Full wwPDB X-ray Structure Validation Report (i)

Aug 8, 2020 – 01:02 PM BST

PDB ID	:	4YN0
Title	:	Crystal structure of APP E2 domain in complex with DR6 CRD domain
Authors	:	Xu, K.; Nikolov, D.
Deposited on	:	2015-03-08
Resolution	:	2.20 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

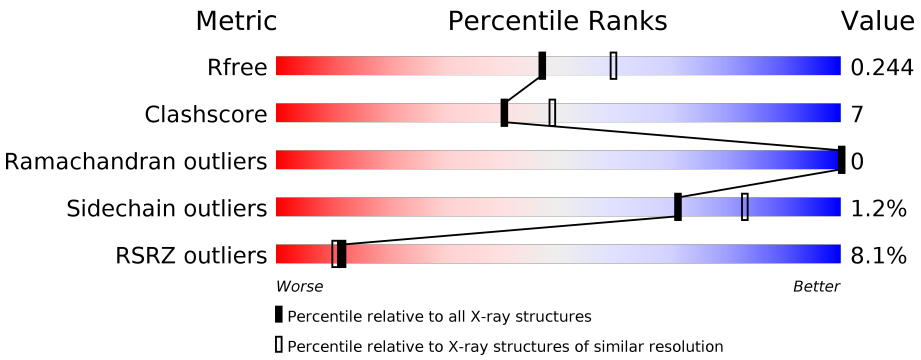
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 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 <=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	190	2%, 78%, 9%, •, 12%
2	B	233	12%, 72%, 14%, 13%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3068 atoms, of which 0 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 Tumor necrosis factor receptor superfamily member 21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	168	1259	762	233	241	23	0	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	40	GLY	-	expression tag	UNP Q9EPU5
A	41	SER	-	expression tag	UNP Q9EPU5
A	221	ALA	-	expression tag	UNP Q9EPU5
A	222	SER	-	expression tag	UNP Q9EPU5
A	223	GLY	-	expression tag	UNP Q9EPU5
A	224	ARG	-	expression tag	UNP Q9EPU5
A	225	GLY	-	expression tag	UNP Q9EPU5
A	226	LEU	-	expression tag	UNP Q9EPU5
A	227	VAL	-	expression tag	UNP Q9EPU5
A	228	PRO	-	expression tag	UNP Q9EPU5
A	229	ARG	-	expression tag	UNP Q9EPU5

- Molecule 2 is a protein called Amyloid beta A4 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	202	1678	1037	318	314	9	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	293	GLY	-	expression tag	UNP P12023
B	294	SER	-	expression tag	UNP P12023
B	518	SER	-	expression tag	UNP P12023
B	519	GLY	-	expression tag	UNP P12023
B	520	ARG	-	expression tag	UNP P12023

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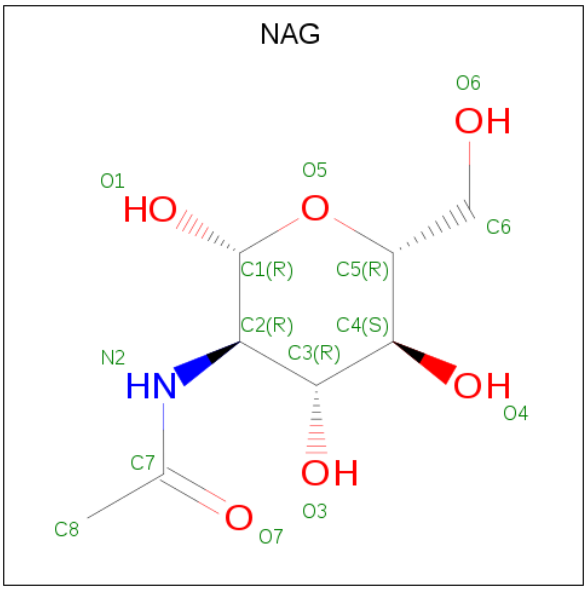
Chain	Residue	Modelled	Actual	Comment	Reference
B	521	GLY	-	expression tag	UNP P12023
B	522	LEU	-	expression tag	UNP P12023
B	523	VAL	-	expression tag	UNP P12023
B	524	PRO	-	expression tag	UNP P12023
B	525	ARG	-	expression tag	UNP P12023

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	14	8	1	5	0	0
			Total	C	N	O		
3	B	1	14	8	1	5	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	A	1	1	1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	53	53	53	0	0

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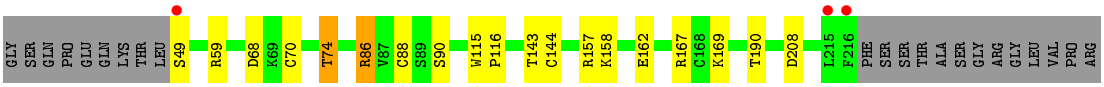
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	B	49	49	49	0	0

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.

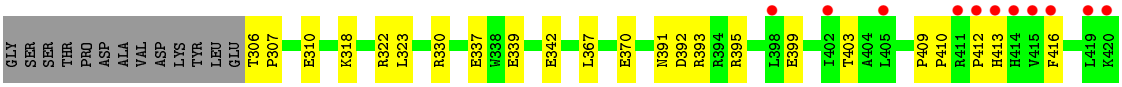
- Molecule 1: Tumor necrosis factor receptor superfamily member 21

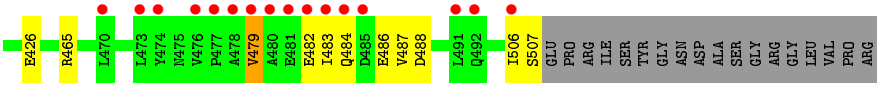
Chain A:



- Molecule 2: Amyloid beta A4 protein

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α, β, γ	67.32Å 67.32Å 226.23Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.60 – 2.20 40.59 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (40.60-2.20) 99.9 (40.59-2.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.11 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1760)	Depositor
R, R_{free}	0.226 , 0.245 0.228 , 0.244	Depositor DCC
R_{free} test set	1421 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å^2)	48.8	Xtriage
Anisotropy	0.412	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 45.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.066 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	3068	wwPDB-VP
Average B, all atoms (Å^2)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: MG, NAG

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	0.57	0/1286	0.68	0/1745
2	B	0.56	0/1706	0.57	0/2293
All	All	0.56	0/2992	0.62	0/4038

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	1259	0	1194	20	0
2	B	1678	0	1664	23	0
3	A	14	0	13	1	0
3	B	14	0	13	0	0
4	A	1	0	0	0	0
5	A	53	0	0	1	0
5	B	49	0	0	2	0
All	All	3068	0	2884	42	0

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 7.

All (42) 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:A:86:ARG:NH1	1:A:88:CYS:SG	2.14	1.20
2:B:426:GLU:OE2	2:B:465:ARG:NE	2.13	0.77
1:A:68:ASP:O	1:A:86:ARG:HD2	1.86	0.74
1:A:86:ARG:O	1:A:86:ARG:HG2	1.86	0.73
1:A:86:ARG:HH11	1:A:86:ARG:HG3	1.56	0.70
1:A:70:CYS:SG	1:A:86:ARG:NH1	2.67	0.66
1:A:158:LYS:HB3	1:A:167:ARG:HB3	1.78	0.65
1:A:70:CYS:HB3	1:A:74:THR:CG2	2.26	0.64
2:B:412:PRO:HG2	2:B:482:GLU:HG2	1.84	0.60
1:A:59:ARG:HH11	1:A:59:ARG:HG2	1.71	0.56
2:B:412:PRO:HG3	2:B:479:VAL:HG13	1.87	0.55
1:A:49:SER:N	5:A:432:HOH:O	2.41	0.54
1:A:70:CYS:HB3	1:A:74:THR:HG22	1.90	0.52
3:A:301:NAG:H3	3:A:301:NAG:H83	1.91	0.52
2:B:392:ASP:OD1	2:B:395:ARG:NH1	2.44	0.51
1:A:86:ARG:NH2	2:B:342:GLU:OE1	2.43	0.51
2:B:318:LYS:NZ	2:B:322:ARG:HE	2.09	0.50
2:B:330:ARG:NH1	2:B:370:GLU:OE1	2.30	0.50
1:A:86:ARG:HH11	1:A:86:ARG:CG	2.24	0.50
2:B:506:ILE:O	2:B:507:SER:OG	2.22	0.48
2:B:337:GLU:OE1	5:B:701:HOH:O	2.20	0.48
1:A:157:ARG:HB2	1:A:169:LYS:HG2	1.96	0.48
1:A:143:THR:OG1	1:A:144:CYS:N	2.47	0.47
2:B:484:GLN:NE2	2:B:488:ASP:OD1	2.47	0.47
2:B:307:PRO:HA	2:B:310:GLU:HG2	1.96	0.47
1:A:190:THR:OG1	1:A:208:ASP:OD2	2.28	0.47
1:A:74:THR:CG2	1:A:88:CYS:HB3	2.45	0.46
2:B:391:ASN:HB3	2:B:395:ARG:NH2	2.31	0.46
2:B:306:THR:HG21	2:B:393:ARG:NH2	2.31	0.45
2:B:416:PHE:HB2	2:B:483:ILE:HG12	1.97	0.45
1:A:74:THR:HG23	1:A:88:CYS:HB3	1.99	0.44
2:B:416:PHE:CZ	2:B:486:GLU:HB3	2.53	0.43
2:B:479:VAL:O	2:B:482:GLU:HB3	2.19	0.43
2:B:330:ARG:NH2	5:B:746:HOH:O	1.93	0.42
2:B:399:GLU:O	2:B:403:THR:HG23	2.18	0.42
2:B:367:LEU:HD23	2:B:367:LEU:HA	1.89	0.42
2:B:483:ILE:HG23	2:B:487:VAL:HG23	2.01	0.42
2:B:323:LEU:HA	2:B:323:LEU:HD12	1.82	0.42
1:A:162:GLU:CD	1:A:162:GLU:H	2.23	0.41
1:A:90:SER:OG	2:B:339:GLU:OE2	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:409:PRO:HA	2:B:410:PRO:HD3	1.96	0.40
1:A:115:TRP:HA	1:A:116:PRO:HA	1.82	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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	166/190 (87%)	156 (94%)	10 (6%)	0	100	100
2	B	200/233 (86%)	194 (97%)	6 (3%)	0	100	100
All	All	366/423 (86%)	350 (96%)	16 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	145/165 (88%)	143 (99%)	2 (1%)	67	80
2	B	181/206 (88%)	179 (99%)	2 (1%)	73	85
All	All	326/371 (88%)	322 (99%)	4 (1%)	71	83

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	74	THR
1	A	86	ARG
2	B	413	HIS
2	B	479	VAL

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

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	$\#\|Z\| > 2$
3	NAG	B	601	2	14,14,15	0.79	0	17,19,21	1.49	4 (23%)
3	NAG	A	301	1	14,14,15	0.74	1 (7%)	17,19,21	1.39	2 (11%)

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
3	NAG	B	601	2	-	0/6/23/26	0/1/1/1
3	NAG	A	301	1	-	3/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	301	NAG	C1-C2	2.39	1.55	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	301	NAG	C2-N2-C7	4.45	129.24	122.90
3	B	601	NAG	O5-C5-C6	-3.09	102.36	107.20
3	B	601	NAG	C3-C4-C5	2.37	114.47	110.24
3	B	601	NAG	C2-N2-C7	-2.20	119.77	122.90
3	B	601	NAG	C6-C5-C4	-2.17	107.93	113.00
3	A	301	NAG	C1-O5-C5	2.06	114.98	112.19

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	NAG	C8-C7-N2-C2
3	A	301	NAG	O7-C7-N2-C2
3	A	301	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	NAG	1	0

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	168/190 (88%)	0.23	3 (1%) 68 66	35, 54, 75, 104	0
2	B	202/233 (86%)	0.76	27 (13%) 3 2	36, 67, 106, 115	0
All	All	370/423 (87%)	0.52	30 (8%) 12 10	35, 61, 100, 115	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	479	VAL	5.7
1	A	216	PHE	5.4
2	B	411	ARG	5.3
2	B	480	ALA	4.8
2	B	416	PHE	4.4
1	A	49	SER	4.3
2	B	405	LEU	4.2
1	A	215	LEU	4.1
2	B	415	VAL	3.8
2	B	485	ASP	3.6
2	B	481	GLU	3.5
2	B	473	LEU	3.5
2	B	412	PRO	3.3
2	B	402	ILE	3.2
2	B	414	HIS	3.1
2	B	474	TYR	3.1
2	B	506	ILE	3.0
2	B	413	HIS	3.0
2	B	419	LEU	2.9
2	B	484	GLN	2.9
2	B	476	VAL	2.8
2	B	491	LEU	2.6
2	B	477	PRO	2.6
2	B	482	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	492	GLN	2.5
2	B	478	ALA	2.3
2	B	398	LEU	2.2
2	B	483	ILE	2.1
2	B	420	LYS	2.1
2	B	470	LEU	2.1

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

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

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(Å^2)	Q<0.9
3	NAG	A	301	14/15	0.74	0.28	79,91,94,97	0
3	NAG	B	601	14/15	0.78	0.35	91,100,105,105	0
4	MG	A	302	1/1	0.95	0.08	45,45,45,45	0

6.5 Other polymers (i)

There are no such residues in this entry.