Full wwPDB X-ray Structure Validation Report (i)

Aug 22, 2023 – 07:33 AM EDT

PDB ID	:	2RHZ
Title	:	Crystal structure of the 3-MBT repeats from human L3MBTL1 with D355N point mutation
Authors	:	Li, H.; Patel, D.J.
Deposited on	:	2007-10-09
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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

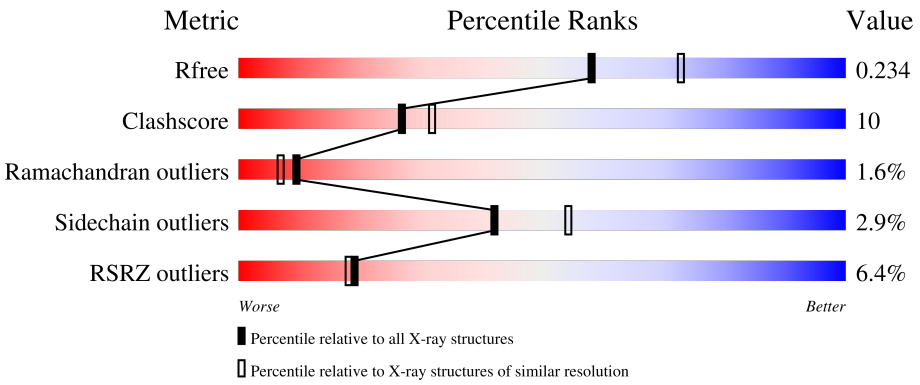
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

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

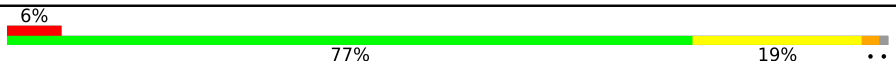
The reported resolution of this entry is 2.20 Å.

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 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 <=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	319	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2931 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.

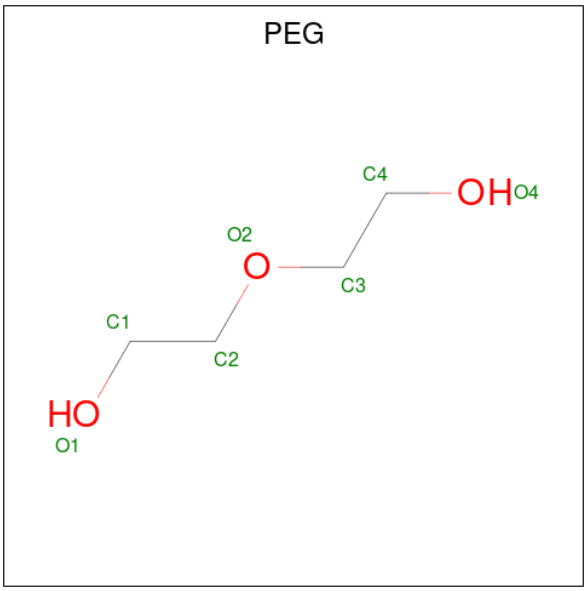
- Molecule 1 is a protein called Lethal(3)malignant brain tumor-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	315	2572	1651	435	474	12	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	GLY	-	expression tag	UNP Q9Y468
A	202	PRO	-	expression tag	UNP Q9Y468
A	203	LEU	-	expression tag	UNP Q9Y468
A	204	GLY	-	expression tag	UNP Q9Y468
A	205	SER	-	expression tag	UNP Q9Y468
A	355	ASN	ASP	engineered mutation	UNP Q9Y468

- Molecule 2 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	7	4	3	0	0

- Molecule 3 is water.

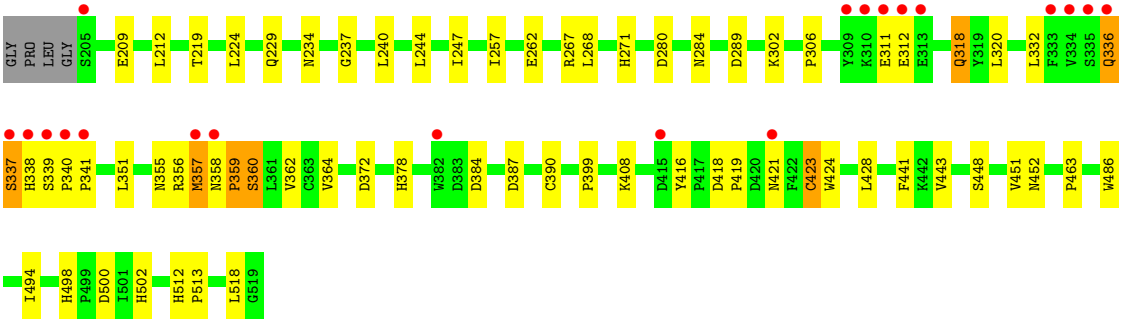
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	352	352	352	0	0

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: Lethal(3)malignant brain tumor-like protein

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	86.02Å 91.18Å 58.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 20.02 – 2.20	Depositor EDS
% Data completeness (in resolution range)	94.6 (20.00-2.20) 94.6 (20.02-2.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	8.28 (at 2.19Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.223 , 0.251 0.203 , 0.234	Depositor DCC
R_{free} test set	1645 reflections (6.87%)	wwPDB-VP
Wilson B-factor (Å^2)	35.6	Xtriage
Anisotropy	0.456	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 53.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	2931	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.02% 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: CML, PEG

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	0.36	1/2641 (0.0%)	0.63	1/3605 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	390	CYS	CB-SG	-5.52	1.72	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	362	VAL	N-CA-C	-5.29	96.73	111.00

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	2572	0	2393	51	0
2	A	7	0	10	0	0
3	A	352	0	0	10	0
All	All	2931	0	2403	51	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 10.

All (51) 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:237:GLY:HA3	1:A:332:LEU:HD11	1.53	0.90
1:A:360:SER:CB	3:A:630:HOH:O	2.33	0.76
1:A:360:SER:HB3	3:A:630:HOH:O	1.87	0.75
1:A:498:HIS:HD2	1:A:500:ASP:H	1.36	0.73
1:A:498:HIS:CD2	1:A:500:ASP:H	2.15	0.63
1:A:209:GLU:OE1	1:A:209:GLU:N	2.27	0.61
1:A:312:GLU:H	1:A:312:GLU:CD	2.05	0.60
1:A:378:HIS:HD2	1:A:387:ASP:OD1	1.85	0.60
1:A:336:GLN:HG2	1:A:337:SER:H	1.66	0.59
1:A:229:GLN:O	1:A:502:HIS:HD2	1.86	0.59
1:A:209:GLU:H	1:A:209:GLU:CD	2.06	0.59
1:A:451:VAL:O	1:A:452:ASN:HB2	2.03	0.58
1:A:318:GLN:HB2	3:A:779:HOH:O	2.02	0.58
1:A:257:ILE:HD12	1:A:306:PRO:HD3	1.85	0.58
1:A:267:ARG:HG2	1:A:284:ASN:HD22	1.69	0.58
1:A:408:LYS:HB3	1:A:408:LYS:NZ	2.19	0.57
1:A:212:LEU:HD21	1:A:219:THR:HG23	1.86	0.57
1:A:355:ASN:CG	1:A:358:ASN:HD22	2.08	0.56
1:A:247:ILE:HG12	1:A:289:ASP:HB3	1.88	0.55
1:A:360:SER:HB2	3:A:630:HOH:O	2.04	0.54
1:A:336:GLN:O	1:A:337:SER:HB2	2.09	0.53
1:A:512:HIS:HD2	1:A:513:PRO:O	1.91	0.53
1:A:443:VAL:HG22	3:A:556:HOH:O	2.09	0.52
1:A:302:LYS:HE2	1:A:311:GLU:OE2	2.10	0.51
1:A:336:GLN:CG	1:A:337:SER:H	2.23	0.51
1:A:372:ASP:HB2	3:A:745:HOH:O	2.09	0.51
1:A:357:MET:HE2	3:A:734:HOH:O	2.12	0.50
1:A:237:GLY:CA	1:A:332:LEU:HD11	2.34	0.48
1:A:355:ASN:O	1:A:358:ASN:N	2.43	0.47
1:A:418:ASP:N	1:A:419:PRO:HD3	2.29	0.47
1:A:338:HIS:CG	1:A:339:SER:N	2.83	0.47
1:A:494:ILE:HD11	1:A:498:HIS:CG	2.50	0.46
1:A:416:TYR:O	1:A:419:PRO:HG3	2.15	0.45
1:A:486:TRP:CZ2	1:A:518:LEU:HD13	2.52	0.45
1:A:486:TRP:CD2	1:A:518:LEU:HD22	2.51	0.44
1:A:224:LEU:HD22	1:A:448:SER:HB2	1.98	0.44
1:A:418:ASP:OD2	1:A:421:ASN:HB2	2.18	0.43
1:A:357:MET:C	1:A:359:PRO:HD3	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:423:CML:H2	3:A:773:HOH:O	2.18	0.43
1:A:240:LEU:HD11	1:A:262:GLU:HA	2.01	0.42
1:A:267:ARG:HH11	1:A:512:HIS:CE1	2.37	0.42
1:A:399:PRO:HG3	1:A:441:PHE:CD1	2.55	0.42
1:A:451:VAL:HG12	1:A:452:ASN:ND2	2.35	0.42
1:A:351:LEU:HD23	1:A:351:LEU:N	2.35	0.41
1:A:341:PRO:HA	1:A:372:ASP:O	2.20	0.41
1:A:364:VAL:HG13	1:A:424:TRP:CH2	2.56	0.41
1:A:339:SER:HA	1:A:340:PRO:HD3	1.76	0.41
1:A:502:HIS:HE1	3:A:532:HOH:O	2.03	0.41
1:A:271:HIS:HD2	1:A:280:ASP:OD1	2.03	0.41
1:A:234:ASN:HB2	3:A:531:HOH:O	2.21	0.40
1:A:312:GLU:CD	1:A:312:GLU:N	2.72	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	311/319 (98%)	297 (96%)	9 (3%)	5 (2%)	9 7

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	337	SER
1	A	336	GLN
1	A	359	PRO
1	A	356	ARG
1	A	463	PRO

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	276/278 (99%)	268 (97%)	8 (3%)	42 54

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	244	LEU
1	A	268	LEU
1	A	318	GLN
1	A	320	LEU
1	A	357	MET
1	A	360	SER
1	A	384	ASP
1	A	428	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	234	ASN
1	A	271	HIS
1	A	279	HIS
1	A	284	ASN
1	A	291	HIS
1	A	318	GLN
1	A	358	ASN
1	A	378	HIS
1	A	414	GLN
1	A	452	ASN
1	A	477	HIS
1	A	498	HIS
1	A	502	HIS
1	A	512	HIS

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	$\#\|Z\| > 2$
1	CML	A	278	1	12,13,14	0.93	0	7,16,18	1.17	0
1	CML	A	423	1	12,13,14	1.08	1 (8%)	7,16,18	1.20	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	CML	A	278	1	-	3/13/15/17	-
1	CML	A	423	1	-	6/13/15/17	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	423	CML	C2-SG	-2.29	1.80	1.83

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	278	CML	SG-C2-C3-C4
1	A	423	CML	C1-C2-SG-CB

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Mol	Chain	Res	Type	Atoms
1	A	423	CML	C2-C3-C4-O4
1	A	423	CML	C2-C3-C4-O5
1	A	423	CML	O1-C1-C2-SG
1	A	278	CML	C2-C3-C4-O5
1	A	423	CML	O1-C1-C2-C3
1	A	278	CML	C2-C3-C4-O4
1	A	423	CML	O2-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	423	CML	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	PEG	A	1	-	6,6,6	0.51	0	5,5,5	0.40	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
2	PEG	A	1	-	-	0/4/4/4	-

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	313/319 (98%)	0.21	20 (6%) 19 18	22, 35, 64, 91	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	334	VAL	11.9
1	A	337	SER	10.6
1	A	338	HIS	10.0
1	A	336	GLN	9.9
1	A	340	PRO	6.1
1	A	312	GLU	5.8
1	A	339	SER	5.7
1	A	341	PRO	5.4
1	A	335	SER	4.8
1	A	311	GLU	4.4
1	A	358	ASN	4.4
1	A	310	LYS	4.2
1	A	309	TYR	3.8
1	A	382	TRP	3.6
1	A	205	SER	3.6
1	A	357	MET	3.5
1	A	333	PHE	3.2
1	A	415	ASP	2.8
1	A	421	ASN	2.7
1	A	313	GLU	2.4

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	CML	A	423	14/15	0.79	0.18	43,53,60,61	0
1	CML	A	278	14/15	0.82	0.17	40,52,65,67	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(Å^2)	Q<0.9
2	PEG	A	1	7/7	0.88	0.18	62,63,63,64	0

6.5 Other polymers (i)

There are no such residues in this entry.