



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:27 AM UTC

PDB ID : 7FTN / pdb_00007ftn
Title : Crystal Structure of human cyclic GMP-AMP synthase in complex with propanedioic acid
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Deposited on : 2023-02-08
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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

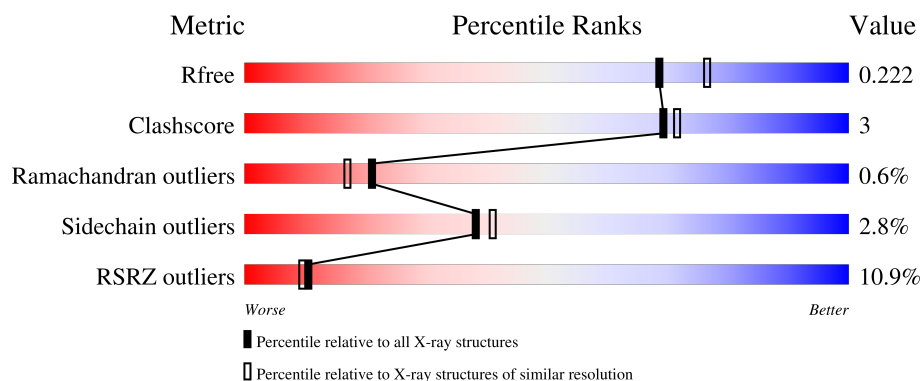
1 Overall quality at a glance

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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (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	362	11% 86% 11% ..
2	B	16	81% 19%
3	C	15	20% 87% 13%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3793 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 Cyclic GMP-AMP synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	353	Total	C	N	O	S	0	3	0
			2925	1869	509	532	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	187	ASN	LYS	conflict	UNP Q8N884
A	195	ARG	LEU	conflict	UNP Q8N884

- Molecule 2 is a DNA chain called DNA (5'-D(*AP*AP*AP*TP*TP*GP*CP*CP*GP*AP*AP*GP*AP*CP*GP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	16	Total	C	N	O	P	0	0	0
			329	157	68	89	15			

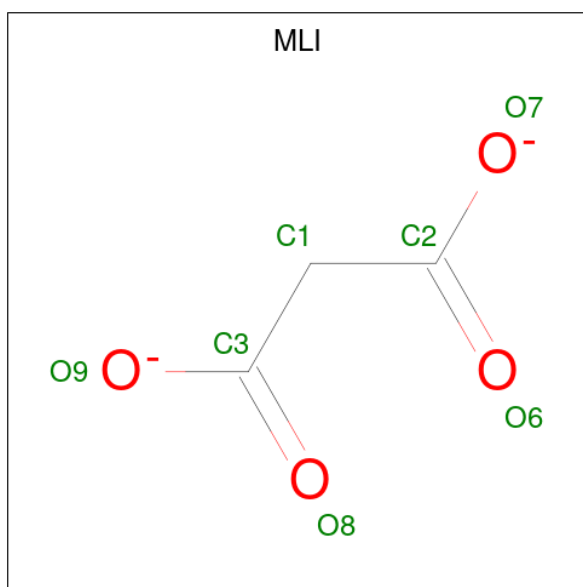
- Molecule 3 is a DNA chain called DNA (5'-D(*TP*CP*GP*TP*CP*TP*TP*CP*GP*GP*CP*AP*AP*TP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	15	Total	C	N	O	P	0	0	0
			301	146	49	92	14			

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

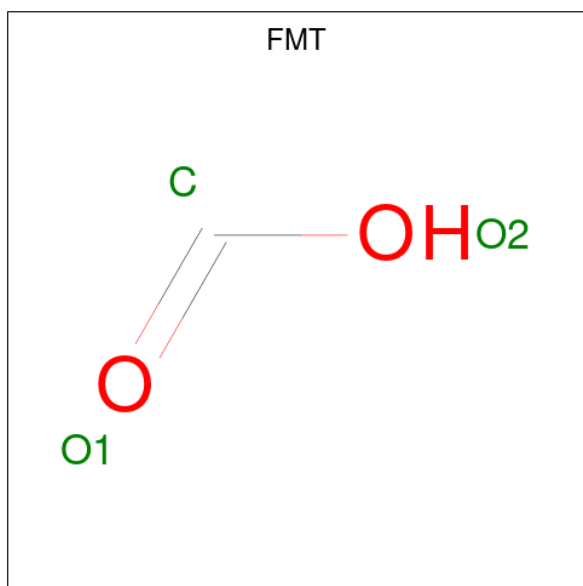
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		

- Molecule 5 is MALONATE ION (CCD ID: MLI) (formula: C₃H₂O₄).



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

- Molecule 6 is FORMIC ACID (CCD ID: FMT) (formula: CH_2O_2).



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

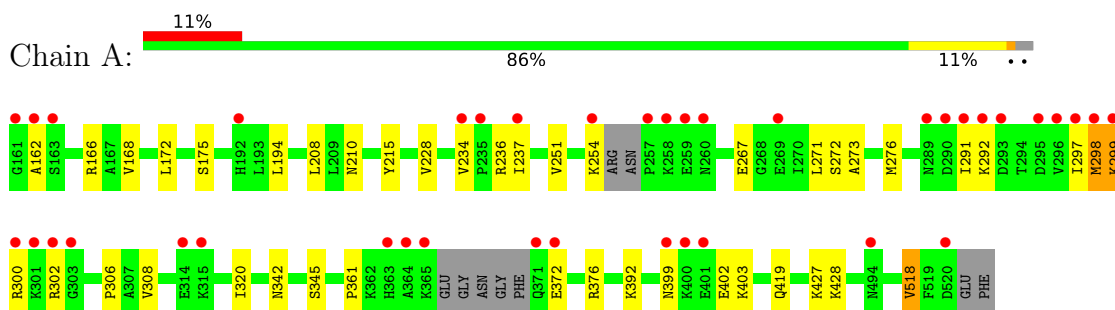
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	190	Total 190	O 190	0	0
7	B	15	Total 15	O 15	0	0
7	C	22	Total 22	O 22	0	0

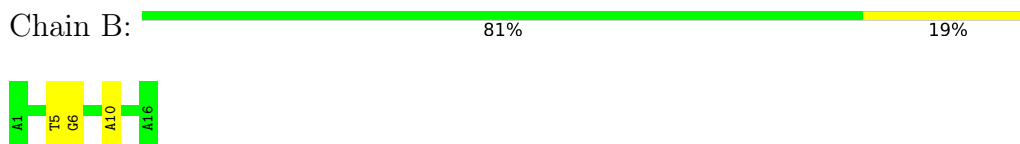
3 Residue-property plots [i](#)

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.

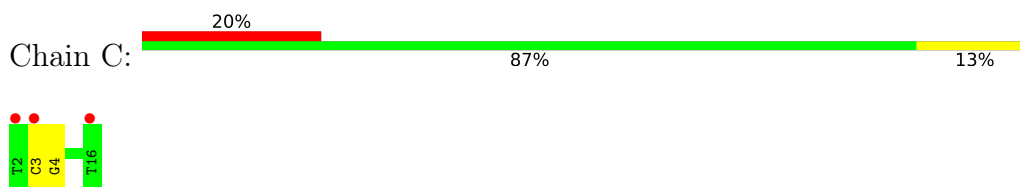
- Molecule 1: Cyclic GMP-AMP synthase



- Molecule 2: DNA (5'-D(*AP*AP*AP*TP*TP*GP*CP*CP*GP*AP*AP*GP*AP*CP*GP*A)-3')



- Molecule 3: DNA (5'-D(*TP*CP*GP*TP*CP*TP*TP*CP*GP*GP*CP*AP*AP*TP*T)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	100.60Å 100.60Å 239.85Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	58.91 – 2.00 58.91 – 2.00	Depositor EDS
% Data completeness (in resolution range)	79.0 (58.91-2.00) 75.1 (58.91-2.00)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.185 , 0.226 0.186 , 0.222	Depositor DCC
R_{free} test set	1912 reflections (3.86%)	wwPDB-VP
Wilson B-factor (Å ²)	30.9	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 54.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3793	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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: MLI, FMT, ZN

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	0.32	0/2990	0.52	0/4005
2	B	0.32	0/371	0.50	0/571
3	C	0.29	0/335	0.54	0/515
All	All	0.31	0/3696	0.52	0/5091

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	2925	0	2983	21	0
2	B	329	0	180	2	0
3	C	301	0	173	1	0
4	A	1	0	0	0	0
5	A	7	0	2	0	0
6	A	3	0	1	0	0
7	A	190	0	0	0	0
7	B	15	0	0	1	0
7	C	22	0	0	0	0
All	All	3793	0	3339	24	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 3.

All (24) 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)
2:B:10:DA:OP1	7:B:101:HOH:O	2.05	0.73
1:A:271:LEU:HD21	1:A:276:MET:HE1	1.80	0.64
1:A:236:ARG:HD3	1:A:254:LYS:HG3	1.79	0.63
1:A:299:LYS:HG3	1:A:302:ARG:HG3	1.86	0.56
1:A:273:ALA:HB1	1:A:361:PRO:HB3	1.92	0.52
1:A:298:MET:O	1:A:300:ARG:N	2.42	0.52
2:B:5:DT:H2''	2:B:6:DG:C8	2.47	0.49
1:A:399:ASN:OD1	1:A:402:GLU:HB2	2.12	0.49
1:A:162:ALA:HB1	1:A:166[B]:ARG:HH21	1.78	0.48
1:A:267:GLU:HG3	1:A:272:SER:HB2	1.95	0.48
3:C:3:DC:H2'	3:C:4:DG:C8	2.49	0.48
1:A:210:ASN:HB3	1:A:215:TYR:CD2	2.49	0.47
1:A:194:LEU:HD11	1:A:208:LEU:HB2	1.96	0.47
1:A:342:ASN:O	1:A:392:LYS:NZ	2.48	0.47
1:A:237:ILE:HG23	1:A:251:VAL:HG13	1.97	0.46
1:A:403:LYS:HE3	1:A:403:LYS:HB3	1.80	0.46
1:A:234:VAL:HG21	1:A:237:ILE:HD11	1.98	0.44
1:A:291:ILE:HG22	1:A:292:LYS:H	1.82	0.43
1:A:299:LYS:HG2	1:A:306:PRO:HG2	1.99	0.43
1:A:168:VAL:O	1:A:172:LEU:HG	2.18	0.43
1:A:419:GLN:HB3	1:A:518:VAL:HG22	2.00	0.43
1:A:162:ALA:HB1	1:A:166[B]:ARG:NH2	2.34	0.42
1:A:308:VAL:HG22	1:A:320:ILE:HB	2.00	0.42
1:A:210:ASN:HB3	1:A:215:TYR:CG	2.57	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	350/362 (97%)	334 (95%)	14 (4%)	2 (1%)	21 17

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	299	LYS
1	A	345	SER

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	330/334 (99%)	321 (97%)	9 (3%)	39 42

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	175	SER
1	A	228	VAL
1	A	297	ILE
1	A	298	MET
1	A	372	GLU
1	A	376	ARG
1	A	427	LYS
1	A	428	LYS
1	A	518	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	192	HIS
1	A	351	GLN
1	A	449	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	$\# Z > 2$
6	FMT	A	603	-	2,2,2	0.79	0	1,1,1	0.32	0
5	MLI	A	602	-	6,6,6	2.68	1 (16%)	7,7,7	2.22	4 (57%)

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
5	MLI	A	602	-	-	0/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	602	MLI	C1-C2	-5.99	1.41	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
5	A	602	MLI	O7-C2-C1	3.00	123.79	114.51
5	A	602	MLI	C3-C1-C2	2.70	122.48	112.95
5	A	602	MLI	O6-C2-C1	-2.60	114.70	122.11
5	A	602	MLI	O9-C3-C1	2.56	122.45	114.51

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

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	353/362 (97%)	0.31	39 (11%) 10 9	16, 36, 87, 142	3 (0%)
2	B	16/16 (100%)	0.30	0 100 100	48, 56, 115, 129	0
3	C	15/15 (100%)	1.00	3 (20%) 3 2	42, 68, 132, 156	0
All	All	384/393 (97%)	0.34	42 (10%) 10 9	16, 38, 95, 156	3 (0%)

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	161	GLY	5.2
1	A	298	MET	5.2
1	A	257	PRO	4.8
1	A	371	GLN	4.7
1	A	292	LYS	4.5
1	A	400	LYS	4.3
1	A	297	ILE	4.3
1	A	162	ALA	4.1
1	A	399	ASN	4.1
1	A	365	LYS	4.1
3	C	16	DT	4.0
1	A	301	LYS	4.0
1	A	302	ARG	3.9
3	C	2	DT	3.9
1	A	314	GLU	3.8
1	A	303	GLY	3.8
1	A	299	LYS	3.8
1	A	260	ASN	3.7
1	A	300	ARG	3.5
1	A	295	ASP	3.4
1	A	234	VAL	3.3
1	A	254	LYS	3.2
1	A	163	SER	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	372	GLU	3.0
1	A	235	PRO	2.9
1	A	259	GLU	2.9
1	A	291	ILE	2.8
1	A	296	VAL	2.8
1	A	290	ASP	2.7
1	A	289	ASN	2.7
1	A	269	GLU	2.6
1	A	363	HIS	2.6
1	A	315	LYS	2.6
1	A	520	ASP	2.5
1	A	258	LYS	2.5
1	A	494	ASN	2.5
1	A	401	GLU	2.4
1	A	192	HIS	2.3
1	A	237	ILE	2.1
1	A	364	ALA	2.1
3	C	3	DC	2.1
1	A	293	ASP	2.0

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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
6	FMT	A	603	3/3	0.86	0.24	68,68,71,73	0
5	MLI	A	602	7/7	0.88	0.14	54,57,64,64	0
4	ZN	A	601	1/1	0.99	0.02	29,29,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.