W O R L D W I D E
wwPDB

PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 28, 2014 – 06:46 PM GMT

PDB ID	:	3KM0
Title	:	17betaHSD1 in complex with 3beta-diol
Authors	:	Mazumdar, M.; Lin, S.-X.
Deposited on	:	2009-11-09
Resolution	:	2.30 Å(reported)

The following versions of software and data (see references) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance ⓘ

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.

Metric	Percentile Ranks	Value
Rfree		0.319
Clashscore		48
Ramachandran outliers		3.0%
Sidechain outliers		15.0%
RSRZ outliers		2.7%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
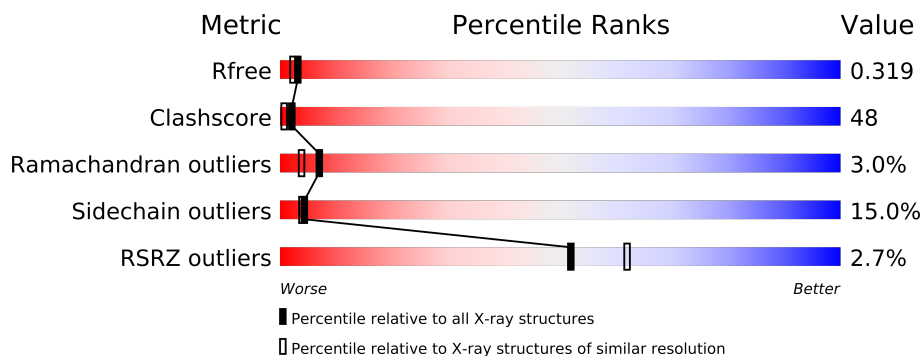
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	2929 (2.30-2.30)
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	327	
1	B	327	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	AOM	C	1	-	X
2	AOM	D	1	-	X
3	NAP	E	360	-	X
3	NAP	F	360	-	X

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2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 4544 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Estradiol 17-beta-dehydrogenase1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	278	Total	C	N	O	S	0	4	0
			2125	1346	378	390	11			
1	B	272	Total	C	N	O	S	0	1	0
			2087	1324	372	380	11			

- Molecule 2 is 5-ALPHA-ANDROSTANE-3-BETA,17BETA-DIOL (three-letter code: AOM) (formula: $C_{19}H_{32}O_2$).
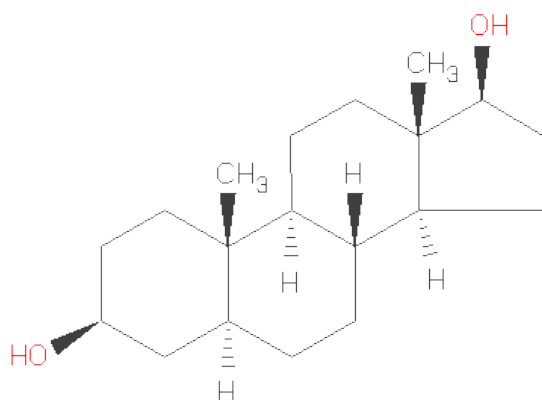
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			21	19	2		
2	D	1	Total	C	O	0	0
			21	19	2		

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDEPHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	E	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	F	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	91	Total	O	0	0
			91	91		
4	B	95	Total	O	0	0
			95	95		
4	E	6	Total	O	0	0
			6	6		
4	F	2	Total	O	0	0
			2	2		

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.
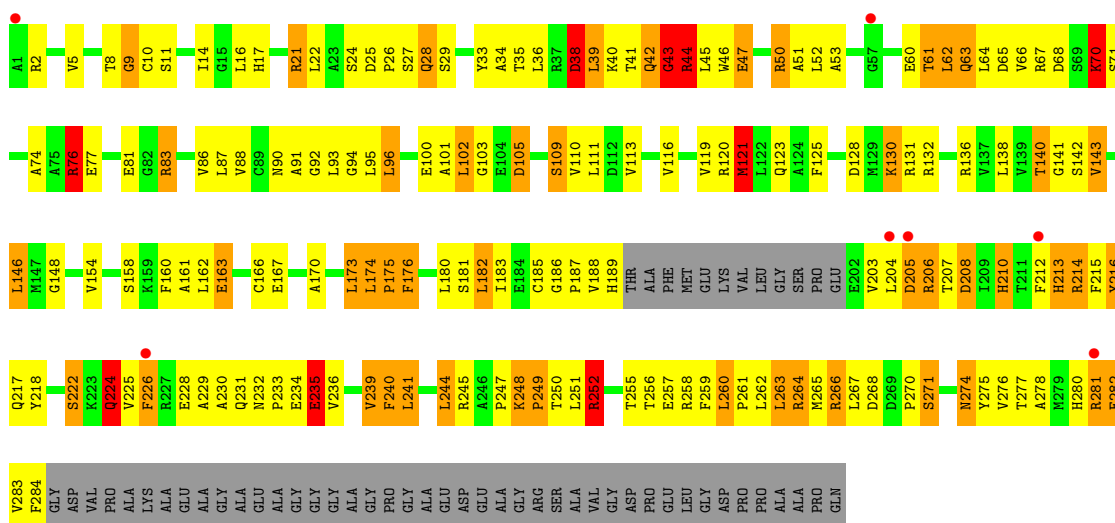
• Molecule 1: Estradiol 17-beta-dehydrogenase1

Chain A:
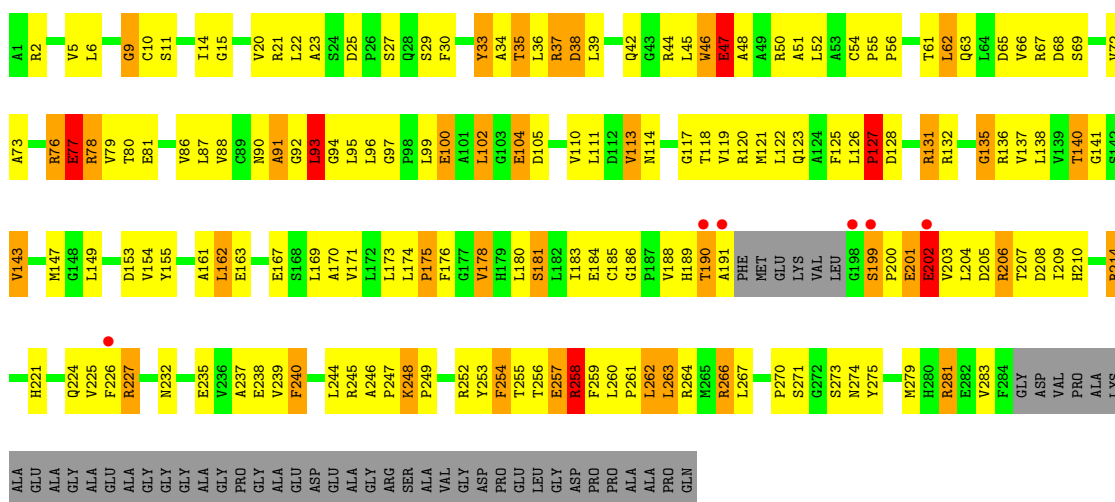
• Molecule 1: Estradiol 17-beta-dehydrogenase1

Chain B:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	154.42Å 43.12Å 121.10Å 90.00° 128.59° 90.00°	Depositor
Resolution (Å)	18.98 – 2.30 18.98 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (18.98-2.30) 91.9 (18.98-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.18 (at 2.30Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.233 , 0.312 0.241 , 0.319	Depositor DCC
R_{free} test set	1286 reflections (5.26%)	DCC
Wilson B-factor (Å^2)	30.5	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 25.8	EDS
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtriage
L-test for twinning	$< |L| > = 0.47, < L^2 > = 0.30$	Xtriage
Outliers	0 of 25732 reflections	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	4544	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.58% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

5　Model quality ⓘ

5.1　Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NAP, AOM

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$|Z|$ >5	RMSZ	#$|Z|$ >5
1	A	1.71	31/2164 (1.4%)	1.53	24/2936 (0.8%)
1	B	1.76	22/2125 (1.0%)	1.62	38/2882 (1.3%)
All	All	1.73	53/4289 (1.2%)	1.58	62/5818 (1.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

The worst 5 of 53 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	100	GLU	CB-CG	-11.94	1.29	1.52
1	A	10	CYS	CB-SG	-10.10	1.65	1.82
1	B	119	VAL	CB-CG1	-8.89	1.34	1.52
1	A	214	ARG	CZ-NH1	7.24	1.42	1.33
1	A	119	VAL	CB-CG1	-7.17	1.37	1.52

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	102	LEU	CB-CG-CD1	-10.81	92.62	111.00
1	B	252	ARG	NE-CZ-NH1	10.74	125.67	120.30
1	A	37[A]	ARG	NE-CZ-NH2	-10.69	114.96	120.30
1	B	146	LEU	CB-CG-CD1	-10.35	93.41	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	102	LEU	CB-CG-CD1	-10.19	93.68	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	79	VAL	Peptide
1	B	270	PRO	Peptide

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2125	0	2157	183	11
1	B	2087	0	2125	231	1
2	C	21	0	32	6	0
2	D	21	0	32	15	0
3	E	48	0	25	42	0
3	F	48	0	25	24	0
4	A	91	0	0	22	1
4	B	95	0	0	36	1
4	E	6	0	0	6	0
4	F	2	0	0	3	0
All	All	4544	0	4396	424	12

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 48.

The worst 5 of 424 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:279:MET:CE	1:A:283:VAL:HG23	1.38	1.51
1:A:279:MET:CE	1:A:283:VAL:CG2	2.02	1.37
1:A:270:PRO:HD3	4:A:402:HOH:O	1.20	1.29
1:B:14:ILE:HD12	3:E:360:NAP:O2N	1.30	1.28
1:A:37[A]:ARG:NH2	1:A:67:ARG:HH22	1.35	1.24

The worst 5 of 12 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:50:ARG:CZ	1:A:255:THR:O[4_454]	0.56	1.64
1:A:50:ARG:NH2	1:A:256:THR:N[4_454]	0.61	1.59
1:A:50:ARG:NH1	1:A:255:THR:O[4_454]	0.78	1.42
1:A:50:ARG:NH2	1:A:255:THR:C[4_454]	0.88	1.32
1:A:50:ARG:CZ	1:A:255:THR:C[4_454]	1.12	1.08

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	274/327 (84%)	245 (89%)	24 (9%)	5 (2%)	13	10
1	B	268/327 (82%)	219 (82%)	38 (14%)	11 (4%)	4	2
All	All	542/654 (83%)	464 (86%)	62 (11%)	16 (3%)	7	4

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	80	THR
1	A	175	PRO
1	A	201	GLU
1	A	202	GLU
1	B	170	ALA

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	229/257 (89%)	197 (86%)	32 (14%)	5	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	225/257 (88%)	189 (84%)	36 (16%)	3	3
All	All	454/514 (88%)	386 (85%)	68 (15%)	4	4

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	264	ARG
1	B	47	GLU
1	B	260	LEU
1	A	281	ARG
1	B	38	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	231	GLN
1	B	123	GLN
1	A	274	ASN
1	A	123	GLN
1	B	17	HIS

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
2	AOM	C	1	-	24,24,24	0.97	1 (4%)	39,39,39	3.17	22 (56%)
2	AOM	D	1	-	24,24,24	0.88	0	39,39,39	2.73	23 (58%)
3	NAP	E	360	-	52,52,52	1.66	6 (11%)	80,80,80	2.36	21 (26%)
3	NAP	F	360	-	52,52,52	1.66	7 (13%)	80,80,80	2.35	21 (26%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	AOM	C	1	-	-	0/0/58/58	0/0/4/4
2	AOM	D	1	-	-	0/0/58/58	0/0/4/4
3	NAP	E	360	-	-	0/35/67/67	0/3/5/5
3	NAP	F	360	-	-	0/35/67/67	0/3/5/5

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	360	NAP	P2B-O2X	-6.23	1.31	1.54
3	F	360	NAP	P2B-O2X	-6.23	1.31	1.54
3	E	360	NAP	P2B-O2B	-4.90	1.44	1.59
3	F	360	NAP	P2B-O2B	-4.87	1.44	1.59
3	F	360	NAP	P2B-O1X	-3.84	1.38	1.51

The worst 5 of 87 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	360	NAP	O4D-C1D-N1N	11.57	119.78	107.95
3	F	360	NAP	O4D-C1D-N1N	11.55	119.77	107.95
3	F	360	NAP	N3A-C2A-N1A	-8.47	121.63	128.71
3	E	360	NAP	N3A-C2A-N1A	-8.45	121.64	128.71
2	C	1	AOM	C14-C13-C17	-6.63	92.15	99.23

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	278/327 (85%)	-0.05	6 (2%)	59	69	13, 30, 45, 83	13 (4%)
1	B	272/327 (83%)	0.05	7 (2%)	53	63	14, 32, 52, 82	10 (3%)
All	All	550/654 (84%)	0.00	13 (2%)	52	66	13, 30, 50, 83	23 (4%)

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	205	ASP	7.1
1	A	190[A]	THR	7.0
1	A	191[A]	ALA	6.2
1	A	198[A]	GLY	4.8
1	B	212	PHE	3.9

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	AOM	C	1	21/21	0.44	9.71	12,27,34,39	21
3	NAP	F	360	48/48	0.46	8.40	17,30,33,34	48
3	NAP	E	360	48/48	0.46	7.80	17,30,33,34	48
2	AOM	D	1	21/21	0.47	7.01	34,37,41,43	21

6.5 Other polymers (i)

There are no such residues in this entry.