
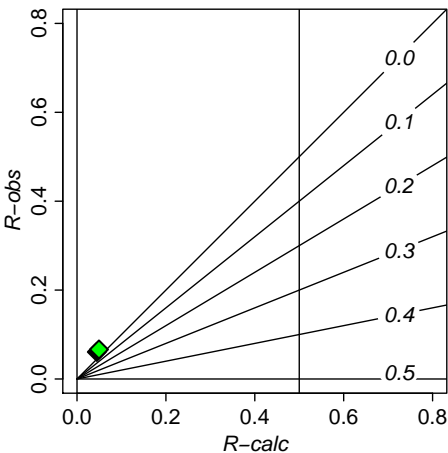
	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	8	4
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		0.23
R	26.3	
R'	26.3	27.2
R-free	32.8	
R'-free	32.9	34.0

s < f/100	3	0.01 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	46.4–3.3	9.9–3.3
unique	59,358	57,135
measured	56,550	54,414
used	49,786	48,210

NCS	translation	rotation
r.m.s.d. (A)	11.09	0.14
angle (o)	26.91	0.14

residues per monomer	DNA	protein
	0	301



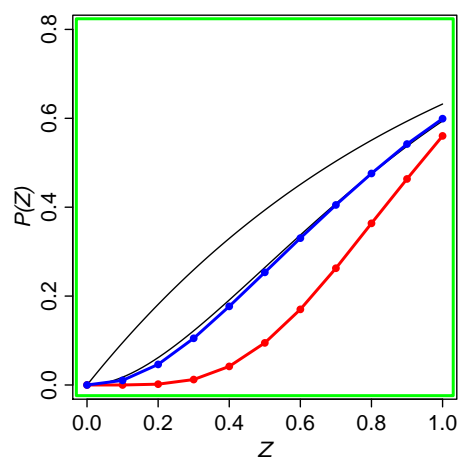
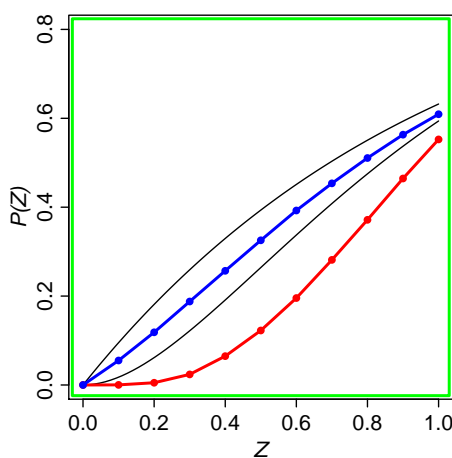
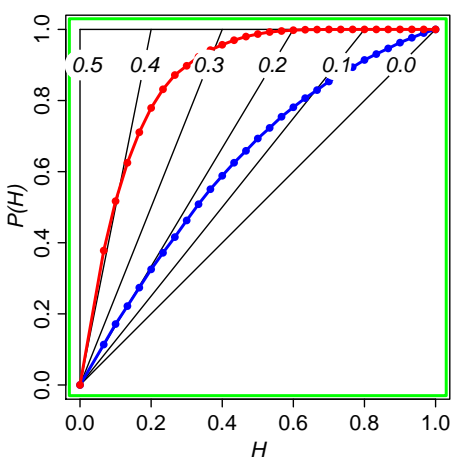
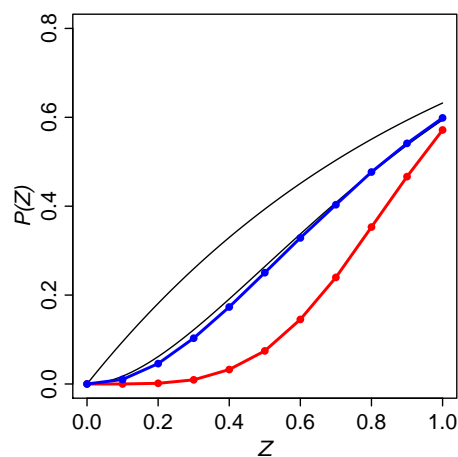
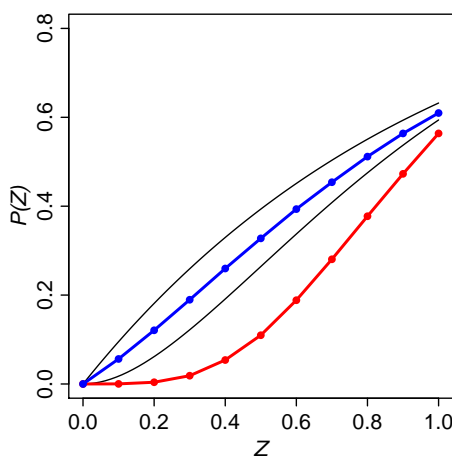
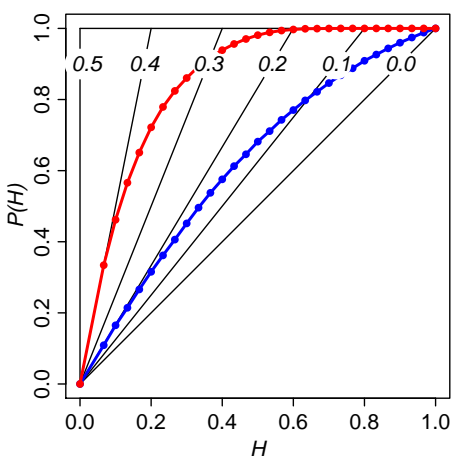
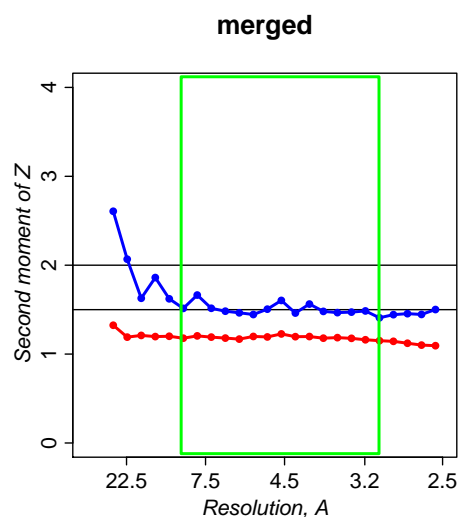
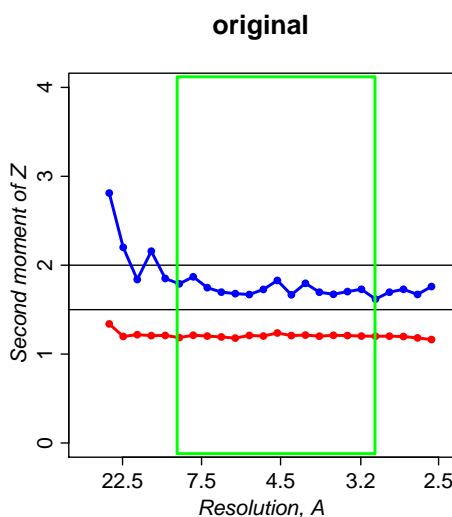
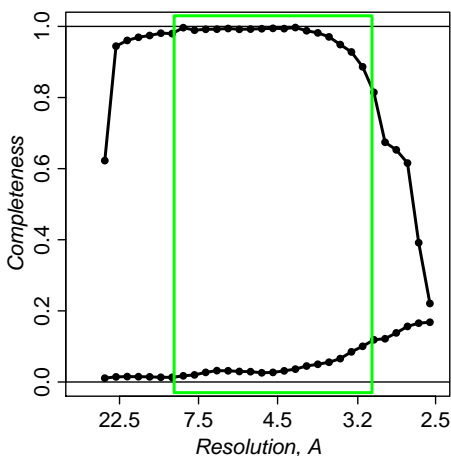
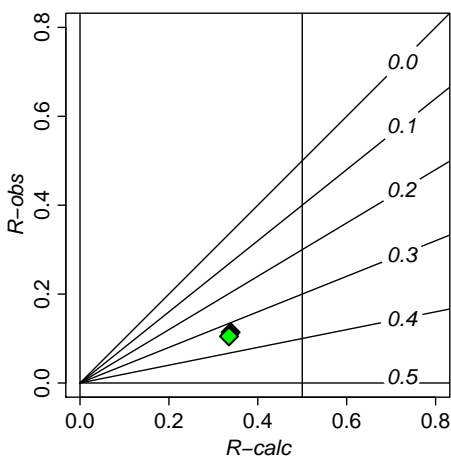
1Inu

	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		8.06
R	27.2	
R'	-	-
R-free	33.1	
R'-free	-	-
residues per monomer	DNA 0	protein 399

s < f/100	1728	3.17 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	46.3–2.5	9.9–3.0
unique	69,050	41,121
measured	54,500	39,261
used	51,134	36,884

NCS	translation	rotation
r.m.s.d. (A)	25.40	0.08
angle (o)	68.97	0.04



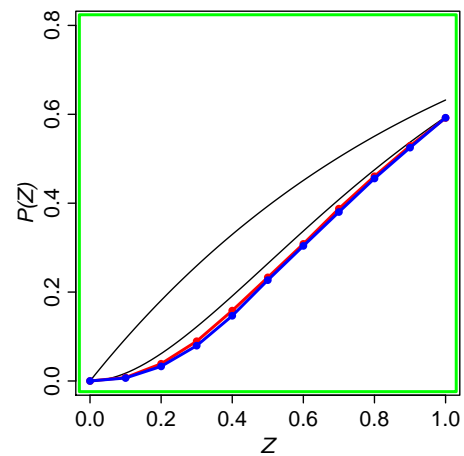
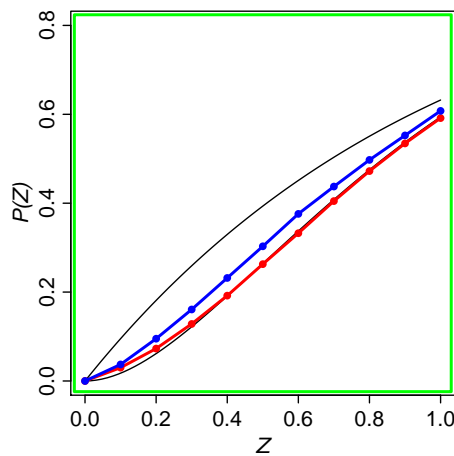
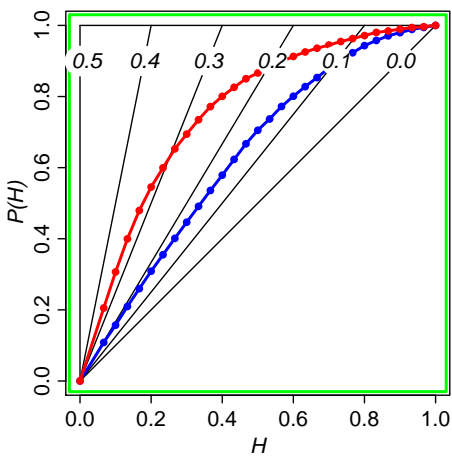
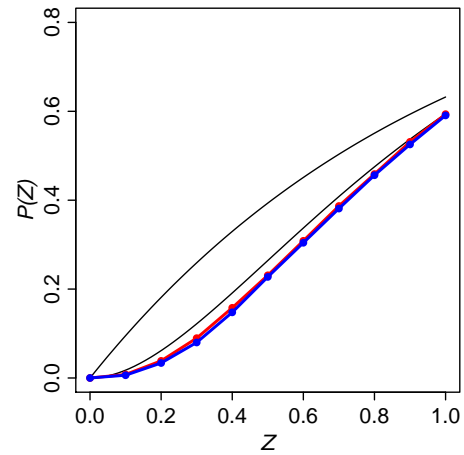
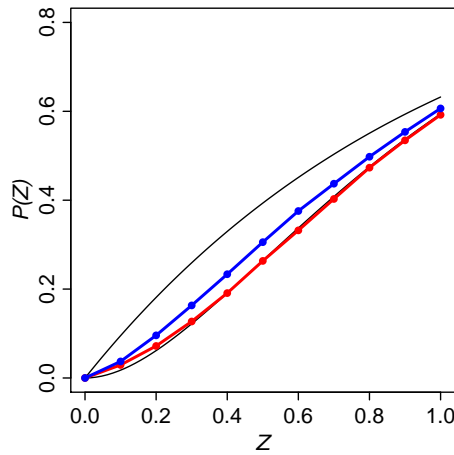
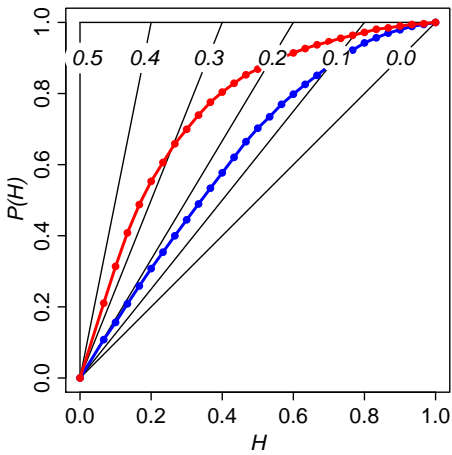
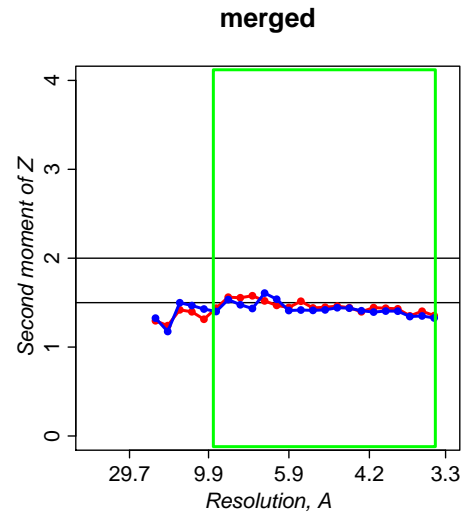
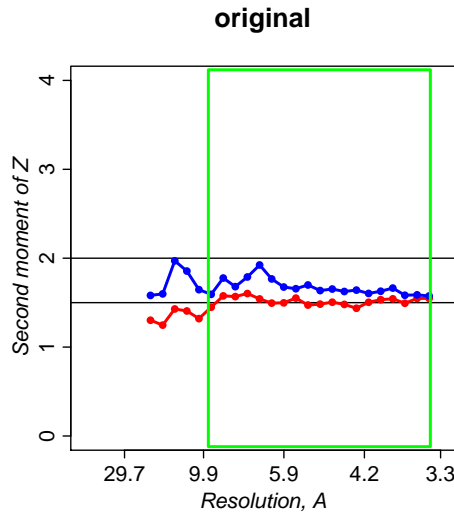
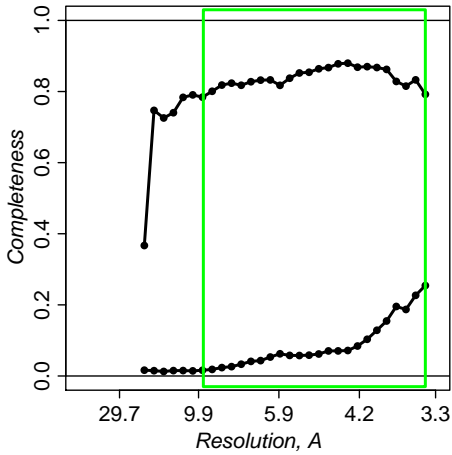
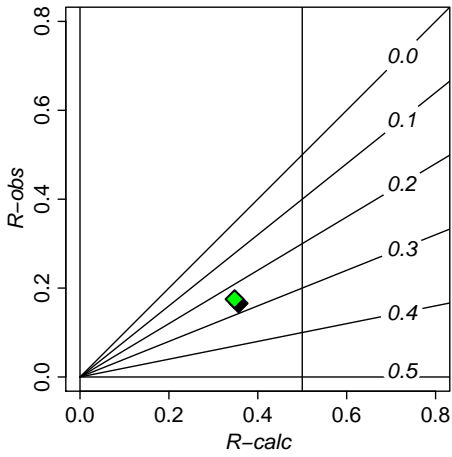
1lqj

	original	merged
s.g.	P 32	P 65
p.g.	10020	12021
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		10.19
R	25.2	
R'	-	-
R-free	33.4	
R'-free	-	-
residues per monomer	DNA 0	protein 224

s < f/100	301	1.59 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.7-3.4	9.9-3.4
unique	22,598	21,829
measured	18,979	18,402
used	15,410	15,036

NCS	translation	rotation
r.m.s.d. (A)	8.05	3.73
angle (o)	37.05	14.09



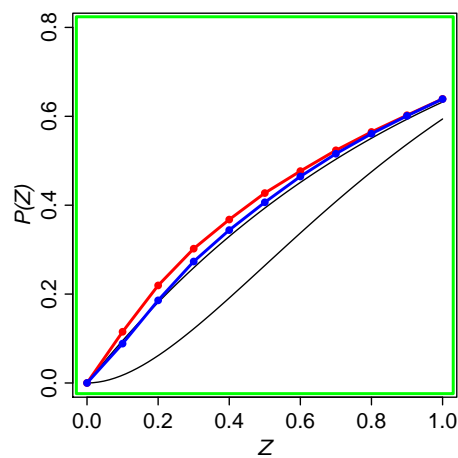
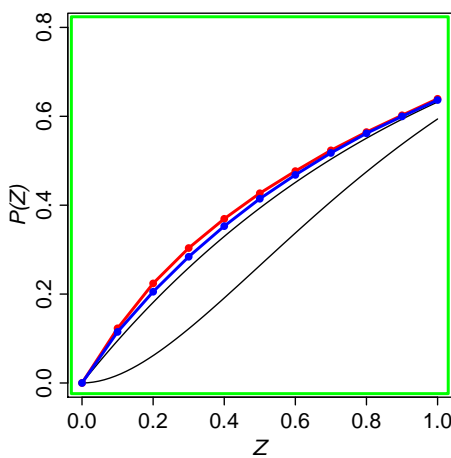
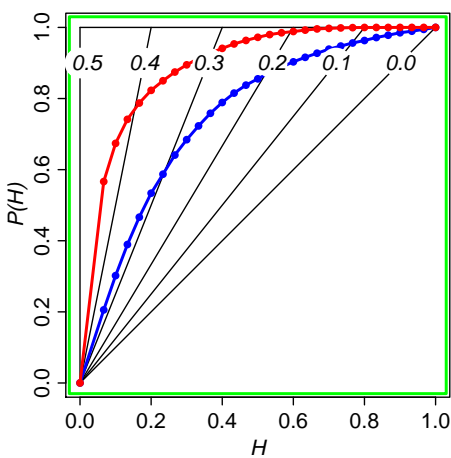
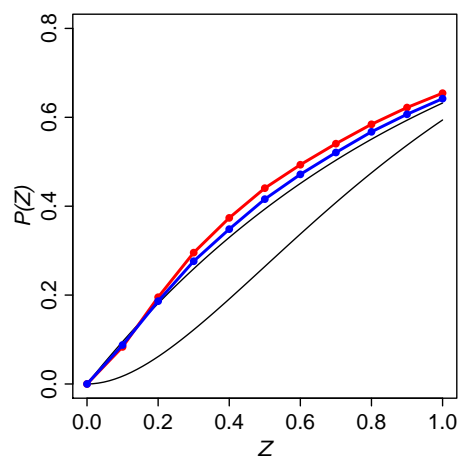
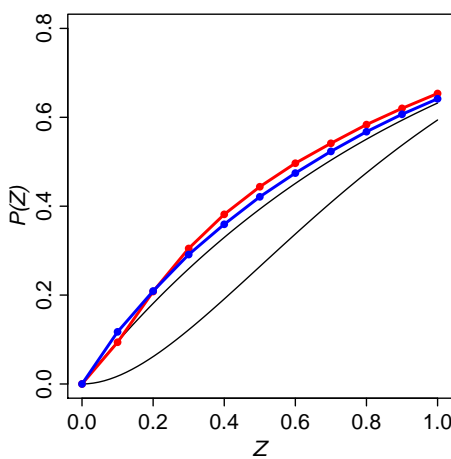
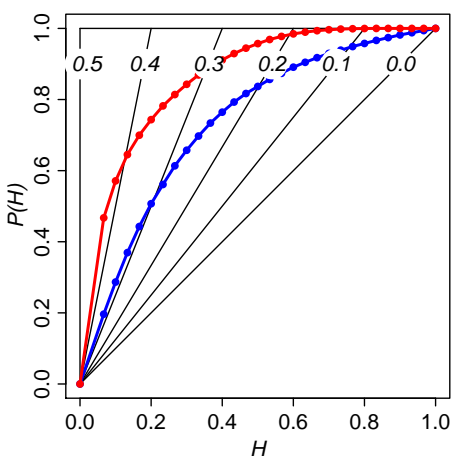
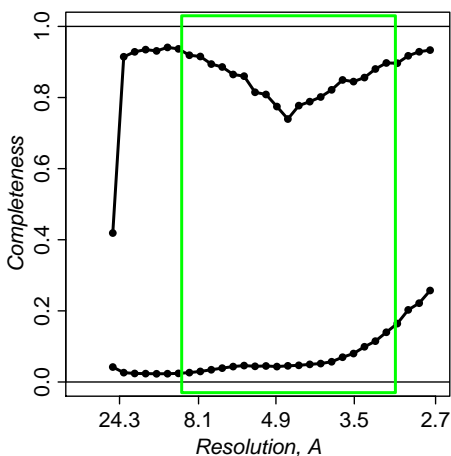
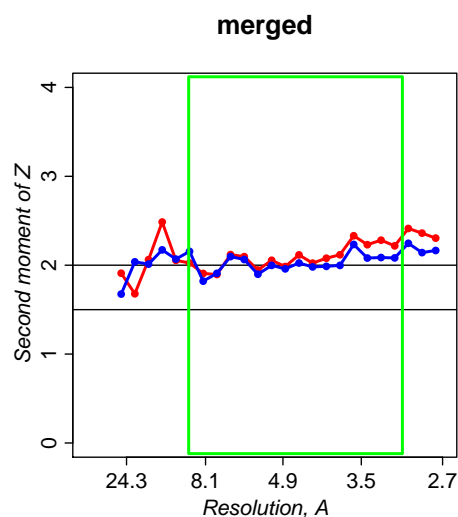
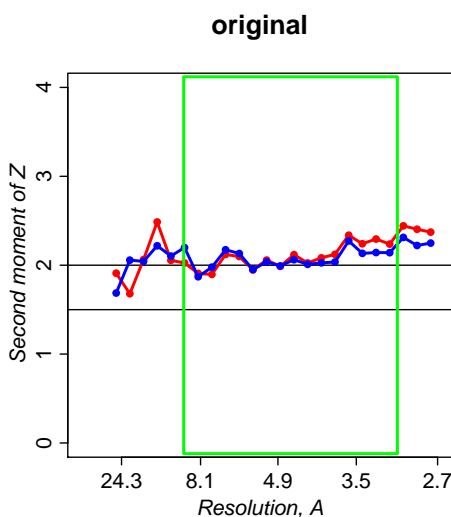
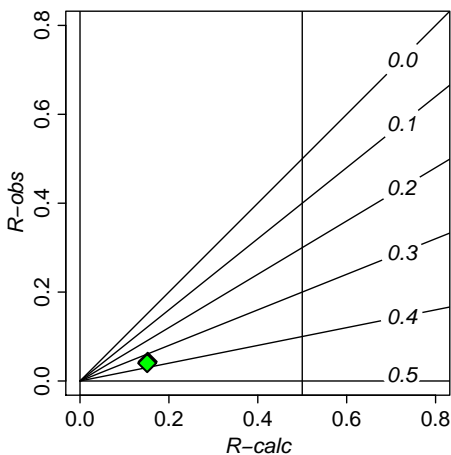
1ls3

	original	merged
s.g.	P 41	P 41 21 2
p.g.	10201	10205
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		0.60
R	25.6	
R'	25.7	26.2
R-free	32.7	
R'-free	33.0	33.1
residues per monomer	DNA 0	protein 448

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	35.2–2.7	9.9–3.0
unique	54,981	38,978
measured	47,665	32,871
used	41,052	27,846

NCS	translation	rotation
r.m.s.d. (A)	15.10	0.20
angle (o)	47.53	0.04



1lv1

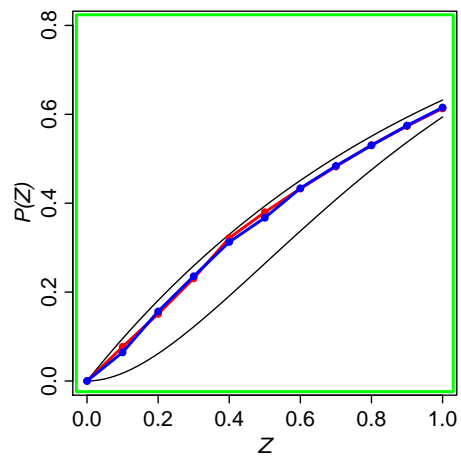
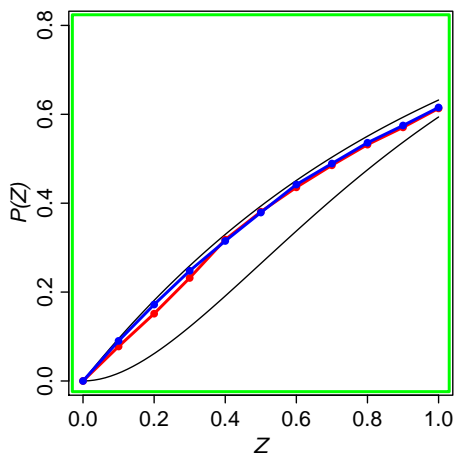
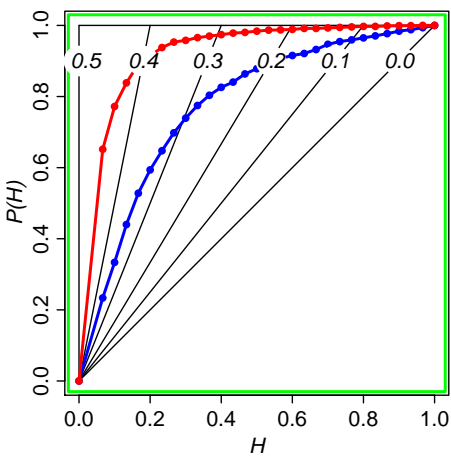
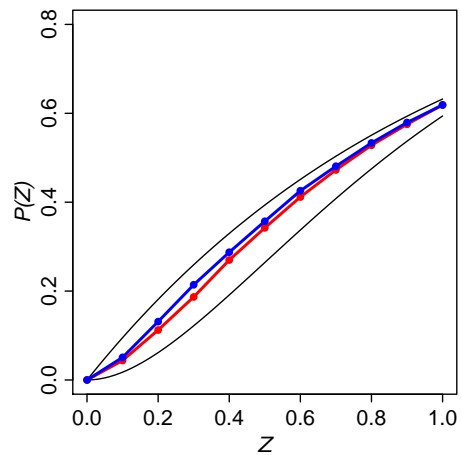
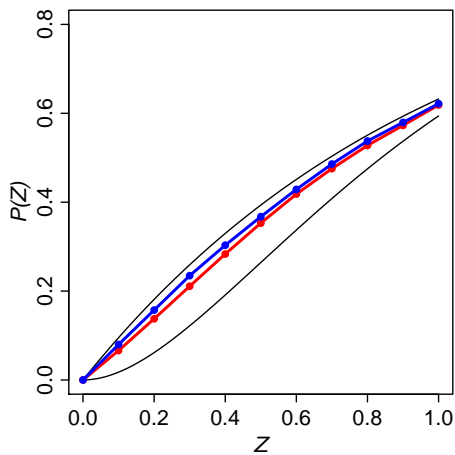
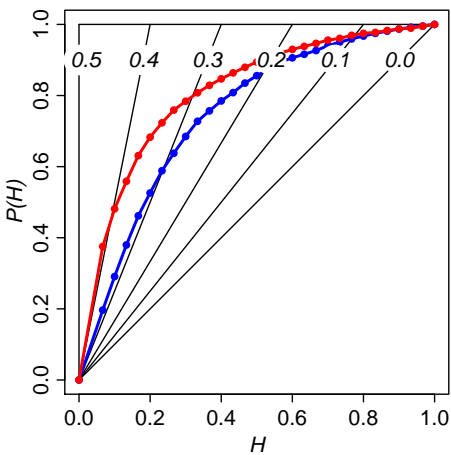
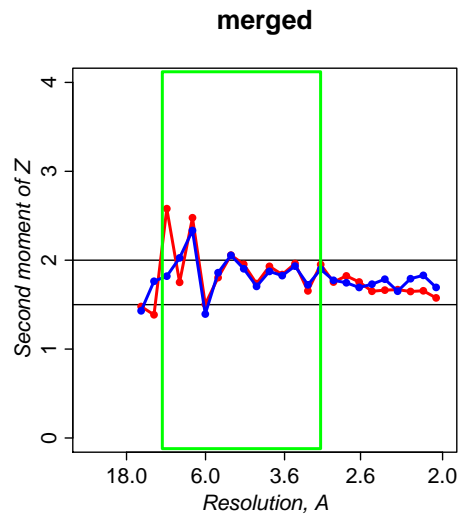
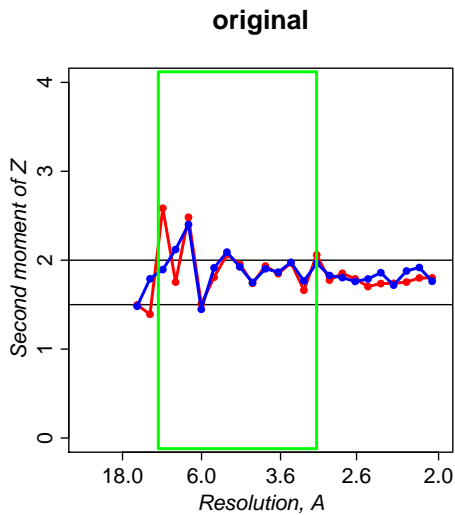
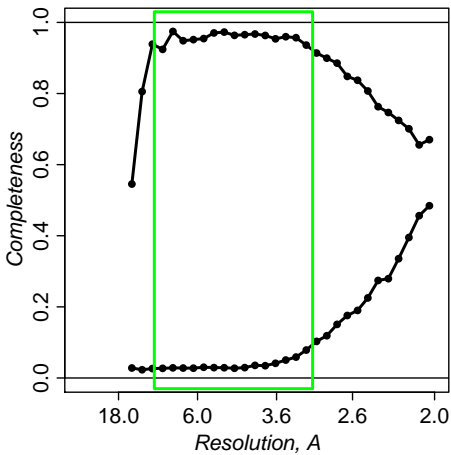
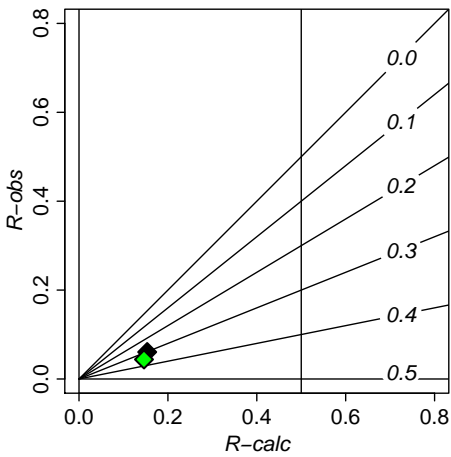
	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.20
R	26.1	
R'	27.3	28.3
R-free	29.8	
R'-free	30.0	30.0

residues per monomer	DNA	protein
	0	94

s < f/100	1246	11.95 %
s <= 0	1246	11.95 %
f <= 0	1246	11.95 %
s,f <= 0	1246	11.95 %

range (A)	translation	rotation
unique	14.9–2.0	9.9–3.0
measured	12,708	3,707
used	10,430	3,538

NCS	translation	rotation
r.m.s.d. (A)	20.90	0.20
angle (o)	179.87	0.23



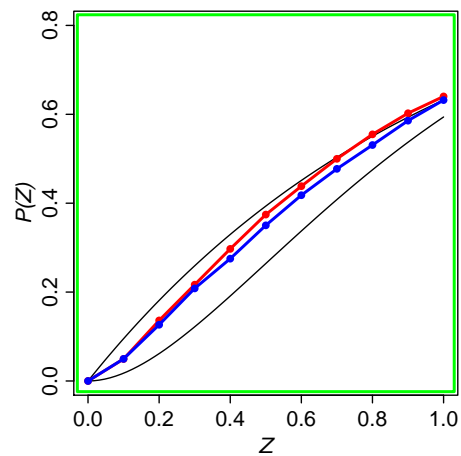
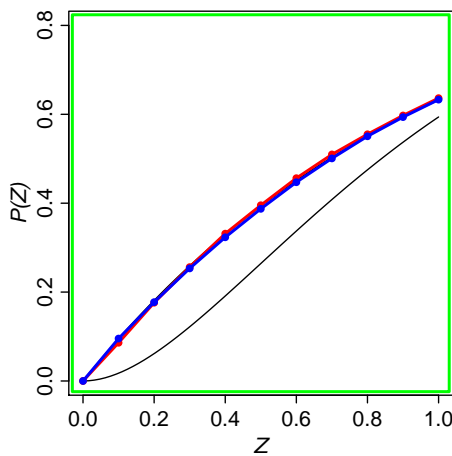
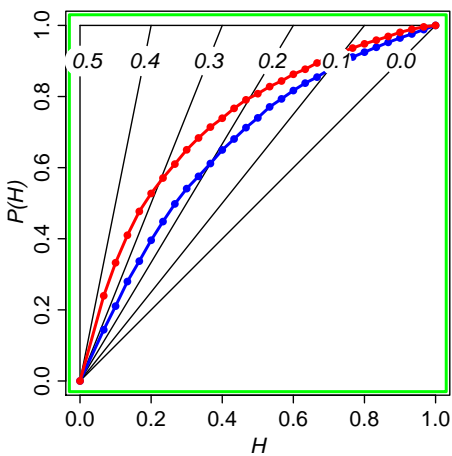
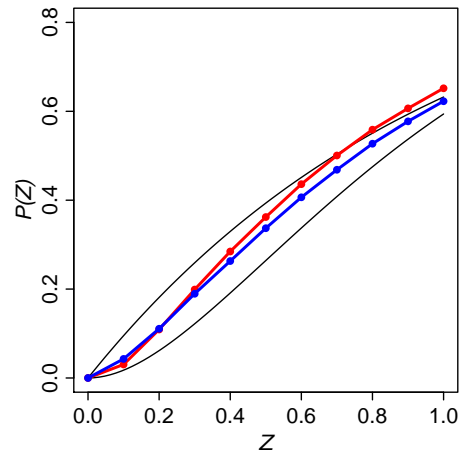
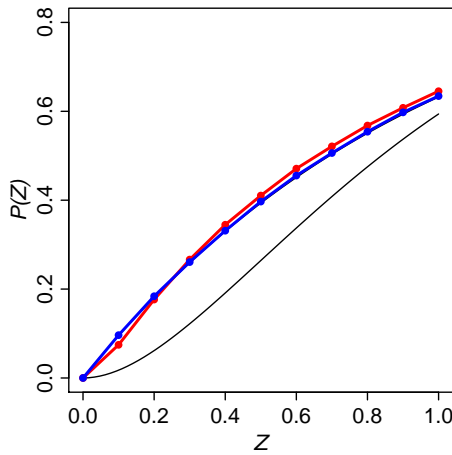
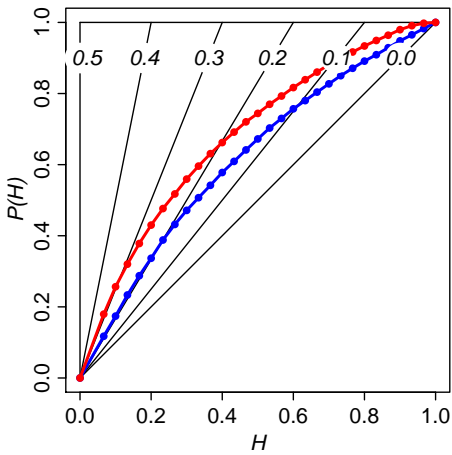
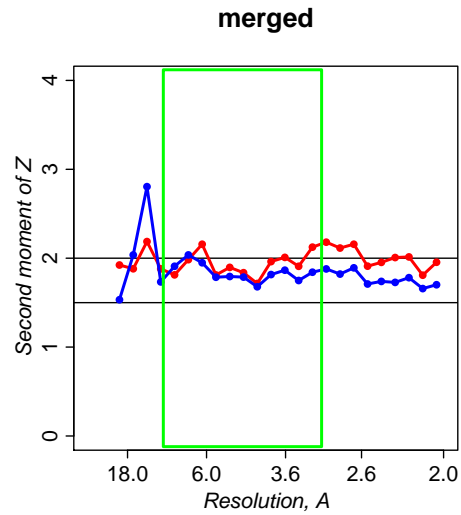
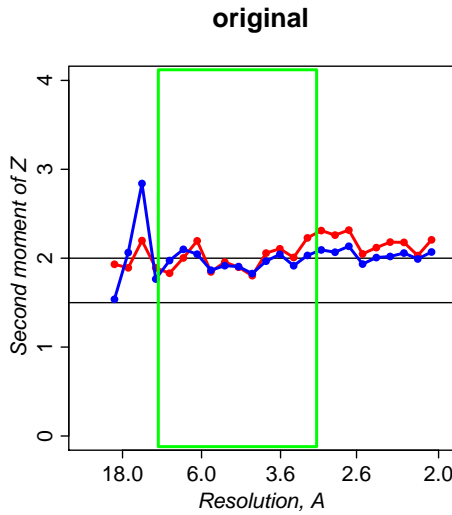
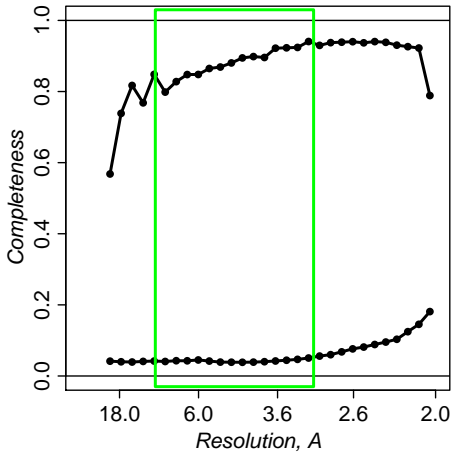
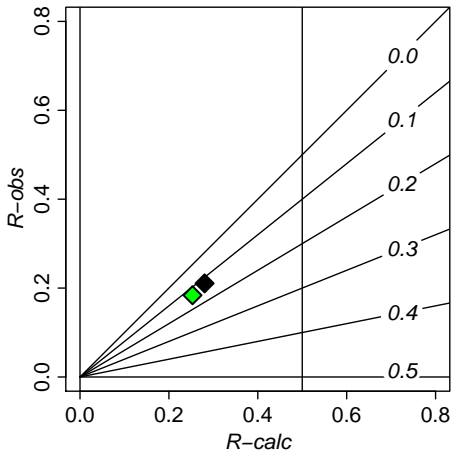
1ly9

	original	merged
s.g.	P 1 21 1	P 21 21 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.71
R	24.1	
R'	24.3	26.3
R-free	27.6	
R'-free	27.7	30.3
residues per monomer	DNA 0	protein 336

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.0–2.0	9.9–3.0
unique	44,166	12,832
measured	40,191	11,561
used	33,906	9,678

NCS	translation	rotation
r.m.s.d. (A)	35.40	0.38
angle (o)	179.61	1.13



1lyc

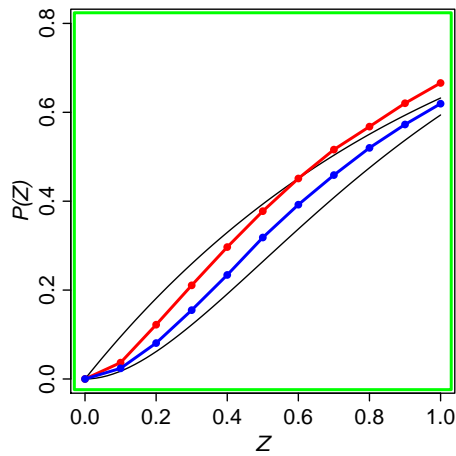
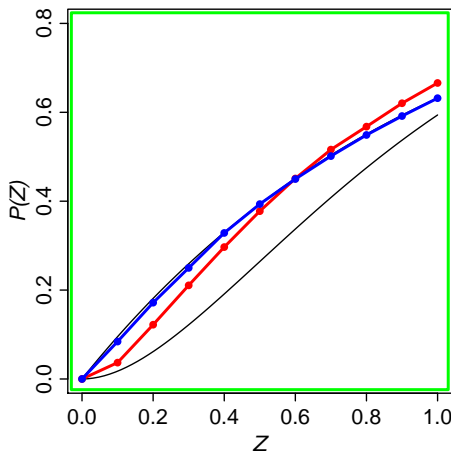
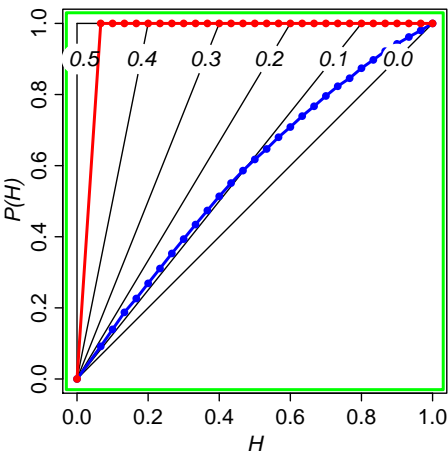
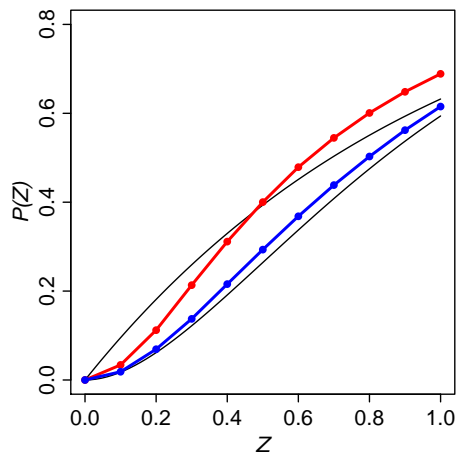
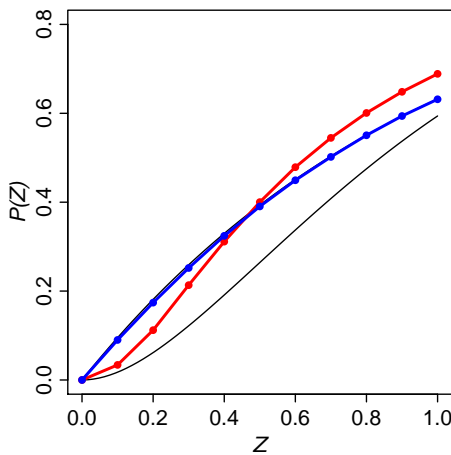
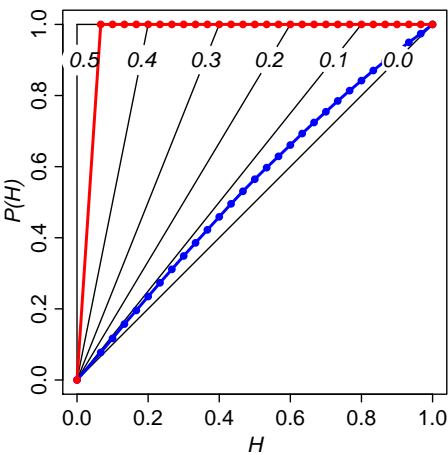
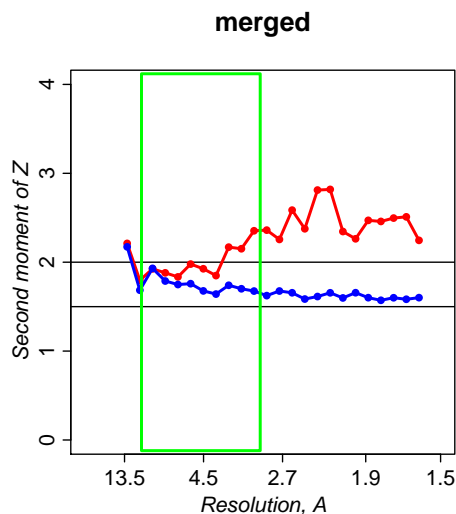
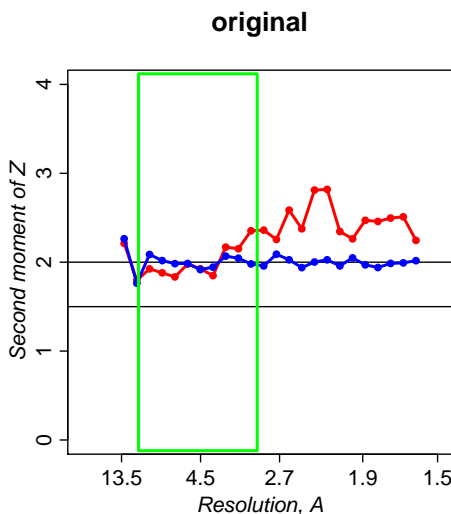
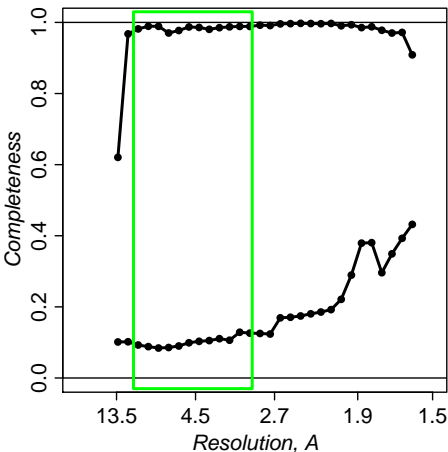
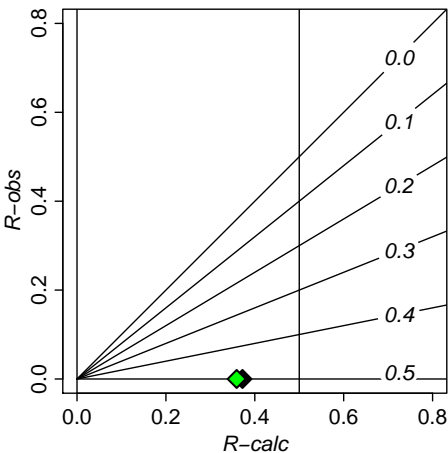
	original	merged
s.g.	P 1 21 1	P 21 21 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		1.04
R	31.9	
R'	31.7	32.1
R-free	34.8	
R'-free	35.3	35.8

residues per monomer	DNA	protein
	0	336

s < f/100	818	0.92 %
s <= 0	818	0.92 %
f <= 0	818	0.92 %
s,f <= 0	818	0.92 %

range (A)	14.9–1.6	9.9–3.0
unique	90,315	12,638
measured	88,500	12,452
used	83,064	11,134

NCS	translation	rotation
r.m.s.d. (A)	35.12	0.25
angle (o)	179.51	0.93



1lyq

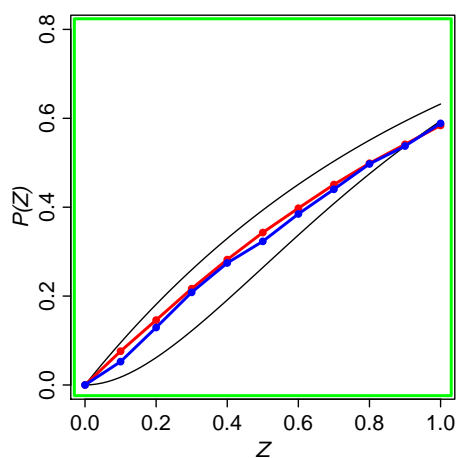
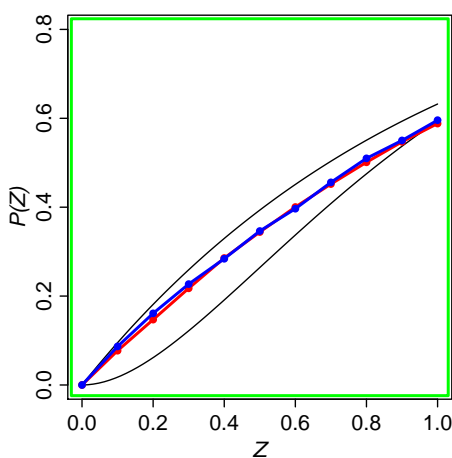
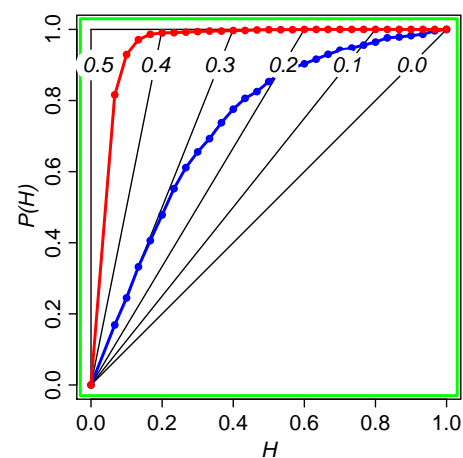
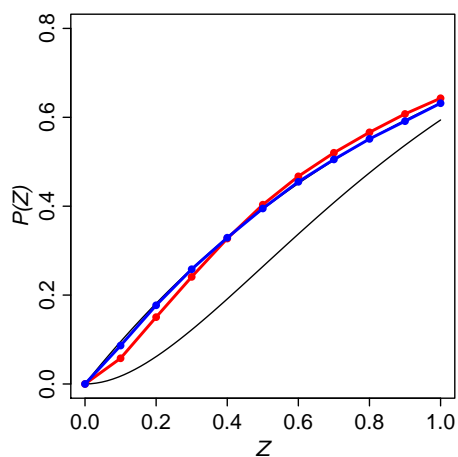
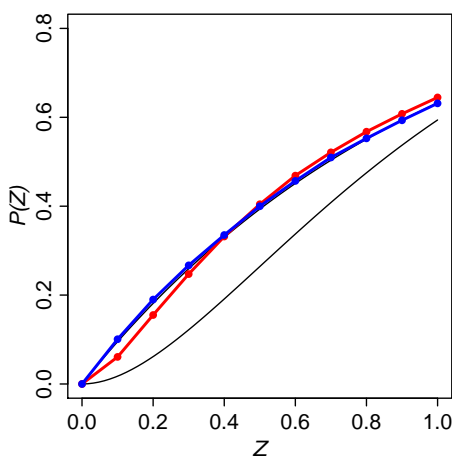
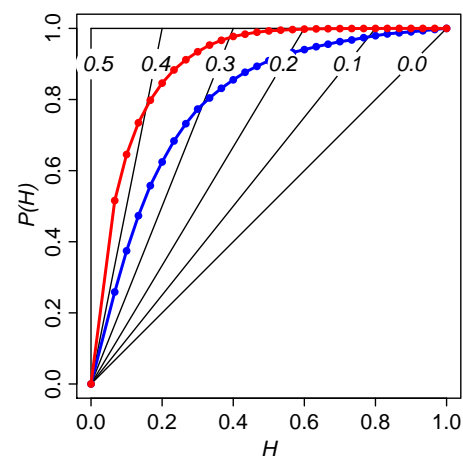
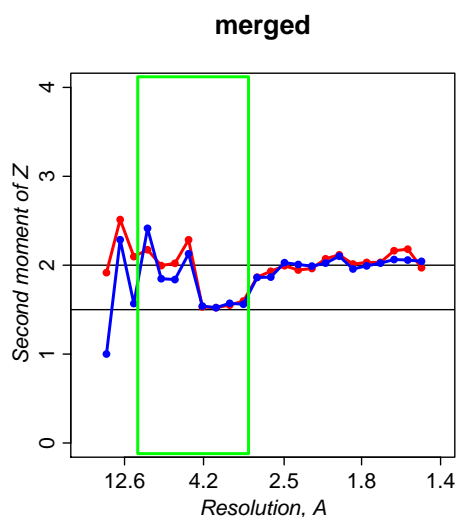
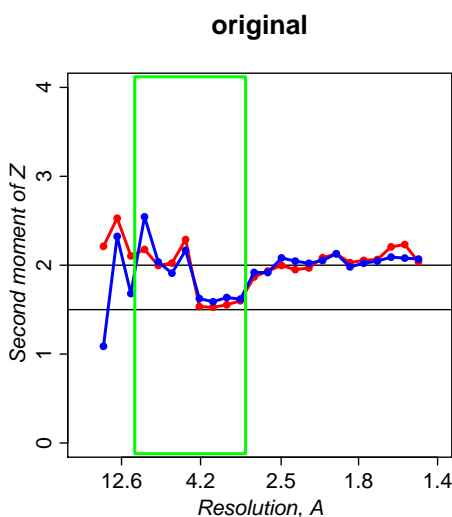
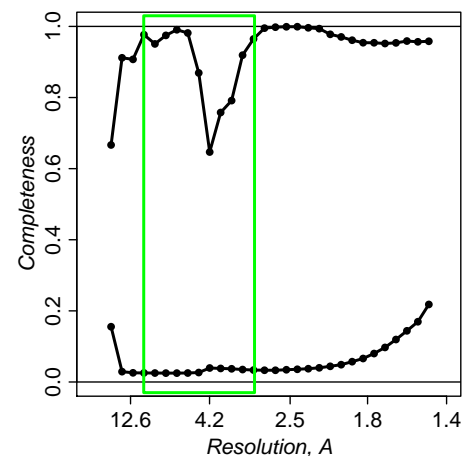
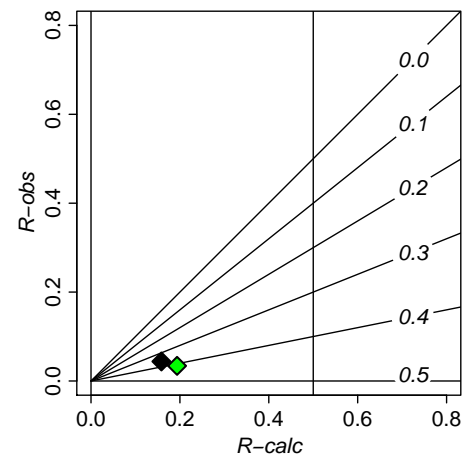
	original	merged
s.g.	P 41	P 41 21 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.16
R	32.3	
R'	32.5	32.8
R-free	33.6	
R'-free	33.1	33.5

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	34.1–1.4	9.9–3.0
unique	33,933	3,822
measured	32,436	3,313
used	28,718	2,616

NCS	translation	rotation
r.m.s.d. (A)	22.79	0.16
angle (o)	179.87	0.13

residues per monomer	DNA	protein
	0	101



1lzq

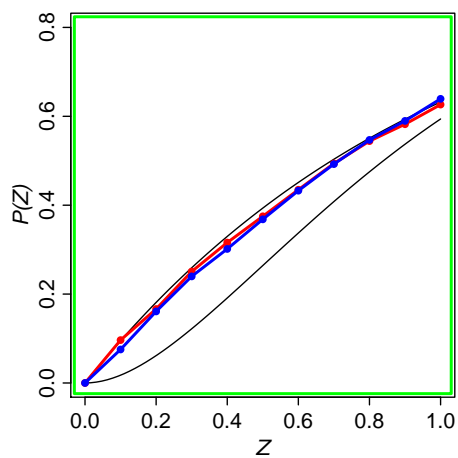
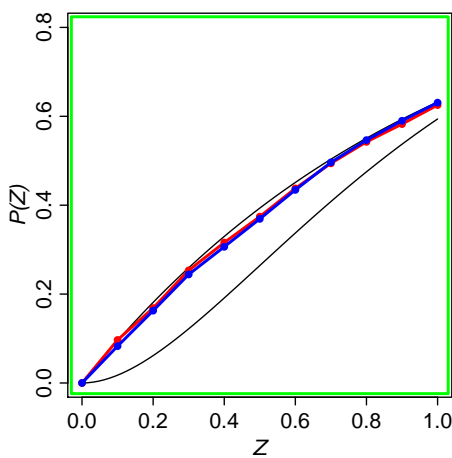
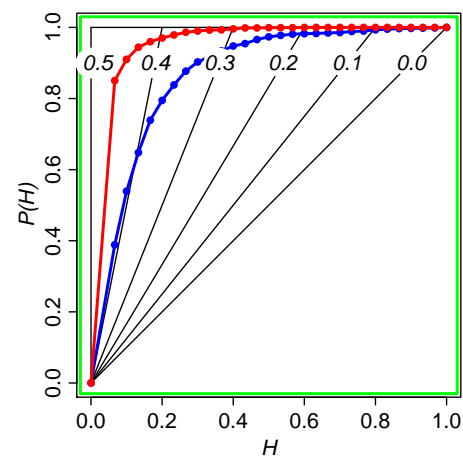
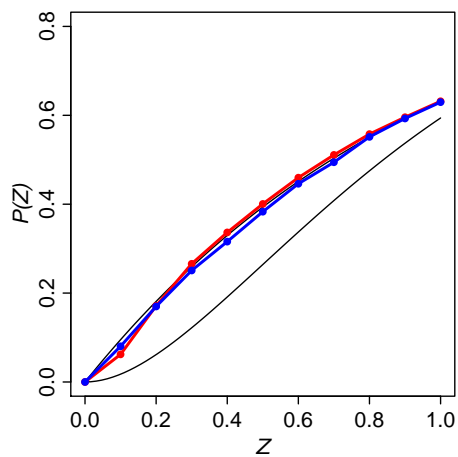
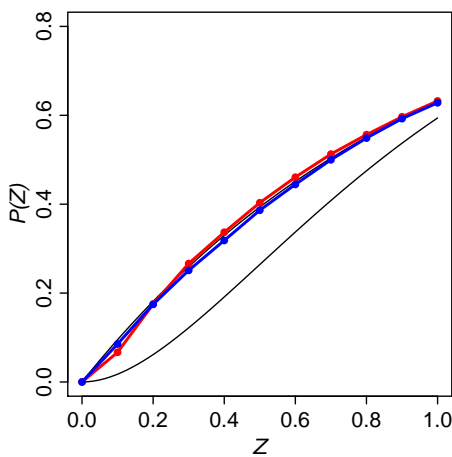
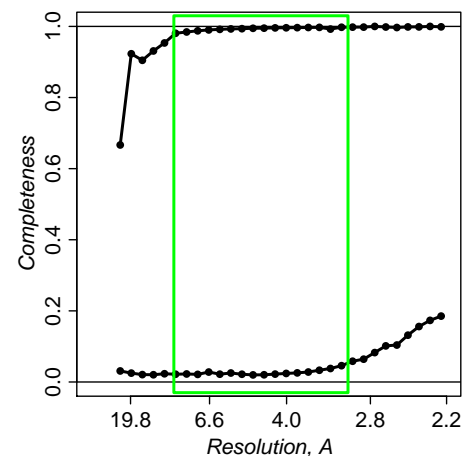
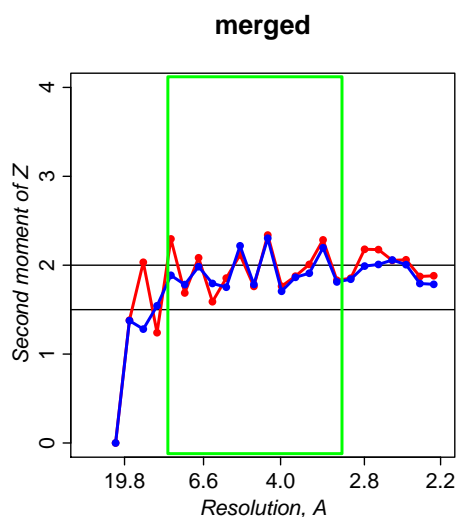
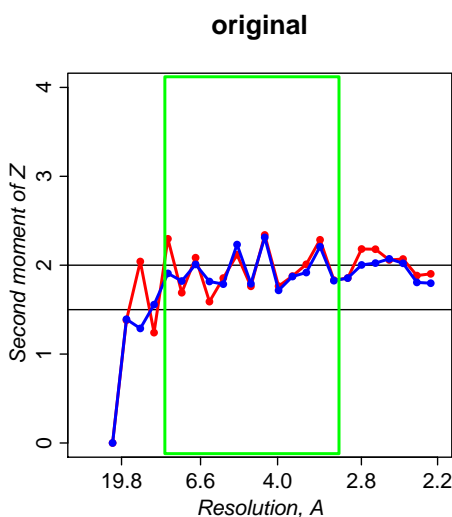
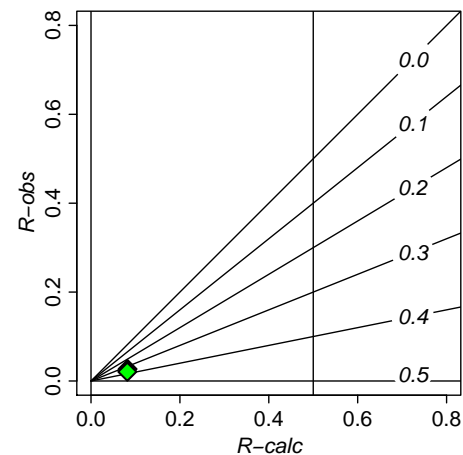
	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.13
R	26.3	
R'	26.7	29.8
R-free	29.8	
R'-free	29.2	29.3

s < f/100	5	0.05 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	33.0–2.2	9.9–3.0
unique	9,523	3,664
measured	9,490	3,646
used	8,018	2,928

NCS	translation	rotation
r.m.s.d. (A)	21.96	0.13
angle (o)	179.76	0.26

residues per monomer	DNA	protein
	0	99



1m0b

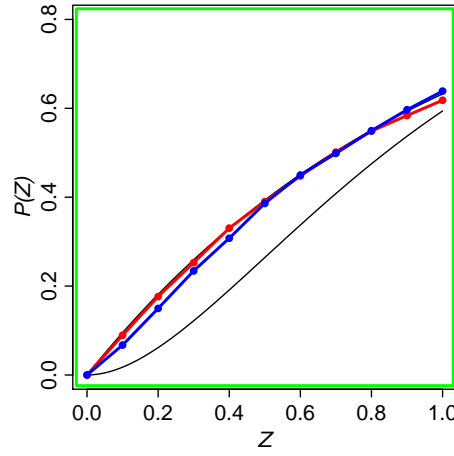
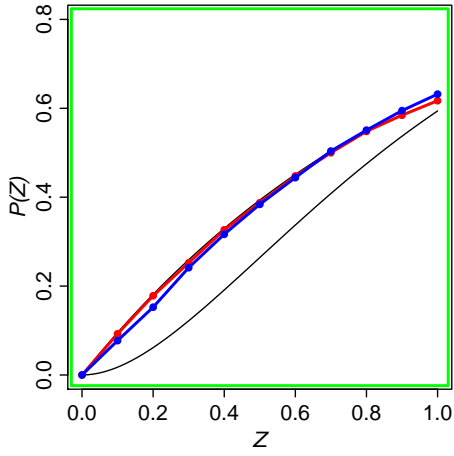
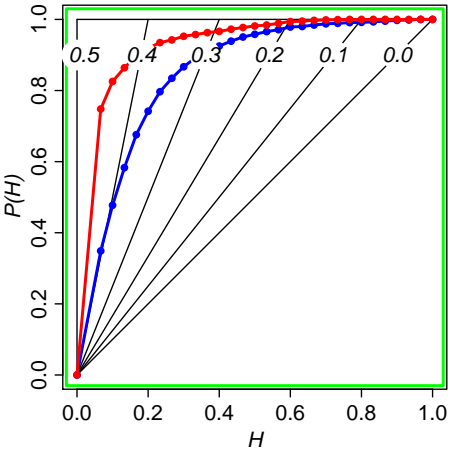
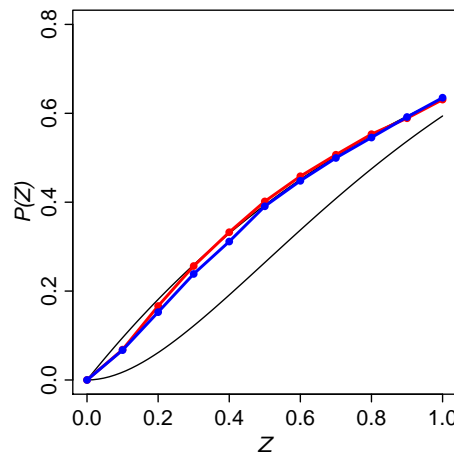
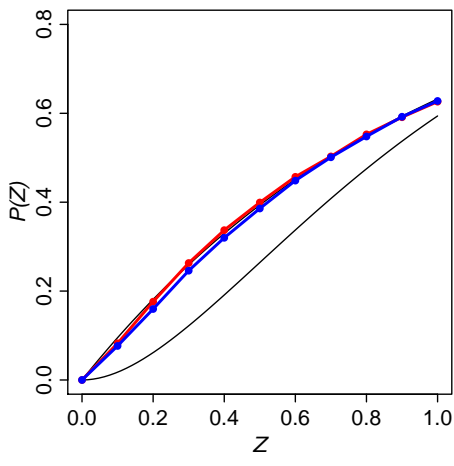
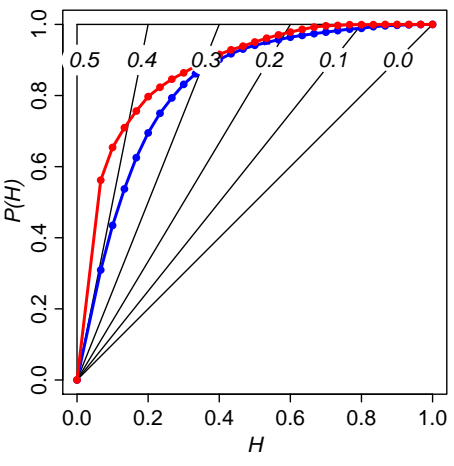
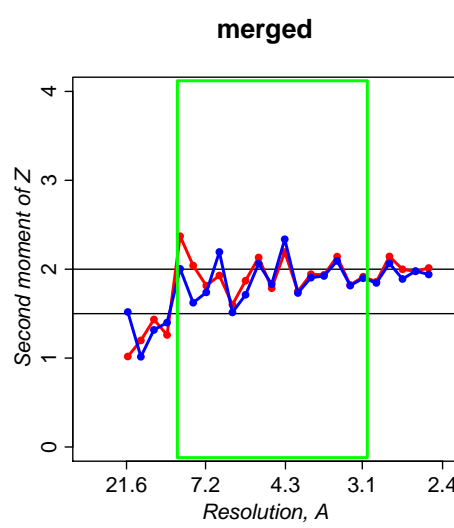
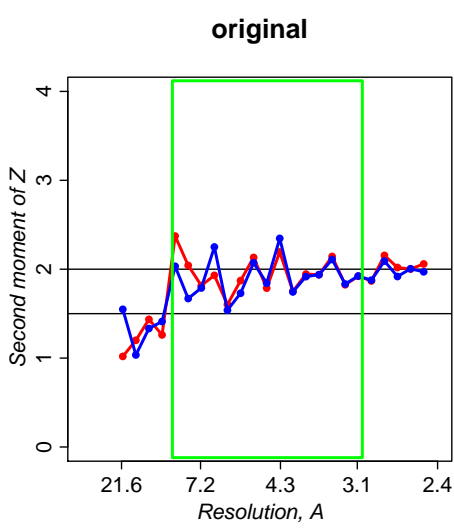
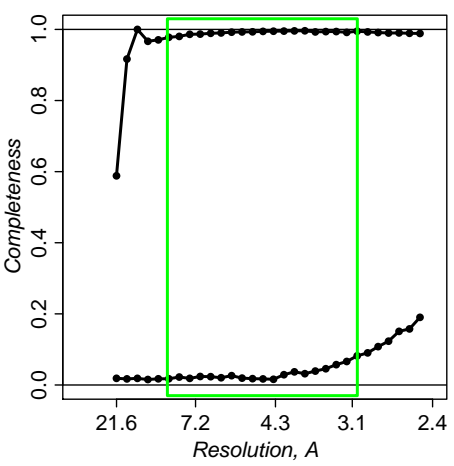
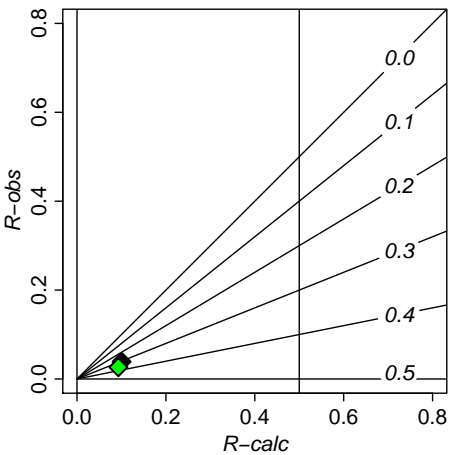
	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.07
R	25.1	
R'	25.2	26.0
R-free	29.3	
R'-free	29.6	30.8

residues per monomer	DNA	protein
	0	99

s < f/100	10	0.15 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	24.9–2.5	9.9–3.0
unique	6,824	3,625
measured	6,765	3,600
used	5,624	2,896

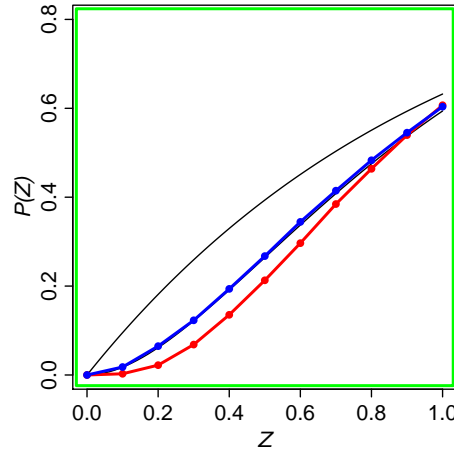
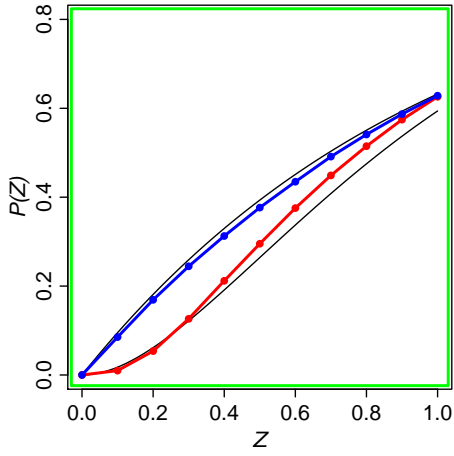
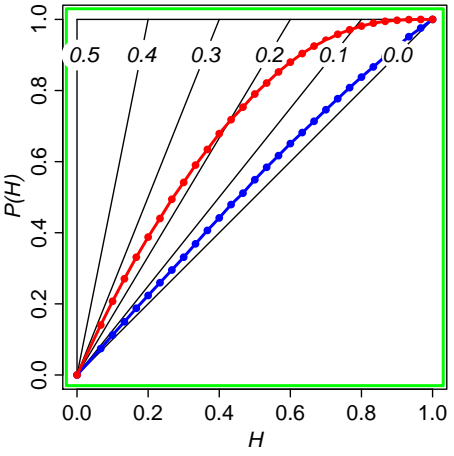
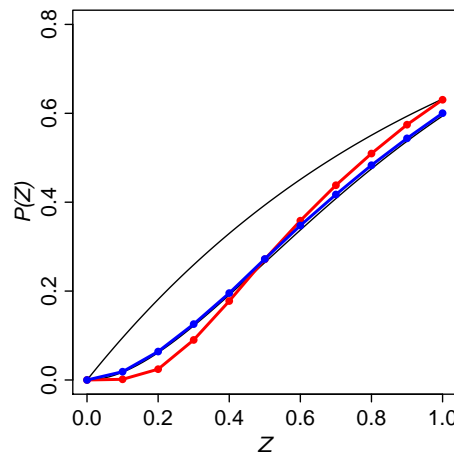
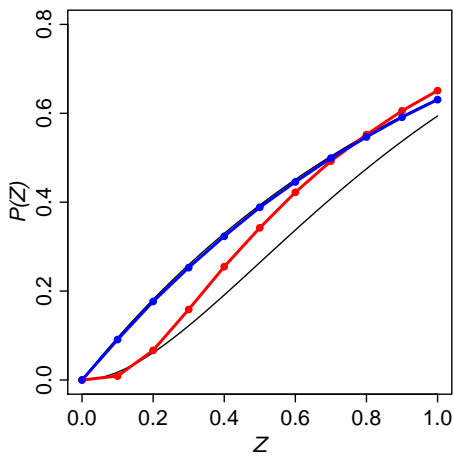
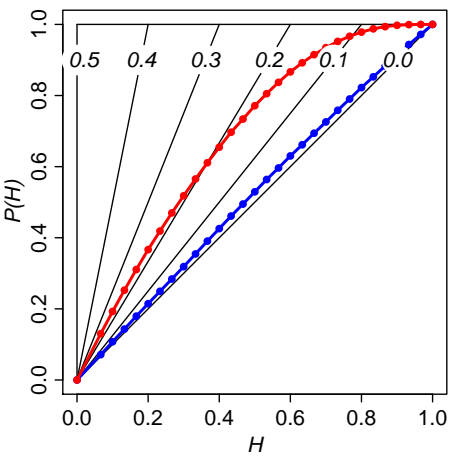
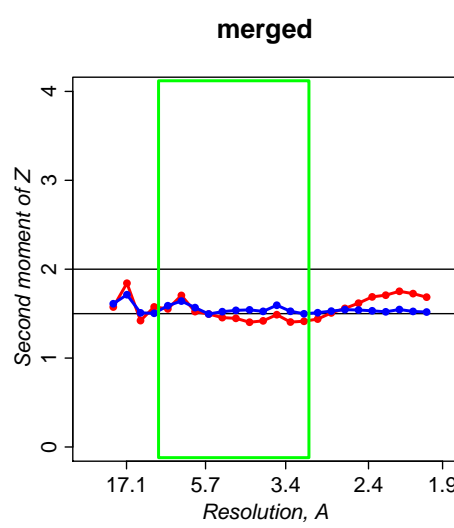
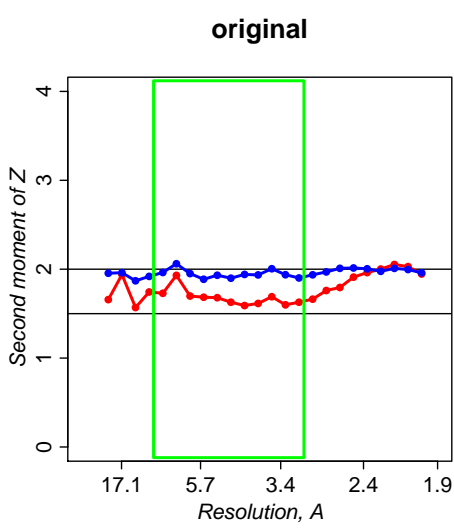
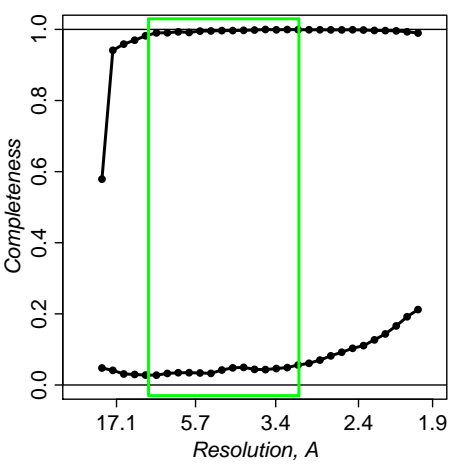
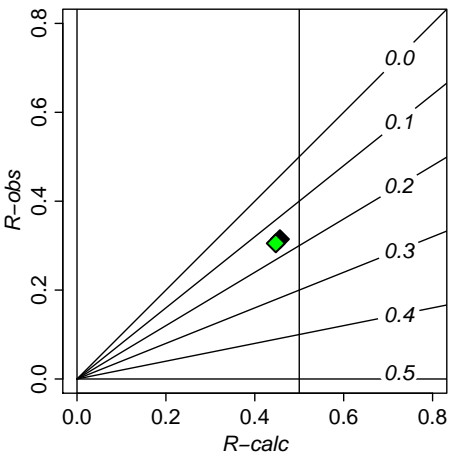
NCS	translation	rotation
r.m.s.d. (A)	20.67	0.07
angle (o)	179.88	0.16



1m1o

	original	merged
s.g.	P 1 21 1	P 21 21 2
p.g.	10001	10003
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		7.51
R	27.7	
R'	-	-
R-free	29.2	
R'-free	-	-
residues per monomer	DNA 0	protein 390

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	34.7-1.9	9.9-3.0
unique	142,162	38,274
measured	141,630	38,173
used	128,896	35,848
NCS	translation	rotation
r.m.s.d. (A)	16.56	1.08
angle (o)	63.69	3.18



1m1t

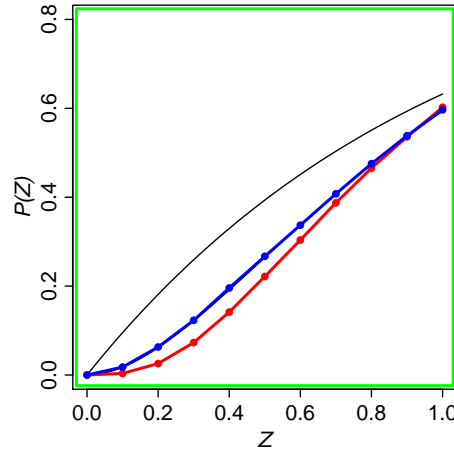
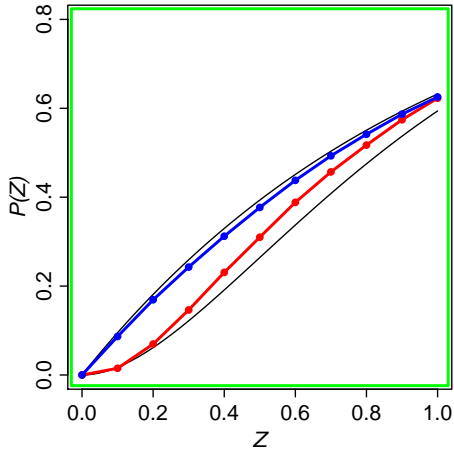
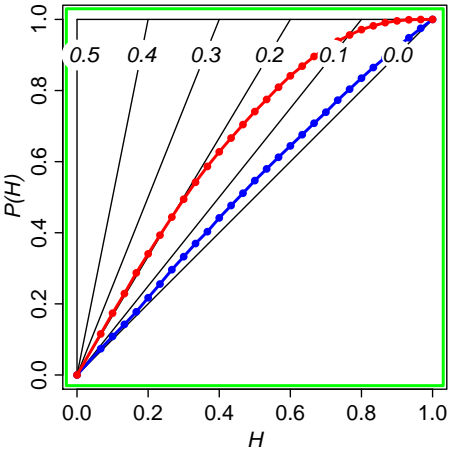
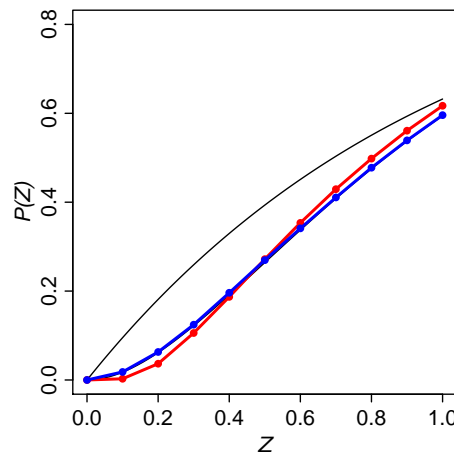
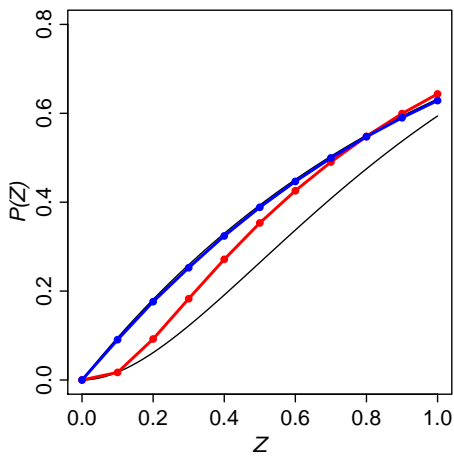
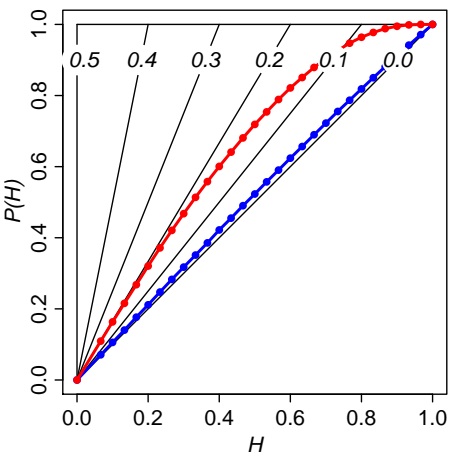
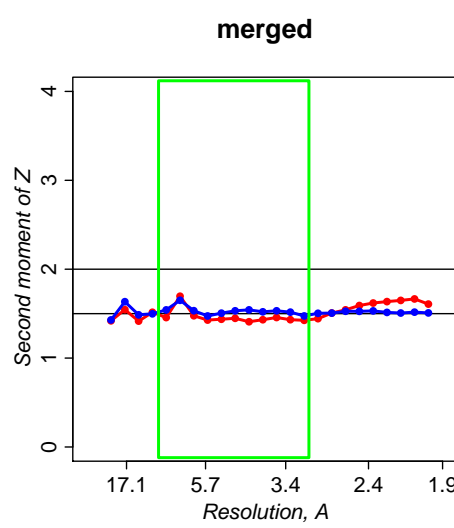
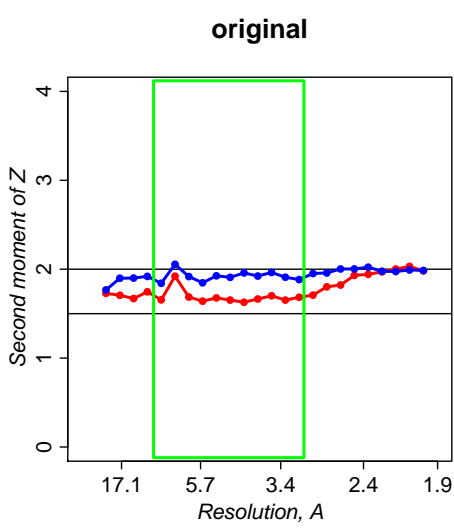
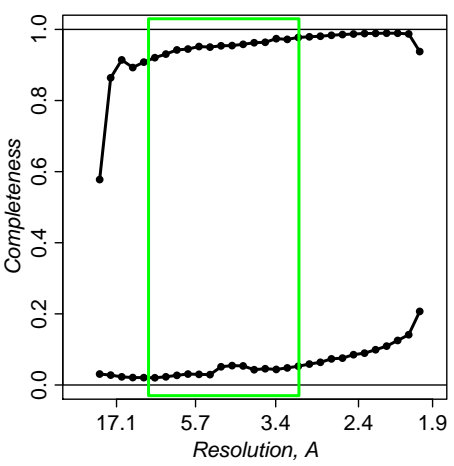
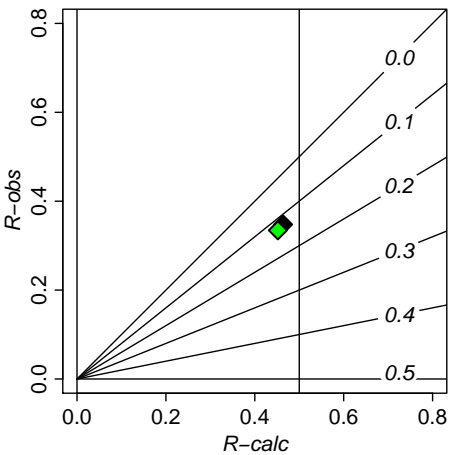
	original	merged
s.g.	P 1 21 1	P 21 21 2
p.g.	10001	10003
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		7.77
R	27.3	
R'	-	-
R-free	29.6	
R'-free	-	-

residues per monomer	DNA	protein
	0	392

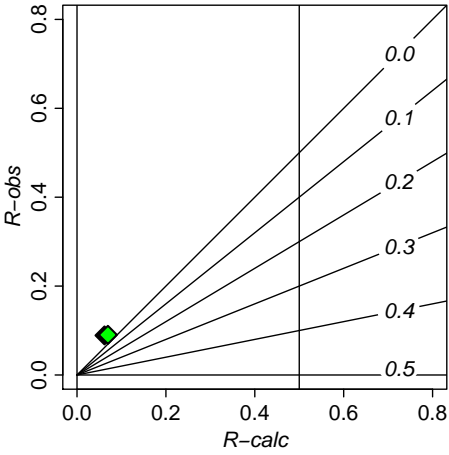
s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	39.5-1.9	9.9-3.0
unique	144,368	38,264
measured	140,702	36,776
used	128,072	34,762

NCS	translation	rotation
r.m.s.d. (A)	16.48	1.19
angle (o)	63.82	3.46



1m21

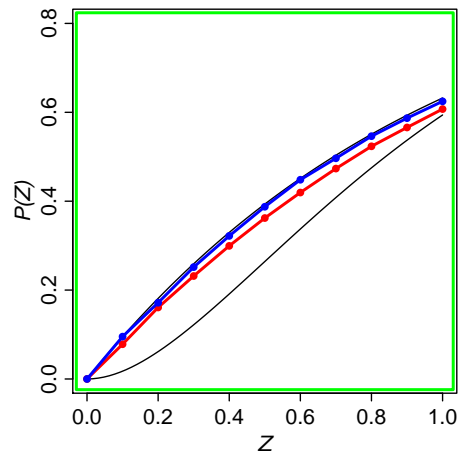
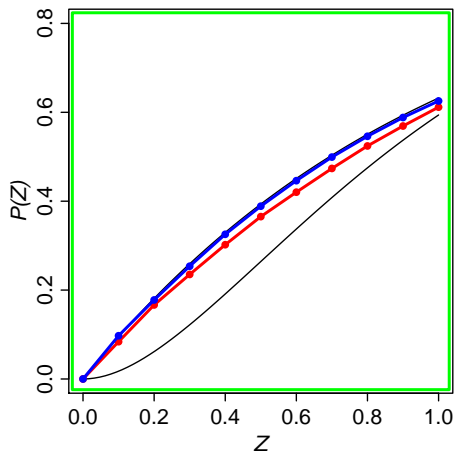
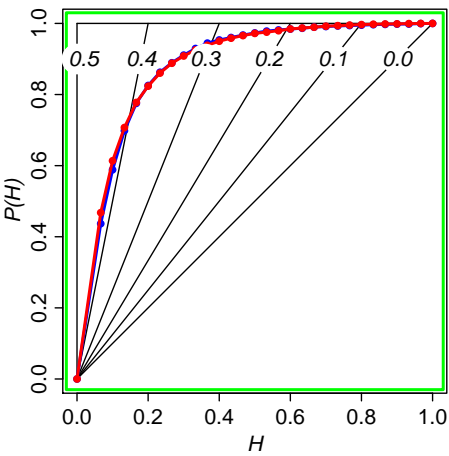
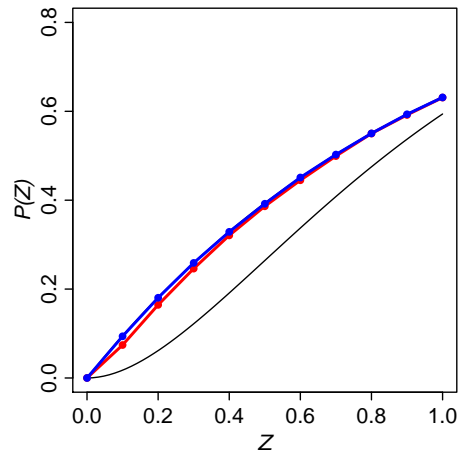
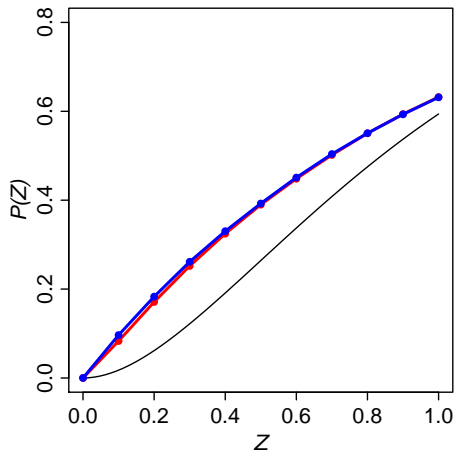
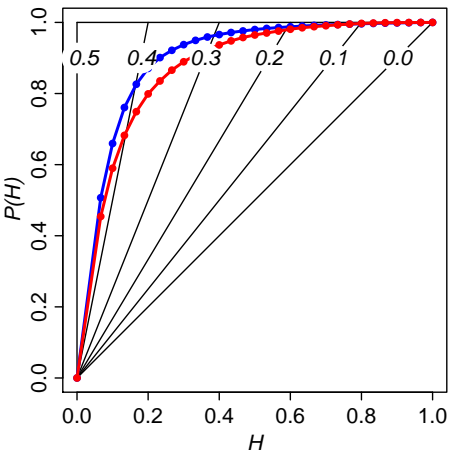
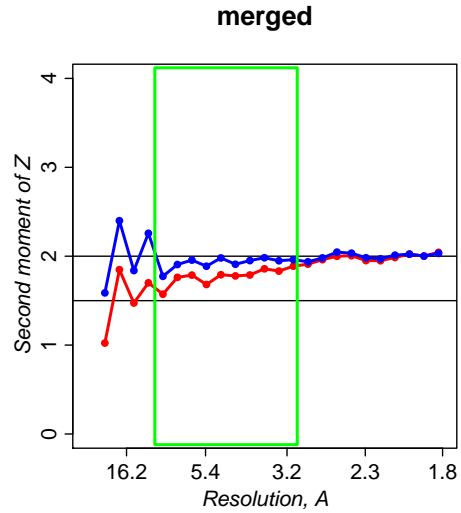
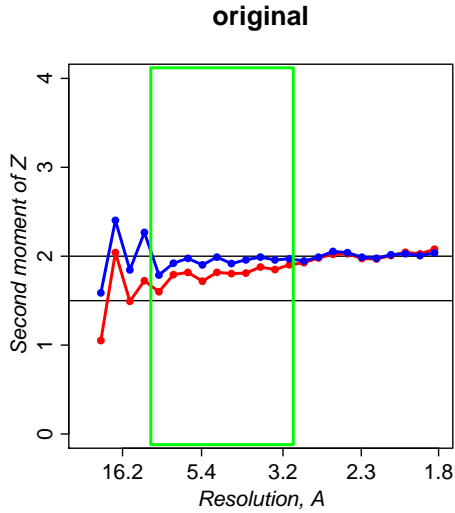
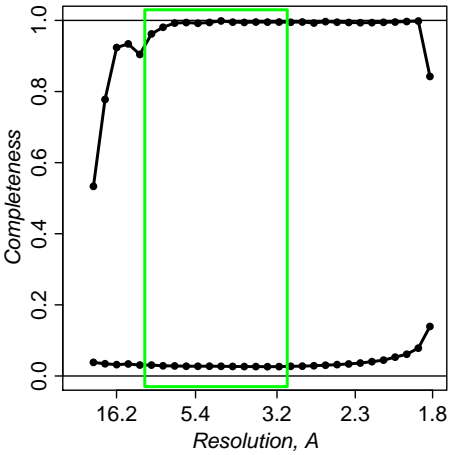


	original	merged
s.g.	P 1 21 1	P 21 21 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.02
R	24.1	
R'	24.1	23.8
R-free	26.5	
R'-free	26.5	26.2
residues per monomer	DNA 0	protein 487

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	60.3–1.8	9.9–3.0
unique	89,972	18,628
measured	88,172	18,506
used	81,548	16,480

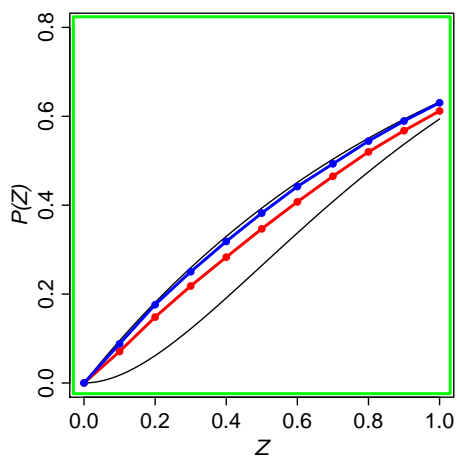
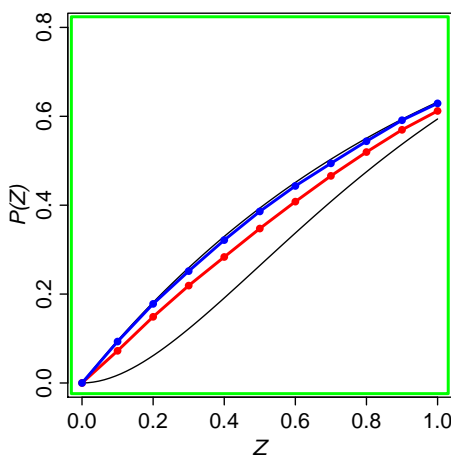
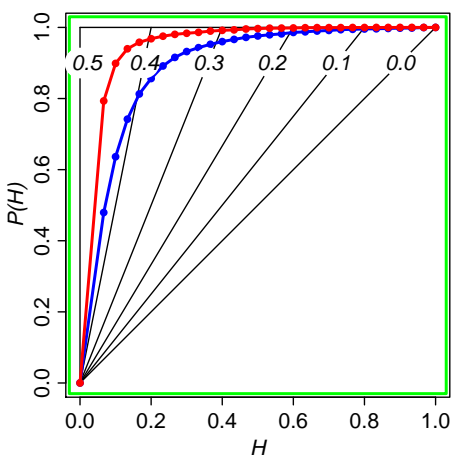
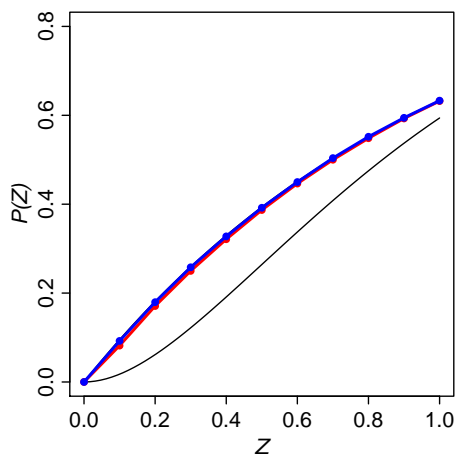
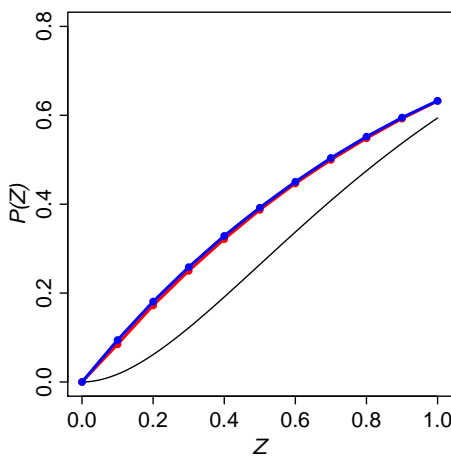
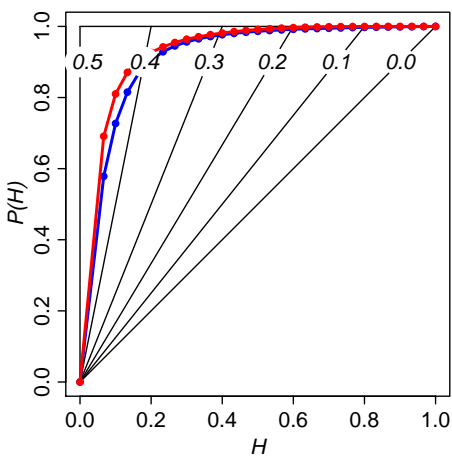
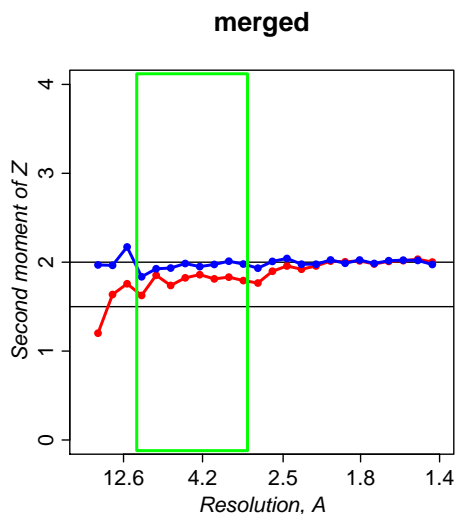
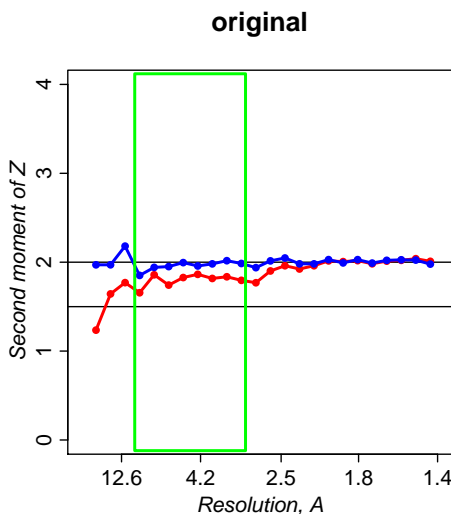
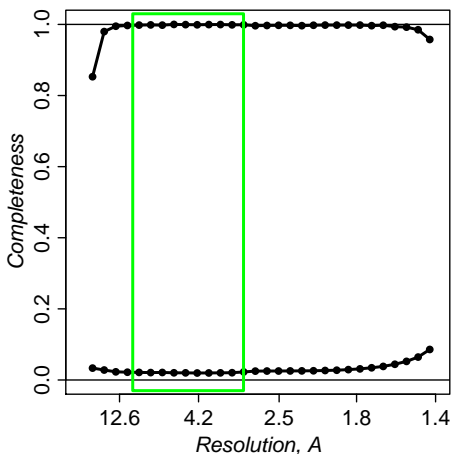
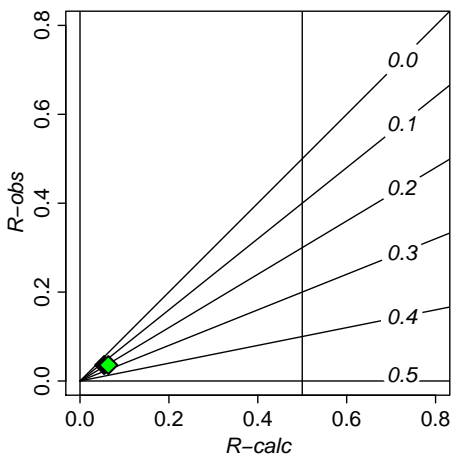
NCS	translation	rotation
r.m.s.d. (A)	32.52	0.02
angle (o)	179.97	0.03



1m22

	original	merged
s.g.	P 1 21 1	P 21 21 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.02
R	25.7	
R'	25.6	25.9
R-free	26.8	
R'-free	26.8	27.1
residues per monomer	DNA 0	protein 487

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	74.2–1.4	9.9–3.0
unique	183,627	18,434
measured	182,174	18,420
used	171,264	16,392
NCS	translation	rotation
r.m.s.d. (A)	32.63	0.02
angle (o)	179.97	0.03



1m3k

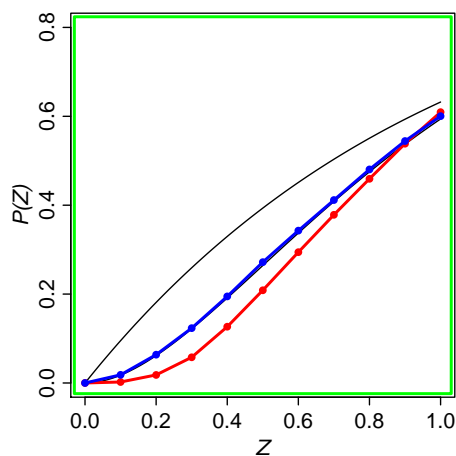
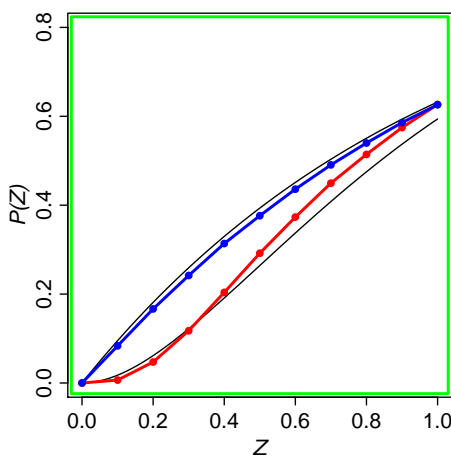
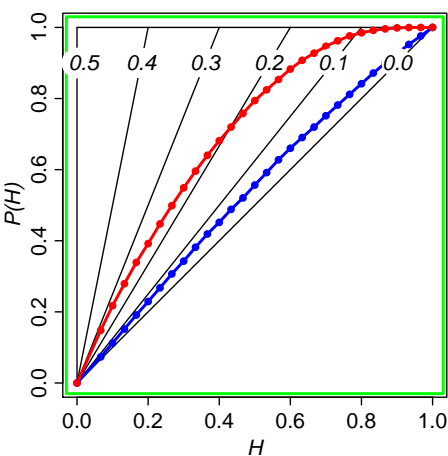
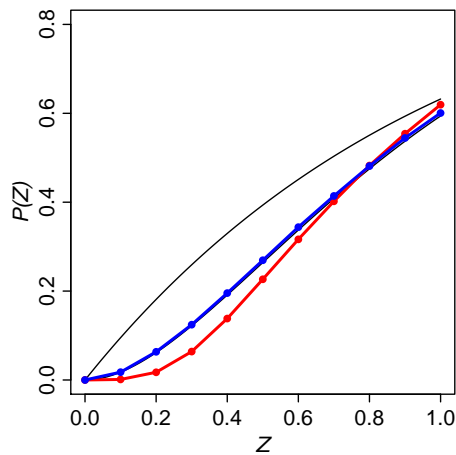
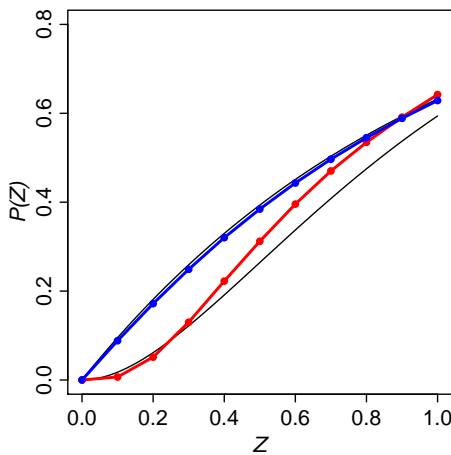
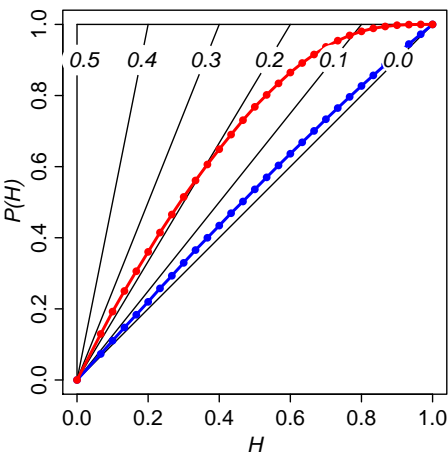
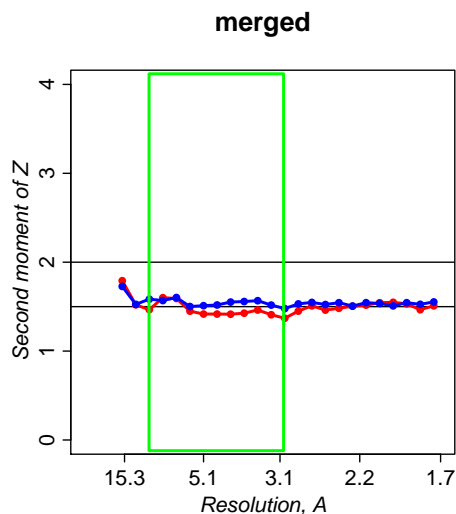
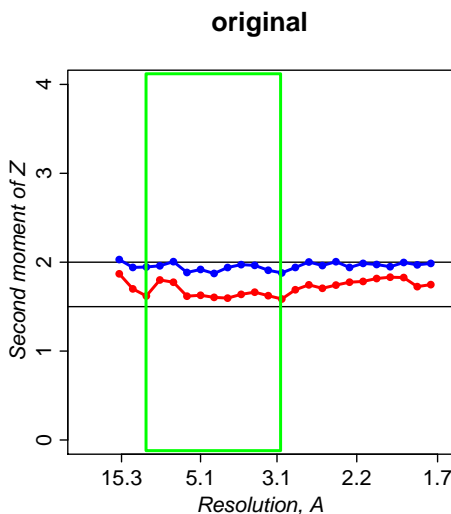
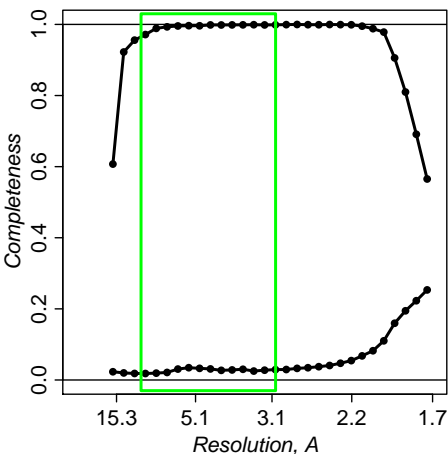
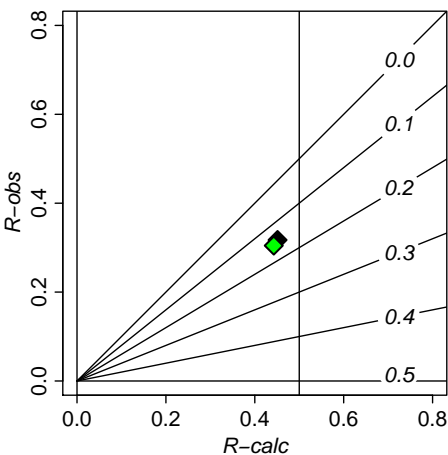
	original	merged
s.g.	P 1 21 1	P 21 21 2
p.g.	10001	10003
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		7.34
R	27.5	
R'	-	-
R-free	29.0	
R'-free	-	-

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.8-1.7	9.9-3.0
unique	211,673	38,479
measured	193,695	38,374
used	174,904	35,884

NCS	translation	rotation
r.m.s.d. (A)	16.48	1.06
angle (o)	63.29	3.11

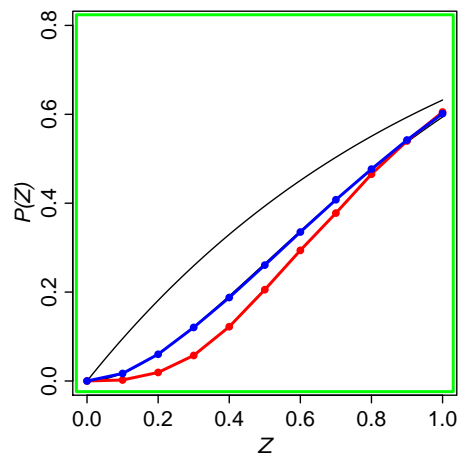
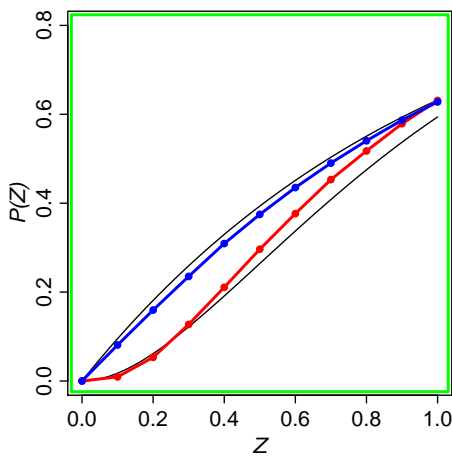
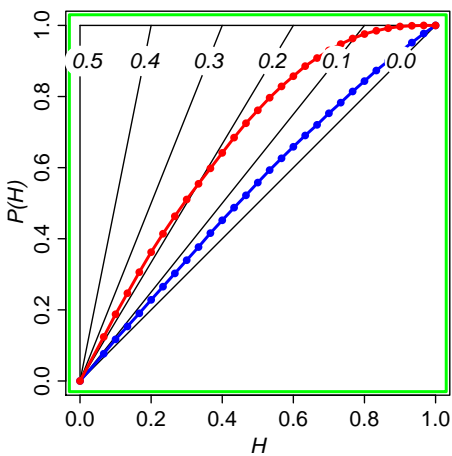
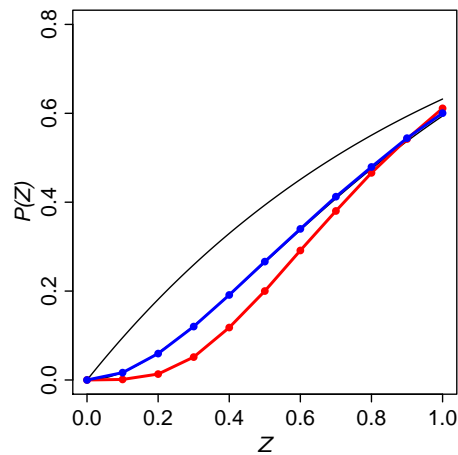
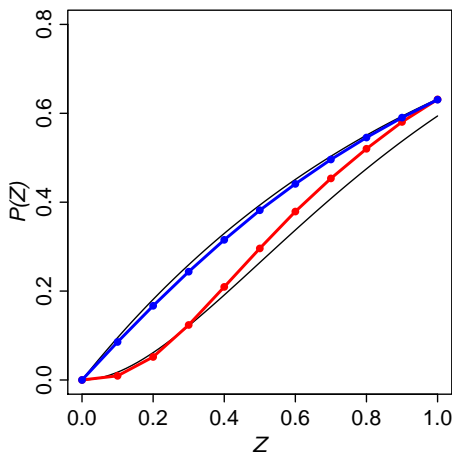
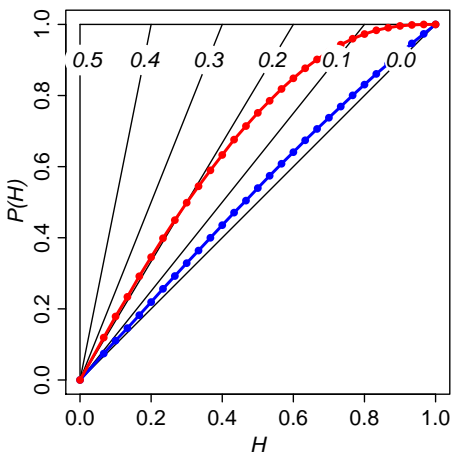
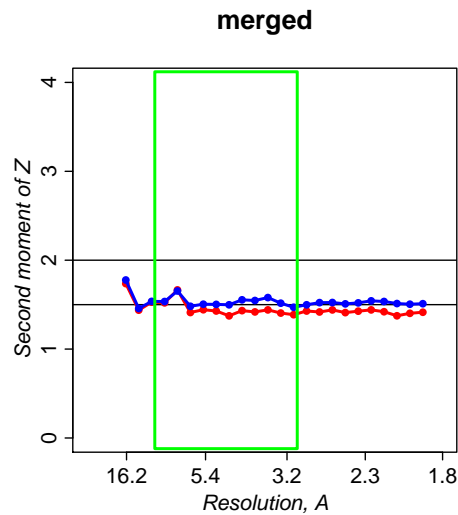
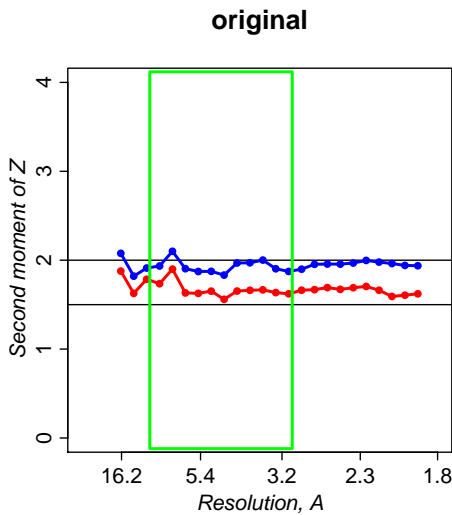
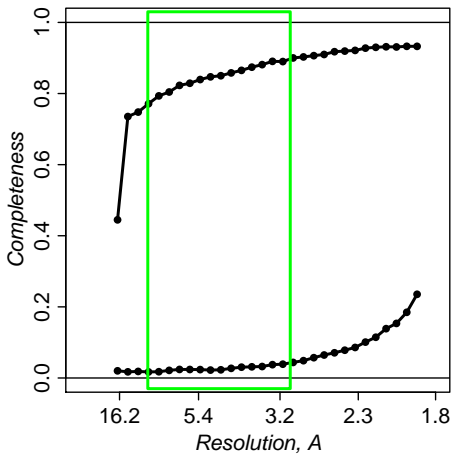
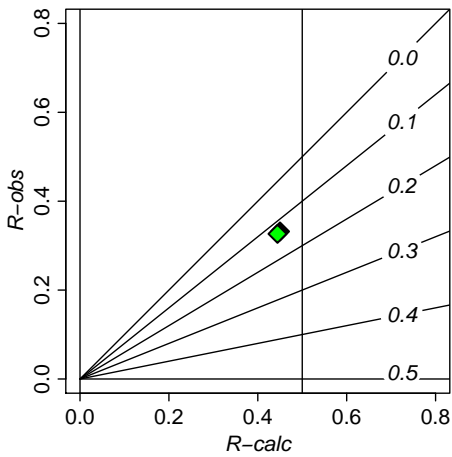
residues per monomer	DNA	protein
	0	392



1m3z

	original	merged
s.g.	P 1 21 1	P 21 21 2
p.g.	10001	10003
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		7.35
R	25.5	
R'	-	-
R-free	27.5	
R'-free	-	-
residues per monomer	DNA 0	protein 390

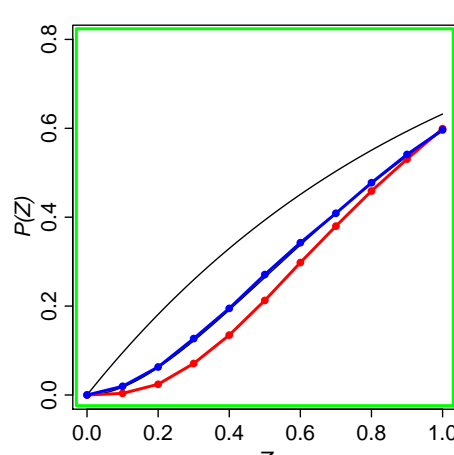
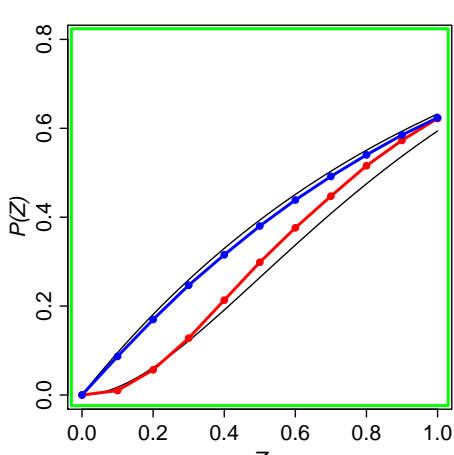
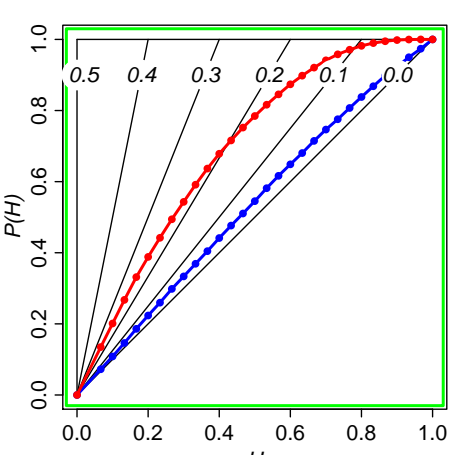
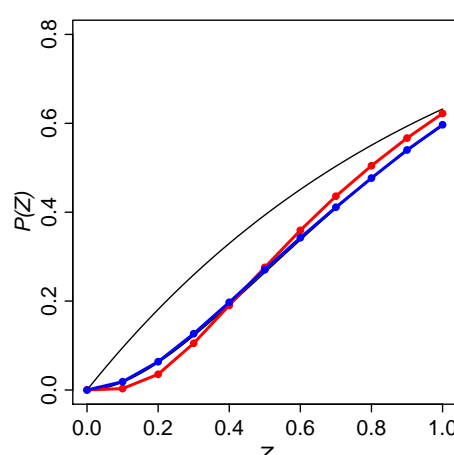
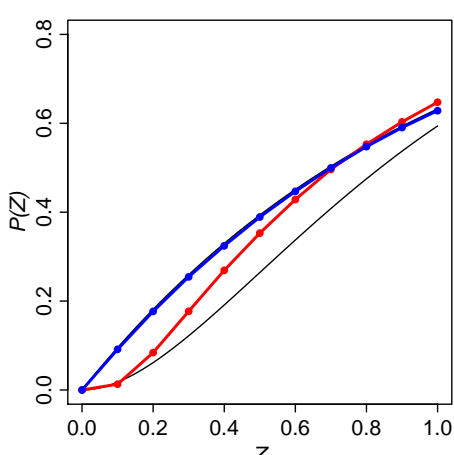
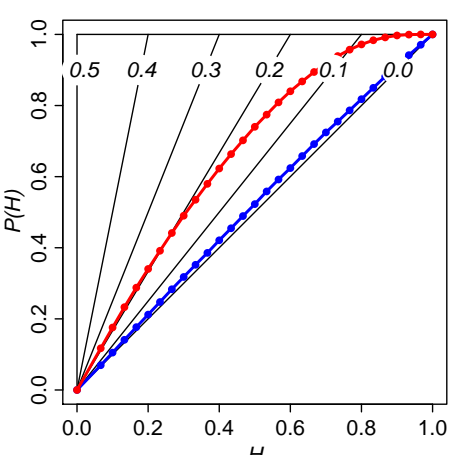
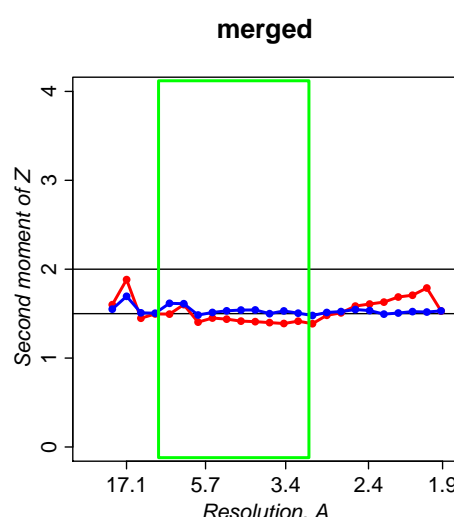
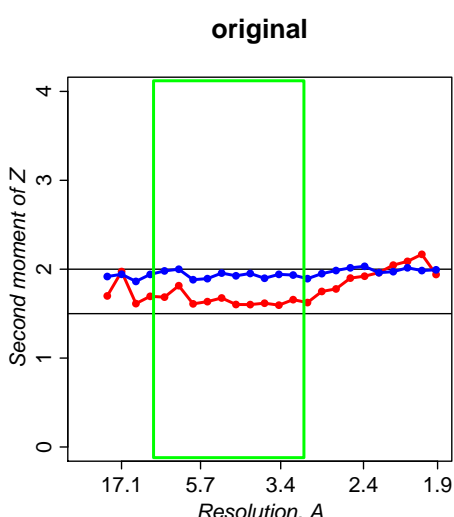
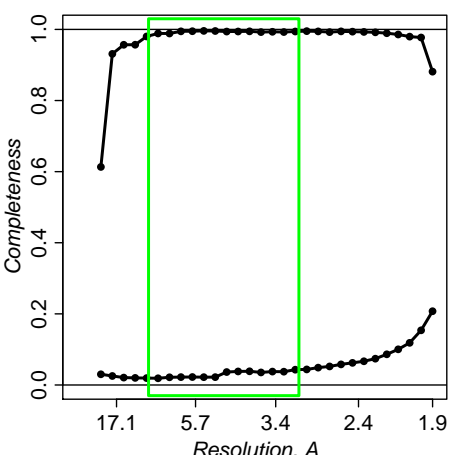
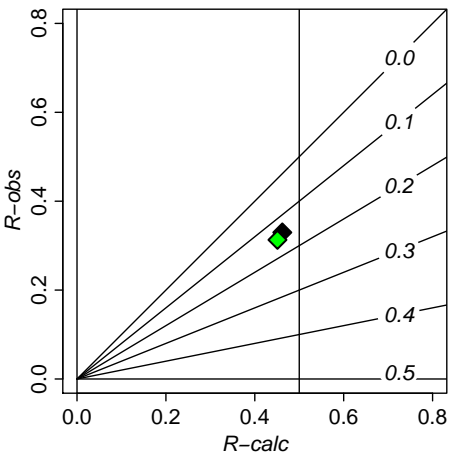
s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	19.8–1.9	9.9–3.0
unique	163,721	38,921
measured	148,800	33,689
used	131,222	31,556
NCS	translation	rotation
r.m.s.d. (A)	16.65	1.27
angle (o)	63.56	3.75



1m4s

	original	merged
s.g.	P 1 21 1	P 21 21 2
p.g.	10001	10003
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		7.43
R	28.1	
R'	-	-
R-free	29.8	
R'-free	-	-
residues per monomer	DNA 0	protein 391

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	37.2-1.9	9.9-3.0
unique	161,726	38,445
measured	158,412	38,200
used	144,180	35,604
NCS	translation	rotation
r.m.s.d. (A)	16.51	1.05
angle (o)	63.48	3.09



1m4v

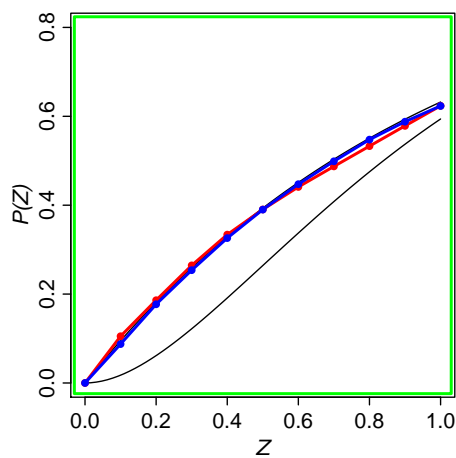
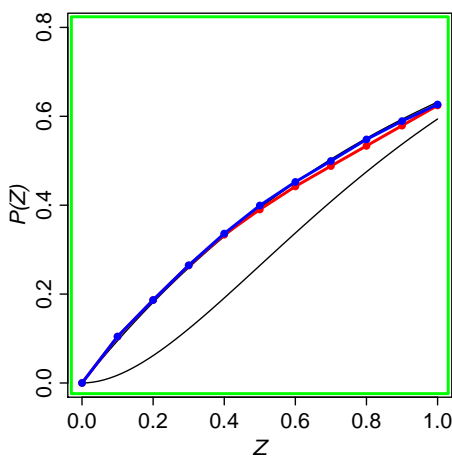
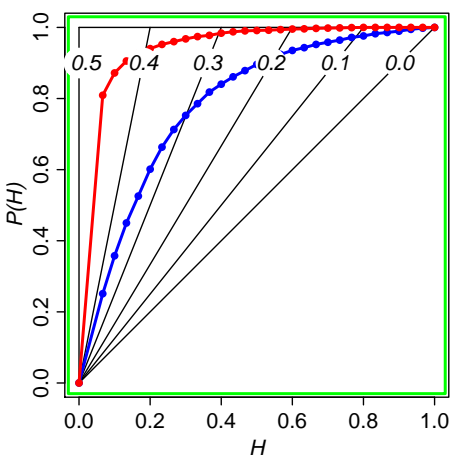
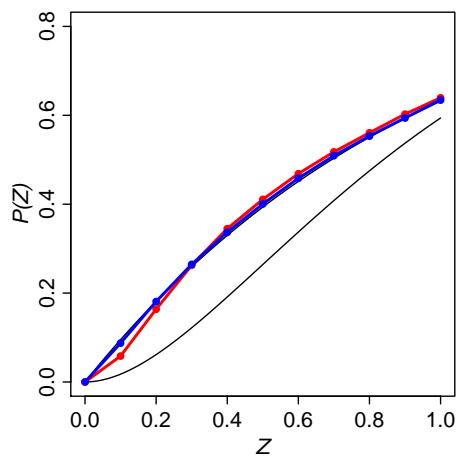
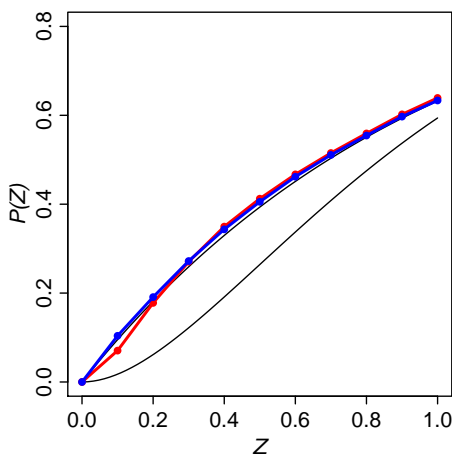
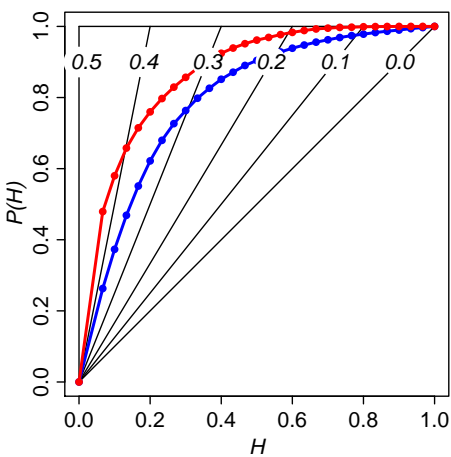
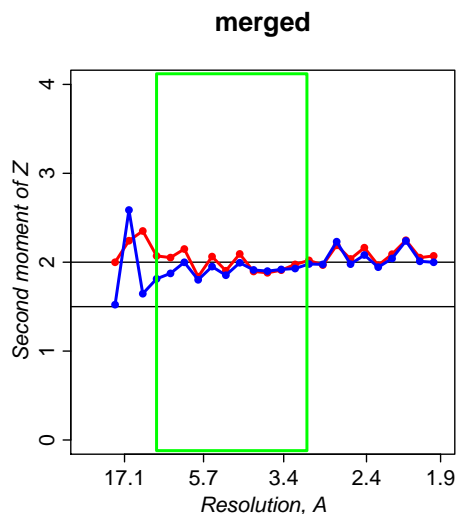
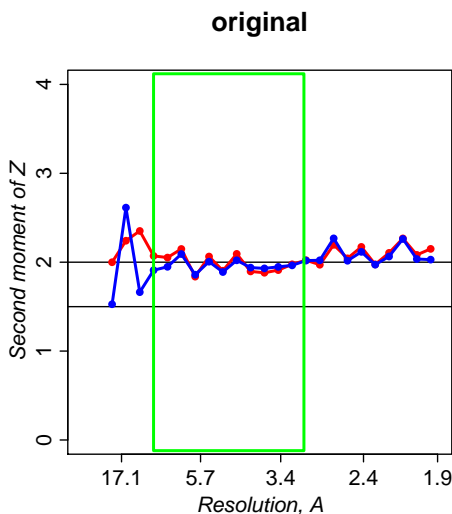
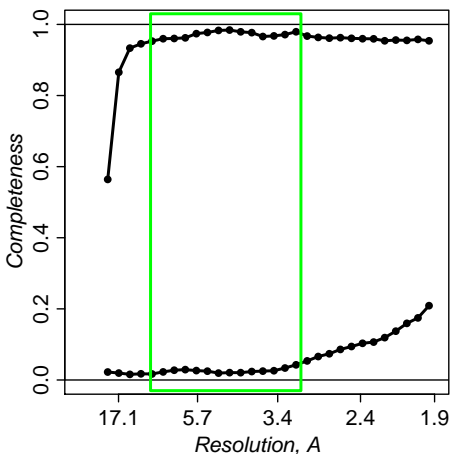
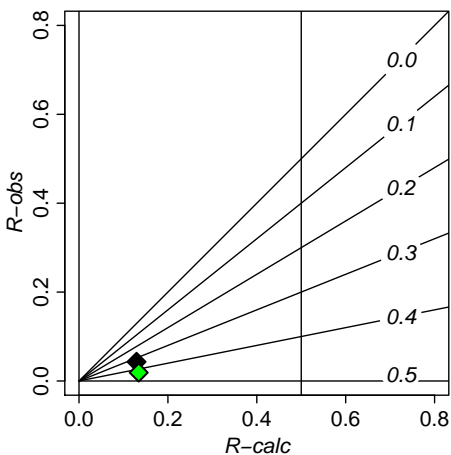
	original	merged
s.g.	P 63	P 63 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.12
R	25.8	
R'	26.0	26.6
R-free	27.4	
R'-free	27.4	28.1

s < f/100	891	2.50 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.2–1.9	9.9–3.0
unique	37,113	9,225
measured	35,694	8,977
used	31,092	7,412

NCS	translation	rotation
r.m.s.d. (A)	30.02	0.12
angle (o)	179.93	0.08

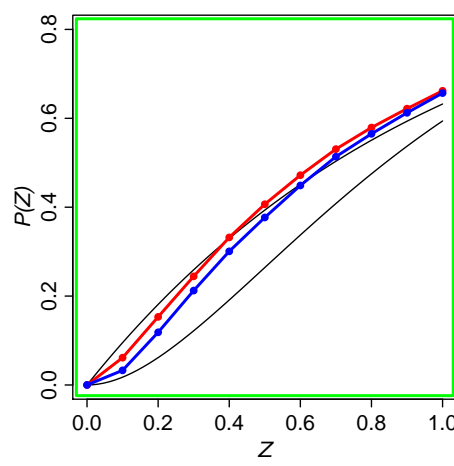
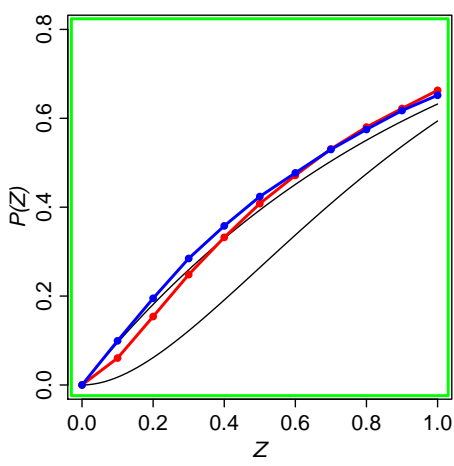
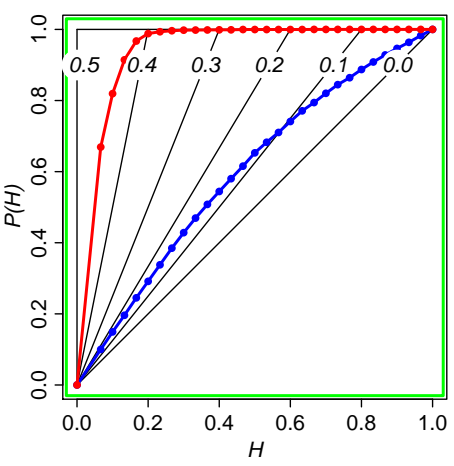
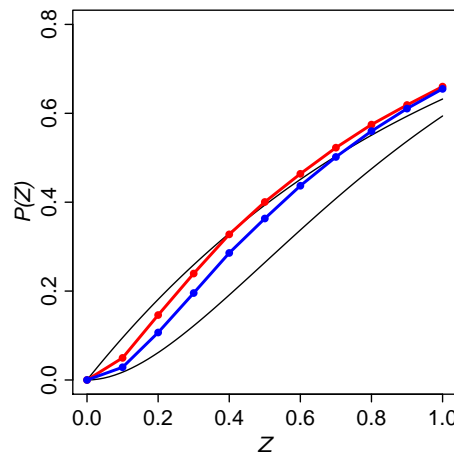
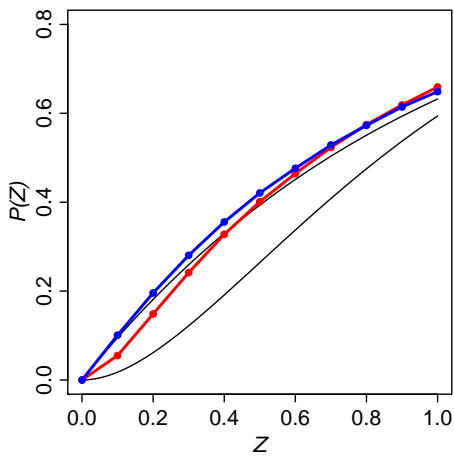
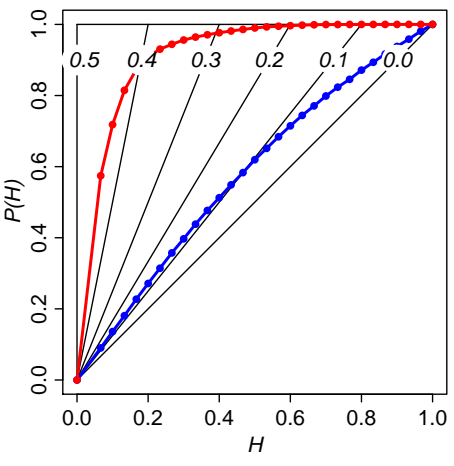
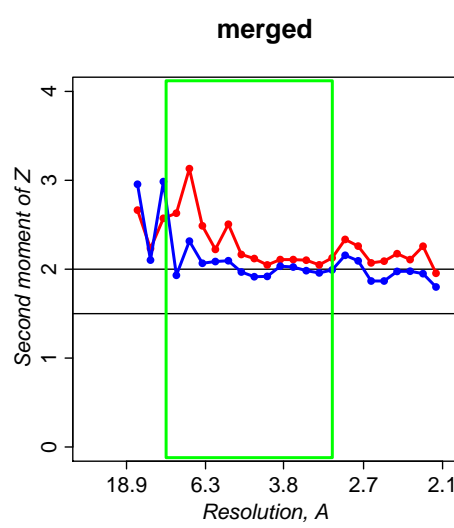
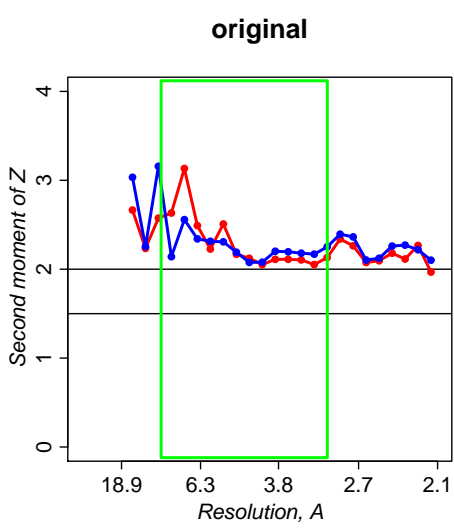
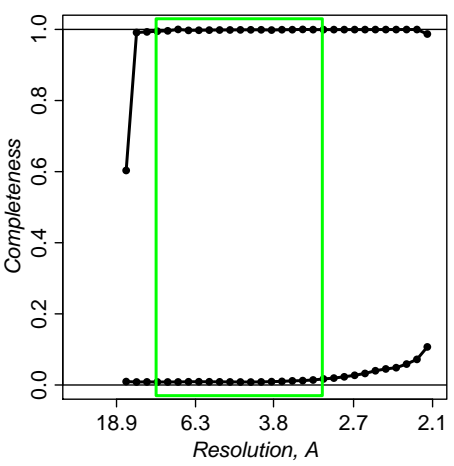
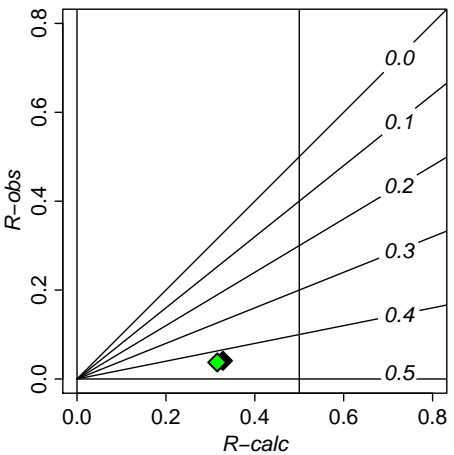
residues per monomer	DNA	protein
	0	196



1m8t

	original	merged
s.g.	P 63	P 63 2 2
p.g.	12021	12027
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		5.69
R	30.4	
R'	-	-
R-free	33.6	
R'-free	-	-
residues per monomer	DNA 0	protein 119

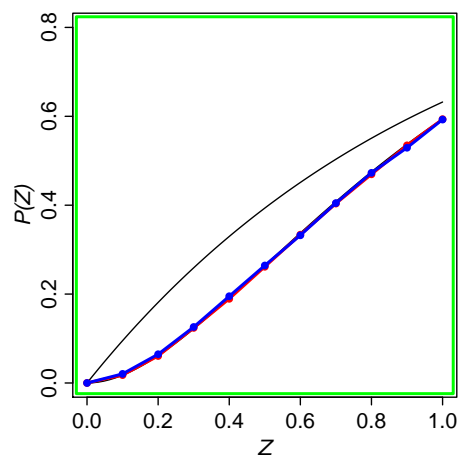
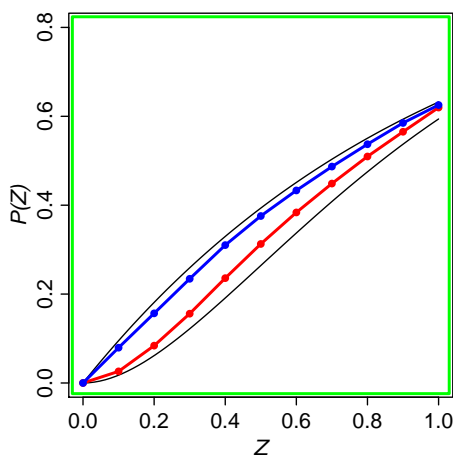
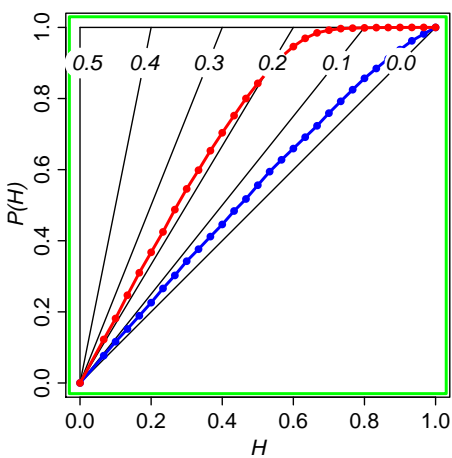
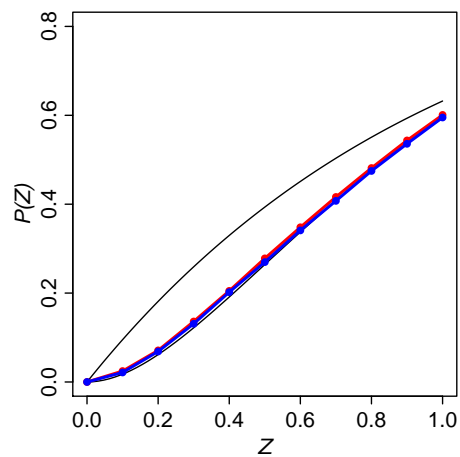
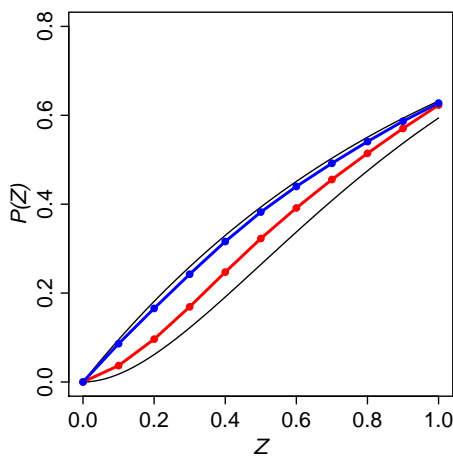
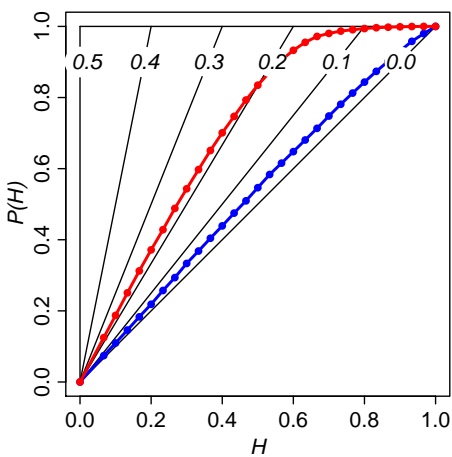
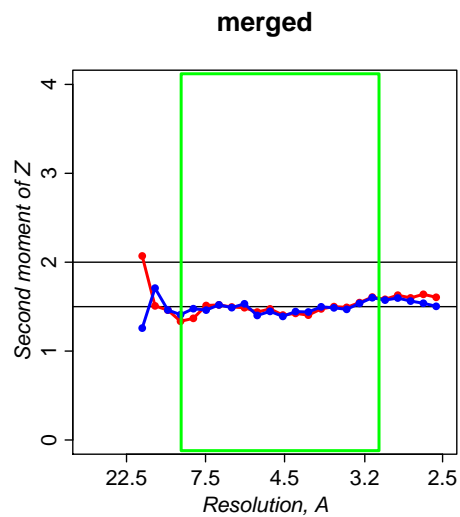
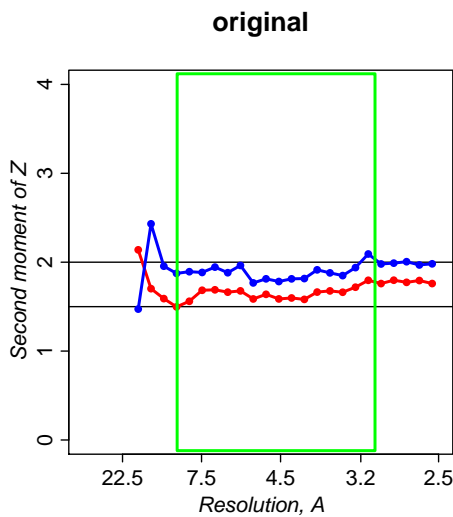
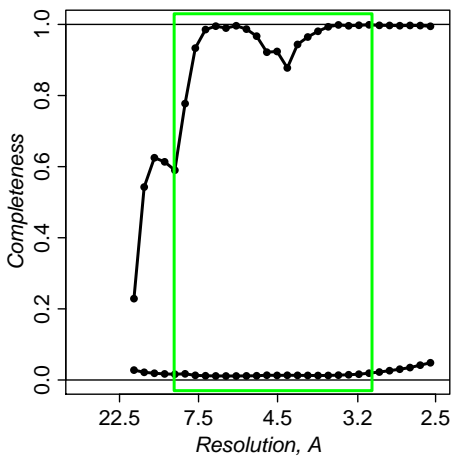
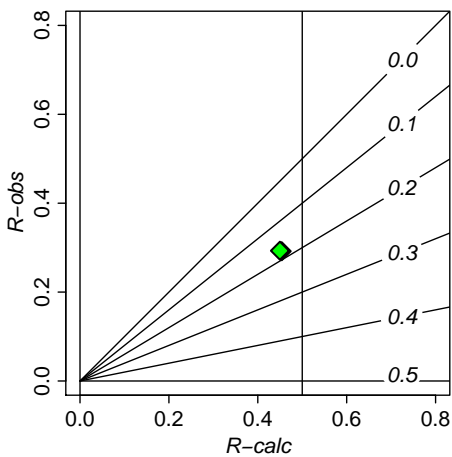
s < f/100	8649	20.62 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	17.0-2.1	9.9-3.0
unique	42,011	14,093
measured	41,938	14,077
used	37,880	12,260
NCS	translation	rotation
r.m.s.d. (A)	0.40	0.30
angle (o)	1.26	0.23



1m9i

	original	merged
s.g.	P 43	-
p.g.	10201	10205
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	25.6	-
R'	-	-
R-free	29.6	-
R'-free	-	-
residues per monomer	DNA 0	protein 664

s < f/100	4409	14.18 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	18.2-2.5	9.9-3.0
unique	31,927	18,038
measured	31,101	17,451
used	27,512	15,058
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



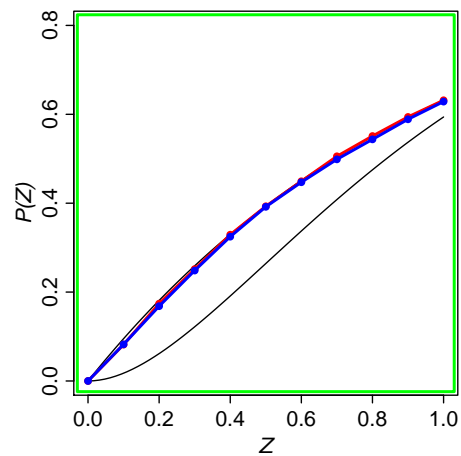
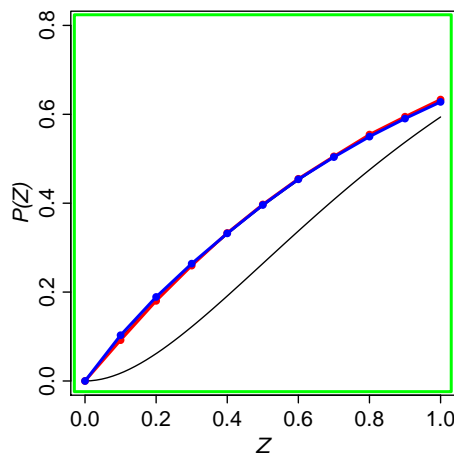
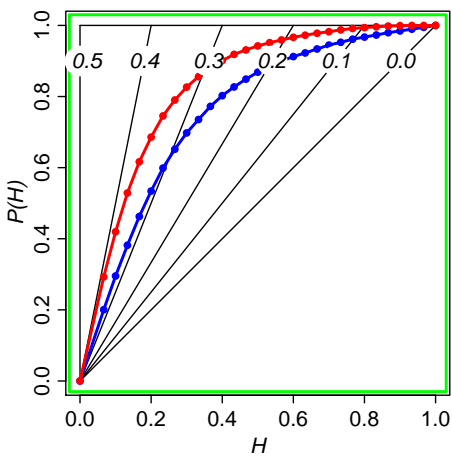
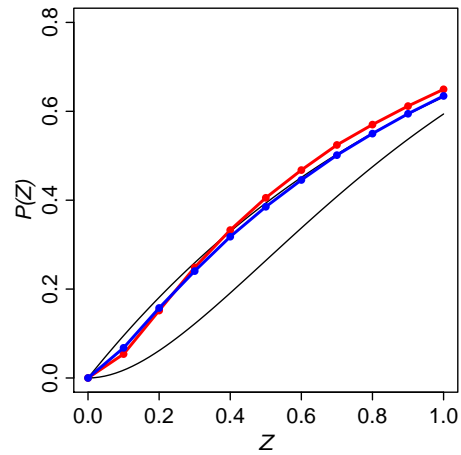
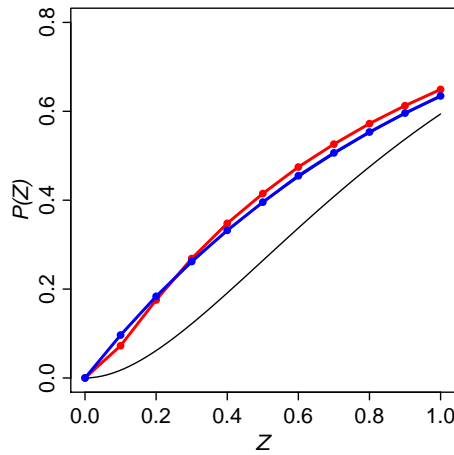
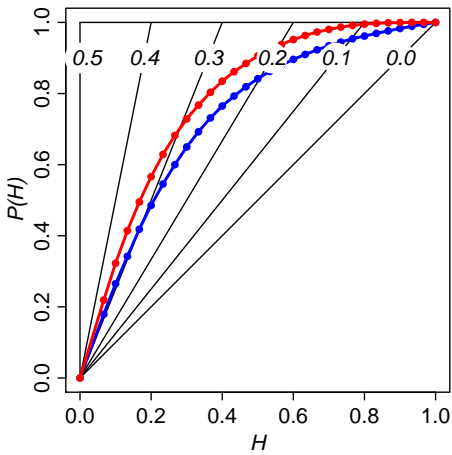
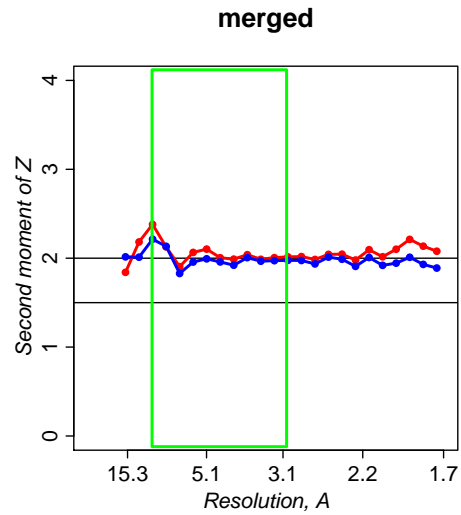
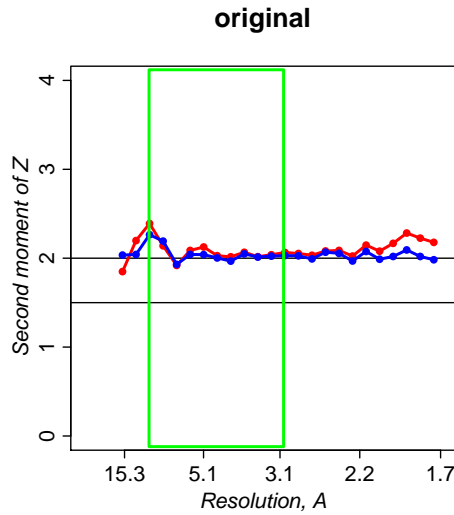
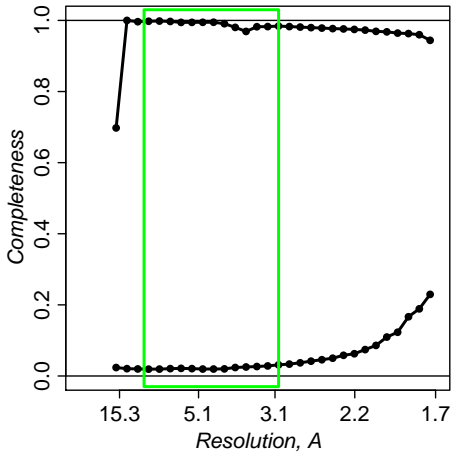
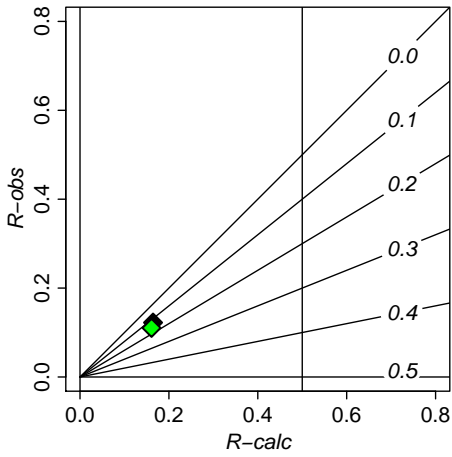
1m9x

	original	merged
s.g.	P 1	P 1 21 1
p.g.	10000	10001
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.13
R	39.8	
R'	39.8	39.3
R-free	41.0	
R'-free	41.3	40.8
residues per monomer	DNA 0	protein 164

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.7–1.7	9.9–3.0
unique	121,117	21,437
measured	117,637	21,130
used	112,782	20,404

NCS	translation	rotation
r.m.s.d. (A)	21.73	0.09
angle (o)	179.93	0.21



1m9y

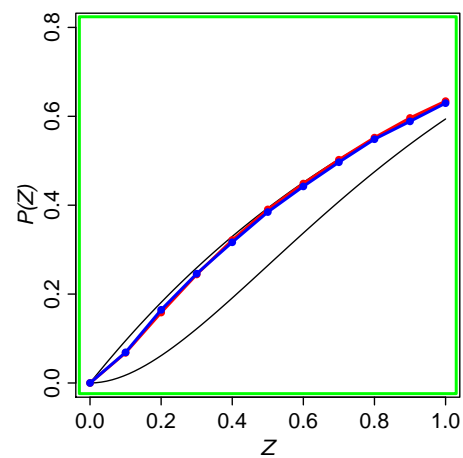
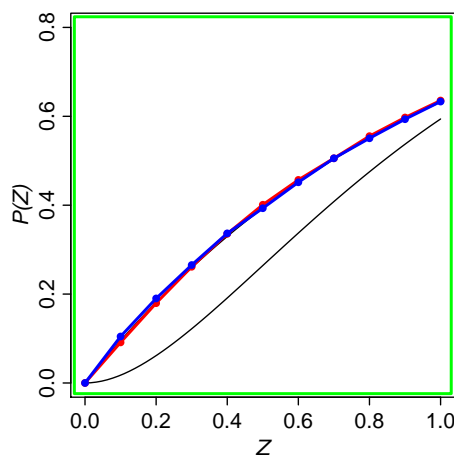
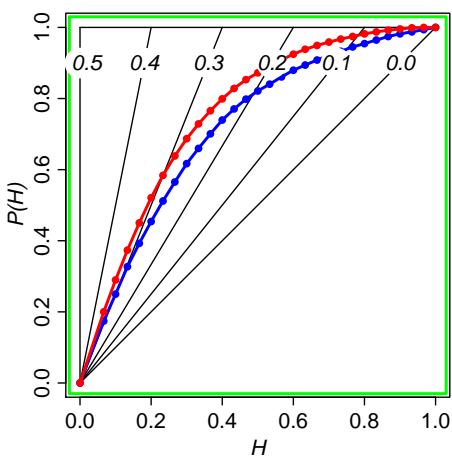
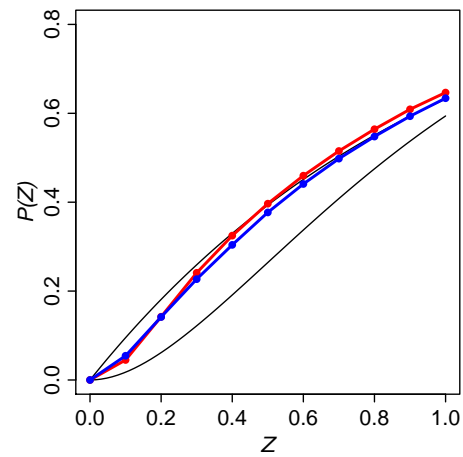
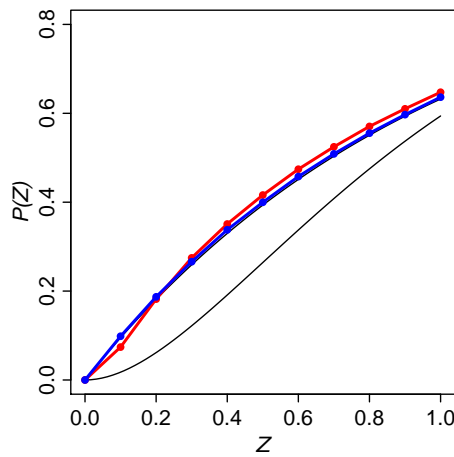
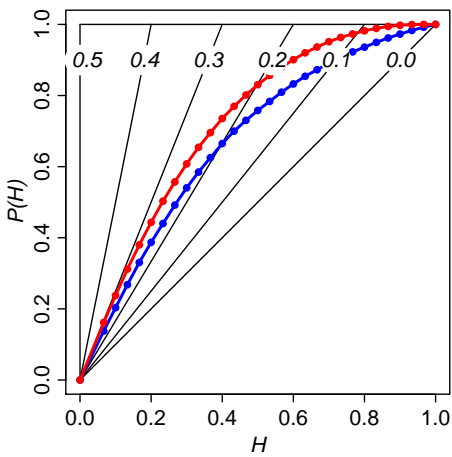
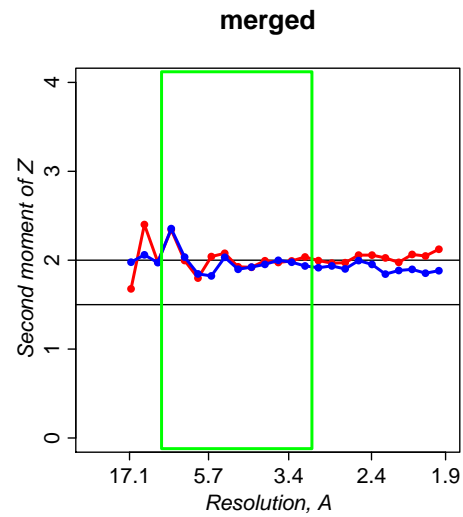
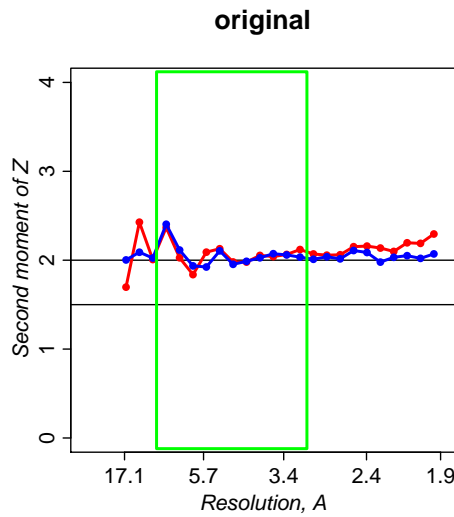
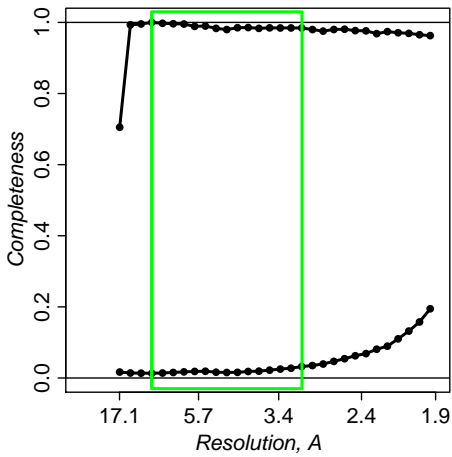
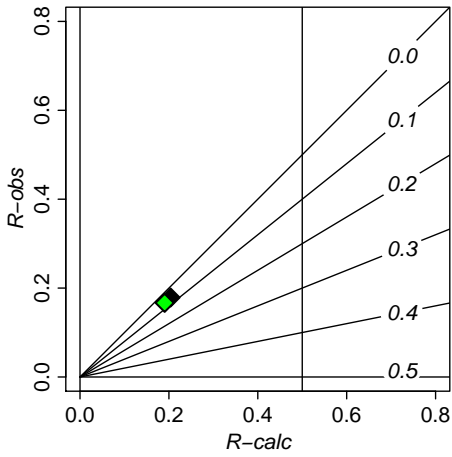
	original	merged
s.g.	P 1	P 1 21 1
p.g.	10000	10001
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.19
R	39.8	
R'	39.9	39.0
R-free	42.3	
R'-free	42.3	41.1

residues per monomer	DNA	protein
	0	164

s < f/100	81	0.10 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.7–1.9	9.9–3.0
unique	86,632	21,417
measured	84,527	21,108
used	81,072	20,374

NCS	translation	rotation
r.m.s.d. (A)	21.71	0.13
angle (o)	179.84	0.34



1mc8

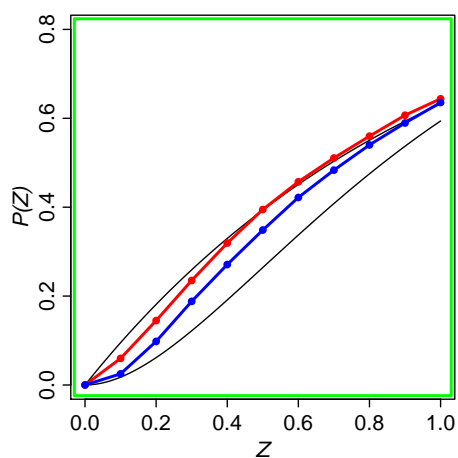
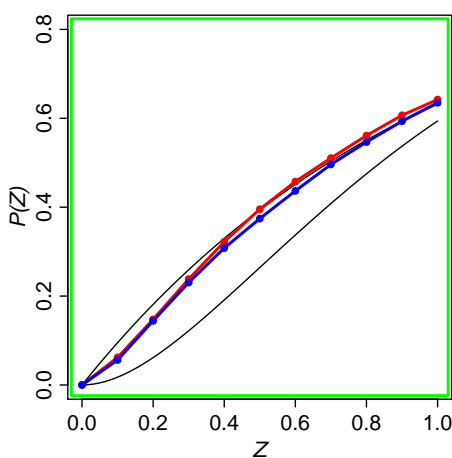
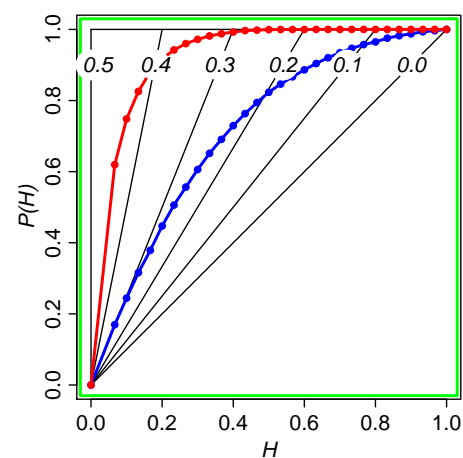
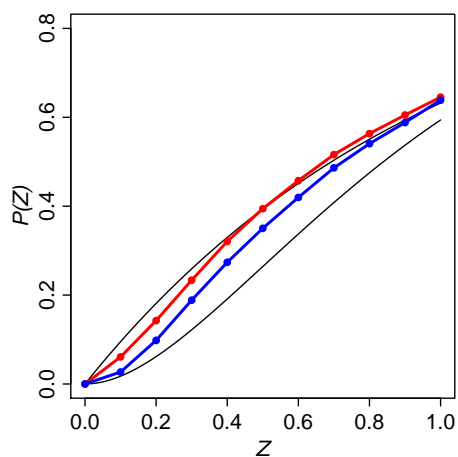
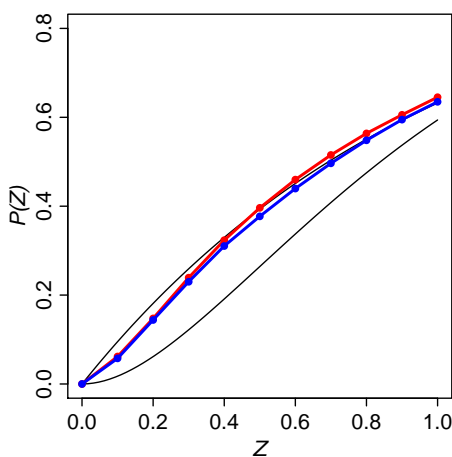
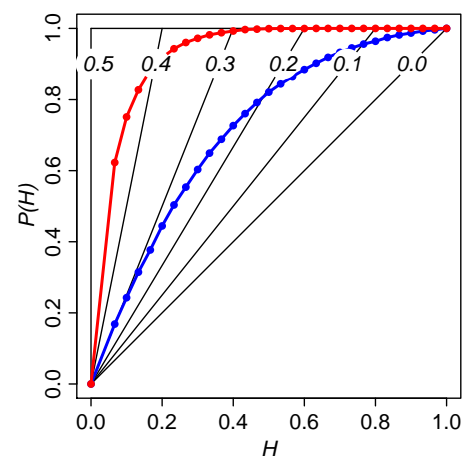
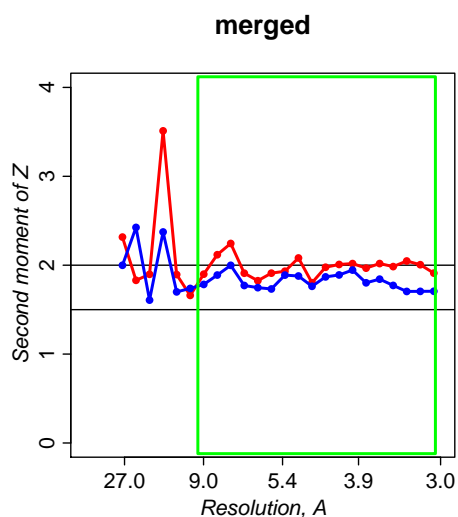
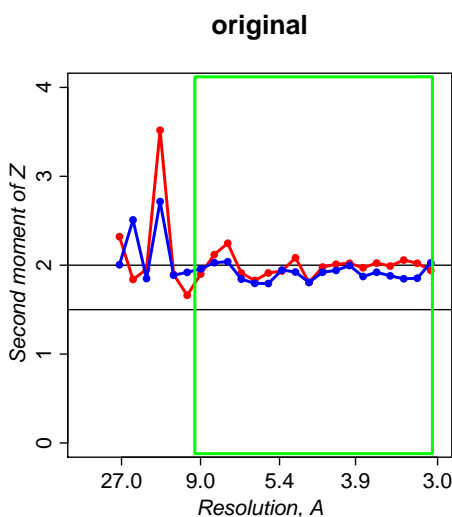
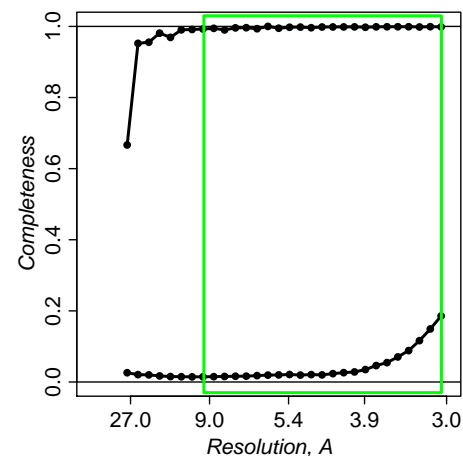
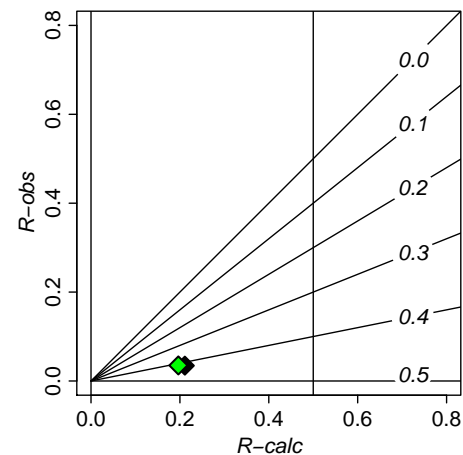
	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		2.17
R	23.7	
R'	25.5	26.8
R-free	32.0	
R'-free	32.8	33.5

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	34.7-3.0	9.9-3.0
unique	15,902	15,461
measured	15,867	15,435
used	14,192	13,898

NCS	translation	rotation
r.m.s.d. (A)	34.93	2.16
angle (o)	179.90	1.77

residues per monomer	DNA	protein
	0	331



1mfh

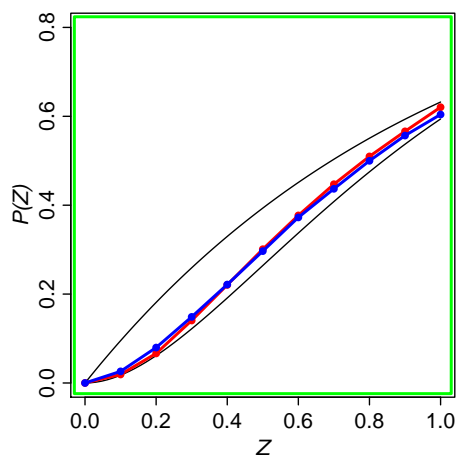
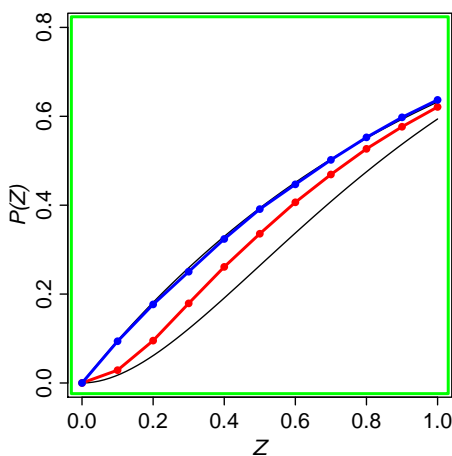
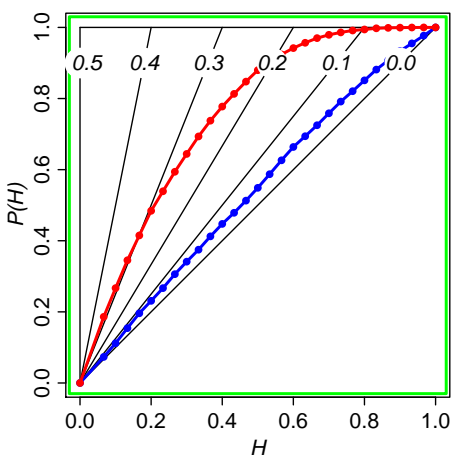
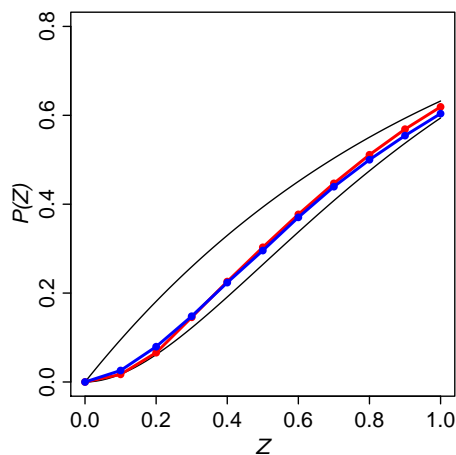
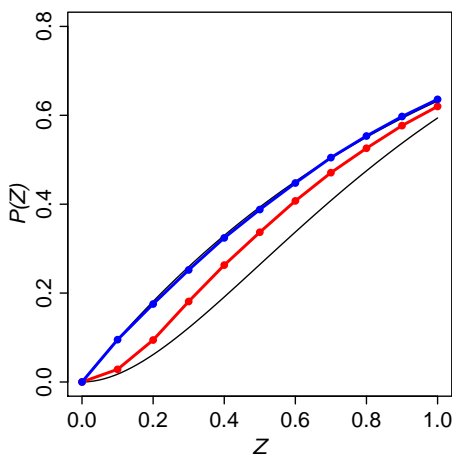
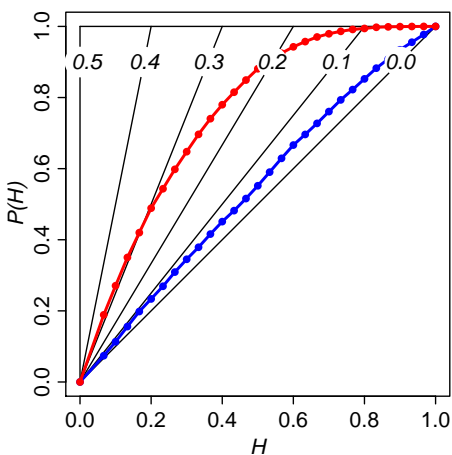
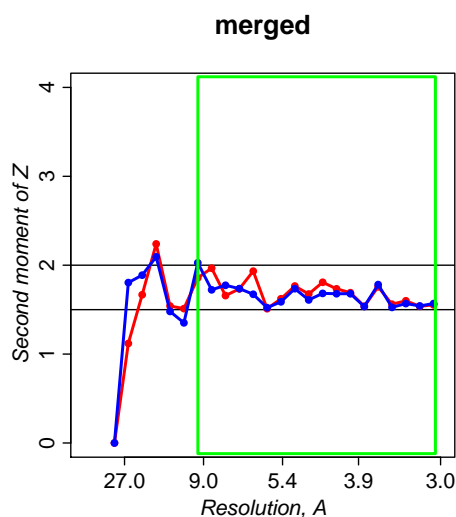
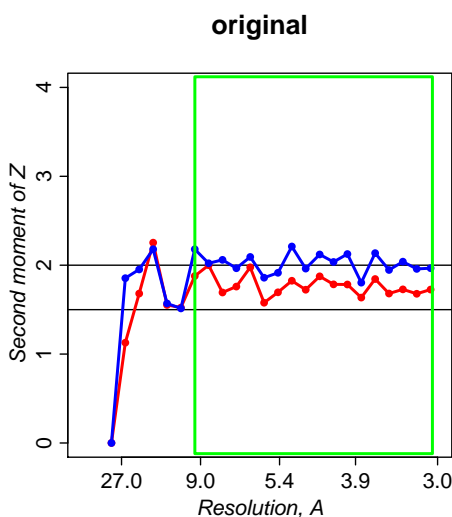
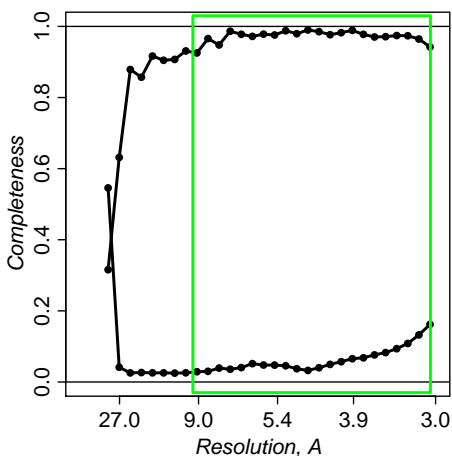
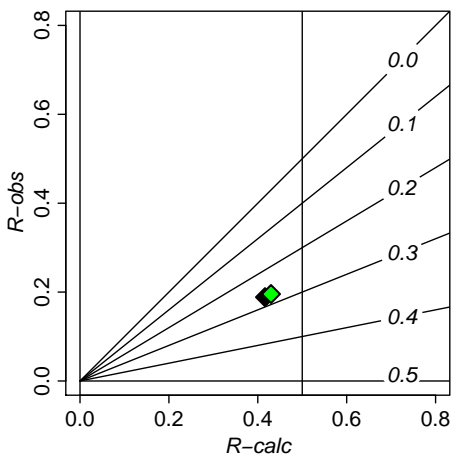
	original	merged
s.g.	P 21 21 21	P 43 21 2
p.g.	10003	10205
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		1.79
R	26.1	
R'	28.5	29.3
R-free	35.9	
R'-free	37.8	39.7

s < f/100	5	0.04 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	47.3-3.0	9.9-3.0
unique	12,855	12,436
measured	12,462	12,094
used	9,828	9,658

NCS	translation	rotation
r.m.s.d. (A)	14.72	0.40
angle (o)	79.98	2.00

residues per monomer	DNA	protein
	0	156



1mh5

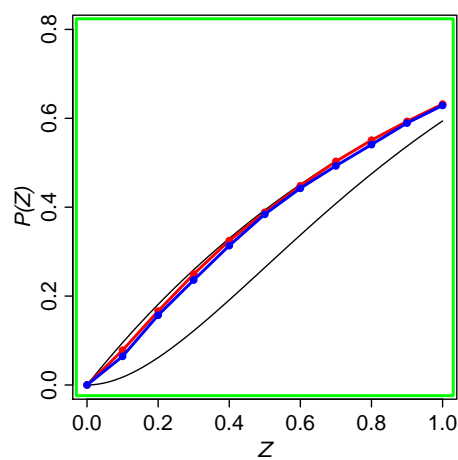
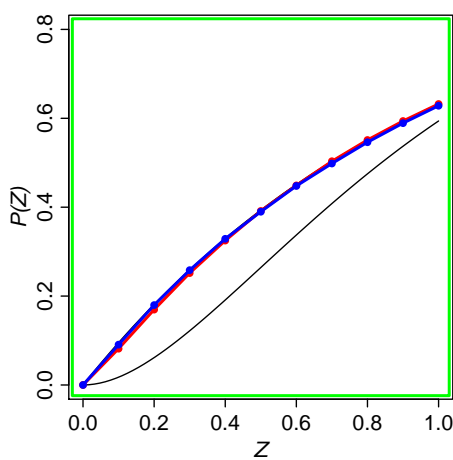
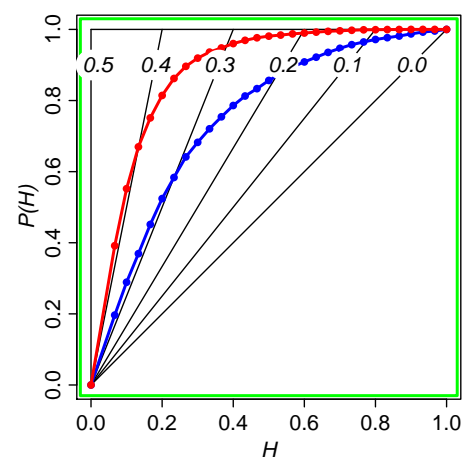
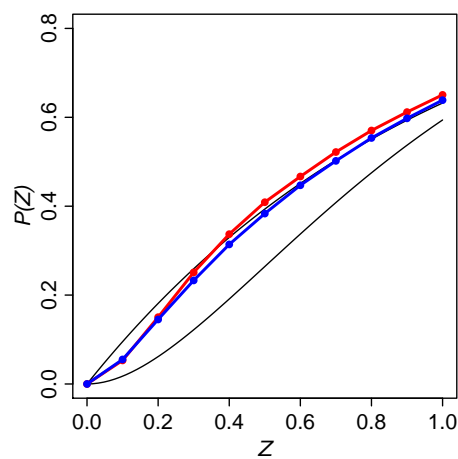
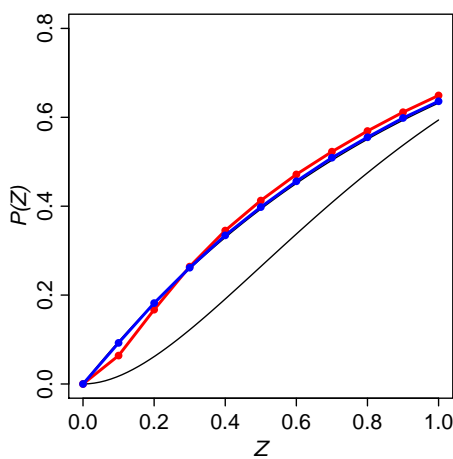
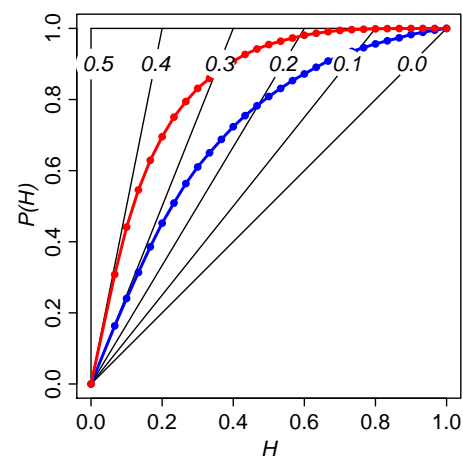
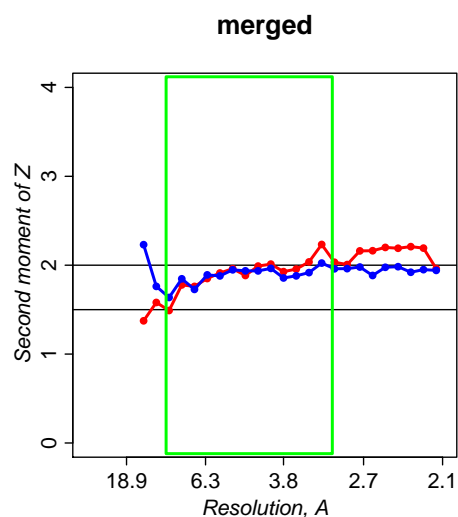
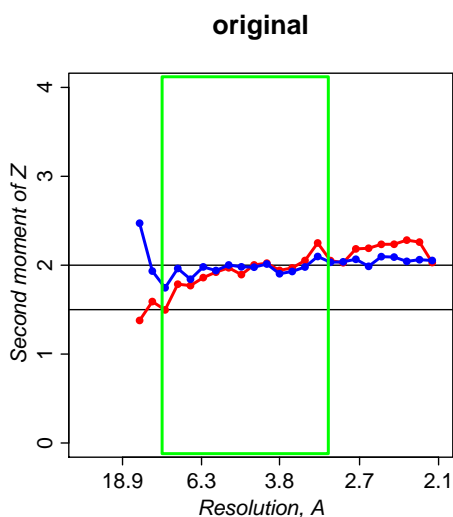
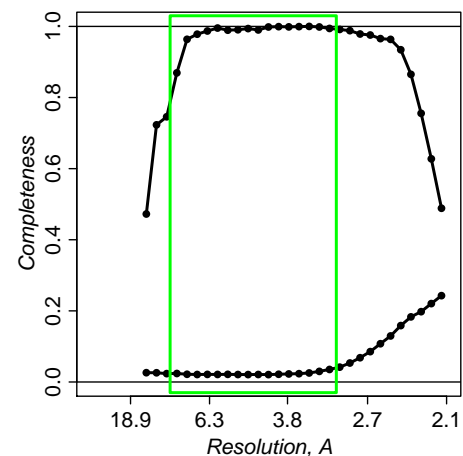
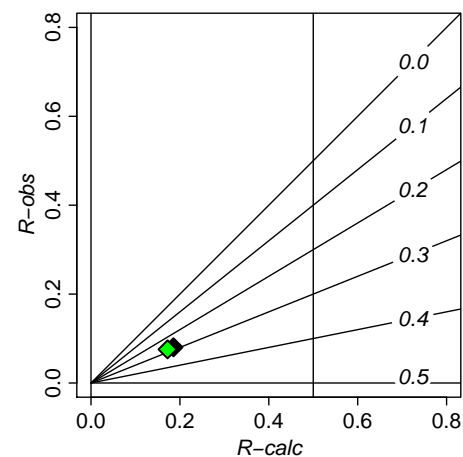
	original	merged
s.g.	C 1 2 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.34
R	28.9	
R'	29.7	29.8
R-free	32.2	
R'-free	32.8	33.0

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	14.9–2.1	9.9–3.0
unique	58,549	19,692
measured	51,796	19,523
used	45,816	17,992

NCS	translation	rotation
r.m.s.d. (A)	39.55	0.33
angle (o)	179.70	0.53

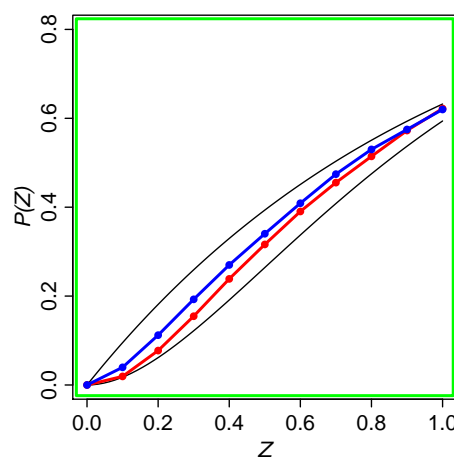
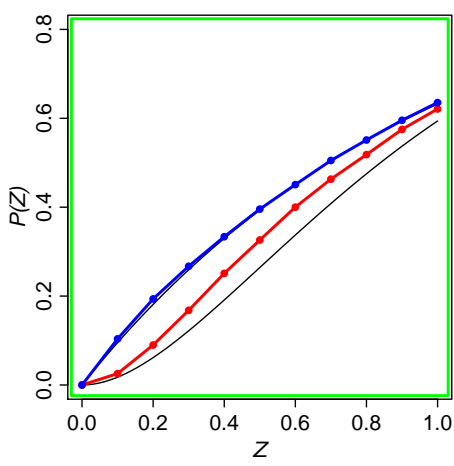
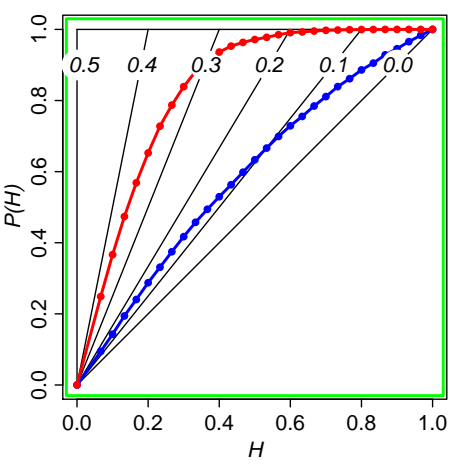
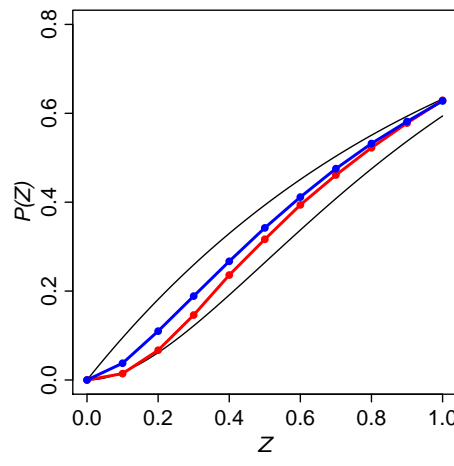
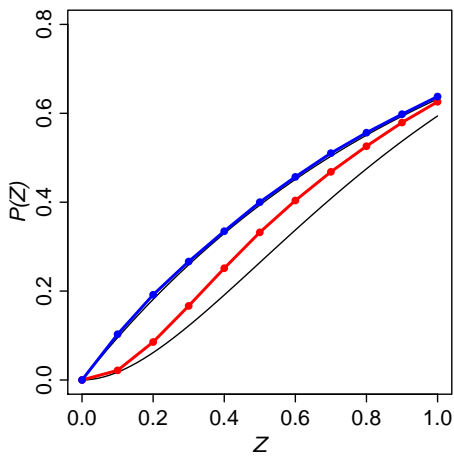
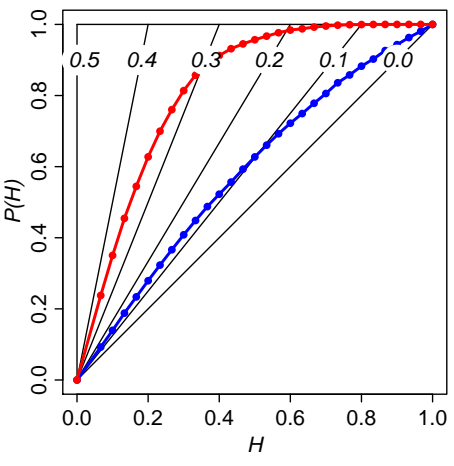
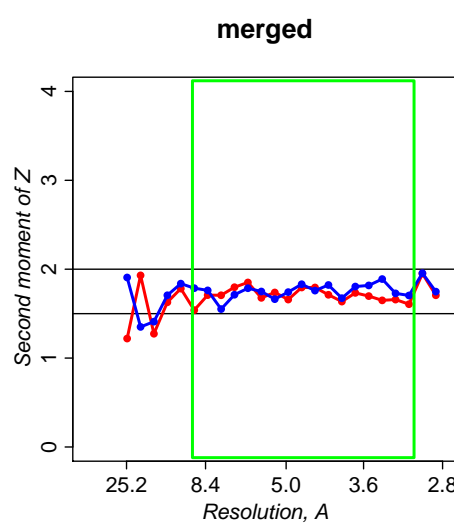
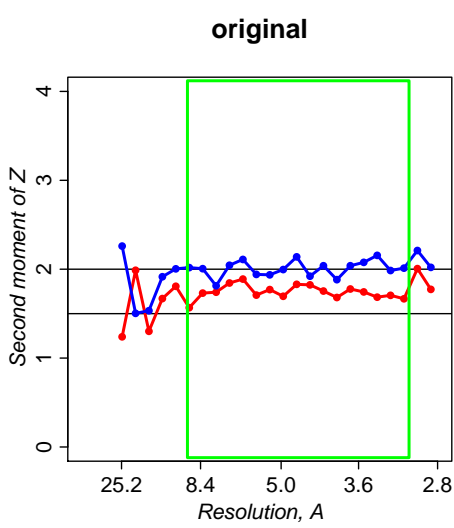
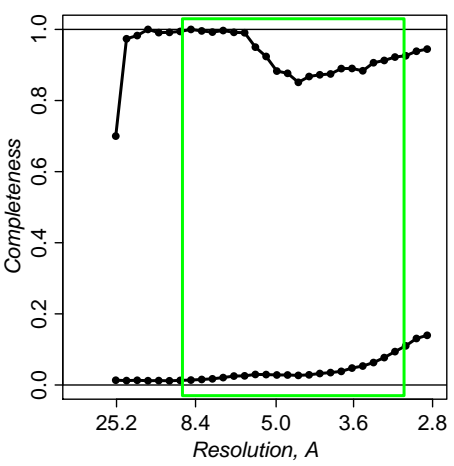
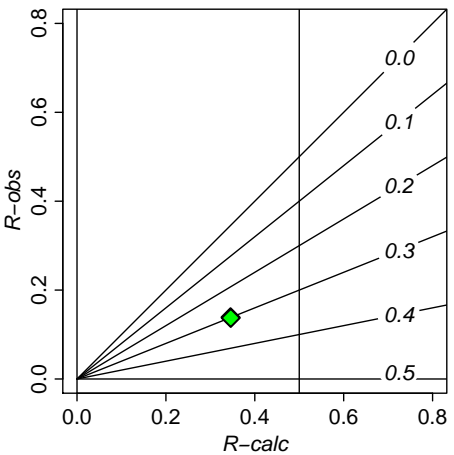
residues per monomer	DNA	protein
	0	368



1mk9

	original	merged
s.g.	P 1 21 1	P 21 21 2
p.g.	10001	10003
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		10.63
R	23.6	
R'	-	-
R-free	33.2	
R'-free	-	-
residues per monomer	DNA 0	protein 197

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	29.8–2.8	9.9–3.0
unique	20,547	16,221
measured	18,821	14,738
used	15,402	11,958
NCS	translation	rotation
r.m.s.d. (A)	13.31	0.29
angle (o)	78.24	0.54



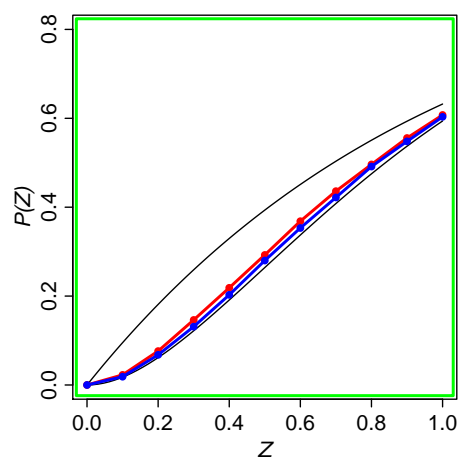
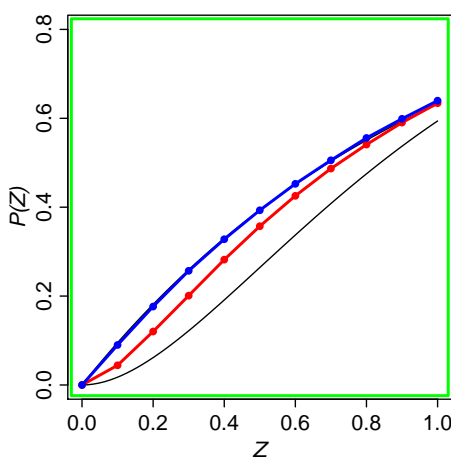
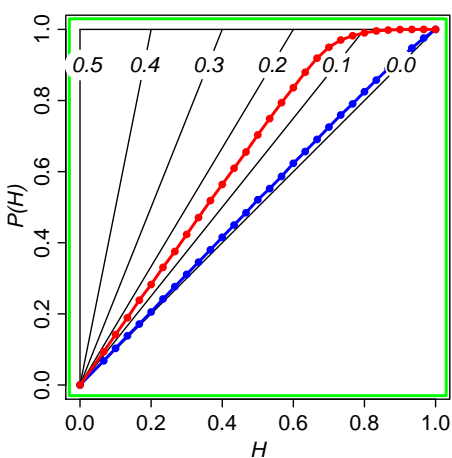
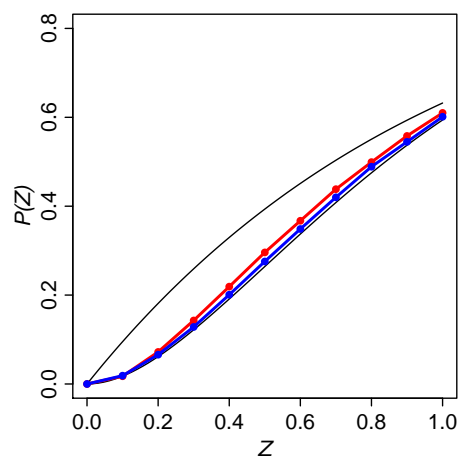
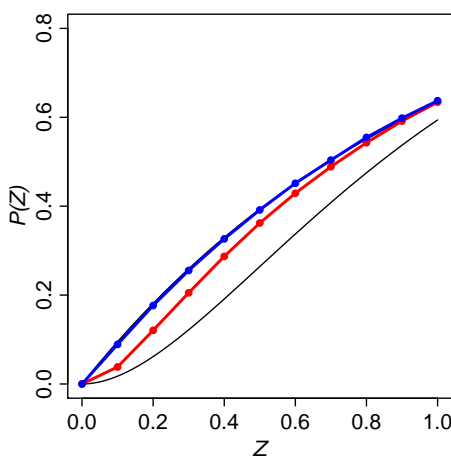
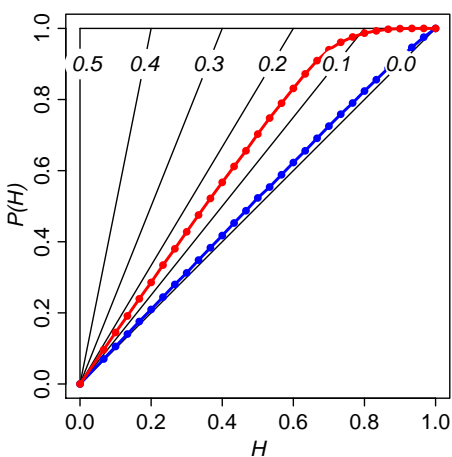
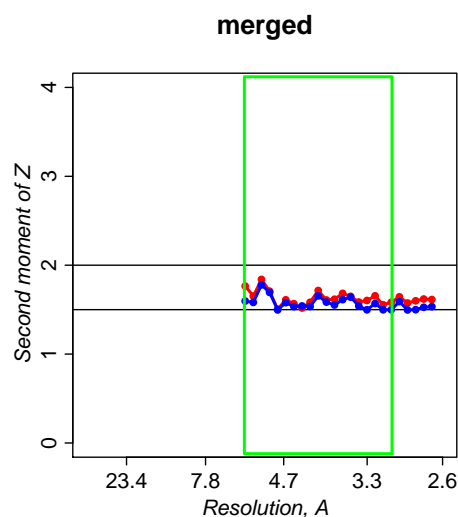
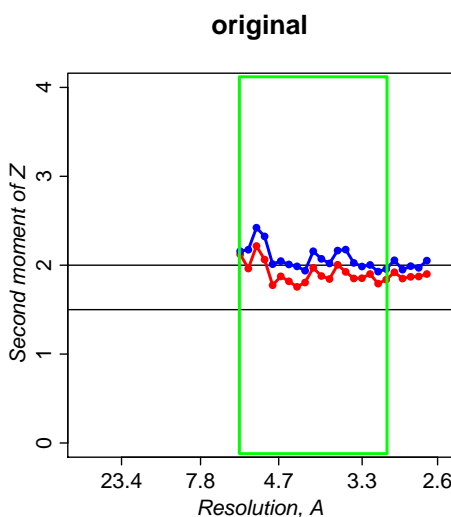
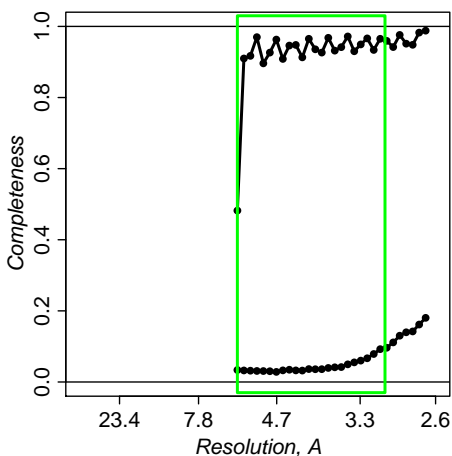
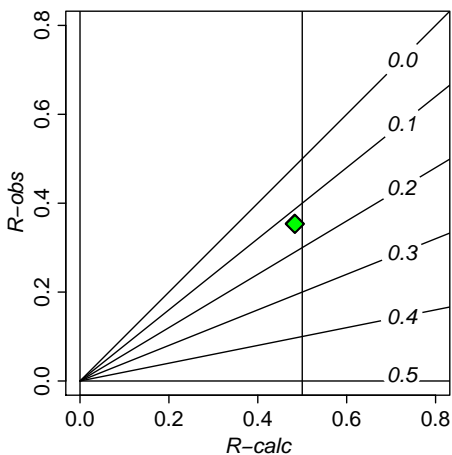
1ml1

	original	merged
s.g.	P 3	P 3 1 2
p.g.	10020	10023
a.u.	6	3
p.t.	3	3
p.o.	3	1
r.m.s.d. (A)		5.59
R	19.6	
R'	-	-
R-free	25.2	
R'-free	-	-
residues per monomer	DNA 0	protein 241

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	6.0-2.6	6.0-3.0
unique	41,452	27,383
measured	39,433	25,866
used	38,526	25,210

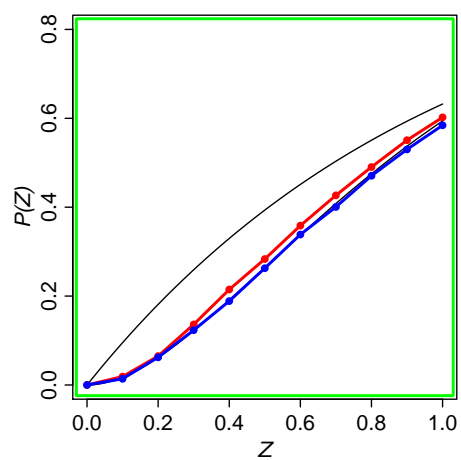
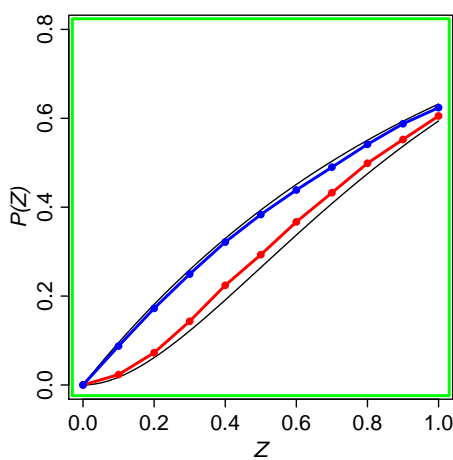
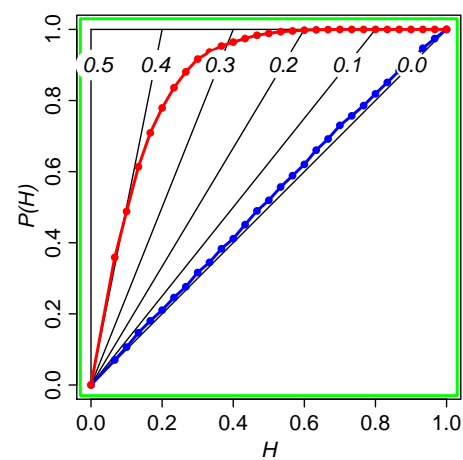
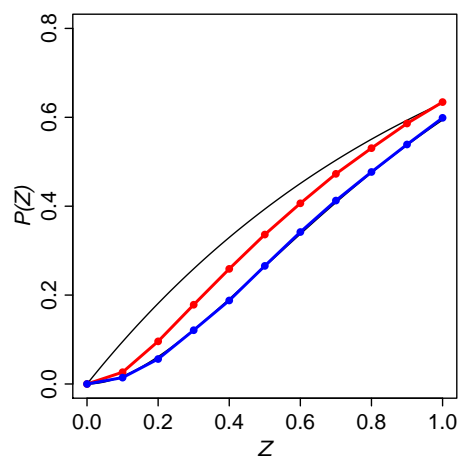
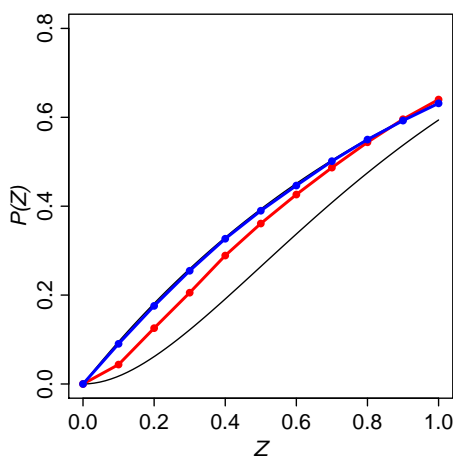
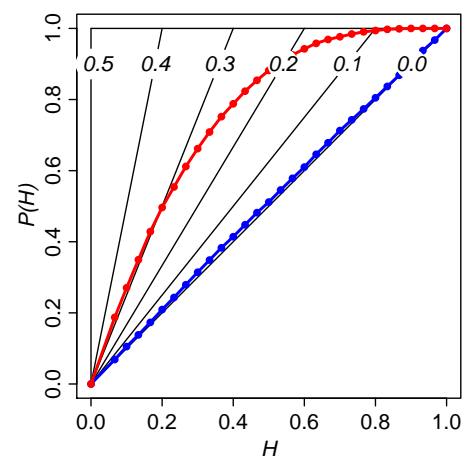
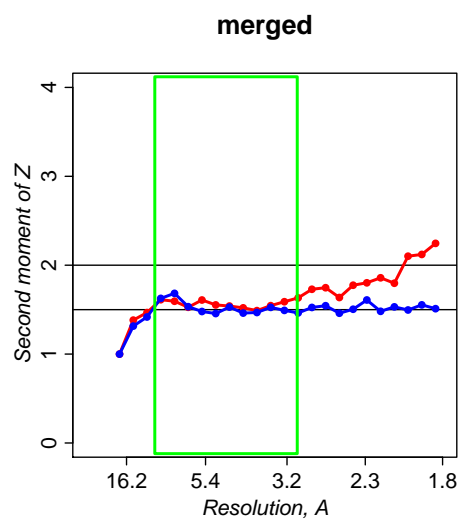
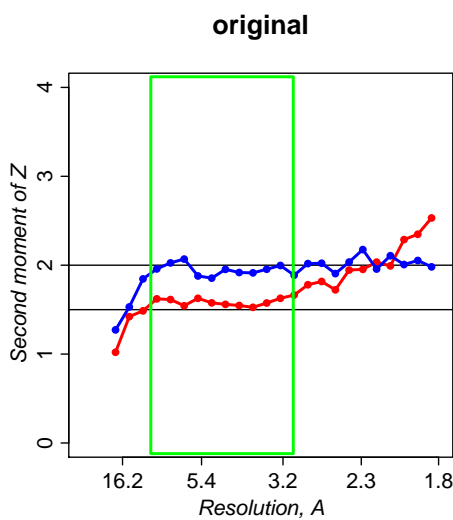
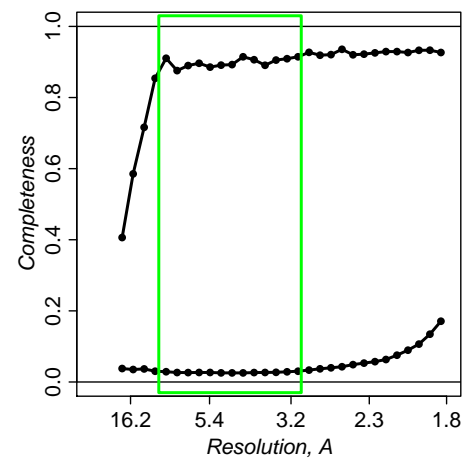
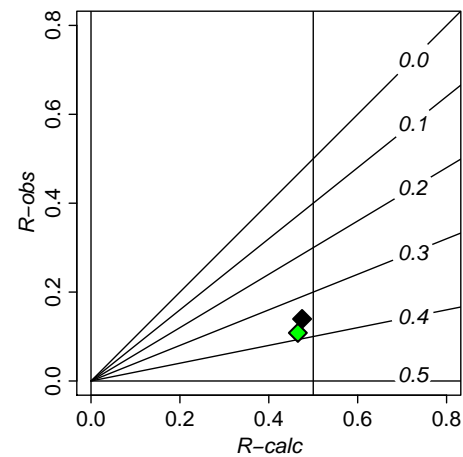
NCS	translation	rotation
r.m.s.d. (A)	1.26	0.58
angle (o)	5.51	2.62



1ml4

	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	28.3	-
R'	-	-
R-free	29.9	-
R'-free	-	-
residues per monomer	DNA 0	protein 307

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
<hr/>		
range (A)	25.0-1.8	9.9-3.0
unique	32,212	6,768
measured	29,666	6,108
used	27,314	5,558
<hr/>		
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1mn7

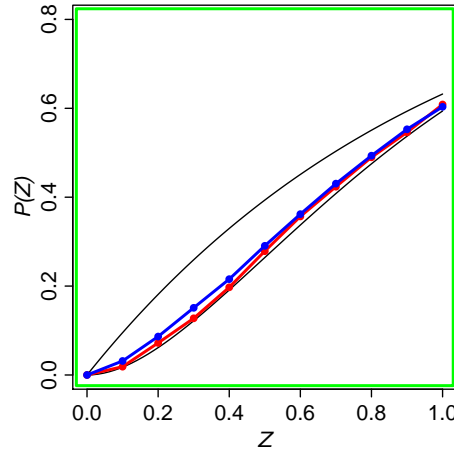
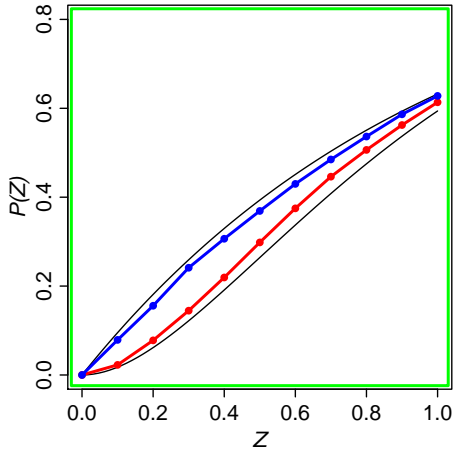
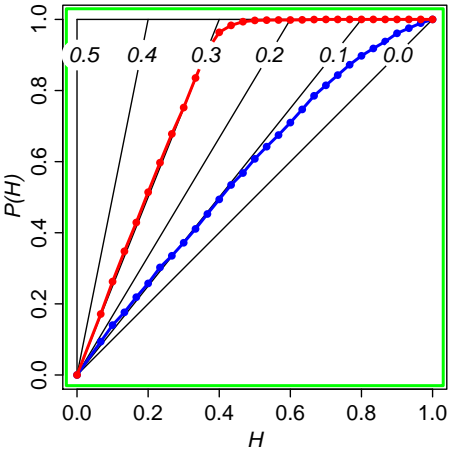
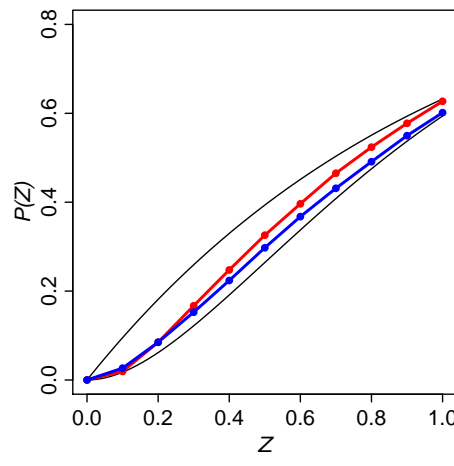
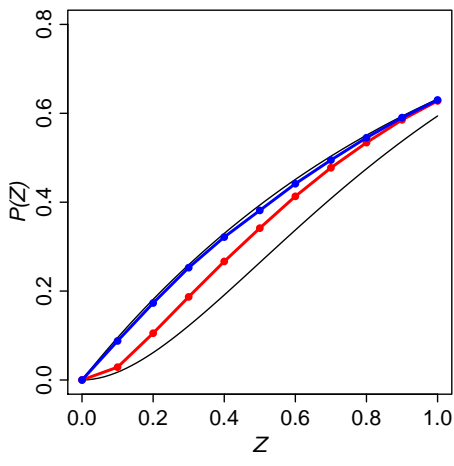
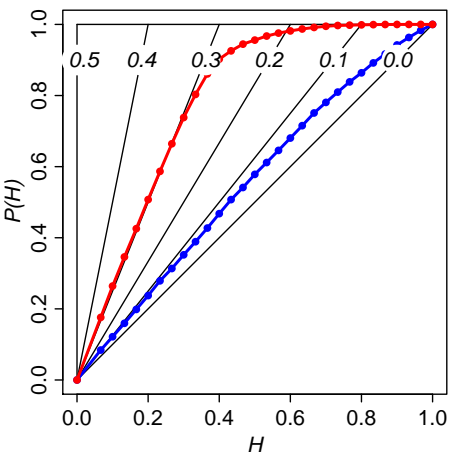
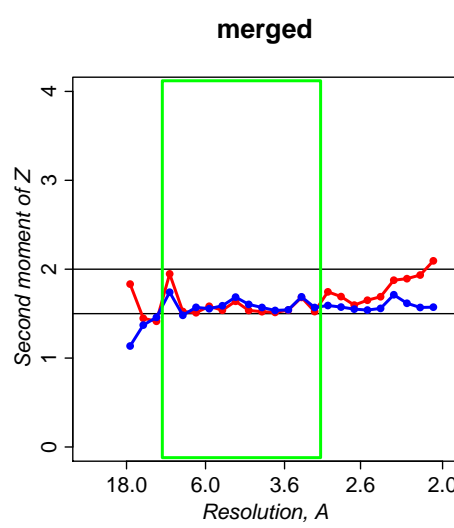
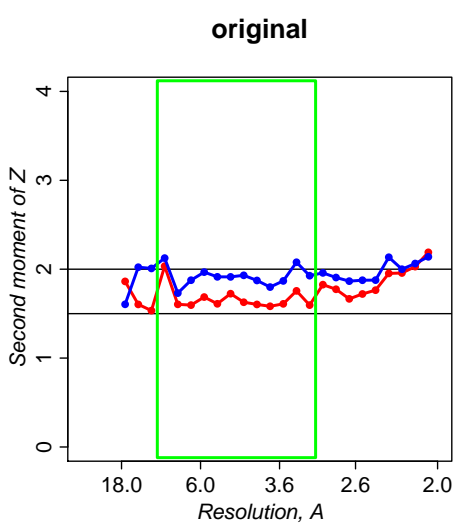
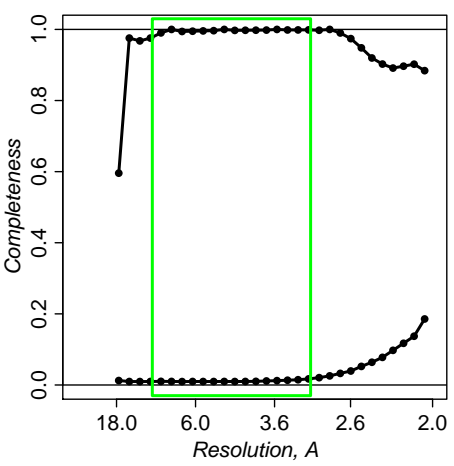
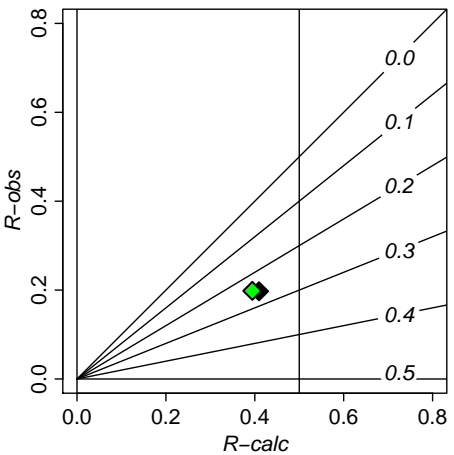
	original	merged
s.g.	P 63	-
p.g.	12021	12027
a.u.	2	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	28.6	-
R'	-	-
R-free	31.8	-
R'-free	-	-

residues per monomer	DNA	protein
	0	150

s < f/100	2879	14.94 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.5-2.0	9.9-3.0
unique	20,311	6,040
measured	19,270	6,026
used	16,250	4,994

NCS	translation	rotation
r.m.s.d. (A)	21.32	5.62
angle (o)	179.68	24.21



1mo1

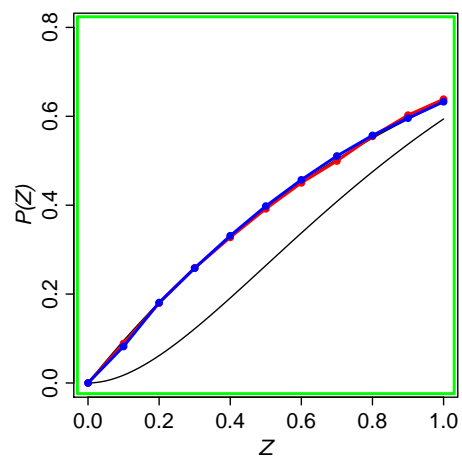
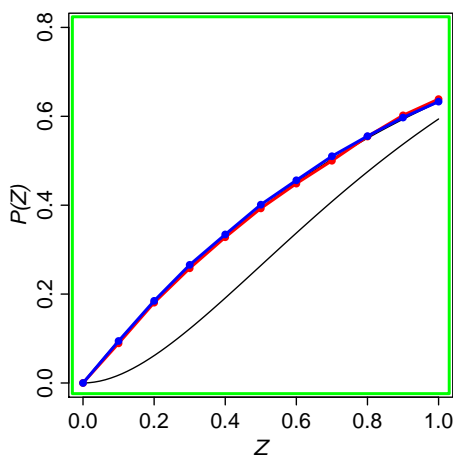
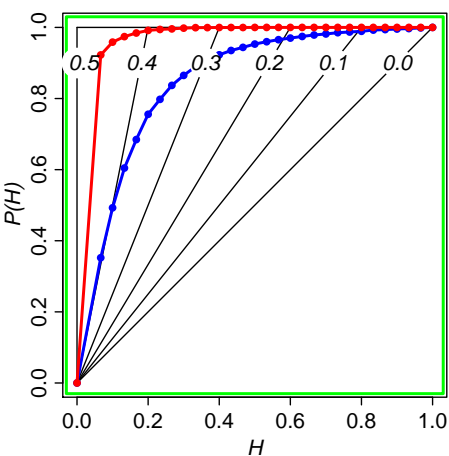
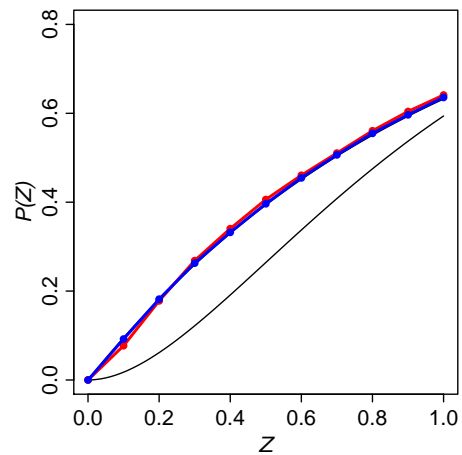
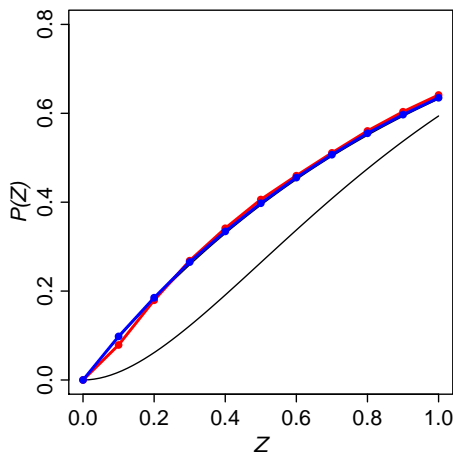
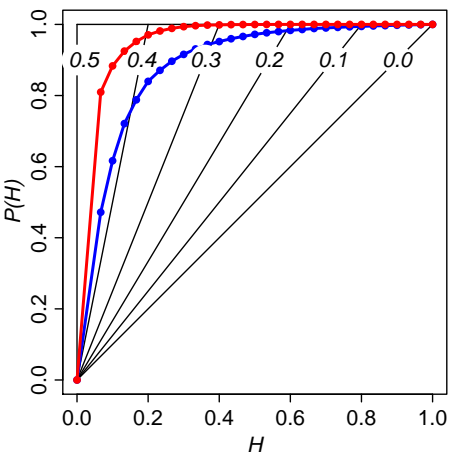
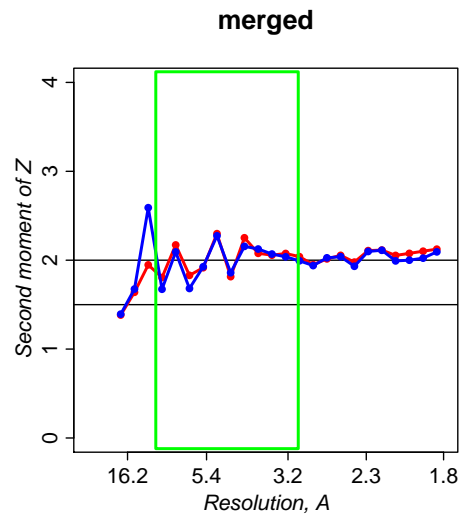
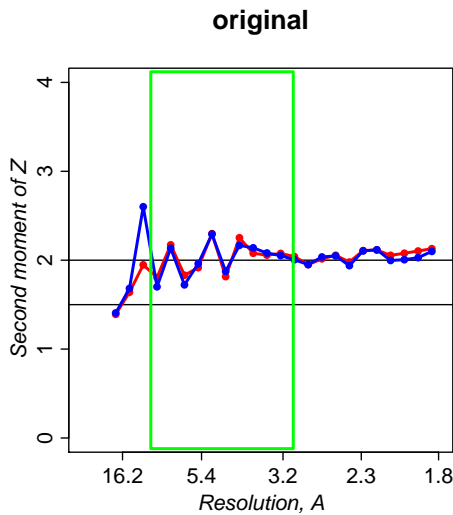
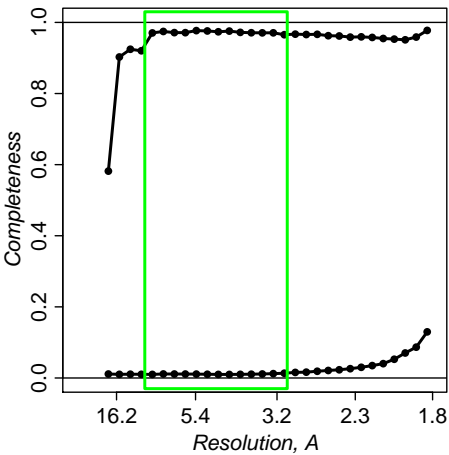
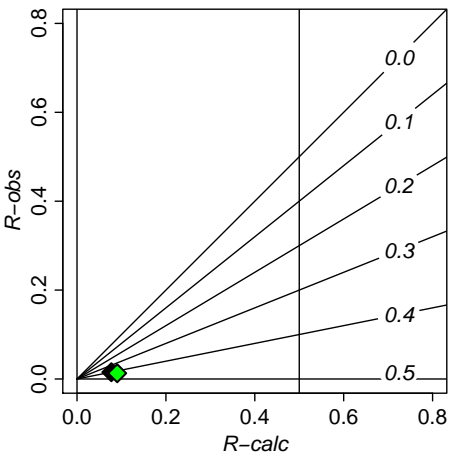
	original	merged
s.g.	P 43	P 43 2 2
p.g.	10201	10205
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.02
R	27.0	
R'	27.3	27.8
R-free	28.1	
R'-free	28.4	29.0

s < f/100	7186	15.35 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	24.8–1.8	9.9–3.0
unique	48,619	10,329
measured	46,800	10,028
used	42,936	8,754

NCS	translation	rotation
r.m.s.d. (A)	11.21	0.02
angle (o)	79.61	0.03

residues per monomer	DNA	protein
	0	86



1mow

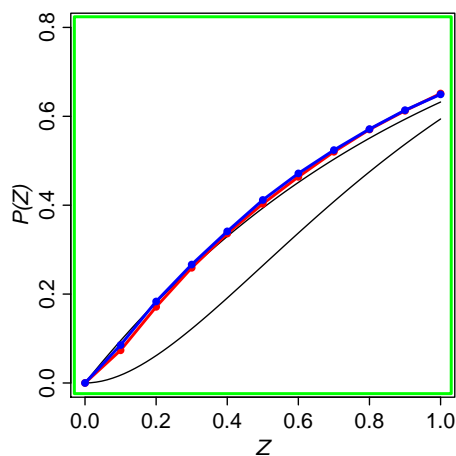
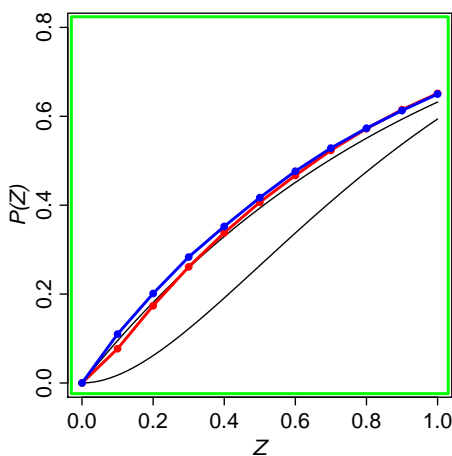
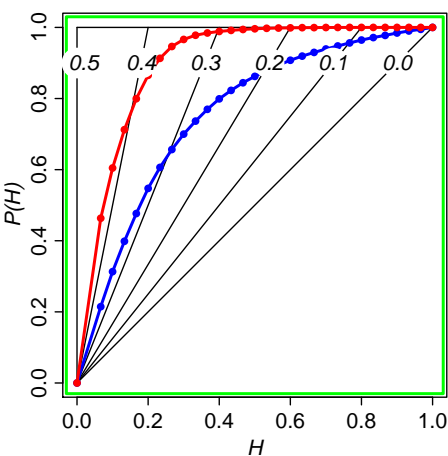
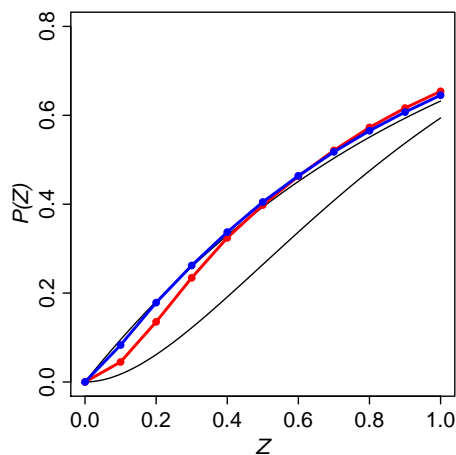
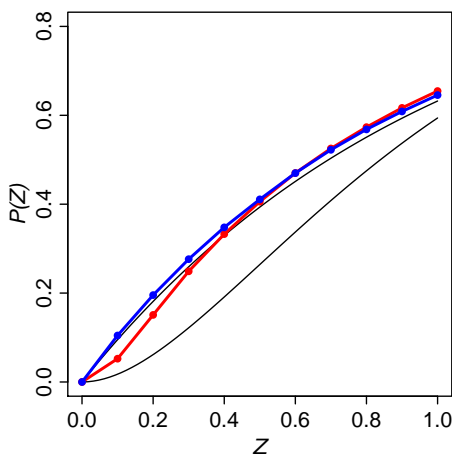
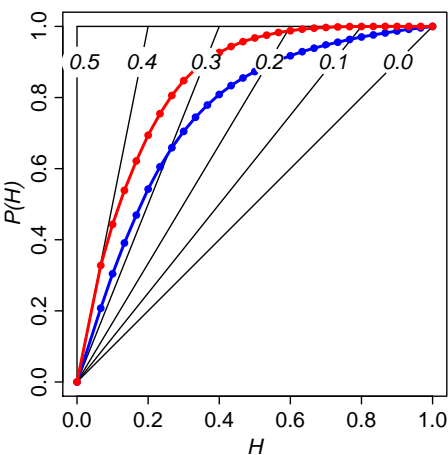
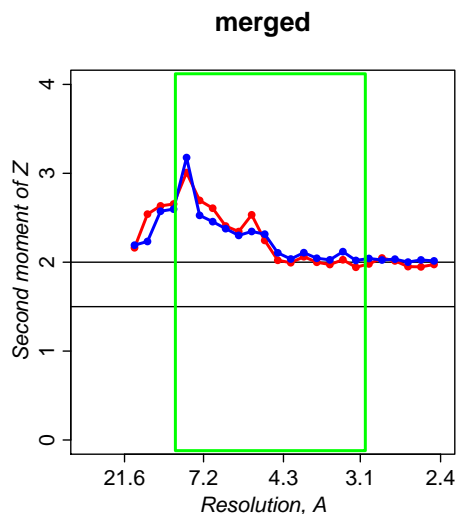
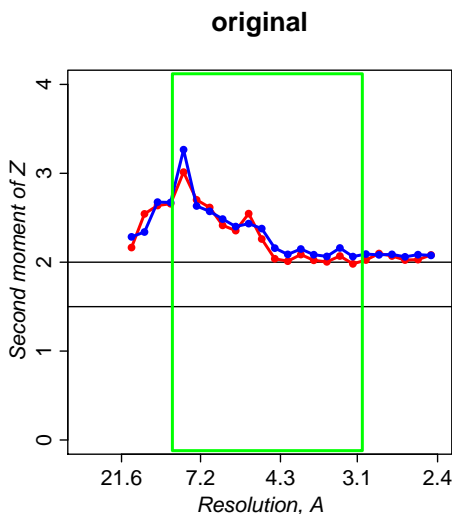
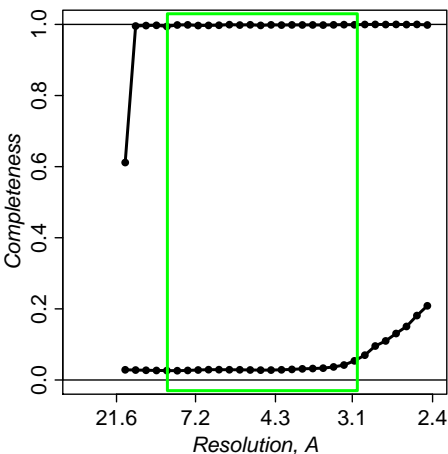
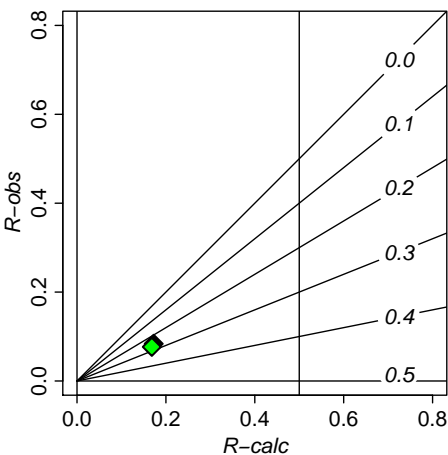
	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.43
R	38.3	
R'	40.1	40.4
R-free	40.2	
R'-free	43.5	43.8

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.9–2.4	9.9–3.0
unique	91,685	45,722
measured	91,595	45,655
used	87,842	43,428

NCS	translation	rotation
r.m.s.d. (A)	0.41	0.09
angle (o)	0.48	0.03

residues per monomer	DNA	protein
	44	224



1mq8

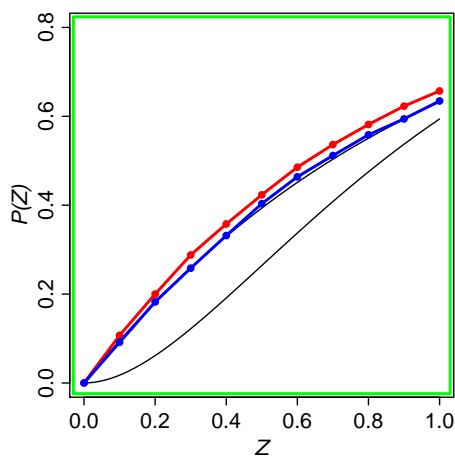
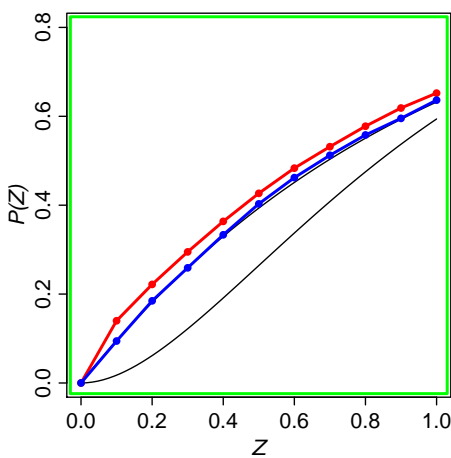
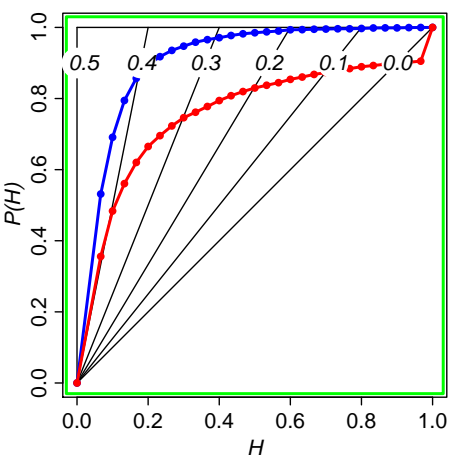
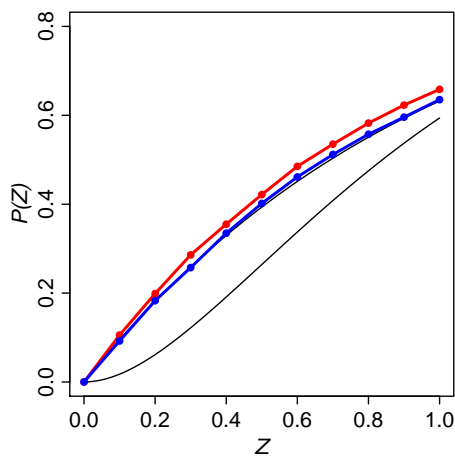
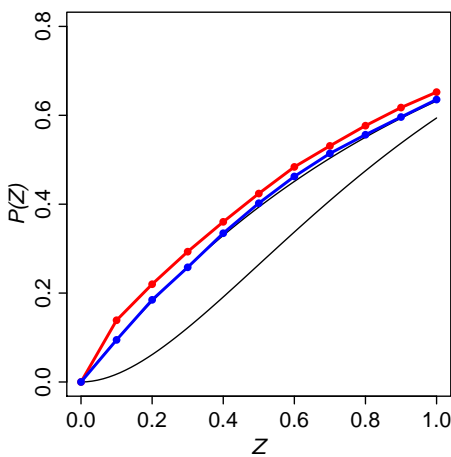
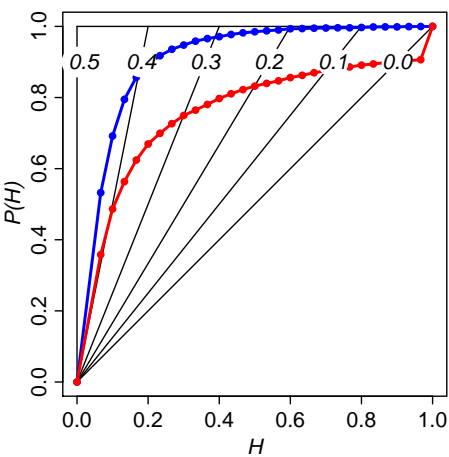
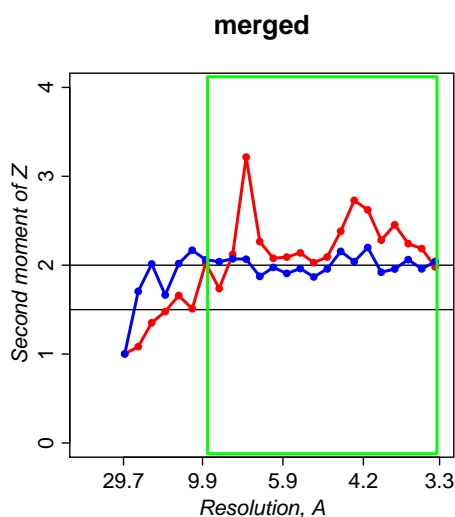
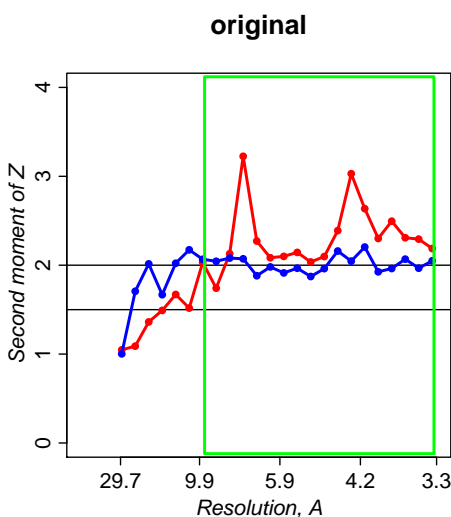
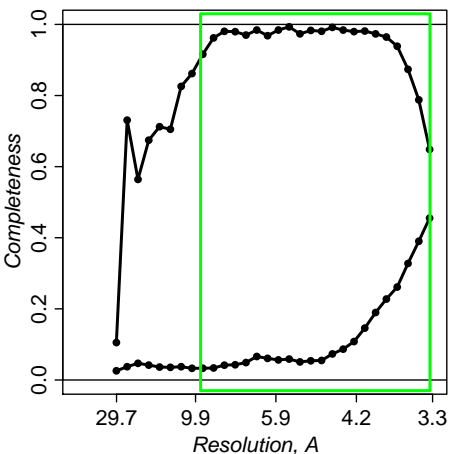
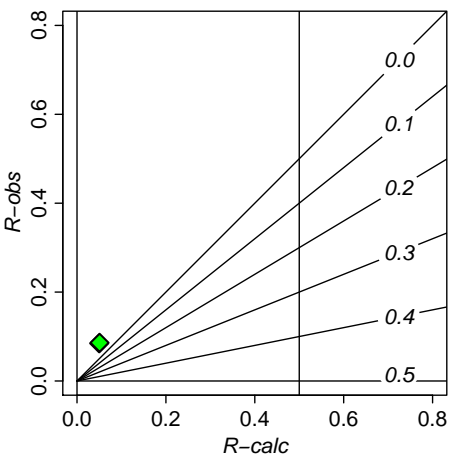
	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.07
R	23.9	
R'	24.1	25.4
R-free	38.5	
R'-free	38.7	40.4

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	824	6.68 %
s,f <= 0	0	0.00 %

range (A)	34.6–3.3	9.9–3.3
unique	13,500	13,021
measured	12,338	11,983
used	11,098	10,858

NCS	translation	rotation
r.m.s.d. (A)	42.32	0.07
angle (o)	179.99	0.01

residues per monomer	DNA	protein
	0	361



1mui

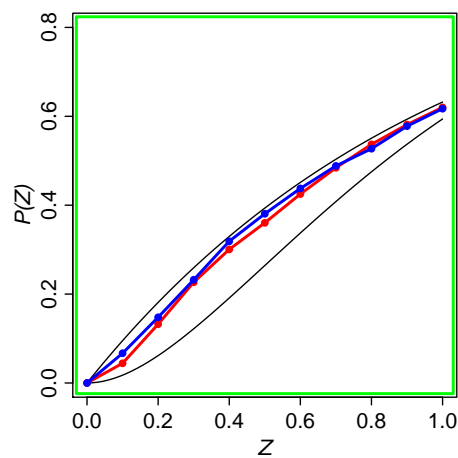
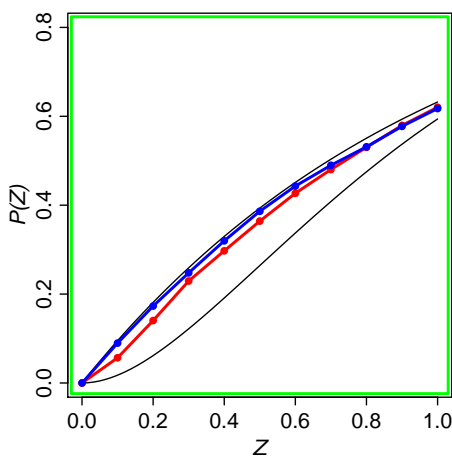
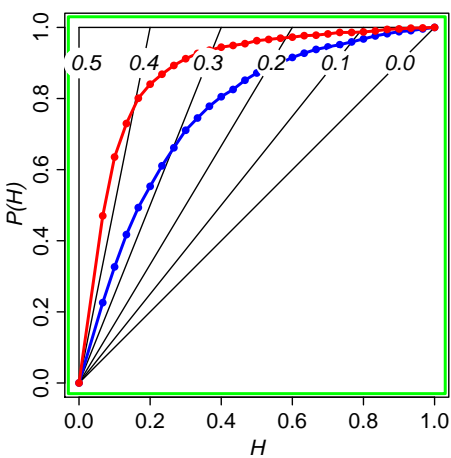
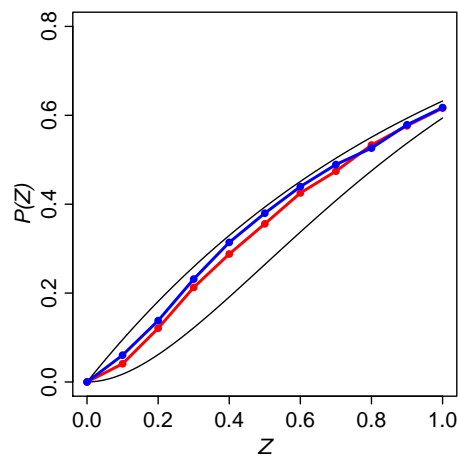
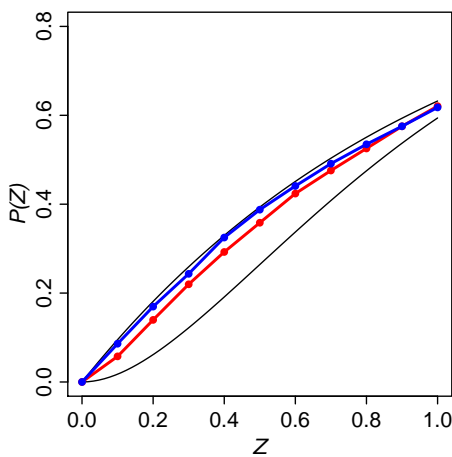
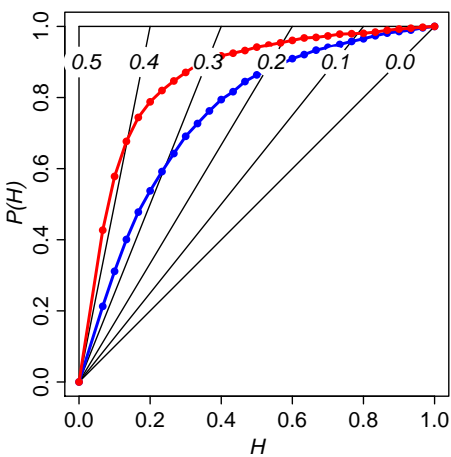
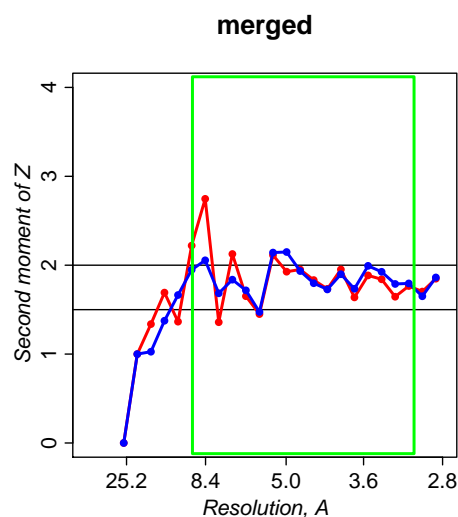
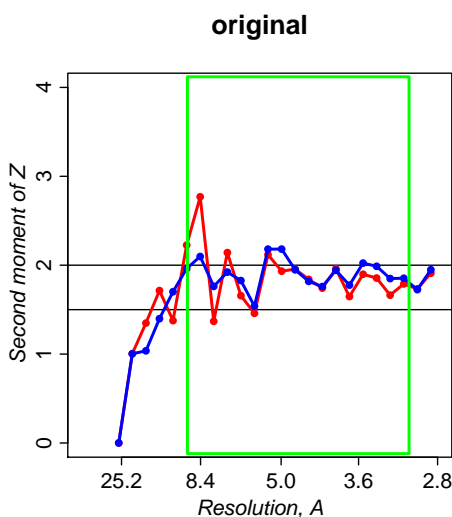
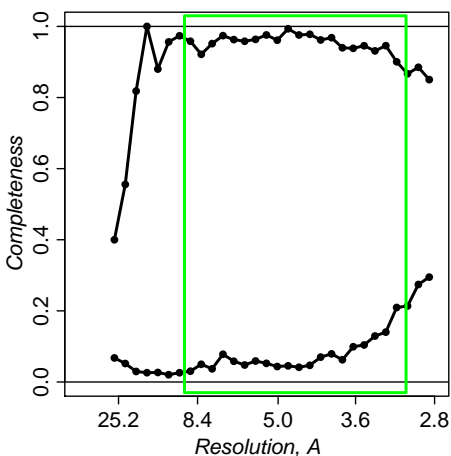
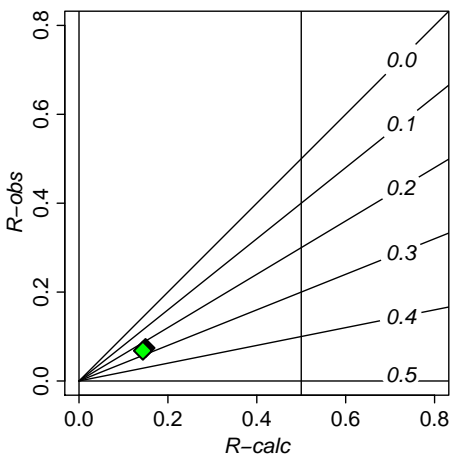
	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.32
R	20.7	
R'	21.3	22.0
R-free	26.6	
R'-free	28.7	28.0

s < f/100	232	5.25 %
s <= 0	232	5.25 %
f <= 0	232	5.25 %
s,f <= 0	232	5.25 %

range (A)	33.2–2.8	9.9–3.0
unique	4,762	3,742
measured	4,417	3,537
used	3,508	2,828

NCS	translation	rotation
r.m.s.d. (A)	22.56	0.32
angle (o)	179.82	0.23

residues per monomer	DNA	protein
	0	99



1mv5

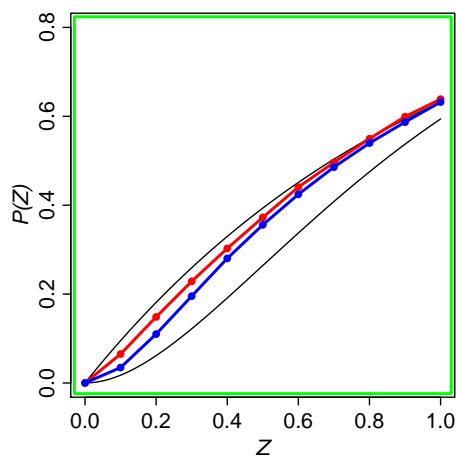
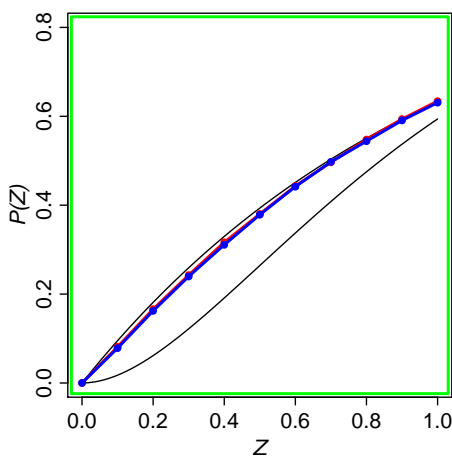
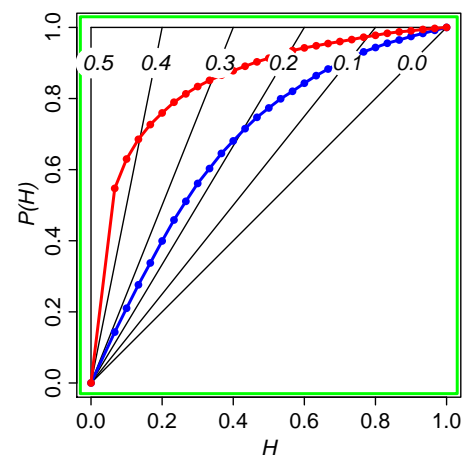
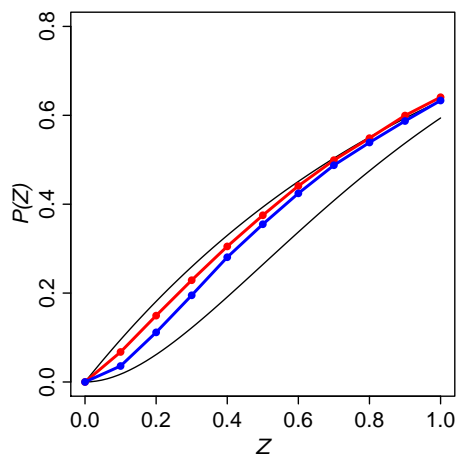
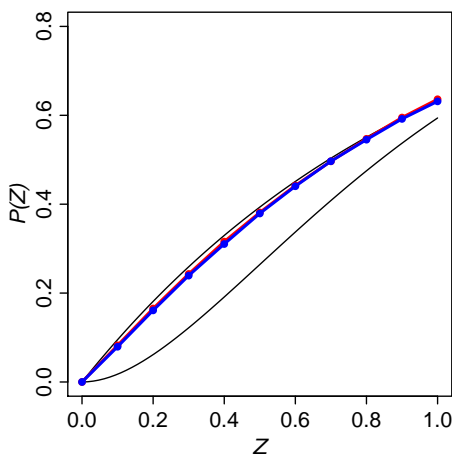
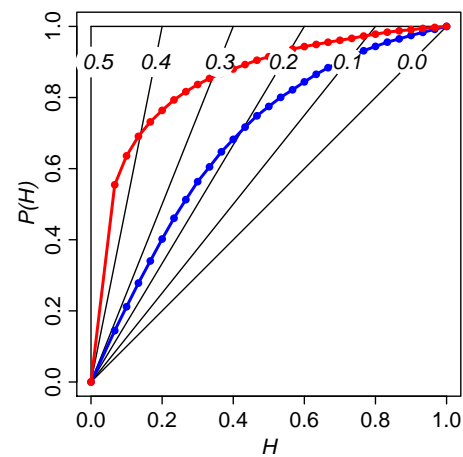
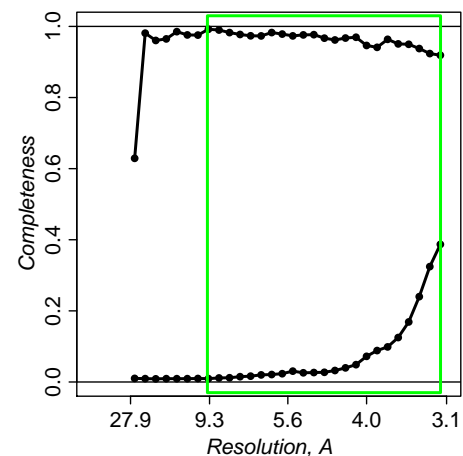
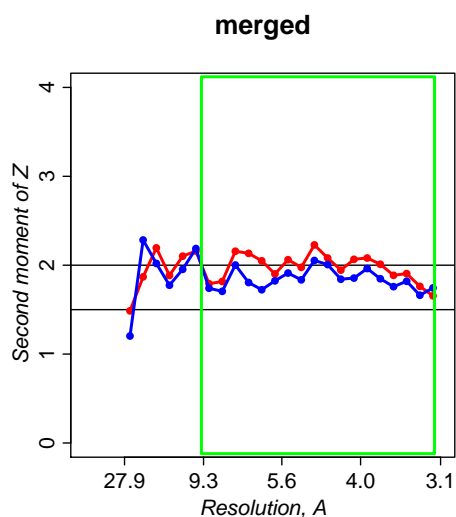
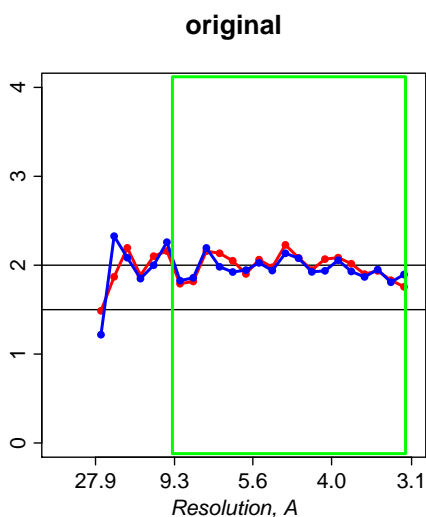
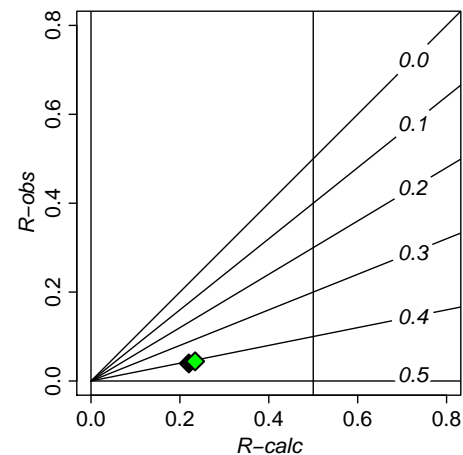
	original	merged
s.g.	P 63	P 63 2 2
p.g.	12021	12027
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		1.51
R	27.8	
R'	29.0	29.8
R-free	37.9	
R'-free	38.0	39.6

s < f/100	1895	7.95 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	28.7–3.1	9.9–3.1
unique	24,956	24,182
measured	23,832	23,077
used	20,896	20,368

NCS	translation	rotation
r.m.s.d. (A)	14.30	0.98
angle (o)	55.55	0.15

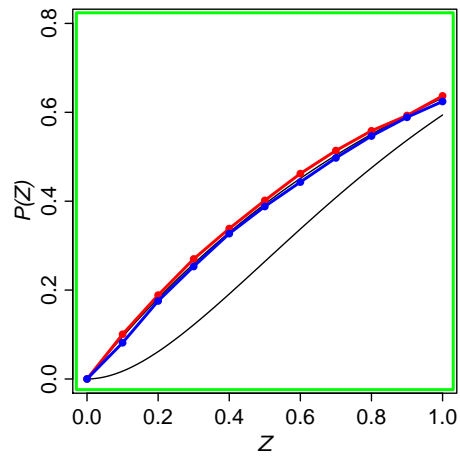
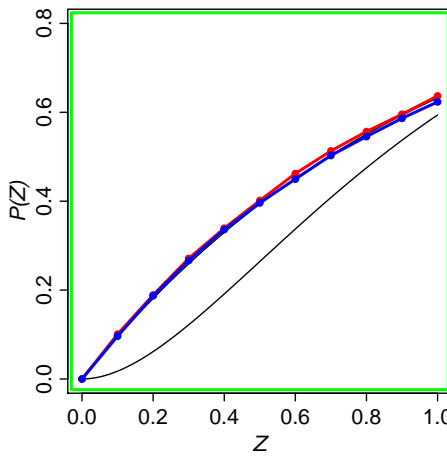
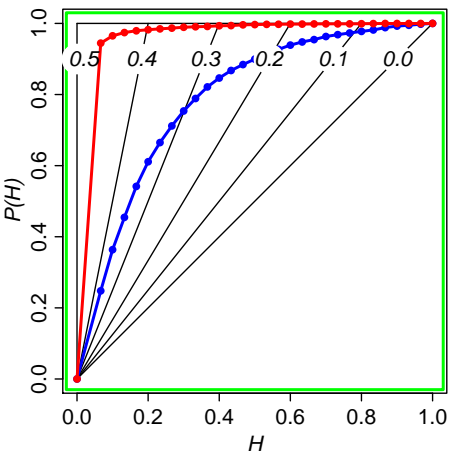
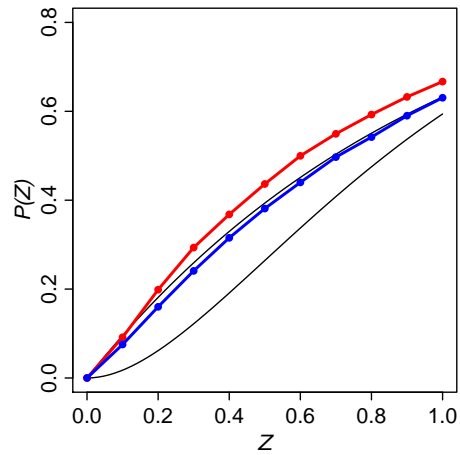
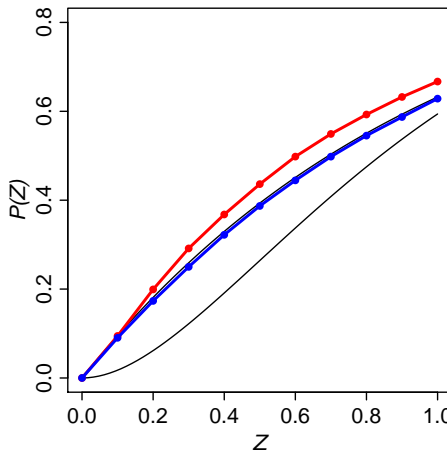
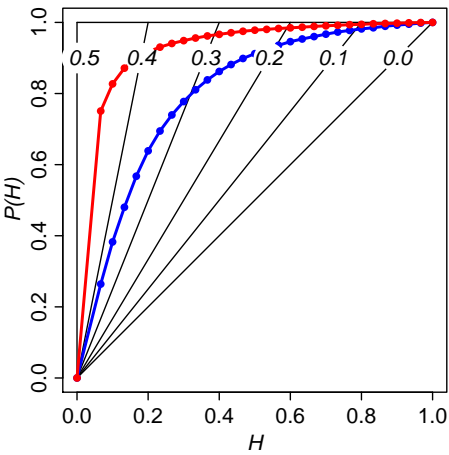
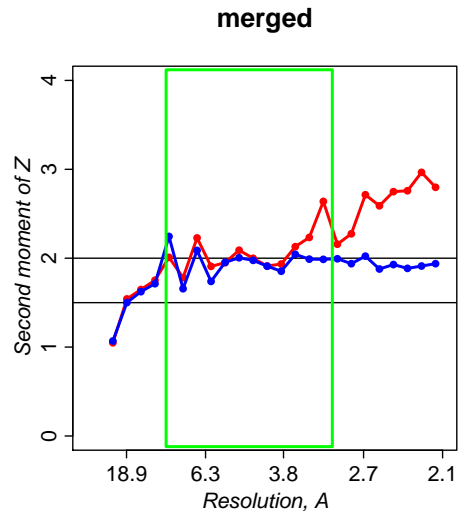
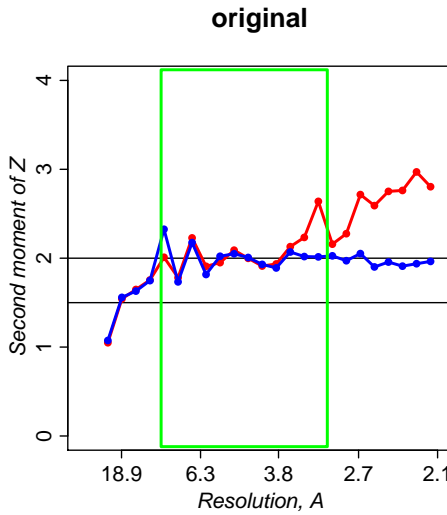
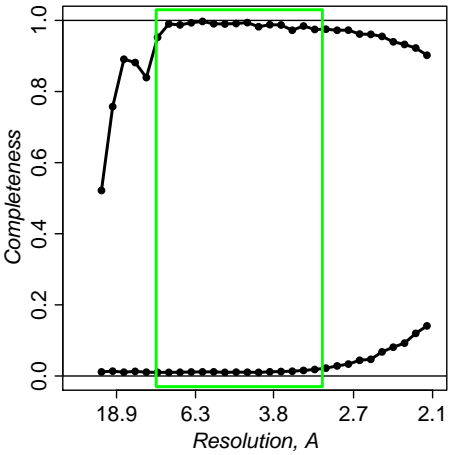
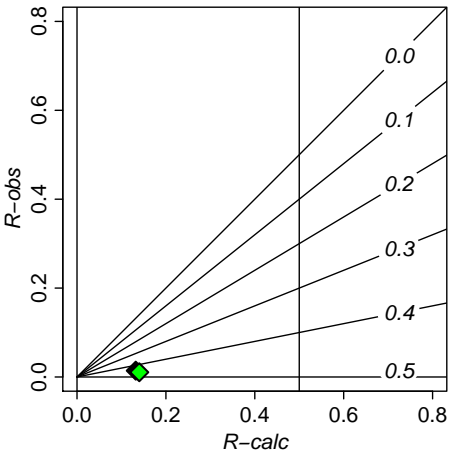
residues per monomer	DNA	protein
	0	241



1mw5

	original	merged
s.g.	P 64	P 64 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.16
R	26.5	
R'	27.3	28.5
R-free	28.6	
R'-free	30.2	31.2
residues per monomer	DNA 0	protein 162

s < f/100	3633	12.71 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	39.6–2.1	9.9–3.0
unique	29,894	10,026
measured	28,580	9,867
used	25,084	8,444
NCS	translation	rotation
r.m.s.d. (A)	36.57	0.16
angle (o)	179.94	0.06



1mwm

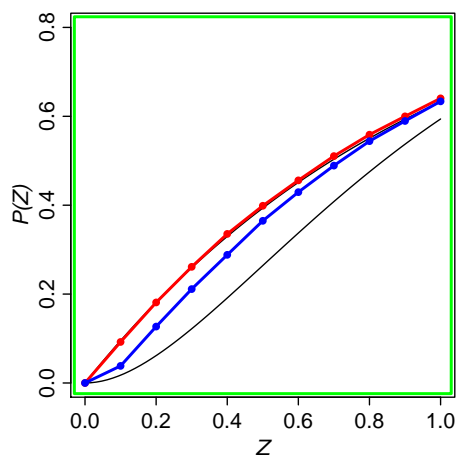
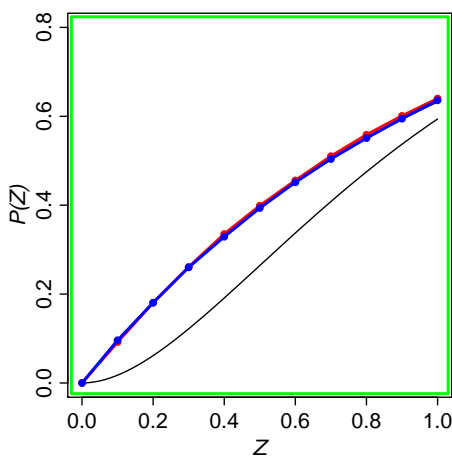
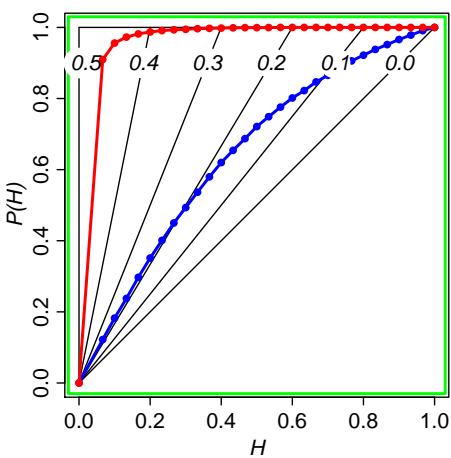
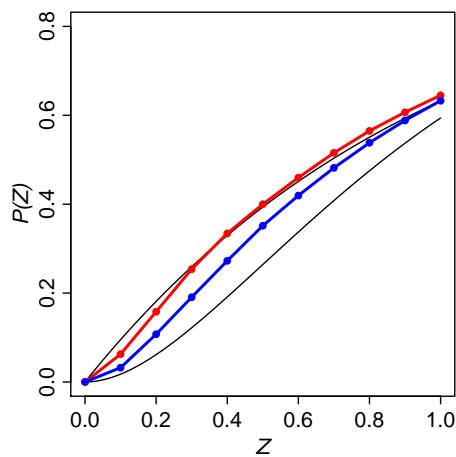
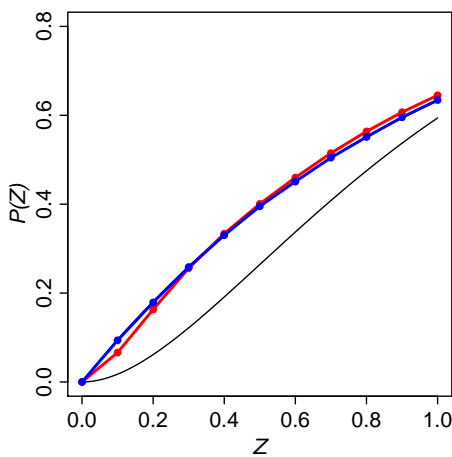
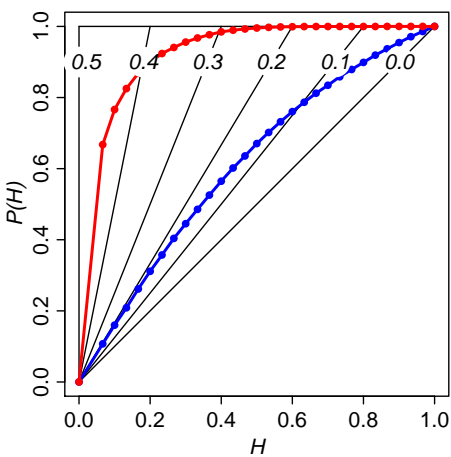
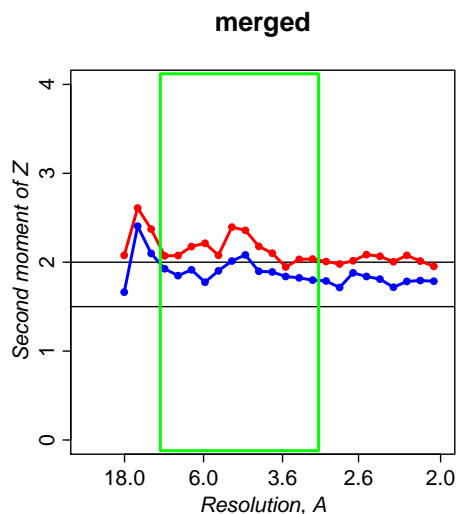
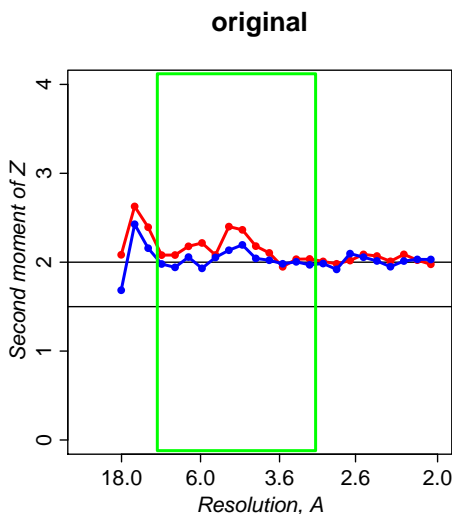
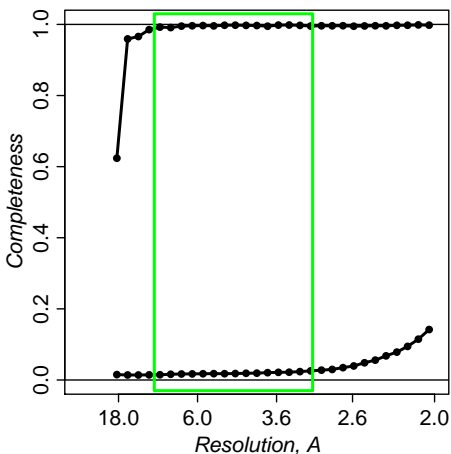
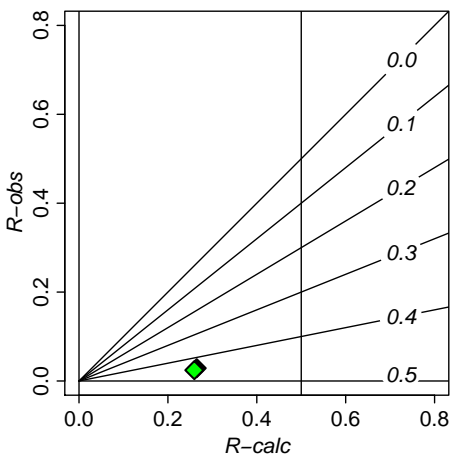
	original	merged
s.g.	P 41	P 41 2 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.61
R	28.1	
R'	28.2	29.0
R-free	31.9	
R'-free	32.3	33.1

s < f/100	109	0.20 %
s <= 0	48	0.09 %
f <= 0	48	0.09 %
s,f <= 0	48	0.09 %

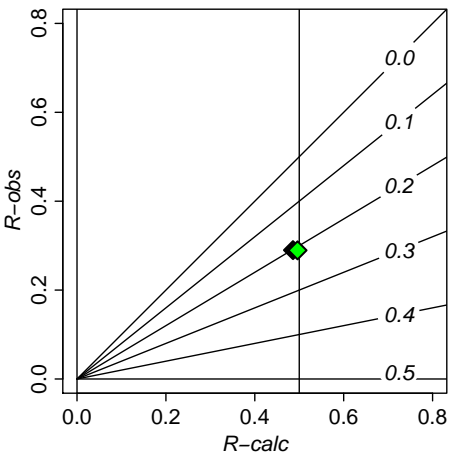
range (A)	21.9–2.0	9.9–3.0
unique	55,165	15,962
measured	54,974	15,908
used	50,024	13,872

NCS	translation	rotation
r.m.s.d. (A)	30.99	0.60
angle (o)	178.57	1.98

residues per monomer	DNA	protein
	0	316



1mzu



	original	merged
s.g.	P 1 21 1	-
p.g.	10001	10003
a.u.	3	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	27.4	-
R'	-	-
R-free	31.4	-
R'-free	-	-

s < f/100	3192	17.19 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

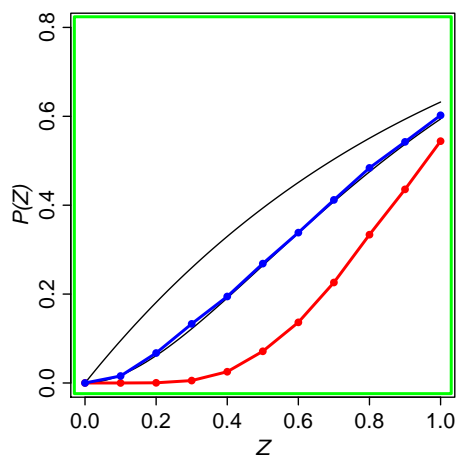
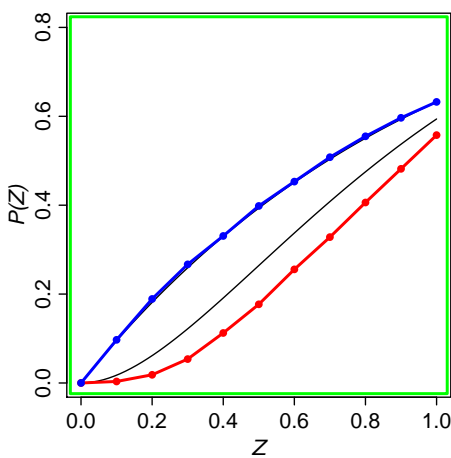
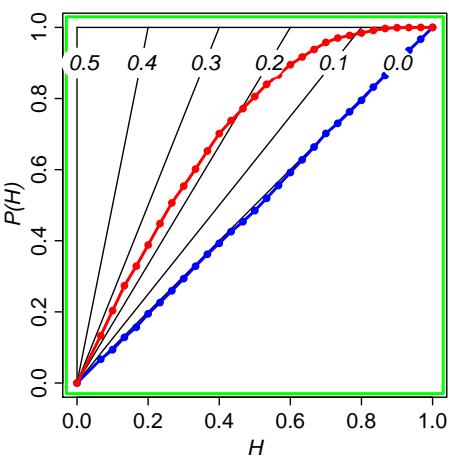
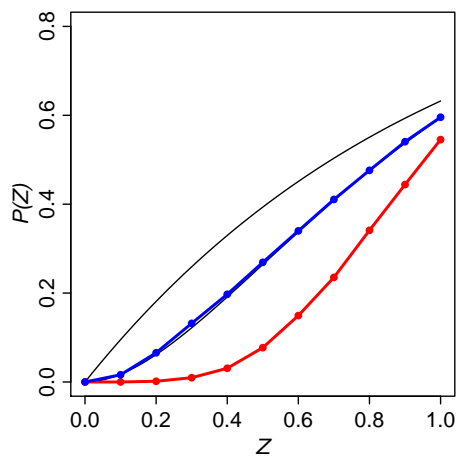
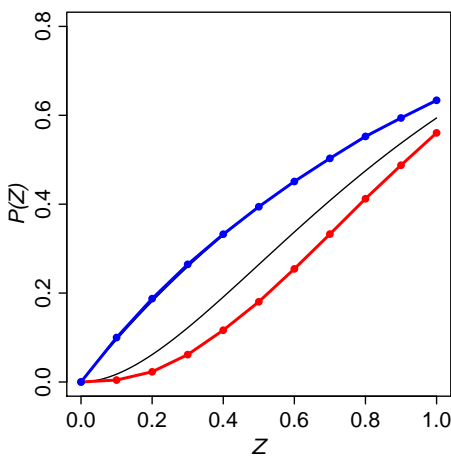
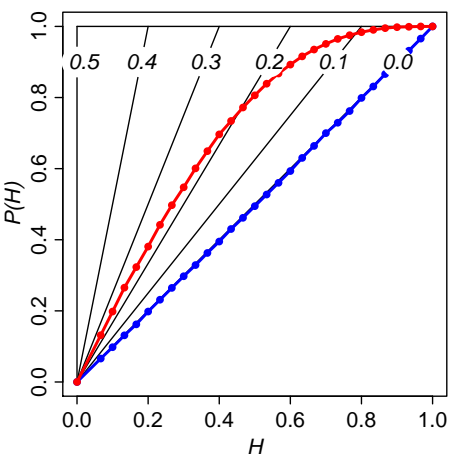
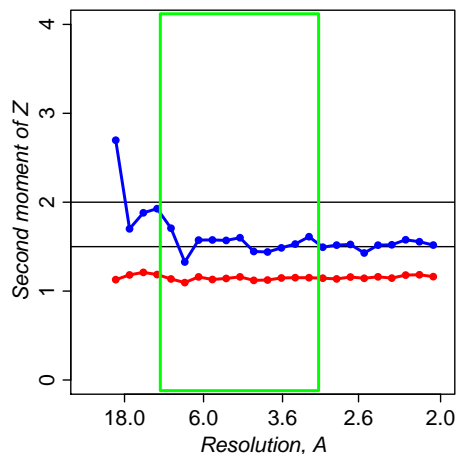
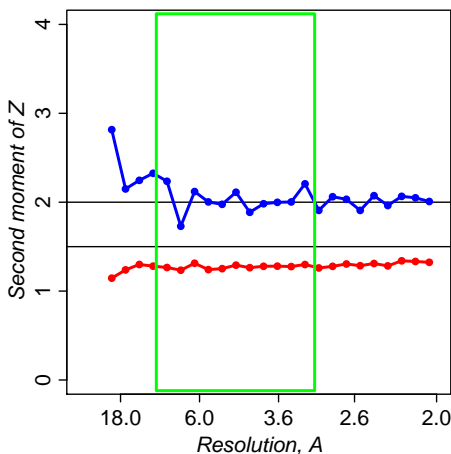
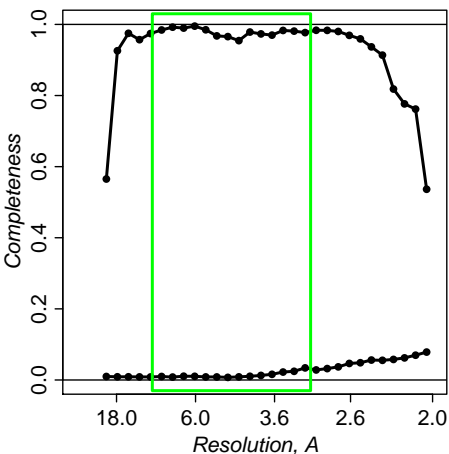
range (A)	29.9-2.0	9.9-3.0
unique	21,014	6,113
measured	18,566	5,966
used	15,394	5,188

NCS	translation	rotation
r.m.s.d. (A)	9.47	19.69
angle (o)	56.63	178.13

residues per monomer	DNA	protein
	0	101

original

merged



1n25

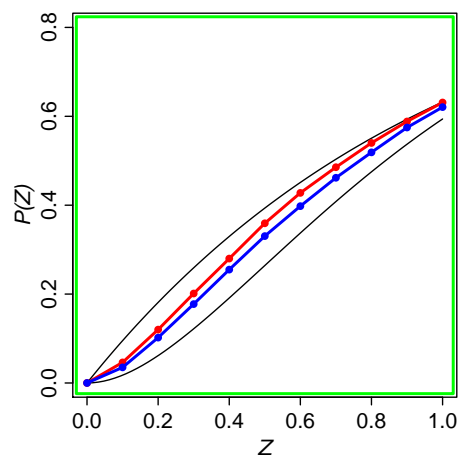
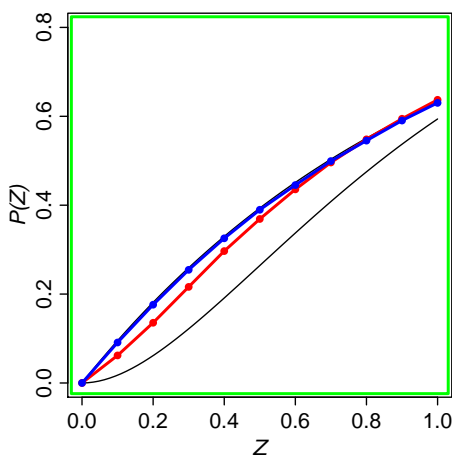
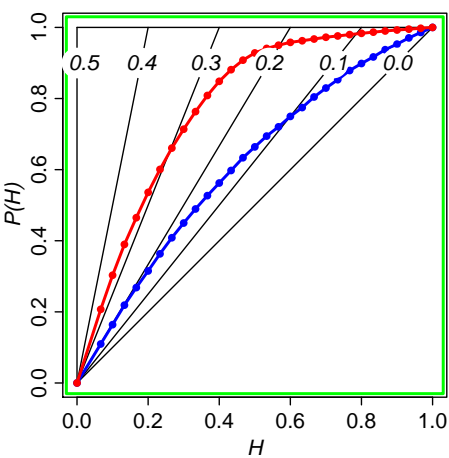
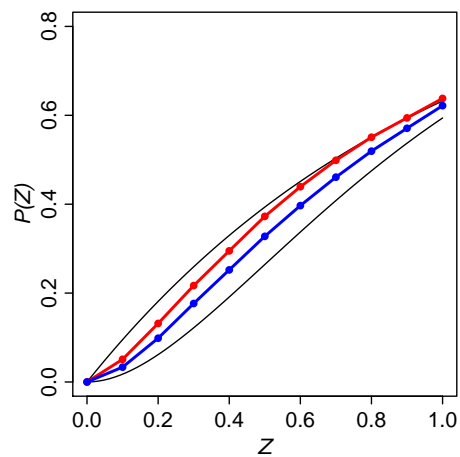
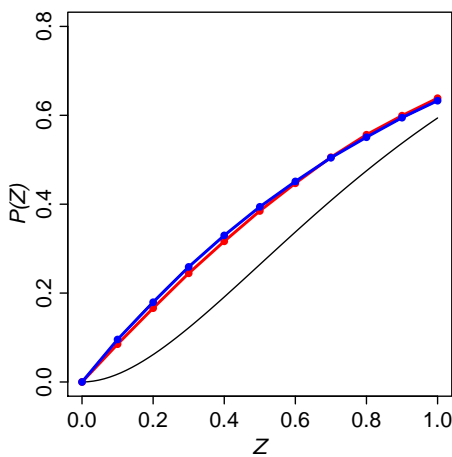
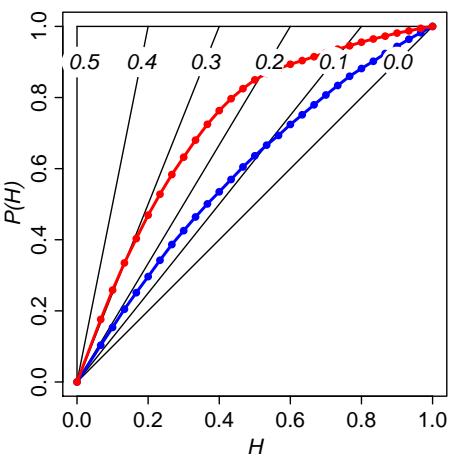
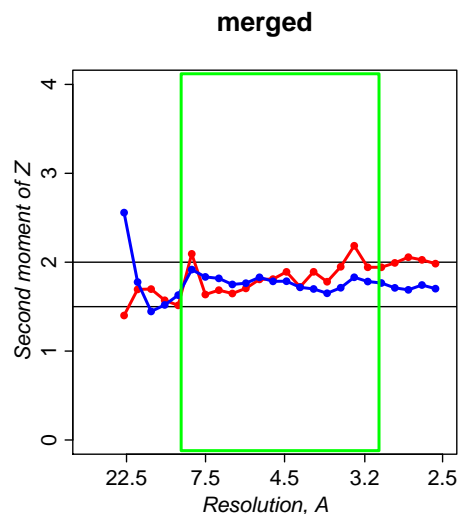
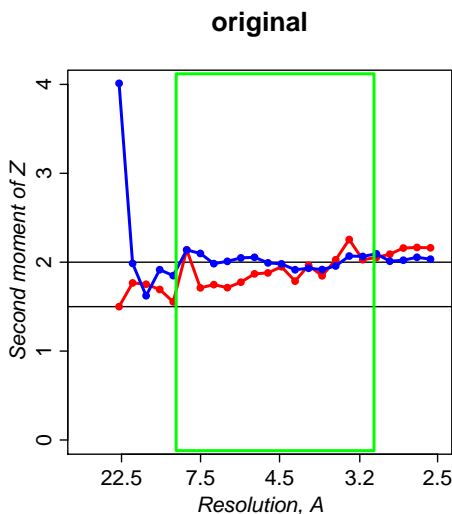
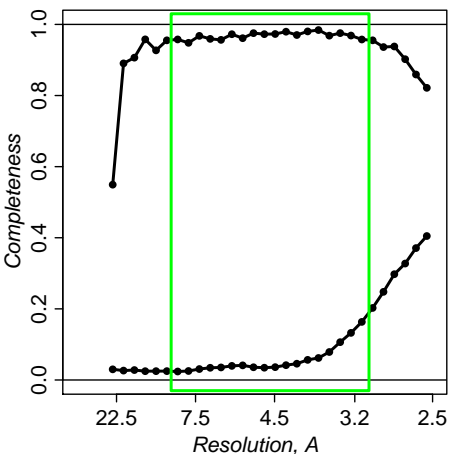
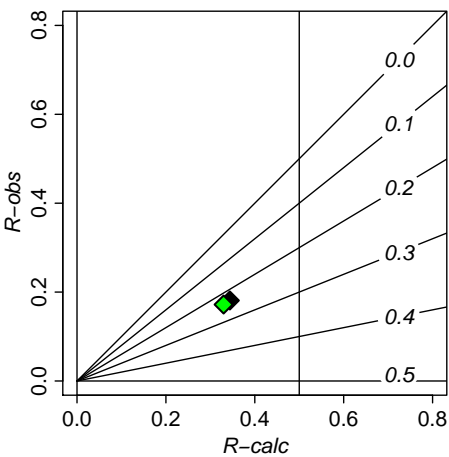
	original	merged
s.g.	P 3 2 1	-
p.g.	10023	12027
a.u.	2	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	26.1	-
R'	-	-
R-free	29.8	-
R'-free	-	-

residues per monomer	DNA	protein
	0	362

s < f/100	1460	4.03 %
s <= 0	1460	4.03 %
f <= 0	1460	4.03 %
s,f <= 0	1460	4.03 %

range (A)	29.4–2.5	9.9–3.0
unique	38,637	21,943
measured	36,187	21,265
used	31,264	18,420

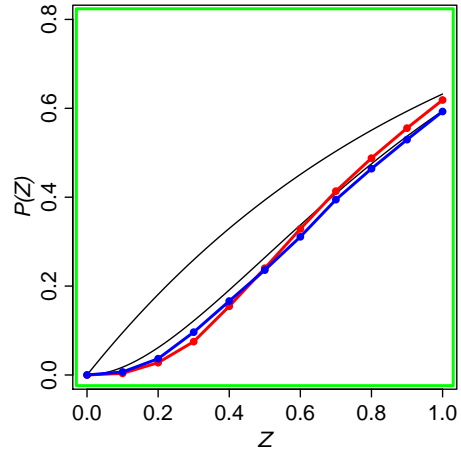
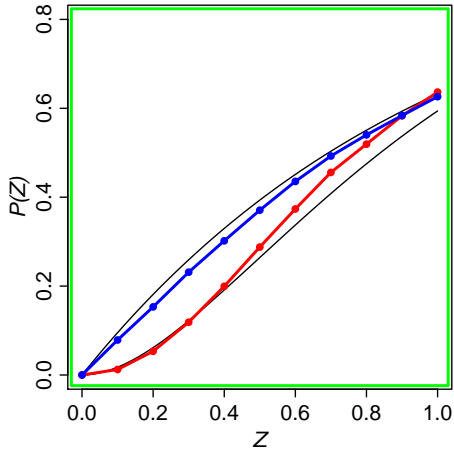
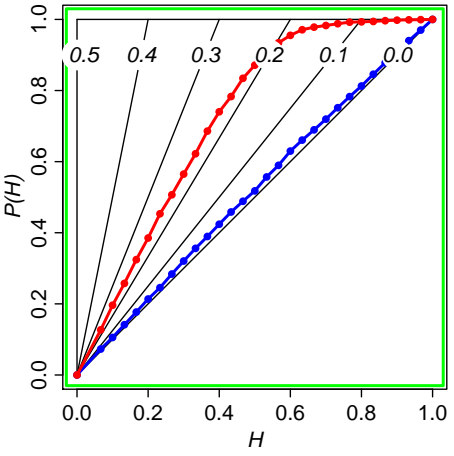
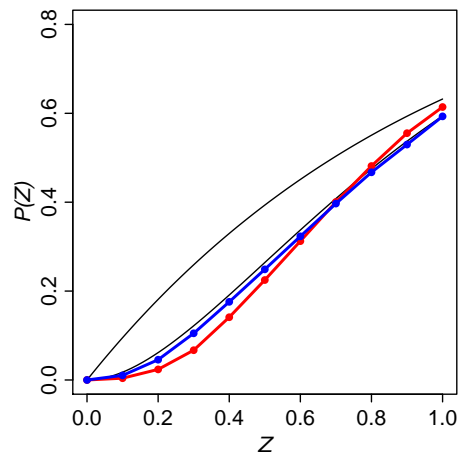
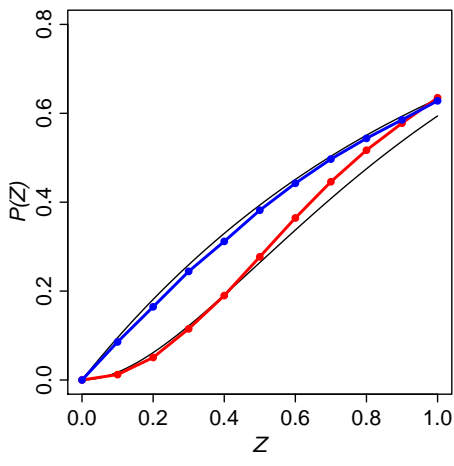
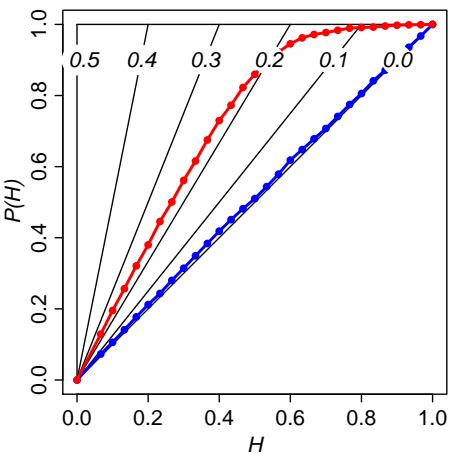
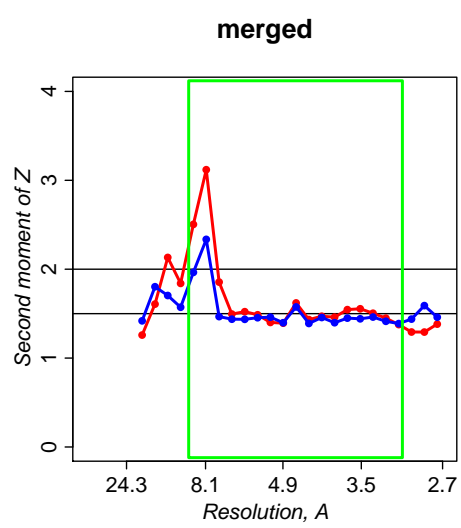
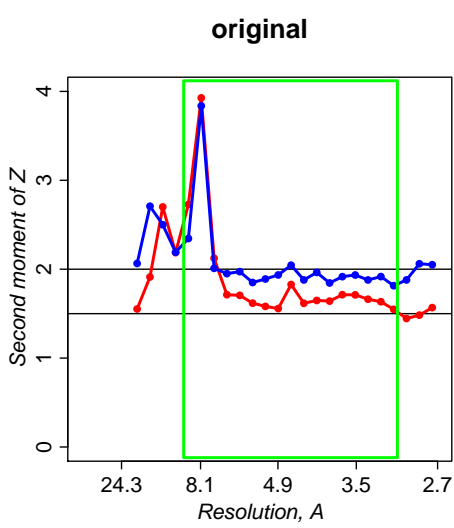
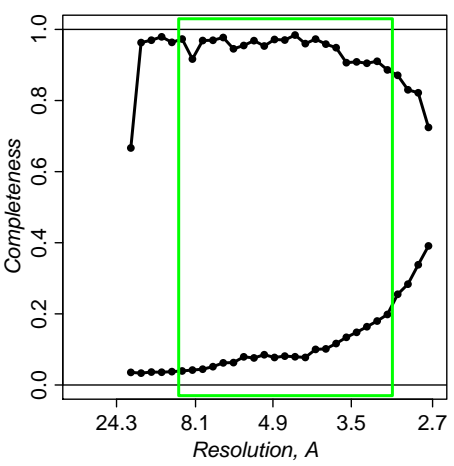
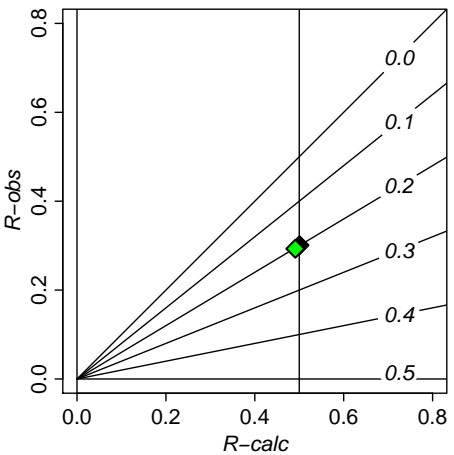
NCS	translation	rotation
r.m.s.d. (A)	16.38	0.42
angle (o)	59.77	0.40



1n44

	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	22.7	-
R'-free	31.6	-
R'-free	-	-
residues per monomer	DNA 0	protein 318

s < f/100	1	0.01 %
s <= 0	1	0.01 %
f <= 0	1	0.01 %
s,f <= 0	1	0.01 %
range (A)	19.7-2.7	9.9-3.0
unique	9,415	6,643
measured	8,459	6,212
used	7,408	5,582
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1n5c

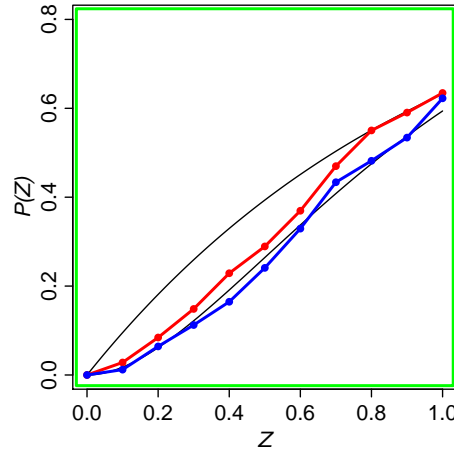
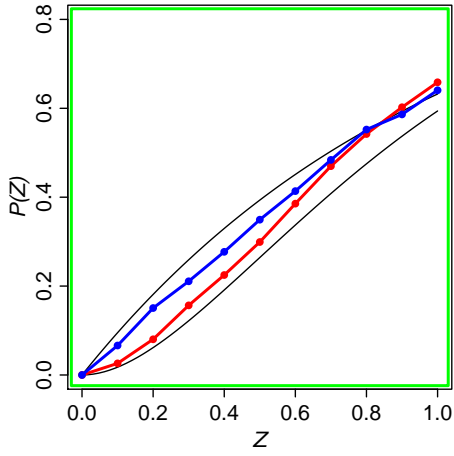
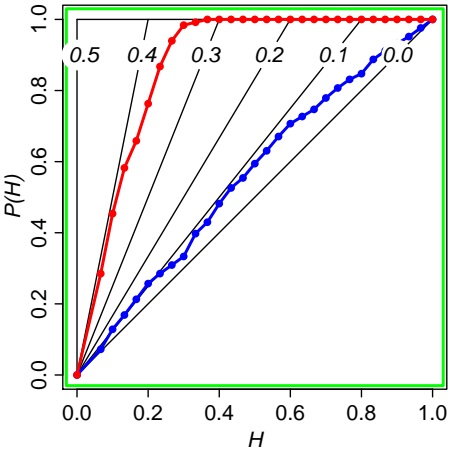
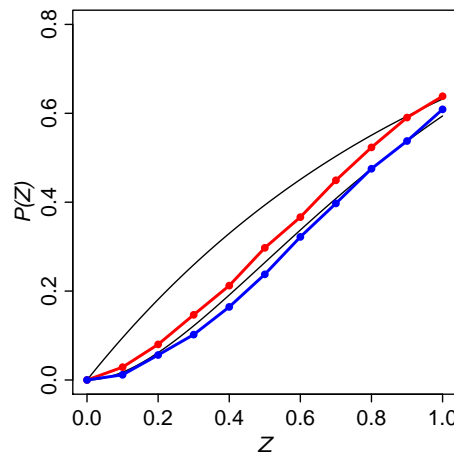
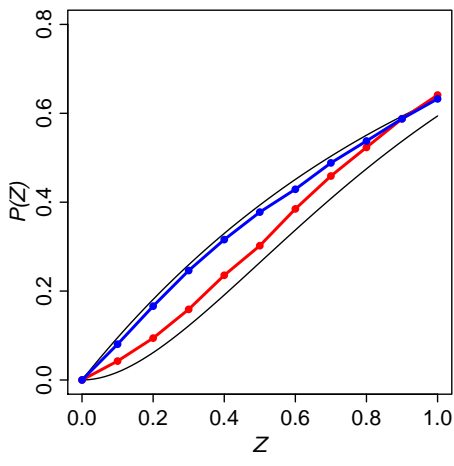
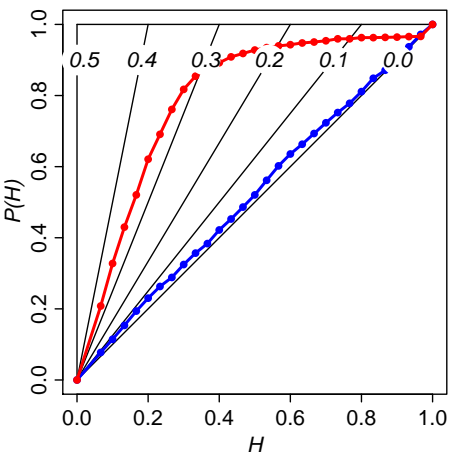
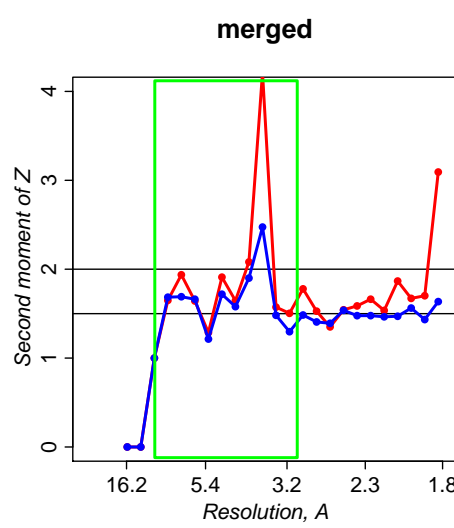
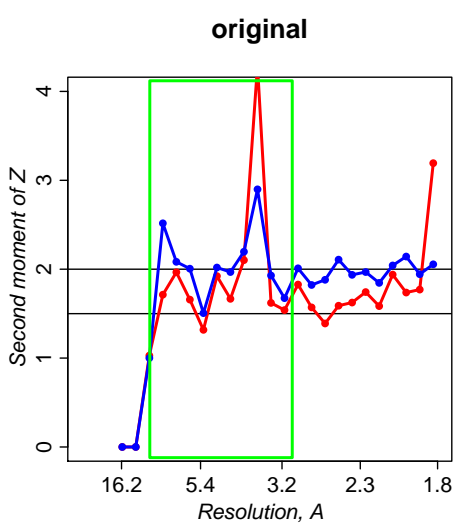
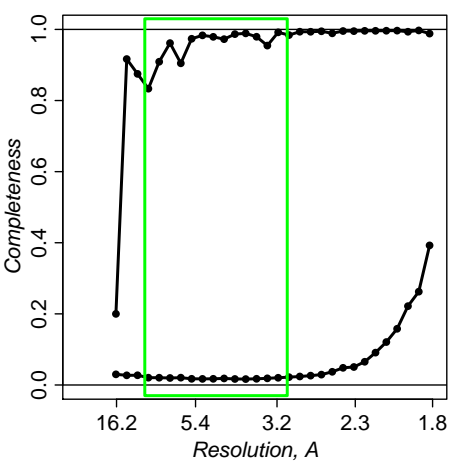
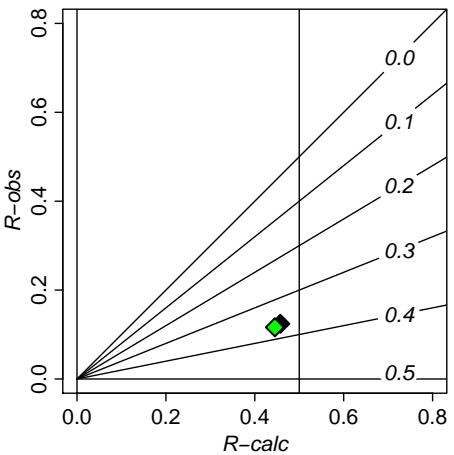
	original	merged
s.g.	P 32 1 2	-
p.g.	10023	12027
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	35.2	-
R'	-	-
R-free	36.9	-
R'-free	-	-

residues per monomer	DNA	protein
	10	0

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	95	2.30 %
s,f <= 0	0	0.00 %

range (A)	19.1-1.8	9.9-3.0
unique	4,175	901
measured	4,124	875
used	2,920	498

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



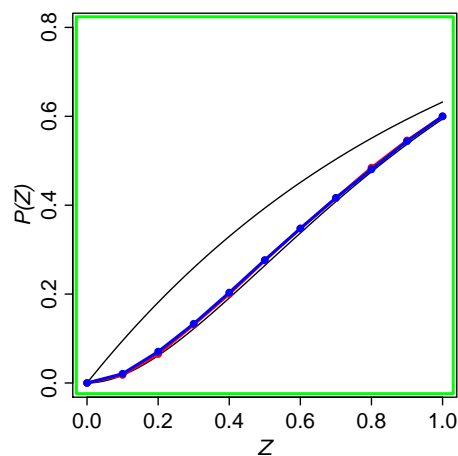
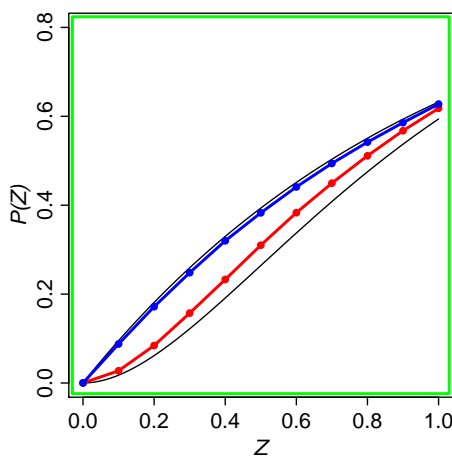
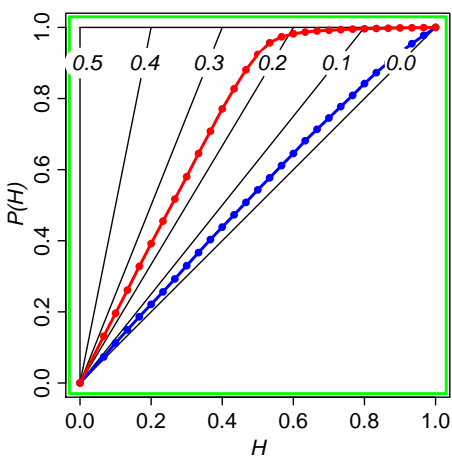
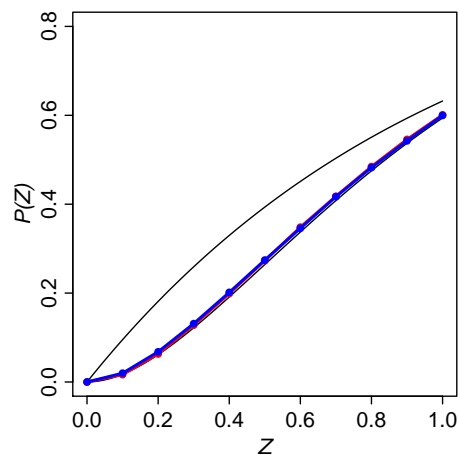
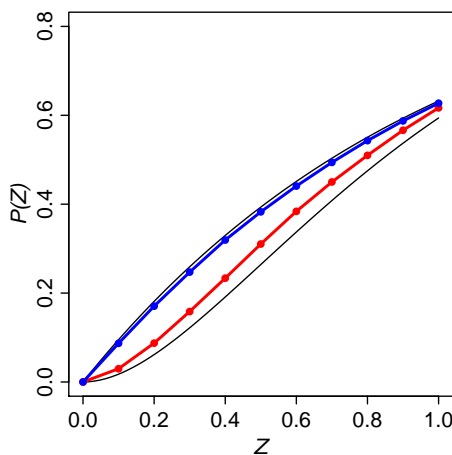
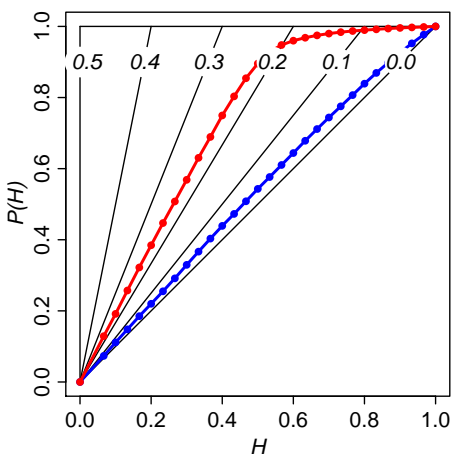
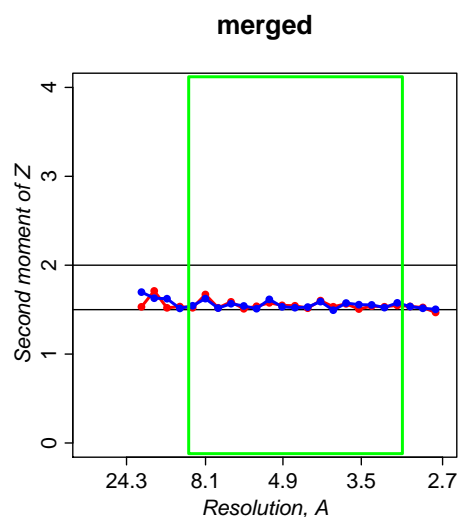
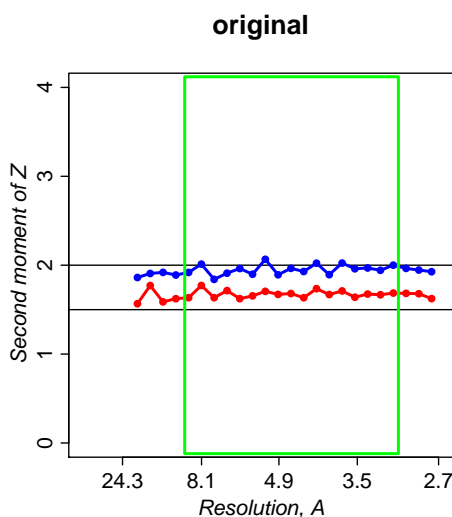
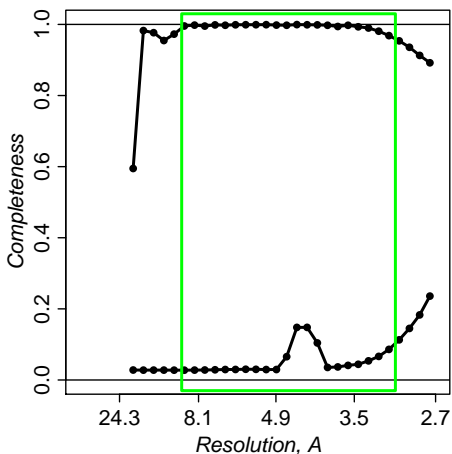
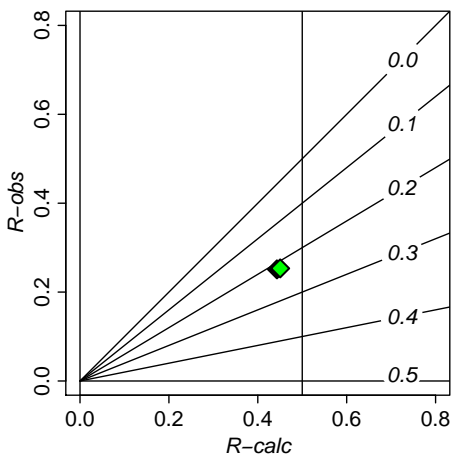
1nex

	original	merged
s.g.	P 32	P 65
p.g.	10020	12021
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		4.03
R	23.5	
R'	-	-
R-free	27.3	
R'-free	-	-
residues per monomer	DNA 0	protein 573

s < f/100	1052	1.82 %
s <= 0	1052	1.82 %
f <= 0	1052	1.82 %
s,f <= 0	1052	1.82 %

range (A)	20.0–2.7	9.9–3.0
unique	59,512	42,482
measured	57,751	42,078
used	55,618	41,216

NCS	translation	rotation
r.m.s.d. (A)	24.55	3.58
angle (o)	53.39	6.74



1nfr

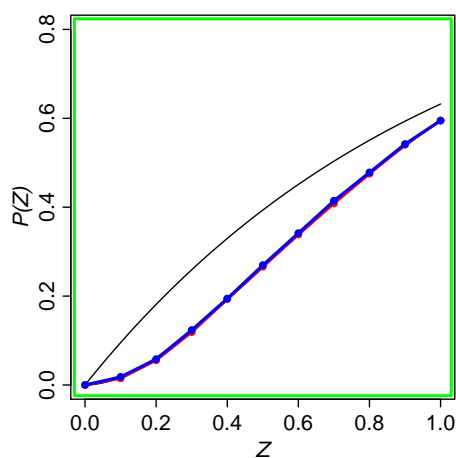
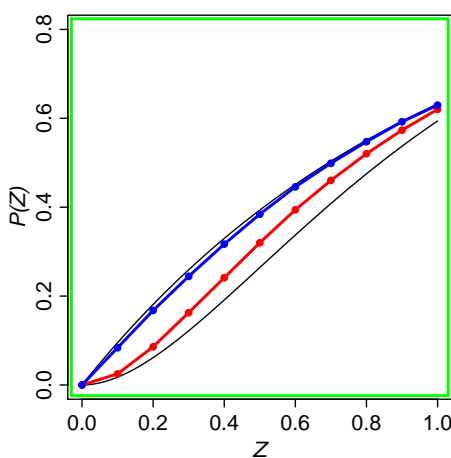
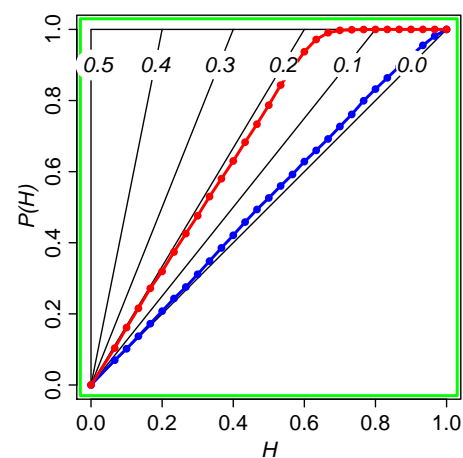
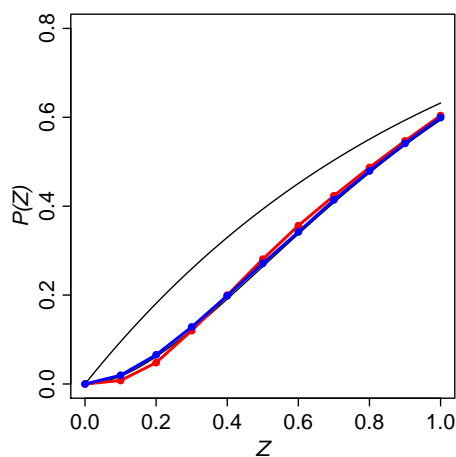
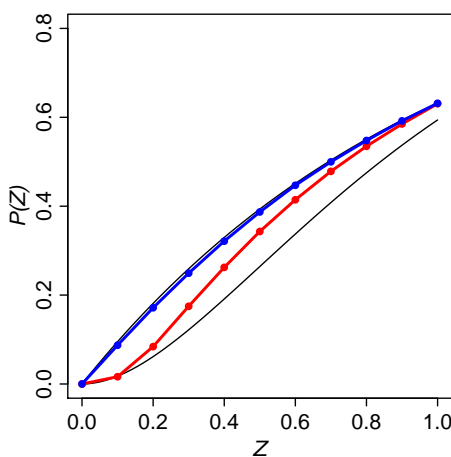
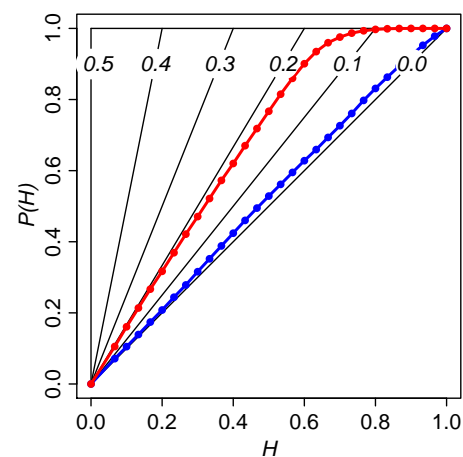
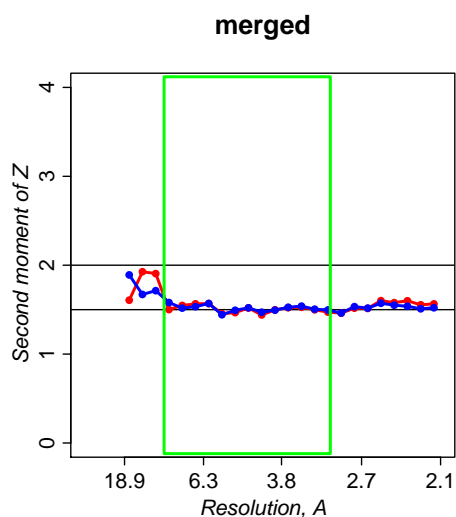
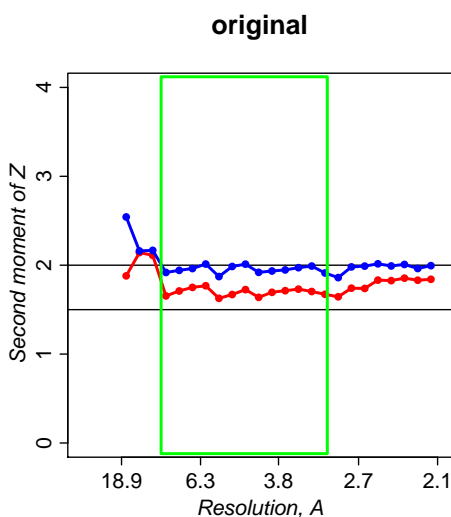
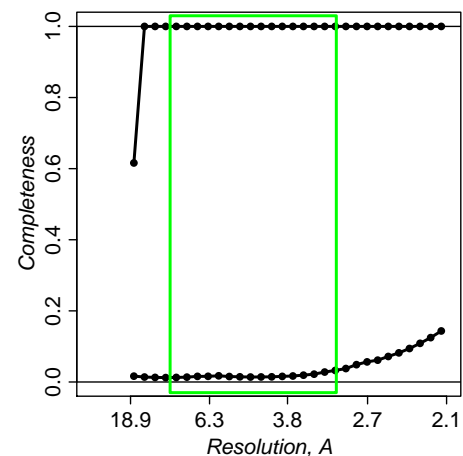
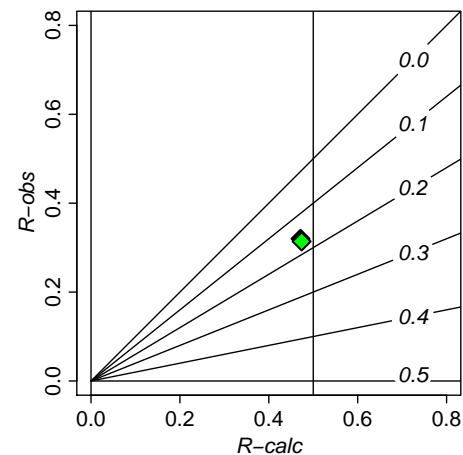
	original	merged
s.g.	14	-
p.g.	10201	10205
a.u.	4	-
p.t.	2	-
p.o.	2	-
r.m.s.d. (A)	-	-
R	23.6	-
R'	-	-
R-free	25.6	-
R'-free	-	-

residues per monomer	DNA	protein
	0	244

s < f/100	981	1.70 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.9–2.1	9.9–3.0
unique	57,607	19,315
measured	57,609	19,315
used	53,846	17,624

NCS	translation	rotation
r.m.s.d. (A)	6.62	1.27
angle (o)	26.53	5.36



1nfz

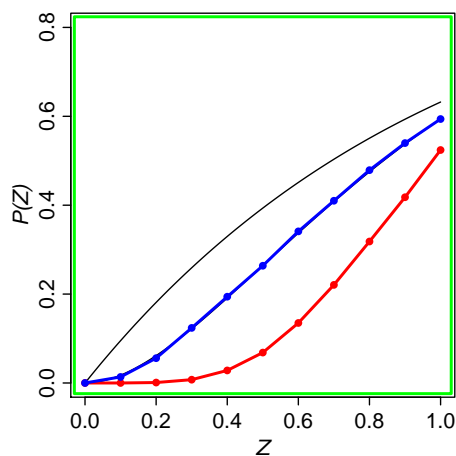
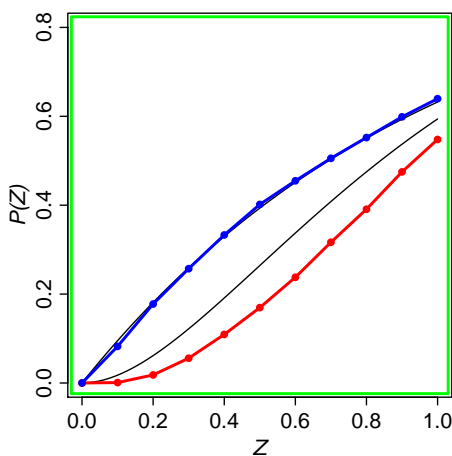
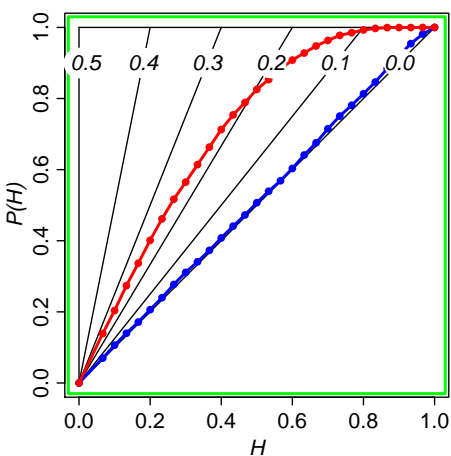
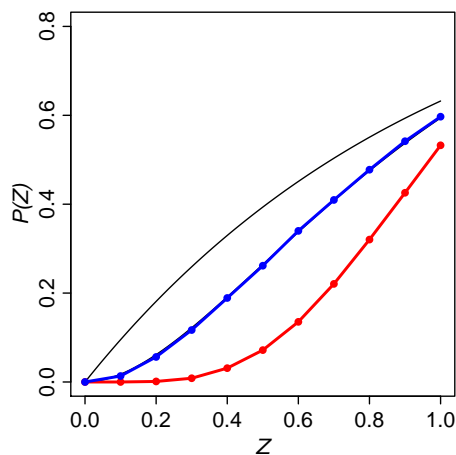
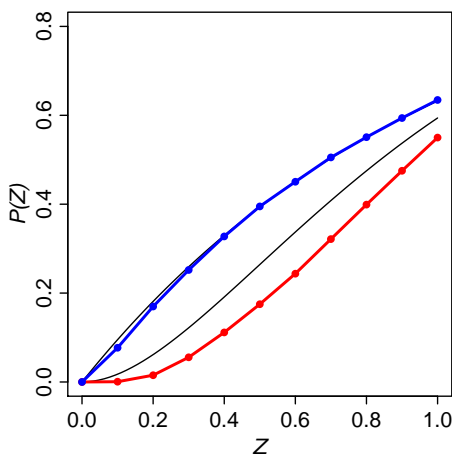
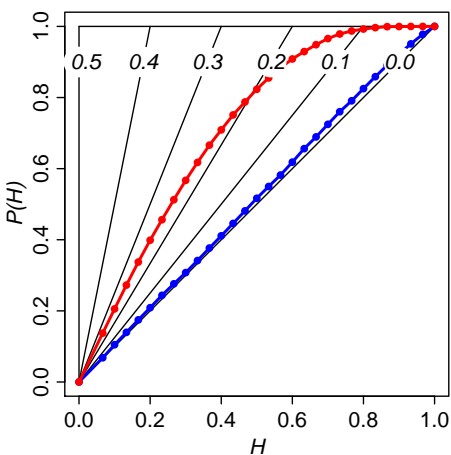
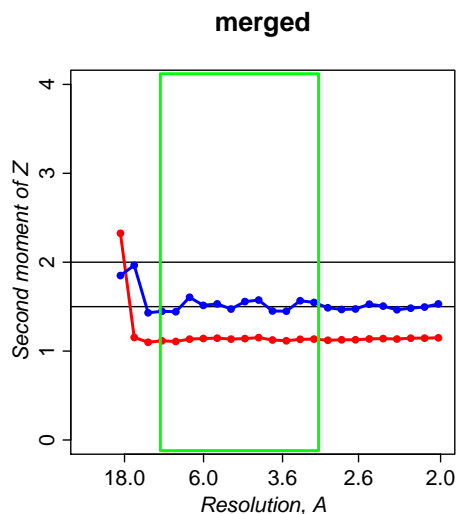
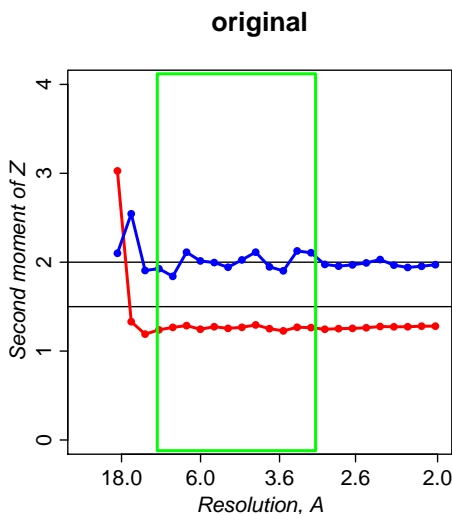
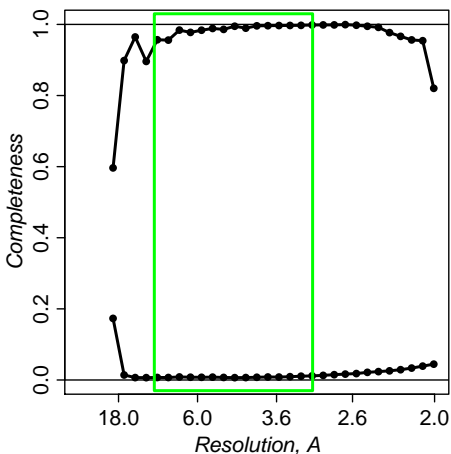
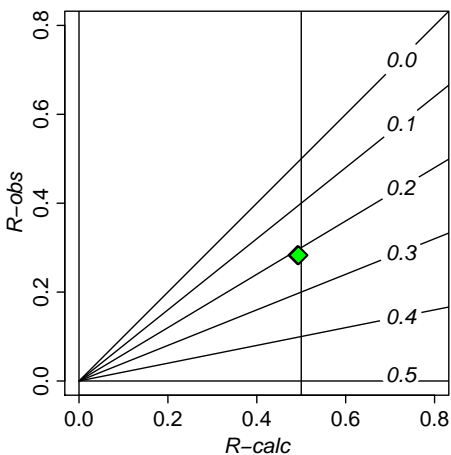
	original	merged
s.g.	P 21 21 21	-
p.g.	10003	10205
a.u.	2	-
p.t.	2	-
p.o.	4	-
r.m.s.d. (A)	-	-
R	28.0	-
R'	-	-
R-free	30.4	-
R'-free	-	-

	11858	37.25 %
s < f/100		
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

	24.9-2.0	9.9-3.0
range (A)		
unique	32,850	9,319
measured	31,834	9,245
used	26,660	7,768

NCS	translation	rotation
r.m.s.d. (A)	11.48	19.34
angle (o)	55.14	98.79

residues per monomer	DNA	protein
	0	176



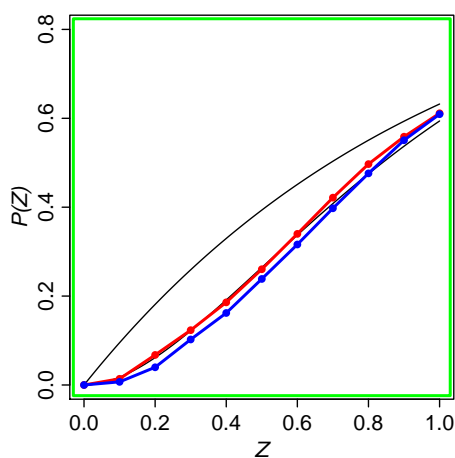
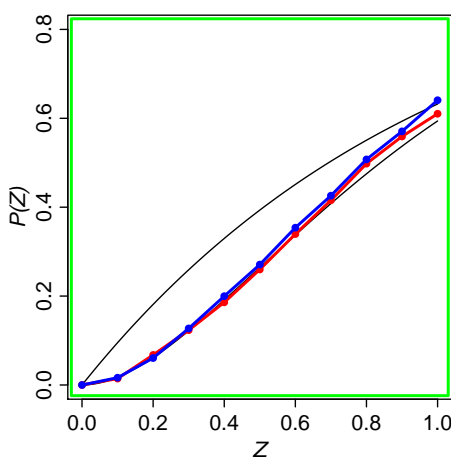
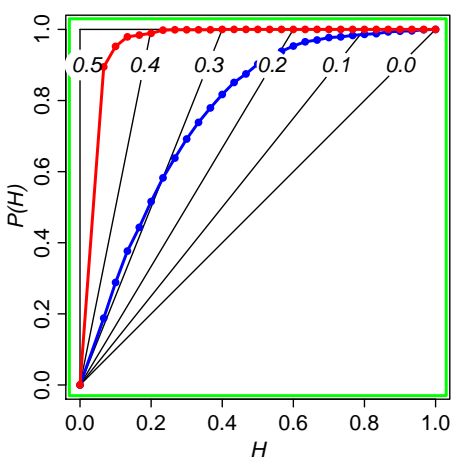
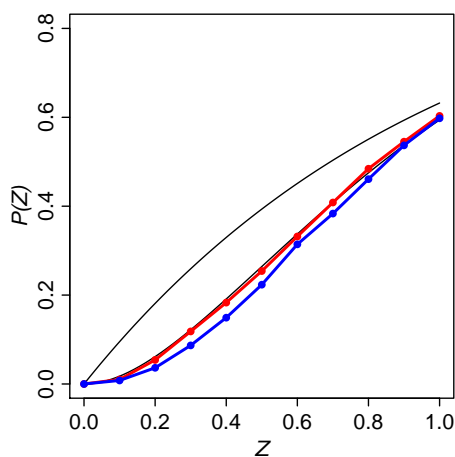
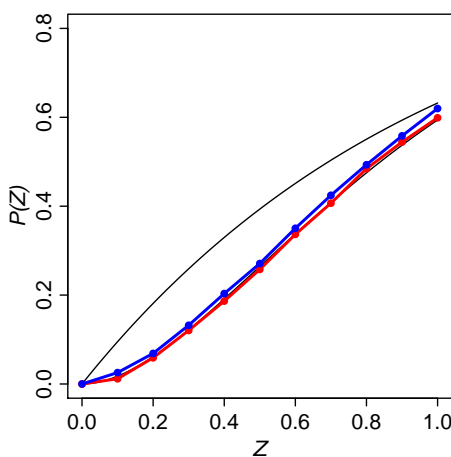
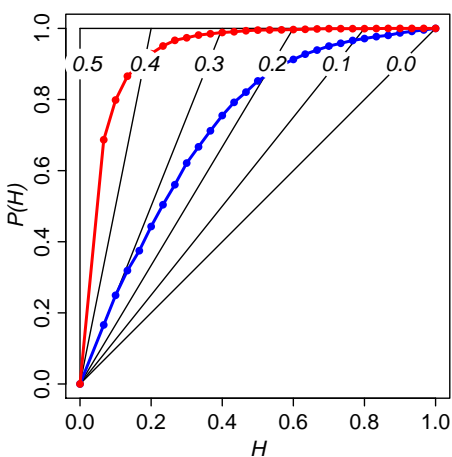
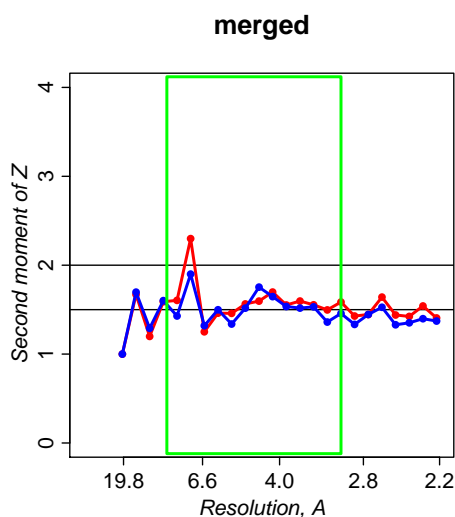
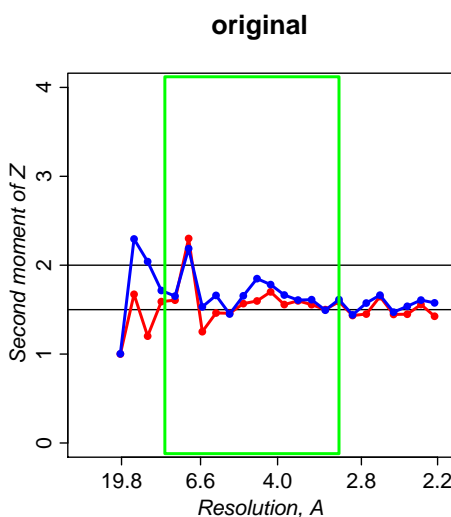
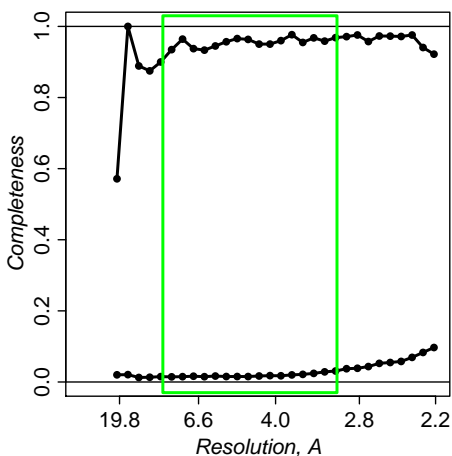
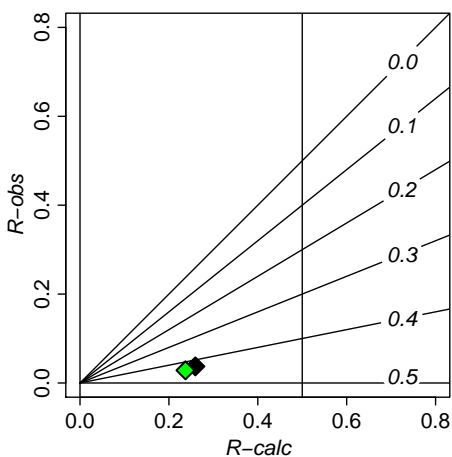
1nr2

	original	merged
s.g.	P 41	P 41 21 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		7.88
R	29.9	
R'	-	-
R-free	33.7	
R'-free	-	-
residues per monomer	DNA 0	protein 62

s < f/100	52	0.78 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	24.8–2.2	9.9–3.0
unique	6,931	2,606
measured	6,647	2,498
used	5,550	1,998

NCS	translation	rotation
r.m.s.d. (A)	18.19	5.13
angle (o)	177.40	30.96



1nsk

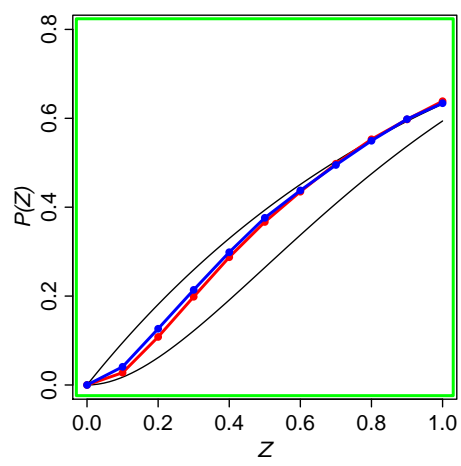
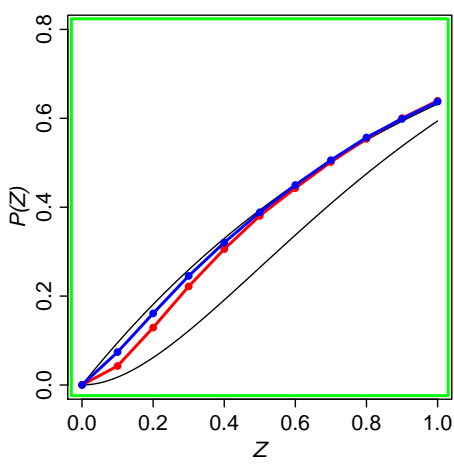
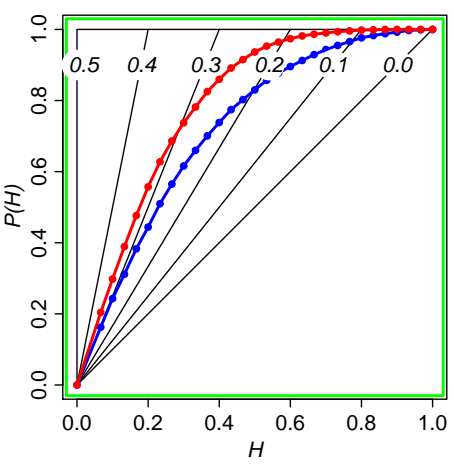
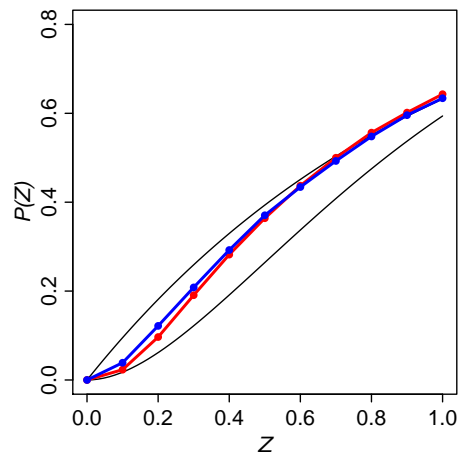
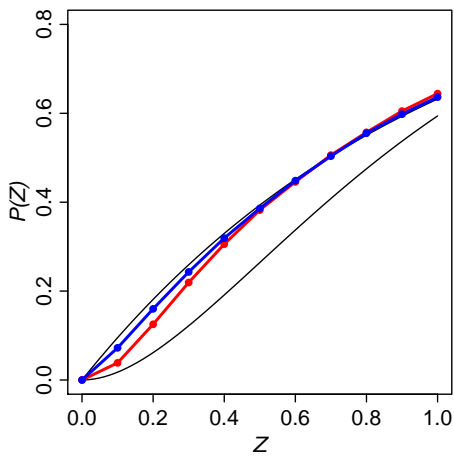
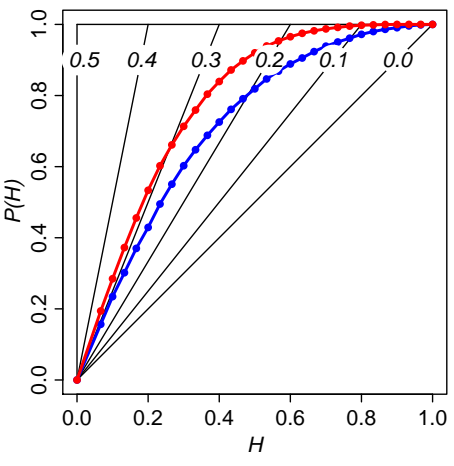
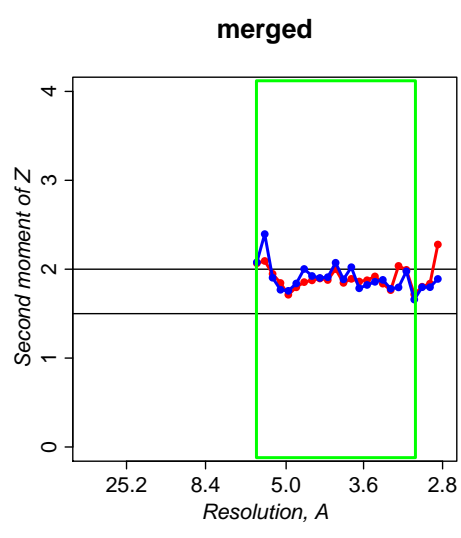
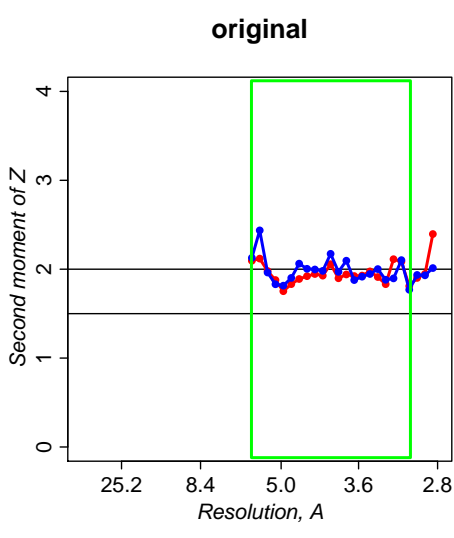
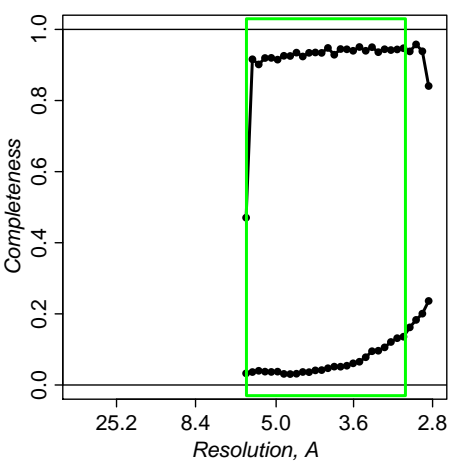
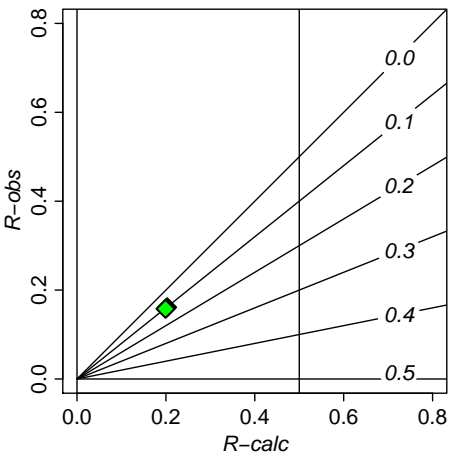
	original	merged
s.g.	P 21 21 21	P 41 21 2
p.g.	10003	10205
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.56
R	23.2	
R'	23.4	23.7
R-free	29.7	
R'-free	30.2	30.4

s < f/100	1	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	6.0–2.8	6.0–3.0
unique	28,434	22,759
measured	26,512	21,321
used	23,066	18,532

NCS	translation	rotation
r.m.s.d. (A)	16.58	0.22
angle (o)	87.99	0.95

residues per monomer	DNA	protein
	0	151



1nt0

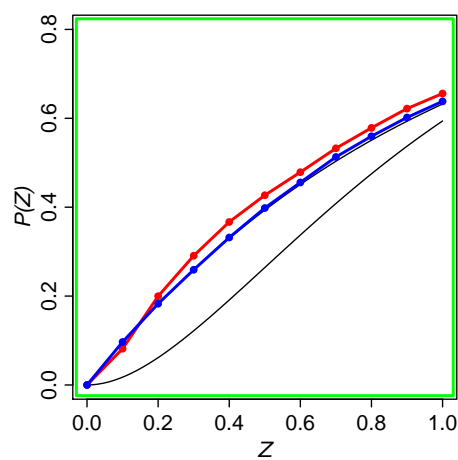
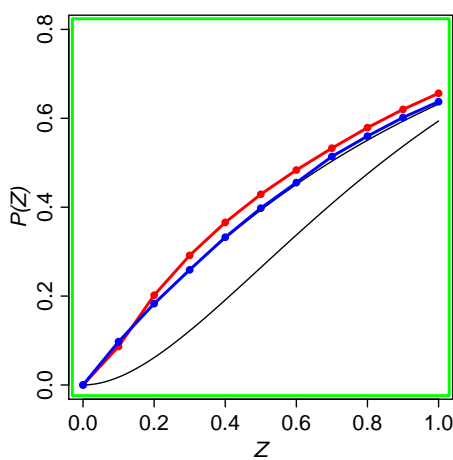
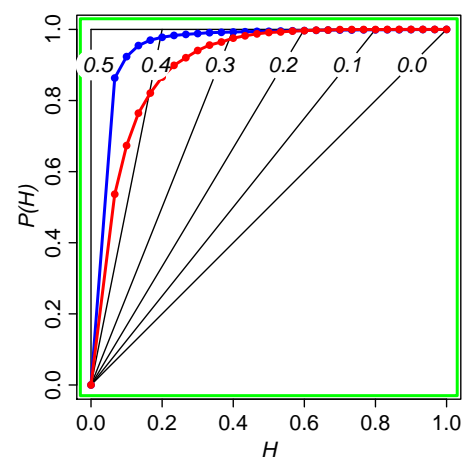
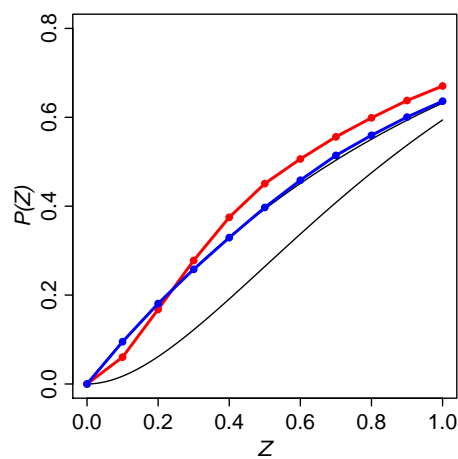
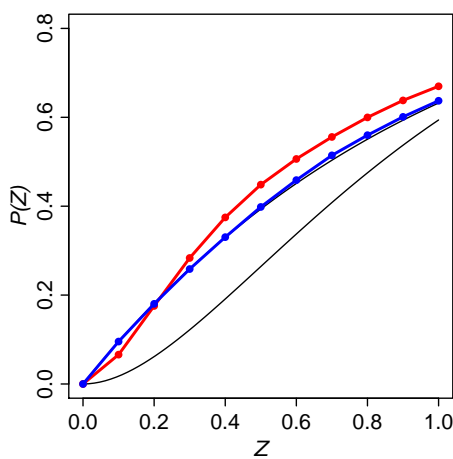
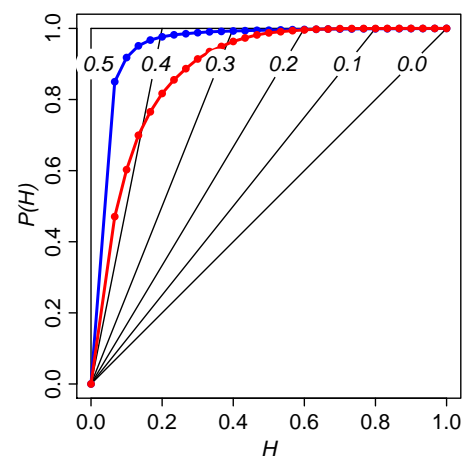
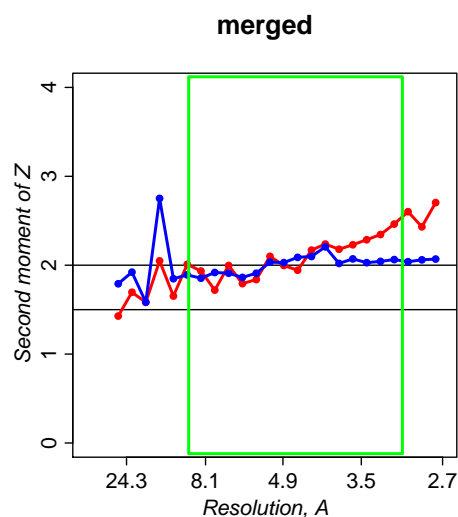
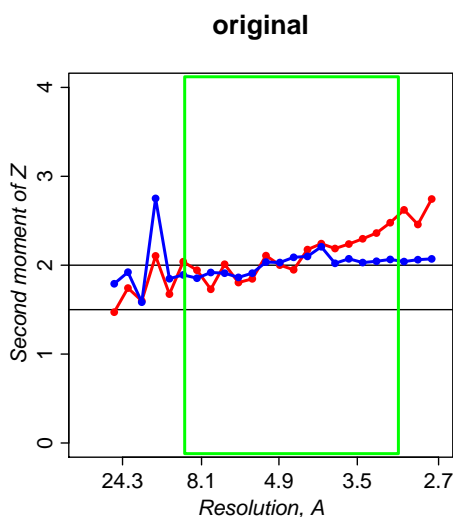
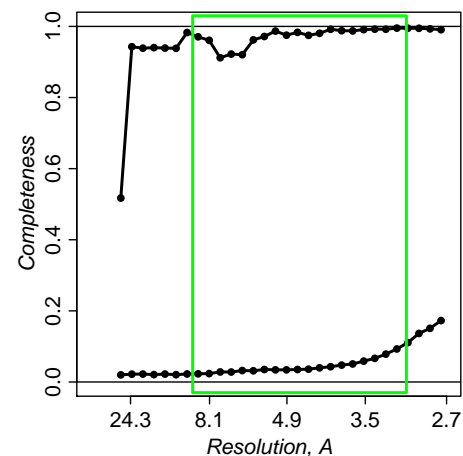
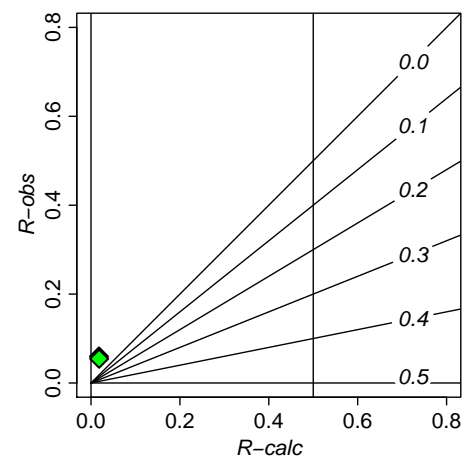
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.05
R	26.2	
R'	26.2	26.5
R-free	30.7	
R'-free	30.6	30.8

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	39.6–2.7	9.9–3.0
unique	24,252	17,203
measured	23,873	16,900
used	21,728	15,304

NCS	translation	rotation
r.m.s.d. (A)	62.99	0.03
angle (o)	179.95	0.09

residues per monomer	DNA	protein
	0	256



1nuj

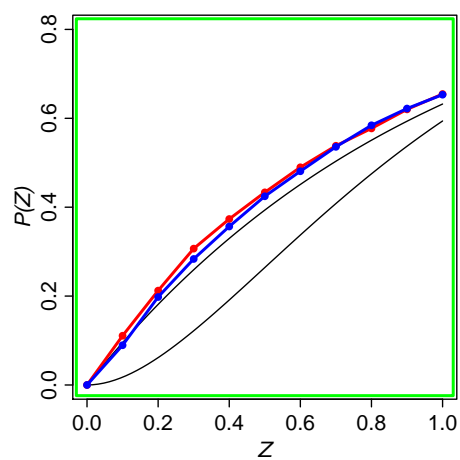
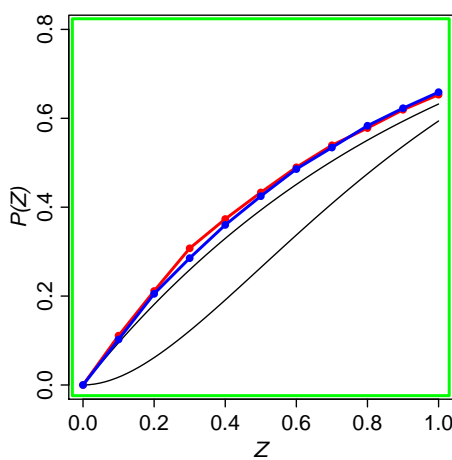
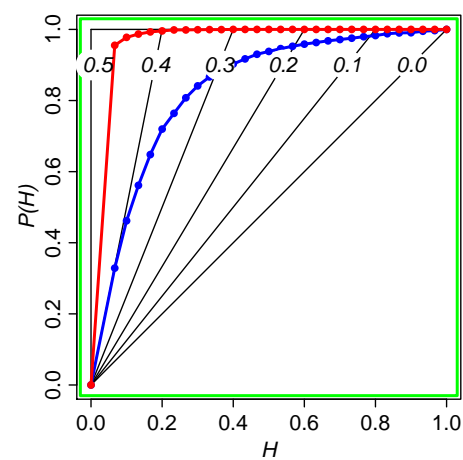
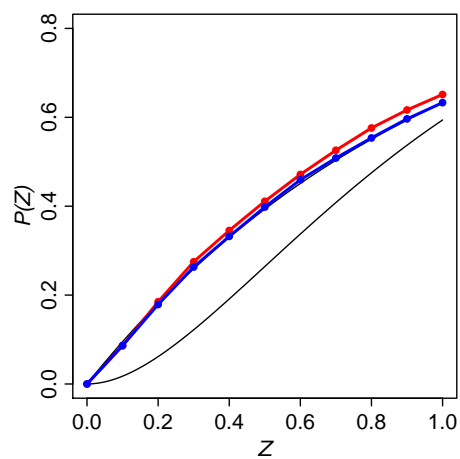
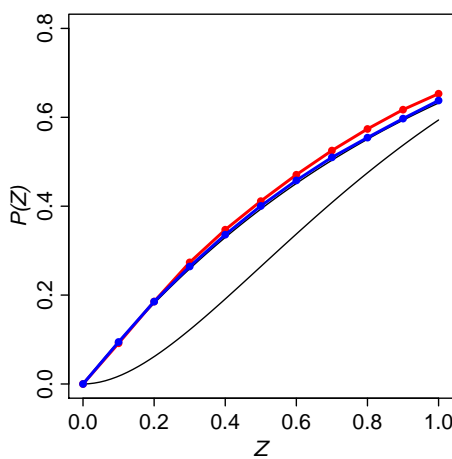
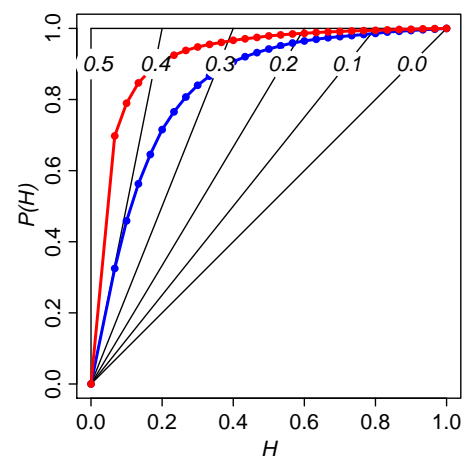
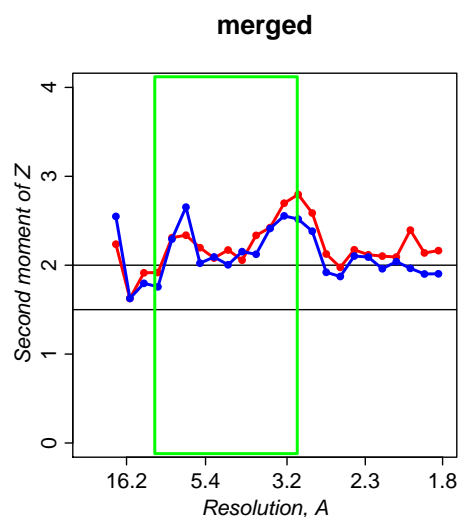
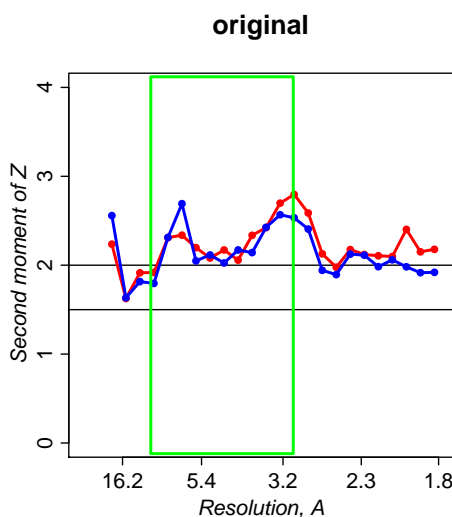
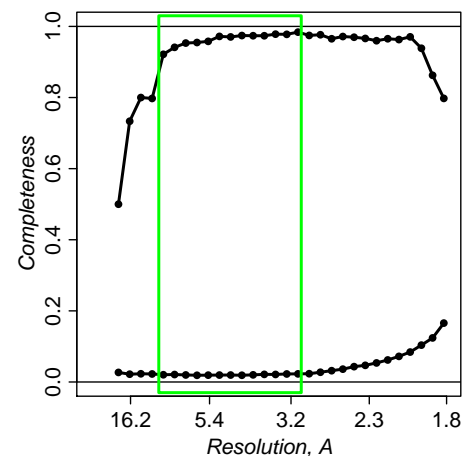
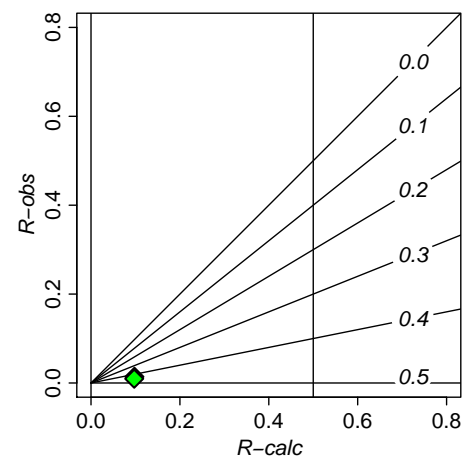
	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		0.08
R	28.7	
R'	28.6	29.8
R-free	31.5	
R'-free	31.3	32.6

s < f/100	198	0.81 %
s <= 0	198	0.81 %
f <= 0	198	0.81 %
s,f <= 0	198	0.81 %

range (A)	29.3–1.8	9.9–3.0
unique	25,843	5,337
measured	24,309	5,181
used	21,130	4,282

NCS	translation	rotation
r.m.s.d. (A)	2.45	0.04
angle (o)	6.95	0.06

residues per monomer	DNA	protein
	22	0



1nuv

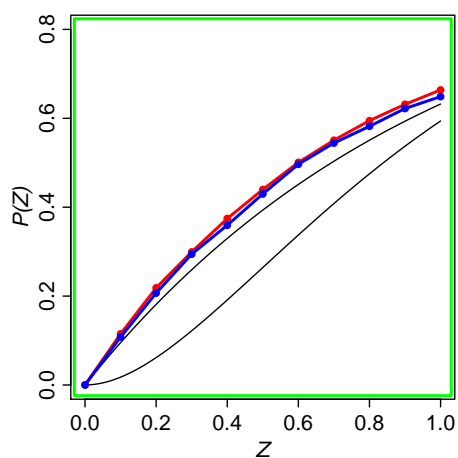
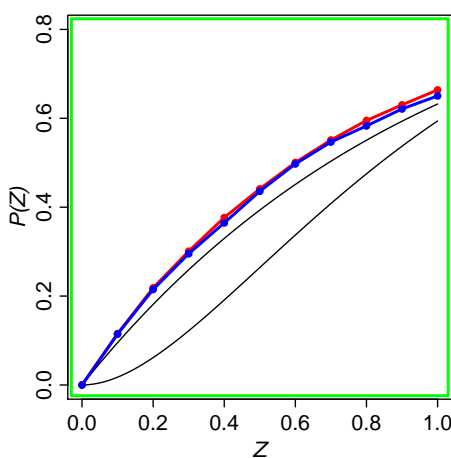
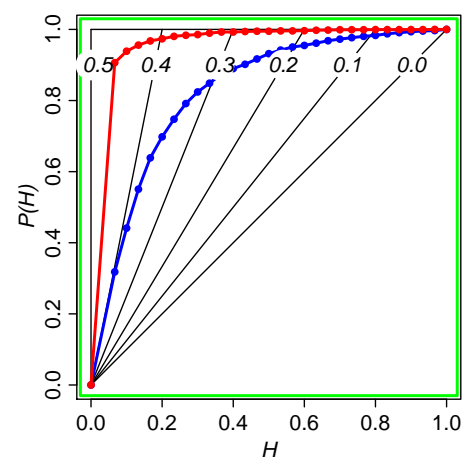
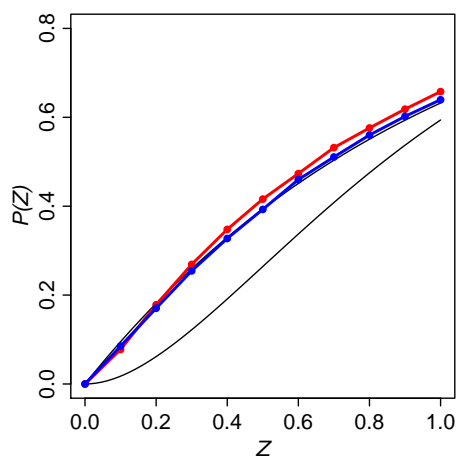
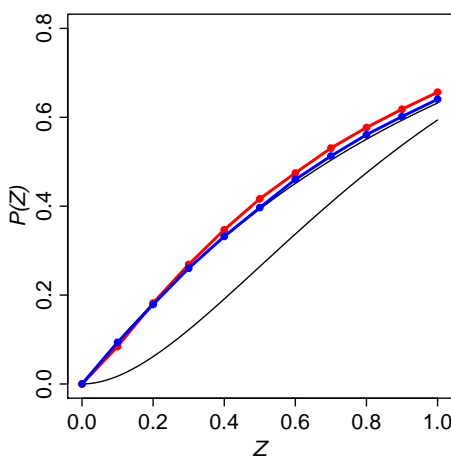
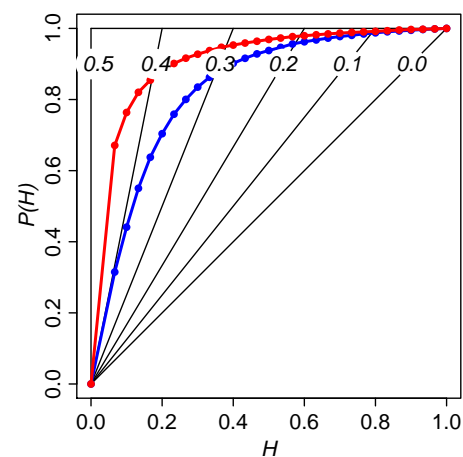
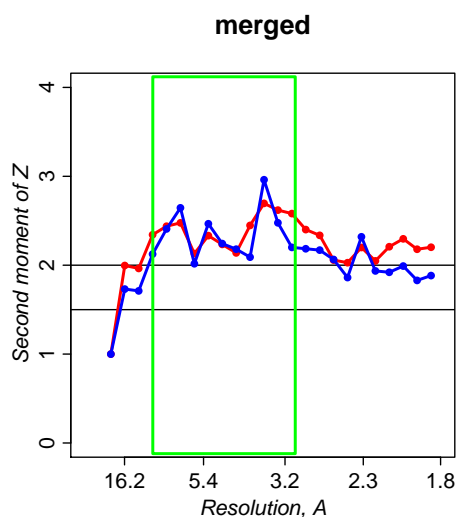
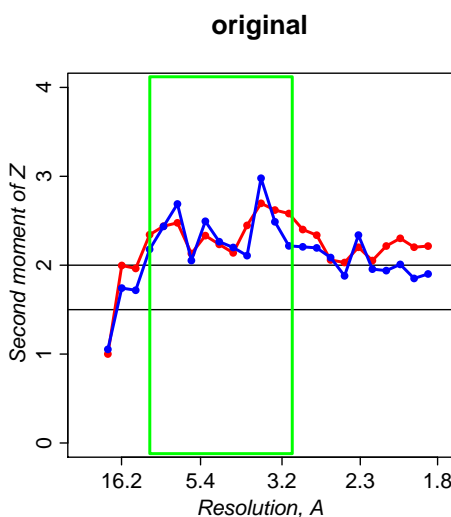
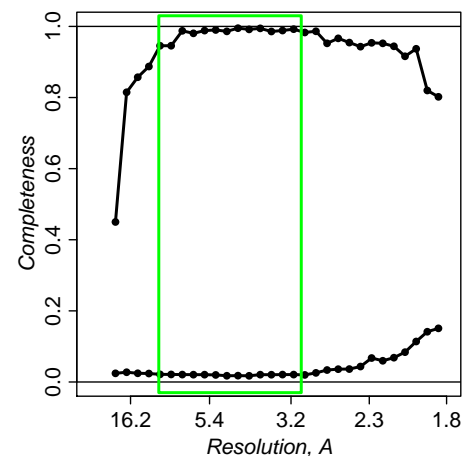
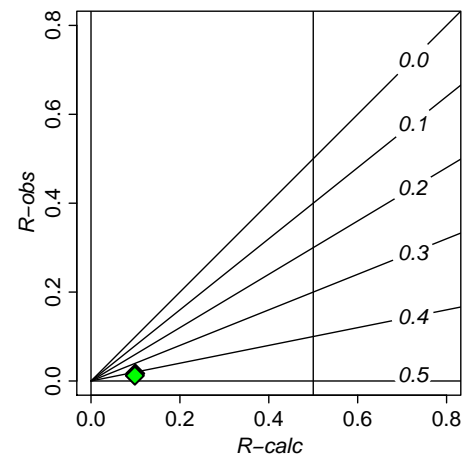
	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		0.08
R	28.7	
R'	28.7	29.7
R-free	33.0	
R'-free	32.9	33.8

residues per monomer	DNA	protein
	22	0

s < f/100	215	0.92 %
s <= 0	136	0.58 %
f <= 0	136	0.58 %
s,f <= 0	136	0.58 %

range (A)	33.9–1.8	9.9–3.0
unique	25,117	5,432
measured	23,407	5,369
used	19,802	4,390

NCS	translation	rotation
r.m.s.d. (A)	2.48	0.06
angle (o)	7.37	0.08



1o0i

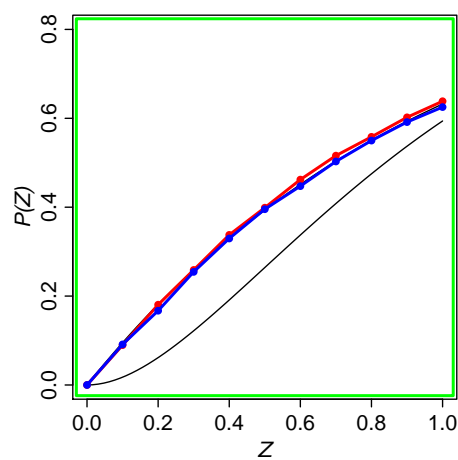
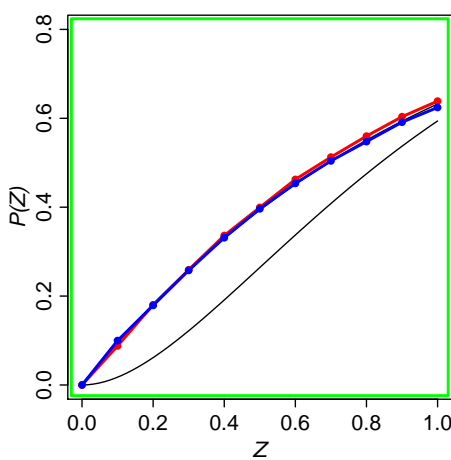
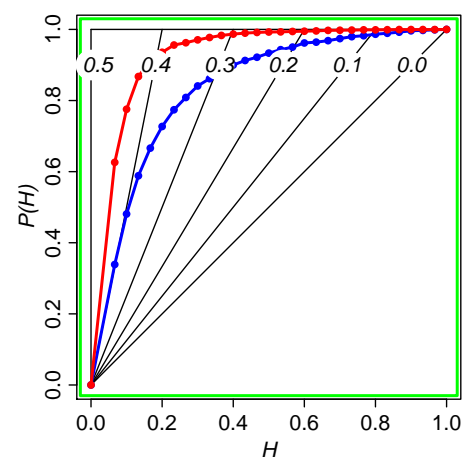
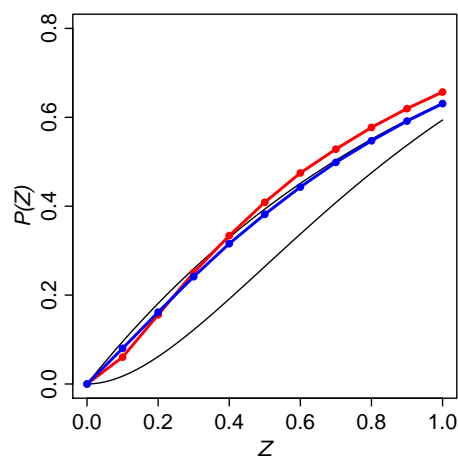
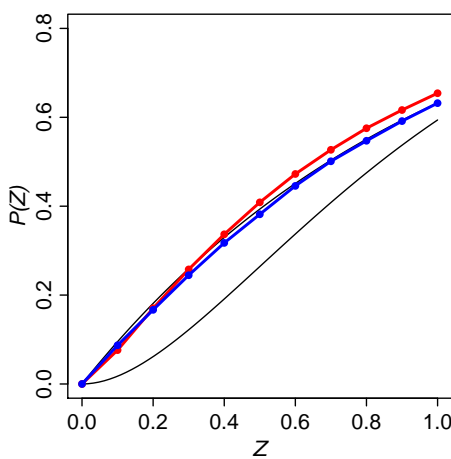
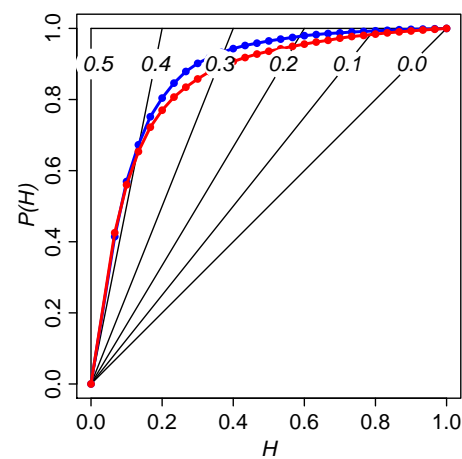
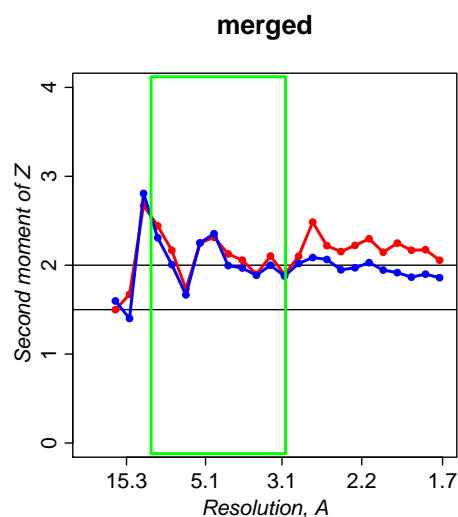
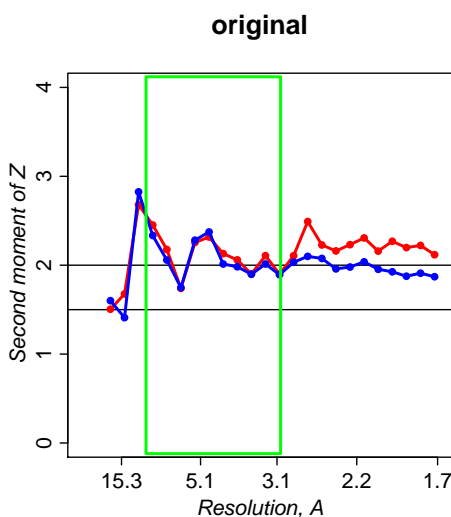
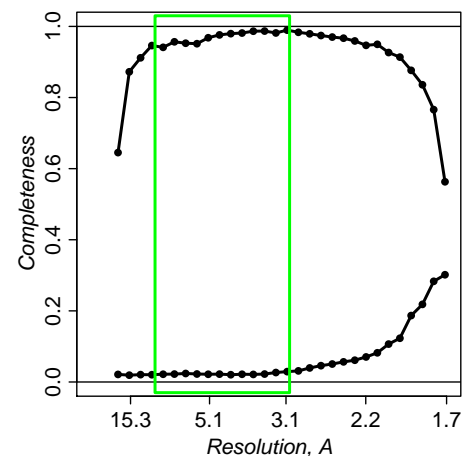
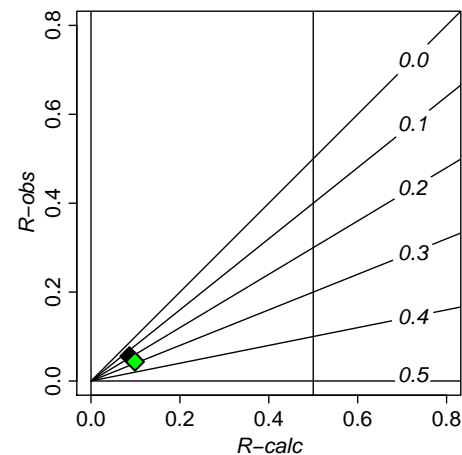
	original	merged
s.g.	C 1 2 1	F 2 2 2
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.09
R	26.3	
R'	26.3	26.3
R-free	27.9	
R'-free	27.5	27.1

s < f/100	1899	6.18 %
s <= 0	1899	6.18 %
f <= 0	1899	6.18 %
s,f <= 0	1899	6.18 %

range (A)	28.3–1.7	9.9–3.0
unique	34,539	5,983
measured	30,744	5,852
used	27,352	5,166

NCS	translation	rotation
r.m.s.d. (A)	26.19	0.09
angle (o)	179.96	0.05

residues per monomer	DNA	protein
	0	137



1o6e

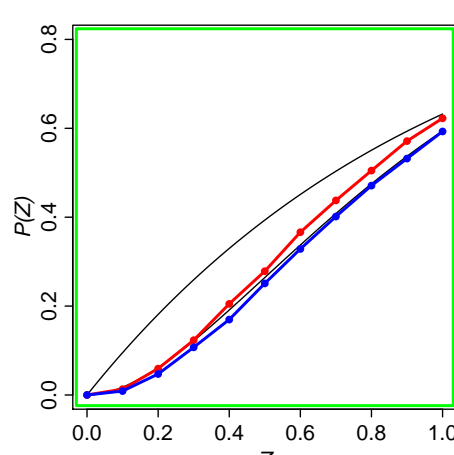
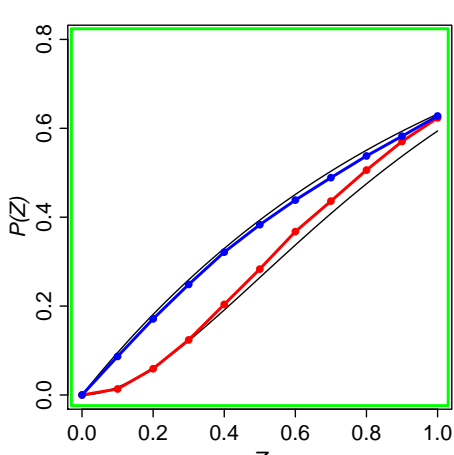
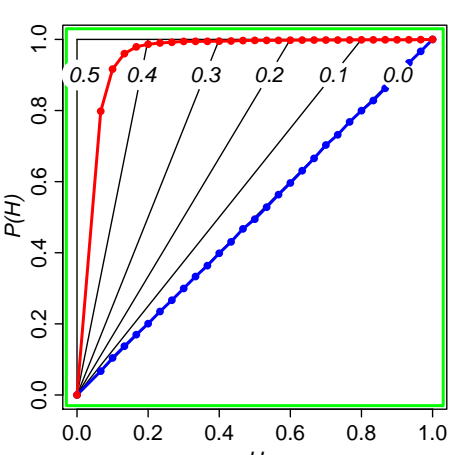
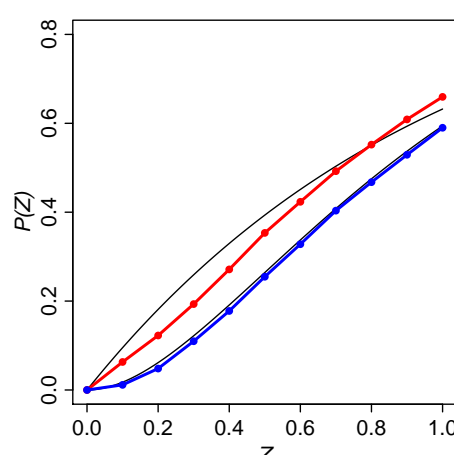
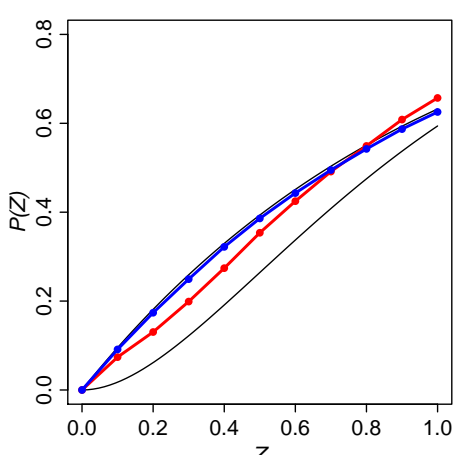
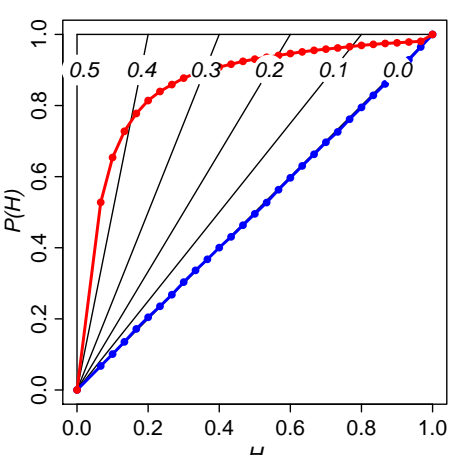
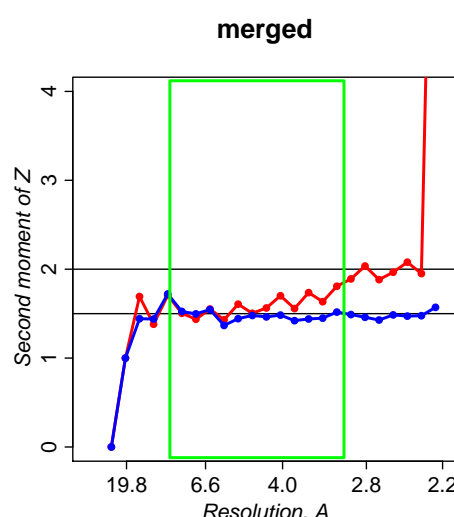
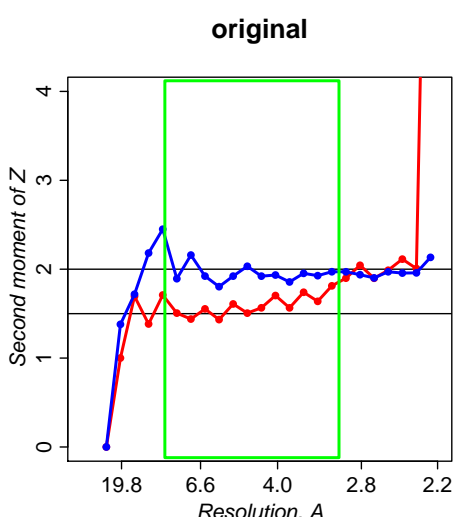
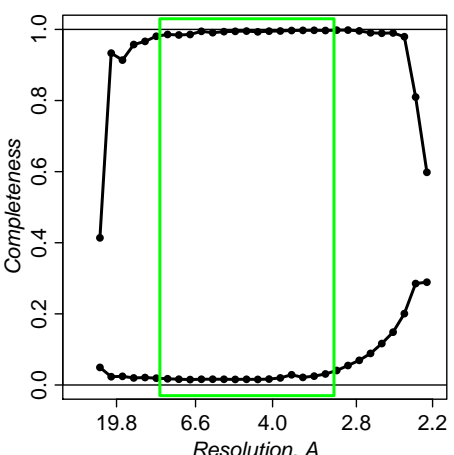
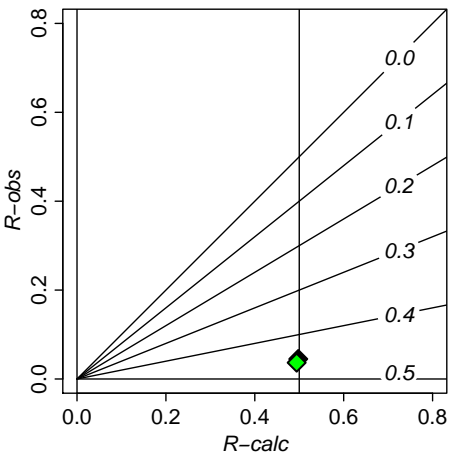
	original	merged
s.g.	P 31 2 1	-
p.g.	10023	12027
a.u.	2	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	35.6	-
R'	-	-
R-free	39.7	-
R'-free	-	-

residues per monomer	DNA	protein
	0	225

s < f/100	184	0.68 %
s <= 0	45	0.17 %
f <= 0	773	2.87 %
s,f <= 0	45	0.17 %

range (A)	45.3-2.2	9.9-3.0
unique	28,581	11,285
measured	26,926	11,229
used	20,602	8,176

NCS	translation	rotation
r.m.s.d. (A)	14.16	8.02
angle (o)	65.79	32.32



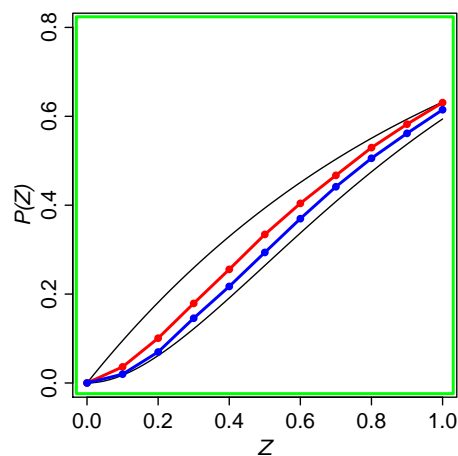
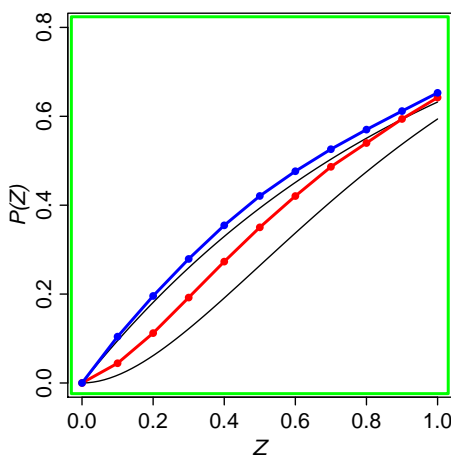
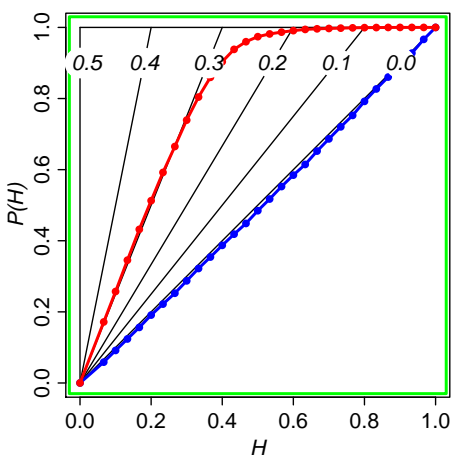
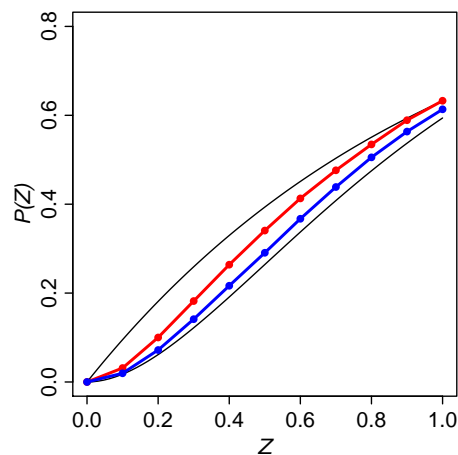
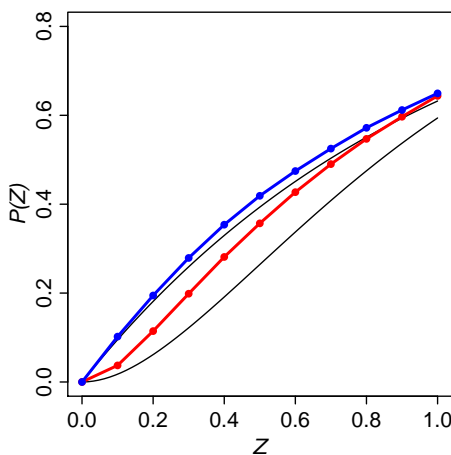
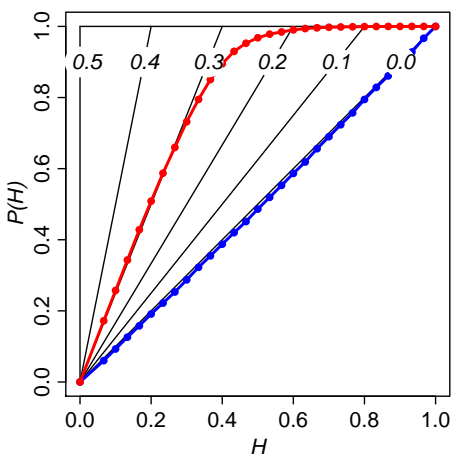
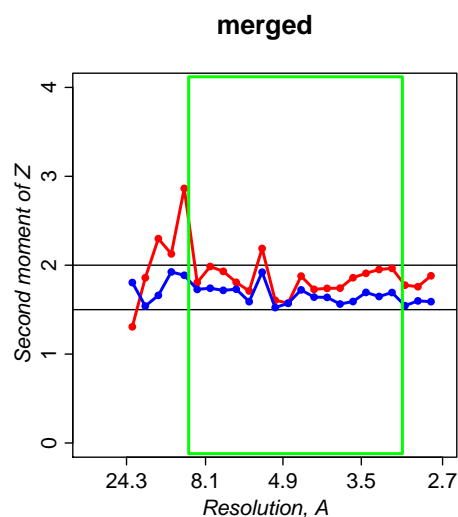
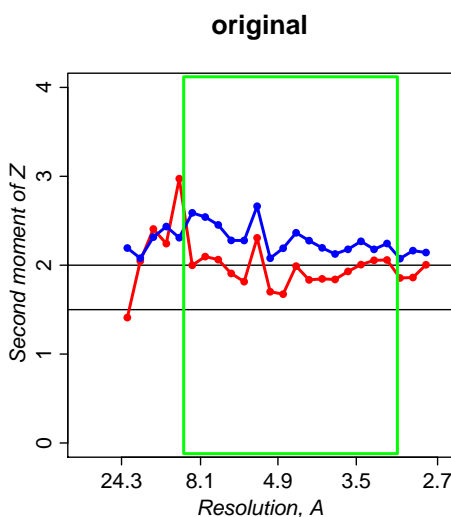
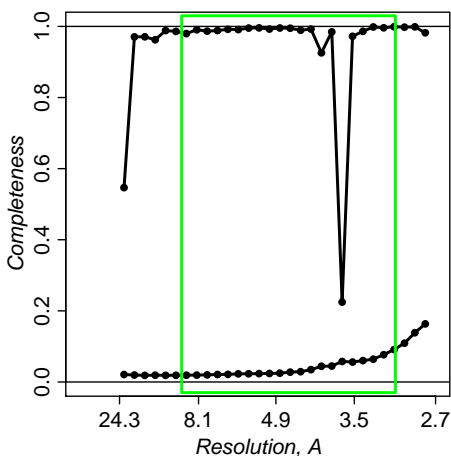
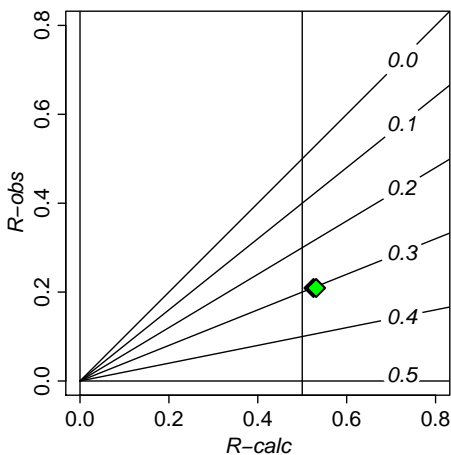
1o7l

	original	merged
s.g.	P 43	P 43 21 2
p.g.	10201	10205
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		17.51
R	28.0	
R'	-	-
R-free	34.5	
R'-free	-	-
residues per monomer	DNA 0	protein 251

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	24.7-2.7	9.9-3.0
unique	31,200	23,165
measured	29,663	21,702
used	26,484	19,274

NCS	translation	rotation
r.m.s.d. (A)	1.39	2.05
angle (o)	2.58	3.75



1oar

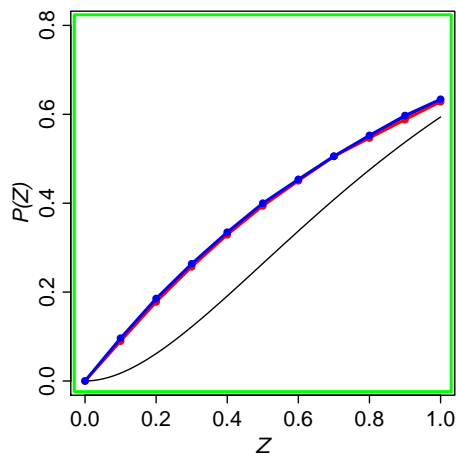
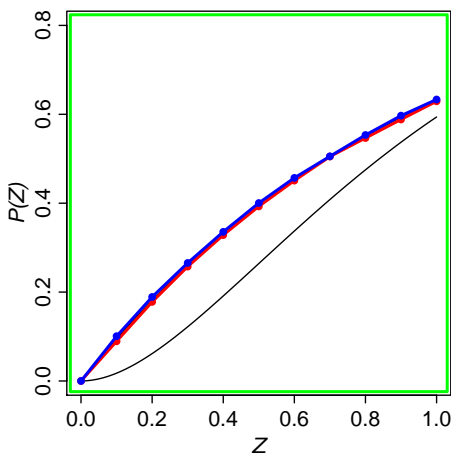
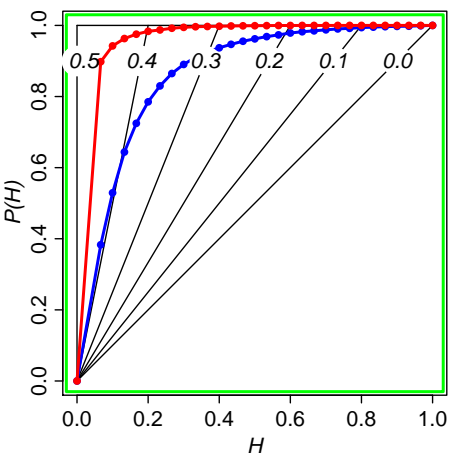
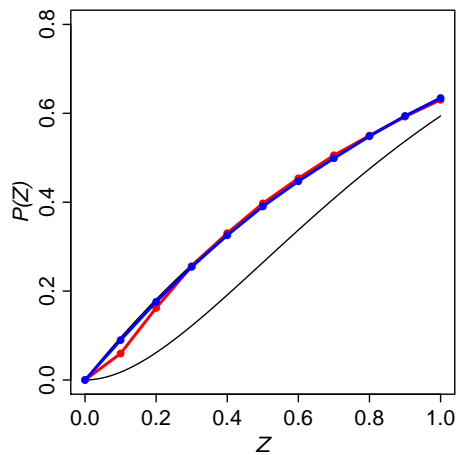
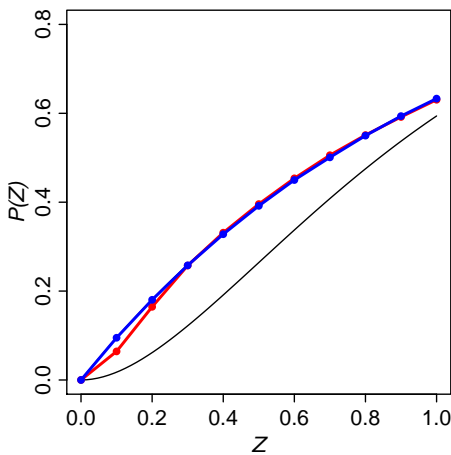
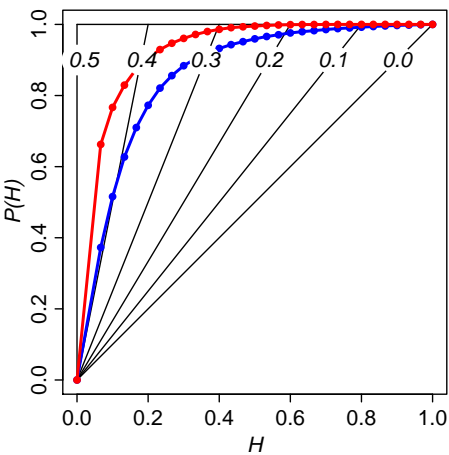
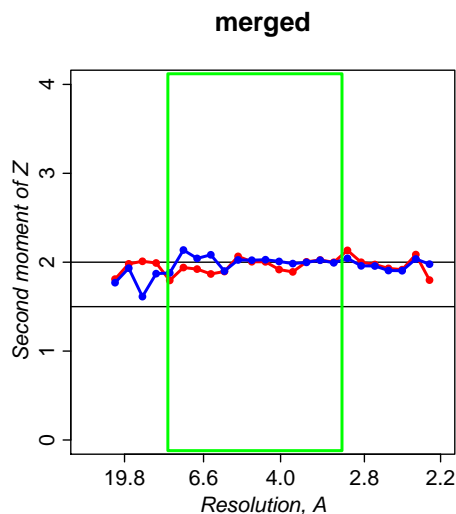
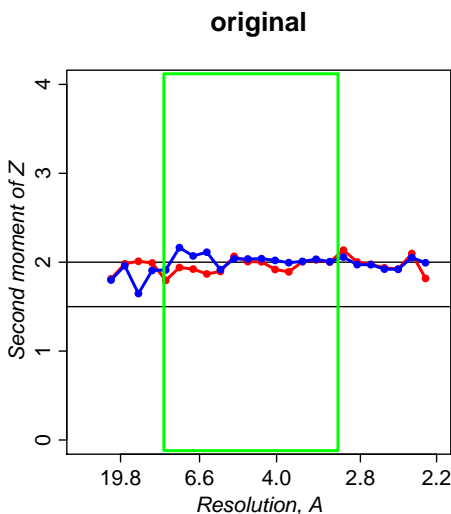
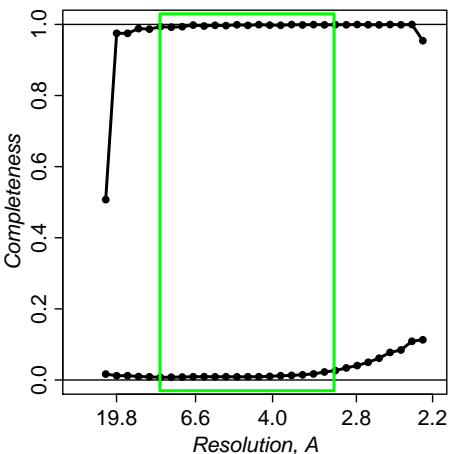
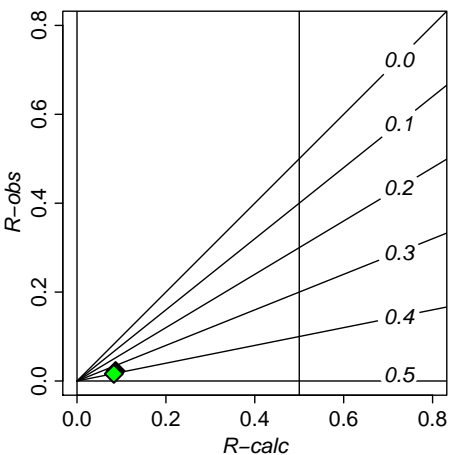
	original	merged
s.g.	P 21 21 21	P 41 21 2
p.g.	10003	10205
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.12
R	31.8	
R'	31.8	32.1
R-free	35.5	
R'-free	35.5	35.9

s < f/100	11516	22.04 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	33.7–2.2	9.9–3.0
unique	52,529	21,169
measured	52,239	21,132
used	45,588	17,824

NCS	translation	rotation
r.m.s.d. (A)	15.04	0.03
angle (o)	63.62	0.08

residues per monomer	DNA	protein
	0	185



10au

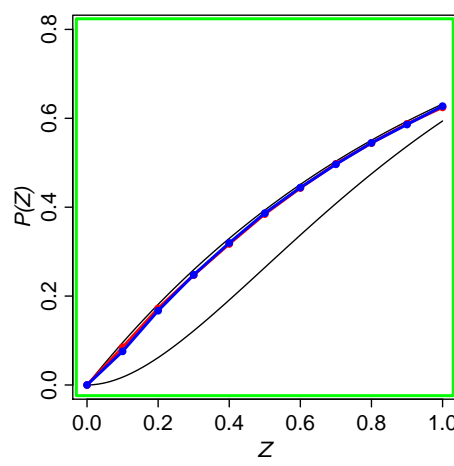
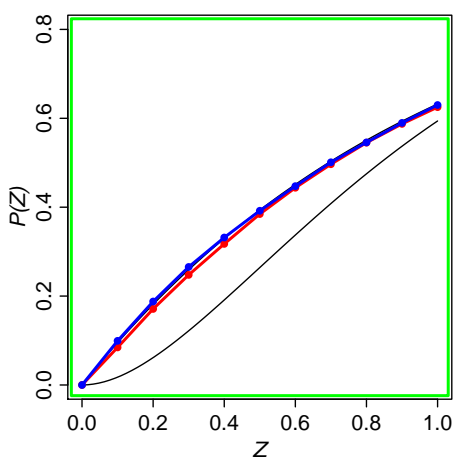
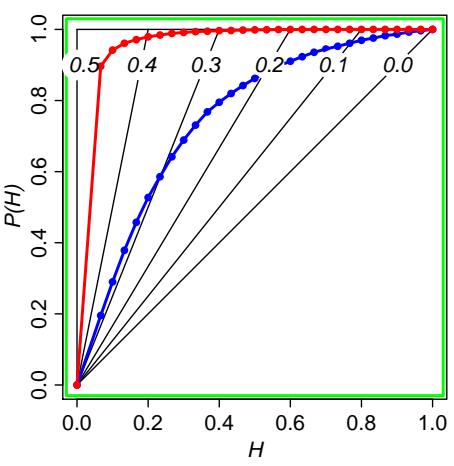
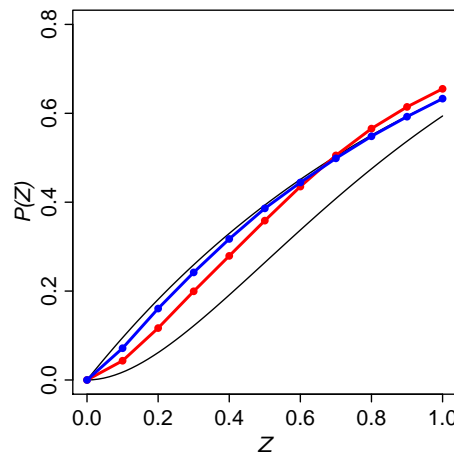
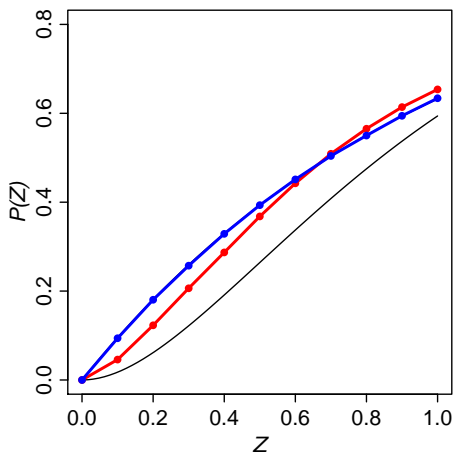
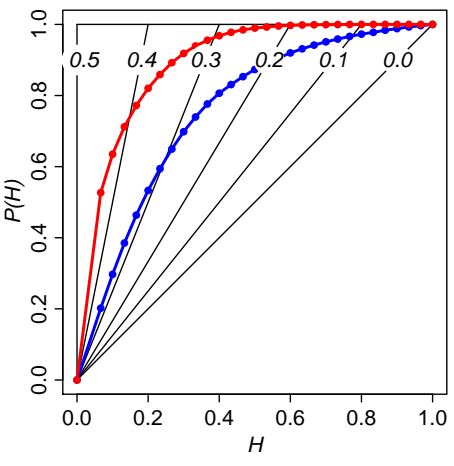
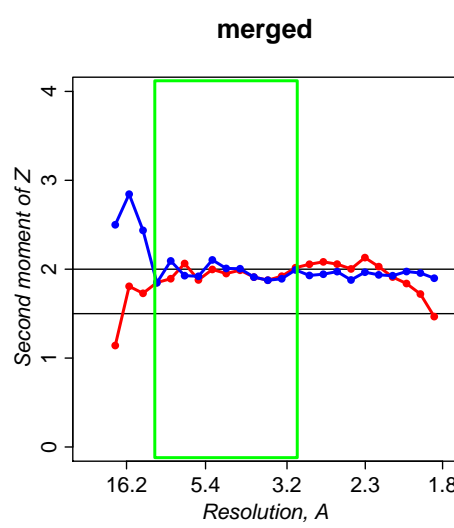
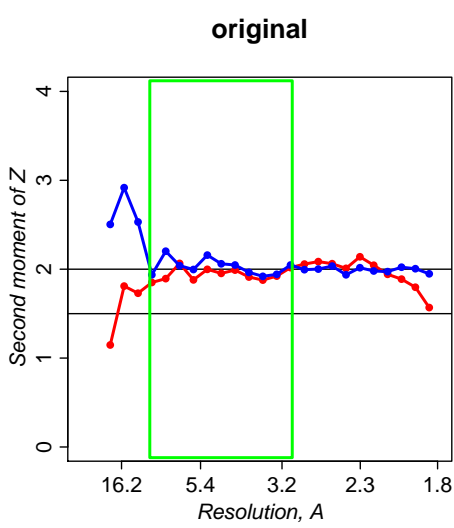
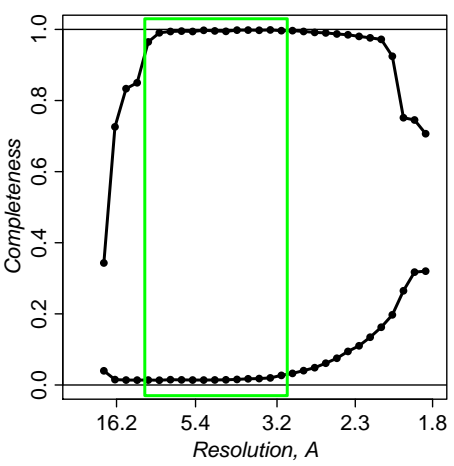
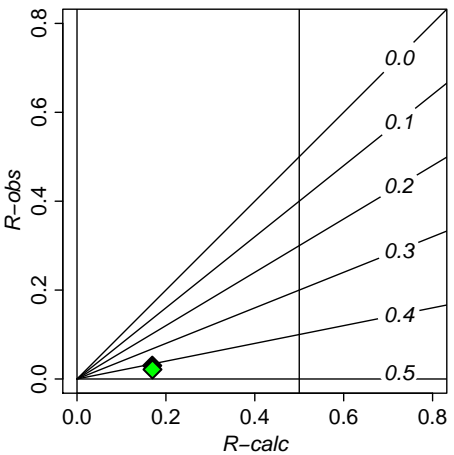
	original	merged
s.g.	P 21 21 21	P 41 21 2
p.g.	10003	10205
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.48
R	47.0	
R'	46.9	47.2
R-free	46.4	
R'-free	46.5	46.7

residues per monomer	DNA	protein
	0	90

s < f/100	323	0.36 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	30.1–1.8	9.9–3.0
unique	98,319	21,463
measured	90,268	21,377
used	76,720	18,092

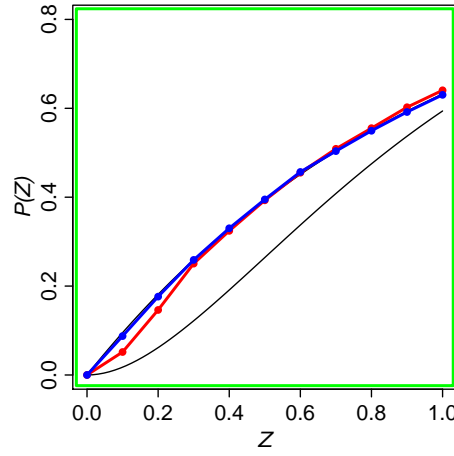
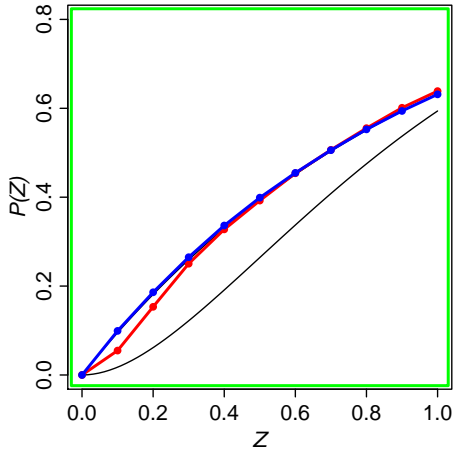
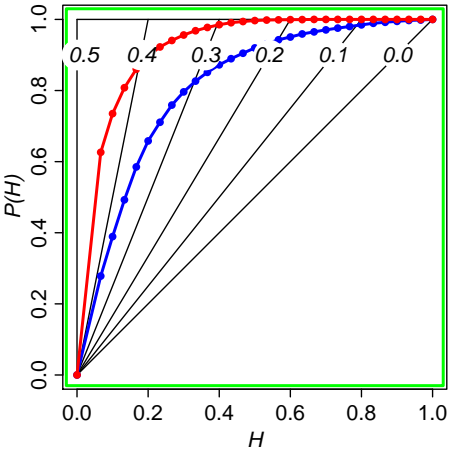
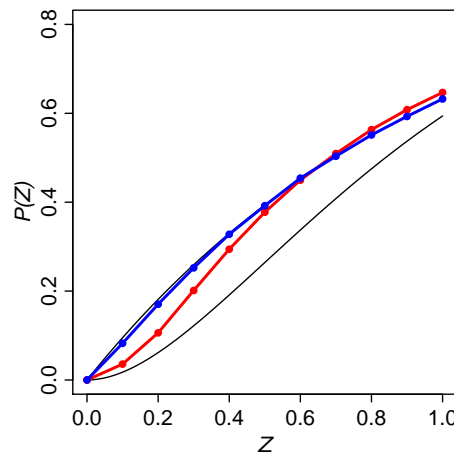
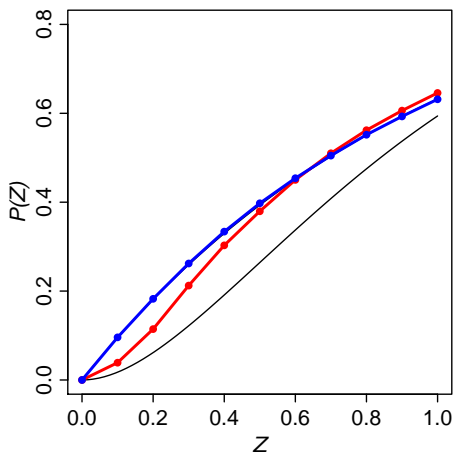
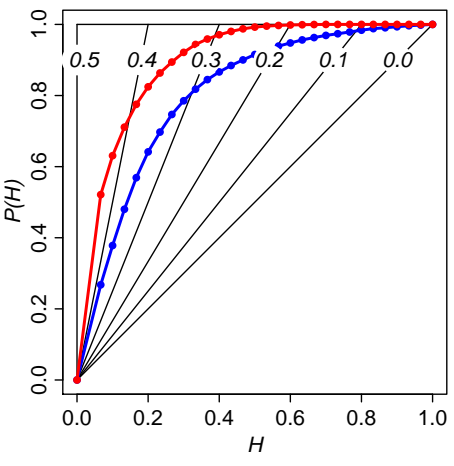
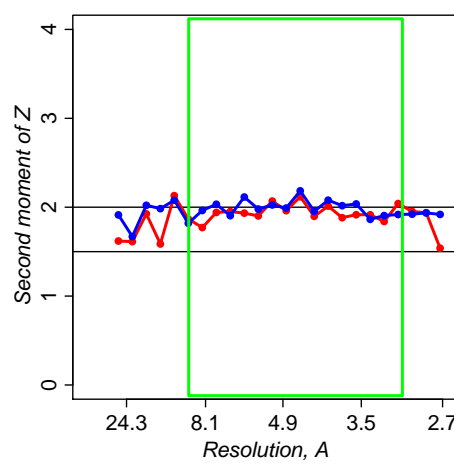
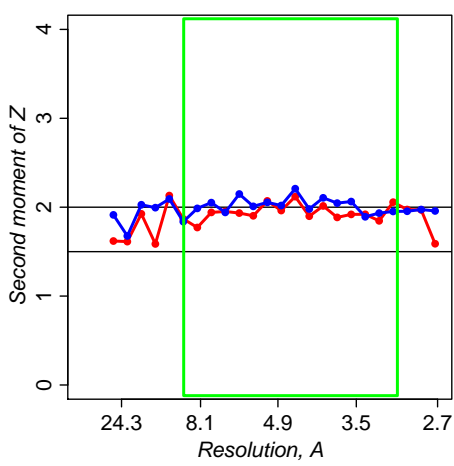
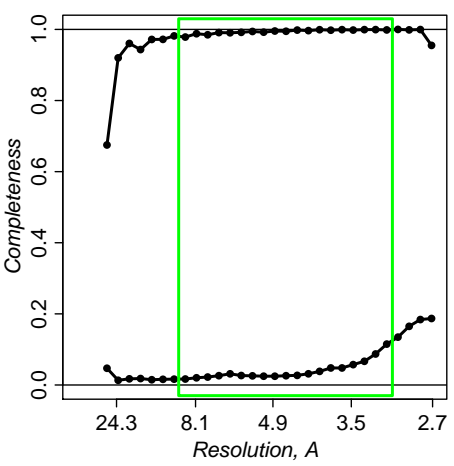
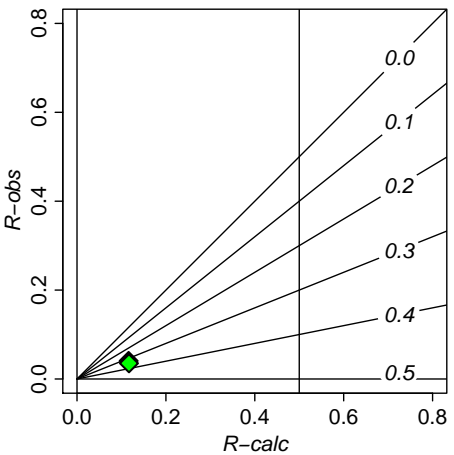
NCS	translation	rotation
r.m.s.d. (A)	9.49	0.01
angle (o)	61.23	0.07



1oax

	original	merged
s.g.	P 21 21 21	P 41 21 2
p.g.	10003	10205
a.u.	4	2
p.t.	2	2
p.o.	4	4
r.m.s.d. (A)		0.40
R	42.9	
R'	43.0	43.2
R-free	46.7	
R'-free	46.0	45.4
residues per monomer	DNA 0	protein 107

s < f/100	545	1.80 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	39.4–2.7	9.9–3.0
unique	30,483	20,864
measured	30,262	20,794
used	25,762	17,554
NCS	translation	rotation
r.m.s.d. (A)	9.58	0.04
angle (o)	61.60	0.19



1oay

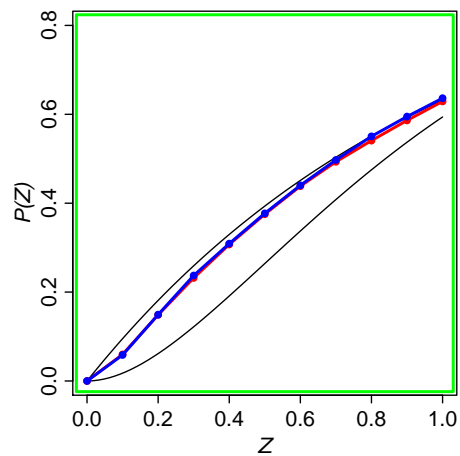
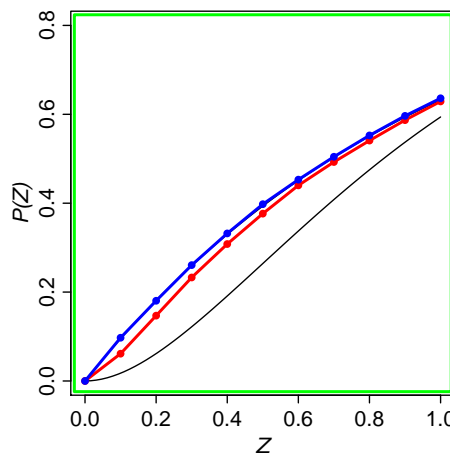
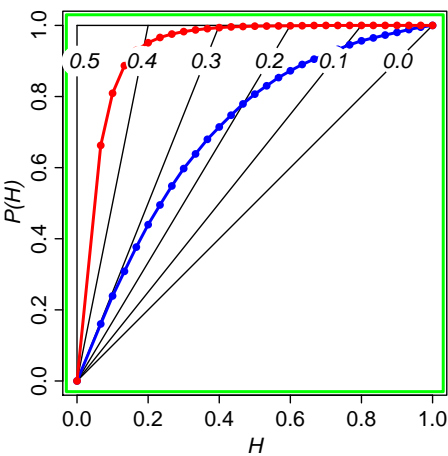
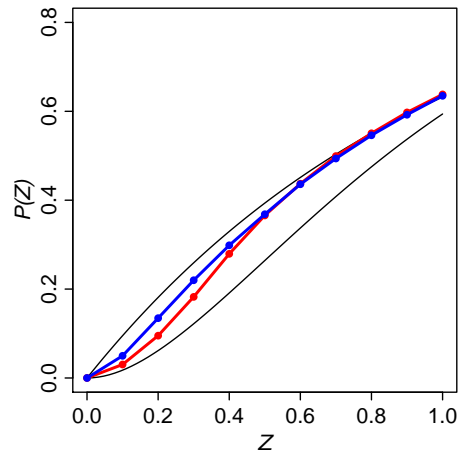
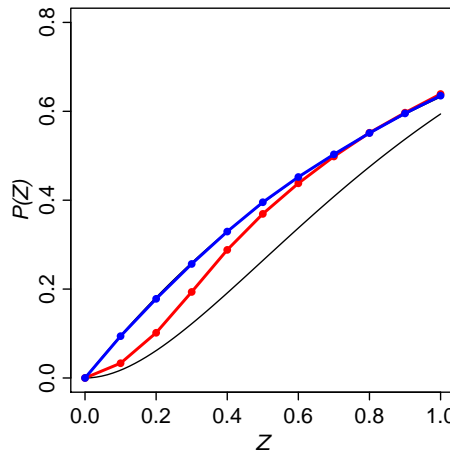
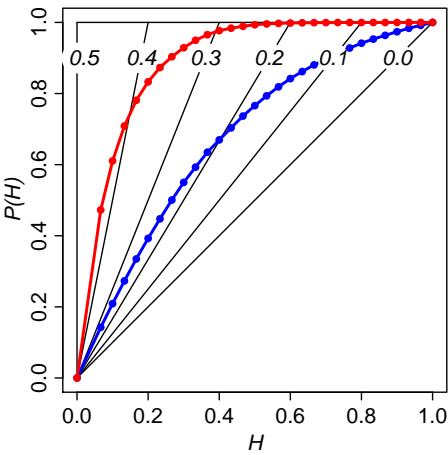
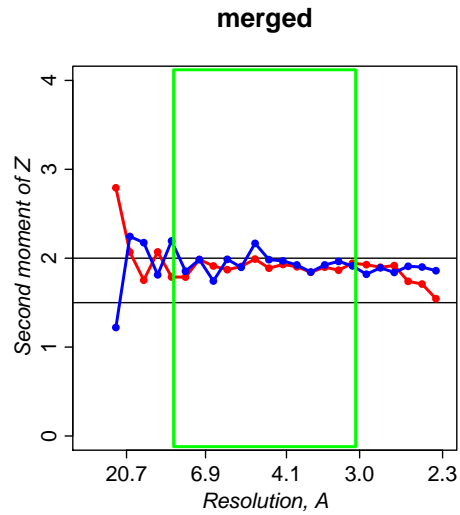
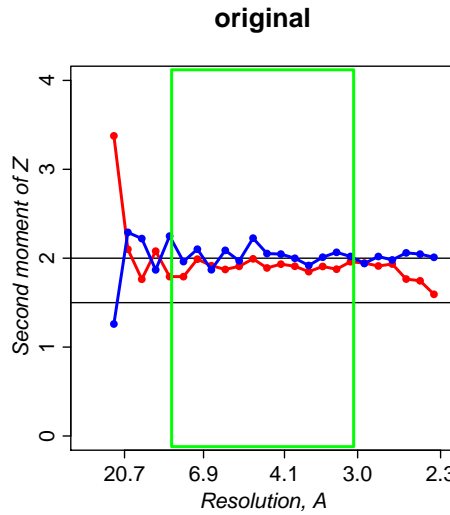
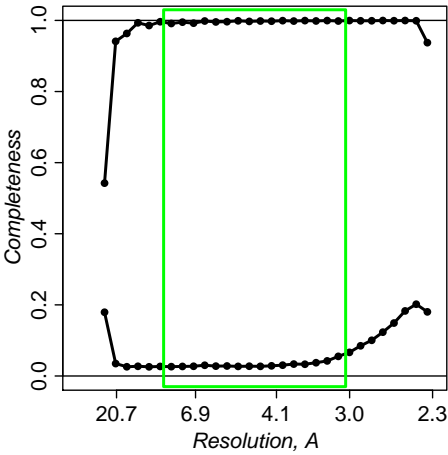
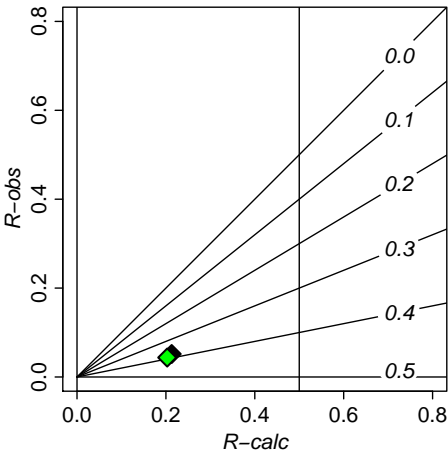
	original	merged
s.g.	P 21 21 21	P 41 21 2
p.g.	10003	10205
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.50
R	46.2	
R'	46.1	46.3
R-free	49.2	
R'-free	49.1	49.2

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	37.3–2.3	9.9–3.0
unique	48,156	21,297
measured	47,811	21,259
used	41,564	17,938

NCS	translation	rotation
r.m.s.d. (A)	8.87	0.13
angle (o)	58.75	0.21

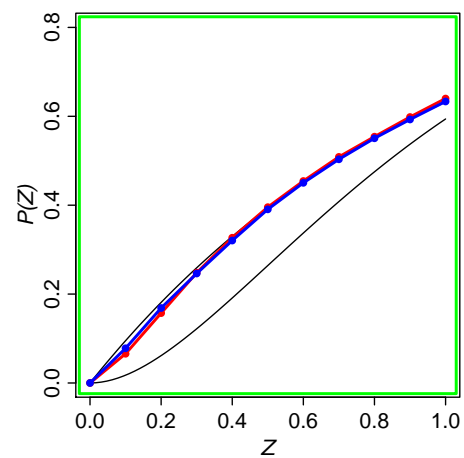
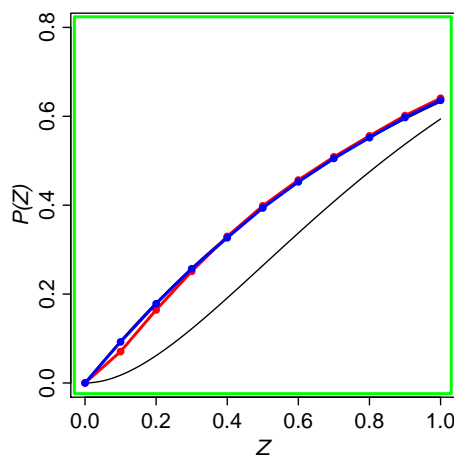
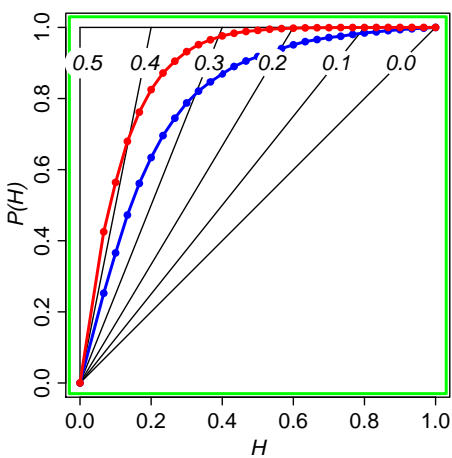
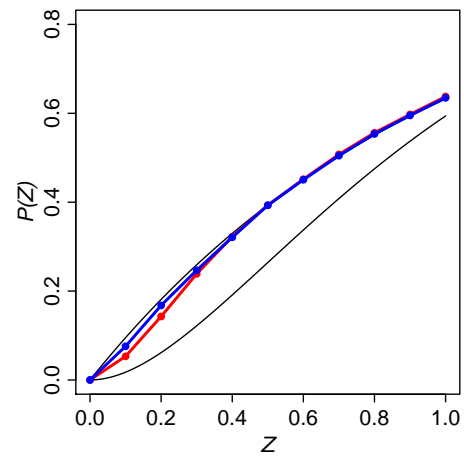
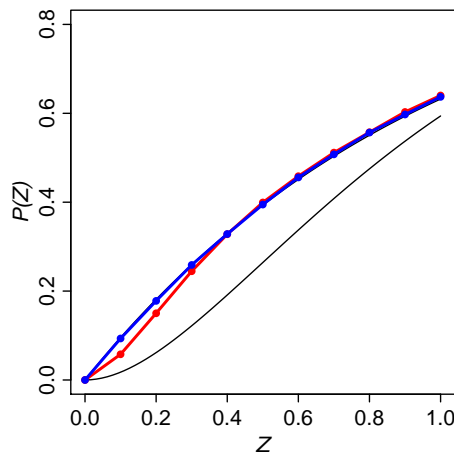
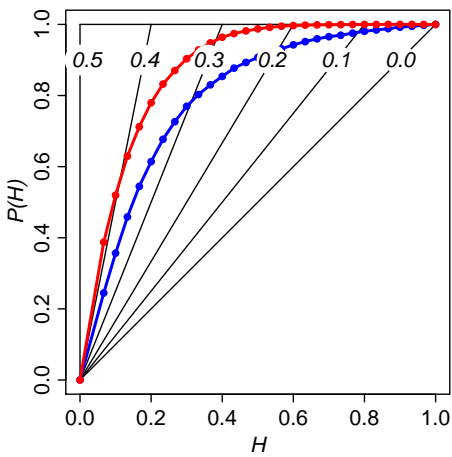
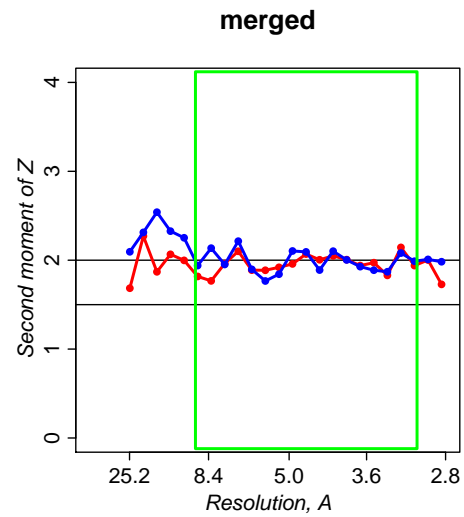
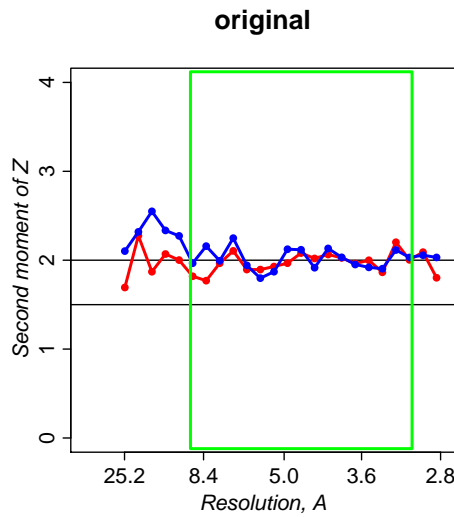
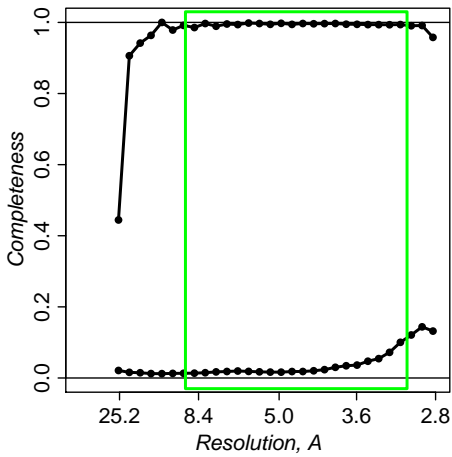
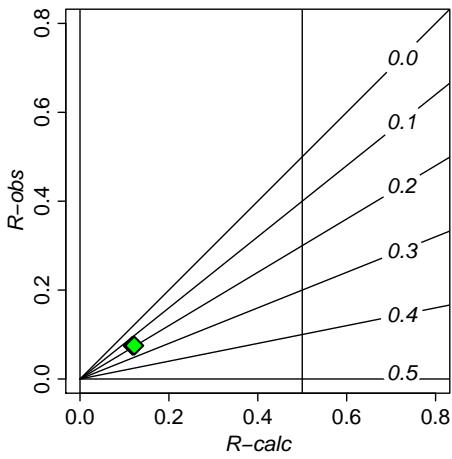
residues per monomer	DNA	protein
	0	82



1oaz

	original	merged
s.g.	P 21 21 21	P 41 21 2
p.g.	10003	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.23
R	27.3	
R'	27.3	27.2
R-free	31.6	
R'-free	31.8	32.6
residues per monomer	DNA 0	protein 345

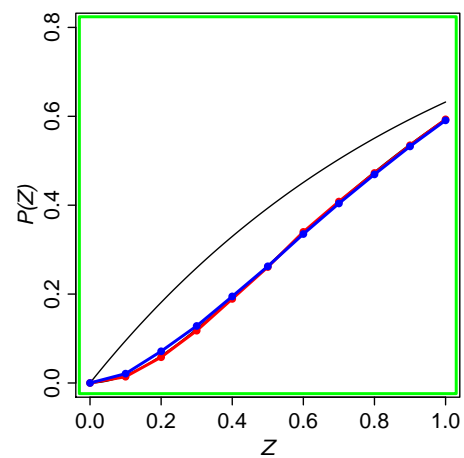
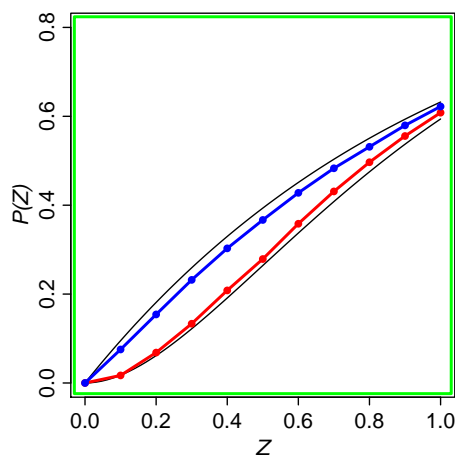
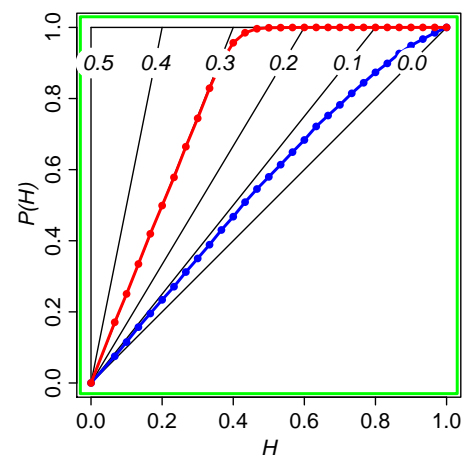
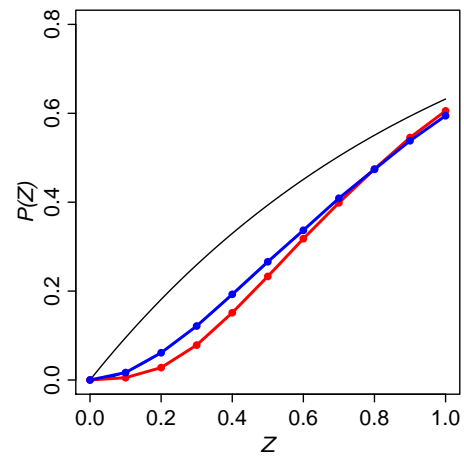
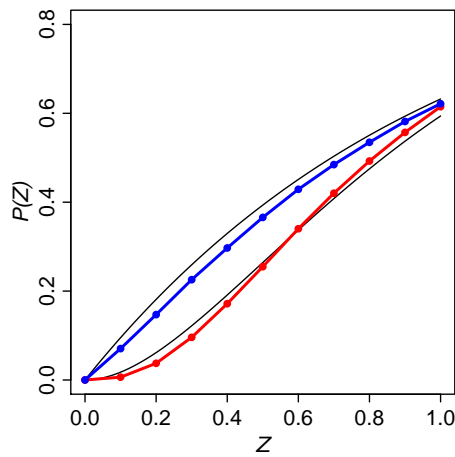
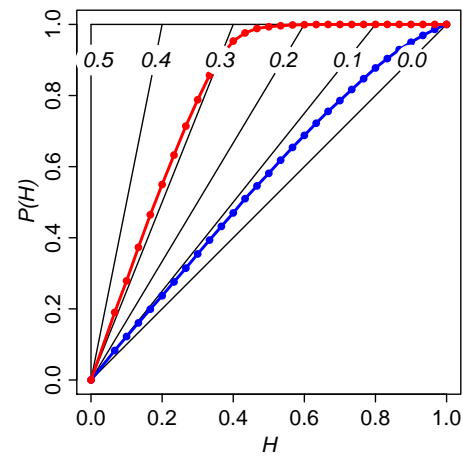
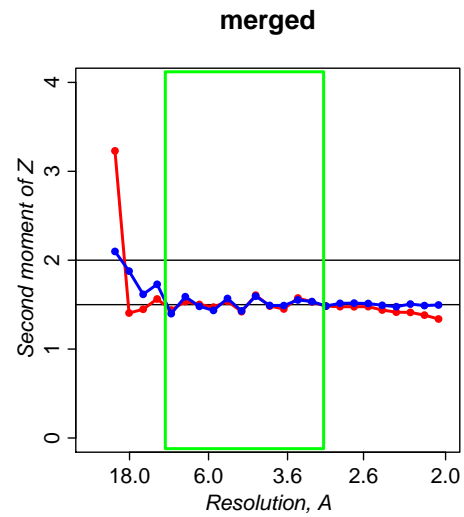
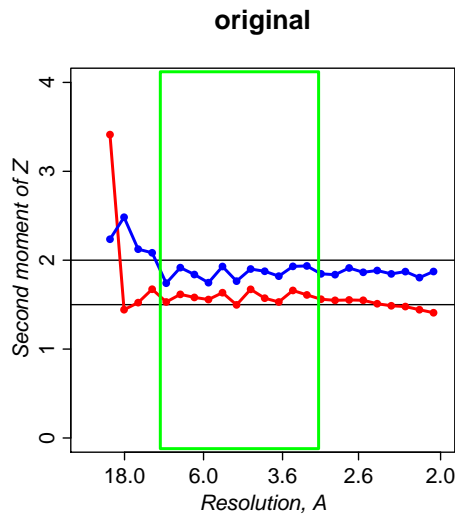
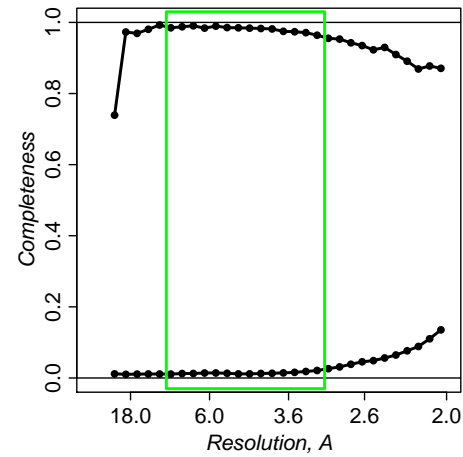
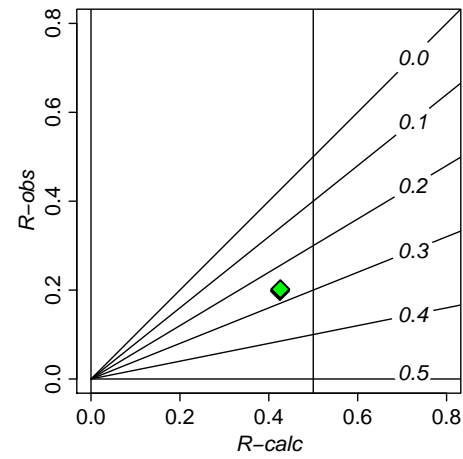
s < f/100	2593	9.36 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	30.1–2.8	9.9–3.0
unique	27,994	21,659
measured	27,717	21,545
used	23,546	18,280
NCS	translation	rotation
r.m.s.d. (A)	20.47	0.20
angle (o)	89.86	0.31



1ocv

	original	merged
s.g.	P 31	-
p.g.	10020	10023
a.u.	4	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	26.5	-
R'	-	-
R-free	28.5	-
R'-free	-	-
residues per monomer	DNA 0	protein 125

s < f/100	2698	7.35 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	39.7-2.0	9.9-3.0
unique	39,575	11,522
measured	36,693	11,251
used	33,698	10,316
NCS	translation	rotation
r.m.s.d. (A)	13.52	2.93
angle (o)	73.60	15.35



1odx

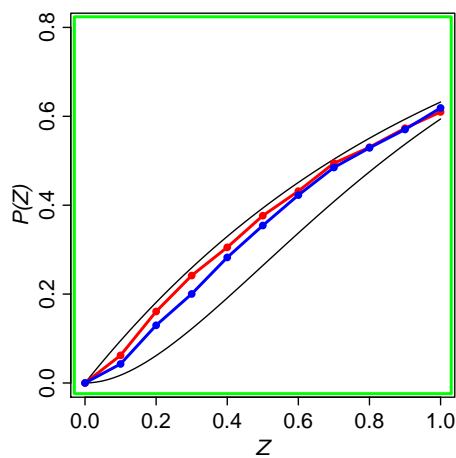
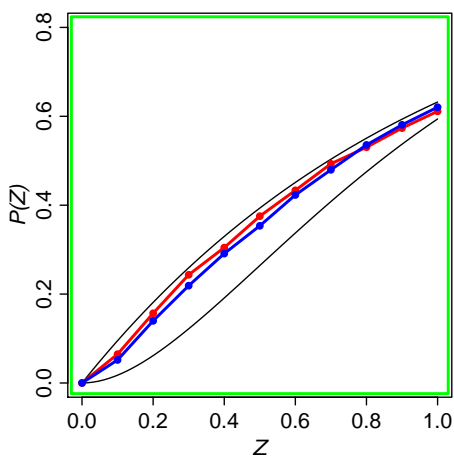
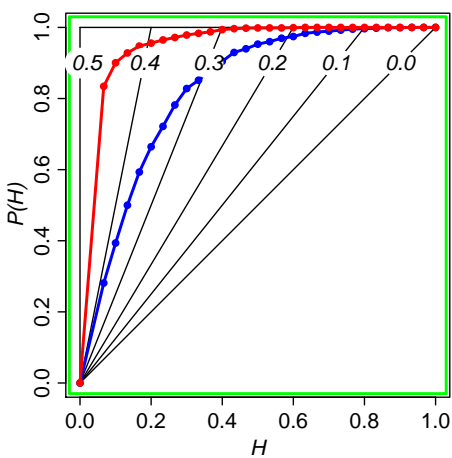
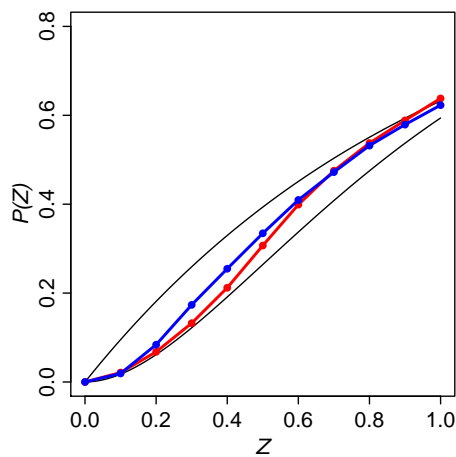
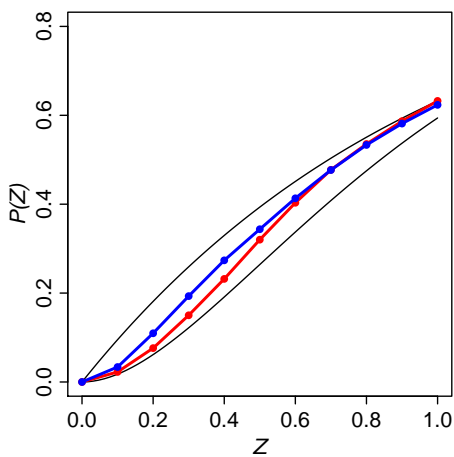
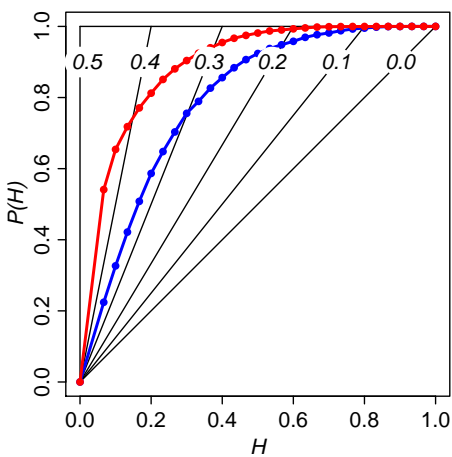
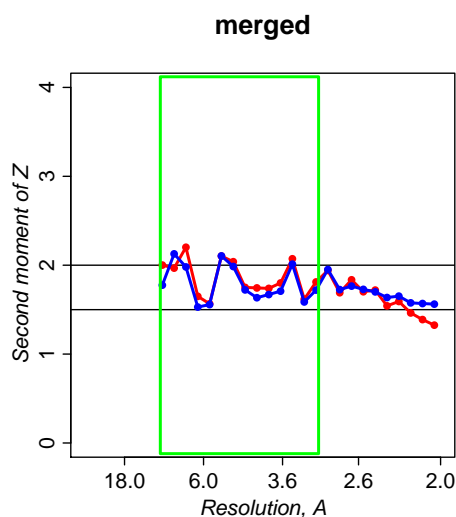
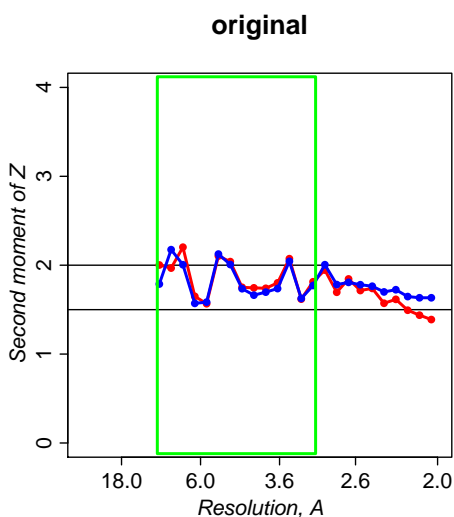
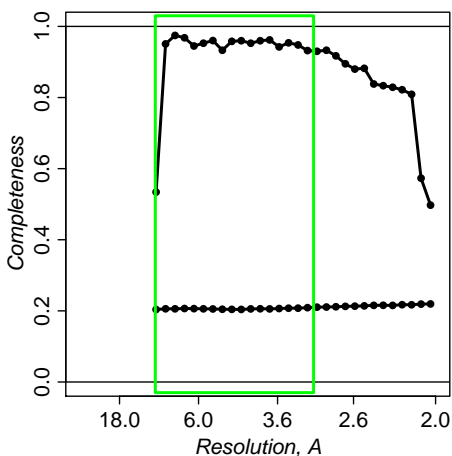
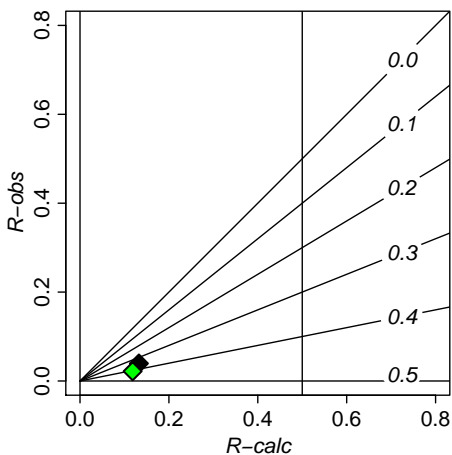
	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.24
R	24.1	
R'	24.8	26.1
R-free	26.2	
R'-free	25.9	26.4

residues per monomer	DNA	protein
	0	99

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	10.0–2.0	9.9–3.0
unique	12,766	3,762
measured	10,696	3,576
used	8,586	2,896

NCS	translation	rotation
r.m.s.d. (A)	19.55	0.24
angle (o)	179.83	0.23



1ody

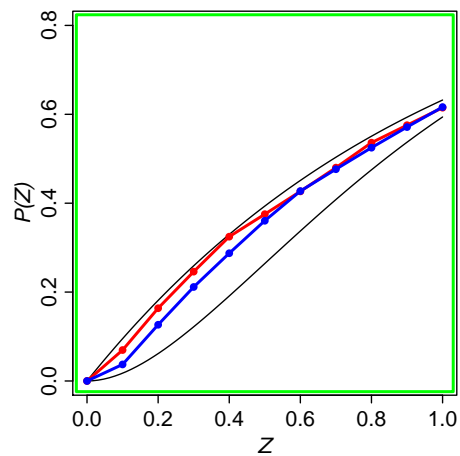
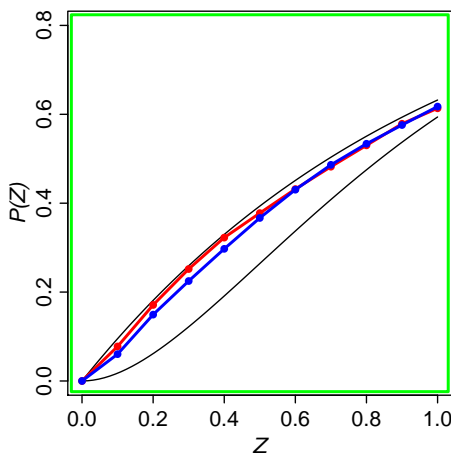
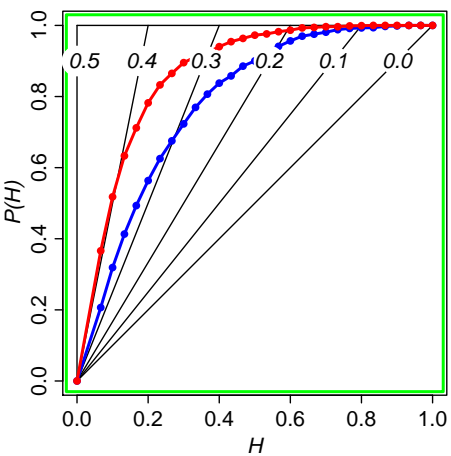
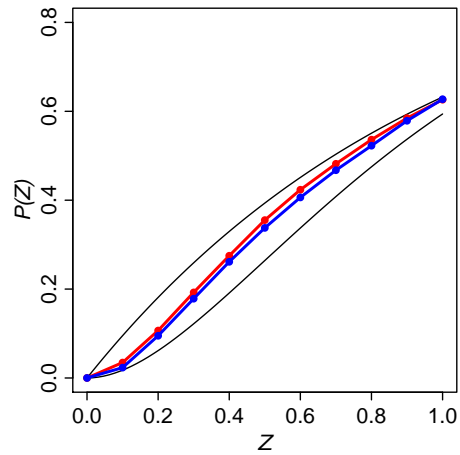
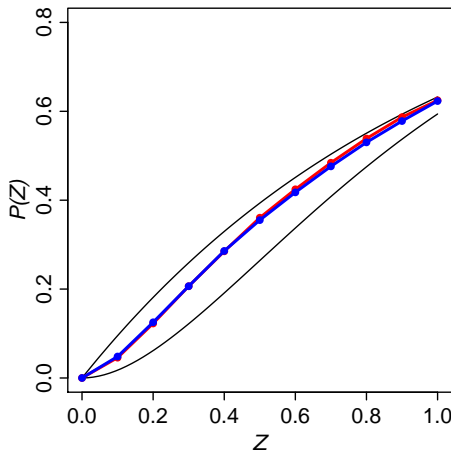
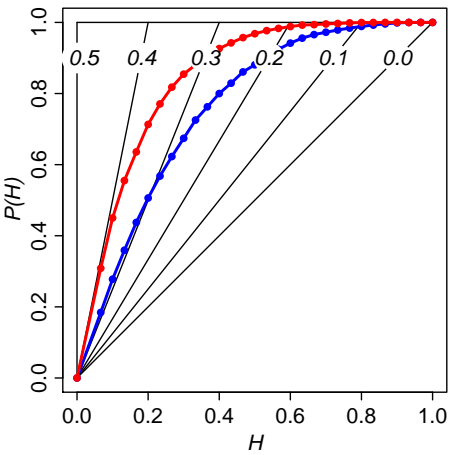
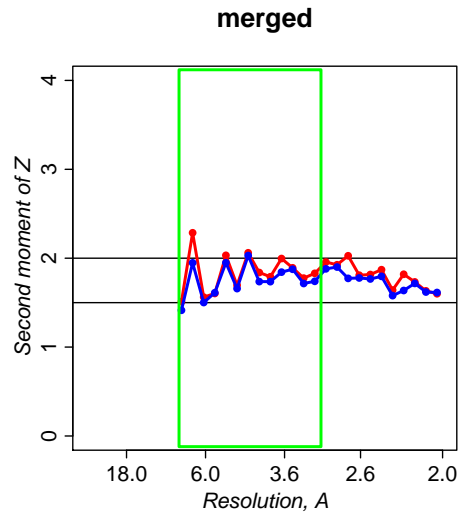
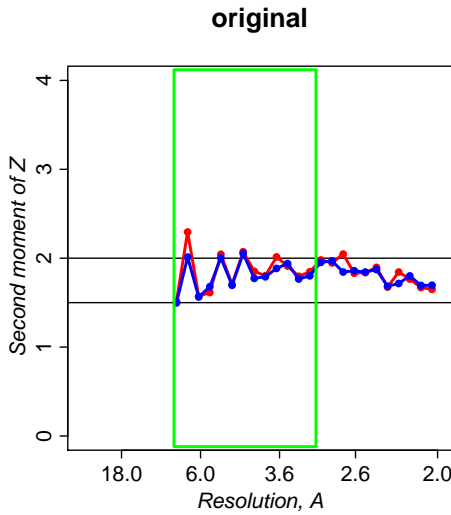
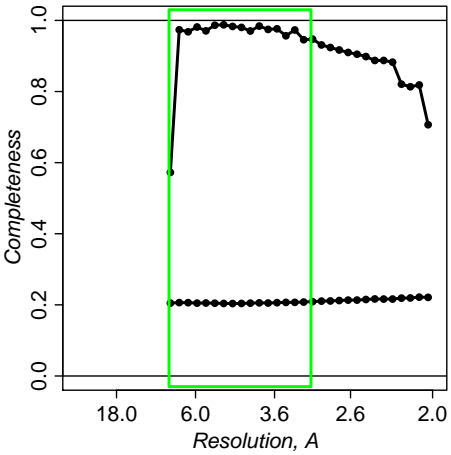
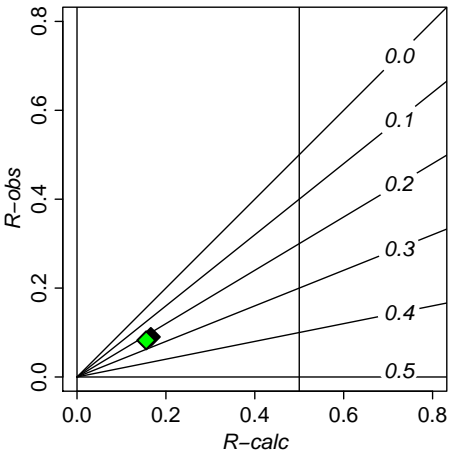
	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.49
R	26.0	
R'	26.7	27.9
R-free	27.9	
R'-free	28.2	28.7

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	8.0–2.0	8.0–3.0
unique	12,396	3,595
measured	11,058	3,490
used	9,280	2,846

NCS	translation	rotation
r.m.s.d. (A)	22.95	0.47
angle (o)	178.97	1.74

residues per monomer	DNA	protein
	0	99



1oe7

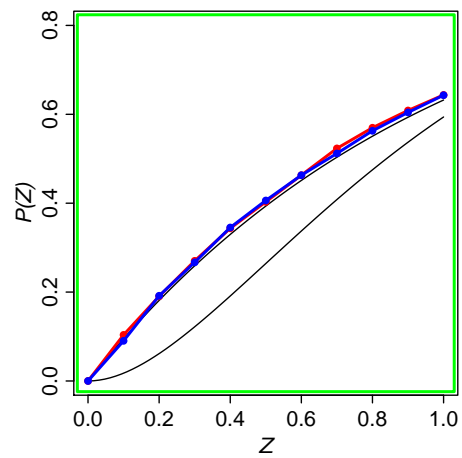
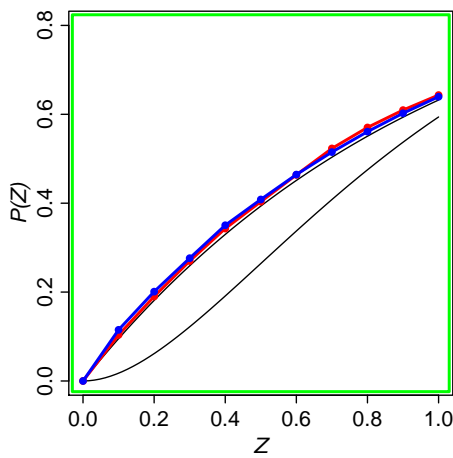
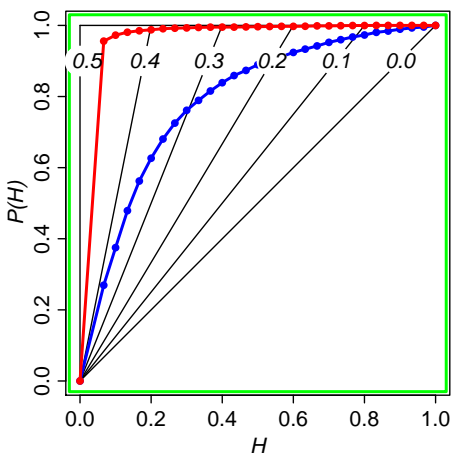
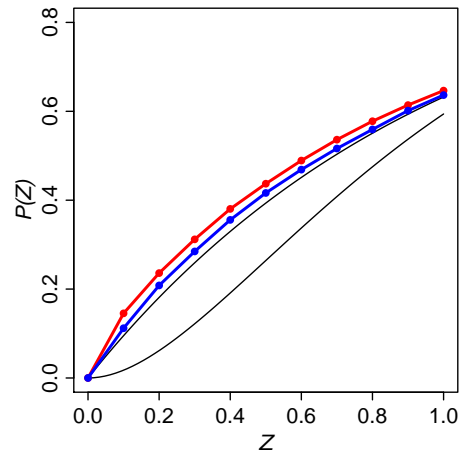
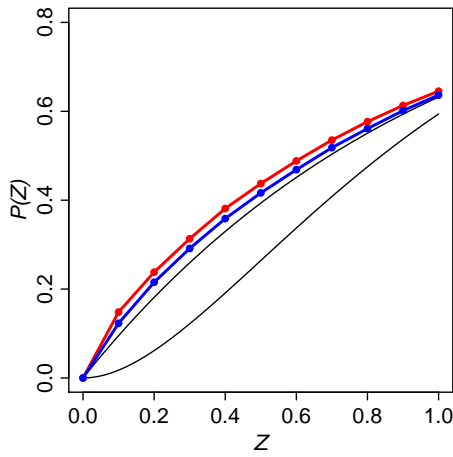
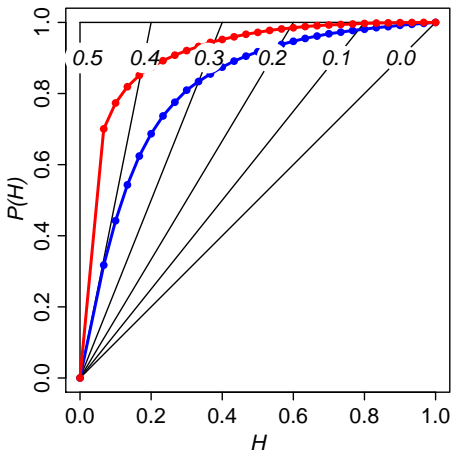
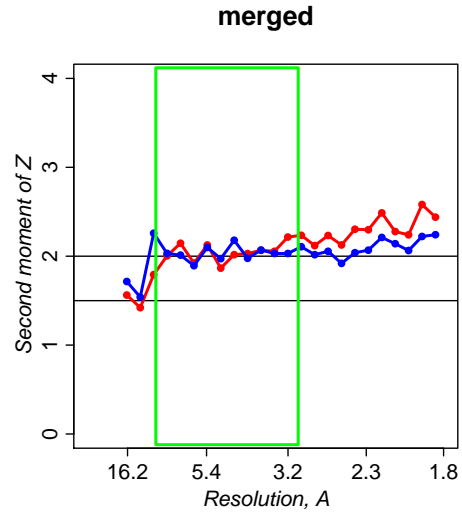
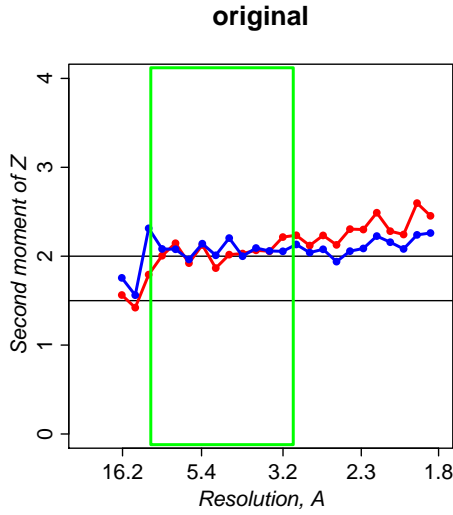
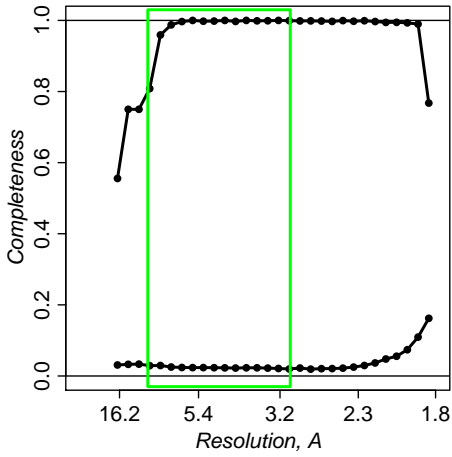
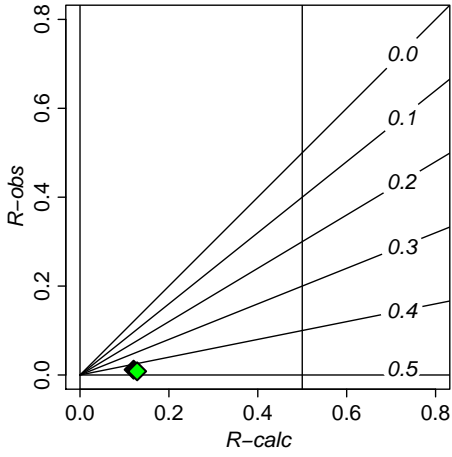
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.08
R	27.7	
R'	27.9	28.1
R-free	30.6	
R'-free	30.9	31.1

residues per monomer	DNA	protein
	0	203

s < f/100	7	0.02 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.9–1.8	9.9–3.0
unique	40,201	8,624
measured	39,157	8,577
used	36,144	7,690

NCS	translation	rotation
r.m.s.d. (A)	27.71	0.08
angle (o)	179.96	0.05



1oe8

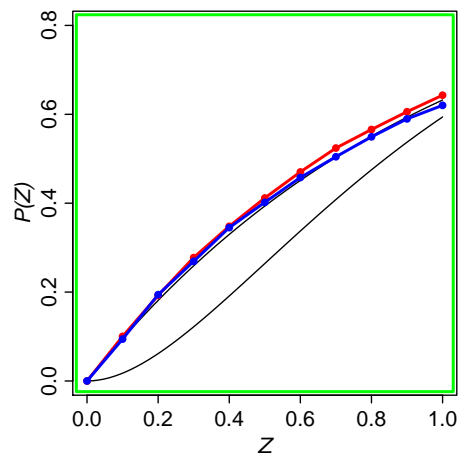
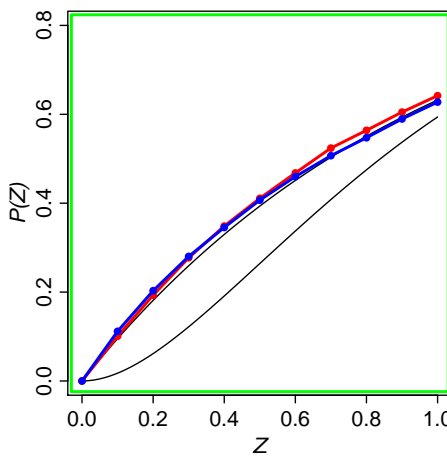
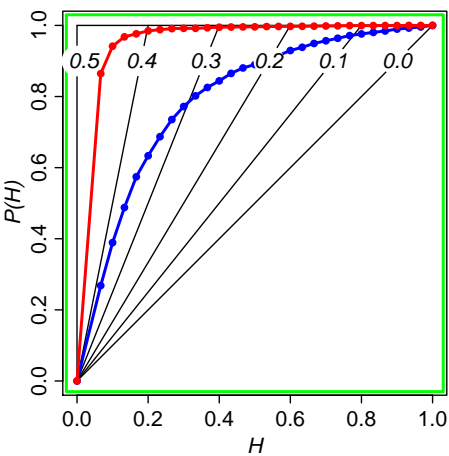
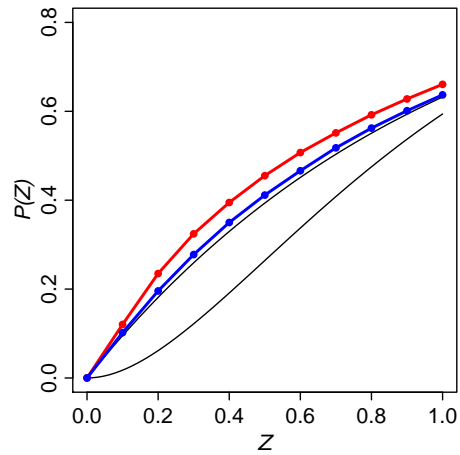
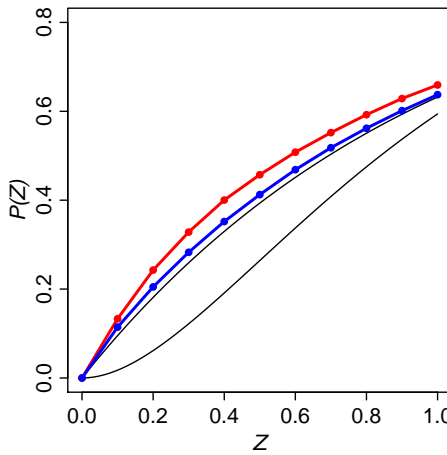
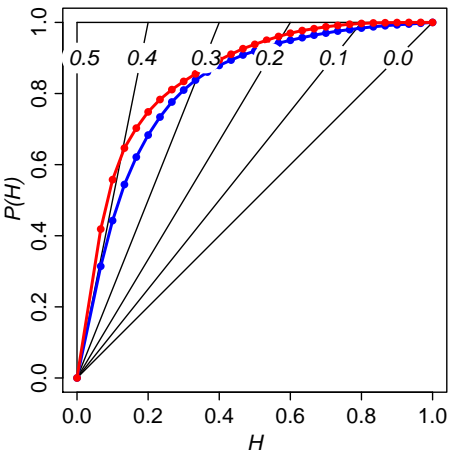
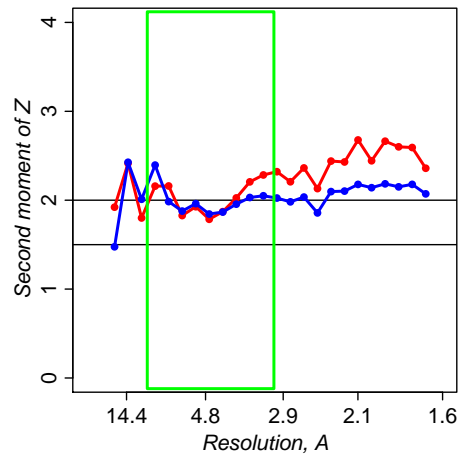
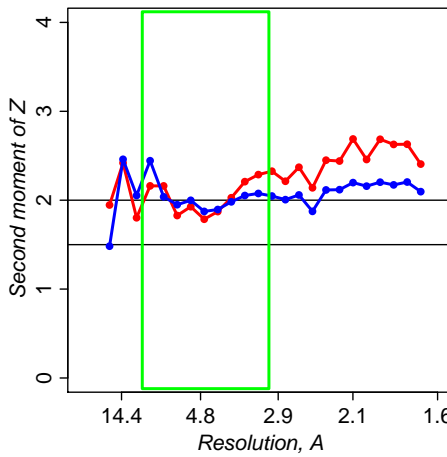
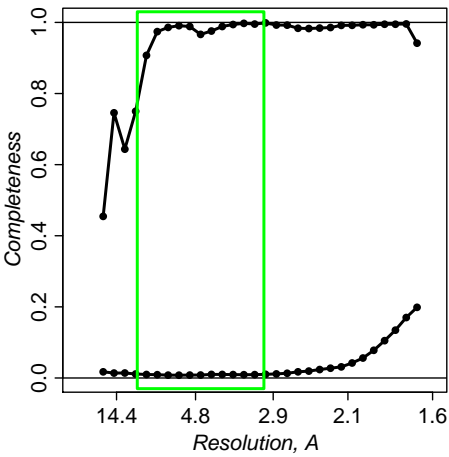
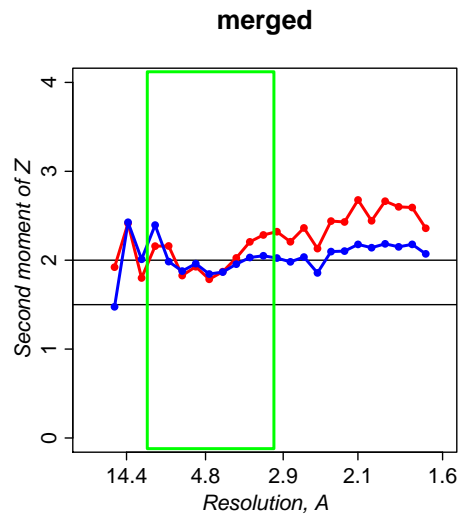
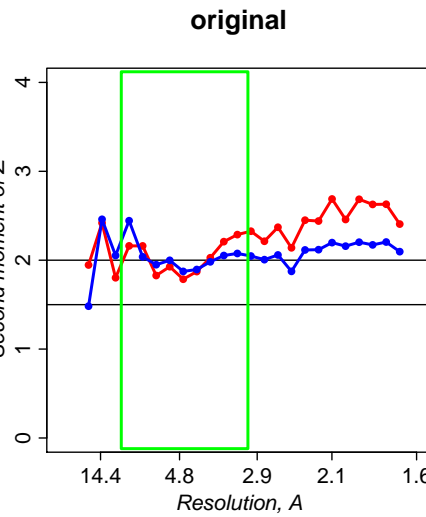
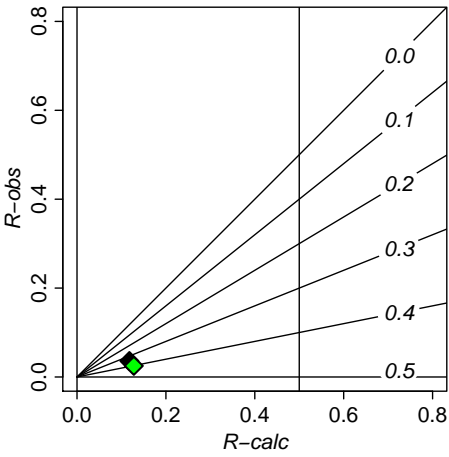
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.07
R	28.8	
R'	29.0	29.2
R-free	29.4	
R'-free	29.6	29.8

s < f/100	9245	17.97 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	27.4–1.6	9.9–3.0
unique	52,254	8,516
measured	51,443	8,385
used	47,988	7,502

NCS	translation	rotation
r.m.s.d. (A)	28.08	0.07
angle (o)	180.00	0.01

residues per monomer	DNA	protein
	0	204



1ojd

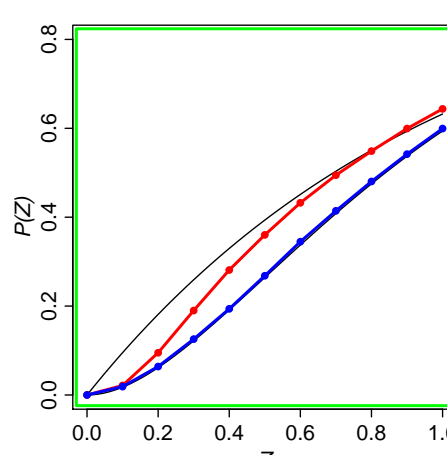
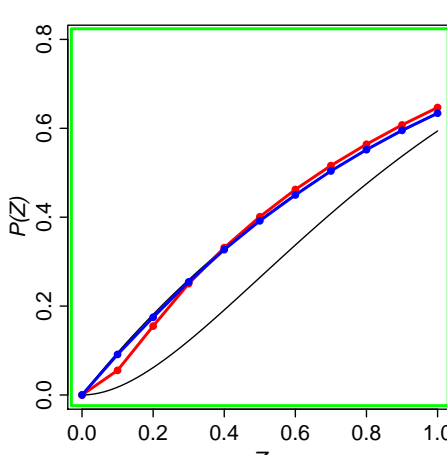
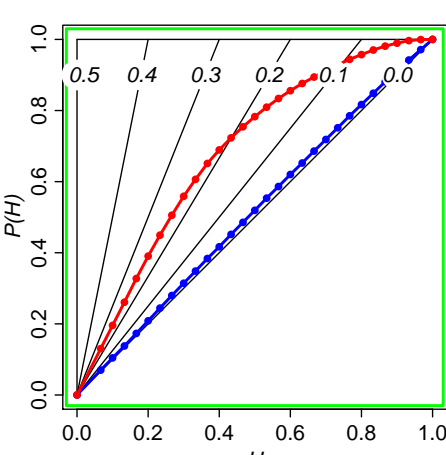
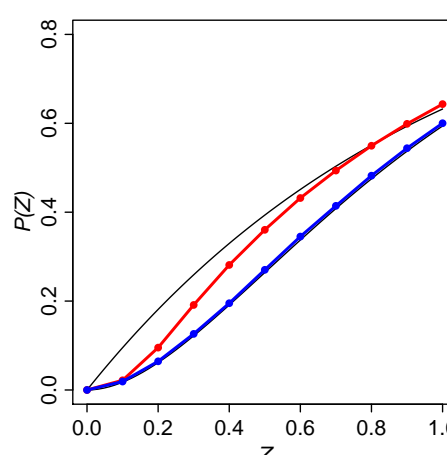
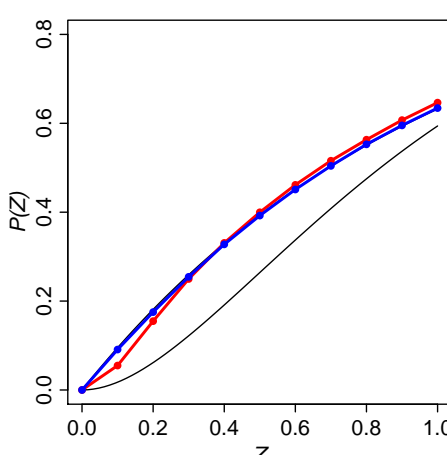
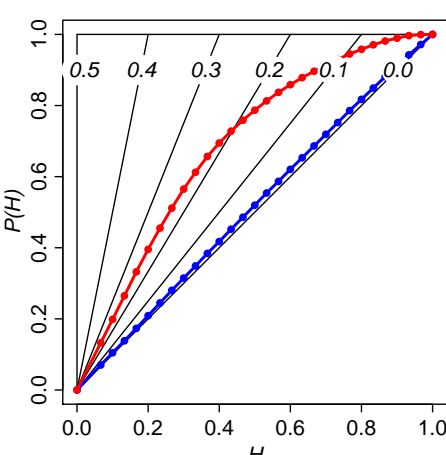
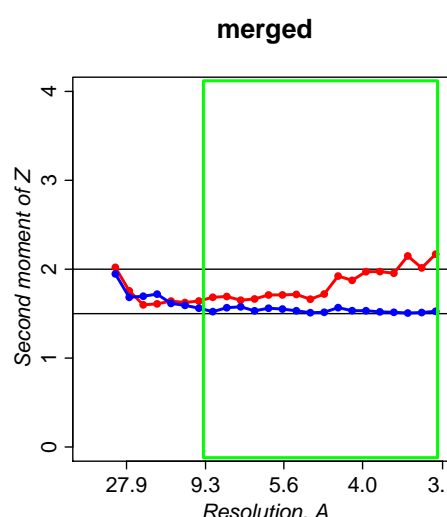
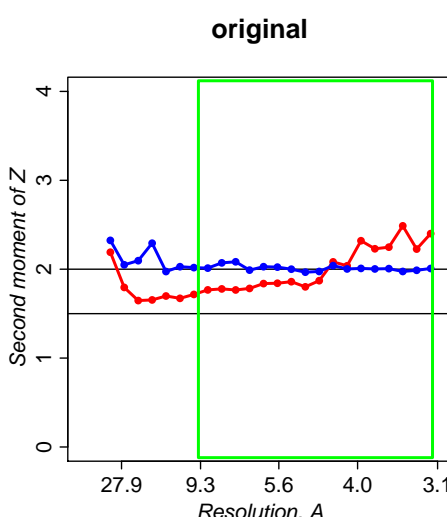
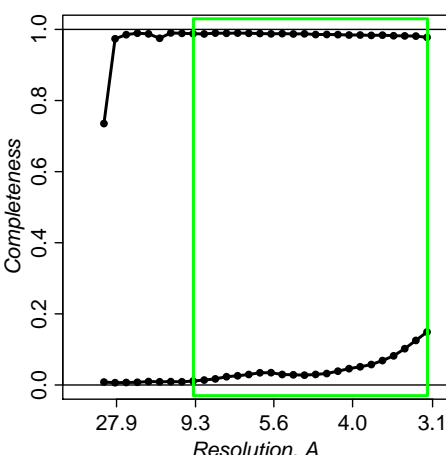
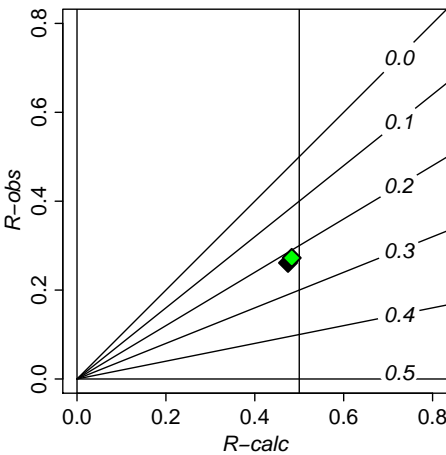
	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	10	5
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		8.00
R	23.0	
R'	-	-
R-free	28.9	
R'-free	-	-

residues per monomer	DNA	protein
	0	494

	8958	6.38 %
s < f/100		
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	51.6-3.1	9.9-3.1
unique	142,700	138,358
measured	140,447	136,167
used	134,424	130,482

NCS	translation	rotation
r.m.s.d. (A)	17.92	1.75
angle (o)	57.28	6.20



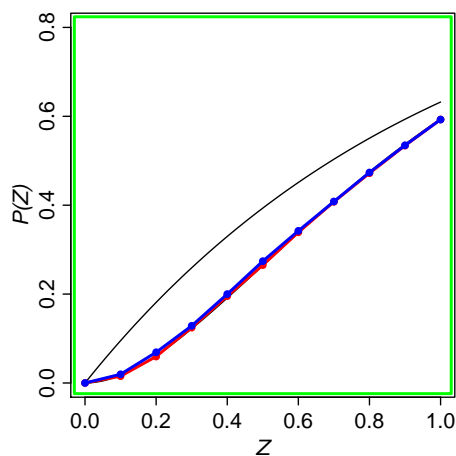
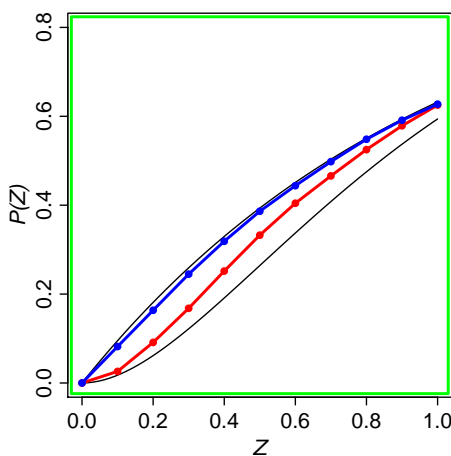
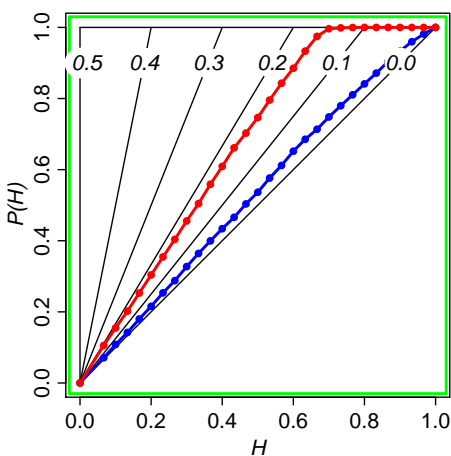
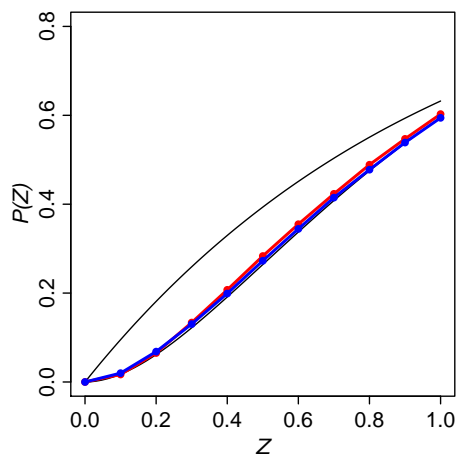
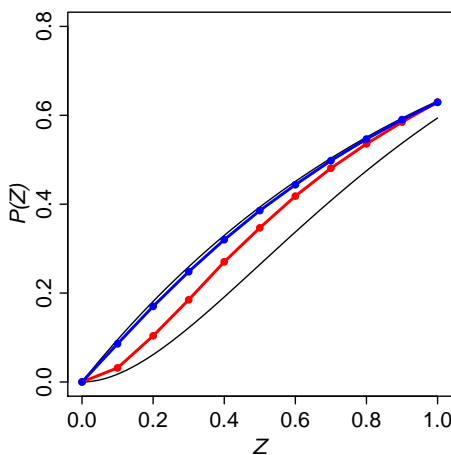
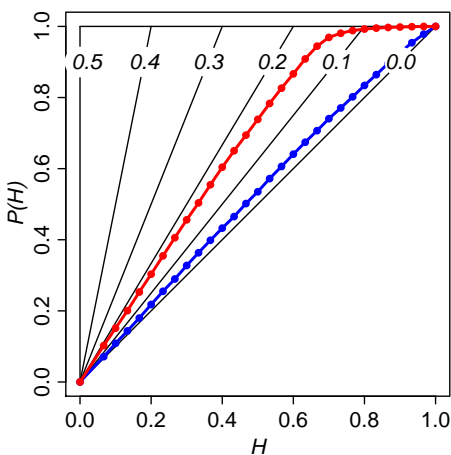
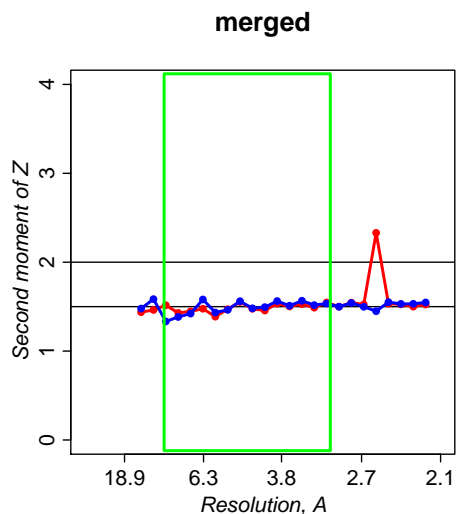
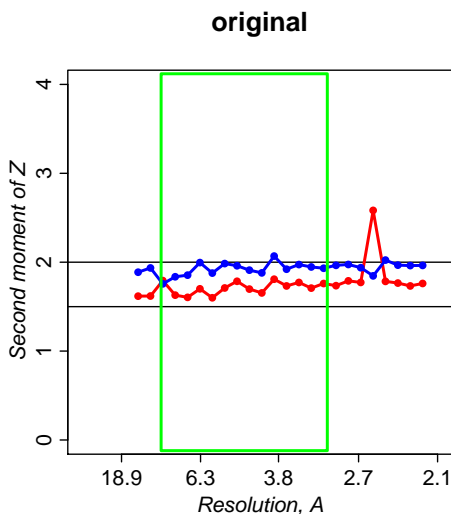
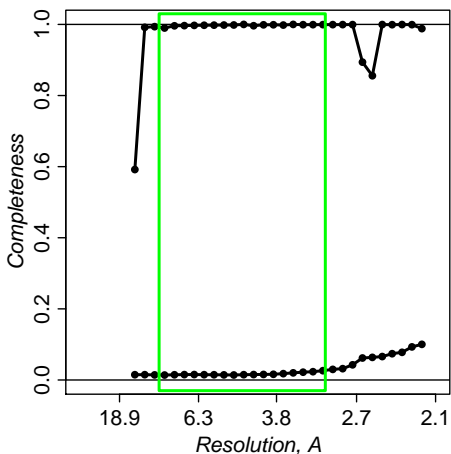
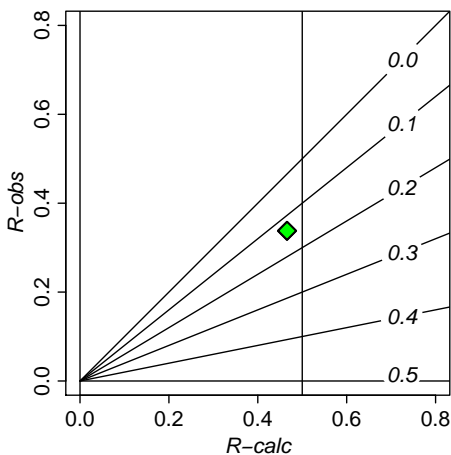
1oji

	original	merged
s.g.	P 65	-
p.g.	12021	12027
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	24.9	-
R'	-	-
R-free	25.8	-
R'-free	-	-
residues per monomer	DNA 0	protein 397

s < f/100	200	0.53 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	15.0-2.2	9.9-3.0
unique	38,074	13,813
measured	37,446	13,794
used	33,610	12,056

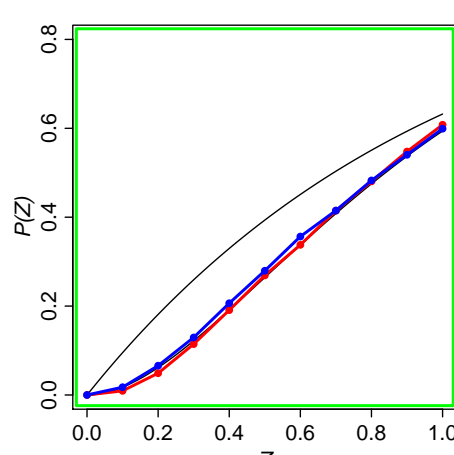
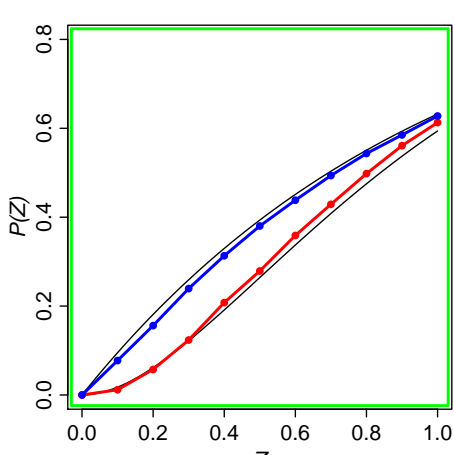
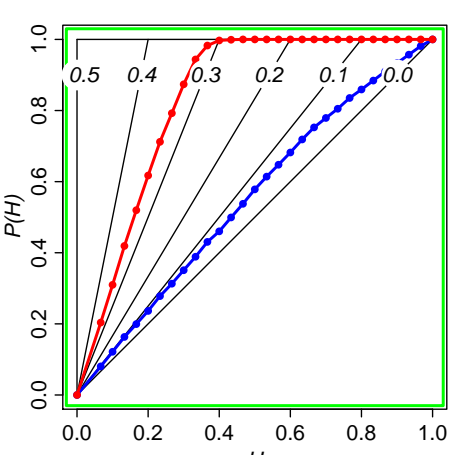
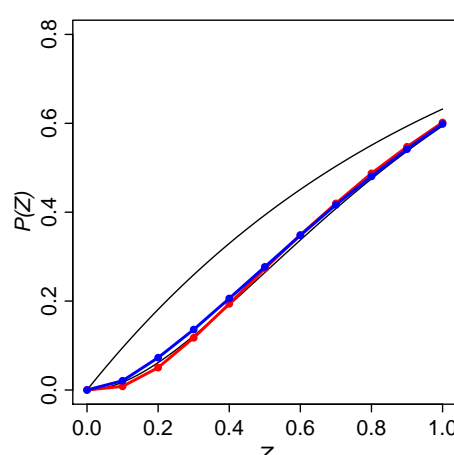
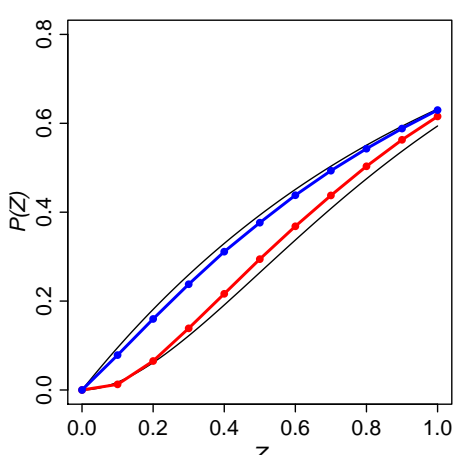
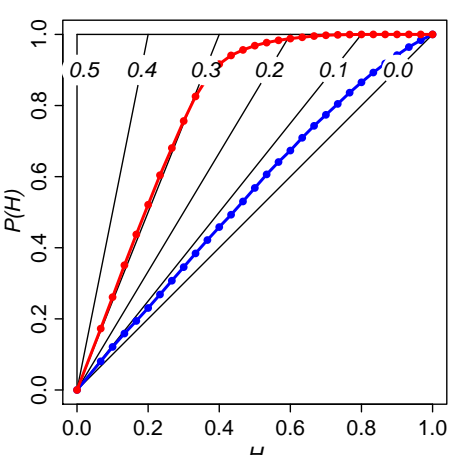
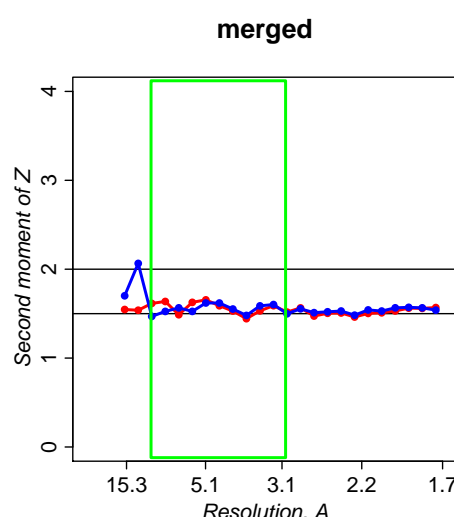
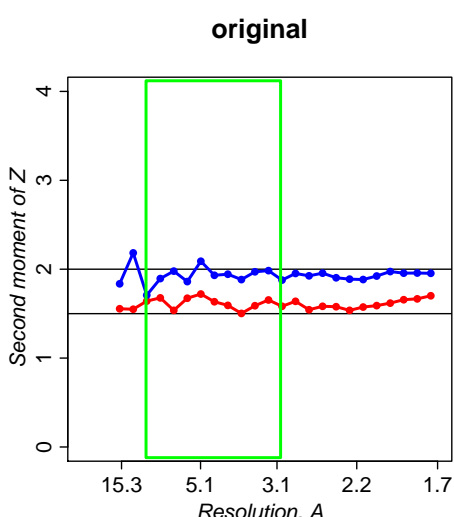
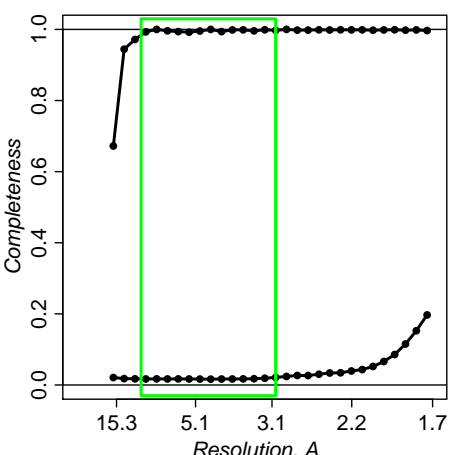
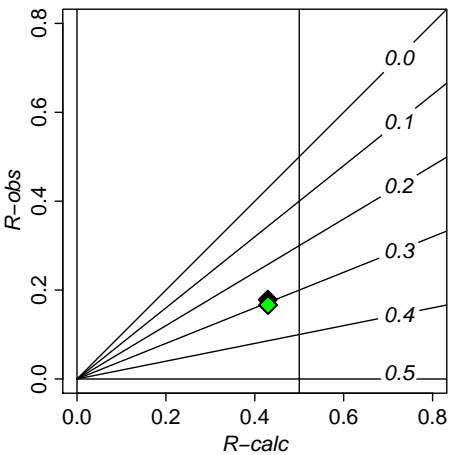
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1olq

	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		3.16
R	26.6	
R'	-	-
R-free	27.5	
R'-free	-	-
residues per monomer	DNA 0	protein 217

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	19.6–1.7	9.9–3.0
unique	42,404	7,517
measured	42,318	7,493
used	40,000	6,820
NCS	translation	rotation
r.m.s.d. (A)	26.43	1.86
angle (o)	173.77	7.31



1om9

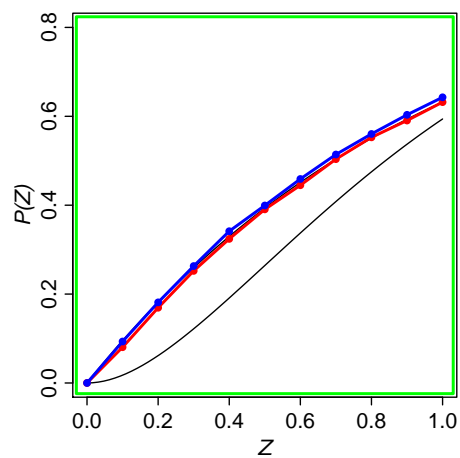
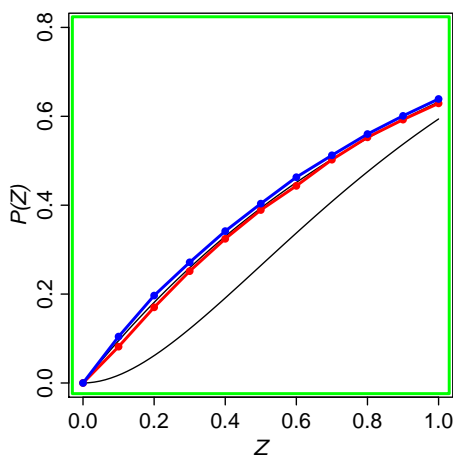
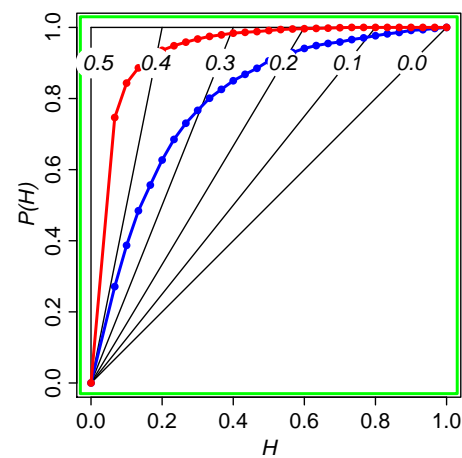
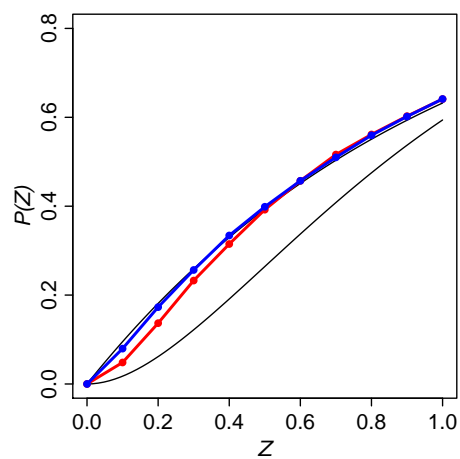
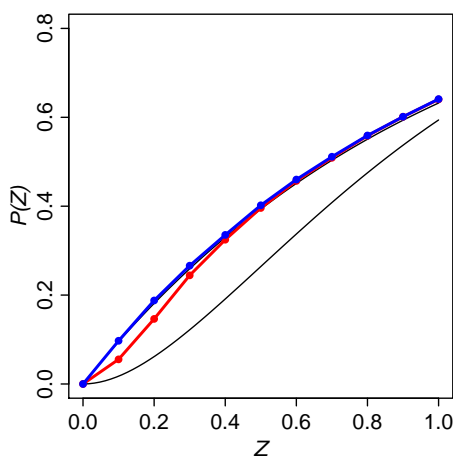
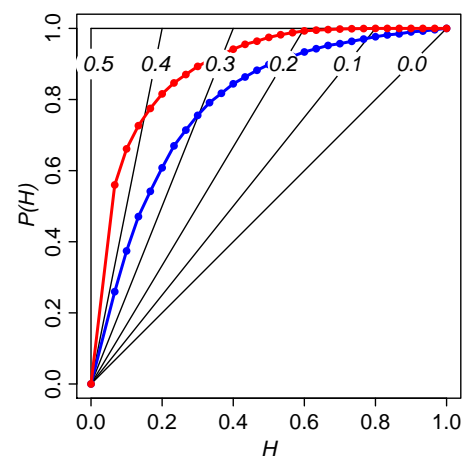
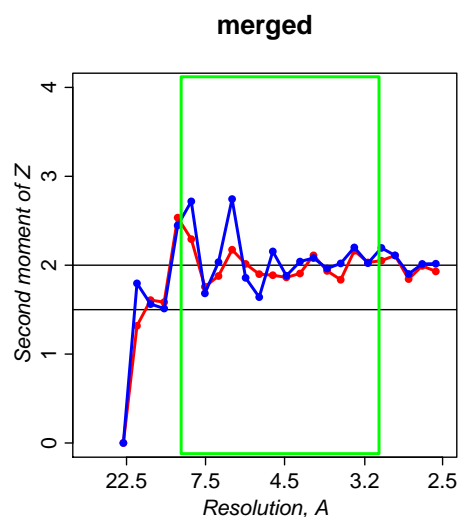
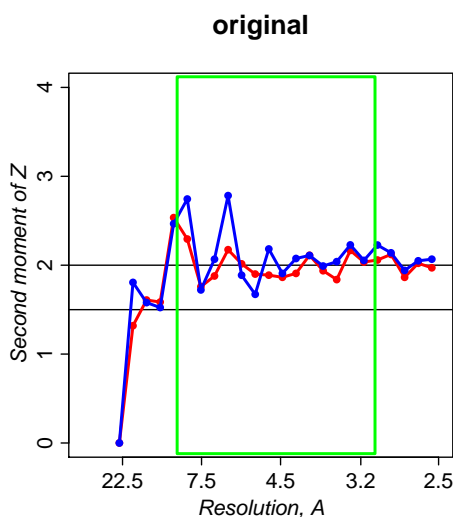
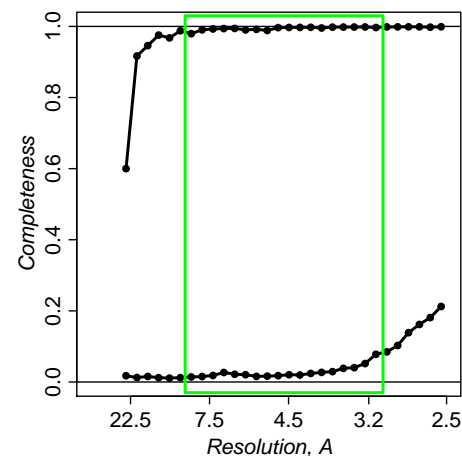
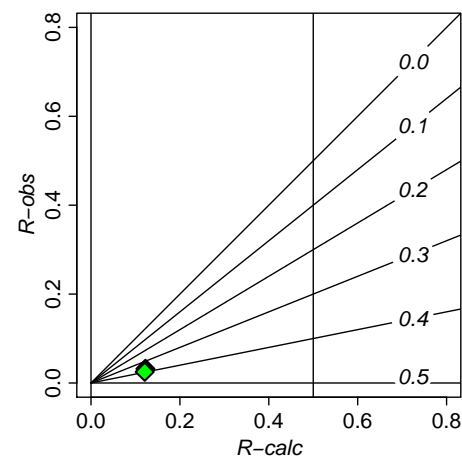
	original	merged
s.g.	P 31 2 1	P 64 2 2
p.g.	10023	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.08
R	25.3	
R'	25.6	25.3
R-free	29.8	
R'-free	30.3	30.1

s < f/100	921	8.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	30.0–2.5	9.9–3.0
unique	11,556	6,589
measured	11,512	6,564
used	8,974	4,950

NCS	translation	rotation
r.m.s.d. (A)	13.91	0.08
angle (o)	59.99	0.05

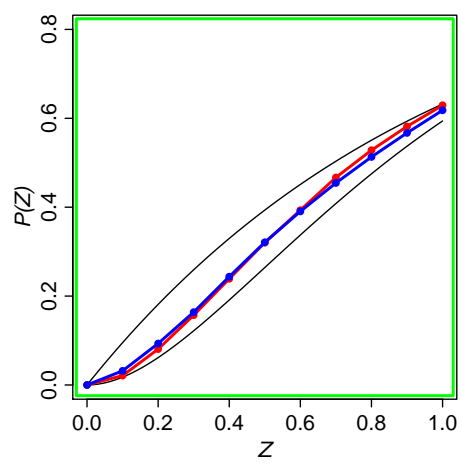
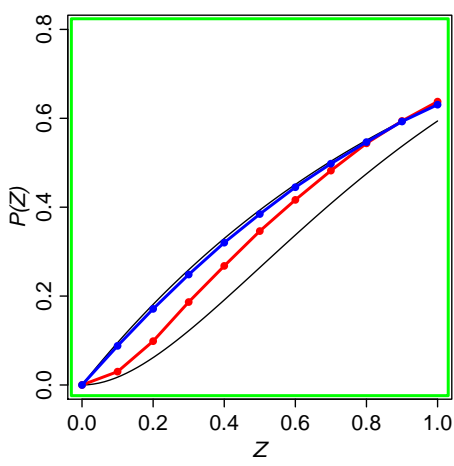
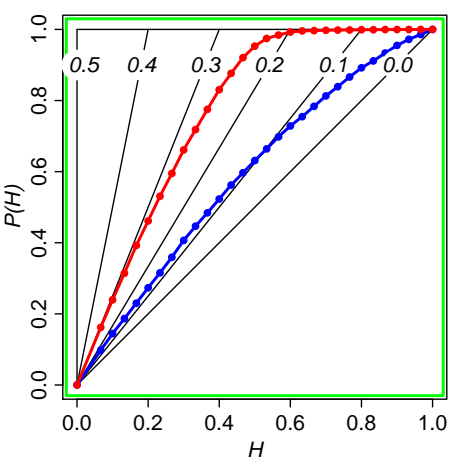
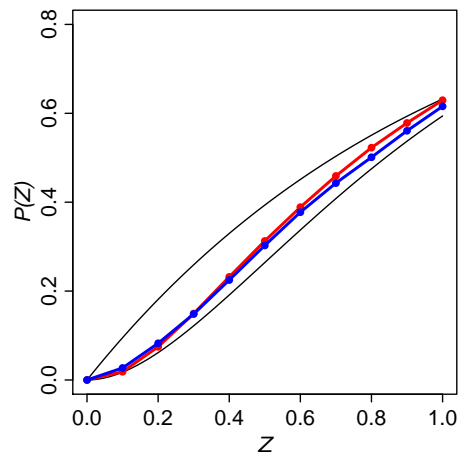
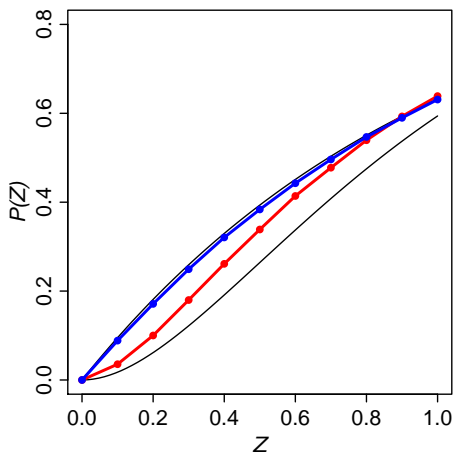
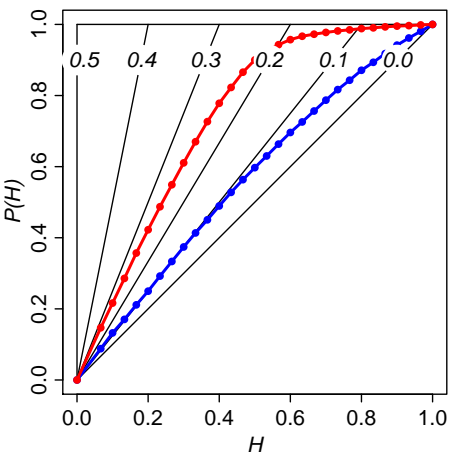
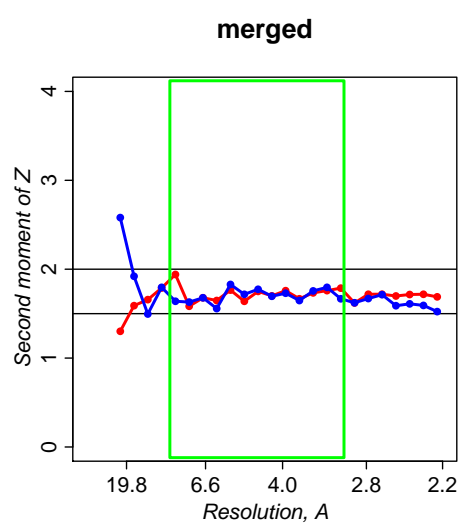
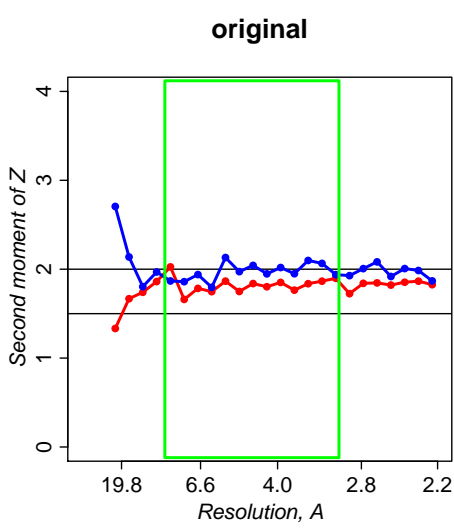
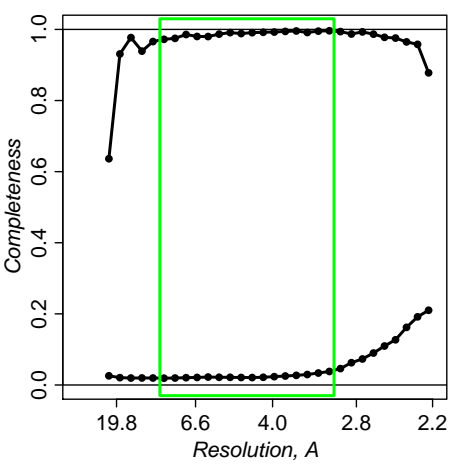
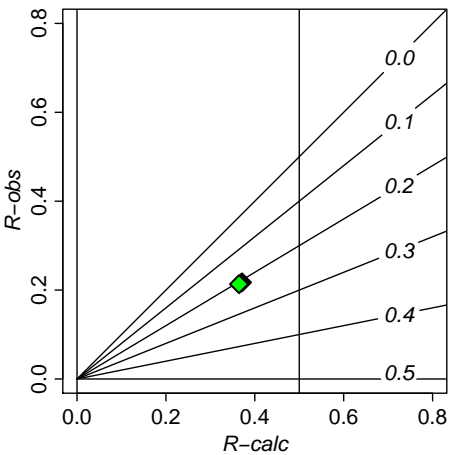
residues per monomer	DNA	protein
	0	152



1on0

	original	merged
s.g.	P 1 2 1 1	C 2 2 2 1
p.g.	10001	10003
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		3.32
R	27.6	
R'	-	-
R-free	30.1	
R'-free	-	-
residues per monomer	DNA 0	protein 156

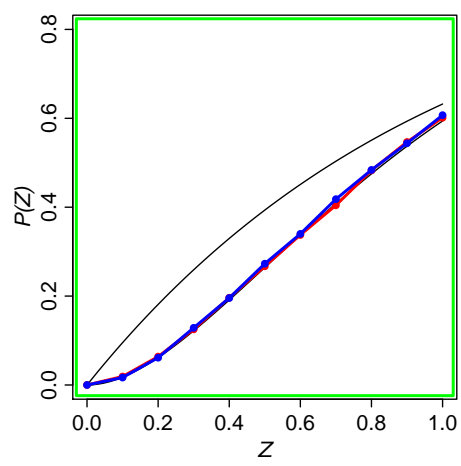
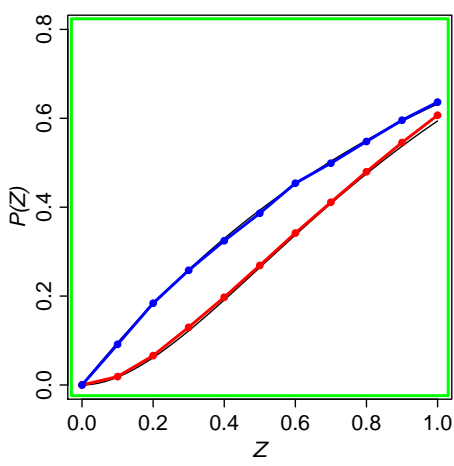
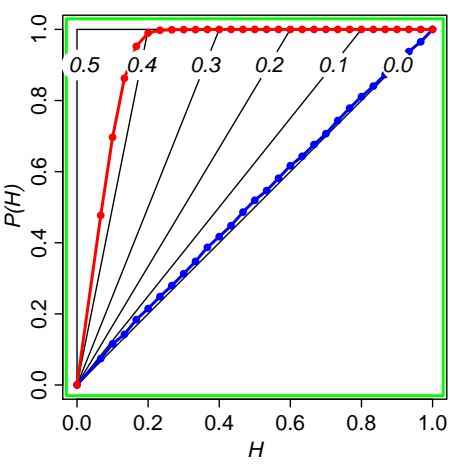
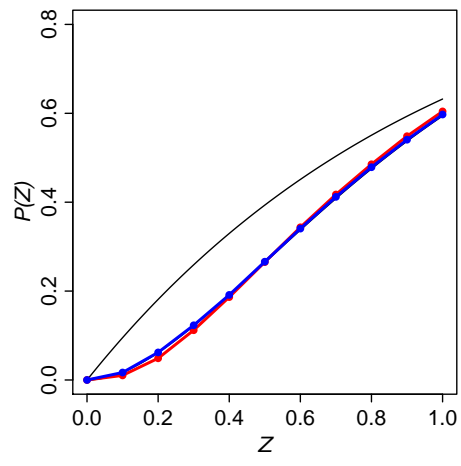
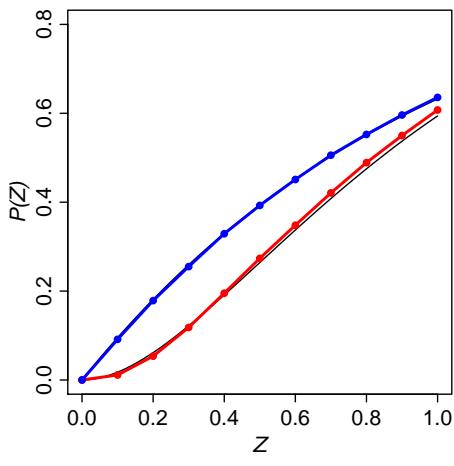
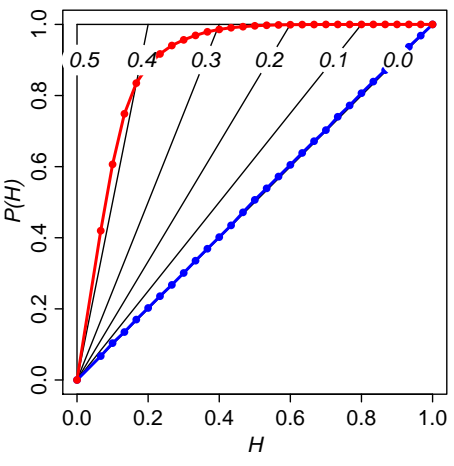
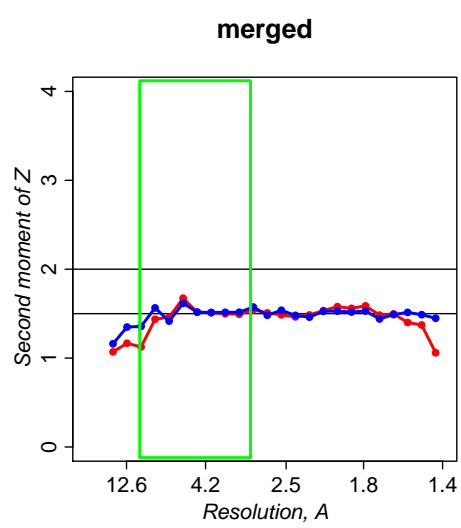
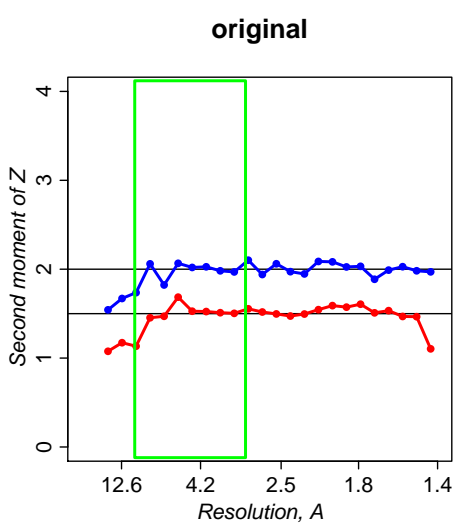
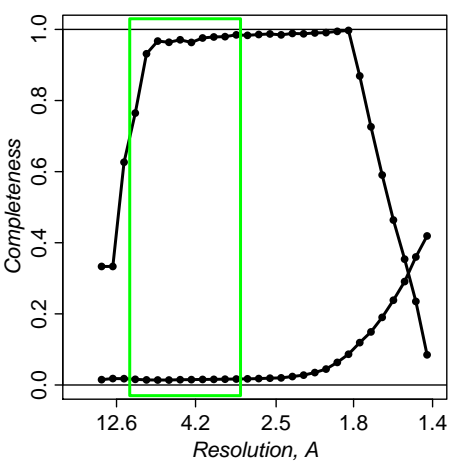
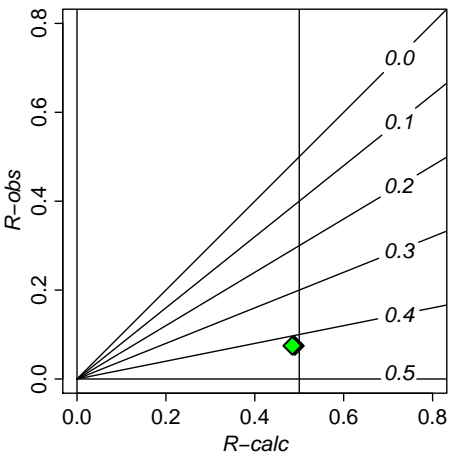
s < f/100	680	1.78 %
s <= 0	680	1.78 %
f <= 0	680	1.78 %
s,f <= 0	680	1.78 %
range (A)	29.7–2.2	9.9–3.0
unique	39,258	14,947
measured	38,218	14,819
used	35,150	13,508
NCS	translation	rotation
r.m.s.d. (A)	6.19	0.69
angle (o)	29.10	1.43



1on2

	original	merged
s.g.	P 32	P 32 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		4.42
R	30.6	
R'	-	-
R-free	32.2	
R'-free	-	-
residues per monomer	DNA 0	protein 135

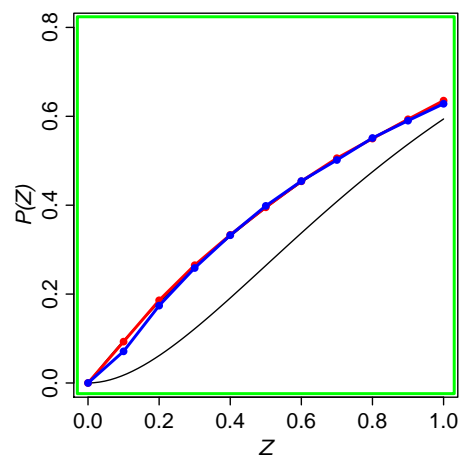
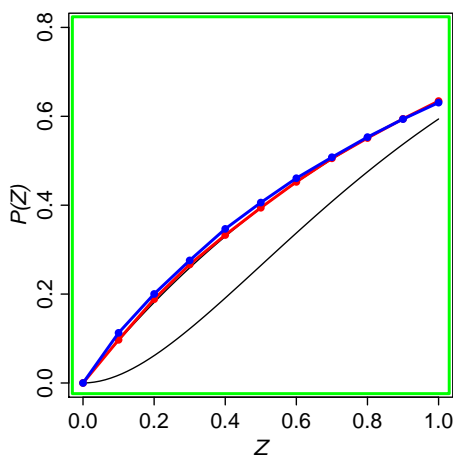
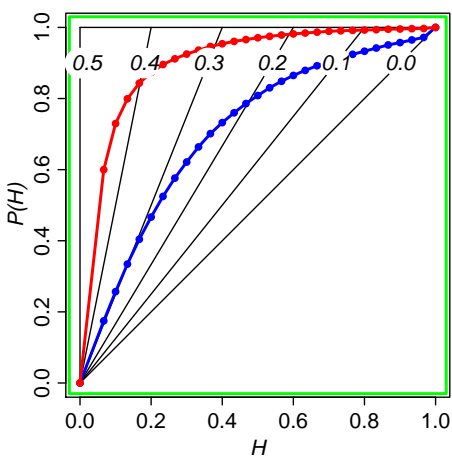
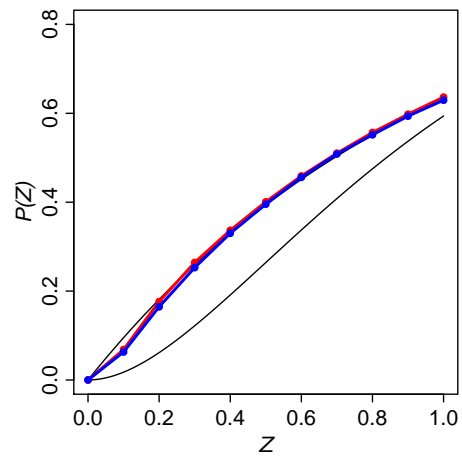
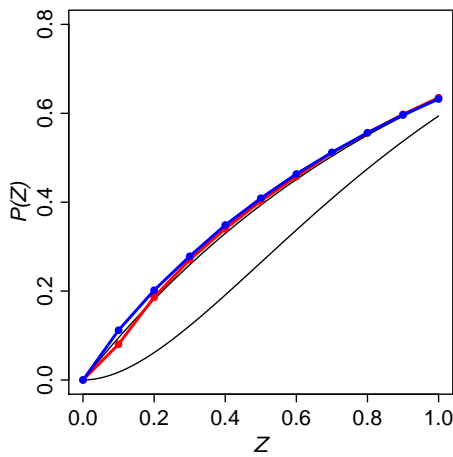
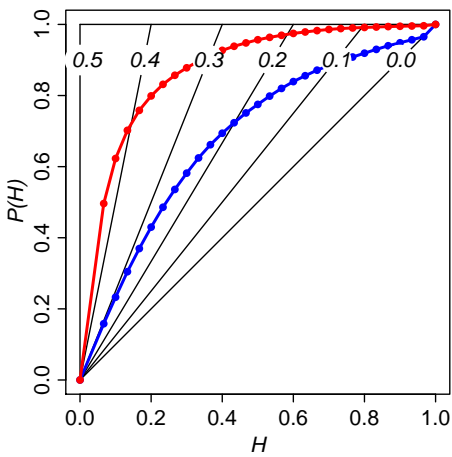
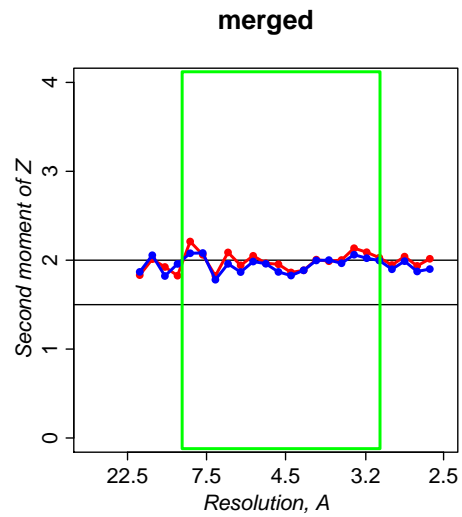
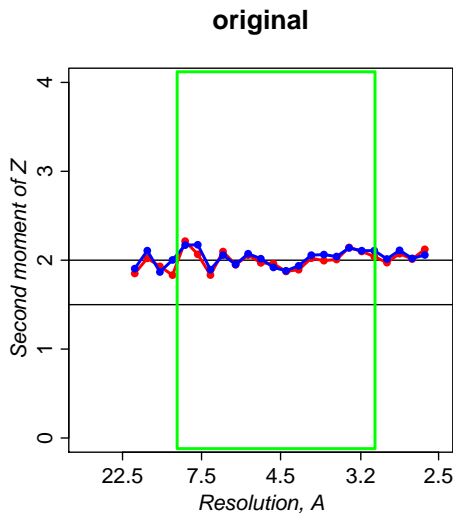
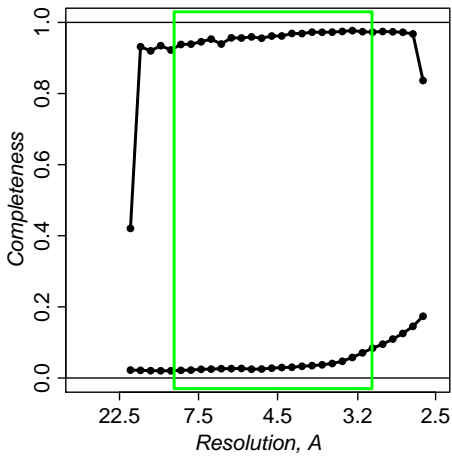
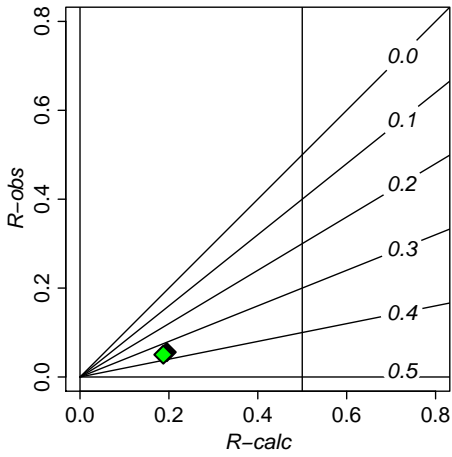
s < f/100	224	0.64 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	26.2-1.4	9.9-3.0
unique	50,516	4,998
measured	35,177	4,833
used	29,534	4,182
NCS	translation	rotation
r.m.s.d. (A)	23.70	3.21
angle (o)	172.72	11.06



1op8

	original	merged
s.g.	P 1	H 3
p.g.	10000	10020
a.u.	6	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.57
R	23.1	
R'	23.1	22.8
R-free	28.6	
R'-free	28.4	27.8
residues per monomer	DNA 0	protein 234

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	19.6–2.6	9.9–3.0
unique	46,601	28,049
measured	44,569	27,118
used	41,622	25,293
NCS	translation	rotation
r.m.s.d. (A)	22.79	0.24
angle (o)	119.80	0.11



1oq7

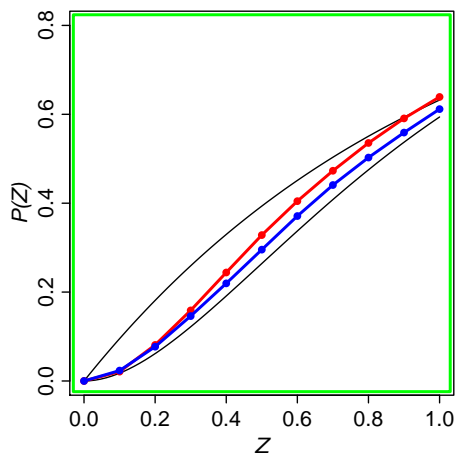
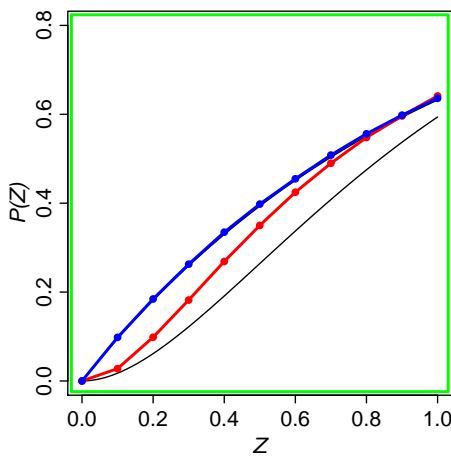
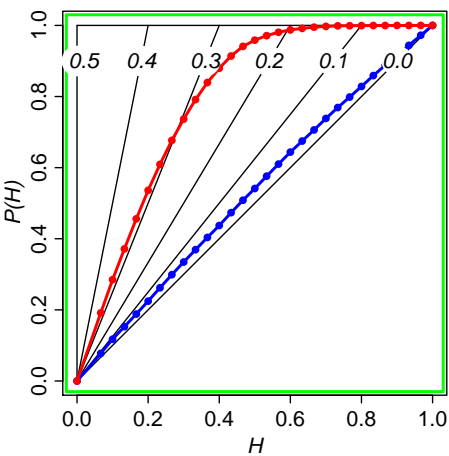
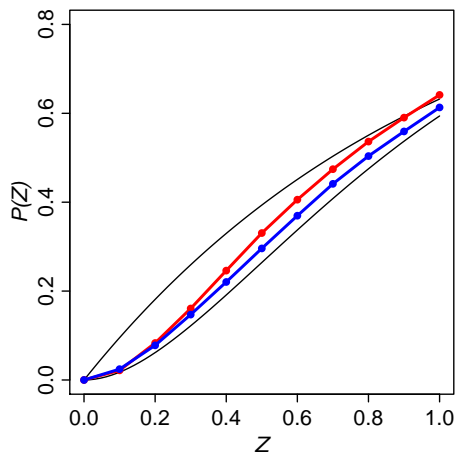
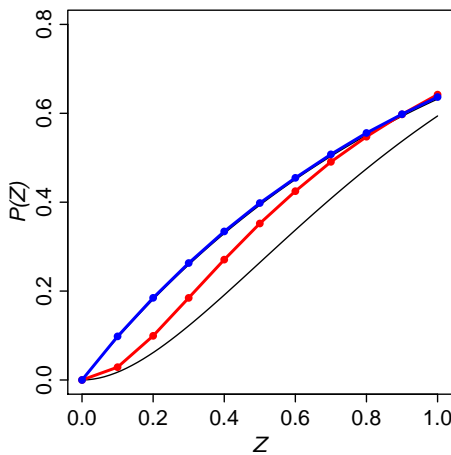
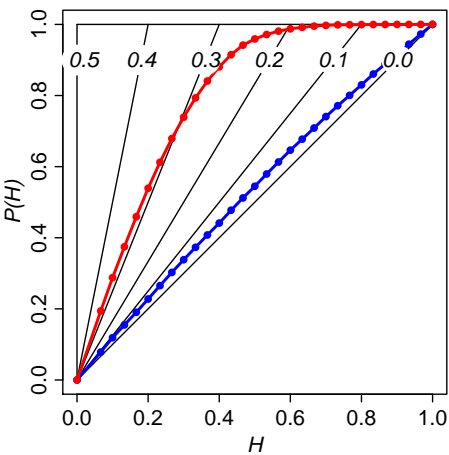
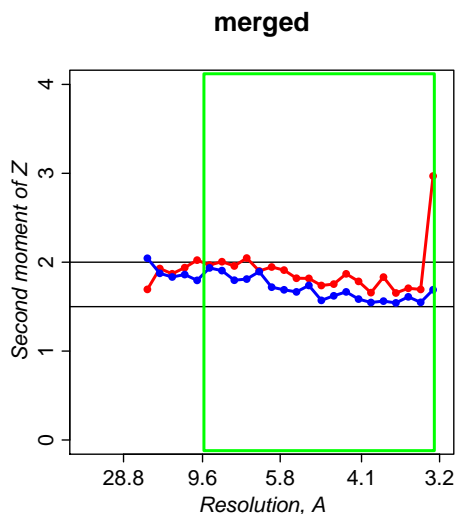
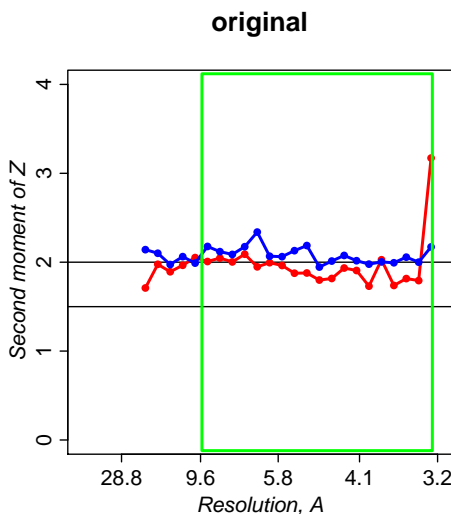
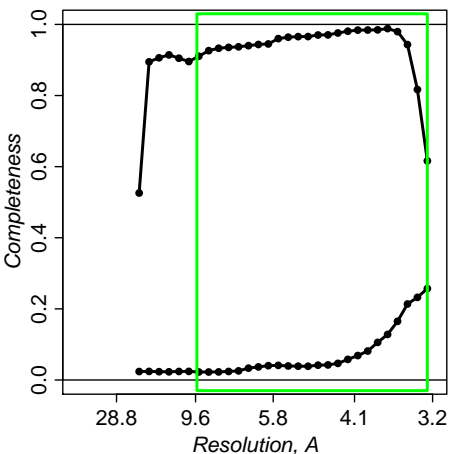
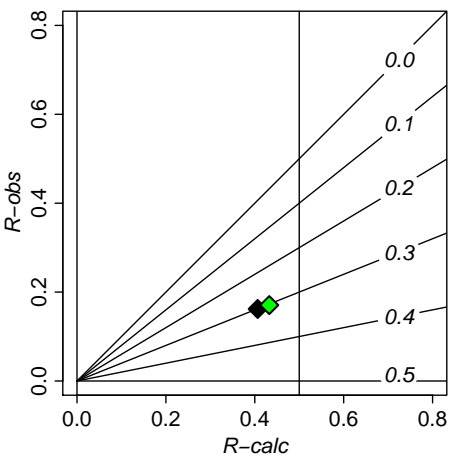
	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		2.16
R	24.4	
R'	25.9	26.9
R-free	32.4	
R'-free	33.1	34.4

residues per monomer	DNA	protein
	0	346

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.9–3.2	9.9–3.2
unique	53,228	51,647
measured	49,227	47,800
used	44,516	43,372

NCS	translation	rotation
r.m.s.d. (A)	7.70	0.62
angle (o)	24.95	1.99



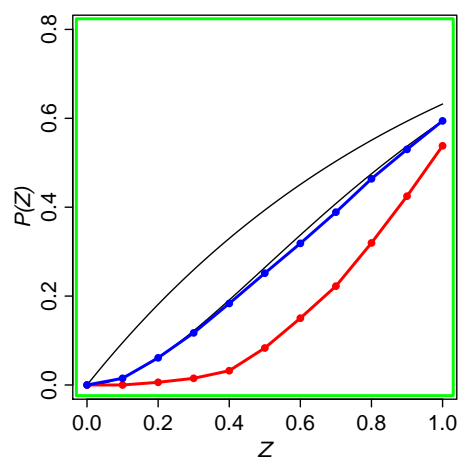
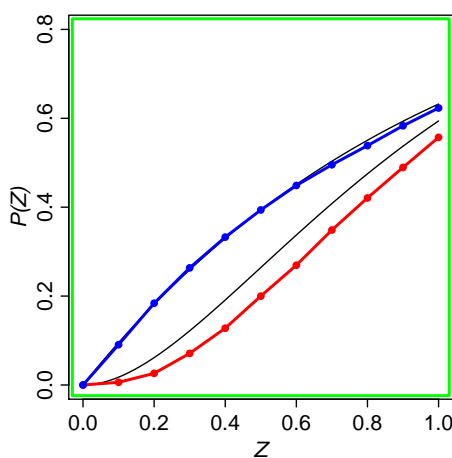
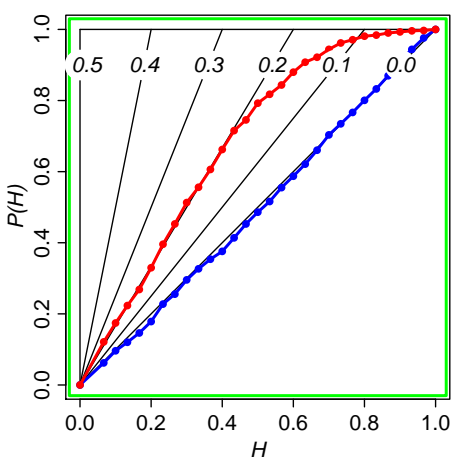
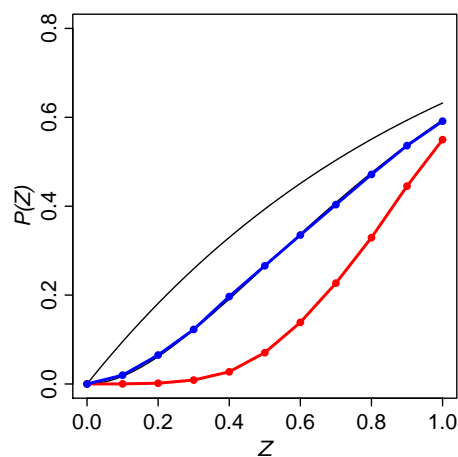
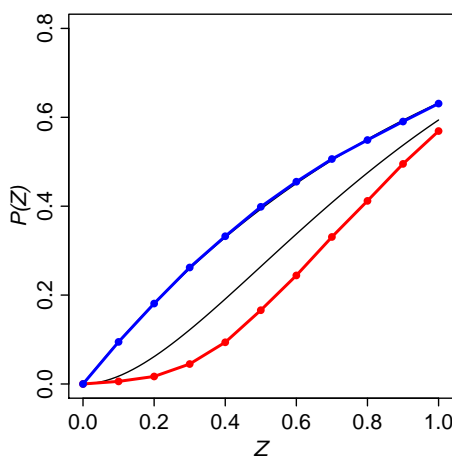
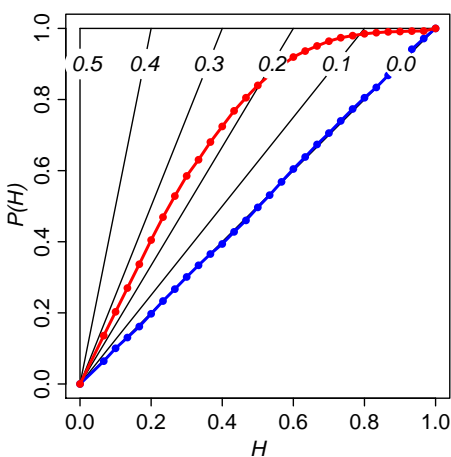
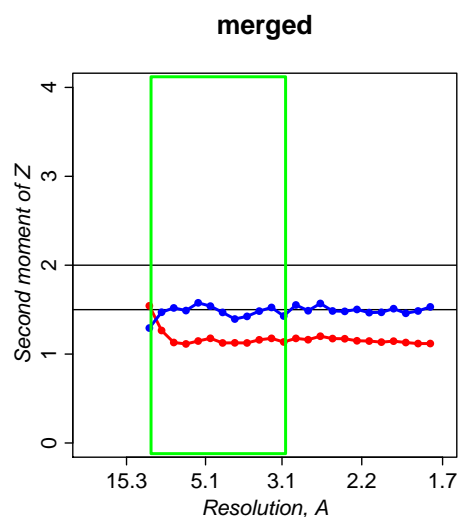
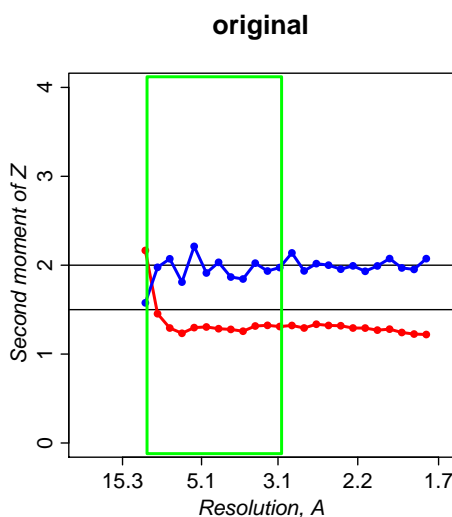
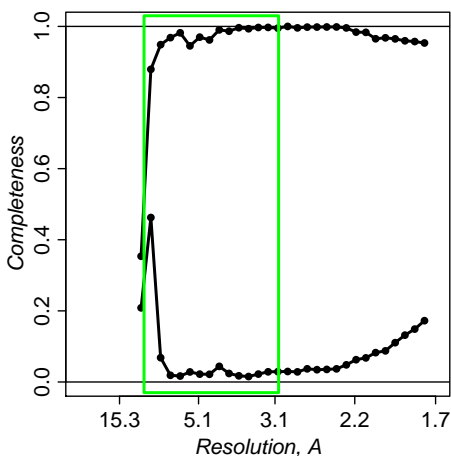
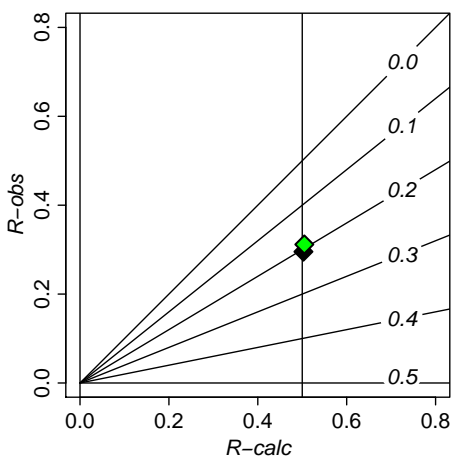
1or3

	original	merged
s.g.	P 31 2 1	-
p.g.	10023	12027
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	30.7	-
R'	-	-
R-free	30.7	-
R'-free	-	-
residues per monomer	DNA 0	protein 136

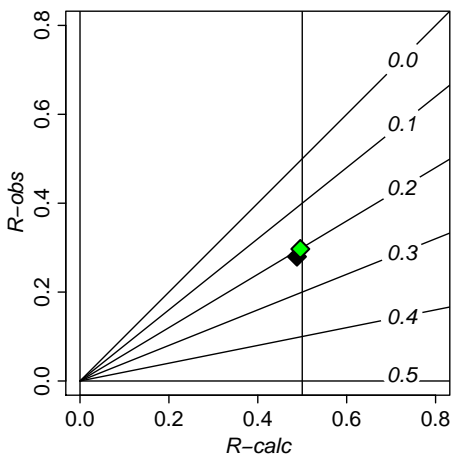
s < f/100	2069	14.35 %
s <= 0	0	0.00 %
f <= 0	73	0.51 %
s,f <= 0	0	0.00 %

range (A)	10.8-1.7	9.9-3.0
unique	14,759	2,899
measured	14,421	2,846
used	11,528	1,990

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1orr



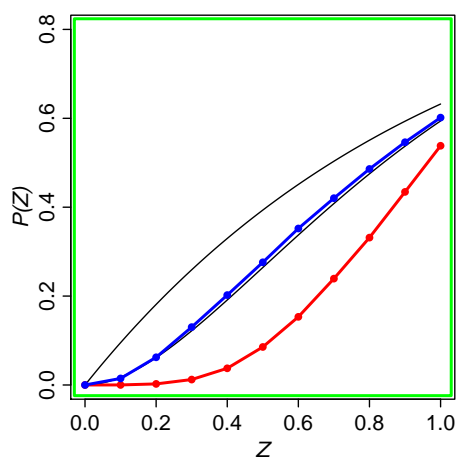
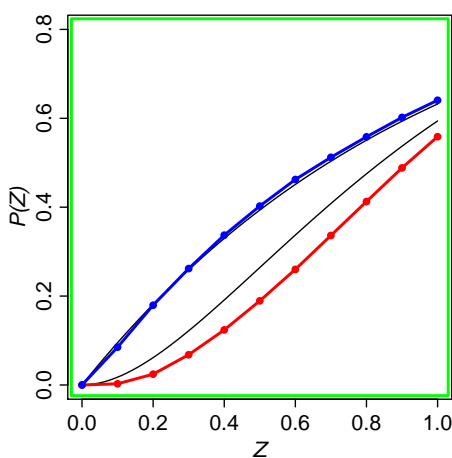
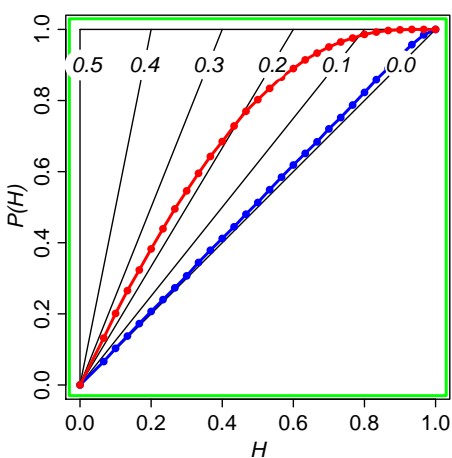
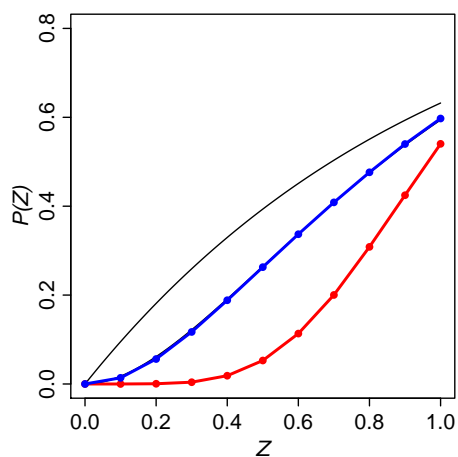
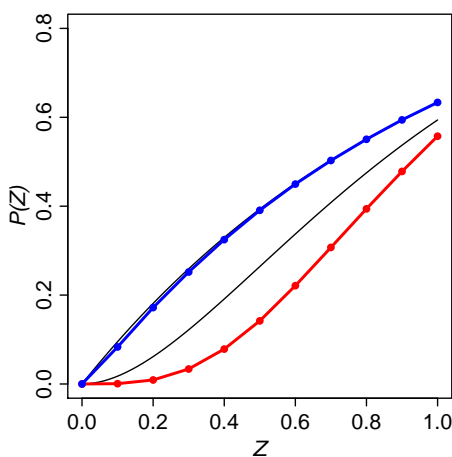
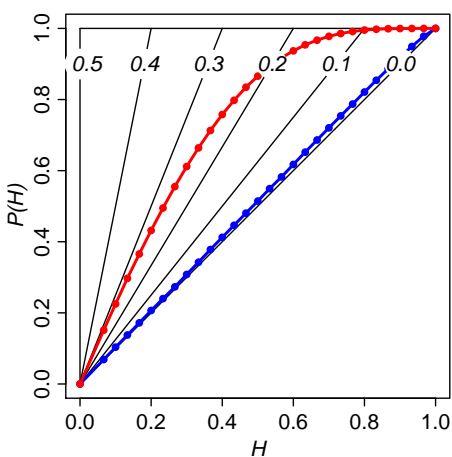
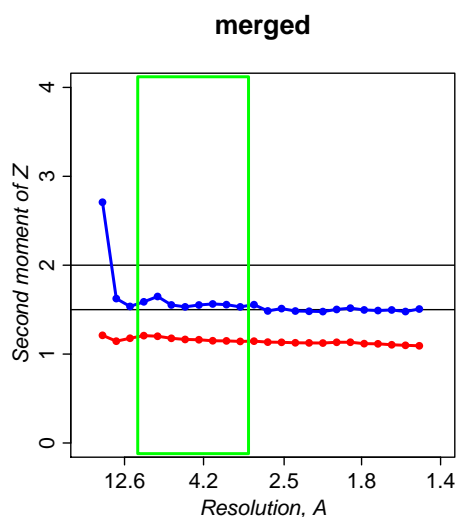
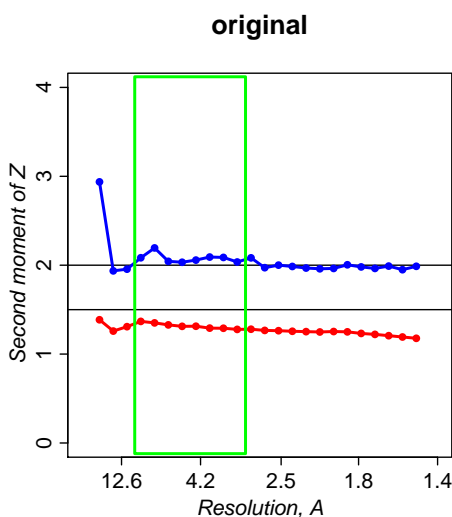
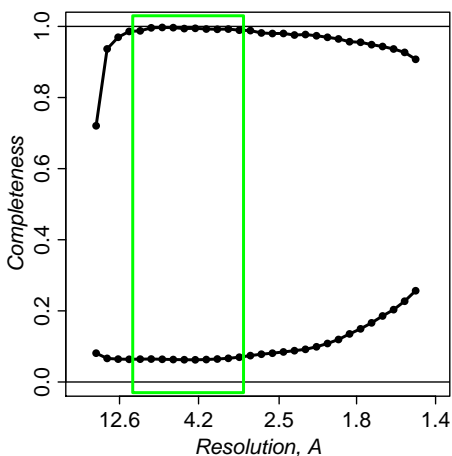
	original	merged
s.g.	P 1 21 1	-
p.g.	10001	10003
a.u.	4	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	27.9	-
R'	-	-
R-free	28.4	-
R'-free	-	-

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	47.0-1.5	9.9-3.0
unique	235,667	26,618
measured	225,493	26,423
used	213,272	24,338

residues per monomer	DNA	protein
	0	335

NCS	translation	rotation
r.m.s.d. (A)	10.39	2.67
angle (o)	41.76	9.50



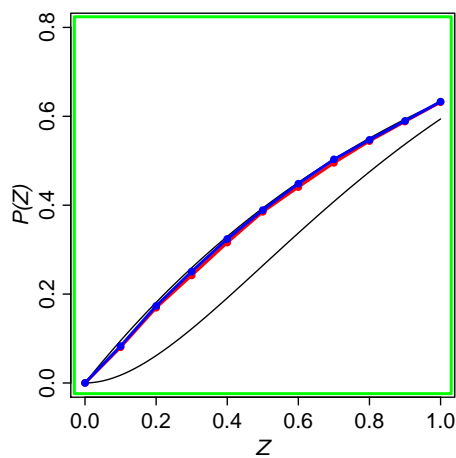
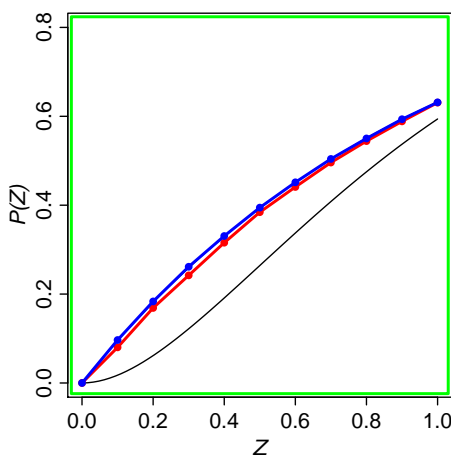
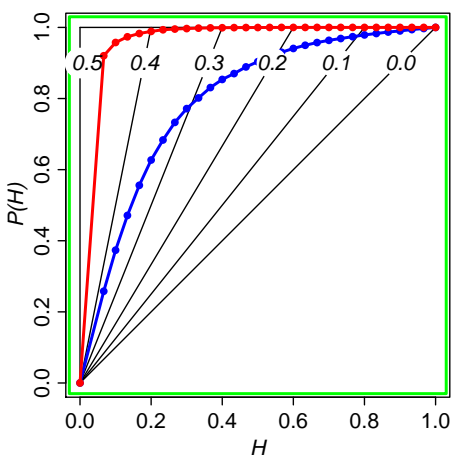
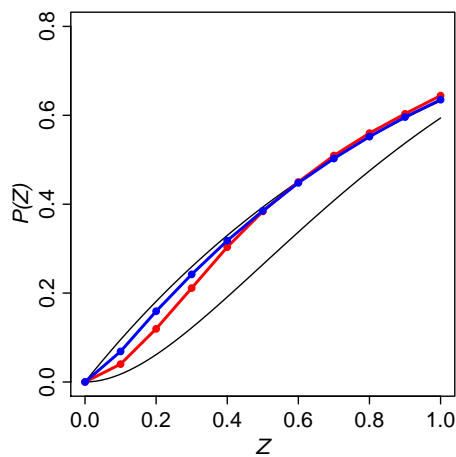
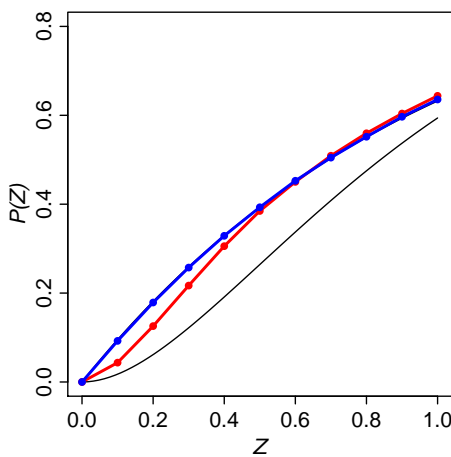
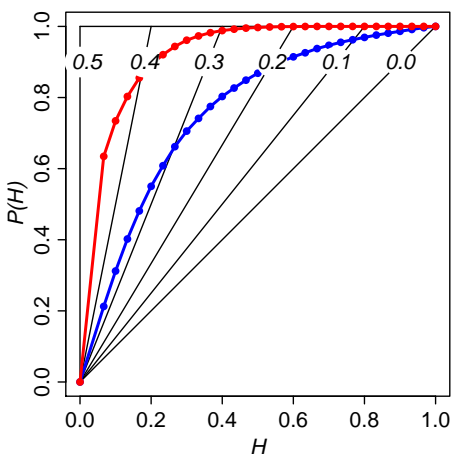
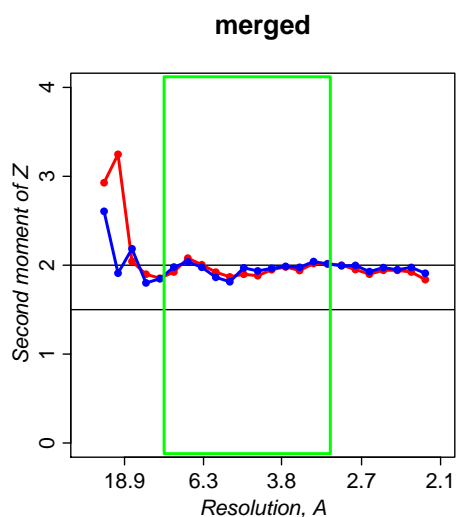
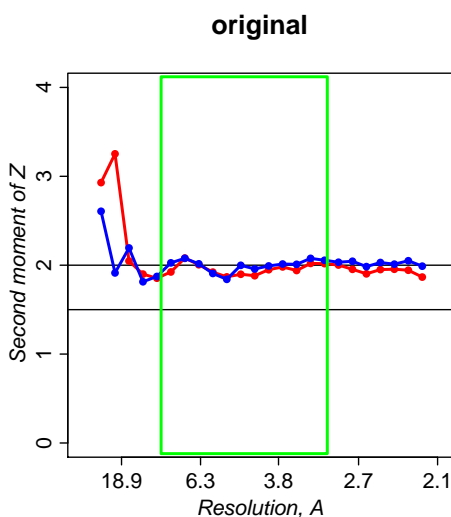
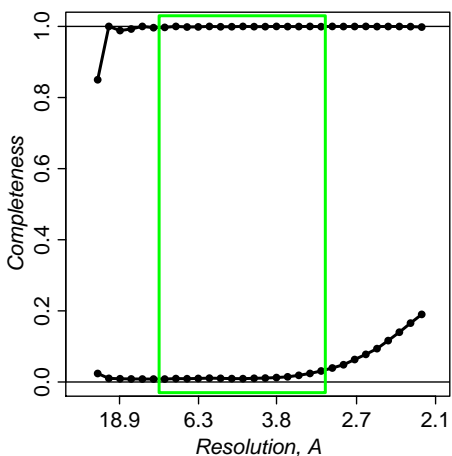
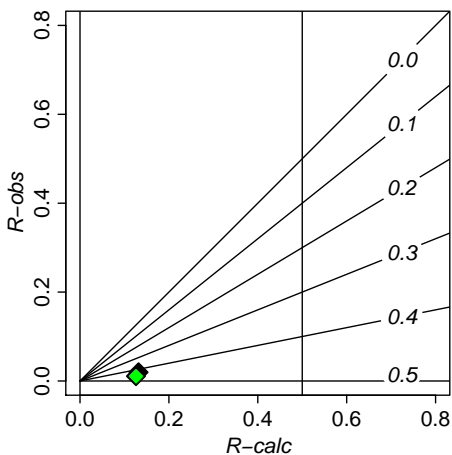
1os2

	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.24
R	28.1	
R'	28.2	28.6
R-free	31.6	
R'-free	31.9	32.8
residues per monomer	DNA 0	protein 165

s < f/100	8754	13.46 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	61.9–2.2	9.9–3.0
unique	65,051	23,311
measured	65,016	23,300
used	62,456	22,108

NCS	translation	rotation
r.m.s.d. (A)	16.83	0.15
angle (o)	85.66	0.07



1os4

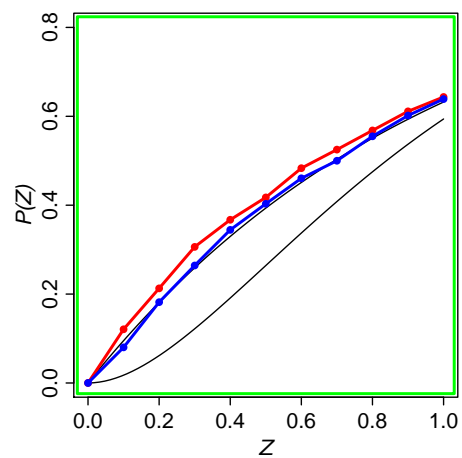
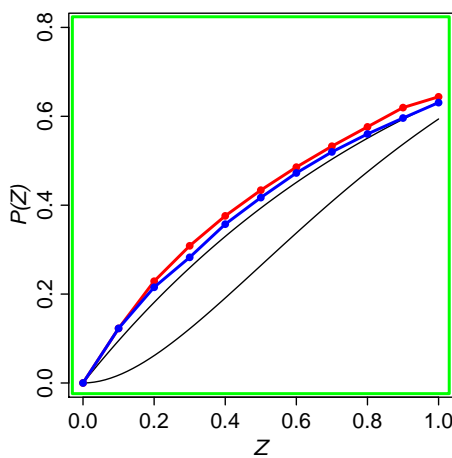
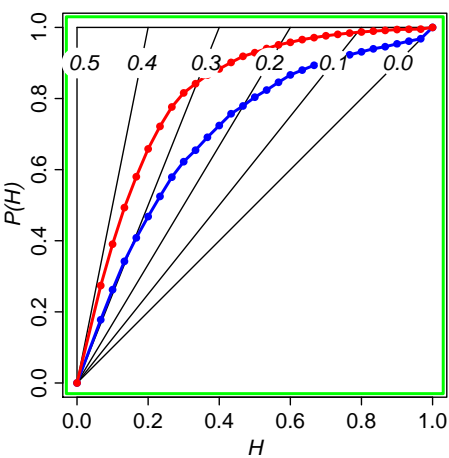
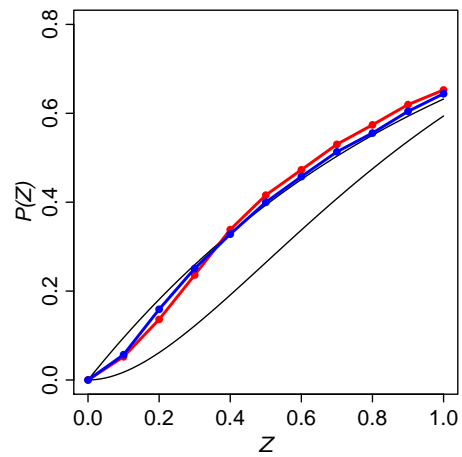
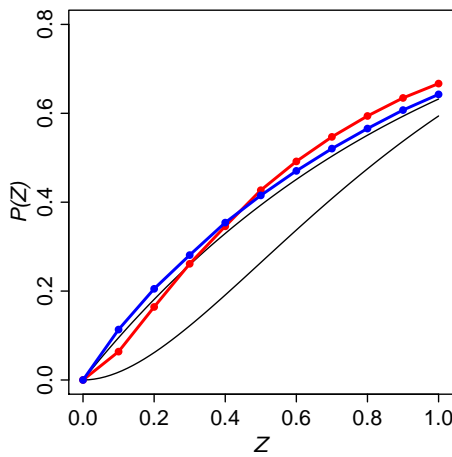
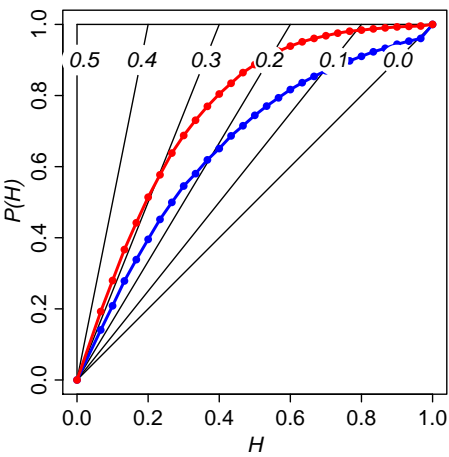
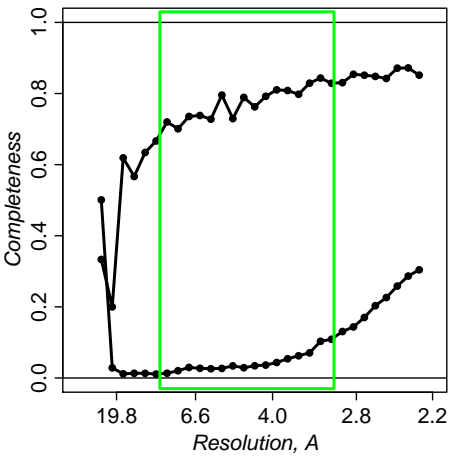
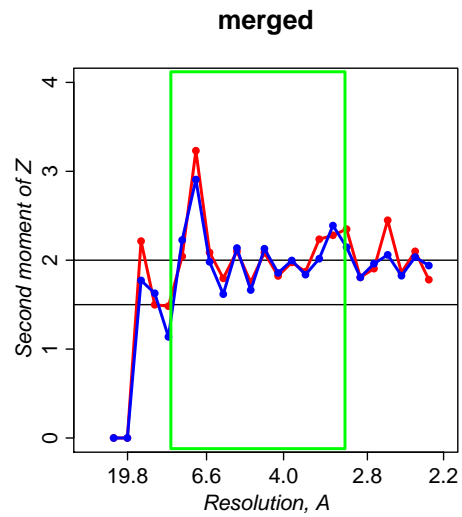
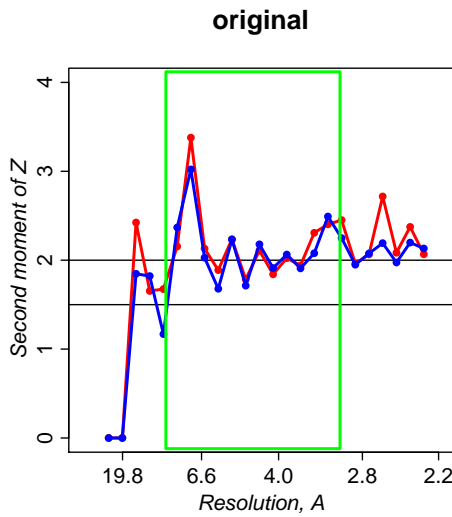
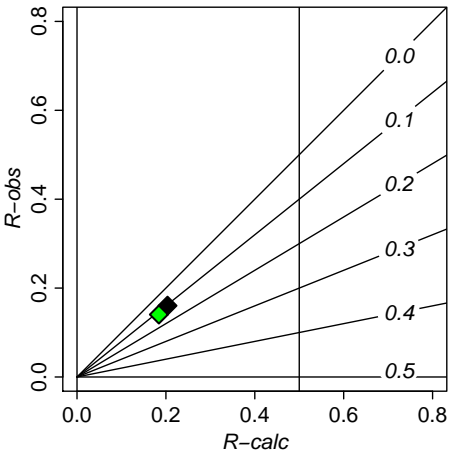
	original	merged
s.g.	P 1	H 3
p.g.	10000	10020
a.u.	6	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.31
R	26.5	
R'	26.2	25.4
R-free	31.4	
R'-free	30.8	29.7

residues per monomer	DNA	protein
	0	48

s < f/100	85	0.83 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	41.6–2.2	9.9–3.0
unique	12,386	5,093
measured	10,248	4,059
used	7,113	2,493

NCS	translation	rotation
r.m.s.d. (A)	11.77	0.23
angle (o)	119.89	0.38



1os9

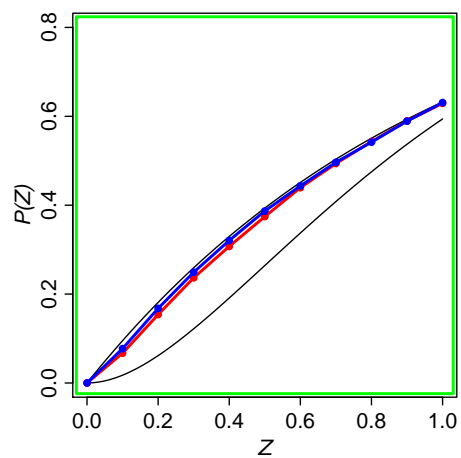
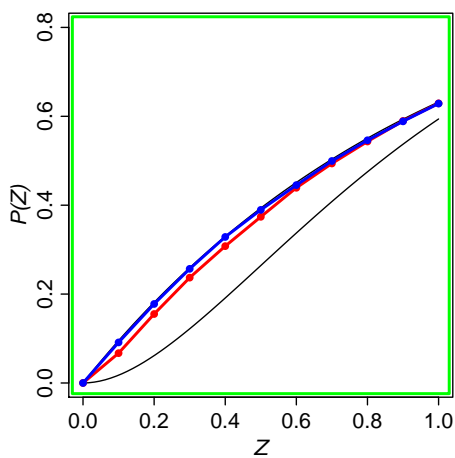
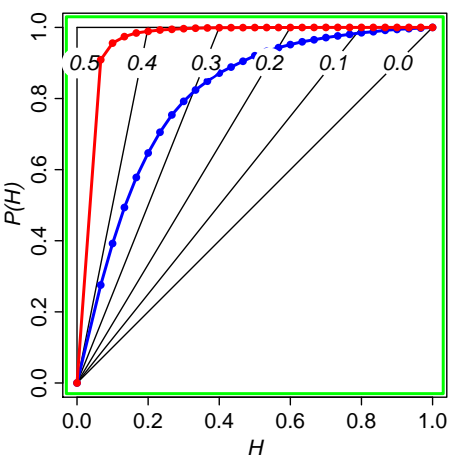
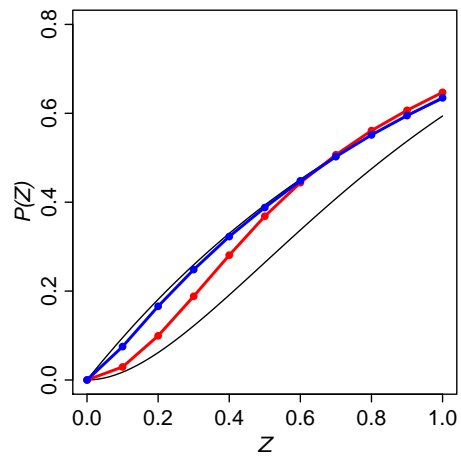
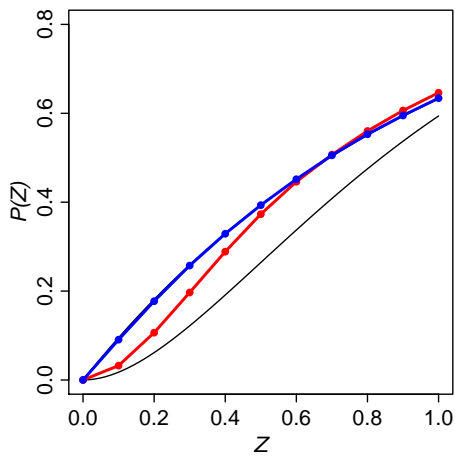
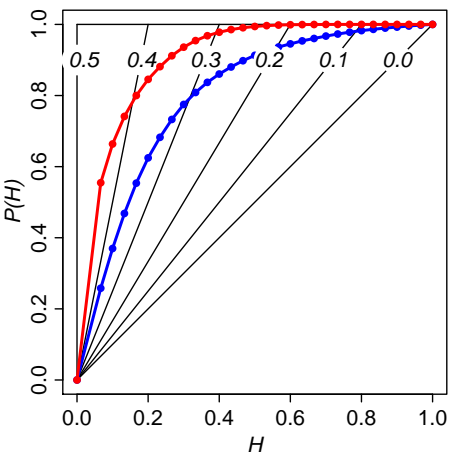
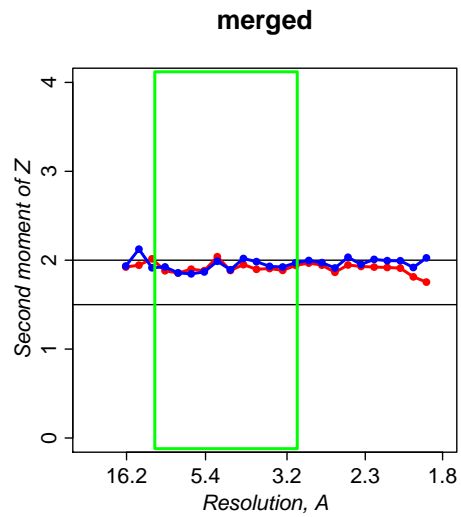
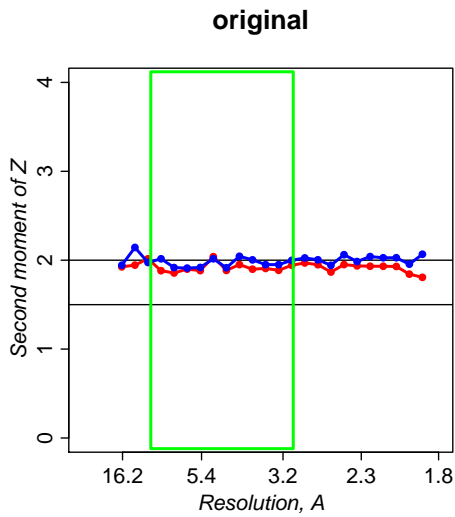
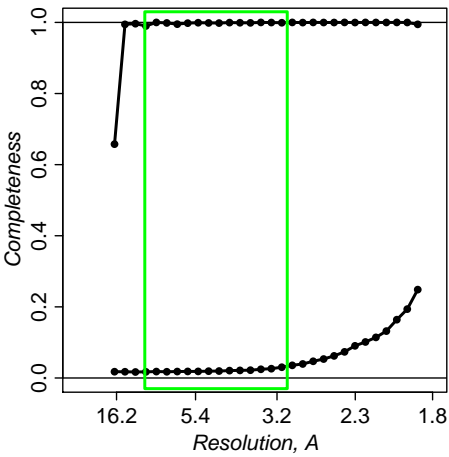
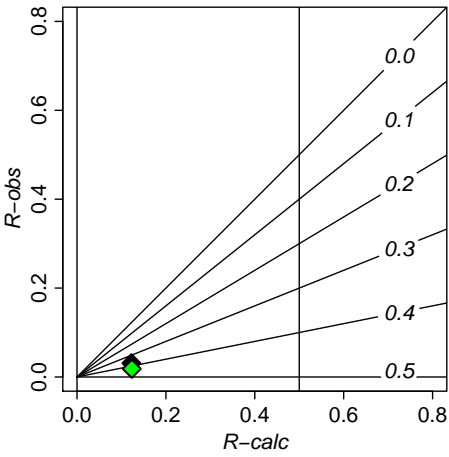
	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.32
R	28.6	
R'	28.8	29.0
R-free	30.2	
R'-free	30.2	30.3

residues per monomer	DNA	protein
	0	165

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.8–1.9	9.9–3.0
unique	108,651	24,783
measured	108,560	24,756
used	104,914	23,492

NCS	translation	rotation
r.m.s.d. (A)	16.07	0.12
angle (o)	80.56	0.08



1osi

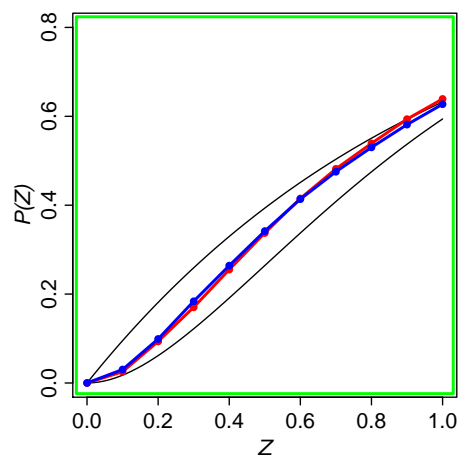
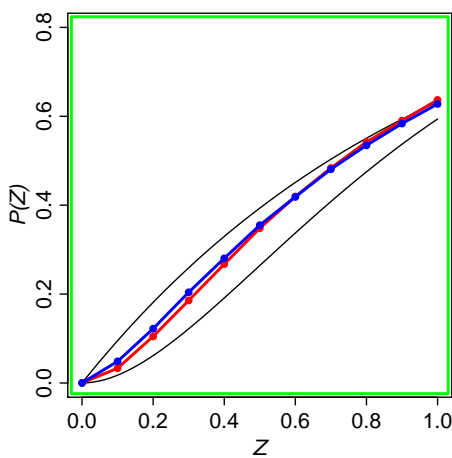
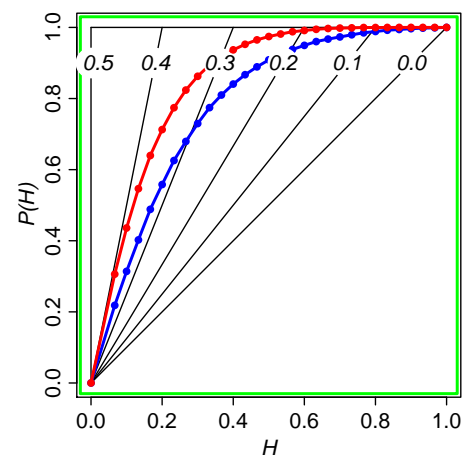
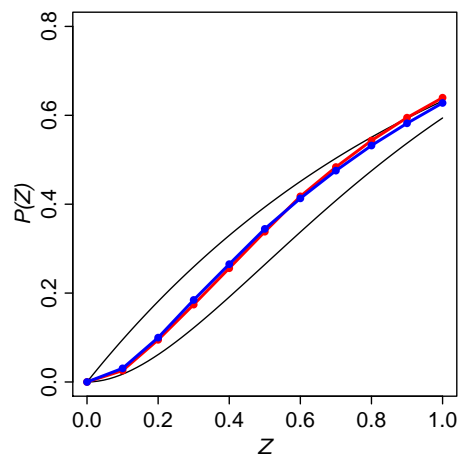
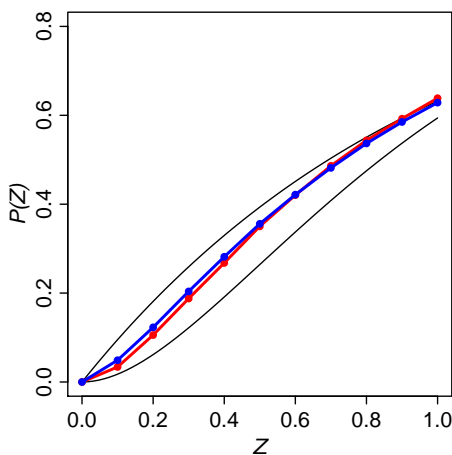
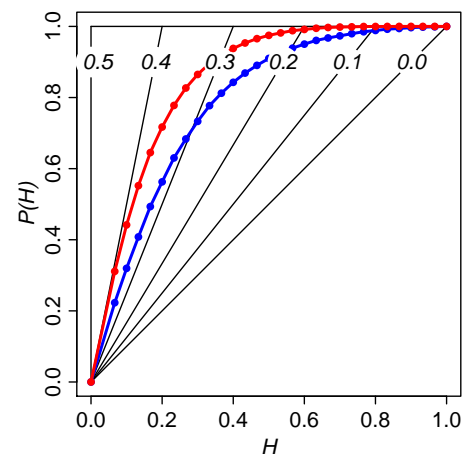
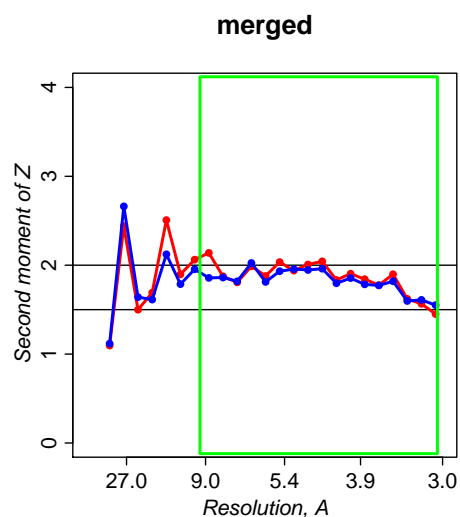
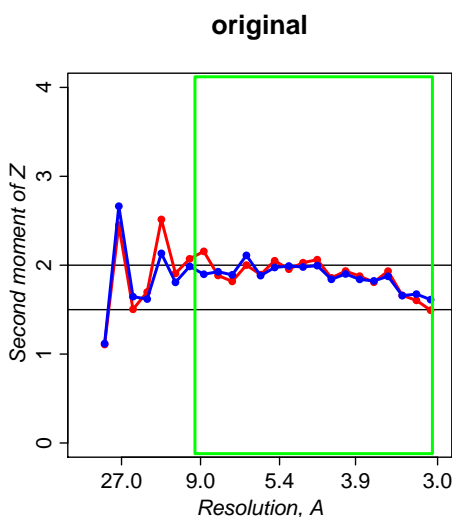
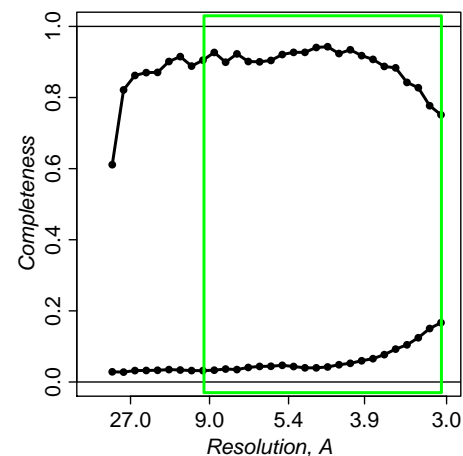
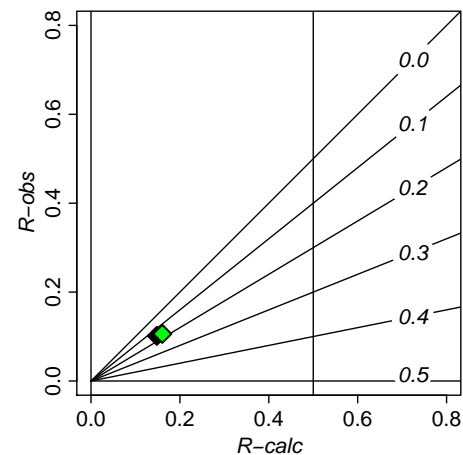
	original	merged
s.g.	P 1 21 1	P 21 21 2
p.g.	10001	10003
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.34
R	16.6	
R'	17.0	17.6
R-free	22.3	
R'-free	22.7	23.7

s < f/100	2	0.01 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	68.6–3.0	9.9–3.0
unique	31,944	30,973
measured	27,925	27,078
used	24,078	23,446

NCS	translation	rotation
r.m.s.d. (A)	22.44	0.24
angle (o)	87.47	0.57

residues per monomer	DNA	protein
	0	345



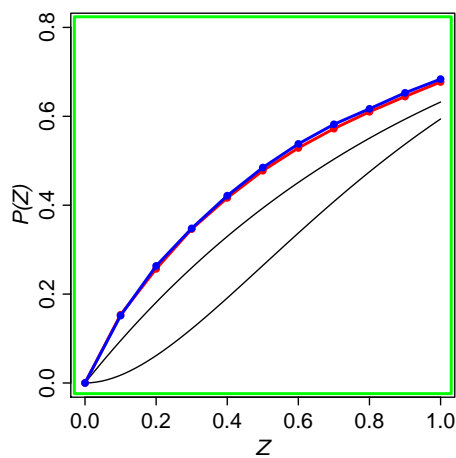
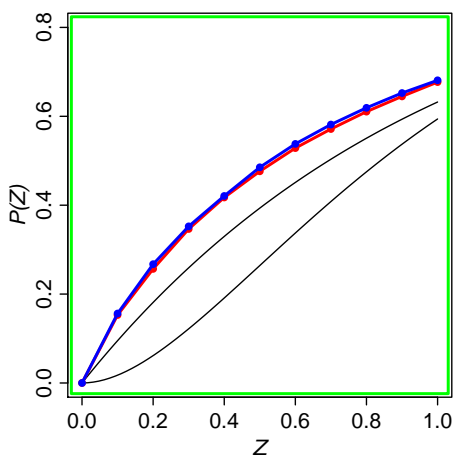
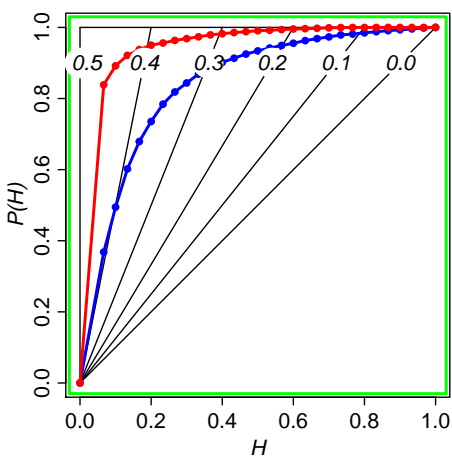
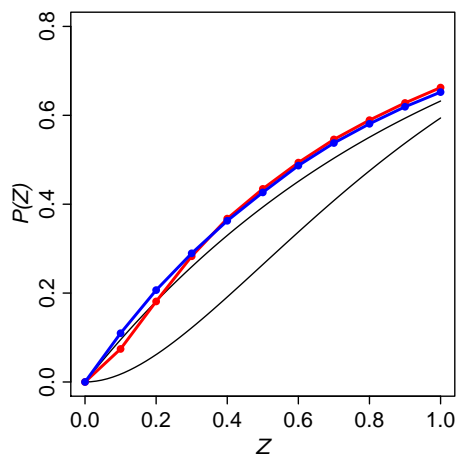
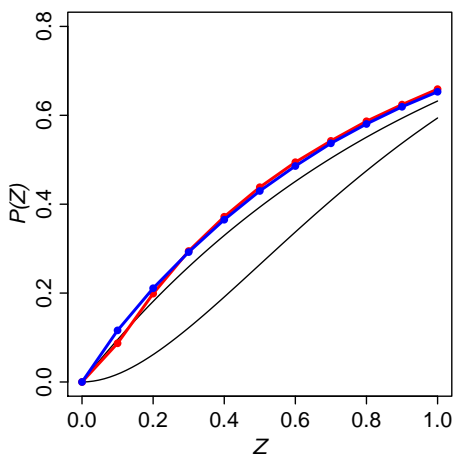
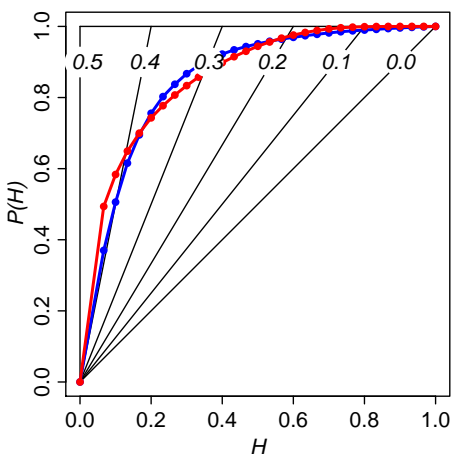
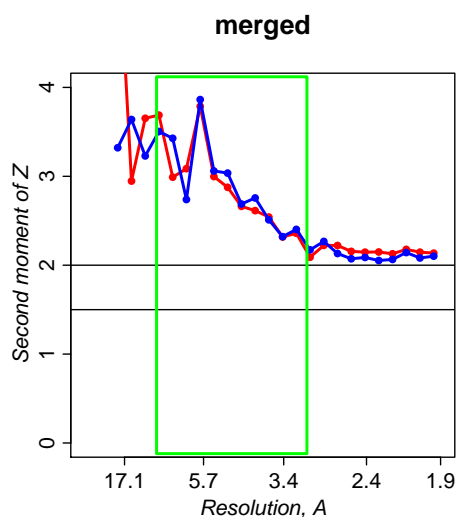
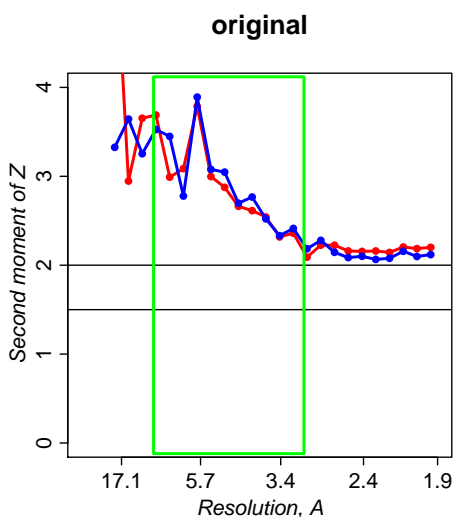
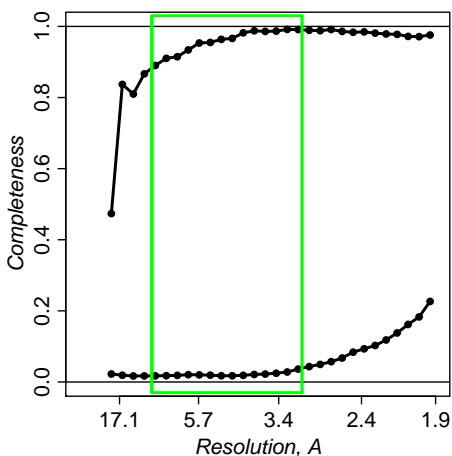
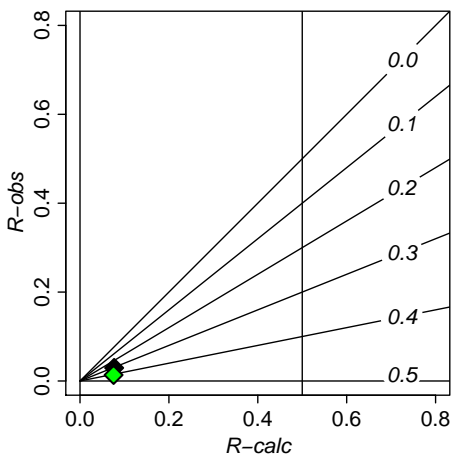
1ov8

	original	merged
s.g.	P 65	P 65 2 2
p.g.	12021	12027
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		0.07
R	28.7	
R'	28.7	28.8
R-free	30.8	
R'-free	30.8	30.9
residues per monomer	DNA 0	protein 139

s < f/100	1	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	26.1–1.9	9.9–3.0
unique	64,804	16,137
measured	63,346	15,723
used	57,846	13,638

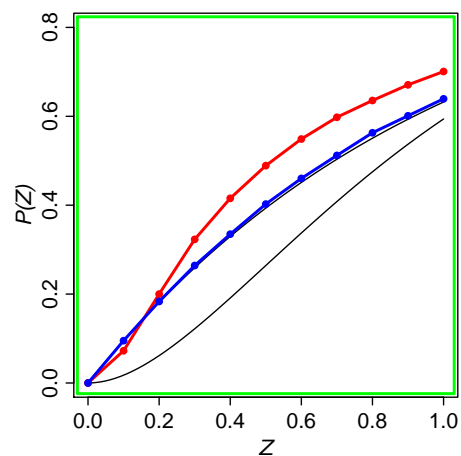
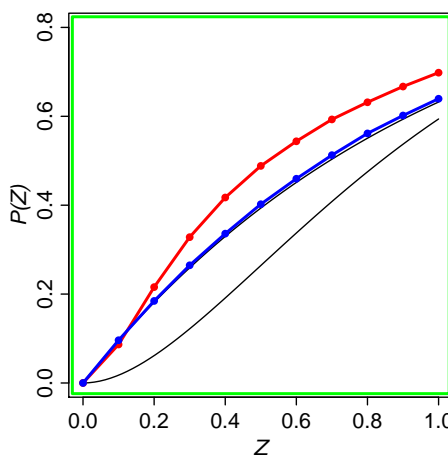
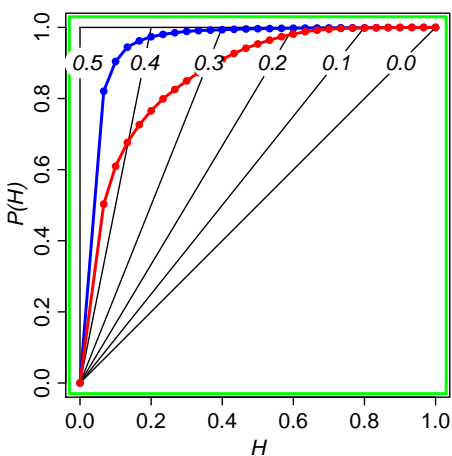
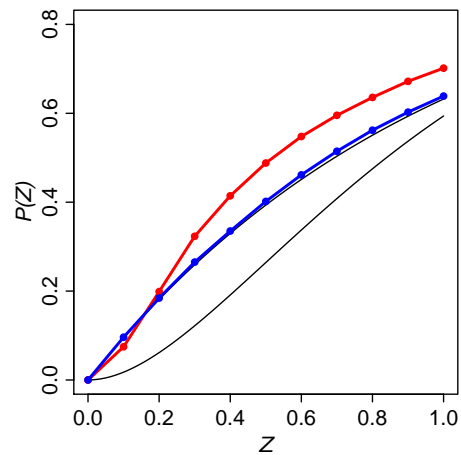
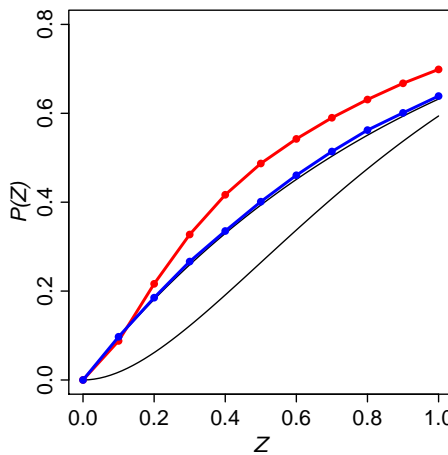
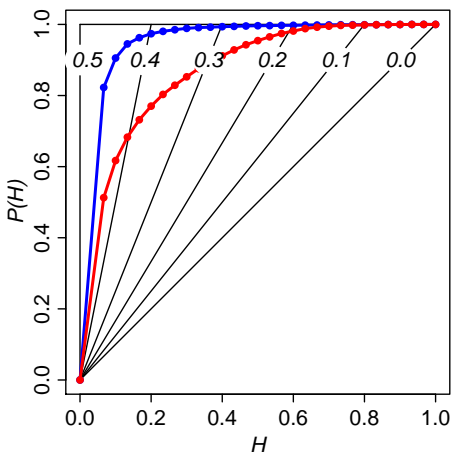
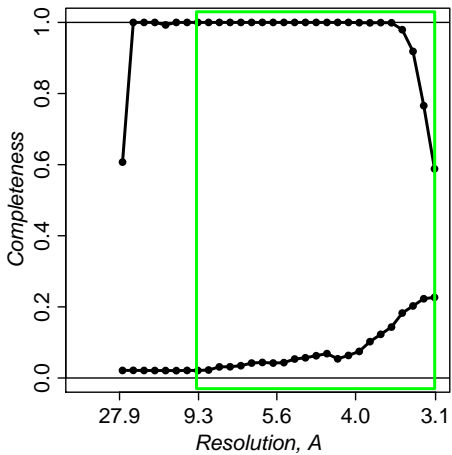
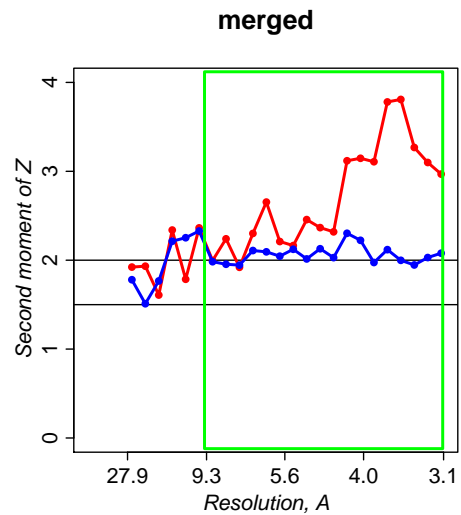
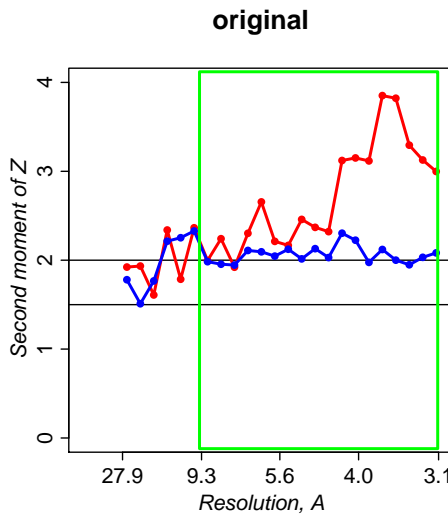
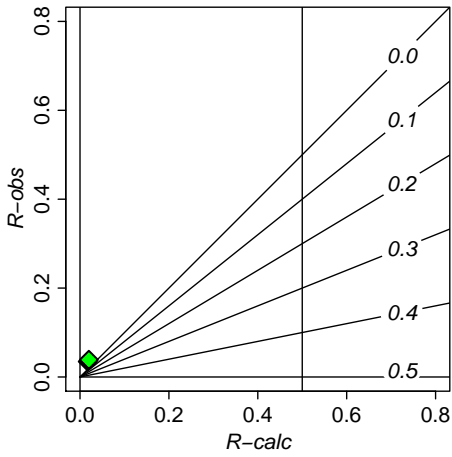
NCS	translation	rotation
r.m.s.d. (A)	0.35	0.05
angle (o)	1.71	0.04



1ow0

	original	merged
s.g.	P 3	P 3 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.03
R	24.5	
R'	24.5	25.0
R-free	28.8	
R'-free	28.8	29.6
residues per monomer	DNA 0	protein 399

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	29.7-3.1	9.9-3.1
unique	29,091	28,272
measured	27,262	26,444
used	25,288	24,592
NCS	translation	rotation
r.m.s.d. (A)	51.39	0.02
angle (o)	179.98	0.05



1oxk

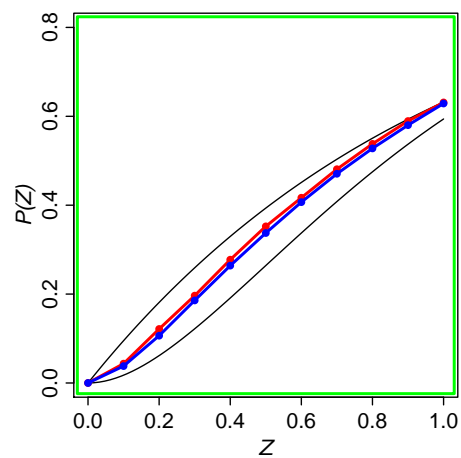
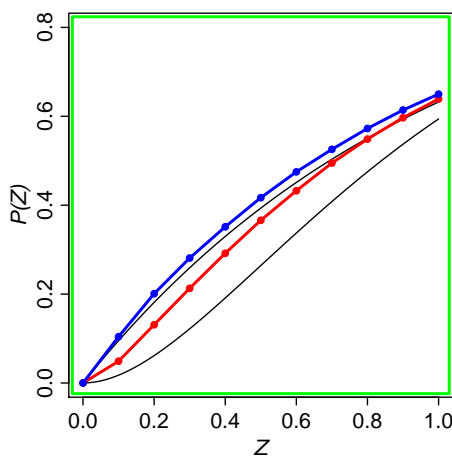
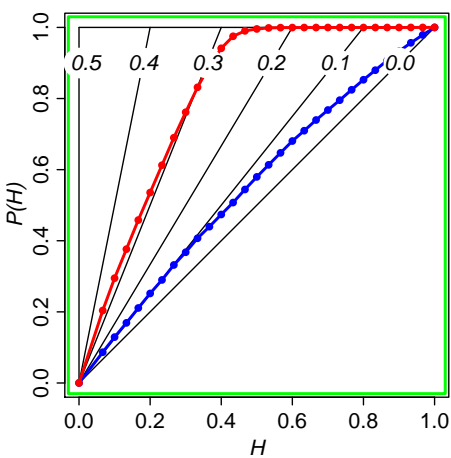
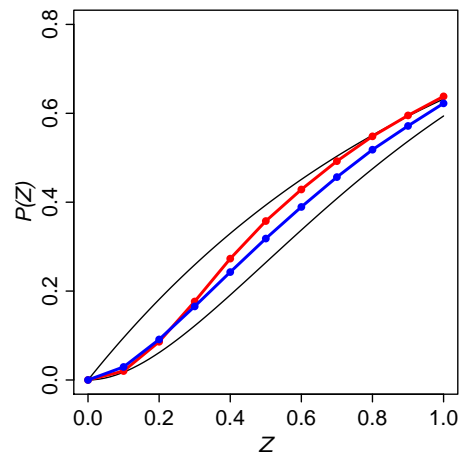
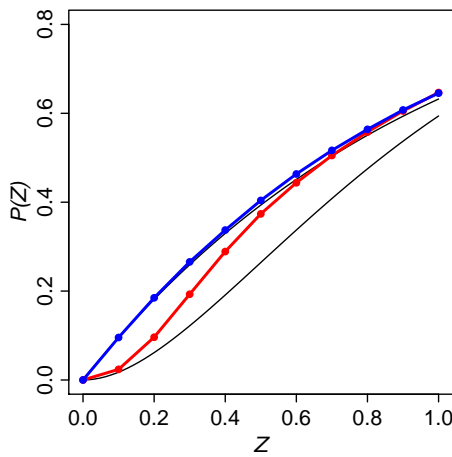
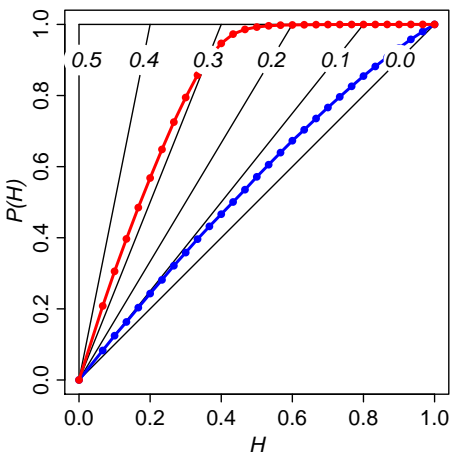
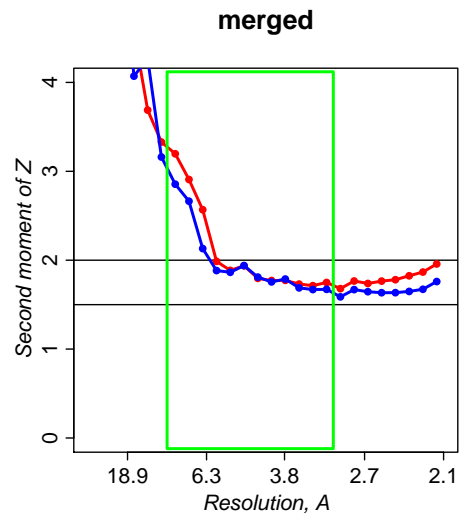
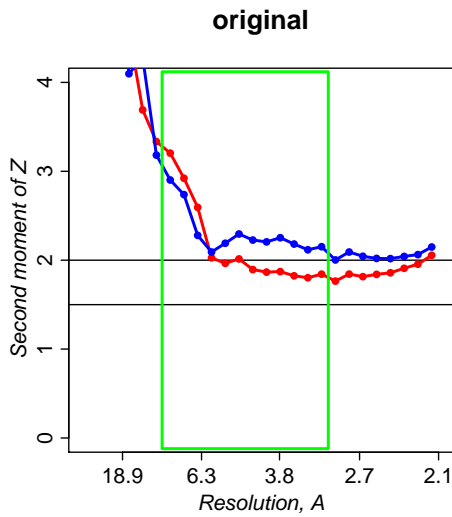
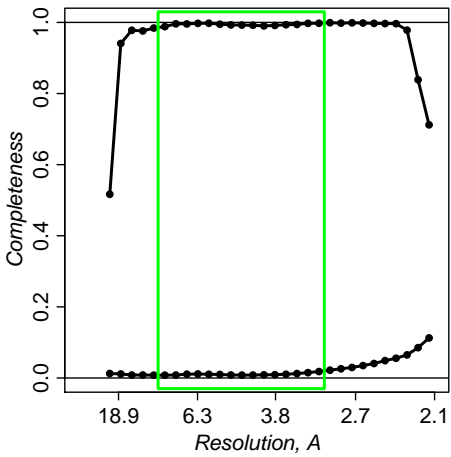
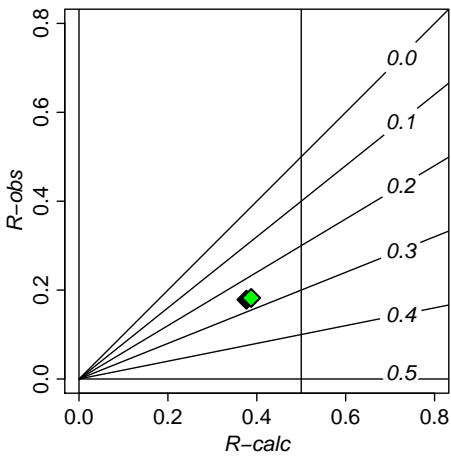
	original	merged
s.g.	P 32	P 32 2 1
p.g.	10020	10023
a.u.	6	3
p.t.	3	3
p.o.	3	9
r.m.s.d. (A)		1.51
R	25.7	
R'	26.4	32.0
R-free	28.2	
R'-free	29.0	36.5

residues per monomer	DNA	protein
	0	284

s < f/100	18195	17.46 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.6–2.1	9.9–3.0
unique	109,074	36,432
measured	104,211	36,235
used	96,250	33,628

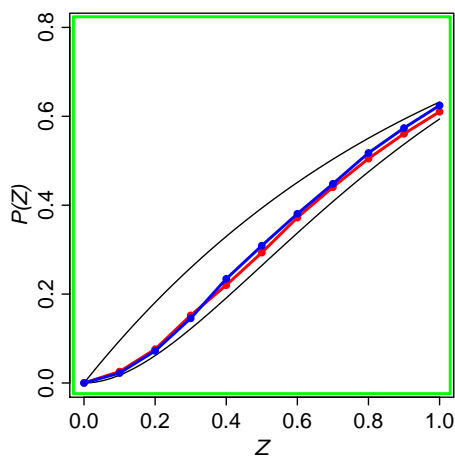
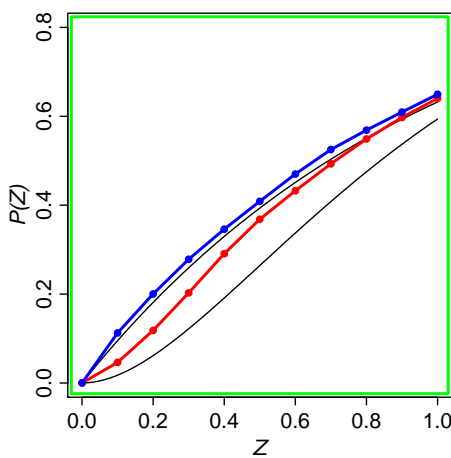
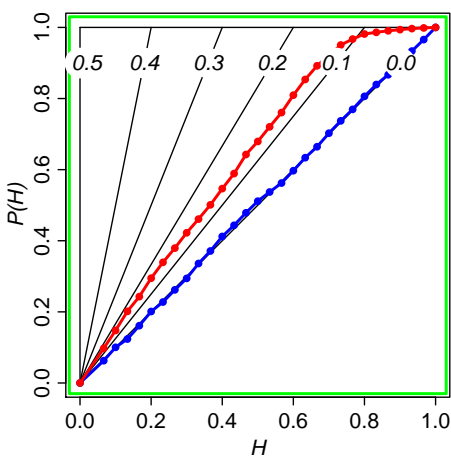
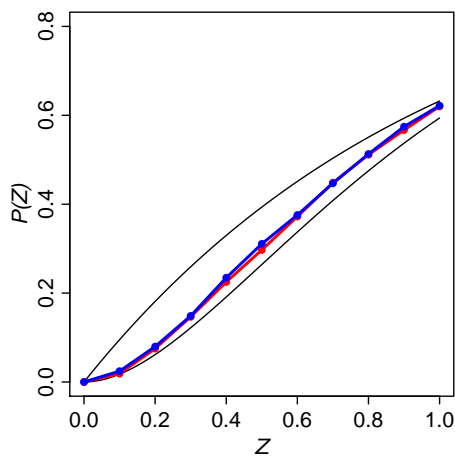
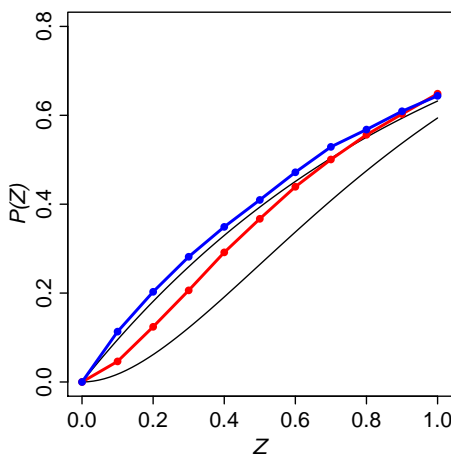
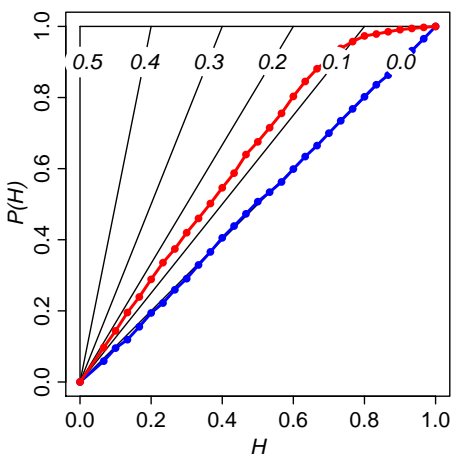
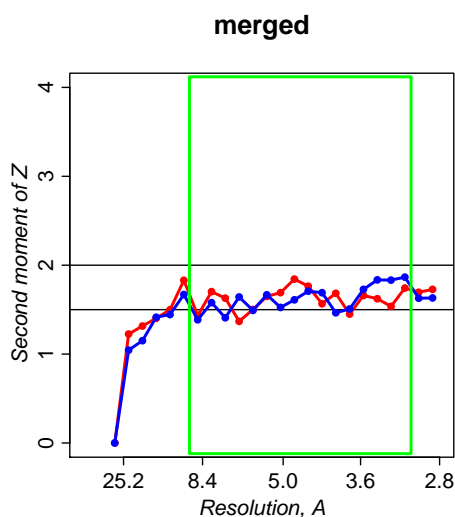
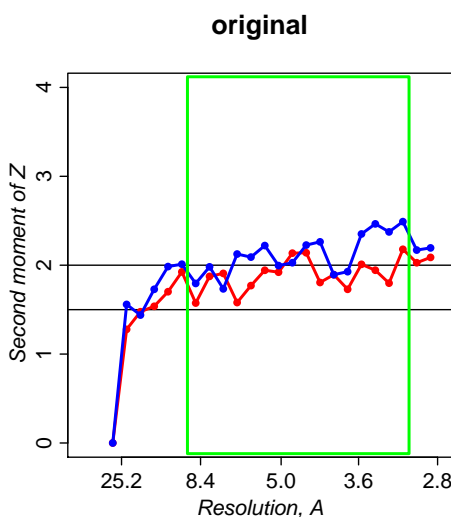
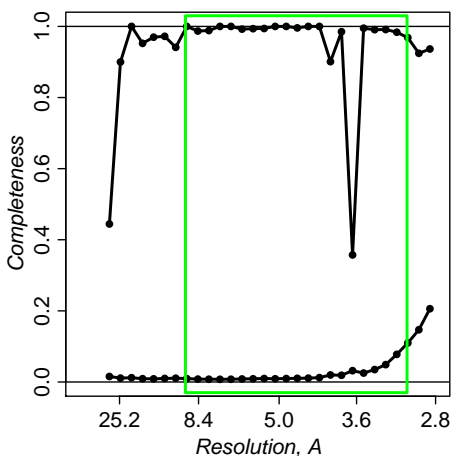
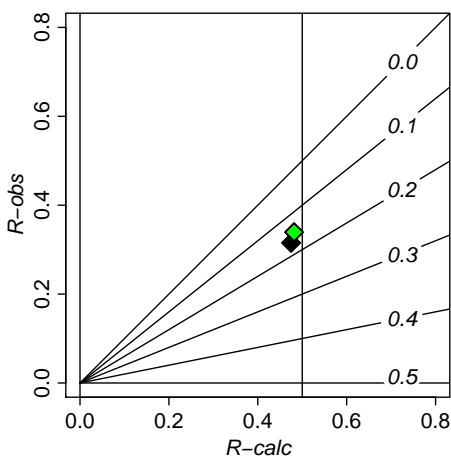
NCS	translation	rotation
r.m.s.d. (A)	1.03	0.60
angle (o)	3.92	2.33



1oxz

	original	merged
s.g.	P 63	-
p.g.	12021	12027
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	26.3	-
R'	-	-
R-free	27.9	-
R'-free	-	-
residues per monomer	DNA 0	protein 132

s < f/100	1546	24.11 %
s <= 0	139	2.17 %
f <= 0	139	2.17 %
s,f <= 0	139	2.17 %
range (A)	41.7-2.8	9.9-3.0
unique	6,824	5,388
measured	6,413	5,071
used	5,244	4,182
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



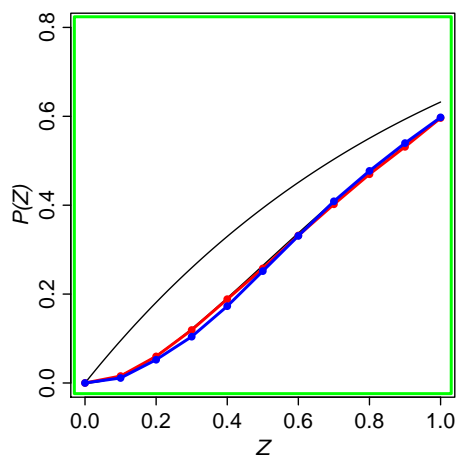
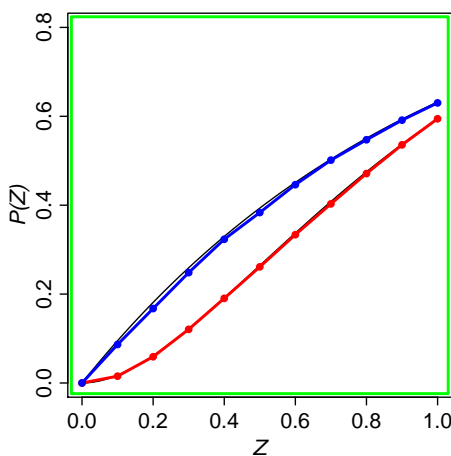
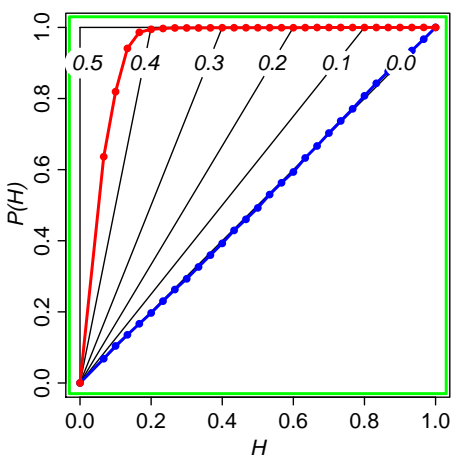
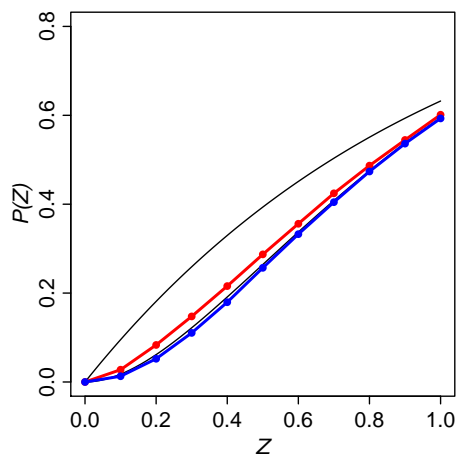
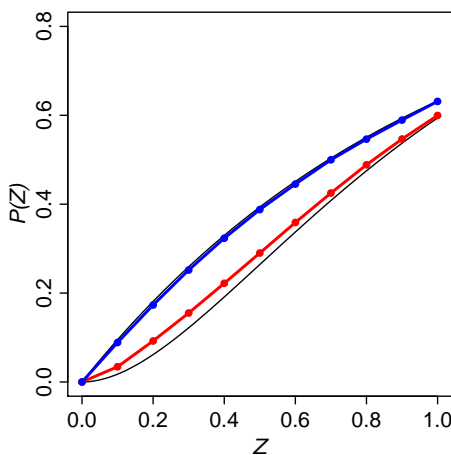
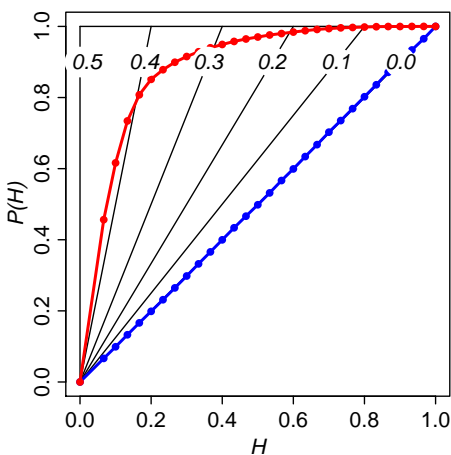
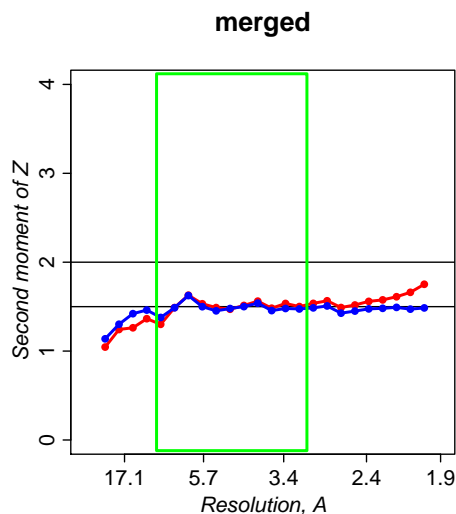
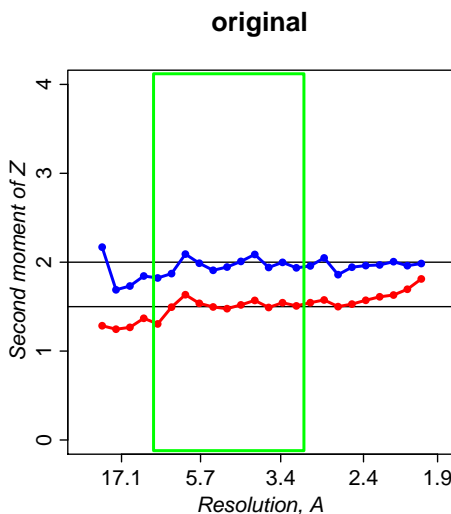
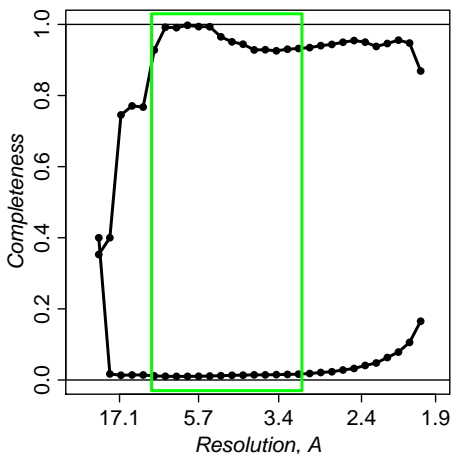
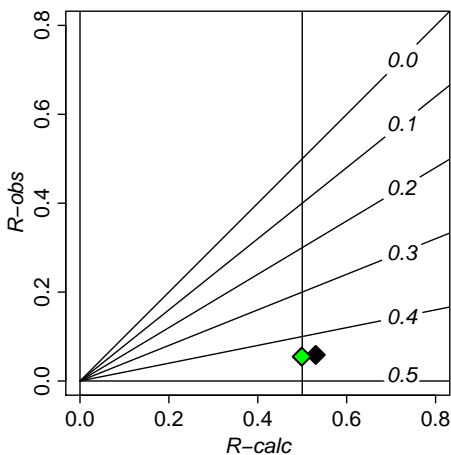
1p15

	original	merged
s.g.	P 31	-
p.g.	10020	10023
a.u.	2	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	32.6	-
R'	-	-
R-free	35.1	-
R'-free	-	-
residues per monomer	DNA 0	protein 244

s < f/100	2252	5.53 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	51.2-2.0	9.9-3.0
unique	43,419	11,624
measured	40,708	10,990
used	36,792	9,808

NCS	translation	rotation
r.m.s.d. (A)	22.37	13.10
angle (o)	124.24	64.89



1p6b

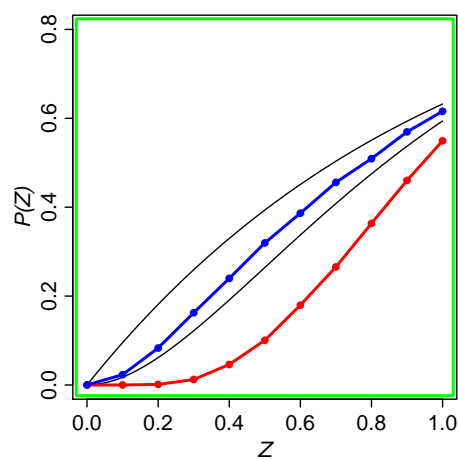
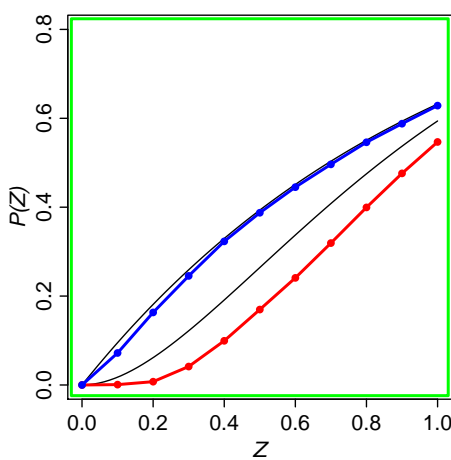
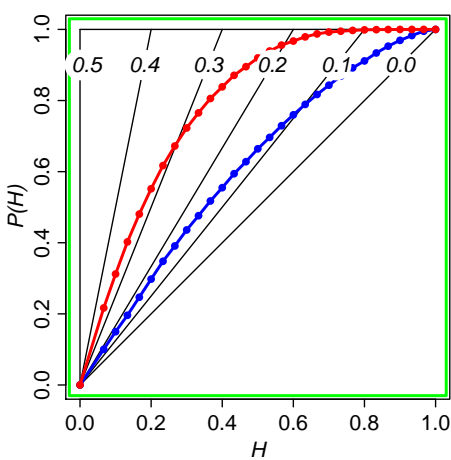
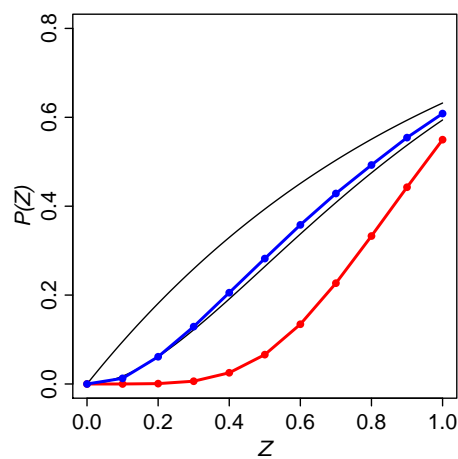
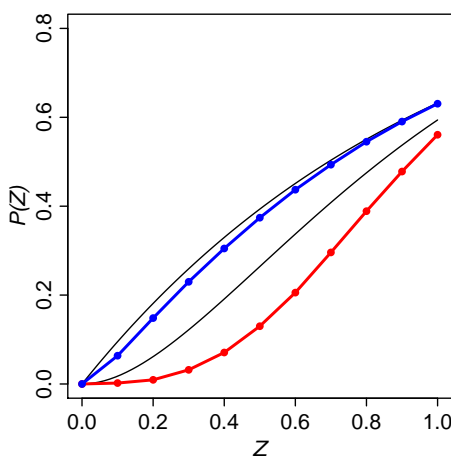
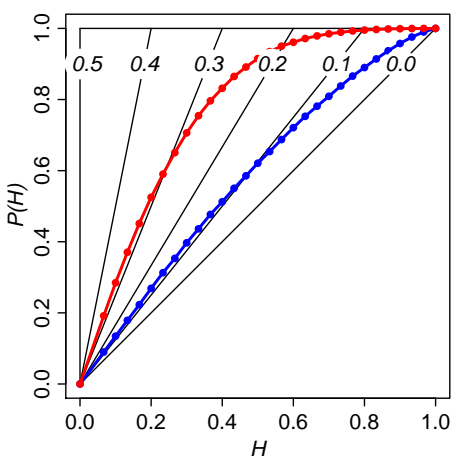
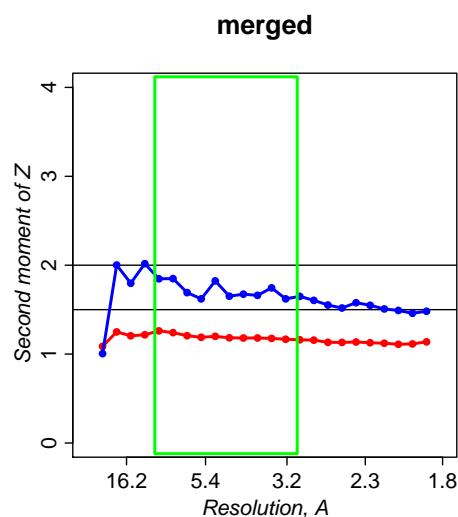
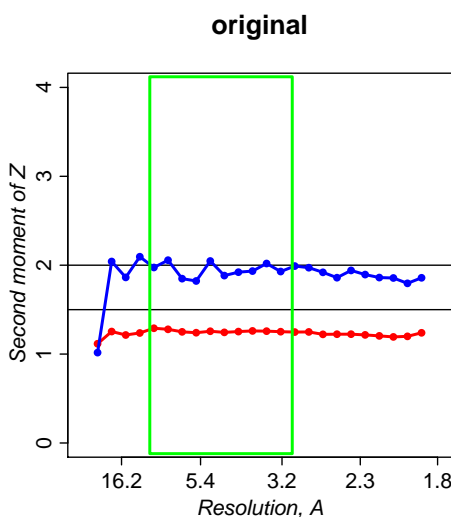
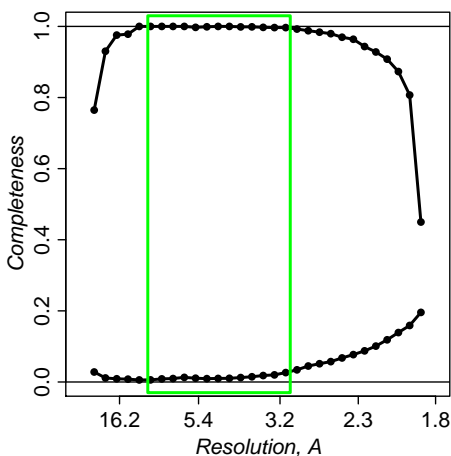
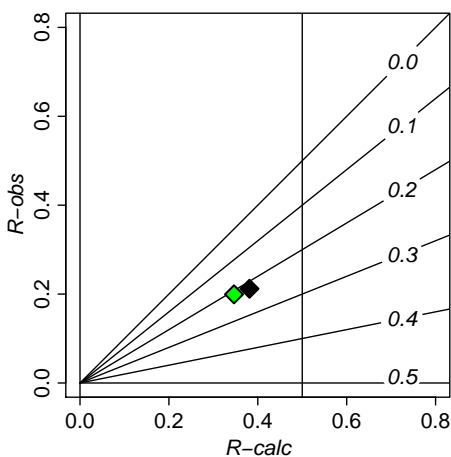
	original	merged
s.g.	C 1 2 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		1.10
R	28.1	
R'	30.2	32.4
R-free	29.5	
R'-free	32.8	34.6

residues per monomer	DNA	protein
	0	329

s < f/100	9302	14.70 %
s <= 0	0	0.00 %
f <= 0	1	0.00 %
s,f <= 0	0	0.00 %

range (A)	75.1–1.8	9.9–3.0
unique	70,465	16,123
measured	63,292	16,094
used	55,148	14,830

NCS	translation	rotation
r.m.s.d. (A)	28.67	0.72
angle (o)	179.19	1.98



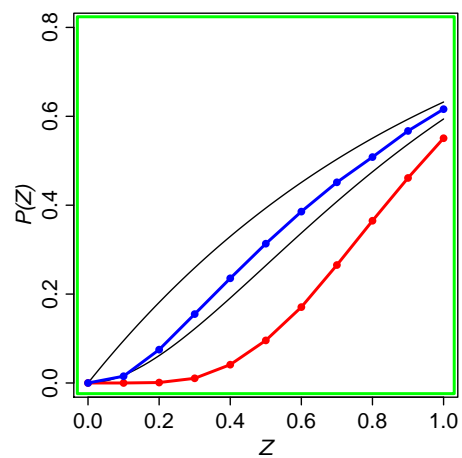
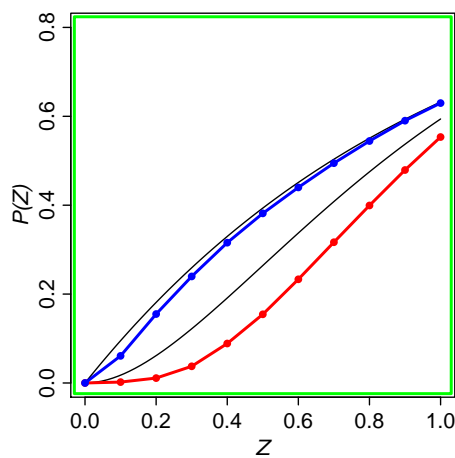
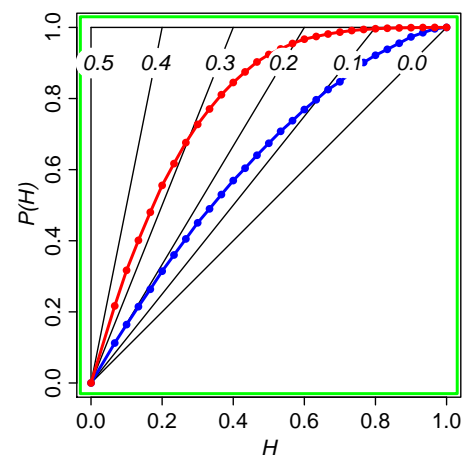
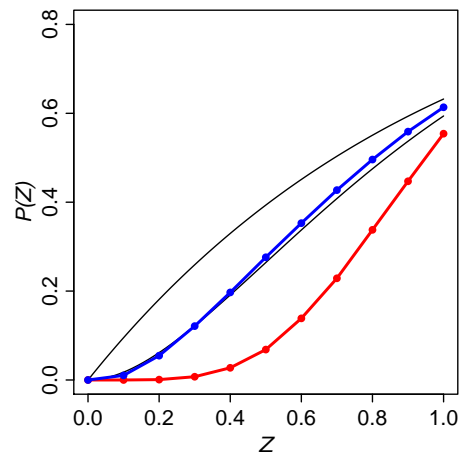
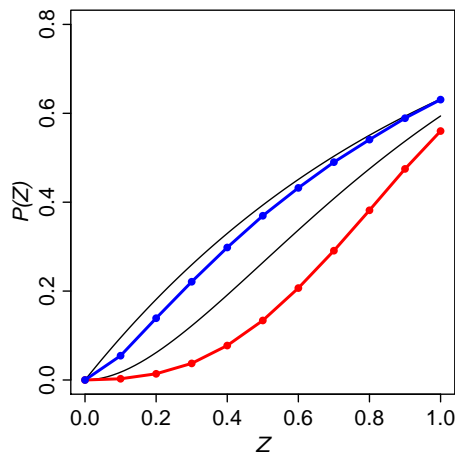
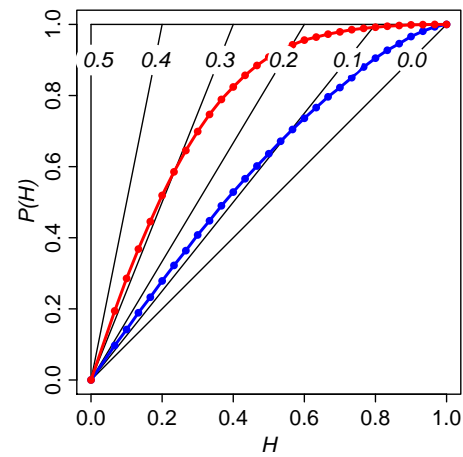
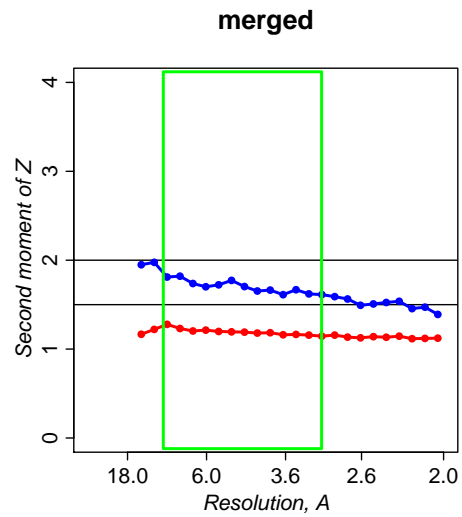
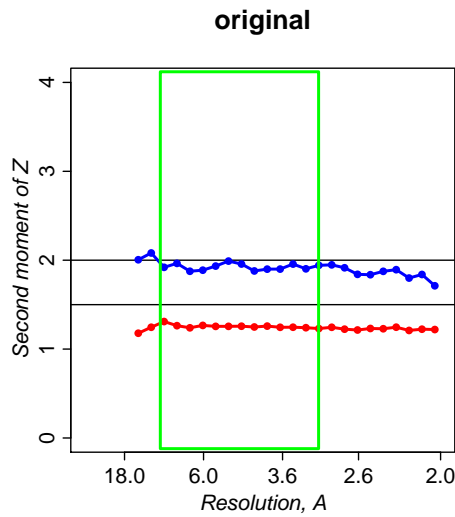
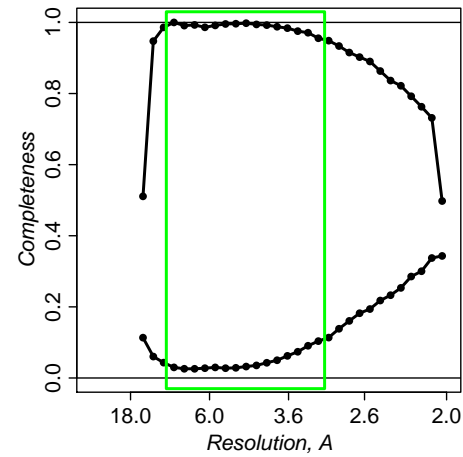
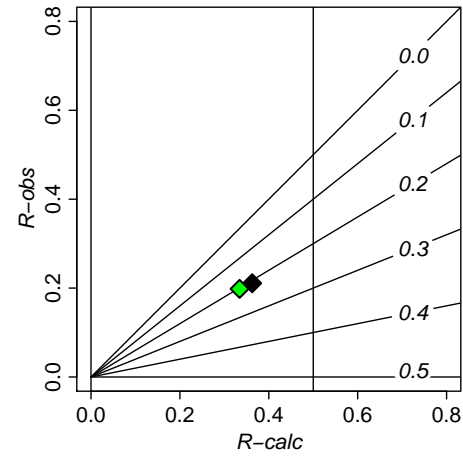
1p6c

	original	merged
s.g.	C 1 2 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		1.09
R	27.3	
R'	29.0	31.2
R-free	30.3	
R'-free	30.3	32.3
residues per monomer	DNA 0	protein 329

s < f/100	3390	7.15 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	15.2–2.0	9.9–3.0
unique	55,741	16,123
measured	47,394	15,819
used	39,986	14,430

NCS	translation	rotation
r.m.s.d. (A)	28.68	0.70
angle (o)	179.27	1.88



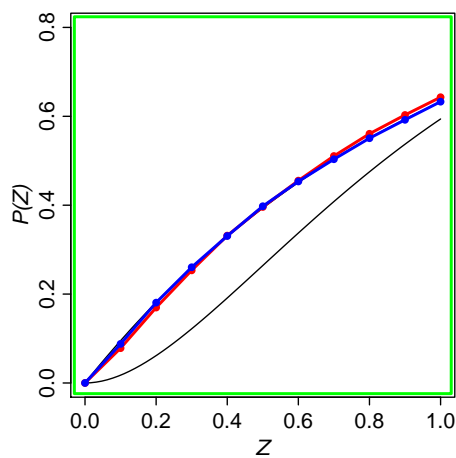
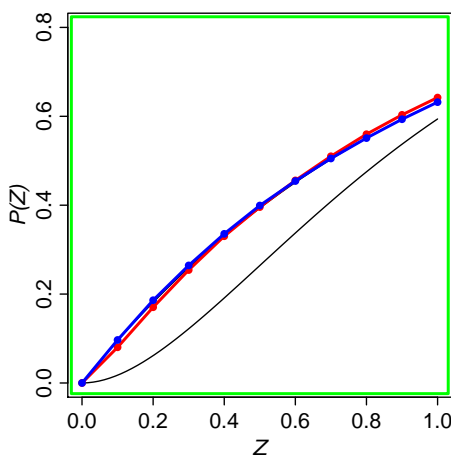
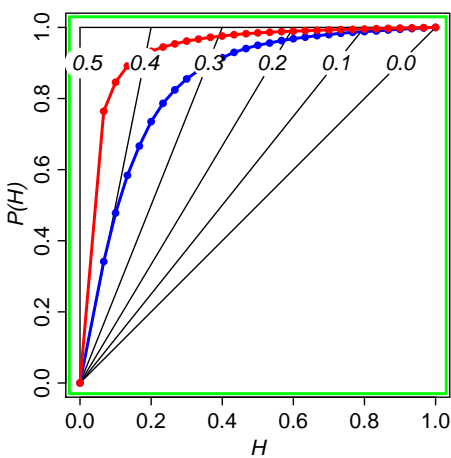
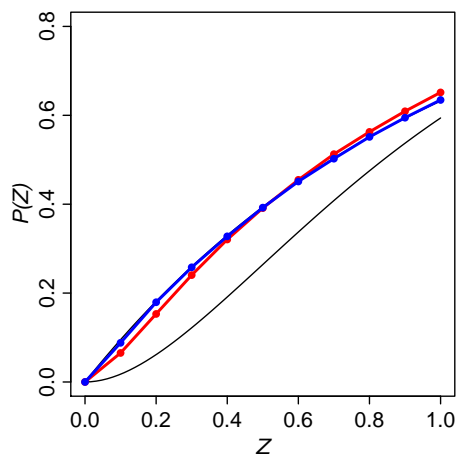
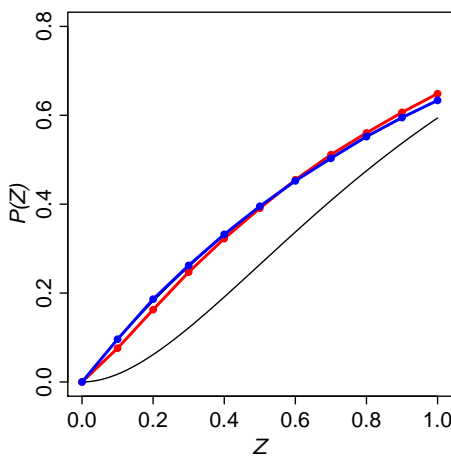
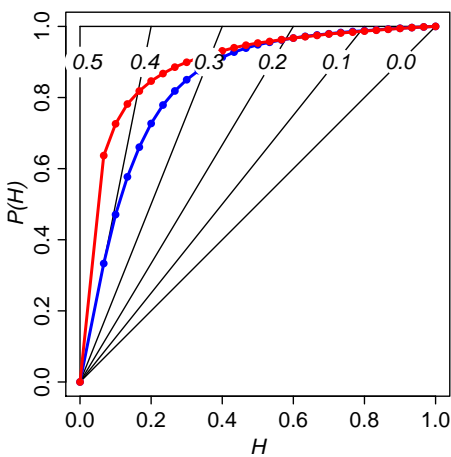
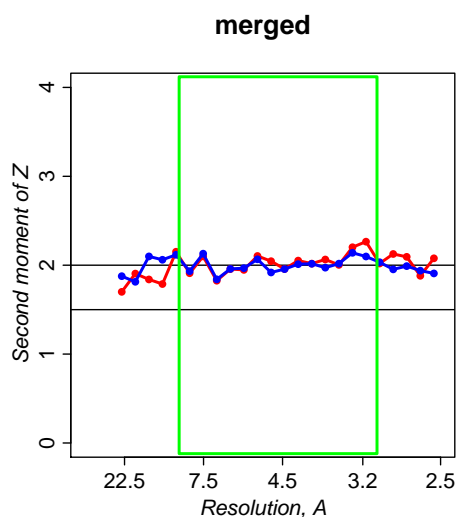
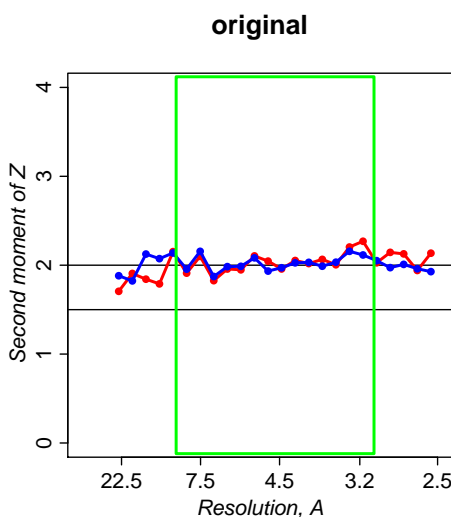
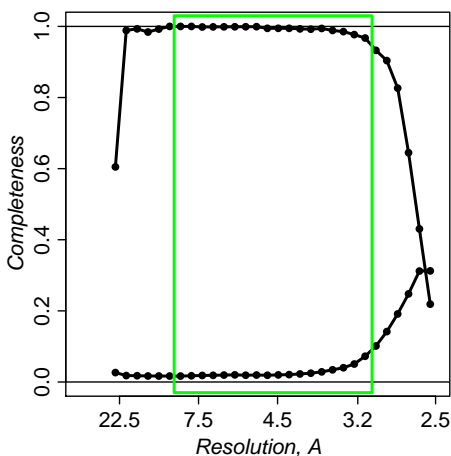
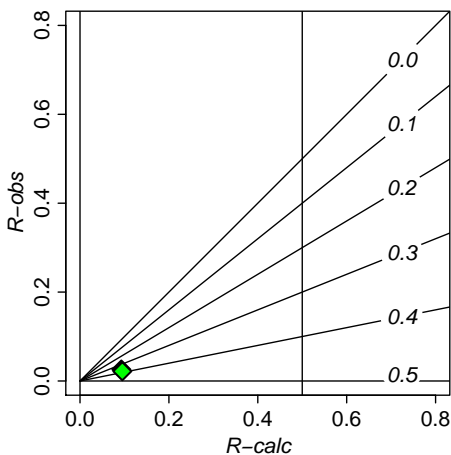
1p7h

	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.02
R	29.8	
R'	29.8	30.2
R-free	36.0	
R'-free	36.0	36.4
residues per monomer	DNA 0	protein 286

s < f/100	2548	5.23 %
s <= 0	2548	5.23 %
f <= 0	2548	5.23 %
s,f <= 0	2548	5.23 %

range (A)	29.7–2.5	9.9–3.0
unique	58,944	33,170
measured	48,681	32,721
used	44,682	31,692

NCS	translation	rotation
r.m.s.d. (A)	30.30	0.02
angle (o)	173.83	0.02



1p90

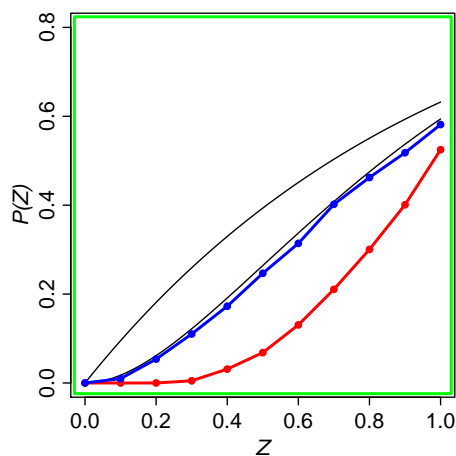
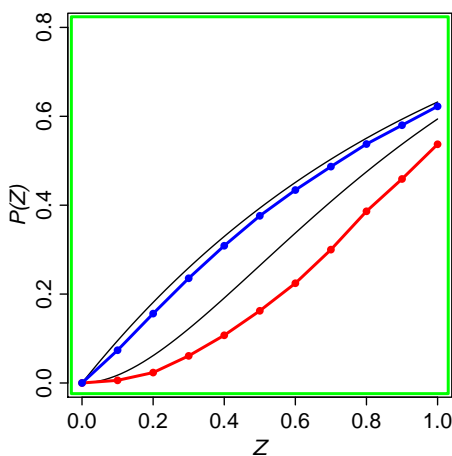
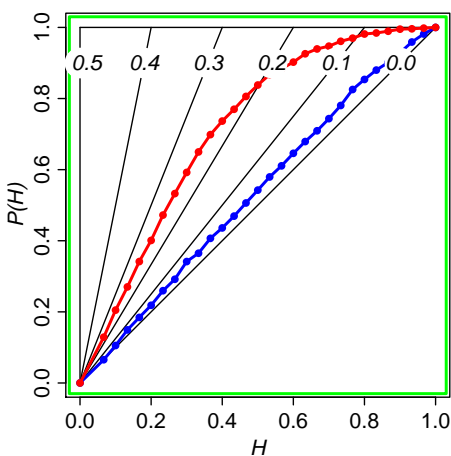
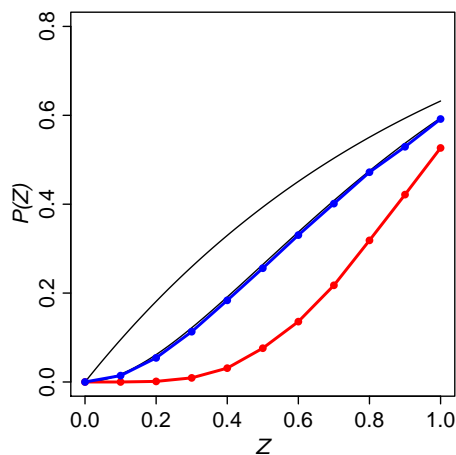
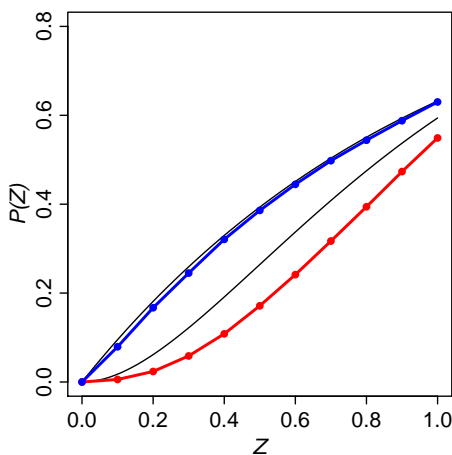
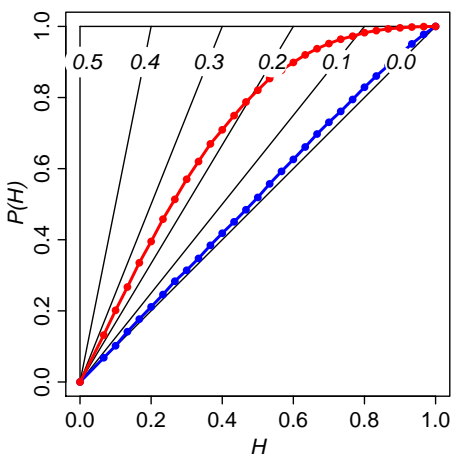
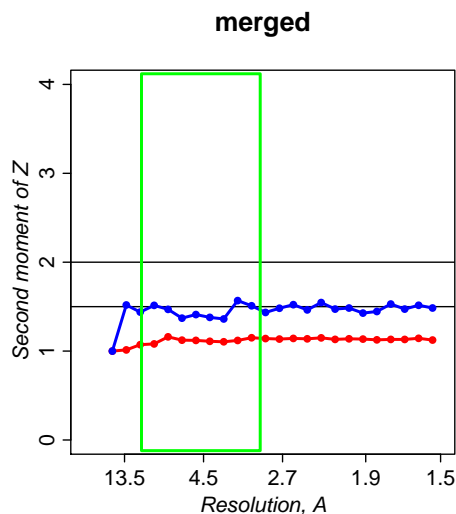
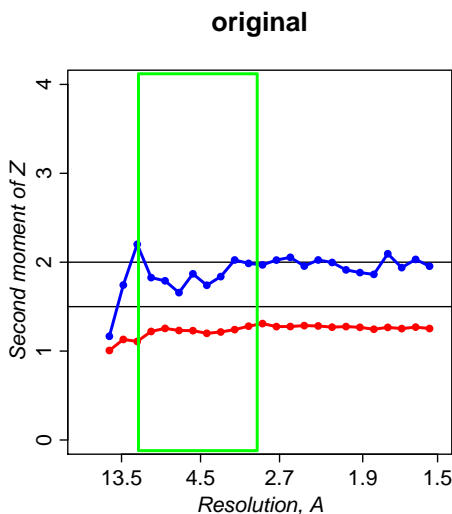
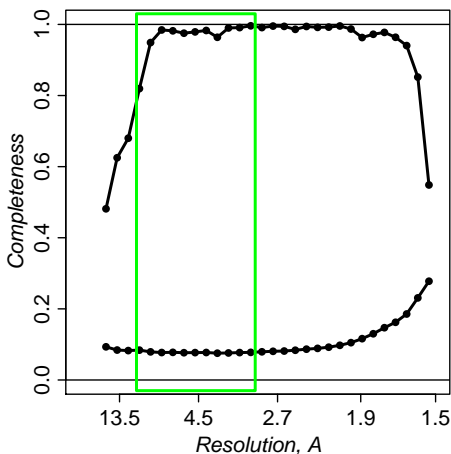
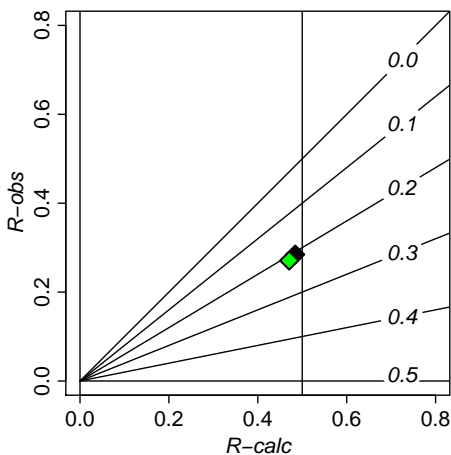
	original	merged
s.g.	P 32 2 1	-
p.g.	10023	12027
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	43.3	-
R'	-	-
R-free	43.6	-
R'-free	-	-

residues per monomer	DNA	protein
	0	123

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	26.1-1.5	9.9-3.0
unique	22,800	2,968
measured	21,149	2,907
used	16,822	2,048

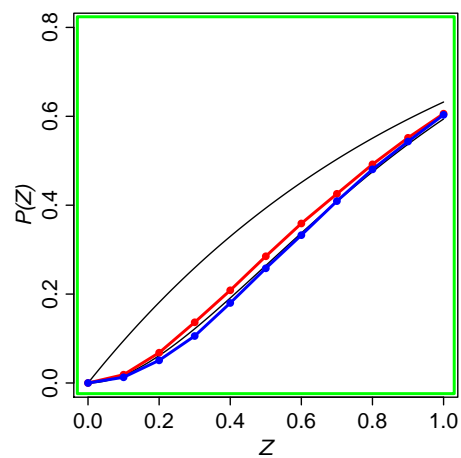
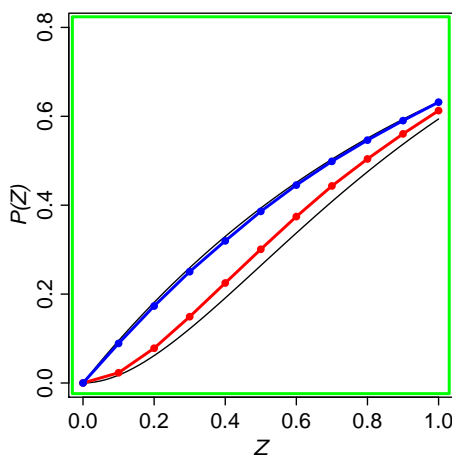
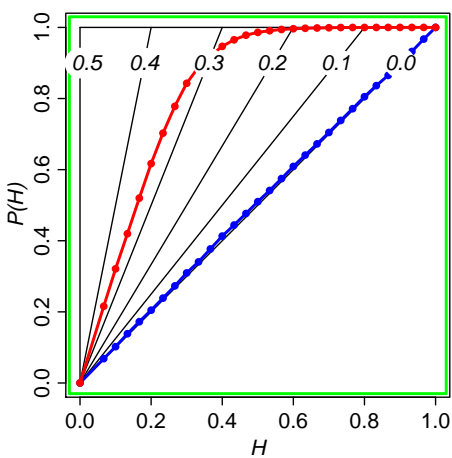
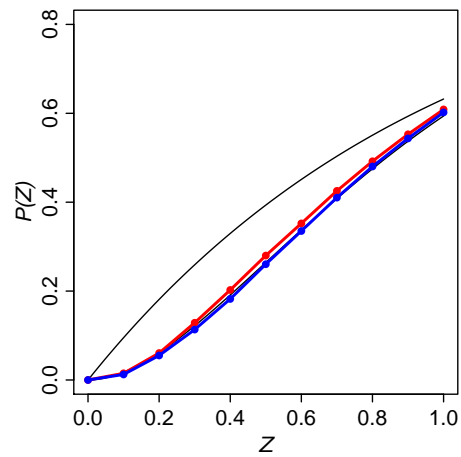
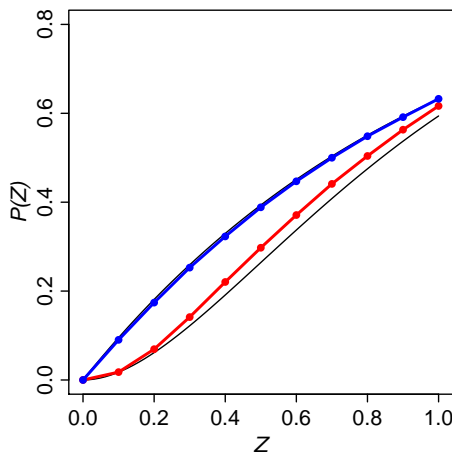
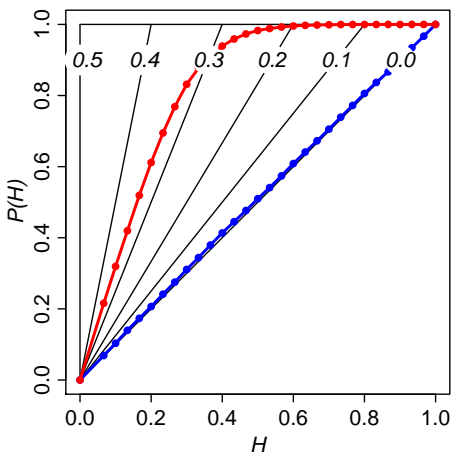
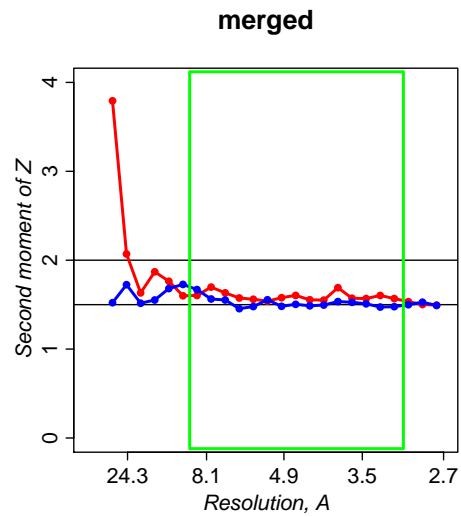
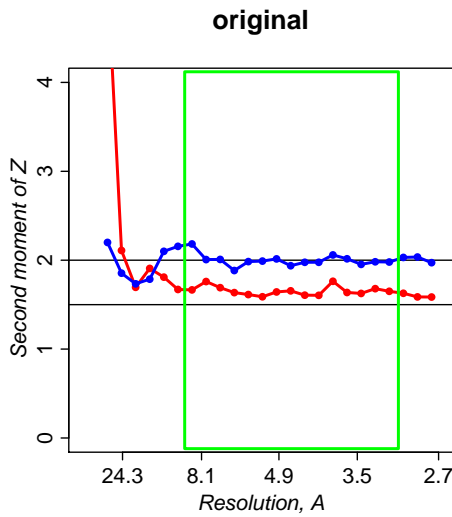
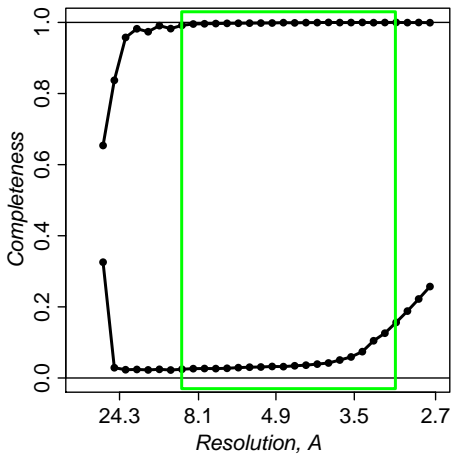
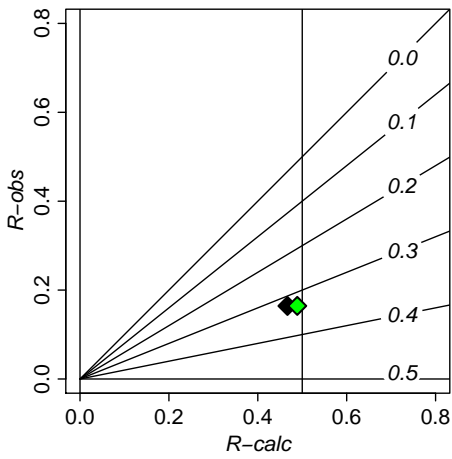
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1p93

	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		3.96
R	27.5	
R'	-	-
R-free	31.8	
R'-free	-	-
residues per monomer	DNA 0	protein 254

s < f/100	1	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	55.2-2.7	9.9-3.0
unique	45,812	32,477
measured	45,751	32,448
used	43,588	30,858
NCS	translation	rotation
r.m.s.d. (A)	15.80	1.49
angle (o)	58.37	5.13



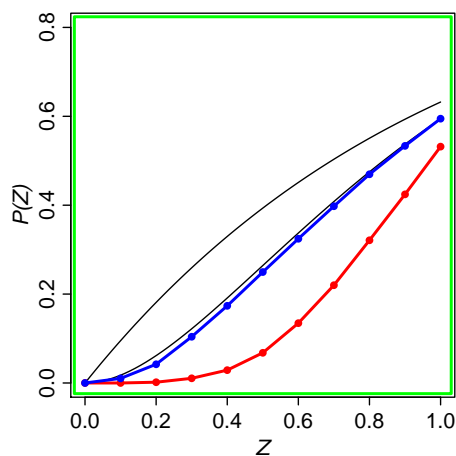
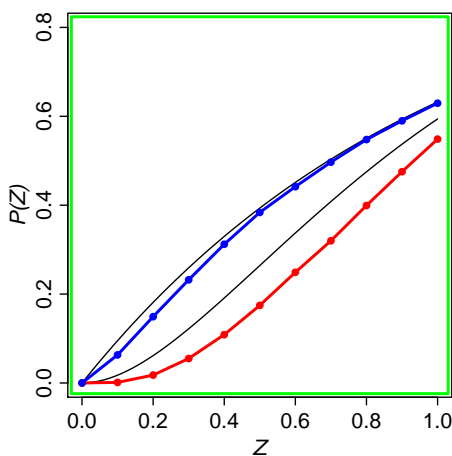
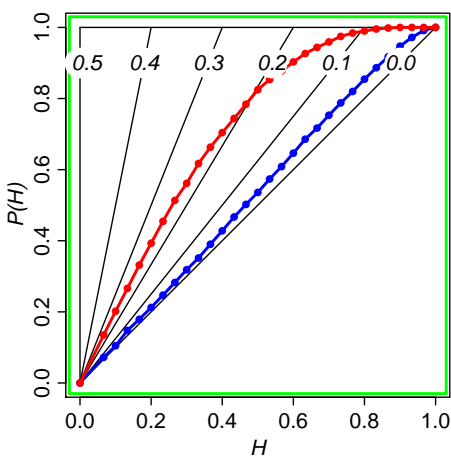
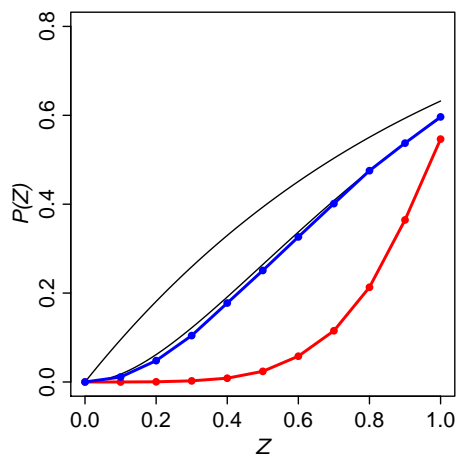
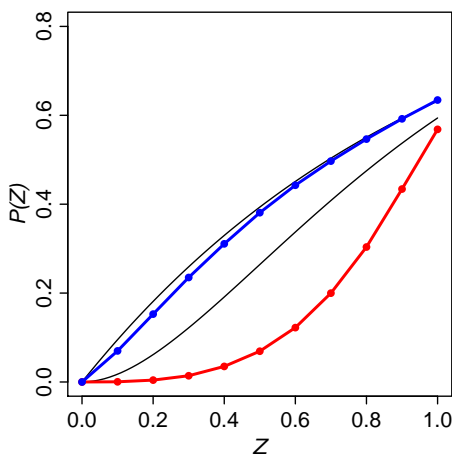
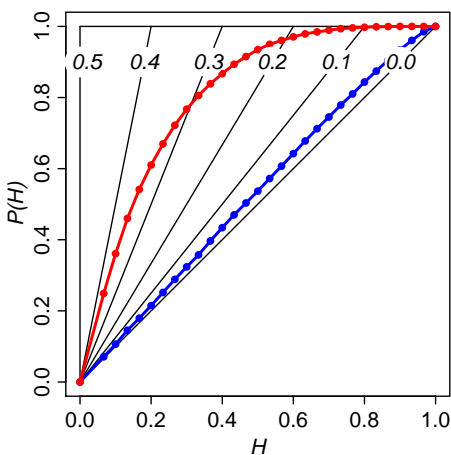
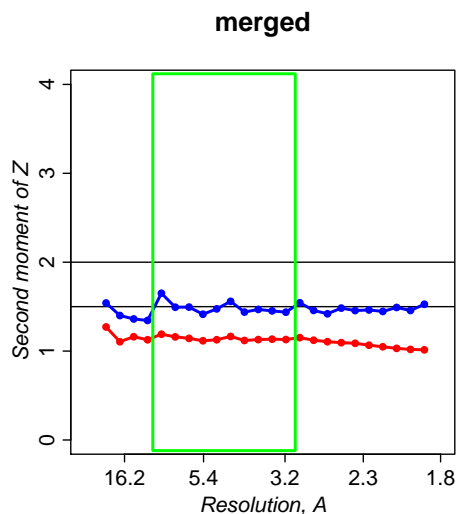
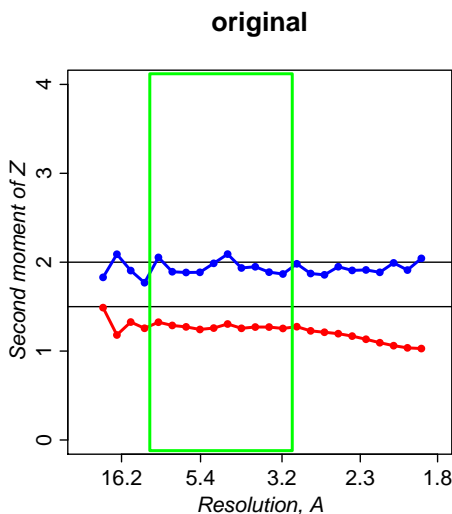
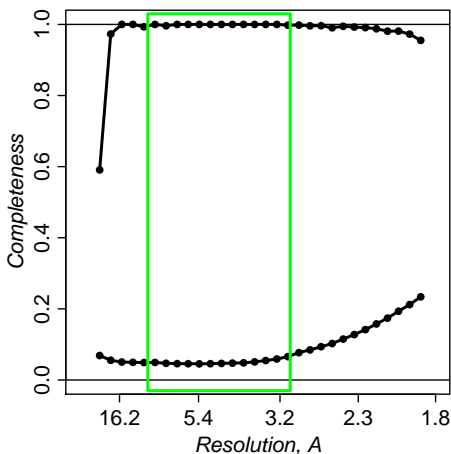
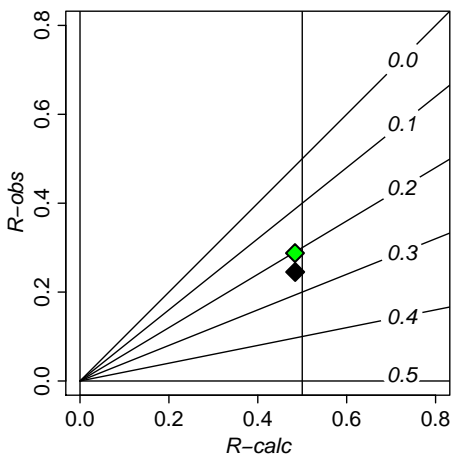
1pie

	original	merged
s.g.	1 2 3	-
p.g.	10083	10689
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	29.5	-
R'	-	-
R-free	31.9	-
R'-free	-	-
residues per monomer	DNA 0	protein 388

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	45.3-1.8	9.9-3.0
unique	41,930	9,682
measured	41,420	9,677
used	37,192	8,312

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1pm7

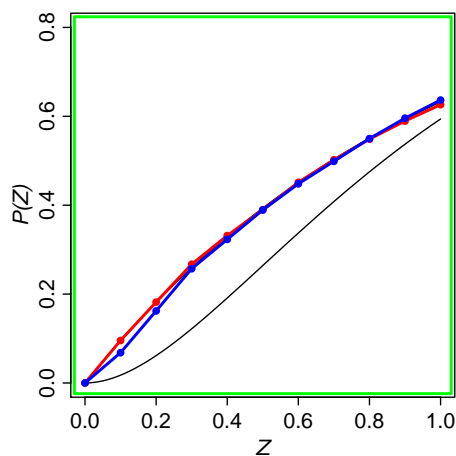
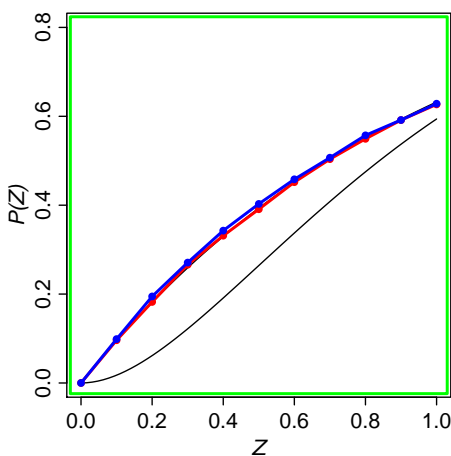
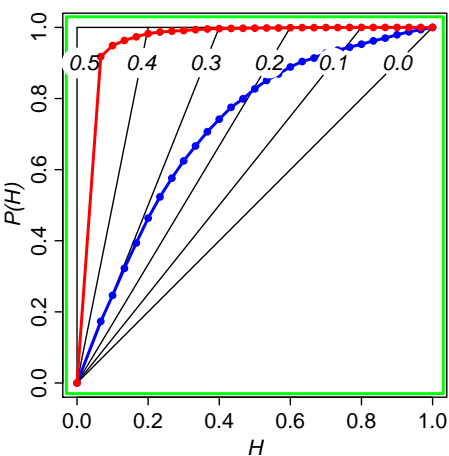
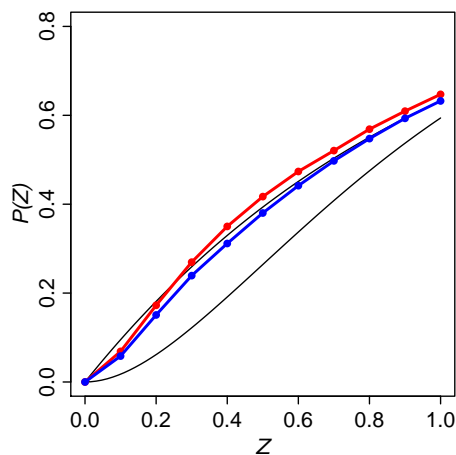
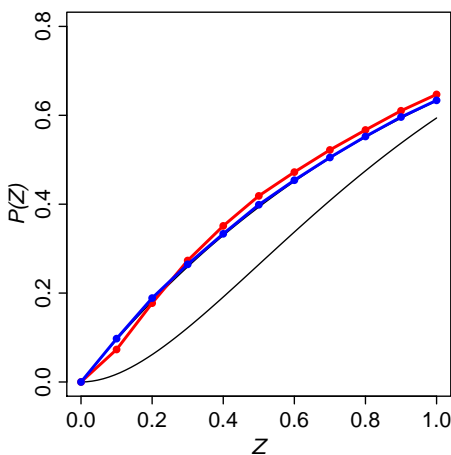
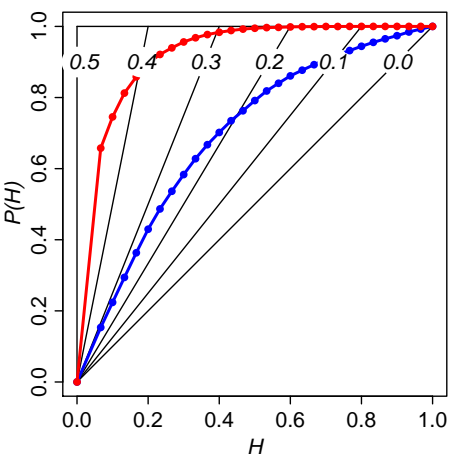
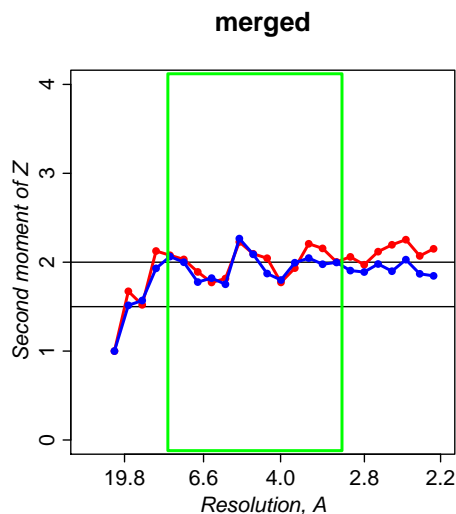
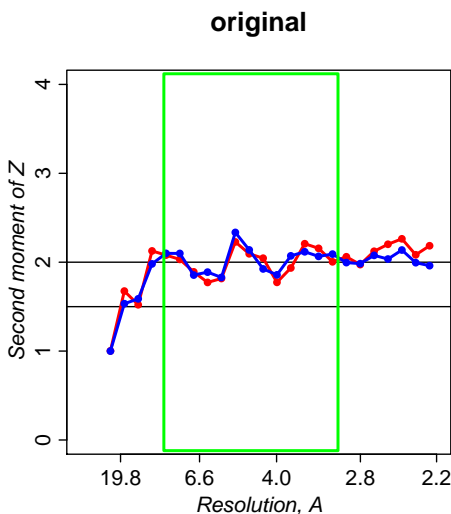
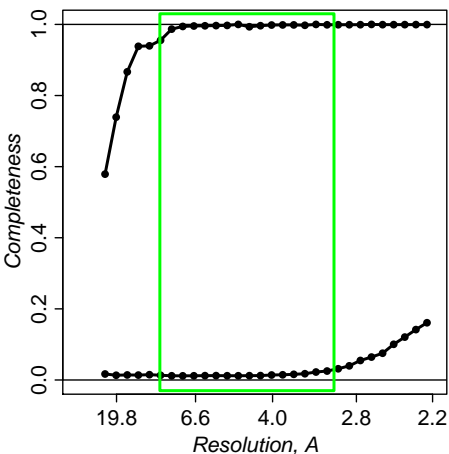
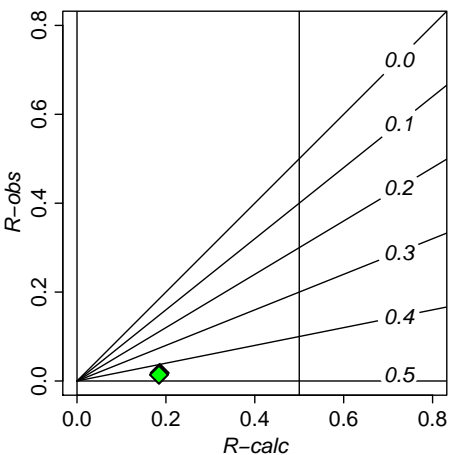
	original	merged
s.g.	P 32	P 32 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.62
R	28.8	
R'	28.9	29.8
R-free	35.1	
R'-free	34.8	35.5

s < f/100	1245	5.75 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	34.8–2.2	9.9–3.0
unique	21,715	8,329
measured	21,661	8,305
used	20,058	7,520

NCS	translation	rotation
r.m.s.d. (A)	24.66	0.62
angle (o)	179.95	0.31

residues per monomer	DNA	protein
	0	199



1pt8

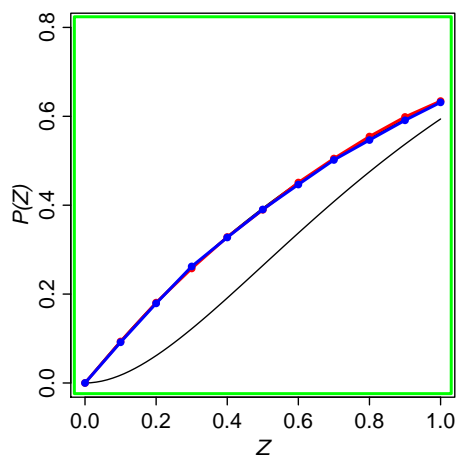
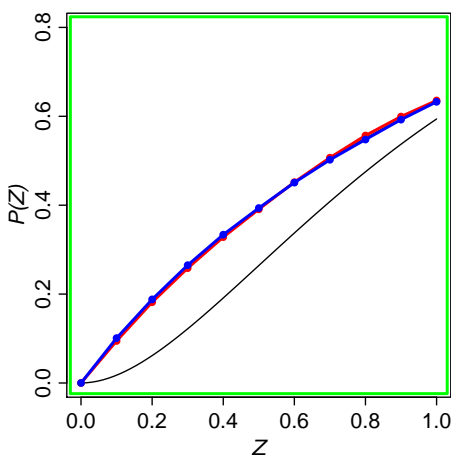
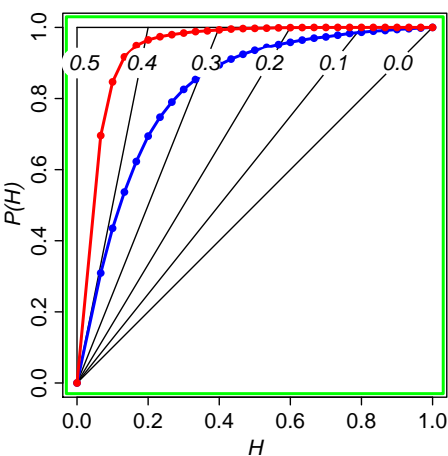
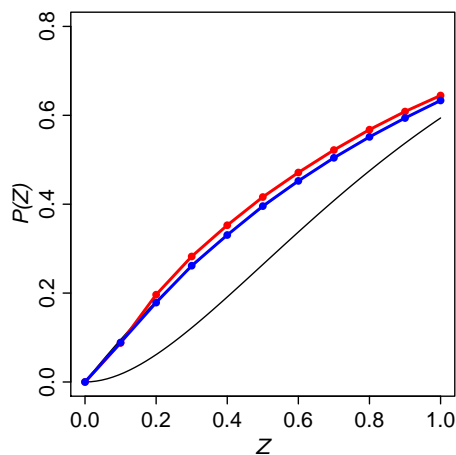
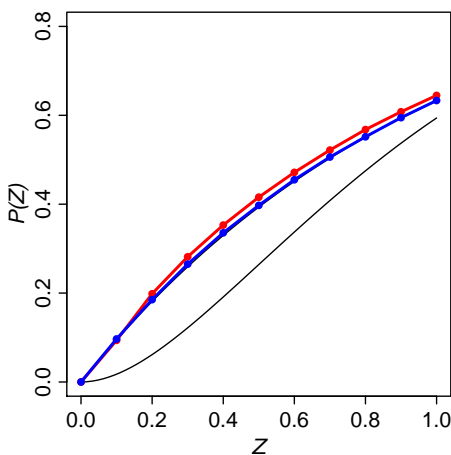
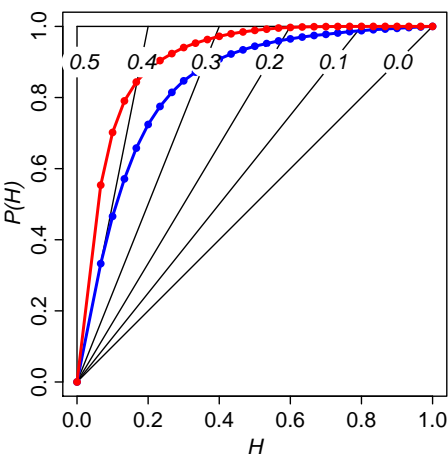
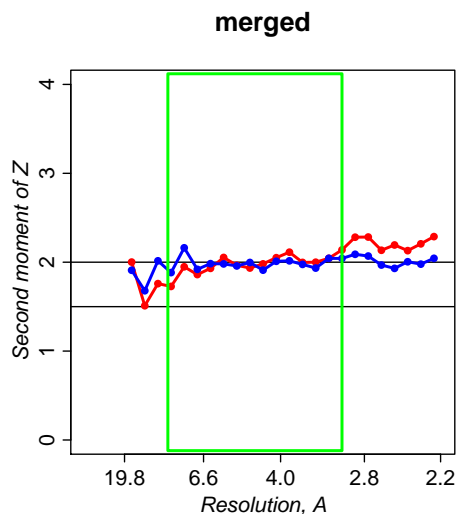
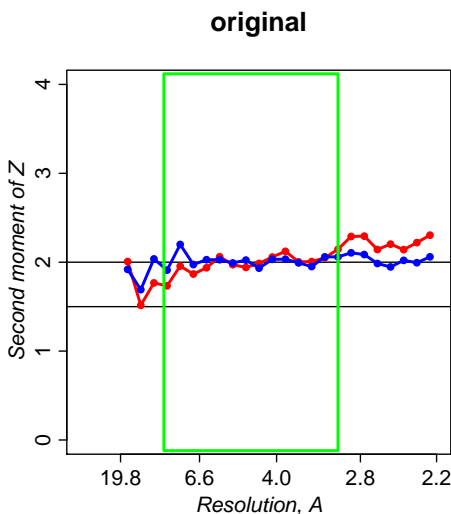
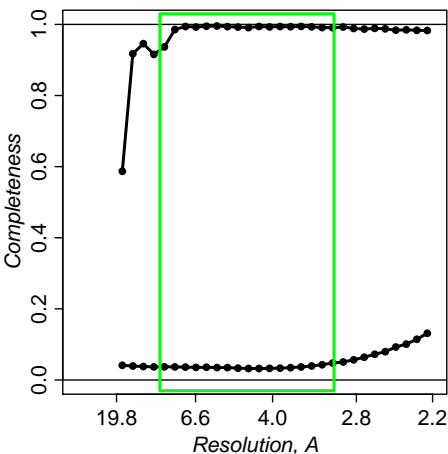
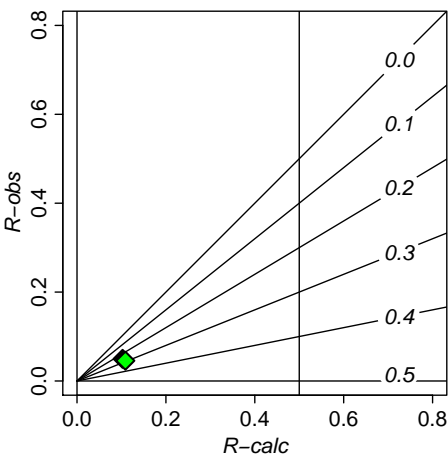
	original	merged
s.g.	P 62	P 62 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.13
R	23.4	
R'	23.8	24.0
R-free	25.3	
R'-free	25.9	26.0

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.5–2.2	9.9–3.0
unique	80,377	30,984
measured	79,388	30,727
used	73,600	27,834

NCS	translation	rotation
r.m.s.d. (A)	37.86	0.13
angle (o)	179.99	0.01

residues per monomer	DNA	protein
	0	415



1pv8

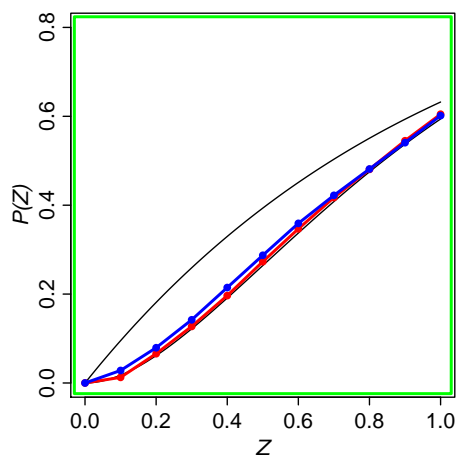
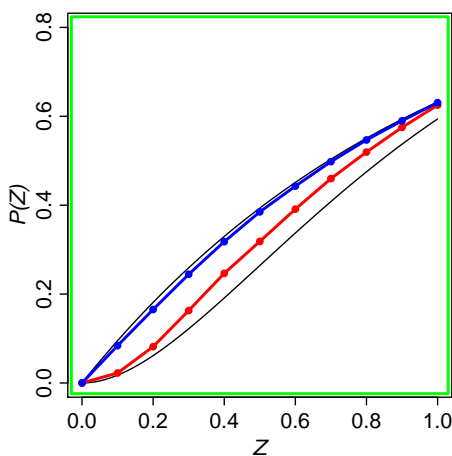
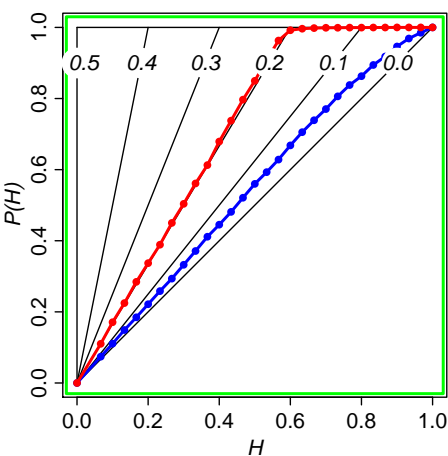
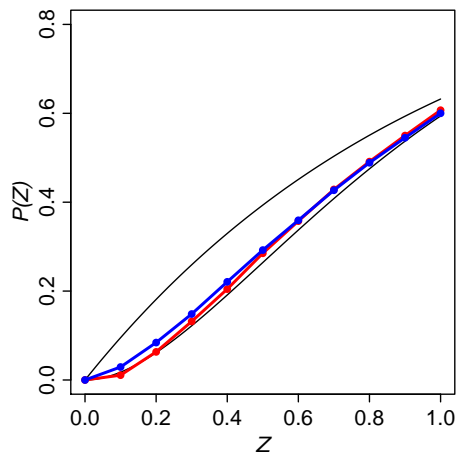
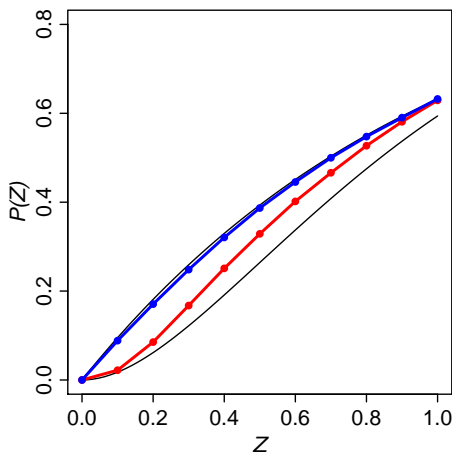
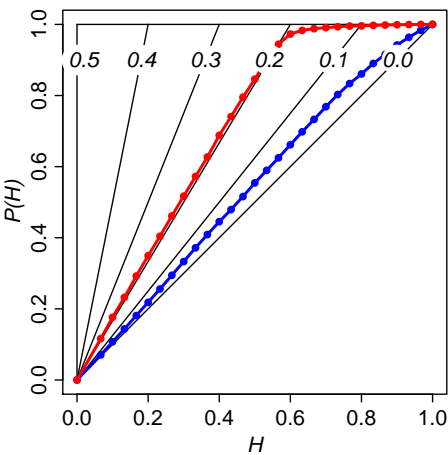
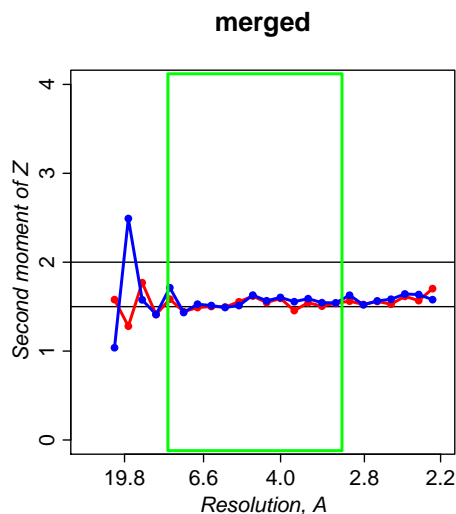
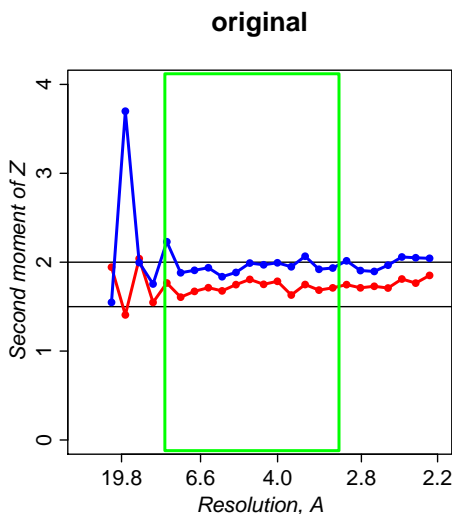
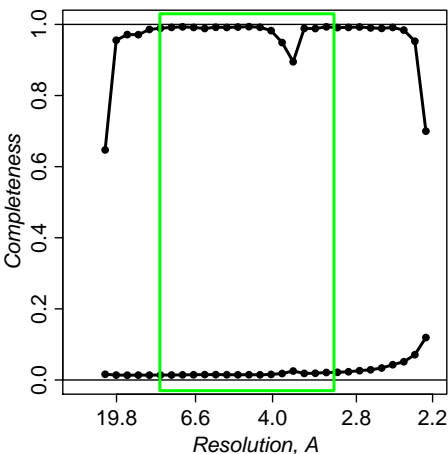
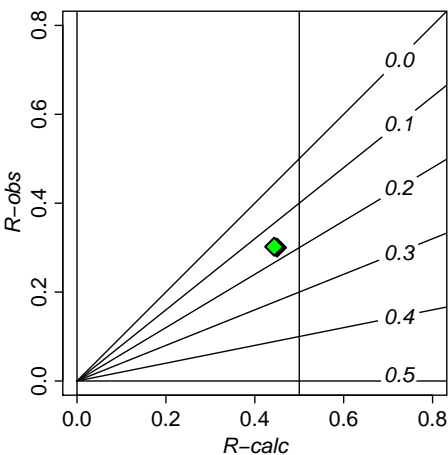
	original	merged
s.g.	P 63	P 63 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		14.24
R	25.1	
R'	-	-
R-free	27.6	
R'-free	-	-

s < f/100	250	0.75 %
s <= 0	181	0.54 %
f <= 0	181	0.54 %
s,f <= 0	181	0.54 %

range (A)	34.6-2.2	9.9-3.0
unique	34,988	13,585
measured	33,434	13,294
used	29,566	11,530

NCS	translation	rotation
r.m.s.d. (A)	31.87	6.51
angle (o)	179.62	27.29

residues per monomer	DNA	protein
	0	272



1pwx

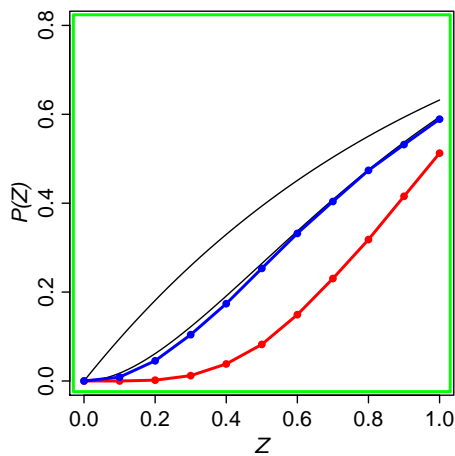
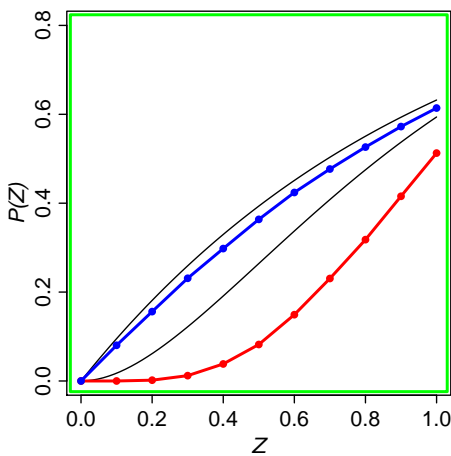
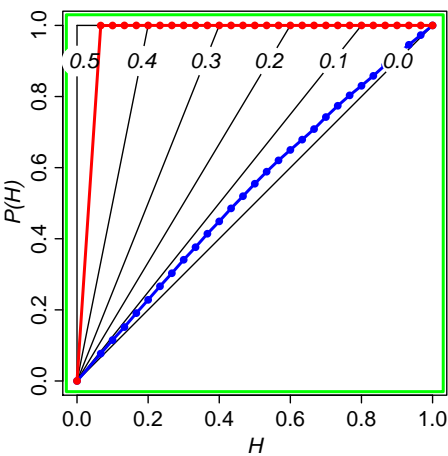
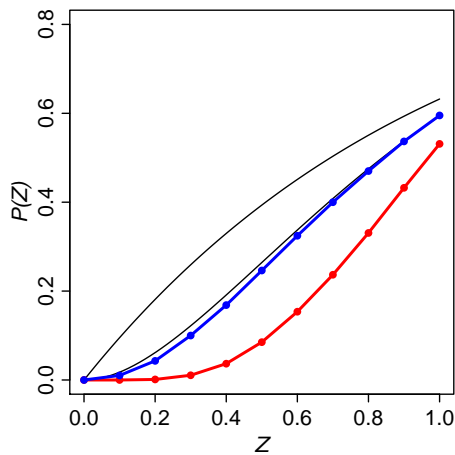
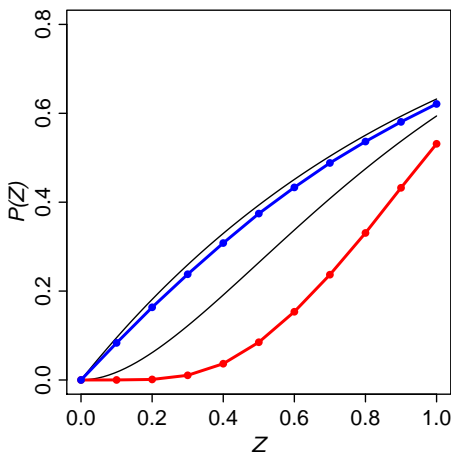
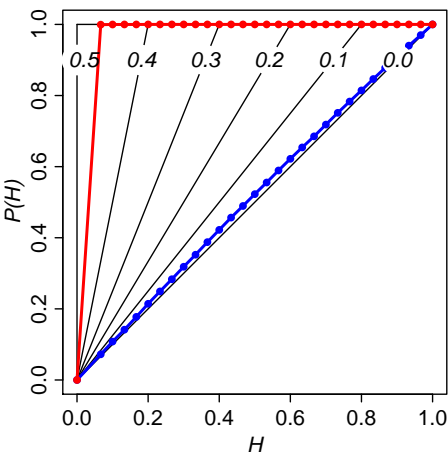
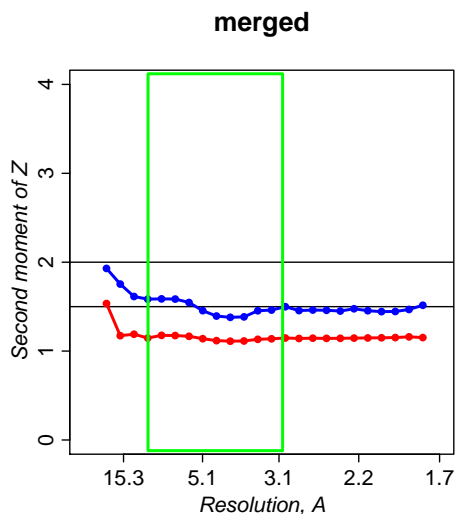
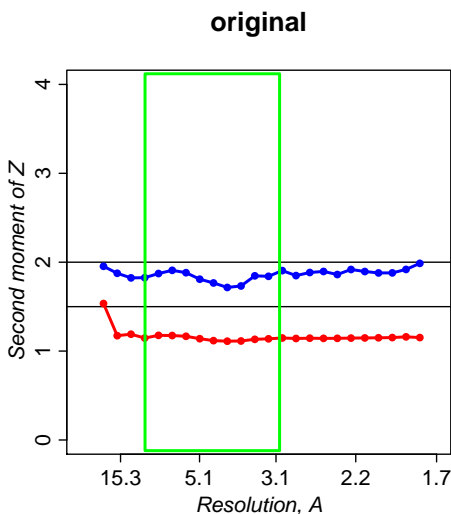
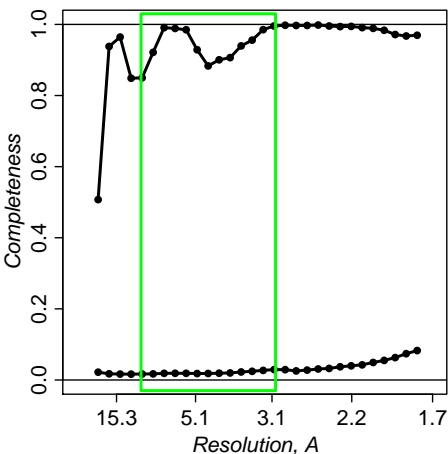
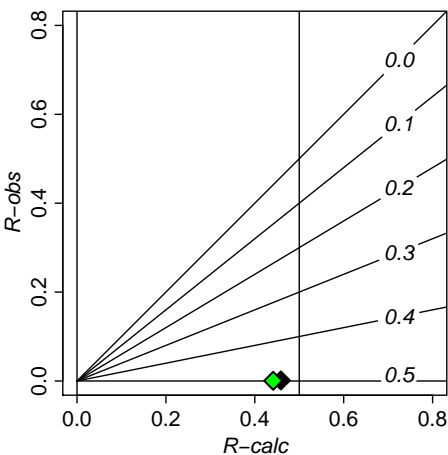
	original	merged
s.g.	P 43	P 43 21 2
p.g.	10201	10205
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		1.16
R	33.4	
R'	33.9	34.4
R-free	35.4	
R'-free	36.0	36.3

s < f/100	1	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	38.8–1.7	9.9–3.0
unique	123,884	24,029
measured	121,118	22,800
used	113,964	20,560

NCS	translation	rotation
r.m.s.d. (A)	17.00	0.86
angle (o)	74.81	2.05

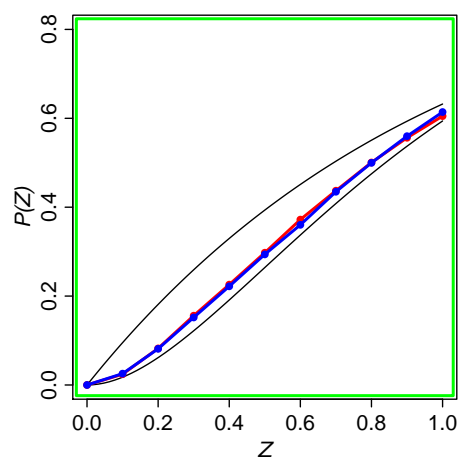
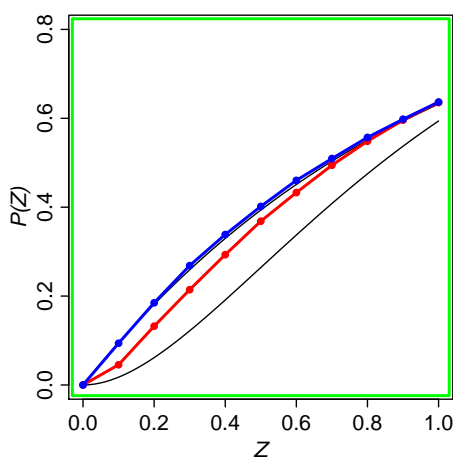
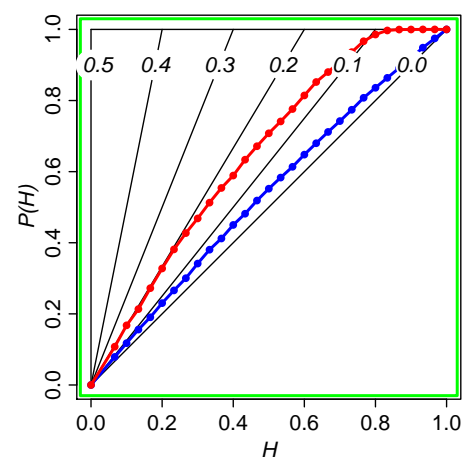
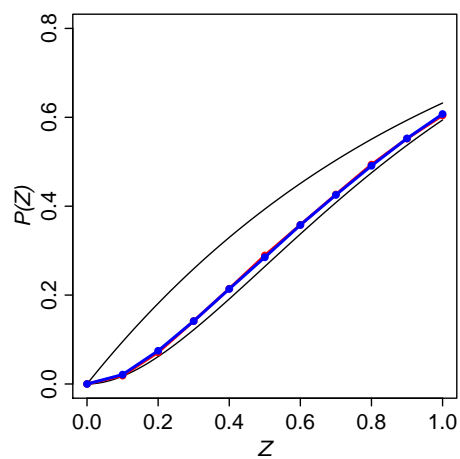
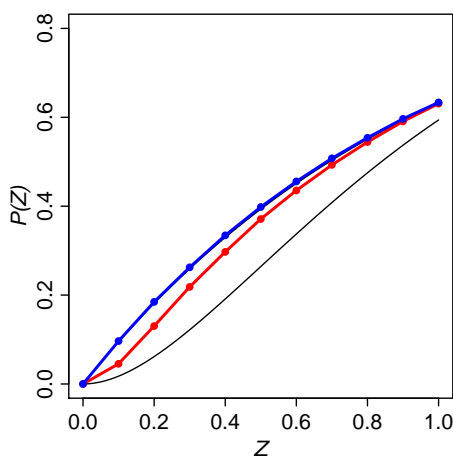
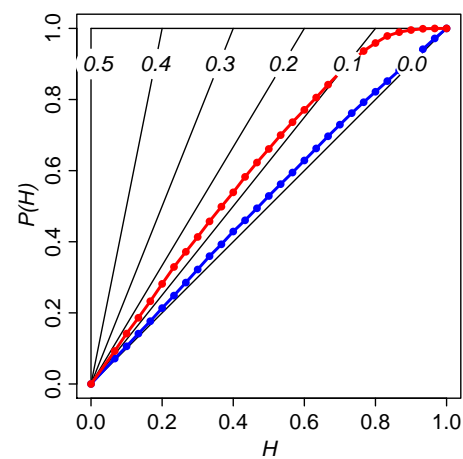
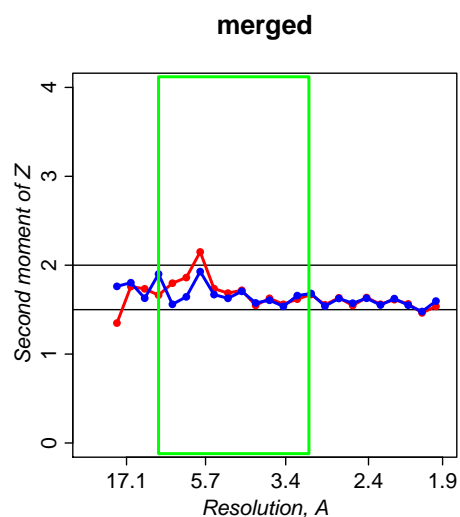
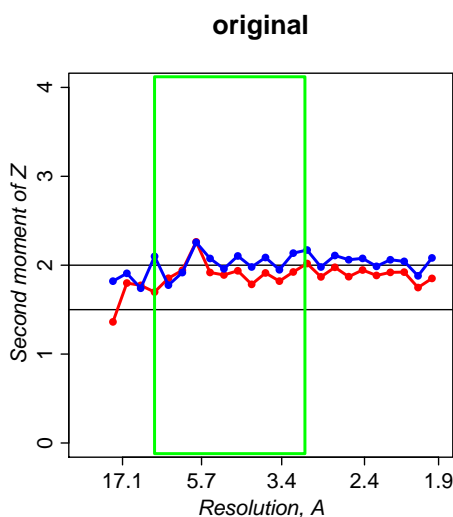
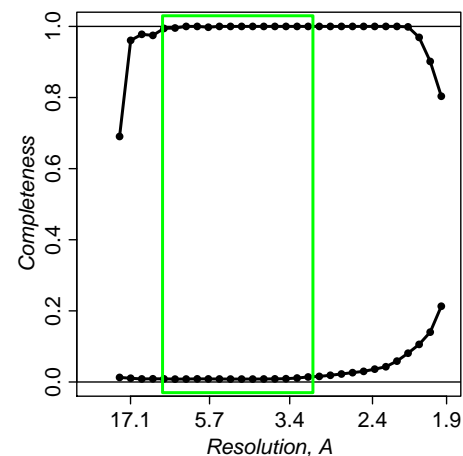
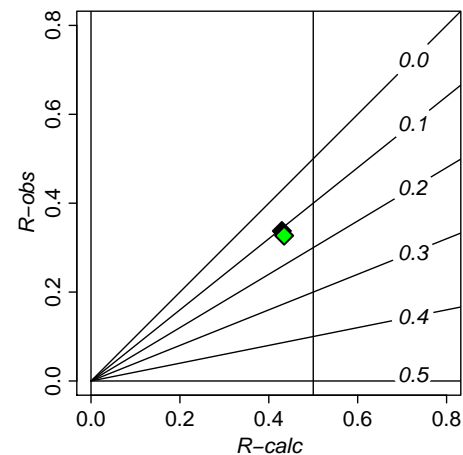
residues per monomer	DNA	protein
	0	252



1q3e

	original	merged
s.g.	14	14 2 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		1.44
R	26.7	
R'	27.2	34.8
R-free	27.7	
R'-free	28.6	38.9
residues per monomer	DNA 0	protein 189

s < f/100	6658	16.09 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	29.3–1.9	9.9–3.0
unique	42,594	10,575
measured	41,374	10,572
used	37,426	9,442
NCS	translation	rotation
r.m.s.d. (A)	31.41	0.76
angle (o)	179.52	3.31



1q4s

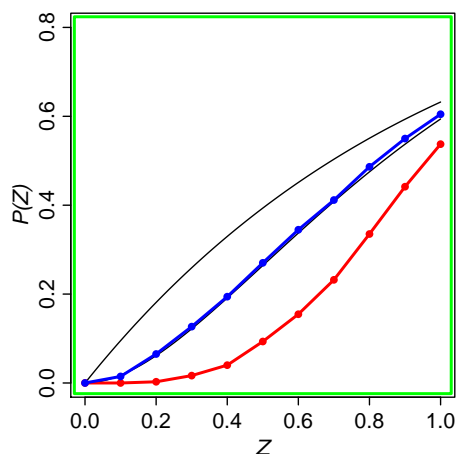
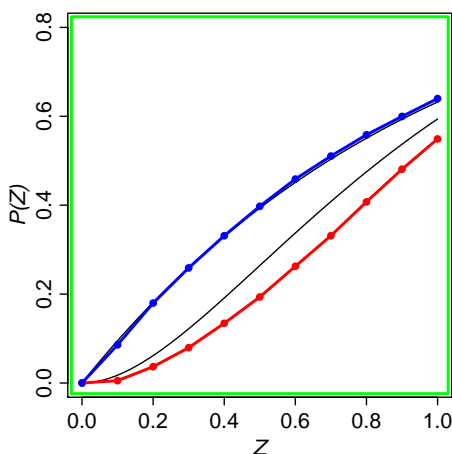
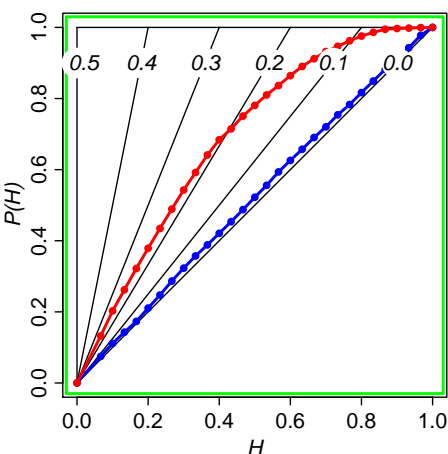
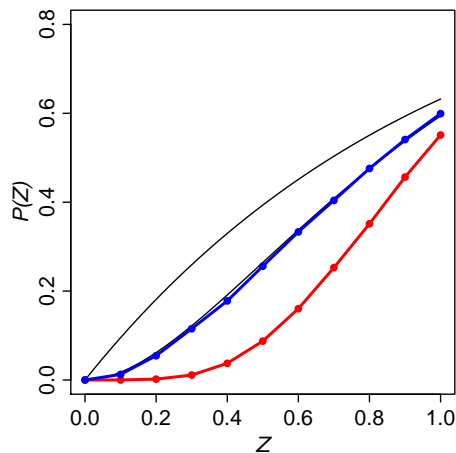
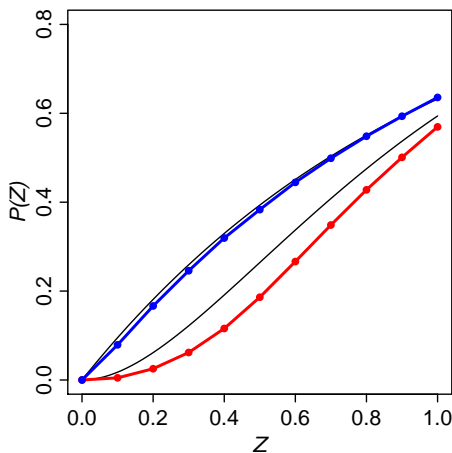
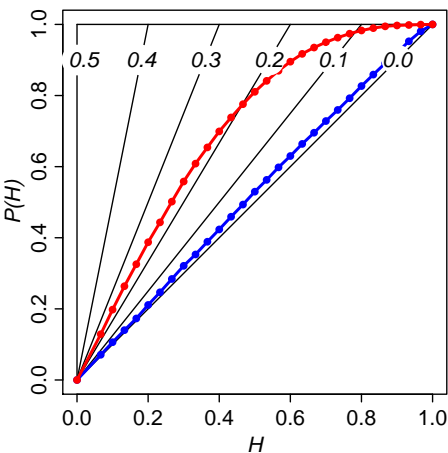
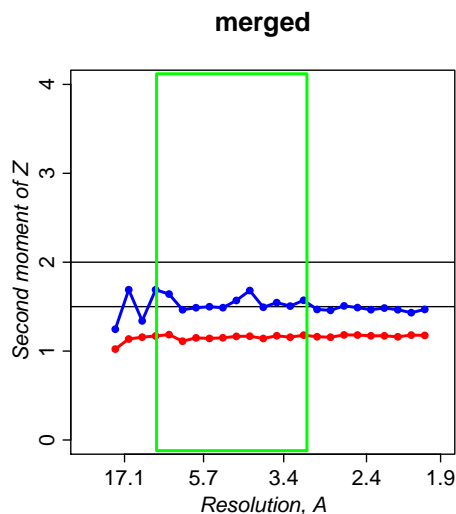
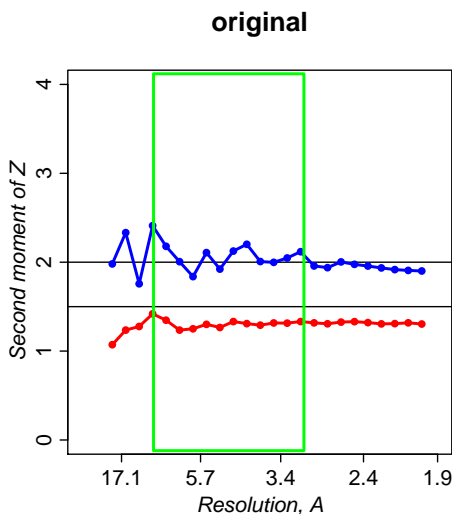
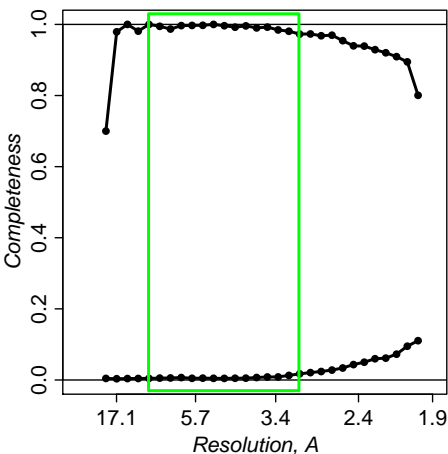
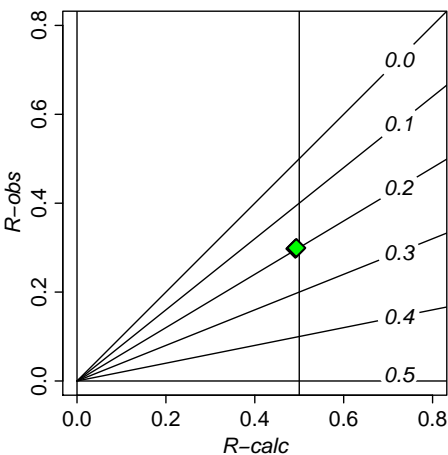
	original	merged
s.g.	P 32 2 1	P 62 2 2
p.g.	10023	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		11.25
R	26.2	
R'	-	-
R-free	27.6	
R'-free	-	-

s < f/100	10769	35.24 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	28.7-1.9	9.9-3.0
unique	32,571	8,837
measured	30,559	8,741
used	25,692	7,288

NCS	translation	rotation
r.m.s.d. (A)	13.88	3.95
angle (o)	64.06	24.04

residues per monomer	DNA	protein
	0	140



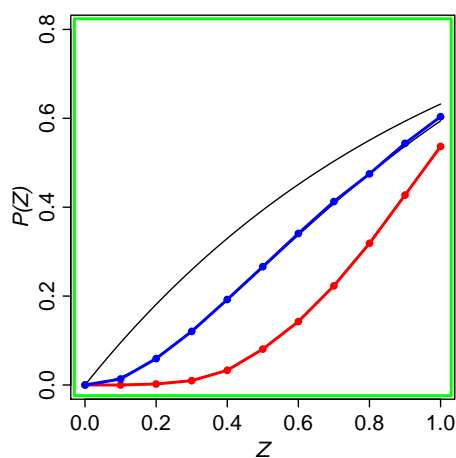
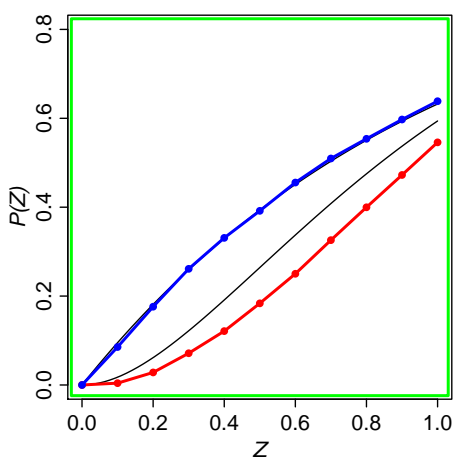
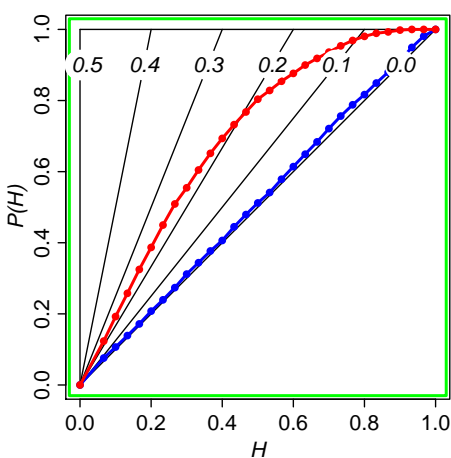
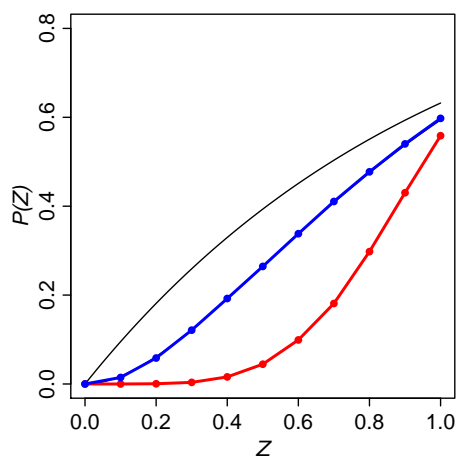
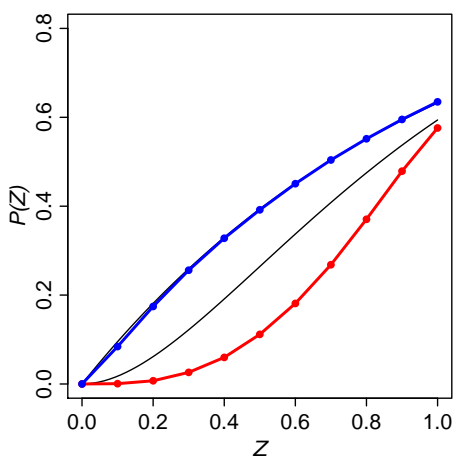
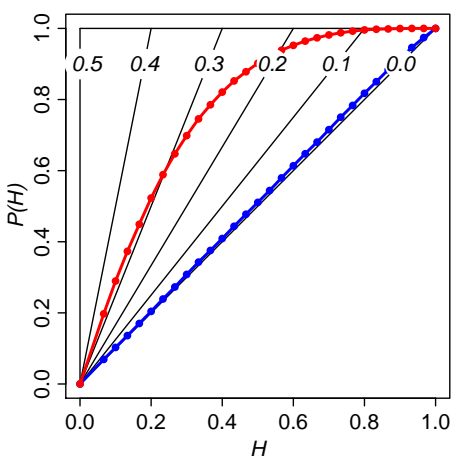
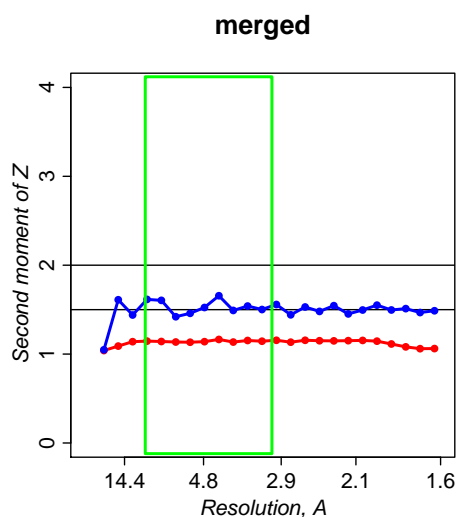
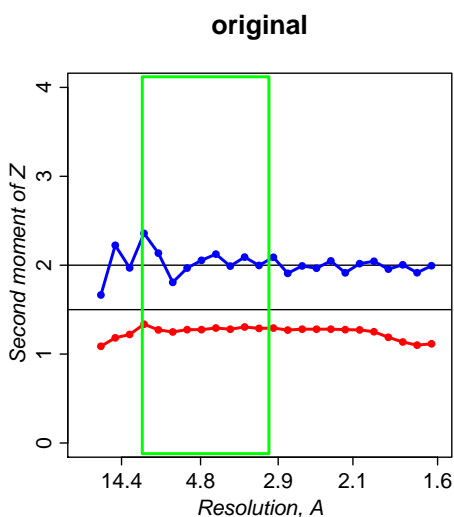
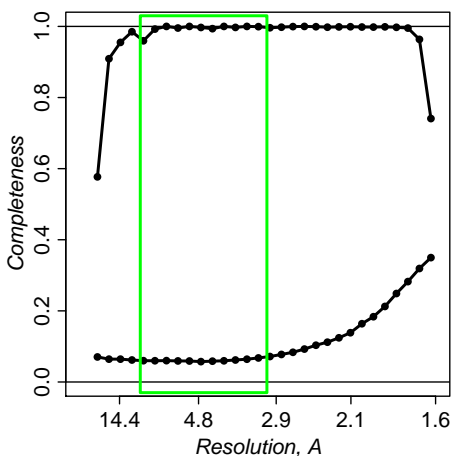
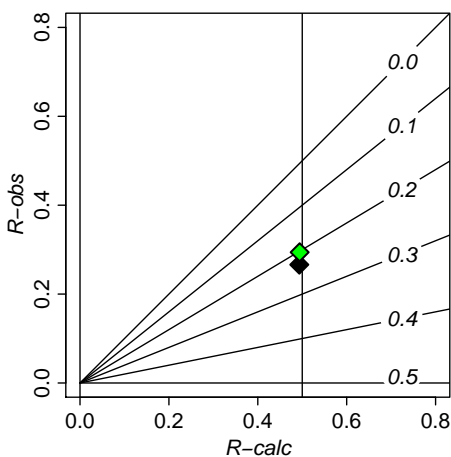
1q4t

	original	merged
s.g.	P 32 2 1	P 62 2 2
p.g.	10023	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		11.11
R	28.9	
R'	-	-
R-free	30.4	
R'-free	-	-
residues per monomer	DNA 0	protein 140

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	48.7-1.6	9.9-3.0
unique	58,959	8,839
measured	57,248	8,812
used	51,318	7,344

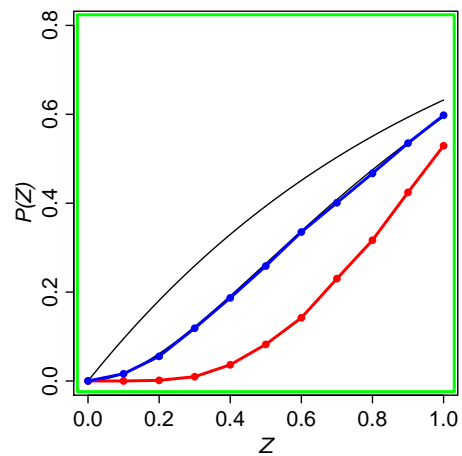
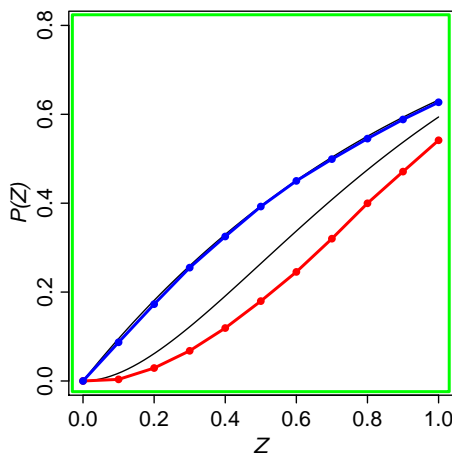
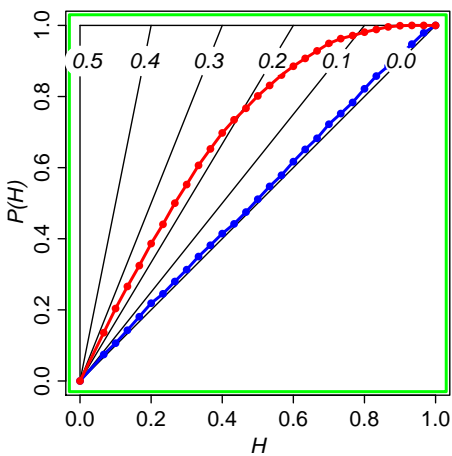
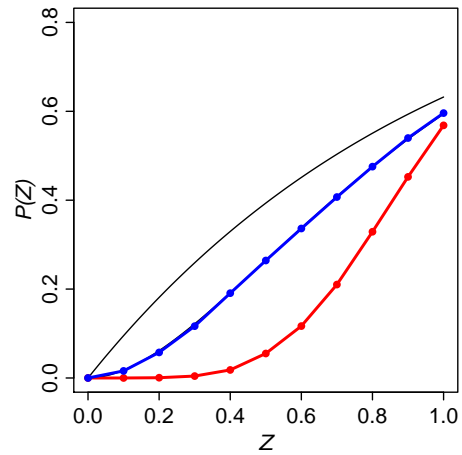
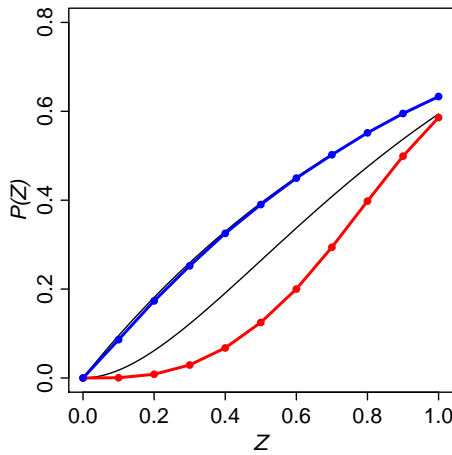
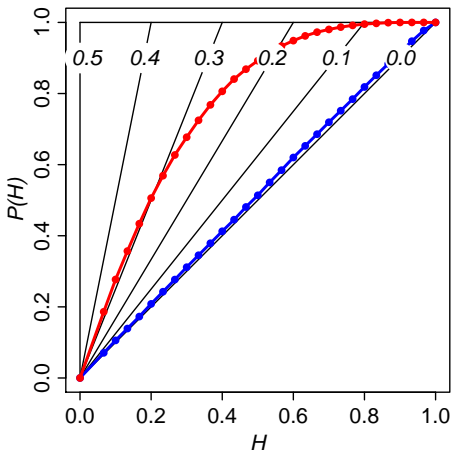
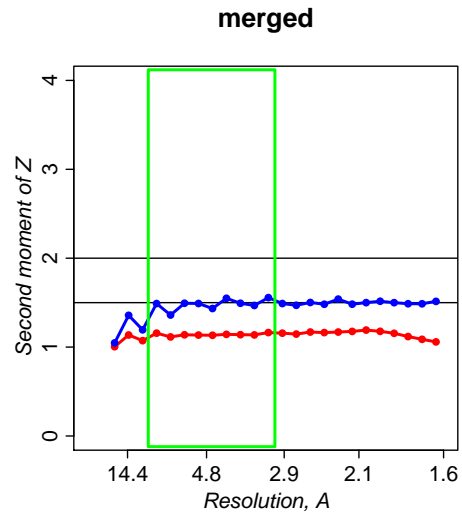
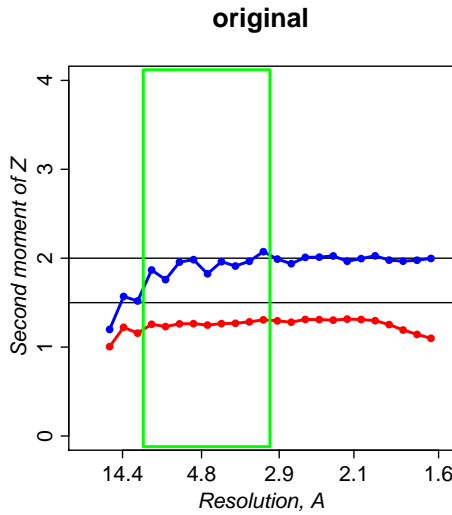
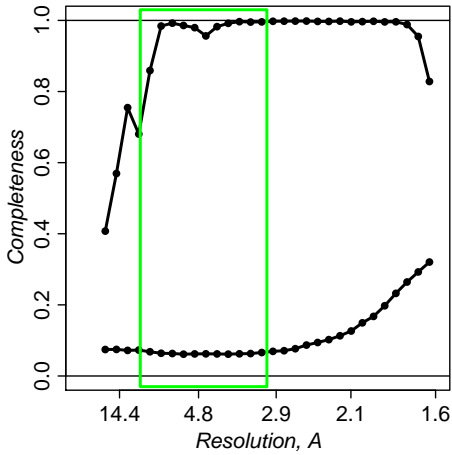
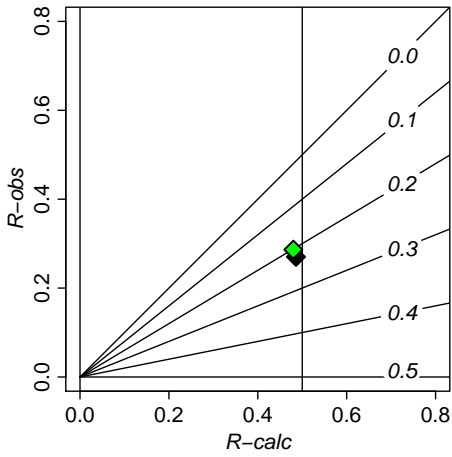
NCS	translation	rotation
r.m.s.d. (A)	13.82	3.75
angle (o)	63.57	22.87



1q4u

	original	merged
s.g.	P 32 2 1	P 62 2 2
p.g.	10023	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		11.37
R	28.1	
R'	-	-
R-free	29.7	
R'-free	-	-
residues per monomer	DNA 0	protein 139

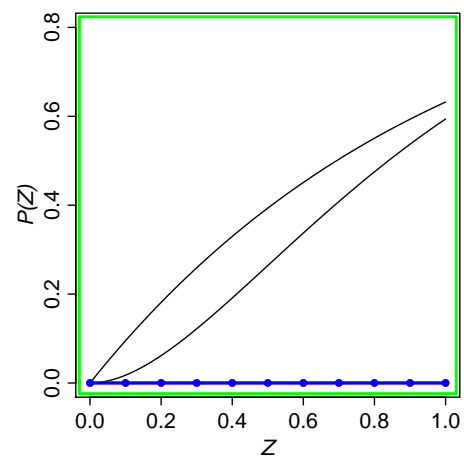
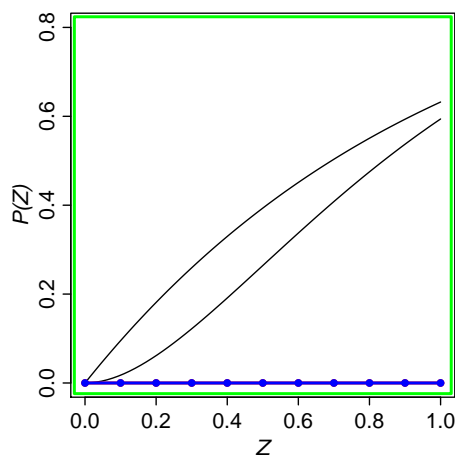
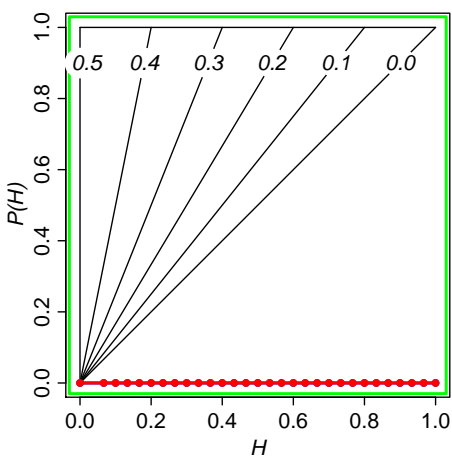
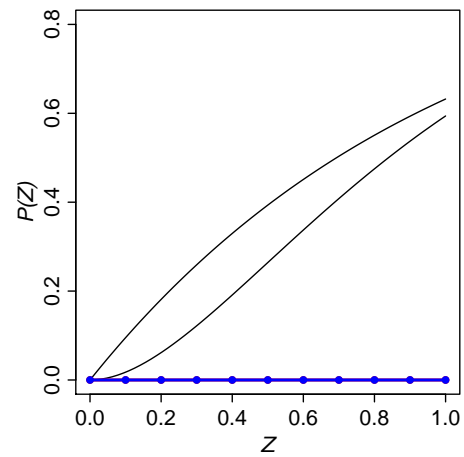
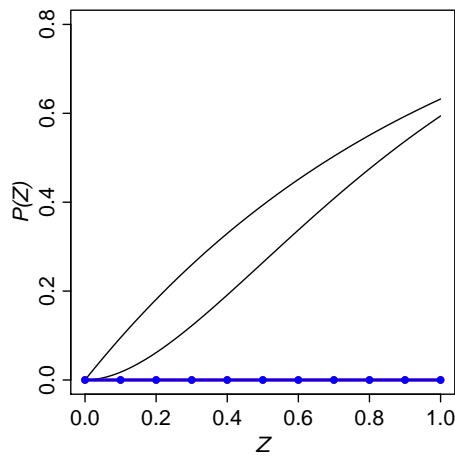
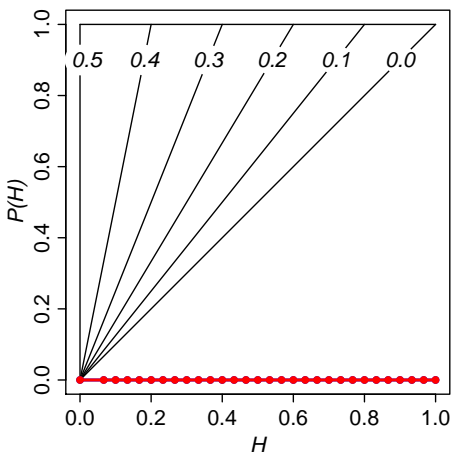
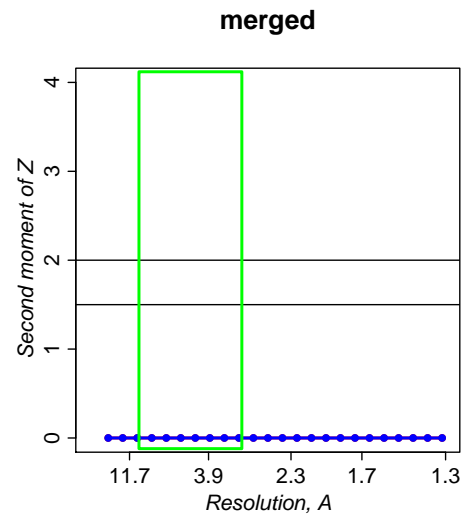
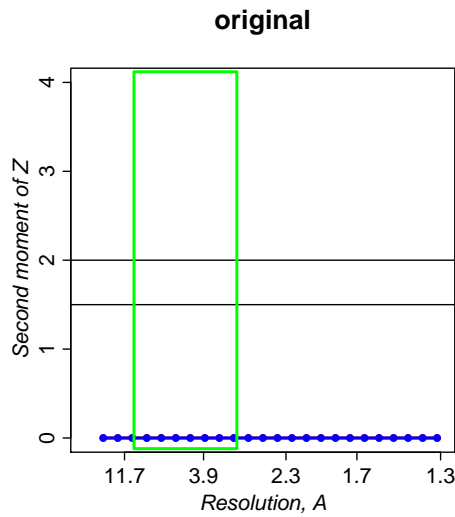
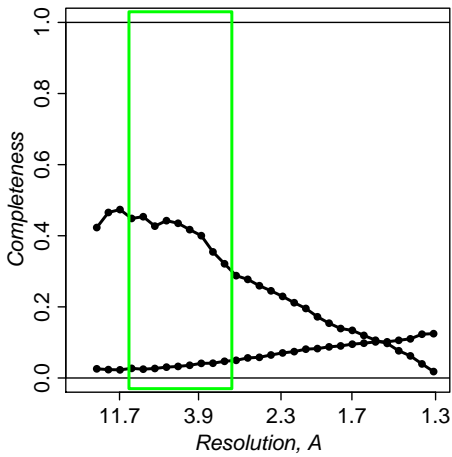
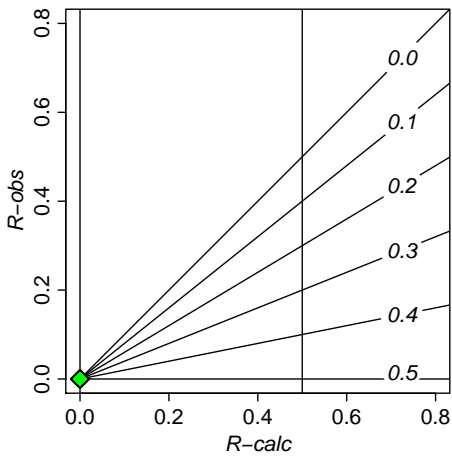
s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	28.9–1.6	9.9–3.0
unique	58,561	8,890
measured	57,011	8,723
used	51,162	7,236
NCS	translation	rotation
r.m.s.d. (A)	13.82	3.89
angle (o)	63.77	23.59



1qaz

	original	merged
s.g.	C 1 2 1	-
p.g.	10001	10003
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	40.2	-
R'	-	-
R-free	44.5	-
R'-free	-	-
residues per monomer	DNA 0	protein 351

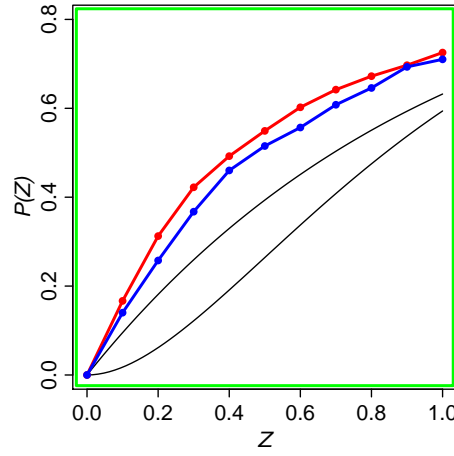
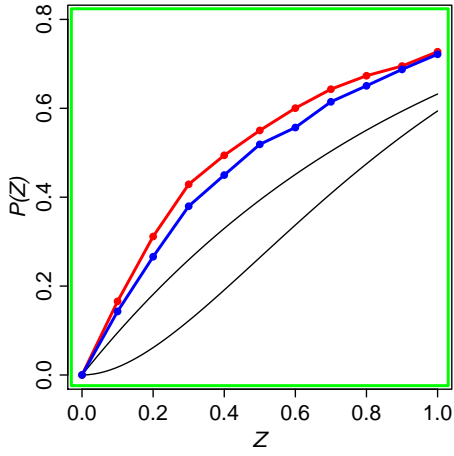
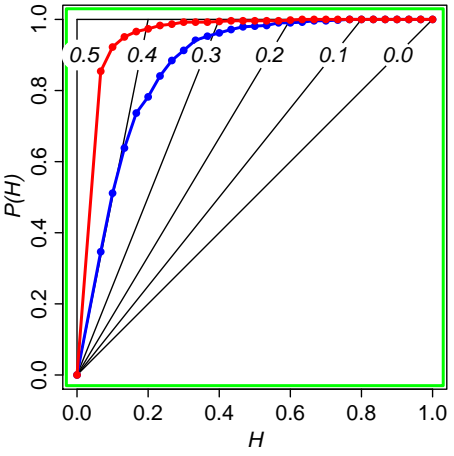
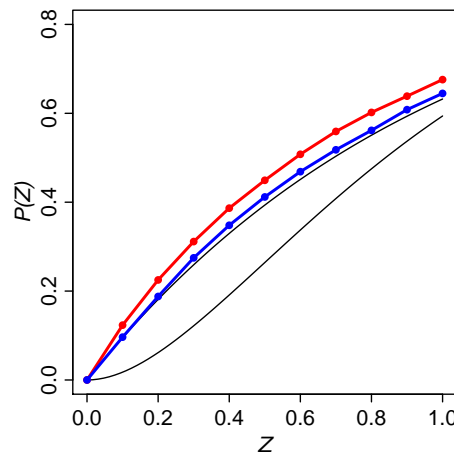
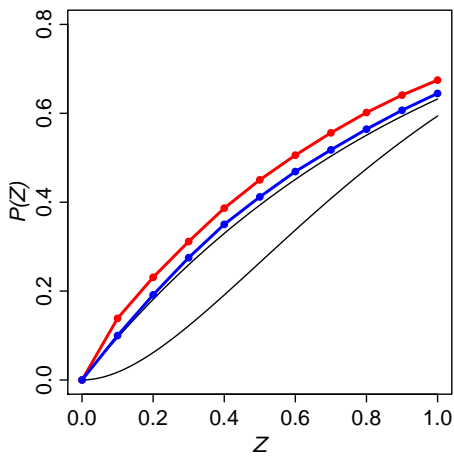
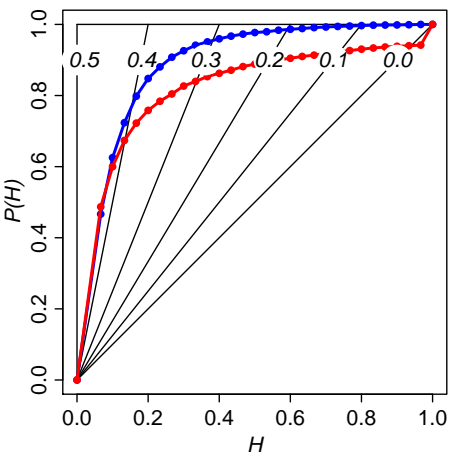
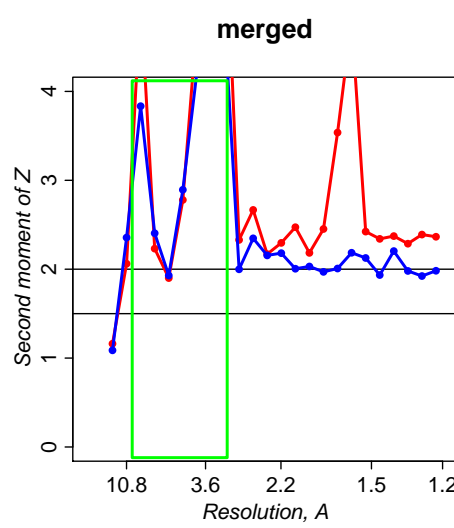
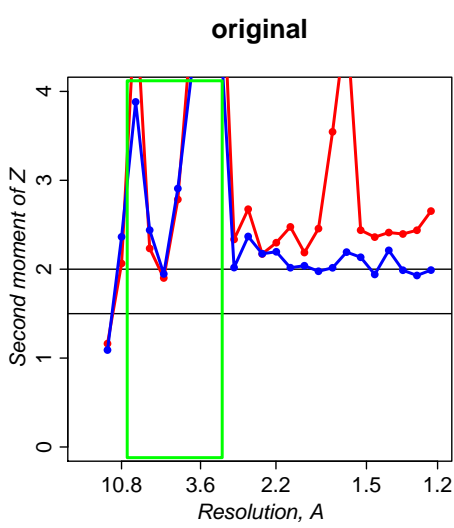
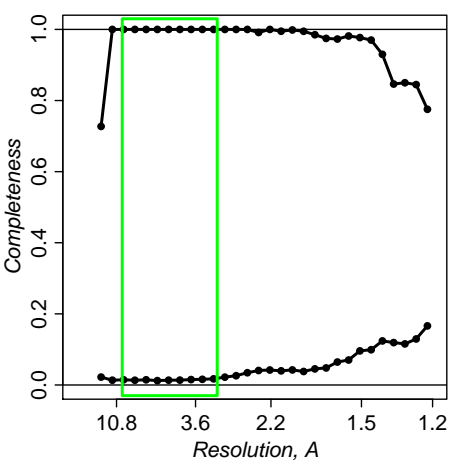
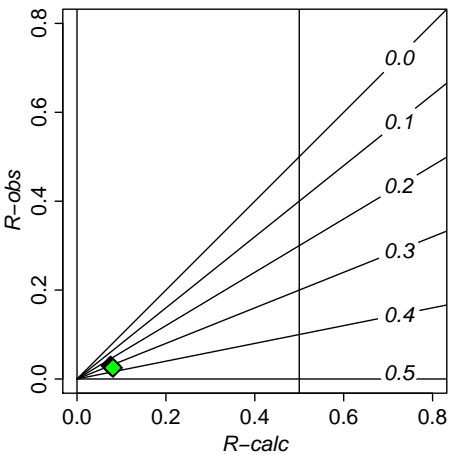
s < f/100	8	0.09 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	42.2-1.3	9.9-3.0
unique	45,915	6,838
measured	8,457	2,612
used	0	0
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1qcu

	original	merged
s.g.	P 3	P 3 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.03
R	26.4	
R'	26.4	25.0
R-free	27.2	
R'-free	27.2	25.3
residues per monomer	DNA 22	protein 0

s < f/100	27	0.15 %
s <= 0	0	0.00 %
f <= 0	787	4.31 %
s,f <= 0	0	0.00 %
range (A)	23.1–1.2	9.9–3.0
unique	19,647	1,229
measured	18,265	1,229
used	16,186	1,048
NCS	translation	rotation
r.m.s.d. (A)	21.22	0.03
angle (o)	179.96	0.04



1qiu

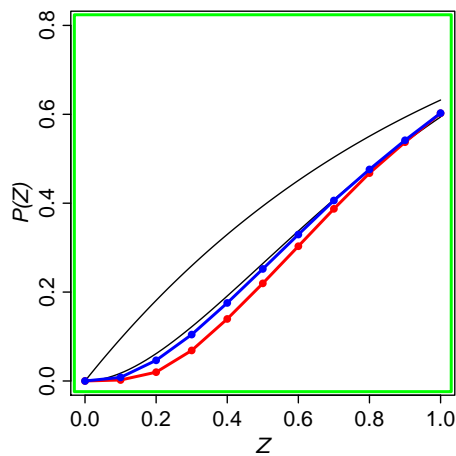
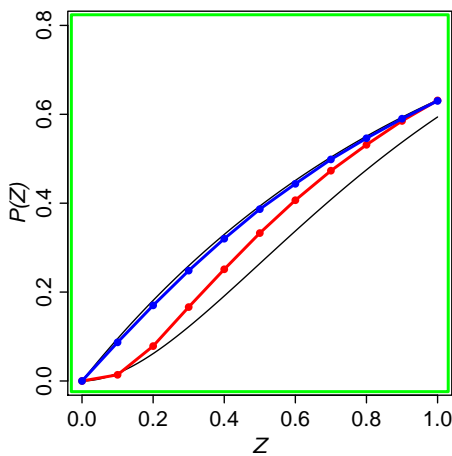
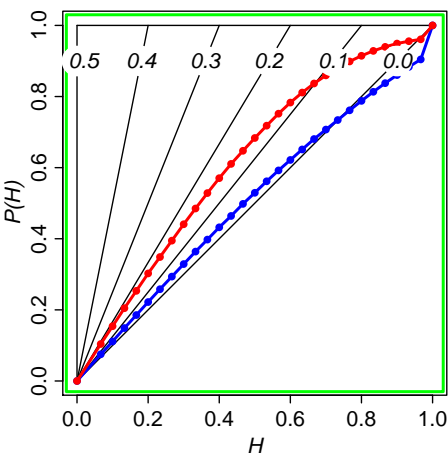
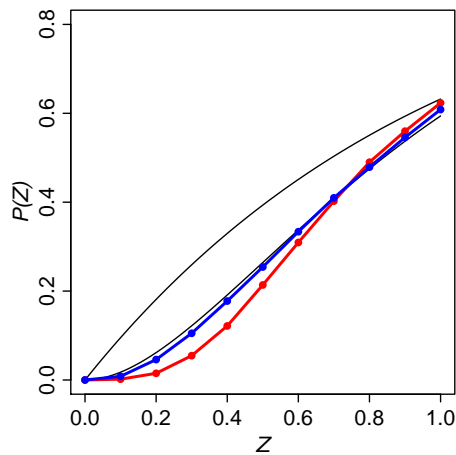
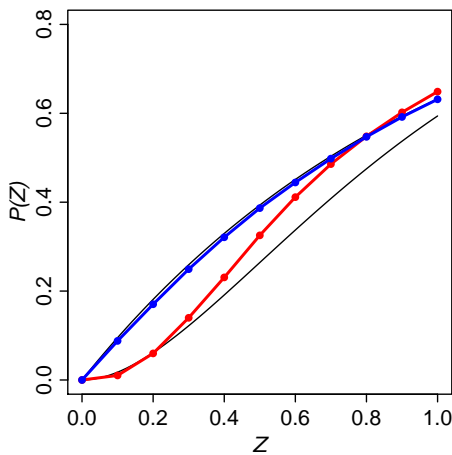
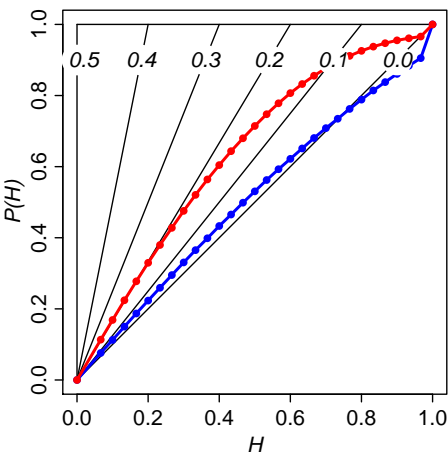
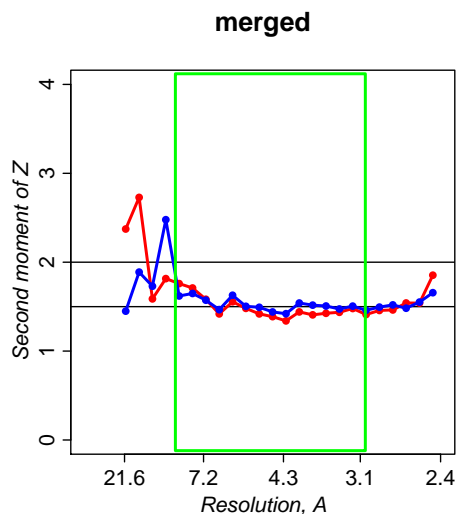
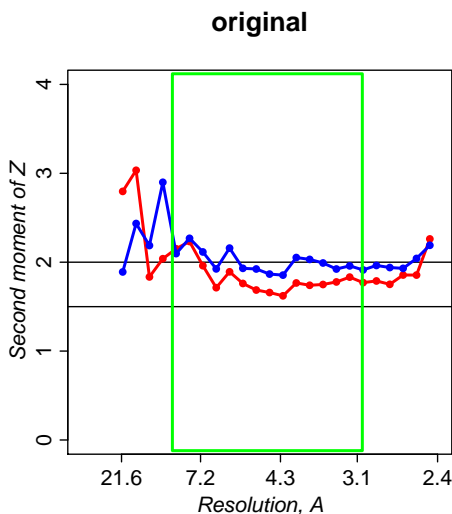
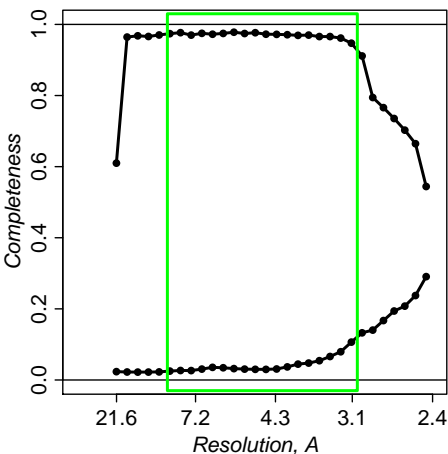
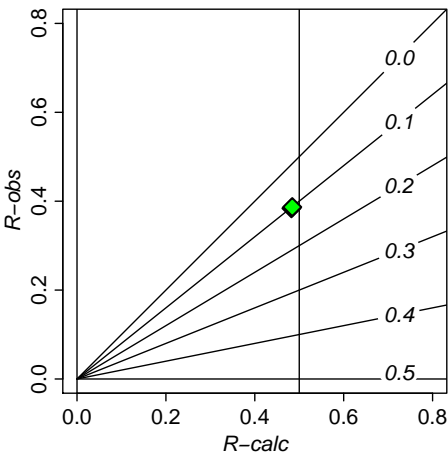
	original	merged
s.g.	C 1 2 1	-
p.g.	10001	10023
a.u.	6	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	25.0	-
R'	-	-
R-free	27.8	-
R'-free	-	-

s < f/100	1038	1.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	25.1-2.4	9.9-3.0
unique	122,875	61,955
measured	103,327	59,836
used	76,821	52,533

NCS	translation	rotation
r.m.s.d. (A)	11.84	1.37
angle (o)	59.53	2.30

residues per monomer	DNA	protein
	0	264



1qow

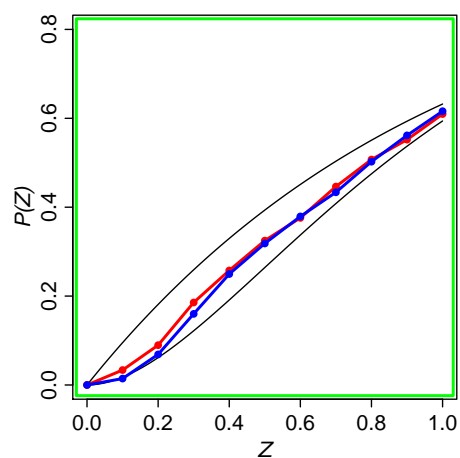
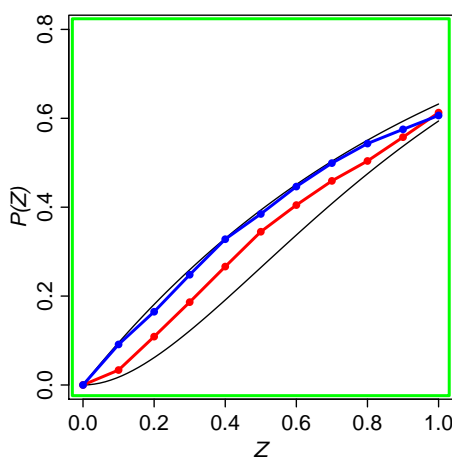
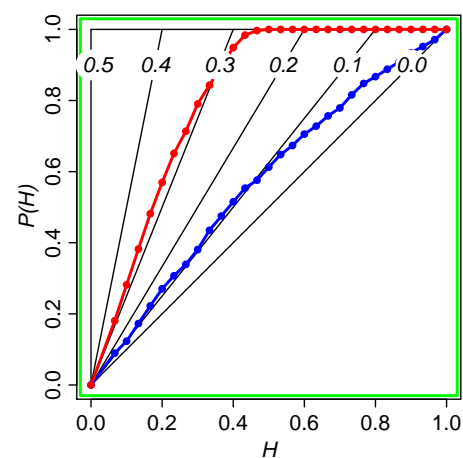
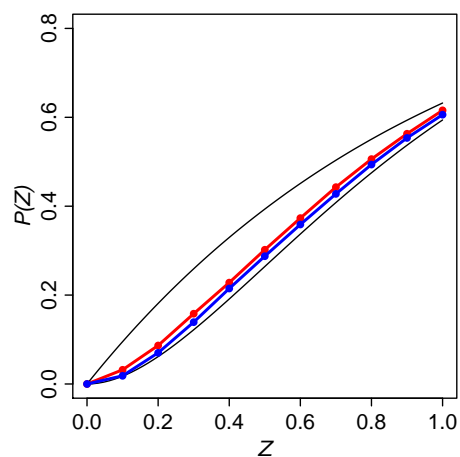
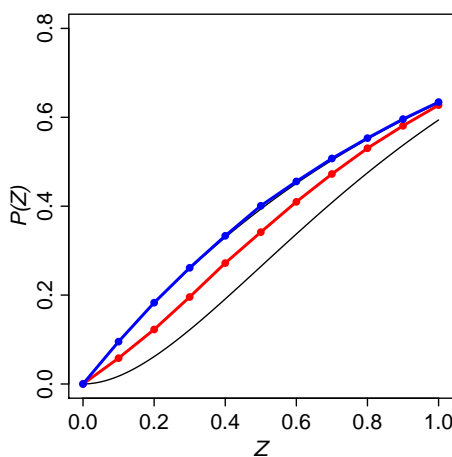
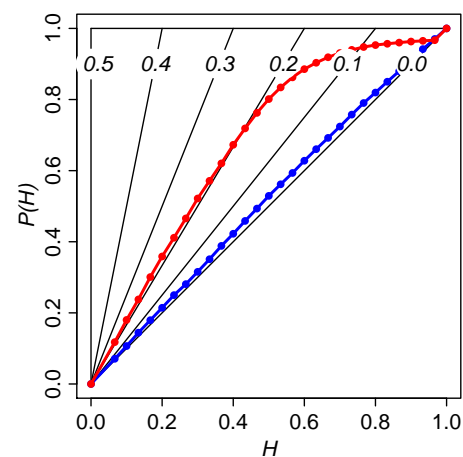
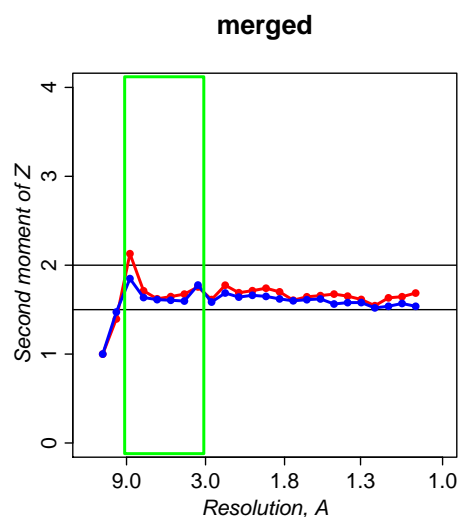
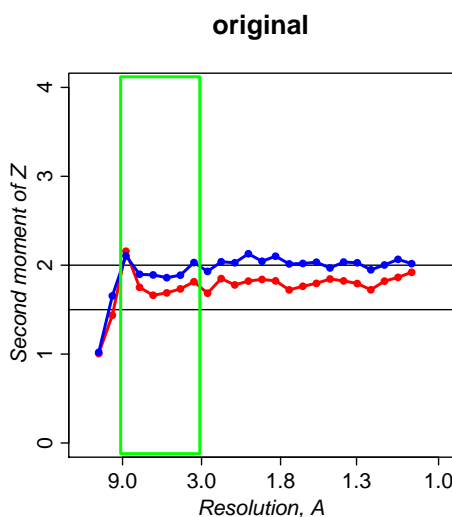
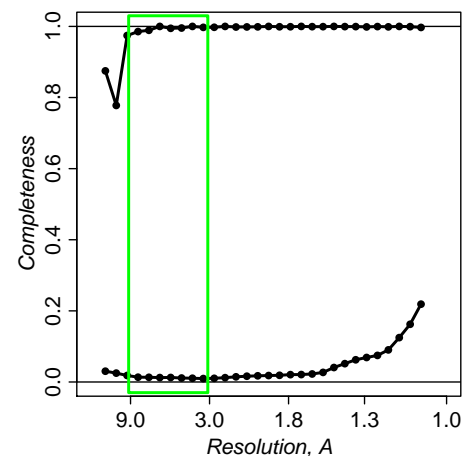
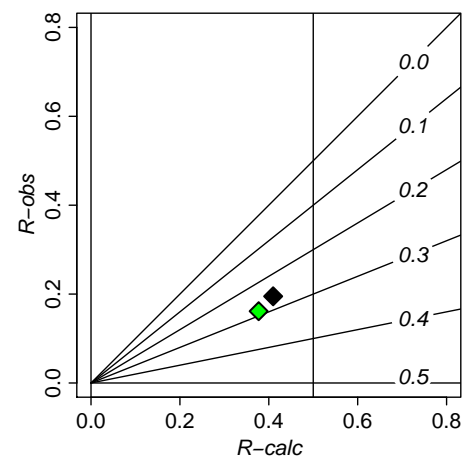
	original	merged
s.g.	P 32	P 32 2 1
p.g.	10020	10023
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		1.10
R	37.8	
R'	39.8	40.8
R-free	37.1	
R'-free	39.7	40.3

s < f/100	864	2.58 %
s <= 0	0	0.00 %
f <= 0	656	1.96 %
s,f <= 0	0	0.00 %

range (A)	39.9–1.1	9.9–3.0
unique	33,485	1,441
measured	33,446	1,436
used	31,706	1,240

NCS	translation	rotation
r.m.s.d. (A)	6.34	0.40
angle (o)	78.08	1.92

residues per monomer	DNA	protein
	0	14



1qrz

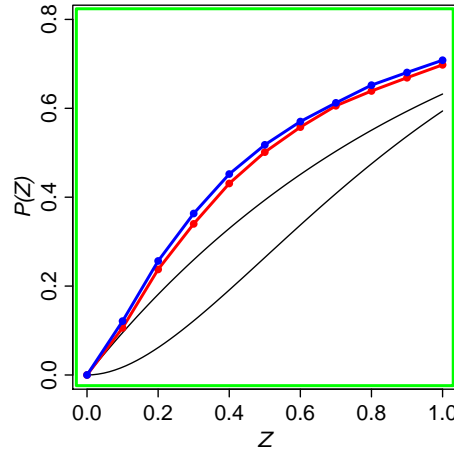
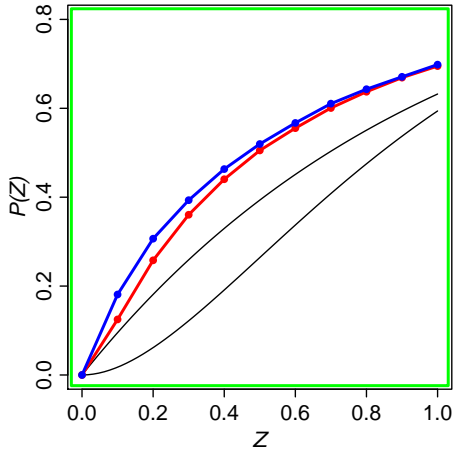
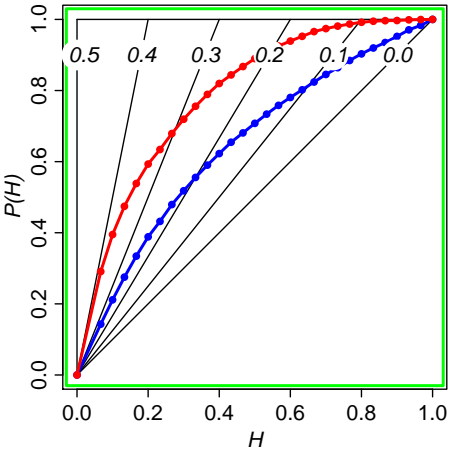
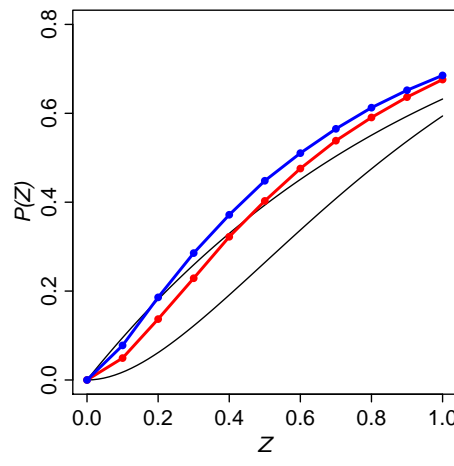
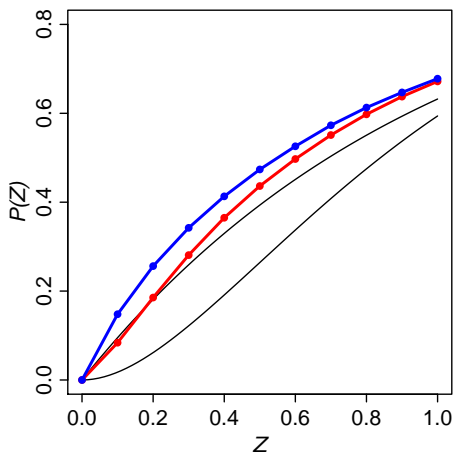
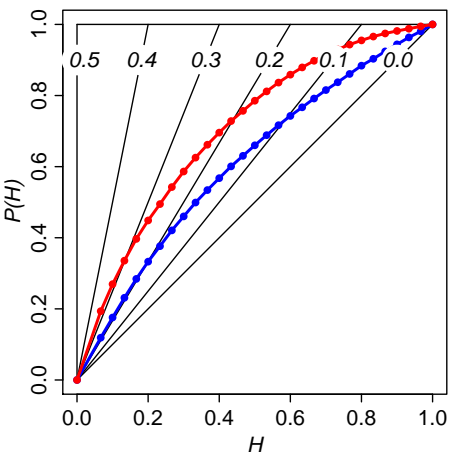
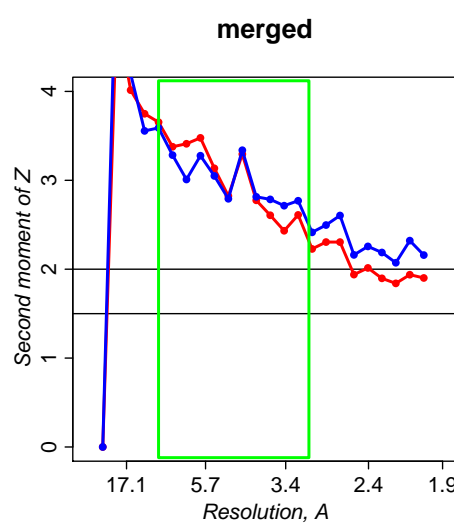
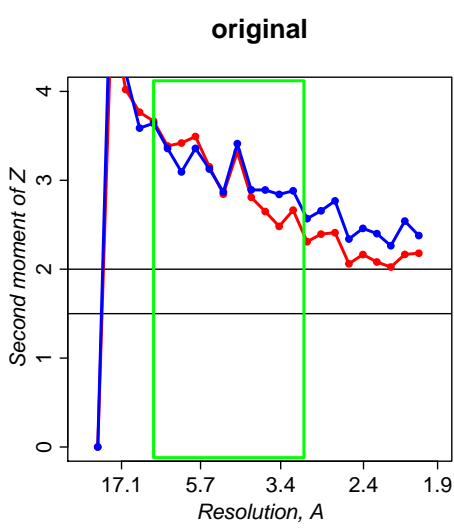
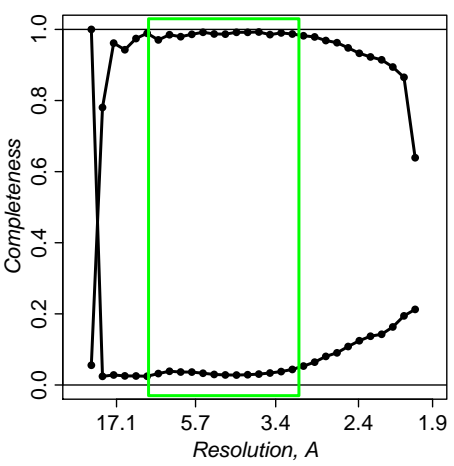
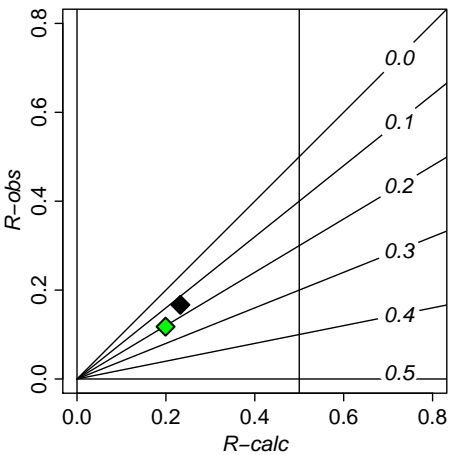
	original	merged
s.g.	P 1 21 1	-
p.g.	10001	10003
a.u.	4	-
p.t.	2	-
p.o.	2	-
r.m.s.d. (A)	-	-
R	28.0	-
R'	-	-
R-free	31.4	-
R'-free	-	-

residues per monomer	DNA	protein
	0	246

s < f/100	3500	5.86 %
s <= 0	3500	5.86 %
f <= 0	3500	5.86 %
s,f <= 0	3500	5.86 %

range (A)	77.3-2.0	9.9-3.0
unique	65,096	17,960
measured	59,708	17,746
used	52,950	16,084

NCS	translation	rotation
r.m.s.d. (A)	0.71	0.25
angle (o)	2.77	0.57



1qsj

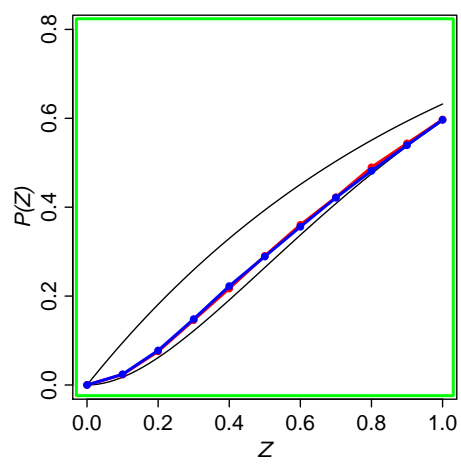
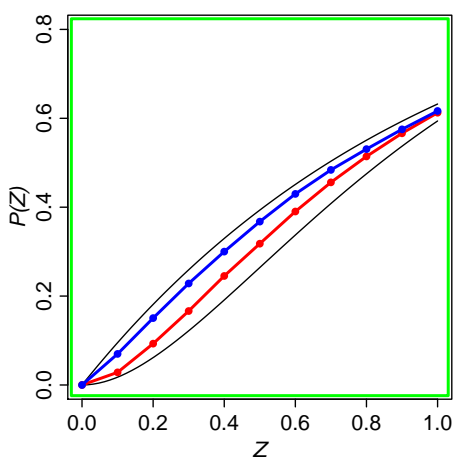
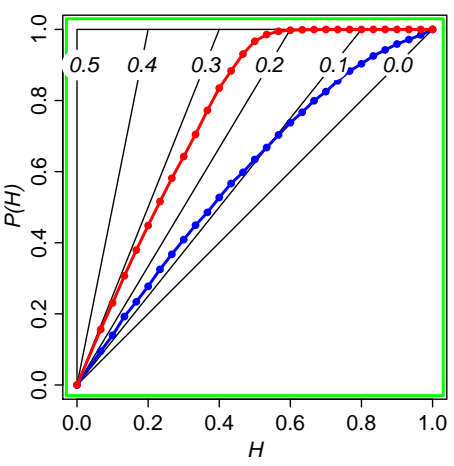
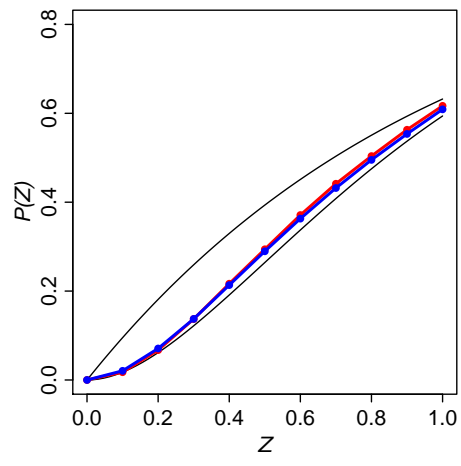
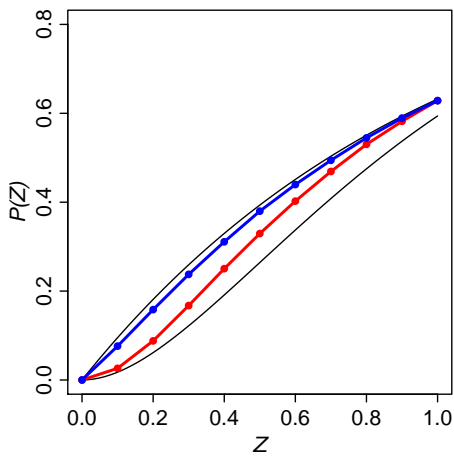
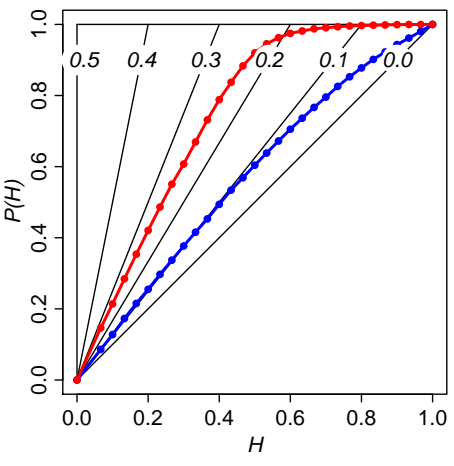
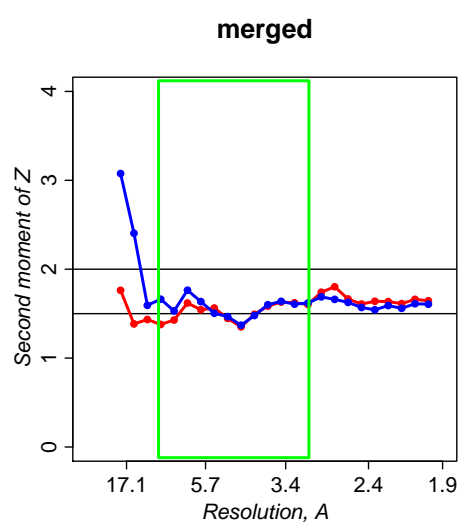
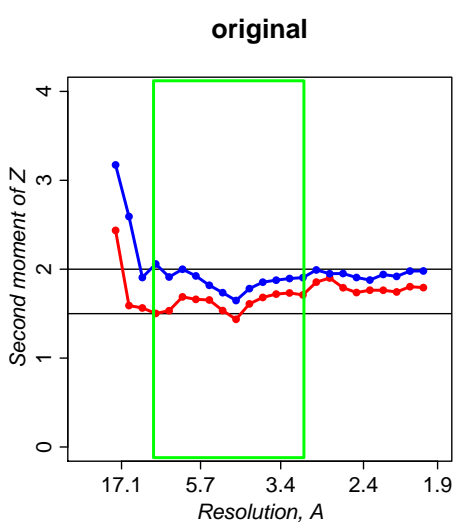
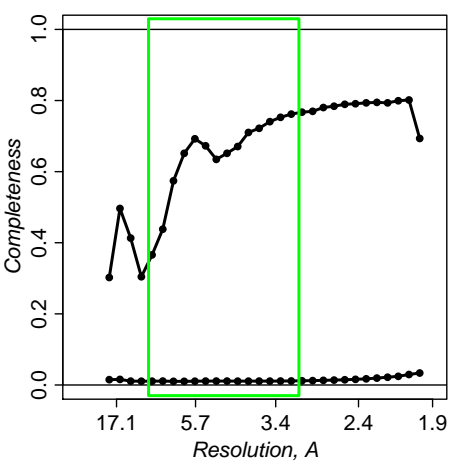
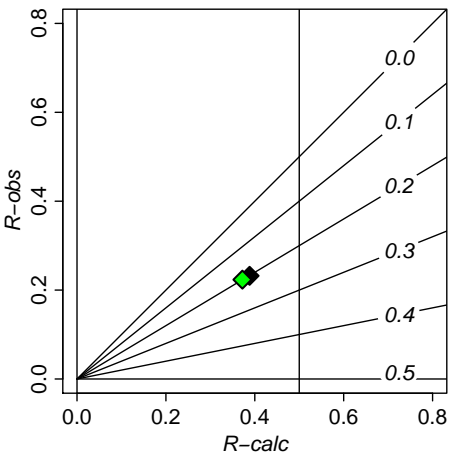
	original	merged
s.g.	P 21 21 21	-
p.g.	10003	10205
a.u.	4	-
p.t.	2	-
p.o.	4	-
r.m.s.d. (A)	-	-
R	26.8	-
R'	-	-
R-free	29.9	-
R'-free	-	-

residues per monomer	DNA	protein
	0	276

s < f/100	16330	25.39 %
s <= 0	0	0.00 %
f <= 0	67	0.10 %
s,f <= 0	0	0.00 %

range (A)	25.1-1.9	9.9-3.0
unique	85,294	22,879
measured	64,312	15,974
used	42,416	9,092

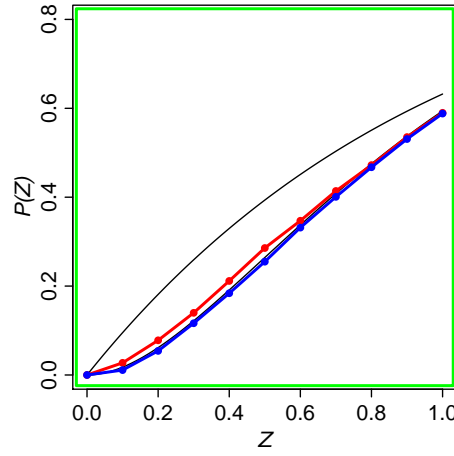
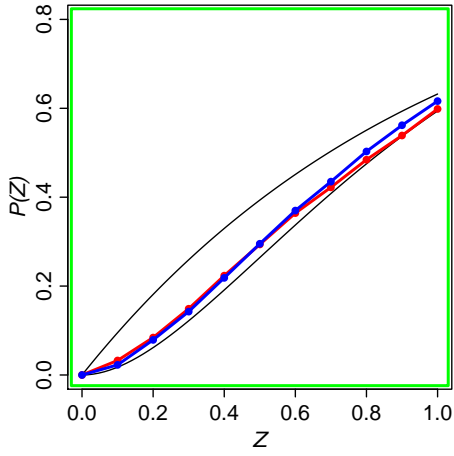
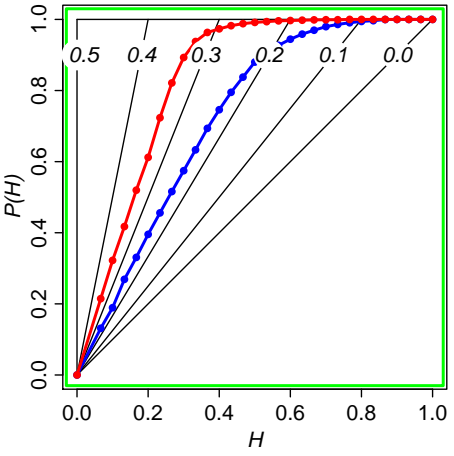
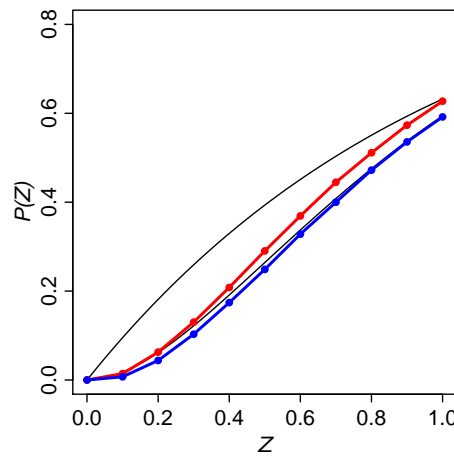
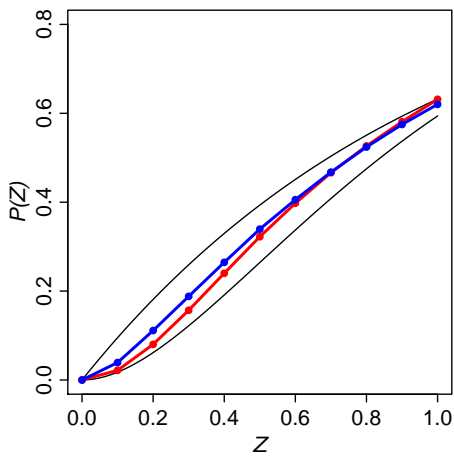
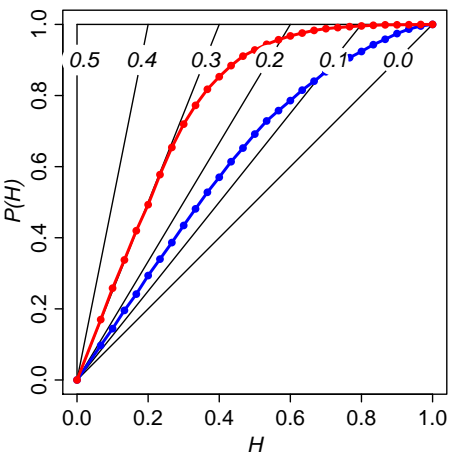
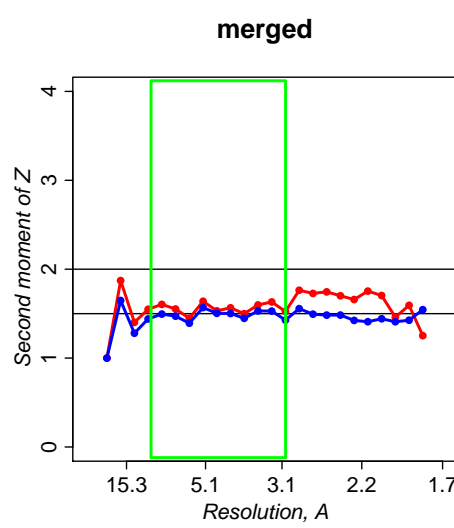
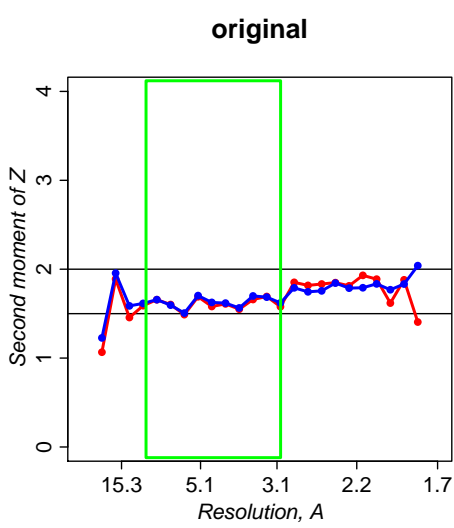
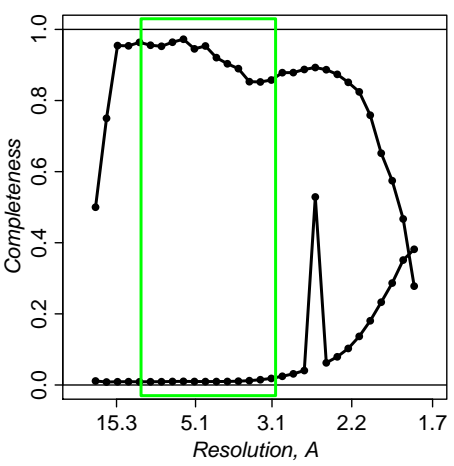
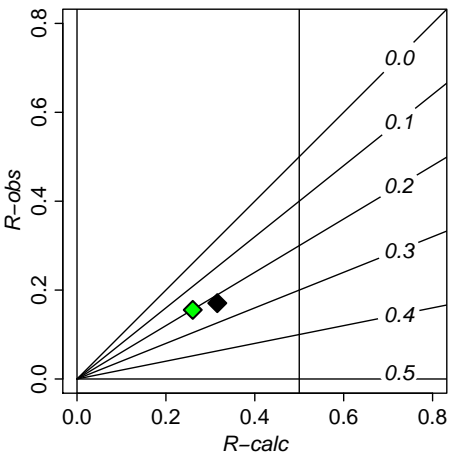
NCS	translation	rotation
r.m.s.d. (A)	1.31	0.24
angle (o)	5.23	0.94



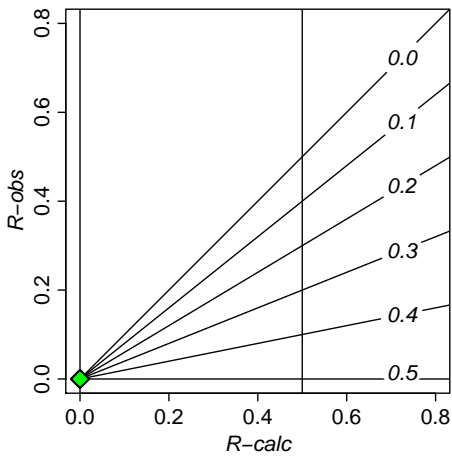
1qth

	original	merged
s.g.	P 31	-
p.g.	10020	10023
a.u.	2	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	26.7	-
R'	-	-
R-free	32.1	-
R'-free	-	-
residues per monomer	DNA 0	protein 162

s < f/100	3063	12.90 %
s <= 0	0	0.00 %
f <= 0	1	0.00 %
s,f <= 0	0	0.00 %
range (A)	46.4-1.8	9.9-3.0
unique	32,246	6,374
measured	23,736	5,724
used	17,712	4,496
NCS	translation	rotation
r.m.s.d. (A)	17.16	20.81
angle (o)	82.21	129.15



1qu7



	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	2	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	37.8	-
R'-free	50.1	-
R'-free	-	-

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	1433	14.55 %
s,f <= 0	0	0.00 %

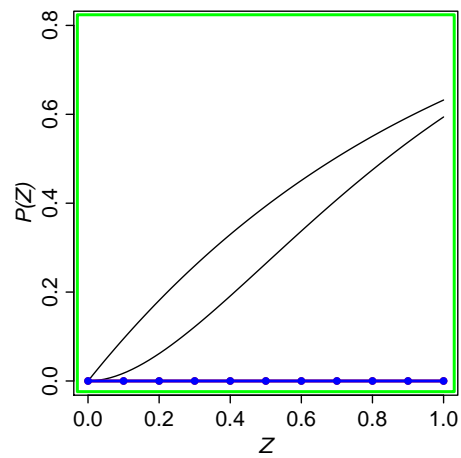
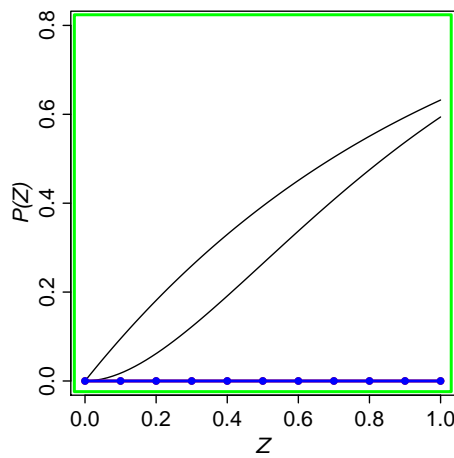
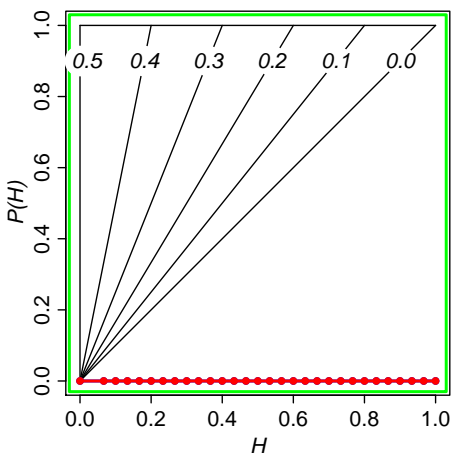
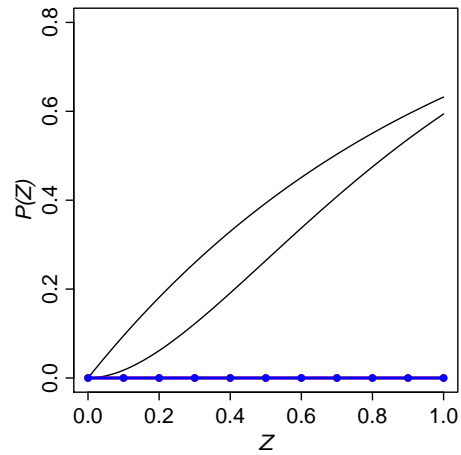
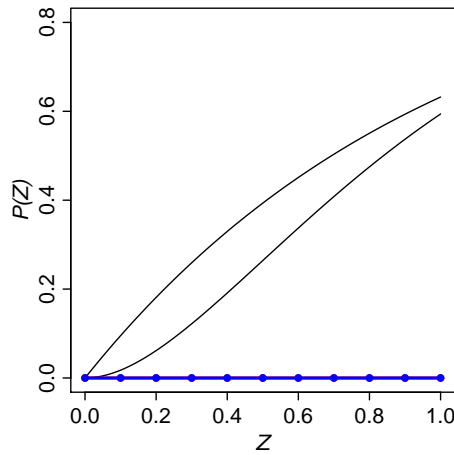
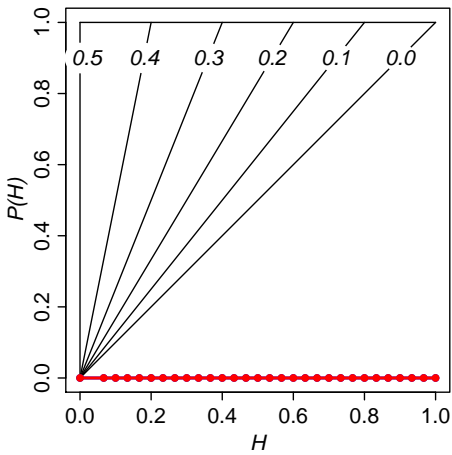
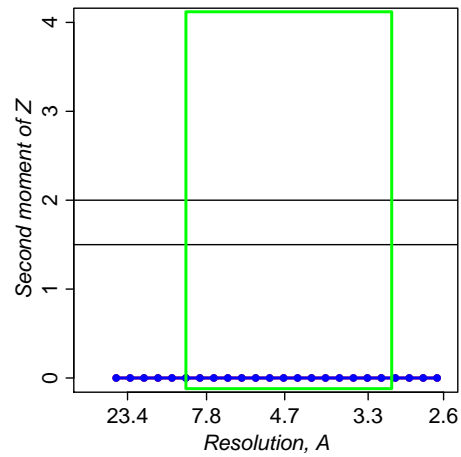
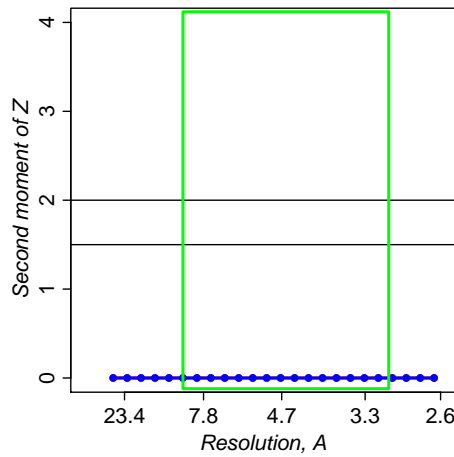
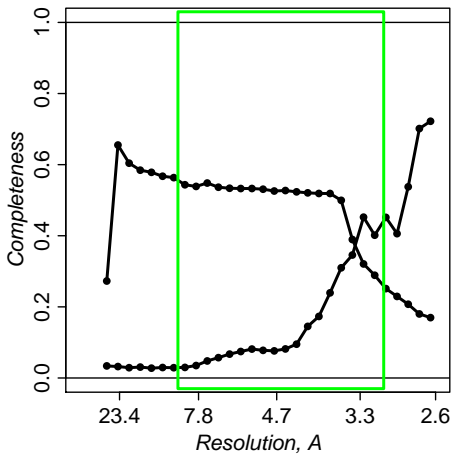
range (A)	43.6-2.6	9.9-3.0
unique	27,170	17,122
measured	9,849	7,681
used	0	0

NCS	translation	rotation
r.m.s.d. (A)	15.88	101.51
angle (o)	42.95	162.24

residues per monomer	DNA	protein
	0	221

original

merged



1qy7

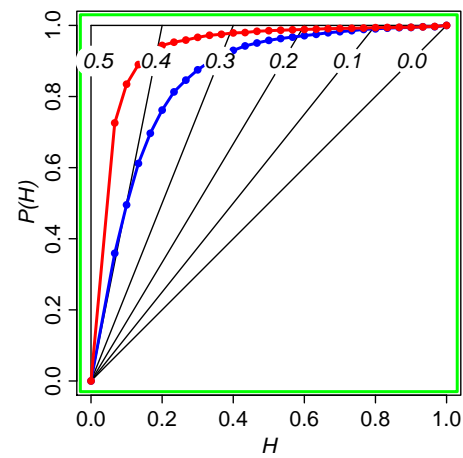
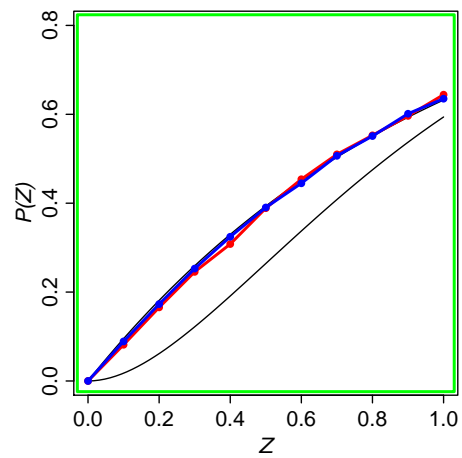
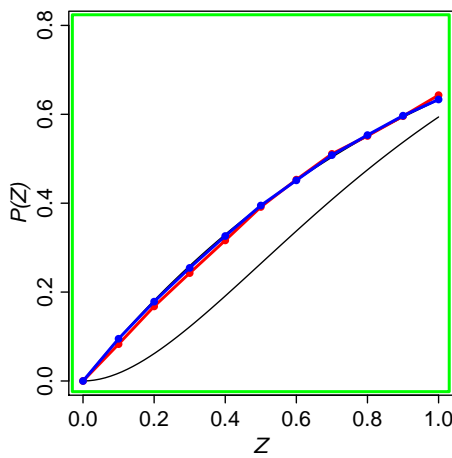
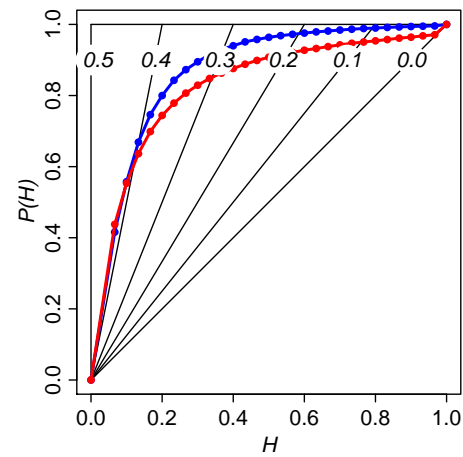
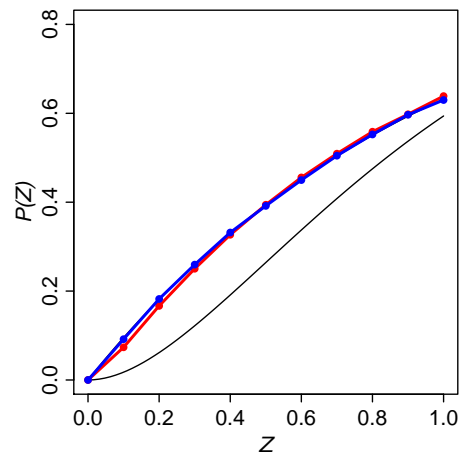
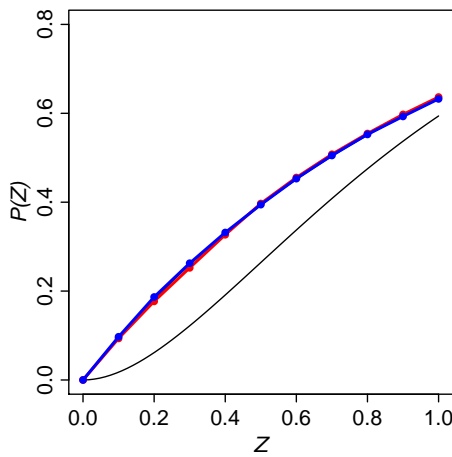
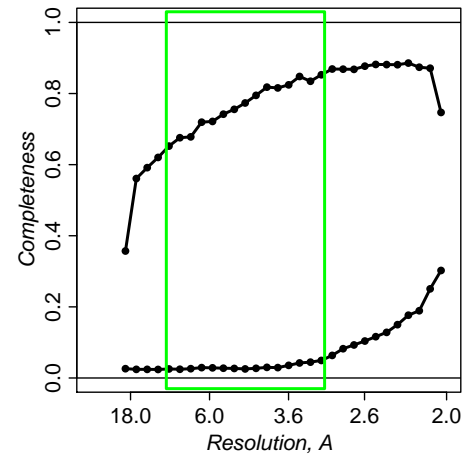
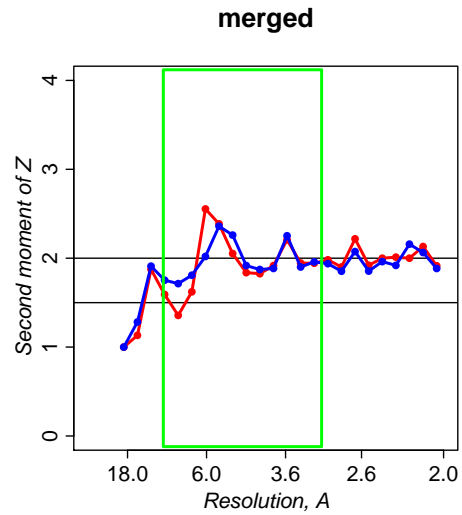
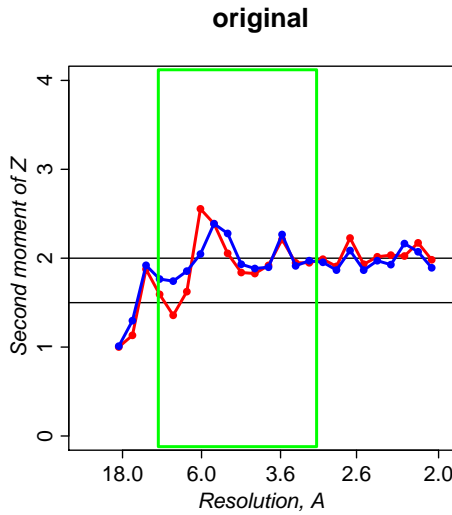
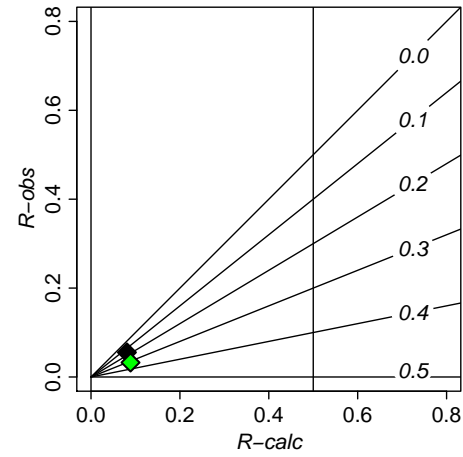
	original	merged
s.g.	1 41 2 2	1 41 3 2
p.g.	10205	10689
a.u.	3	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.01
R	25.0	
R'	24.9	25.1
R-free	26.1	
R'-free	25.9	25.7

residues per monomer	DNA	protein
	0	112

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	348	1.81 %
s,f <= 0	0	0.00 %

range (A)	24.5–2.0	9.9–3.0
unique	22,913	6,766
measured	19,247	5,426
used	13,626	3,627

NCS	translation	rotation
r.m.s.d. (A)	13.83	0.01
angle (o)	90.00	0.02



1qzw

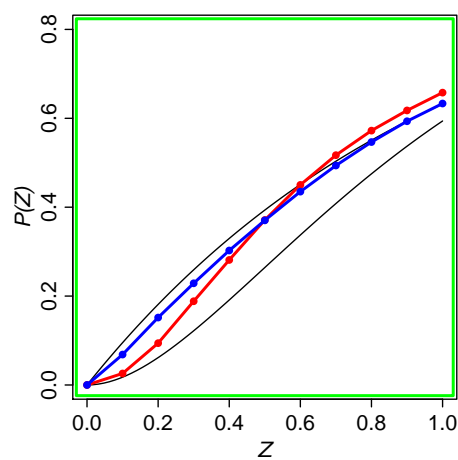
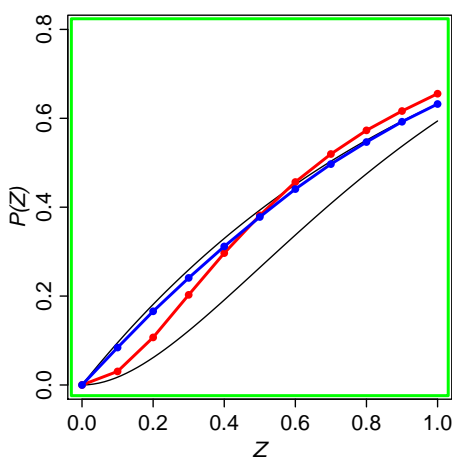
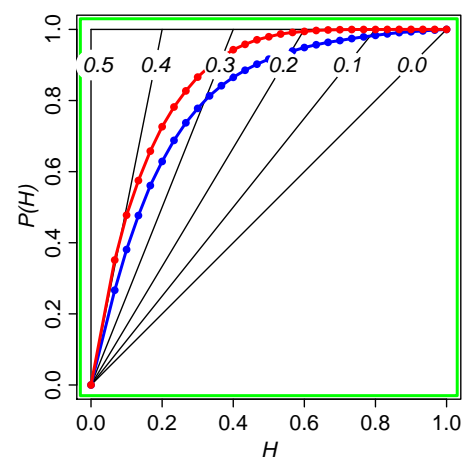
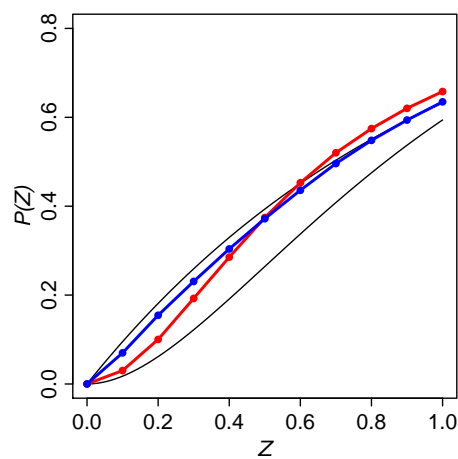
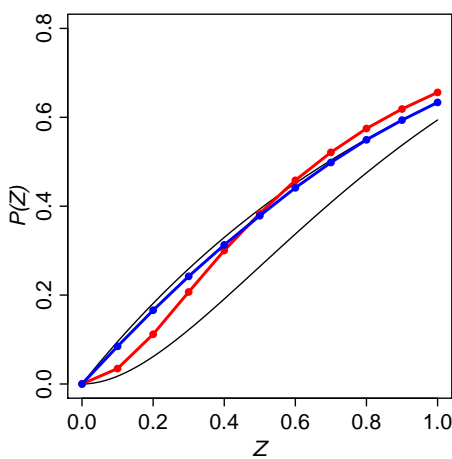
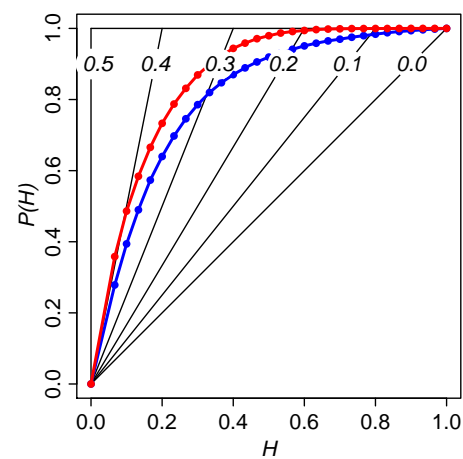
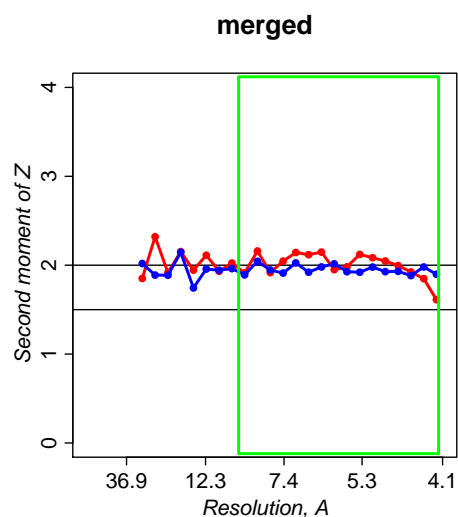
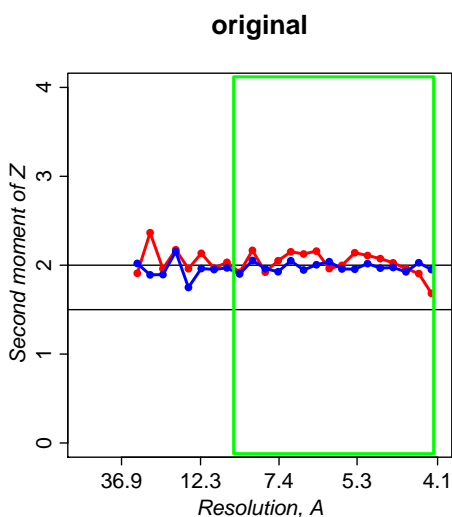
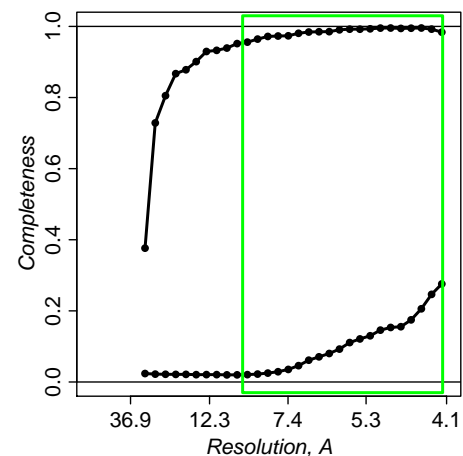
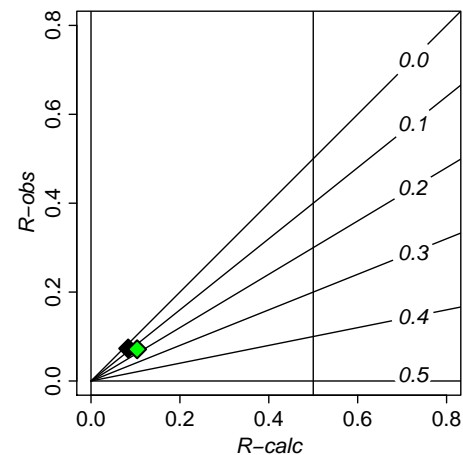
	original	merged
s.g.	P 31	P 31 1 2
p.g.	10020	10023
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.37
R	31.0	
R'	31.0	31.0
R-free	36.7	
R'-free	36.6	36.5

s < f/100	11	0.02 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.8–4.1	9.9–4.1
unique	51,325	47,814
measured	50,404	47,259
used	47,820	45,166

NCS	translation	rotation
r.m.s.d. (A)	26.31	0.23
angle (o)	59.60	0.53

residues per monomer	DNA	protein
	45	432



1qzx

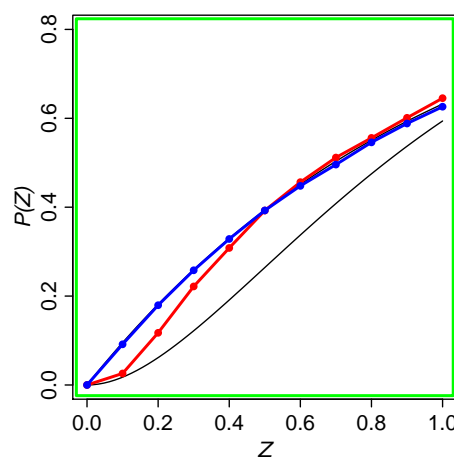
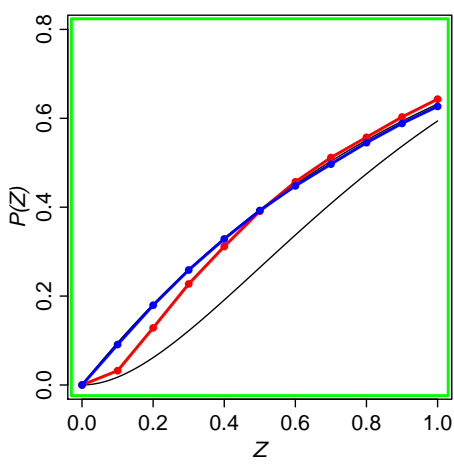
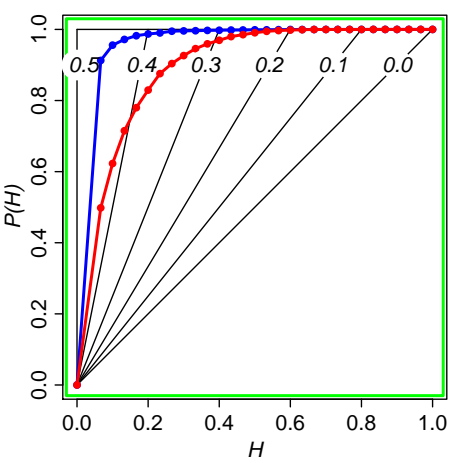
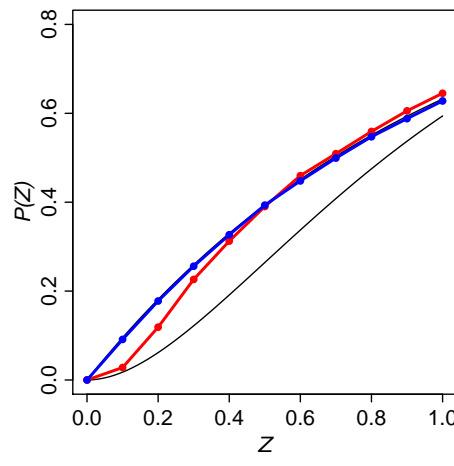
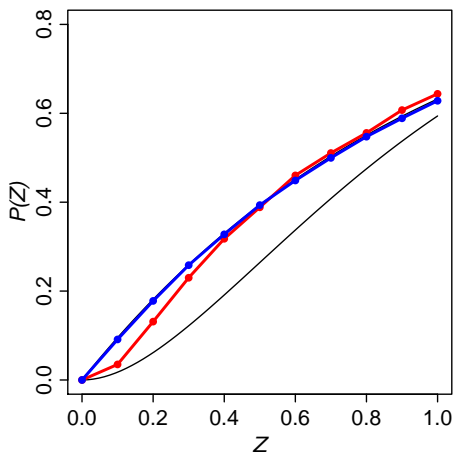
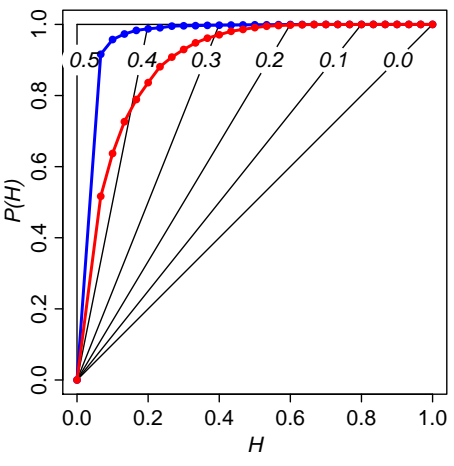
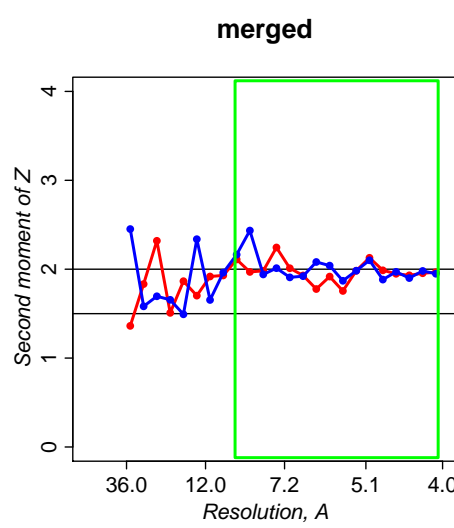
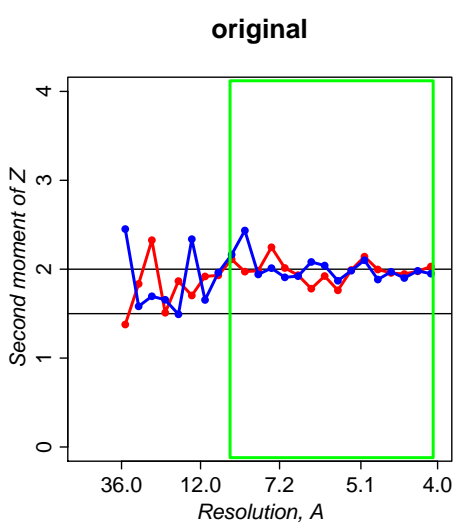
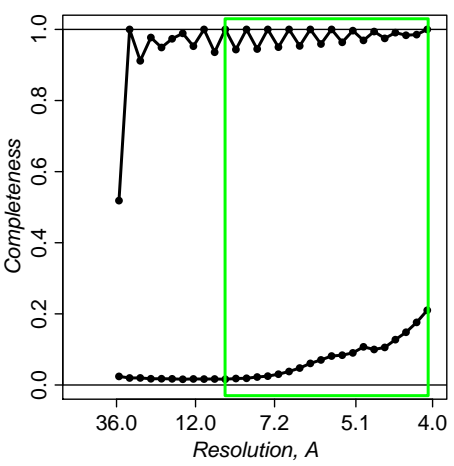
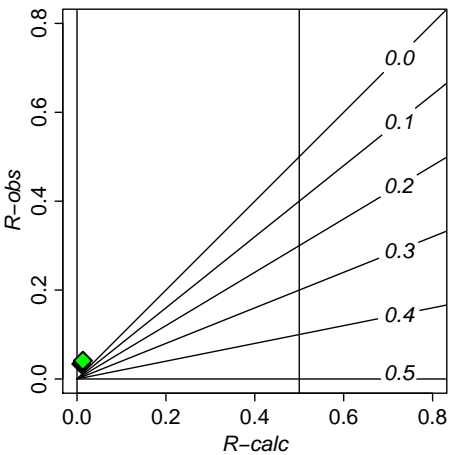
	original	merged
s.g.	14	14 2 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.03
R	28.3	
R'	28.2	29.7
R-free	40.6	
R'-free	40.4	42.0

s < f/100	111	1.05 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	38.8–4.0	9.9–4.0
unique	10,746	10,000
measured	10,545	9,828
used	9,140	8,632

NCS	translation	rotation
r.m.s.d. (A)	46.48	0.03
angle (o)	179.98	0.07

residues per monomer	DNA	protein
	0	425



1r19

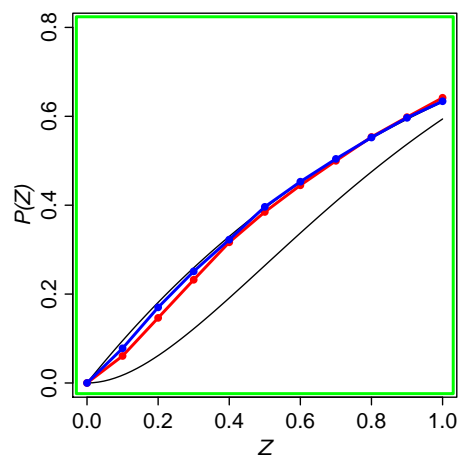
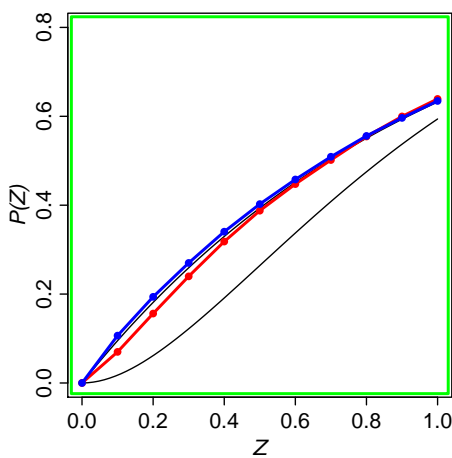
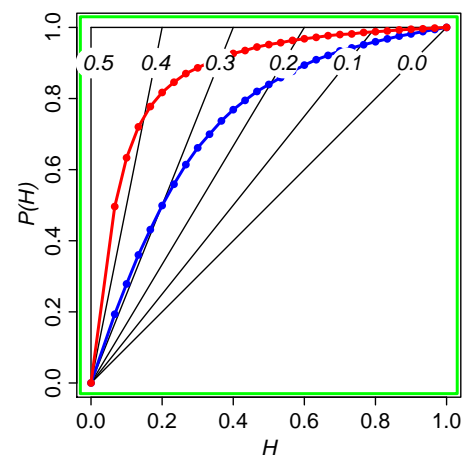
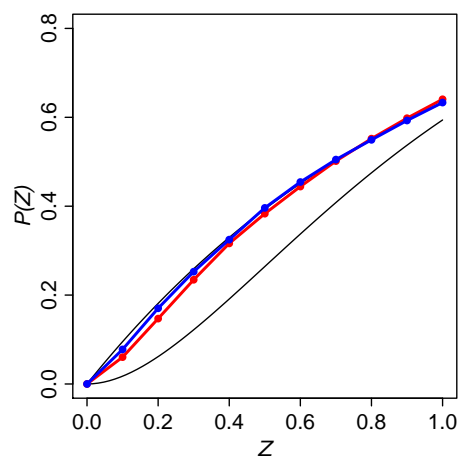
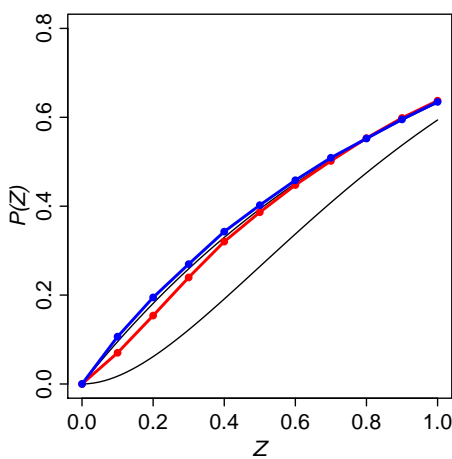
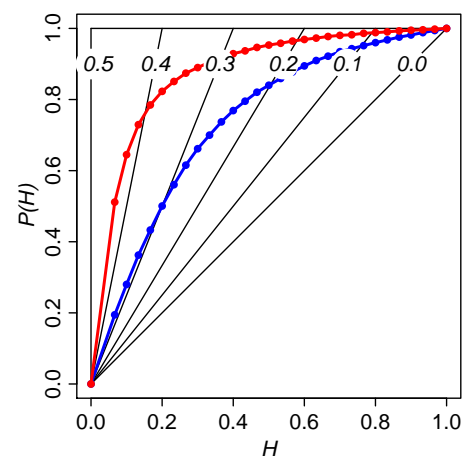
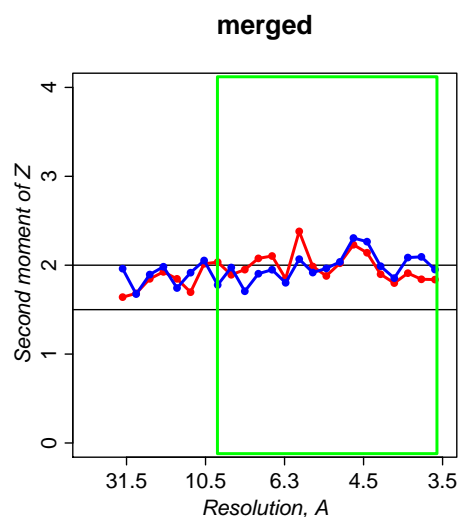
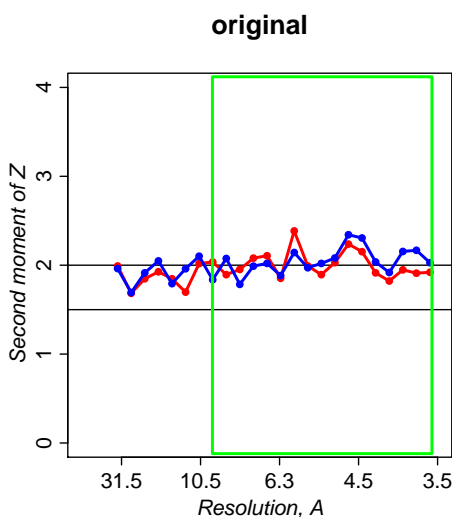
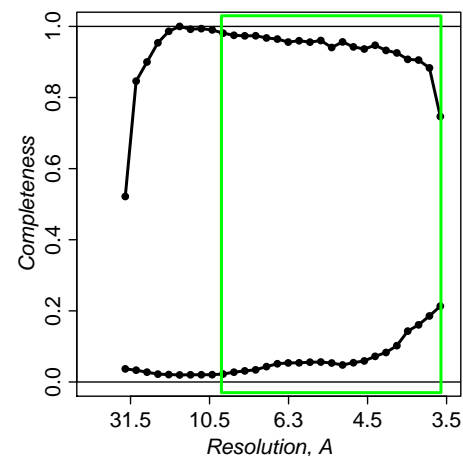
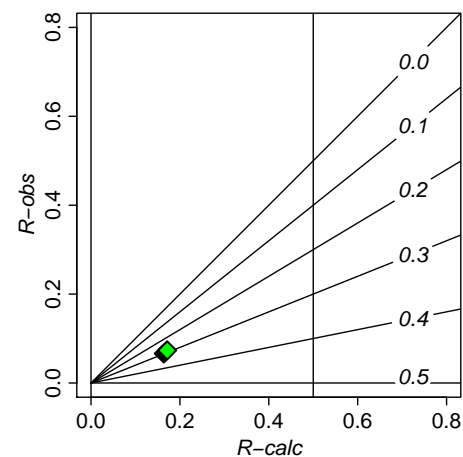
	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.28
R	27.0	
R'	27.0	27.8
R-free	35.0	
R'-free	35.2	36.2

s < f/100	728	4.37 %
s <= 0	728	4.37 %
f <= 0	728	4.37 %
s,f <= 0	728	4.37 %

range (A)	43.2–3.5	9.9–3.5
unique	18,103	17,297
measured	16,651	15,867
used	14,902	14,244

NCS	translation	rotation
r.m.s.d. (A)	18.94	0.25
angle (o)	99.08	0.08

residues per monomer	DNA	protein
	0	274



1r2j

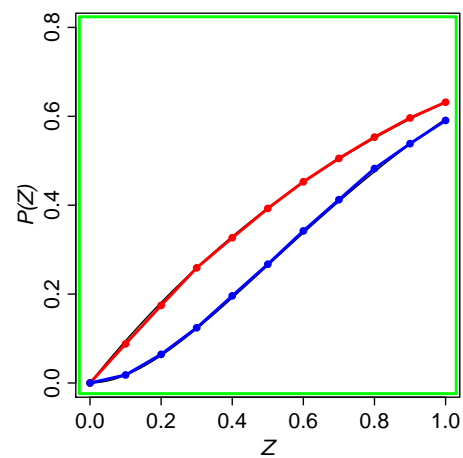
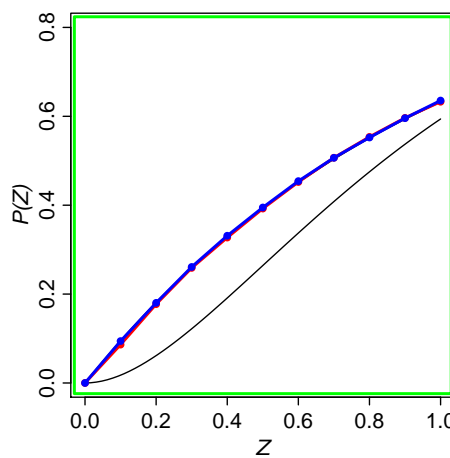
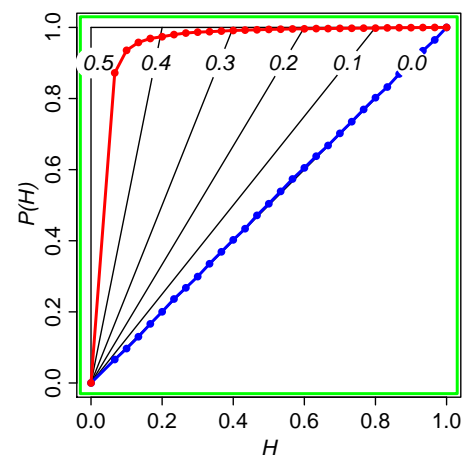
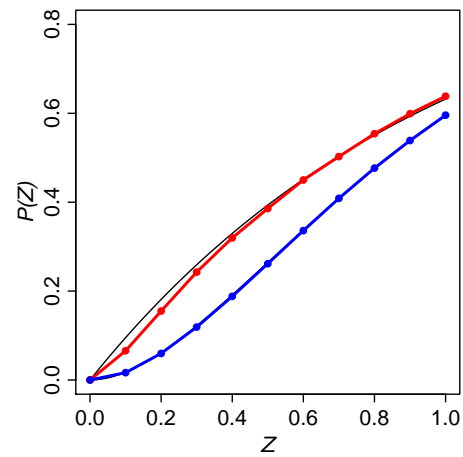
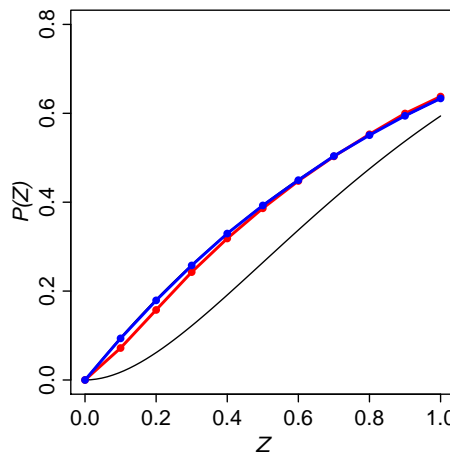
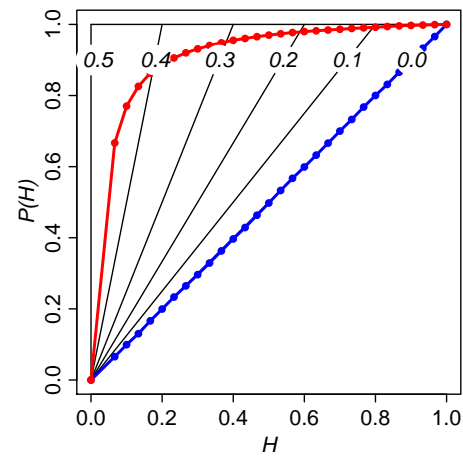
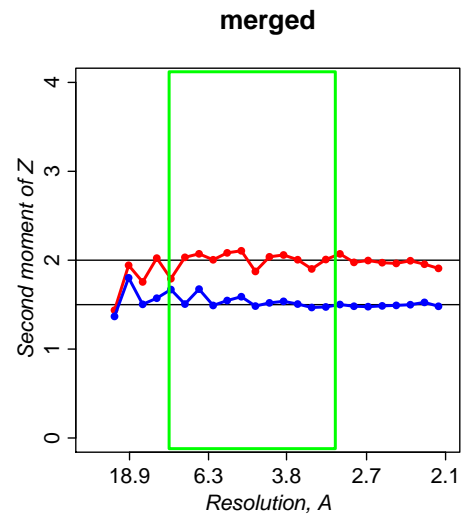
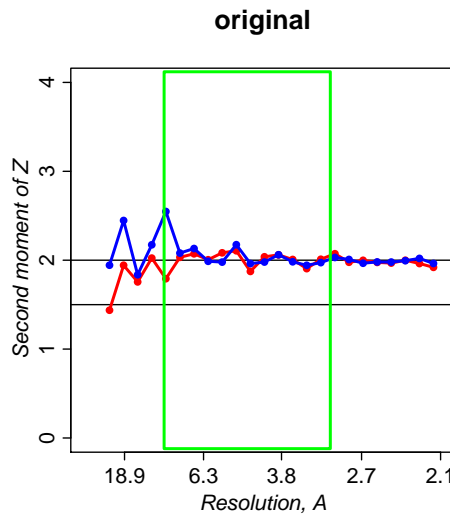
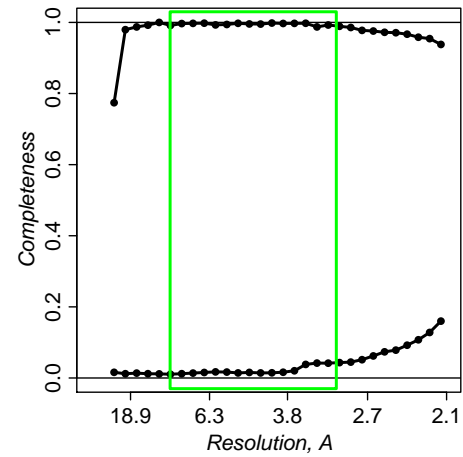
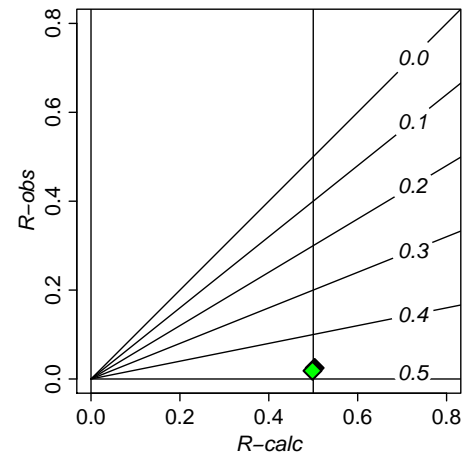
	original	merged
s.g.	141	-
p.g.	10201	10205
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	43.2	-
R'	-	-
R-free	46.7	-
R'-free	-	-

residues per monomer	DNA	protein
	0	353

s < f/100	2675	5.59 %
s <= 0	1199	2.51 %
f <= 0	1199	2.51 %
s,f <= 0	1199	2.51 %

range (A)	42.8-2.1	9.9-3.0
unique	49,075	16,429
measured	47,859	16,338
used	43,934	14,838

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1r52

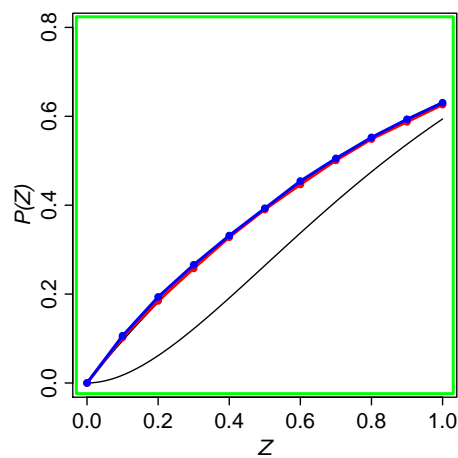
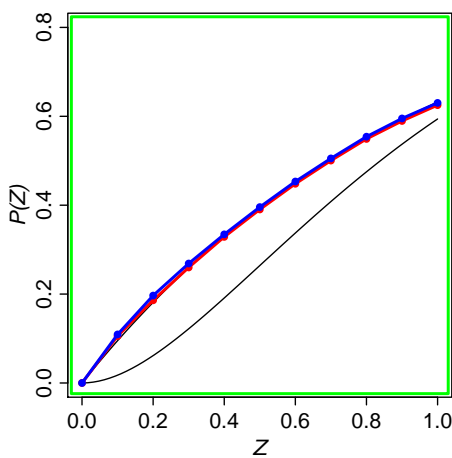
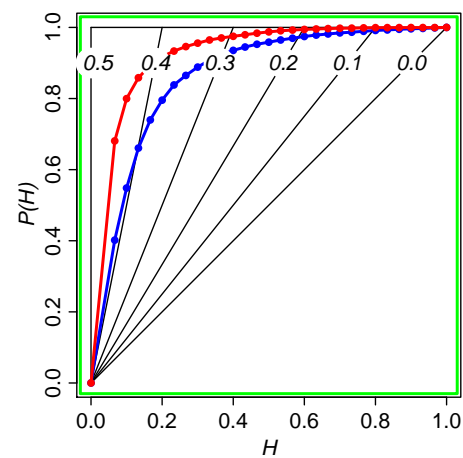
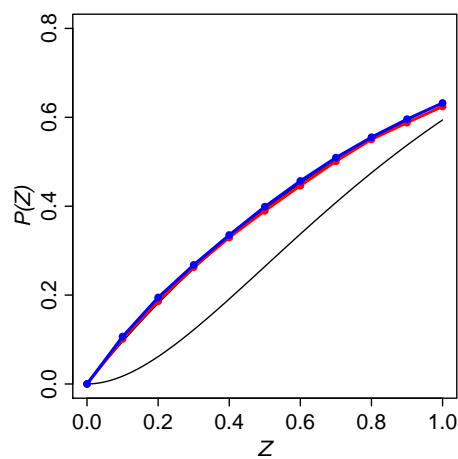
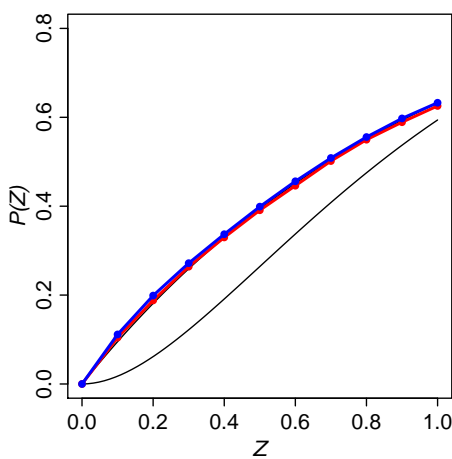
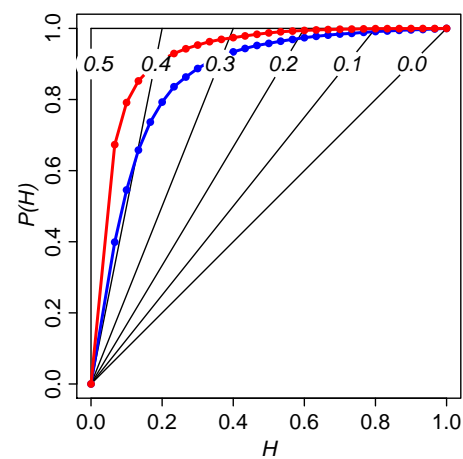
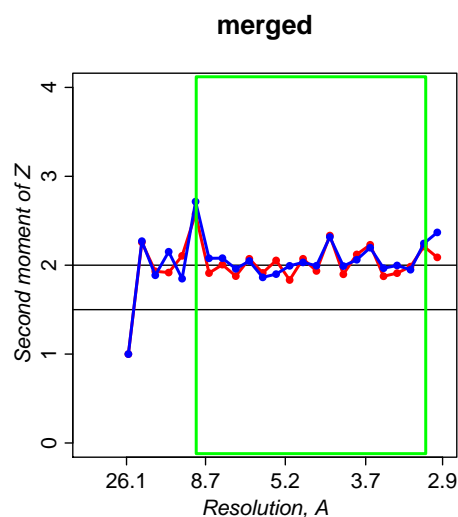
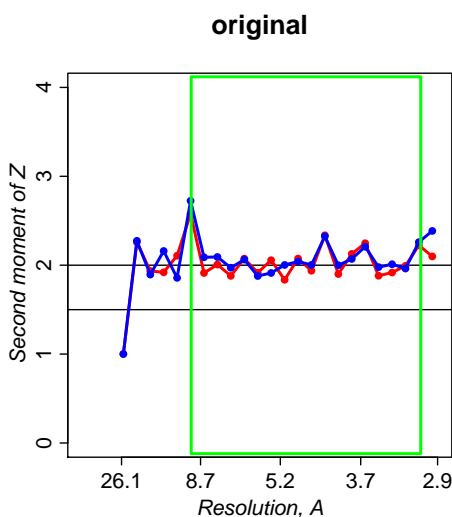
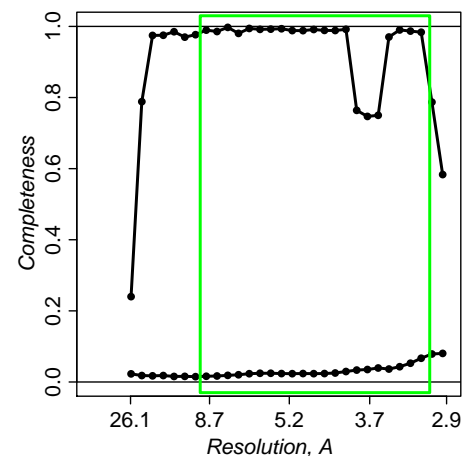
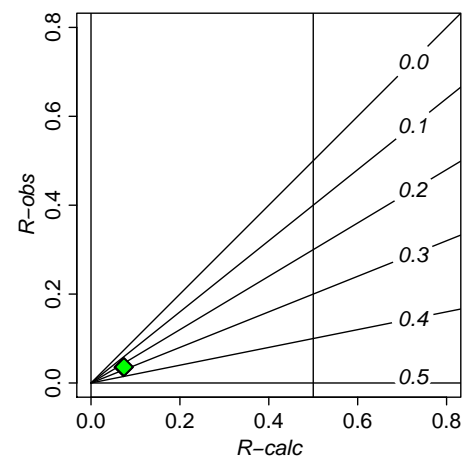
	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	4	2
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.05
R	19.7	
R'	19.8	20.3
R-free	25.8	
R'-free	26.0	26.5

s < f/100	26	0.10 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	29.7–2.9	9.9–3.0
unique	29,599	25,705
measured	26,514	23,904
used	23,982	22,294

NCS	translation	rotation
r.m.s.d. (A)	27.59	0.05
angle (o)	179.96	0.04

residues per monomer	DNA	protein
	0	281



1r8h

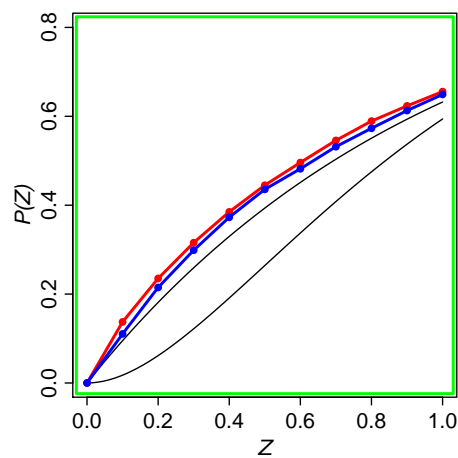
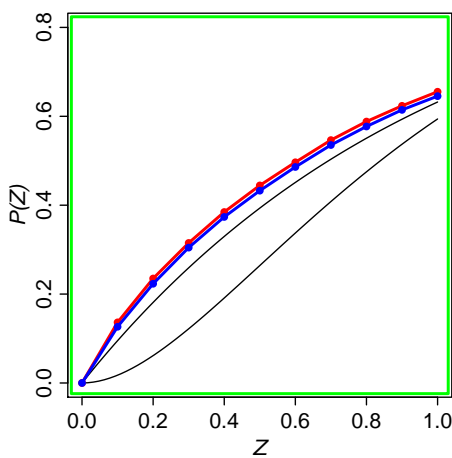
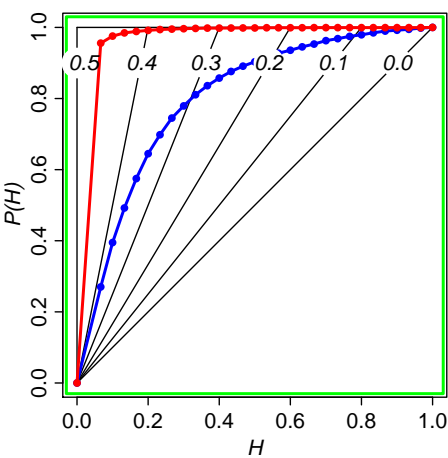
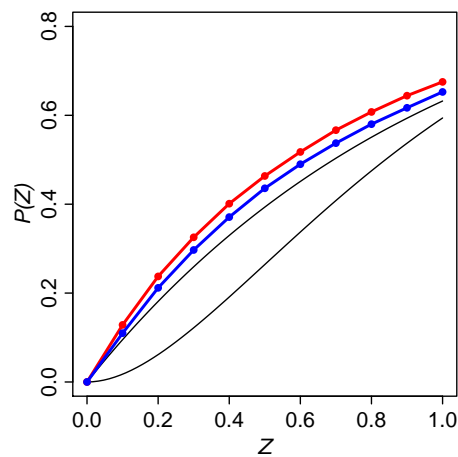
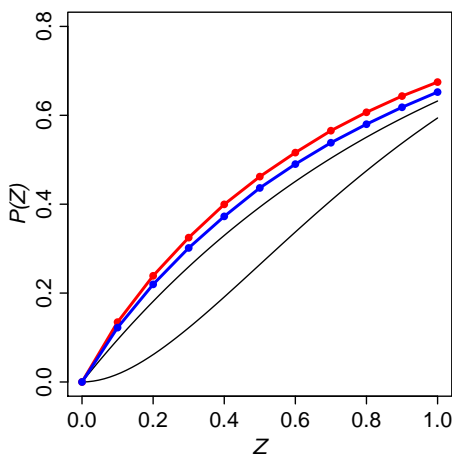
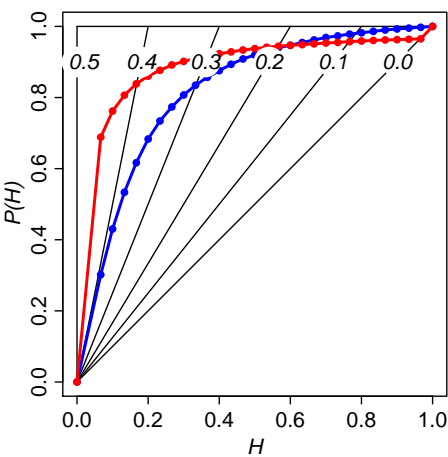
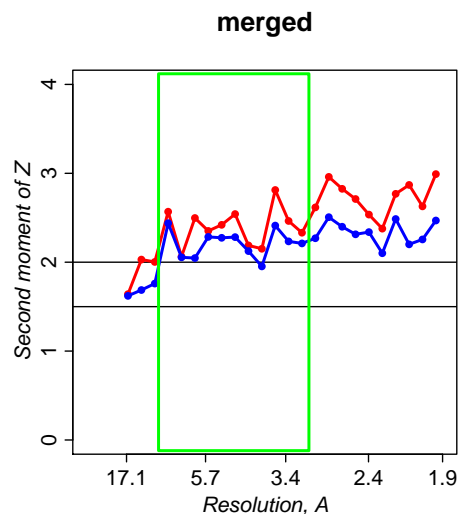
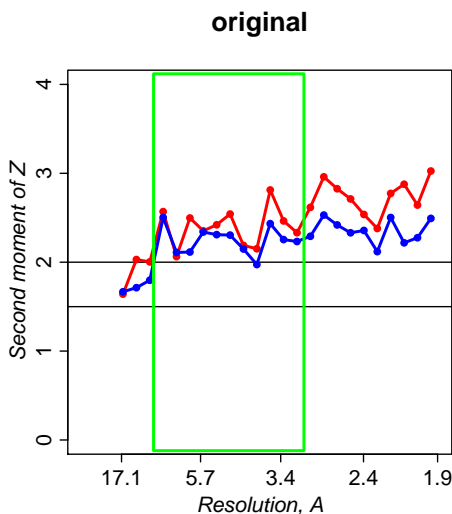
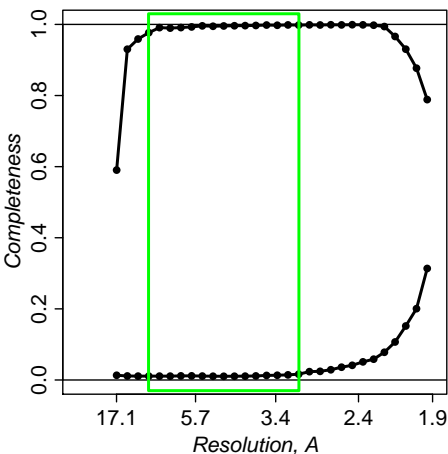
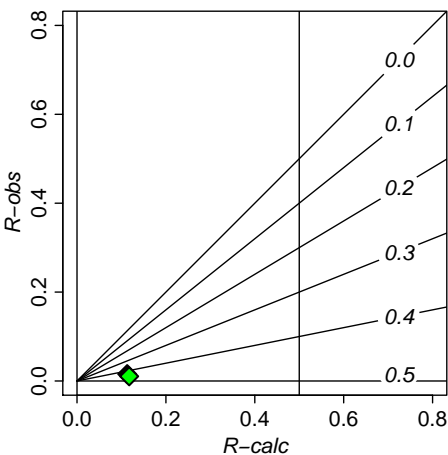
	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.12
R	28.0	
R'	28.3	29.7
R-free	29.3	
R'-free	29.4	30.7

s < f/100	4059	9.52 %
s <= 0	0	0.00 %
f <= 0	1168	2.74 %
s,f <= 0	0	0.00 %

range (A)	19.7–1.9	9.9–3.0
unique	44,331	11,041
measured	42,648	10,999
used	37,400	9,310

NCS	translation	rotation
r.m.s.d. (A)	0.45	0.09
angle (o)	0.77	0.12

residues per monomer	DNA	protein
	0	83



1rjf

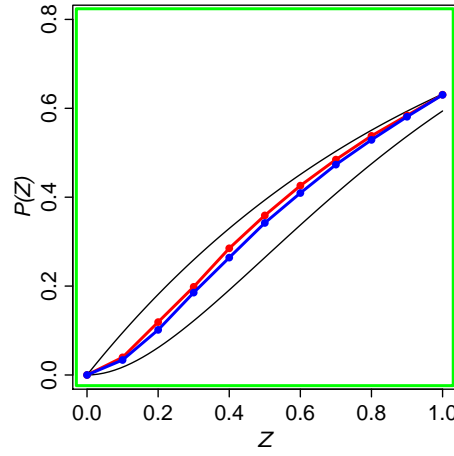
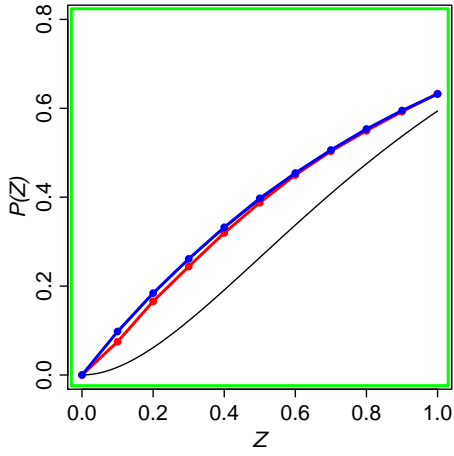
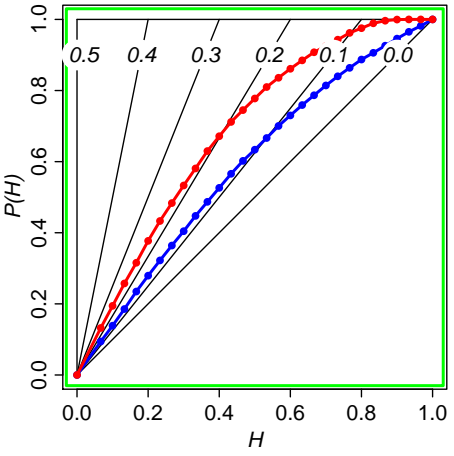
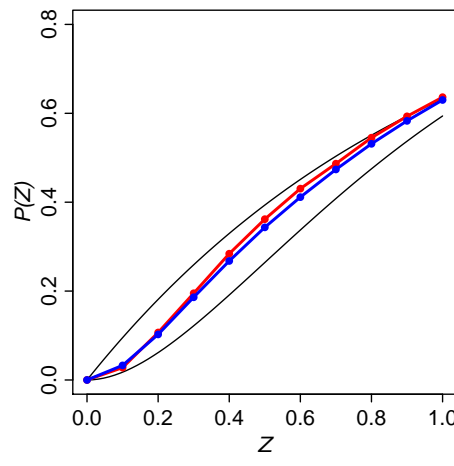
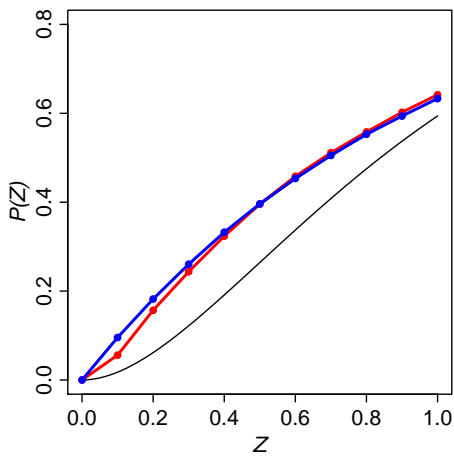
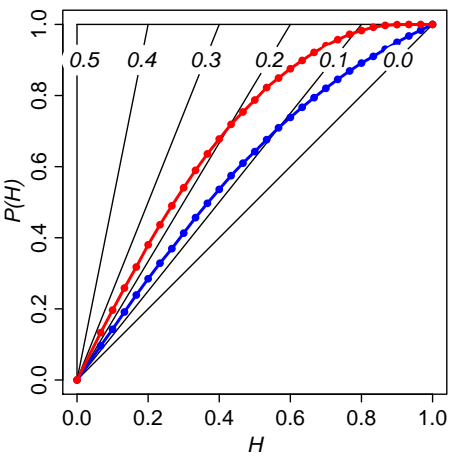
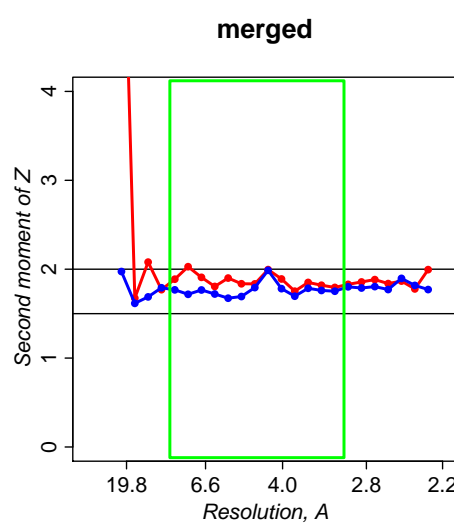
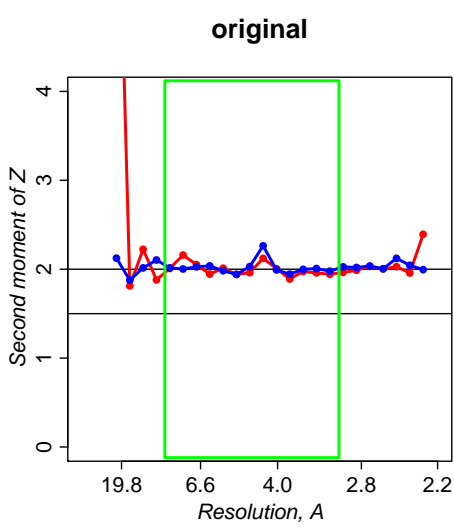
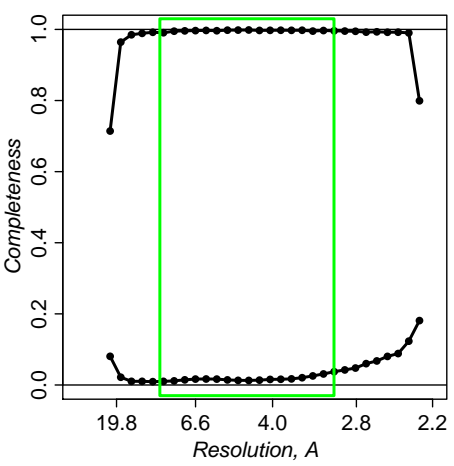
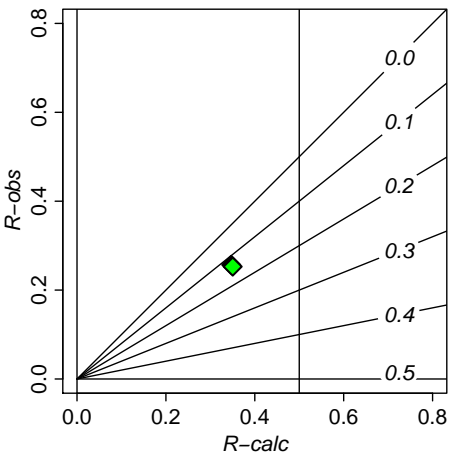
	original	merged
s.g.	P 65	-
p.g.	12021	12027
a.u.	3	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	23.9	-
R'	-	-
R-free	26.6	-
R'-free	-	-

residues per monomer	DNA	protein
	0	321

s < f/100	5244	9.73 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	28.2-2.2	9.9-3.0
unique	55,107	22,720
measured	53,873	22,648
used	49,124	20,172

NCS	translation	rotation
r.m.s.d. (A)	5.46	0.34
angle (o)	20.51	0.55



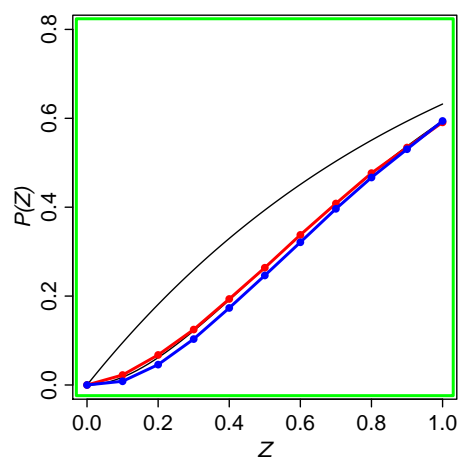
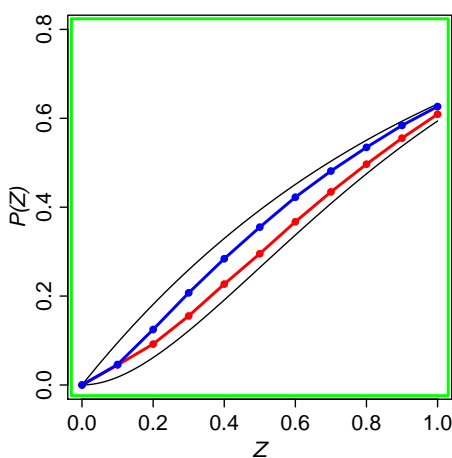
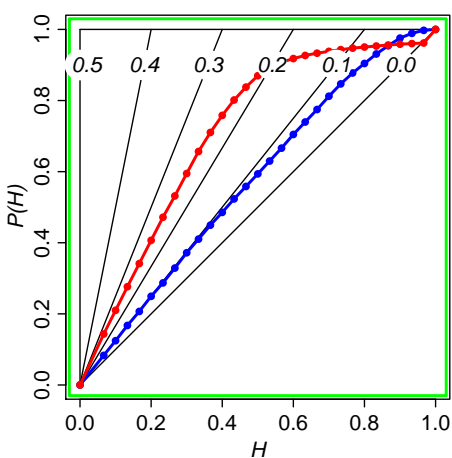
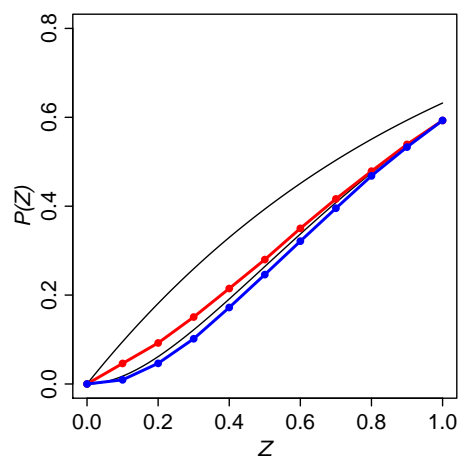
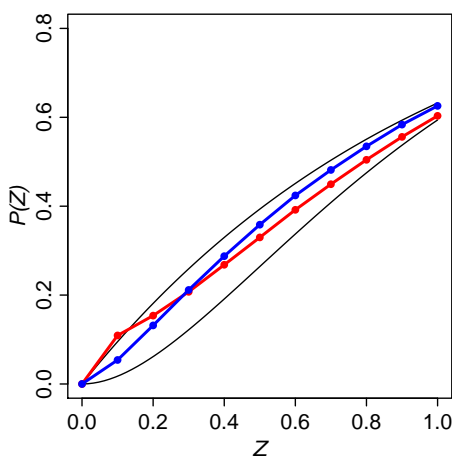
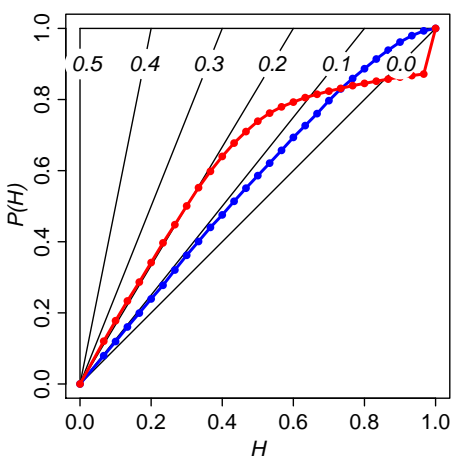
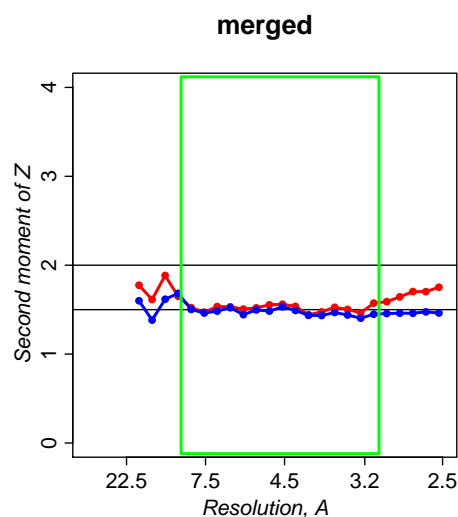
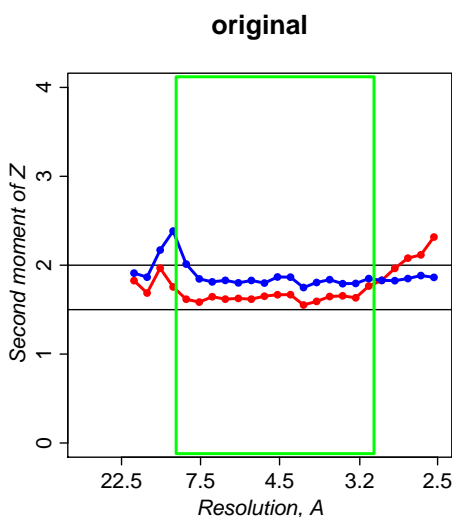
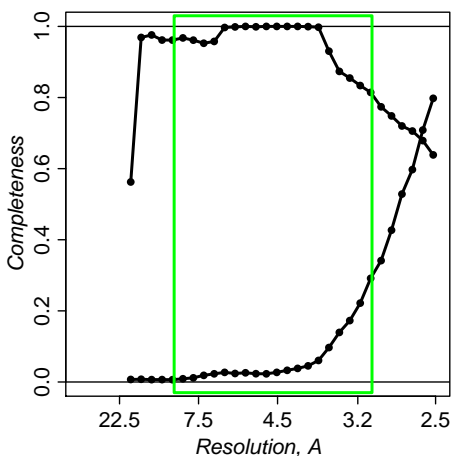
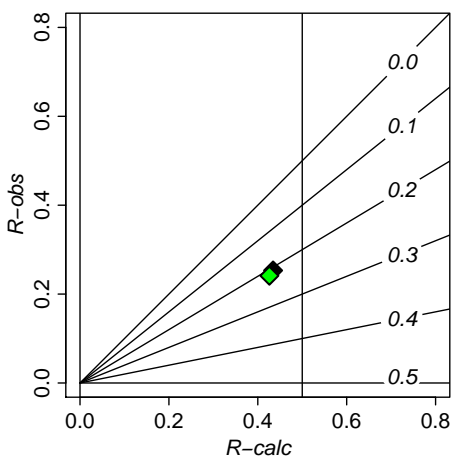
1rlid

	original	merged
s.g.	14	14 2 2
p.g.	10201	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		4.94
R	23.2	
R'	-	-
R-free	28.3	
R'-free	-	-
residues per monomer	DNA 0	protein 564

s < f/100	1968	5.10 %
s <= 0	0	0.00 %
f <= 0	3405	8.83 %
s,f <= 0	0	0.00 %

range (A)	19.5–2.5	9.9–3.0
unique	46,271	25,495
measured	38,575	23,736
used	33,646	21,436

NCS	translation	rotation
r.m.s.d. (A)	43.98	2.22
angle (o)	179.98	7.67



1rpm

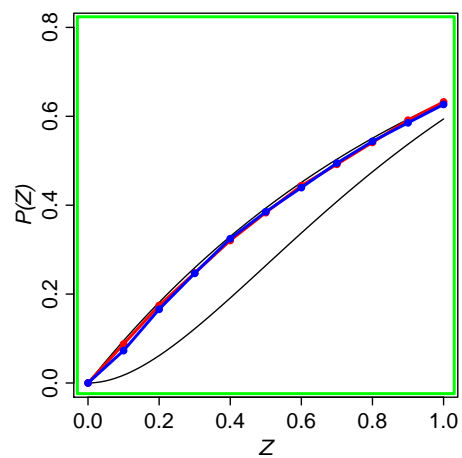
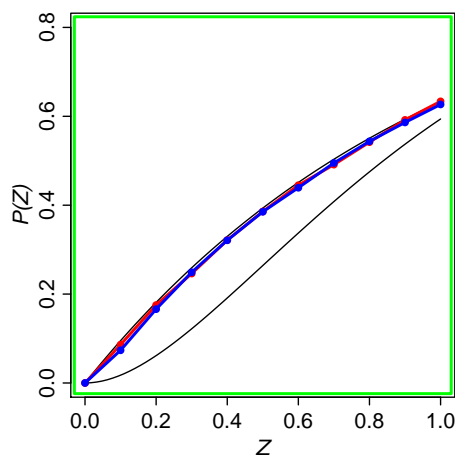
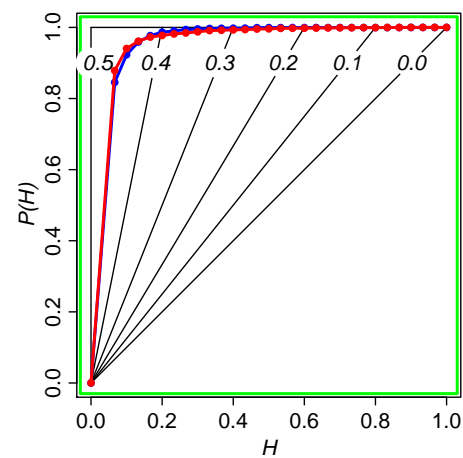
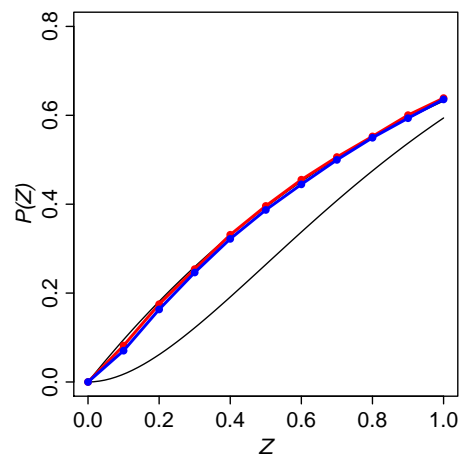
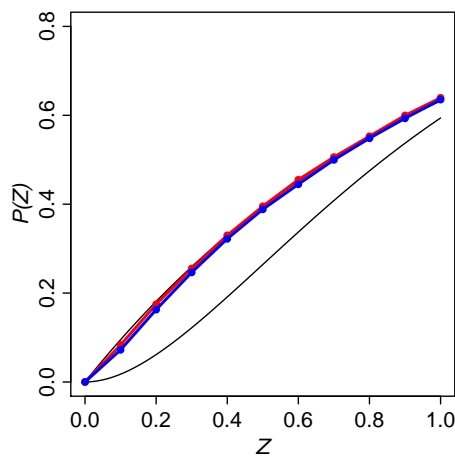
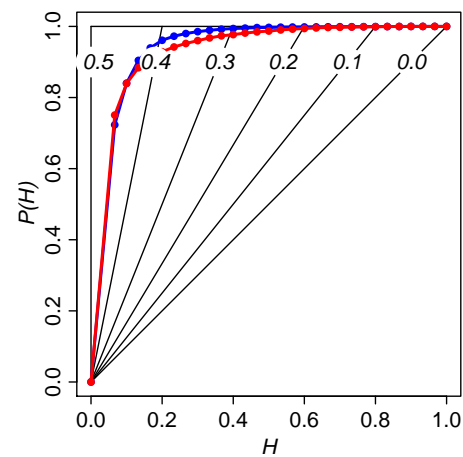
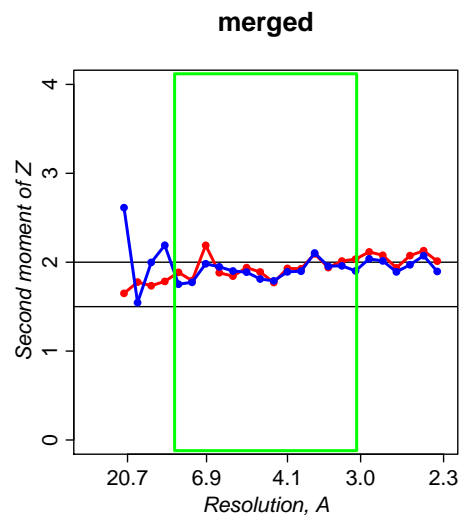
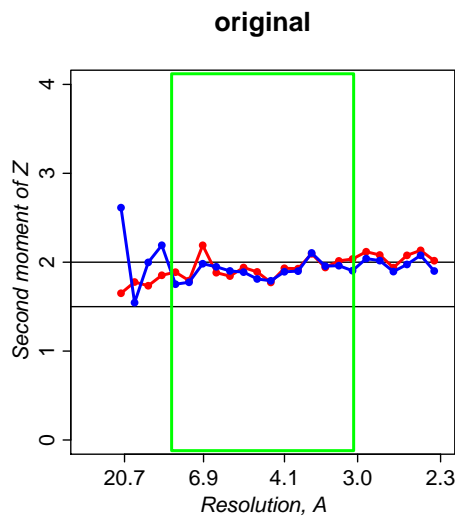
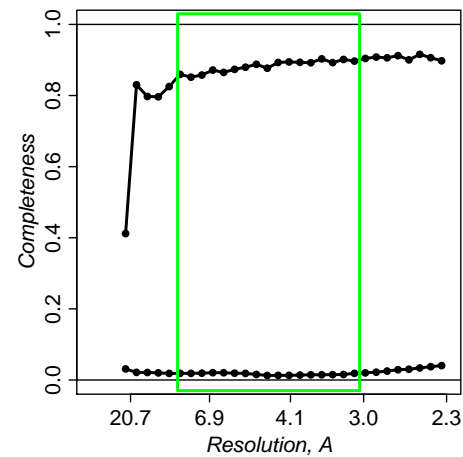
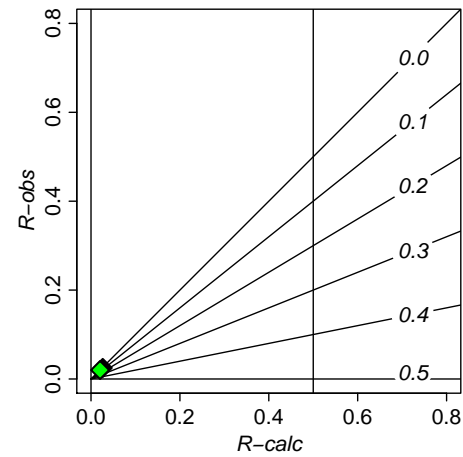
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.03
R	24.1	
R'	24.1	24.4
R-free	26.5	
R'-free	26.5	26.9

s < f/100	3016	11.28 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	28.1–2.3	9.9–3.0
unique	29,786	13,107
measured	26,737	11,655
used	22,310	9,470

NCS	translation	rotation
r.m.s.d. (A)	25.04	0.03
angle (o)	179.97	0.03

residues per monomer	DNA	protein
	0	278



1ru8

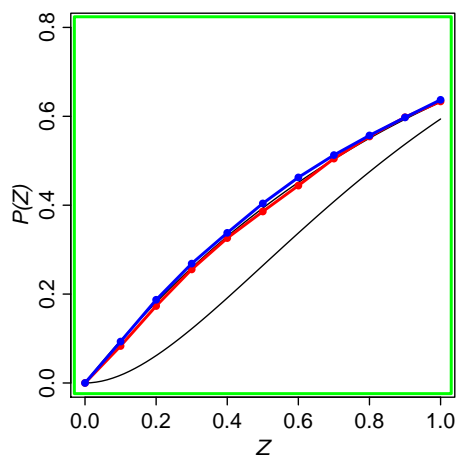
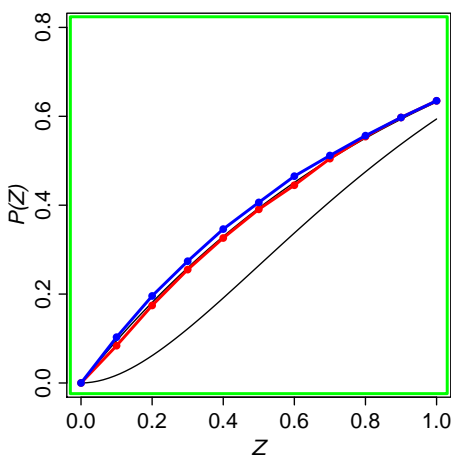
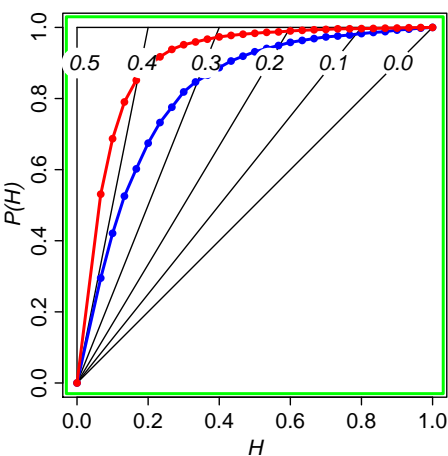
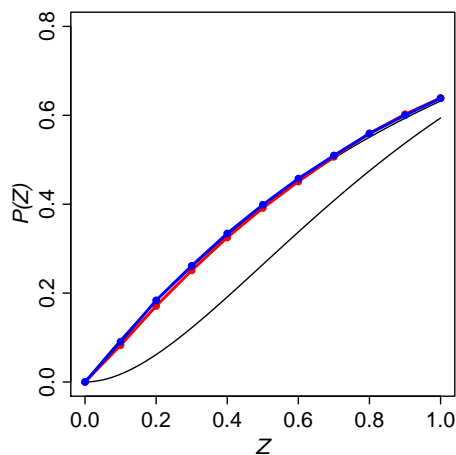
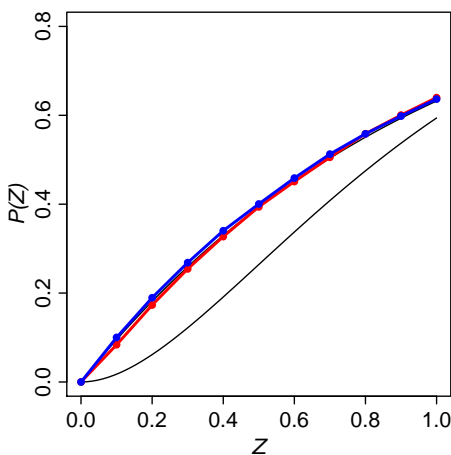
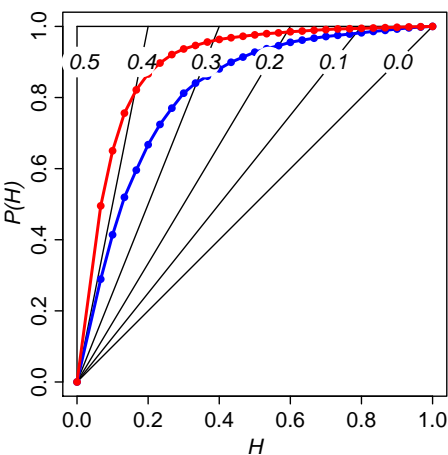
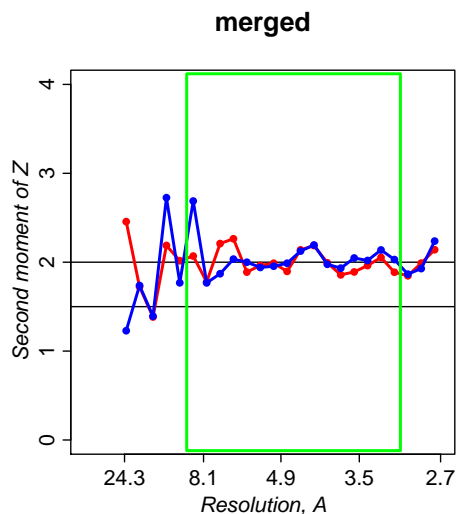
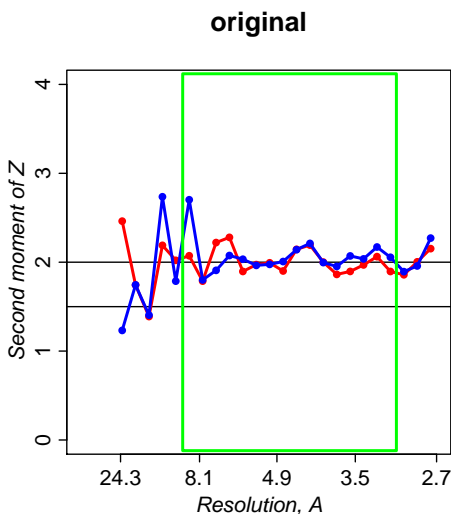
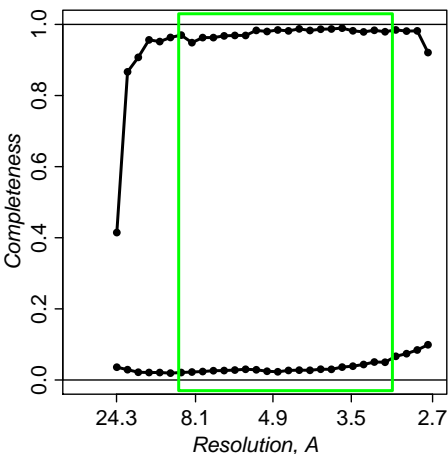
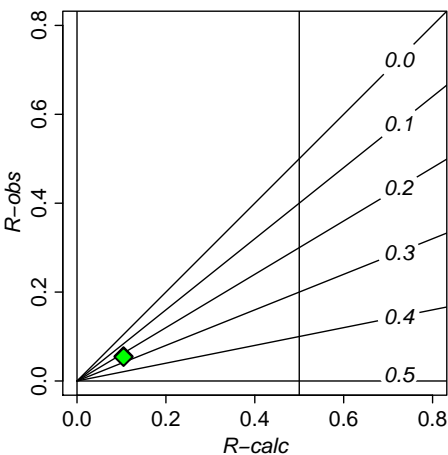
	original	merged
s.g.	P 21 21 21	P 41 21 2
p.g.	10003	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.01
R	25.5	
R'	25.5	25.9
R-free	30.2	
R'-free	30.2	30.4

s < f/100	184	1.22 %
s <= 0	184	1.22 %
f <= 0	184	1.22 %
s,f <= 0	184	1.22 %

range (A)	27.9–2.7	9.9–3.0
unique	15,495	10,946
measured	15,103	10,737
used	12,622	8,936

NCS	translation	rotation
r.m.s.d. (A)	20.26	0.01
angle (o)	89.99	0.02

residues per monomer	DNA	protein
	0	227



1rx1f

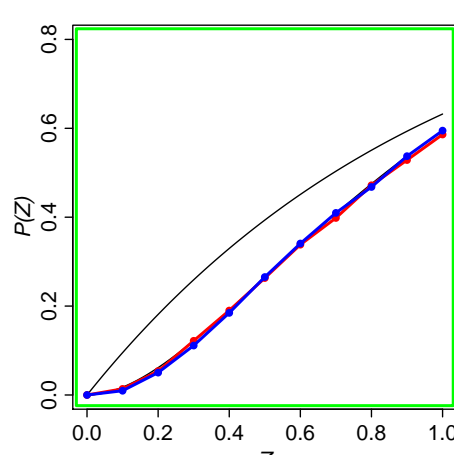
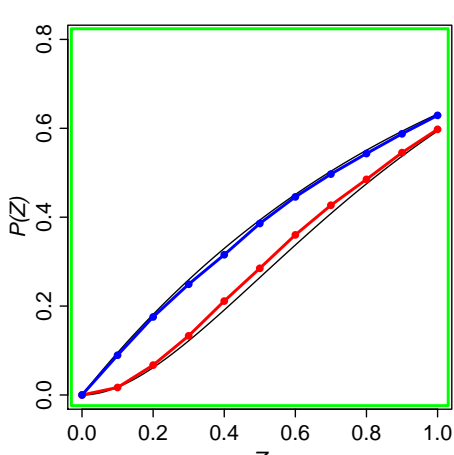
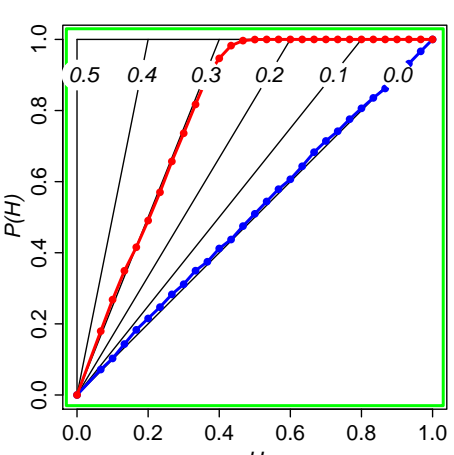
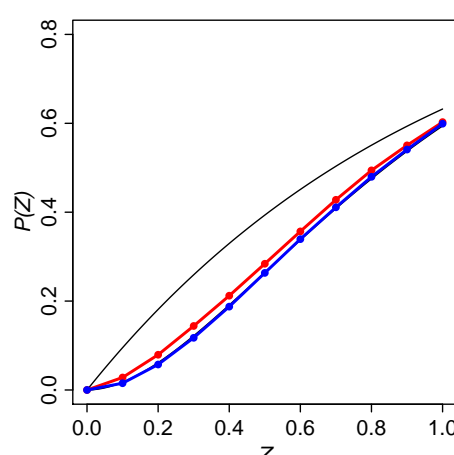
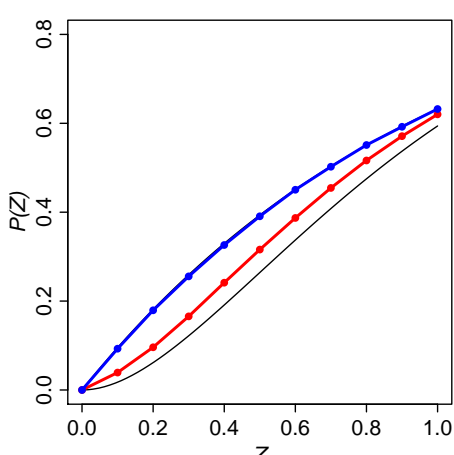
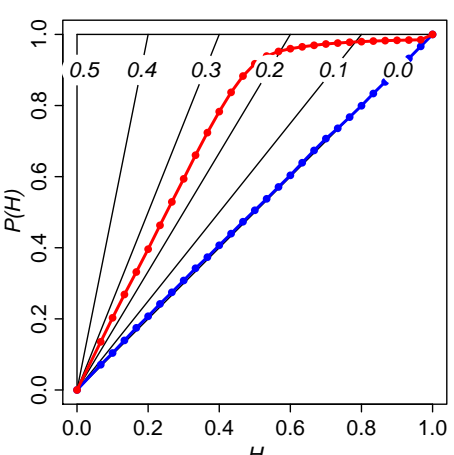
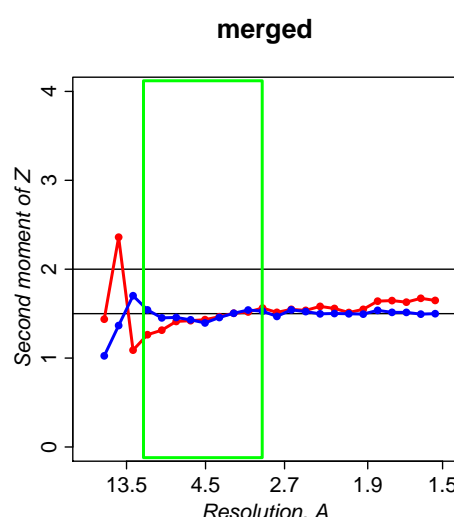
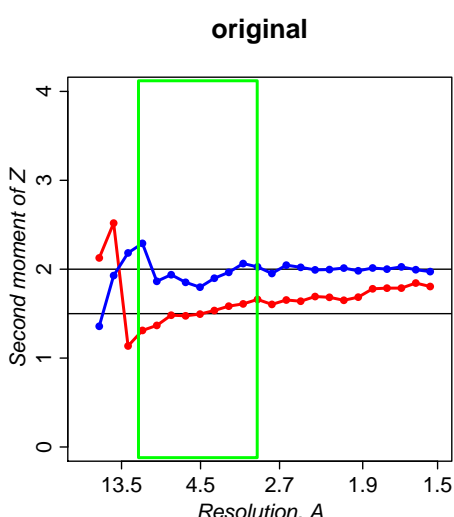
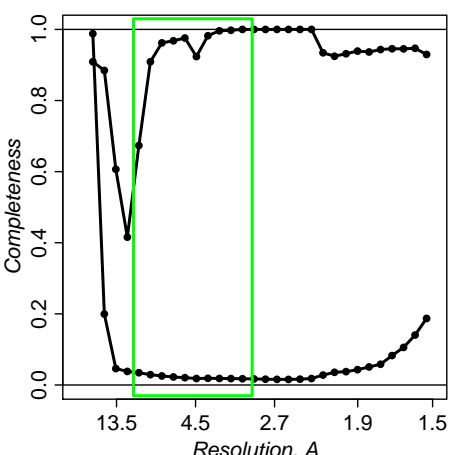
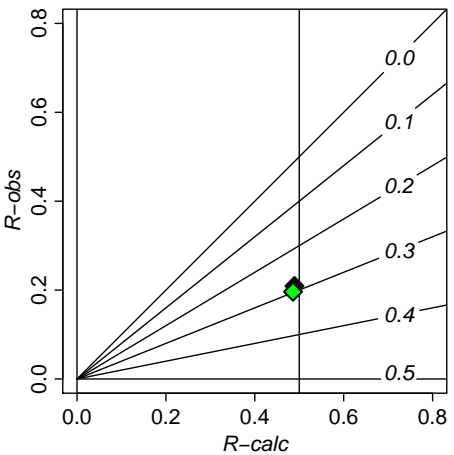
	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	28.4	-
R'	-	-
R-free	29.0	-
R'-free	-	-

residues per monomer	DNA	protein
	0	264

s < f/100	172	0.38 %
s <= 0	0	0.00 %
f <= 0	464	1.02 %
s,f <= 0	0	0.00 %

range (A)	53.0-1.5	9.9-3.0
unique	47,772	5,818
measured	45,509	5,653
used	42,634	5,238

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



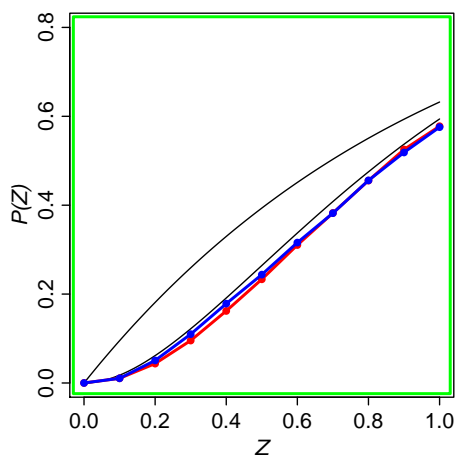
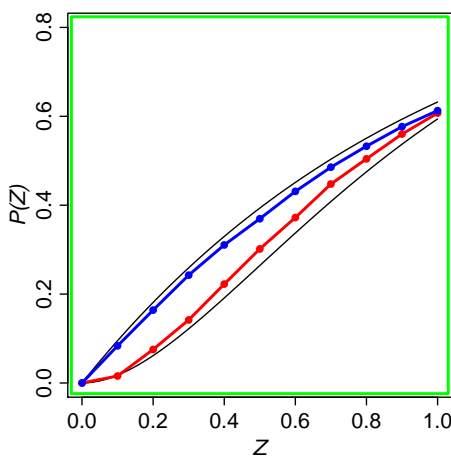
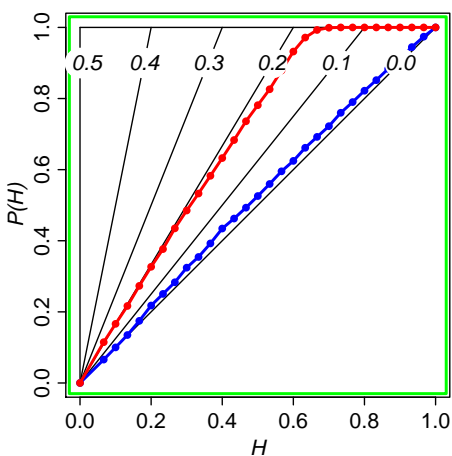
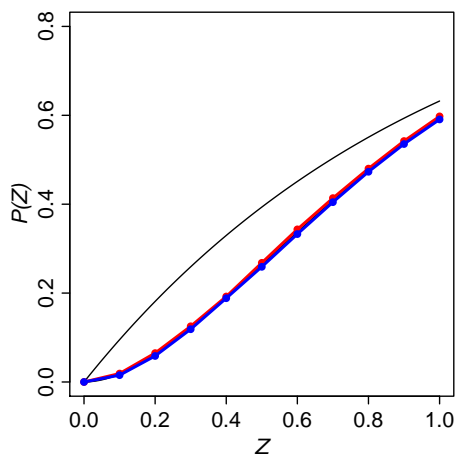
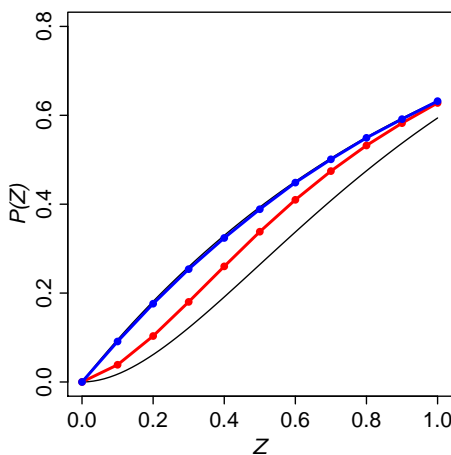
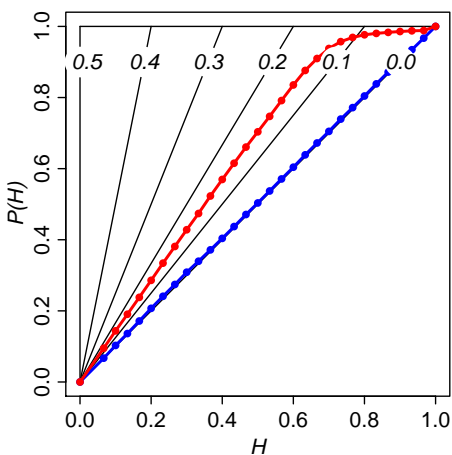
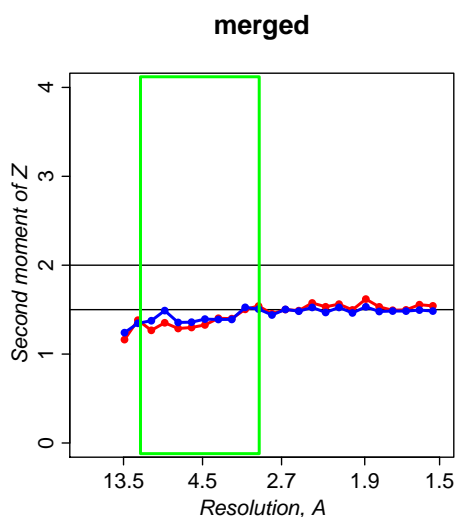
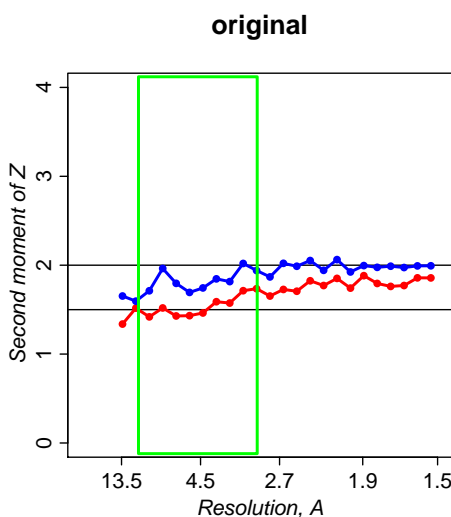
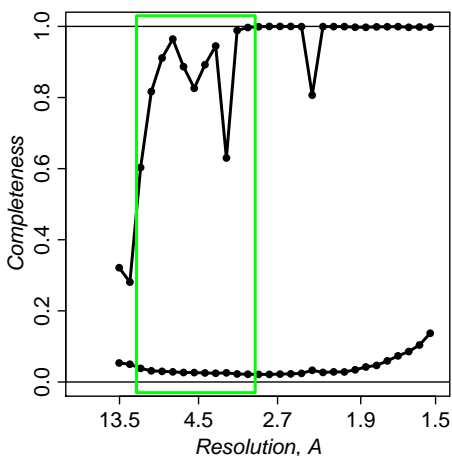
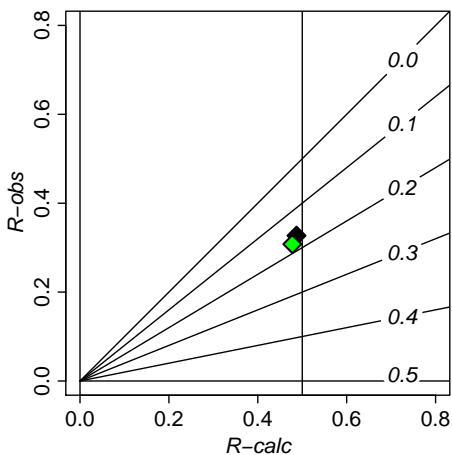
1rxg

	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	26.6	-
R'	-	-
R-free	27.9	-
R'-free	-	-
residues per monomer	DNA 0	protein 275

s < f/100	1	0.00 %
s <= 0	0	0.00 %
f <= 0	295	0.61 %
s,f <= 0	0	0.00 %

range (A)	15.8-1.5	9.9-3.0
unique	49,149	5,976
measured	48,010	5,341
used	46,110	4,768

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



1sma

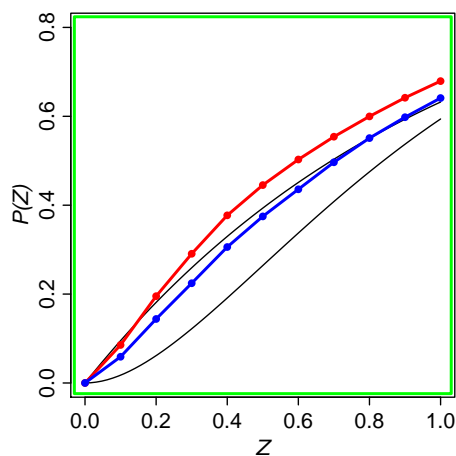
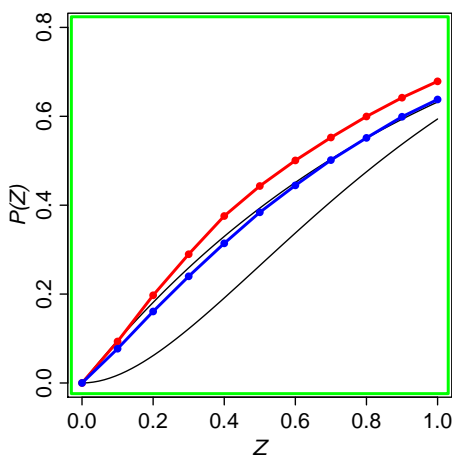
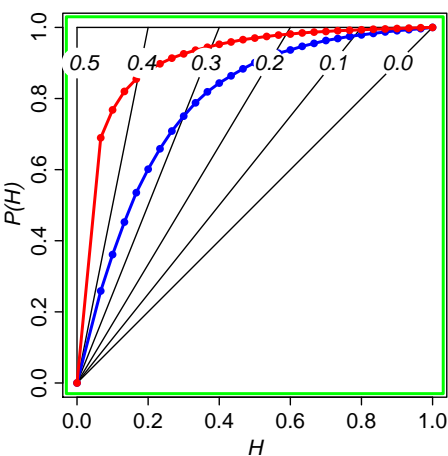
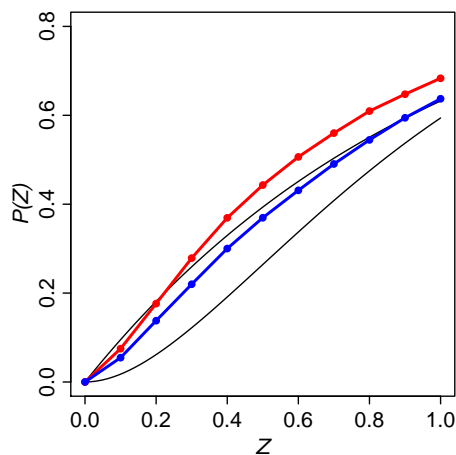
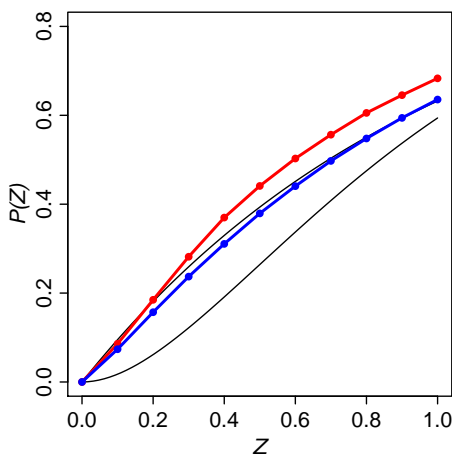
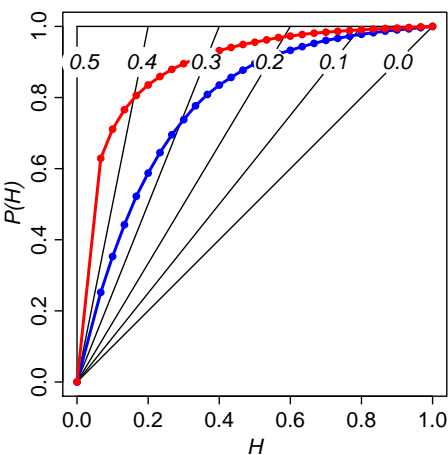
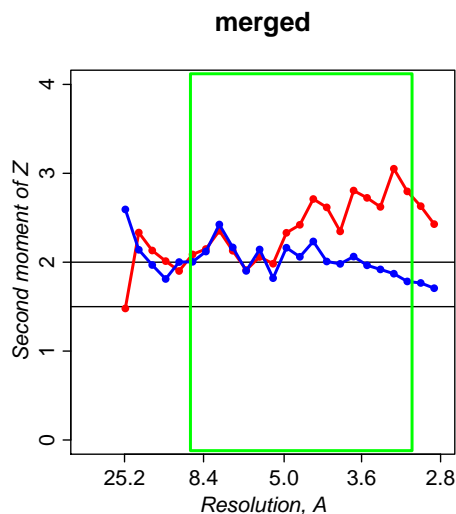
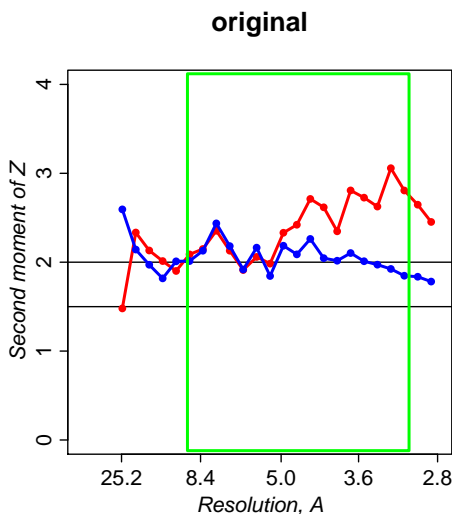
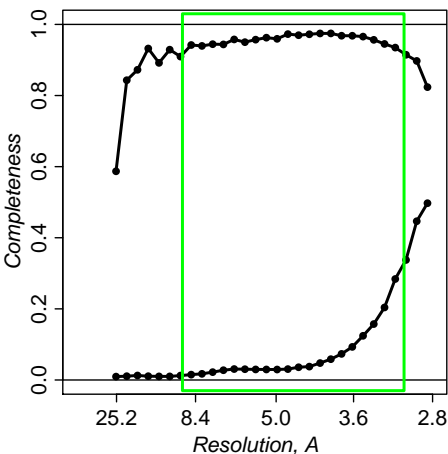
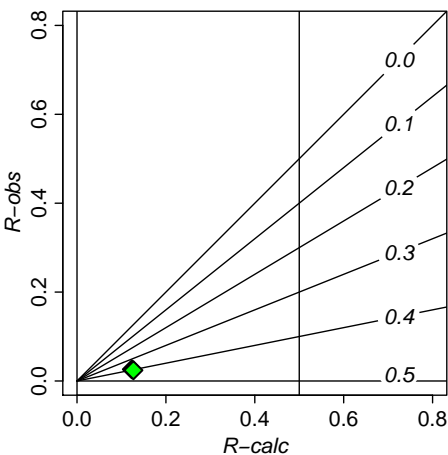
	original	merged
s.g.	P 61	P 61 2 2
p.g.	12021	12027
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.33
R	22.9	
R'	23.0	23.9
R-free	26.7	
R'-free	26.7	27.3

s < f/100	3822	7.84 %
s <= 0	38	0.08 %
f <= 0	38	0.08 %
s,f <= 0	38	0.08 %

range (A)	29.6–2.8	9.9–3.0
unique	52,015	41,054
measured	48,757	39,251
used	42,062	34,260

NCS	translation	rotation
r.m.s.d. (A)	42.93	0.00
angle (o)	179.99	0.01

residues per monomer	DNA	protein
	0	588



1trq

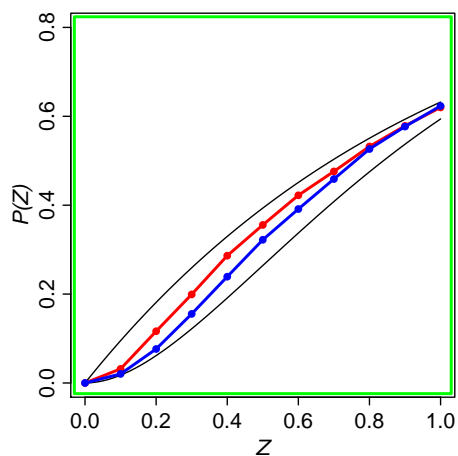
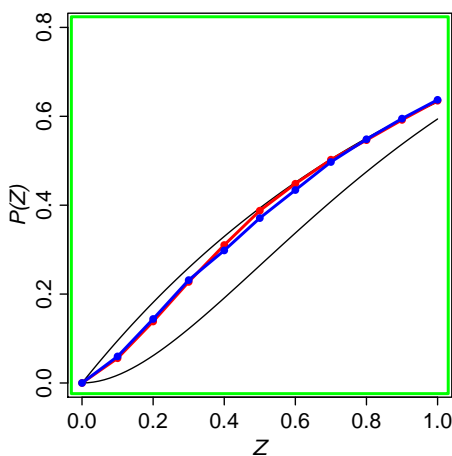
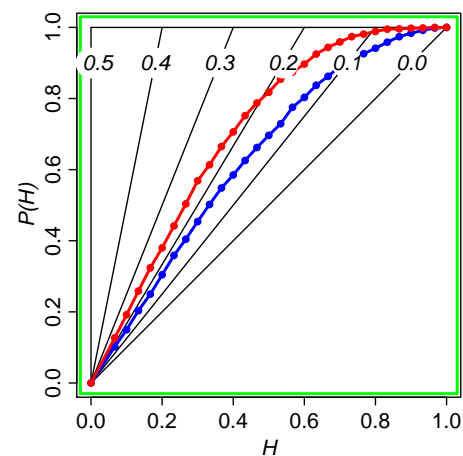
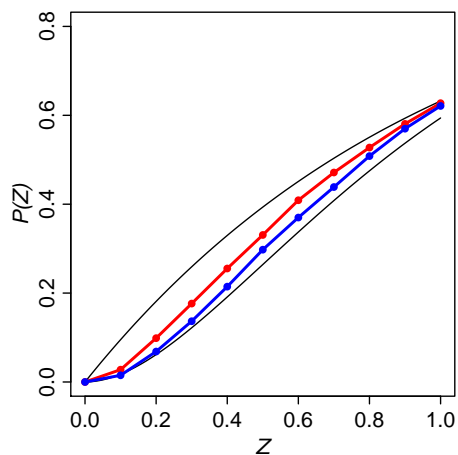
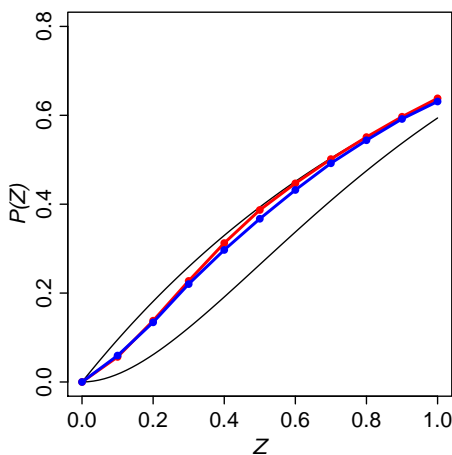
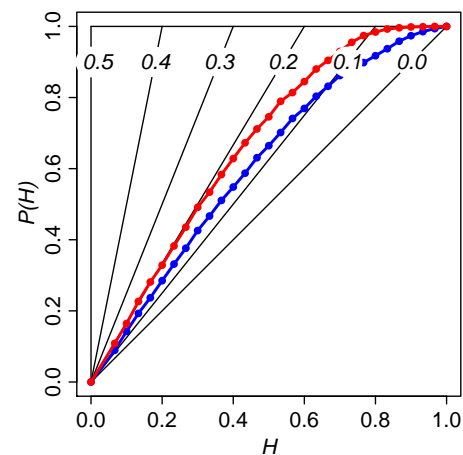
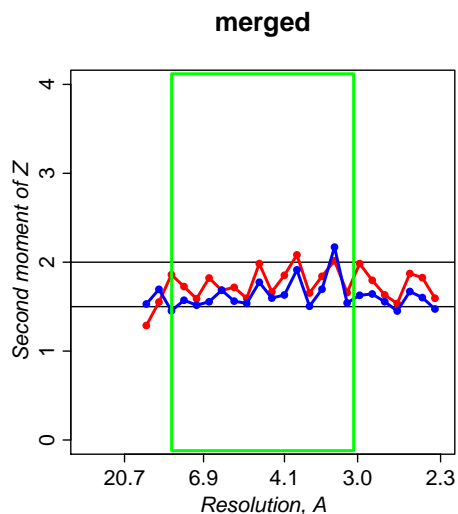
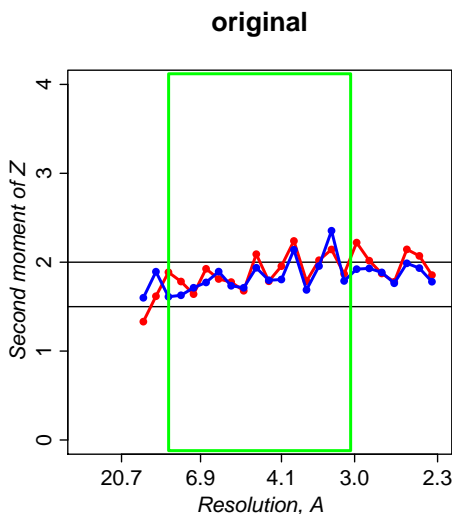
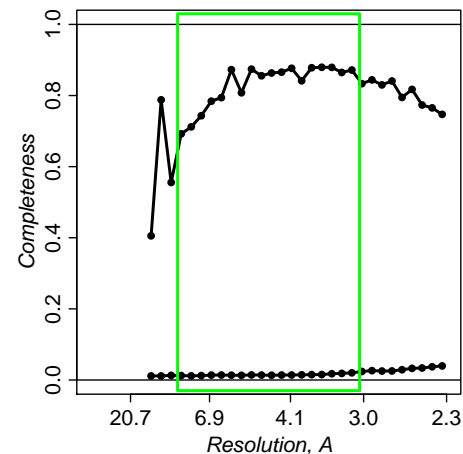
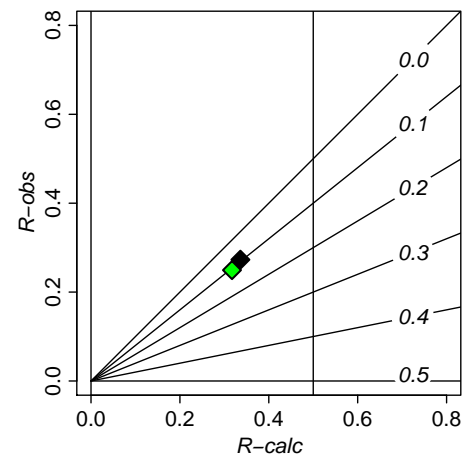
	original	merged
s.g.	P 1 21 1	P 21 21 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		1.15
R	22.6	
R'	23.7	28.8
R-free	25.0	
R'-free	28.2	36.9

s < f/100	97	1.39 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	14.9–2.3	9.9–3.0
unique	8,483	3,763
measured	6,965	3,205
used	5,194	2,450

NCS	translation	rotation
r.m.s.d. (A)	20.76	1.02
angle (o)	174.95	5.12

residues per monomer	DNA	protein
	0	104



1tvx

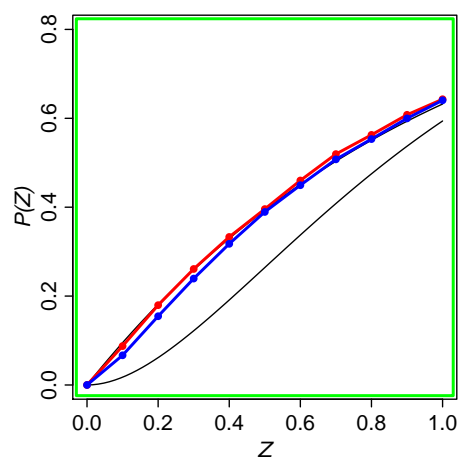
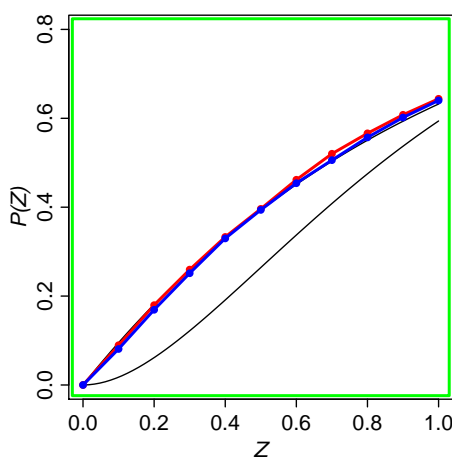
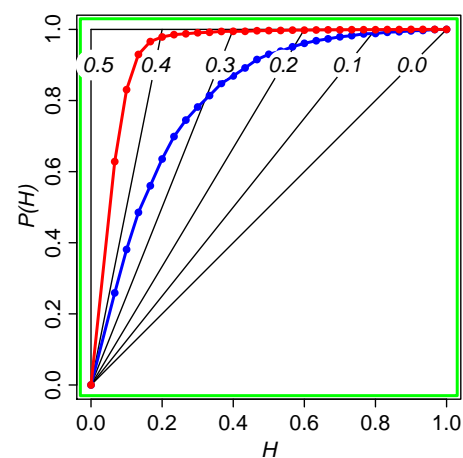
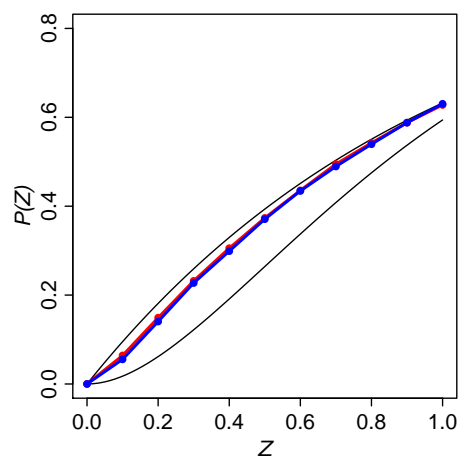
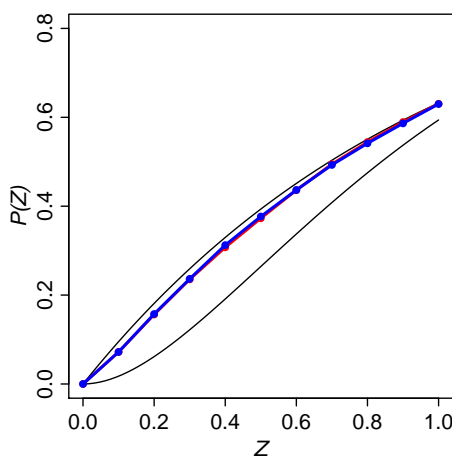
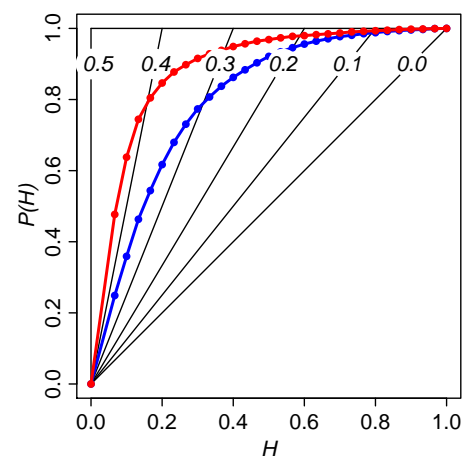
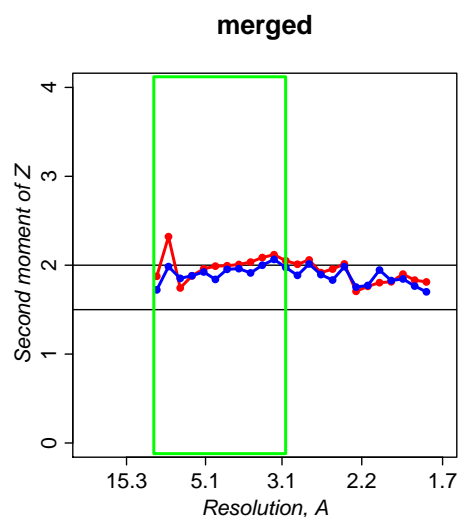
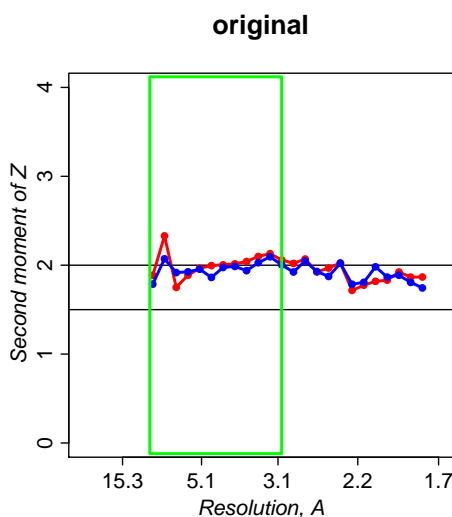
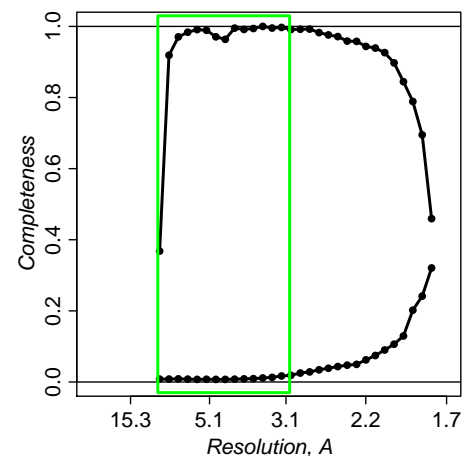
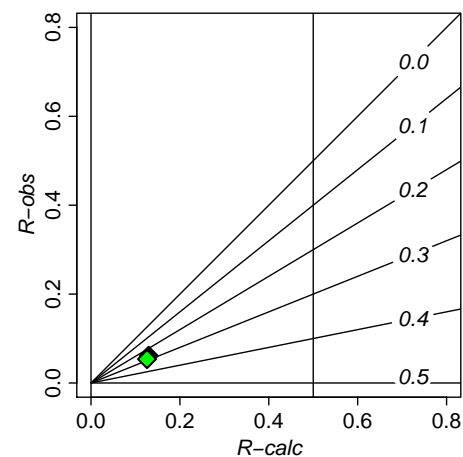
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		0.16
R	29.0	
R'	29.2	29.7
R-free	30.2	
R'-free	30.5	30.6

s < f/100	3690	14.57 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	9.5–1.8	9.5–3.0
unique	28,672	5,658
measured	25,326	5,563
used	21,604	4,912

NCS	translation	rotation
r.m.s.d. (A)	6.07	0.13
angle (o)	33.12	0.05

residues per monomer	DNA	protein
	0	64



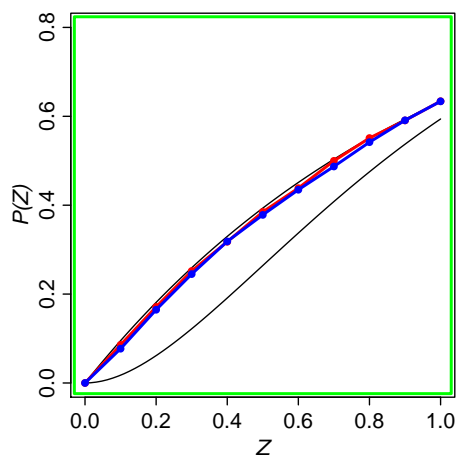
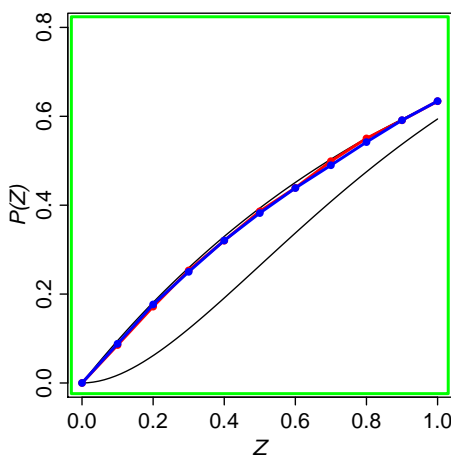
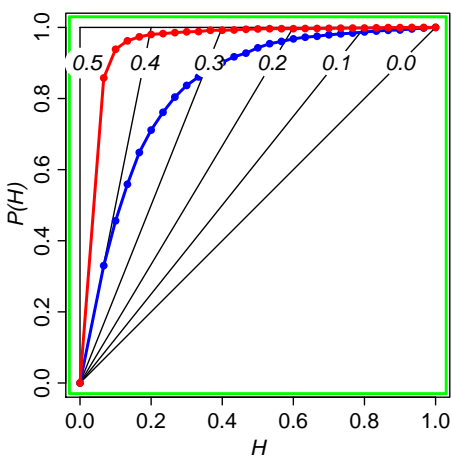
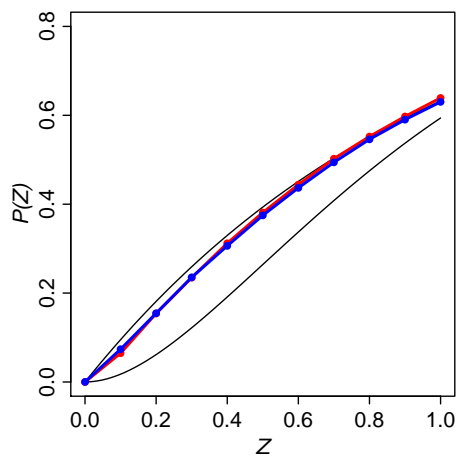
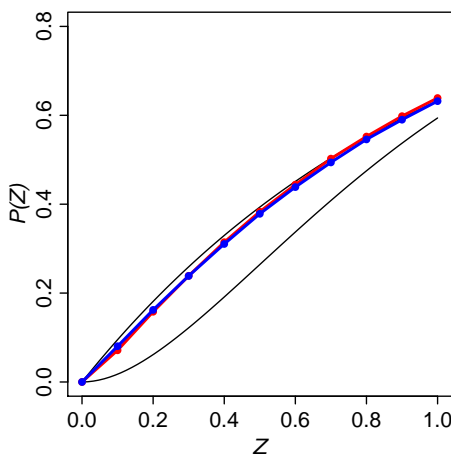
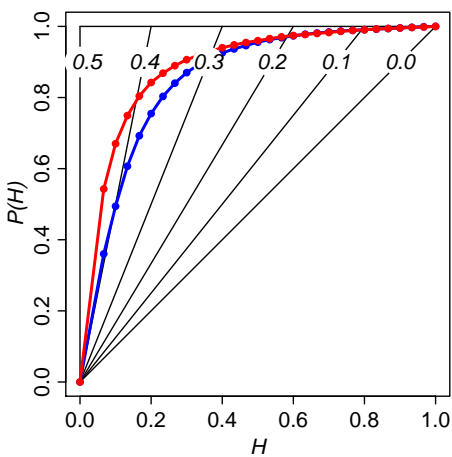
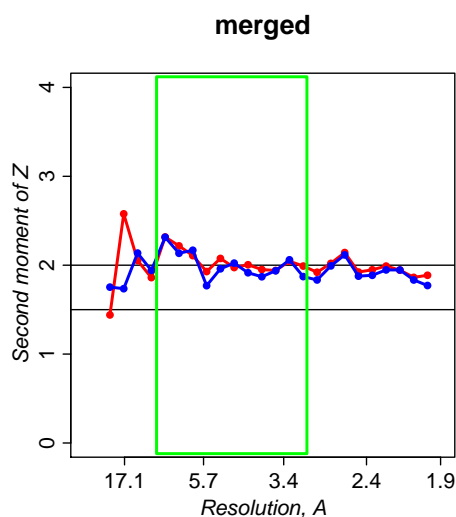
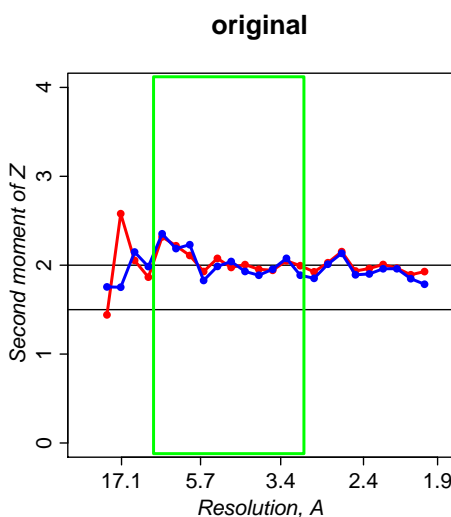
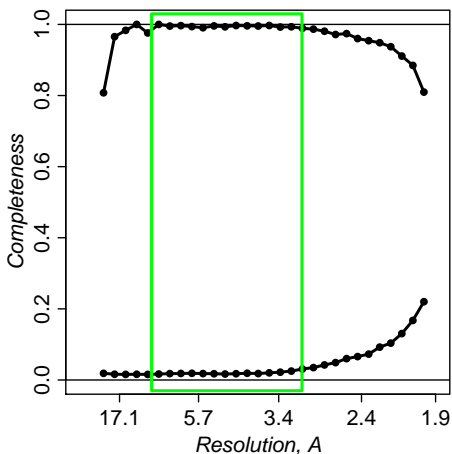
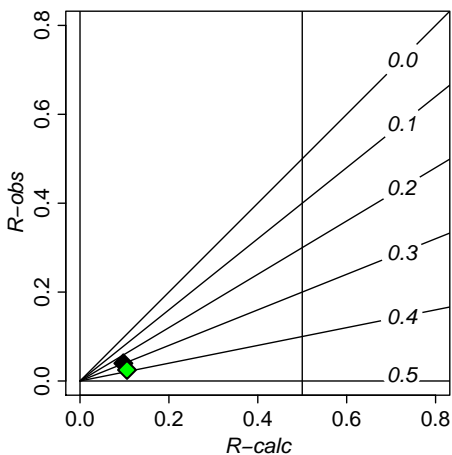
1ucf

	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.05
R	22.7	
R'	22.8	23.2
R-free	26.1	
R'-free	26.4	26.5
residues per monomer	DNA 0	protein 188

s < f/100	1083	3.24 %
s <= 0	1083	3.24 %
f <= 0	1083	3.24 %
s,f <= 0	1083	3.24 %

range (A)	37.5–1.9	9.9–3.0
unique	35,295	9,153
measured	33,380	9,097
used	30,430	8,326

NCS	translation	rotation
r.m.s.d. (A)	23.30	0.05
angle (o)	179.98	0.03



1upp

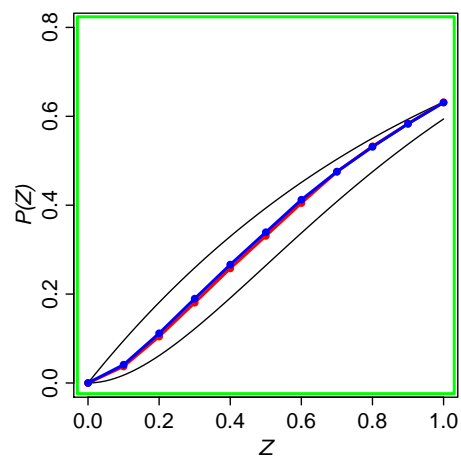
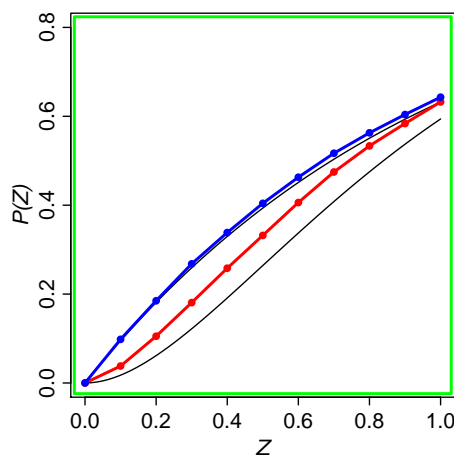
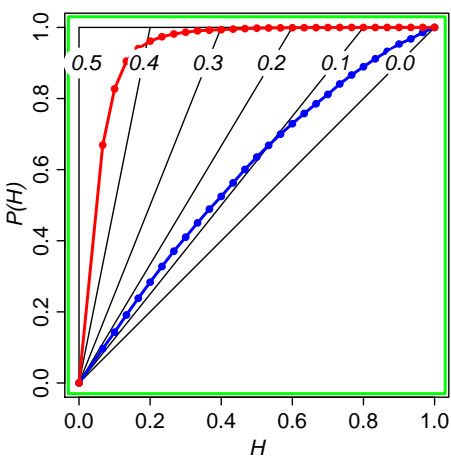
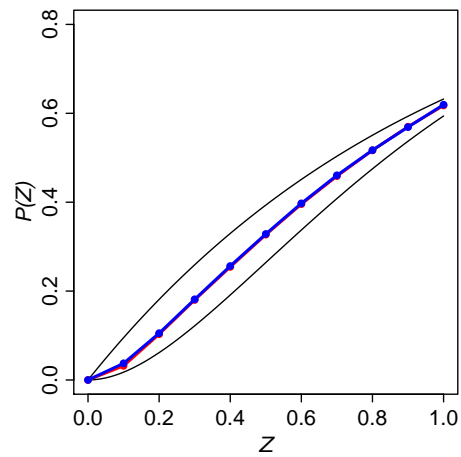
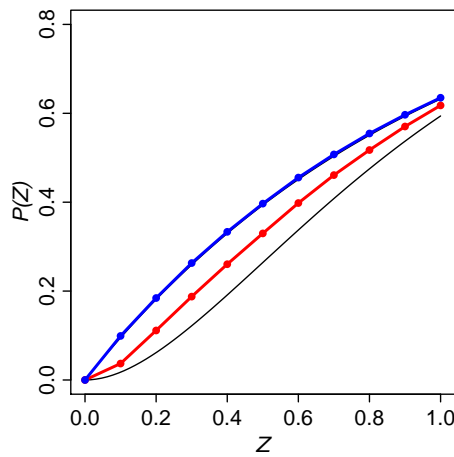
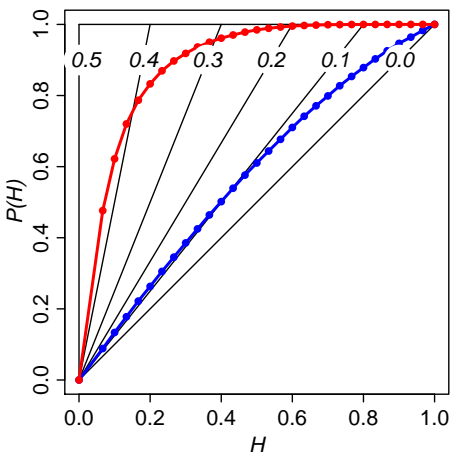
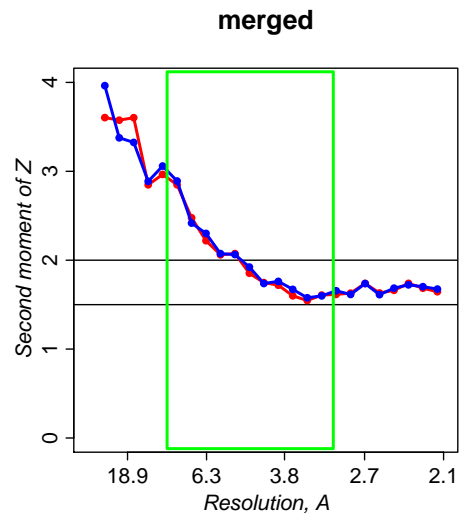
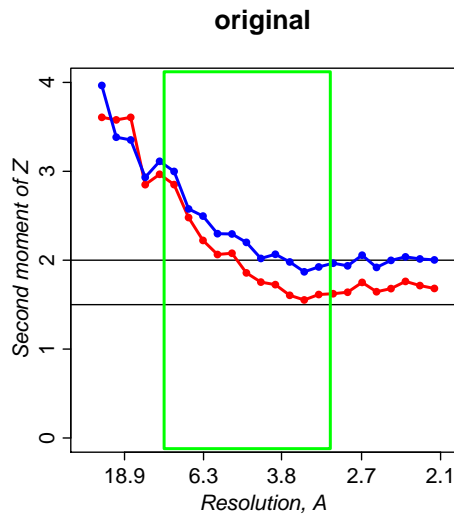
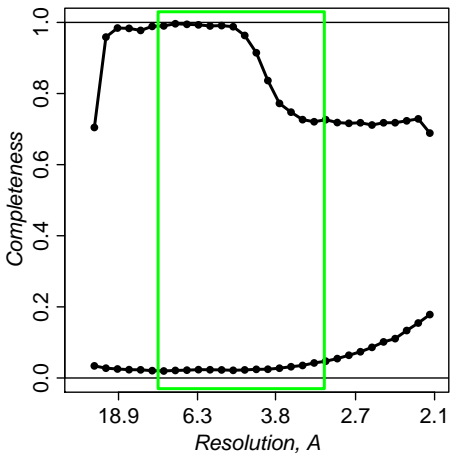
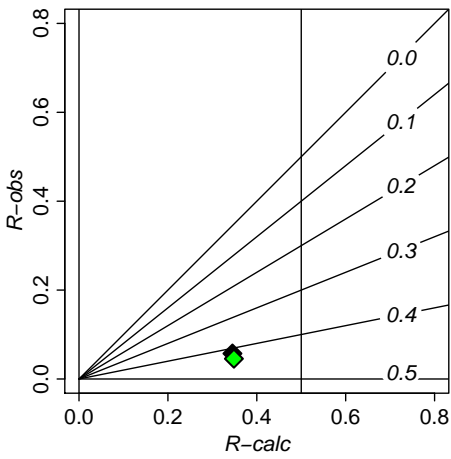
	original	merged
s.g.	C 2 2 21	P 42 21 2
p.g.	10003	10205
a.u.	4	2
p.t.	2	2
p.o.	4	4
r.m.s.d. (A)		2.30
R	28.0	
R'	38.2	43.5
R-free	32.2	
R'-free	44.1	49.4

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	78.1–2.1	9.9–3.0
unique	142,658	47,589
measured	108,167	39,795
used	90,654	33,558

NCS	translation	rotation
r.m.s.d. (A)	1.40	0.95
angle (o)	3.41	2.36

residues per monomer	DNA	protein
	0	589



1vgz

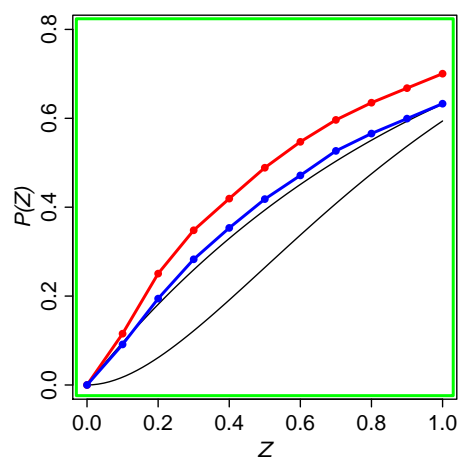
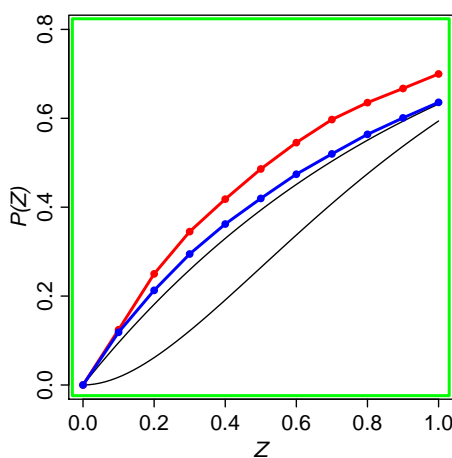
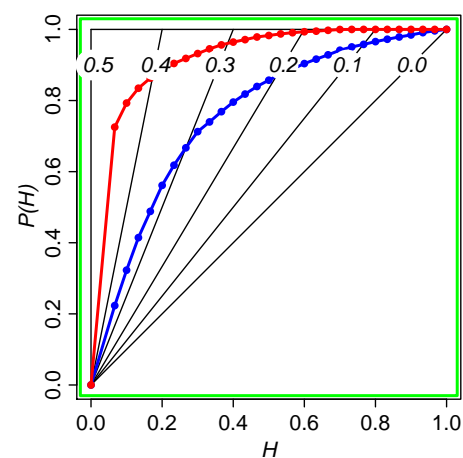
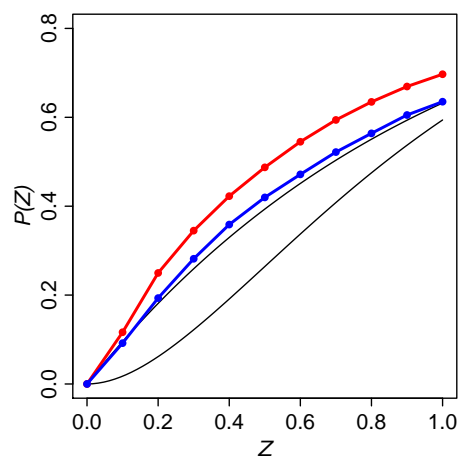
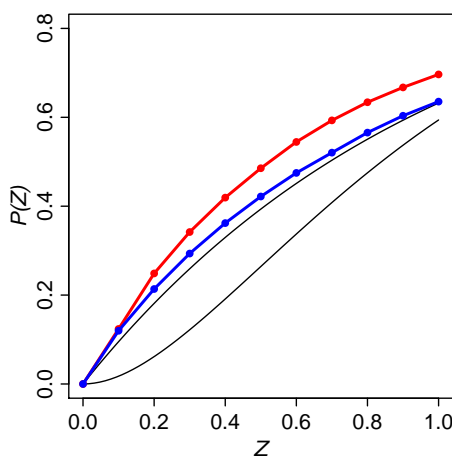
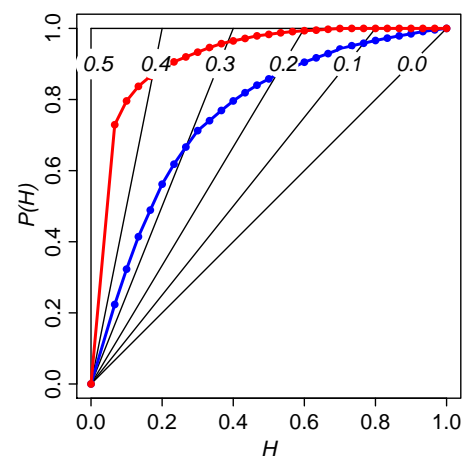
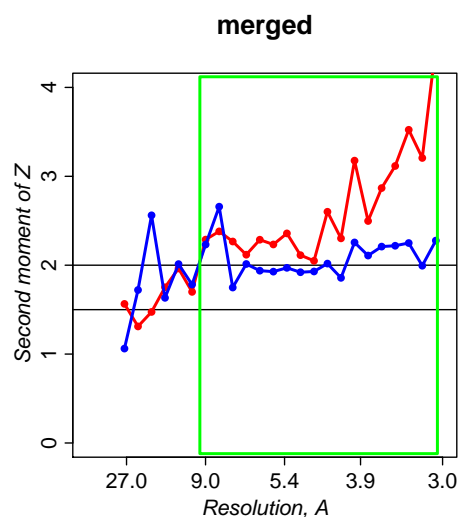
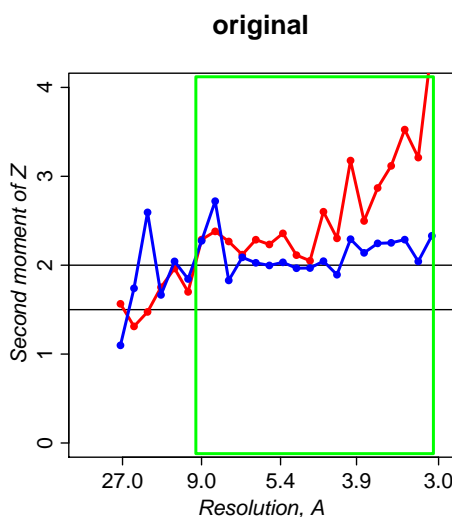
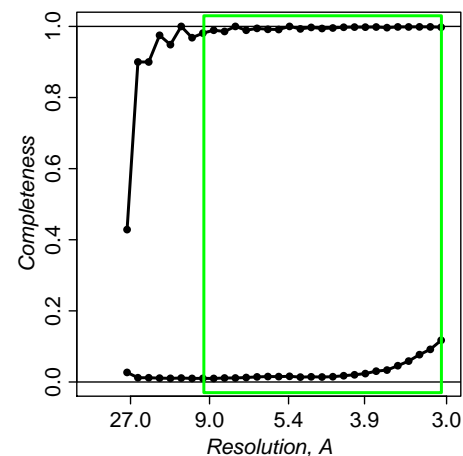
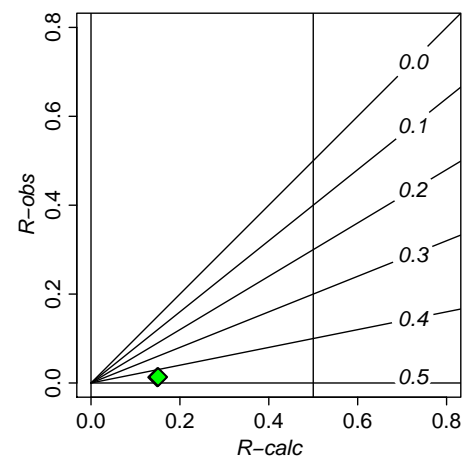
	original	merged
s.g.	P 31	P 31 1 2
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.20
R	23.2	
R'	23.3	23.9
R-free	28.8	
R'-free	29.1	28.6

s < f/100	728	7.42 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	34.8-3.0	9.9-3.0
unique	9,857	9,590
measured	9,816	9,559
used	9,072	8,876

NCS	translation	rotation
r.m.s.d. (A)	27.71	0.20
angle (o)	179.96	0.07

residues per monomer	DNA	protein
	0	209



1vh0

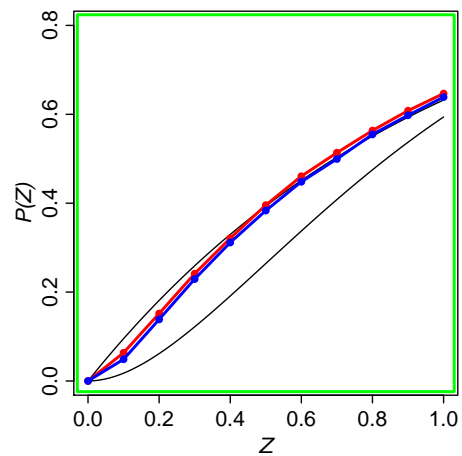
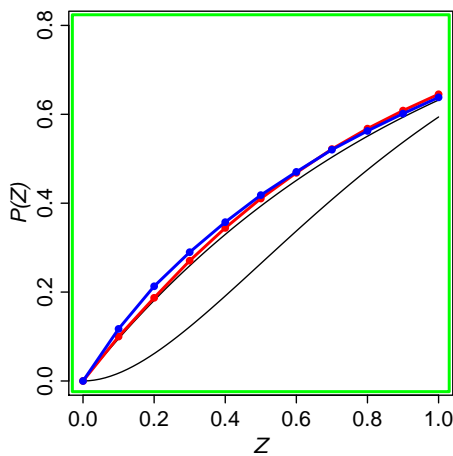
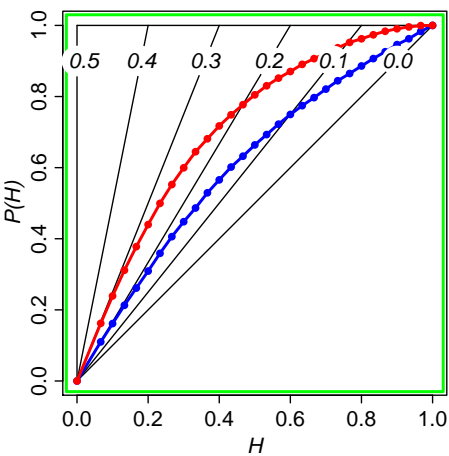
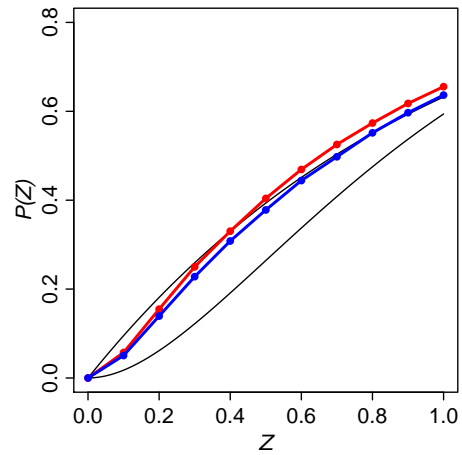
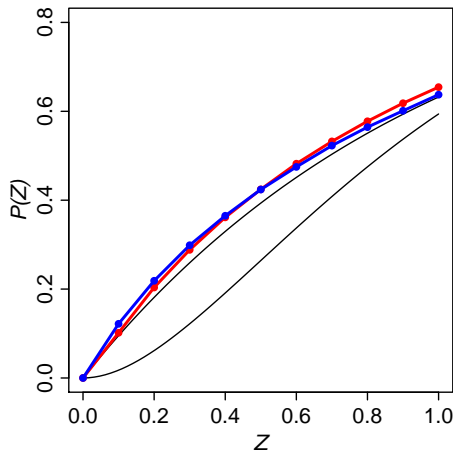
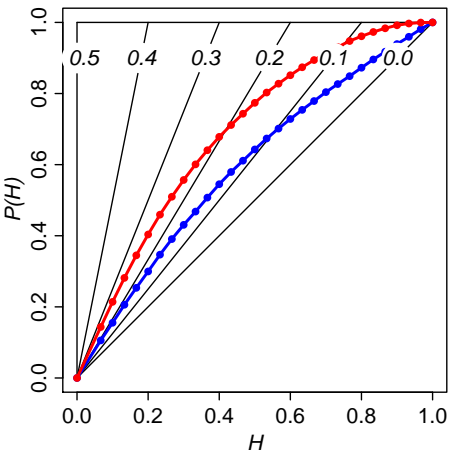
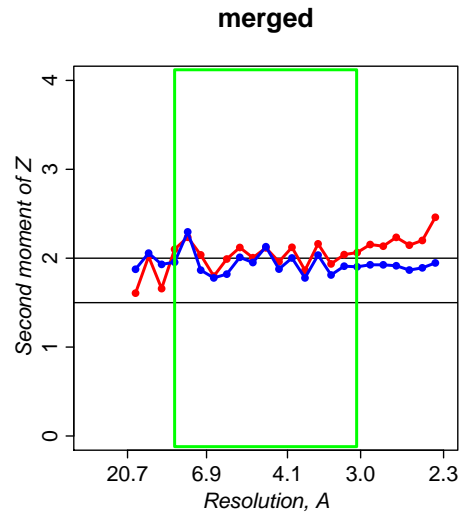
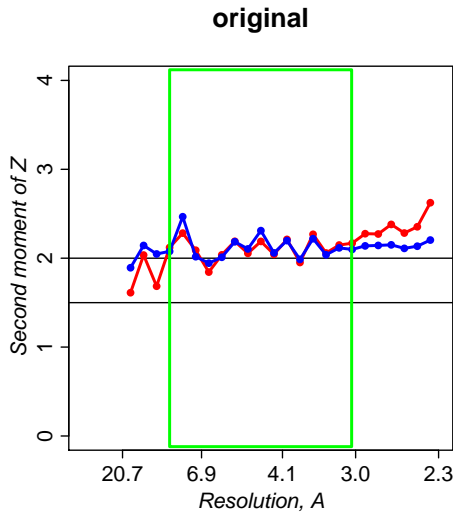
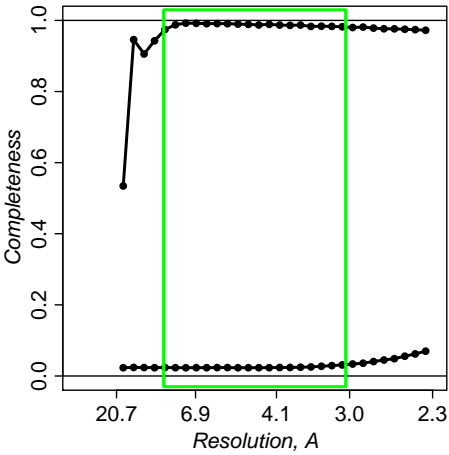
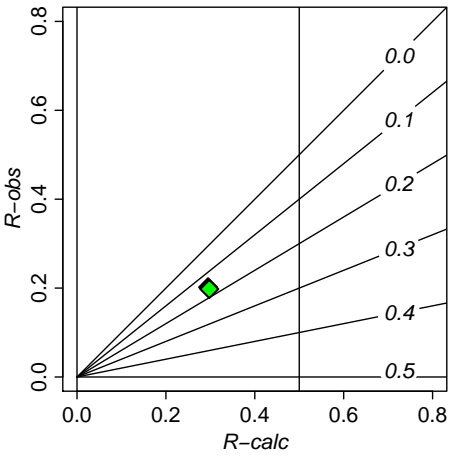
	original	merged
s.g.	P 1	C 1 2 1
p.g.	10000	10001
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.94
R	29.8	
R'	30.3	30.0
R-free	34.1	
R'-free	34.4	33.3

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.9–2.3	9.9–3.0
unique	47,682	21,246
measured	46,732	20,945
used	44,020	19,676

NCS	translation	rotation
r.m.s.d. (A)	13.40	0.32
angle (o)	64.54	0.65

residues per monomer	DNA	protein
	0	148



1vhb

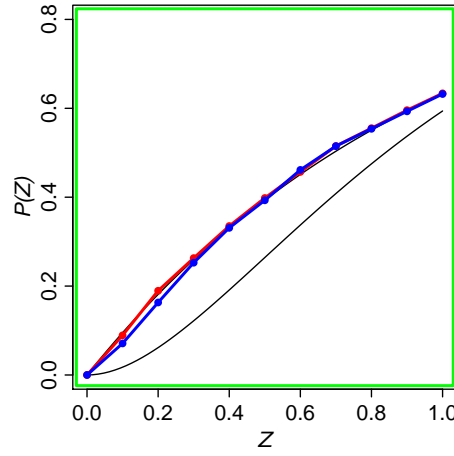
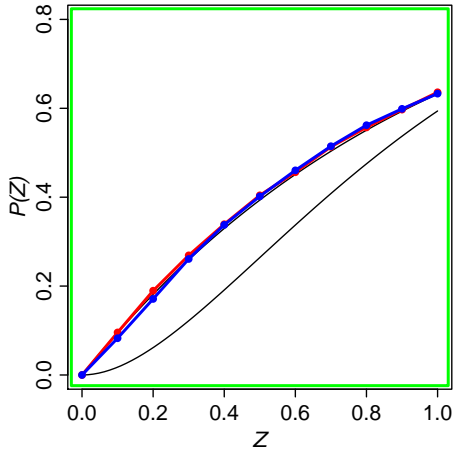
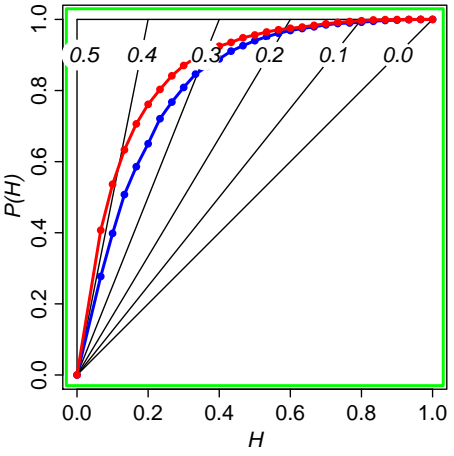
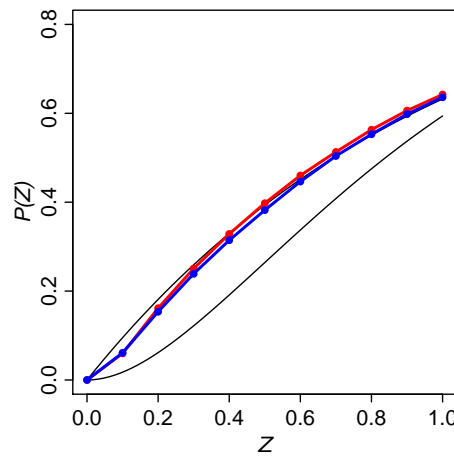
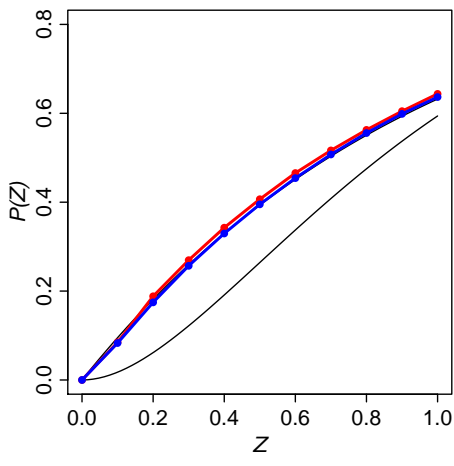
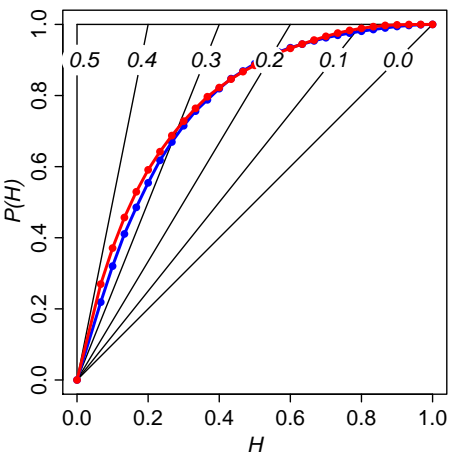
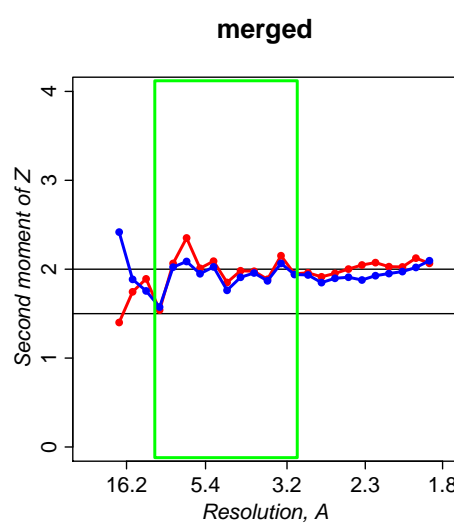
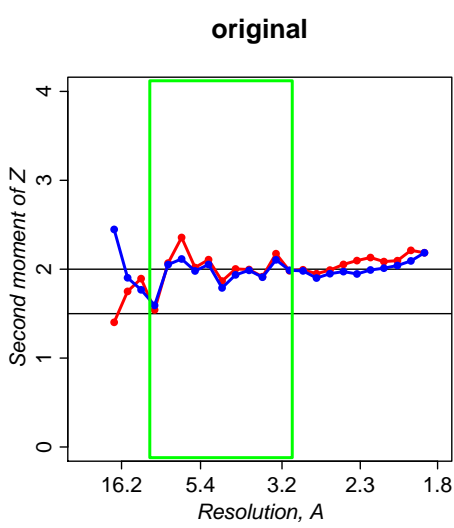
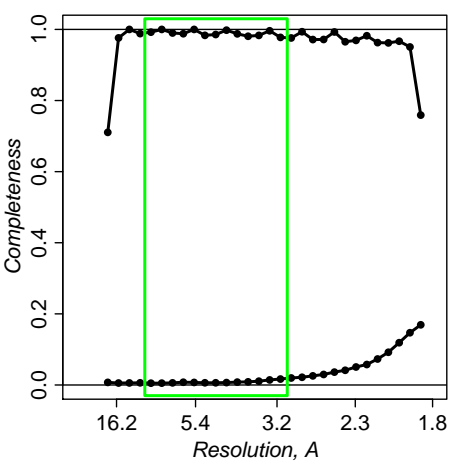
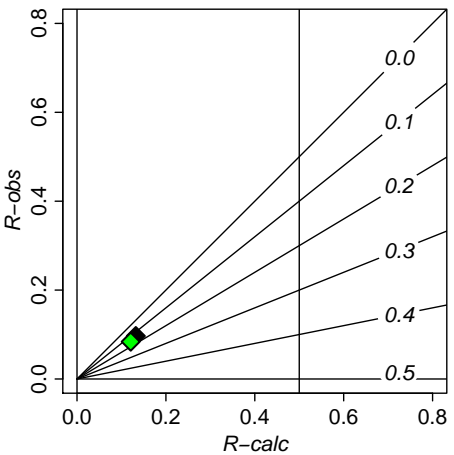
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.35
R	28.0	
R'	28.1	28.0
R-free	31.1	
R'-free	30.9	31.0

residues per monomer	DNA	protein
	0	135

s < f/100	5003	18.86 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	25.2-1.8	9.9-3.0
unique	27,761	6,282
measured	26,526	6,208
used	23,880	5,346

NCS	translation	rotation
r.m.s.d. (A)	24.03	0.28
angle (o)	179.69	0.89



1vhj

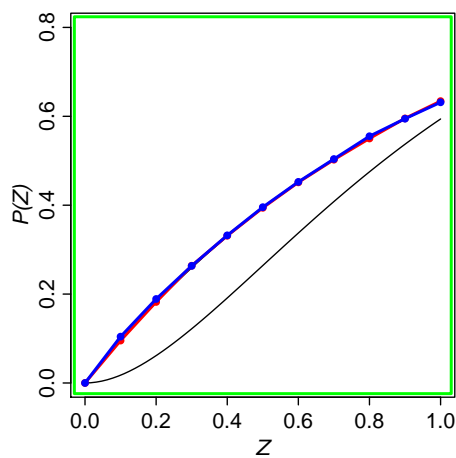
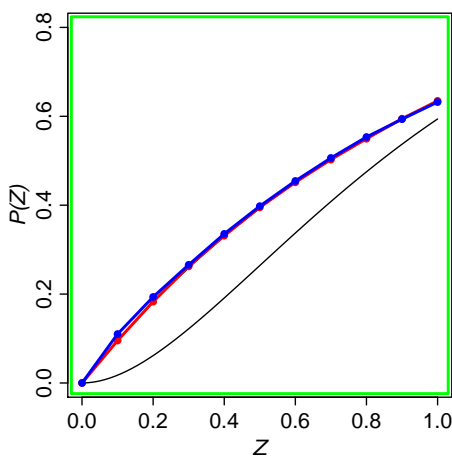
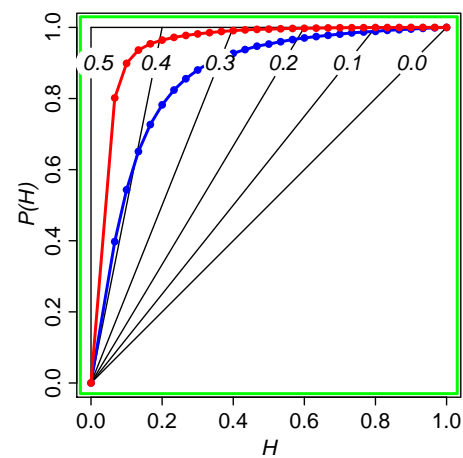
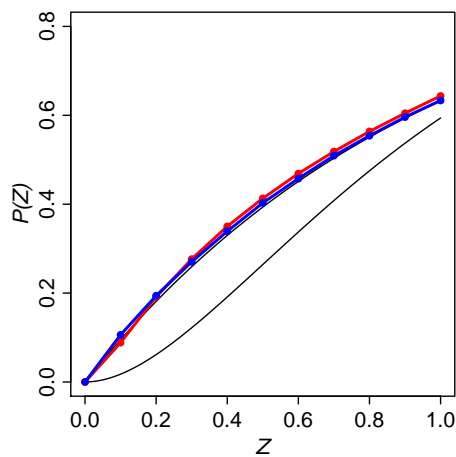
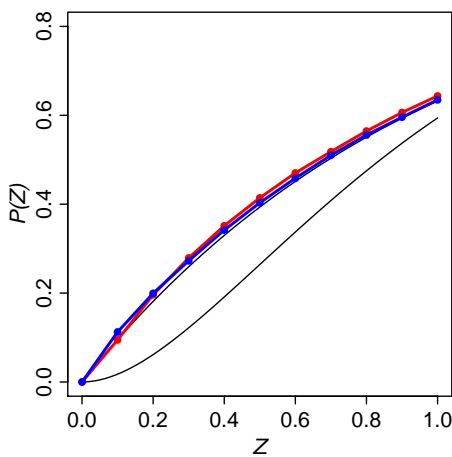
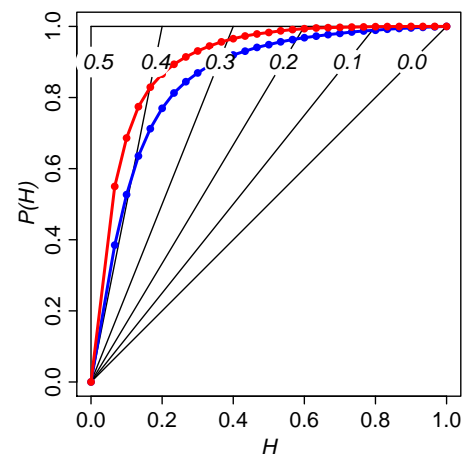
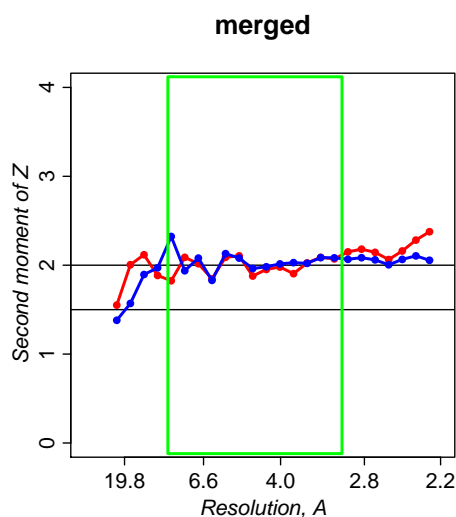
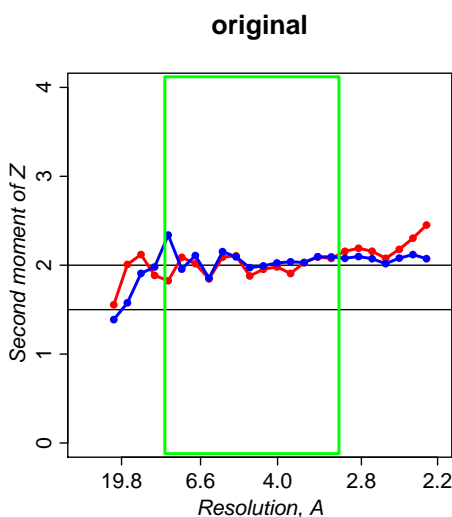
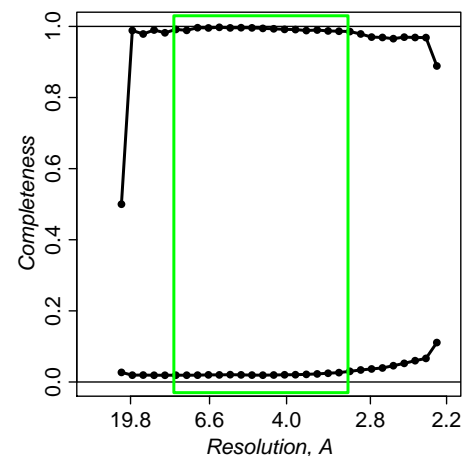
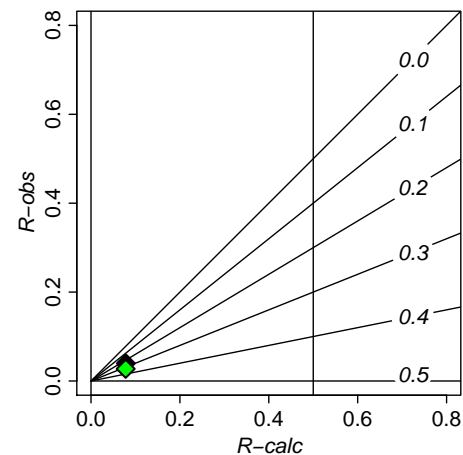
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.06
R	22.7	
R'	22.8	23.2
R-free	26.4	
R'-free	26.1	26.6

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	31.3–2.2	9.9–3.0
unique	64,333	25,727
measured	62,482	25,492
used	58,198	23,396

NCS	translation	rotation
r.m.s.d. (A)	12.95	0.05
angle (o)	60.51	0.02

residues per monomer	DNA	protein
	0	232



1vhw

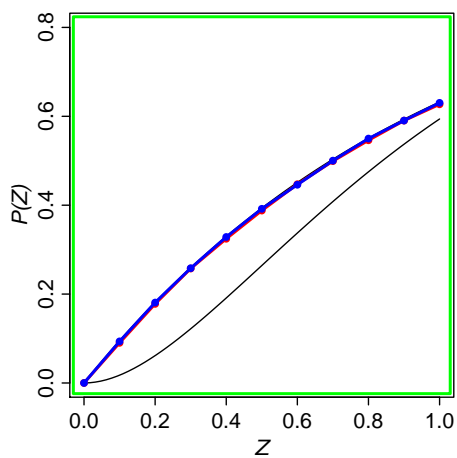
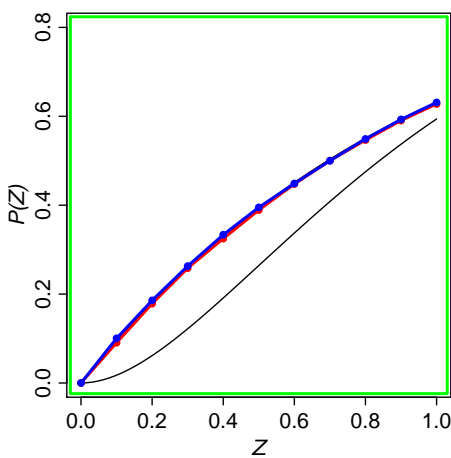
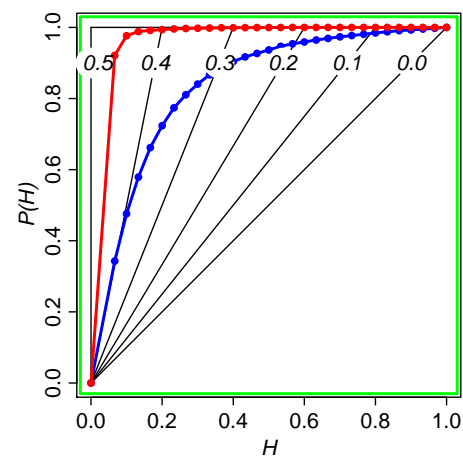
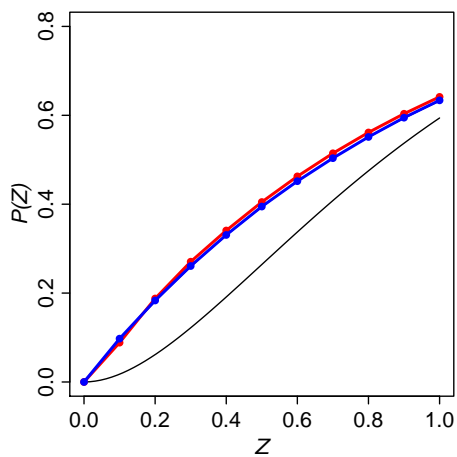
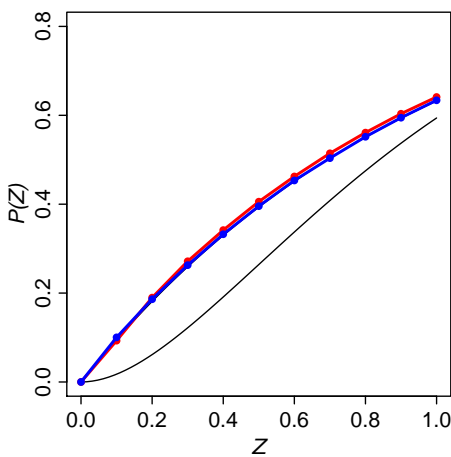
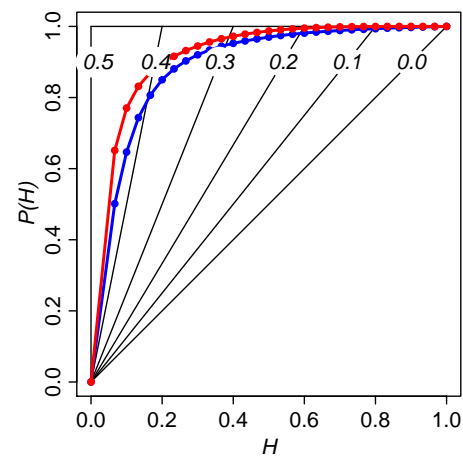
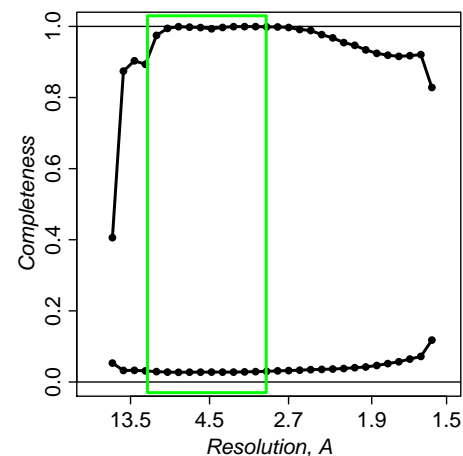
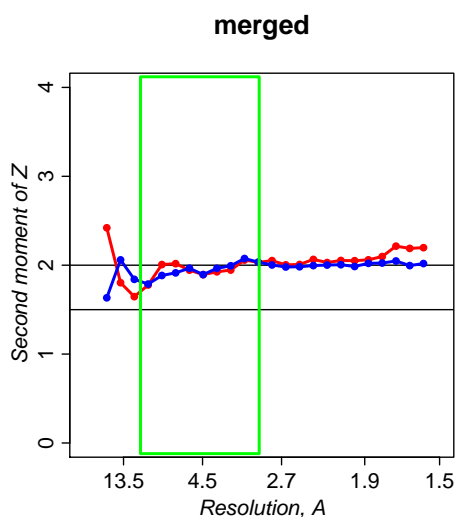
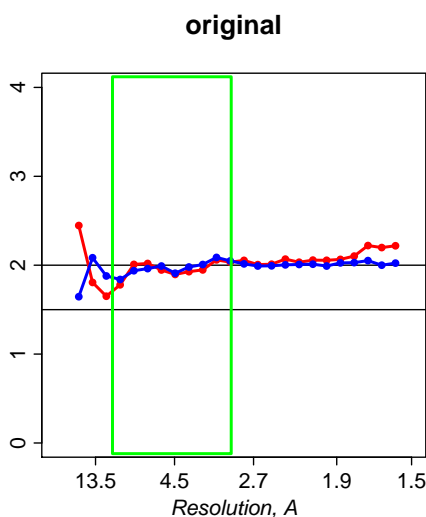
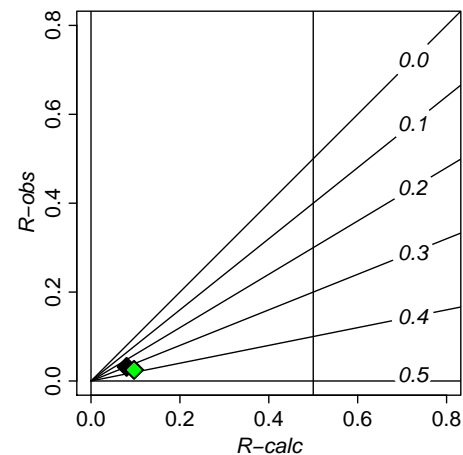
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	6	3
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.06
R	25.1	
R'	25.1	25.4
R-free	25.7	
R'-free	25.7	25.9

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	33.6–1.5	9.9–3.0
unique	192,910	25,554
measured	181,396	25,470
used	168,094	23,410

NCS	translation	rotation
r.m.s.d. (A)	12.82	0.05
angle (o)	60.21	0.02

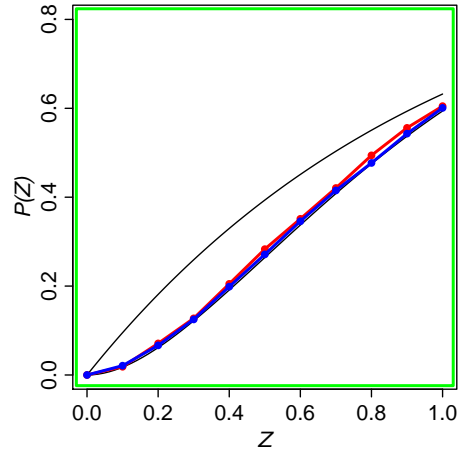
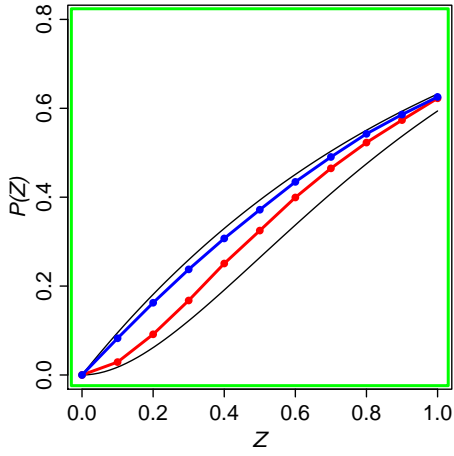
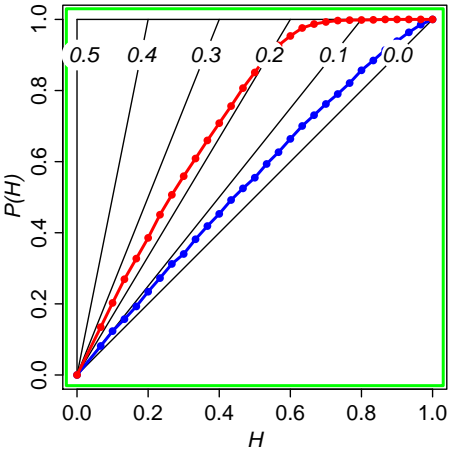
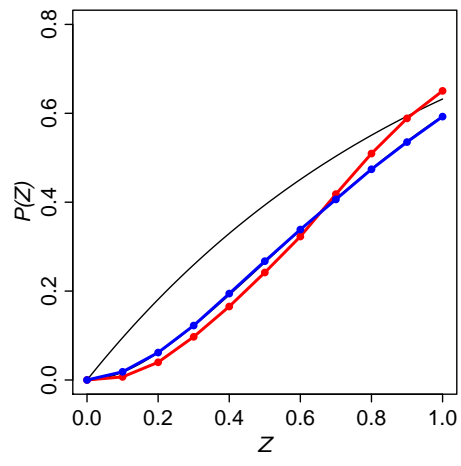
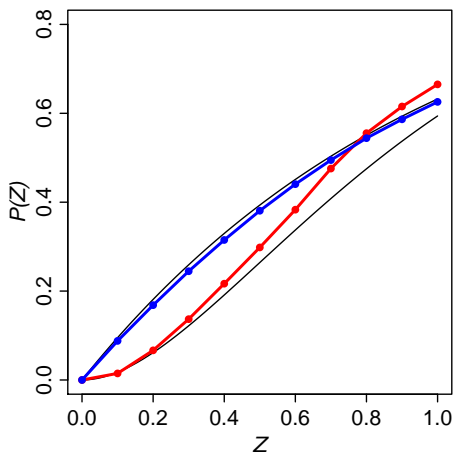
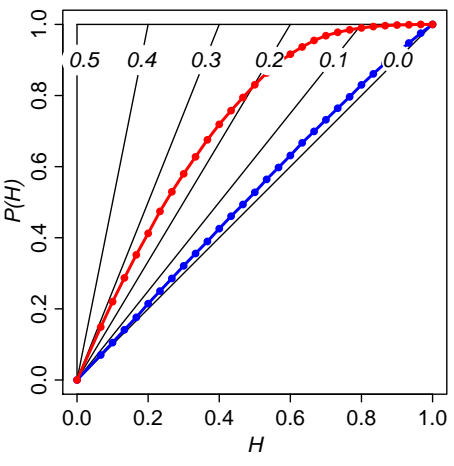
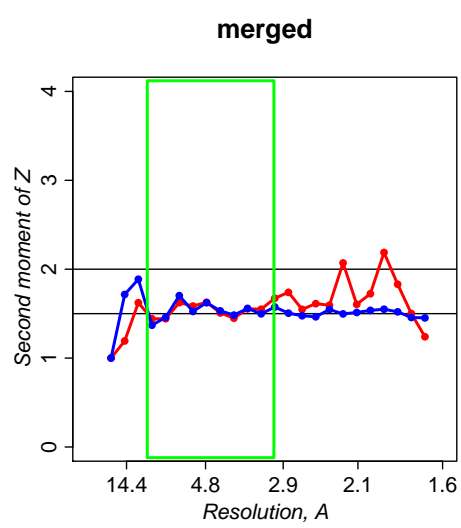
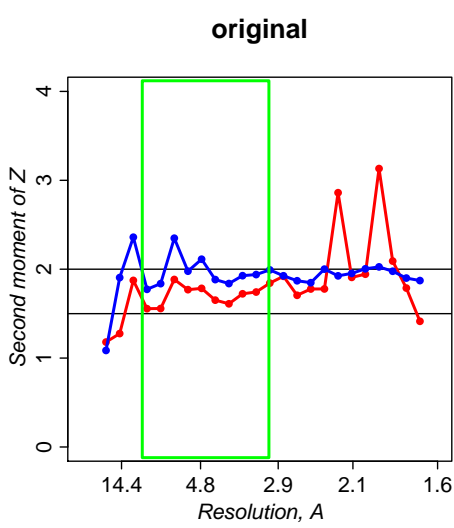
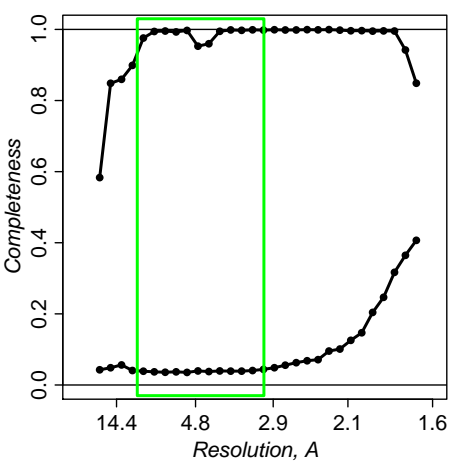
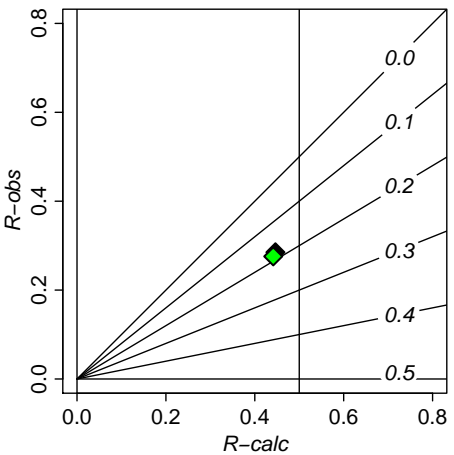
residues per monomer	DNA	protein
	0	233



1vj2

	original	merged
s.g.	P 32	P 32 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		2.92
R	27.1	
R'	39.4	40.9
R-free	28.8	
R'-free	45.1	46.5
residues per monomer	DNA 0	protein 114

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	33.1–1.7	9.9–3.0
unique	35,818	5,818
measured	34,991	5,755
used	32,126	5,038
NCS	translation	rotation
r.m.s.d. (A)	22.30	1.86
angle (o)	171.72	9.31



1wgt

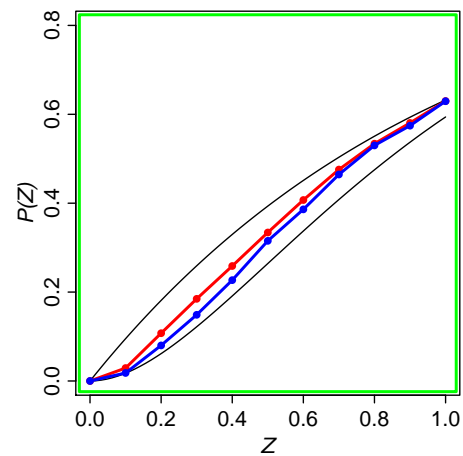
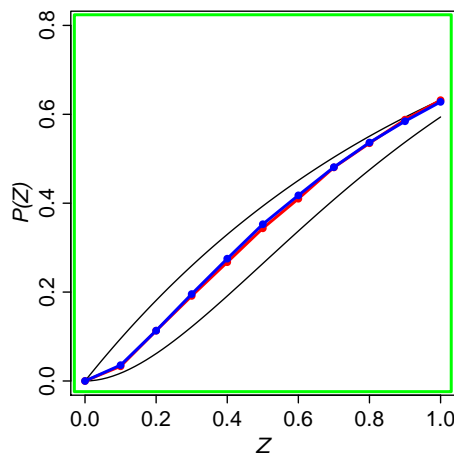
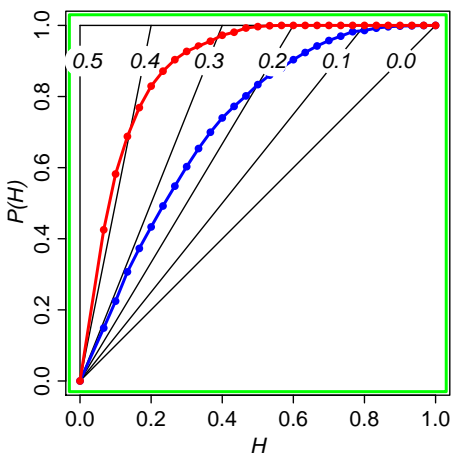
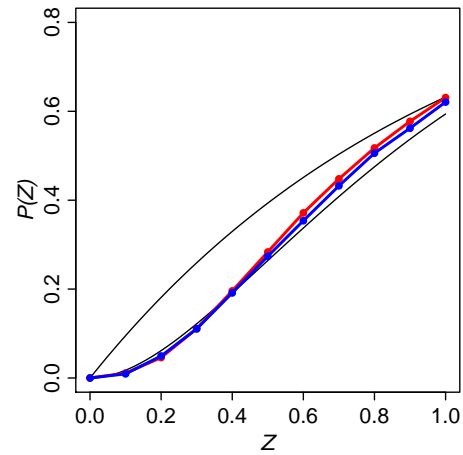
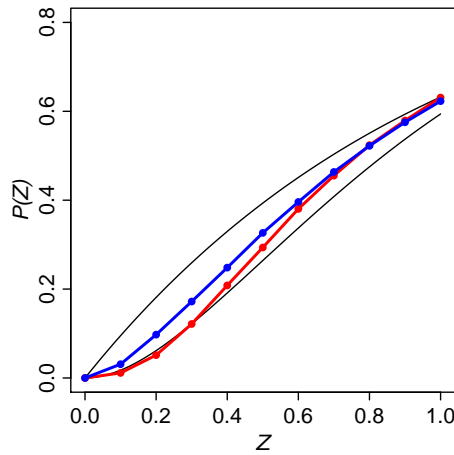
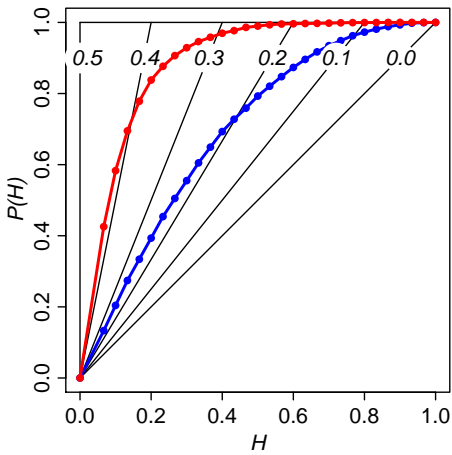
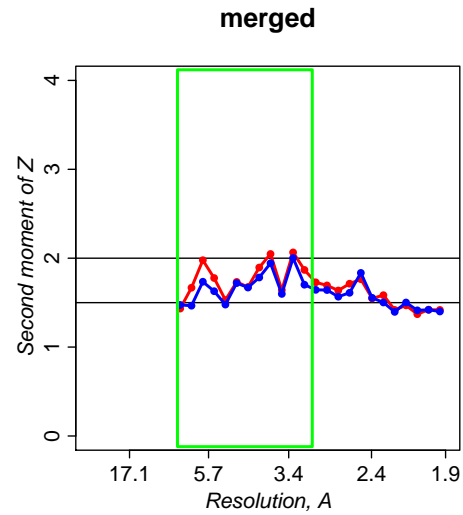
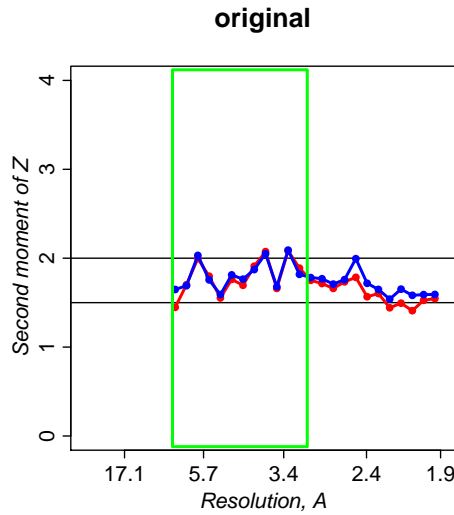
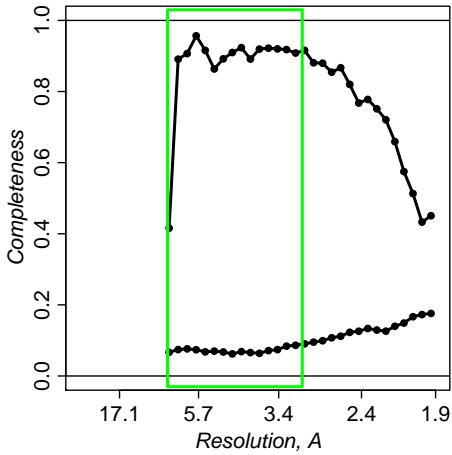
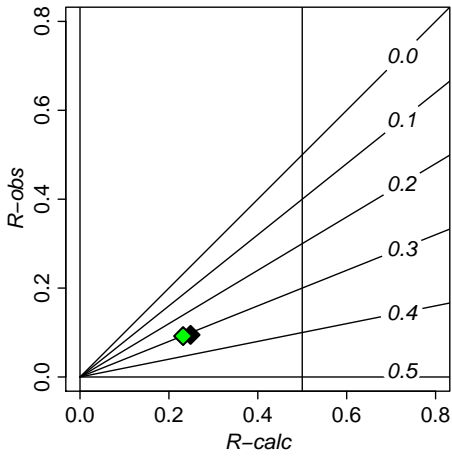
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		6.04
R	24.2	
R'	-	-
R-free	26.9	
R'-free	-	-

residues per monomer	DNA	protein
	0	170

s < f/100	73	0.38 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	8.0-1.9	8.0-3.0
unique	26,277	6,446
measured	19,330	5,867
used	15,946	5,226

NCS	translation	rotation
r.m.s.d. (A)	24.49	0.36
angle (o)	179.83	0.21



1yfo

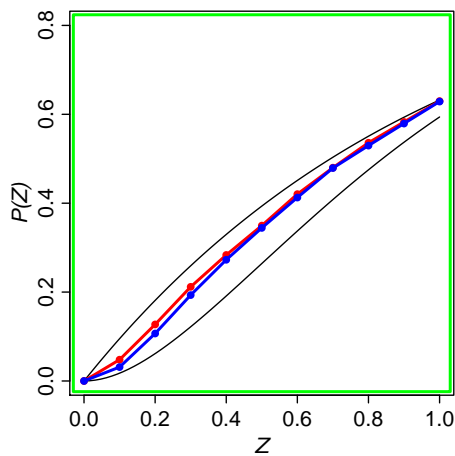
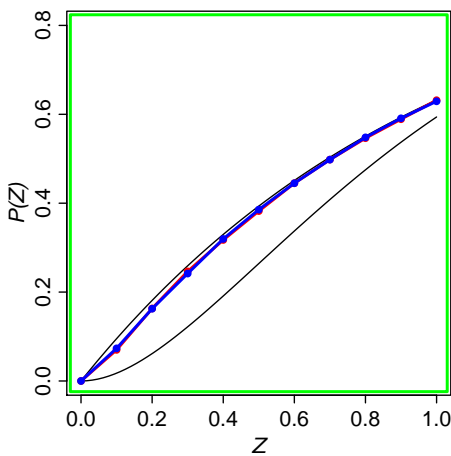
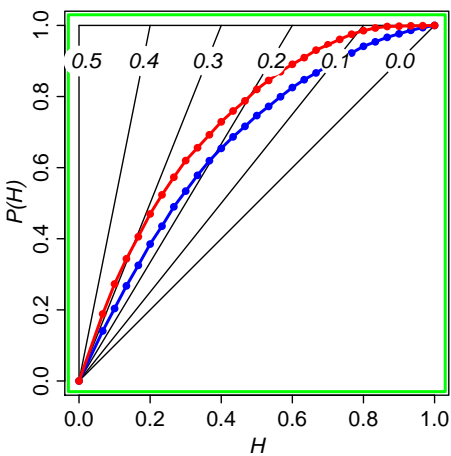
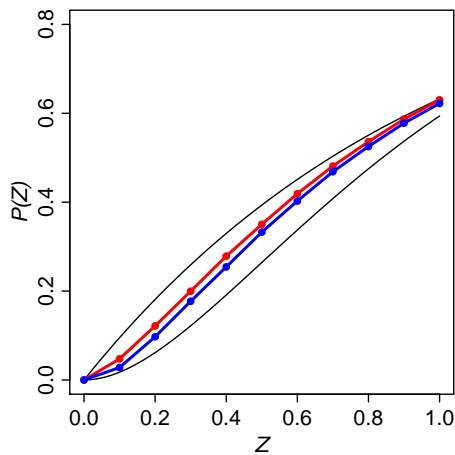
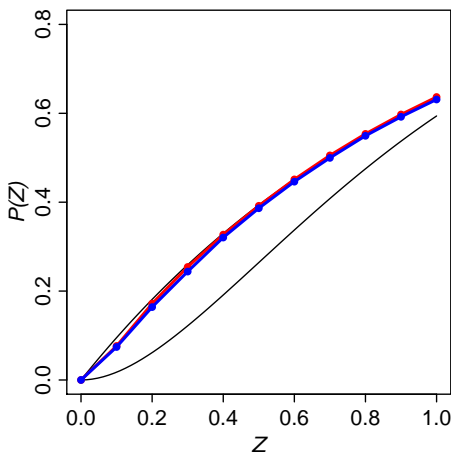
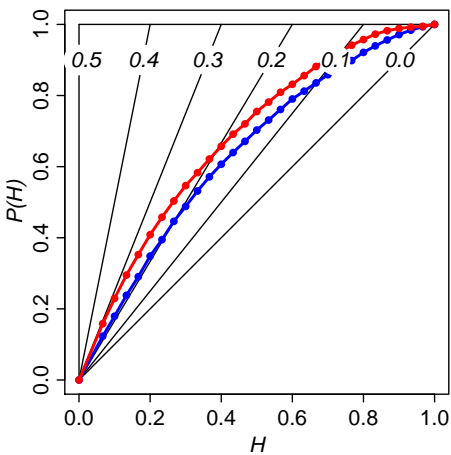
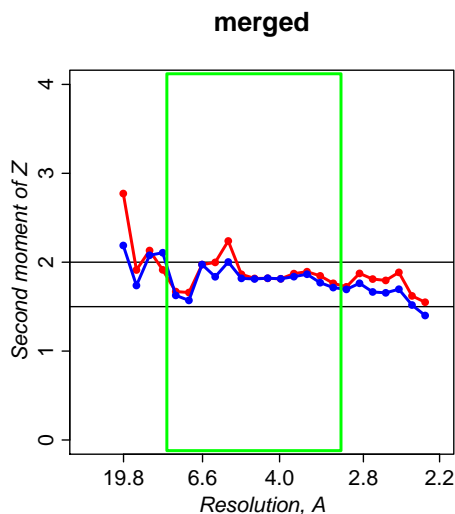
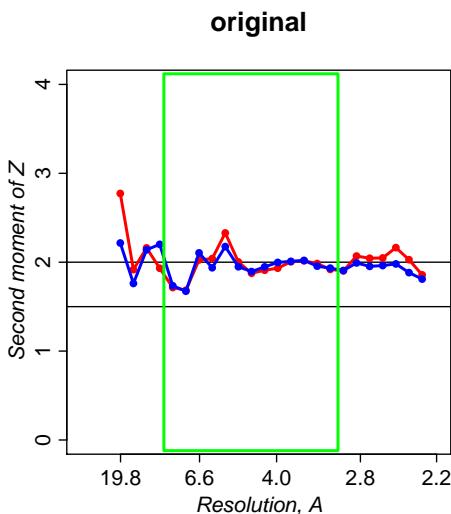
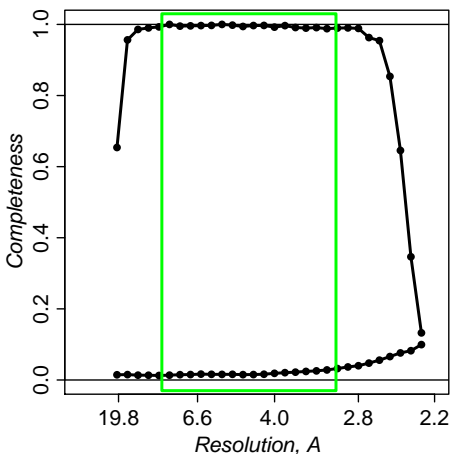
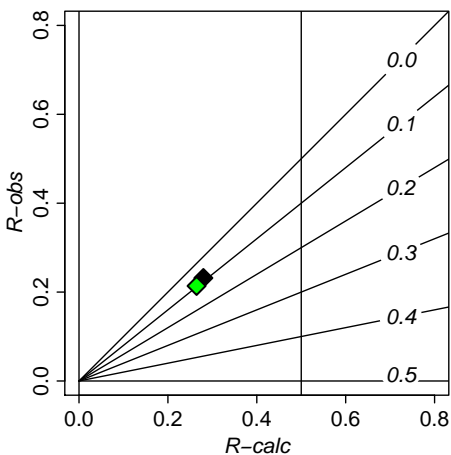
	original	merged
s.g.	P 1 2 1 1	C 2 2 2 1
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.67
R	23.4	
R'	23.8	25.4
R-free	29.4	
R'-free	30.7	32.8

s < f/100	55	0.25 %
s <= 0	0	0.00 %
f <= 0	68	0.31 %
s,f <= 0	0	0.00 %

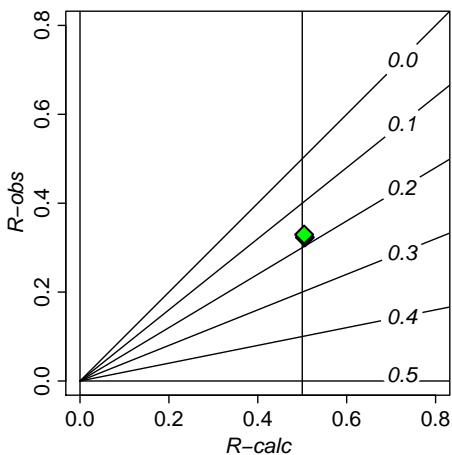
range (A)	23.9–2.2	9.9–3.0
unique	27,049	11,152
measured	22,292	11,073
used	19,042	9,920

NCS	translation	rotation
r.m.s.d. (A)	31.98	0.18
angle (o)	179.88	0.22

residues per monomer	DNA	protein
	0	279



2bcc



	original	merged
s.g.	P 21 21 21	-
p.g.	10003	10205
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	33.7	-
R'	-	-
R-free	37.9	-
R'-free	-	-

s < f/100	9753	8.21 %
s <= 0	0	0.00 %
f <= 0	12232	10.30 %
s,f <= 0	0	0.00 %

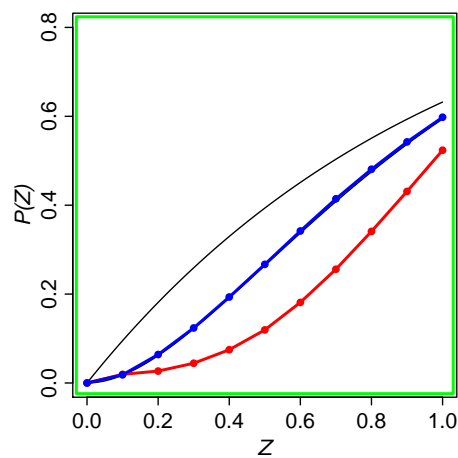
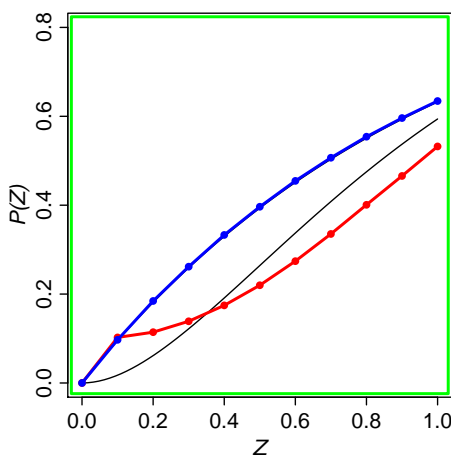
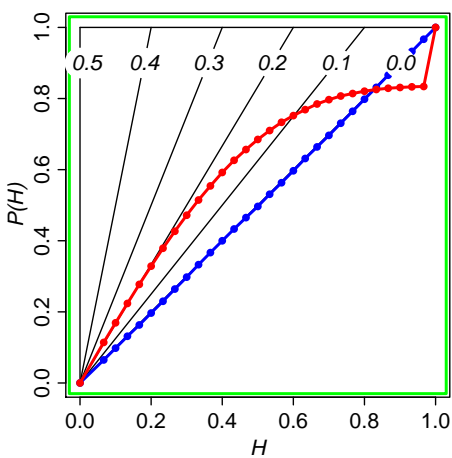
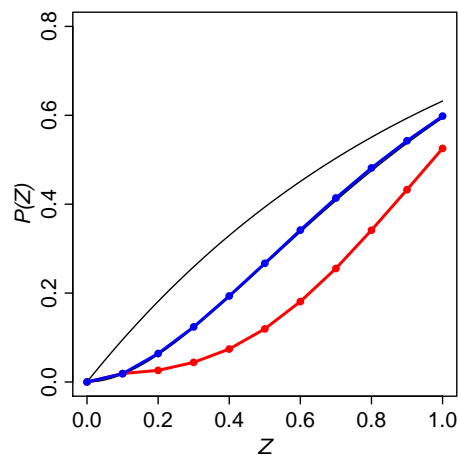
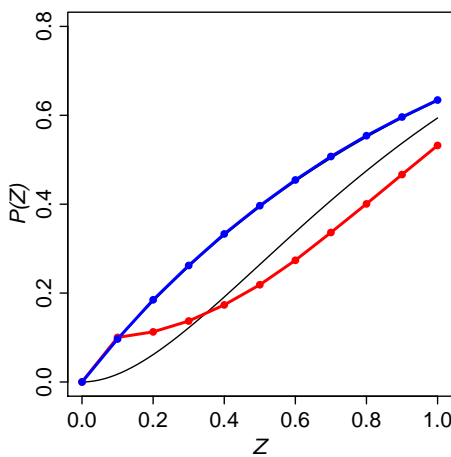
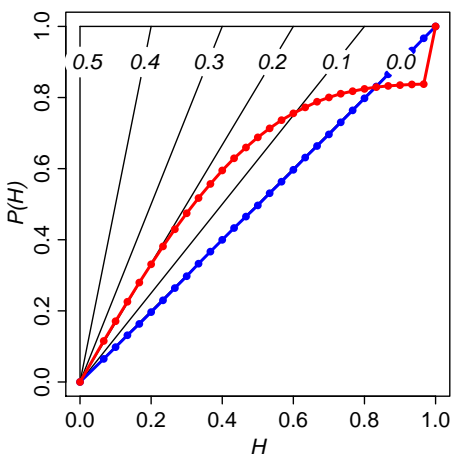
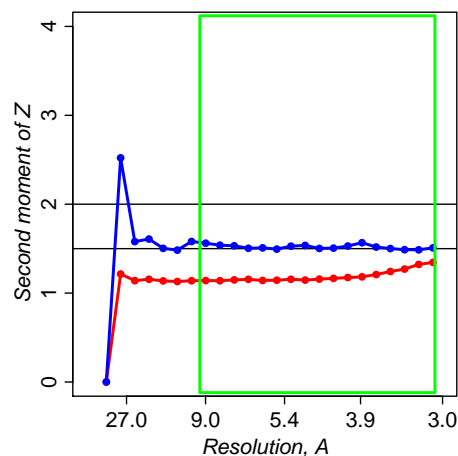
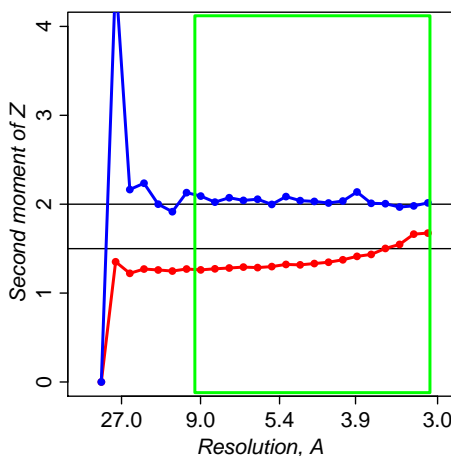
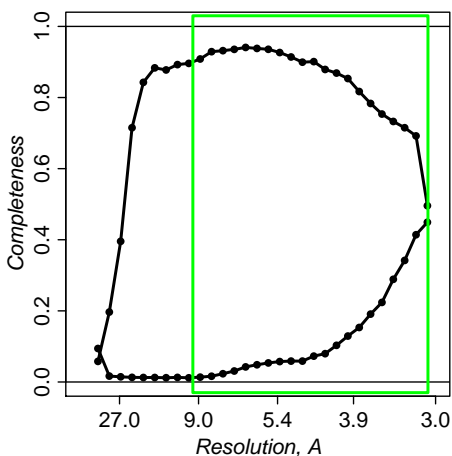
range (A)	87.1-3.0	9.9-3.0
unique	149,855	145,250
measured	118,814	115,065
used	91,158	88,220

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-

residues per monomer	DNA	protein
	0	1967

original

merged



2dbv

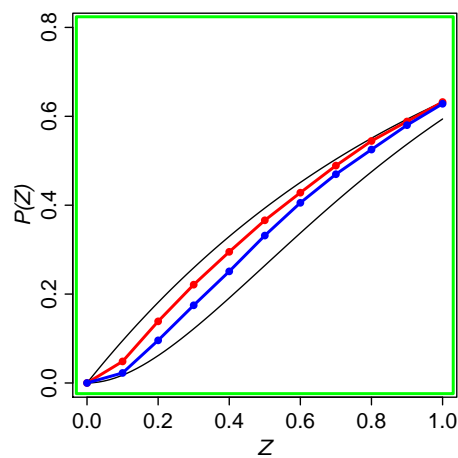
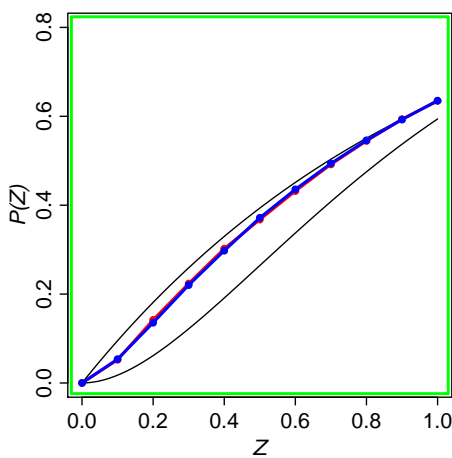
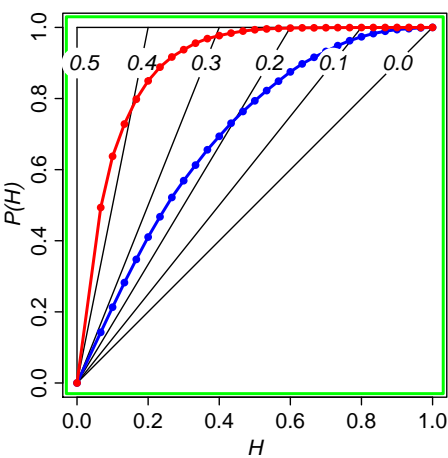
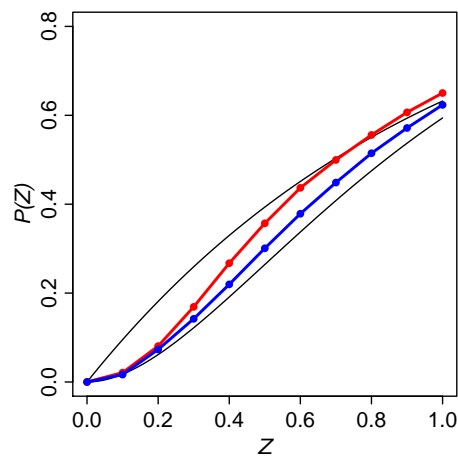
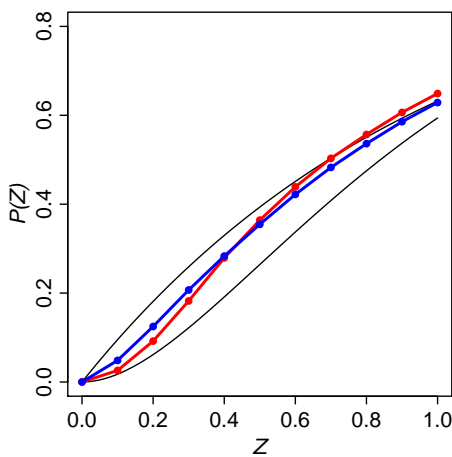
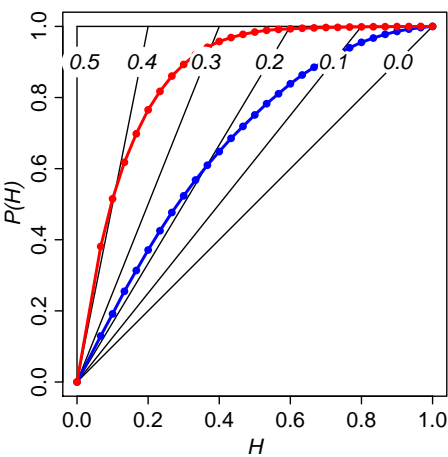
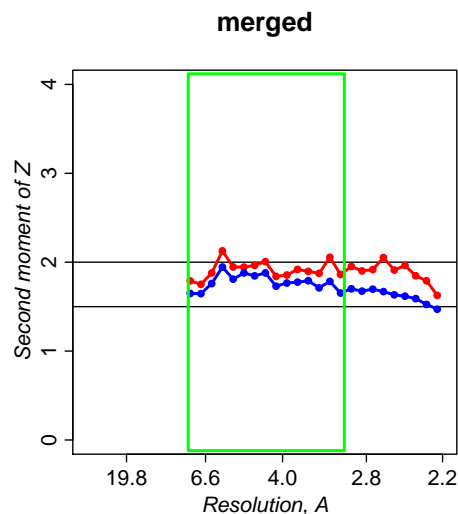
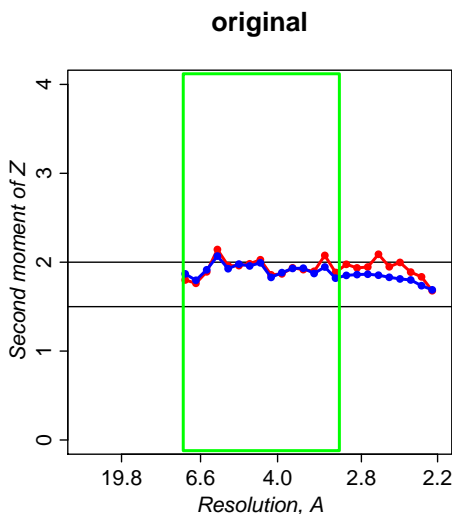
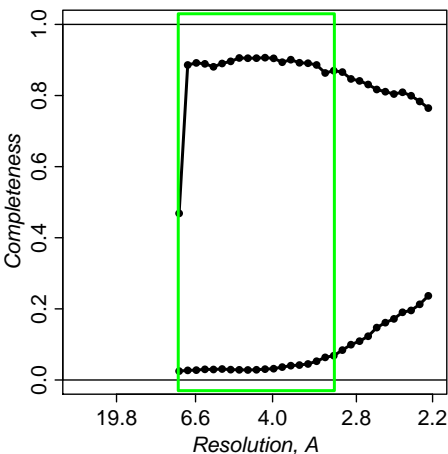
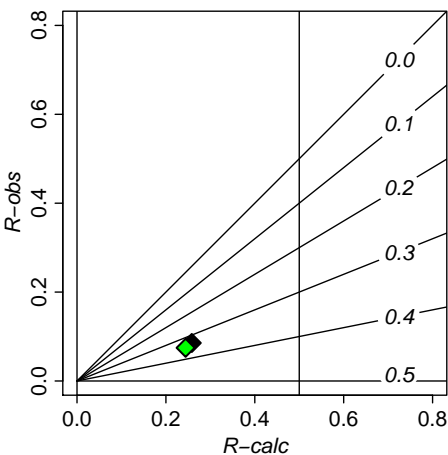
	original	merged
s.g.	P 1 21 1	C 2 2 21
p.g.	10001	10003
a.u.	4	2
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		3.02
R	25.6	
R'	-	-
R-free	29.3	
R'-free	-	-

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	8.0-2.2	8.0-3.0
unique	77,887	29,819
measured	65,528	26,530
used	52,448	21,956

NCS	translation	rotation
r.m.s.d. (A)	3.30	0.28
angle (o)	11.87	0.28

residues per monomer	DNA	protein
	0	334



2fiv

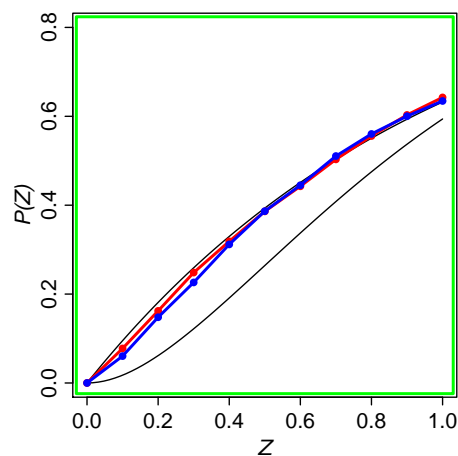
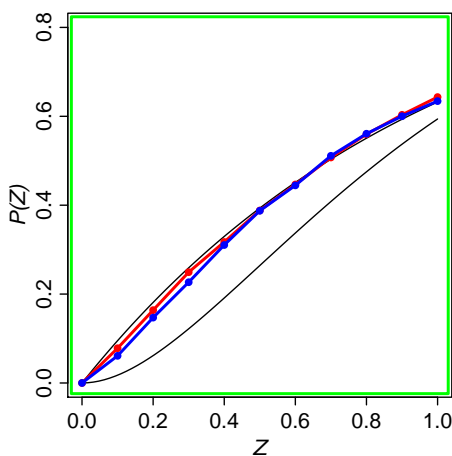
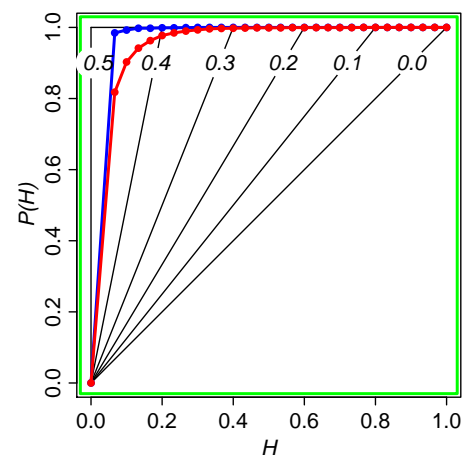
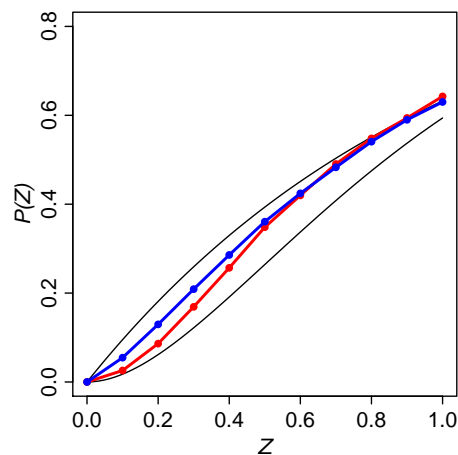
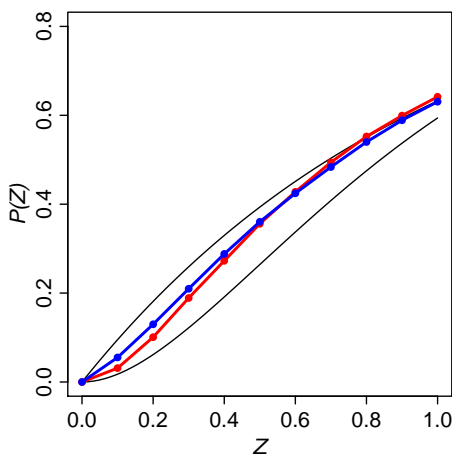
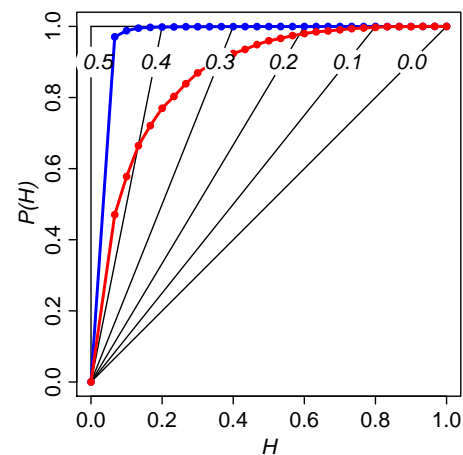
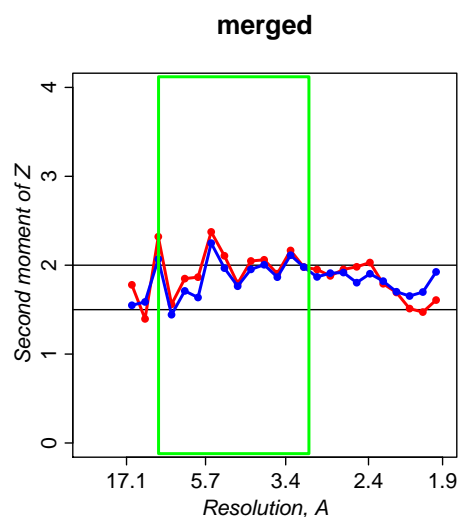
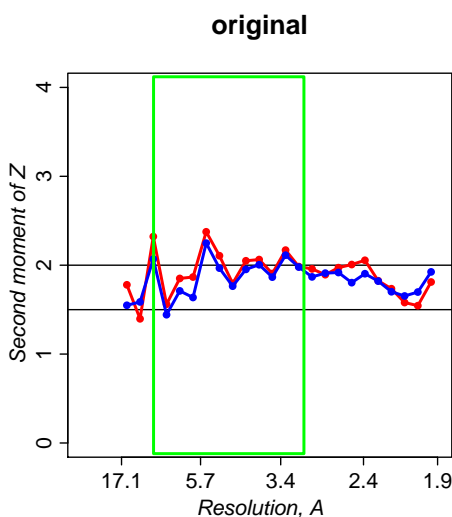
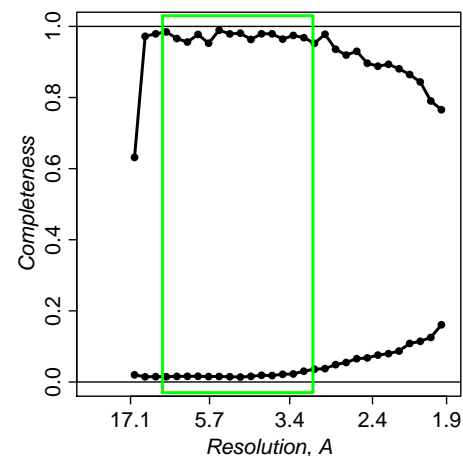
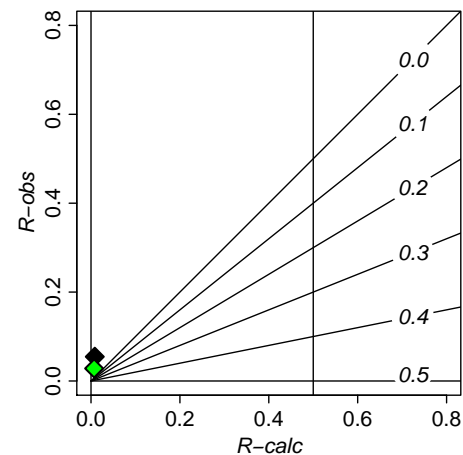
	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.00
R	25.8	
R'	25.9	26.8
R-free	29.2	
R'-free	29.5	30.1

s < f/100	39	0.26 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	17.7–1.9	9.9–3.0
unique	16,726	4,129
measured	14,974	4,010
used	12,654	3,482

NCS	translation	rotation
r.m.s.d. (A)	20.36	0.00
angle (o)	180.00	0.01

residues per monomer	DNA	protein
	0	115



2vhb

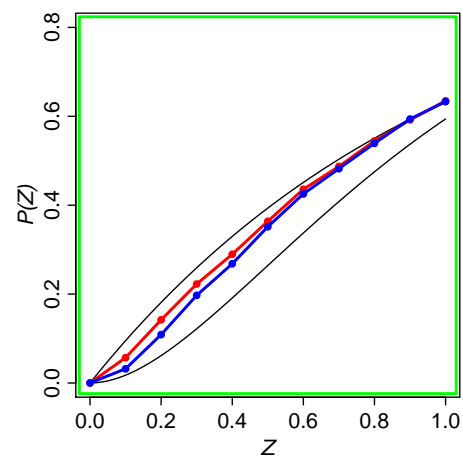
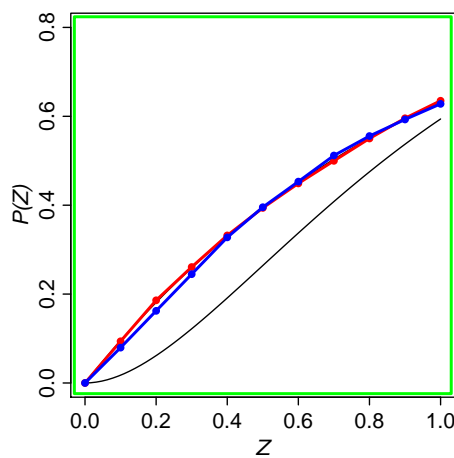
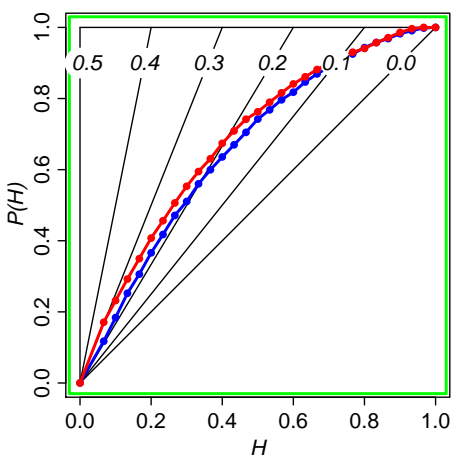
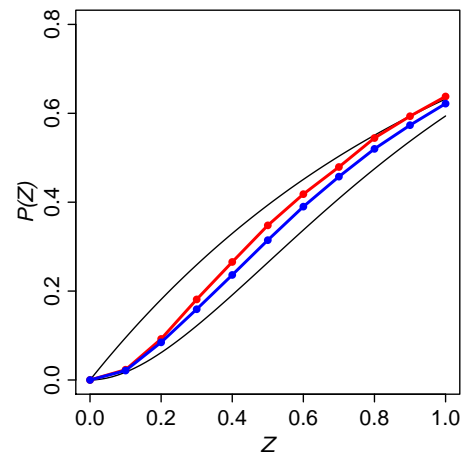
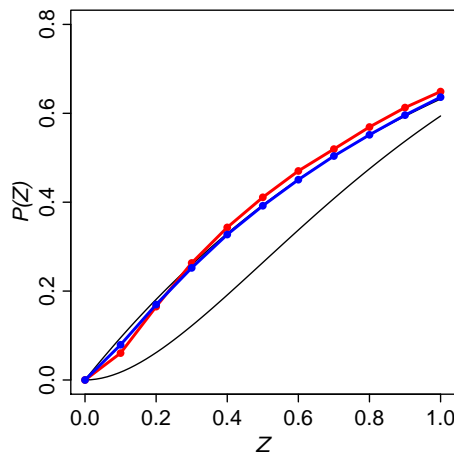
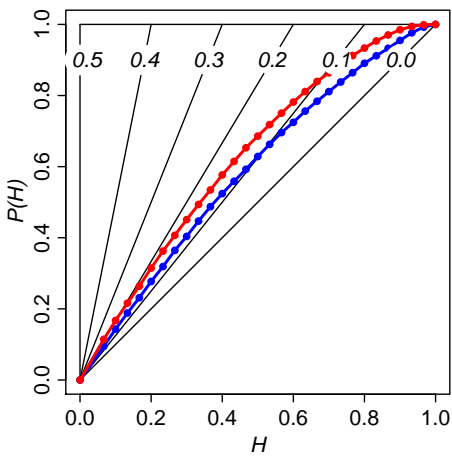
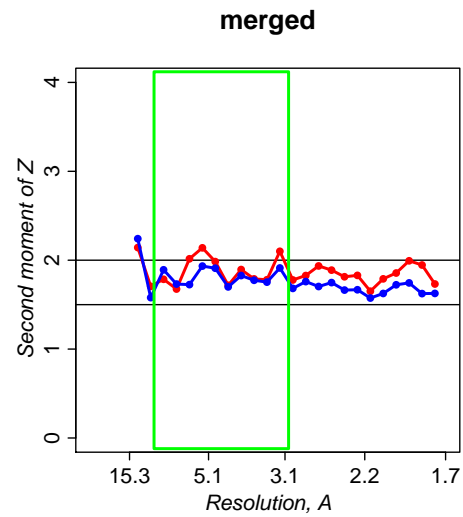
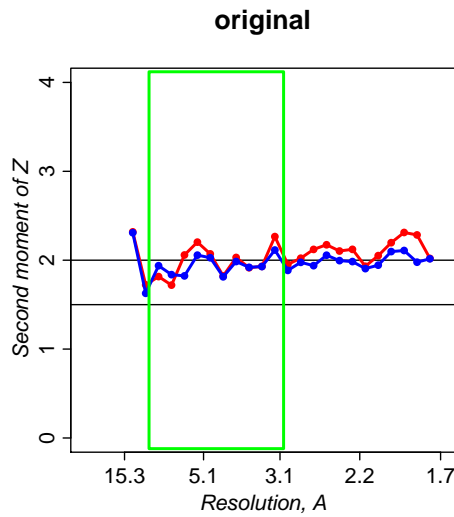
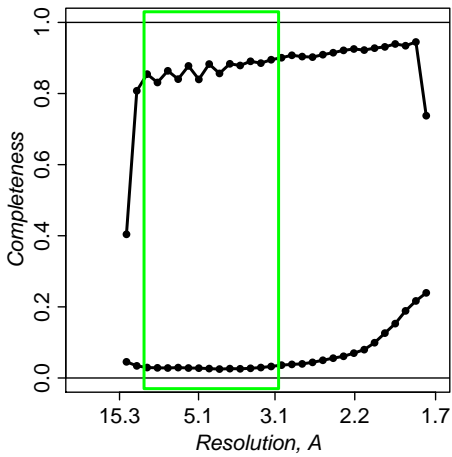
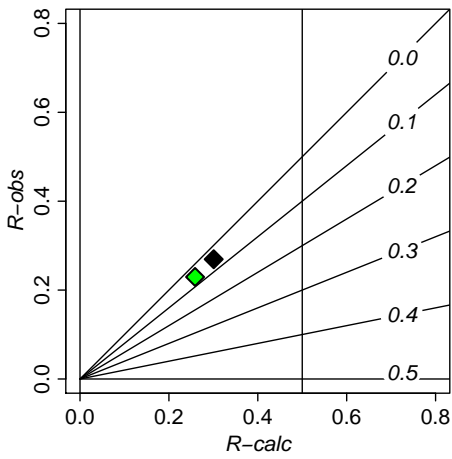
	original	merged
s.g.	P 1 2 1 1	C 2 2 2 1
p.g.	10001	10003
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.79
R	29.3	
R'	29.7	30.4
R-free	30.2	
R'-free	30.8	31.4

residues per monomer	DNA	protein
	0	136

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	14.6–1.7	9.9–3.0
unique	32,265	6,023
measured	29,016	5,287
used	24,952	4,364

NCS	translation	rotation
r.m.s.d. (A)	23.99	0.70
angle (o)	179.34	2.82



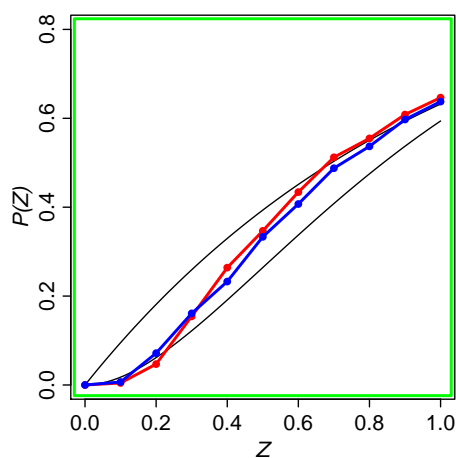
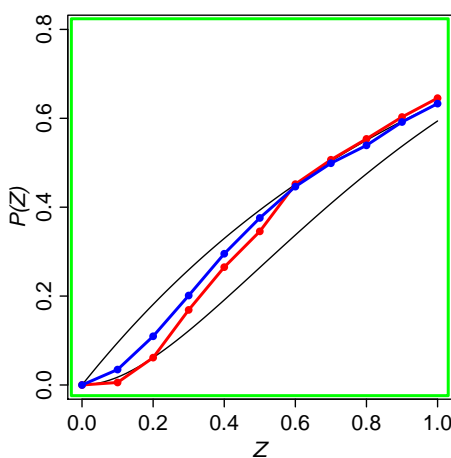
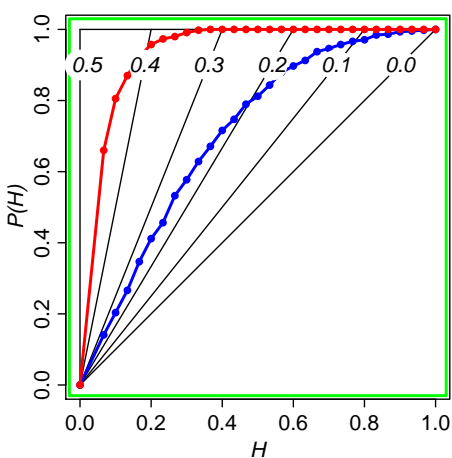
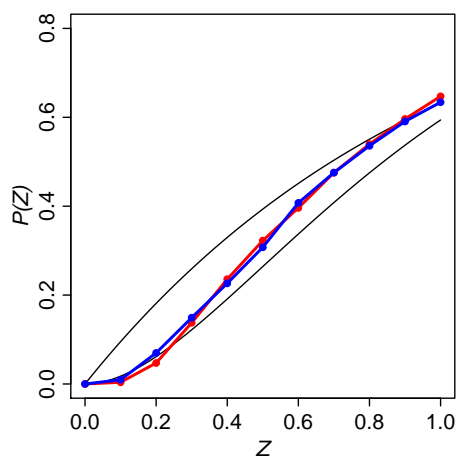
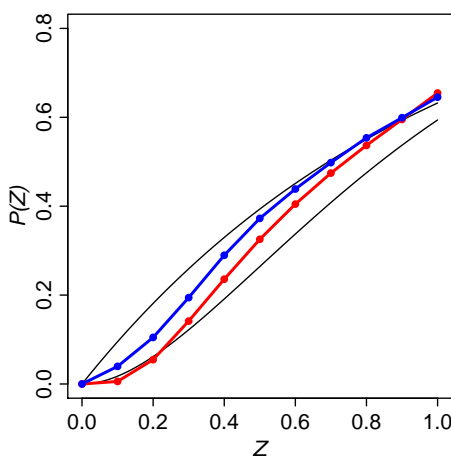
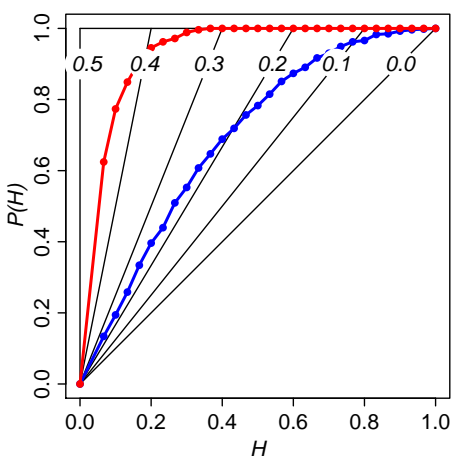
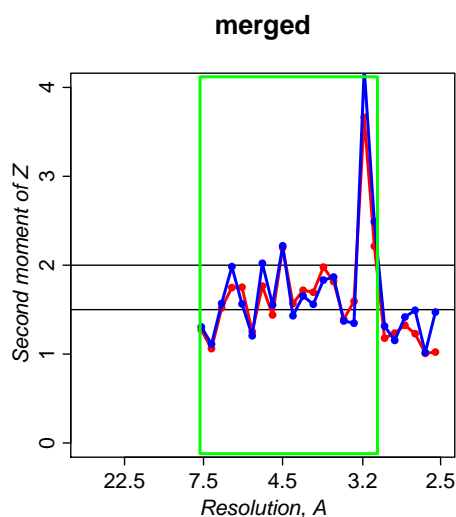
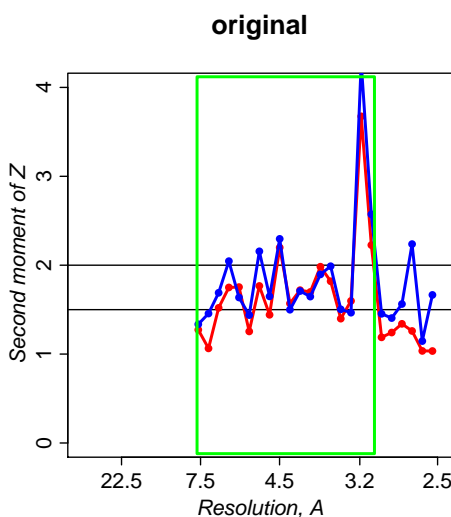
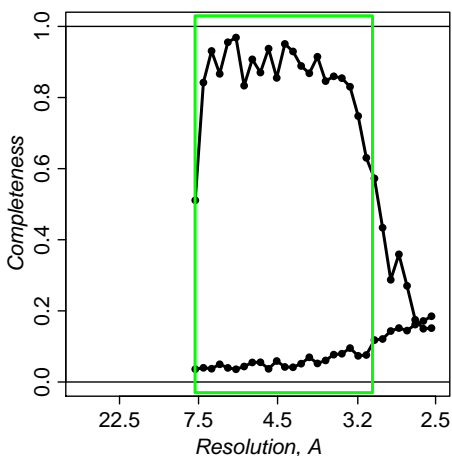
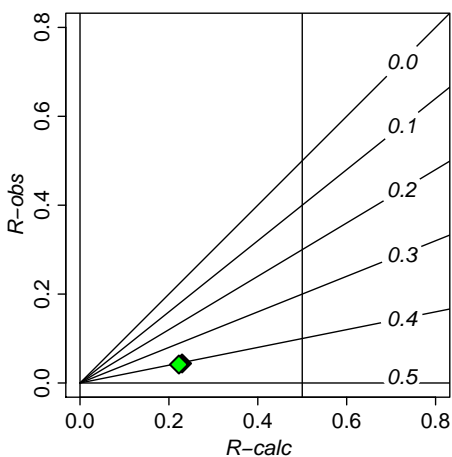
358d

	original	merged
s.g.	P 61	-
p.g.	12021	12027
a.u.	2	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	40.5	-
R'	-	-
R-free	42.1	-
R'-free	-	-
residues per monomer	DNA 3	protein 0

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	8.0-2.5	8.0-3.0
unique	2,835	1,630
measured	1,667	1,352
used	1,060	894

NCS	translation	rotation
r.m.s.d. (A)	2.69	10.38
angle (o)	28.58	151.46



3fiv

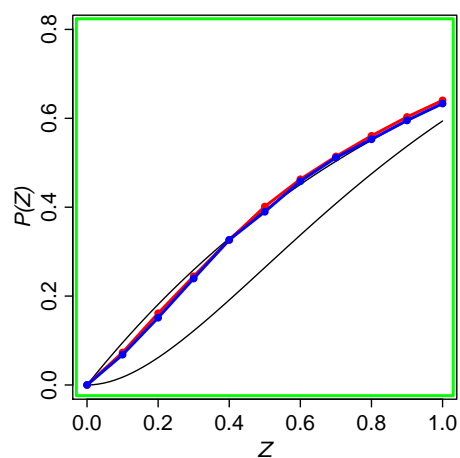
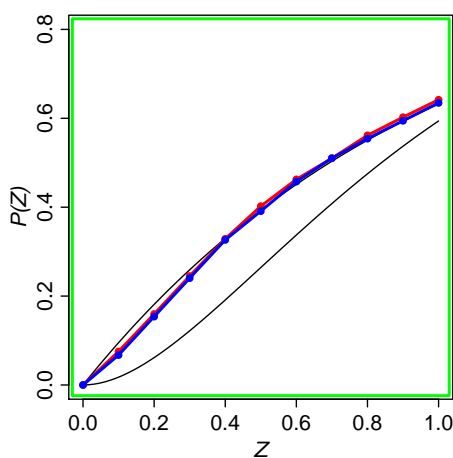
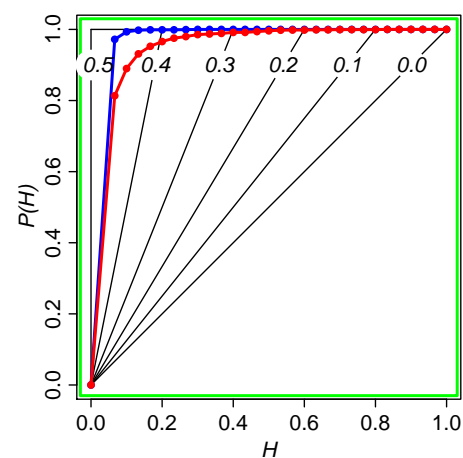
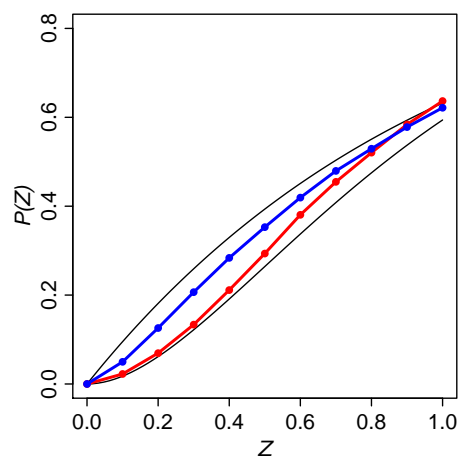
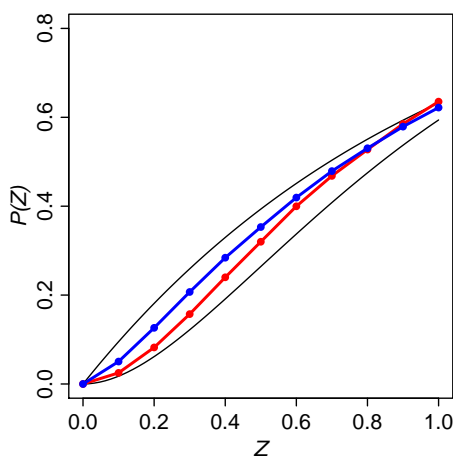
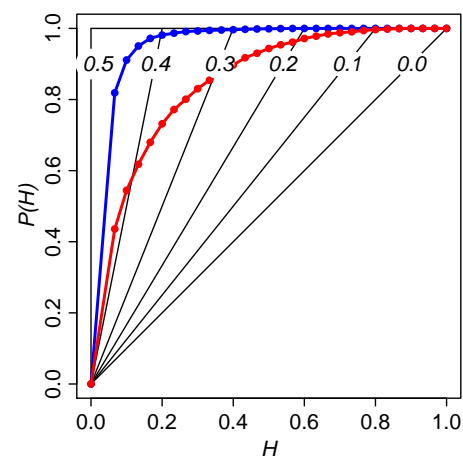
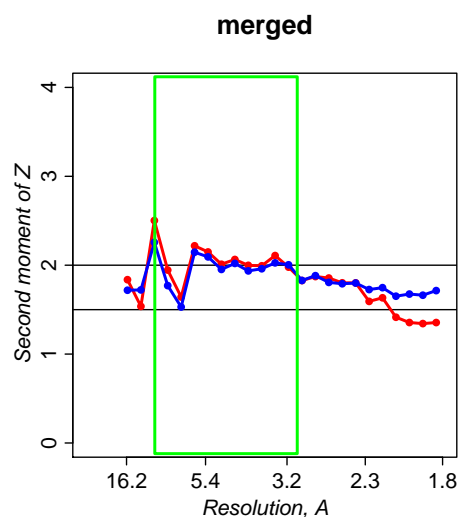
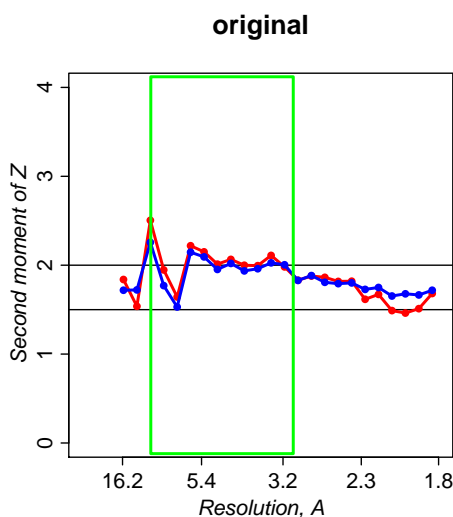
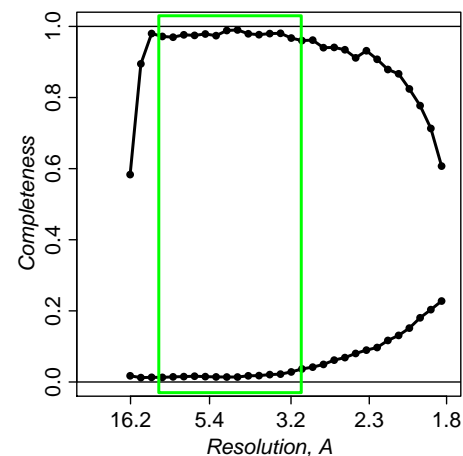
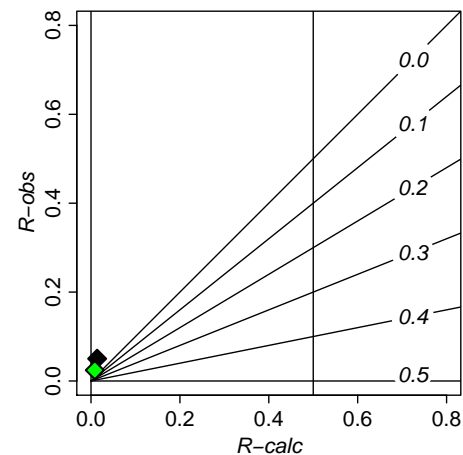
	original	merged
s.g.	P 31	P 31 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.01
R	25.6	
R'	25.6	26.7
R-free	28.2	
R'-free	28.2	28.7

s < f/100	135	0.78 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	19.0–1.8	9.9–3.0
unique	20,091	4,189
measured	17,411	4,088
used	14,578	3,566

NCS	translation	rotation
r.m.s.d. (A)	21.82	0.01
angle (o)	179.99	0.01

residues per monomer	DNA	protein
	0	114



3ng1

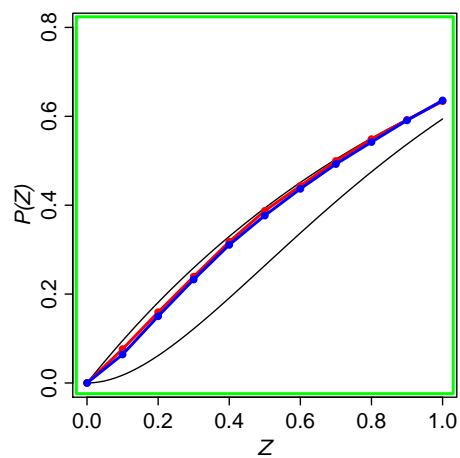
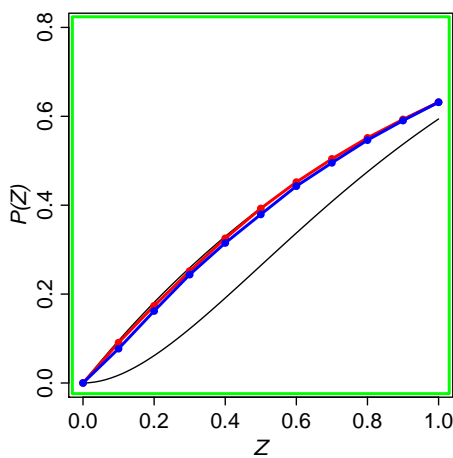
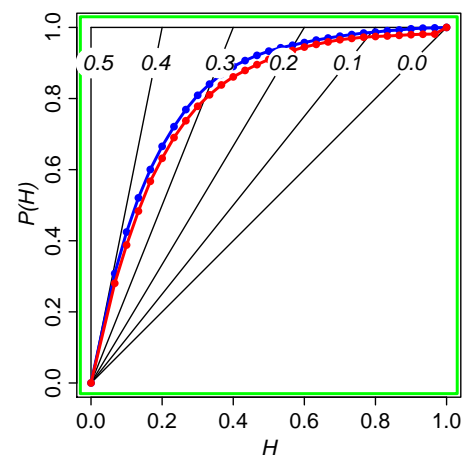
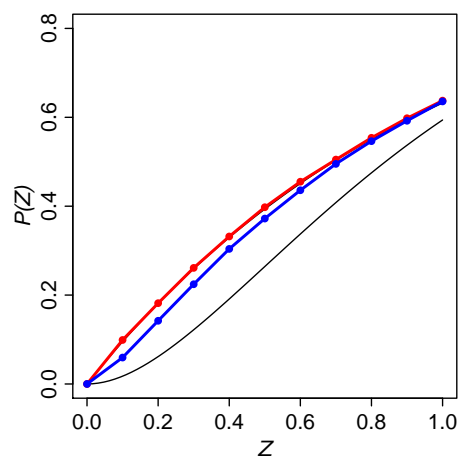
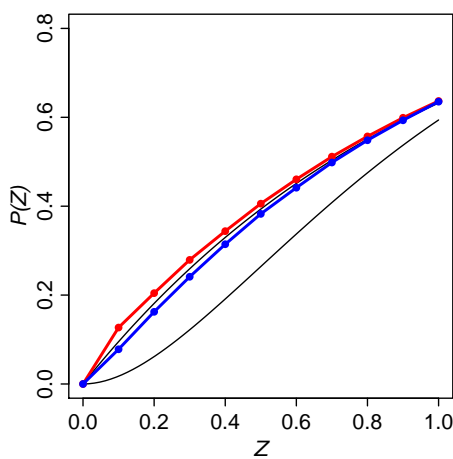
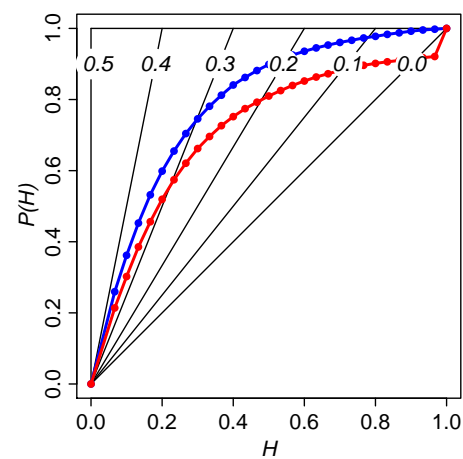
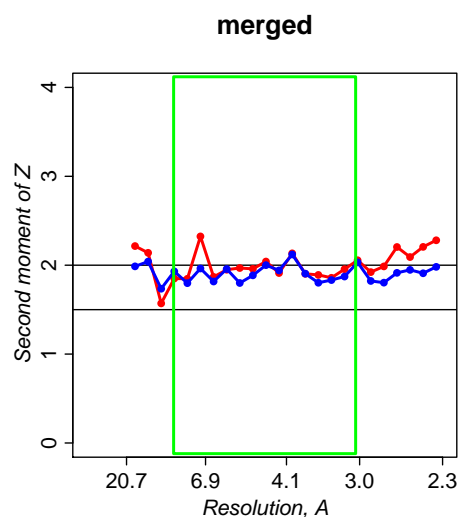
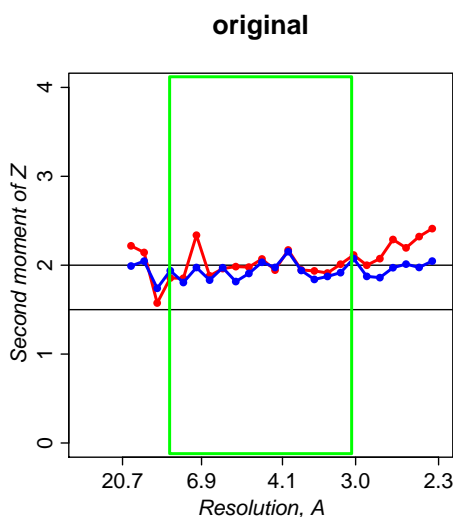
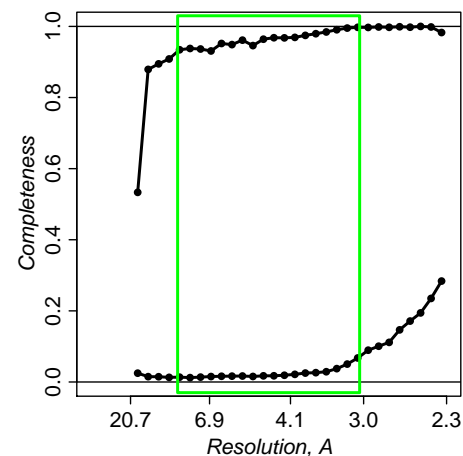
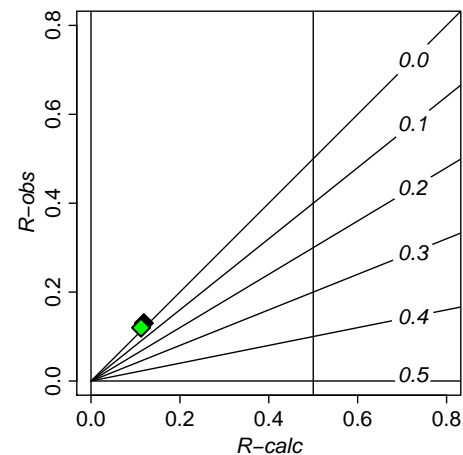
	original	merged
s.g.	P 21 21 21	P 43 21 2
p.g.	10003	10205
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.28
R	27.0	
R'	27.0	27.2
R-free	29.9	
R'-free	29.9	29.8

s < f/100	1380	4.25 %
s <= 0	0	0.00 %
f <= 0	2050	6.31 %
s,f <= 0	0	0.00 %

range (A)	19.7–2.3	9.9–3.0
unique	33,000	14,635
measured	32,508	14,260
used	28,458	12,344

NCS	translation	rotation
r.m.s.d. (A)	29.01	0.21
angle (o)	89.67	0.33

residues per monomer	DNA	protein
	0	294



3sxl

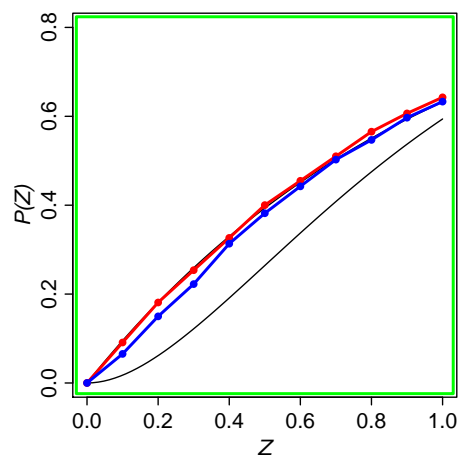
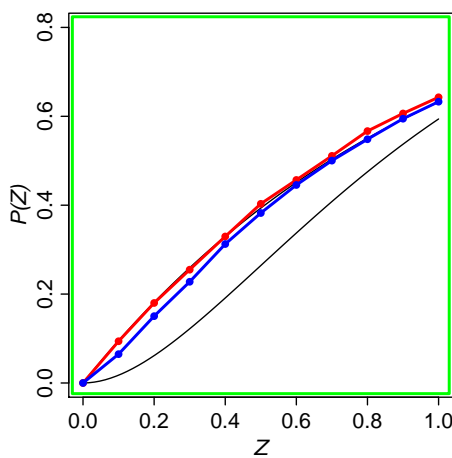
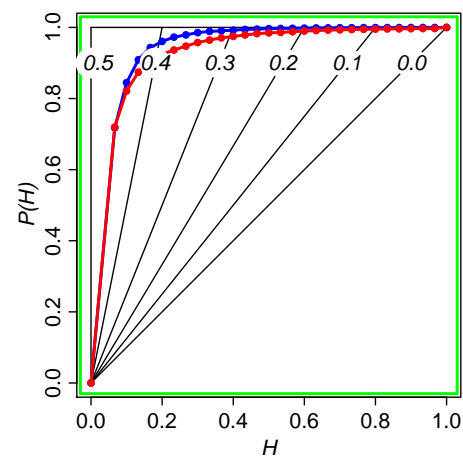
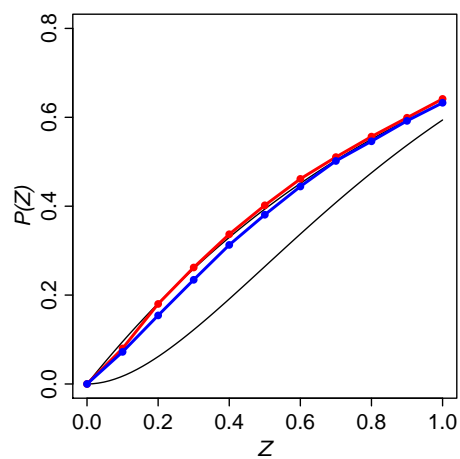
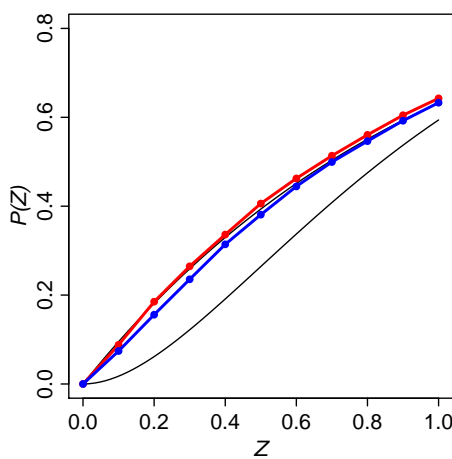
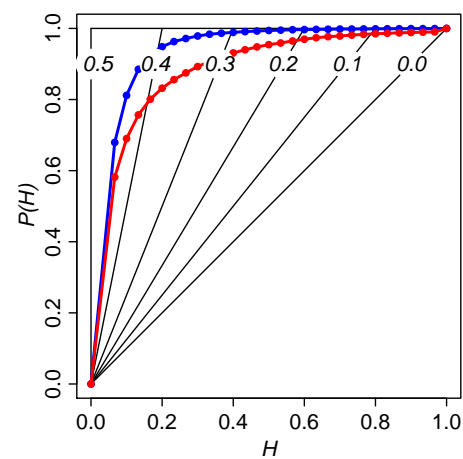
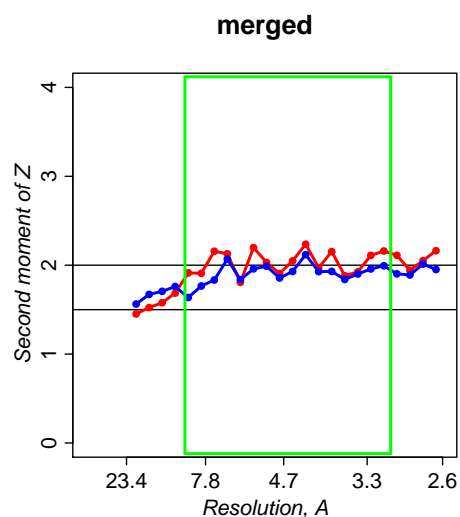
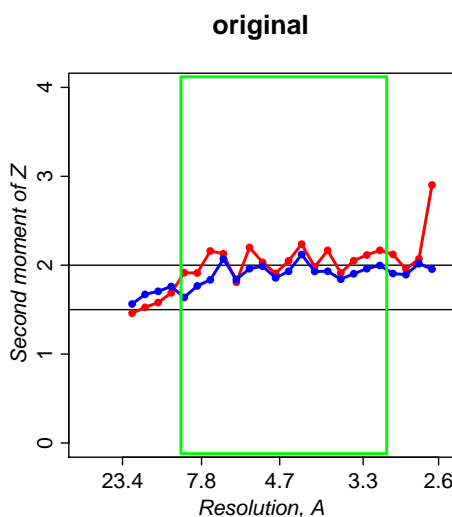
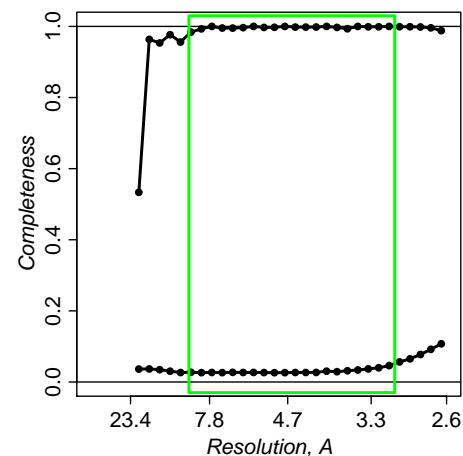
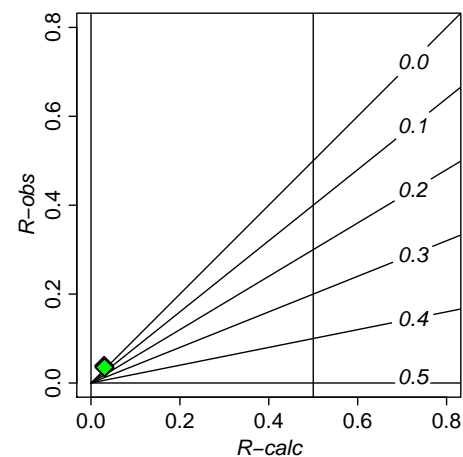
	original	merged
s.g.	P 1 21 1	P 65
p.g.	10001	12021
a.u.	3	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.04
R	24.2	
R'	24.2	23.8
R-free	31.1	
R'-free	31.0	31.0

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	193	1.15 %
s,f <= 0	0	0.00 %

range (A)	21.7–2.6	9.9–3.0
unique	16,907	10,688
measured	16,847	10,667
used	16,278	10,299

NCS	translation	rotation
r.m.s.d. (A)	18.40	0.03
angle (o)	59.98	0.04

residues per monomer	DNA	protein
	0	157



405d

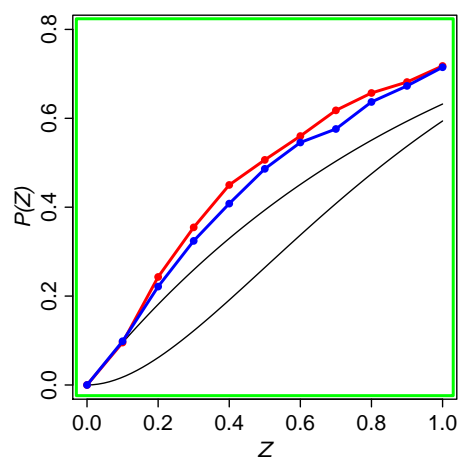
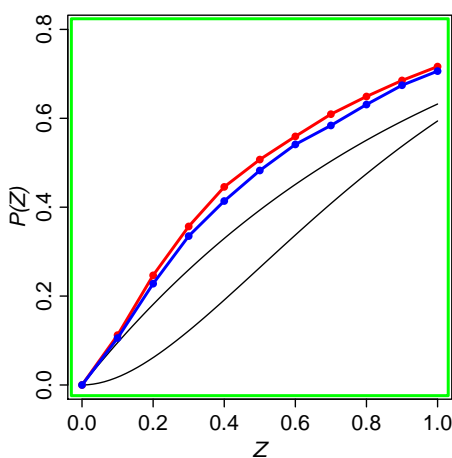
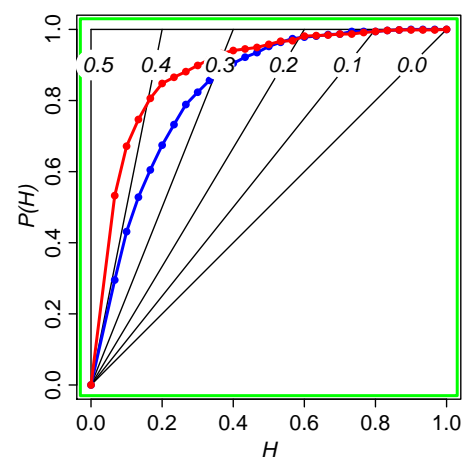
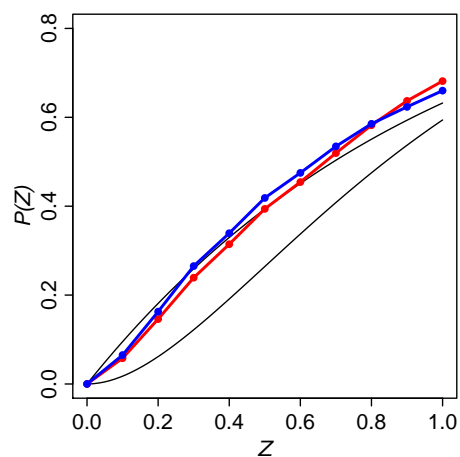
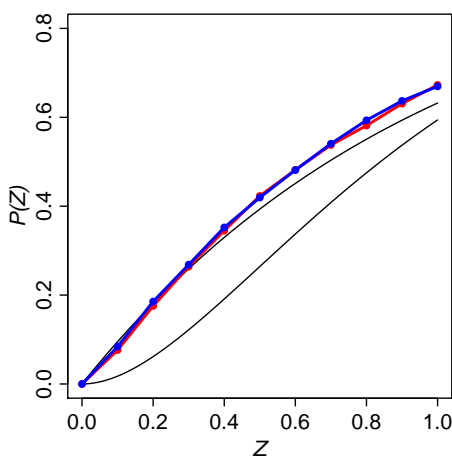
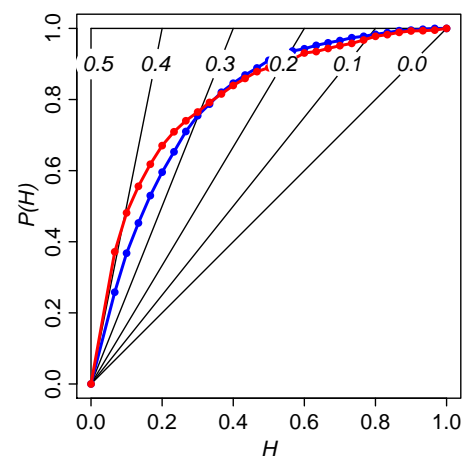
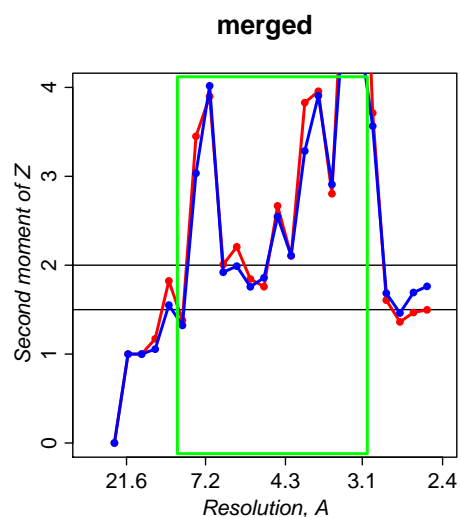
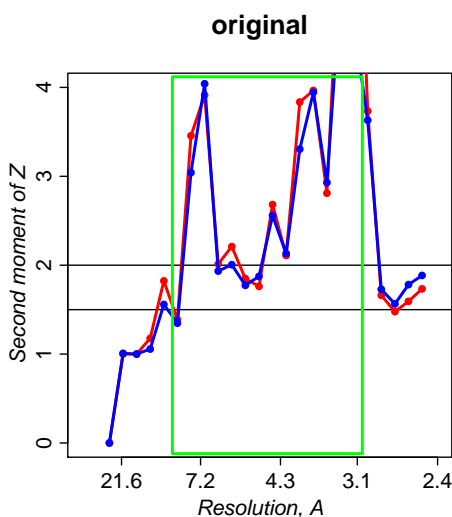
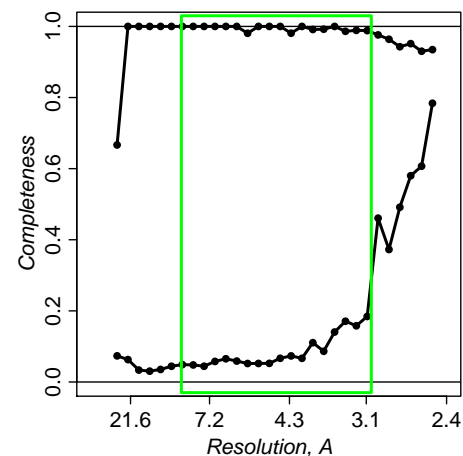
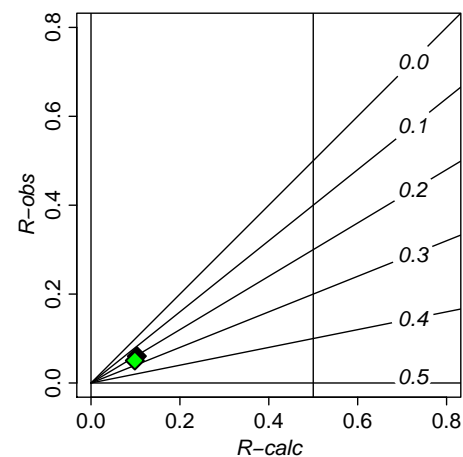
	original	merged
s.g.	H 3	H 3 2
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.22
R	17.4	
R'	17.4	17.7
R-free	19.4	
R'-free	19.6	18.6

s < f/100	2	0.07 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	41.4–2.5	9.9–3.0
unique	3,057	1,637
measured	2,972	1,625
used	2,518	1,374

NCS	translation	rotation
r.m.s.d. (A)	26.12	0.21
angle (o)	179.73	0.28

residues per monomer	DNA	protein
	15	0



406d

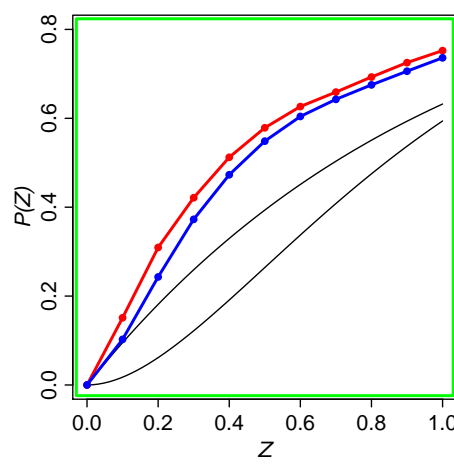
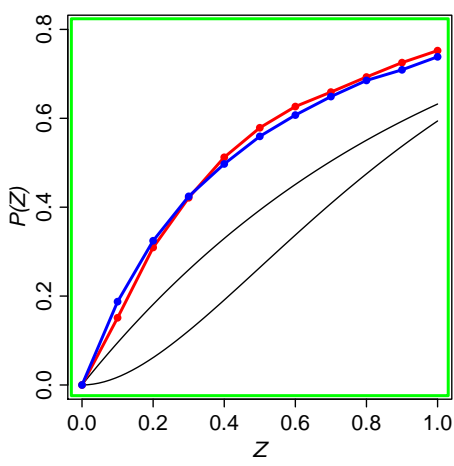
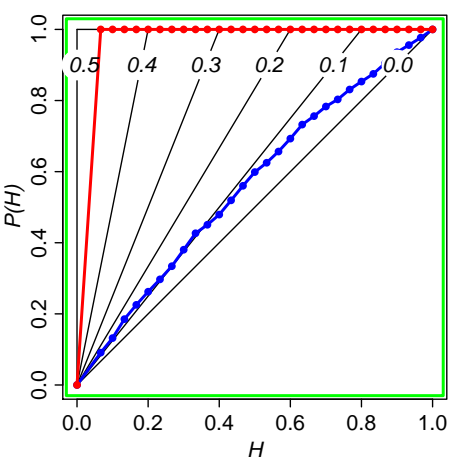
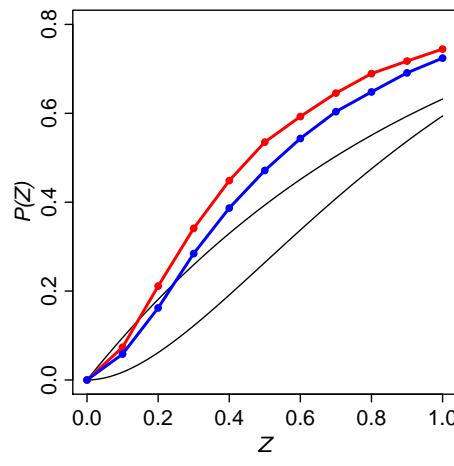
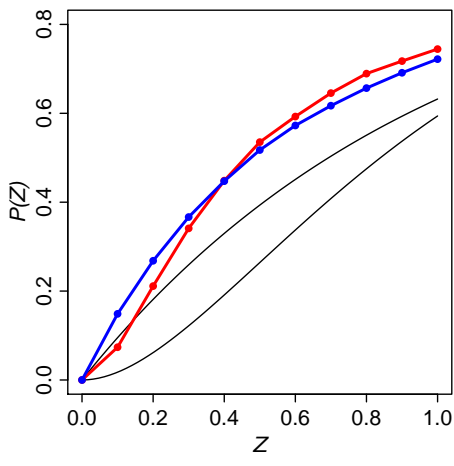
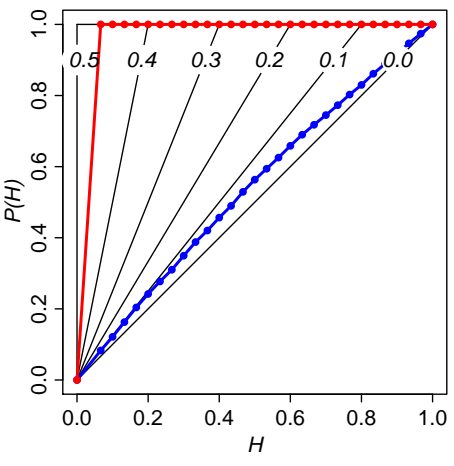
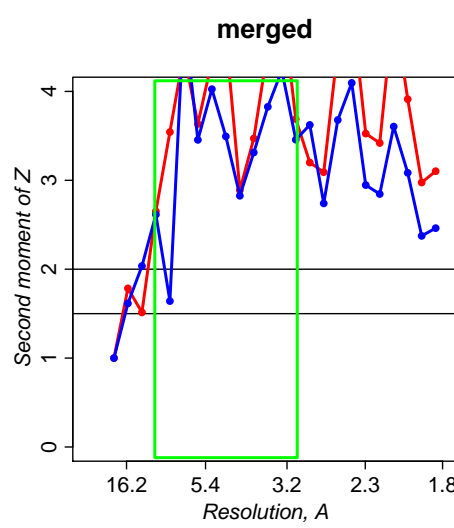
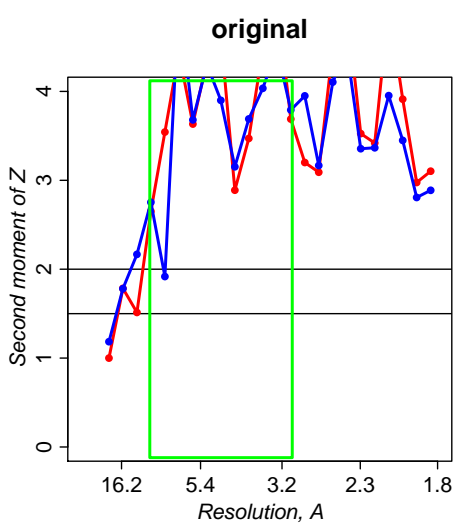
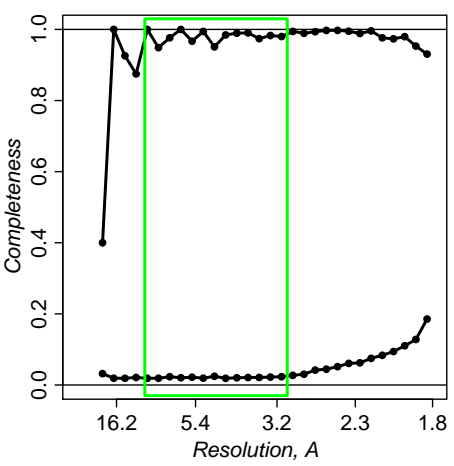
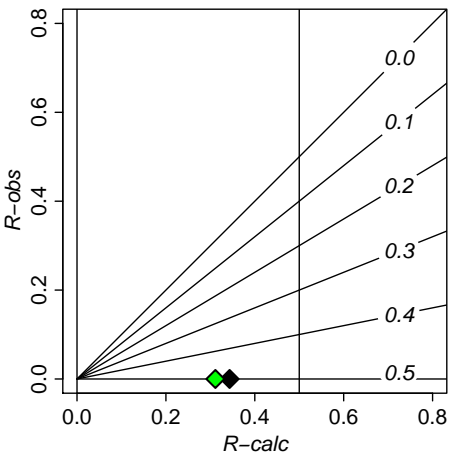
	original	merged
s.g.	P 3	P 3 2 1
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		0.52
R	44.4	
R'	44.7	46.0
R-free	48.1	
R'-free	48.6	49.4

residues per monomer	DNA	protein
	15	0

s < f/100	112	0.77 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	32.1–1.8	9.9–3.0
unique	14,848	3,119
measured	14,516	3,060
used	13,106	2,586

NCS	translation	rotation
r.m.s.d. (A)	28.84	0.49
angle (o)	179.36	0.93



464d

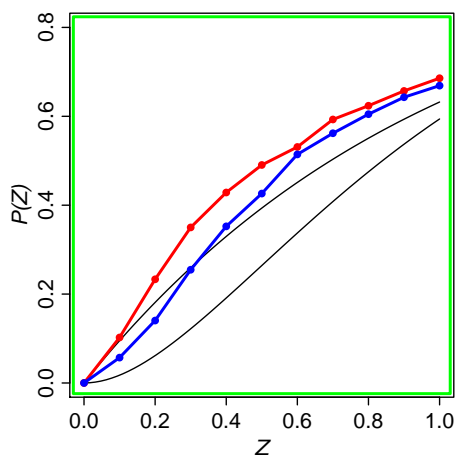
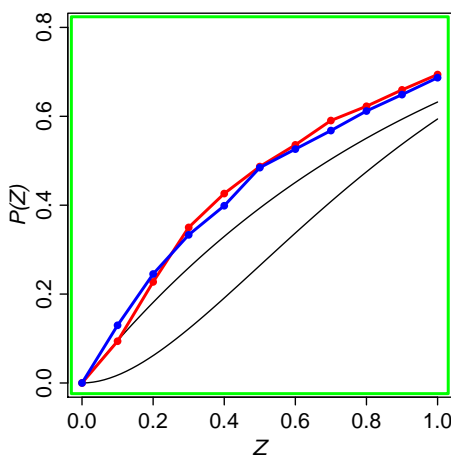
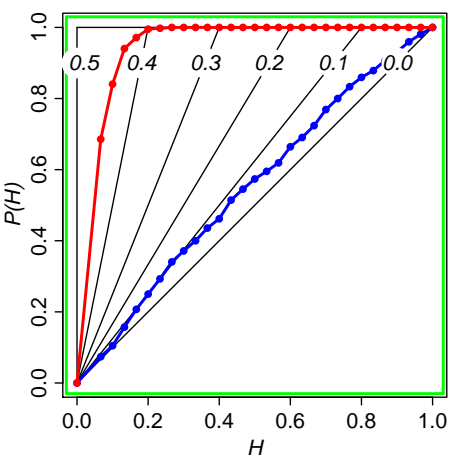
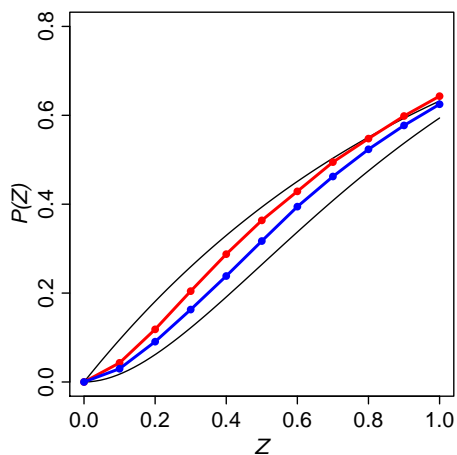
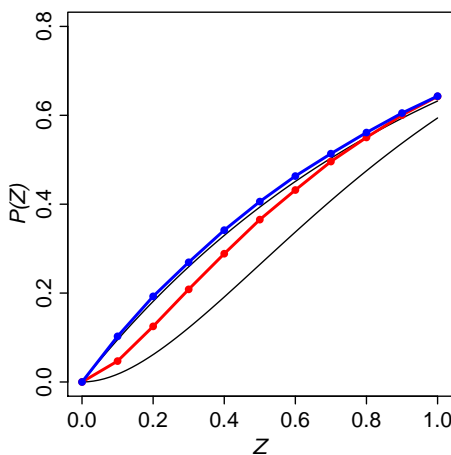
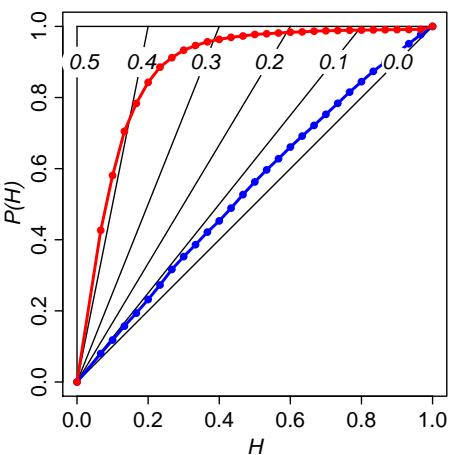
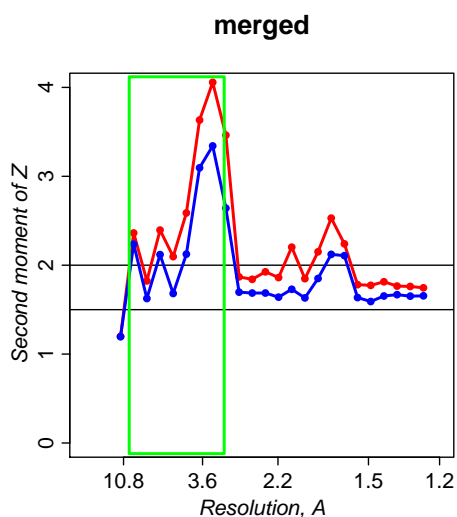
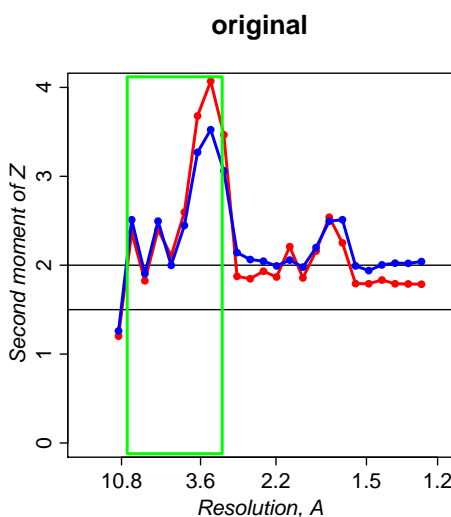
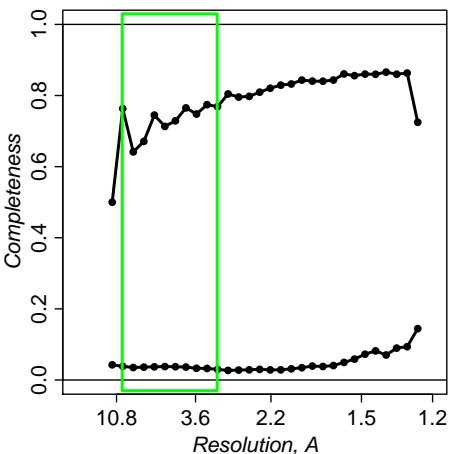
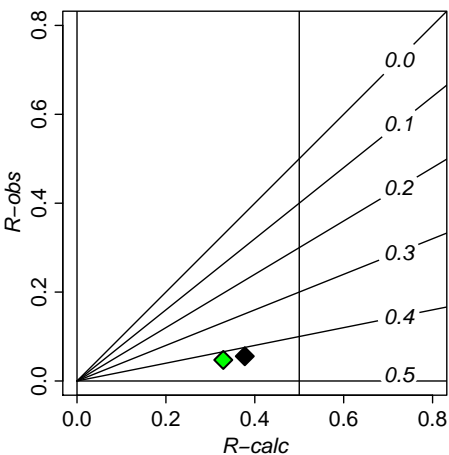
	original	merged
s.g.	P 1	-
p.g.	10000	10001
a.u.	2	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	37.3	-
R'	-	-
R-free	38.9	-
R'-free	-	-

residues per monomer	DNA	protein
	11	0

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	126	0.67 %
s,f <= 0	0	0.00 %

range (A)	14.3-1.2	9.9-3.0
unique	22,726	1,539
measured	18,836	1,152
used	15,350	834

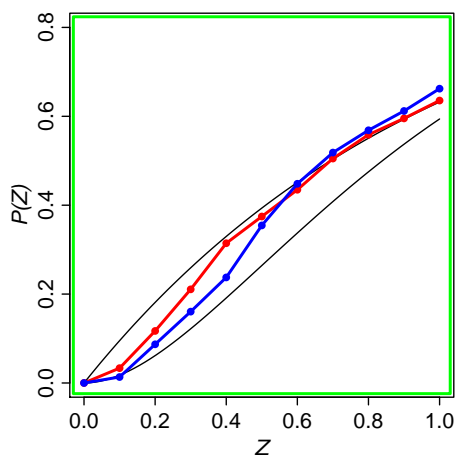
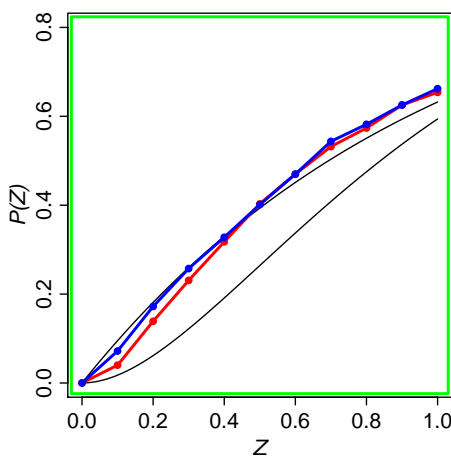
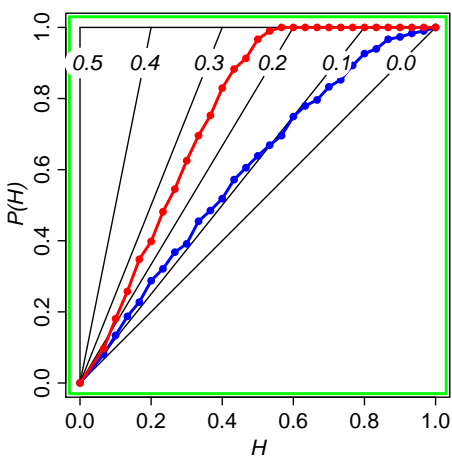
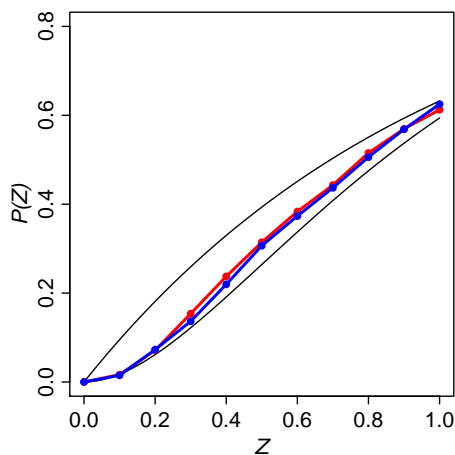
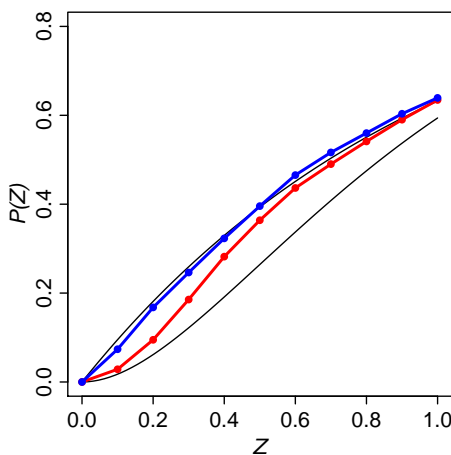
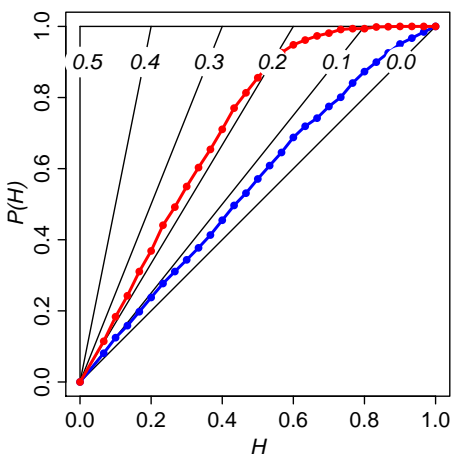
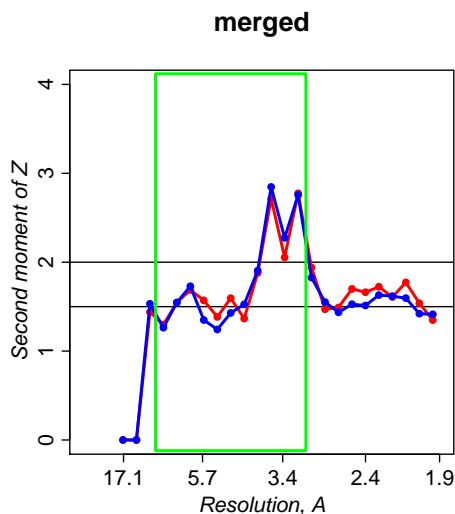
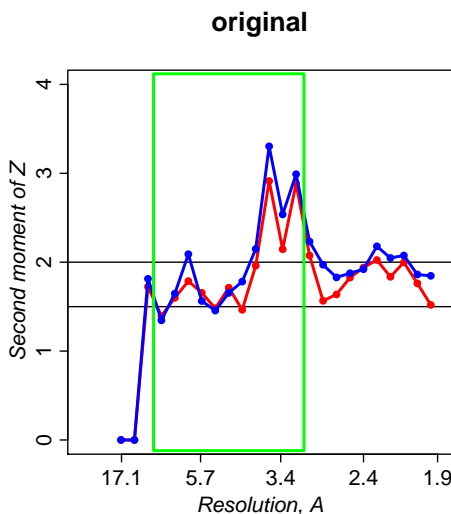
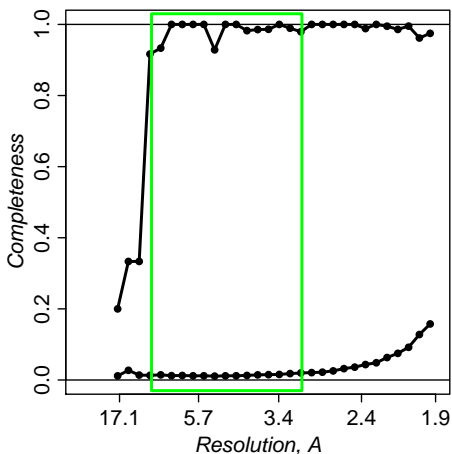
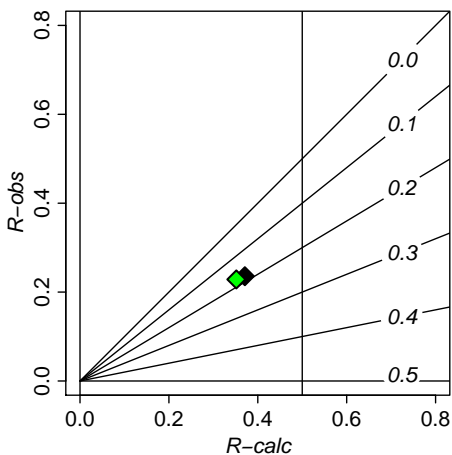
NCS	translation	rotation
r.m.s.d. (A)	16.52	17.51
angle (o)	179.22	179.36



472d

	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	25.0	-
R'	-	-
R-free	29.7	-
R'-free	-	-
residues per monomer	DNA 14	protein 0

s < f/100	90	3.14 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %
range (A)	21.0-1.9	9.9-3.0
unique	2,905	721
measured	2,862	710
used	2,550	596
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



485d

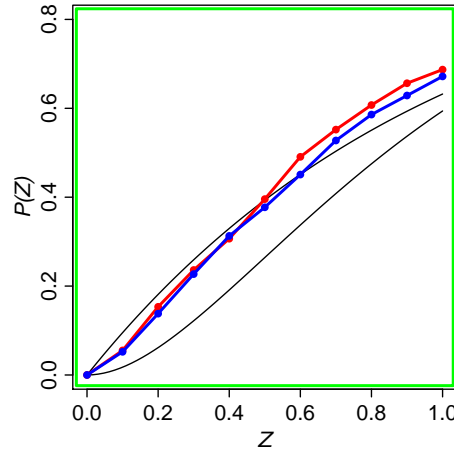
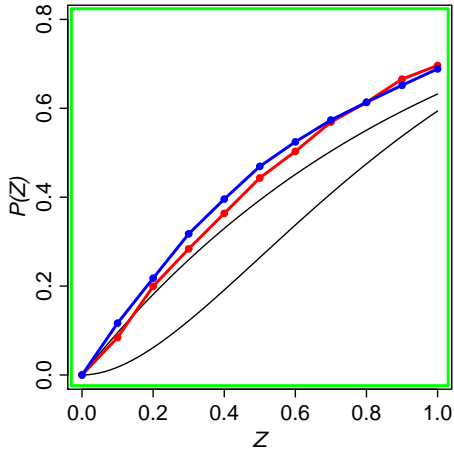
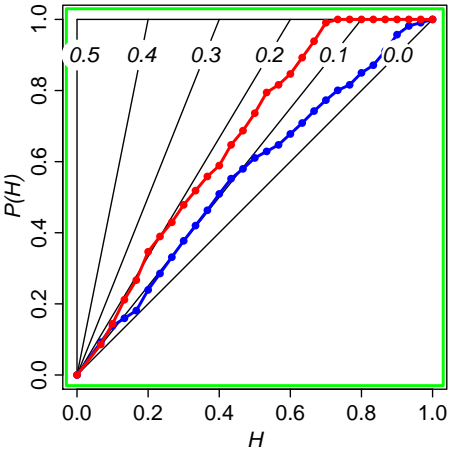
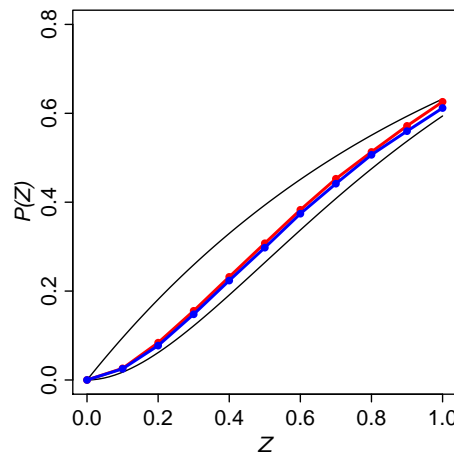
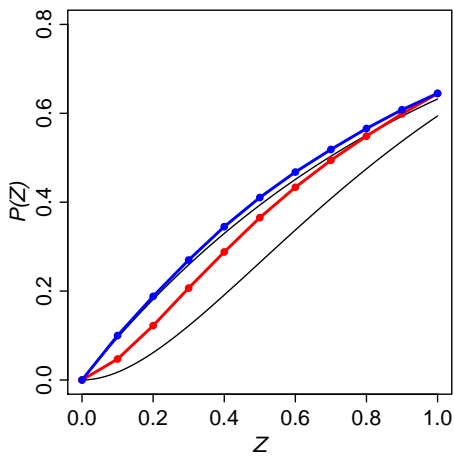
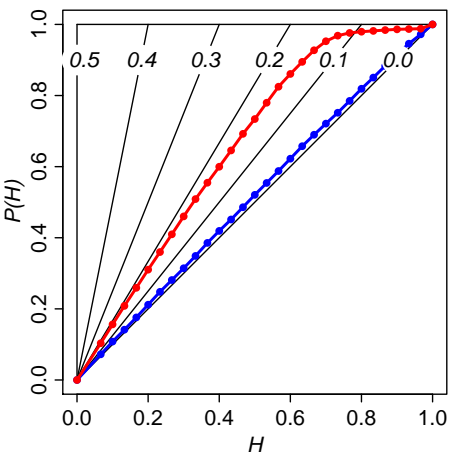
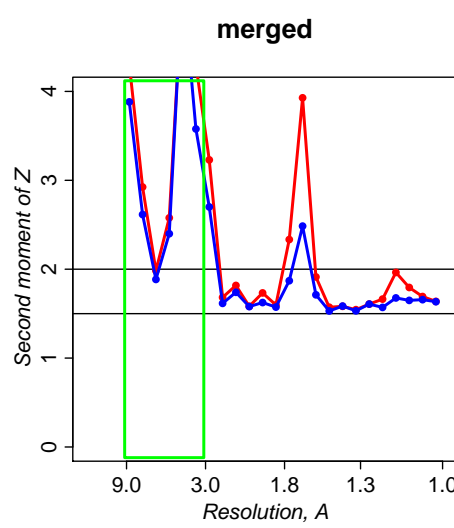
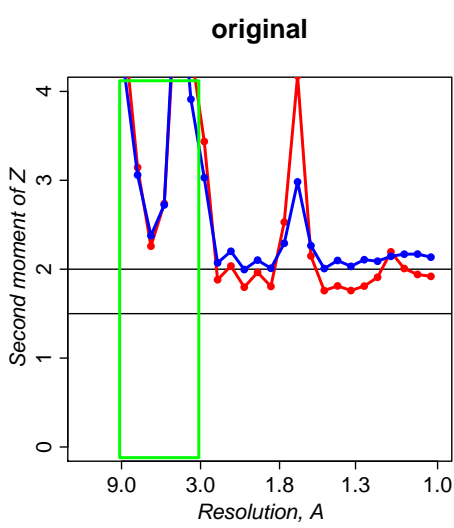
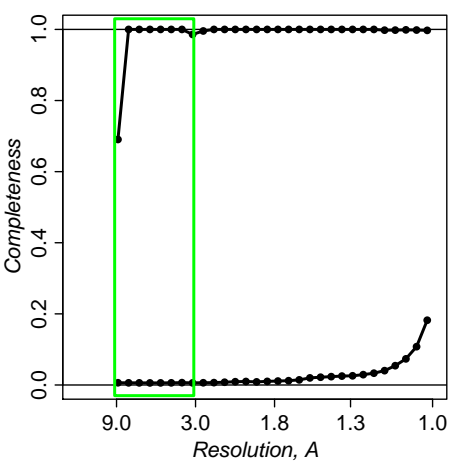
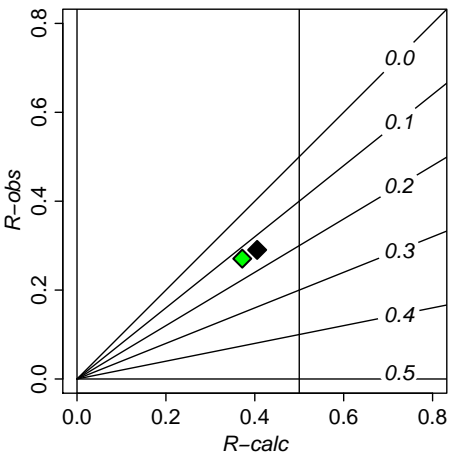
	original	merged
s.g.	H 3	H 3 2
p.g.	10020	10023
a.u.	2	1
p.t.	1	1
p.o.	1	1
r.m.s.d. (A)		5.23
R	26.4	
R'	-	-
R-free	26.6	
R'-free	-	-

residues per monomer	DNA	protein
	8	0

s < f/100	2987	13.79 %
s <= 0	0	0.00 %
f <= 0	147	0.68 %
s,f <= 0	0	0.00 %

range (A)	10.0-1.0	9.9-3.0
unique	21,679	782
measured	21,659	779
used	20,422	652

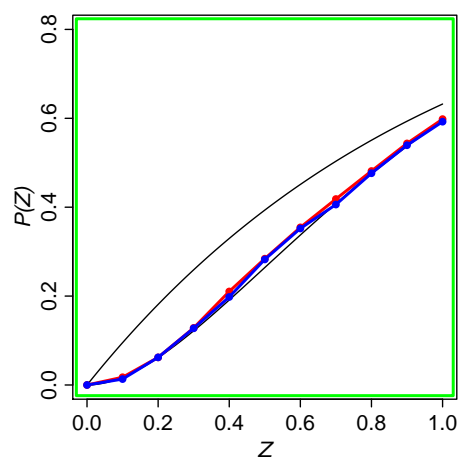
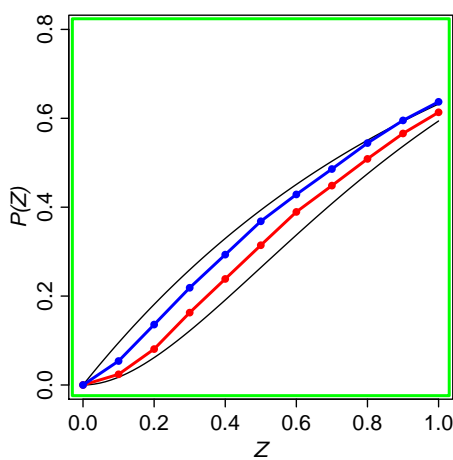
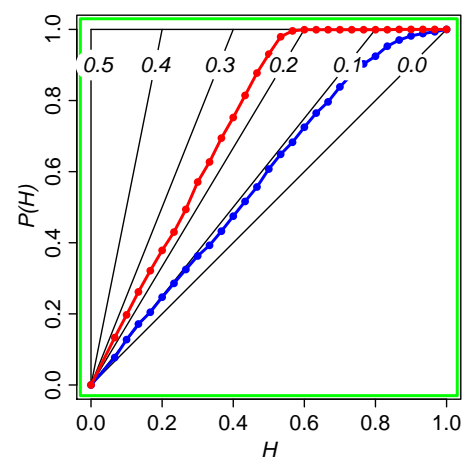
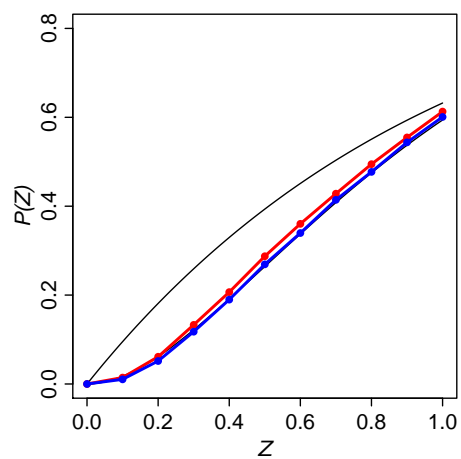
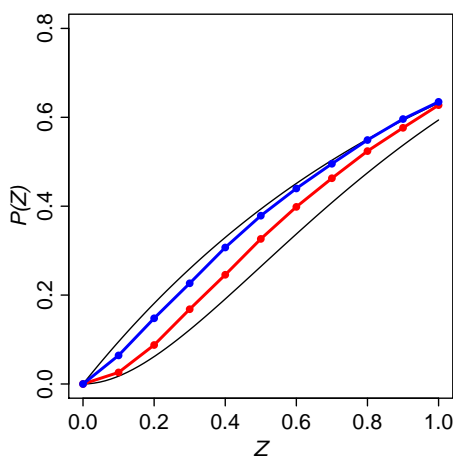
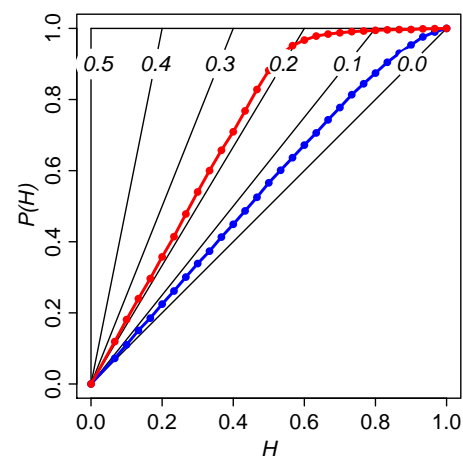
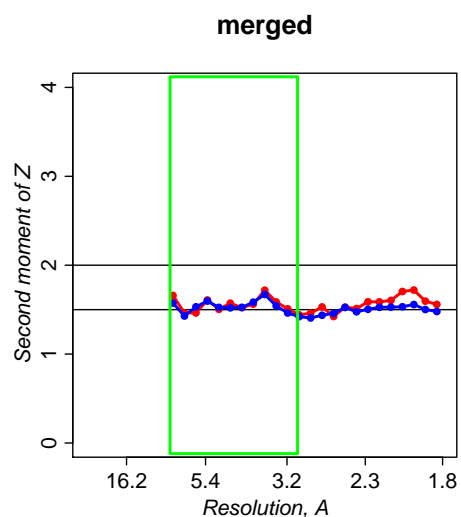
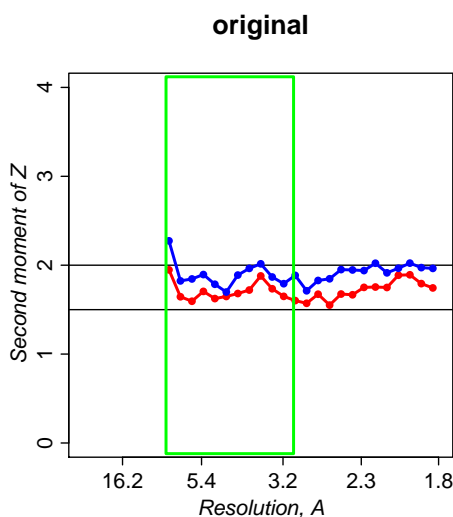
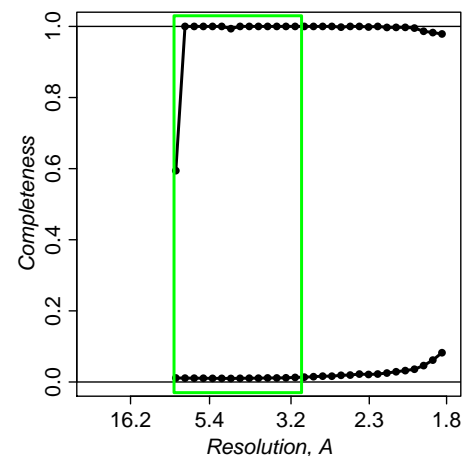
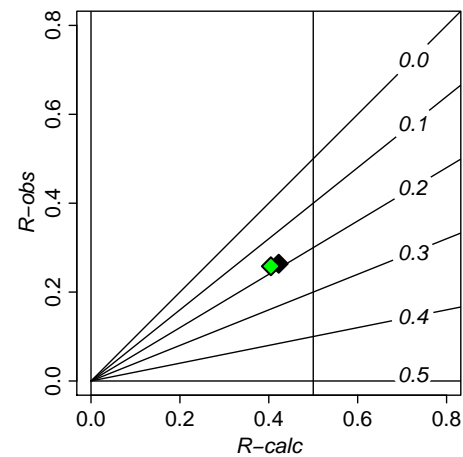
NCS	translation	rotation
r.m.s.d. (A)	16.69	4.85
angle (o)	178.22	31.83



4tsv

	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	25.3	-
R'	-	-
R-free	28.5	-
R'-free	-	-
residues per monomer	DNA 0	protein 148

s < f/100	990	7.68 %
s <= 0	59	0.46 %
f <= 0	59	0.46 %
s,f <= 0	59	0.46 %
range (A)	8.0-1.8	8.0-3.0
unique	12,944	2,668
measured	12,884	2,667
used	12,074	2,414
NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-



5pgm

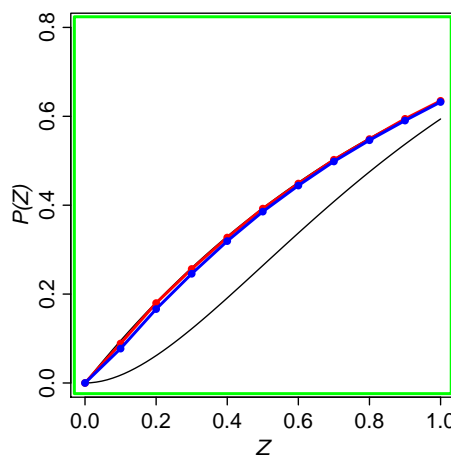
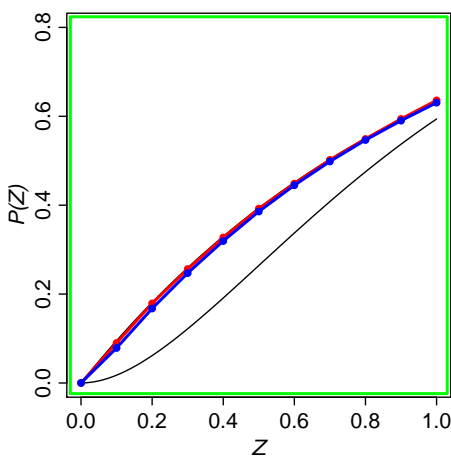
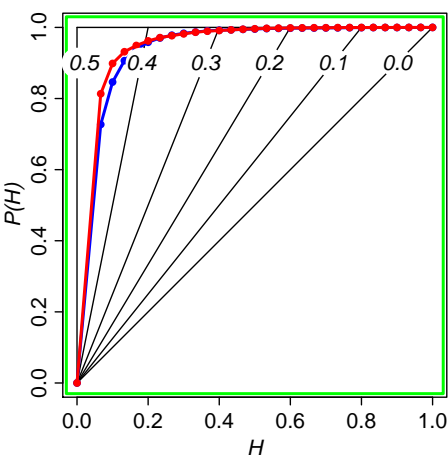
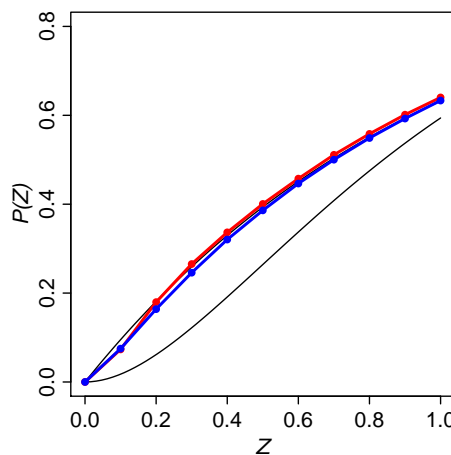
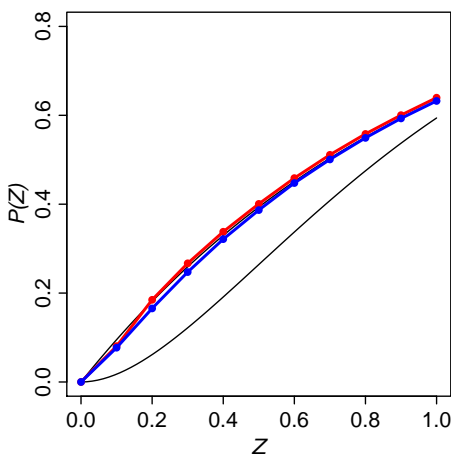
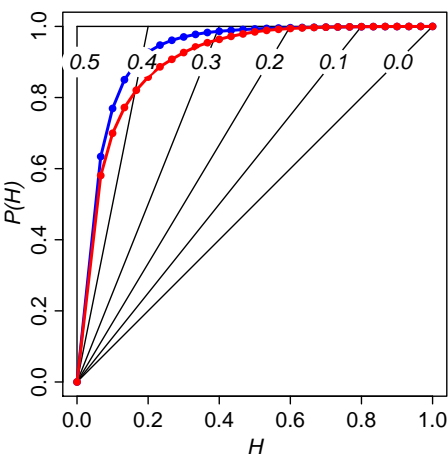
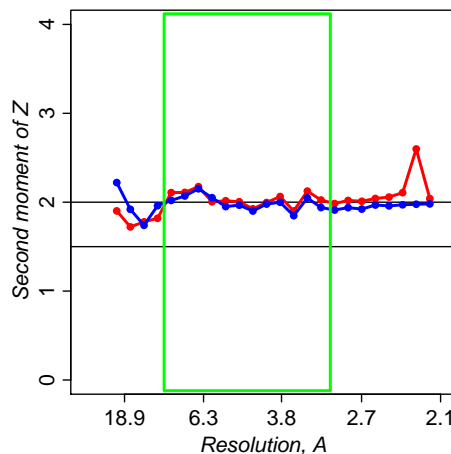
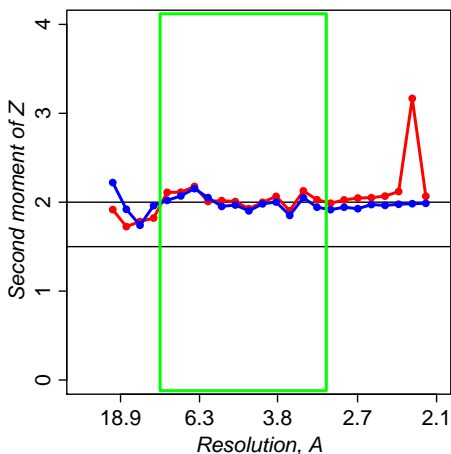
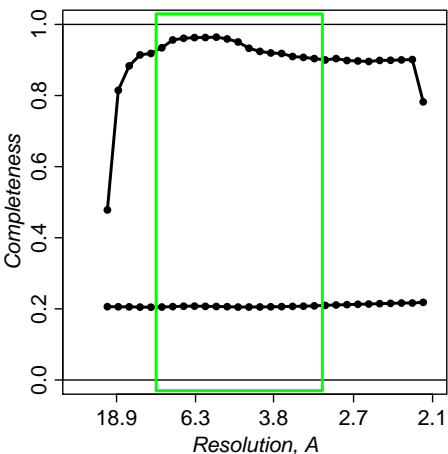
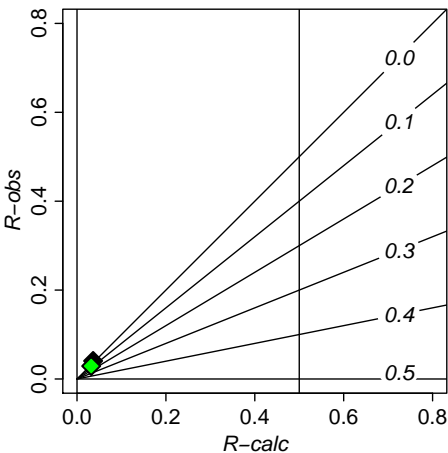
	original	merged
s.g.	P 1 21 1	P 21 21 2
p.g.	10001	10003
a.u.	8	4
p.t.	2	2
p.o.	2	4
r.m.s.d. (A)		0.07
R	25.1	
R'	25.1	25.3
R-free	28.4	
R'-free	28.4	28.4

s < f/100	0	0.00 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	30.0–2.1	9.9–3.0
unique	126,060	43,708
measured	113,169	40,438
used	96,824	34,554

NCS	translation	rotation
r.m.s.d. (A)	8.02	0.03
angle (o)	32.64	0.02

residues per monomer	DNA	protein
	0	234



7prn

	original	merged
s.g.	H 3	-
p.g.	10020	10023
a.u.	1	-
p.t.	1	-
p.o.	1	-
r.m.s.d. (A)	-	-
R	24.7	-
R'	-	-
R-free	28.0	-
R'-free	-	-

residues per monomer	DNA	protein
	0	289

s < f/100	590	2.47 %
s <= 0	0	0.00 %
f <= 0	0	0.00 %
s,f <= 0	0	0.00 %

range (A)	32.9-2.3	9.9-3.0
unique	23,983	9,830
measured	23,933	9,797
used	22,714	9,160

NCS	translation	rotation
r.m.s.d. (A)	-	-
angle (o)	-	-

