



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:36 AM UTC

PDB ID : 4JLX / pdb_00004jlx
Title : Structure of porcine cyclic GMP-AMP synthase (cGAS)
Authors : Civril, F.; Hopfner, K.P.
Deposited on : 2013-03-13
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

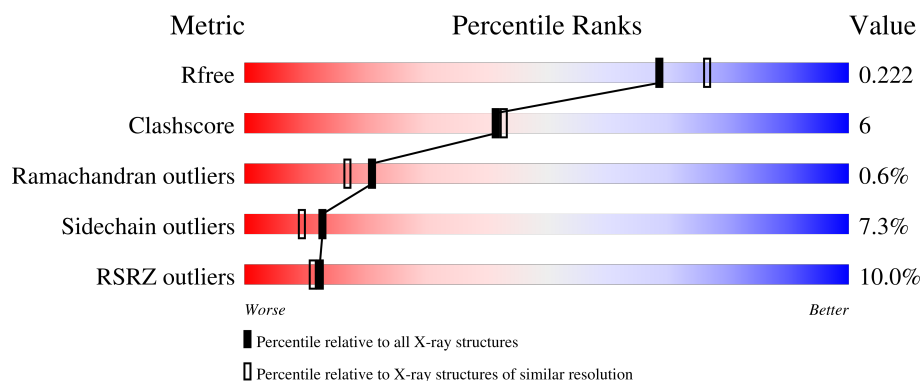
1 Overall quality at a glance

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	366	

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
5	PG4	A	505	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3058 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 Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	351	Total	C	N	O	S	161	3	0
			2878	1847	503	512	16			

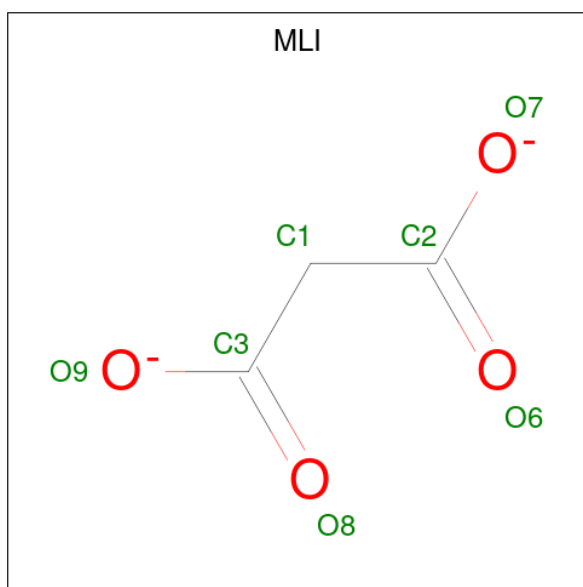
There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	132	GLY	-	expression tag	UNP I3LM39
A	133	ALA	-	expression tag	UNP I3LM39
A	134	MET	-	expression tag	UNP I3LM39
A	268	ASP	-	SEE REMARK 999	UNP I3LM39
A	269	THR	-	SEE REMARK 999	UNP I3LM39

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

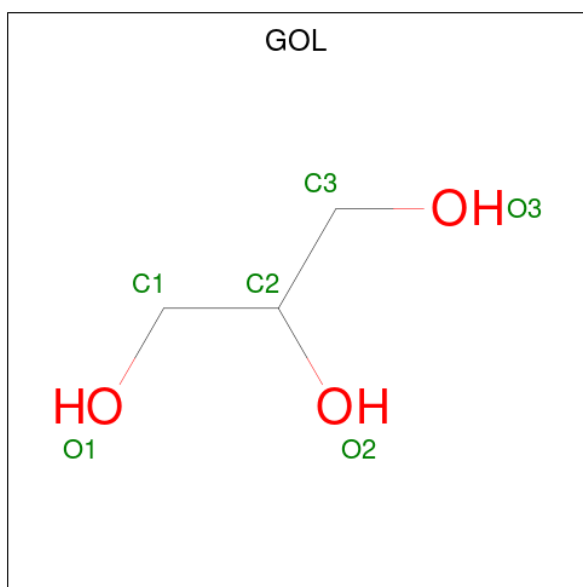
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is MALONATE ION (CCD ID: MLI) (formula: C₃H₂O₄).



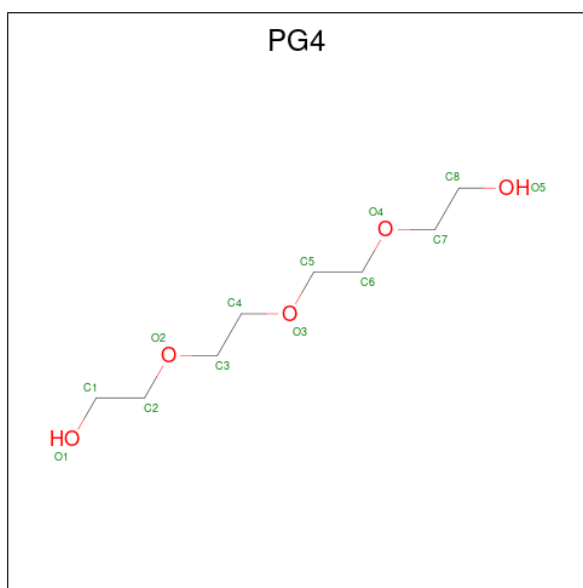
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	3	4		
3	A	1	Total	C	O	0	0
			7	3	4		
3	A	1	Total	C	O	0	0
			7	3	4		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 5 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			13	8	5		
5	A	1	Total	C	O	0	0
			13	8	5		

- Molecule 6 is water.

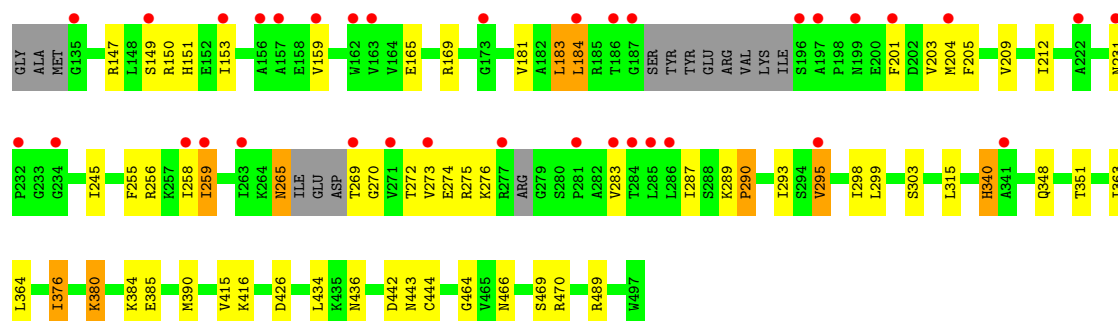
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	126	Total	O	0	0
			126	126		

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: Uncharacterized protein

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	47.40Å 118.01Å 142.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.46 – 2.00 45.46 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (45.46-2.00) 99.6 (45.46-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.188 , 0.215 0.197 , 0.222	Depositor DCC
R_{free} test set	1364 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	37.1	Xtriage
Anisotropy	0.454	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 57.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3058	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.39% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MLI, ZN, PG4

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	0.52	0/2944	0.78	0/3953

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

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	2878	0	2912	35	0
2	A	1	0	0	0	0
3	A	21	0	6	0	0
4	A	6	0	8	0	0
5	A	26	0	36	11	0
6	A	126	0	0	1	0
All	All	3058	0	2962	35	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.

All (35) 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:376:ILE:HG12	6:A:664:HOH:O	1.87	0.74
1:A:256:ARG:NH2	1:A:274:GLU:O	2.23	0.72
1:A:380:LYS:HD2	1:A:434:LEU:HD22	1.73	0.71
1:A:464:GLY:O	5:A:505:PG4:H61	2.03	0.58
1:A:165:GLU:O	1:A:169:ARG:HG2	2.03	0.58
1:A:340:HIS:NE2	1:A:351:THR:O	2.37	0.57
1:A:287:ILE:HB	1:A:293:ILE:HB	1.86	0.56
1:A:259:ILE:HG12	1:A:283:VAL:HG11	1.89	0.55
1:A:390[B]:MET:HE2	1:A:415:VAL:HB	1.90	0.54
1:A:426:ASP:OD2	5:A:506:PG4:H32	2.11	0.51
1:A:466:ASN:HD22	5:A:505:PG4:H31	1.77	0.49
1:A:390[B]:MET:SD	1:A:444:CYS:HB3	2.52	0.49
1:A:436:ASN:CB	5:A:506:PG4:H72	2.43	0.49
1:A:364:LEU:HD11	1:A:416:LYS:HE2	1.93	0.49
1:A:442:ASP:OD1	1:A:489:ARG:HD2	2.13	0.49
1:A:443:ASN:OD1	5:A:506:PG4:H11	2.13	0.48
1:A:255:PHE:O	1:A:259:ILE:HG23	2.14	0.48
1:A:289:LYS:HA	1:A:290:PRO:C	2.38	0.48
1:A:380:LYS:NZ	1:A:385:GLU:OE2	2.40	0.48
1:A:269:THR:OG1	1:A:270:GLY:N	2.42	0.47
1:A:183:LEU:HD22	1:A:184:LEU:H	1.79	0.46
1:A:466:ASN:HD22	5:A:505:PG4:C3	2.29	0.46
1:A:340:HIS:HB3	1:A:348:GLN:HG2	1.99	0.44
1:A:466:ASN:CB	5:A:505:PG4:H51	2.48	0.44
1:A:315:LEU:HD11	1:A:363:ILE:HD11	2.00	0.44
1:A:201:PHE:O	1:A:295:VAL:HA	2.18	0.44
1:A:466:ASN:HB3	5:A:505:PG4:H51	2.01	0.43
1:A:265:ASN:HB2	1:A:269:THR:N	2.34	0.43
1:A:212:ILE:HD12	1:A:303:SER:HB2	2.01	0.43
1:A:470:ARG:H	5:A:505:PG4:C1	2.32	0.42
1:A:469:SER:HA	5:A:505:PG4:H11	2.02	0.42
1:A:147:ARG:HH11	1:A:147:ARG:HG2	1.85	0.42
1:A:181:VAL:CG2	1:A:205:PHE:HB3	2.50	0.41
1:A:470:ARG:H	5:A:505:PG4:H11	1.85	0.41
1:A:204:MET:HG3	1:A:298:ILE:HB	2.03	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	346/366 (94%)	338 (98%)	6 (2%)	2 (1%)	21	17

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	149	SER
1	A	290	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	319/329 (97%)	296 (93%)	23 (7%)	13	10

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	150	ARG
1	A	151	HIS
1	A	153	ILE
1	A	159	VAL
1	A	183	LEU
1	A	184	LEU
1	A	203	VAL
1	A	209	VAL
1	A	231	ASN

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Mol	Chain	Res	Type
1	A	245	ILE
1	A	258	ILE
1	A	259	ILE
1	A	265	ASN
1	A	272	THR
1	A	273	VAL
1	A	275	ARG
1	A	276	LYS
1	A	295	VAL
1	A	299	LEU
1	A	340	HIS
1	A	376	ILE
1	A	380	LYS
1	A	384	LYS

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	332	GLN
1	A	433	HIS
1	A	436	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](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 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	GOL	A	503	-	5,5,5	0.64	0	5,5,5	1.23	0
5	PG4	A	505	-	12,12,12	0.54	0	11,11,11	1.57	2 (18%)
5	PG4	A	506	-	12,12,12	0.61	0	11,11,11	1.54	1 (9%)
3	MLI	A	504	-	6,6,6	1.14	0	7,7,7	1.49	0
3	MLI	A	502	-	6,6,6	1.16	0	7,7,7	1.48	0
3	MLI	A	507	-	6,6,6	1.49	2 (33%)	7,7,7	1.25	1 (14%)

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	GOL	A	503	-	-	1/4/4/4	-
5	PG4	A	505	-	-	7/10/10/10	-
5	PG4	A	506	-	-	5/10/10/10	-
3	MLI	A	504	-	-	0/4/4/4	-
3	MLI	A	502	-	-	2/4/4/4	-
3	MLI	A	507	-	-	0/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	507	MLI	O7-C2	-2.55	1.22	1.30
3	A	507	MLI	O9-C3	-2.34	1.23	1.30

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	505	PG4	O4-C7-C8	2.40	120.69	110.11
5	A	505	PG4	O4-C6-C5	2.40	121.28	110.35
3	A	507	MLI	O9-C3-C1	2.10	121.03	114.51
5	A	506	PG4	O4-C7-C8	2.02	118.99	110.11

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	505	PG4	C8-C7-O4-C6
5	A	505	PG4	O1-C1-C2-O2
5	A	505	PG4	C4-C3-O2-C2
5	A	506	PG4	O2-C3-C4-O3
4	A	503	GOL	O1-C1-C2-O2
3	A	502	MLI	C2-C1-C3-O9
3	A	502	MLI	C2-C1-C3-O8
5	A	505	PG4	C1-C2-O2-C3
5	A	505	PG4	C6-C5-O3-C4
5	A	506	PG4	C3-C4-O3-C5
5	A	506	PG4	C4-C3-O2-C2
5	A	506	PG4	O4-C7-C8-O5
5	A	505	PG4	C3-C4-O3-C5
5	A	505	PG4	O2-C3-C4-O3
5	A	506	PG4	C1-C2-O2-C3

There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	505	PG4	8	0
5	A	506	PG4	3	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 ⓘ

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	351/366 (95%)	0.47	35 (9%) 12 11	15, 43, 92, 111	65 (18%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	232	PRO	4.9
1	A	231	ASN	4.5
1	A	197	ALA	4.1
1	A	196	SER	3.7
1	A	341	ALA	3.7
1	A	295	VAL	3.2
1	A	153	ILE	3.1
1	A	263	ILE	3.1
1	A	259	ILE	2.8
1	A	201	PHE	2.7
1	A	173	GLY	2.6
1	A	234	GLY	2.6
1	A	277	ARG	2.6
1	A	199	ASN	2.5
1	A	184	LEU	2.5
1	A	285	LEU	2.5
1	A	135	GLY	2.5
1	A	281	PRO	2.5
1	A	273	VAL	2.4
1	A	186	THR	2.4
1	A	283	VAL	2.4
1	A	162	TRP	2.4
1	A	269	THR	2.4
1	A	157	ALA	2.3
1	A	258	ILE	2.3
1	A	284	THR	2.3
1	A	159	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	204	MET	2.2
1	A	222	ALA	2.2
1	A	271	VAL	2.2
1	A	149	SER	2.2
1	A	156	ALA	2.1
1	A	163	VAL	2.1
1	A	187	GLY	2.0
1	A	286	LEU	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(Å ²)	Q<0.9
3	MLI	A	504	7/7	0.72	0.12	89,94,98,102	0
3	MLI	A	507	7/7	0.78	0.39	20,20,20,20	0
4	GOL	A	503	6/6	0.78	0.13	87,90,94,95	0
5	PG4	A	506	13/13	0.78	0.14	38,56,71,73	0
5	PG4	A	505	13/13	0.79	0.16	38,51,58,67	0
3	MLI	A	502	7/7	0.81	0.11	55,57,73,74	0
2	ZN	A	501	1/1	0.99	0.02	31,31,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.