wwPDB X-ray Structure Validation Summary Report (i)

May 15, 2020 – 04:19 pm BST

PDB ID	:	4QXH
Title	:	Crystal structure of histone demethylase KDM2A-H3K36ME1 with NOG
Authors	:	Cheng, Z.J.; Patel, D.J.
Deposited on	:	2014-07-20
Resolution	:	2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

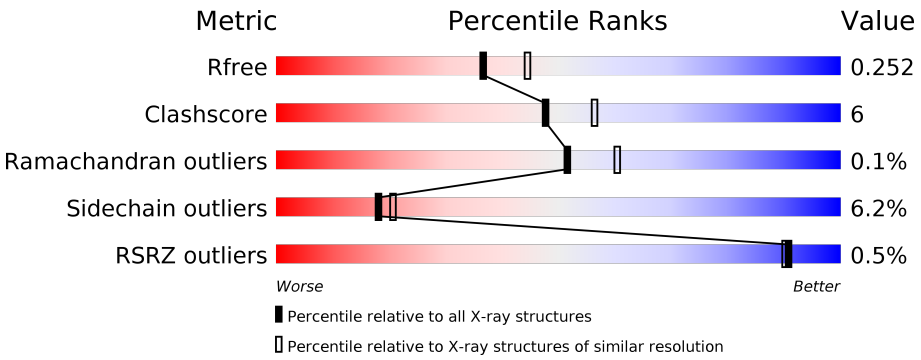
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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	329	86% 12% •
1	C	329	% 86% 12% •
2	B	68	81% 18% •
2	D	68	84% 15% •
3	E	15	7% 47% 33% 7% 13%
3	F	15	67% 33%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 7157 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 Lysine-specific demethylase 2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	329	2754	1766	458	509	21	0	2	0
1	C	329	2757	1766	462	508	21	0	2	0

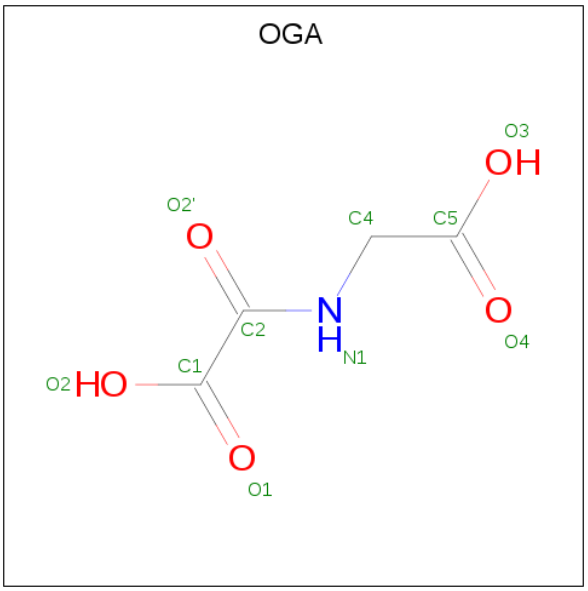
- Molecule 2 is a protein called Lysine-specific demethylase 2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	68	528	341	85	100	2	0	0	0
2	D	68	531	343	85	100	3	0	1	0

- Molecule 3 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	E	13	98	63	20	15	0	0	0
3	F	10	70	45	14	11	0	0	0

- Molecule 4 is N-OXALYLGLYCINE (three-letter code: OGA) (formula: $C_4H_5NO_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	10	4	1	5	0	0
4	C	1	10	4	1	5	0	0

- Molecule 5 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ni		
5	A	1	1	1	0	0
5	C	1	1	1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	182	182	182	0	0
6	B	34	34	34	0	0
6	C	148	148	148	0	0
6	D	24	24	24	0	0
6	E	5	5	5	0	0

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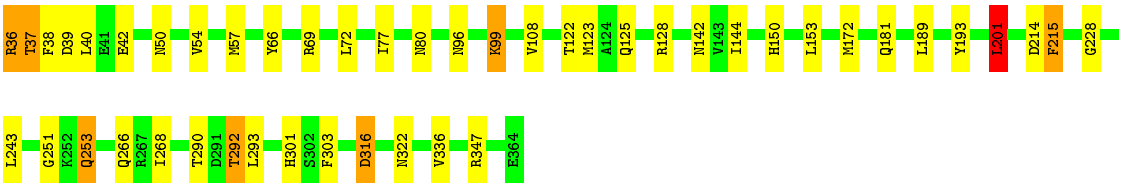
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	F	4	4	4	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

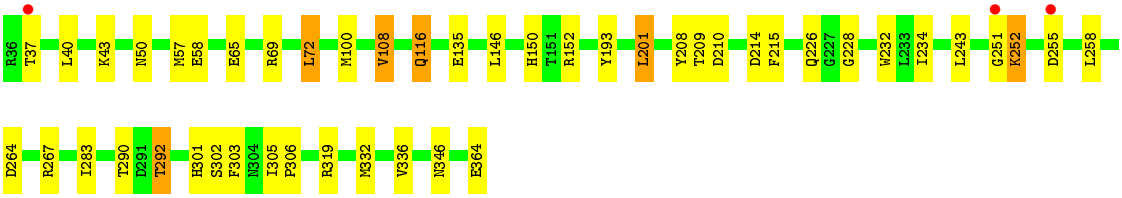
- Molecule 1: Lysine-specific demethylase 2A

Chain A:



- Molecule 1: Lysine-specific demethylase 2A

Chain C:

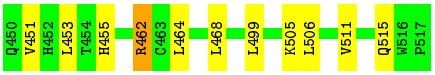


- Molecule 2: Lysine-specific demethylase 2A

Chain B:

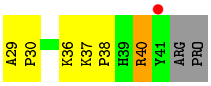
- Molecule 2: Lysine-specific demethylase 2A

Chain D:



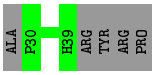
- Molecule 3: Histone H3.2

Chain E:



- Molecule 3: Histone H3.2

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	54.59Å 86.76Å 171.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	85.43 – 2.20 47.65 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.1 (85.43-2.20) 96.2 (47.65-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	2.68 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.5.0093	Depositor
R, R_{free}	0.187 , 0.243 0.202 , 0.252	Depositor DCC
R_{free} test set	2047 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	30.8	Xtriage
Anisotropy	0.801	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 38.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7157	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.21 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.1777e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: MLZ, NI, OGA

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	0.67	0/2836	0.81	6/3839 (0.2%)
1	C	0.66	0/2836	0.80	3/3839 (0.1%)
2	B	0.65	0/538	0.81	0/733
2	D	0.59	0/544	0.74	0/741
3	E	0.66	0/90	0.89	0/120
3	F	0.53	0/61	0.61	0/80
All	All	0.66	0/6905	0.80	9/9352 (0.1%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	201	LEU	CA-CB-CG	7.23	131.92	115.30
1	C	152	ARG	NE-CZ-NH2	5.82	123.21	120.30
1	A	201[A]	LEU	CB-CG-CD2	5.43	120.24	111.00
1	A	201[B]	LEU	CB-CG-CD2	5.43	120.24	111.00
1	C	152	ARG	NE-CZ-NH1	-5.35	117.62	120.30

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	2754	0	2654	34	0
1	C	2757	0	2656	31	0
2	B	528	0	546	8	0
2	D	531	0	551	9	0
3	E	98	0	101	4	0
3	F	70	0	74	0	0
4	A	10	0	3	1	0
4	C	10	0	3	0	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	A	182	0	0	8	0
6	B	34	0	0	2	0
6	C	148	0	0	6	0
6	D	24	0	0	2	0
6	E	5	0	0	0	0
6	F	4	0	0	0	0
All	All	7157	0	6588	82	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 6.

The worst 5 of 82 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:37:THR:HG21	6:A:846:HOH:O	1.91	0.70
1:C:43:LYS:O	1:C:267:ARG:NH1	2.24	0.70
2:B:497:GLU:HG3	6:B:633:HOH:O	1.92	0.69
6:A:839:HOH:O	2:D:505:LYS:CG	2.42	0.68
1:C:37:THR:HB	1:C:255:ASP:HA	1.74	0.68

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	329/329 (100%)	320 (97%)	9 (3%)	0	100	100
1	C	329/329 (100%)	317 (96%)	11 (3%)	1 (0%)	41	46
2	B	66/68 (97%)	64 (97%)	2 (3%)	0	100	100
2	D	67/68 (98%)	64 (96%)	3 (4%)	0	100	100
3	E	10/15 (67%)	9 (90%)	1 (10%)	0	100	100
3	F	7/15 (47%)	6 (86%)	1 (14%)	0	100	100
All	All	808/824 (98%)	780 (96%)	27 (3%)	1 (0%)	51	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	116	GLN

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	307/305 (101%)	285 (93%)	22 (7%)	14	15
1	C	307/305 (101%)	290 (94%)	17 (6%)	21	26
2	B	61/61 (100%)	58 (95%)	3 (5%)	25	31
2	D	62/61 (102%)	57 (92%)	5 (8%)	11	12
3	E	8/10 (80%)	7 (88%)	1 (12%)	4	4
3	F	6/10 (60%)	6 (100%)	0	100	100
All	All	751/752 (100%)	703 (94%)	48 (6%)	18	20

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	322	ASN
1	C	50	ASN
2	D	468	LEU
2	B	464	LEU

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Mol	Chain	Res	Type
2	B	511	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	50	ASN
1	C	116	GLN
1	C	301	HIS
1	A	346	ASN
1	C	346	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 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	$\#\|Z\| > 2$
3	MLZ	E	36	3	8,9,10	0.65	0	4,9,11	2.08	1 (25%)
3	MLZ	F	36	3	8,9,10	0.61	0	4,9,11	1.85	1 (25%)

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	MLZ	E	36	3	-	2/7/8/10	-
3	MLZ	F	36	3	-	1/7/8/10	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	36	MLZ	CM-NZ-CE	4.10	123.81	111.95
3	F	36	MLZ	CM-NZ-CE	3.49	122.04	111.95

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	36	MLZ	CD-CE-NZ-CM
3	F	36	MLZ	CG-CD-CE-NZ
3	E	36	MLZ	CA-CB-CG-CD

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	36	MLZ	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 are 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	$\#\|Z\| > 2$
4	OGA	A	600	5	3,9,9	0.31	0	4,11,11	3.14	1 (25%)
4	OGA	C	600	5	3,9,9	0.48	0	4,11,11	2.86	2 (50%)

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
4	OGA	A	600	5	-	0/3/9/9	-
4	OGA	C	600	5	-	1/3/9/9	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	600	OGA	C1-C2-N1	5.86	121.43	115.60
4	C	600	OGA	C1-C2-N1	4.99	120.56	115.60
4	C	600	OGA	C4-N1-C2	2.73	128.28	121.81

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	600	OGA	C5-C4-N1-C2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	600	OGA	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	329/329 (100%)	-0.58	0 100 100	22, 31, 49, 60	0
1	C	329/329 (100%)	-0.20	3 (0%) 84 83	25, 34, 59, 87	0
2	B	68/68 (100%)	-0.44	0 100 100	26, 35, 48, 54	0
2	D	68/68 (100%)	-0.29	0 100 100	29, 40, 56, 74	0
3	E	12/15 (80%)	0.09	1 (8%) 11 10	28, 33, 71, 77	0
3	F	9/15 (60%)	0.34	0 100 100	44, 49, 58, 63	0
All	All	815/824 (98%)	-0.37	4 (0%) 91 90	22, 34, 55, 87	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	251	GLY	5.2
1	C	255	ASP	2.9
1	C	37	THR	2.9
3	E	41	TYR	2.6

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
3	MLZ	F	36	10/11	0.77	0.18	40,45,52,58	0
3	MLZ	E	36	10/11	0.95	0.12	30,36,40,40	0

6.3 Carbohydrates (i)

There are no carbohydrates 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
4	OGA	A	600	10/10	0.93	0.15	35,38,46,48	0
4	OGA	C	600	10/10	0.93	0.17	34,44,51,54	0
5	NI	C	601	1/1	0.97	0.05	61,61,61,61	0
5	NI	A	601	1/1	0.98	0.04	51,51,51,51	0

6.5 Other polymers (i)

There are no such residues in this entry.