



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 22, 2025 – 01:55 PM EDT

PDB ID : 7JXN
Title : Beta hairpin derived from Abeta17-36 with an F20Cha mutation
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Deposited on : 2020-08-27
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.21
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.004 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

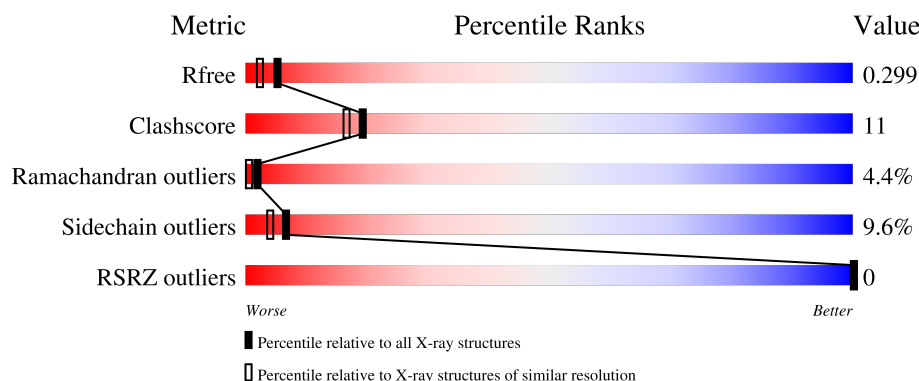
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	21	 62% 33% 5%
1	B	21	 76% 19% 5%
1	C	21	 67% 29% 5%
1	D	21	 52% 43% 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CL	A	101	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 1360 atoms, of which 684 are hydrogens and 0 are deuteriums.

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 Amyloid-beta 17-36 peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	21	Total	C	H	N	O	0	0	0
			325	102	171	25	27			
1	B	21	Total	C	H	N	O	0	0	0
			325	102	171	25	27			
1	C	21	Total	C	H	N	O	0	0	0
			325	102	171	25	27			
1	D	21	Total	C	H	N	O	0	0	0
			325	102	171	25	27			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	VAL	GLN	conflict	UNP P05067
A	2	ORN	LYS	conflict	UNP P05067
A	6	H7V	PHE	conflict	UNP P05067
A	21	ORN	MET	conflict	UNP P05067
B	1	VAL	GLN	conflict	UNP P05067
B	2	ORN	LYS	conflict	UNP P05067
B	6	H7V	PHE	conflict	UNP P05067
B	21	ORN	MET	conflict	UNP P05067
C	1	VAL	GLN	conflict	UNP P05067
C	2	ORN	LYS	conflict	UNP P05067
C	6	H7V	PHE	conflict	UNP P05067
C	21	ORN	MET	conflict	UNP P05067
D	1	VAL	GLN	conflict	UNP P05067
D	2	ORN	LYS	conflict	UNP P05067
D	6	H7V	PHE	conflict	UNP P05067
D	21	ORN	MET	conflict	UNP P05067

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl 1 1	0	0
2	D	1	Total Cl 1 1	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Na 1 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	16	Total O 16 16	0	0
4	B	12	Total O 12 12	0	0
4	C	18	Total O 18 18	0	0
4	D	11	Total O 11 11	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: Amyloid-beta 17-36 peptide

Chain A:  62% 33% 5%



- Molecule 1: Amyloid-beta 17-36 peptide

Chain B:  76% 19% 5%



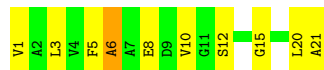
- Molecule 1: Amyloid-beta 17-36 peptide

Chain C:  67% 29% 5%



- Molecule 1: Amyloid-beta 17-36 peptide

Chain D:  52% 43% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	37.17Å 37.17Å 116.99Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.19 – 2.00 32.19 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (32.19-2.00) 99.7 (32.19-2.00)	Depositor EDS
R_{merge}	0.01	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 1.70Å)	Xtriage
Refinement program	PHENIX dev_3908	Depositor
R, R_{free}	0.277 , 0.301 0.276 , 0.299	Depositor DCC
R_{free} test set	5574 reflections (9.91%)	wwPDB-VP
Wilson B-factor (Å ²)	20.5	Xtriage
Anisotropy	0.481	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 72.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.489 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.490 for h,-h-k,-l	Depositor
Outliers	0 of 10063 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	1360	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.53% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, CL, H7V, ORN

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	0.27	0/124	0.52	0/163
1	B	0.25	0/124	0.45	0/163
1	C	0.27	0/124	0.50	0/163
1	D	0.23	0/124	0.51	0/163
All	All	0.26	0/496	0.49	0/652

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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 hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	154	171	150	6	0
1	B	154	171	150	2	0
1	C	154	171	149	4	0
1	D	154	171	151	4	0
2	A	1	0	0	3	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
4	A	16	0	0	1	2
4	B	12	0	0	1	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	18	0	0	0	0
4	D	11	0	0	1	0
All	All	676	684	600	14	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (14) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:8:GLU:O	4:D:201:HOH:O	2.02	0.76
1:B:12:SER:OG	4:B:101:HOH:O	1.96	0.68
1:A:9:ASP:OD2	4:A:202:HOH:O	2.13	0.67
1:A:16:ALA:N	2:A:101:CL:CL	2.58	0.63
1:A:17:ILE:HD11	1:D:6:H7V:C05	2.39	0.53
1:A:12:SER:HB3	2:A:101:CL:CL	2.47	0.52
1:D:5:PHE:N	1:D:20:LEU:O	2.43	0.51
1:D:1:VAL:N	1:D:3:LEU:O	2.45	0.49
1:B:17:ILE:O	1:C:17:ILE:N	2.44	0.47
1:C:1:VAL:O	1:C:1:VAL:HG12	2.13	0.47
1:C:1:VAL:HB	1:C:5:PHE:CE1	2.51	0.46
1:A:7:ALA:HB3	1:A:18:ILE:HG13	1.99	0.45
1:A:16:ALA:CB	2:A:101:CL:CL	3.04	0.43
1:C:4:VAL:O	1:C:4:VAL:HG12	2.18	0.42

All (2) 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	Interatomic distance (Å)	Clash overlap (Å)
4:A:212:HOH:O	4:A:215:HOH:O[3_675]	2.06	0.14
4:A:206:HOH:O	4:B:108:HOH:O[4_774]	2.13	0.07

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	17/21 (81%)	16 (94%)	1 (6%)	0	100	100
1	B	17/21 (81%)	16 (94%)	0	1 (6%)	1	0
1	C	17/21 (81%)	11 (65%)	6 (35%)	0	100	100
1	D	17/21 (81%)	11 (65%)	4 (24%)	2 (12%)	0	0
All	All	68/84 (81%)	54 (79%)	11 (16%)	3 (4%)	2	0

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	19	GLY
1	D	15	GLY
1	D	10	VAL

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	13/13 (100%)	12 (92%)	1 (8%)	10	7
1	B	13/13 (100%)	12 (92%)	1 (8%)	10	7
1	C	13/13 (100%)	11 (85%)	2 (15%)	2	1
1	D	13/13 (100%)	12 (92%)	1 (8%)	10	7
All	All	52/52 (100%)	47 (90%)	5 (10%)	7	4

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	SER
1	B	12	SER
1	C	5	PHE
1	C	12	SER
1	D	12	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

12 non-standard protein/DNA/RNA residues 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
1	ORN	D	2	1	6,7,8	0.61	0	2,7,9	0.14	0
1	ORN	A	2	1	6,7,8	0.59	0	2,7,9	0.22	0
1	ORN	B	2	1	6,7,8	0.58	0	2,7,9	0.07	0
1	H7V	B	6	1	11,12,13	0.65	0	13,14,16	1.66	3 (23%)
1	ORN	C	2	1	6,7,8	0.62	0	2,7,9	0.20	0
1	H7V	C	6	1	11,12,13	0.63	0	13,14,16	1.85	3 (23%)
1	ORN	A	21	1	6,7,8	2.55	1 (16%)	2,7,9	0.88	0
1	ORN	C	21	1	6,7,8	2.53	1 (16%)	2,7,9	0.83	0
1	ORN	D	21	1	6,7,8	2.59	1 (16%)	2,7,9	0.68	0
1	H7V	A	6	1	11,12,13	0.69	0	13,14,16	2.34	4 (30%)
1	H7V	D	6	1	11,12,13	0.66	0	13,14,16	1.49	3 (23%)
1	ORN	B	21	1	6,7,8	2.54	1 (16%)	2,7,9	0.78	0

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
1	ORN	D	2	1	-	1/5/6/8	-
1	ORN	A	2	1	-	1/5/6/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	ORN	B	2	1	-	1/5/6/8	-
1	H7V	B	6	1	-	2/5/16/18	0/1/1/1
1	ORN	C	2	1	-	1/5/6/8	-
1	H7V	C	6	1	-	0/5/16/18	0/1/1/1
1	ORN	A	21	1	-	2/5/6/8	-
1	ORN	C	21	1	-	2/5/6/8	-
1	ORN	D	21	1	-	0/5/6/8	-
1	H7V	A	6	1	-	3/5/16/18	0/1/1/1
1	H7V	D	6	1	-	2/5/16/18	0/1/1/1
1	ORN	B	21	1	-	1/5/6/8	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	21	ORN	CA-N	-6.21	1.30	1.48
1	A	21	ORN	CA-N	-6.13	1.30	1.48
1	B	21	ORN	CA-N	-6.10	1.31	1.48
1	C	21	ORN	CA-N	-6.04	1.31	1.48

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	6	H7V	CB-CA-N	5.36	118.73	110.59
1	C	6	H7V	CB-CA-N	4.18	116.94	110.59
1	C	6	H7V	C01-CB-CA	-3.90	109.28	114.52
1	D	6	H7V	CB-CA-N	3.44	115.82	110.59
1	B	6	H7V	CB-CA-N	3.36	115.70	110.59
1	B	6	H7V	CB-C01-C06	-3.09	104.53	111.71
1	A	6	H7V	CB-CA-C	-2.98	106.40	110.99
1	A	6	H7V	CB-C01-C02	2.79	118.21	111.71
1	A	6	H7V	C05-C06-C01	-2.74	106.31	112.08
1	D	6	H7V	C01-CB-CA	-2.72	110.86	114.52
1	B	6	H7V	CB-CA-C	-2.17	107.65	110.99
1	D	6	H7V	C05-C06-C01	-2.12	107.61	112.08
1	C	6	H7V	C05-C06-C01	-2.02	107.83	112.08

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	2	ORN	C-CA-CB-CG
1	A	6	H7V	O-C-CA-CB
1	A	6	H7V	C02-C01-CB-CA
1	B	6	H7V	C-CA-CB-C01
1	A	21	ORN	N-CA-CB-CG
1	A	21	ORN	C-CA-CB-CG
1	B	21	ORN	O-C-CA-CB
1	C	21	ORN	C-CA-CB-CG
1	B	6	H7V	N-CA-CB-C01
1	A	6	H7V	C06-C01-CB-CA
1	D	6	H7V	C-CA-CB-C01
1	B	2	ORN	C-CA-CB-CG
1	C	21	ORN	N-CA-CB-CG
1	D	6	H7V	N-CA-CB-C01
1	C	2	ORN	CA-CB-CG-CD
1	D	2	ORN	C-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	6	H7V	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	18/21 (85%)	-1.26	0 100 100	20, 24, 34, 34	0
1	B	18/21 (85%)	-1.40	0 100 100	16, 21, 32, 36	0
1	C	18/21 (85%)	-1.12	0 100 100	16, 26, 40, 41	0
1	D	18/21 (85%)	-1.23	0 100 100	18, 26, 31, 31	0
All	All	72/84 (85%)	-1.25	0 100 100	16, 25, 34, 41	0

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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. 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	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	ORN	A	2	8/9	0.98	0.05	31,38,43,43	0
1	ORN	C	2	8/9	0.98	0.06	39,48,51,51	0
1	H7V	A	6	12/13	0.98	0.05	30,36,38,40	0
1	H7V	D	6	12/13	0.98	0.05	25,30,30,33	0
1	ORN	C	21	8/9	0.98	0.05	30,41,49,49	0
1	ORN	D	21	8/9	0.98	0.04	23,29,36,36	0
1	H7V	C	6	12/13	0.99	0.05	20,24,28,28	0
1	ORN	D	2	8/9	0.99	0.04	25,31,33,33	0
1	ORN	A	21	8/9	0.99	0.04	13,25,34,40	0
1	ORN	B	21	8/9	0.99	0.05	16,23,30,32	0
1	ORN	B	2	8/9	0.99	0.04	25,35,43,43	0
1	H7V	B	6	12/13	0.99	0.04	23,28,32,32	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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. 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	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CL	A	101	1/1	0.99	0.04	21,21,21,21	0
2	CL	D	101	1/1	0.99	0.03	23,23,23,23	0
3	NA	A	102	1/1	0.99	0.02	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.